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(54) FLAGELLIN RELATED POLYPEPTIDES AND USES THEREOF

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Related U.S. Application Data

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A61K 45/06	(2006.01)
A61K 38/16	(2006.01)

(52) **U.S. Cl.**

CPC ***C07K 14/255*** (2013.01); ***A61K 38/164*** (2013.01); ***A61K 45/06*** (2013.01)

(57) ABSTRACT

The use of flagellin and flagellin related polypeptides for the protection of mammals from the effects of apoptosis is described.

Fig. 1

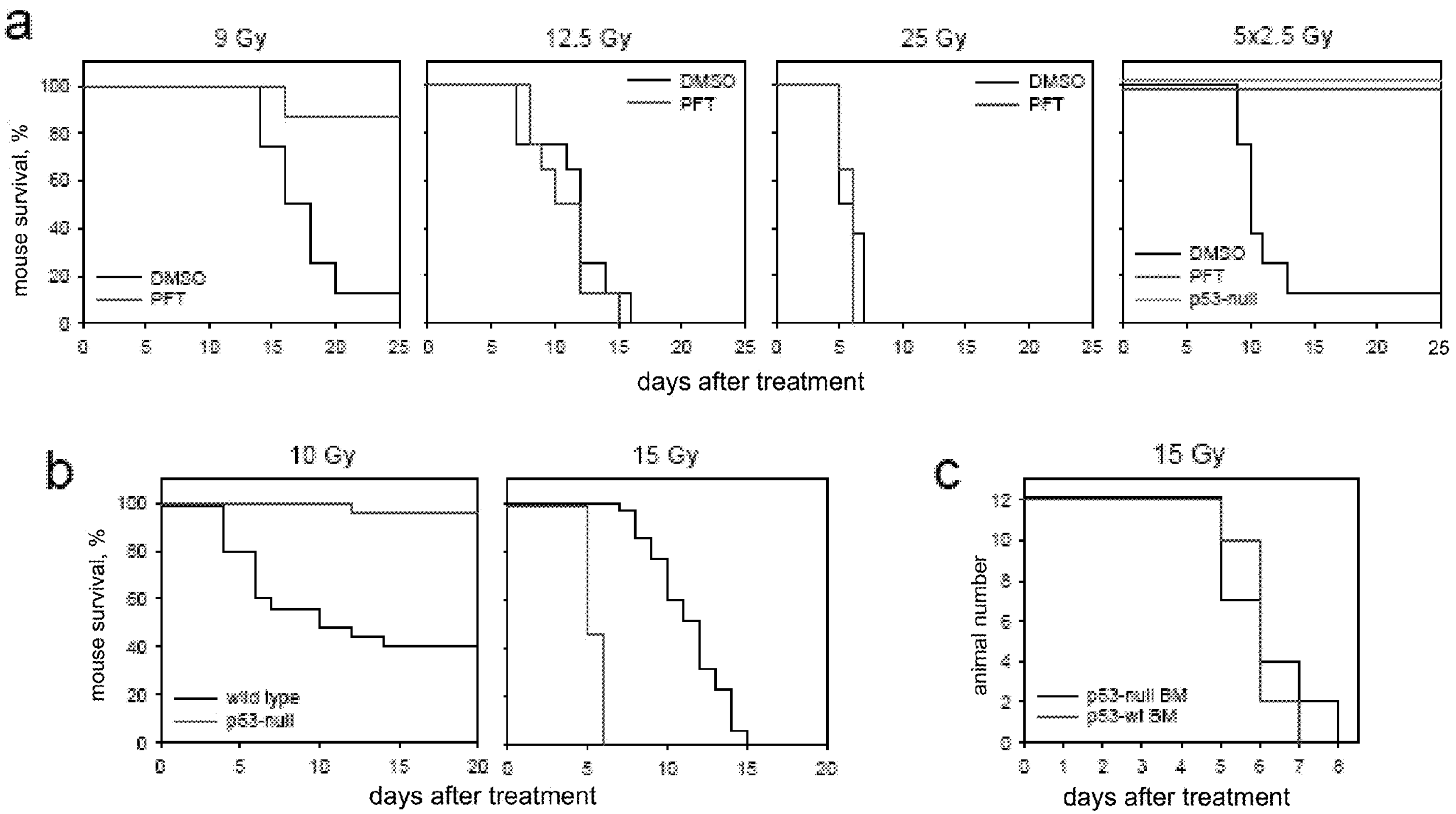
a
9 Gy
12.5 Gy
25 Gy
5x2.5 Gy
mouse survival, %
100
80
60
40
20
0
0
5
10
15
20
25
DMSO
PFT
p53-null
days after treatment
b
10 Gy
15 Gy
wild type
p53-null
c
15 Gy
animal number
12
10
8
6
4
2
0
1
2
3
4
5
6
7
8
p53-null BM
p53-wt BM

Fig. 1, CONTINUED

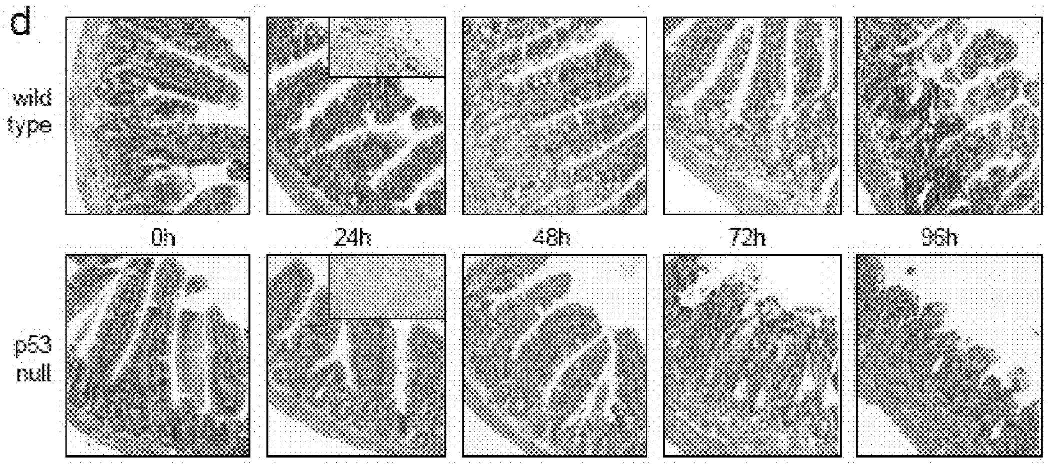

Fig. 2

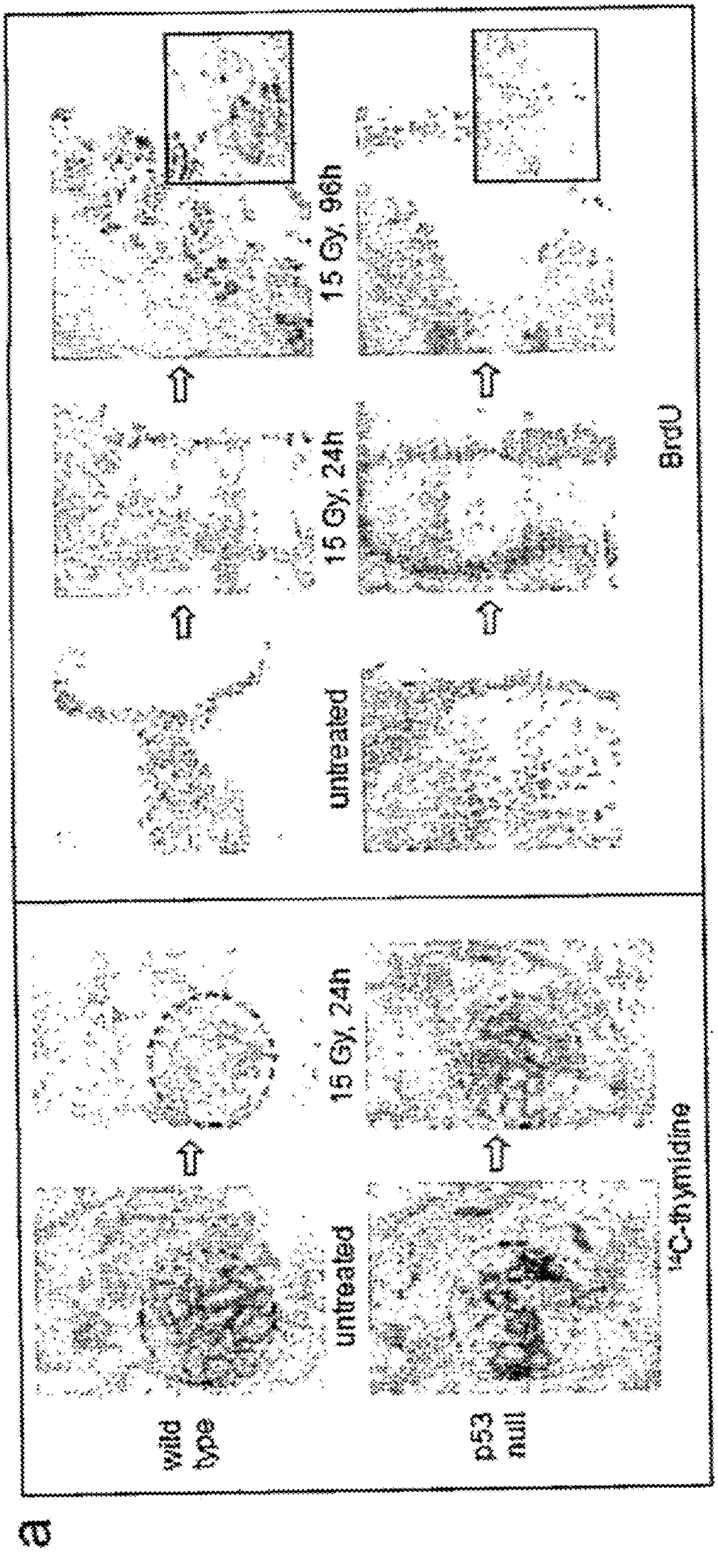
a
wild type
p53 null
untreated
15 Gy, 24h
^{14}C-thymidine
untreated
15 Gy, 24h
15 Gy, 96h
BrdU

Fig. 2, continued

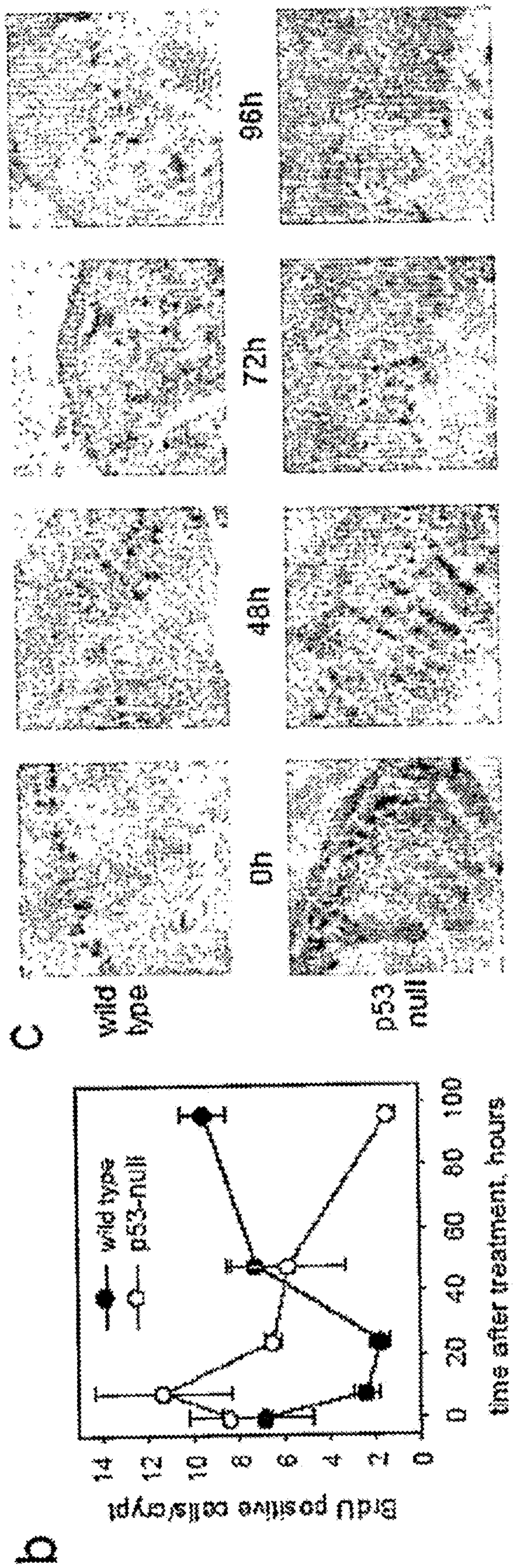

Fig. 3

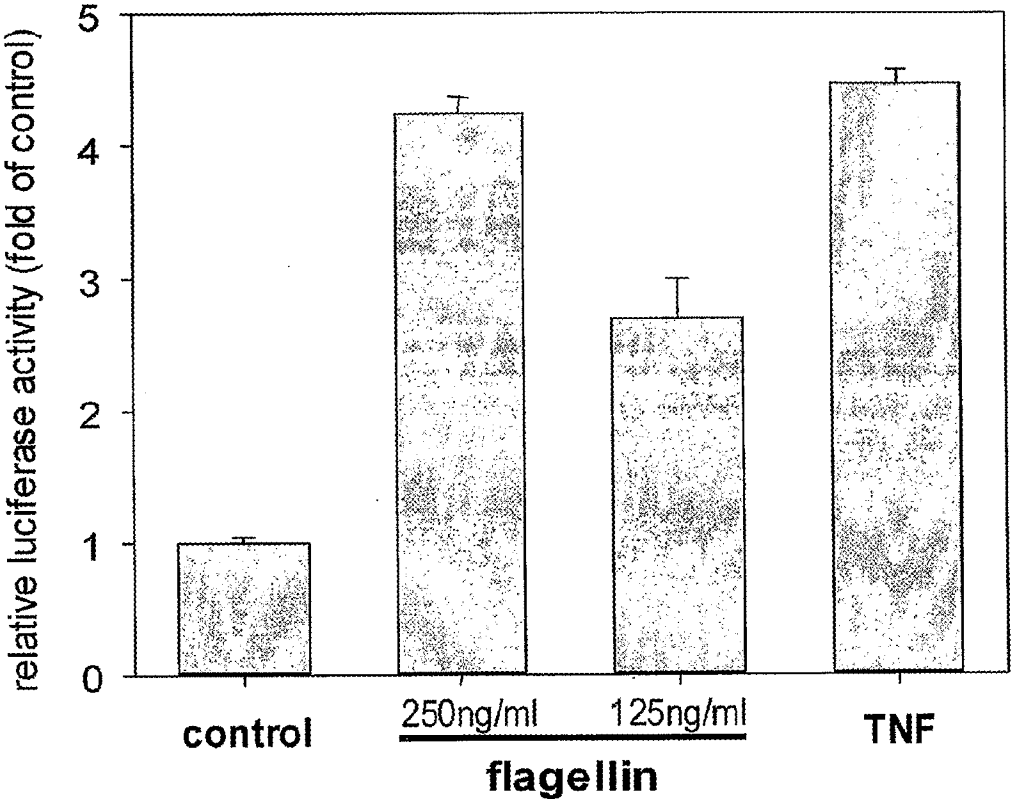
relative luciferase activity (fold of control)
0
1
2
3
4
5
control
250ng/ml
125ng/ml
flagellin
TNF

Fig. 4

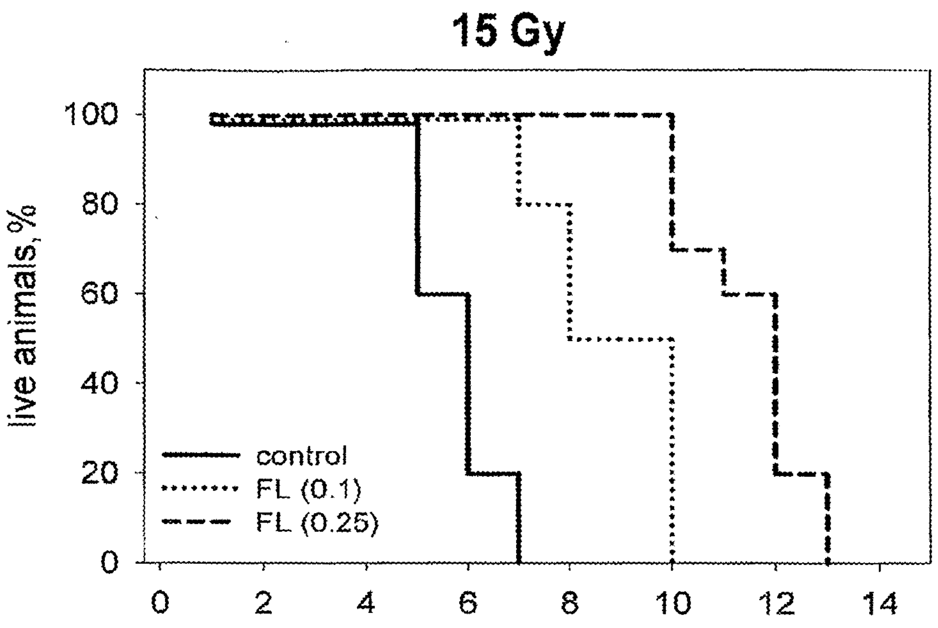
15 Gy
live animals, %
100
80
60
40
20
0
0
2
4
6
8
10
12
14
control
FL (0.1)
FL (0.25)

Fig. 5

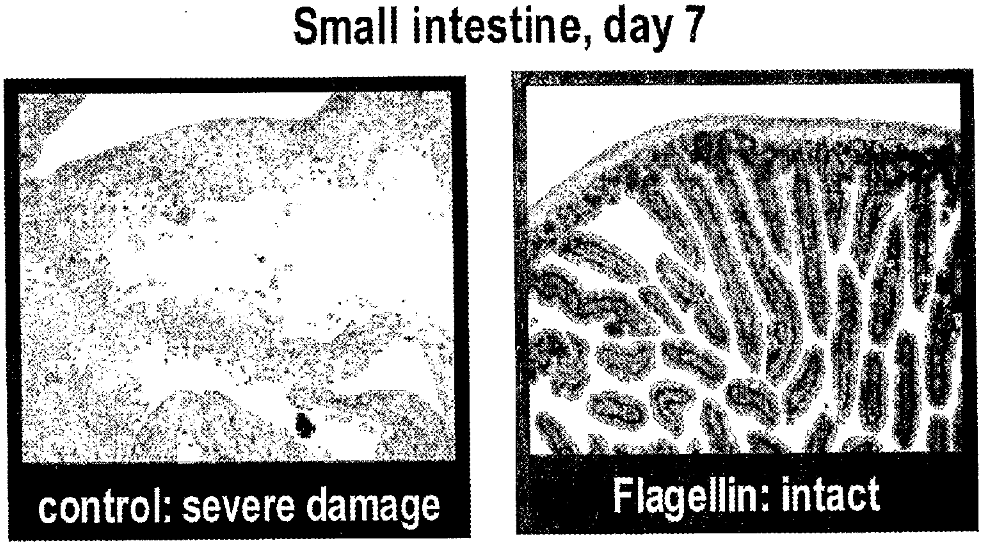
Small intestine, day 7
control: severe damage
Flagellin: intact

Fig. 6

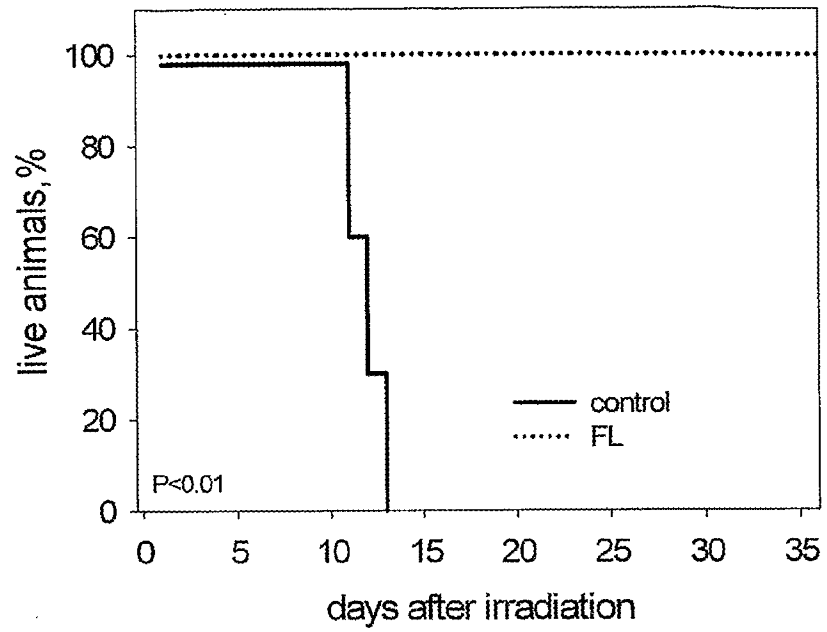
live animals, %
100
80
60
40
20
0
0
5
10
15
20
25
30
35
days after irradiation
control
FL
P<0.01

Fig. 7

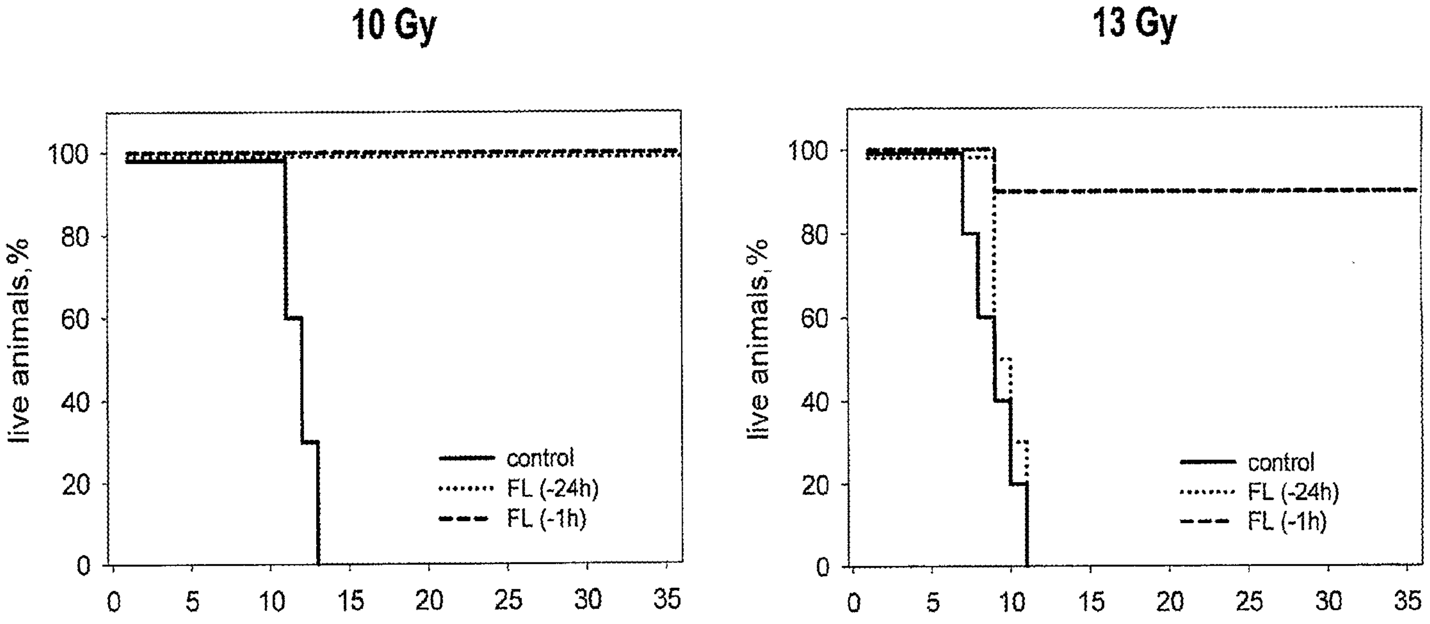
10 Gy
13 Gy
live animals,%
100
80
60
40
20
0
0
5
10
15
20
25
30
35
control
FL (-24h)
FL (-1h)

Fig. 8

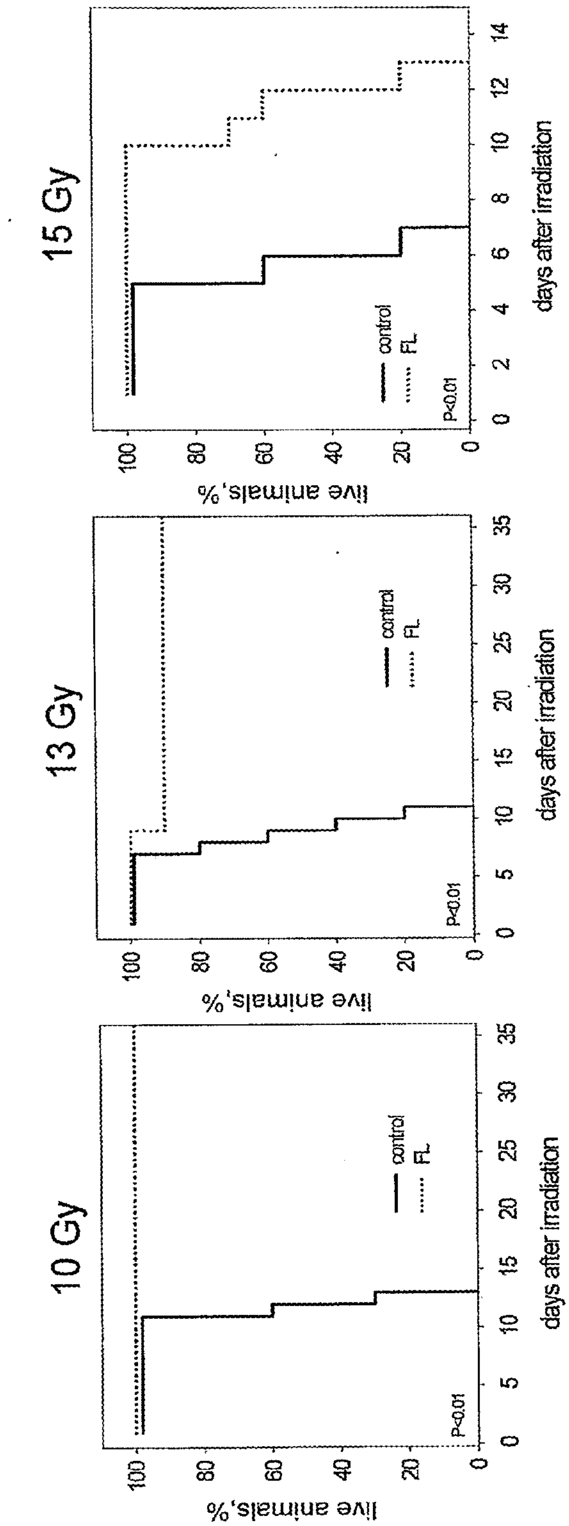
10 Gy
13 Gy
15 Gy
live animals,%
days after irradiation
control
FL
P<0.01
100
80
60
40
20
0
0
5
10
15
20
25
30
35
2
4
6
8
12
14

Fig. 9

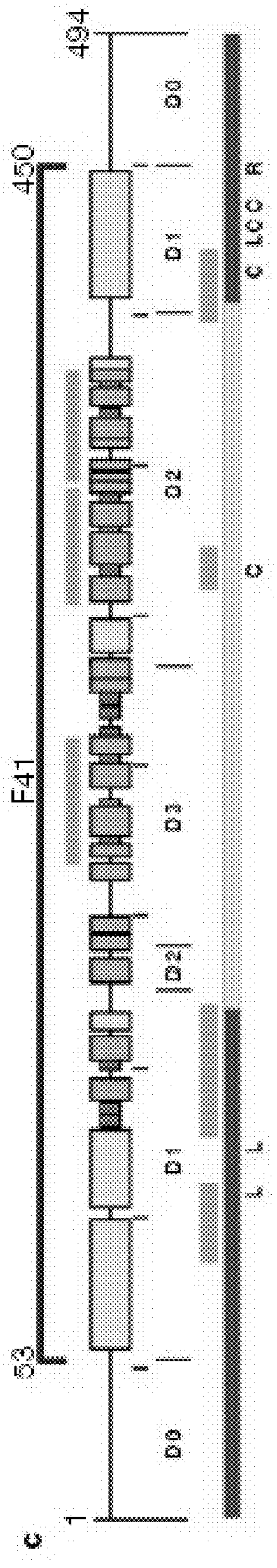

Fig. 10

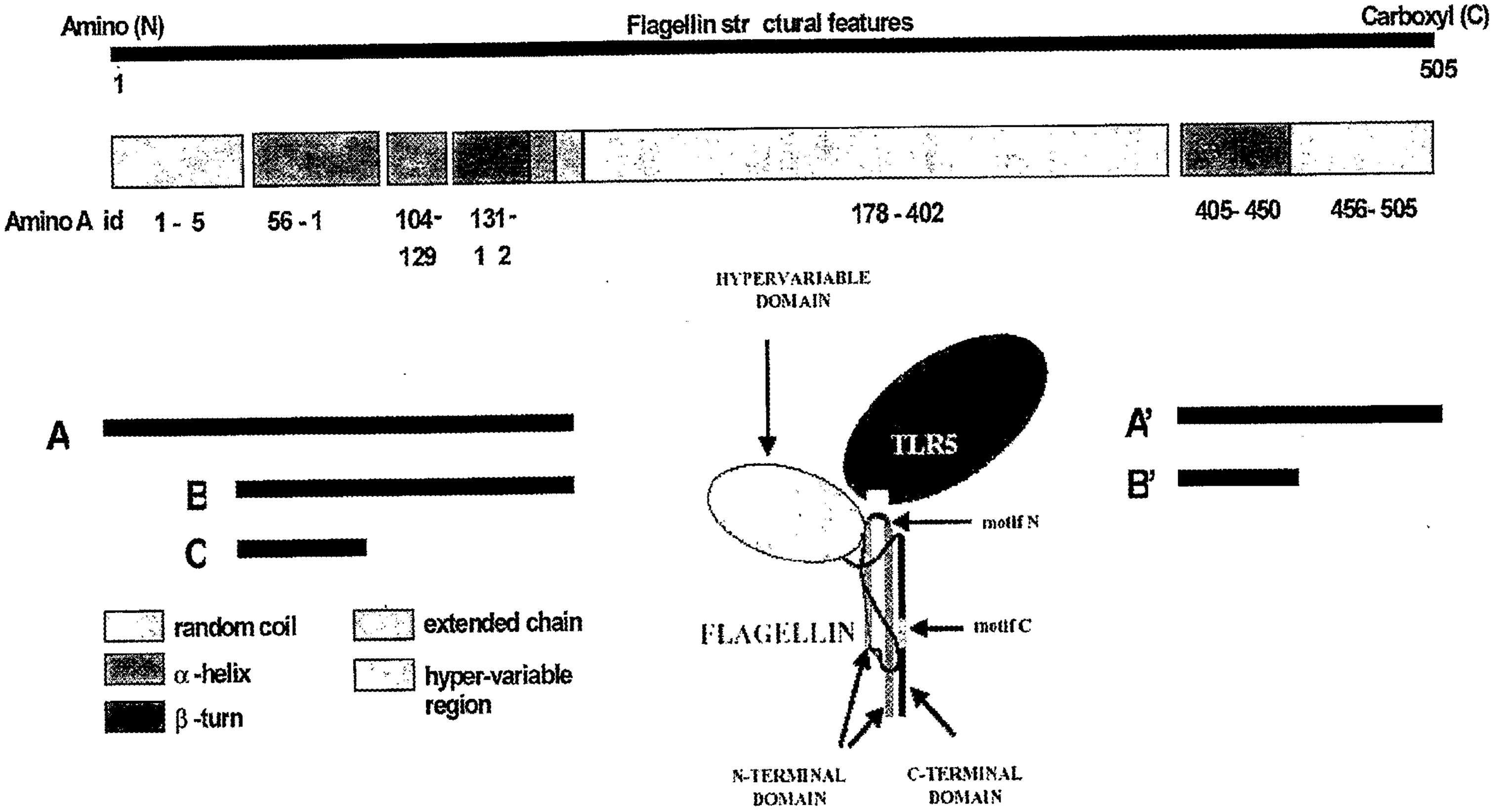
Amino (N)
Flagellin str ctural features
Carboxyl (C)
1
505
Amino A id
1 - 5
56 - 1
104-
129
131-
1 2
178 - 402
405- 450
456- 505
HYPERVARIABLE DOMAIN
TLR5
motif N
motif C
FLAGELLIN
N-TERMINAL DOMAIN
C-TERMINAL DOMAIN
A
B
C
A'
B'
random coil
α -helix
β -turn
extended chain
hyper-variable region

Fig. 11

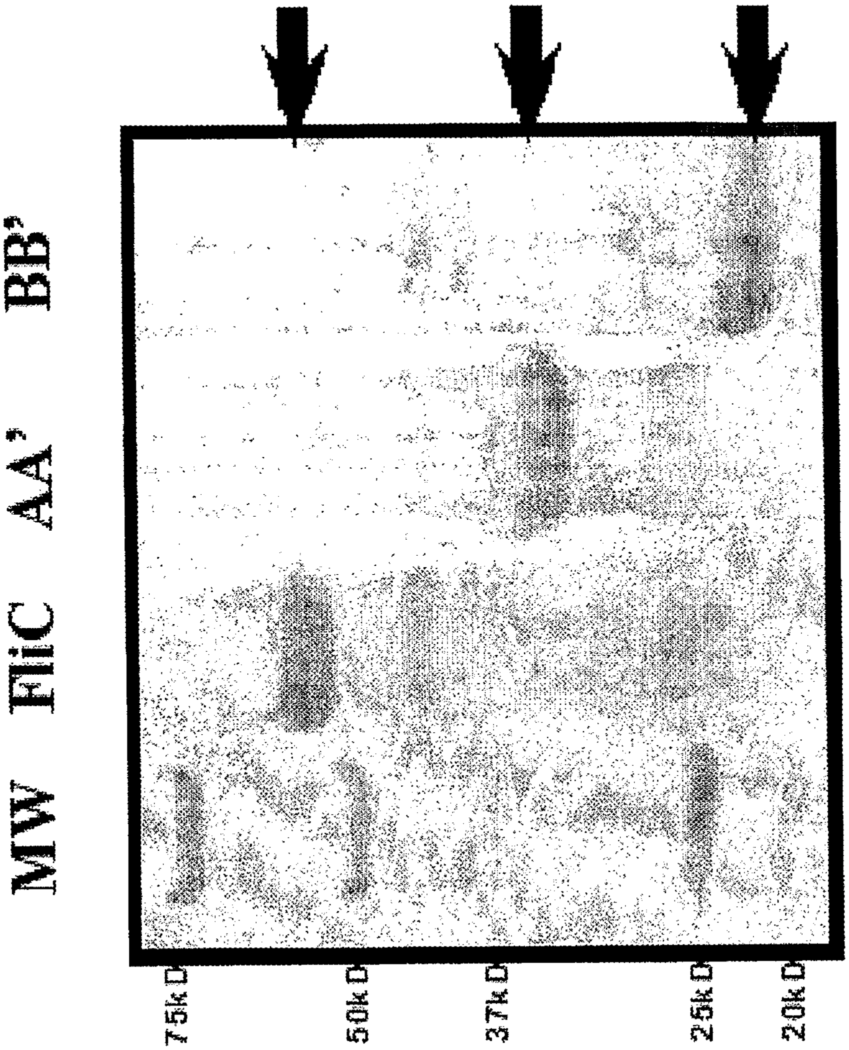

Fig. 12

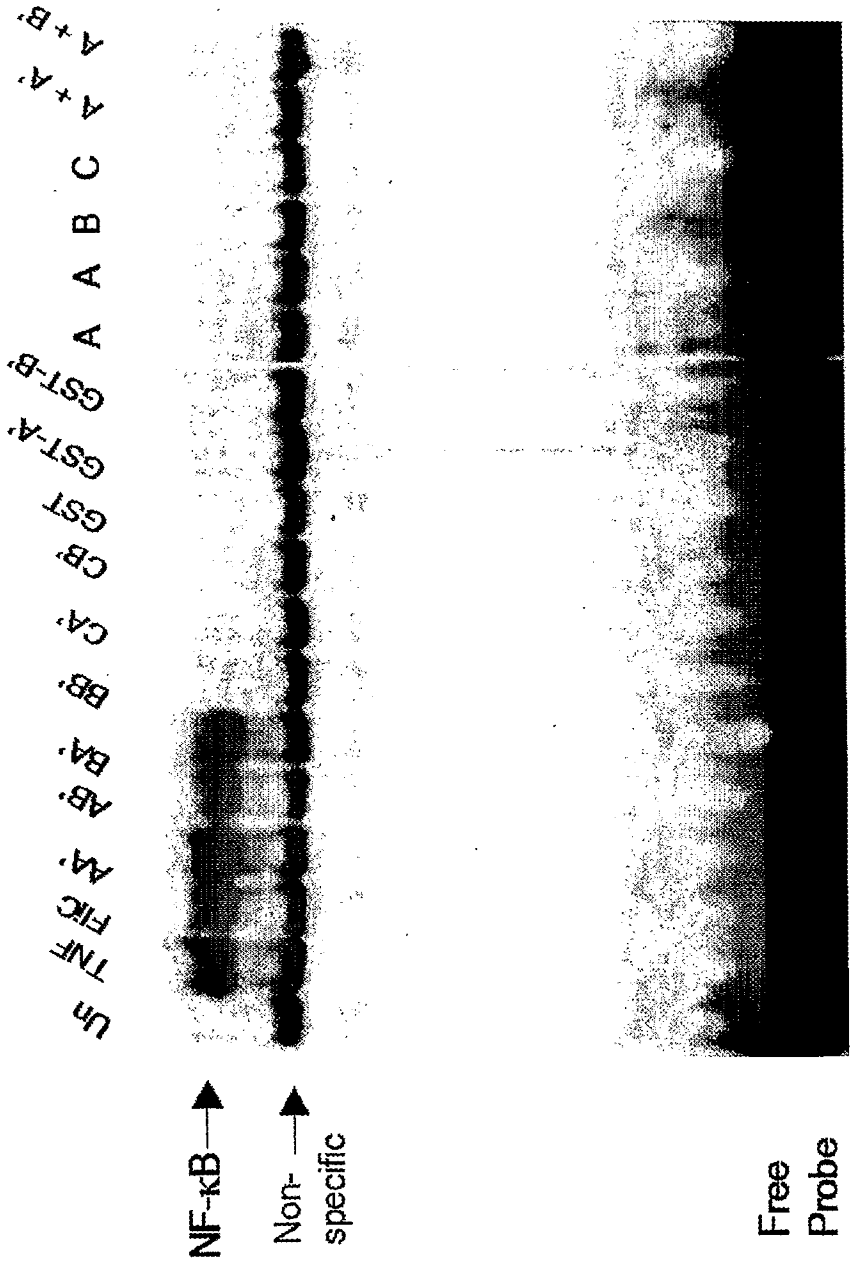
Un
TNF
FIC
AA'
AB'
BA'
BB'
CA'
CB'
GST
GST-A'
GST-B'
A
A
B
C
A + A'
A + B'
NF-κB
Non-specific
Free Probe

Fig. 13

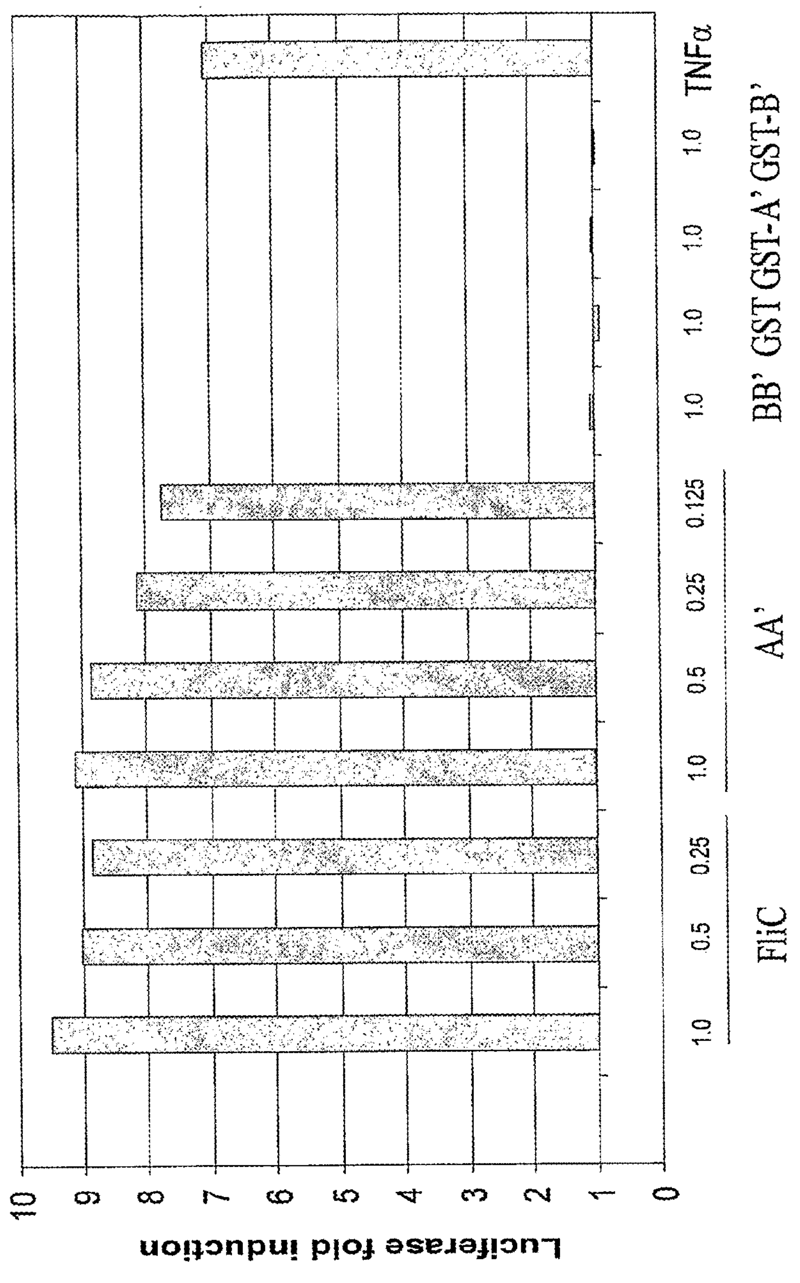
Luciferase fold induction
10
9
8
7
6
5
4
3
2
1
0
1.0
0.5
0.25
FliC
1.0
0.5
0.25
0.125
AA'
1.0
1.0
1.0
1.0
BB' GST GST-A' GST-B'
TNFα

Fig. 14

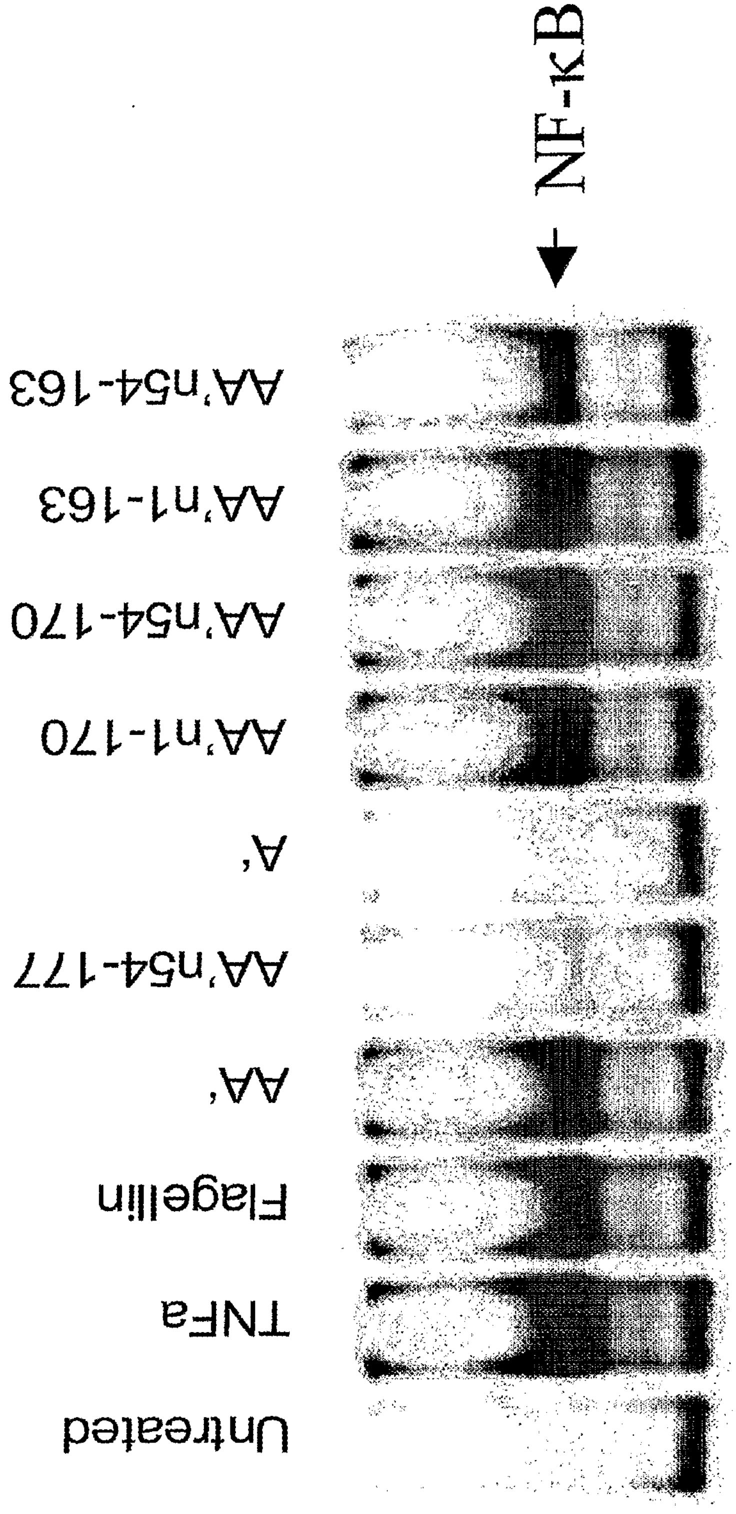
NF-κB
AA'n54-163
AA'n1-163
AA'n54-170
AA'n1-170
A'
AA'n54-177
AA'
Flagellin
TNFa
Untreated

Fig. 15

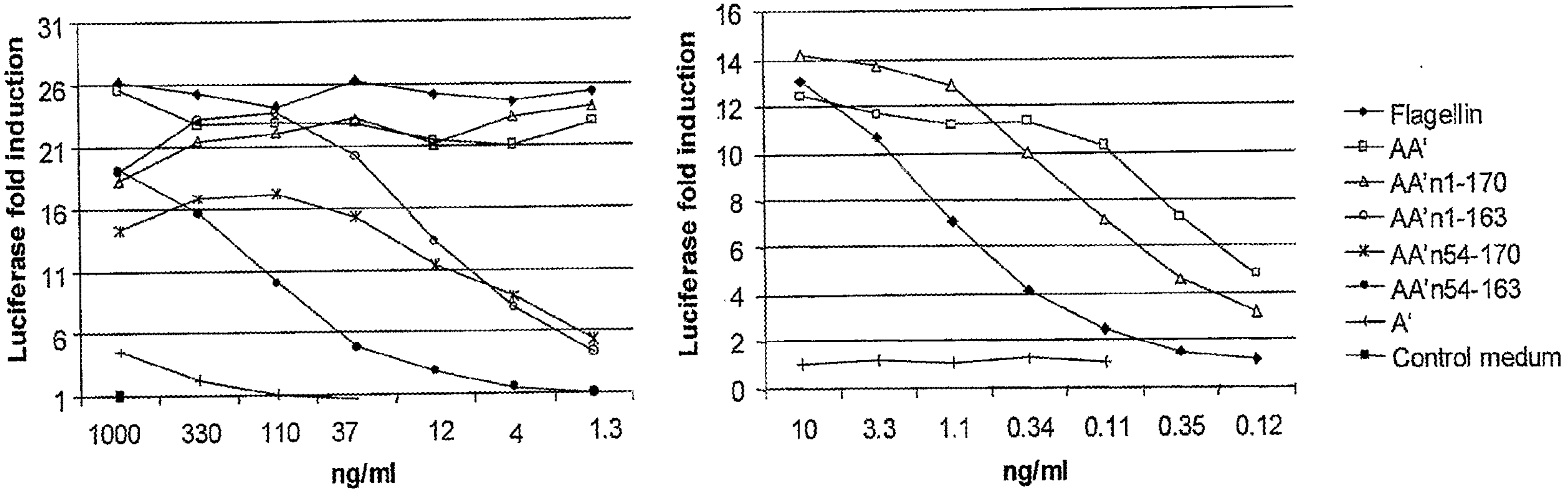
Luciferase fold induction
31
26
21
16
11
6
1
1000
330
110
37
12
4
1.3
ng/ml
Luciferase fold induction
16
14
12
10
8
6
4
2
0
10
3.3
1.1
0.34
0.11
0.35
0.12
ng/ml
Flagellin
AA'
AA'n1-170
AA'n1-163
AA'n54-170
AA'n54-163
A'
Control medum

Fig. 16

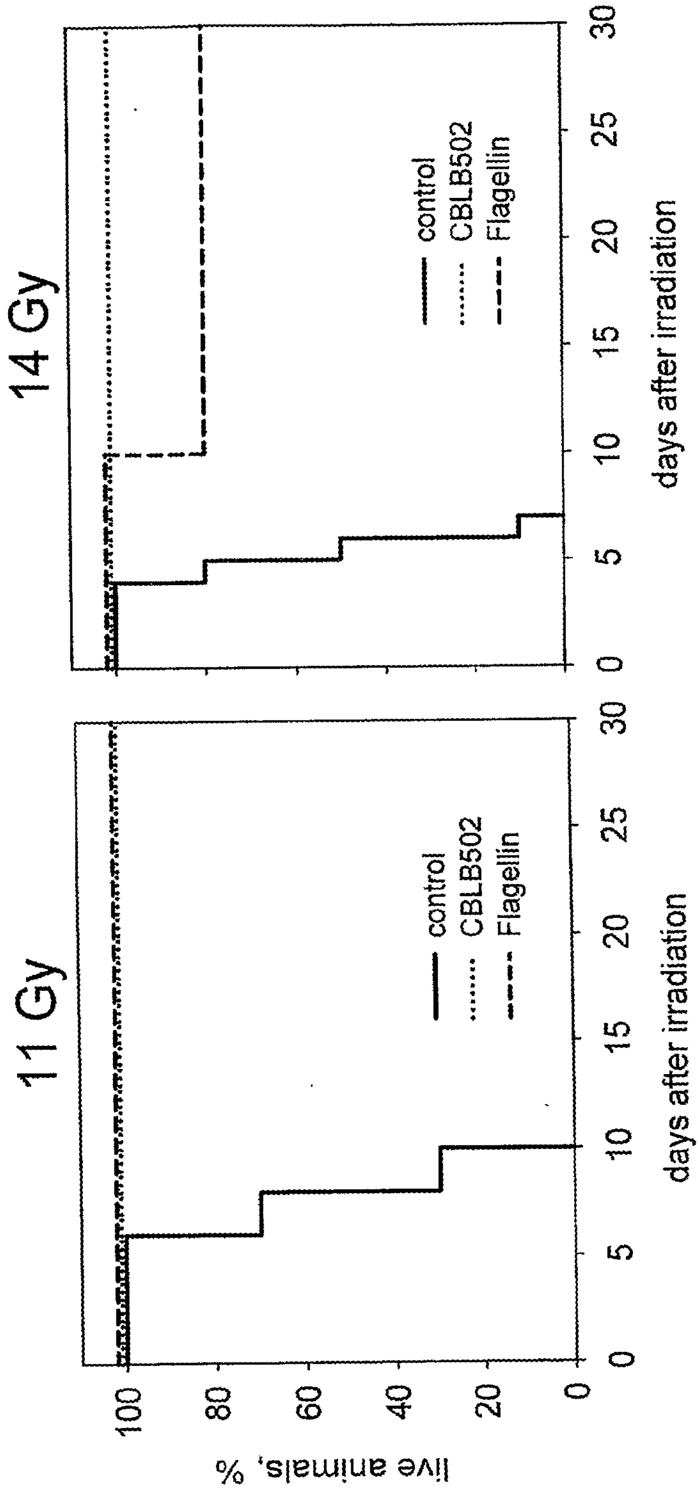
11 Gy
14 Gy
control
CBLB502
Flagellin
live animals, %
100
80
60
40
20
0
days after irradiation
0
5
10
15
20
25
30

Fig. 17

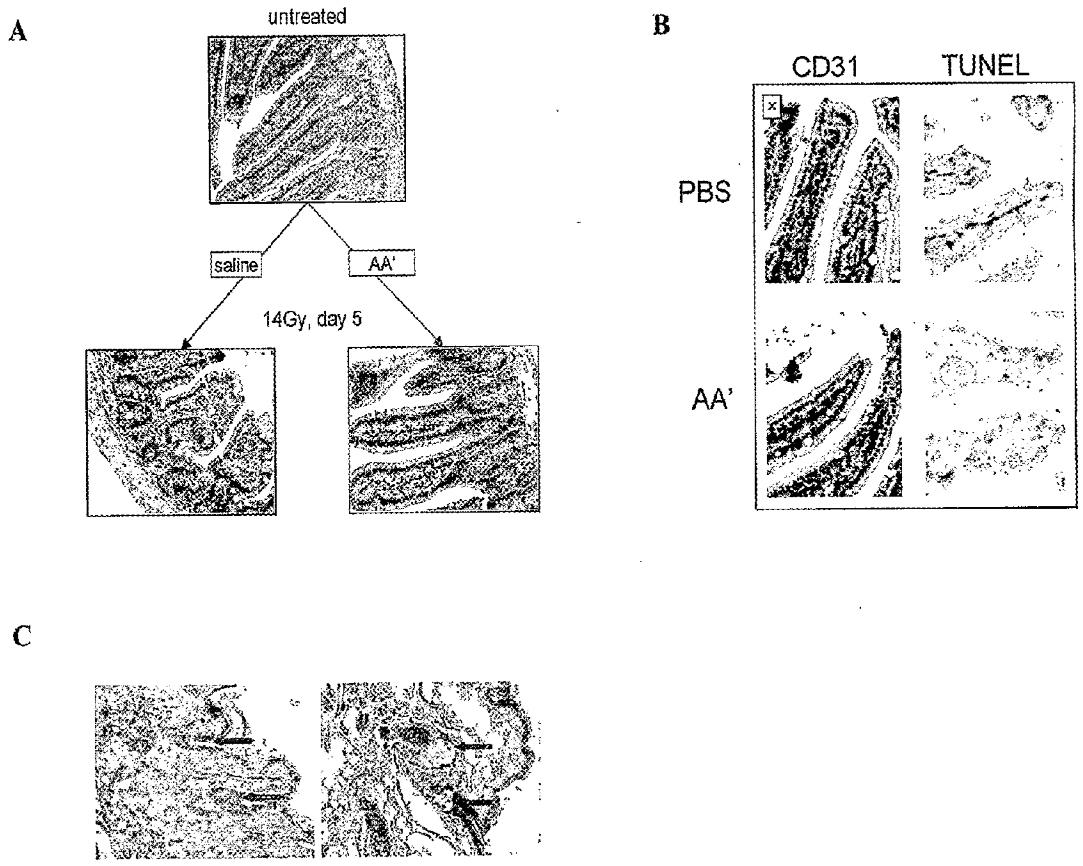

Fig. 18

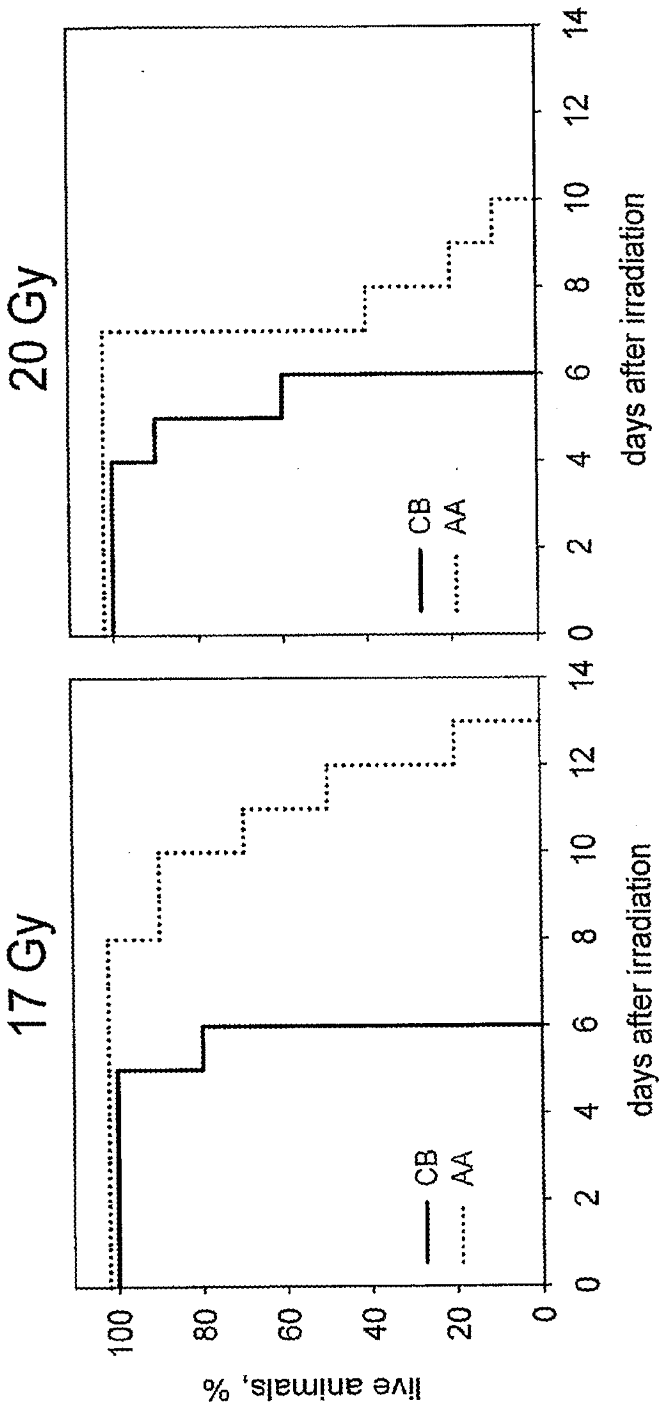
17 Gy
20 Gy
live animals, %
100
80
60
40
20
0
0
2
4
6
8
10
12
14
days after irradiation
CB
AA

Fig. 19

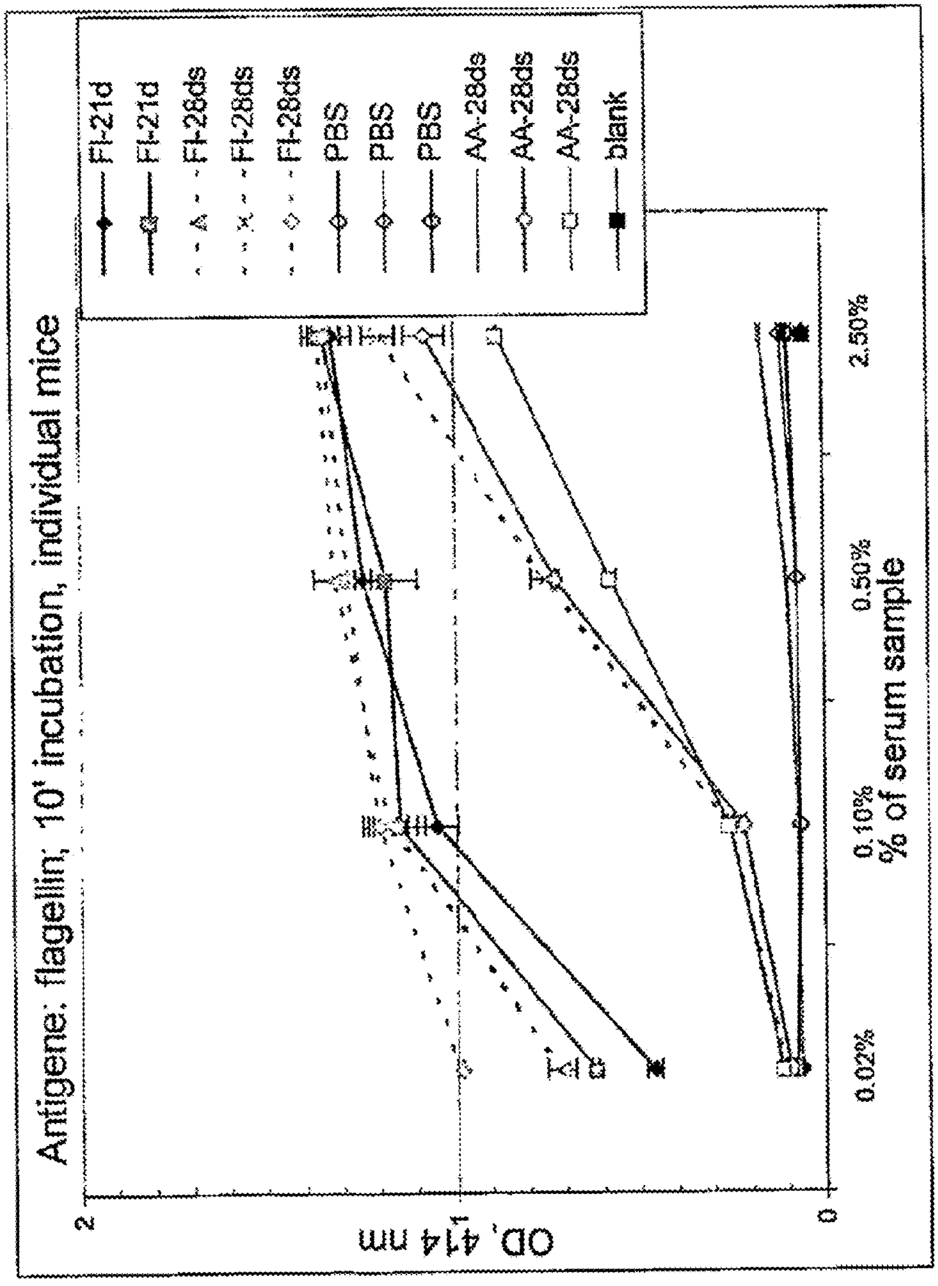
Antigene: flagellin; 10' incubation, individual mice
OD, 414 nm
2
1
0
0.02%
0.10%
0.50%
2.50%
% of serum sample
Fl-21d
Fl-21d
Fl-28ds
Fl-28ds
Fl-28ds
PBS
PBS
PBS
AA-28ds
AA-28ds
AA-28ds
blank

Fig. 19, continued

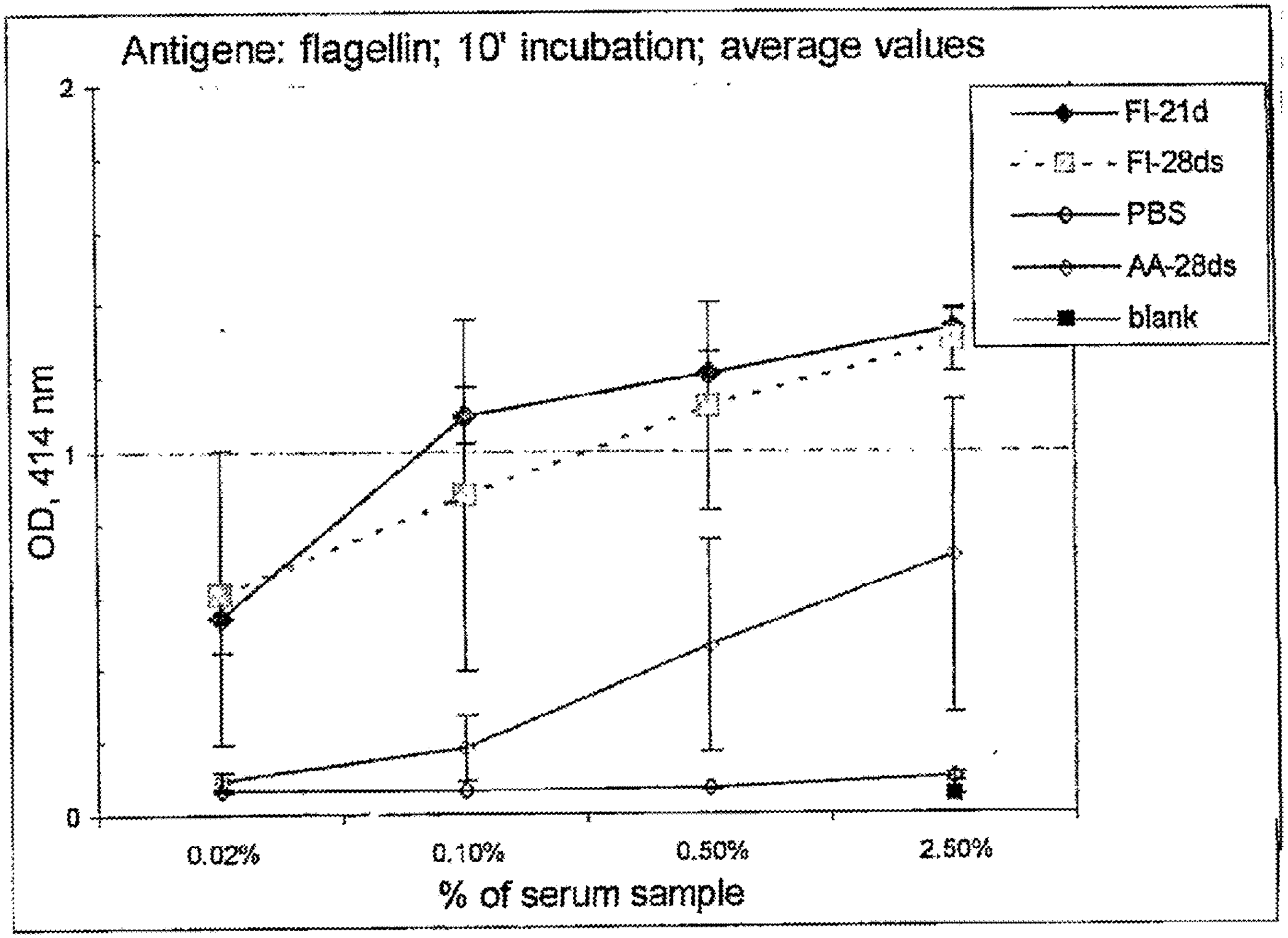

Fig. 20

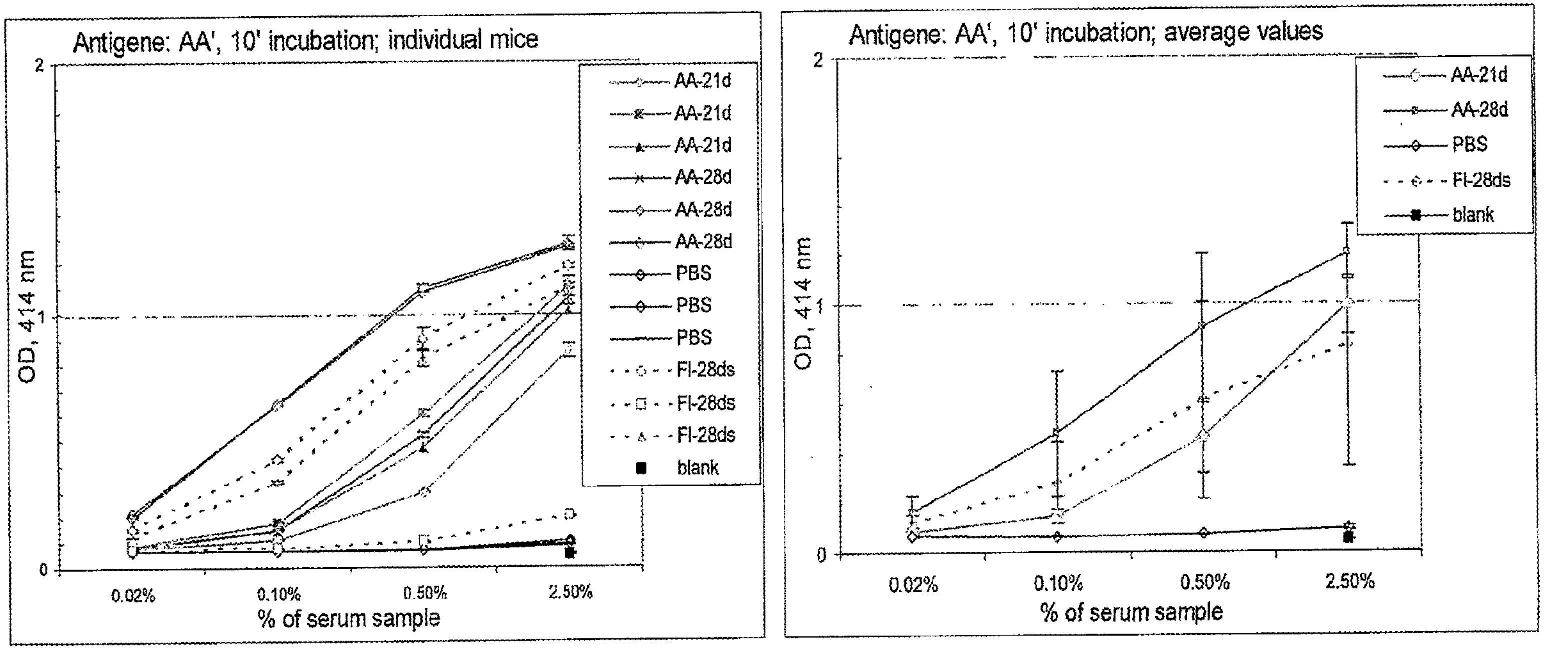
Antigene: AA', 10' incubation; individual mice
OD, 414 nm
0
1
2
0.02%
0.10%
0.50%
2.50%
% of serum sample
AA-21d
AA-21d
AA-21d
AA-28d
AA-28d
AA-28d
PBS
PBS
PBS
FI-28ds
FI-28ds
FI-28ds
blank
Antigene: AA', 10' incubation; average values
OD, 414 nm
0
1
2
0.02%
0.10%
0.50%
2.50%
% of serum sample
AA-21d
AA-28d
PBS
FI-28ds
blank

Fig. 21

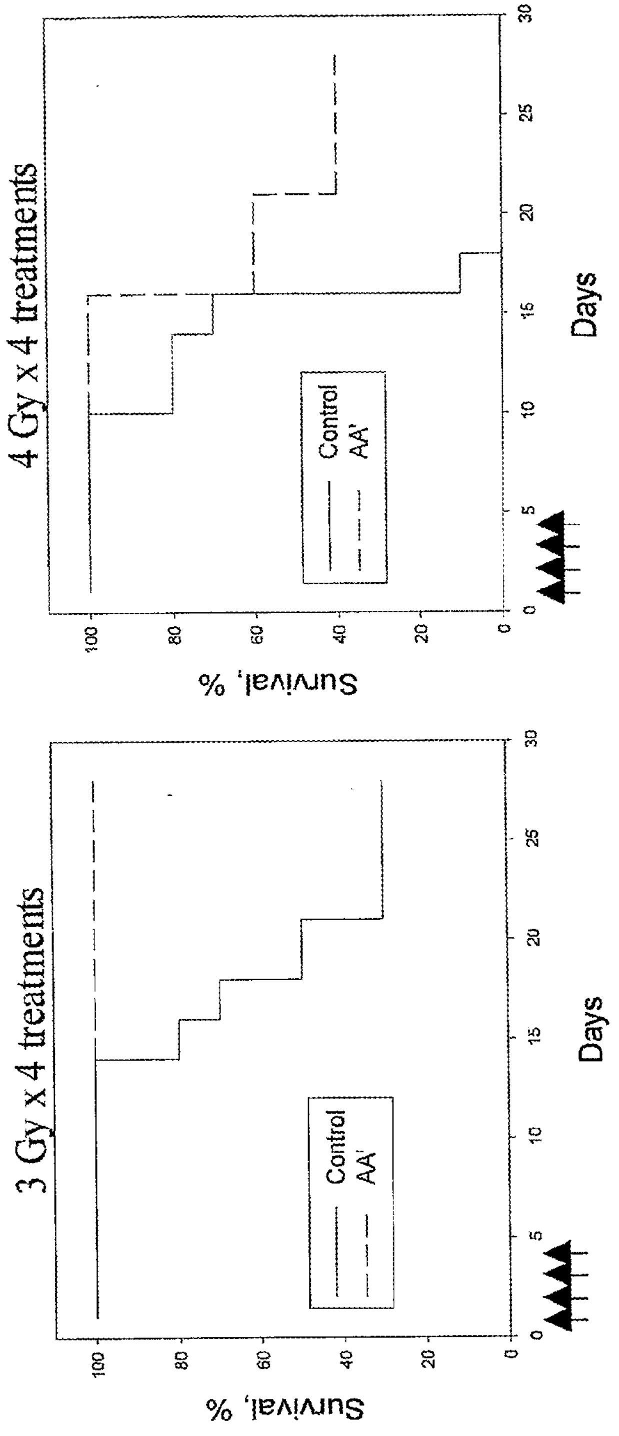
3 Gy x 4 treatments
Survival, %
100
80
60
40
20
0
0
5
10
15
20
25
30
Days
Control
AA'
4 Gy x 4 treatments
Survival, %
100
80
60
40
20
0
0
5
10
15
20
25
30
Days
Control
AA'

Fig. 22

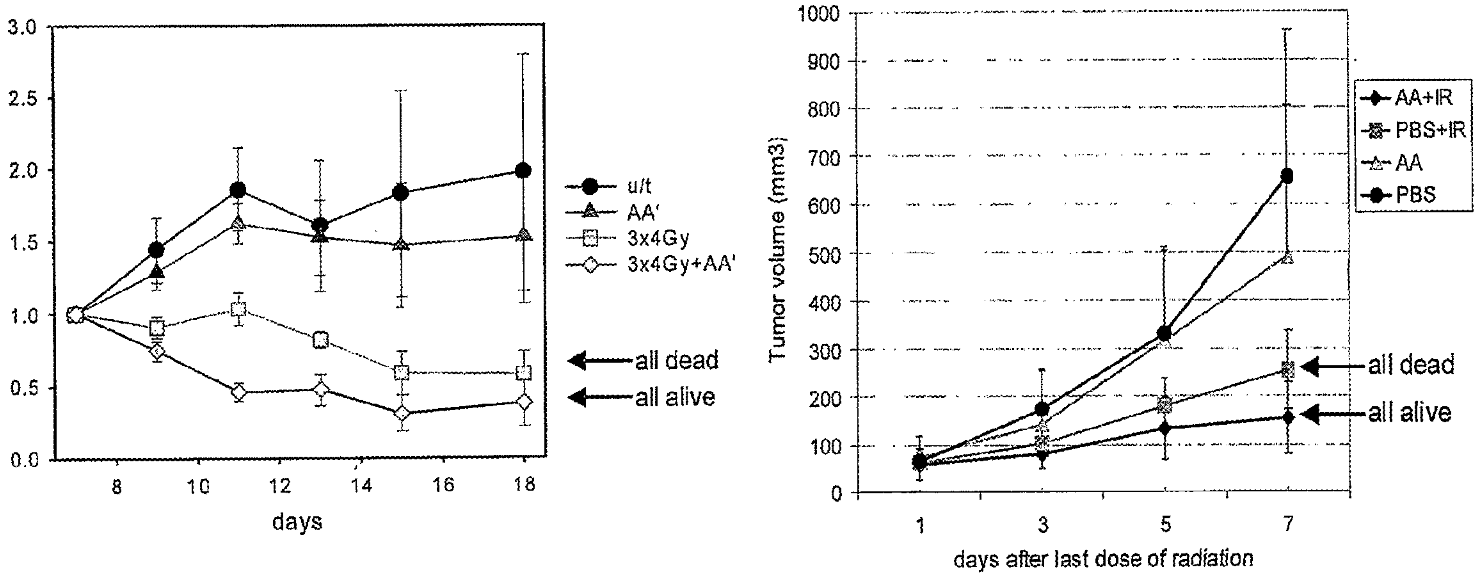
3.0
2.5
2.0
1.5
1.0
0.5
0.0
8
10
12
14
16
18
days
u/t
AA'
3x4Gy
3x4Gy+AA'
all dead
all alive
Tumor volume (mm3)
1000
900
800
700
600
500
400
300
200
100
0
1
3
5
7
days after last dose of radiation
AA+IR
PBS+IR
AA
PBS
all dead
all alive

Fig. 23

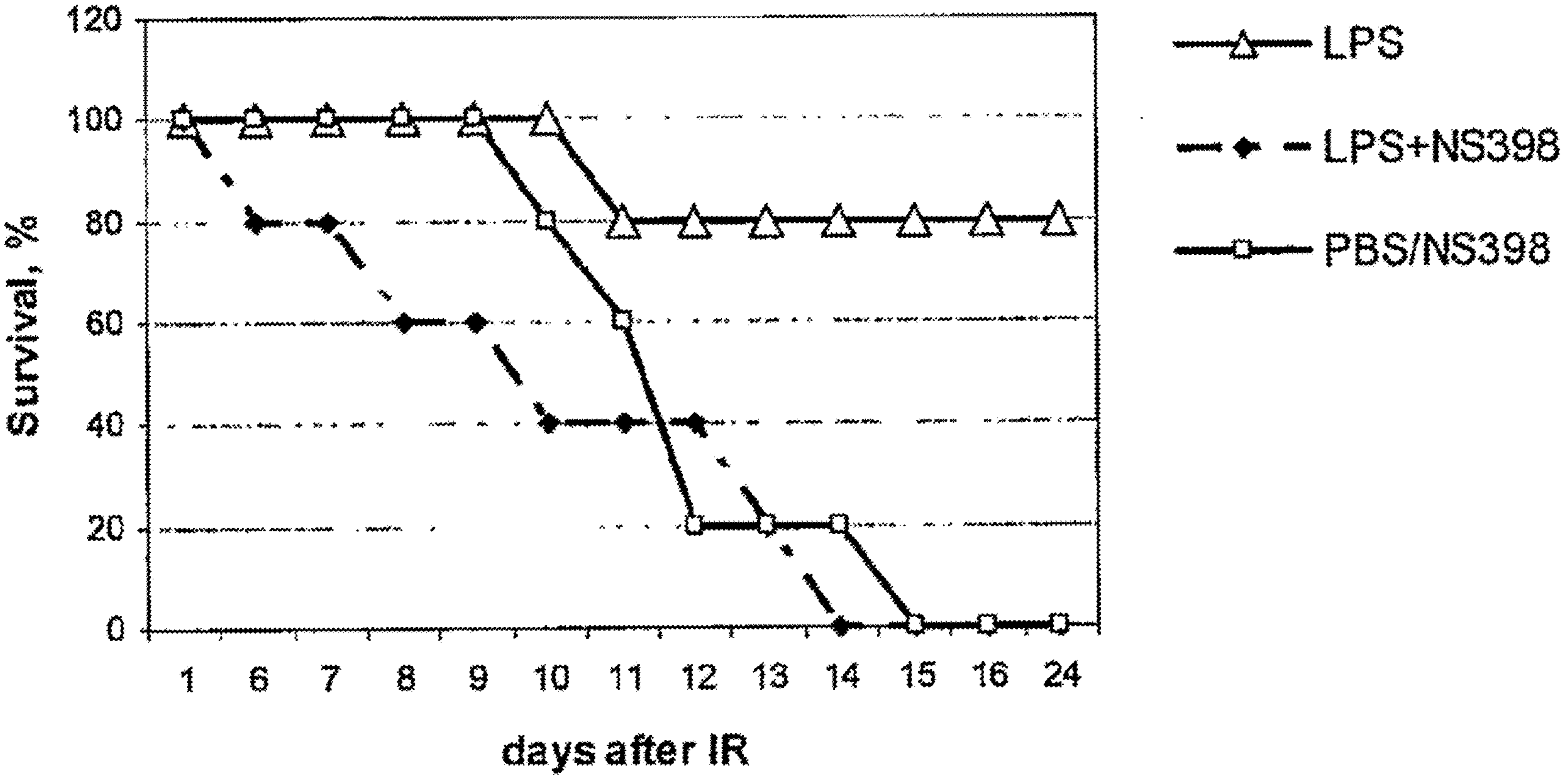
120
100
80
60
40
20
0
Survival, %
1
6
7
8
9
10
11
12
13
14
15
16
24
days after IR
LPS
LPS+NS398
PBS/NS398

Fig. 23, continued

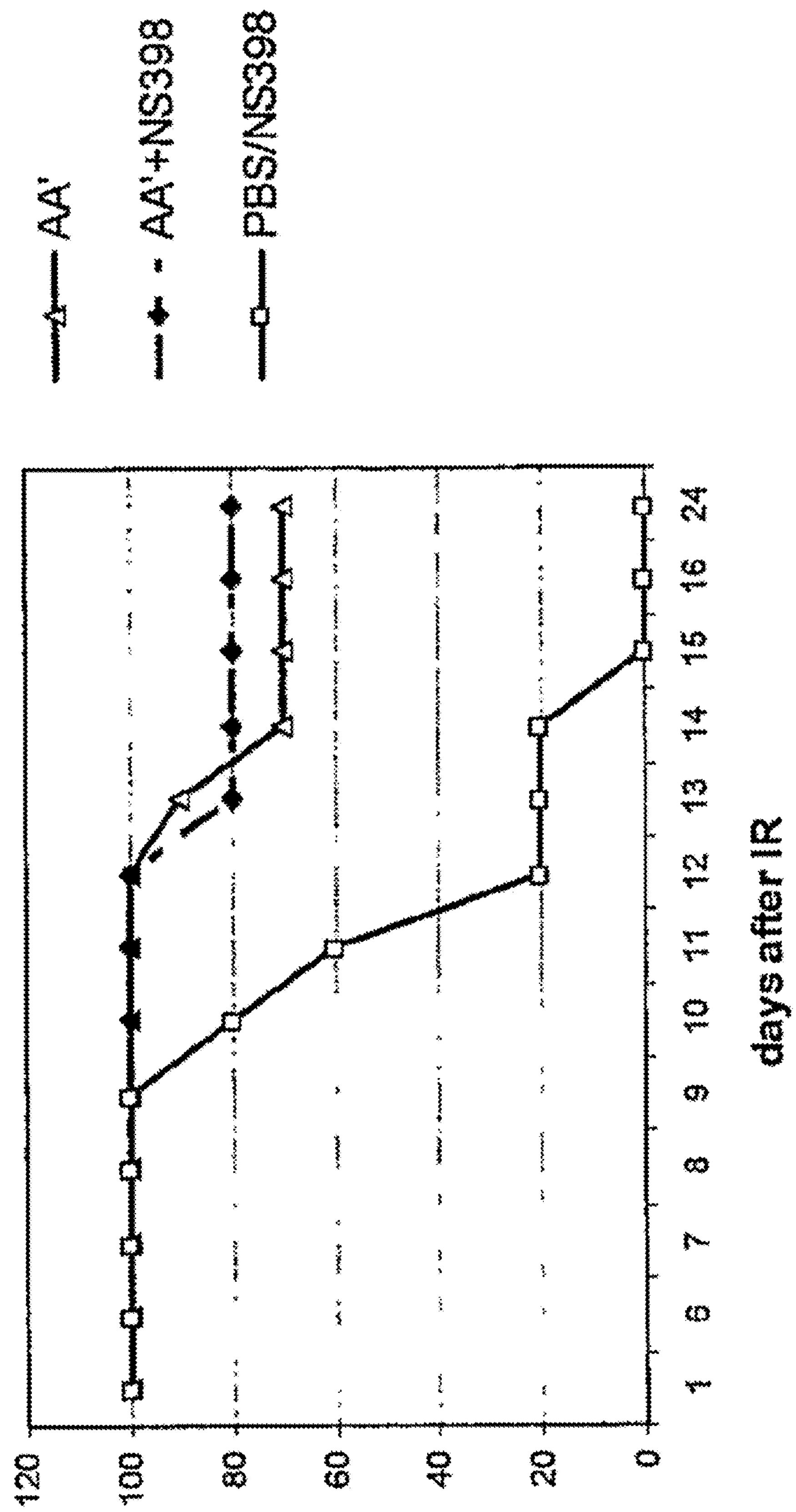

Fig. 24(A)

```
                         |         |         |         |         |         |         |
Q53970        1 MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTSNIKGLTQASRNAND
P72151        1 MALTVNTNIASLNTQRNLNASSNDLNTSLQRLTTGYRINSAKDDAAGLQISNRLSNQISGLNVATRNAND
Q5X5M6        1 MAQVININVASLTAQRNLGVSGNMMQTSIQRLSSGLRINSAKDDAAGLAISQRMTAQIRGMNQAVRNAND
Q6VMV6        1 MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTANIKGLTQASRNAND
P13713        1 MAQVINTNSLSLMAQNNLNKSQSSLGTAIERLSSGLRINSAKDDAAGQAISNRFTANIKGLTQASRNAND
Q93RK8        1 --MRINHNIAALNTSRQLNAGSNSAAKNMEKLSSGLRINRAGDDAAGLAISEKMRSQIRGLDMASKNAQD
Q02551        1 --MKVNTNIISLKTQEYLRKNNEGMTQAQERLASGKRINSSLDDAAGLAVVTRMNVKSTGLDAASKNSSM
Q09012        1 MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSSGLRINSAKDDAAGQAIANRFTANIKGLTQASRNAND
Q8GNT8        1 MAQVINTNSLSLMAQNNLNKSQSALGTAIERLSSGLRINSAKDDAAGQAISNRFTANINGLTQASRNAND
Q9FAE7        1 MASTINTNVSSLTAQRNLSLSQSSLNTSIQRLSSGLRINSAKDDAAGLAISERFTSQIRGLNQAVRNAND
Q8ZF76        1 MA-VINTNSLSLLTQNNLNKSQSSLGTAIERLSSGLRINSAKDDAAGQAIANRFTSNIKGLTQAARNAND
Q7N5J4        1 MAQVINTNSLSLLTQNNLNRSQGTLGSAIERLSSGLRINSAKDDAAGQAIANRFTANVRGLTQAARNAND
O33578        1 -MTTINTNIGAIAAQANMTKVNDQFNTAMTRLSTGLRINAAKDDAAGMAIGEKMTAQVMGLNQAIRNAQD
Q56826        1 MASVINTNDSALLAQNNLTKSKGILGSAIERLSSGLRINSAKDDAAGQAIANRFTANVKGLTQAARNAND
P42273        1 MAQVINTNYLSLVTQNNLNRSQSALGNAIERLSSGMRINSAKDDAAGQAIANRFTSNINGLTQASRNAND
O31059        1 --MVVQHNMQAANASRMLGITTGDQSKSTEKLSSGFKINRAADDAAGLSISEKMRKQIRGLDQASTNASD
Q7VZC2        1 MAAVINTNYLSLVAQNNLNKSQSALGSAIERLSSGLRINSAKDDAAGQAIANRFTANVKGLTQAARNAND
Q9F4A4        1 --MIINHNMMALNAHRNMMGNIATAGKSMEKLSSGLRINRAGDDAAGLAISEKMRGQIRGLDQASRNAQD
Q8P9C4        1 MAQVINTNVMSLNAQRNLNTNSSSMALSIQQLSSGKRITSASVDAAGLAISERFTTQIRGLDVASRNAND
Q82UA3        1 MPQVINTNIASLNAQRNLNVSQNSLSTALQRLSSGLRINSAKDDAAGLAISERMTSQIRGMNQAARNAND
Q84IC5        1 -GFRINTNGASLNAQVNAGLNSRNLDSSLARLSSGLRINSAADDASGLAIADSLKTQANSLGQAINNAND
                    :: *  :  :                :*::* :*. :  **:*  :   :  :  .:  *  *:.

                         |         |         |         |         |         |         |
Q53970       71 GISIAQTTEGALNEINNNLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQ
P72151       71 GISLAQTAEGALQQSTNILQRIRDLALQSANGSNSDADRAALQKEVAAQQAELTRISDTTTFGGRKLLDG
Q5X5M6       71 GISLAQVAEGAMQETTNILQRMRELSVQAANSTNNSSDRASIQSEISQLKSELERIAQNTEFNGQRILDG
Q6VMV6       71 GISVAQTTEGALNEINNNLQRVRELTVQATNGTNSDSDLSSIQAEITQRLEEIDRVSEQTQFNGVKVLAE
P13713       71 GISLAQTTEGALNEVNDNLQNIRRLTVQAQNGSNSTSDLKSIQDEITQRLSEINRISEQTDFNGVKVLSS
Q93RK8       69 GISLIQTSEGALNETHSILQRMSELATQAANDTNTDSDRSELQKEMDQLASEVTRISTDTEFNTKKLLDG
Q02551       71 GIDLLQTADSALSSMSSILQRMRQLAVQSSNGSFSDEDRKQYTAEFGSLIKELDHVADTTNYNNIKLLDQ
Q09012       69 GISVAQTTEGALSEINNNLQRIRELSVQATNGTNSDSDLNSIQDEITQRLSEIDRVSNQTQFNGVKVLAS
Q8GNT8       71 GISLAQTTEGALNEVNDNLQNIRRLTVQAQNGSNSSSDLQSIQDEITQRLSEIDRISQQTDFNGVKVLSK
Q9FAE7       71 GISLAQTAEGALKSTGDILQRVRELAVQSANATNSSGDRKAIQAEVGQLLSEMDRIAGNTEFNGQKLLDG
Q8ZF76       70 GISIAQTTEGSLNEINNNLQRVRELTVQAQNGSNSSSDLDSIQDEISLRLAEIDRVSDQTQFNGKKVLAE
Q7N5J4       71 GISIAQTTEGALNEINTNLQRIRELTVQSQNGSNSESDIKSIQEEVTQRLKEIDRISEQTQFNGVRVLRE
O33578       70 GKNLVDTTEGAHVEVSSMLQRLRELAVQSSNDTNTAADRGSLAAEGKQLIAEINRVAESTTFNGMKVLDG
Q56826       71 GISIAQTTEGALNEINNNLQRIRELTVQSENGSNSKSDLDSIQKEVTQRLEEIDRISTQTQFNGIKVLNG
P42273       71 GISVSQTTEGALNEINNNLQRIRELTVQAKNGTNSNSDINSIQNEVNQRLDEINRVSEQTQFNGVKVLSG
O31059       69 GISAVQTAEGALTEVHSMLQRMNELAVQAANGTNSESDRSSIQDEINQLTTEIDRVAETTKFNETYLLKG
Q7VZC2       71 GISIAQTTEGALNEINNNLQRIRELTVQASNGTNSASDIDSIQQEVNQRLEEINRIAEQTDFNGIKVLKS
Q9F4A4       69 GISLIQTAEGALAETHSILQRMRELSVQSANDTNVAVDRTAIQDEINSLTEEINRISGDTEFNTQKLLDG
Q8P9C4       71 GISLAQTAEGAMVEIGNNLQRIRELSVQSANATNSATDREALNSEVKQLTSEIDRVANQTSFNGTKLLNG
Q82UA3       71 GISLAQTAEGALVEIGNNLQRIRELAVQSANATNSEDDREALQKEVTQLIDEIQRVGEQTSFNGTKLLDG
Q84IC5       70 ANSMLQIADKAMDEQLKILDTIKVKATQAACDGQTAKTRAMIQGEINKLMEELDNIANTTTYNGKQLLSG
                . .  : :: :  .    *: :   : *: :             *      *: .:.  *: .   :*
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Fig. 24 (A) Continued

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                          |                        |                        |
Q53970    141 DNQ-MK--IQVGANDG---------------ETITIDLQ----------KID-VKSLG----LDGFN
P72151    141 SFGTTS--FQVGSNAY---------------ETIDISLQNASASAIGSYQVG-SNGAGTVASVAGTA
Q5X5M6    141 SFSGAS--FQVGANSN---------------QTINFSIG----------SIK-ASSIGGIATATGTE
Q6VMV6    141 NNE-MK--IQVGANDG---------------ETITINLA----------KID-AKTLG----LDGFN
P13713    141 DQK-LT--IQVGANDG---------------ETTDIDLK----------KID-AKQLG----MDTF-
Q93RK8    139 TAQNLT--FQIGANEG---------------QTMSLSIN----------KMD-SE---------SLK
Q02551    139 TATGAATQVSIQASDKAN-------------DLINIDLFNAKGLSAGTITLGSGSTVAGYSALSVAD
Q09012    141 DQT-MK--IQVGANDG---------------ETIEIALD----------KID-AKTLG----LDNFS
Q8GNT8    141 DQK-LT--IQVGANDG---------------ETIDIDLK----------NIN-AQSLG----LDKFN
Q9FAE7    141 SFGSAT--FQVGANAN---------------QTITATTGNFRTNNY-GAQLT-ASASG--AATSGAS
Q8ZF76    140 NTT-MS--IQVGANDG---------------ETIDINLQ----------KID-SKSLG----LGSYS
Q7N5J4    141 DSK-MT--IQVGANDN---------------EVIDIDLK----------KID-KEALN----LGKFT
O33578    140 SFTGKQ--LQIGADSG---------------QTMAINVDSAAATDIGAHKISSASTVVADAALTDTT
Q56826    141 DVTEMK--IQVGANDN---------------ETIGIKLG----------KIN-SEKLN----LKEFS
P42273    141 EKSKMT--IQVGTNDN---------------EVIEFNLD----------KID-NDTLG----VASDK
O31059    139 GNGDRT--VRVYAHDAGLVGSLSQNTTKATFQMRKLEIGDSYTIGGTTYKIG-AETVK--EAMTALK
Q7VZC2    141 NATDMTLSIQVGAKDN---------------ETIDIKID----------RNS-NWNLY----DAVGT
Q9F4A4    139 GFKG-E--FQIGANSN---------------QTVKLDIG----------NMS-AA---------SLG
Q8P9C4    141 DFSGAL--FQVGADAG---------------QTIGINS---------IVDAN-VDSLG--KANFAAS
Q82UA3    141 SFASQI--FQVGANEG---------------ETIDFTD-----------------------------
Q84IC5    140 SFSNAQ--FQIGDKAN---------------QTVNATIG----------STN-SAKVGQTRFETGAV
                      . :                    :
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Fig. 24 (B)

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                     |         |         |         |         |         |         |         |         |
Q53970    418 PLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR--
P72151    401 AIAVVDNALAAIDAQRADLGAVQNRFKNTIDNLTNISENATNARSRIKDTDFAAETAALSKNQVLQQAGTAILAQANQLPQAVLSLLR--
Q5X5M6    387 AIKRIDAALNSVNSNRANMGALQNRFESTIANLQNVSDNLSAARSRIQDADYAAEMASLTKNQILQQAGTAMLAQANSLPQSVLSLLGR-
Q6VMV6    400 PLETIDKALAKVDNLRSDLGAVQNRFDSAITNLGNTVNNLSSARSRIEDADYATEVSNMSRAQILQQAGTSVLAQANQTTQNVLSLLQG-
P13713    264 PLATLDKALAQVDGLRSSLGAVQNRFDSVINNLNSTVNNLSASQSRIQDADYATEVSNMSRANILQQAGTSVLAQANQSTQNVLSLLR--
Q93RK8    245 ALTTIKTAIDTVSSERAKLGAVQNRLEHTINNLGTSSENLTSAESRIRDVDMASEMMEYTKNNILTQASQAMLAQANQQPQQVLQLLKG-
Q02551    481 VIGLADAALTKIMKQRADMGAYYNRLEYTAKGLMGAYENMQASESRIRDADMAEEVVSLTTKQILVQSGTAMLAQANMKPNSVLKLLQQI
Q09012    437 PLSKLDEALAKVDKLRSSLGAVQNRFDSAITNLGNTVNDLSSARSRIEDADYATEVSNMSRAQILQQAGTSVLAQANQTTQNVLSLLR--
Q8GNT8    329 PLATLDKALSQVDDLRSGLGAVQNRFDSVINNLNSTVNNLSASRSRIQDADYATEVSNMSRAQILQQAGTSVLAQANQSTQNVLSLLR--
Q9FAE7    405 ALKIIDAALSAVNGQRASFGALQSRFETTVNNLQSTSENMSASRSRIQDADFAAETANLSRSQILQQAGTAMVAQANQLPQGVLSLLK--
Q8ZF76    282 PLETLDDAIKQVDGLRSSLGAVQNRFESAVTNLNNTVTNLTSARSRIEDADYATEVSNMSRAQILQQAGTSVLSQANQVPQTVLSLLN--
Q7N5J4    268 PLETLDSALAQVDSLRSSLGAIQNRLESTVNNLNNTVNNLSAARSRIEDADYATEVSNMSRGQILQQAGTAVLAQANQVPQNVMSLLR--
O33578    405 AIGVIDVALSKISQSRSELGAVSNRLDSTISNLTNISTSVQAAKSQVMDADFAAESTNLARSQILSQASTAMLAQANSSKQNVLSLLRG-
Q56826    226 PLDTLDKALAQVDDMRSSIGAVQNRLESTVNNLNNTVNNLSAARSRIEDADYAVEVSNMSRGQILQQAGTSVLAQANQVPQTVLSLLR--
P42273    280 ALATLDNAISKVDESRSKLGAIQNRFQSTINNLNNTVNNLSASRSRILDADYATEVSNMSKNQILQQAGTAVLAQANQVPQTVLSLLR--
O31059    385 AIDAISDALAKVSAQRSALGSIQNRLEHSIANLDNVVENTNAAESRIRDTDMADEMVTYSKNNILMQAGQSMLAQANQATQGVLSILQ--
Q7VZC2    304 ALSKLDDAMKAVDEQRSSLGAIQNRFESTVANLNNTITNLSAARSRIEDSDYATEVSNMTKNQILQQAGTSVLAQANQVPQNVLSLLR--
Q9F4A4    326 SIKTINSAIEQVSTQRSKLGAVQNRLEHTINNLNTSSENLTAAESRVRDVDMAKEMMAFSKNNILSQAAQAMLGQANQQPQGVLQLLR--
Q8P9C4    312 ALEIVDKALTSVNSSRADMGAVQNRFTSTIANLAATSENLTASRSRIADTDYAKTTAELTRTQILQQAGTAMLAQAKSVPQNVLSLLQ--
Q82UA3    192 ----IDDALKIVNSTRADLGAIQNRFSSAIANLQTSAENLSASRSRIQDADFAAETAALTRAQILQQAGVAMLSQANALPNNVLSLLR--
Q84IC5    403 VMDIADTAIANLDTIRANIGATQNQITSTINNISVTQVNVKAAESQIRDVDFASESANYSKANILAQSGSYAMAQANAASQNVLRLLQ--
                   . *:  :    *: :*:   .::     .:     .    :.*:: * * *       :   ::* *:.   :.**:   : *: :*
```

Fig. 25A

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AJ605765	1050	386	1.00E-107	348	215	61
AJ536600	1050	385	1.00E-106	348	214	61
AY249989	1050	384	1.00E-106	348	213	61
AJ605764	1050	384	1.00E-106	348	213	61
AB028472	1433	384	1.00E-106	348	213	61
AJ605766	1050	383	1.00E-106	348	214	61
AJ515904	1243	382	1.00E-105	348	213	61
AY743588	829	378	1.00E-104	284	201	70
X91047	2820	369	1.00E-101	313	206	65
D32256	1240	367	1.00E-101	356	214	60
BX571865	348813	364	1.00E-100	355	207	58
AF221596	7867	356	8.00E-98	367	213	58
AF221596	7867	355	1.00E-97	365	211	57
AY649742	1518	336	1.00E-91	178	177	99
AY649742	1518	194	5.00E-49	106	104	98
AY649741	1518	336	1.00E-91	178	177	99
AY649741	1518	194	5.00E-49	106	104	98
AY649715	1518	336	1.00E-91	178	177	99
AY649715	1518	197	5.00E-50	227	126	55
AY649714	1518	336	1.00E-91	178	177	99
AY649714	1518	195	2.00E-49	227	125	55
AY649713	1518	336	1.00E-91	178	177	99
AY649713	1518	196	2.00E-49	227	126	55
AY649712	1518	336	1.00E-91	178	177	99
AY649712	1518	194	5.00E-49	106	104	98
AY649711	1518	336	1.00E-91	178	177	99
AY649711	1518	194	5.00E-49	106	104	98
AY649710	1518	336	1.00E-91	178	177	99
AY649710	1518	194	5.00E-49	106	104	98
AY649709	1518	336	1.00E-91	178	177	99
AY649709	1518	194	5.00E-49	106	104	98
AY649708	1518	336	1.00E-91	178	177	99
AY649708	1518	194	5.00E-49	106	104	98
AY649707	1518	336	1.00E-91	178	177	99
AY649707	1518	197	8.00E-50	227	126	55
AY649706	1518	336	1.00E-91	178	177	99
AY649706	1518	194	4.00E-49	227	125	55
AY649705	1518	336	1.00E-91	178	177	99
AY649705	1518	197	8.00E-50	227	126	55
AY353534	1518	336	1.00E-91	178	177	99
AY353534	1518	194	4.00E-49	227	125	55
AY353533	1527	336	1.00E-91	178	177	99
AY353533	1527	197	5.00E-50	324	142	43
AY353532	1527	336	1.00E-91	178	177	99
AY353532	1527	197	5.00E-50	324	142	43
AY353416	1515	336	1.00E-91	178	177	99
AY353416	1515	194	4.00E-49	309	141	45
AY353415	1515	336	1.00E-91	178	177	99
AY353415	1515	194	4.00E-49	309	141	45
AY353412	1527	336	1.00E-91	178	177	99
AY353412	1527	194	5.00E-49	106	104	98
AY353411	1527	336	1.00E-91	178	177	99
AY353411	1527	194	5.00E-49	106	104	98
AY353410	1527	336	1.00E-91	178	177	99
AY353410	1527	194	5.00E-49	106	104	98
AY353409	1527	336	1.00E-91	178	177	99
AY353409	1527	194	5.00E-49	106	104	98
AY353408	1518	336	1.00E-91	178	177	99
AY353408	1518	194	4.00E-49	227	125	55
AY353407	1518	336	1.00E-91	178	177	99
AY353407	1518	197	5.00E-50	227	126	55
AY353406	1518	336	1.00E-91	178	177	99
AY353406	1518	197	5.00E-50	227	126	55
AY353405	1518	336	1.00E-91	178	177	99
AY353405	1518	197	5.00E-50	227	126	55
AY353404	1518	336	1.00E-91	178	177	99
AY353404	1518	194	5.00E-49	106	104	98
AY353403	1518	336	1.00E-91	178	177	99

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY353403	1518	196	2.00E-49	227	126	55
AY353402	1518	336	1.00E-91	178	177	99
AY353402	1518	194	5.00E-49	106	104	98
AY353401	1518	336	1.00E-91	178	177	99
AY353401	1518	194	5.00E-49	106	104	98
AY353400	1518	336	1.00E-91	178	177	99
AY353400	1518	194	5.00E-49	106	104	98
AY353399	1518	336	1.00E-91	178	177	99
AY353399	1518	194	5.00E-49	106	104	98
AY353398	1518	336	1.00E-91	178	177	99
AY353398	1518	194	5.00E-49	106	104	98
AY353397	1515	336	1.00E-91	178	177	99
AY353397	1515	193	1.00E-48	106	103	97
AY353396	1515	336	1.00E-91	178	177	99
AY353396	1515	193	1.00E-48	106	103	97
AY353395	1518	336	1.00E-91	178	177	99
AY353395	1518	194	5.00E-49	106	104	98
AY353394	1518	336	1.00E-91	178	177	99
AY353394	1518	194	5.00E-49	106	104	98
AY353393	1518	336	1.00E-91	178	177	99
AY353393	1518	194	5.00E-49	106	104	98
AY353392	1518	336	1.00E-91	178	177	99
AY353392	1518	194	5.00E-49	106	104	98
AY353391	1518	336	1.00E-91	178	177	99
AY353391	1518	194	5.00E-49	106	104	98
AY353389	1518	336	1.00E-91	178	177	99
AY353389	1518	194	5.00E-49	106	104	98
AY353388	1518	336	1.00E-91	178	177	99
AY353388	1518	194	5.00E-49	106	104	98
AY353387	1518	336	1.00E-91	178	177	99
AY353387	1518	194	5.00E-49	106	104	98
AY353386	1518	336	1.00E-91	178	177	99
AY353386	1518	194	5.00E-49	106	104	98
AY353385	1518	336	1.00E-91	178	177	99
AY353385	1518	197	8.00E-50	227	126	55
AY353384	1518	336	1.00E-91	178	177	99
AY353384	1518	197	8.00E-50	227	126	55
AY353383	1518	336	1.00E-91	178	177	99
AY353383	1518	197	8.00E-50	227	126	55
AY353381	1518	336	1.00E-91	178	177	99
AY353381	1518	197	8.00E-50	227	126	55
AY353380	1518	336	1.00E-91	178	177	99
AY353380	1518	197	8.00E-50	227	126	55
D78639	1530	336	1.00E-91	178	177	99
D78639	1530	194	5.00E-49	106	104	98
M84980	1518	336	1.00E-91	178	177	99
M84980	1518	194	5.00E-49	106	104	98
M84979	1518	336	1.00E-91	178	177	99
M84979	1518	194	5.00E-49	106	104	98
M84972	1518	336	1.00E-91	178	177	99
M84972	1518	194	5.00E-49	106	104	98
M84976	1518	336	1.00E-91	178	177	99
M84976	1518	194	5.00E-49	106	104	98
M84975	1518	336	1.00E-91	178	177	99
M84975	1518	191	6.00E-48	106	103	97
M84973	1518	336	1.00E-91	178	177	99
M84973	1518	194	5.00E-49	106	104	98
U06455	1867	336	1.00E-91	178	177	99
U06455	1867	194	5.00E-49	106	104	98
U06227	1876	336	1.00E-91	178	177	99
U06227	1876	197	5.00E-50	324	142	43
U06225	1867	336	1.00E-91	178	177	99
U06225	1867	197	8.00E-50	227	126	55
U06205	1864	336	1.00E-91	178	177	99
U06205	1864	193	1.00E-48	106	103	97
U06204	1876	336	1.00E-91	178	177	99
U06204	1876	194	4.00E-49	227	125	55
U06203	1867	336	1.00E-91	178	177	99

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
U06203	1867	197	5.00E-50	227	126	55
U06202	1876	336	1.00E-91	178	177	99
U06202	1876	194	5.00E-49	106	104	98
U06201	1876	336	1.00E-91	178	177	99
U06201	1876	194	5.00E-49	106	104	98
U06200	1876	336	1.00E-91	178	177	99
U06200	1876	197	8.00E-50	305	140	45
U06197	1867	336	1.00E-91	178	177	99
U06197	1867	194	4.00E-49	227	125	55
M84974	1867	336	1.00E-91	178	177	99
M84974	1867	194	5.00E-49	106	104	98
AY353535	1518	335	2.00E-91	178	176	98
AY353535	1518	194	4.00E-49	227	125	55
U06206	1876	335	2.00E-91	178	176	98
U06206	1876	193	1.00E-48	106	103	97
AY353537	1515	334	3.00E-91	178	176	98
AY353537	1515	189	2.00E-47	106	101	95
AY353536	1515	334	3.00E-91	178	176	98
AY353536	1515	190	7.00E-48	280	139	49
AY353382	1518	334	3.00E-91	178	176	98
AY353382	1518	194	4.00E-49	227	125	55
AY649717	1515	334	4.00E-91	178	176	98
AY649717	1515	191	6.00E-48	301	136	45
AY649716	1515	334	4.00E-91	178	176	98
AY649716	1515	191	6.00E-48	301	136	45
Z15086	1515	334	4.00E-91	177	176	99
Z15086	1515	196	2.00E-49	227	126	55
Z15072	1515	334	4.00E-91	177	176	99
Z15072	1515	197	5.00E-50	227	126	55
Z15071	1515	334	4.00E-91	177	176	99
Z15071	1515	194	5.00E-49	106	104	98
Z15070	1524	334	4.00E-91	177	176	99
Z15070	1524	194	5.00E-49	106	104	98
Z15069	1515	334	4.00E-91	177	176	99
Z15069	1515	194	5.00E-49	106	104	98
Z15068	1515	334	4.00E-91	177	176	99
Z15068	1515	194	5.00E-49	106	104	98
Z15057	1515	334	4.00E-91	177	176	99
Z15067	1516	194	5.00E-49	106	104	98
Z15066	1515	334	4.00E-91	177	176	99
Z15066	1515	197	8.00E-50	227	126	55
Z15065	1515	334	4.00E-91	177	176	99
Z15065	1515	197	5.00E-50	227	126	55
Z15064	1524	334	4.00E-91	177	176	99
Z15064	1524	197	5.00E-50	324	142	43
AY353414	1515	334	4.00E-91	178	176	98
AY353414	1515	191	6.00E-48	301	136	45
U05303	1515	334	4.00E-91	177	176	99
U05303	1515	197	5.00E-50	227	126	55
U05302	1524	334	4.00E-91	177	176	99
U05302	1524	194	5.00E-49	106	104	98
U05300	1515	334	4.00E-91	177	176	99
U05300	1515	194	5.00E-49	106	104	98
U05299	1515	334	4.00E-91	177	176	99
U05299	1515	194	5.00E-49	106	104	98
U05297	1515	334	4.00E-91	177	176	99
U05297	1515	194	5.00E-49	106	104	98
U05296	1524	334	4.00E-91	177	176	99
U05296	1524	194	5.00E-49	106	104	98
U05295	1515	334	4.00E-91	177	176	99
U05295	1515	196	1.00E-49	227	126	55
U06226	1864	334	4.00E-91	178	176	98
U06226	1864	191	6.00E-48	301	136	45
U06198	1864	334	4.00E-91	178	176	98
U06198	1864	191	6.00E-48	301	136	45
AY649696	1518	333	5.00E-91	178	176	98
AY649696	1518	194	5.00E-49	106	104	98
M84978	1518	333	5.00E-91	178	176	98

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
M84978	1518	192	1.00E-48	106	103	97
M84977	1518	333	5.00E-91	178	176	98
M84977	1518	194	5.00E-49	106	104	98
M27219	1544	333	7.00E-91	354	196	55
U05298	1398	330	5.00E-90	177	175	98
U05298	1398	171	6.00E-42	91	91	100
AY353413	1515	330	6.00E-90	178	173	97
AY353413	1515	187	6.00E-47	227	120	52
U06199	1864	330	6.00E-90	178	173	97
U06199	1864	187	6.00E-47	227	120	52
U05301	1512	328	2.00E-89	177	172	97
U05301	1512	187	6.00E-47	227	120	52
BX950851	5064019	327	5.00E-89	302	187	61
BX950851	5064019	131	4.00E-30	126	71	56
BX950851	5064019	88.6	4.00E-17	152	63	41
L33468	1282	319	1.00E-86	365	203	55
AE017132	290155	318	3.00E-86	368	202	54
AJ414150	335050	318	3.00E-86	368	202	54
AE013850	10283	318	3.00E-86	368	202	54
BX936398	4744671	318	3.00E-86	368	202	54
BX936398	4744671	98.2	5.00E-20	207	61	29
BX936398	4744671	60.1	2.00E-08	115	37	32
AY244565	1515	315	2.00E-85	368	201	54
U12963	1484	315	3.00E-85	166	165	99
U12963	1484	194	5.00E-49	106	104	98
AY337465	1467	311	2.00E-84	263	178	67
AY337465	1467	160	8.00E-39	103	83	80
AY353477	1518	311	2.00E-84	244	175	71
AY353477	1518	175	3.00E-43	140	96	68
AY353476	1518	311	2.00E-84	244	175	71
AY353476	1518	175	3.00E-43	140	96	68
AY353475	1518	311	2.00E-84	244	175	71
AY353475	1518	175	3.00E-43	140	96	68
AY353474	1518	311	2.00E-84	244	175	71
AY353474	1518	175	3.00E-43	140	96	68
AB108532	3325	310	5.00E-84	273	180	65
AB108532	3326	166	2.00E-40	280	121	43
L33467	1300	310	8.00E-84	359	194	54
AY337472	1467	309	1.00E-83	263	177	67
AY337472	1467	160	8.00E-39	103	83	80
AF345848	1464	308	2.00E-83	256	177	69
AF345848	1464	158	4.00E-38	103	82	79
AJ567919	1392	306	3.00E-83	262	173	66
AJ567919	1392	117	6.00E-26	75	59	78
AY353479	1518	308	3.00E-83	244	172	70
AY353479	1518	171	5.00E-42	140	94	67
AY353478	1518	308	3.00E-83	244	172	70
AY353478	1518	173	9.00E-43	140	95	67
AY337475	1578	306	9.00E-83	299	184	61
AY337475	1578	149	2.00E-35	92	76	82
AB128919	1996	306	9.00E-83	299	184	61
AB128919	1996	150	7.00E-36	92	77	83
AY337476	1578	305	2.00E-82	299	184	61
AY337476	1578	149	2.00E-35	92	76	82
U47614	1762	305	2.00E-82	274	170	62
U47614	1762	142	3.00E-33	115	74	64
AE005174	5528445	305	3.00E-82	274	169	61
AE005174	5528445	142	3.00E-33	115	74	64
AE005174	5528445	51.6	5.00E-06	299	66	22
AE005174	5528445	33.5	1.5	185	42	22
AY337468	1758	305	3.00E-82	274	169	61
AY337468	1758	142	3.00E-33	115	74	64
AY249992	1758	305	3.00E-82	267	168	62
AY249992	1758	142	3.00E-33	115	74	64
BA000007	5498450	305	3.00E-82	274	169	61
BA000007	5498450	142	3.00E-33	115	74	64
BA000007	5498450	51.6	5.00E-06	299	66	22
BA000007	5498450	33.5	1.5	185	42	22

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF228496	1758	305	3.00E-82	274	169	61
AF228496	1758	142	3.00E-33	115	74	64
AF228494	1758	305	3.00E-82	267	168	62
AF228494	1758	142	3.00E-33	115	74	64
AF228493	1758	305	3.00E-82	267	168	62
AF228493	1758	142	3.00E-33	115	74	64
AF228492	1758	305	3.00E-82	267	168	62
AF228492	1758	142	3.00E-33	115	74	64
AF228491	1758	305	3.00E-82	267	168	62
AF228491	1758	142	3.00E-33	115	74	64
AF228490	1758	305	3.00E-82	267	168	62
AF228490	1758	142	3.00E-33	115	74	64
AF228489	1758	305	3.00E-82	274	169	61
AF228489	1758	142	3.00E-33	115	74	64
AF228488	1758	305	3.00E-82	274	169	61
AF228488	1758	142	3.00E-33	115	74	64
AF228487	1758	305	3.00E-82	274	169	61
AF228487	1758	142	3.00E-33	115	74	64
D16821	2006	305	3.00E-82	299	183	61
D16821	2006	148	3.00E-35	92	76	82
D16820	1851	305	3.00E-82	299	183	61
D16820	1851	148	3.00E-35	92	76	82
AB028474	2329	305	3.00E-82	267	168	62
AB028474	2329	142	3.00E-33	115	74	64
AY337477	1578	304	4.00E-82	299	183	61
AY337477	1578	149	2.00E-35	92	76	82
AF228495	1758	304	5.00E-82	274	169	61
AF228495	1758	142	3.00E-33	115	74	64
AY337478	1578	303	1.00E-81	299	183	61
AY337478	1578	145	4.00E-34	92	74	80
L07388	1755	303	1.00E-81	267	169	63
L07388	1755	141	5.00E-33	115	73	63
AB128917	8242	301	4.00E-81	296	186	62
AB128917	8242	141	5.00E-33	87	75	86
AY337481	1604	300	9.00E-81	177	157	88
AY337481	1604	147	7.00E-35	92	75	81
AY249991	1647	300	9.00E-81	266	171	64
AY249991	1647	140	7.00E-33	102	69	67
AY250013	1668	299	1.00E-80	295	171	57
AY250013	1668	140	7.00E-33	116	71	61
AY337474	1788	298	2.00E-80	223	157	70
AY337474	1788	137	7.00E-32	113	71	62
AY337471	1788	298	2.00E-80	223	157	70
AY337471	1788	137	7.00E-32	113	71	62
AY250023	1707	298	2.00E-80	223	160	71
AY250023	1707	140	7.00E-33	114	74	64
AY249997	1788	298	2.00E-80	223	157	70
AY249997	1788	137	7.00E-32	113	71	62
AE016752	311143	298	2.00E-80	223	157	70
AE016762	311143	138	3.00E-32	255	106	41
AB028477	2277	298	2.00E-80	223	160	71
AB028477	2277	141	4.00E-33	270	104	38
AB028475	2359	298	2.00E-80	223	157	70
AB028475	2359	137	7.00E-32	113	71	62
AB028471	2351	298	2.00E-80	223	157	70
AB028471	2351	138	3.00E-32	255	106	41
L07387	1788	298	2.00E-80	223	157	70
L07387	1788	139	2.00E-32	255	106	41
AJ566339	1634	298	3.00E-80	246	163	66
AJ566339	1634	89.7	2.00E-17	83	44	53
AJ566338	1634	298	3.00E-80	246	163	66
AJ566338	1634	89.7	2.00E-17	83	44	53
AY250005	1767	297	6.00E-80	219	162	73
AY250005	1767	142	2.00E-33	149	83	55
AB028476	2338	297	6.00E-80	219	162	73
AB028476	2338	142	2.00E-33	149	83	55
AY337466	1344	296	7.00E-80	290	172	59
AY337466	1344	135	2.00E-31	181	87	48

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY250027	1818	296	7.00E-80	222	157	70
AY250027	1818	139	2.00E-32	163	81	49
AB028481	2168	296	7.00E-80	222	157	70
AB028481	2168	139	2.00E-32	163	81	49
AY250029	1311	296	1.00E-79	300	175	58
AY250029	1311	135	4.00E-31	92	67	72
AF345847	1497	296	1.00E-79	178	155	87
AF345847	1497	155	2.00E-37	174	94	54
AY380836	1714	296	1.00E-79	223	159	71
AY380836	1714	140	7.00E-33	114	74	64
AB028480	2269	296	1.00E-79	302	176	58
AB028480	2269	133	1.00E-30	102	66	64
L07389	1788	296	1.00E-79	223	156	69
L07389	1788	135	3.00E-31	113	70	61
AY250001	1665	296	1.00E-79	237	161	67
AY250001	1665	141	5.00E-33	295	105	35
AF194946	1664	296	1.00E-79	237	161	67
AF194946	1664	139	2.00E-32	293	104	35
AY337480	1512	295	2.00E-79	178	155	87
AY337480	1512	158	4.00E-38	265	111	41
AY250016	1638	295	2.00E-79	218	157	72
AY250016	1638	140	7.00E-33	172	85	49
Z36877	1925	295	2.00E-79	222	156	70
Z36877	1925	133	1.00E-30	102	66	64
AY337483	1674	295	2.00E-79	284	169	59
AY337483	1674	141	5.00E-33	115	71	61
AY250028	1344	295	2.00E-79	274	171	62
AY250028	1344	134	6.00E-31	92	67	72
AY250010	1740	295	2.00E-79	236	161	68
AY250010	1740	140	9.00E-33	116	72	62
AY250008	1674	295	2.00E-79	284	169	59
AY250008	1674	142	3.00E-33	115	71	61
AY249999	1689	295	2.00E-79	257	168	65
AY249999	1689	142	2.00E-33	273	102	37
AY249990	1311	295	3.00E-79	291	174	59
AY249990	1311	135	4.00E-31	92	67	72
AF345850	1638	295	3.00E-79	218	157	72
AF345850	1638	140	7.00E-33	172	85	49
AB028473	1867	295	3.00E-79	291	174	59
AB028473	1867	135	4.00E-31	92	67	72
AY337473	1344	294	4.00E-79	290	171	58
AY337473	1344	137	7.00E-32	314	115	36
AY250018	1344	294	4.00E-79	290	171	58
AY250018	1344	137	1.00E-31	314	114	36
AY249994	2013	294	4.00E-79	247	162	65
AY249994	2013	147	9.00E-35	312	104	33
AF079163	2078	294	4.00E-79	247	162	65
AF079163	2078	147	9.00E-35	312	104	33
AY250026	1695	294	5.00E-79	222	156	70
AY250026	1695	133	1.00E-30	102	66	64
AF345851	1695	294	5.00E-79	222	156	70
AF345851	1695	132	2.00E-30	102	65	64
AE005674	4607203	293	6.00E-79	202	154	76
AE005674	4607203	140	7.00E-33	116	71	61
AY337485	1323	293	6.00E-79	288	177	61
AY337485	1323	137	1.00E-31	312	109	34
AF543692	1497	293	6.00E-79	178	153	85
AF543692	1497	156	2.00E-37	174	94	54
AE016984	290582	293	6.00E-79	202	154	76
AE016984	290582	140	7.00E-33	116	71	61
AY250003	1731	293	6.00E-79	299	171	57
AY250003	1731	142	2.00E-33	287	111	38
D16819	1966	293	6.00E-79	202	154	76
D16819	1966	140	7.00E-33	116	71	61
AY250024	1719	293	8.00E-79	229	160	69
AY250024	1719	144	8.00E-34	116	73	62
AY249998	1653	293	8.00E-79	202	154	76
AY249998	1653	140	7.00E-33	116	71	61

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF169321	1653	293	8.00E-79	202	154	76
AF169321	1653	138	4.00E-32	276	102	36
AY337469	1311	293	1.00E-78	291	169	58
AY337469	1311	134	5.00E-31	92	67	72
AY250020	1680	292	1.00E-78	179	149	83
AY250020	1680	139	3.00E-32	113	69	61
AY250012	1332	291	2.00E-78	288	176	61
AY250012	1332	135	3.00E-31	315	107	33
D26166	3294	291	2.00E-78	234	159	67
D26166	3294	134	6.00E-31	100	66	66
AF543693	1497	291	3.00E-78	178	152	85
AF543693	1497	155	2.00E-37	174	94	54
AY353496	1242	291	3.00E-78	275	175	63
AY353496	1242	150	9.00E-36	100	79	79
AY353486	1266	291	3.00E-78	276	170	61
AY353486	1266	152	3.00E-36	102	79	77
AY353485	1266	291	3.00E-78	276	170	61
AY353485	1266	152	3.00E-36	102	79	77
D26165	2520	291	3.00E-78	263	159	60
D26165	2520	140	7.00E-33	114	74	64
AY337479	1851	291	4.00E-78	191	151	79
AY337479	1851	145	3.00E-34	287	109	37
AY250014	1713	291	4.00E-78	179	150	83
AY250014	1713	139	2.00E-32	234	88	37
AY250002	1842	291	4.00E-78	191	151	79
AY250002	1842	146	2.00E-34	285	109	38
AJ567918	1359	291	4.00E-78	251	164	65
AJ567918	1359	117	6.00E-26	75	59	78
AJ271930	1713	291	4.00E-78	179	150	83
AJ271930	1713	139	2.00E-32	234	88	37
AB028478	2284	290	7.00E-78	229	159	69
AB028478	2284	144	8.00E-34	116	73	62
AB128916	11067	290	7.00E-78	296	177	59
AB128916	11067	151	5.00E-36	293	112	38
AY250019	1299	290	9.00E-78	286	169	59
AY250019	1299	136	1.00E-31	253	102	40
AY250015	1287	290	9.00E-78	267	166	62
AY250015	1287	134	6.00E-31	127	74	58
AF345849	1287	290	9.00E-78	267	166	62
AF345849	1287	131	4.00E-30	127	73	57
AY353488	1266	290	9.00E-78	271	170	62
AY353488	1266	152	3.00E-36	102	79	77
AY353487	1266	290	9.00E-78	271	170	62
AY353487	1266	152	3.00E-36	102	79	77
AY353483	1266	290	9.00E-78	175	153	87
AY353484	1266	289	1.00E-77	175	153	87
AY353484	1266	152	3.00E-36	102	79	77
AY353482	1266	289	1.00E-77	175	153	87
AY250017	1686	289	2.00E-77	233	162	69
AY250017	1686	150	9.00E-36	279	102	36
AY353547	1269	289	2.00E-77	284	175	61
AY353547	1269	150	7.00E-36	100	79	79
AY353546	1269	289	2.00E-77	284	175	61
AY353546	1269	150	7.00E-36	100	79	79
AY353545	1269	289	2.00E-77	284	175	61
AY353545	1269	150	7.00E-36	100	79	79
AY353332	1503	288	2.00E-77	208	157	75
AY353332	1503	155	3.00E-37	100	81	81
AY250021	1281	288	3.00E-77	258	164	63
AY250021	1281	138	4.00E-32	232	93	40
AY250011	1713	288	3.00E-77	179	149	83
AY250011	1713	139	3.00E-32	237	91	38
AF169322	1281	288	3.00E-77	258	164	63
AF169322	1281	136	2.00E-31	92	69	75
AY353498	1269	288	3.00E-77	237	164	69
AY353498	1269	148	3.00E-35	100	78	78
AY353493	1269	288	3.00E-77	237	164	69
AY353493	1269	148	3.00E-35	100	78	78

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY649737	1281	288	3.00E-77	214	161	75
AY649737	1281	150	7.00E-36	100	79	79
AY649736	1269	288	3.00E-77	214	161	75
AY649736	1269	148	3.00E-35	100	78	78
AY649735	1275	288	3.00E-77	214	161	75
AY649735	1275	150	7.00E-36	100	79	79
AY649704	1509	288	3.00E-77	220	160	72
AY649704	1509	157	7.00E-38	100	82	82
AY649703	1509	288	3.00E-77	220	160	72
AY649703	1509	157	7.00E-38	100	82	82
AY250022	1506	288	3.00E-77	220	156	70
AY250022	1506	134	8.00E-31	151	77	50
AF169323	1506	288	3.00E-77	220	156	70
AF169323	1506	134	8.00E-31	151	77	50
AY353549	1269	288	3.00E-77	214	161	75
AY353549	1269	148	3.00E-35	100	78	78
AY353548	1269	288	3.00E-77	214	161	75
AY353548	1269	150	7.00E-36	100	79	79
AY353544	1269	288	3.00E-77	214	161	75
AY353544	1269	148	3.00E-35	100	78	78
AY353507	1269	288	3.00E-77	214	161	75
AY353507	1269	150	7.00E-36	100	79	79
AY353506	1269	288	3.00E-77	214	161	75
AY353506	1269	150	7.00E-36	100	79	79
AY353505	1281	288	3.00E-77	214	161	75
AY353505	1281	151	5.00E-36	174	92	52
AY353503	1281	288	3.00E-77	214	161	75
AY353503	1281	149	1.00E-35	174	91	52
AY353499	1269	288	3.00E-77	214	161	75
AY353499	1269	150	7.00E-36	100	79	79
AY353497	1275	288	3.00E-77	214	161	75
AY353497	1275	150	7.00E-36	100	79	79
AY353495	1269	288	3.00E-77	214	161	75
AY353495	1269	150	7.00E-36	100	79	79
AY353494	1269	288	3.00E-77	214	161	75
AY353494	1269	150	7.00E-36	100	79	79
AY353492	1269	288	3.00E-77	214	161	75
AY353492	1269	150	7.00E-36	100	79	79
AY353454	1506	288	3.00E-77	216	158	73
AY353454	1506	156	1.00E-37	100	82	82
AY353447	1503	288	3.00E-77	208	157	75
AY353447	1503	156	1.00E-37	100	82	82
AY353446	1503	288	3.00E-77	208	157	75
AY353446	1503	156	1.00E-37	100	82	82
AY353379	1509	288	3.00E-77	220	160	72
AY353379	1509	157	7.00E-38	100	82	82
AY353377	1509	288	3.00E-77	220	160	72
AY353377	1509	157	7.00E-38	100	82	82
AY353331	1503	288	3.00E-77	208	157	75
AY353331	1503	154	5.00E-37	100	81	81
AY353455	1506	287	4.00E-77	216	158	73
AY353455	1506	156	1.00E-37	100	82	82
AY337470	1281	287	6.00E-77	258	163	63
AY337470	1281	136	4.00E-32	232	93	40
AY649725	1503	287	6.00E-77	206	157	76
AY649725	1503	152	2.00E-36	98	79	80
AY649724	1503	287	6.00E-77	198	154	77
AY649724	1503	156	1.00E-37	100	82	82
AY649723	1503	287	6.00E-77	198	154	77
AY649723	1503	156	1.00E-37	100	82	82
AY250025	1497	287	6.00E-77	177	146	82
AY250025	1497	149	2.00E-35	151	80	52
X17440	2526	287	6.00E-77	177	146	82
X17440	2526	151	4.00E-36	244	101	41
U00096	4639675	287	6.00E-77	177	146	82
U00096	4639675	149	2.00E-35	151	80	52
U00096	4639675	33.1	2	147	37	25
AY353543	1269	287	6.00E-77	211	159	75

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY353543	1269	150	7.00E-36	100	79	79
AY353457	1482	287	6.00E-77	198	154	77
AY353457	1482	156	1.00E-37	100	82	82
AY353456	1446	287	6.00E-77	245	162	66
AY353456	1446	156	1.00E-37	100	82	82
AY353453	1506	287	6.00E-77	206	157	76
AY353453	1506	156	1.00E-37	100	82	82
AY353452	1506	287	6.00E-77	206	157	76
AY353452	1506	154	5.00E-37	100	81	81
AY353451	1503	287	6.00E-77	198	154	77
AY353451	1503	156	1.00E-37	100	82	82
AY353450	1503	287	6.00E-77	206	157	76
AY353450	1503	156	1.00E-37	100	82	82
AY353449	1503	287	6.00E-77	206	157	76
AY353449	1503	152	2.00E-36	98	79	80
AY353448	1503	287	6.00E-77	198	154	77
AY353448	1503	156	1.00E-37	100	82	82
AY353444	1503	287	6.00E-77	198	154	77
AY353444	1503	156	1.00E-37	100	82	82
AY353443	1503	287	6.00E-77	198	154	77
AY353443	1503	156	1.00E-37	100	82	82
AY353378	1509	287	6.00E-77	220	160	72
AY353378	1509	157	7.00E-38	100	82	82
D90833	15605	287	6.00E-77	177	146	82
D90833	15605	149	2.00E-35	151	80	52
AB028479	2060	287	6.00E-77	177	146	82
AB028479	2060	149	2.00E-35	151	80	52
M14358	1667	287	6.00E-77	177	146	82
M14358	1667	149	2.00E-35	151	80	52
AY353509	1266	286	8.00E-77	175	152	86
AY353509	1268	150	9.00E-36	100	79	79
AY353501	1266	286	8.00E-77	175	152	86
AY353501	1266	150	9.00E-36	100	79	79
AY353500	1266	286	8.00E-77	175	152	86
AY353500	1266	150	9.00E-36	100	79	79
AY353445	1503	286	8.00E-77	198	154	77
AY353445	1503	152	2.00E-36	98	79	80
AY337467	1281	286	1.00E-76	258	163	63
AY337467	1281	136	1.00E-31	232	92	39
AY353334	1506	286	1.00E-76	206	157	76
AY353334	1506	156	1.00E-37	100	82	82
AY353333	1506	286	1.00E-76	206	157	76
AY353333	1506	156	1.00E-37	100	82	82
AB128918	12979	286	1.00E-76	291	170	58
AB128918	12979	146	2.00E-34	95	75	78
AY649702	1509	286	1.00E-76	220	159	72
AY649702	1509	157	7.00E-38	100	82	82
AY353350	1500	286	1.00E-76	209	158	75
AY353350	1500	158	3.00E-38	338	127	37
AY353349	1500	286	1.00E-76	209	158	75
AY353349	1500	158	4.00E-38	338	127	37
AY353348	1500	286	1.00E-76	209	158	75
AY353348	1500	158	3.00E-38	338	127	37
AY353347	1500	286	1.00E-76	209	158	75
AY353347	1500	158	4.00E-38	338	127	37
AY353346	1500	286	1.00E-76	209	158	75
AY353346	1500	157	5.00E-38	338	127	37
AY353345	1500	286	1.00E-76	209	158	75
AY353345	1500	158	4.00E-38	338	127	37
AF169320	1263	285	2.00E-76	269	160	59
AF169320	1263	135	4.00E-31	138	77	55
AY353502	1266	285	2.00E-76	175	151	86
AY353502	1266	150	9.00E-36	100	79	79
AY353360	1488	285	2.00E-76	306	176	57
AY353360	1488	149	2.00E-35	89	76	85
AJ566341	1223	285	3.00E-76	179	145	81
AJ566341	1223	85.1	4.00E-16	284	81	28
AJ566340	1223	285	3.00E-76	179	145	81
AJ566340	1223	85.1	4.00E-16	284	81	28
AY649698	1488	285	3.00E-76	306	176	57
AY549698	1488	151	4.00E-36	96	78	81
AY249995	1263	285	3.00E-76	189	147	77
AY249995	1263	137	1.00E-31	138	78	56
AY657001	1488	285	3.00E-76	306	176	57
AY657001	1488	151	4.00E-36	96	78	81
BX321861	298050	285	3.00E-76	297	159	53
AY353508	1269	285	3.00E-76	211	158	74
AY353508	1269	150	7.00E-36	100	79	79
AY353363	1488	285	3.00E-76	306	175	57
AY353363	1488	151	4.00E-36	96	78	81
AY353362	1488	285	3.00E-76	306	176	57
AY353362	1488	151	4.00E-36	96	78	81
AY353361	1488	285	3.00E-76	306	176	57
AY353361	1488	151	4.00E-36	96	76	81
AY353359	1488	285	3.00E-76	306	176	57
AY353359	1488	151	4.00E-36	96	76	81
AY353358	1488	285	3.00E-76	306	176	57
AY353358	1488	151	4.00E-36	96	78	81
AY353303	1506	285	3.00E-76	175	150	85
AY353303	1506	155	3.00E-37	100	81	81
AY353517	1506	284	4.00E-76	215	157	73
AY353517	1506	152	2.00E-36	98	79	80
AY353516	1506	284	4.00E-76	215	157	73
AY353516	1506	152	2.00E-36	98	79	80
AY353504	1281	284	4.00E-76	214	160	74
AY353504	1281	149	1.00E-35	174	91	52
AY353490	1500	284	4.00E-76	192	152	79
AY353490	1500	153	1.00E-36	100	80	80
AY353489	1500	284	4.00E-76	192	152	79
AY353489	1500	153	1.00E-36	100	80	80
AY337482	1263	284	5.00E-76	189	147	77
AY337482	1263	135	4.00E-31	138	77	55
AY649732	1521	284	5.00E-76	175	150	85
AY649732	1521	149	2.00E-35	91	76	83
AY649701	1521	284	5.00E-76	175	150	85
AY649701	1521	149	2.00E-35	91	76	83
AY649700	1521	284	5.00E-76	175	150	85
AY649700	1521	150	9.00E-36	91	77	84
AE016837	300247	284	5.00E-76	175	150	85
AE016637	300247	149	2.00E-35	91	75	83
X03395	1530	284	5.00E-76	175	150	85
X03395	1530	149	2.00E-35	91	76	83
AL627272	245050	284	5.00E-76	175	150	85
AL627272	245050	149	2.00E-35	91	76	83
AY353434	1260	284	5.00E-76	175	150	85
AY353434	1260	149	2.00E-35	91	76	83
AY353433	1260	284	5.00E-76	175	150	85
AY353433	1260	149	2.00E-35	91	76	83
AY353376	1521	284	5.00E-76	175	150	85
AY353376	1521	150	9.00E-36	91	77	84
AY353375	1521	284	5.00E-76	175	150	85
AY353375	1521	149	2.00E-35	91	76	83
AY353374	1521	284	5.00E-76	175	150	85
AY353374	1521	149	2.00E-35	91	76	83
AY353373	1521	284	5.00E-76	175	150	85
AY353373	1521	149	2.00E-35	91	76	83
AY353372	1521	284	5.00E-76	175	150	85
AY353372	1521	149	2.00E-35	91	76	83
AY353371	1521	284	5.00E-76	175	150	85
AY353371	1521	149	2.00E-35	91	76	83
AY353302	1521	284	5.00E-76	175	150	85
AY353302	1521	150	9.00E-36	91	77	84
L21912	2001	284	5.00E-76	175	150	85
L21912	2001	149	2.00E-35	91	76	83
CP0000264585229		283	6.00E-76	279	165	59
CP0000264585229		278	2.00E-74	175	147	84

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
CP000026	4585229	156	1.00E-37	100	82	82
CP000026	4585229	155	3.00E-37	100	81	81
AE008826	20513	283	6.00E-76	232	160	68
AE008826	20513	155	3.00E-37	100	81	81
AY353521	1521	283	6.00E-76	232	160	68
AY353521	1521	155	3.00E-37	100	81	81
AY353271	1521	283	6.00E-76	232	160	68
AY353271	1521	155	3.00E-37	100	81	81
AY353269	1521	283	6.00E-76	232	160	68
AY353269	1521	155	3.00E-37	100	81	81
AY353268	1521	283	6.00E-76	232	160	68
AY353268	1521	155	3.00E-37	100	81	81
AY353267	1521	283	6.00E-76	232	160	68
AY353267	1521	155	3.00E-37	100	81	81
AY353266	1521	283	6.00E-76	232	160	68
AY353266	1521	155	3.00E-37	100	81	81
AY353264	1521	283	6.00E-76	232	160	68
AY353264	1521	155	3.00E-37	100	81	81
AY353259	1506	283	6.00E-76	295	159	57
AY353259	1506	151	4.00E-36	98	78	79
AF045151	1521	283	6.00E-76	232	160	68
AF045151	1521	155	3.00E-37	100	81	81
U17177	1521	283	6.00E-76	232	160	68
U17177	1621	155	3.00E-37	100	81	81
U17176	1521	283	6.00E-76	232	160	68
U17176	1621	155	3.00E-37	100	81	81
U17173	1521	283	6.00E-76	232	160	68
U17173	1521	155	3.00E-37	100	81	81
AY353272	1521	283	6.00E-76	232	160	68
AY353272	1521	155	3.00E-37	100	81	81
AJ243796	1368	283	1.00E-75	247	162	65
AJ243796	1368	137	6.00E-32	87	70	80
AJ243795	1368	283	1.00E-75	247	162	65
AJ243795	1368	137	6.00E-32	87	70	80
AY353525	1521	283	1.00E-75	229	160	69
AY353525	1521	154	6.00E-37	150	87	58
AY353524	1521	283	1.00E-75	229	160	69
AY353524	1521	154	6.00E-37	150	87	58
AY363523	1521	283	1.00E-75	229	160	69
AY353523	1521	154	8.00E-37	100	80	80
AY353522	1521	283	1.00E-75	229	160	69
AY353522	1521	154	8.00E-37	100	80	80
AY353491	1500	282	1.00E-75	199	154	77
AY353491	1500	151	5.00E-36	98	78	79
AY353287	1521	282	1.00E-75	275	164	59
AY353287	1521	155	3.00E-37	100	81	81
AY353286	1521	282	1.00E-75	275	164	59
AY353286	1521	155	3.00E-37	100	81	81
AY353285	1521	282	1.00E-75	275	164	59
AY353285	1521	155	3.00E-37	100	81	81
AJ430202	8179	282	2.00E-75	296	167	56
AY353527	1521	282	2.00E-75	217	156	71
AY353527	1521	154	5.00E-37	100	80	80
AY353300	1521	282	2.00E-75	232	159	68
AY353300	1521	155	3.00E-37	100	81	81
AY353299	1521	282	2.00E-75	232	159	68
AY353299	1521	155	3.00E-37	100	81	81
AY353298	1521	282	2.00E-75	232	159	68
AY353298	1521	155	3.00E-37	100	81	81
AY353297	1521	282	2.00E-75	232	159	68
AY353297	1521	155	3.00E-37	100	81	81
AY353296	1521	282	2.00E-75	232	159	68
AY353296	1521	155	3.00E-37	100	81	81
AY353277	1521	282	2.00E-75	232	159	68
AY353277	1521	155	3.00E-37	100	81	81
AY353276	1521	282	2.00E-75	232	159	68
AY353276	1521	155	3.00E-37	100	81	81
AY353275	1521	282	2.00E-75	232	159	68
AY353275	1521	155	3.00E-37	100	81	81
U17172	1521	282	2.00E-75	232	159	68
U17172	1521	155	3.00E-37	100	81	81
AY353292	1521	281	2.00E-75	268	163	60
AY353292	1521	155	3.00E-37	100	81	81
AY353283	1521	281	2.00E-75	268	162	60
AY353283	1521	155	3.00E-37	100	81	81
AY353263	1521	281	2.00E-75	268	163	60
AY353263	1521	155	3.00E-37	100	81	81
U17175	1521	281	2.00E-75	228	156	68
U17175	1521	155	3.00E-37	100	81	81
AY353542	1485	281	3.00E-75	175	148	84
AY353542	1486	152	2.00E-36	98	79	80
AY353541	1485	281	3.00E-75	175	148	84
AY353541	1485	152	2.00E-36	98	79	80
AY353540	1485	281	3.00E-75	175	148	84
AY353540	1485	152	2.00E-36	98	79	80
AY353539	1488	281	3.00E-75	175	148	84
AY353539	1488	148	4.00E-35	98	77	78
AY353538	1488	281	3.00E-75	175	148	84
AY353538	1488	152	2.00E-36	98	79	80
AY353531	1521	281	3.00E-75	175	148	84
AY353531	1521	155	3.00E-37	100	81	81
AY353530	1521	281	3.00E-75	175	148	84
AY353530	1521	155	3.00E-37	100	81	81
AY353529	1521	281	3.00E-75	175	148	84
AY353529	1521	154	8.00E-37	100	80	80
AY353528	1521	281	3.00E-75	175	148	84
AY353528	1521	155	3.00E-37	100	81	81
AY353518	1488	281	3.00E-75	175	148	84
AY353518	1488	155	3.00E-37	245	105	42
AY353512	1485	281	3.00E-75	175	148	84
AY353512	1485	158	3.00E-38	272	108	39
AY353470	1500	281	3.00E-75	175	148	84
AY353470	1500	154	8.00E-37	100	80	80
AY353469	1500	281	3.00E-75	175	148	84
AY353469	1500	154	8.00E-37	100	80	80
AY353439	1485	281	3.00E-75	175	148	84
AY353439	1485	152	2.00E-36	98	79	80
AY353438	1485	281	3.00E-75	175	148	84
AY353438	1485	152	2.00E-36	98	79	80
AY353436	1488	281	3.00E-75	175	148	84
AY353436	1488	152	2.00E-36	98	79	80
AY353355	1521	281	3.00E-75	175	148	84
AY353355	1521	155	3.00E-37	100	81	81
AY353354	1503	281	3.00E-75	175	148	84
AY353354	1503	157	9.00E-38	100	82	82
AY353353	1503	281	3.00E-76	175	148	84
AY353353	1503	157	9.00E-38	100	82	82
AY353352	1503	281	3.00E-75	175	148	84
AY353352	1503	155	3.00E-37	100	81	81
AY353330	1488	281	3.00E-75	175	148	84
AY353330	1488	155	3.00E-37	100	81	81
AY353329	1488	281	3.00E-75	175	148	84
AY353329	1488	155	3.00E-37	100	81	81
AY353328	1488	281	3.00E-75	175	148	84
AY353328	1488	155	3.00E-37	100	81	81
AY353327	1506	281	3.00E-75	175	148	84
AY353327	1506	155	3.00E-37	100	81	81
AY353326	1506	281	3.00E-75	175	148	84
AY353326	1506	155	3.00E-37	100	81	81
AY353325	1506	281	3.00E-75	175	148	84
AY353325	1506	155	3.00E-37	100	81	81
AY353324	1506	281	3.00E-75	175	148	84
AY353324	1506	155	3.00E-37	100	81	81
AY353323	1506	281	3.00E-75	175	148	84
AY353323	1506	155	3.00E-37	100	81	81
AY353320	1506	281	3.00E-75	175	148	84

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY353320	1506	155	3.00E-37	100	81	81
AY353319	1506	281	3.00E-75	175	148	84
AY353319	1506	155	3.00E-37	100	81	81
AY353318	1506	281	3.00E-75	175	148	84
AY353318	1506	155	3.00E-37	100	81	81
AY353317	1506	281	3.00E-75	175	148	84
AY353317	1506	155	3.00E-37	100	81	81
AY353316	1506	281	3.00E-75	175	148	84
AY353316	1506	155	3.00E-37	100	81	81
AY353315	1506	281	3.00E-75	175	148	84
AY353315	1506	155	3.00E-37	100	81	81
AY353314	1506	281	3.00E-75	175	148	84
AY353314	1506	155	3.00E-37	100	81	81
AY353311	1506	281	3.00E-75	175	148	84
AY353311	1506	155	3.00E-37	100	81	81
AY353309	1506	281	3.00E-75	175	148	84
AY353309	1506	155	3.00E-37	100	81	81
AY353308	1506	281	3.00E-75	175	148	84
AY353308	1506	155	3.00E-37	100	81	81
AY353306	1506	281	3.00E-75	175	148	84
AY353306	1506	155	3.00E-37	100	81	81
AY353305	1506	281	3.00E-75	175	148	84
AY353305	1506	155	3.00E-37	100	81	81
AY353295	1521	281	3.00E-75	175	148	84
AY353295	1521	155	3.00E-37	100	81	81
AY353294	1521	281	3.00E-75	175	148	84
AY353294	1521	155	3.00E-37	100	81	81
AY353293	1398	281	3.00E-75	175	148	84
AY353293	1398	155	3.00E-37	100	81	81
AY353289	1521	281	3.00E-75	175	148	84
AY353289	1521	155	3.00E-37	100	81	81
AY353284	1521	281	3.00E-75	175	148	84
AY353284	1521	155	3.00E-37	100	81	81
AY353282	1521	281	3.00E-75	175	148	84
AY353282	1521	155	3.00E-37	100	81	81
AY353280	1521	281	3.00E-75	175	148	84
AY353280	1521	155	3.00E-37	100	81	81
U17174	1521	281	3.00E-75	175	148	84
U17174	1521	155	3.00E-37	100	81	81
U17171	1521	281	3.00E-75	175	148	84
U17171	1521	154	5.00E-37	100	81	81
AY353462	1482	281	4.00E-75	229	160	69
AY353462	1482	147	7.00E-35	98	77	78
AY353461	1482	281	4.00E-75	229	160	69
AY353461	1482	152	2.00E-36	98	79	80
AY353460	1482	281	4.00E-75	229	160	69
AY353460	1482	152	2.00E-36	98	79	80
AY353339	1500	281	4.00E-75	217	157	72
AY353339	1500	155	3.00E-37	100	81	81
AY353338	1500	281	4.00E-75	217	157	72
AY353338	1500	155	3.00E-37	100	81	81
AY353337	1500	281	4.00E-75	217	157	72
AY353337	1500	155	3.00E-37	100	81	81
AY353336	1500	281	4.00E-75	217	157	72
AY353336	1500	155	3.00E-37	100	81	81
AY353335	1500	281	4.00E-75	217	157	72
AY353335	1500	155	3.00E-37	100	81	81
AY649740	1506	280	5.00E-75	175	148	84
AY649740	1506	154	5.00E-37	100	81	81
AY649739	1500	280	5.00E-75	175	148	84
AY649739	1500	155	3.00E-37	100	81	81
AY649734	1500	280	5.00E-75	175	148	84
AY649734	1500	154	6.00E-37	98	80	81
AY649733	1488	280	5.00E-75	175	148	84
AY649733	1488	152	2.00E-36	98	79	80
AY649731	1482	280	5.00E-75	175	148	84
AY649731	1482	152	2.00E-36	98	79	80
AY649730	1482	280	5.00E-75	175	148	84

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY649730	1482	152	2.00E-36	98	79	80
AY649729	1482	280	5.00E-75	175	148	84
AY649729	1482	152	2.00E-36	98	79	80
AY649728	1482	280	5.00E-75	175	148	84
AY649728	1482	152	2.00E-36	98	79	80
AY649727	1482	280	5.00E-75	175	148	84
AY649727	1482	152	2.00E-36	98	79	80
AY649726	1482	280	5.00E-75	175	148	84
AY649726	1482	152	2.00E-36	98	79	80
AY649722	1488	280	5.00E-75	175	148	84
AY649722	1486	156	1.00E-37	245	106	43
AY649721	1488	280	6.00E-75	175	148	84
AY649721	1488	152	2.00E-36	98	79	80
AY649720	1488	280	5.00E-75	175	148	84
AY649720	1488	152	2.00E-36	98	79	80
AY649719	1488	280	5.00E-75	175	148	84
AY649719	1488	152	2.00E-36	98	79	80
AY649718	1488	280	5.00E-75	175	148	84
AY649718	1488	152	2.00E-36	98	79	80
AY649699	1506	280	5.00E-75	175	148	84
AY649699	1506	154	5.00E-37	100	81	81
AY649697	1488	280	5.00E-75	175	148	84
AY649697	1488	156	1.00E-37	100	82	82
AE008787	24186	280	5.00E-75	175	148	84
AE008787	24186	152	2.00E-36	98	79	80
X03394	1482	280	5.00E-75	175	148	84
X03394	1482	154	8.00E-37	329	126	38
X03393	1497	280	5.00E-75	175	148	84
X03393	1497	157	5.00E-38	100	83	83
AY657000	1474	280	5.00E-75	175	148	84
AY657000	1474	136	1.00E-31	90	71	78
X04505	1479	280	5.00E-75	175	148	84
X04505	1479	152	2.00E-36	98	79	80
AF336929	1506	280	5.00E-75	175	148	84
AF336929	1506	154	8.00E-37	100	80	80
AF420425	1460	280	5.00E-75	175	148	84
AF420425	1460	129	3.00E-29	85	66	77
AY353526	1521	280	5.00E-75	175	148	84
AY353526	1521	155	3.00E-37	100	81	81
AY353519	1503	280	5.00E-75	175	148	84
AY353519	1603	152	2.00E-36	98	79	80
AY353515	1488	280	5.00E-75	175	148	84
AY353515	1488	156	1.00E-37	245	106	43
AY353513	1491	280	5.00E-75	175	148	84
AY353513	1491	155	3.00E-37	100	81	81
AY353511	1491	280	5.00E-75	175	148	84
AY353511	1491	153	1.00E-36	100	80	80
AY353510	1491	280	5.00E-75	175	148	84
AY353510	1491	152	2.00E-36	98	79	80
AY353481	1488	280	5.00E-75	175	148	84
AY353481	1488	154	5.00E-37	100	81	81
AY353480	1488	280	5.00E-75	175	148	84
AY353480	1488	152	2.00E-36	98	79	80
AY353472	1500	280	5.00E-75	175	148	84
AY353472	1500	154	6.00E-37	98	80	81
AY353471	1500	280	5.00E-75	175	148	84
AY353471	1500	154	6.00E-37	98	80	81
AY353468	1500	280	5.00E-75	175	148	84
AY353468	1500	155	3.00E-37	100	81	81
AY353467	1500	280	5.00E-75	175	148	84
AY353467	1500	155	3.00E-37	100	81	81
AY353466	1521	280	5.00E-75	175	148	84
AY353466	1521	159	2.00E-38	100	83	83
AY353465	1521	280	5.00E-75	175	148	84
AY353465	1521	158	3.00E-38	98	82	83
AY353464	1476	280	5.00E-75	175	148	84
AY353464	1476	152	2.00E-36	98	79	80
AY353463	1476	280	5.00E-75	175	148	84

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY353463	1476	152	2.00E-36	98	79	80
AY353459	1482	280	5.00E-75	175	148	84
AY353459	1482	152	2.00E-36	98	79	80
AY353458	1482	280	5.00E-75	175	148	84
AY353458	1482	152	2.00E-36	98	79	80
AY353442	1488	280	5.00E-75	175	148	84
AY353442	1488	156	1.00E-37	245	106	43
AY353441	1488	280	5.00E-75	175	148	84
AY353441	1488	157	9.00E-38	245	106	43
AY353432	1488	280	5.00E-75	175	148	84
AY353432	1488	152	2.00E-36	98	79	80
AY353431	1488	280	5.00E-75	175	148	84
AY353431	1488	152	2.00E-36	98	79	80
AY353430	1488	280	5.00E-75	175	148	84
AY353430	1488	152	2.00E-36	98	79	80
AY353429	1488	280	5.00E-75	175	148	84
AY353429	1488	152	2.00E-36	98	79	80
AY353428	1488	280	5.00E-75	175	148	84
AY353428	1488	152	2.00E-36	98	79	80
AY353427	1488	280	5.00E-75	175	148	84
AY353427	1488	152	2.00E-36	98	79	80
AY353426	1488	280	5.00E-75	175	148	84
AY353426	1488	152	2.00E-36	98	79	80
AY353425	1488	280	5.00E-75	175	148	84
AY353425	1488	152	2.00E-36	98	79	80
AY353424	1488	280	5.00E-75	175	148	84
AY353424	1488	152	2.00E-36	98	79	80
AY353423	1488	280	5.00E-75	175	148	84
AY353423	1488	152	2.00E-36	98	79	80
AY353422	1488	280	5.00E-75	175	148	84
AY353422	1488	152	2.00E-36	98	79	80
AY353421	1488	280	5.00E-75	175	148	84
AY353421	1488	152	2.00E-36	98	79	80
AY353420	1488	280	5.00E-75	175	148	84
AY353420	1488	152	2.00E-36	98	79	80
AY353419	1488	280	5.00E-75	175	148	84
AY353419	1488	152	2.00E-36	98	79	80
AY353418	1488	280	5.00E-75	175	148	84
AY353418	1488	152	2.00E-36	98	79	80
AY353417	1488	280	5.00E-75	175	148	84
AY353417	1488	152	2.00E-36	98	79	80
AY353369	1506	280	5.00E-75	175	148	84
AY353369	1506	152	2.00E-36	98	79	80
AY353368	1506	280	5.00E-75	175	148	84
AY353368	1506	154	5.00E-37	100	81	81
AY353367	1506	280	5.00E-75	175	148	84
AY353367	1506	154	5.00E-37	100	81	81
AY353366	1506	280	5.00E-75	175	148	84
AY353366	1506	152	2.00E-36	98	79	80
AY353365	1506	280	5.00E-75	175	148	84
AY353365	1506	154	5.00E-37	100	81	81
AY353364	1506	280	5.00E-75	175	148	84
AY353364	1506	154	5.00E-37	100	81	81
AY353357	1488	280	5.00E-75	175	148	84
AY353357	1488	156	1.00E-37	100	82	82
AY353356	1488	280	5.00E-75	175	148	84
AY353356	1488	156	1.00E-37	100	82	82
AY353351	1497	280	5.00E-75	175	148	84
AY353351	1497	155	3.00E-37	100	81	81
AY353343	1488	280	5.00E-75	175	148	84
AY353343	1488	155	3.00E-37	100	81	81
AY353342	1488	280	5.00E-75	175	148	84
AY353342	1488	155	3.00E-37	100	81	81
AY353341	1488	280	5.00E-75	175	148	84
AY353341	1488	155	3.00E-37	100	81	81
AY353340	1488	280	5.00E-75	175	148	84
AY353340	1488	155	3.00E-37	100	81	81
AY353322	1506	280	5.00E-75	175	148	84

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY353322	1506	155	3.00E-37	100	81	81
AY353321	1506	280	5.00E-75	175	148	84
AY353321	1506	155	3.00E-37	100	81	81
AY353313	1506	280	5.00E-75	175	148	84
AY353313	1506	155	3.00E-37	100	81	81
AY353312	1506	280	5.00E-75	175	148	84
AY353312	1506	155	3.00E-37	100	81	81
AY353307	1506	280	5.00E-75	175	148	84
AY353307	1506	155	3.00E-37	100	81	81
AY353301	1488	280	5.00E-75	175	148	84
AY353301	1488	155	3.00E-37	100	81	81
AY353291	1521	280	5.00E-75	175	148	84
AY353291	1521	154	5.00E-37	98	80	81
AY353290	1521	280	5.00E-75	175	148	84
AY353290	1521	154	5.00E-37	98	80	81
AY353281	1521	280	5.00E-75	175	148	84
AY353281	1521	154	5.00E-37	98	80	81
AY353279	1521	280	5.00E-75	175	148	84
AY353279	1521	154	5.00E-37	98	80	81
AY353278	1521	280	5.00E-75	175	148	84
AY353278	1521	154	5.00E-37	98	80	81
AY353274	1521	280	5.00E-75	175	148	84
AY353274	1521	154	5.00E-37	98	80	81
AY353273	1521	280	5.00E-75	175	148	84
AY353273	1521	154	5.00E-37	98	80	81
AY353262	1488	280	5.00E-75	175	148	84
AY353262	1488	155	3.00E-37	100	81	81
AF332601	1515	280	5.00E-75	173	148	85
AF332601	1515	149	2.00E-35	91	76	83
D13689	1826	280	5.00E-75	175	148	84
D13689	1826	152	2.00E-36	98	79	80
AF159459	1602	280	7.00E-75	175	146	84
AF159459	1602	154	5.00E-37	100	81	81
AY353440	1488	280	9.00E-75	175	147	84
AY353440	1488	152	2.00E-36	98	79	80
AY353261	1485	280	9.00E-75	175	147	84
AY353261	1485	153	1.00E-36	100	80	80
AY353260	1485	280	9.00E-75	175	147	84
AY353260	1485	152	2.00E-36	98	79	80
AY337484	1472	194	9.00E-75	114	97	85
AY337484	1472	163	1.00E-39	258	114	44
AY337484	1472	113	9.00E-75	66	60	90
D13690	3471	279	1.00E-74	175	147	84
D13690	3471	155	3.00E-37	100	81	81
AY649738	1491	279	2.00E-74	175	147	84
AY649738	1491	153	1.00E-36	100	80	80
AY249996	1368	279	2.00E-74	245	160	65
AY249996	1368	142	2.00E-33	90	73	81
AY353520	1503	279	2.00E-74	175	147	84
AY353520	1503	153	1.00E-36	100	80	80
AY353473	1500	279	2.00E-74	175	147	84
AY353473	1500	152	2.00E-36	98	79	80
AY353265	1521	279	2.00E-74	232	158	68
AY353265	1521	155	3.00E-37	100	81	81
AY353258	1494	279	2.00E-74	175	147	84
AY353258	1494	165	2.00E-37	273	112	41
AY353370	1506	278	2.00E-74	175	147	84
AY353370	1506	152	2.00E-36	98	79	80
AY353344	1488	278	2.00E-74	175	147	84
AY353344	1488	155	3.00E-37	100	81	81
AB128921	2358	278	3.00E-74	158	145	91
AB128921	2358	136	1.00E-31	85	72	84
AY249993	1383	278	4.00E-74	244	157	64
AY249993	1383	142	2.00E-33	90	73	81
AY353437	1488	278	4.00E-74	175	147	84
AY353437	1488	152	2.00E-36	98	79	80
M11332	1485	277	5.00E-74	175	146	83
M11332	1485	153	1.00E-36	100	80	80

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF128953	1668	276	1.00E-73	258	154	59
AF128953	1668	123	1.00E-27	103	64	62
AF128950	1681	276	1.00E-73	258	154	59
AF128950	1681	132	3.00E-30	107	68	63
AF487406	1656	275	2.00E-73	222	151	68
AF487406	1656	143	1.00E-33	335	118	35
AY250009	1365	275	2.00E-73	238	159	66
AY250009	1365	140	9.00E-33	90	72	80
AF517662	1348	275	3.00E-73	243	158	65
AF517662	1348	126	2.00E-28	85	65	76
AY250004	1380	274	4.00E-73	158	141	89
AY250004	1380	142	2.00E-33	90	73	81
AF517661	1361	274	4.00E-73	242	155	64
AF517661	1361	124	7.00E-28	84	64	76
AY250000	1506	273	7.00E-73	281	166	59
AY250000	1506	144	8.00E-34	88	73	82
AF128952	1695	273	1.00E-72	208	143	68
AF128952	1695	117	1.00E-25	99	60	60
AF517665	1365	272	1.00E-72	158	140	88
AF517665	1365	130	9.00E-30	294	104	35
AY353514	1500	272	1.00E-72	197	149	75
AY353514	1500	152	2.00E-36	98	79	80
BX640427	348997	272	1.00E-72	392	180	45
BX640427	348997	54.3	8.00E-07	136	42	30
AF128948	1569	272	2.00E-72	251	156	62
AF128948	1569	128	5.00E-29	93	62	66
AF517664	1343	271	3.00E-72	236	157	66
AF517664	1343	119	2.00E-26	84	61	72
AF517663	1356	270	7.00E-72	156	139	89
AF517663	1356	124	7.00E-28	84	64	76
AF128958	1665	268	3.00E-71	253	151	59
AF128958	1665	132	3.00E-30	107	68	63
AF128951	1665	268	3.00E-71	253	151	59
AF128951	1665	132	3.00E-30	107	68	63
BX640413	349028	268	4.00E-71	391	182	46
BX640444	349008	266	1.00E-70	391	183	46
BX640444	349008	54.3	8.00E-07	136	42	30
L13034	1572	266	1.00E-70	391	183	46
AF128954	1680	265	2.00E-70	204	140	68
AF128954	1680	114	9.00E-25	97	58	59
AF128947	1649	265	2.00E-70	254	149	58
AF128947	1649	117	6.00E-26	100	62	62
AF128955	1524	265	3.00E-70	247	153	61
AF128955	1524	112	3.00E-24	82	53	64
AY249138	1398	253	7.00E-70	160	137	85
AY249138	1398	138	4.00E-32	161	84	52
AF128956	1551	262	2.00E-69	245	152	62
AF128956	1551	126	1.00E-28	93	62	66
AF128949	1563	259	2.00E-68	246	151	61
AF128949	1563	121	6.00E-27	90	58	64
AF425736	1351	254	3.00E-67	160	133	83
AF425736	1351	92.4	3.00E-18	64	46	71
AF128957	1668	254	3.00E-67	248	143	57
AF128957	1668	129	2.00E-29	106	67	63
AY534751	1404	253	7.00E-67	158	135	85
AY534751	1404	123	1.00E-27	117	70	59
AY250006	1383	251	4.00E-66	177	133	75
AY250006	1383	118	5.00E-26	280	93	33
AY534750	1380	250	8.00E-66	158	133	84
AY534750	1380	123	1.00E-27	189	82	43
AF002709	3434	250	8.00E-66	303	140	46
AF002709	3434	239	2.00E-62	304	139	45
AY250007	1197	249	2.00E-65	158	127	80
AY250007	1197	107	6.00E-23	304	93	30
AE016923	303642	248	4.00E-65	297	137	46
AE016923	303642	246	1.00E-64	297	137	46
AF420426	1364	248	4.00E-65	157	130	82
AF420426	1364	114	5.00E-25	77	58	75

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF077601	831	243	1.00E-63	292	136	46
AF198617	6830	242	2.00E-63	304	141	46
AF198617	6830	238	4.00E-62	305	142	46
AF105060	3785	236	1.00E-61	296	129	43
AE015761	14255	236	2.00E-61	297	140	47
AE015761	14255	233	1.00E-60	297	138	46
AE015761	14255	55.1	5.00E-07	136	36	26
AE015761	14255	34.3	0.89	89	26	29
BA000043	3544776	234	4.00E-61	307	134	43
BA000043	3544776	142	2.00E-33	269	96	35
BA000043	3544776	103	2.00E-21	179	62	34
BA000043	3544776	80.5	1.00E-14	288	69	23
AB061233	849	233	1.00E-60	299	137	45
AF077600	834	232	2.00E-60	296	137	46
AF399739	6492	231	5.00E-60	300	138	46
AF232939	1045	230	6.00E-60	348	157	45
AF232941	1051	230	8.00E-60	350	154	44
AY590666	874	229	1.00E-59	289	127	43
AY590679	873	229	1.00E-59	289	127	43
AY590678	873	229	1.00E-59	289	127	43
AY590677	873	229	1.00E-59	289	127	43
AY590676	873	229	1.00E-59	289	127	43
AY590675	873	229	1.00E-59	289	127	43
AY590674	864	229	1.00E-59	289	127	43
AY590673	873	229	1.00E-59	289	127	43
AY590672	873	229	1.00E-59	289	127	43
AY590671	873	229	1.00E-59	289	127	43
AY590670	873	229	1.00E-59	289	127	43
AY590669	873	229	1.00E-59	289	127	43
AE017180	3814139	228	3.00E-59	298	133	44
AE017180	3814139	90.1	1.00E-17	293	76	25
AB128920	2676	228	3.00E-59	127	121	95
AB128920	2676	167	7.00E-41	313	124	39
AB128920	2676	85.9	3.00E-16	51	40	78
AB061232	849	227	5.00E-59	299	131	43
AB106910	15284	226	1.00E-58	299	131	43
AB061230	19187	226	1.00E-58	299	131	43
AB061230	19187	59.3	3.00E-08	130	38	29
AE016862	310266	223	8.00E-58	297	129	43
AF095238	846	222	2.00E-57	291	129	44
AB061231	849	222	2.00E-57	297	129	43
AE013021	10029	220	7.00E-57	298	134	44
BA000021	697724	219	1.00E-56	181	109	60
BA000021	697724	120	9.00E-27	345	109	31
AF077341	874	219	1.00E-56	292	124	42
AF095237	873	219	2.00E-56	292	123	42
AB080999	348	218	3.00E-56	115	115	100
AB033501	1210	217	6.00E-56	330	134	40
CP000002	4222334	215	3.00E-55	313	135	43
CP000002	4222334	33.9	1.2	87	22	25
AE017333	4222645	215	3.00E-55	313	135	43
AE017333	4222645	33.9	1.2	87	22	25
BA000004	4202352	214	6.00E-55	294	124	42
BA000004	4202352	130	1.00E-29	135	70	51
BA000004	4202352	95.9	2.00E-19	169	57	33
D10063	1064	214	6.00E-55	294	124	42
AF232940	1045	213	1.00E-54	273	137	50
AF065259	1631	211	3.00E-54	300	125	41
AF095236	873	211	3.00E-54	300	125	41
AF011370	1300	211	5.00E-54	381	141	37
AE015942	300171	209	1.00E-53	296	125	42
AE015942	300171	68.2	6.00E-11	284	68	23
BA000028	3630528	209	1.00E-53	338	131	38
BA000028	3630528	91.3	6.00E-18	293	75	25
AF080260	1149	209	2.00E-53	380	141	37
AF080259	1149	209	2.00E-53	380	141	37
Z99122	200690	208	3.00E-53	306	130	42
U56901	20320	208	3.00E-53	306	130	42

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
M26946	2360	208	3.00E-53	306	130	42
M26947	1474	208	3.00E-53	306	130	42
AB058936	884	207	4.00E-53	294	123	41
BA000032	1877212	207	6.00E-53	301	119	39
BA000032	1877212	36.6	0.18	116	29	25
AF124349	42050	207	6.00E-53	299	120	40
AE007720	7354	207	8.00E-53	295	122	41
AF064086	1020	207	8.00E-53	295	122	41
AE008692	2056416	206	1.00E-52	296	119	40
U52957	9544	206	2.00E-52	301	119	39
L06176	3724	206	2.00E-52	301	119	39
BA000031	3288558	201	3.00E-51	376	131	34
BA000031	3288558	173	9.00E-43	384	125	32
BA000031	3288558	167	9.00E-41	377	125	33
BA000031	3288558	167	9.00E-41	377	126	33
BA000031	3288558	167	9.00E-41	377	126	33
BA000031	3288558	109	2.00E-23	148	60	40
BA000031	3288558	74.3	8.00E-13	217	61	28
AB058937	820	199	1.00E-50	287	118	41
AJ748317	3009	199	2.00E-50	295	124	42
BX842647	346357	199	2.00E-50	295	124	42
BX842647	346357	196	2.00E-49	292	120	41
BX842647	346357	188	3.00E-47	301	117	38
BX842647	346357	186	2.00E-46	292	115	39
AE011832	13074	196	2.00E-49	212	113	53
AE011832	13074	103	9.00E-22	307	87	28
AE011832	13074	62.4	3.00E-09	134	40	29
AB039913	921	195	3.00E-49	302	118	39
AF081500	1152	194	4.00E-49	380	136	35
AF078155	1146	194	5.00E-49	379	136	35
AF078153	1146	194	5.00E-49	379	136	35
AJ748319	3196	194	5.00E-49	291	119	40
AJ748319	3196	90.1	1.00E-17	101	49	48
AE012298	12693	193	9.00E-49	241	119	49
AE012298	12693	104	7.00E-22	319	93	29
AE012298	12693	58.2	6.00E-08	134	38	28
AY514454	9258	193	9.00E-49	379	140	36
AY514454	9258	174	4.00E-43	370	126	34
AY514454	9258	174	4.00E-43	377	126	33
AY514454	9258	153	1.00E-36	218	89	40
AY514454	9258	57	1.00E-07	60	27	45
AB039905	921	193	9.00E-49	302	117	38
AB058938	817	192	1.00E-48	287	119	41
CR522870	3523383	192	2.00E-48	252	120	47
CR522870	3523383	177	8.00E-44	231	108	46
CR522870	3523383	115	3.00E-25	227	81	35
CR522870	3523383	107	1.00E-22	254	79	31
CR522870	3523383	51.6	5.00E-06	130	40	30
CR522870	3523383	34.3	0.89	148	33	22
AB039911	927	191	3.00E-48	304	119	39
AB039907	927	191	4.00E-48	304	119	39
AE011409	10859	190	7.00E-48	302	111	36
AE011409	10859	176	2.00E-43	300	107	35
AE017293	301124	190	7.00E-48	302	111	36
AE017293	301124	176	1.00E-43	300	107	35
AE017293	301124	33.9	1.2	59	18	30
AB039910	927	190	1.00E-47	304	119	39
M20983	1031	190	1.00E-47	304	121	39
AE004290	10581	189	1.00E-47	375	130	34
AE004290	10581	175	2.00E-43	377	129	34
CP000010	3510148	189	1.00E-47	385	136	35
CP000010	3510148	34.3	0.89	76	24	31
BX571965	4074542	189	1.00E-47	385	136	35
BX571965	4074542	40	0.016	335	74	22
BX571965	4074542	34.3	0.89	76	24	31
U73848	2046	189	1.00E-47	385	136	35
AF084815	1951	189	1.00E-47	385	136	35
AF084814	1951	189	1.00E-47	385	136	35

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF084813	1952	189	1.00E-47	385	136	35
AF084812	1952	189	1.00E-47	385	136	35
AF019213	7256	189	1.00E-47	375	130	34
AF030239	1167	189	1.00E-47	385	136	35
U82287	1199	189	1.00E-47	385	136	35
U82286	1199	189	1.00E-47	385	136	35
AE017003	347456	189	2.00E-47	296	114	38
AE017003	347456	180	1.00E-44	298	115	38
AE017003	347456	165	3.00E-40	271	98	36
AE017003	347456	140	9.00E-33	291	95	32
AE017003	347456	56.6	2.00E-07	243	57	23
AF111790	1161	189	2.00E-47	384	136	35
AF098793	1167	189	2.00E-47	385	134	34
AF078161	1161	189	2.00E-47	384	136	35
AP006840	3566135	189	2.00E-47	296	114	38
AF078152	1161	188	3.00E-47	384	136	35
AJ748315	3011	188	3.00E-47	301	117	38
AE017029	290525	188	4.00E-47	292	112	38
AE017334	5227419	188	4.00E-47	292	112	38
AE017225	5228663	188	4.00E-47	292	112	38
Y18889	5040	187	5.00E-47	300	111	37
Y18889	5040	174	7.00E-43	304	103	33
AF078154	1161	187	5.00E-47	384	135	35
AF007121	4400	187	5.00E-47	375	129	34
AF007121	4400	175	2.00E-43	377	129	34
AE017251	301045	187	6.00E-47	300	113	37
AE017251	301045	172	3.00E-42	304	106	34
AB110834	1155	187	8.00E-47	382	131	34
AJ851165	2169	186	2.00E-46	292	115	39
X67138	5206	185	3.00E-46	292	107	36
X67138	5206	182	3.00E-45	292	107	36
X67138	5206	180	1.00E-44	298	107	36
AB039909	750	185	3.00E-46	269	114	42
U52198	5354	184	5.00E-46	375	128	34
U52198	5354	155	3.00E-37	182	80	43
U52198	5354	150	9.00E-36	376	119	31
AB040140	1479	184	5.00E-46	235	116	49
AB040140	1479	114	9.00E-25	251	80	31
AB039906	756	184	5.00E-46	270	111	41
CR378665	347213	184	5.00E-46	382	130	34
CR378665	347213	145	3.00E-34	213	82	38
CR378665	347213	90.5	1.00E-17	203	63	31
AE001250	14793	183	1.00E-45	298	114	38
AY331139	686	182	2.00E-45	251	102	40
AB110832	1155	182	2.00E-45	381	132	34
AE007665	12205	182	2.00E-45	292	115	39
AE017314	300029	182	2.00E-45	311	119	38
AE004287	14585	182	3.00E-45	375	133	35
AE004287	14585	176	1.00E-43	377	134	35
AE004287	14585	169	1.00E-41	379	127	33
AF069392	39101	182	3.00E-45	376	124	32
AF069392	39101	167	9.00E-41	377	125	33
AF069392	39101	167	9.00E-41	377	126	33
AF007122	4700	182	3.00E-45	375	133	35
AF007122	4700	176	1.00E-43	377	134	35
AF007122	4700	171	6.00E-42	379	127	33
X63965	2072	181	3.00E-45	301	112	37
X63965	2072	181	6.00E-45	304	107	35
AB040139	1479	181	3.00E-45	236	111	47
AB040139	1479	115	3.00E-25	264	83	29
AY331140	686	181	6.00E-45	251	105	41
AE001257	13979	181	6.00E-45	301	111	36
AE001257	13979	181	6.00E-45	304	107	35
AY331141	686	180	8.00E-45	251	105	41
M94015	1198	180	8.00E-45	304	113	37
AB110833	1155	180	1.00E-44	381	131	34
AB110831	1155	179	1.00E-44	381	131	34
CR628336	3503610	179	1.00E-44	309	124	40

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
CR628336	3503610	110	7.00E-24	200	77	38
L47122	2101	179	1.00E-44	379	129	34
L34686	2350	179	1.00E-44	304	116	38
AE017355	5237682	179	2.00E-44	365	125	34
AE017355	5237682	142	3.00E-33	292	97	33
AY166716	1608	179	2.00E-44	335	120	35
AY028400	8125	179	2.00E-44	296	109	36
AF348135	3834	179	2.00E-44	301	109	36
AF348135	3834	172	2.00E-42	301	109	36
AE017354	3397754	178	3.00E-44	309	125	40
AE017354	3397754	109	2.00E-23	198	78	39
AJ496278	1490	178	3.00E-44	309	123	39
AJ496278	1490	109	2.00E-23	198	78	39
AB022132	1011	178	3.00E-44	342	116	33
AE011374	11076	177	6.00E-44	300	107	35
AE011374	11076	162	3.00E-39	301	100	33
AE017249	301384	177	6.00E-44	304	109	35
AE017294	300207	177	6.00E-44	300	107	35
AE017294	300207	161	4.00E-39	301	99	32
gi|94646	107	2.00E-22	181	65	35	
AB022136	1011	177	6.00E-44	342	115	33
AE016918	302178	177	8.00E-44	299	104	34
AE016918	302178	35.4	0.4	266	61	22
X69609	1011	177	8.00E-44	342	114	33
AE017317	302040	177	8.00E-44	310	113	36
AJ496382	1548	176	1.00E-43	309	122	39
AJ496382	1548	110	1.00E-23	251	88	35
AJ496283	1468	176	1.00E-43	309	122	39
AJ496283	1468	110	1.00E-23	251	88	35
AJ496281	1472	176	1.00E-43	309	122	39
AJ496281	1472	95.9	2.00E-19	84	46	54
AJ496276	1493	176	1.00E-43	309	122	39
AJ496276	1493	92.8	2.00E-18	136	61	44
X83232	1755	176	1.00E-43	309	122	39
X83232	1755	109	2.00E-23	251	87	34
AJ496282	1482	176	1.00E-43	309	122	39
AJ496282	1482	110	1.00E-23	251	88	35
CR628337	3345687	176	1.00E-43	309	122	39
CR628337	3345687	110	1.00E-23	251	88	35
AB022133	1011	176	1.00E-43	342	115	33
AJ748316	3730	176	1.00E-43	295	110	37
BX842655	349965	176	1.00E-43	295	110	37
CP000013	904246	176	2.00E-43	342	113	33
CP000013	904246	35	0.52	77	18	23
AE001126	11037	176	2.00E-43	342	113	33
X69597	1011	176	2.00E-43	342	114	33
X69611	1008	176	2.00E-43	342	113	33
X69607	1008	176	2.00E-43	342	114	33
AB039908	843	176	2.00E-43	285	113	39
X84699	2178	175	2.00E-43	228	105	46
X84699	2178	107	8.00E-23	214	79	36
X53940	1005	175	2.00E-43	340	116	34
X75202	1123	175	2.00E-43	342	114	33
X15660	1011	175	2.00E-43	342	113	33
X56334	1426	175	2.00E-43	342	113	33
AL646078	203050	175	2.00E-43	297	109	36
AF241832	1300	175	2.00E-43	296	107	36
L42881	1011	175	2.00E-43	342	113	33
L42876	1011	175	2.00E-43	342	113	33
D43777	1398	175	2.00E-43	337	115	34
M86838	1736	175	2.00E-43	340	116	34
X69608	1008	175	3.00E-43	342	113	33
AF283285	1371	175	3.00E-43	300	111	37
AJ496275	1487	174	4.00E-43	310	122	39
AJ496275	1487	99.8	2.00E-20	191	72	37
X75201	1112	174	4.00E-43	333	113	33
X69598	1011	174	4.00E-43	342	113	33
X75203	1087	174	5.00E-43	342	113	33

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF320637	1685	174	5.00E-43	300	107	35
L42885	1011	174	5.00E-43	342	113	33
X69614	1011	174	7.00E-43	342	112	32
X69610	1011	174	7.00E-43	342	113	33
AB022138	974	174	7.00E-43	329	114	34
AE016803	300045	173	9.00E-43	375	121	32
AE016803	300045	169	1.00E-41	376	122	32
AE016803	300045	151	5.00E-36	376	119	31
AY660550	864	173	9.00E-43	296	107	36
AY660549	864	173	9.00E-43	296	107	36
X63413	1011	173	9.00E-43	342	113	33
X65624	1498	173	9.00E-43	296	107	36
X16833	1435	173	9.00E-43	342	112	32
X15661	1011	173	9.00E-43	342	112	32
BA000037	3354505	173	9.00E-43	375	121	32
BA000037	3354505	153	1.00E-36	376	118	31
BA000037	3354505	151	5.00E-36	376	119	31
BA000037	3354505	149	2.00E-35	178	80	44
BA000037	3354505	148	4.00E-35	376	111	29
BA000037	3354505	121	4.00E-27	374	108	28
BA000037	3354505	102	3.00E-21	301	92	30
AL591976	250050	173	9.00E-43	296	107	36
AL596166	260050	173	9.00E-43	296	107	36
X69612	1011	173	9.00E-43	342	113	33
X69513	1008	173	9.00E-43	342	113	33
AE017324	290242	173	9.00E-43	296	107	36
AY275679	1223	173	1.00E-42	314	118	37
AY275679	1223	122	3.00E-27	182	73	40
AB022137	960	173	1.00E-42	323	113	34
AE016822	2584158	172	2.00E-42	299	105	35
AE016822	2584158	99.8	2.00E-20	308	85	27
AJ496277	1486	172	2.00E-42	160	92	55
AJ496277	1486	109	2.00E-23	198	78	39
AJ748318	3949	172	2.00E-42	295	109	36
BX842654	344249	172	2.00E-42	295	109	36
CR555306	4296230	171	4.00E-42	151	89	58
AB039912	843	171	4.00E-42	280	110	39
AY445112	990	171	5.00E-42	314	117	37
L81147	1272	171	5.00E-42	314	117	37
D82864	978	171	5.00E-42	325	109	33
AB014678	963	171	5.00E-42	323	111	34
AY660548	864	171	6.00E-42	296	106	35
AE007717	14157	171	6.00E-42	290	104	35
AY275678	1223	171	6.00E-42	314	117	37
AY275678	1223	122	3.00E-27	182	73	40
AY275677	1222	171	6.00E-42	314	117	37
AY275677	1222	122	3.00E-27	182	73	40
AB014677	973	171	6.00E-42	323	111	34
AE015941	299511	170	8.00E-42	294	105	35
AE015941	299511	142	2.00E-33	270	80	29
X75200	1117	170	8.00E-42	342	111	32
D82853	987	170	8.00E-42	335	111	33
D82852	987	170	8.00E-42	335	111	33
AE017316	300704	169	1.00E-41	295	101	34
D82856	987	169	1.00E-41	335	110	32
AJ496279	1495	169	2.00E-41	314	122	38
AJ496279	1495	109	2.00E-23	198	78	39
X75204	1121	169	2.00E-41	334	112	33
L81146	1272	169	2.00E-41	300	114	38
U54775	2745	168	3.00E-41	242	104	42
U54775	2745	113	1.00E-24	335	100	29
AY380808	1011	168	4.00E-41	342	110	32
D82855	987	168	4.00E-41	335	108	32
AE016920	305584	167	5.00E-41	369	122	33
AE016920	305584	58.9	3.00E-08	299	62	20
D82854	987	167	5.00E-41	335	108	32
D82848	987	167	5.00E-41	335	109	32
D82847	987	167	5.00E-41	335	109	32

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AB022134	987	167	5.00E-41	335	109	32
AE004540	15833	167	7.00E-41	242	103	42
AE004540	15833	113	2.00E-24	335	100	29
AF034764	1170	167	7.00E-41	271	105	38
AY275676	1229	167	7.00E-41	271	105	38
AY275675	1228	167	7.00E-41	271	105	38
AY275674	1243	167	7.00E-41	271	105	38
D82862	981	167	7.00E-41	333	109	32
D82858	987	167	7.00E-41	335	108	32
D82857	987	167	7.00E-41	335	108	32
AF034768	1434	167	9.00E-41	225	101	44
AF034768	1434	111	4.00E-24	278	83	29
D63372	987	167	9.00E-41	335	107	31
D63366	987	167	9.00E-41	335	108	32
D63365	987	167	9.00E-41	335	108	32
D63364	987	167	9.00E-41	335	107	31
D82851	987	167	9.00E-41	335	107	31
D82850	987	167	9.00E-41	335	107	31
D82849	987	167	9.00E-41	335	107	31
AB022139	976	167	9.00E-41	323	109	33
D63374	987	166	1.00E-40	335	107	31
D63373	987	166	1.00E-40	335	107	31
D63371	987	166	1.00E-40	335	107	31
D63370	987	166	1.00E-40	335	107	31
D63369	987	166	1.00E-40	335	107	31
D63368	987	166	1.00E-40	335	107	31
D63367	987	166	1.00E-40	335	107	31
D63363	987	166	1.00E-40	335	107	31
D82846	987	166	1.00E-40	335	107	31
D82861	981	166	1.00E-40	333	110	33
M57501	1596	166	2.00E-40	271	105	38
M57501	1596	107	1.00E-22	197	73	37
AF307102	981	165	3.00E-40	333	108	32
AF307101	981	165	3.00E-40	333	108	32
U12817	19811	165	3.00E-40	377	125	33
U12817	19811	147	6.00E-35	188	78	41
U12817	19811	107	6.00E-23	160	61	38
U12817	19811	75.9	3.00E-13	217	59	27
U28496	1085	165	3.00E-40	334	111	33
D82863	981	165	3.00E-40	333	108	32
AE016790	300242	164	6.00E-40	252	103	40
AE016790	300242	96.3	2.00E-19	129	53	41
AE016790	300242	56.2	2.00E-07	130	41	31
L15366	2531	164	6.00E-40	252	103	40
L15366	2531	95.9	2.00E-19	92	46	50
AB017479	952	164	7.00E-40	323	108	33
AF064056	852	163	1.00E-39	301	100	33
AJ537492	1203	162	3.00E-39	103	84	81
AJ537491	1202	162	3.00E-39	103	84	81
AJ537490	1203	162	3.00E-39	103	84	81
AJ537489	1204	162	3.00E-39	103	84	81
AJ537488	1203	162	3.00E-39	103	84	81
AJ537487	1202	162	3.00E-39	103	84	81
AJ537486	1201	162	3.00E-39	103	84	81
AJ537485	1204	162	3.00E-39	103	84	81
X63513	1035	161	4.00E-39	307	109	35
AF064057	852	161	5.00E-39	301	99	32
M81344	1207	161	5.00E-39	301	99	32
AF034765	1179	160	6.00E-39	300	108	36
BA000040	9105828	160	8.00E-39	295	95	32
BA000040	9105828	85.1	4.00E-16	311	73	23
BA000040	9105828	80.9	8.00E-15	317	74	23
BA000040	9105828	58.5	4.00E-08	273	72	26
BA000040	9105828	57.4	1.00E-07	255	72	28
BA000040	9105828	55.1	5.00E-07	250	63	25
BA000040	9105828	53.9	1.00E-06	186	47	25
BA000040	9105828	38.5	0.047	233	50	21
BA000040	9105828	37.7	0.08	134	39	29

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
BA000040	9105828	36.2	0.23	109	29	26
BA000040	9105828	35.4	0.4	121	28	23
BA000040	9105828	34.7	0.68	109	29	26
BA000040	9105828	34.3	0.89	109	29	26
BA000040	9105828	33.9	1.2	109	29	26
BA000040	9105828	33.1	2	62	19	30
AF014114	852	160	1.00E-38	301	98	32
AF034766	1458	160	1.00E-38	232	99	42
AF034766	1458	100	8.00E-21	346	89	25
AJ277361	822	159	2.00E-38	273	94	34
D86618	984	159	2.00E-38	327	106	32
D89073	1560	159	2.00E-38	256	101	39
D89073	1560	89.7	2.00E-17	173	60	34
D82859	984	159	2.00E-38	327	106	32
AB058931	1313	159	2.00E-38	256	101	39
AB058931	1313	89.7	2.00E-17	173	60	34
AF034767	2007	159	2.00E-38	260	105	40
AF034767	2007	108	3.00E-23	273	74	27
AY424358	705	158	3.00E-38	217	92	42
AJ277358	822	158	3.00E-38	273	95	34
AF064055	852	158	3.00E-38	301	98	32
AY744156	858	158	4.00E-38	304	106	34
AB022135	934	158	4.00E-38	313	103	32
AB058932	1313	156	1.00E-37	278	102	36
AB058932	1313	85.1	4.00E-16	108	45	41
AJ277360	822	156	2.00E-37	273	93	34
AF011371	1515	156	2.00E-37	246	97	39
AF011371	1515	92	4.00E-18	87	46	52
AB058934	1150	155	2.00E-37	374	115	30
AJ277359	813	152	2.00E-36	268	91	33
BX572595	349260	152	2.00E-36	295	92	31
BX572595	349260	35	0.52	261	58	22
AE016797	301380	151	4.00E-36	376	120	31
AE016797	301380	149	2.00E-35	178	80	44
AE016797	301380	121	4.00E-27	374	108	28
AE016797	301380	102	3.00E-21	301	92	30
AB058933	1217	151	4.00E-36	169	82	48
AY192720	724	151	5.00E-36	263	96	36
AB058935	1156	151	5.00E-36	169	82	48
AB058935	1156	79.7	2.00E-14	291	83	28
CR378663	348044	151	5.00E-36	251	106	42
CR378663	348044	89.4	2.00E-17	149	55	36
U28499	1093	150	9.00E-36	335	102	30
AF011372	1620	150	1.00E-35	266	100	37
AF011372	1620	51.2	7.00E-06	147	43	29
U52199	2471	149	1.00E-35	376	116	30
AY192721	724	149	2.00E-35	263	95	36
AJ277355	661	149	2.00E-35	238	90	37
D90832	19662	149	2.00E-35	151	80	52
AB018734	603	149	2.00E-35	214	90	42
AE017340	2839318	148	3.00E-35	170	82	48
AE017340	2839318	99.4	2.00E-20	267	77	28
AE017340	2839318	44.7	7.00E-04	130	35	26
AJ277351	667	147	7.00E-35	237	85	35
AY192718	724	147	9.00E-35	267	96	35
AE017269	294300	145	3.00E-34	292	96	32
AE017269	294300	126	1.00E-28	221	77	34
AE017269	294300	75.1	5.00E-13	84	41	48
AY192722	724	145	4.00E-34	263	91	34
AJ277350	667	145	4.00E-34	237	84	35
U28498	1089	145	4.00E-34	330	102	30
AB018732	606	145	4.00E-34	217	91	41
AY192719	724	144	5.00E-34	264	93	35
AJ242662	1131	144	5.00E-34	377	112	29
AJ277356	660	144	6.00E-34	238	89	37
AY331135	1880	143	1.00E-33	263	99	37
AY331135	1880	70.9	9.00E-12	68	35	51
D85070	876	143	1.00E-33	291	94	32

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
D85069	876	143	1.00E-33	291	94	32
AY192716	724	143	1.00E-33	264	92	34
AY192717	724	142	2.00E-33	264	89	33
D83764	876	142	2.00E-33	291	94	32
D83763	876	142	2.00E-33	291	94	32
D83762	876	142	2.00E-33	291	94	32
D88295	876	142	2.00E-33	291	93	31
AJ277352	667	142	2.00E-33	237	86	36
AF515472	674	142	2.00E-33	125	80	64
AF515472	674	57.8	8.00E-08	58	33	56
D85071	876	142	3.00E-33	291	92	31
D88291	866	142	3.00E-33	291	92	31
AB001704	876	142	3.00E-33	291	92	31
AB167766	746	141	4.00E-33	267	88	32
X98463	998	141	4.00E-33	332	107	32
D85076	876	141	4.00E-33	291	92	31
D85075	876	141	4.00E-33	291	92	31
D85074	876	141	4.00E-33	291	92	31
D85072	876	141	4.00E-33	291	92	31
D88293	876	141	4.00E-33	291	92	31
AB001718	876	141	4.00E-33	291	92	31
AB001717	876	141	4.00E-33	291	92	31
AB001716	876	141	4.00E-33	291	92	31
AB001715	876	141	4.00E-33	291	92	31
AB001714	876	141	4.00E-33	291	92	31
AB001713	876	141	4.00E-33	291	92	31
AB001712	876	141	4.00E-33	291	92	31
AB001711	876	141	4.00E-33	291	92	31
AB001710	876	141	4.00E-33	291	92	31
AB001709	876	141	4.00E-33	291	92	31
AB001708	876	141	4.00E-33	291	92	31
AB001707	876	141	4.00E-33	291	92	31
AB001706	876	141	4.00E-33	291	92	31
AB001705	876	141	4.00E-33	291	92	31
AB030271	746	141	4.00E-33	267	87	32
AB030270	746	141	4.00E-33	267	88	32
AB027180	746	141	4.00E-33	267	88	32
AB027175	746	141	4.00E-33	267	88	32
AB027166	746	141	4.00E-33	267	87	32
AB027161	746	141	4.00E-33	267	88	32
AB091716	746	141	5.00E-33	267	87	32
AB031516	746	141	5.00E-33	267	87	32
AB031515	746	141	5.00E-33	267	87	32
AB031513	746	141	5.00E-33	267	87	32
AB031512	746	141	5.00E-33	267	87	32
AB031511	746	141	5.00E-33	267	87	32
AB031510	746	141	5.00E-33	267	87	32
AB031509	746	141	5.00E-33	267	87	32
AB031508	746	141	5.00E-33	267	87	32
AB018733	624	141	5.00E-33	214	87	40
AB027186	746	141	5.00E-33	267	87	32
AB027185	746	141	5.00E-33	267	87	32
AB027184	746	141	5.00E-33	267	87	32
AB027183	746	141	5.00E-33	267	87	32
AB027182	746	141	5.00E-33	267	87	32
AB027179	746	141	5.00E-33	267	87	32
AB027178	746	141	5.00E-33	267	87	32
AB027177	746	141	5.00E-33	267	87	32
AB027174	746	141	5.00E-33	267	87	32
AB027172	746	141	5.00E-33	267	87	32
AB027171	746	141	5.00E-33	267	87	32
AB027170	746	141	5.00E-33	267	87	32
AB027168	746	141	5.00E-33	267	87	32
AB027167	746	141	5.00E-33	267	87	32
AB027165	746	141	5.00E-33	267	87	32
AB027164	746	141	5.00E-33	267	87	32
AB027162	746	141	5.00E-33	267	87	32
AB027160	746	141	5.00E-33	267	87	32

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AB027159	746	141	5.00E-33	267	87	32
AB027158	746	141	5.00E-33	267	87	32
AB027157	746	141	5.00E-33	267	87	32
AY192726	724	140	7.00E-33	267	92	34
AY192725	724	140	7.00E-33	267	92	34
CP000001	5300915	140	7.00E-33	292	95	32
CP000001	5300915	137	6.00E-32	289	96	33
CP000001	5300915	80.9	8.00E-15	111	46	41
CP000001	5300915	57.8	8.00E-08	242	57	23
Y14687	2026	140	7.00E-33	166	74	44
Y14687	2026	97.1	1.00E-19	176	63	35
AF274346	699	140	7.00E-33	166	74	44
D85073	876	140	7.00E-33	291	92	31
AB174780	746	140	9.00E-33	267	87	32
AB174779	746	140	9.00E-33	267	87	32
AB174778	746	140	9.00E-33	267	87	32
AB174777	746	140	9.00E-33	267	87	32
AB174776	746	140	9.00E-33	267	87	32
AB174775	746	140	9.00E-33	267	87	32
AB174774	746	140	9.00E-33	267	87	32
AB031514	746	140	9.00E-33	267	87	32
AB027181	746	140	9.00E-33	267	87	32
AB027176	746	140	9.00E-33	267	87	32
AB027173	746	140	9.00E-33	267	87	32
AB027169	746	140	9.00E-33	267	87	32
AB027163	746	140	9.00E-33	267	87	32
AY192723	724	140	1.00E-32	267	92	34
AE001746	18364	140	1.00E-32	392	119	30
AF336830	772	140	1.00E-32	273	87	31
AB030272	746	140	1.00E-32	267	87	32
AB018737	600	139	2.00E-32	218	89	40
AB018736	600	139	2.00E-32	218	89	40
AY331136	1863	139	3.00E-32	258	96	37
AY331136	1863	63.2	2.00E-09	64	31	48
AY192727	722	139	3.00E-32	266	91	34
AJ277362	703	139	3.00E-32	248	85	34
AB058939	1685	138	4.00E-32	136	71	52
AB058939	1685	99.8	2.00E-20	291	82	28
AE007672	10661	137	7.00E-32	292	89	30
AY192724	723	135	2.00E-31	266	90	33
AY331137	1411	134	5.00E-31	233	86	36
AY331137	1411	65.1	5.00E-10	264	68	25
AF017113	47739	134	6.00E-31	206	81	39
Z99121	194692	134	6.00E-31	206	81	39
L15367	1666	130	7.00E-31	132	69	52
L15367	1666	97.4	9.00E-20	280	77	27
L15367	1666	29.6	7.00E-31	24	13	54
AB030273	746	134	8.00E-31	268	84	31
AJ277353	703	132	3.00E-30	248	83	33
AY551006	1380	132	3.00E-30	139	70	50
AY551006	1380	87.4	9.00E-17	159	57	35
AF026811	3031	131	4.00E-30	265	93	35
AF026811	3031	98.2	5.00E-20	153	63	41
AJ277363	669	131	5.00E-30	241	78	32
AB018735	600	130	9.00E-30	216	85	39
AY129557	9117	129	2.00E-29	251	82	32
AY129557	9117	49.3	3.00E-05	87	34	39
AJ277364	669	129	3.00E-29	241	79	32
AY551005	1482	129	3.00E-29	140	68	48
AY551005	1482	94	9.00E-19	195	67	34
AF026812	1863	128	5.00E-29	150	68	45
AF026812	1863	86.7	2.00E-16	158	58	36
AF312378	687	126	1.00E-28	248	79	31
AY331138	1293	124	7.00E-28	165	67	40
AY331138	1293	60.1	2.00E-08	92	33	35
AJ131736	2833	124	9.00E-28	81	63	77
AJ277357	670	122	3.00E-27	240	77	32
AY278534	577	122	3.00E-27	182	73	40

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY278531	566	122	3.00E-27	182	73	40
AF529084	780	121	4.00E-27	260	83	31
L81176	5735	119	2.00E-26	195	77	39
AY278546	607	119	2.00E-26	195	77	39
AY278537	599	119	2.00E-26	195	77	39
X98462	1301	119	2.00E-26	197	78	39
X98462	1301	92.4	3.00E-18	309	90	29
AF416443	388	118	4.00E-26	117	60	51
X98280	1301	118	4.00E-26	196	78	39
X98280	1301	98.6	4.00E-20	326	91	27
AF416435	381	118	5.00E-26	120	59	49
AB181529	1701	118	5.00E-26	180	68	37
AB181529	1701	75.9	3.00E-13	84	34	40
AB018719	1449	118	5.00E-26	254	87	34
AB018719	1449	58.5	4.00E-08	221	60	27
AF416449	395	117	8.00E-26	117	59	50
AF416448	399	117	8.00E-26	117	59	50
AF416447	399	117	8.00E-26	117	59	50
AF416446	394	117	8.00E-26	117	59	50
AF416445	396	117	8.00E-26	117	59	50
AF416444	399	117	8.00E-26	117	59	50
AF416442	389	117	8.00E-26	117	59	50
AF416441	397	117	8.00E-26	117	59	50
AF416440	393	117	8.00E-26	117	59	50
AF416439	393	117	8.00E-26	117	59	50
AF416438	396	117	8.00E-26	117	59	50
AF416436	399	117	8.00E-26	117	59	50
AF416434	399	117	8.00E-26	117	59	50
AF416433	397	117	8.00E-26	117	59	50
AB181536	1698	117	1.00E-25	180	68	37
AB181536	1698	75.5	3.00E-13	83	34	40
AB181530	1701	117	1.00E-25	180	68	37
AB181530	1701	74.7	6.00E-13	83	34	40
AB181528	1701	117	1.00E-25	180	68	37
AB181528	1701	74.7	6.00E-13	83	34	40
AB181524	1701	117	1.00E-25	180	68	37
AB181524	1701	74.7	6.00E-13	83	34	40
AB181522	1698	117	1.00E-25	180	68	37
AB181522	1698	75.5	3.00E-13	83	34	40
AB181521	1698	117	1.00E-25	180	68	37
AB181521	1698	75.5	3.00E-13	83	34	40
AB105426	3847	116	1.00E-25	132	58	43
AB105426	3847	102	2.00E-21	297	90	30
AJ277354	663	116	1.00E-25	238	74	31
AB181523	1701	116	1.00E-25	180	68	37
AB181523	1701	74.7	6.00E-13	83	34	40
AB181525	1689	116	2.00E-25	180	67	37
AB181525	1689	76.6	2.00E-13	173	50	28
AB181532	1695	115	2.00E-25	180	67	37
AB181532	1695	78.2	5.00E-14	127	45	35
AF016231	1302	115	2.00E-25	196	76	38
AF016231	1302	103	1.00E-21	327	93	28
AF016230	1302	115	2.00E-25	196	76	38
AF016230	1302	102	3.00E-21	327	93	28
AF016229	1302	115	2.00E-25	196	76	38
AF016229	1302	102	3.00E-21	327	93	28
AF003906	1004	115	2.00E-25	265	87	32
AF003906	1004	110	1.00E-23	174	66	37
AB181527	1698	115	3.00E-25	180	67	37
AB181527	1698	75.5	3.00E-13	83	34	40
AF416437	379	114	5.00E-25	127	61	48
AY024344	763	114	7.00E-25	257	80	31
X98465	2099	114	7.00E-25	301	93	30
X98465	2099	99.8	2.00E-20	297	91	30
AJ297533	1319	113	1.00E-24	237	83	35
AJ297533	1319	103	1.00E-21	254	79	31
AB181535	1713	113	2.00E-24	180	66	36
AB181535	1713	74.7	6.00E-13	83	33	39

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
U76543	1023	113	2.00E-24	225	76	33
U76543	1023	107	6.00E-23	187	70	37
AF003905	1023	113	2.00E-24	225	76	33
AF003905	1023	105	3.00E-22	187	69	36
AB018711	1194	113	2.00E-24	215	86	40
AB018711	1194	55.8	3.00E-07	130	43	33
X98464	1019	112	2.00E-24	225	76	33
X98464	1019	105	4.00E-22	186	69	37
AF016232	1302	112	2.00E-24	196	73	37
AF016232	1302	102	3.00E-21	327	93	28
X98461	1301	112	3.00E-24	196	75	38
X98461	1301	95.5	3.00E-19	326	90	27
AB018724	510	111	4.00E-24	125	61	48
AB018722	450	111	4.00E-24	125	61	48
X98281	1301	110	7.00E-24	196	74	37
X98281	1301	89	3.00E-17	321	85	26
AB018714	528	110	7.00E-24	174	74	42
AB181534	1704	110	1.00E-23	180	64	35
AB181534	1704	75.5	3.00E-13	83	34	40
BX571662	349859	109	2.00E-23	294	89	30
BX571662	349859	73.2	2.00E-12	122	44	36
AB181533	1704	109	2.00E-23	180	64	35
AB181533	1704	75.5	3.00E-13	83	34	40
AB181526	1704	109	2.00E-23	180	63	35
AB181526	1704	74.7	6.00E-13	83	34	40
AF290503	1728	109	2.00E-23	184	63	34
AF290503	1728	79	3.00E-14	107	43	40
AF290502	1728	109	2.00E-23	184	63	34
AF290502	1728	79	3.00E-14	107	43	40
AF290501	1728	109	2.00E-23	184	63	34
AF290501	1728	79	3.00E-14	107	43	40
AF290500	1722	109	2.00E-23	184	63	34
AF290500	1722	79.3	2.00E-14	124	47	37
AF290499	1722	109	2.00E-23	184	63	34
AF290499	1722	79.3	2.00E-14	124	47	37
AF290498	1722	109	2.00E-23	184	63	34
AF290498	1722	79.3	2.00E-14	124	47	37
AF290497	1722	109	2.00E-23	184	63	34
AF290497	1722	79.3	2.00E-14	124	47	37
AF290496	1722	109	2.00E-23	184	63	34
AF290496	1722	79.3	2.00E-14	124	47	37
AF202168	7756	109	2.00E-23	184	63	34
AF202168	7756	105	3.00E-22	184	63	34
AF202168	7756	77	1.00E-13	83	37	44
AF202168	7756	77	1.00E-13	83	37	44
AF202168	7756	73.6	1.00E-12	83	34	40
AF202168	7756	63.5	1.00E-09	133	36	27
AF202168	7756	47	1.00E-04	52	26	50
AF050191	1731	109	2.00E-23	184	62	33
AF050191	1731	77.4	9.00E-14	156	52	33
AJ297532	1370	108	3.00E-23	144	65	45
AJ297532	1370	98.6	4.00E-20	275	84	30
AB181531	1704	108	4.00E-23	180	63	35
AB181531	1704	75.5	3.00E-13	83	34	40
AB098070	1713	108	4.00E-23	181	66	36
AB098070	1713	72	4.00E-12	83	34	40
AB098067	1725	108	4.00E-23	184	63	34
AB098067	1725	77.4	9.00E-14	159	55	34
AF140252	2031	108	4.00E-23	184	63	34
AF140252	2031	77	1.00E-13	83	37	44
AF270499	1146	108	4.00E-23	215	72	33
AF050195	1731	108	4.00E-23	184	62	33
AF050195	1731	77.4	9.00E-14	83	37	44
AF050190	1731	108	4.00E-23	184	63	34
AF050190	1731	77.4	9.00E-14	124	44	35
AF050184	1731	108	4.00E-23	184	62	33
AF050184	1731	77	1.00E-13	83	37	44
AB070578	1458	108	4.00E-23	183	67	36

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AB070578	1458	80.1	1.00E-14	83	38	45
M64671	4200	108	4.00E-23	184	63	34
M64671	4200	105	3.00E-22	184	64	34
M64671	4200	79.7	2.00E-14	124	46	37
M64671	4200	73.9	1.00E-12	124	43	34
J05635	3832	108	4.00E-23	184	62	33
J05635	3832	106	3.00E-22	184	63	34
J05635	3832	77	1.00E-13	83	37	44
J05635	3832	71.6	5.00E-12	83	33	39
M64670	4200	108	4.00E-23	184	63	34
M64670	4200	105	3.00E-22	184	64	34
M64670	4200	79.7	2.00E-14	124	46	37
M64670	4200	73.9	1.00E-12	124	43	34
AE000533	11152	108	5.00E-23	187	67	35
AE000533	11152	77.4	8.00E-14	121	47	38
AB073915	1458	108	5.00E-23	183	66	36
AB073915	1458	80.1	1.00E-14	83	38	45
AY304577	1545	107	6.00E-23	166	62	37
AY304577	1545	77.4	9.00E-14	121	47	38
AB098069	1722	107	6.00E-23	181	65	35
AB098069	1722	82	4.00E-15	162	56	34
AB098058	1722	107	6.00E-23	181	65	35
AB098058	1722	79	3.00E-14	83	37	44
AF050186	1728	107	6.00E-23	181	65	35
AF050186	1728	82	4.00E-15	162	56	34
AY714226	1545	107	8.00E-23	187	67	35
AY714226	1545	77.4	9.00E-14	121	47	38
AY319299	1545	107	8.00E-23	187	67	35
AY319299	1545	77.4	9.00E-14	121	47	38
AF479024	1545	107	8.00E-23	187	67	35
AF479024	1545	77.4	9.00E-14	121	47	38
Z29327	3879	107	8.00E-23	182	67	36
Z29327	3879	103	9.00E-22	182	69	37
Z29327	3879	79.3	2.00E-14	107	43	40
Z29327	3879	73.9	1.00E-12	107	40	37
Y11602	1900	107	8.00E-23	249	79	31
Y11602	1900	75.1	5.00E-13	148	50	33
AY155232	1545	107	8.00E-23	187	67	35
AY155232	1545	77.4	9.00E-14	121	47	38
AB103061	1725	107	8.00E-23	171	64	37
AB103061	1725	79.7	2.00E-14	121	44	36
M74578	1800	107	8.00E-23	182	67	36
M74578	1800	73.9	1.00E-12	107	40	37
AE001449	13631	107	8.00E-23	187	67	35
AE001449	13631	77.4	9.00E-14	121	47	38
L08907	1800	107	8.00E-23	187	67	35
L08907	1800	77.4	9.00E-14	121	47	38
X57173	1731	107	1.00E-22	181	65	35
X57173	1731	82	4.00E-15	162	56	34
AF050197	1719	107	1.00E-22	171	64	37
AF050197	1719	77.8	7.00E-14	132	48	36
AF050196	1719	107	1.00E-22	181	65	35
AF050196	1719	78.2	5.00E-14	132	48	36
AF050192	1719	107	1.00E-22	181	65	35
AF050192	1719	79.3	2.00E-14	132	48	36
AF050188	1719	107	1.00E-22	181	65	35
AF050188	1719	78.6	4.00E-14	83	37	44
AB103060	1716	106	1.00E-22	184	61	33
AB103060	1716	79.7	2.00E-14	124	46	37
AL139078	263335	106	2.00E-22	171	63	36
AL139078	263335	102	3.00E-21	181	66	36
AL139078	263335	79.3	2.00E-14	132	48	36
AL139078	263335	72.8	2.00E-12	132	45	34
AB018730	375	106	2.00E-22	125	57	45
AB018728	393	106	2.00E-22	125	57	45
AB103058	1461	105	2.00E-22	183	64	34
AB103058	1461	80.1	1.00E-14	83	38	45
AB018716	495	105	2.00E-22	165	68	41

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
U28497	1055	105	3.00E-22	308	87	28
AB018726	372	105	3.00E-22	124	57	45
M35141	1932	105	3.00E-22	184	64	34
M35141	1932	72.8	2.00E-12	124	43	34
AY102622	7647	105	4.00E-22	184	62	33
AY102622	7647	73.6	1.00E-12	83	34	40
AY278540	560	105	4.00E-22	186	69	37
AE017149	266956	104	5.00E-22	188	67	35
AE017149	266956	97.8	7.00E-20	170	60	35
AE017149	266956	76.3	2.00E-13	297	74	24
AE017149	266956	68.9	3.00E-11	115	40	34
AB103059	1461	104	5.00E-22	183	65	35
AB103059	1461	80.1	1.00E-14	83	38	45
AB103056	1461	104	5.00E-22	183	65	35
AB103056	1461	79	3.00E-14	83	37	44
AB103053	1461	104	5.00E-22	183	65	35
AB103053	1461	79	3.00E-14	83	37	44
AB073918	1473	104	5.00E-22	180	63	35
AB073918	1473	81.6	5.00E-15	174	54	31
L08908	1800	104	5.00E-22	189	63	33
L08908	1800	80.5	1.00E-14	123	48	39
AE005820	14021	104	7.00E-22	297	76	25
AE005820	14021	99.4	2.00E-20	298	76	25
AE005820	14021	99	3.00E-20	292	75	25
AB084912	1461	104	7.00E-22	183	64	34
AB084912	1461	82.8	2.00E-15	170	56	32
AB084911	1461	104	7.00E-22	183	64	34
AB084911	1461	82.8	2.00E-15	170	56	32
AF050185	1731	104	7.00E-22	181	64	35
AF050185	1731	79.3	2.00E-14	121	44	36
AB080202	1473	104	7.00E-22	181	63	34
AB080202	1473	83.2	2.00E-15	174	55	31
AB103052	1473	103	9.00E-22	184	63	34
AB103052	1473	82.8	2.00E-15	174	59	33
AF050194	1728	103	9.00E-22	171	62	36
AF050194	1728	78.6	4.00E-14	107	43	40
BX571661	346613	103	1.00E-21	192	63	32
BX571661	346613	94.7	6.00E-19	333	85	25
Y11762	4057	103	1.00E-21	181	64	35
Y11762	4057	102	3.00E-21	183	65	35
Y11762	4057	79.3	2.00E-14	148	50	33
Y11762	4057	71.2	7.00E-12	105	38	36
AF050193	1719	103	1.00E-21	181	67	37
AF050193	1719	72.8	2.00E-12	132	45	34
M82917	2236	103	1.00E-21	192	63	32
M82917	2236	94.7	6.00E-19	333	85	25
AB073917	1461	103	1.00E-21	183	63	34
AB073917	1461	80.1	1.00E-14	83	38	45
AB103055	1473	103	2.00E-21	219	68	31
AB103055	1473	84	1.00E-15	171	56	32
AF089835	2310	103	2.00E-21	297	75	25
AF089835	2310	99	3.00E-20	292	75	25
AE017138	290924	102	2.00E-21	223	67	30
AE017138	290924	47.8	8.00E-05	66	22	33
AE013947	10446	102	2.00E-21	223	67	30
AE013947	10446	57.4	1.00E-07	84	28	33
AJ414144	208050	102	2.00E-21	223	67	30
AJ414144	208050	95.9	2.00E-19	295	76	25
AJ414144	208050	92	4.00E-18	309	79	25
AY751741	1630	102	3.00E-21	169	61	36
AY751741	1630	62	4.00E-09	141	42	29
AB103054	1470	102	3.00E-21	219	68	31
AB103054	1470	83.6	1.00E-15	171	59	34
AB018720	360	102	3.00E-21	119	55	46
AF369587	1671	101	5.00E-21	178	59	33
AF369587	1671	70.1	1.00E-11	113	41	36
AF050187	1728	101	5.00E-21	181	65	35
AF050187	1728	77.8	7.00E-14	296	78	26

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
Y11601	1900	101	6.00E-21	240	73	30
Y11601	1900	77.8	7.00E-14	329	89	27
AB103051	1476	101	6.00E-21	174	61	35
AB103051	1476	82.8	2.00E-15	175	58	33
AF369581	1671	101	6.00E-21	178	59	33
AF369581	1671	70.1	1.00E-11	113	41	36
AF050189	1719	101	6.00E-21	181	66	36
AF050189	1719	71.6	5.00E-12	132	45	34
AE000767	13413	100	8.00E-21	209	62	29
AE000767	13413	62	4.00E-09	129	39	30
AB103050	1500	100	8.00E-21	153	61	39
AB103050	1500	85.9	3.00E-16	316	82	25
AF369584	1668	100	1.00E-20	175	62	35
AF369584	1668	71.6	5.00E-12	287	73	25
AF369583	1674	100	1.00E-20	175	62	35
AF369583	1674	74.7	6.00E-13	287	72	25
AF369580	582	100	1.00E-20	175	62	35
AF369586	1662	100	1.00E-20	175	61	34
AF369586	1662	58.6	4.00E-11	74	31	41
AF369585	1662	100	1.00E-20	175	61	34
AF369585	1662	58.6	4.00E-11	74	31	41
AF369582	1662	100	1.00E-20	175	61	34
AF368582	1662	68.6	4.00E-11	74	31	41
AF369579	582	100	1.00E-20	175	61	34
AF369578	582	100	1.00E-20	175	61	34
AF369577	582	100	1.00E-20	175	61	34
AB018712	345	99.8	2.00E-20	115	58	50
AB073916	1476	99.8	2.00E-20	174	59	33
AB073916	1476	85.9	3.00E-16	172	57	33
AE005755	12263	99	3.00E-20	292	72	24
AE005755	12263	98.6	4.00E-20	292	72	24
AE005755	12263	97.4	9.00E-20	292	70	23
M26945	1719	99	3.00E-20	171	58	33
M26945	1719	79.7	2.00E-14	124	46	37
AF040268	3447	99	3.00E-20	292	72	24
AF040268	3447	98.6	4.00E-20	292	72	24
AF040268	3447	95.5	3.00E-19	292	70	23
AE013020	10181	98.2	5.00E-20	290	83	28
BX294139	287650	98.2	5.00E-20	284	88	30
BX294139	287650	81.3	6.00E-15	143	57	39
AB018718	1191	98.2	5.00E-20	188	67	35
AB018718	1191	51.2	7.00E-06	91	27	29
AE017148	317022	97.8	7.00E-20	170	60	35
AE017148	317022	76.3	2.00E-13	297	74	24
BX294140	307050	97.4	9.00E-20	257	76	29
BX294140	307050	79.3	2.00E-14	250	70	28
BX294140	307050	34.3	0.89	120	34	28
BX294140	307050	33.1	2	116	34	29
X60746	1800	97.1	1.00E-19	170	57	33
X60746	1800	82.4	3.00E-15	311	78	25
AB103057	1500	97.1	1.00E-19	222	73	32
AB103057	1500	82.4	3.00E-15	174	65	31
AY304576	1533	96.3	2.00E-19	170	57	33
AY304576	1533	83.2	2.00E-15	311	79	25
AY714225	1533	96.3	2.00E-19	170	57	33
AY714225	1533	82	4.00E-15	311	78	25
AJ297530	1280	96.3	2.00E-19	251	76	30
AJ297530	1280	91.7	5.00E-18	270	73	27
AY155231	1533	96.3	2.00E-19	170	57	33
AY155231	1533	82.4	3.00E-15	311	78	25
AE000574	10042	96.3	2.00E-19	170	57	33
AE000574	10042	82.4	3.00E-15	311	78	25
AE001487	17223	96.3	2.00E-19	170	57	33
AE001487	17223	82.4	3.00E-15	311	78	25
L36137	1548	96.3	2.00E-19	172	69	40
L36137	1548	45.8	3.00E-04	69	33	47
L36137	1548	45.4	4.00E-04	60	31	51
AY319298	1533	95.9	2.00E-19	170	57	33

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY319298	1533	82	4.00E-15	311	78	25
AY278532	503	94.7	6.00E-19	164	59	35
Z25773	404	93.6	1.00E-18	154	59	38
BX294145	300350	92.8	2.00E-18	169	62	36
BX294145	300350	85.5	3.00E-16	126	55	43
AJ297534	1512	92.4	3.00E-18	208	66	31
AJ297534	1512	66.2	2.00E-10	252	61	24
X96435	3919	91.3	6.00E-18	313	77	24
X96435	3919	79.7	2.00E-14	313	75	23
X96435	3919	71.6	5.00E-12	324	75	23
AE009023	9808	91.3	6.00E-18	313	77	24
AE009023	9808	79.7	2.00E-14	313	75	23
AE009023	9808	71.6	5.00E-12	324	75	23
AE007989	10029	91.3	6.00E-18	313	77	24
AE007989	10029	79.7	2.00E-14	313	75	23
AE007989	10029	71.6	5.00E-12	324	75	23
U95165	21846	91.3	6.00E-18	313	77	24
U95165	21846	79.7	2.00E-14	313	75	23
U95165	21846	71.6	5.00E-12	324	75	23
U95165	21846	53.5	1.00E-06	256	60	23
U95165	21846	46.2	2.00E-04	140	34	24
X80701	4423	91.3	6.00E-18	313	77	24
X80701	4423	79.7	2.00E-14	313	75	23
X80701	4423	71.6	5.00E-12	324	75	23
AB110835	909	90.5	1.00E-17	301	81	26
L38478	1446	90.5	1.00E-17	150	51	34
U17575	2803	90.5	1.00E-17	200	57	28
U17575	2803	56.6	2.00E-07	146	47	32
AE001699	13774	89.7	2.00E-17	248	63	25
AE014292	1207381	88.6	4.00E-17	298	76	25
U42432	305	88.6	4.00E-17	87	45	51
AF019251	3817	88.6	4.00E-17	298	76	25
AY751740	1595	87.4	9.00E-17	142	52	36
AY751740	1595	63.9	1.00E-09	94	34	36
AE009654	10807	86.7	2.00E-16	298	75	25
BA000012	7036071	84.7	6.00E-16	329	75	22
BA000012	7036071	59.7	2.00E-08	356	80	22
AB110836	909	84.3	7.00E-16	92	44	47
U42431	305	84	1.00E-15	87	43	49
J01556	1193	82.4	3.00E-15	298	70	23
AJ418317	1384	79	3.00E-14	149	49	32
AJ418317	1384	63.9	1.00E-09	109	39	35
AJ418316	1384	79	3.00E-14	149	49	32
AJ418316	1384	63.9	1.00E-09	109	39	35
AJ418322	1376	77.8	7.00E-14	136	45	33
AJ418322	1376	67.8	7.00E-11	294	70	23
AJ418321	1376	77.8	7.00E-14	136	45	33
AJ418321	1376	65.9	3.00E-10	294	69	23
AJ418320	1377	77.8	7.00E-14	136	45	33
AJ418320	1377	65.9	3.00E-10	294	69	23
AJ418319	1377	77.8	7.00E-14	136	45	33
AJ418319	1377	65.9	3.00E-10	294	69	23
AJ418318	1377	77.8	7.00E-14	136	45	33
AJ418318	1377	65.9	3.00E-10	294	69	23
AY134860	420	77.4	9.00E-14	74	38	51
AJ297531	1299	77.4	9.00E-14	315	74	23
AB035615	600	77.4	9.00E-14	134	46	34
AB035614	600	77.4	9.00E-14	134	46	34
AB035613	600	77.4	9.00E-14	134	46	34
AF398973	437	77	1.00E-13	158	53	33
AB091714	600	77	1.00E-13	134	46	34
AB091713	600	77	1.00E-13	134	46	34
AB091712	600	77	1.00E-13	134	46	34
AB091711	600	77	1.00E-13	134	46	34
AB091710	600	77	1.00E-13	134	46	34
AB091709	600	77	1.00E-13	134	46	34
AB091708	600	77	1.00E-13	134	46	34
AB091707	600	77	1.00E-13	134	46	34

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AB091706	600	77	1.00E-13	134	46	34
AB091705	600	77	1.00E-13	134	46	34
AB091704	600	77	1.00E-13	134	46	34
AB091703	600	77	1.00E-13	134	46	34
AB091702	600	77	1.00E-13	134	46	34
AB091701	600	77	1.00E-13	134	46	34
AB091700	600	77	1.00E-13	134	46	34
AB037130	600	77	1.00E-13	134	46	34
AB037129	600	77	1.00E-13	134	46	34
AB037128	600	77	1.00E-13	134	46	34
AB037127	600	77	1.00E-13	134	46	34
AY505350	209	76.6	2.00E-13	69	39	56
AB052665	600	75.9	3.00E-13	134	45	33
AB035621	600	75.9	3.00E-13	134	45	33
AB035620	600	75.9	3.00E-13	134	46	33
AB035619	600	75.9	3.00E-13	134	45	33
AB035618	600	75.9	3.00E-13	134	45	33
AB035617	600	75.9	3.00E-13	134	45	33
AB035616	600	75.9	3.00E-13	134	45	33
AB035612	600	75.9	3.00E-13	134	45	33
AB035611	600	75.9	3.00E-13	134	45	33
AB035610	600	75.9	3.00E-13	134	45	33
AB035609	600	75.9	3.00E-13	134	46	33
AB035608	600	75.9	3.00E-13	134	45	33
AB035607	600	75.9	3.00E-13	134	45	33
AB035606	600	75.9	3.00E-13	134	45	33
AB035605	600	75.9	3.00E-13	134	45	33
AB035604	600	75.9	3.00E-13	134	45	33
AB035603	600	75.9	3.00E-13	134	45	33
AB035602	600	75.9	3.00E-13	134	45	33
AB035601	600	75.9	3.00E-13	134	45	33
AB035600	600	75.9	3.00E-13	134	45	33
AB035599	600	75.9	3.00E-13	134	45	33
AB035598	600	75.9	3.00E-13	134	45	33
AB035597	600	75.9	3.00E-13	134	45	33
AB035596	600	75.9	3.00E-13	134	45	33
AB035595	600	75.9	3.00E-13	134	45	33
AB091808	597	75.5	3.00E-13	133	45	33
AB091806	597	75.5	3.00E-13	133	45	33
AB178780	597	75.5	3.00E-13	133	45	33
AB178779	597	75.5	3.00E-13	133	45	33
AB178335	597	75.5	3.00E-13	133	45	33
AB178334	597	75.5	3.00E-13	133	45	33
AB091812	597	75.1	5.00E-13	133	45	33
AB091811	597	75.1	6.00E-13	133	45	33
AB091810	597	75.1	5.00E-13	133	46	33
AB091809	597	75.1	5.00E-13	133	45	33
AB091805	597	75.1	5.00E-13	133	45	33
AB178333	597	75.1	5.00E-13	133	45	33
AB091715	600	74.7	6.00E-13	134	45	33
BX571659	349970	74.3	8.00E-13	278	65	23
AB109246	596	74.3	8.00E-13	133	44	33
AB109245	596	74.3	8.00E-13	133	44	33
AB109244	596	74.3	8.00E-13	133	44	33
AB109243	596	74.3	8.00E-13	133	44	33
AB109242	596	74.3	8.00E-13	133	44	33
AB109241	596	74.3	8.00E-13	133	44	33
AB091814	597	73.9	1.00E-12	133	44	33
AB091813	597	73.9	1.00E-12	133	44	33
AB091807	597	73.9	1.00E-12	133	44	33
AB189460	597	73.9	1.00E-12	133	44	33
AB178331	597	73.9	1.00E-12	133	44	33
AB178332	597	73.9	1.00E-12	133	44	33
AB178330	597	73.9	1.00E-12	133	44	33
AB178329	597	73.9	1.00E-12	133	44	33
AB178328	597	73.9	1.00E-12	133	44	33
AB178327	597	73.9	1.00E-12	133	44	33
AB178326	597	73.9	1.00E-12	133	44	33

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AB178325	597	73.9	1.00E-12	133	44	33
AY278543	479	73.2	2.00E-12	162	54	33
AB189459	597	72	4.00E-12	133	43	32
CR354386	888	71.6	5.00E-12	294	67	22
AF072133	582	71.2	7.00E-12	100	41	41
AY278539	474	71.2	7.00E-12	160	53	33
AY278536	463	71.2	7.00E-12	160	53	33
AY278544	468	69.7	2.00E-11	159	52	32
CR354387	852	69.7	2.00E-11	284	61	21
AF030241	751	68.9	3.00E-11	186	50	26
AF030241	751	38.5	0.047	49	20	40
U85622	1105	68.9	3.00E-11	288	68	23
AL139076	317511	68.6	4.00E-11	288	66	22
AF461538	7599	68.2	6.00E-11	257	63	24
AY278541	466	67.4	9.00E-11	158	52	32
U26705	641	67.4	9.00E-11	221	58	26
U26704	641	67.4	9.00E-11	221	58	26
AF398975	351	67	1.00E-10	129	46	35
AF398974	351	67	1.00E-10	129	46	35
AE017253	302836	66.6	2.00E-10	285	65	22
V01370	1149	66.2	2.00E-10	37	34	91
AF398982	378	65.1	5.00E-10	130	41	31
AF398981	378	65.1	5.00E-10	130	41	31
AF398976	378	65.1	5.00E-10	130	42	32
AE001695	13302	65.1	5.00E-10	256	62	24
AF030240	766	63.5	1.00E-09	202	51	25
AF030240	766	38.5	0.047	49	20	40
AE001240	14244	63.2	2.00E-09	268	60	22
AY342020	584	63.2	2.00E-09	190	50	26
AL591784	300000	62.4	3.00E-09	321	68	21
AL591784	300000	50.4	1.00E-05	87	29	33
AL591784	300000	45.8	3.00E-04	245	56	22
AL591784	300000	40	0.016	87	24	27
AJ297535	949	62.4	3.00E-09	141	46	32
AJ297535	949	40.4	1.00E-04	57	26	45
AJ297535	949	31.2	1.00E-04	78	21	26
L49337	19824	62	4.00E-09	321	65	20
L49337	19824	50.4	1.00E-05	149	43	28
L49337	19824	45.1	5.00E-04	146	38	26
L49337	19824	40	0.016	87	24	27
AF264897	608	61.2	7.00E-09	208	52	25
AF264883	608	61.2	7.00E-09	208	52	25
AY342021	584	61.2	7.00E-09	190	49	25
AY342019	584	61.2	7.00E-09	190	48	25
AF264899	608	60.8	9.00E-09	208	51	24
AF264898	608	60.8	9.00E-09	208	51	24
AF264896	608	60.5	1.00E-08	208	50	24
AF264895	608	60.5	1.00E-08	208	50	24
AF264894	608	60.5	1.00E-08	208	50	24
AF264893	608	60.5	1.00E-08	208	50	24
AF264892	608	60.5	1.00E-08	208	50	24
AF264891	608	60.5	1.00E-08	208	50	24
AF264890	608	60.5	1.00E-08	208	50	24
AF264888	608	60.5	1.00E-08	208	50	24
AF264887	608	60.5	1.00E-08	208	50	24
AY342027	584	60.5	1.00E-08	190	48	25
AY342026	584	60.5	1.00E-08	190	48	25
AY342025	584	60.5	1.00E-08	190	48	25
AY342024	584	60.5	1.00E-08	190	48	25
AY342023	584	60.5	1.00E-08	190	48	25
AY342022	584	60.5	1.00E-08	190	48	25
AY342018	584	60.5	1.00E-08	190	48	25
AB001703	584	60.5	1.00E-08	190	48	25
AB001701	584	60.5	1.00E-08	190	48	25
AB001700	584	60.5	1.00E-08	190	48	25
AF398984	378	60.1	2.00E-08	124	41	33
AF398983	378	60.1	2.00E-08	124	41	33
AF264886	608	60.1	2.00E-08	208	49	23

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AE007721	8198	60.1	2.00E-08	289	65	22
AE007721	8198	42.4	0.003	310	69	22
AF264889	608	60.1	2.00E-08	208	49	23
AF264885	608	60.1	2.00E-08	208	49	23
AF264882	608	60.1	2.00E-08	208	49	23
AF264881	608	60.1	2.00E-08	208	49	23
AF264880	608	60.1	2.00E-08	208	49	23
AF264879	608	60.1	2.00E-08	208	49	23
AF398980	378	59.7	2.00E-08	138	44	31
AF398979	378	59.7	2.00E-08	138	44	31
AF398978	378	59.7	2.00E-08	138	44	31
AF398977	378	59.7	2.00E-08	138	44	31
AB001702	584	59.7	2.00E-08	190	48	25
AF264884	608	59.3	3.00E-08	208	49	23
AF264901	602	58.5	4.00E-08	206	50	24
AB018725	537	58.5	4.00E-08	69	29	42
AB018723	408	58.5	4.00E-08	69	29	42
M21445	867	58.5	4.00E-08	46	28	60
M21445	867	41.6	0.006	307	79	25
AY083505	621	58.2	6.00E-08	161	41	25
AY083504	621	58.2	6.00E-08	161	41	25
AJ297537	384	57.8	8.00E-08	64	28	43
AF264900	608	57.8	8.00E-08	208	51	24
AY450560	570	57.4	1.00E-07	185	47	25
AY278538	432	57	1.00E-07	149	47	31
AY278533	417	57	1.00E-07	135	41	30
U62056	2236	56.2	2.00E-07	47	27	57
AJ297536	340	52.8	2.00E-07	43	27	62
AJ297536	340	28.5	2.00E-07	31	13	41
AF332547	19758	55.8	3.00E-07	132	36	27
M34710	684	55.8	3.00E-07	63	27	42
AJ251711	1260	55.1	5.00E-07	193	48	24
AJ251711	1260	39.7	0.021	72	22	30
AB018721	282	55.1	5.00E-07	49	23	46
AE011584	11491	54.7	6.00E-07	110	34	30
AY083503	615	54.7	6.00E-07	156	41	26
AY083502	615	54.7	6.00E-07	156	41	26
AE017300	358408	54.7	6.00E-07	110	34	30
BX640415	347071	54.7	6.00E-07	136	43	31
Y15093	506	53.9	1.00E-06	159	39	24
AB018731	363	53.9	1.00E-06	92	32	34
AB018729	363	53.9	1.00E-06	92	32	34
AB018727	369	53.9	1.00E-06	92	32	34
AE009025	11897	53.5	1.00E-06	256	60	23
AE009025	11897	46.2	2.00E-04	140	34	24
AE007991	9626	53.5	1.00E-06	256	60	23
AE007991	9626	46.2	2.00E-04	140	34	24
AB018713	369	53.5	1.00E-06	108	33	30
AF515473	528	53.1	2.00E-06	92	37	40
AF515473	528	49.7	2.00E-05	132	41	31
AY357714	479	52.4	3.00E-06	150	40	26
AY362359	436	52	4.00E-06	144	38	26
Y15088	506	52	4.00E-06	159	38	23
U26679	1573	52	4.00E-06	108	32	29
AF497995	544	51.6	5.00E-06	181	44	24
AB018715	468	51.6	5.00E-06	88	27	30
BX572605	349746	50.8	9.00E-06	284	69	24
BX572605	349746	44.7	7.00E-04	194	49	25
BX572600	349640	50.8	9.00E-06	284	70	24
M57565	3608	50.4	1.00E-05	87	29	33
M57565	3608	45.8	3.00E-04	245	56	22
M24526	3530	50.4	1.00E-05	149	43	28
M24526	3530	42	0.004	87	23	26
AY533375	7214	49.3	3.00E-05	134	34	25
AY533375	7214	48.5	5.00E-05	130	34	26
AB018717	234	48.9	3.00E-05	74	28	37
D26168	866	47.8	8.00E-05	24	24	100
D26167	832	47.8	8.00E-05	24	24	100

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AY366539	426	47	1.00E-04	132	36	27
AE004539	25022	46.6	2.00E-04	134	34	25
AY007305	1233	46.6	2.00E-04	116	29	25
AF408410	423	46.2	2.00E-04	126	35	27
AJ311998	235	46.2	2.00E-04	71	25	35
AJ311997	235	46.2	2.00E-04	71	25	35
AJ311996	235	46.2	2.00E-04	71	25	35
AJ311995	235	46.2	2.00E-04	71	25	35
AJ311993	235	46.2	2.00E-04	71	25	35
AE001532	11113	46.2	2.00E-04	149	40	26
AF015108	267	46.2	2.00E-04	77	21	27
Y15098	477	45.8	3.00E-04	139	33	23
Y15095	463	45.8	3.00E-04	139	33	23
Y15094	481	45.8	3.00E-04	139	33	23
Y15091	463	45.8	3.00E-04	139	33	23
AF015109	267	45.8	3.00E-04	77	21	27
AY365212	402	45.4	4.00E-04	132	35	26
Y15101	490	45.4	4.00E-04	139	33	23
Y15099	466	45.4	4.00E-04	139	33	23
Y15097	479	45.4	4.00E-04	139	33	23
Y15092	463	45.4	4.00E-04	139	33	23
Y15090	473	45.4	4.00E-04	139	33	23
Y15089	478	45.4	4.00E-04	139	33	23
AF116904	467	45.4	4.00E-04	143	36	25
Y15100	456	45.1	5.00E-04	139	33	23
X89239	1310	45.1	5.00E-04	105	29	27
AF228032	476	45.1	5.00E-04	146	37	25
D12510	832	45.1	6.00E-04	24	23	95
AY226590	321	44.7	7.00E-04	94	24	25
BX571966	3173005	44.7	7.00E-04	292	64	21
BX571966	3173005	42.7	0.002	320	69	21
BX571966	3173005	40.4	0.012	278	59	21
BX571966	3173005	40.4	0.012	291	65	22
BX571966	3173005	39.3	0.028	302	59	19
AF228034	476	44.7	7.00E-04	146	37	25
AF228033	476	44.7	7.00E-04	146	37	25
AF354560	321	44.7	7.00E-04	94	24	25
AF354559	321	44.7	7.00E-04	94	24	25
AF354558	321	44.7	7.00E-04	94	24	25
AF355599	321	44.7	7.00E-04	94	24	25
Y15096	480	44.3	9.00E-04	139	33	23
AE006319	10302	44.3	9.00E-04	287	50	17
AF119150	18605	44.3	9.00E-04	228	52	22
M33808	852	44.3	9.00E-04	30	21	70
M33808	852	37.4	0.1	31	18	58
AE004223	24353	43.9	0.001	228	52	22
AF354561	321	43.9	0.001	94	24	25
AF015104	267	43.9	0.001	77	21	27
AY226588	321	43.5	0.001	91	28	30
AY226587	321	43.5	0.001	91	28	30
AF354554	321	43.5	0.001	91	28	30
AF354553	321	43.5	0.001	91	28	30
AF354548	321	43.5	0.001	91	28	30
AF015105	267	43.5	0.001	77	20	25
AF015101	267	43.5	0.001	77	20	25
AF015097	267	43.5	0.001	77	20	25
AF015089	267	43.5	0.001	77	20	25
AY226589	321	43.1	0.002	91	27	29
X51740	1766	43.1	0.002	21	21	100
BA000038	1857073	43.1	0.002	289	63	21
BA000038	1857073	33.1	2	120	30	25
AF354555	321	43.1	0.002	91	27	29
AF354550	321	43.1	0.002	91	27	29
AF354549	321	43.1	0.002	91	27	29
AF354547	321	43.1	0.002	91	27	29
AF354546	321	43.1	0.002	91	27	29
X89238	1310	42.7	0.002	99	27	27
AF354552	321	42.7	0.002	81	26	32

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AF354551	321	42.7	0.002	81	26	32
AF015106	267	42.7	0.002	77	20	25
BX248358	348408	42.4	0.003	169	38	22
BX571658	346792	42.4	0.003	168	37	22
AL591982	295050	42.4	0.003	273	58	21
AF354557	321	42.4	0.003	81	25	30
AF354556	321	42.4	0.003	81	25	30
AY007306	1236	42.4	0.003	116	27	23
AF015103	267	42.4	0.003	77	20	25
AL935252	343050	42	0.004	285	64	22
AL646086	92509	42	0.004	264	60	22
AL646086	92509	36.2	0.23	260	56	21
AL646086	92509	35.8	0.31	247	57	23
AJ311994	206	41.6	0.006	65	24	36
J01801	1094	41.6	0.006	20	20	100
AF015095	267	41.6	0.006	74	24	32
AF015090	267	41.6	0.006	74	24	32
M58145	224	41.6	0.006	20	20	100
J01800	349	41.6	0.006	20	20	100
BA000018	2814816	41.2	0.007	332	72	21
AF015115	267	41.2	0.007	74	23	31
AF015113	267	41.2	0.007	74	23	31
AF015112	267	41.2	0.007	74	23	31
AF015102	267	41.2	0.007	74	23	31
AF015100	267	41.2	0.007	74	23	31
AF015099	267	41.2	0.007	74	23	31
AF015098	267	41.2	0.007	74	23	31
AF015096	267	41.2	0.007	74	23	31
AF015094	267	41.2	0.007	74	23	31
AF015091	267	41.2	0.007	74	23	31
AP003362	346300	41.2	0.007	332	72	21
Z54217	2262	40.8	0.009	20	20	100
AY575004	136	40.8	0.009	38	18	47
AY575002	136	40.8	0.009	38	18	47
AY575001	136	40.8	0.009	38	18	47
AF270112	3067	40.8	0.009	262	58	22
AF269857	3319	40.8	0.009	262	58	22
AF269729	3867	40.8	0.009	262	58	22
S62783	193	40.4	0.012	32	20	62
S62780	191	40.4	0.012	32	20	62
S62779	191	40.4	0.012	32	20	62
S62776	191	40.4	0.012	32	20	62
S62775	192	40.4	0.012	32	20	62
S62773	200	40.4	0.012	32	20	62
AF525505	11500	40.4	0.012	278	64	23
AF525505	11500	39.3	0.028	321	76	23
AY575003	136	40.4	0.012	38	18	47
AF015114	267	40.4	0.012	64	21	32
AF015110	267	40.4	0.012	64	21	32
AF015107	267	40.4	0.012	64	21	32
AF015093	267	40.4	0.012	64	21	32
AF015092	267	40.4	0.012	64	21	32
CP000024	1796226	40	0.016	302	64	21
CP000023	1796846	40	0.016	302	64	21
J01607	351	40	0.016	20	18	90
U96166	19841	39.7	0.021	278	48	17
U96239	390	39.7	0.021	97	26	26
U96238	390	39.7	0.021	97	26	26
U96237	390	39.7	0.021	97	26	26
U96236	390	39.7	0.021	97	26	26
U96235	390	39.7	0.021	97	26	26
AY374137	491	39.7	0.021	97	26	26
AY374135	485	39.7	0.021	97	26	26
AY374134	485	39.7	0.021	97	26	26
AY374133	485	39.7	0.021	97	26	26
AY374132	485	39.7	0.021	97	26	26
BX571857	2799802	39.3	0.028	283	66	23
BA000033	2820462	39.3	0.028	283	66	23

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
BA000033	2820462	34.3	0.89	299	60	20
U96234	390	39.3	0.028	97	26	26
AL596163	231450	38.9	0.036	261	57	21
U25727	108	38.9	0.036	34	21	61
AY708387	1232	38.5	0.047	260	55	21
AY708385	1250	38.5	0.047	260	55	21
AF386506	441	38.5	0.047	95	25	26
AF386505	442	38.5	0.047	95	25	26
AE016747	300892	38.5	0.047	169	43	25
AE016747	300892	34.7	0.68	302	60	19
U25820	108	38.5	0.047	36	19	52
AF015111	267	38.5	0.047	74	22	29
AE005766	10091	38.1	0.062	73	21	28
Z31376	4192	38.1	0.062	29	19	65
X86999	186	37.7	0.08	43	16	37
X86998	186	37.7	0.08	43	16	37
X86997	186	37.7	0.08	43	16	37
X86996	186	37.7	0.08	43	16	37
X86995	186	37.7	0.08	43	16	37
X86994	186	37.7	0.08	43	16	37
X86993	186	37.7	0.08	43	16	37
X86992	186	37.7	0.08	43	16	37
X86990	186	37.7	0.08	43	16	37
X86989	186	37.7	0.08	43	16	37
X86988	186	37.7	0.08	43	16	37
X86987	186	37.7	0.08	43	16	37
X86986	186	37.7	0.08	43	16	37
X86985	186	37.7	0.08	43	16	37
X86984	186	37.7	0.08	43	16	37
X86983	186	37.7	0.08	43	16	37
X86982	186	37.7	0.08	43	16	37
X86981	186	37.7	0.08	43	16	37
X86980	186	37.7	0.08	43	16	37
X86979	186	37.7	0.08	43	16	37
X87005	186	37.7	0.08	43	16	37
X87004	186	37.7	0.08	43	16	37
X87003	186	37.7	0.08	43	16	37
X87002	186	37.7	0.08	43	16	37
X87001	186	37.7	0.08	43	16	37
X87000	186	37.7	0.08	43	16	37
AL596172	248050	37.7	0.08	292	64	21
AE004867	15356	36.6	0.18	201	49	24
X86991	186	36.6	0.18	43	15	34
AY603345	483	36.6	0.18	166	34	20
AY603344	483	36.6	0.18	166	34	20
AY603342	483	35.6	0.18	166	34	20
AY278535	360	36.6	0.18	115	31	26
AE016827	2314078	35.2	0.23	273	58	21
AE016827	2314078	36.2	0.23	273	58	21
AE016827	2314078	35.8	0.31	274	61	22
AY603343	483	36.2	0.23	166	34	20
AY458638	19060	36.2	0.23	146	39	26
AE016968	302070	35.8	0.31	183	40	21
BA000019	6413771	35.8	0.31	286	59	20
M12293	181	35.8	0.31	17	17	100
AF459093	6852	35.4	0.4	259	58	21
BX294135	340750	35.4	0.4	240	52	21
AY278547	377	35.4	0.4	129	35	27
AE016940	304230	35	0.52	150	44	29
AE001129	10845	35	0.52	77	18	23
AY275838	27297	35	0.52	239	49	20
AF045472	7263	34.7	0.68	95	25	26
AE001578	29838	34.7	0.68	114	30	26
BA000016	3031430	34.7	0.68	232	49	21
BA000045	4659019	34.7	0.68	73	24	32
U40259	8013	34.7	0.68	95	25	26
AE016864	310325	34.3	0.89	128	31	24
AE014627	10029	34.3	0.89	271	54	19

Fig. 25A-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AE017201	300478	33.9	1.2	125	28	22
AE011395	10368	33.9	1.2	59	18	30
AE015945	89370	33.9	1.2	103	24	23
AL935255	269050	33.9	1.2	299	58	19
CR378673	349814	33.9	1.2	73	16	21
AE017310	300343	33.9	1.2	171	36	21
AB015410	3519	33.9	1.2	283	55	19
AE016858	312839	33.1	2	162	41	25
AE016813	336182	33.1	2	120	30	25
gi|42627766	3786	33.1	2	62	19	30
AE016748	300029	33.1	2	148	30	20
CR378667	349080	33.1	2	137	31	22
AF113610	3246	33.1	2	240	48	20
AF322013	230573	33.1	2	62	19	30
D90775	16902	33.1	2	147	37	25
D90774	18700	33.1	2	147	37	25
CR378676	343529	33.1	2	107	27	25
AE017135	291326	32.7	2.6	290	61	21
AY708386	1203	32.7	2.6	254	52	20
AJ414152	313050	32.7	2.6	290	61	21
AE013773	10520	32.7	2.6	290	61	21
AE005723	10573	32.7	2.6	235	47	20
AE017240	299986	32.7	2.6	70	21	30

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S

Fig. 25B

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
CAE53942	349	386	1.00E-106	348	215	61
CAD60547	349	385	1.00E-106	348	214	61
AAP13297	349	384	1.00E-106	348	213	61
CAE53943	349	383	1.00E-105	348	214	61
CAD56695	349	382	1.00E-105	348	213	61
AAU90046	271	379	1.00E-104	284	202	71
CAA62509	313	369	1.00E-101	313	206	65
BAA06987	348	367	1.00E-101	356	214	60
NP_929221	355	364	1.00E-100	355	207	58
AAA62397	367	356	1.00E-97	367	213	58
AAA62396	365	355	2.00E-97	365	211	57
ZP_00169997361		343	1.00E-93	361	201	55
AAT81649	505	336	2.00E-91	178	177	99
AAT81649	505	194	8.00E-49	106	104	98
AAT81648	505	336	2.00E-91	178	177	99
AAT81648	505	194	8.00E-49	106	104	98
AAT81622	505	336	2.00E-91	178	177	99
AAT81622	505	197	7.00E-50	227	126	55
AAT81621	505	336	2.00E-91	178	177	99
AAT81621	505	195	4.00E-49	227	125	55
AAT81620	505	336	2.00E-91	178	177	99
AAT81620	505	196	3.00E-49	227	126	55
AAT81619	505	336	2.00E-91	178	177	99
AAT81619	505	194	8.00E-49	106	104	98
AAT81618	505	336	2.00E-91	178	177	99
AAT81618	505	194	8.00E-49	106	104	98
AAT81617	505	336	2.00E-91	178	177	99
AAT81617	505	194	8.00E-49	106	104	98
AAT81614	505	336	2.00E-91	178	177	99
AAT81614	505	197	1.00E-49	227	126	55
AAT81613	505	336	2.00E-91	178	177	99
AAT81613	505	194	6.00E-49	227	125	55
AAT81612	505	336	2.00E-91	178	177	99
AAT81612	505	197	1.00E-49	227	126	55
AAR10745	508	336	2.00E-91	178	177	99
AAR10745	508	197	7.00E-50	324	142	43
AAR10628	504	336	2.00E-91	178	177	99
AAR10628	504	194	6.00E-49	309	141	45
AAR10624	508	336	2.00E-91	178	177	99
AAR10624	508	194	8.00E-49	106	104	98
AAR10622	508	336	2.00E-91	178	177	99
AAR10622	508	194	8.00E-49	106	104	98
AAR10621	508	336	2.00E-91	178	177	99
AAR10621	508	194	8.00E-49	106	104	98
AAR10619	505	336	2.00E-91	178	177	99
AAR10619	505	197	7.00E-50	227	126	55
AAR10618	505	336	2.00E-91	178	177	99
AAR10618	505	197	7.00E-50	227	126	55
AAR10616	505	336	2.00E-91	178	177	99
AAR10616	505	194	8.00E-49	106	104	98
AAR10610	505	336	2.00E-91	178	177	99
AAR10610	505	194	8.00E-49	106	104	98
AAR10609	504	336	2.00E-91	178	177	99
AAR10609	504	193	2.00E-48	106	103	97
AAR10608	504	336	2.00E-91	178	177	99
AAR10608	504	193	2.00E-48	106	103	97
AAR10604	505	336	2.00E-91	178	177	99
AAR10604	505	194	8.00E-49	106	104	98
O52959	505	336	2.00E-91	178	177	99
O52959	505	194	8.00E-49	106	104	98
AAA27092	505	336	2.00E-91	178	177	99
AAA27092	505	194	8.00E-49	106	104	98
AAA27090	505	336	2.00E-91	178	177	99
AAA27090	505	194	8.00E-49	106	104	98
AAA27085	494	336	2.00E-91	178	177	99
AAA27085	494	174	9.00E-43	95	93	97
AAA17863	508	336	2.00E-91	178	177	99
AAA17863	508	194	6.00E-49	227	125	55

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAA17862	505	336	2.00E-91	178	177	99
AAA17862	505	197	7.00E-50	227	126	55
AAA17859	508	336	2.00E-91	178	177	99
AAA17859	508	197	1.00E-49	305	140	45
AAR10747	505	335	4.00E-91	178	176	98
AAR10747	505	194	6.00E-49	227	125	55
AAA17865	508	335	4.00E-91	178	176	98
AAA17865	508	193	2.00E-48	106	103	97
AAR10749	504	334	5.00E-91	178	176	98
AAR10749	504	189	3.00E-47	106	101	95
AAR10748	504	334	5.00E-91	178	176	98
AAR10748	504	190	1.00E-47	280	139	49
AAR10594	505	334	5.00E-91	178	176	98
AAR10594	505	194	6.00E-49	227	125	55
AAT81624	504	334	7.00E-91	178	176	98
AAT81624	504	191	9.00E-48	301	136	45
AAT81623	504	334	7.00E-91	178	176	98
AAT81623	504	191	9.00E-48	301	136	45
CAA78794	504	334	7.00E-91	177	176	99
CAA78794	504	196	3.00E-49	227	126	55
CAA78781	504	334	7.00E-91	177	176	99
CAA78781	504	197	7.00E-50	227	126	55
CAA78780	504	334	7.00E-91	177	176	99
CAA78780	504	194	8.00E-49	106	104	98
CAA78779	507	334	7.00E-91	177	176	99
CAA78779	507	194	8.00E-49	106	104	98
CAA78778	504	334	7.00E-91	177	176	99
CAA78778	504	194	8.00E-49	106	104	98
CAA78777	504	334	7.00E-91	177	176	99
CAA78777	504	194	8.00E-49	106	104	98
CAA78776	504	334	7.00E-91	177	176	99
CAA78776	504	194	8.00E-49	106	104	98
CAA78775	504	334	7.00E-91	177	176	99
CAA78775	504	197	1.00E-49	227	126	55
CAA78774	504	334	7.00E-91	177	176	99
CAA78774	504	197	7.00E-50	227	126	55
CAA78773	507	334	7.00E-91	177	176	99
CAA78773	507	197	7.00E-50	324	142	43
S33187	504	334	7.00E-91	177	176	99
S33187	504	197	1.00E-49	227	126	55
AAA53497	507	334	7.00E-91	177	176	99
AAA53497	507	194	8.00E-49	106	104	98
AAA53495	504	334	7.00E-91	177	176	99
AAA53495	504	194	8.00E-49	106	104	98
AAA53491	507	334	7.00E-91	177	176	99
AAA53491	507	194	8.00E-49	106	104	98
AAA53490	504	334	7.00E-91	177	176	99
AAA53490	504	196	2.00E-49	227	126	55
AAT81603	505	333	9.00E-91	178	176	98
AAT81603	505	194	8.00E-49	106	104	98
AAA27088	505	333	9.00E-91	178	176	98
AAA27088	505	192	2.00E-48	106	103	97
JU0056	351	333	1.00E-90	354	196	55
AAA53493	465	330	7.00E-90	177	175	98
AAA53493	465	171	1.00E-41	91	91	100
AAR10625	504	330	1.00E-89	178	173	97
AAR10625	504	187	1.00E-46	227	120	52
AAA53496	503	328	4.00E-89	177	172	97
AAA53496	503	187	1.00E-46	227	120	52
YP_049831	290	327	8.00E-89	302	187	61
S78461	364	319	2.00E-86	365	203	55
NP_992909	369	318	5.00E-86	368	202	54
NP_405406	369	318	5.00E-86	368	202	54
AAO85383	369	315	2.00E-85	368	201	54
AAA64387	493	315	4.00E-85	166	165	99
AAA64387	493	194	8.00E-49	106	104	98
AAQ22673	488	311	4.00E-84	263	178	67
AAQ22673	488	160	1.00E-38	103	83	80

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAR10689	505	311	4.00E-84	244	175	71
AAR10689	505	175	5.00E-43	140	96	68
BAD16577	488	310	8.00E-84	273	180	65
BAD16577	488	166	3.00E-40	280	121	43
S78460	358	310	1.00E-83	359	194	54
AAQ22680	488	309	2.00E-83	263	177	67
AAQ22680	488	160	1.00E-38	103	83	80
AAL30165	487	308	4.00E-83	256	177	69
AAL30165	487	158	7.00E-38	103	82	79
CAD99230	464	308	5.00E-83	262	173	66
CAD99230	464	117	1.00E-25	75	59	78
AAR10691	505	308	5.00E-83	244	172	70
AAR10691	505	171	7.00E-42	140	94	67
AAR10690	505	308	5.00E-83	244	172	70
AAR10690	505	173	2.00E-42	140	95	67
AAQ22683	525	306	1.00E-82	299	184	61
AAQ22683	525	149	4.00E-35	92	76	82
BAD14980	524	306	1.00E-82	299	184	61
BAD14980	524	150	1.00E-35	92	77	83
AAQ22684	525	305	3.00E-82	299	184	61
AAQ22684	525	149	4.00E-35	92	76	82
AAB17947	585	305	3.00E-82	274	170	62
AAB17947	585	142	5.00E-33	115	74	64
S44982	524	305	4.00E-82	299	183	61
S44982	524	148	5.00E-35	92	75	82
AAG56938	585	305	4.00E-82	274	169	61
AAG56938	585	142	5.00E-33	115	74	64
AAQ22676	585	305	4.00E-82	274	169	61
AAQ22676	585	142	5.00E-33	115	74	64
AAP13300	585	305	4.00E-82	267	168	62
AAP13300	585	142	5.00E-33	115	74	64
AAF71897	585	305	4.00E-82	267	168	62
AAF71897	585	142	5.00E-33	115	74	64
AAQ22685	525	304	6.00E-82	299	183	61
AAQ22685	525	149	4.00E-35	92	76	82
AAF71901	585	304	7.00E-82	274	169	61
AAF71901	585	142	6.00E-33	115	74	64
C48658	584	303	2.00E-81	267	169	63
C48658	584	141	8.00E-33	115	73	63
BAD14967	423	301	6.00E-81	296	186	62
BAD14967	423	141	8.00E-33	87	75	86
AAP13299	548	300	1.00E-80	266	171	64
AAP13299	548	140	1.00E-32	102	69	67
AAP13321	555	299	2.00E-80	295	171	57
AAP13321	555	140	1.00E-32	116	71	61
B48658	595	298	3.00E-80	223	157	70
B48658	595	139	3.00E-32	255	106	41
AAQ22682	595	298	3.00E-80	223	157	70
AAQ22682	595	137	1.00E-31	113	71	62
AAQ22679	595	298	3.00E-80	223	157	70
AAQ22679	595	137	1.00E-31	113	71	62
NP_754230	595	298	3.00E-80	223	157	70
NP_754230	595	138	5.00E-32	255	106	41
AAP13331	568	298	3.00E-80	223	160	71
AAP13331	568	140	1.00E-32	114	74	64
AAP13305	595	298	3.00E-80	223	157	70
AAP13305	595	137	1.00E-31	113	71	62
BAA85086	568	298	3.00E-80	223	160	71
BAA85086	568	141	6.00E-33	270	104	38
CAD97427	545	298	5.00E-80	246	163	66
CAD97427	545	91.3	1.00E-17	84	45	53
AAP13313	588	297	9.00E-80	219	162	73
AAP13313	588	142	3.00E-33	149	83	55
AAQ22674	447	296	1.00E-79	290	172	59
AAQ22674	447	135	3.00E-31	181	87	48
AAP13335	605	296	1.00E-79	222	157	70
AAP13335	605	139	3.00E-32	163	81	49
A48658	595	296	2.00E-79	223	156	69
A48658	595	135	5.00E-31	113	70	61
AAP13337	436	296	2.00E-79	300	175	58
AAP13337	436	135	6.00E-31	92	67	72
AAL30164	498	296	2.00E-79	178	155	87
AAL30164	498	155	3.00E-37	174	94	54
AAR97969	376	296	2.00E-79	223	159	71
BAA85089	565	296	2.00E-79	302	176	58
BAA85089	565	133	2.00E-30	102	66	64
AAP13309	554	296	2.00E-79	237	161	67
AAP13309	554	141	8.00E-33	295	105	35
AAF85764	554	296	2.00E-79	237	161	67
AAF85764	554	139	3.00E-32	293	104	35
AAQ22687	503	295	3.00E-79	178	155	87
AAQ22687	503	158	7.00E-38	265	111	41
AAP13324	545	295	3.00E-79	218	157	72
AAP13324	545	140	1.00E-32	172	85	49
AAP13324	545	32	7.10E+00	219	51	23
CAA85351	565	295	3.00E-79	222	156	70
CAA85351	565	133	2.00E-30	102	66	64
AAQ22689	557	295	3.00E-79	284	169	59
AAQ22689	557	141	8.00E-33	115	71	61
AAP13336	447	295	3.00E-79	274	171	62
AAP13336	447	134	1.00E-30	92	67	72
AAP13318	579	295	3.00E-79	236	161	68
AAP13318	579	140	1.00E-32	116	72	62
AAP13316	557	295	3.00E-79	284	169	59
AAP13316	557	142	5.00E-33	115	71	61
AAP13307	562	295	3.00E-79	257	168	65
AAP13307	562	142	3.00E-33	273	102	37
AAP13298	436	295	4.00E-79	291	174	59
AAP13298	436	135	6.00E-31	92	67	72
AAL30167	545	295	4.00E-79	218	157	72
AAL30167	545	140	1.00E-32	172	85	49
AAQ22681	447	294	6.00E-79	290	171	58
AAQ22681	447	137	1.00E-31	314	115	36
AAP13326	447	294	6.00E-79	290	171	58
AAP13326	447	137	2.00E-31	314	114	36
AAP13302	670	294	6.00E-79	247	162	65
AAP13302	670	147	2.00E-34	312	104	33
AAP13334	564	294	8.00E-79	222	156	70
AAP13334	564	133	2.00E-30	102	66	64
AAL30168	564	294	8.00E-79	222	156	70
AAL30168	564	132	4.00E-30	102	66	64
NP_707809	550	293	1.00E-78	202	154	76
NP_707809	550	140	1.00E-32	116	71	61
AAQ22690	440	293	1.00E-78	288	177	61
AAQ22690	440	137	2.00E-31	312	109	34
AAN34779	498	293	1.00E-78	178	153	85
AAN34779	498	155	3.00E-37	174	94	54
AAP13311	576	293	1.00E-78	299	171	57
AAP13311	576	142	4.00E-33	287	111	38
AAP13332	572	293	1.00E-78	229	160	69
AAP13332	572	144	1.00E-33	116	73	62
AAP13332	572	32	7.10E+00	221	44	19
AAP13306	550	293	1.00E-78	202	154	76
AAP13306	550	140	1.00E-32	116	71	61
AAF32260	550	293	1.00E-78	202	154	76
AAF32260	550	138	7.00E-32	276	102	36
AAQ22677	436	293	2.00E-78	291	169	58
AAQ22677	436	134	8E-31	92	67	72
AAP13328	559	292	2.00E-78	179	149	83
AAP13328	559	139	4.00E-32	113	69	61
AAP13320	443	291	4.00E-78	288	176	61
AAP13320	443	135	6.00E-31	315	107	33
AAN34780	498	291	5.00E-78	178	152	85
AAN34780	498	155	3.00E-37	174	94	54
AAR10708	413	291	5.00E-78	275	175	63
AAR10708	413	150	1E-35	100	79	79

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAR10698	421	291	5.00E-78	276	170	61
AAR10698	421	152	5.00E-36	102	79	77
BAA05151	568	291	5.00E-78	263	159	60
BAA05151	568	140	1.00E-32	114	74	64
AAQ22686	610	291	6.00E-78	191	151	79
AAQ22686	610	145	4.00E-34	287	109	37
AAP13322	570	291	6.00E-78	179	150	83
AAP13322	570	139	3.00E-32	234	88	37
AAP13310	613	291	6.00E-78	191	151	79
AAP13310	613	146	3.00E-34	285	109	38
CAD99229	453	291	6.00E-78	251	164	65
CAD99229	453	117	1.00E-25	75	59	78
BAA85087	570	290	1.00E-77	229	159	69
BAA85087	570	144	1.00E-33	116	73	62
BAA85087	570	32	7.10E+00	221	44	19
BAD14961	529	290	1.00E-77	296	177	59
BAD14961	529	151	8.00E-36	293	112	38
AAP13327	432	290	1.00E-77	286	169	59
AAP13327	432	136	2.00E-31	253	102	40
AAP13323	428	290	1.00E-77	267	166	62
AAP13323	428	134	1.00E-30	127	74	58
AAL30166	428	290	1.00E-77	267	166	62
AAL30166	428	131	7.00E-30	127	73	57
AAR10700	421	290	1.00E-77	271	170	62
AAR10700	421	152	5.00E-36	102	79	77
AAR10699	421	290	1.00E-77	271	170	62
AAR10699	421	152	5.00E-36	102	79	77
AAR10695	421	290	1.00E-77	175	153	87
AAR10696	421	289	2.00E-77	175	153	87
AAR10696	421	152	5.00E-36	102	79	77
AAR10694	421	289	2.00E-77	175	153	87
AAP13325	561	289	2.00E-77	233	162	69
AAP13325	561	150	1.00E-35	279	102	36
AAR10759	422	289	2.00E-77	284	175	61
AAR10759	422	150	1.00E-35	100	79	79
AAR10544	500	288	3.00E-77	208	157	75
AAR10544	500	155	4.00E-37	100	81	81
BAA05153	549	288	3.00E-77	234	159	67
BAA05153	549	135	6.00E-31	240	86	35
AAP13329	426	288	4.00E-77	258	164	63
AAP13329	426	138	7.00E-32	232	93	40
AAP13319	570	288	4.00E-77	179	149	83
AAP13319	570	139	4.00E-32	237	91	38
AAF32261	426	288	4.00E-77	258	164	63
AAF32261	426	136	3.00E-31	92	69	75
AAR10710	422	288	4.00E-77	237	164	69
AAR10710	422	148	5.00E-35	100	78	78
AAT81644	426	288	5.00E-77	214	161	75
AAT81644	426	150	1.00E-35	100	79	79
AAT81643	422	288	5.00E-77	214	161	75
AAT81643	422	148	5.00E-35	100	78	78
AAT81642	424	288	5.00E-77	214	161	75
AAT81642	424	150	1.00E-35	100	79	79
AAT81611	502	288	5.00E-77	220	160	72
AAT81611	502	157	1.00E-37	100	82	82
AAT81610	502	288	5.00E-77	220	160	72
AAT81610	502	157	1.00E-37	100	82	82
AAP13330	501	288	5.00E-77	220	156	70
AAP13330	501	134	1.00E-30	151	77	50
AAR10761	422	288	5.00E-77	214	161	75
AAR10761	422	148	5.00E-35	100	78	78
AAR10760	422	288	5.00E-77	214	161	75
AAR10760	422	150	1.00E-35	100	79	79
AAR10719	422	288	5.00E-77	214	161	75
AAR10719	422	150	1.00E-35	100	79	79
AAR10717	426	288	5.00E-77	214	161	75
AAR10717	426	151	8.00E-36	174	92	52
AAR10715	426	288	5.00E-77	214	161	75
AAR10715	426	149	2.00E-35	174	91	52
AAR10711	422	288	5.00E-77	214	161	75
AAR10711	422	150	1.00E-35	100	79	79
AAR10706	422	288	5.00E-77	214	161	75
AAR10706	422	150	1.00E-35	100	79	79
AAR10666	501	288	5.00E-77	216	158	73
AAR10666	501	156	2.00E-37	100	82	82
AAR10659	500	288	5.00E-77	208	157	75
AAR10659	500	156	2.00E-37	100	82	82
AAR10658	500	288	5.00E-77	208	157	75
AAR10658	500	156	2.00E-37	100	82	82
AAR10543	500	288	5.00E-77	208	157	75
AAR10543	500	154	7.00E-37	100	81	81
AAR10667	501	287	7.00E-77	216	158	73
AAR10667	501	156	2.00E-37	100	82	82
NP_416433	498	287	9.00E-77	177	146	82
NP_416433	498	149	4.00E-35	151	80	52
AAQ22678	426	287	9.00E-77	258	163	63
AAQ22678	426	138	7.00E-32	232	93	40
AAT81632	500	287	9.00E-77	206	157	76
AAT81632	500	152	4.00E-36	98	79	80
AAT81631	500	287	9.00E-77	198	154	77
AAT81631	500	156	2.00E-37	100	82	82
CAA35488	498	287	9.00E-77	177	146	82
CAA35488	498	151	6.00E-36	244	101	41
AAR10755	422	287	9.00E-77	211	159	75
AAR10755	422	150	1.00E-35	100	79	79
AAR10669	493	287	9.00E-77	198	154	77
AAR10669	493	156	2.00E-37	100	82	82
AAR10668	481	287	9.00E-77	245	162	66
AAR10668	481	156	2.00E-37	100	82	82
AAR10665	501	287	9.00E-77	206	157	76
AAR10665	501	156	2.00E-37	100	82	82
AAR10664	501	287	9.00E-77	206	157	76
AAR10664	501	154	7.00E-37	100	81	81
AAR10662	500	287	9.00E-77	206	157	76
AAR10662	500	156	2.00E-37	100	82	82
AAR10660	500	287	9.00E-77	198	154	77
AAR10660	500	156	2.00E-37	100	82	82
AAR10590	502	287	9.00E-77	220	160	72
AAR10590	502	157	1.00E-37	100	82	82
AAR10721	421	286	1.00E-76	175	152	86
AAR10721	421	150	1.00E-35	100	79	79
AAR10713	421	286	1.00E-76	175	152	86
AAR10713	421	150	1.00E-35	100	79	79
AAR10657	500	286	1.00E-76	198	154	77
AAR10657	500	152	4.00E-36	98	79	80
AAQ22675	426	286	2.00E-76	258	163	63
AAQ22675	426	136	2.00E-31	232	92	39
AAR10546	501	286	2.00E-76	206	157	76
AAR10546	501	156	2.00E-37	100	82	82
BAD14977	516	286	2.00E-76	291	170	58
BAD14977	516	146	3.00E-34	95	75	78
AAT81609	502	286	2.00E-76	220	159	72
AAT81609	502	157	1.00E-37	100	82	82
AAR10562	499	286	2.00E-76	209	158	75
AAR10562	499	158	5.00E-38	338	127	37
AAR10561	499	286	2.00E-76	209	158	75
AAR10561	499	158	7.00E-38	338	127	37
AAR10559	499	286	2.00E-76	209	158	75
AAR10559	499	158	7.00E-38	338	127	37
AAR10558	499	286	2.00E-76	209	158	75
AAR10558	499	157	9.00E-38	338	127	37
AAR10557	499	286	2.00E-76	209	158	75
AAR10557	499	158	7.00E-38	338	127	37
AAF32259	420	285	4.00E-76	269	160	59
AAF32259	420	135	6.00E-31	138	77	55
AAR10714	421	285	4.00E-76	175	151	86

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAR10714	421	150	1.00E-35	100	79	79
AAR10572	495	285	4.00E-76	306	176	57
AAR10572	495	149	3.00E-35	89	76	85
NP_841632	275	285	5.00E-76	297	159	63
CAD97429	408	285	5.00E-76	179	145	81
CAD97429	408	85.7	2.00E-16	285	82	28
AAT81605	495	285	5.00E-76	306	176	57
AAT81605	495	151	6.00E-36	96	78	81
AAP13303	420	285	5.00E-76	189	147	77
AAP13303	420	137	2.00E-31	138	78	55
AAR10720	422	285	5.00E-76	211	158	74
AAR10720	422	150	1.00E-35	100	79	79
AAR10575	495	285	5.00E-76	306	175	57
AAR10575	495	151	6.00E-36	96	78	81
AAR10574	495	285	5.00E-76	306	176	57
AAR10574	495	151	6.00E-36	96	78	81
AAR10515	501	285	5.00E-76	175	150	85
AAR10515	501	155	4.00E-37	100	81	81
AAR10729	501	284	6.00E-76	215	157	73
AAR10729	501	152	4.00E-36	98	79	80
AAR10728	501	284	6.00E-76	215	157	73
AAR10728	501	152	4.00E-36	96	79	80
AAR10716	426	284	6.00E-76	214	160	74
AAR10716	426	149	2.00E-35	174	91	52
AAR10702	499	284	6.00E-76	192	152	79
AAR10702	499	153	2.00E-36	100	80	80
CAA27130	509	284	8.00E-76	175	150	85
CAA27130	509	149	4.00E-35	91	76	83
NP_456520	506	284	8.00E-76	175	150	85
NP_456520	506	149	4.00E-35	91	76	83
AAQ22688	420	284	8.00E-76	189	147	77
AAQ22688	420	135	6.00E-31	138	77	55
AAT81639	506	284	8.00E-76	175	150	85
AAT81639	506	149	4.00E-35	91	76	83
AAT81608	506	284	8.00E-76	175	150	85
AAT81608	506	149	4.00E-35	91	76	83
AAT81607	506	284	8.00E-76	175	150	85
AAT81607	506	150	1.00E-35	91	77	84
AAR10646	419	284	8.00E-76	175	150	85
AAR10646	419	149	4.00E-35	91	76	83
AAR10588	506	284	8.00E-76	175	150	85
AAR10588	506	150	1.00E-35	91	77	84
AAR10514	506	284	8.00E-76	175	150	85
AAR10514	506	150	1.00E-35	91	77	84
S09638	505	284	8.00E-76	175	150	85
S09638	505	149	4.00E-35	91	76	83
NP_461698	506	283	1.00E-75	232	160	68
NP_461698	506	155	4.00E-37	100	81	81
YP_151805	506	283	1.00E-75	279	165	59
YP_151805	506	155	4.00E-37	100	81	81
AAR10471	501	283	1.00E-75	295	169	57
AAR10471	501	151	6.00E-36	98	78	79
AAR10484	506	283	1.00E-75	232	160	68
AAR10484	506	155	4.00E-37	100	81	81
CAB65960	456	283	2.00E-75	247	162	65
CAB65960	456	139	3.00E-32	88	71	80
AAR10737	506	283	2.00E-75	229	160	69
AAR10737	506	154	9.00E-37	150	87	58
AAR10735	506	283	2.00E-75	229	160	69
AAR10735	506	154	1.00E-36	100	80	80
AAR10703	499	282	2.00E-75	199	154	77
AAR10703	499	151	8.00E-36	98	78	79
AAR10499	506	282	2.00E-75	275	164	59
AAR10499	506	155	4.00E-37	100	81	81
AAR10509	506	282	3.00E-75	232	159	68
AAR10509	506	155	4.00E-37	100	81	81
CAD22870	280	282	3.00E-75	296	167	56
AAR10739	506	282	3.00E-75	217	156	71

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAR10739	506	154	7.00E-37	100	80	80
AAR10512	506	282	3.00E-75	232	159	68
AAR10512	506	155	4.00E-37	100	81	81
AAR10511	506	282	3.00E-75	232	159	68
AAR10511	506	155	4.00E-37	100	81	81
AAR10489	506	282	3.00E-75	232	159	68
AAR10489	506	155	4.00E-37	100	81	81
AAR10488	506	282	3.00E-75	232	159	68
AAR10488	506	155	4.00E-37	100	81	81
AAC43352	506	281	4.00E-75	228	156	68
AAC43352	506	155	4.00E-37	100	81	81
AAR10504	506	281	4.00E-75	268	163	60
AAR10504	505	155	4.00E-37	100	81	81
AAR10495	506	281	4.00E-75	268	162	60
AAR10495	506	155	4.00E-37	100	81	81
AAR10754	494	281	5.00E-75	175	148	84
AAR10754	494	152	4.00E-36	98	79	80
AAC43351	506	281	5.00E-75	175	148	84
AAC43351	506	155	4.00E-37	100	81	81
AAC43348	506	281	5.00E-75	175	148	84
AAC43348	506	154	7.00E-37	100	81	81
AAR10751	495	281	5.00E-75	175	148	84
AAR10751	495	148	7.00E-35	98	77	78
AAR10750	495	281	5.00E-75	175	148	84
AAR10750	495	152	4.00E-36	98	79	80
AAR10743	506	281	5.00E-75	175	148	84
AAR10743	506	155	4.00E-37	100	81	81
AAR10742	506	281	5.00E-75	175	148	84
AAR10742	506	155	4.00E-37	100	81	81
AAR10741	506	281	5.00E-75	175	148	84
AAR10741	506	154	1.00E-36	100	80	80
AAR10740	506	281	5.00E-75	175	148	84
AAR10740	506	155	6.00E-37	100	81	81
AAR10730	495	281	5.00E-75	175	148	84
AAR10730	495	155	6.00E-37	245	105	42
AAR10724	494	281	5.00E-75	175	148	84
AAR10724	494	158	5.00E-38	272	108	39
AAR10682	499	281	5.00E-75	175	148	84
AAR10682	499	154	1.00E-36	100	80	80
AAR10681	499	281	5.00E-75	175	148	84
AAR10681	499	154	1.00E-36	100	80	80
AAR10648	495	281	5.00E-75	175	148	84
AAR10648	495	152	4.00E-36	98	79	80
AAR10567	506	281	5.00E-75	175	148	84
AAR10567	506	155	4.00E-37	100	81	81
AAR10566	500	281	5.00E-75	175	148	84
AAR10566	500	157	1.00E-37	100	82	82
AAR10564	500	281	5.00E-75	175	148	84
AAR10564	500	155	4.00E-37	100	81	81
AAR10542	495	281	5.00E-75	175	148	84
AAR10542	495	155	6.00E-37	100	81	81
AAR10539	501	281	5.00E-75	175	148	84
AAR10539	501	155	4.00E-37	100	81	81
AAR10538	501	281	5.00E-75	175	148	84
AAR10538	501	155	4.00E-37	100	81	81
AAR10536	501	281	5.00E-75	175	148	84
AAR10536	501	155	4.00E-37	100	81	81
AAR10532	501	281	5.00E-75	175	148	84
AAR10532	501	155	4.00E-37	100	81	81
AAR10530	501	281	5.00E-75	175	148	84
AAR10530	501	155	4.00E-37	100	81	81
AAR10527	501	281	5.00E-75	175	148	84
AAR10527	501	155	4.00E-37	100	81	81
AAR10523	501	281	5.00E-75	175	148	84
AAR10523	501	155	4.00E-37	100	81	81
AAR10521	501	281	5.00E-75	175	148	84
AAR10521	501	155	6E-37	100	81	81
AAR10518	501	281	5.00E-75	175	148	84

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAR10518	501	155	6.00E-37	100	81	81
AAR10505	465	281	5.00E-75	175	148	84
AAR10505	465	155	4.00E-37	100	81	81
AAR10501	506	281	5.00E-75	175	148	84
AAR10501	506	155	4.00E-37	100	81	81
AAR10496	506	281	5.00E-75	175	148	84
AAR10496	506	155	4.00E-37	100	81	81
AAR10494	506	281	5.00E-75	175	148	84
AAR10494	506	155	4.00E-37	100	81	81
AAR10674	493	281	7.00E-75	229	160	69
AAR10674	493	147	1.00E-34	98	77	78
AAR10673	493	281	7.00E-75	229	160	69
AAR10673	493	152	4.00E-36	98	79	80
AAR10551	499	281	7.00E-75	217	157	72
AAR10551	499	155	6.00E-37	100	81	81
AAR10548	499	281	7.00E-75	217	157	72
AAR10548	499	155	6.00E-37	100	81	81
CAA27129	493	280	9.00E-75	175	148	84
CAA27129	493	154	1.00E-36	329	126	38
CAA27128	498	280	9.00E-75	175	148	84
CAA27128	498	157	9.00E-38	100	83	83
AAR10534	501	280	9.00E-75	175	148	84
AAR10534	501	155	4.00E-37	100	81	81
AAR10503	506	280	9.00E-75	175	148	84
AAR10503	506	154	7.00E-37	98	80	81
NP_460912	495	280	9.00E-75	175	148	84
NP_460912	495	152	4.00E-36	98	79	80
AAT81647	501	280	9.00E-75	175	148	84
AAT81647	501	154	7.00E-37	100	81	81
AAT81646	499	280	9.00E-75	175	148	84
AAT81646	499	155	4.00E-37	100	81	81
AAT81641	499	280	9.00E-75	175	148	84
AAT81641	499	154	9.00E-37	98	80	81
AAT81640	495	280	9.00E-75	175	148	84
AAT81640	495	152	4.00E-36	98	79	80
AAT81638	493	280	9.00E-75	175	148	84
AAT81638	493	152	4.00E-36	98	79	80
AAT81629	495	280	9.00E-75	175	148	84
AAT81629	495	156	2.00E-37	245	106	43
AAT81627	495	280	9.00E-75	175	148	84
AAT81627	495	152	4.00E-36	98	79	80
AAT81606	501	280	9.00E-75	175	148	84
AAT81606	501	154	7.00E-37	100	81	81
AAT81604	495	280	9.00E-75	175	148	84
AAT81604	495	156	2.00E-37	100	82	82
AAT68767	491	280	9.00E-75	175	148	84
AAT68767	491	136	2.00E-31	90	71	78
CAA28190	493	280	9.00E-75	175	148	84
CAA28190	493	152	4.00E-36	98	79	80
AAO13791	501	280	9.00E-75	175	148	84
AAO13791	501	154	1.00E-36	100	80	80
AAL16053	487	280	9.00E-75	175	148	84
AAL16053	487	129	4.00E-29	85	66	77
AAR10738	506	280	9.00E-75	175	148	84
AAR10738	506	155	6.00E-37	100	81	81
AAR10731	500	280	9.00E-75	175	148	84
AAR10731	500	152	4.00E-36	98	79	80
AAR10725	496	280	9.00E-75	175	148	84
AAR10725	496	155	4.00E-37	100	81	81
AAR10723	496	280	9.00E-75	175	148	84
AAR10723	496	153	2.00E-36	100	80	80
AAR10722	496	280	9.00E-75	175	148	84
AAR10722	496	152	3.00E-36	98	79	80
AAR10693	495	280	9.00E-75	175	148	84
AAR10693	495	154	7.00E-37	100	81	81
AAR10692	495	280	9.00E-75	175	148	84
AAR10692	495	152	4.00E-36	98	79	80
AAR10684	499	280	9.00E-75	175	148	84
AAR10684	499	154	9.00E-37	98	80	81
AAR10683	499	280	9.00E-75	175	148	84
AAR10683	499	154	9.00E-37	98	80	81
AAR10679	499	280	9.00E-75	175	148	84
AAR10679	499	155	4.00E-37	100	81	81
AAR10678	506	280	9.00E-75	175	148	84
AAR10678	506	159	4.00E-38	100	83	83
AAR10677	506	280	9.00E-75	175	148	84
AAR10677	506	158	5.00E-38	98	82	83
AAR10676	491	280	9.00E-75	175	148	84
AAR10676	491	152	4.00E-36	98	79	80
AAR10675	491	280	9.00E-75	175	148	84
AAR10675	491	152	4.00E-36	98	79	80
AAR10653	495	280	9.00E-75	175	148	84
AAR10653	495	157	1.00E-37	245	106	43
AAR10644	495	280	9.00E-75	175	148	84
AAR10644	495	152	4.00E-36	98	79	80
AAR10637	495	280	9.00E-75	175	148	84
AAR10637	495	152	4.00E-36	98	79	80
AAR10633	495	280	9.00E-75	175	148	84
AAR10633	495	152	4.00E-36	98	79	80
AAR10581	501	280	9.00E-75	175	148	84
AAR10581	501	152	4.00E-36	98	79	80
AAR10579	501	280	9.00E-75	175	148	84
AAR10579	501	154	7.00E-37	100	81	81
AAR10576	501	280	9.00E-75	175	148	84
AAR10576	501	154	7.00E-37	100	81	81
AAR10569	495	280	9.00E-75	175	148	84
AAR10569	495	156	2.00E-37	100	82	82
AAR10568	495	280	9.00E-75	175	148	84
AAR10568	495	156	2.00E-37	100	82	82
AAR10563	498	280	9.00E-75	175	148	84
AAR10563	498	155	6.00E-37	100	81	81
AAR10555	495	280	9.00E-75	175	148	84
AAR10555	495	155	6.00E-37	100	81	81
AAR10553	495	280	9.00E-75	175	148	84
AAR10553	495	155	4.00E-37	100	81	81
AAR10525	501	280	9.00E-75	175	148	84
AAR10525	501	155	6.00E-37	100	81	81
AAR10524	501	280	9.00E-75	175	148	84
AAR10524	501	155	6.00E-37	100	81	81
AAR10513	495	280	9.00E-75	175	148	84
AAR10513	495	155	6.00E-37	100	81	81
AAK20804	504	280	9.00E-75	173	148	85
AAK20804	504	149	4.00E-35	91	76	83
S07276	494	280	9.00E-75	175	148	84
S07276	494	157	9.00E-38	100	83	83
S09637	489	280	9.00E-75	175	148	84
S09637	489	154	1.00E-36	329	126	38
AAF80752	501	280	1.00E-74	175	148	84
AAF80752	501	154	7.00E-37	100	81	81
AAR10652	495	280	1.00E-74	175	147	84
AAR10652	495	152	4.00E-36	98	79	80
AAR10473	494	280	1.00E-74	175	147	84
AAR10473	494	153	2.00E-36	100	80	80
AAR10472	494	280	1.00E-74	175	147	84
AAR10472	494	152	3.00E-36	98	79	80
AAB33953	397	280	1.00E-74	276	169	61
P52615	501	279	2.00E-74	175	147	84
P52615	501	155	4.00E-37	100	81	81
AAT81645	496	279	3.00E-74	175	147	84
AAT81645	496	153	2.00E-36	100	80	80
AAP13304	456	279	3.00E-74	245	160	65
AAP13304	456	142	3.00E-33	90	73	81
AAR10732	500	279	3.00E-74	175	147	84
AAR10732	500	153	2.00E-36	100	80	80
AAR10685	499	279	3.00E-74	175	147	84
AAR10685	499	152	4.00E-36	98	79	80

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAR10477	506	279	3.00E-74	232	158	68
AAR10477	506	155	4.00E-37	100	81	81
AAR10470	497	279	3.00E-74	175	147	84
AAR10470	497	155	3.00E-37	273	112	41
YP_150203	495	278	3.00E-74	175	147	84
YP_150203	495	156	2.00E-37	100	82	82
AAR10582	501	278	3.00E-74	175	147	84
AAR10582	501	152	4.00E-36	98	79	80
AAR10556	495	278	3.00E-74	175	147	84
AAR10556	495	155	6.00E-37	100	81	81
1UCU	494	278	3.00E-74	174	147	84
1UCU	494	150	1.00E-35	98	78	79
AAB33952	405	278	3.00E-74	174	147	84
S16121	494	278	3.00E-74	174	147	84
S16121	494	152	4.00E-36	98	79	80
AAP13301	461	278	6.00E-74	244	157	64
AAP13301	461	142	3.00E-33	90	73	81
AAR10649	495	278	6.00E-74	175	147	84
AAR10649	495	152	4.00E-36	98	79	80
A24262	490	277	7.00E-74	175	146	83
A24262	490	153	2.00E-36	100	80	80
AAD28524	556	276	2.00E-73	258	154	59
AAD28524	556	123	2.00E-27	103	64	62
AAD28521	560	276	2.00E-73	258	154	59
AAD28521	560	132	5.00E-30	107	68	63
AAN52540	416	275	3.00E-73	222	151	68
AAN52540	416	143	2.00E-33	335	118	35
AAP13317	455	275	3.00E-73	238	159	66
AAP13317	455	140	1.00E-32	90	72	80
AAN77106	449	275	5.00E-73	243	158	65
AAN77106	449	126	3.00E-28	85	65	76
AAP13312	460	274	6.00E-73	158	141	89
AAP13312	460	142	3.00E-33	90	73	81
AAN77105	454	274	6.00E-73	242	155	64
AAN77105	454	126	3.00E-28	85	65	76
AAP13308	502	273	1:00E-72	281	166	59
AAP13308	502	144	1.00E-33	88	73	82
AAD28523	565	273	2.00E-72	208	143	68
AAD28523	565	117	2.00E-25	99	60	60
NP_883763	392	272	2.00E-72	392	180	45
AAN77109	455	272	2.00E-72	158	140	88
AAN77109	455	130	1.00E-29	294	104	35
AAR10726	499	272	2.00E-72	197	149	75
AAR10726	499	152	4.00E-36	98	79	80
AAD28519	523	272	3.00E-72	251	156	62
AAD28519	523	128	7.00E-29	93	62	66
AAN77108	448	271	5.00E-72	236	157	66
AAN77108	448	121	9.00E-27	85	62	72
AAN77107	452	270	1.00E-71	156	139	89
AAN77107	452	124	1.00E-27	84	64	76
AAD28529	555	268	5.00E-71	253	151	59
AAD28529	555	132	5.00E-30	107	68	63
NP_879790	391	268	6.00E-71	391	182	46
NP_889078	391	266	2.00E-70	391	183	46
AAD28525	560	265	4.00E-70	204	140	68
AAD28525	560	114	1.00E-24	97	58	59
AAD28518	550	265	4.00E-70	254	149	58
AAD28518	550	119	3.00E-26	101	63	62
AAD28526	508	265	5.00E-70	247	153	61
AAD28526	508	112	5.00E-24	82	53	64
AAO65441	466	263	1.00E-69	160	137	85
AAO65441	466	138	7.00E-32	161	84	52
AAD28527	517	262	3.00E-69	245	152	62
AAD28527	517	126	2.00E-28	93	62	66
AAD28520	521	259	3.00E-68	246	151	61
AAD28520	521	121	9.00E-27	90	58	64
AAL30512	450	254	5.00E-67	160	133	83
AAL30512	450	92.4	4.00E-18	64	46	71

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAD28528	555	254	5.00E-67	248	143	57
AAD28528	555	129	3.00E-29	106	67	63
ZP_00091764573		254	9.00E-67	262	144	54
ZP_00091764573		139	4.00E-32	90	71	78
AAT06391	468	253	2.00E-66	158	134	84
AAT06391	468	123	2.00E-27	117	70	59
AAP13314	461	251	6.00E-66	177	133	75
AAP13314	461	118	8.00E-26	280	93	33
AAC45643	303	250	1.00E-65	303	140	46
ZP_00173465285		249	2.00E-65	297	145	48
AAT06390	460	249	2.00E-65	158	132	83
AAT06390	460	123	2.00E-27	189	82	43
AAP13315	399	249	3.00E-65	158	127	80
AAP13315	399	107	1.00E-22	304	93	30
AAQ61541	282	248	6.00E-65	297	137	46
AAL16054	455	248	6.00E-65	157	130	82
AAL16054	455	116	3.00E-25	78	59	75
ZP_00288126272		247	8.00E-65	296	145	48
AAQ61540	282	246	2.00E-64	297	137	46
AAC72199	277	243	2.00E-63	292	136	46
AAF19180	306	242	3.00E-63	304	141	46
AAC45642	305	239	3.00E-62	304	139	45
ZP_00289013269		238	5.00E-62	292	133	45
AAF19179	306	238	7.00E-62	305	142	46
ZP_00149772273		236	1.00E-61	296	131	44
AAC79723	281	236	2.00E-61	296	129	43
ZP_00289014271		236	2.00E-61	296	133	44
NP_718792	272	236	2.00E-61	297	140	47
ZP_00274388386		236	2.00E-61	167	122	73
ZP_00274388386		135	6.00E-31	92	68	73
ZP_00289011271		235	3.00E-61	296	133	44
ZP_00288132271		235	4.00E-61	295	136	46
ZP_00288131271		234	6.00E-61	295	136	46
ZP_00299645314		234	7.00E-61	296	137	46
ZP_00288133271		233	1.00E-60	295	135	45
YP_148984	297	233	2.00E-60	303	133	43
NP_718793	273	233	2.00E-60	297	138	46
BAD06421	282	233	2.00E-60	299	137	45
AAC72198	278	232	3.00E-60	296	137	46
AAL67341	283	231	8.00E-60	300	138	46
ZP_00288136271		230	1.00E-59	296	132	44
AAK14995	348	230	1.00E-59	348	157	45
AAK14997	350	230	1.00E-59	350	154	44
AAT86134	274	229	2.00E-59	289	127	43
ZP_00211492272		229	2.00E-59	291	134	46
AAT86133	274	229	2.00E-59	289	127	43
ZP_00289022272		228	4.00E-59	296	136	45
NP_954080	276	228	5.00E-59	298	133	44
BAD06420	282	227	9.00E-59	299	131	43
BAD01155	282	226	2.00E-58	299	131	43
NP_791772	282	223	1.00E-57	297	129	43
AAG15516	281	222	3.00E-57	291	129	44
BAD06419	282	222	4.00E-57	297	129	43
BAC54116	116	220	1.00E-56	116	116	100
NP_622175	276	220	1.00E-56	296	134	45
ZP_00302555327		219	2.00E-56	329	133	40
NP_871067	421	219	2.00E-56	181	109	60
NP_871067	421	120	2.00E-26	345	109	31
AAD46086	291	219	2.00E-55	292	124	42
AAG15515	290	219	3.00E-56	292	123	42
ZP_00127282271		218	4.00E-56	283	128	45
BAB58972	333	217	9.00E-56	330	134	40
YP_080862	310	215	5.00E-55	313	135	43
S69767	378	215	5.00E-55	307	147	47
NP_244483	272	214	1.00E-54	294	124	42
AAK14996	348	213	2.00E-54	273	137	50
ZP_00263336255		213	2.00E-54	269	125	46
AAF09167	290	211	5.00E-54	300	126	41

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAC38199	384	211	9.00E-54	381	141	37
ZP_00183380275		210	1.00E-53	299	128	42
NP_782313	275	209	2.00E-53	296	125	42
NP_693649	338	209	2.00E-53	338	131	38
ZP_00289017266		209	2.00E-53	285	125	43
ZP_00289012373		209	3.00E-53	282	117	41
AAD12054	383	209	3.00E-53	380	141	37
NP_391416	304	208	6.00E-53	306	130	42
BAB87734	270	207	7.00E-53	294	123	41
NP_801058	284	207	9.00E-53	301	119	39
AAD19738	279	207	9.00E-53	299	120	40
NP_348820	275	207	1.00E-52	295	122	41
YP_162364	284	206	2.00E-52	296	119	40
AAB07350	284	206	3.00E-52	301	119	39
NP_798640	377	202	2.00E-51	376	132	35
ZP_00313276273		201	9.00E-51	295	120	40
ZP_00236467307		200	1.00E-50	309	119	38
BAB87735	263	199	2.00E-50	287	118	41
NP_967402	282	199	3.00E-50	295	124	42
NP_967404	277	196	3.00E-49	292	120	41
NP_642301	399	196	3.00E-49	212	113	53
NP_642301	399	103	1.00E-21	307	87	28
ZP_00236470278		196	3.00E-49	293	117	39
ZP_00236469286		195	4.00E-49	292	118	40
ZP_00244371402		195	5.00E-49	400	144	36
BAB58986	306	195	5.00E-49	302	118	39
AAC31966	383	194	6.00E-49	380	136	35
AAD24680	382	194	8.00E-49	379	136	35
AAD24678	382	194	8.00E-49	379	136	35
CAG38109	277	194	8.00E-49	291	119	40
ZP_00313275272		193	1.00E-48	292	118	40
ZP_00335280609		193	1.00E-48	290	120	41
ZP_00335280609		114	1.00E-24	159	67	42
NP_637306	399	193	1.00E-48	241	119	49
NP_637306	399	104	1.00E-21	319	93	29
ZP_00244372404		193	1.00E-48	404	150	37
AAS91569	379	193	1.00E-48	379	140	36
BAB58978	306	193	1.00E-48	302	117	38
BAB87737	265	192	2.00E-48	287	119	41
YP_065397	1128	192	3.00E-48	252	120	47
YP_065397	1128	107	2.00E-22	254	79	31
YP_001491	285	192	4.00E-48	302	112	37
NP_712598	285	192	4.00E-48	302	112	37
BAB58984	308	191	5.00E-48	304	119	39
BAB58980	308	191	7.00E-48	304	119	39
B32010	293	190	2.00E-47	304	121	39
BAB58983	308	190	2.00E-47	304	119	39
AAF95333	379	189	2.00E-47	375	130	34
YP_109915	388	189	2.00E-47	385	136	35
AAP08635	272	189	3.00E-47	296	114	38
AAD27808	387	189	3.00E-47	384	136	35
1IO1	398	189	3.00E-47	122	98	80
1IO1	398	72.4	5.00E-12	54	36	66
AAC71051	388	189	3.00E-47	385	134	34
YP_076801	275	189	3.00E-47	296	114	38
NP_967579	277	188	5.00E-47	301	117	38
AAD24677	387	188	5.00E-47	384	136	35
YP_027849	287	188	6.00E-47	292	112	38
CAB67250	285	187	8.00E-47	300	111	37
AAD24679	387	187	8.00E-47	384	135	35
AAC01552	379	187	8.00E-47	375	129	34
NP_972081	285	187	1.00E-46	300	113	37
ZP_00236468284		187	1.00E-46	295	111	37
BAC98371	384	187	1.00E-46	382	131	34
ZP_00288129272		186	2.00E-46	296	112	37
NP_967577	274	186	3.00E-46	292	115	39
CAA47619	276	185	5.00E-46	292	107	36
BAB58982	249	185	5.00E-46	269	114	42

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
ZP_00200889296		184	7.00E-46	300	110	36
YP_129125	382	184	9.00E-46	382	130	34
Q56572	376	184	9.00E-46	375	128	34
BAB16757	492	184	9.00E-46	235	116	49
BAB16757	492	114	1.00E-24	251	80	31
BAB58979	251	184	9.00E-46	270	111	41
AAC65757	286	183	2.00E-45	298	114	38
AAC27808	377	183	2.00E-45	376	125	33
AAQ96738	228	182	3.00E-45	251	102	40
NP_348162	278	182	3.00E-45	292	115	39
YP_010660	298	182	3.00E-45	311	119	38
BAC98369	384	182	3.00E-45	381	132	34
AAF95287	376	182	4.00E-45	375	133	35
CAG25467	277	182	4.00E-45	292	107	36
CAA45382	285	181	6.00E-45	301	112	37
ZP_00130180299		181	6.00E-45	295	107	36
BAB16756	492	181	6.00E-45	236	111	47
BAB16756	492	115	5.00E-25	284	83	29
AAC65834	286	181	9.00E-45	304	107	35
AAQ96739	228	181	9.00E-45	251	105	41
AAC65835	285	181	9.00E-45	301	111	36
P21989	286	180	1.00E-44	304	113	37
AAQ96740	228	180	1.00E-44	251	105	41
AAP08636	273	180	2.00E-44	298	115	38
BAC98370	384	180	2.00E-44	381	131	34
CAG25466	280	180	2.00E-44	296	107	35
AAA68044	290	179	2.00E-44	304	116	38
JC6021	379	179	2.00E-44	379	129	34
YP_123618	475	179	2.00E-44	309	124	40
YP_123618	475	110	1.00E-23	200	77	38
BAC98368	384	179	2.00E-44	381	131	34
S24986	280	179	3.00E-44	296	107	36
YP_035879	367	179	3.00E-44	365	125	34
AAN86121	328	179	4.00E-44	335	120	35
AAK20919	279	179	4.00E-44	296	109	36
AAK57644	281	179	4.00E-44	301	109	36
YP_095369	475	178	5.00E-44	309	125	40
YP_095369	475	109	3.00E-23	198	78	39
CAD42896	475	178	5.00E-44	309	123	39
CAD42896	475	109	3.00E-23	198	78	39
BAA82629	336	178	5.00E-44	342	116	33
YP_001839	281	177	1.00E-43	300	107	35
NP_971613	286	177	1.00E-43	304	109	35
BAA82633	336	177	1.00E-43	342	115	33
AAQ60166	265	177	1.00E-43	299	104	34
YP_066429	857	177	1.00E-43	231	108	46
YP_066429	857	115	5.00E-25	227	81	35
YP_011656	297	177	1.00E-43	310	113	36
CAA49317	336	177	1.00E-43	342	114	33
YP_126643	475	176	2.00E-43	309	122	39
YP_126643	475	110	2.00E-23	251	88	35
YP_001490	282	176	2.00E-43	300	107	35
CAD43143	475	176	2.00E-43	309	122	39
CAD43143	475	110	2.00E-23	251	88	35
CAD42899	327	176	2.00E-43	309	122	39
CAD42894	361	176	2.00E-43	309	122	39
CAA58234	475	176	2.00E-43	309	122	39
CAA58234	475	109	3.00E-23	251	87	34
CAD42900	489	176	2.00E-43	309	122	39
CAD42900	489	110	2.00E-23	251	88	35
BAA82630	336	176	2.00E-43	342	115	33
NP_970090	277	176	2.00E-43	295	110	37
AAF95289	378	176	2.00E-43	377	134	35
AAC01555	378	176	2.00E-43	377	134	35
AAU07006	336	176	3.00E-43	342	113	33
NP_212281	336	176	3.00E-43	342	113	33
NP_712599	282	176	3.00E-43	300	107	35
CAA49307	336	176	3.00E-43	342	114	33

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
BAB58981	280	176	3.00E-43	285	113	39
CAA53013	336	175	4.00E-43	342	114	33
BAA07832	334	175	4.00E-43	337	115	34
CAA33695	336	175	4.00E-43	342	113	33
CAA37884	334	175	4.00E-43	340	116	34
NP_521943	273	175	4.00E-43	297	109	36
AAF95332	377	175	4.00E-43	377	129	34
CAA59172	474	175	4.00E-43	228	105	46
CAA59172	474	107	1.00E-22	214	79	36
AAB37005	336	175	4.00E-43	342	113	33
CAA49316	336	175	5.00E-43	342	113	33
AAF87586	273	175	5.00E-43	300	111	37
AAG34566	280	175	5.00E-43	294	107	36
CAA53012	334	174	7.00E-43	333	113	33
CAD42893	493	174	7.00E-43	310	122	39
CAD42893	493	99.8	3.00E-20	191	72	37
CAA49308	336	174	7.00E-43	342	113	33
AAS91572	375	174	7.00E-43	370	126	34
AAS91571	400	174	7.00E-43	377	126	33
CAA53014	336	174	9.00E-43	342	113	33
AAK01040	282	174	9.00E-43	300	107	35
CAB67249	286	174	1.00E-42	304	103	33
CAA49322	336	174	1.00E-42	342	112	32
CAA49318	336	174	1.00E-42	342	113	33
BAA82635	323	174	1.00E-42	329	114	34
CAA34735	336	173	2.00E-42	342	112	32
YP_013330	287	173	2.00E-42	296	107	36
CAA45011	336	173	2.00E-42	342	113	33
NP_470041	287	173	2.00E-42	296	107	36
NP_464217	287	173	2.00E-42	296	107	36
NP_797167	384	173	2.00E-42	384	125	32
AAO10326	376	173	2.00E-42	375	121	32
AAU95795	287	173	2.00E-42	296	107	36
CAA49321	336	173	2.00E-42	342	113	33
AAP33175	387	173	2.00E-42	314	118	37
AAP33175	387	122	5.00E-27	182	73	40
BAA82634	319	173	2.00E-42	323	113	34
AAK57645	286	172	3.00E-42	301	109	36
NP_969824	277	172	3.00E-42	295	109	36
YP_061686	277	172	3.00E-42	299	105	35
CAD42895	491	172	3.00E-42	166	92	55
CAD42895	491	109	3.00E-23	198	78	39
NP_972083	286	172	4.00E-42	304	106	34
YP_159591	306	171	6.00E-42	151	89	58
BAB58985	280	171	6.00E-42	280	110	39
AAR16426	329	171	7.00E-42	314	117	37
AAO10324	377	171	7.00E-42	376	123	32
ZP_00346385295		171	7.00E-42	292	98	33
AAC28557	387	171	7.00E-42	314	117	37
BAA11613	326	171	7.00E-42	325	109	33
BAA28607	320	171	7.00E-42	323	111	34
NP_348785	283	171	1.00E-41	290	104	35
AAU95794	287	171	1.00E-41	296	106	35
AAP33174	387	171	1.00E-41	314	117	37
AAP33174	387	122	5.00E-27	182	73	40
AAC01556	377	171	1.00E-41	379	127	33
BAA28606	323	171	1.00E-41	323	111	34
NP_782278	280	170	1.00E-41	294	105	35
ZP_00279040381		170	1.00E-41	378	127	33
CAA53011	336	170	1.00E-41	342	111	32
BAA11602	329	170	1.00E-41	335	111	33
AAF95288	377	169	2.00E-41	379	127	33
YP_011295	297	169	2.00E-41	295	101	34
BAA11605	329	169	2.00E-41	335	110	32
CAA53015	335	169	3.00E-41	334	112	33
CAD42897	476	169	3.00E-41	314	122	38
CAD42897	476	109	3.00E-23	198	78	39
AAC28556	387	169	4.00E-41	300	114	38

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAA99807	488	168	5.00E-41	242	104	42
AAA99807	488	113	2.00E-24	335	100	29
AAR00324	336	168	6.00E-41	342	110	32
BAA11604	329	168	6.00E-41	335	108	32
AAQ60680	372	167	8.00E-41	359	122	33
BAA11603	329	167	8.00E-41	335	108	32
BAA11597	329	167	8.00E-41	335	109	32
BAA82631	329	167	8.00E-41	335	109	32
BAA11611	327	167	1.00E-40	333	109	32
NP_249783	488	167	1.00E-40	242	103	42
NP_249783	488	113	2.00E-24	335	100	29
P21184	394	167	1.00E-40	271	105	38
ZP_00138680488		167	1.00E-40	242	103	42
ZP_00138680488		113	2.00E-24	335	100	29
ZP_00130923288		167	1.00E-40	284	103	36
AAC63946	390	167	1.00E-40	271	105	38
AAP33170	394	167	1.00E-40	271	106	38
BAA11607	329	167	1.00E-40	335	108	32
AAC27800	378	167	1.00E-40	377	126	33
NP_798637	376	167	1.00E-40	377	125	33
NP_798638	378	167	1.00E-40	377	126	33
AAC63950	478	167	1.00E-40	225	101	44
AAC63950	478	111	7.00E-24	278	83	29
BAA09687	329	167	1.00E-40	335	107	31
BAA09681	329	167	1.00E-40	335	108	32
BAA11600	329	167	1.00E-40	335	107	31
BAA82636	324	167	1.00E-40	323	109	33
BAA09689	329	166	2.00E-40	335	107	31
BAA09688	329	166	2.00E-40	335	107	31
BAA09686	329	166	2.00E-40	335	107	31
BAA09684	329	166	2.00E-40	335	107	31
BAA09678	329	166	2.00E-40	335	107	31
BAA11610	327	165	2.00E-40	333	110	33
A37853	394	166	3.00E-40	271	105	38
A37853	394	107	2.00E-22	197	73	37
AAD10272	378	165	5.00E-40	377	125	33
AAG29830	327	165	5.00E-40	333	108	32
AAP08637	249	165	5.00E-40	271	98	36
AAB03518	335	165	5.00E-40	334	111	33
ZP_00317212580		164	7.00E-40	222	101	45
ZP_00317212580		99.4	4.00E-20	182	66	36
AAA62843	688	164	9.00E-40	252	103	40
AAA62843	688	95.9	4.00E-19	92	46	50
NP_746492	687	164	9.00E-40	252	103	40
NP_746492	687	96.3	3.00E-19	129	53	41
BAA33017	316	164	1.00E-39	323	108	33
ZP_00100062385		163	2.00E-39	385	128	33
AAC99335	283	163	2.00E-39	301	100	33
ZP_00317210587		162	5.00E-39	254	105	41
ZP_00317210587		95.9	4.00E-19	129	55	42
NP_712200	283	162	5.00E-39	301	100	33
CAD65866	268	162	5.00E-39	103	84	81
YP_001838	283	161	6.00E-39	301	99	32
AAC99336	283	161	8.00E-39	301	99	32
AAC63947	393	160	1.00E-38	300	108	36
NP_770335	274	160	1.00E-38	295	95	32
AAB94024	283	160	2.00E-38	301	98	32
AAC63948	486	160	2.00E-38	232	99	42
AAC63948	486	100	1.00E-20	346	89	25
CAA45081	285	159	2.00E-38	304	108	35
BAA23224	328	159	3.00E-38	327	106	32
CAC35206	274	159	3.00E-38	273	94	34
BAB13814	413	159	3.00E-38	256	101	39
BAB13814	413	89.7	3.00E-17	173	60	34
BAA11608	328	159	3.00E-38	327	106	32
AAC63949	669	159	4.00E-38	260	105	40
AAC63949	669	108	5.00E-23	273	74	27
AAR08139	235	158	5.00E-38	217	92	42

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
CAC36204	274	158	5.00E-38	273	95	34
AAC99334	283	158	5.00E-38	301	98	32
AAU93692	286	158	7.00E-38	304	106	34
BAA82632	311	158	7.00E-38	313	103	32
ZP_00218989614		156	2.00E-37	242	97	40
ZP_00218989614		90.1	2.00E-17	86	46	53
BAB87728	413	156	2.00E-37	278	102	36
BAB87728	413	85.1	7.00E-16	108	45	41
CAC36205	274	156	2.00E-37	273	93	34
AAC38200	504	156	2.00E-37	246	97	39
AAC38200	504	92	6.00E-18	87	46	52
BAB87730	375	155	3.00E-37	374	115	30
AAB09433	377	155	6.00E-37	182	80	43
ZP_00270146298		154	1.00E-36	305	107	35
NP_935285	396	153	2.00E-36	376	118	31
AAS91570	377	153	2.00E-36	218	89	40
CAC36223	271	152	3.00E-36	268	91	33
NP_945993	274	152	4.00E-36	295	92	31
AAO08751	377	151	6.00E-36	376	120	31
BAB87729	384	151	6.00E-36	169	82	48
AAO61408	241	151	8.00E-36	263	96	36
AAC10325	377	151	8.00E-36	376	119	31
YP_128298	426	151	8.00E-36	251	106	42
YP_128298	426	89.4	4.00E-17	149	55	36
BAB87732	377	151	8.00E-36	169	82	48
BAB87732	377	79.7	3.00E-14	291	83	28
AAB09434	377	150	1.00E-35	376	119	31
AAB03521	334	150	1.00E-35	335	102	30
AAC38201	540	150	2.00E-35	266	100	37
AAC38201	540	51.2	1.00E-05	147	43	29
ZP_00329901380		149	2.00E-35	382	125	32
NP_935286	377	149	2.00E-35	376	112	29
Q56574	377	149	2.00E-35	376	116	30
AAO61409	241	149	3.00E-35	263	95	36
NP_933764	385	149	4.00E-35	178	80	44
NP_933764	385	102	6.00E-21	301	92	30
CAC36218	220	149	4.00E-35	238	90	37
BAA15744	340	149	4.00E-35	151	80	52
BAA77322	201	149	4.00E-35	214	90	42
YP_155525	471	148	5.00E-35	170	82	48
YP_155525	471	99.4	4.00E-20	267	77	28
AAD10271	384	147	9.00E-35	188	78	41
CAC36221	222	147	1.00E-34	237	85	35
AAO61406	241	147	2.00E-34	267	96	35
CAC36220	222	147	2.00E-34	237	84	35
ZP_00273972629		146	3.00E-34	199	85	42
ZP_00273972629		104	9.00E-22	92	57	61
YP_129126	393	145	4.00E-34	213	82	38
YP_129126	393	90.5	2.00E-17	203	63	31
NP_978099	266	145	4.00E-34	292	96	32
AAO61410	241	145	6.00E-34	263	91	34
AAB03520	334	145	6.00E-34	330	102	30
BAA77320	202	145	6.00E-34	217	91	41
AAO61407	241	144	8.00E-34	264	93	35
CAB44444	377	144	8.00E-34	377	112	29
CAA67103	333	144	1.00E-33	333	108	32
CAC36219	220	144	1.00E-33	238	89	37
AAQ96734	626	143	2.00E-33	263	99	37
AAQ96734	626	70.9	1.00E-11	68	35	51
BAA12718	292	143	2.00E-33	291	94	32
AAO61404	241	143	2.00E-33	264	92	34
AAO61405	241	142	3.00E-33	264	89	33
BAA12102	292	142	3.00E-33	291	94	32
BAA13584	292	142	3.00E-33	291	93	31
YP_148995	604	142	4.00E-33	269	96	35
YP_148995	604	103	3.00E-21	179	62	34
CAC36224	222	142	4.00E-33	237	86	36
ZP_00287990272		142	5.00E-33	280	85	30

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
YP_035878	266	142	5.00E-33	292	97	33
BAA12719	292	142	5.00E-33	291	92	31
BAA20904	289	142	5.00E-33	291	92	31
BAA19430	292	142	5.00E-33	291	92	31
AAO08752	374	141	6.00E-33	167	76	45
AAO08752	374	102	6.00E-21	301	92	30
NP_782259	268	141	6.00E-33	266	79	29
BAD12778	248	141	6E-33	267	88	32
BAA20481	292	141	6.00E-33	291	92	31
BAA20479	292	141	6.00E-33	291	92	31
BAA20477	292	141	6.00E-33	291	92	31
BAA13582	292	141	6.00E-33	291	92	31
BAA19444	292	141	6.00E-33	291	92	31
BAA19443	292	141	6.00E-33	291	92	31
BAA19439	292	141	6.00E-33	291	92	31
BAA89303	248	141	6.00E-33	267	87	32
BAA89302	248	141	6.00E-33	267	88	32
BAA77944	248	141	6.00E-33	267	87	32
BAC16349	248	141	8.00E-33	267	87	32
BAA77321	208	141	8.00E-33	214	87	40
AAO61414	241	140	1.00E-32	267	92	34
ZP_00004597493		140	1.00E-32	166	74	44
ZP_00004597493		97.1	2.00E-19	176	63	35
YP_083129	266	140	1.00E-32	292	95	32
CAA75001	493	140	1.00E-32	166	74	44
CAA75001	493	97.1	2.00E-19	176	63	35
AAG21990	170	140	1.00E-32	166	74	44
BAA20478	292	140	1.00E-32	291	92	31
AAP08634	266	140	1.00E-32	291	95	32
BAD13295	248	140	1.00E-32	267	87	32
AAO61411	241	140	2.00E-32	267	92	34
NP_228567	387	140	2.00E-32	392	119	30
AAK31137	257	140	2.00E-32	273	87	31
BAA89304	248	140	2.00E-32	267	87	32
BAA77325	200	139	3.00E-32	218	89	40
AAQ96735	620	139	4.00E-32	258	96	37
AAQ96735	620	63.2	3.00E-09	64	31	48
AAO61415	240	139	4.00E-32	266	91	34
CAC36207	234	139	4.00E-32	248	85	34
ZP_00236466266		138	5.00E-32	292	96	32
BAB87738	554	138	7.00E-32	136	71	52
BAB87738	554	99.8	3.00E-20	291	82	28
YP_083130	460	137	9.00E-32	289	96	33
YP_083130	460	80.9	1.00E-14	111	46	41
NP_348261	269	137	1.00E-31	292	89	30
AAO61412	240	135	3.00E-31	266	90	33
AAQ96736	470	134	8.00E-31	233	86	36
AAQ96736	470	65.1	8.00E-10	264	68	25
BAA89305	248	134	1.00E-30	268	84	31
CAC36202	234	132	5E-30	248	83	33
AAT06255	459	132	5.00E-30	139	70	50
AAT06255	459	87.4	1E-16	159	57	35
YP_050963	484	131	7.00E-30	126	71	56
YP_050963	484	88.6	6.00E-17	152	63	41
AAB82610	472	131	7.00E-30	265	93	35
AAB82610	472	98.2	8.00E-20	153	63	41
CAC36217	223	131	9.00E-30	241	78	32
AAA62844	479	130	1.00E-29	132	69	52
AAA62844	479	97.4	1.00E-19	280	77	27
BAA77323	200	130	1.00E-29	216	85	39
NP_242343	464	130	2.00E-29	135	70	51
NP_242343	464	95.9	4.00E-19	169	57	33
CAC36201	223	129	4.00E-29	241	79	32
AAT06254	493	129	4.00E-29	140	68	48
AAT06254	493	94	2.00E-18	195	67	34
AAB82613	508	128	7.00E-29	150	68	45
AAB82613	508	86.7	2.00E-16	168	58	36
NP_978100	465	126	2.00E-28	221	77	34

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_978100	465	75.1	7.00E-13	84	41	48
AAL26808	229	126	2.00E-28	248	79	31
AAQ96737	430	124	1.00E-27	165	67	40
AAQ96737	430	60.1	2.00E-08	92	33	35
CAB46359	81	124	1E-27	81	63	77
CAC36222	223	122	5.00E-27	240	77	32
AAP34182	184	122	5.00E-27	182	73	40
AAP34179	185	122	5.00E-27	182	73	40
AAO08750	375	121	7.00E-27	374	108	28
AAP44578	259	121	7.00E-27	260	83	31
NP_933768	375	121	7.00E-27	374	108	28
AAC09389	259	119	3.00E-26	195	77	39
AAP34194	195	119	3.00E-26	195	77	39
AAP34185	194	119	3.00E-26	195	77	39
CAA67102	434	119	3.00E-26	197	78	39
CAA67102	434	95.1	7.00E-19	310	91	29
AAQ03611	128	118	6.00E-26	117	60	51
CAA66927	434	118	6.00E-26	196	78	39
CAA66927	434	101	1.00E-20	327	92	28
AAQ03603	127	118	8.00E-26	120	59	49
BAD22842	567	118	8.00E-26	180	68	37
BAD22842	567	75.9	4.00E-13	84	34	40
BAA77307	483	118	8.00E-26	254	87	34
BAA77307	483	58.5	7.00E-08	221	60	27
AAQ03617	132	117	1.00E-25	117	59	50
AAQ03616	133	117	1.00E-25	117	59	50
AAQ03614	131	117	1.00E-25	117	59	50
AAQ03610	129	117	1.00E-25	117	59	50
BAD22849	566	117	2.00E-25	180	68	37
BAD22849	566	75.5	6.00E-13	83	34	40
BAD22843	567	117	2.00E-25	180	68	37
BAD22843	567	74.7	1.00E-12	83	34	40
BAD22841	567	117	2.00E-25	180	68	37
BAD22841	567	74.7	1.00E-12	83	34	40
BAD22837	567	117	2.00E-25	180	68	37
BAD22837	567	74.7	1.00E-12	83	34	40
BAD22835	566	117	2.00E-25	180	68	37
BAD22835	566	75.5	6.00E-13	83	34	40
BAD22834	566	117	2.00E-25	180	68	37
BAD22834	566	75.5	6.00E-13	83	34	40
CAC36203	221	116	2.00E-25	238	74	31
BAD22836	567	116	2.00E-25	180	68	37
BAD22836	567	74.7	1.00E-12	83	34	40
NP_391395	160	116	3.00E-25	179	68	37
BAD22838	563	116	3.00E-25	180	67	37
BAD22838	563	76.6	3.00E-13	173	50	28
BAD22845	565	115	4.00E-25	180	67	37
BAD22845	565	78.2	9.00E-14	127	45	35
AAB69135	434	115	4E-25	196	76	38
AAB69135	434	103	2.00E-21	327	93	28
AAB69134	434	115	4.00E-25	196	76	38
AAB69134	434	102	4.00E-21	327	93	28
I40573	195	115	4.00E-25	165	65	39
BAD22840	566	115	5.00E-25	180	67	37
BAD22840	566	75.5	6.00E-13	83	34	40
AAQ03605	126	114	8E-25	127	61	48
AAG61259	253	114	1.00E-24	257	80	31
CAA67105	700	114	1.00E-24	301	93	30
CAA67105	700	102	4.00E-21	298	92	30
CAC03724	440	113	2.00E-24	237	83	35
CAC03724	440	106	3.00E-22	255	80	31
BAD22848	571	113	2E-24	180	66	36
BAD22848	571	74.7	1.00E-12	83	33	39
AAB66595	340	113	2E-24	225	76	33
AAB66595	340	107	1E-22	187	70	37
AAB66597	340	113	2.00E-24	225	76	33
AAB66597	340	105	5.00E-22	187	69	36
BAA77299	398	113	2.00E-24	215	86	40

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
BAA77299	398	55.8	5.00E-07	130	43	33
CAA67104	340	112	3.00E-24	225	76	33
CAA67104	340	107	1.00E-22	187	70	37
CAA67101	434	112	5.00E-24	196	75	38
CAA67101	434	98.2	8.00E-20	327	91	27
BAA77312	170	111	7.00E-24	125	61	48
BAA77310	150	111	7.00E-24	125	61	48
CAA66928	434	110	1.00E-23	196	74	37
CAA66928	434	91.7	8.00E-18	322	86	26
BAA77302	176	110	1.00E-23	174	74	42
BAD22847	568	110	2.00E-23	180	64	35
BAD22847	568	75.5	6.00E-13	83	34	40
NP_797170	374	109	3.00E-23	148	60	40
NP_797170	374	74.3	1.00E-12	217	61	28
NP_908288	513	109	3.00E-23	294	89	30
NP_908288	513	73.2	3.00E-12	122	44	36
BAD22846	568	109	3.00E-23	180	64	35
BAD22846	568	75.5	6.00E-13	83	34	40
BAD22839	568	109	3.00E-23	180	63	35
BAD22839	568	74.7	1.00E-12	83	34	40
AAK12380	576	109	3.00E-23	184	63	34
AAK12380	576	79	5.00E-14	107	43	40
AAK12377	574	109	3.00E-23	184	63	34
AAK12377	574	79.3	4.00E-14	124	47	37
AAF25214	576	109	3.00E-23	184	63	34
AAF25214	576	77	2.00E-13	83	37	44
AAC25644	576	109	3.00E-23	184	62	33
AAC25644	576	77.4	1.00E-13	156	52	33
S41310	575	109	3.00E-23	182	68	37
S41310	575	79.3	4.00E-14	107	43	40
CAC03725	457	108	5.00E-23	144	65	45
CAC03725	457	101	1.00E-20	276	85	30
A42474	573	108	6.00E-23	184	63	34
A42474	573	79.7	3.00E-14	124	46	37
A39228	576	108	6.00E-23	184	62	33
A39228	576	77	2.00E-13	83	37	44
BAD22844	568	108	6.00E-23	180	63	35
BAD22844	568	75.5	6.00E-13	83	34	40
BAC44988	571	108	6.00E-23	181	66	36
BAC44988	571	72	6.00E-12	83	34	40
BAC44985	575	108	6.00E-23	184	63	34
BAC44985	575	77.4	1.00E-13	159	55	34
AAF05902	574	108	6.00E-23	184	63	34
AAF05902	574	77	2.00E-13	83	37	44
AAN75633	196	108	6.00E-23	215	72	33
AAC25648	576	108	6.00E-23	184	62	33
AAC25648	576	77.4	1.00E-13	83	37	44
AAC25643	576	108	6.00E-23	184	63	34
AAC25643	576	77.4	1.00E-13	124	44	35
AAC25637	576	108	6.00E-23	184	62	33
AAC25637	576	77	2.00E-13	83	37	44
P27053	573	108	6.00E-23	184	63	34
P27053	573	79.7	3.00E-14	124	46	37
BAB63937	486	108	6.00E-23	183	67	36
BAB63937	486	80.1	2.00E-14	83	38	45
NP_206915	514	108	8.00E-23	187	67	35
NP_206915	514	77.4	1.00E-13	121	47	38
BAB71798	486	108	8.00E-23	183	66	36
BAB71798	486	80.1	2.00E-14	83	38	45
AAP72265	514	107	1.00E-22	166	62	37
AAP72265	514	77.4	1.00E-13	121	47	38
BAC44987	574	107	1.00E-22	181	65	35
BAC44987	574	82	6.00E-15	162	56	34
BAC44986	574	107	1.00E-22	181	65	35
BAC44986	574	79	5.00E-14	83	37	44
AAD10273	374	107	1.00E-22	160	61	38
AAD10273	374	75.9	4.00E-13	217	59	27
AAP34188	183	107	1.00E-22	187	70	37

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAC25639	575	107	1.00E-22	181	66	35
AAC25639	575	82	6.00E-15	162	56	34
AAA25016	514	107	1.00E-22	187	67	35
AAA25016	514	77.4	1.00E-13	121	47	38
NP_222828	514	107	1.00E-22	187	67	35
NP_222828	514	77.4	1.00E-13	121	47	38
AAL86894	514	107	1.00E-22	187	67	35
AAL86894	514	77.4	1.00E-13	121	47	38
CAA82523	575	107	1.00E-22	182	67	36
CAA82523	575	79.3	4.00E-14	107	43	40
CAB46859	514	107	1.00E-22	249	79	31
CAB46859	514	75.1	7.00E-13	148	50	33
AAN74969	514	107	1.00E-22	187	67	35
AAN74969	514	77.4	1.00E-13	121	47	38
BAC56997	575	107	1.00E-22	171	64	37
BAC56997	575	79.7	3.00E-14	121	44	36
AAA17046	575	107	1.00E-22	182	67	36
AAA17046	575	73.9	2.00E-12	107	40	37
CAA40460						
CAA40460	576	82	6.00E-15	162	56	34
AAC25650	572	107	2.00E-22	171	64	37
AAC25650	572	77.8	1E-13	132	48	36
AAC25649	572	107	2.00E-22	181	65	35
AAC25649	572	78.2	9.00E-14	132	48	36
AAC25645	572	107	2.00E-22	181	65	35
AAC25645	572	79.3	4.00E-14	132	48	36
AAC25641	572	107	2.00E-22	181	65	35
AAC25641	572	78.6	7.00E-14	83	37	44
BAC56996	572	106	2.00E-22	184	61	33
BAC56996	572	79.7	3.00E-14	124	46	37
NP_282485	572	106	3.00E-22	171	63	36
NP_282485	572	79.3	4.00E-14	132	48	36
BAA77318	125	106	3.00E-22	125	57	45
BAA77316	131	106	3.00E-22	125	57	45
BAC56994	487	105	4.00E-22	183	64	34
BAC56994	487	80.1	2.00E-14	83	38	45
BAA77304	165	105	4.00E-22	165	68	41
B39228	576	105	5.00E-22	184	63	34
B39228	576	71.6	8.00E-12	83	33	39
AAB03519	328	105	5.00E-22	308	87	28
AAF25216	576	105	5.00E-22	184	63	34
AAF25216	576	73.6	2.00E-12	83	34	40
B42474	573	105	5E-22	184	64	34
B42474	573	73.9	2.00E-12	124	43	34
A35146	573	105	5.00E-22	184	64	34
A35146	573	72.8	4.00E-12	124	43	34
P18245	573	105	5.00E-22	184	64	34
P18245	573	73.9	2.00E-12	124	43	34
BAA77314	124	105	5.00E-22	124	57	45
AAA23020	573	105	5.00E-22	184	64	34
AAA23020	573	72.8	4.00E-12	124	43	34
1814303A	556	105	5.00E-22	182	66	36
1814303A	556	45.4	6.00E-04	75	24	32
AAM76286	576	105	7.00E-22	184	62	33
AAM76286	576	73.6	2.00E-12	83	34	40
B40586	514	104	9.00E-22	189	63	33
B40586	514	80.5	2.00E-14	123	48	39
AAP78393	514	104	9.00E-22	188	67	35
AAP78393	514	68.9	5.00E-11	115	40	34
BAC56995	487	104	9.00E-22	183	65	35
BAC56995	487	80.1	2.00E-14	83	38	45
BAC56992	487	104	9.00E-22	183	65	35
BAC56992	487	79	5.00E-14	83	37	44
BAC56989	487	104	9.00E-22	183	65	35
BAC56989	487	79	5.00E-14	83	37	44
BAB71801	491	104	9.00E-22	180	63	35
BAB71801	491	81.6	8.00E-15	174	54	31

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_420273	273	104	1.00E-21	297	76	25
AAC25638	576	104	1.00E-21	181	64	35
AAC25638	576	79.3	4.00E-14	121	44	36
BAB85480	491	104	1.00E-21	181	63	34
BAB85480	491	83.2	3.00E-15	174	55	31
CAA82524	575	103	1.00E-21	182	69	37
CAA82524	575	73.9	2.00E-12	107	40	37
BAC56988	491	103	1.00E-21	184	63	34
BAC56988	491	82.8	4.00E-15	174	59	33
AAC25647	575	103	1.00E-21	171	62	36
AAC25647	575	78.6	7.00E-14	107	43	40
NP_907654	518	103	2.00E-21	192	63	32
NP_907654	518	94.7	9.00E-19	333	85	25
CAA72431	630	103	2.00E-21	181	64	35
CAA72431	630	71.2	1.00E-11	105	38	36
AAC25646	572	103	2.00E-21	181	67	37
AAC25646	572	72.8	4.00E-12	132	45	34
BAB71800	487	103	2.00E-21	183	63	34
BAB71800	487	80.1	2.00E-14	83	38	45
BAC56991	491	103	3.00E-21	219	68	31
BAC56991	491	84	2.00E-15	171	56	32
AAC35988	273	103	3.00E-21	297	75	25
NP_404368	404	102	3.00E-21	223	67	30
NP_670739	401	102	3.00E-21	223	67	30
NP_670739	401	57.4	2.00E-07	84	28	33
AAV35033	543	102	4.00E-21	169	61	36
AAV35033	543	62	6.00E-09	141	42	29
BAC56990	490	102	4.00E-21	219	68	31
BAC56990	490	83.6	2.00E-15	171	59	34
BAA77308	120	102	4.00E-21	119	55	46
NP_282484	572	102	6.00E-21	181	66	36
NP_282484	572	72.8	4.00E-12	132	45	34
CAA72430	626	102	6.00E-21	183	65	35
CAA72430	626	79.3	4.00E-14	148	50	33
AAK73706	557	101	7.00E-21	178	59	33
AAK73706	557	70.1	2.00E-11	113	41	36
AAC25640	575	101	7.00E-21	181	65	35
AAC25640	575	77.8	1.00E-13	296	78	26
CAB46858	513	101	1.00E-20	240	73	30
CAB46858	513	77.8	1.00E-13	329	89	27
BAC56987	492	101	1.00E-20	174	61	35
BAC56987	492	82.8	4.00E-15	175	58	33
AAK73700	557	101	1.00E-20	178	59	33
AAK73700	557	70.1	2.00E-11	113	41	36
AAC25642	572	101	1.00E-20	181	66	36
AAC25642	572	71.6	8.00E-12	132	45	34
NP_214372	518	100	1.00E-20	209	62	29
NP_214372	518	62	6.00E-09	129	39	30
BAC56986	500	100	1.00E-20	153	61	39
BAC56986	500	85.9	4.00E-16	316	82	25
AAK73703	556	100	2.00E-20	175	62	35
AAK73703	556	71.6	8.00E-12	287	73	25
AAK73702	558	100	2.00E-20	175	62	35
AAK73702	558	74.7	1.00E-12	287	72	25
AAK73699	194	100	2.00E-20	175	62	35
AAK73705	554	100	2.00E-20	175	61	34
AAK73705	554	68.6	7.00E-11	74	31	41
AAK73698	194	100	2.00E-20	175	61	34
AAK73697	194	100	2.00E-20	175	61	34
YP_061683	290	99.8	3.00E-20	308	85	27
BAA77300	115	99.8	3.00E-20	115	58	50
BAB71799	492	99.8	3.00E-20	174	59	33
BAB71799	492	85.9	4.00E-16	172	57	33
ZP_00313281302		99.4	4.00E-20	274	69	25
ZP_00100043955		99.4	4.00E-20	270	82	30
ZP_00100043955		63.5	2.00E-09	154	47	30
A44757	572	99	5.00E-20	171	58	33
A44757	572	79.7	3.00E-14	124	46	37

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_420274	273	99	5.00E-20	292	75	25
NP_419609	273	99	5.00E-20	292	72	24
AAA23021	572	99	5.00E-20	171	58	33
AAA23021	572	79.7	3.00E-14	124	46	37
NP_419611	273	98.6	6.00E-20	292	72	24
YP_071817	400	98.2	8.00E-20	207	61	29
YP_071817	400	60.1	2.00E-08	115	37	32
NP_865696	718	98.2	8.00E-20	284	88	30
NP_865696	718	81.3	1.00E-14	143	57	39
NP_622171	296	98.2	8.00E-20	290	83	28
BAA77306	397	98.2	8.00E-20	188	67	35
BAA77306	397	51.2	1.00E-05	91	27	29
AAP78250	508	97.8	1.00E-19	170	60	35
AAP78250	508	76.3	3.00E-13	297	74	24
NP_419610	273	97.4	1.00E-19	292	70	23
NP_866107	739	97.4	1.00E-19	257	76	29
NP_866107	739	79.3	4.00E-14	250	70	28
CAA43148	510	97.1	2.00E-19	170	57	33
CAA43148	510	82.4	5.00E-15	311	78	25
BAC56993	500	97.1	2.00E-19	222	73	32
BAC56993	500	82.4	5.00E-15	174	55	31
NP_223266	510	96.3	3.00E-19	170	57	33
NP_223266	510	82.4	5.00E-15	311	78	25
AAP72264	510	96.3	3.00E-19	170	57	33
AAP72264	510	83.2	3.00E-15	311	79	25
AAU21201	510	96.3	3.00E-19	170	57	33
AAU21201	510	82	6.00E-15	311	78	25
CAC03721	427	96.3	3.00E-19	251	76	30
CAC03721	427	94.4	1.00E-18	271	74	27
NP_404369	399	95.9	4.00E-19	295	75	25
AAQ82717	510	95.9	4.00E-19	170	57	33
AAQ82717	510	82	6.00E-15	311	78	25
ZP_00299642294		95.5	5.00E-19	295	75	25
A55864	518	95.5	5.00E-19	197	65	32
A55864	518	94.7	9.00E-19	333	85	25
AAB95381	273	95.5	5.00E-19	292	70	23
AAP34180	167	94.7	9.00E-19	164	59	35
P50612	494	94.4	1.00E-18	166	56	33
P50612	494	61.2	1.00E-08	299	71	23
CAA81035	134	93.6	2.00E-18	154	59	38
NP_867573	685	92.8	3.00E-18	169	62	36
NP_867573	685	85.5	5.00E-16	126	55	43
CAC03723	503	92.4	4.00E-18	208	66	31
CAC03723	503	66.2	3.00E-10	252	61	24
NP_404370	401	92	6.00E-18	309	79	25
ZP_00329910306		91.7	8.00E-18	285	73	25
ZP_00196929279		91.7	8.00E-18	288	79	27
NP_353572	306	91.3	1.00E-17	313	77	24
NP_693427	293	91.3	1.00E-17	293	75	25
ZP_00098298321		90.9	1.00E-17	302	85	28
AAA88923	501	90.5	2.00E-17	200	57	28
AAA88923	501	56.6	3.00E-07	146	47	32
BAC98372	302	90.5	2.00E-17	301	81	26
AAC41457	482	90.5	2.00E-17	150	51	34
AAC41457	482	61.2	1.00E-08	299	71	23
NP_227947	258	89.7	3.00E-17	248	63	25
NP_954084	298	89.7	3.00E-17	290	75	25
ZP_00289010110		89.7	3.00E-17	87	47	54
NP_700301	282	88.6	6.00E-17	298	76	25
AAA85132	102	88.6	6.00E-17	87	45	51
AAV35032	531	87.4	1.00E-16	142	52	36
AAV35032	531	63.9	2.00E-09	94	34	36
NP_391420	298	86.7	2.00E-16	288	80	27
NP_541127	282	86.7	2.00E-16	298	75	25
ZP_00288130268		85.5	5.00E-16	295	76	25
NP_773506	313	85.1	7.00E-16	311	73	23
NP_104150	328	84.7	9E-16	329	75	22
BAC98373	302	84.3	1E-15	92	44	47

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
ZP_00339045281		84	2E-15	296	75	25
AAA85133	102	84	2E-15	87	43	49
YP_080866	303	83.2	3E-15	281	70	24
FLQL2C	276	82.4	5E-15	298	70	23
NP_773505	314	80.9	1E-14	317	73	23
YP_148989	297	80.5	2E-14	288	69	23
NP_353570	313	79.7	3.00E-14	313	75	23
ZP_00339044282		79.3	4.00E-14	298	72	24
CAD11203	461	79	5.00E-14	149	49	32
CAD11203	461	63.9	2.00E-09	109	39	35
CAD11202	461	79	5.00E-14	149	49	32
CAD11202	461	63.9	2.00E-09	109	39	35
ZP_00007767281		78.6	7.00E-14	302	70	23
NP_840399	299	77.8	1.00E-13	290	71	24
CAD11208	458	77.8	1.00E-13	136	45	33
CAD11208	458	67.8	1.00E-10	294	70	23
CAD11207	458	77.8	1.00E-13	136	45	33
CAD11207	458	65.9	4.00E-10	294	69	23
CAD11206	458	77.8	1.00E-13	136	45	33
CAD11206	458	65.9	4.00E-10	294	69	23
ZP_00339046273		77.4	1.00E-13	280	73	26
ZP_00338034282		77.4	1.00E-13	294	72	24
AAN08500	139	77.4	1.00E-13	74	38	51
CAC03722	433	77.4	1.00E-13	315	74	23
CAC03722	433	31.6	9.30E+00	199	49	24
BAB18964	200	77.4	1.00E-13	134	46	34
AAM90627	145	77	2.00E-13	158	53	33
BAC16347	200	77	2.00E-13	134	46	34
BAC16341	200	77	2.00E-13	134	46	34
BAC16340	200	77	2.00E-13	134	46	34
ZP_00193517283		76.6	3.00E-13	290	65	22
AAR98527	69	76.6	3E-13	69	39	56
ZP_00337030282		76.3	3.00E-13	299	69	23
BAB19647	200	75.9	4.00E-13	134	45	33
BAB18970	200	75.9	4.00E-13	134	45	33
BAB18969	200	75.9	4.00E-13	134	45	33
BAB18968	200	75.9	4.00E-13	134	45	33
BAB18961	200	75.9	4.00E-13	134	45	33
BAB18959	200	75.9	4.00E-13	134	45	33
BAB18950	200	75.9	4.00E-13	134	45	33
BAB18949	200	75.9	4.00E-13	134	45	33
BAB18948	200	75.9	4.00E-13	134	45	33
BAB18946	200	75.9	4.00E-13	134	45	33
BAC16528	199	75.5	6.00E-13	133	45	33
BAC16532	199	75.1	7.00E-13	133	45	33
BAC16525	199	75.1	7.00E-13	133	45	33
BAC16348	200	74.7	1.00E-12	134	45	33
NP_907272	253	74.3	1.00E-12	278	65	23
BAC76096	198	74.3	1.00E-12	133	44	33
BAC76095	198	74.3	1.00E-12	133	44	33
BAC16534	199	73.9	2.00E-12	133	44	33
BAC16533	199	73.9	2.00E-12	133	44	33
BAC16527	199	73.9	2.00E-12	133	44	33
BAD18056	199	73.9	2.00E-12	133	44	33
BAD18057	193	73.9	2.00E-12	133	44	33
BAD18055	199	73.9	2.00E-12	133	44	33
AAP34191	169	73.2	3.00E-12	162	54	33
ZP_00270458289		72.8	4.00E-12	302	69	22
ZP_00289016275		72	6.00E-12	275	64	23
BAD38984	199	72	6.00E-12	133	43	32
YP_162339	285	71.6	8.00E-12	282	56	19
NP_353571	337	71.6	8.00E-12	324	75	23
NP_531244	320	71.6	8.00E-12	324	75	23
ZP_00183364320		71.6	8.00E-12	321	74	23
CAF74789	295	71.6	8.00E-12	294	67	22
AAD41622	127	71.2	1.00E-11	100	41	41
AAP34187	157	71.2	1.00E-11	160	53	33
AAP34184	154	71.2	1.00E-11	160	53	33

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAP34192	155	69.7	3.00E-11	159	52	32
CAF74790	283	69.7	3.00E-11	284	61	21
AAB48473	249	68.9	5.00E-11	288	68	23
AAC27443	249	68.9	5.00E-11	186	50	26
AAC27443	249	38.5	7.60E-02	49	20	40
AAA99141	214	68.9	5.00E-11	222	59	26
NP_281892	249	68.6	7.00E-11	288	66	22
NP_782319	316	68.2	9.00E-11	284	68	23
ZP_00337274271		67.4	2.00E-10	284	64	22
AAP34189	154	67.4	2.00E-10	158	52	32
ZP_00335243300		67	2.00E-10	302	74	24
AAM90629	117	67	2.00E-10	129	46	35
ZP_00149794326		67	2.00E-10	322	67	20
NP_972952	415	66.6	3.00E-10	285	65	22
CAA24655	38	66.2	3.00E-10	37	34	91
NP_227898	304	65.1	8.00E-10	256	62	24
AAM90636	126	65.1	8.00E-10	130	41	31
AAM90630	126	65.1	8.00E-10	130	42	32
AAQ75042	195	64.7	1.00E-09	202	52	25
YP_013346	291	64.3	1.00E-09	288	61	21
ZP_00049388242		63.9	2.00E-09	188	52	27
NP_464233	291	63.9	2.00E-09	288	61	21
ZP_00229464291		63.5	2.00E-09	288	61	21
AAO33575	375	63.5	2.00E-09	305	71	23
AAC27442	254	63.5	2.00E-09	202	51	25
AAC27442	254	38.5	7.60E-02	49	20	40
AAC65633	416	63.2	3.00E-09	268	60	22
AAQ75043	195	62.8	4.00E-09	202	51	25
NP_384778	321	62.4	5.00E-09	321	68	21
NP_642302	401	62.4	5.00E-09	134	40	29
NP_642302	401	40.8	1.50E-02	118	31	26
AAO33576	375	62.4	5.00E-09	305	71	23
CAC03720	316	62.4	5.00E-09	141	46	32
CAD11201	281	62.4	5.00E-09	108	38	35
CAD11199	281	62.4	5.00E-09	108	38	35
AAQ75041	195	62.4	5.00E-09	202	50	24
NP_470057	291	62	6.00E-09	286	60	20
AAB81422	321	62	6.00E-09	321	65	20
AAM75948	452	61.6	8.00E-09	231	55	23
AAQ75049	195	61.6	8.00E-09	202	50	24
AAQ75048	195	61.6	8.00E-09	202	50	24
AAQ75047	195	61.6	8.00E-09	202	50	24
AAQ75044	195	61.6	8.00E-09	202	50	24
AAQ75040	195	61.6	8.00E-09	202	50	24
BAA20927	195	61.6	8.00E-09	202	50	24
AAK58558	202	61.2	1.00E-08	208	52	25
ZP_00237160287		60.8	1.00E-08	243	62	25
AAK58560	202	60.8	1.00E-08	208	51	24
BAA20929	195	60.8	1.00E-08	202	50	24
AAU13836	416	60.5	2.00E-08	124	36	29
AAU13836	416	38.5	7.60E-02	260	55	21
AAK58557	202	60.5	2.00E-08	208	50	24
AAK58548	202	60.5	2.00E-08	208	50	24
NP_348828	425	60.1	2.00E-08	289	65	22
NP_348828	425	42.4	5.00E-03	310	69	22
YP_126585	411	60.1	2.00E-08	147	39	26
YP_095257	411	60.1	2.00E-08	147	39	26
AAM90638	126	60.1	2.00E-08	124	41	33
AAK58547	202	60.1	2.00E-08	208	49	23
AAK58550	202	60.1	2.00E-08	208	49	23
NP_104151	356	59.7	3.00E-08	357	81	22
AAL99376	207	59.7	3.00E-08	162	42	25
AAM90634	126	59.7	3.00E-08	138	44	31
YP_123558	411	59.3	4.00E-08	147	38	25
YP_123558	411	32	7.10E+00	83	25	30
BAC75963	530	59.3	4.00E-08	130	38	29
AAK58545	202	59.3	4.00E-08	208	49	23
AAA86521	414	58.9	5.00E-08	270	64	23

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
AAA86521	414	52	7.00E-06	108	32	29
AAQ60546	309	58.9	5.00E-08	299	62	20
ZP_00127287530		58.9	5.00E-08	135	40	29
AAA23951	288	58.5	7.00E-08	46	28	60
AAA23951	288	41.6	9.00E-03	307	79	25
NP_772484	757	58.5	7.00E-08	273	72	26
NP_772484	757	34.7	1.10E+00	109	29	26
AAK58562	200	58.5	7.00E-08	205	50	24
BAA77313	179	58.5	7.00E-08	69	29	42
BAA77311	136	58.5	7.00E-08	69	29	42
NP_637307	401	58.2	9.00E-08	134	38	28
NP_637307	401	35.8	4.90E-01	119	31	26
AAU13838	410	58.2	9.00E-08	121	35	28
AAU13838	410	38.5	7.60E-02	260	55	21
YP_083110	287	57.8	1.00E-07	242	57	23
NP_978079	287	57.8	1.00E-07	241	60	24
AAK58561	202	57.8	1.00E-07	208	51	24
NP_772486	757	57.4	2.00E-07	255	72	28
NP_772486	757	34.3	1.40E+00	109	29	26
AAS14965	190	57.4	2.00E-07	185	47	25
NP_212316	424	57.4	2.00E-07	132	38	28
NP_212316	424	35	8.40E-01	77	18	23
AAB81420	395	57.4	2.00E-07	138	38	27
AAB81420	395	50.4	2.00E-05	149	43	28
AAG14364	410	57.4	2.00E-07	418	87	20
NP_384775	394	57	2.00E-07	138	38	27
NP_384775	394	50.4	2.00E-05	87	29	33
AAS91573	80	57	2.00E-07	60	27	45
AAP34186	144	57	2.00E-07	149	47	31
AAP34181	139	57	2.00E-07	135	41	30
AAU07039	424	56.6	3.00E-07	157	46	29
AAU07039	424	35	8.40E-01	77	18	23
AAP08616	287	56.6	3.00E-07	243	57	23
ZP_00128974504		56.6	3.00E-07	113	32	28
ZP_00128974504		43.5	2.00E-03	238	50	21
A32808	395	56.2	4.00E-07	138	37	26
A32808	395	50.4	2.00E-05	149	43	28
NP_521913	316	56.2	4.00E-07	305	65	21
NP_746494	521	56.2	4.00E-07	130	41	31
NP_746494	521	41.6	9.00E-03	149	37	24
AAL99374	205	56.2	4.00E-07	157	42	26
ZP_00173445304		56.2	4.00E-07	301	68	22
AAU13837	400	55.8	5.00E-07	115	34	29
AAU13837	400	32.7	4.20E+00	254	52	20
AAK15325	433	55.8	5.00E-07	132	36	27
AAK15325	433	36.6	2.90E-01	167	45	26
AAA65584	64	55.8	5.00E-07	63	27	42
ZP_00278994407		55.5	6.00E-07	250	55	22
NP_718794	403	55.1	8.00E-07	136	36	26
NP_718794	403	34.3	1.40E+00	89	26	29
NP_791768	530	55.1	8.00E-07	130	36	27
NP_772485	757	55.1	8.00E-07	250	63	25
NP_772485	757	33.9	1.90E+00	109	29	26
CAB64773	399	55.1	8.00E-07	193	48	24
CAB64773	399	39.7	3.40E-02	72	22	30
BAA77309	94	55.1	8.00E-07	49	23	46
NP_880130	510	54.7	1.00E-06	136	43	31
YP_003353	422	54.7	1.00E-06	110	34	30
NP_992941	337	54.3	1.00E-06	310	73	23
NP_883789	510	54.3	1.00E-06	136	42	30
NP_405374	326	54.3	1.00E-06	310	73	23
ZP_00212998398		54.3	1.00E-06	111	29	26
NP_799784	299	53.9	2.00E-06	258	55	21
NP_772483	763	53.9	2.00E-06	186	47	25
NP_772483	763	36.2	3.80E-01	109	29	26
NP_244487	395	53.9	2.00E-06	126	33	26
CAA75368	168	53.9	2.00E-06	159	39	24
BAA77319	121	53.9	2.00E-06	92	32	34

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
BAA77315	123	53.9	2.00E-06	92	32	34
NP_353593	436	53.5	2.00E-06	256	59	23
NP_353593	436	46.2	4.00E-04	140	34	24
NP_753263	317	53.5	2.00E-06	299	67	22
NP_531268	430	53.5	2.00E-06	256	59	23
NP_531268	430	46.2	4.00E-04	140	34	24
AAB81421	395	53.5	2.00E-06	232	54	23
AAB81421	395	40	2.60E-02	87	24	27
BAA77301	123	53.5	2.00E-06	108	33	30
ZP_00317213517		53.1	3.00E-06	100	31	31
ZP_00317213517		40	2.60E-02	91	24	26
ZP_00273669412		52.8	4.00E-06	311	67	21
ZP_00273669412		35.8	4.90E-01	146	35	23
ZP_00056435521		52.8	4.00E-06	185	40	21
NP_384777	401	52.8	4.00E-06	189	48	25
NP_384777	401	40	2.60E-02	87	24	27
AAQ63645	159	52.4	5.00E-06	150	40	26
NP_415601	317	52	7.00E-06	305	70	22
AAQ62964	145	52	7.00E-06	144	38	26
NP_421770	424	52	7.00E-06	164	35	21
CAA75363	168	52	7.00E-06	159	38	23
AAG55829	317	51.6	9.00E-06	299	66	22
NP_967522	361	51.6	9.00E-06	178	44	24
YP_066426	757	61.6	9.00E-06	130	40	30
AAM27194	181	51.6	9.00E-06	181	44	24
BAA77303	156	51.6	9.00E-06	88	27	30
B32808	396	51.2	1.00E-05	285	66	23
B32808	396	42	7.00E-03	87	23	26
YP_111446	2634	51.2	1.00E-05	287	60	20
YP_111446	2634	50.8	1.00E-05	281	59	20
YP_111446	2634	47	2.00E-04	296	63	21
YP_111446	2634	46.2	4.00E-04	291	60	20
YP_111446	2634	45.1	8.00E-04	292	58	19
YP_111446	2634	43.5	2.00E-03	284	58	20
YP_111446	2634	43.5	2.00E-03	283	58	20
YP_111446	2634	43.5	2.00E-03	289	59	20
YP_111446	2634	43.1	3.00E-03	292	59	20
YP_111446	2634	42	7.00E-03	281	63	22
YP_111446	2634	40	2.60E-02	295	59	20
YP_111446	2634	40	2.60E-02	298	59	19
YP_111446	2634	39.3	4.40E-02	302	59	19
YP_111446	2634	38.9	5.80E-02	283	53	18
YP_111446	2634	37.4	1.70E-01	278	48	17
YP_111446	2634	35.8	4.90E-01	235	50	21
YP_105520	459	51.2	1.00E-05	248	57	22
YP_105520	459	41.6	9.00E-03	298	60	20
YP_027819	207	51.2	1.00E-05	115	30	26
NP_866849	651	51.2	1.00E-05	129	34	26
NP_947642	935	50.8	1.00E-05	284	70	24
NP_947642	935	34.3	1.40E+00	93	22	23
NP_949266	888	50.8	1.00E-05	284	69	24
NP_949266	888	38.9	5.80E-02	305	63	20
YP_009743	523	50.4	2.00E-05	123	32	26
YP_009743	523	33.9	1.90E+00	171	36	21
ZP_00129084282		50.4	2.00E-05	285	68	23
NP_282040	750	50.1	3.00E-05	129	36	27
NP_282040	750	41.6	9.00E-03	229	48	20
ZP_00242042398		49.7	3.00E-05	215	53	24
ZP_00242042398		39.7	3.40E-02	140	35	25
AAS66690	430	49.3	4.00E-05	134	34	25
AAS66690	430	48.5	7.00E-05	130	33	25
BAA77305	78	48.9	6.00E-05	74	28	37
ZP_00263356523		48.5	7.00E-05	162	43	26
ZP_00263356523		35	6.40E-01	106	23	21
NP_460155	317	48.5	7.00E-05	140	38	27
YP_150904	317	48.5	7.00E-05	140	38	27
YP_128296	304	48.5	7.00E-05	293	53	18
YP_040849	10746	48.5	7.00E-05	303	63	20
YP_040849	10746	42.4	5.00E-03	340	71	20
YP_040849	10746	36.6	2.90E-01	297	58	19
YP_040849	10746	36.6	2.90E-01	332	69	20
YP_040849	10746	35.8	4.90E-01	301	63	20
YP_040849	10746	33.5	2.40E+00	279	55	19
YP_040849	10746	33.1	3.20E+00	317	68	21
YP_040849	10746	31.6	9.30E+00	297	57	19
AAB81423	395	48.5	7.00E-05	285	66	23
AAB81423	395	45.1	8.00E-04	146	38	26
1ORY	65	48.5	7.00E-05	50	24	48
ZP_00167907404		48.5	7.00E-05	121	37	30
ZP_00167907404		35.4	6.40E-01	99	23	23
AAB69136	37	48.5	7.00E-05	36	23	63
AAG14365	411	48.1	1.00E-04	207	51	24
AAG14365	411	42.4	6.00E-03	116	27	23
NP_384776	394	47.8	1.00E-04	137	34	24
NP_384776	394	45.8	5.00E-04	245	56	22
AAF34780	3381	47.8	1.00E-04	286	55	19
AAF34780	3381	45.1	8.00E-04	295	58	19
AAF34780	3381	44.7	1.00E-03	274	50	18
AAF34780	3381	42.7	4.00E-03	285	51	17
AAF34780	3381	41.2	1.20E-02	300	56	15
AAF34780	3381	39.7	3.40E-02	278	48	17
BAA05156	24	47.8	1.00E-04	24	24	100
NP_562800	451	47.4	2.00E-04	220	53	24
NP_455677	317	47.4	2.00E-04	140	38	27
NP_646141	9904	47	2.00E-04	306	64	20
NP_646141	9904	43.1	3.00E-03	153	36	23
NP_646141	9904	39.7	3.40E-02	332	71	21
NP_646141	9904	39.3	4.40E-02	283	66	23
NP_646141	9904	38.1	9.90E-02	279	56	20
NP_646141	9904	35.4	6.40E-01	317	66	20
NP_646141	9904	33.9	1.90E+00	297	57	19
AAQ73340	142	47	2.00E-04	132	36	27
YP_012160	282	47	2.00E-04	223	53	23
AAB21164	31	47	2.00E-04	31	24	77
NP_249778	439	46.6	3.00E-04	134	34	25
NP_249778	439	32	7.10E+00	257	50	19
ZP_00138675439		46.6	3.00E-04	134	34	25
ZP_00314296822		46.2	4.00E-04	267	54	21
NP_223759	267	46.2	4.00E-04	149	40	26
YP_108306	1606	46.2	4.00E-04	296	66	22
YP_108306	1506	38.1	9.90E-02	281	57	20
YP_108306	1606	38.1	9.90E-02	228	54	23
YP_108306	1606	38.1	9.90E-02	309	60	19
YP_108306	1606	37.4	1.70E-01	256	58	22
AAK97535	140	46.2	4.00E-04	126	35	27
CAC84733	78	46.2	4.00E-04	71	25	35
CAC84731	78	46.2	4.00E-04	71	25	35
AAB69371	89	46.2	4.00E-04	78	21	26
AAB69370	89	46.2	4.00E-04	77	21	27
ZP_00290372765		45.8	5.00E-04	280	56	20
CAA75373	158	45.8	5.00E-04	139	33	23
CAA75370	154	45.8	5.00E-04	139	33	23
CAA75369	159	45.8	5.00E-04	139	33	23
NP_267773	1072	45.4	6.00E-04	287	53	18
NP_267773	1072	33.6	2.40E+00	91	21	23
AAQ64681	134	45.4	6.00E-04	132	35	26
NP_228520	407	45.4	6.00E-04	290	63	21
ZP_003230792334		45.4	6.00E-04	274	50	18
ZP_003230792334		39.7	3.40E-02	276	49	17
ZP_003230792334		39.3	4.40E-02	293	54	18
ZP_003230792334		38.5	7.60E-02	294	53	18
ZP_003230792334		37	2.20E-01	280	52	18
ZP_003230792334		34.7	1.10E+00	261	50	19
CAA75376	163	45.4	6.00E-04	139	33	23
CAA75374	155	45.4	6.00E-04	139	33	23
CAA75372	159	45.4	6.00E-04	139	33	23

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
CAA75367	154	45.4	6.00E-04	139	33	23
CAA75365	157	45.4	6.00E-04	139	33	23
CAA75364	159	45.4	6.00E-04	139	33	23
AAD25047	156	45.4	6.00E-04	143	36	25
BAA02072	24	45.1	8.00E-04	24	23	95
YP_111449	1530	45.1	8.00E-04	295	64	21
YP_111449	1530	44.7	1.00E-03	292	64	21
YP_111449	1530	44.3	1.00E-03	278	59	21
YP_111449	1530	42.7	4.00E-03	320	69	21
YP_111449	1530	41.6	9.00E-03	288	59	20
YP_111449	1530	41.2	1.20E-02	284	60	21
YP_111449	1530	40	2.60E-02	250	51	20
YP_111449	1530	37.7	1.30E-01	250	50	20
YP_111449	1530	37	2.20E-01	263	52	19
YP_111449	1530	34.7	1.10E+00	257	55	21
CAA75375	151	45.1	8.00E-04	139	33	23
CAA61528	436	45.1	8.00E-04	105	29	27
AAF67137	159	45.1	8.00E-04	146	37	25
NP_949252	886	44.7	1.00E-03	194	49	25
NP_949252	886	33.9	1.90E+00	102	25	24
YP_155526	404	44.7	1.00E-03	130	35	26
YP_155526	404	32	7.10E+00	196	41	20
NP_929192	321	44.7	1.00E-03	318	74	23
NP_647392	2275	44.7	1.00E-03	287	53	18
NP_647392	2275	34.3	1.40E+00	216	42	19
NP_647392	2275	34.3	1.40E+00	299	60	20
NP_371958	6713	44.7	1.00E-03	303	61	20
NP_371958	6713	42	7.00E-03	153	36	23
NP_371958	6713	41.2	1.20E-02	332	72	21
NP_371958	6713	35.4	6.40E-01	276	53	19
NP_371958	6713	33.1	3.20E+00	297	57	19
AAP48612	107	44.7	1.00E-03	94	24	25
NP_374548	6713	44.7	1.00E-03	303	61	20
NP_374548	6713	42	7.00E-03	153	36	23
NP_374548	6713	41.2	1.20E-02	332	72	21
NP_374548	6713	35.4	6.40E-01	276	53	19
NP_374548	6713	33.1	3.20E+00	297	57	19
YP_106908	410	44.7	1.00E-03	124	28	22
YP_044654	2275	44.7	1.00E-03	287	53	18
YP_044654	2275	34.3	1.40E+00	216	42	19
AAF67139	159	44.7	1.00E-03	146	37	25
AAK39536	107	44.7	1.00E-03	94	24	25
AAK39541	107	44.7	1.00E-03	94	24	25
AAA27080	284	44.3	1.00E-03	30	21	70
AAA27080	284	37.4	1.70E-01	31	18	58
YP_110805	1653	44.3	1.00E-03	269	58	21
YP_110805	1653	40	2.60E-02	254	56	22
YP_110805	1653	37	2.20E-01	287	58	20
YP_110805	1653	36.2	3.80E-01	274	56	20
YP_110805	1653	34.7	1.10E+00	265	52	19
CAA75371	159	44.3	1.00E-03	139	33	23
AAD21057	4545	44.3	1.00E-03	228	52	22
ZP_001627551140		44.3	1.00E-03	295	62	21
T30822	1365	44.3	1.00E-03	284	53	18
AAF94608	4558	43.9	2.00E-03	228	52	22
CAA57229	962	43.9	2.00E-03	284	53	18
CAA57228	1344	43.9	2.00E-03	284	53	18
CAA57228	1344	43.9	2.00E-03	284	53	18
CAA57228	1344	43.5	2.00E-03	284	53	18
CAA57228	1344	43.1	3.00E-03	269	50	18
AAK39539	107	43.9	2.00E-03	94	24	25
AAB69366	89	43.9	2.00E-03	77	21	27
AAA81014	716	43.9	2.00E-03	284	53	18
AAA81014	716	43.1	3.00E-03	269	50	18
CAF74791	410	43.9	2.00E-03	224	46	20
AAP48610	107	43.5	2.00E-03	91	28	30
AAP48609	107	43.5	2.00E-03	91	28	30
AAB69367	89	43.5	2.00E-03	77	20	26

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
ZP_00326048609		43.1	3.00E-03	273	63	23
ZP_00326048609		32	7.10E+00	99	20	20
CAA36029	21	43.1	3.00E-03	21	21	100
ZP_00051799172		43.1	3.00E-03	136	31	22
AAP48611	107	43.1	3.00E-03	91	27	29
NP_207286	295	43.1	3.00E-03	150	42	28
NP_936893	989	43.1	3.00E-03	289	63	21
AAK39533	107	43.1	3.00E-03	91	27	29
AAQ59385	302	42.7	4.00E-03	282	55	19
NP_267008	1063	42.7	4.00E-03	291	56	19
NP_267008	1063	37	2.20E-01	231	42	18
NP_267008	1063	36.6	2.90E-01	281	63	22
YP_042074	1351	42.7	4.00E-03	304	59	19
CAA61527	436	42.7	4.00E-03	99	27	27
AAK39530	107	42.7	4.00E-03	81	26	32
AAB69368	89	42.7	4.00E-03	77	20	25
NP_939992	1254	42.4	5.00E-03	169	38	22
YP_105401	1535	42.4	5.00E-03	300	63	21
YP_105401	1535	36.2	3.80E-01	307	64	20
YP_105401	1535	35.8	4.90E-01	217	46	21
YP_065260	567	42.4	5.00E-03	263	54	20
NP_906736	846	42.4	5.00E-03	168	37	22
ZP_001432362005		42.4	5.00E-03	256	59	23
AAK39535	107	42.4	5.00E-03	81	25	30
AAK39534	107	42.4	5.00E-03	81	25	30
AAB69365	89	42.4	5.00E-03	77	20	25
NP_523179	1309	42	7.00E-03	264	60	22
NP_523179	1309	36.2	3.80E-01	260	56	21
NP_523179	1309	35.8	4.90E-01	247	57	23
AAF95046	672	42	7.00E-03	320	64	20
NP_488975	661	42	7.00E-03	268	63	23
NP_784110	1377	42	7.00E-03	285	64	22
AAL58470	2283	42	7.00E-03	299	55	18
AAL58470	2283	35.4	6.40E-01	269	58	21
AAL58470	2283	33.9	1.90E+00	285	52	18
AAL58470	2283	33.5	2.40E+00	270	44	16
AAQ97872	309	41.6	9.00E-03	306	71	23
YP_129124	396	41.6	9.00E-03	119	25	21
CAC84729	68	41.6	9.00E-03	65	24	36
AAA27074	20	41.6	9.00E-03	20	20	100
AAB69357	89	41.6	9.00E-03	74	24	32
ZP_00089080401		41.6	9.00E-03	122	36	29
ZP_00089080401		38.5	7.60E-02	139	36	25
NP_465811	1787	41.2	1.20E-02	268	58	21
ZP_002143701439		41.2	1.20E-02	297	72	24
ZP_002143701439		32.3	5.40E+00	272	56	20
AAB69377	89	41.2	1.20E-02	74	23	31
AAP07456	953	40.8	1.50E-02	263	49	18
CAA90950	20	40.8	1.50E-02	20	20	100
AAS91596	44	40.8	1.50E-02	38	18	47
ZP_00063096901		40.8	1.50E-02	241	60	24
NP_251152	5627	40.4	2.00E-02	329	67	20
NP_251152	5627	34.3	1.40E+00	235	50	21
NP_251152	5627	32.7	4.20E+00	312	60	19
AAM90995	3692	40.4	2.00E-02	278	64	23
AAM90995	3692	39.3	4.40E-02	321	76	23
AAS91595	44	40.4	2.00E-02	38	18	47
AAB69376	89	40.4	2.00E-02	64	21	32
AAB69369	89	40.4	2.00E-02	64	21	32
AAB69354	89	40.4	2.00E-02	64	21	32
ZP_00288079749		40	2.60E-02	236	51	21
AAA92491	20	40	2.60E-02	20	18	90
YP_142319	789	40	2.60E-02	302	64	21
YP_140402	710	40	2.60E-02	302	64	21
NP_373178	2271	40	2.60E-02	287	52	18
NP_373178	2271	34.3	1.40E+00	216	42	19
NP_373178	2271	32	7.10E+00	303	62	20
AAO08483	623	40	2.60E-02	114	31	27

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
YP_114536	437	40	2.60E-02	83	27	32
YP_034700	953	40	2.60E-02	301	58	19
NP_936493	623	40	2.60E-02	114	31	27
NP_764683	9439	40	2.60E-02	130	27	20
NP_764683	9439	38.5	7.60E-02	169	43	25
NP_764683	9439	36.2	3.80E-01	265	55	20
NP_764683	9439	36.2	3.80E-01	288	61	21
NP_764683	9439	36.2	3.80E-01	255	48	18
NP_764683	9439	35.4	6.40E-01	316	61	19
NP_764683	9439	34.7	1.10E+00	302	60	19
NP_764683	9439	33.9	1.90E+00	314	65	20
NP_764683	9439	33.9	1.90E+00	146	40	27
NP_764683	9439	33.1	3.20E+00	181	46	25
NP_764683	9439	33.1	3.20E+00	151	38	25
NP_764683	9439	32.3	5.40E+00	329	68	20
NP_764683	9439	31.6	9.30E+00	292	53	18
AAN08647	402	39.7	3.40E-02	148	34	22
ZP_00123691638		39.7	3.40E-02	352	74	21
ZP_000642471003		39.7	3.40E-02	307	71	23
AAC09051	130	39.7	3.40E-02	97	26	26
AAC09050	130	39.7	3.40E-02	97	26	26
AAC09048	130	39.7	3.40E-02	97	26	26
AAB52741	425	39.7	3.40E-02	136	34	25
AAB62741	425	32	7.10E+00	78	18	23
AAR21284	163	39.7	3.40E-02	97	26	26
AAR21282	161	39.7	3.40E-02	97	26	26
ZP_00319871233		39.3	4.40E-02	139	37	26
NP_908061	118	39.3	4.40E-02	103	29	28
ZP_002335911787		39.3	4.40E-02	261	60	22
AAC09046	130	39.3	4.40E-02	97	26	26
1QOY	318	39.3	4.40E-02	77	27	35
NP_798012	3240	38.9	5.80E-02	269	58	21
YP_015833	662	38.9	5.80E-02	167	43	25
ZP_002814314726		38.9	5.80E-02	310	62	20
ZP_002814314726		38.1	9.90E-02	308	61	19
ZP_002814314726		37.4	1.70E-01	272	54	19
ZP_002814314726		36.6	2.90E-01	275	56	20
ZP_002814314726		36.6	2.90E-01	254	53	20
ZP_002814314726		35.4	6.40E-01	279	55	19
ZP_002814314726		35	8.40E-01	319	59	18
ZP_002814314726		34.3	1.40E+00	324	59	18
ZP_00211493472		38.9	5.80E-02	274	60	21
ZP_002047941979		38.9	5.80E-02	235	47	20
ZP_002047941979		34.7	1.10E+00	235	50	21
ZP_002047941979		33.1	3.20E+00	312	61	19
AAC43555	35	38.9	5.80E-02	34	21	61
ZP_00208729459		38.5	0.076	278	63	22
NP_928380	567	38.5	0.076	257	58	22
YP_115646	750	38.5	7.60E-02	144	32	22
YP_087940	5399	38.5	7.60E-02	312	72	23
YP_087940	5399	37.4	1.70E-01	256	45	17
YP_087940	5399	37.4	1.70E-01	256	45	17
YP_087940	5399	36.2	3.80E-01	273	58	21
YP_087940	5399	36.2	3.80E-01	273	58	21
YP_087940	5399	35.8	4.90E-01	274	61	22
YP_087940	5399	35	8.40E-01	294	58	19
YP_087940	5399	33.9	1.90E+00	289	57	19
YP_087940	5399	33.5	2.40E+00	289	57	19
NP_781518	518	38.5	7.60E-02	302	64	21
AAM46179	146	38.5	7.60E-02	95	25	26
AAM46178	147	38.5	7.60E-02	95	25	26
CAC51118	1564	38.5	7.60E-02	275	60	21
ZP_00213493557		38.5	7.60E-02	223	51	22
ZP_00224552561		38.5	7.60E-02	223	53	23
ZP_00355727801		38.5	7.60E-02	317	71	22
ZP_001404443443		38.5	7.60E-02	286	62	21
AAC43560	36	38.5	7.60E-02	36	19	52
AAB69373	89	38.5	7.60E-02	74	22	29

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_419715	307	38.1	9.90E-02	73	21	28
NP_207906	228	38.1	9.90E-02	110	32	29
ZP_003235731130		38.1	9.90E-02	292	65	22
ZP_003235731130		32.3	5.40E+00	281	57	20
ZP_00317192676		37.7	1.30E-01	169	35	20
CAA60556	61	37.7	1.30E-01	43	16	37
NP_771092	696	37.7	1.30E-01	134	39	29
NP_214145	422	37.7	1.30E-01	186	40	21
NP_765958	681	37.7	1.30E-01	176	45	25
ZP_003125671475		37.7	1.30E-01	273	58	21
ZP_00240971564		37.7	1.30E-01	107	24	22
ZP_00195263572		37.7	1.30E-01	183	41	22
BAD13429	718	37.7	1.30E-01	89	18	20
AAB19816	20	37.7	1.30E-01	20	18	90
NP_949268	623	37.4	1.70E-01	277	53	19
ZP_00315446537		37.4	1.70E-01	263	54	20
ZP_0028945115245		37.4	1.70E-01	272	65	23
ZP_00273576527		37.4	1.70E-01	90	25	27
ZP_00273576527		33.9	1.90E+00	83	22	26
NP_800021	623	37.4	1.70E-01	117	31	26
NP_772493	627	37.4	1.70E-01	229	49	21
AAP78292	855	37.4	1.70E-01	138	32	23
ZP_00281310507		37.4	1.70E-01	119	31	26
ZP_00289133779		37	2.20E-01	198	38	19
ZP_00289133779		36.2	3.80E-01	89	26	29
NP_471790	927	37	2.20E-01	281	59	20
NP_471790	927	31.6	9.30E+00	210	46	21
NP_622634	3322	37	2.20E-01	228	52	22
NP_404364	307	37	2.20E-01	253	52	20
NP_336479	342	37	2.20E-01	87	25	28
NP_248731	3535	37	2.20E-01	286	62	21
YP_066441	693	37	2.20E-01	120	30	25
NP_757754	161	37	2.20E-01	77	23	29
NP_670743	308	37	2.20E-01	253	52	20
NP_603291	1724	37	2.20E-01	131	34	25
ZP_00290800910		37	2.20E-01	260	53	20
ZP_00219646252		37	2.20E-01	74	21	28
ZP_00063136721		37	2.20E-01	298	58	19
NP_799785	346	36.6	2.90E-01	116	29	25
NP_739300	290	36.6	2.90E-01	122	30	24
AAP96352	1119	36.6	2.90E-01	143	35	24
NP_359656	1902	36.6	2.90E-01	282	60	21
NP_253231	1417	36.6	2.90E-01	201	49	24
NP_932208	603	36.6	2.90E-01	53	17	32
CAA60548	61	36.6	2.90E-01	43	15	34
AAT28336	160	36.6	2.90E-01	166	34	20
AAT28335	160	36.6	2.90E-01	166	34	20
AAT28333	160	36.6	2.90E-01	166	34	20
ZP_00218988486		36.6	2.90E-01	259	56	21
ZP_00149774452		36.6	2.90E-01	264	56	21
AAP34183	119	36.6	2.90E-01	115	31	26
ZP_00319246821		36.2	3.80E-01	65	19	29
ZP_00284479601		36.2	3.80E-01	262	52	19
ZP_00005278425		36.2	3.80E-01	193	50	25
NP_522101	3552	36.2	3.80E-01	209	45	21
NP_964415	1096	36.2	3.80E-01	265	56	21
AAG31286	1363	36.2	3.80E-01	193	50	25
ZP_00313063880		36.2	3.80E-01	181	39	21
AAT28334	160	36.2	3.80E-01	166	34	20
ZP_00182337425		36.2	3.80E-01	245	41	16
ZP_00160617717		36.2	3.80E-01	289	62	21
ZP_00160617717		31.6	9.30E+00	248	46	18
ZP_001380311417		36.2	3.80E-01	201	49	24
AAR37720	394	36.2	3.80E-01	146	39	26
NP_561526	1109	35.8	4.90E-01	287	53	18
NP_561526	1109	32	7.10E+00	181	40	22
NP_349224	664	35.8	4.90E-01	272	59	21
AAP56614	499	35.8	4.90E-01	183	40	21

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
YP_133518	665	35.8	4.90E-01	111	33	29
YP_071943	3378	35.8	4.90E-01	289	61	21
YP_049813	317	35.8	4.90E-01	266	61	22
AAT28337	160	35.8	4.90E-01	166	34	20
AAA27141	17	35.8	4.90E-01	17	17	100
ZP_00270453727		35.4	6.40E-01	239	49	20
AAQ59977	458	35.4	6.40E-01	266	61	22
NP_773497	491	35.4	6.40E-01	121	28	23
NP_267038	799	35.4	6.40E-01	301	71	23
NP_478503	1487	35.4	6.40E-01	249	49	19
YP_086339	564	35.4	6.40E-01	107	23	21
NP_207948	1230	35.4	6.40E-01	292	62	21
YP_039058	564	35.4	6.40E-01	107	23	21
NP_864533	7716	35.4	6.40E-01	240	52	21
NP_765804	2310	35.4	6.40E-01	290	52	17
NP_765787	676	35.4	6.40E-01	117	33	28
ZP_00323296769		35.4	6.40E-01	148	35	23
ZP_00288038997		35.4	6.40E-01	294	56	19
CAE46764	510	35.4	6.40E-01	95	29	30
CAE46762	506	35.4	6.40E-01	95	29	30
T08613	619	35.4	6.40E-01	173	37	21
AAP34195	125	35.4	6.40E-01	129	35	27
ZP_00338261589		35	8.40E-01	62	20	32
NP_718836	667	35	8.40E-01	98	20	20
YP_128297	361	35	8.40E-01	358	69	19
YP_132326	529	35	8.40E-01	332	69	20
NP_812240	868	35	8.40E-01	150	44	29
NP_964984	4734	35	8.40E-01	316	66	20
NP_964984	4734	33.1	3.20E+00	153	40	26
AAN33150	434	35	8.40E-01	127	35	27
ZP_00144637646		35	8.40E-01	243	44	18
ZP_00222048485		35	8.40E-01	88	23	26
ZP_00220113501		35	8.40E-01	88	23	26
ZP_00137782629		35	8.40E-01	245	43	17
ZP_00121836231		35	8.40E-01	165	39	23
AAQ19127	2343	35	8.40E-01	239	49	20
NP_946001	587	34.7	1.10E+00	121	36	29
ZP_00319892754		34.7	1.10E+00	284	62	21
ZP_00319892754		33.1	3.20E+00	261	51	19
ZP_00311897602		34.7	1.10E+00	269	56	20
YP_160437	862	34.7	1.10E+00	68	24	35
ZP_00336629824		34.7	1.10E+00	149	35	23
NP_802026	593	34.7	1.10E+00	118	33	27
NP_924800	1241	34.7	1.10E+00	73	24	32
NP_463823	500	34.7	1.10E+00	233	47	20
NP_645581	946	34.7	1.10E+00	219	44	20
NP_792426	633	34.7	1.10E+00	283	50	17
NP_561978	344	34.7	1.10E+00	232	49	21
NP_350172	783	34.7	1.10E+00	129	29	22
NP_349191	722	34.7	1.10E+00	143	36	25
NP_349191	722	33.1	3.20E+00	292	57	19
AAO10484	626	34.7	1.10E+00	299	52	17
NP_642322	396	34.7	1.10E+00	123	22	17
YP_133410	577	34.7	1.10E+00	317	61	19
NP_259527	594	34.7	1.10E+00	118	33	27
YP_060520	593	34.7	1.10E+00	118	33	27
YP_042878	928	34.7	1.10E+00	219	44	20
YP_012922	500	34.7	1.10E+00	233	47	20
NP_051325	222	34.7	1.10E+00	114	30	26
NP_782459	569	34.7	1.10E+00	305	61	20
NP_607532	594	34.7	1.10E+00	118	33	27
ZP_00233976541		34.7	1.10E+00	233	47	20
ZP_00212291306		34.7	1.10E+00	130	38	29
AAK84427	542	34.7	1.10E+00	233	47	20
AAA67447	232	34.7	1.10E+00	149	33	22
YP_162386	564	34.3	1.40E+00	242	55	22
NP_469464	1788	34.3	1.40E+00	290	65	22
NP_792292	629	34.3	1.40E+00	128	31	24

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_695350	459	34.3	1.40E+00	271	54	19
NP_348729	570	34.3	1.40E+00	162	36	22
YP_046173	335	34.3	1.40E+00	117	26	22
NP_252997	632	34.3	1.40E+00	245	43	17
YP_066477	393	34.3	1.40E+00	148	33	22
YP_064761	880	34.3	1.40E+00	126	30	23
YP_064723	674	34.3	1.40E+00	248	48	19
NP_935137	626	34.3	1.40E+00	299	52	17
NP_866060	3056	34.3	1.40E+00	120	34	28
NP_866060	3056	33.1	3.20E+00	116	34	29
ZP_003233981656		34.3	1.4	187	41	21
ZP_00308827366		34.3	1.40E+00	138	35	25
ZP_00137780616		34.3	1.40E+00	245	43	17
ZP_00124017629		34.3	1.40E+00	254	46	18
ZP_00110825475		34.3	1.40E+00	140	35	25
ZP_00046942967		33.9	1.90E+00	134	35	26
YP_080405	660	33.9	1.90E+00	87	22	25
NP_470074	599	33.9	1.90E+00	288	59	20
NP_927898	4582	33.9	1.90E+00	257	61	23
NP_815456	533	33.9	1.90E+00	125	35	28
NP_562046	933	33.9	1.90E+00	259	51	19
NP_267826	901	33.9	1.90E+00	281	56	19
YP_126425	657	33.9	1.90E+00	121	29	23
YP_131301	638	33.9	1.90E+00	73	16	21
YP_030040	660	33.9	1.90E+00	105	25	23
NP_981473	564	33.9	1.90E+00	109	24	22
NP_784971	983	33.9	1.9	299	58	19
NP_783077	417	33.9	1.90E+00	103	24	23
NP_965011	912	33.9	1.90E+00	214	49	22
NP_964462	1000	33.9	1.90E+00	125	28	22
AAP02960	599	33.9	1.90E+00	119	30	25
BAB20920	1172	33.9	1.90E+00	283	55	19
ZP_002991151200		33.5	2.4	61	17	27
ZP_00056271661		33.5	2.40E+00	278	54	19
AAG56007	973	33.5	2.40E+00	185	42	22
AAF81209	277	33.5	2.40E+00	199	45	22
NP_794375	539	33.5	2.40E+00	128	23	17
YP_115527	534	33.5	2.40E+00	80	24	30
AAK93934	736	33.5	2.40E+00	89	20	22
NP_309677	971	33.5	2.4	185	42	22
NP_936396	542	33.5	2.40E+00	300	62	20
NP_637327	396	33.5	2.40E+00	123	21	17
NP_964159	982	33.5	2.40E+00	203	47	23
ZP_00217082977		33.5	2.40E+00	109	32	29
ZP_00106667978		33.5	2.40E+00	112	29	25
AAB21165	20	33.5	2.40E+00	20	16	80
BAA23410	632	33.5	2.40E+00	229	43	18
ZP_00290912684		33.1	3.20E+00	130	24	18
ZP_00290912684		32.3	5.40E+00	188	35	18
YP_147975	435	33.1	3.20E+00	121	32	26
ZP_00338277837		33.1	3.20E+00	109	26	23
AAU01878	1363	33.1	3.20E+00	175	40	22
NP_798538	678	33.1	3.20E+00	127	27	21
NP_790701	498	33.1	3.20E+00	162	41	25
NP_768559	816	33.1	3.20E+00	62	19	30
NP_415890	1122	33.1	3.20E+00	147	37	25
AAO08482	622	33.1	3.20E+00	120	30	25
AAO10918	675	33.1	3.20E+00	125	29	23
NP_889112	632	33.1	3.20E+00	250	48	19
YP_129467	640	33.1	3.20E+00	137	31	22
YP_133516	467	33.1	3.20E+00	127	26	20
YP_132040	542	33.1	3.20E+00	107	27	25
YP_076807	558	33.1	3.20E+00	118	30	25
NP_253000	629	33.1	3.20E+00	245	42	17
YP_063897	576	33.1	3.20E+00	263	46	17
YP_041192	424	33.1	3.20E+00	147	36	24
NP_936490	622	33.1	3.20E+00	120	30	25
NP_786249	1106	33.1	3.20E+00	330	64	19

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_777771	638	33.1	3.20E+00	121	29	23
NP_764984	3692	33.1	3.2	148	30	20
NP_764984	3692	32.3	5.40E+00	264	52	19
NP_600104	441	33.1	3.20E+00	280	63	22
NP_693909	466	33.1	3.20E+00	126	24	19
NP_608047	400	33.1	3.20E+00	108	29	26
NP_604026	1193	33.1	3.20E+00	253	52	20
NP_541885	131	33.1	3.20E+00	62	24	38
gi|42627767|tpe|CAD89361.1| TPA: SbcC exonuclease [Bradyrhizobium japonicum]	1261	33.1	3.20E+00	62	19	30
CAA64859	624	33.1	3.20E+00	284	47	16
CAA81206	955	33.1	3.20E+00	239	47	19
BAB98269	413	33.1	3.20E+00	280	63	22
AAD43469	912	33.1	3.20E+00	240	48	20
ZP_00137783633		33.1	3.20E+00	245	42	17
ZP_00123950634		33.1	3.20E+00	96	24	25
ZP_00128148551		33.1	3.20E+00	256	46	17
ZP_003460801463		33.1	3.20E+00	274	69	25
AAG60897	896	33.1	3.20E+00	62	19	30
PC6003	624	33.1	3.2	284	47	16
P76072	1120	33.1	3.20E+00	147	37	25
BAA23413	629	33.1	3.20E+00	245	42	17
ZP_00326431563		32.7	4.20E+00	307	70	22
CAA79304	933	32.7	4.20E+00	145	30	20
NP_252999	629	32.7	4.20E+00	127	32	25
AAM01202	183	32.7	4.20E+00	121	29	23
ZP_000531851136		32.7	4.20E+00	223	51	22
NP_993634	2578	32.7	4.20E+00	290	61	21
YP_081346	561	32.7	4.20E+00	99	20	20
NP_471252	1186	32.7	4.20E+00	316	63	20
NP_469482	290	32.7	4.20E+00	82	21	25
NP_464250	601	32.7	4.20E+00	193	39	20
NP_929013	190	32.7	4.20E+00	133	34	25
NP_793014	6274	32.7	4.2	246	51	20
NP_790315	541	32.7	4.20E+00	93	28	30
NP_769573	564	32.7	4.20E+00	157	36	22
NP_563507	721	32.7	4.20E+00	112	25	22
NP_406024	2535	32.7	4.20E+00	290	61	21
NP_939703	888	32.7	4.20E+00	123	31	25
AAP56776	742	32.7	4.20E+00	186	40	21
NP_882071	1175	32.7	4.20E+00	65	18	27
NP_419323	622	32.7	4.20E+00	235	47	20
YP_108428	634	32.7	4.20E+00	266	52	19
NP_109825	228	32.7	4.20E+00	154	29	18
YP_013363	601	32.7	4.20E+00	193	39	20
NP_669014	2579	32.7	4.20E+00	290	61	21
ZP_00284267481		32.7	4.20E+00	77	21	27
ZP_00280424428		32.7	4.20E+00	196	50	25
AAM01201	183	32.7	4.20E+00	121	29	23
BAA23412	629	32.7	4.20E+00	127	32	25
NP_326456	750	32.3	5.40E+00	121	27	22
CAA55199	545	32.3	5.40E+00	238	47	19
NP_391003	662	32.3	5.40E+00	322	60	18
A42292	818	32.3	5.40E+00	103	29	28
BAA02196	777	32.3	5.40E+00	134	35	26
AAP08880	1658	32.3	5.40E+00	149	33	22
AAP08880	1658	32.3	5.40E+00	139	27	19
NP_646487	424	32.3	5.40E+00	147	36	24
NP_718941	169	32.3	5.40E+00	160	36	22
NP_716901	706	32.3	5.40E+00	273	59	21
NP_801002	542	32.3	5.40E+00	304	58	19
AAQ60540	2373	32.3	5.40E+00	255	55	21
AAQ58389	690	32.3	5.40E+00	110	25	22
NP_770343	582	32.3	5.4	270	50	18
AAF96820	652	32.3	5.40E+00	120	31	25
AAF94794	596	32.3	5.40E+00	80	19	23
NP_404241	3295	32.3	5.40E+00	289	61	21
YP_032604	1872	32.3	5.40E+00	118	31	26
NP_782523	471	32.3	5.40E+00	107	20	18
NP_765908	300	32.3	5.40E+00	132	29	21
NP_765785	952	32.3	5.40E+00	195	37	18
NP_606940	628	32.3	5.40E+00	271	60	22
CAF32691	1828	32.3	5.40E+00	228	56	24
CAD56598	1184	32.3	5.40E+00	270	49	18
ZP_002394591038		32.3	5.40E+00	243	52	21
ZP_00236267289		32.3	5.40E+00	156	31	19
ZP_002326811066		32.3	5.40E+00	277	57	20
CAB99193	326	32.3	5.40E+00	104	27	25
AAT41983	427	32.3	5.40E+00	245	48	19
AAF25839	177	32.3	5.40E+00	86	23	26
AAS93940	693	32.3	5.40E+00	137	29	21
ZP_002188313513		32.3	5.40E+00	204	51	25
ZP_00171926505		32.3	5.40E+00	253	48	18
ZP_00201727822		32.3	5.40E+00	306	59	19
P55116	953	32.3	5.40E+00	233	48	20
ZP_00149920505		32.3	5.40E+00	139	31	22
ZP_00133930158		32.3	5.40E+00	106	26	24
ZP_00098108451		32.3	5.40E+00	139	33	23
AAK27341	3241	32.3	5.40E+00	102	24	23
ZP_00312864422		32	7.10E+00	142	36	25
ZP_00298543733		32	7.10E+00	278	50	17
ZP_003410411311		32	7.10E+00	230	37	16
ZP_00208461932		32	7.10E+00	211	43	20
ZP_00046132979		32	7.10E+00	143	32	22
NP_464751	1066	32	7.10E+00	277	56	20
NP_885521	1195	32	7.10E+00	65	18	27
AAQ60246	251	32	7.10E+00	98	30	30
NP_768828	432	32	7.10E+00	164	35	21
NP_699533	317	32	7.10E+00	56	22	39
NP_346950	371	32	7.1	147	35	23
NP_207534	493	32	7.1	122	32	26
NP_249777	683	32	7.1	303	72	23
YP_060448	1039	32	7.1	193	42	21
YP_041227	2189	32	7.10E+00	149	35	23
YP_010811	580	32	7.10E+00	206	44	21
NP_784951	3360	32	7.10E+00	76	21	27
NP_765498	495	32	7.10E+00	74	16	21
NP_757771	1378	32	7.10E+00	73	22	30
NP_688862	443	32	7.10E+00	66	17	25
AAO19442	5431	32	7.10E+00	206	44	21
ZP_002842243286		32	7.10E+00	283	62	21
CAA05367	577	32	7.10E+00	163	32	19
BAD51767	1173	32	7.10E+00	283	53	18
BAC57543	269	32	7.1	135	33	24
ZP_00356478659		32	7.1	128	32	25
ZP_00216525494		32	7.1	118	25	21
ZP_00215989433		32	7.1	61	20	32
ZP_00211381462		32	7.1	89	23	25
ZP_00220828371		32	7.1	116	31	26
ZP_00154800558		32	7.1	139	31	22
ZP_00348486544		32	7.1	93	22	23
ZP_00138674683		32	7.1	303	72	23
ZP_00274787513		31.6	9.3	247	48	19
NP_326524	1125	31.6	9.3	174	37	21
CAA41384	1134	31.6	9.3	147	31	21
AAD02406	269	31.6	9.3	81	21	25
ZP_00054847736		31.6	9.3	272	53	19
NP_941106	1062	31.6	9.3	221	48	21
NP_813981	522	31.6	9.3	137	33	24
NP_794891	647	31.6	9.3	119	27	22
NP_766736	691	31.6	9.3	101	30	29
NP_562167	327	31.6	9.3	253	47	18
NP_561782	2104	31.6	9.3	126	23	18
NP_358633	1091	31.6	9.3	137	31	22
NP_349987	570	31.6	9.3	300	64	21

Fig. 25B-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_223662	668	31.6	9.3	138	32	23
YP_084257	1041	31.6	9.3	243	51	20
YP_130345	561	31.6	9.3	303	57	18
YP_130208	521	31.6	9.3	273	61	22
YP_071037	2550	31.6	9.3	290	61	21
YP_070267	808	31.6	9.3	249	53	21
AAK93939	733	31.6	9.3	89	19	21
NP_072757	398	31.6	9.3	156	36	23
YP_056420	529	31.6	9.3	94	25	26
YP_030044	959	31.6	9.3	276	57	20
YP_028999	810	31.6	9.3	243	52	21
NP_600558	288	31.6	9.3	63	18	28
NP_657914	598	31.6	9.3	276	57	20
NP_656819	807	31.6	9.3	243	52	21
NP_965588	1218	31.0	9.3	246	40	16
ZP_00305598305		31.6	9.3	69	21	30
ZP_00267783642		31.6	9.3	232	47	20
ZP_00235052646		31.6	9.3	176	34	19
ZP_00233607236		31.6	9.3	121	27	22
BAC98831	1083	31.6	9.3	147	31	21
FCSOAG	1164	31.6	9.3	147	31	21
CAA42442	1164	31.6	9.3	147	31	21
AAT10376	1158	31.6	9.3	147	31	21
AAC18948	269	31.6	9.3	81	21	25
ZP_001698191318		31.6	9.3	233	54	23
ZP_00203712834		31.6	9.3	112	28	25
ZP_00125435646		31.6	9.3	225	42	18
ZP_00127280469		31.6	9.3	275	54	19
ZP_001224603554		31.6	9.3	284	59	20
AAK11617	437	31.6	9.3	108	29	26

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S

Fig. 25C

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_929221	355	364	1.00E-100	355	207	58
ZP_00169997	361	343	1.00E-93	361	201	55
NP_992909	369	318	4.00E-86	368	202	54
NP_405406	369	318	4.00E-86	368	202	54
NP_288384	585	305	4.00E-82	274	169	61
NP_288384	585	142	4.00E-33	115	74	64
NP_310689	585	305	4.00E-82	274	169	61
NP_310689	585	142	4.00E-33	115	74	64
NP_754230	595	298	3.00E-80	223	157	70
NP_754230	595	138	5.00E-32	255	106	41
NP_707809	550	293	9.00E-79	202	154	76
NP_707809	550	140	9.00E-33	116	71	61
NP_416433	498	287	8.00E-77	177	146	82
NP_416433	498	149	3.00E-35	151	80	52
NP_841632	275	285	4.00E-76	297	159	53
NP_456520	506	284	7.00E-76	175	150	85
NP_456520	506	149	3.00E-35	91	76	83
NP_461698	506	283	9.00E-76	232	160	68
NP_461698	506	155	4.00E-37	100	81	81
NP_460912	495	280	8.00E-75	175	148	84
NP_460912	495	152	3.00E-36	98	79	80
NP_883763	392	272	2.00E-72	392	180	45
NP_879790	391	268	5.00E-71	391	182	46
NP_889078	391	266	1.00E-70	391	183	46
ZP_00091764	573	254	8.00E-67	262	144	54
ZP_00091764	573	139	4.00E-32	90	71	78
ZP_00173465	285	249	1.00E-65	297	145	48
NP_903549	282	248	6.00E-65	297	137	46
ZP_00288126	272	247	7.00E-65	296	145	48
NP_903548	282	246	2.00E-64	297	137	46
ZP_00289013	269	238	4.00E-62	292	133	45
ZP_00149772	273	236	1.00E-61	296	131	44
ZP_00289014	271	236	2.00E-61	296	133	44
NP_718792	272	236	2.00E-61	297	140	47
ZP_00274388	386	236	2.00E-61	167	122	73
ZP_00274388	386	135	5.00E-31	92	68	73
ZP_00289011	271	235	3.00E-61	296	133	44
ZP_00288132	271	235	4.00E-61	295	136	46
ZP_00288131	271	234	5.00E-61	295	136	46
ZP_00299645	314	234	6.00E-61	296	137	46
ZP_00288133	271	233	1.00E-60	295	135	45
NP_718793	273	233	1.00E-60	297	138	46
ZP_00288136	271	230	9.00E-60	296	132	44
ZP_00211492	272	229	2.00E-59	291	134	46
ZP_00289022	272	228	3.00E-59	296	136	45
NP_954080	276	228	5.00E-59	298	133	44
NP_791772	282	223	1.00E-57	297	129	43
NP_622175	276	220	1.00E-56	296	134	45
ZP_00302555	327	219	2.00E-56	329	133	40
NP_871067	421	219	2.00E-56	181	109	60
NP_871067	421	120	1.00E-26	345	109	31
ZP_00127282	271	218	4.00E-56	283	128	45
YP_080662	310	215	4.00E-55	313	135	43
NP_244483	272	214	9.00E-55	294	124	42
ZP_00263336	255	213	2.00E-54	269	125	46
ZP_00183380	275	210	1.00E-53	299	128	42
NP_782313	275	209	2.00E-53	296	125	42
NP_693649	338	209	2.00E-53	338	131	38
ZP_00289017	266	209	2.00E-53	285	125	43
ZP_00289012	373	209	3.00E-53	282	117	41
NP_391416	304	208	5.00E-53	306	130	42
NP_801058	284	207	8.00E-53	301	119	39
NP_348820	275	207	1.00E-52	295	122	41
NP_798640	377	202	2.00E-51	376	132	35
ZP_00313276	273	201	8.00E-51	295	120	40
ZP_00236467	307	200	1.00E-50	309	119	38
NP_957402	282	199	3.00E-50	295	124	42
NP_967404	277	196	2.00E-49	292	120	41

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_642301	399	196	2.00E-49	212	113	53
NP_642301	399	103	1.00E-21	307	87	28
ZP_00236470	278	196	2.00E-49	293	117	39
ZP_00236469	286	195	3.00E-49	292	118	40
ZP_00244371	402	195	4.00E-49	400	144	36
ZP_00313275	272	193	1.00E-48	292	118	40
ZP_00335280	609	193	1.00E-48	290	120	41
ZP_00335280	609	114	1.00E-24	159	67	42
NP_637306	399	193	1.00E-48	241	119	49
NP_637306	399	104	1.00E-21	319	93	29
ZP_00244372	404	193	1.00E-48	404	150	37
YP_065397	1128	192	3.00E-48	252	120	47
YP_065397	1128	107	2.00E-22	254	79	31
YP_001491	285	192	4.00E-48	302	112	37
NP_712598	285	192	4.00E-48	302	112	37
NP_231819	379	189	2.00E-47	375	130	34
YP_109915	388	189	2.00E-47	385	136	35
NP_831434	272	189	2.00E-47	296	114	38
YP_076801	275	189	3.00E-47	296	114	38
NP_967579	277	188	4.00E-47	301	117	38
YP_027849	287	188	5.00E-47	292	112	38
NP_972081	285	187	9.00E-47	300	113	37
ZP_00236468	284	187	1.00E-46	295	111	37
ZP_00288129	272	186	2.00E-46	296	112	37
NP_967577	274	186	3.00E-46	292	115	39
ZP_00200889	296	184	6.00E-46	300	110	36
YP_129125	382	184	7.00E-46	382	130	34
NP_219229	286	183	2.00E-45	298	114	38
NP_348182	278	182	3.00E-45	292	115	39
YP_010660	298	182	3.00E-45	311	119	38
NP_231773	376	182	4.00E-45	375	133	35
ZP_00130180	299	181	5.00E-45	295	107	36
NP_219303	286	181	8.00E-45	304	107	35
NP_219305	285	181	8.00E-45	301	111	36
NP_831435	273	180	1.00E-44	298	115	38
YP_123618	475	179	2.00E-44	309	124	40
YP_123618	475	110	1.00E-23	200	77	38
YP_035879	367	179	2.00E-44	365	125	34
YP_095369	475	178	4.00E-44	309	125	40
YP_095369	475	109	2.00E-23	198	78	39
YP_001839	281	177	9.00E-44	300	107	35
NP_971613	286	177	9.00E-44	304	109	35
NP_902165	285	177	1.00E-43	299	104	34
YP_066429	857	177	1.00E-43	231	108	46
YP_066429	857	115	4.00E-25	227	81	35
YP_011656	297	177	1.00E-43	310	113	36
YP_126643	475	176	2.00E-43	309	122	39
YP_126643	475	110	1.00E-23	251	88	35
YP_001490	282	176	2.00E-43	300	107	35
NP_970090	277	176	2.00E-43	295	110	37
NP_231775	378	176	2.00E-43	377	134	35
YP_072597	336	176	3.00E-43	342	113	33
NP_212281	336	176	3.00E-43	342	113	33
NP_712599	282	176	3.00E-43	300	107	35
NP_521943	273	175	3.00E-43	297	109	36
NP_231818	377	175	3.00E-43	377	129	34
YP_013330	287	173	1.00E-42	296	107	36
NP_470041	287	173	1.00E-42	296	107	36
NP_464217	287	173	1.00E-42	296	107	36
NP_797167	384	173	1.00E-42	384	125	32
NP_935284	376	173	1.00E-42	375	121	32
NP_969824	277	172	3.00E-42	295	109	36
NP_972083	286	172	4.00E-42	304	106	34
NP_760797	377	171	7.00E-42	376	123	32
ZP_00346385	295	171	7.00E-42	292	98	33
NP_348785	283	171	9.00E-42	290	104	35
NP_782278	280	170	1.00E-41	294	105	35
ZP_00279040	381	170	1.00E-41	378	127	33

Fig. 25C-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_231774	377	169	2.00E-41	379	127	33
YP_011295	297	169	2.00E-41	295	101	34
NP_902681	372	167	7.00E-41	369	122	33
NP_249785	488	167	9.00E-41	242	103	42
NP_249783	488	113	2.00E-24	335	100	29
ZP_00138680488		167	9.00E-41	242	103	42
ZP_00138680488		113	2.00E-24	335	100	29
ZP_00130923288		167	9.00E-41	284	103	36
NP_798637	376	167	1.00E-40	377	125	33
NP_798638	378	167	1.00E-40	377	126	33
AAP08637	249	165	5.00E-40	271	98	36
ZP_00317212580		164	6.00E-40	222	101	45
ZP_00317212580		99.4	3.00E-20	162	66	36
NP_746492	687	164	8.00E-40	252	103	40
NP_746492	687	96.3	3.00E-19	129	53	41
ZP_00100062385		163	1.00E-39	385	128	33
ZP_00317210587		162	4.00E-39	254	105	41
ZP_00317210587		95.9	3.00E-19	129	55	42
NP_712200	283	162	4.00E-39	301	100	33
YP_001838	283	161	5.00E-39	301	99	32
NP_770335	274	160	1.00E-38	295	95	32
ZP_00218989614		156	2.00E-37	242	97	40
ZP_00218989614		90.1	2.00E-17	86	46	53
ZP_00270146298		154	1.00E-36	305	107	35
NP_936285	396	153	1.00E-36	376	118	31
NP_945993	274	152	3.00E-36	295	92	31
NP_759224	377	151	5.00E-36	376	120	31
NP_933767	377	151	7.00E-36	376	119	31
YP_128298	426	151	7.00E-36	251	106	42
YP_128298	426	89.4	3.00E-17	149	55	36
ZP_00329901380		149	2.00E-35	382	125	32
NP_935286	377	149	2.00E-35	376	112	29
NP_933764	385	149	3.00E-35	178	80	44
NP_933764	385	102	5.00E-21	301	92	30
ZP_00273972629		146	2.00E-34	199	85	42
ZP_00273972629		104	8.00E-22	92	57	61
YP_129126	393	145	4.00E-34	213	82	38
YP_129126	393	90.5	1.00E-17	203	63	31
NP_978099	266	145	4.00E-34	292	96	32
ZP_00287990272		142	4.00E-33	280	85	30
YP_035878	266	142	4.00E-33	292	97	33
NP_759225	374	141	6.00E-33	167	76	45
NP_759225	374	102	5.00E-21	301	92	30
NP_782289	268	141	6.00E-33	256	79	29
ZP_00004597493		140	9.00E-33	166	74	44
ZP_00004597493		97.1	2.00E-19	176	63	35
YP_083129	266	140	9.00E-33	292	95	32
AAP08634	266	140	1.00E-32	291	95	32
NP_228567	387	140	2.00E-32	392	119	30
ZP_00236466266		138	5.00E-32	292	96	32
YP_083130	460	137	8.00E-32	289	96	33
YP_083130	460	80.9	1.00E-14	111	46	41
NP_348261	269	137	1.00E-31	292	89	30
NP_242343	464	130	2.00E-29	135	70	51
NP_242343	464	95.9	3.00E-19	169	57	33
NP_978100	465	126	2.00E-28	221	77	34
NP_978100	465	75.1	6.00E-13	84	41	48
AAO08750	375	121	6.00E-27	374	108	28
NP_933768	375	121	6.00E-27	374	108	28
NP_391395	160	116	2.00E-25	179	68	37
NP_797170	374	109	2.00E-23	148	60	40
NP_797170	374	74.3	1.00E-12	217	61	28
NP_908288	513	109	2.00E-23	294	89	30
NP_908288	513	73.2	2.00E-12	122	44	36
NP_206915	514	108	7.00E-23	187	67	35
NP_206915	514	77.4	1.00E-13	121	47	38
NP_222828	514	107	1.00E-22	187	67	35
NP_222828	514	77.4	1.00E-13	121	47	38

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_282485	572	106	3.00E-22	171	63	36
NP_282485	572	79.3	3.00E-14	132	48	36
AAP78393	514	104	8.00E-22	188	67	35
AAP78393	514	68.9	5.00E-11	115	40	34
NP_420273	273	104	1.00E-21	297	76	25
NP_907654	518	103	2.00E-21	192	63	32
NP_907654	518	94.7	8.00E-19	333	85	25
NP_404368	404	102	3.00E-21	223	67	30
NP_670739	401	102	3.00E-21	223	67	30
NP_670739	401	57.4	1.00E-07	84	28	33
NP_282484	572	102	5.00E-21	181	66	36
NP_282484	572	72.8	3.00E-12	132	45	34
NP_214372	518	100	1.00E-20	209	62	29
NP_214372	516	62	6.00E-09	129	39	30
ZP_00313281302		99.4	3.00E-20	274	69	25
ZP_00100043955		99.4	3.00E-20	270	82	30
ZP_00100043955		63.5	2.00E-09	154	47	30
NP_420274	273	99	4.00E-20	292	75	25
NP_419609	273	99	4.00E-20	292	72	24
NP_419611	273	98.6	5.00E-20	292	72	24
YP_071817	400	98.2	7.00E-20	207	61	29
YP_071817	400	60.1	2.00E-08	115	37	32
NP_865696	718	98.2	7.00E-20	284	88	30
NP_865696	718	81.3	9.00E-15	143	57	39
NP_622171	296	98.2	7.00E-20	290	83	28
AAP78250	508	97.8	9.00E-20	170	60	35
AAP78250	508	76.3	3.00E-13	297	74	24
NP_419610	273	97.4	1.00E-19	292	70	23
NP_866107	739	97.4	1.00E-19	257	76	29
NP_866107	739	79.3	3.00E-14	250	70	28
NP_223266	510	96.3	3.00E-19	170	57	33
NP_223266	510	82.4	4.00E-15	311	78	25
NP_404369	399	95.9	3.00E-19	295	76	25
ZP_00299642294		95.5	5.00E-19	295	75	25
NP_867573	685	92.8	3.00E-18	169	62	36
NP_867573	685	85.5	5.00E-16	126	55	43
NP_404370	401	92	5.00E-18	309	79	25
ZP_00329910305		91.7	7.00E-18	285	73	25
ZP_00196929279		91.7	7.00E-18	288	79	27
NP_353672	306	91.3	9.00E-18	313	77	24
NP_693427	293	91.3	9.00E-18	293	75	25
ZP_00098298321		90.9	1.00E-17	302	85	28
NP_227947	258	89.7	3.00E-17	248	63	25
NP_954084	298	89.7	3.00E-17	290	75	25
ZP_00289010110		89.7	3.00E-17	87	47	54
NP_700301	282	88.6	6.00E-17	298	76	25
NP_391420	298	86.7	2.00E-16	288	80	27
NP_541127	282	86.7	2.00E-16	298	75	25
ZP_00288130268		85.5	5.00E-16	295	76	25
NP_773506	313	85.1	6.00E-16	311	73	23
NP_104150	328	84.7	8.00E-16	329	75	22
ZP_00339045281		84	1.00E-15	296	75	25
YP_080866	303	83.2	2.00E-15	281	70	24
NP_773505	314	80.9	1.00E-14	317	73	23
NP_353570	313	79.7	3.00E-14	313	75	23
ZP_00339044282		79.3	3.00E-14	298	72	24
ZP_00007767281		78.6	6.00E-14	302	70	23
NP_840399	299	77.8	1.00E-13	290	71	24
ZP_00339046273		77.4	1.00E-13	280	73	26
ZP_00338034282		77.4	1E-13	294	72	24
ZP_00193517283		76.6	2.00E-13	290	65	22
ZP_00337030282		76.3	3.00E-13	299	69	23
NP_907272	253	74.3	1.00E-12	278	65	23
ZP_00270458289		72.8	3.00E-12	302	69	22
ZP_00289016275		72	5.00E-12	275	64	23
NP_353571	337	71.6	7.00E-12	324	75	23
NP_531244	320	71.6	7.00E-12	324	75	23
ZP_00183364320		71.6	7E-12	321	74	23

Fig. 25C-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_281892	249	68.6	6.00E-11	288	66	22
NP_782319	316	68.2	8.00E-11	284	68	23
ZP_00337274271		67.4	1.00E-10	284	64	22
ZP_00335243300		67	2.00E-10	302	74	24
ZP_00149794326		67	2.00E-10	322	67	20
NP_972952	415	66.6	2.00E-10	285	65	22
NP_227898	304	65.1	7.00E-10	256	62	24
YP_013346	291	64.3	1.00E-09	288	61	21
ZP_00049388242		63.9	1.00E-09	188	52	27
NP_464233	291	63.9	1.00E-09	288	61	21
ZP_00229464291		63.5	2.00E-09	288	61	21
AAC65633	416	63.2	3.00E-09	268	60	22
NP_384778	321	62.4	4.00E-09	321	68	21
NP_642302	401	62.4	4.00E-09	134	40	29
NP_642302	401	40.8	1.30E-02	118	31	26
NP_470057	291	62	6.00E-09	288	60	20
ZP_00237160287		60.8	1.00E-08	243	52	25
NP_348828	425	60.1	2.00E-08	289	65	22
NP_348828	425	42.4	5.00E-03	310	69	22
YP_126585	411	60.1	2.00E-08	147	39	26
YP_095257	411	60.1	2.00E-08	147	39	26
NP_104151	356	59.7	3.00E-08	357	81	22
YP_123558	411	59.3	4.00E-08	147	38	25
YP_123558	411	32	6.20E+00	83	25	30
AAQ60546	309	58.9	5.00E-08	299	62	20
ZP_00127287530		58.9	5.00E-08	135	40	29
NP_772484	757	58.5	6.00E-08	273	72	26
NP_772484	757	34.7	9.60E-01	109	29	26
NP_637307	401	58.2	8.00E-08	134	38	28
NP_637307	401	35.8	4.30E-01	119	31	26
YP_083110	287	57.8	1.00E-07	242	57	23
NP_978079	287	57.8	1.00E-07	241	60	24
NP_772486	757	57.4	1.00E-07	255	72	28
NP_772486	757	34.3	1.20E+00	109	29	26
NP_212316	424	57.4	1.00E-07	132	38	28
NP_212316	424	35	7.30E-01	77	18	23
NP_384775	394	57	2.00E-07	138	38	27
NP_384775	394	50.4	2.00E-05	87	29	33
YP_072631	424	56.6	2.00E-07	157	46	29
YP_072631	424	35	7.30E-01	77	18	23
AAP08616	287	56.6	2.00E-07	243	57	23
ZP_00128974504		56.6	2.00E-07	113	32	28
ZP_00128974504		43.5	2.00E-03	238	50	21
NP_521913	316	56.2	3.00E-07	305	65	21
NP_746494	521	56.2	3.00E-07	130	41	31
NP_746494	521	41.6	8.00E-03	149	37	24
ZP_00173445304		56.2	3.00E-07	301	68	22
ZP_00278994407		55.5	5.00E-07	250	55	22
NP_718794	403	55.1	7.00E-07	136	36	26
NP_718794	403	34.3	1.20E+00	89	26	29
NP_791768	530	55.1	7.00E-07	130	36	27
NP_772485	757	55.1	7.00E-07	250	63	25
NP_772485	757	33.9	1.60E+00	109	29	26
NP_880130	510	54.7	9.00E-07	136	43	31
YP_003353	422	54.7	9.00E-07	110	34	30
NP_992941	337	54.3	1.00E-06	310	73	23
NP_883789	510	54.3	1.00E-06	136	42	30
NP_405374	326	54.3	1.00E-06	310	73	23
ZP_00212998398		54.3	1.00E-06	111	29	26
NP_799784	299	53.9	2.00E-06	258	55	21
NP_772483	763	53.9	2.00E-06	186	47	25
NP_772483	763	36.2	3.30E-01	109	29	26
NP_244487	395	53.9	2.00E-06	126	33	26
NP_353593	436	53.5	2.00E-06	256	59	23
NP_353593	436	46.2	3.00E-04	140	34	24
NP_753263	317	53.5	2.00E-06	299	67	22
NP_531268	430	53.5	2.00E-06	255	59	23
NP_531268	430	46.2	3.00E-04	140	34	24

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
ZP_00317213517		53.1	3.00E-06	100	31	31
ZP_00317213517		40	2.30E-02	91	24	26
ZP_00273669412		52.8	3.00E-06	311	67	21
ZP_00273669412		35.8	4.30E-01	146	35	23
ZP_00056435521		52.8	3.00E-06	185	40	21
NP_384777	401	52.8	3.00E-06	189	48	25
NP_384777	401	40	2.30E-02	87	24	27
NP_415601	317	52	5.00E-06	305	70	22
NP_421770	424	52	6.00E-06	164	35	21
NP_287217	317	51.6	8.00E-06	299	66	22
NP_967522	361	51.6	8.00E-06	178	44	24
YP_066426	757	51.6	8.00E-06	130	40	30
YP_111446	2634	51.2	1.00E-05	287	60	20
YP_111446	2634	50.8	1.00E-05	281	59	20
YP_111446	2634	47	2.00E-04	296	63	21
YP_111446	2634	46.2	3.00E-04	291	60	20
YP_111446	2634	45.1	7.00E-04	292	58	19
YP_111446	2634	43.5	2.00E-03	284	58	20
YP_111446	2634	43.5	2.00E-03	283	58	20
YP_111446	2634	43.5	2.00E-03	289	59	20
YP_111446	2634	43.1	3.00E-03	292	59	20
YP_111446	2634	42	6.00E-03	281	63	22
YP_111446	2634	40	2.30E-02	295	59	20
YP_111446	2634	40	2.30E-02	298	59	19
YP_111446	2634	39.3	3.90E-02	302	59	19
YP_111446	2634	38.9	5.10E-02	283	53	18
YP_111446	2634	37.4	1.50E-01	278	48	17
YP_111446	2634	35.8	4.30E-01	235	50	21
YP_105520	459	51.2	1.00E-05	248	57	22
YP_105520	459	41.6	8.00E-03	296	60	20
YP_027819	207	51.2	1.00E-05	115	30	26
NP_866849	651	51.2	1.00E-05	129	34	26
NP_947642	935	50.8	1.00E-05	284	70	24
NP_947642	935	34.3	1.20E+00	93	22	23
NP_949266	888	50.8	1.00E-05	284	69	24
NP_949266	888	38.9	5.10E-02	305	63	20
YP_009743	523	50.4	2.00E-05	123	32	26
YP_009743	523	33.9	1.60E+00	171	36	21
ZP_00129084282		50.4	2.00E-05	285	68	23
NP_282040	750	50.1	2.00E-05	129	36	27
NP_282040	750	41.6	8.00E-03	229	48	20
ZP_00242042398		49.7	3.00E-05	215	53	24
ZP_00242042398		39.7	3.00E-02	140	35	25
ZP_00263356523		48.5	6.00E-05	162	43	26
ZP_00263356523		35	7.30E-01	106	23	21
NP_460155	317	48.5	6.00E-05	140	38	27
YP_128296	304	48.5	6.00E-05	293	53	18
YP_040849	10746	48.5	6.00E-05	303	63	20
YP_040849	10746	42.4	5.00E-03	340	71	20
YP_040849	10746	36.6	2.50E-01	297	58	19
YP_040849	10746	36.6	2.50E-01	332	69	20
YP_040849	10746	35.8	4.30E-01	301	63	20
YP_040849	10746	33.5	2.10E+00	279	55	19
YP_040849	10746	33.1	2.80E+00	317	68	21
YP_040849	10746	31.6	8.10E+00	297	57	19
ZP_00167907404		48.5	6.00E-05	121	37	30
ZP_00167907404		35.4	5.60E-01	99	23	23
NP_384776	394	47.8	1.00E-04	137	34	24
NP_384776	394	45.8	4.00E-04	245	56	22
NP_562800	451	47.4	1.00E-04	220	53	24
NP_455677	317	47.4	1.00E-04	140	38	27
NP_646141	9904	47	2.00E-04	306	64	20
NP_646141	9904	43.1	3.00E-03	153	36	23
NP_646141	9904	39.7	3.00E-02	332	71	21
NP_646141	9904	39.3	3.90E-02	283	66	23
NP_646141	9904	38.1	8.60E-02	279	56	20
NP_646141	9904	35.4	5.60E-01	317	66	20
NP_646141	9904	33.9	1.60E+00	297	57	19

Fig. 25C-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
YP_012160	282	47	2.00E-04	223	53	23
NP_249778	439	46.6	2.00E-04	134	34	25
NP_249778	439	32	6.20E+00	257	50	19
ZP_00138675439		46.6	2.00E-04	134	34	25
ZP_00314296822		46.2	3.00E-04	257	54	21
NP_223759	267	46.2	3.00E-04	149	40	26
YP_108306	1606	46.2	3.00E-04	296	66	22
YP_108306	1606	38.1	8.60E-02	281	57	20
YP_108306	1606	38.1	8.60E-02	228	54	23
YP_108306	1606	38.1	8.60E-02	309	60	19
YP_108306	1606	37.4	1.50E-01	256	58	22
ZP_00290372765		45.8	4.00E-04	280	56	20
NP_267773	1072	45.4	5.00E-04	287	53	18
NP_267773	1072	33.5	2.10E+00	91	21	23
NP_228520	407	45.4	5.00E-04	290	63	21
ZP_003230792334		45.4	5.00E-04	274	50	18
ZP_003230792334		39.7	3.00E-02	276	49	17
ZP_003230792334		39.3	3.90E-02	293	54	18
ZP_003230792334		38.5	6.60E-02	294	53	18
ZP_003230792334		37	1.90E-01	280	52	18
ZP_003230792334		34.7	9.60E-01	261	50	19
YP_111449	1530	45.1	7.00E-04	295	64	21
YP_111449	1530	44.7	1.00E-03	292	64	21
YP_111449	1530	44.3	1.00E-03	278	59	21
YP_111449	1530	42.7	4.00E-03	320	69	21
YP_111449	1530	41.6	8.00E-03	288	59	20
YP_111449	1530	41.2	1.00E-02	284	60	21
YP_111449	1530	40	2.30E-02	250	51	20
YP_111449	1530	37.7	1.10E-01	250	50	20
YP_111449	1530	37	1.90E-01	263	52	19
YP_111449	1530	34.7	9.60E-01	257	55	21
NP_949252	886	44.7	1.00E-03	194	49	25
NP_949252	886	33.9	1.60E+00	102	25	24
NP_929192	321	44.7	1.00E-03	318	74	23
NP_647392	2275	44.7	1.00E-03	287	53	18
NP_647392	2275	34.3	1.20E+00	216	42	19
NP_647392	2275	34.3	1.20E+00	299	60	20
NP_371958	6713	44.7	1.00E-03	303	61	20
NP_371958	6713	42	6.00E-03	153	36	23
NP_371958	6713	41.2	1.00E-02	332	72	21
NP_371958	6713	35.4	5.60E-01	276	53	19
NP_371958	6713	33.1	2.80E+00	297	57	19
NP_374548	6713	44.7	1.00E-03	303	61	20
NP_374548	6713	42	6.00E-03	153	36	23
NP_374548	6713	41.2	1.00E-02	332	72	21
NP_374548	6713	35.4	5.60E-01	276	53	19
NP_374548	6713	33.1	2.80E+00	297	57	19
YP_106908	410	44.7	1.00E-03	124	28	22
YP_044654	2275	44.7	1.00E-03	287	53	18
YP_044654	2275	34.3	1.20E+00	216	42	19
YP_110805	1653	44.3	1.00E-03	269	58	21
YP_110805	1653	40	2.30E-02	254	56	22
YP_110805	1653	37	1.90E-01	287	58	20
YP_110805	1653	36.2	3.30E-01	274	56	20
YP_110805	1653	34.7	9.60E-01	265	52	19
ZP_001627551140		44.3	1.00E-03	295	62	21
AAF94608	4558	43.9	2.00E-03	228	52	22
ZP_00326048609		43.1	3.00E-03	273	63	23
ZP_00326048609		32	6.20E+00	99	20	20
ZP_00051799172		43.1	3.00E-03	136	31	22
NP_207286	295	43.1	3.00E-03	150	42	28
NP_936893	989	43.1	3.00E-03	289	63	21
AAQ59385	302	42.7	4.00E-03	282	55	19
NP_267008	1063	42.7	4.00E-03	291	56	19
NP_267008	1063	37	1.90E-01	231	42	18
NP_267008	1063	36.6	2.50E-01	281	63	22
YP_042074	1351	42.7	4.00E-03	304	59	19
NP_939992	1254	42.4	5.00E-03	169	38	22

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
YP_105401	1535	42.4	5.00E-03	300	63	21
YP_105401	1535	36.2	3.30E-01	307	64	20
YP_105401	1535	35.8	4.30E-01	217	46	21
YP_065260	567	42.4	5.00E-03	263	54	20
NP_906736	846	42.4	5.00E-03	168	37	22
ZP_001432362005		42.4	5.00E-03	256	59	23
NP_523179	1309	42	6.00E-03	264	60	22
NP_523179	1309	36.2	3.30E-01	260	56	21
NP_523179	1309	35.8	4.30E-01	247	57	23
AAF95046	672	42	6.00E-03	320	64	20
NP_468975	661	42	6.00E-03	268	63	23
NP_784110	1377	42	6.00E-03	285	64	22
YP_129124	396	41.6	8.00E-03	119	25	21
ZP_00089080401		41.6	8.00E-03	122	36	29
ZP_00089080401		38.5	6.60E-02	139	36	25
NP_465811	1787	41.2	1.00E-02	268	58	21
ZP_002143701439		41.2	1.00E-02	297	72	24
ZP_002143701439		32.3	4.70E+00	272	56	20
AAP07456	953	40.8	1.30E-02	263	49	18
ZP_00063096901		40.8	1.30E-02	241	60	24
ZP_00296669699		40.4	1.70E-02	292	54	18
ZP_00296669699		32	6.20E+00	133	26	19
NP_251152	5627	40.4	1.70E-02	329	67	20
NP_251152	5627	34.3	1.20E+00	235	50	21
NP_251152	5627	32.7	3.60E+00	312	60	19
ZP_00288079749		40	2.30E-02	236	51	21
YP_142319	789	40	2.30E-02	302	64	21
YP_140402	710	40	2.30E-02	302	64	21
NP_373178	2271	40	2.30E-02	287	52	18
NP_373178	2271	34.3	1.20E+00	216	42	19
NP_373178	2271	32	6.20E+00	303	62	20
AAO08483	623	40	2.30E-02	114	31	27
YP_114536	437	40	2.30E-02	83	27	32
YP_034700	953	40	2.30E-02	301	58	19
NP_936493	623	40	2.30E-02	114	31	27
NP_764683	9439	40	2.30E-02	130	27	20
NP_764683	9439	38.5	6.60E-02	169	43	25
NP_764683	9439	36.2	3.30E-01	265	55	20
NP_764683	9439	36.2	3.30E-01	288	61	21
NP_764683	9439	36.2	3.30E-01	255	48	18
NP_764683	9439	35.4	5.60E-01	316	61	19
NP_764683	9439	34.7	9.60E-01	302	60	19
NP_764683	9439	33.9	1.60E+00	314	65	20
NP_764683	9439	33.9	1.60E+00	146	40	27
NP_764683	9439	33.1	2.80E+00	181	46	25
NP_764683	9439	33.1	2.80E+00	151	38	25
NP_764683	9439	32.3	4.70E+00	329	68	20
NP_764683	9439	31.6	8.10E+00	292	53	18
ZP_00123691638		39.7	3.00E-02	352	74	21
ZP_000642471003		39.7	3.00E-02	307	71	23
ZP_00319871233		39.3	3.90E-02	139	37	26
NP_908061	118	39.3	3.90E-02	103	29	28
ZP_002335911787		39.3	3.90E-02	261	60	22
NP_798012	3240	38.9	5.10E-02	269	58	21
YP_015833	662	38.9	5.10E-02	167	43	25
ZP_002814314726		38.9	5.10E-02	310	62	20
ZP_002814314726		38.1	8.60E-02	308	61	19
ZP_002814314726		37.4	1.50E-01	272	54	19
ZP_002814314726		36.6	2.50E-01	275	56	20
ZP_002814314726		36.6	2.50E-01	254	53	20
ZP_002814314726		35.4	5.60E-01	279	55	19
ZP_002814314726		35	7.30E-01	319	59	18
ZP_002814314726		34.3	1.20E+00	324	59	18
ZP_00211493472		38.9	5.10E-02	274	60	21
ZP_002047941979		38.9	5.10E-02	235	47	20
ZP_002047941979		34.7	9.60E-01	235	50	21
ZP_002047941979		33.1	2.8	312	61	19
ZP_00208729459		38.5	6.60E-02	278	63	22

Fig. 25C-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_928380	567	38.5	6.60E-02	257	58	22
YP_115646	750	38.5	6.60E-02	144	32	22
YP_087940	5399	38.5	6.60E-02	312	72	23
YP_087940	5399	37.4	1.50E-01	256	45	17
YP_087940	5399	37.4	1.50E-01	256	45	17
YP_087940	5399	36.2	3.30E-01	273	58	21
YP_087940	5399	36.2	3.30E-01	273	58	21
YP_087940	5399	35.8	4.30E-01	274	61	22
YP_087940	5399	35	7.30E-01	294	58	19
YP_087940	5399	33.9	1.60E+00	289	57	19
YP_087940	5399	33.5	2.10E+00	289	57	19
NP_781518	518	38.5	6.60E-02	302	64	21
ZP_00213493557		38.5	6.60E-02	223	51	22
ZP_00224552561		38.5	6.60E-02	223	53	23
ZP_00355727801		38.5	6.60E-02	317	71	22
ZP_001404443443		38.5	6.60E-02	286	62	21
NP_419715	307	38.1	8.60E-02	73	21	28
NP_207906	228	38.1	8.60E-02	110	32	29
ZP_003235731130		38.1	8.60E-02	292	65	22
ZP_003235731130		32.3	4.70E+00	281	57	20
ZP_00317192676		37.7	1.10E-01	169	35	20
NP_771092	696	37.7	1.10E-01	134	39	29
NP_214145	422	37.7	1.10E-01	186	40	21
NP_766958	681	37.7	1.10E-01	176	45	25
ZP_003125671475		37.7	1.10E-01	273	58	21
ZP_00240971564		37.7	1.10E-01	107	24	22
ZP_00195263572		37.7	1.10E-01	183	41	22
NP_949268	623	37.4	1.50E-01	277	53	19
ZP_00315446537		37.4	1.50E-01	263	54	20
ZP_0028945115245		37.4	1.50E-01	272	65	23
ZP_00273576527		37.4	1.50E-01	90	25	27
ZP_00273576527		33.9	1.60E+00	83	22	26
NP_800021	623	37.4	1.50E-01	117	31	26
NP_772493	627	37.4	1.50E-01	229	49	21
AAP78292	855	37.4	1.50E-01	138	32	23
ZP_00281310507		37.4	1.50E-01	119	31	26
ZP_00289133779		37	1.90E-01	198	38	19
ZP_00289133779		36.2	3.30E-01	89	26	29
NP_471790	927	37	1.90E-01	281	59	20
NP_471790	927	31.6	8.10E+00	210	46	21
NP_522634	3322	37	1.90E-01	228	52	22
NP_404364	307	37	1.90E-01	253	52	20
NP_336479	342	37	1.90E-01	87	25	28
NP_248731	3536	37	1.90E-01	286	62	21
YP_066441	693	37	1.90E-01	120	30	25
NP_757754	161	37	1.90E-01	77	23	29
NP_670743	308	37	1.90E-01	253	52	20
NP_603291	1724	37	1.90E-01	131	34	25
ZP_00290800910		37	1.90E-01	260	53	20
ZP_00219646252		37	1.90E-01	74	21	28
ZP_00063136721		37	1.90E-01	298	58	19
NP_799785	346	36.6	2.50E-01	116	29	25
NP_739300	290	36.6	2.50E-01	122	30	24
AAP96352	1119	36.6	2.50E-01	143	35	24
NP_359656	1902	36.6	2.50E-01	282	60	21
NP_253231	1417	36.6	2.50E-01	201	49	24
NP_932208	603	36.6	2.50E-01	53	17	32
ZP_00218988486		36.6	2.50E-01	259	56	21
ZP_00149774452		36.6	2.50E-01	264	56	21
ZP_00319246821		36.2	3.30E-01	65	19	29
ZP_00284479601		36.2	3.30E-01	262	52	19
ZP_00005278425		36.2	3.30E-01	193	50	25
NP_280332	643	36.2	3.30E-01	233	50	21
NP_522101	3552	36.2	3.30E-01	209	45	21
NP_964415	1096	36.2	3.30E-01	265	56	21
ZP_00313063880		36.2	3.30E-01	181	39	21
ZP_00182337425		36.2	3.30E-01	245	41	16
ZP_00160617717		36.2	3.30E-01	289	62	21

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
ZP_00160617717		31.6	8.10E+00	248	46	18
ZP_001380311417		36.2	3.30E-01	201	49	24
NP_561526	1109	35.8	4.30E-01	287	53	18
NP_561526	1109	32	6.20E+00	181	40	22
NP_349224	664	35.8	4.30E-01	272	59	21
AAP56614	499	35.8	4.30E-01	183	40	21
YP_133618	665	35.8	4.30E-01	111	33	29
YP_071943	3378	35.8	4.30E-01	289	61	21
ZP_00270453727		35.4	5.60E-01	239	49	20
AAQ59977	458	35.4	5.60E-01	266	61	22
NP_773497	491	35.4	5.60E-01	121	28	23
NP_267038	799	35.4	5.60E-01	301	71	23
NP_478603	1487	35.4	5.60E-01	249	49	19
YP_086339	564	35.4	5.60E-01	107	23	21
NP_207948	1230	35.4	5.60E-01	292	62	21
YP_039058	564	35.4	5.60E-01	107	23	21
NP_864533	7716	35.4	5.60E-01	240	52	21
NP_765804	2310	35.4	5.60E-01	290	52	17
NP_765787	676	35.4	5.60E-01	117	33	28
ZP_00323296769		35.4	5.60E-01	148	35	23
ZP_00288038997		35.4	6.60E-01	294	56	19
ZP_00338261589		35	7.30E-01	62	20	32
NP_718836	667	35	7.30E-01	98	20	20
YP_128297	361	35	7.30E-01	358	69	19
YP_132326	529	35	7.30E-01	332	69	20
NP_812240	868	35	7.30E-01	150	44	29
NP_964984	4734	35	7.30E-01	316	66	20
NP_964984	4734	33.1	2.80E+00	153	40	26
ZP_00144637646		35	7.30E-01	243	44	18
ZP_00222048485		35	7.30E-01	88	23	26
ZP_00220113501		35	7.30E-01	88	23	26
ZP_00137782629		35	7.30E-01	245	43	17
ZP_00121836231		35	7.30E-01	165	39	23
NP_946001	587	34.7	9.60E-01	121	36	29
ZP_00319892754		34.7	9.60E-01	284	62	21
ZP_00319892754		33.1	2.80E+00	261	51	19
ZP_00311897602		34.7	9.60E-01	269	56	20
ZP_00336629824		34.7	9.60E-01	149	35	23
NP_802026	593	34.7	9.60E-01	118	33	27
NP_924800	1241	34.7	9.60E-01	73	24	32
NP_463823	500	34.7	9.60E-01	233	47	20
NP_645681	946	34.7	9.60E-01	219	44	20
NP_792425	633	34.7	9.60E-01	283	50	17
NP_561978	344	34.7	9.60E-01	232	49	21
NP_350172	783	34.7	9.60E-01	129	29	22
NP_349191	722	34.7	9.60E-01	143	36	25
NP_349191	722	33.1	2.80E+00	292	57	19
AAO10484	626	34.7	9.60E-01	299	52	17
NP_642322	396	34.7	9.60E-01	123	22	17
YP_133410	677	34.7	9.60E-01	317	61	19
NP_269527	594	34.7	9.60E-01	118	33	27
YP_042878	928	34.7	9.60E-01	219	44	20
YP_012922	500	34.7	9.60E-01	233	47	20
NP_051325	222	34.7	9.60E-01	114	30	26
NP_782459	569	34.7	9.60E-01	305	61	20
NP_607532	594	34.7	9.60E-01	118	33	27
ZP_00233976541		34.7	9.60E-01	233	47	20
ZP_00212291306		34.7	9.60E-01	130	38	29
NP_469464	1788	34.3	1.20E+00	290	65	22
NP_792292	629	34.3	1.20E+00	128	31	24
NP_695350	459	34.3	1.20E+00	271	54	19
NP_348729	570	34.3	1.20E+00	162	36	22
NP_252997	632	34.3	1.20E+00	245	43	17
YP_066477	393	34.3	1.20E+00	148	33	22
YP_064761	880	34.3	1.20E+00	126	30	23
YP_064723	674	34.3	1.20E+00	248	48	19
NP_935137	626	34.3	1.20E+00	299	52	17
NP_866060	3056	34.3	1.20E+00	120	34	28

Fig. 25C-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_866060	3056	33.1	2.80E+00	116	34	29
NP_616105	1074	34.3	1.20E+00	257	49	19
ZP_003233981656		34.3	1.20E+00	187	41	21
ZP_00308827366		34.3	1.20E+00	138	35	25
ZP_00137780616		34.3	1.20E+00	246	43	17
ZP_00124017629		34.3	1.20E+00	254	46	18
ZP_00110825475		34.3	1.20E+00	140	35	26
ZP_00046942967		33.9	1.60E+00	134	35	26
YP_080405	660	33.9	1.60E+00	87	22	25
NP_470074	599	33.9	1.60E+00	288	59	20
NP_927898	4582	33.9	1.60E+00	257	61	23
NP_815456	533	33.9	1.60E+00	125	35	28
NP_562046	933	33.9	1.60E+00	259	51	19
NP_267626	901	33.9	1.60E+00	281	56	19
YP_135620	471	33.9	1.60E+00	121	30	24
YP_126425	657	33.9	1.60E+00	121	29	23
YP_131301	638	33.9	1.60E+00	73	16	21
NP_987908	720	33.9	1.60E+00	95	27	28
YP_030040	660	33.9	1.60E+00	105	25	23
NP_981473	564	33.9	1.60E+00	109	24	22
NP_784971	983	33.9	1.60E+00	299	58	19
NP_783077	417	33.9	1.60E+00	103	24	23
NP_965011	912	33.9	1.60E+00	214	49	22
NP_964462	1000	33.9	1.60E+00	125	28	22
ZP_002991151200		33.5	2.10E+00	61	17	27
ZP_00056271661		33.5	2.10E+00	278	54	19
NP_287395	973	33.5	2.10E+00	185	42	22
NP_794375	539	33.5	2.10E+00	128	23	17
YP_137657	727	33.5	2.10E+00	86	25	29
YP_115527	534	33.5	2.10E+00	80	24	30
NP_309677	971	33.5	2.10E+00	185	42	22
NP_936396	542	33.5	2.10E+00	300	62	20
NP_637327	396	33.5	2.10E+00	123	21	17
NP_616912	1052	33.5	2.10E+00	132	36	27
NP_964159	982	33.5	2.10E+00	203	47	23
ZP_00296785641		33.5	2.10E+00	275	60	21
ZP_00217082977		33.5	2.10E+00	109	32	29
ZP_00106667978		33.5	2.10E+00	112	29	25
ZP_00290912684		33.1	2.80E+00	130	24	18
ZP_00290912684		32.3	4.70E+00	188	35	18
ZP_00338277837		33.1	2.80E+00	109	26	23
NP_798538	678	33.1	2.80E+00	127	27	21
NP_790701	498	33.1	2.80E+00	162	41	25
NP_768559	816	33.1	2.80E+00	62	19	30
NP_415890	1122	33.1	2.80E+00	147	37	25
AAO08482	622	33.1	2.80E+00	120	30	25
AAO10918	675	33.1	2.80E+00	125	29	23
NP_889112	532	33.1	2.80E+00	250	48	19
YP_129457	640	33.1	2.80E+00	137	31	22
YP_133516	467	33.1	2.80E+00	127	26	20
YP_132040	542	33.1	2.80E+00	107	27	25
YP_076807	558	33.1	2.80E+00	118	30	25
NP_987607	729	33.1	2.80E+00	95	26	27
NP_378194	467	33.1	2.80E+00	53	17	32
NP_253000	629	33.1	2.80E+00	245	42	17
YP_063897	576	33.1	2.80E+00	263	46	17
YP_041192	424	33.1	2.80E+00	147	36	24
NP_936490	622	33.1	2.80E+00	120	30	26
NP_786249	1106	33.1	2.80E+00	330	64	19
NP_777771	638	33.1	2.80E+00	121	29	23
NP_764984	3692	33.1	2.80E+00	148	30	20
NP_764984	3692	32.3	4.70E+00	264	52	19
NP_600104	441	33.1	2.80E+00	280	63	22
NP_693909	466	33.1	2.80E+00	126	24	19
NP_608047	400	33.1	2.80E+00	108	29	26
NP_604026	1193	33.1	2.80E+00	253	52	20
NP_559170	396	33.1	2.80E+00	119	29	24
NP_541885	131	33.1	2.80E+00	62	24	38
ZP_00147410749		33.1	2.80E+00	131	34	25
ZP_00137783633		33.1	2.80E+00	245	42	17
ZP_00123950634		33.1	2.80E+00	96	24	25
ZP_00128148551		33.1	2.80E+00	256	46	17
ZP_003460801463		33.1	2.80E+00	274	69	25
ZP_00326431563		32.7	3.60E+00	307	70	22
NP_252999	629	32.7	3.60E+00	127	32	25
ZP_000531851136		32.7	3.60E+00	223	51	22
NP_993634	2578	32.7	3.60E+00	290	61	21
YP_081346	561	32.7	3.60E+00	99	20	20
NP_471252	1186	32.7	3.60E+00	315	63	20
NP_469482	290	32.7	3.60E+00	82	21	25
NP_464250	601	32.7	3.60E+00	193	39	20
NP_929013	190	32.7	3.60E+00	133	34	25
NP_793014	6274	32.7	3.60E+00	246	51	20
NP_790315	541	32.7	3.60E+00	93	28	30
NP_769573	564	32.7	3.60E+00	157	36	22
NP_563507	721	32.7	3.60E+00	112	25	22
NP_406024	2535	32.7	3.60E+00	290	61	21
NP_939703	888	32.7	3.60E+00	123	31	25
AAP56776	742	32.7	3.60E+00	186	40	21
NP_882071	1175	32.7	3.60E+00	65	18	27
NP_419323	622	32.7	3.60E+00	235	47	20
YP_134634	596	32.7	3.60E+00	63	14	22
YP_108428	634	32.7	3.60E+00	266	52	19
NP_109825	228	32.7	3.60E+00	154	29	18
YP_013363	601	32.7	3.60E+00	193	39	20
NP_669014	2579	32.7	3.60E+00	290	61	21
ZP_00284267481		32.7	3.60E+00	77	21	27
ZP_00280424428		32.7	3.60E+00	196	50	25
NP_326456	750	32.3	4.70E+00	121	27	22
NP_391003	662	32.3	4.70E+00	322	60	18
NP_852542	1658	32.3	4.70E+00	149	33	22
NP_852542	1658	32.3	4.70E+00	139	27	19
NP_646487	424	32.3	4.70E+00	147	36	24
NP_718941	169	32.3	4.70E+00	160	36	22
NP_716901	706	32.3	4.70E+00	273	59	21
NP_801002	542	32.3	4.70E+00	304	58	19
AAQ60540	2373	32.3	4.70E+00	255	55	21
AAQ58389	690	32.3	4.70E+00	110	26	22
NP_770343	582	32.3	4.70E+00	270	50	18
AAF96820	652	32.3	4.70E+00	120	31	25
AAF94794	596	32.3	4.70E+00	80	19	23
NP_404241	3295	32.3	4.70E+00	289	61	21
YP_137110	536	32.3	4.70E+00	199	47	23
YP_032604	1872	32.3	4.70E+00	118	31	26
NP_782523	471	32.3	4.70E+00	107	20	18
NP_765908	300	32.3	4.70E+00	132	29	21
NP_765785	952	32.3	4.70E+00	195	37	18
NP_606940	628	32.3	4.70E+00	271	60	22
ZP_002394591038		32.3	4.70E+00	243	52	21
ZP_00236267289		32.3	4.70E+00	156	31	19
ZP_002326811086		32.3	4.70E+00	277	57	20
ZP_002168313513		32.3	4.70E+00	204	51	25
ZP_00171926505		32.3	4.70E+00	253	48	18
ZP_00201727822		32.3	4.70E+00	306	59	19
ZP_00149920505		32.3	4.70E+00	139	31	22
ZP_00133930158		32.3	4.70E+00	106	26	24
ZP_00098108451		32.3	4.70E+00	139	33	23
ZP_00312864422		32	6.20E+00	142	36	25
ZP_00298543733		32	6.20E+00	278	50	17
ZP_003410411311		32	6.20E+00	230	37	16
ZP_00208461932		32	6.20E+00	211	43	20
ZP_00046132979		32	6.20E+00	143	32	22
NP_279901	636	32	6.20E+00	244	53	21
NP_464751	1066	32	6.20E+00	277	56	20
NP_885521	1195	32	6.20E+00	65	18	27
AAQ60246	251	32	6.20E+00	98	30	30

Fig. 25C-Continued

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S
NP_768828	432	32	6.20E+00	164	35	21
NP_699533	317	32	6.20E+00	56	22	39
NP_346950	371	32	6.20E+00	147	35	23
NP_207534	493	32	6.20E+00	122	32	26
NP_249777	683	32	6.20E+00	303	72	23
YP_041227	2189	32	6.20E+00	149	35	23
YP_010811	580	32	6.20E+00	206	44	21
NP_784951	3360	32	6.20E+00	76	21	27
NP_765498	495	32	6.20E+00	74	16	21
NP_757771	1378	32	6.20E+00	73	22	30
NP_688862	443	32	6.20E+00	66	17	25
ZP_002842243286		32	6.20E+00	283	62	21
ZP_00356478659		32	6.20E+00	128	32	25
ZP_00216525494		32	6.20E+00	118	25	21
ZP_00215989433		32	6.20E+00	61	20	32
ZP_00211381462		32	6.20E+00	89	23	25
ZP_00220828371		32	6.20E+00	116	31	26
ZP_00154800558		32	6.20E+00	139	31	22
ZP_00348486544		32	6.20E+00	93	22	23
ZP_00138674683		32	6.20E+00	303	72	23
ZP_00274787513		31.6	8.10E+00	247	48	19
NP_326524	1125	31.6	8.10E+00	174	37	21
ZP_00054847736		31.6	8.10E+00	272	53	19
NP_813981	522	31.6	8.10E+00	137	33	24
NP_794891	647	31.6	8.10E+00	119	27	22
NP_766736	691	31.6	8.10E+00	101	30	29
NP_562167	327	31.6	8.10E+00	253	47	18
NP_561782	2104	31.6	8.10E+00	126	23	18
NP_358633	1091	31.6	8.10E+00	137	31	22
NP_349987	570	31.6	8.10E+00	300	64	21
YP_138060	1562	31.6	8.10E+00	103	23	22
NP_223662	668	31.6	8.10E+00	138	32	23
YP_084257	1041	31.6	8.10E+00	243	51	20
YP_130345	561	31.6	8.10E+00	303	57	18
YP_130208	521	31.6	8.10E+00	273	61	22
YP_071037	2550	31.6	8.10E+00	290	61	21
YP_070267	808	31.6	8.10E+00	249	53	21
NP_072757	398	31.6	8.10E+00	156	36	23
YP_056420	529	31.6	8.10E+00	94	25	26
YP_030044	959	31.6	8.10E+00	276	57	20
YP_028999	810	31.6	8.10E+00	243	52	21
NP_600558	288	31.6	8.10E+00	63	18	28
NP_657914	598	31.6	8.10E+00	276	57	20
NP_656819	807	31.6	8.10E+00	243	52	21
NP_965588	1218	31.6	8.10E+00	246	40	16
ZP_00305598305		31.6	8.10E+00	69	21	30
ZP_00267783642		31.6	8.10E+00	232	47	20
ZP_00235052646		31.6	8.10E+00	176	34	19
ZP_00233607236		31.6	8.10E+00	121	27	22
ZP_001698191318		31.6	8.10E+00	233	54	23
ZP_00203712834		31.6	8.10E+00	112	28	25
ZP_00125435646		31.6	8.10E+00	225	42	18
ZP_00127280469		31.6	8.10E+00	275	54	19
ZP_001224603554		31.6	8.10E+00	284	59	20

Hit_ID	Length	Bitscore	Expected	Length	#Ident	%S

Fig. 25D

Hit_ID	Expected	Length	#Ident	%S
AADY01000001	1.00E-100	373	213	57
NZ_AADY01000001	1.00E-100	373	213	57
NC_005126	1.00E-100	355	207	58
Yersinia	7.00E-89	364	202	55
Yersinia	9.00E-89	367	200	54
Yersinia	7.00E-59	308	149	48
Yersinia	2.00E-31	294	107	36
NC_005810	5.00E-86	368	202	54
NC_005810	3.00E-21	223	67	30
NC_005810	1.00E-04	66	22	33
NC_003143	5.00E-86	368	202	54
NC_003143	3.00E-21	223	67	30
NC_003143	4.00E-19	295	76	25
NC_003143	6.00E-18	309	79	25
NC_006155	5.00E-86	368	202	54
NC_006155	9.00E-20	207	61	29
NC_006155	3.00E-08	115	37	32
NC_004088	5.00E-86	368	202	54
NC_004088	3.00E-21	223	67	30
NC_004088	2.00E-07	84	28	33
NC_002655	5.00E-82	274	169	61
NC_002655	5.00E-33	115	74	64
NC_002655	9.00E-06	299	66	22
NC_002655	2.60E+00	185	42	22
NC_002695	5.00E-82	274	169	61
NC_002695	5.00E-33	115	74	64
NC_002695	9.00E-06	299	66	22
NC_002695	2.60E+00	185	42	22
senteritdis_716_10.21	5.00E-82	161	160	99
shig277d06.q1k	5.00E-82	299	183	61
shig277d06.q1k	6.00E-35	92	76	82
Epath054a03.p1k	1.00E-80	266	171	64
Epath054a03.p1k	1.00E-32	102	69	57
NC_004431	3.00E-80	223	157	70
NC_004431	6.00E-32	255	106	41
Eagg66e09.q1k	2.00E-79	237	161	67
Eagg66e09.q1k	9.00E-33	295	105	35
NC_004337	1.00E-78	202	154	76
NC_004337	1.00E-32	116	71	61
NC_004741	1.00E-78	202	154	76
NC_004741	1.00E-32	116	71	61
dys055h06.q1k	2.00E-78	237	159	67
dys055h06.q1k	2.00E-31	100	67	67
NC_000913	1.00E-76	177	146	82
NC_000913	4.00E-35	151	80	52
NC_004757	5.00E-76	297	159	53
NC_003198	8.00E-76	175	150	85
NC_003198	4.00E-35	91	76	83
NC_004631	8.00E-76	175	150	85
NC_004631	4.00E-35	91	76	83
NC_006511	1.00E-75	279	165	59
NC_006511	4.00E-74	175	147	84
NC_006511	2.00E-37	100	82	82
NC_006511	5.00E-37	100	81	81
NC_003197	1.00E-75	232	160	68
NC_003197	9.00E-75	175	148	84
NC_003197	5.00E-37	100	81	81
NC_003197	4.00E-36	98	79	80
spara_B_SPA.0.15635	1.00E-75	279	165	59
spara_B_SPA.0.15635	1.00E-31	74	65	87
spara_B_SPA.0.15635	1.00E-31	26	16	61
salt7-76a12.p1k	1.00E-75	232	160	68
salt7-76a12.p1k	5.00E-37	100	81	81
NC_003916	3.00E-75	296	167	56
salt11-469e08.p1k	9.00E-75	175	148	84
salt11-469e08.p1k	4.00E-36	98	79	80
bong465h05.q1k	3.00E-74	175	147	84
bong465h05.q1k	2.00E-36	100	80	80

Hit_ID	Expected	Length	#Ident	%S
spara_B_SPA.0.22632	4.00E-74	175	147	84
spara_B_SPA.0.22632	2.00E-37	100	82	82
NC_002928	3.00E-72	392	180	45
NC_002928	1.00E-06	136	42	30
NC_002929	6.00E-71	391	182	46
NC_002929	1.00E-06	136	43	31
NC_002927	2.00E-70	391	183	46
NC_002927	1.00E-06	136	42	30
NZ_AAAI02000003	1.00E-67	179	134	74
NZ_AAAI02000003	6.00E-31	92	68	73
AAAI02000003	1.00E-67	179	134	74
AAAI02000003	6.00E-31	92	68	73
NZ_AAAU02000002	9.00E-67	262	144	54
NZ_AAAU02000002	4.00E-32	90	71	78
AAAU02000002	9.00E-67	262	144	54
AAAU02000002	4.00E-32	90	71	78
AADX01000003	2.00E-65	297	145	48
NZ_AADX01000003	2.00E-65	297	145	48
NC_005085	7.00E-65	297	137	46
NC_005085	3.00E-64	297	137	46
NC_005085	1.00E-43	299	104	34
NC_005085	9.00E-41	369	122	33
NC_005085	6.00E-08	299	62	20
NC_005085	6.80E-01	266	61	22
NZ_AAAN02000069	9.00E-65	296	145	48
NZ_AAAN02000069	5.00E-61	295	136	46
NZ_AAAN02000069	6.00E-61	295	136	46
NZ_AAAN02000069	1.00E-60	295	135	45
NZ_AAAN02000069	1.00E-59	296	132	44
NZ_AAAN02000069	1.00E-59	296	132	44
NZ_AAAN02000069	2.00E-46	296	112	37
AAAN02000069	9.00E-65	296	145	48
AAAN02000069	5.00E-61	295	136	46
AAAN02000069	6.00E-61	295	136	46
AAAN02000069	1.00E-60	295	135	45
AAAN02000069	1.00E-59	296	132	44
AAAN02000069	1.00E-59	296	132	44
AAAN02000069	2.00E-46	296	112	37
NZ_AAAN02000032	1.00E-62	296	134	45
NZ_AAAN02000032	3.00E-61	296	133	44
NZ_AAAN02000032	3.00E-61	296	133	44
NZ_AAAN02000032	4.00E-59	296	136	45
NZ_AAAN02000032	7.00E-56	295	130	44
NZ_AAAN02000032	3.00E-53	282	117	41
NZ_AAAN02000032	3.00E-17	87	47	54
NZ_AAAN02000032	7.00E-12	275	64	23
AAAN02000032	1.00E-62	296	134	45
AAAN02000032	3.00E-61	296	133	44
AAAN02000032	3.00E-61	296	133	44
AAAN02000032	4.00E-59	296	136	45
AAAN02000032	7.00E-56	295	130	44
AAAN02000032	3.00E-53	282	117	41
AAAN02000032	3.00E-17	87	47	54
AAAN02000032	7.00E-12	275	64	23
AAAT03000008	4.00E-62	297	138	46
NZ_AAAT03000008	4.00E-62	297	138	46
AADF01000011	2.00E-61	296	131	44
AADF01000011	2.00E-10	322	67	20
AADF01000011	3.10E-01	264	56	21
NZ_AADF01000011	2.00E-61	296	131	44
NZ_AADF01000011	2.00E-10	322	67	20
NZ_AADF01000011	3.10E-01	264	56	21
NC_004347	3.00E-61	297	140	47
NC_004347	2.00E-60	297	135	46
NC_004347	8.00E-07	136	36	28
NC_004347	1.50E+00	89	26	29
NZ_AAAS02000027	8.00E-61	296	137	46
AAAS02000027	8.00E-61	296	137	46

Fig. 25D-Continued

Hit_ID	Expected	Length	#Ident	%S
NC_006510	8.00E-61	307	134	43
NC_006510	4.00E-33	269	96	35
NC_006510	3.00E-21	179	62	34
NC_006510	2.00E-14	288	69	23
contig:3337:p_fluorescens	7.00E-60	300	134	44
contig:3337:p_fluorescens	5.00E-06	130	37	28
NZ_AABP02000008	1.00E-59	297	135	45
NZ_AABP02000008	4.00E-08	138	41	29
AABP02000008	1.00E-59	297	135	45
AABP02000008	4.00E-08	138	41	29
AAEI01000040	2.00E-59	291	134	46
NZ_AAEI01000040	2.00E-59	291	134	46
bstearo.fasta.screen.Contig	4.00E-59	292	131	44
bstearo.fasta.screen.Contig	1.00E-54	327	133	40
bstearo.fasta.screen.Contig	1.00E-14	291	68	23
NC_002939	6.00E-59	298	133	44
NC_002939	2.00E-17	293	76	25
contig:4013:c_hydrogenoform	2.00E-56	298	133	44
contig:4013:c_hydrogenoform	6.00E-21	288	81	28
NC_004578	1.00E-57	297	129	43
NC_004578	1.50E+00	128	31	24
NC_003869	1.00E-56	298	134	44
NC_003869	9.00E-20	290	83	28
NZ_AAAV02000005	3.00E-56	329	133	40
AAAV02000005	3.00E-56	329	133	40
NC_004344	3.00E-56	181	109	60
NC_004344	2.00E-26	345	109	31
NC_006270	5.00E-55	313	135	43
NC_006270	2.00E+00	87	22	25
NC_006322	5.00E-55	313	135	43
NC_006322	2.00E+00	87	22	25
Cbot440b12.q1c	6.00E-55	298	127	42
Cbot440b12.q1c	1.00E-54	298	127	42
Cbot440b12.q1c	4.00E-40	304	103	33
Cbot440b12.q1c	2.00E-37	280	84	30
Cbot440b12.q1c	3.00E-11	305	63	20
NC_002570	1.00E-54	294	124	42
NC_002570	2.00E-29	135	70	51
NC_002570	4.00E-19	169	57	33
Cd183h6.p1t	5.00E-54	300	125	41
Cd183h6.p1t	3.00E-08	293	62	21
Cd183h6.p1t	1.50E+00	309	55	17
Cd183h6.p1t	2.00E+00	113	24	21
AADW01000019	1.00E-53	299	128	42
AADW01000019	7.00E-46	300	110	36
AADW01000019	9.00E-12	321	74	23
NZ_AADW01000019	1.00E-53	299	128	42
NZ_AADW01000019	7.00E-46	300	110	36
NZ_AADW01000019	9.00E-12	321	74	23
NC_004557	2.00E-53	296	125	42
NC_004557	1.00E-41	294	106	35
NC_004557	3.00E-33	270	80	29
NC_004557	1.00E-10	284	68	23
NC_004557	2.00E+00	103	24	23
NC_004193	2.00E-53	338	131	38
NC_004193	1.00E-17	293	75	25
BC10B5Le10.q1ka	2.00E-53	381	141	37
BC10B5Le10.q1ka	4.00E-07	183	45	24
NC_000964	6.00E-53	306	130	42
NC_000964	1.00E-30	206	81	39
NC_004605	1.00E-52	301	119	39
NC_004605	3.10E-01	116	29	25
NC_003030	1.00E-52	295	122	41
NC_003030	3.00E-45	292	115	39
NC_003030	1.00E-41	290	104	35
NC_003030	1.00E-31	292	89	30
NC_003030	3.00E-08	289	65	22
NC_003030	6.00E-03	310	69	22

Hit_ID	Expected	Length	#Ident	%S
J10164Af04.p1k	1.00E-51	300	115	38
NC_004603	6.00E-51	376	131	34
NC_004603	2.00E-42	384	125	32
NC_004603	2.00E-40	377	125	33
NC_004603	2.00E-40	377	126	33
NC_004603	2.00E-40	377	126	33
NC_004603	3.00E-23	148	60	40
NC_004603	1.00E-12	217	61	28
NZ_AABG03000012	9.00E-51	295	120	40
NZ_AABG03000012	2.00E-48	292	118	40
NZ_AABG03000012	4.00E-20	274	59	25
AABG03000012	9.00E-51	295	120	40
AABG03000012	2.00E-48	292	118	40
AABG03000012	4.00E-20	274	69	25
NZ_AAEK01000005	1.00E-50	309	119	38
NZ_AAEK01000005	3.00E-49	293	117	39
NZ_AAEK01000005	4.00E-49	292	118	40
NZ_AAEK01000005	1.00E-46	295	111	37
NZ_AAEK01000005	6.00E-32	292	96	32
AAEK01000005	1.00E-50	309	119	38
AAEK01000005	3.00E-49	293	117	39
AAEK01000005	4.00E-49	292	118	40
AAEK01000005	1.00E-46	295	111	37
AAEK01000005	6.00E-32	292	96	32
NC_005363	4.00E-50	295	124	42
NC_005363	3.00E-49	292	120	41
NC_005363	5.00E-47	301	117	38
NC_005363	3.00E-46	292	115	39
NC_005363	2.00E-43	295	110	37
NC_005363	4.00E-42	295	109	36
AAEM01000002	8.00E-50	404	146	36
AAEM01000002	2.00E-48	404	150	37
NZ_AAEM01000002	8.00E-50	404	146	36
NZ_AAEM01000002	2.00E-48	404	150	37
NC_003919	3.00E-49	212	113	53
NC_003919	2.00E-21	307	87	28
NC_003919	5.00E-09	134	40	29
contig:492:b_thailandensis	7.00E-49	380	136	35
contig:492:b_thailandensis	8.90E-01	49	18	36
sdublin_Contig2945_12.23	9.00E-49	105	104	98
senteritdis_1988_10.21	9.00E-49	106	104	98
NZ_AAFH01000001	2.00E-48	290	120	41
NZ_AAFH01000001	2.00E-24	159	67	42
AAFH01000001	2.00E-48	290	120	41
AAFH01000001	2.00E-24	159	67	42
NC_003902	2.00E-48	241	119	49
NC_003902	1.00E-21	319	93	29
NC_003902	1.00E-07	134	38	28
NC_006138	3.00E-48	252	120	47
NC_006138	1.00E-43	231	108	46
NC_006138	5.00E-25	227	81	35
NC_006138	2.00E-22	254	79	31
NC_006138	9.00E-06	130	40	30
NC_006138	1.50E+00	148	33	22
NC_005823	1.00E-47	302	111	36
NC_005823	1.00E-43	300	107	35
NC_005823	2.00E-43	300	107	35
NC_005823	6.00E-39	301	99	32
NC_005823	1.00E-06	110	34	30
NC_005823	2	59	18	30
NC_004342	1.00E-47	302	111	36
NC_004342	1.00E-43	300	107	35
NC_004342	3.00E-43	300	107	35
NC_004342	5.00E-39	301	100	33
NC_004342	1.00E-06	110	34	30
NC_004342	2.00E+00	59	18	30
NC_002505	2.00E-47	375	130	34
NC_002505	5E-45	375	133	35

Fig. 25D-Continued

Hit_ID	Expected	Length	#Ident	%S
NC_002505	2.00E-43	377	134	35
NC_002505	4.00E-43	377	129	34
NC_002506	2.00E-41	379	127	33
NC_002505	2.00E-03	228	52	22
NC_006348	2.00E-47	385	136	35
NC_006348	1.50E+00	76	24	31
Burkholderia	2.00E-47	385	136	35
Burkholderia	2.80E-02	335	74	22
Burkholderia	1.50E+00	76	24	31
NC_004722	3.00E-47	296	114	38
NC_004722	2.00E-44	298	115	38
NC_004722	6.00E-40	271	98	36
NC_004722	2.00E-32	291	95	32
NC_004722	3.00E-07	243	57	23
NC_006177	4.00E-47	296	114	38
NZ_AAER01000023	6.00E-47	292	112	38
NZ_AAES01000034	6.00E-47	292	112	38
NZ_AAEO01000025	6.00E-47	292	112	38
NZ_AAEN01000011	6.00E-47	292	112	38
NZ_AAEP01000035	6.00E-47	292	112	38
NZ_AAEQ01000029	6.00E-47	292	112	38
AAES01000034	6.00E-47	292	112	38
AAER01000023	6.00E-47	292	112	38
AAEQ01000029	6.00E-47	292	112	38
AAEP01000035	6.00E-47	292	112	38
AAEO01000025	6.00E-47	292	112	38
AAEN01000011	6.00E-47	292	112	38
NC_005945	6.00E-47	292	112	38
NC_007530	6.00E-47	292	112	38
NC_003997	6.00E-47	292	112	38
NC_003995	6.00E-47	292	112	38
NC_002967	1.00E-46	300	113	37
NC_002967	1.00E-43	304	109	35
NC_002967	5.00E-42	304	106	34
NC_002967	3.00E-10	285	65	22
NC_006370	9.00E-46	382	130	34
NC_006370	9.00E-36	251	106	42
NC_006370	5.00E-34	213	82	38
NC_006370	2.00E-17	203	63	31
NC_006370	4.00E-17	149	55	36
NC_006370	2.00E+00	73	16	21
NC_000919	2.00E-45	298	114	38
NC_000919	1.00E-44	301	111	36
NC_000919	1.00E-44	304	107	35
NC_000919	3.00E-09	268	60	22
NC_002937	3.00E-45	311	119	38
NC_002937	1.00E-43	310	113	36
NC_002937	2.00E-41	295	101	34
NC_002937	2.00E+00	171	36	21
NZ_AABN02000006	6.00E-45	295	107	36
NZ_AABN02000006	3.00E-03	46	21	45
AABN02000006	6.00E-45	295	107	36
AABN02000006	3.00E-03	46	21	45
sdublin_Contig1652_12.23	1.00E-44	97	97	100
NC_006368	2.00E-44	309	124	40
NC_006368	1.00E-23	200	77	38
NC_005957	3.00E-44	365	125	34
NC_005957	5.00E-33	292	97	33
NC_002942	5.00E-44	309	125	40
NC_002942	3.00E-23	198	78	39
NC_006369	2.00E-43	309	122	39
NC_006369	2.00E-23	251	88	35
NC_006156	3.00E-43	342	113	33
NC_006155	8.90E-01	77	18	23
NC_001318	3.00E-43	342	113	33
NC_001318	8.90E-01	77	18	23
NC_003296	4.00E-43	297	109	36
NC_003296	7.00E-03	264	60	22

Hit_ID	Expected	Length	#Ident	%S
NC_003296	4.00E-01	260	56	21
NC_003296	5.20E-01	247	57	23
NZ_AABN02000015	9.00E-43	300	108	36
NZ_AABN02000015	2.00E-42	295	99	33
AABN02000015	9.00E-43	300	108	36
AABN02000015	2.00E-42	295	99	33
NZ_AADQ01000005	2.00E-42	296	107	36
NZ_AADR01000002	2.00E-42	296	107	36
AADR01000002	2.00E-42	296	107	36
AADQ01000005	2.00E-42	296	107	36
NC_003212	2.00E-42	296	107	36
NC_003212	6.20E-02	261	57	21
NC_003212	1.40E-01	292	64	21
NC_003210	2.00E-42	296	107	36
NC_003210	6.00E-03	273	58	21
NC_002973	2.00E-42	296	107	36
NC_005139	2.00E-42	375	121	32
NC_005139	2.00E-36	376	118	31
NC_005139	9.00E-36	376	119	31
NC_005139	4.00E-35	178	80	44
NC_005139	7.00E-35	376	111	29
NC_005139	7.00E-27	374	108	28
NC_005139	6.00E-21	301	92	30
NC_004459	2.00E-42	375	121	32
NC_004459	2.00E-41	376	122	32
NC_004459	7.00E-36	376	120	31
NC_004459	9.00E-36	376	119	31
NC_004459	4.00E-35	178	80	44
NC_004459	7.00E-27	374	108	28
NC_004459	6.00E-21	301	92	30
NC_006087	4.00E-42	299	105	35
NC_006087	3.00E-20	308	85	27
NC_006513	6.00E-42	151	89	58
Eagg631c06.q1k	8.00E-42	310	107	34
Eagg631c06.q1k	8.00E-08	309	62	20
NZ_AAAJ03000013	1.00E-41	378	127	33
AAAJ03000013	1.00E-41	378	127	33
NZ_AABQ07000002	1.00E-40	242	103	42
NZ_AABQ07000002	3.00E-24	335	100	29
NZ_AABQ07000002	3.00E-04	134	34	25
AABQ07000002	1.00E-40	242	103	42
AABQ07000002	3.00E-24	335	100	29
AABQ07000002	3.00E-04	134	34	25
NC_002516	1.00E-40	242	103	42
NC_002516	3.00E-24	335	100	29
NC_002516	3.00E-04	134	34	25
NC_002516	3.10E-01	201	49	24
AABI03000002	7.00E-40	222	101	45
AABI03000002	5.00E-39	254	105	41
AABI03000002	4.00E-20	182	66	36
AABI03000002	4.00E-19	129	55	42
AABI03000002	1.00E-06	128	33	25
AABI03000002	2.80E-02	91	24	26
AABI03000002	1.40E-01	169	35	20
NZ_AABI03000002	7.00E-40	222	101	45
NZ_AABI03000002	5.00E-39	254	105	41
NZ_AABI03000002	4.00E-20	182	66	36
NZ_AABI03000002	4.00E-19	129	55	42
NZ_AABI03000002	1.00E-06	128	33	25
NZ_AABI03000002	2.80E-02	91	24	26
NZ_AABI03000002	1.40E-01	169	35	20
contig:1731:c_psychroerythr	7.00E-40	259	108	41
contig:1731:c_psychroerythr	6.00E-39	259	108	41
contig:1731:c_psychroerythr	6.00E-24	263	82	31
contig:1731:c_psychroerythr	1.00E-21	263	78	29
contig:1731:c_psychroerythr	8.00E-07	136	32	23
NC_002947	1.00E-39	252	103	40
NC_002947	3.00E-19	129	53	41

Fig. 25D-Continued

Hit_ID	Expected	Length	#Ident	%S
NC_002947	4.00E-07	130	41	31
AAAW02000007	2.00E-39	385	128	33
AAAW02000007	8.00E-23	298	89	29
AAAW02000007	2.00E-09	154	47	30
NZ_AAAW02000007	2.00E-39	385	128	33
NZ_AAAW02000007	8.00E-23	298	89	29
NZ_AAAW02000007	2.00E-09	154	47	30
NC_004463	1.00E-38	295	95	32
NC_004463	8.00E-16	311	73	23
NC_004463	1.00E-14	317	74	23
NC_004463	8.00E-08	273	72	26
NC_004463	2.00E-07	255	72	28
NC_004463	8.00E-07	250	63	25
NC_004463	2.00E-06	186	47	25
NC_004463	8.10E-02	233	50	21
NC_004463	1.40E-01	134	39	29
NC_004463	4.00E-01	109	29	26
NC_004463	6.80E-01	121	28	23
NC_004463	1.20E+00	109	29	26
NC_004463	1.50E+00	109	29	26
NC_004463	2.00E+00	109	29	26
Pflu019c02.p1c	2.00E-38	230	97	42
Pflu019c02.p1c	2.00E-17	330	81	24
contig:491:b_thailandensis	3.00E-38	305	107	35
AAEH01000086	2.00E-37	242	97	40
AAEH01000086	2.00E-17	86	46	53
NZ_AAEH01000086	2.00E-37	242	97	40
NZ_AAEH01000086	2.00E-17	86	46	53
AAAG02000001	1.00E-36	305	107	35
AAAG02000001	4.00E-12	302	69	22
AAAG02000001	6.80E-01	239	49	20
NZ_AAAG02000001	1.00E-36	305	107	35
NZ_AAAG02000001	4.00E-12	302	69	22
NZ_AAAG02000001	6.80E-01	239	49	20
NC_005296	4.00E-36	295	92	31
NC_005296	2.00E-05	284	70	24
NC_005296	2.00E-05	284	69	24
NC_005296	1.00E-03	194	49	25
NC_005296	8.90E-01	261	58	22
sdublin_Contig993_12.23	4.00E-36	81	81	100
stdt38a03.p1k	4.00E-36	98	79	80
stdt23f04.p1k	4.00E-36	98	79	80
NZ_AADT02000011	2.00E-35	382	125	32
NZ_AADT02000011	8.00E-18	285	73	25
AADT02000011	2.00E-35	382	125	32
AADT02000011	8.00E-18	285	73	25
NC_006512	6.00E-35	170	82	48
NC_006512	4.00E-20	267	77	28
NC_006512	1.00E-03	130	35	26
NZ_AAAI02000004	3.00E-34	199	85	42
NZ_AAAI02000004	9.00E-22	92	57	61
AAAI02000004	3.00E-34	199	85	42
AAAI02000004	9.00E-22	92	57	61
NC_003909	5.00E-34	292	96	32
NC_003909	2.00E-28	221	77	34
NC_003909	8.00E-13	84	41	48
NZ_AAAN02000082	5.00E-33	280	85	30
AAAN02000082	5.00E-33	280	85	30
NZ_AAAE01000066	1.00E-32	166	74	44
NZ_AAAE01000066	2.00E-19	176	63	35
AAAE01000066	1.00E-32	166	74	44
AAAE01000066	2.00E-19	176	63	35
NC_006274	1.00E-32	292	95	32
NC_006274	1.00E-31	289	96	33
NC_006274	1.00E-14	111	46	41
NC_006274	1.00E-07	242	57	23
NC_000853	2.00E-32	392	119	30
NC_000853	3.00E-17	248	63	25

Hit_ID	Expected	Length	#Ident	%S
NC_000853	8.00E-10	256	62	24
pputidprs_GPPBG16TR	7.00E-28	123	66	53
stdt25b06.p1k	9.00E-25	77	58	75
AAEF01000080	3.00E-24	245	76	31
AAEF01000080	7.00E-20	195	65	33
AAEF01000080	3.00E-13	301	76	25
NZ_AAEF01000080	3.00E-24	245	76	31
NZ_AAEF01000080	7.00E-20	195	65	33
NZ_AAEF01000080	3.00E-13	301	76	25
NC_005090	3.00E-23	294	89	30
NC_005090	2.00E-21	192	63	32
NC_005090	9.00E-19	333	85	25
NC_005090	1.00E-12	278	65	23
NC_005090	3.00E-12	122	44	36
NC_005090	6.00E-03	168	37	22
contig:521:c_jejuni	3.00E-23	181	66	36
contig:521:c_jejuni	1.00E-21	181	66	36
contig:521:c_jejuni	2.00E-14	156	53	33
contig:521:c_jejuni	2.00E-12	156	50	32
contig:521:c_jejuni	6.00E-11	288	68	23
NC_000915	8.00E-23	187	67	35
NC_000915	3.00E-19	170	57	33
NC_000915	5.00E-15	311	78	25
NC_000915	2.00E-13	121	47	38
NC_000921	1.00E-22	187	67	35
NC_000921	3.00E-19	170	57	33
NC_000921	5.00E-15	311	78	25
NC_000921	2.00E-13	121	47	38
NC_000921	4.00E-04	149	40	26
NC_002163	3.00E-22	171	63	36
NC_002163	6.00E-21	181	66	36
NC_002163	4.00E-14	132	48	36
NC_002163	4.00E-12	132	45	34
NC_002163	7.00E-11	288	66	22
NC_004917	9.00E-22	188	67	35
NC_004917	1.00E-19	170	60	35
NC_004917	1.00E-19	170	60	35
NC_004917	3.00E-13	297	74	24
NC_004917	3.00E-13	297	74	24
NC_004917	6.00E-11	115	40	34
NC_002696	1.00E-21	297	76	25
NC_002696	4.00E-20	298	76	25
NC_002696	5.00E-20	292	75	25
NC_002696	5.00E-20	292	72	24
NC_002696	7.00E-20	292	72	24
NC_002696	1.00E-19	292	70	23
NC_002696	1.10E-01	73	21	28
NC_000918	1.00E-20	209	62	29
NC_000918	7.00E-09	129	39	30
contig:4798:g_obscuriglobus	7.00E-20	139	57	41
contig:4798:g_obscuriglobus	3.00E-12	157	52	33
AAED01000008	9.00E-20	294	80	27
AAED01000008	8.00E-15	297	68	22
NZ_AAED01000008	9.00E-20	294	80	27
NZ_AAED01000008	8.00E-15	297	68	22
NC_005027	9.00E-20	284	88	30
NC_005027	1.00E-19	257	76	29
NC_005027	4.00E-18	169	62	36
NC_005027	6.00E-16	126	55	43
NC_005027	1.00E-14	143	57	39
NC_005027	4.00E-14	250	70	28
NC_005027	6.80E-01	240	52	21
NC_005027	1.50E+00	120	34	28
rhiz573a05.p1n	2.00E-19	303	84	27
AAAW02000158	2.00E-18	314	89	28
NZ_AAAW02000158	2.00E-18	314	89	28
NC_003062	1E-17	313	77	24
NC_003062	3.00E-14	313	75	23

Fig. 25D-Continued

Hit_ID	Expected	Length	#Ident	%S
NC_003062	9.00E-12	324	75	23
NC_003062	2.00E-06	256	60	23
NC_003062	4.00E-04	140	34	24
NC_003304	1.00E-17	313	77	24
NC_003304	3.00E-14	313	75	23
NC_003304	9.00E-12	324	75	23
NC_003304	2.00E-06	256	60	23
NC_003304	4.00E-04	140	34	24
NC_004311	7.00E-17	298	76	25
NC_003318	3.00E-16	298	75	25
sdublin_Contig1019_12.23	3.00E-16	80	49	61
rhiz606c07.p1n	4.00E-16	303	78	25
rhiz606c07.p1n	5.00E-15	304	76	25
rhiz606c07.p1n	1.00E-05	317	66	20
NC_002678	1.00E-15	329	75	22
NC_002678	3.00E-08	356	80	22
NZ_AAFG01000002	2.00E-15	296	75	25
NZ_AAFG01000002	4.00E-14	298	72	24
AAFG01000002	2.00E-15	296	75	25
AAFG01000002	4.00E-14	298	72	24
rhiz24d12.p1k	3.00E-14	310	77	24
NZ_AAAE01000155	7.00E-14	302	70	23
AAAE01000155	7.00E-14	302	70	23
NZ_AAFG01000004	2.00E-13	294	72	24
AAFG01000004	2.00E-13	294	72	24
NZ_AAFG01000007	3.00E-13	299	69	23
AAFG01000007	3.00E-13	299	69	23
contig:519:c_jejuni	6.00E-11	288	68	23
NZ_AAAP01001822	1.00E-10	276	72	26
AAAP01001822	1.00E-10	276	72	26
Cbot389c10.p2c412	1.00E-10	257	63	24
NC_003047	5.00E-09	321	68	21
NC_003047	2.00E-05	87	29	33
NC_003047	5.00E-04	245	56	22
NC_003047	2.80E-02	87	24	27
NZ_AAEK01000008	2.00E-08	243	62	25
AAEK01000008	2.00E-08	243	62	25
NZ_AABN02000001	3.00E-07	113	32	28
NZ_AABN02000001	3.00E-03	238	50	21
AABN02000001	3.00E-07	113	32	28
AABN02000001	3.00E-03	238	50	21
contig:2663:s_pomeroyi	4.00E-07	278	64	23
contig:2663:s_pomeroyi	4.00E-03	180	36	20
contig:1062:h_neptunium	6.00E-07	153	39	26
NZ_AAAI02000005	3.00E-06	326	70	21
NZ_AAAI02000005	2.00E+00	93	28	30
AAAI02000005	3.00E-06	326	70	21
AAAI02000005	2.00E+00	93	28	30
Bcep1110a03.q2kb4087	3.00E-05	298	66	22
Bcep1110a03.q2kb4087	5.00E-05	299	67	22
Bcep1110a03.q2kb4087	3.00E-04	286	66	23
Bcep1110a03.q2kb4087	4.00E-01	226	52	23
AADY01000003	8.00E-05	121	37	30
NZ_AADY01000003	8.00E-05	121	37	30
NZ_AABG03000053	2.00E-04	83	28	33
AAEI01000016	2.00E-04	291	67	23
AAEI01000016	9.00E-04	289	59	20
AABG03000053	2.00E-04	83	28	33
NZ_AAEI01000016	2.00E-04	291	67	23
NZ_AAEI01000016	9.00E-04	289	59	20
NZ_AABG03000001	4.00E-04	257	54	21
AABG03000001	4.00E-04	257	54	21
contig:313:m_arthritidis	4.00E-04	263	60	22
contig:313:m_arthritidis	1.40E-01	127	32	25
contig:313:m_arthritidis	1.80E-01	124	33	26
contig:313:m_arthritidis	1.50E+00	137	32	23
Bcep825a04.p2n33	4.00E-04	255	58	22
contig:510:v_spinosum	7.00E-04	262	66	25

Hit_ID	Expected	Length	#Ident	%S
AAEA01000001	1.00E-03	295	62	21
NZ_AAEA01000001	1.00E-03	295	62	21
NC_002662	1.00E-03	287	50	17
Pflu552a01.p1kz	3.00E-03	277	69	24
AABK03000008	3.00E-03	273	63	23
NZ_AABK03000008	3.00E-03	273	63	23
AAEH01000003	3.00E-03	284	62	21
AAEH01000003	2.10E-02	282	56	19
AAEH01000003	2.80E-02	287	60	20
AAEH01000003	2.80E-02	295	59	20
AAEH01000003	3.60E-02	285	61	21
AAEH01000003	4.70E-02	285	61	21
AAEH01000003	8.10E-02	285	59	20
AAEH01000003	1.10E-01	285	60	21
AAEH01000003	1.10E-01	322	67	20
NZ_AAEH01000003	3.00E-03	284	62	21
NZ_AAEH01000003	2.10E-02	282	56	19
NZ_AAEH01000003	2.80E-02	287	60	20
NZ_AAEH01000003	2.80E-02	295	59	20
NZ_AAEH01000003	3.60E-02	285	61	21
NZ_AAEH01000003	4.70E-02	285	61	21
NZ_AAEH01000003	8.10E-02	285	59	20
NZ_AAEH01000003	1.10E-01	285	60	21
NZ_AAEH01000003	1.10E-01	322	67	20
NC_005140	3.00E-03	289	63	21
NZ_AADQ01000014	4.00E-03	258	56	21
AADQ01000014	4.00E-03	258	56	21
AAEI01000009	4.00E-03	304	61	20
AAEI01000009	4.00E-03	298	64	21
AAEI01000009	8.10E-02	292	62	21
AAEI01000009	1.80E-01	278	57	20
NZ_AAEI01000009	4.00E-03	304	61	20
NZ_AAEI01000009	4.00E-03	298	64	21
NZ_AAEI01000009	8.10E-02	292	62	21
NZ_AAEI01000009	1.80E-01	278	57	20
NC_002935	6.00E-03	169	38	22
NC_004567	7.00E-03	285	64	22
NC_004567	2.00E+00	299	58	19
NZ_AAAU02000026	1.00E-02	122	36	29
AAAU02000026	1.00E-02	122	36	29
AAEI01000011	1.20E-02	297	72	24
NZ_AAEI01000011	1.20E-02	297	72	24
NC_002758	1.20E-02	332	72	21
NC_002745	1.20E-02	332	72	21
NZ_AABH02000009	1.60E-02	241	60	24
AABH02000009	1.60E-02	241	60	24
NZ_AAAR02000005	2.10E-02	292	54	18
AAAR02000005	2.10E-02	292	54	18
NC_006449	2.80E-02	302	64	21
NC_006448	2.80E-02	302	64	21
sdublin_Contig4745_12.23	2.80E-02	19	18	94
sdublin_Contig3450_12.23	2.80E-02	19	18	94
mar499b01.q1k	3.60E-02	87	25	28
NZ_AAAM01000127	4.70E-02	57	21	36
NZ_AACK01000006	4.70E-02	146	38	26
AACK01000006	4.70E-02	146	38	26
AAAM01000127	4.70E-02	57	21	36
NC_003923	4.70E-02	283	66	23
NC_003923	1.50E+00	299	60	20
NC_002953	4.70E-02	283	66	23
ap5.fasta.screen.Contig207	4.70E-02	146	38	26
NZ_AAAN02000006	6.20E-02	294	57	19
NZ_AAAJ03000006	6.20E-02	310	62	20
NZ_AAAJ03000006	1.10E-01	308	61	19
NZ_AAAJ03000006	1.80E-01	272	54	19
NZ_AAAJ03000006	3.10E-01	275	56	20
NZ_AAAJ03000006	3.10E-01	254	53	20
NZ_AAAJ03000006	6.80E-01	279	55	19

Fig. 25D-Continued

Hit_ID	Expected	Length	#Ident	%S
NZ_AAAJ03000006	8.90E-01	319	59	18
NZ_AAAJ03000006	1.50E+00	324	59	18
AAAN02000006	6.20E-02	294	57	19
AAAJ03000006	6.20E-02	310	62	20
AAAJ03000006	1.10E-01	308	61	19
AAAJ03000006	1.80E-01	272	54	19
AAAJ03000006	3.10E-01	275	56	20
AAAJ03000006	3.10E-01	254	53	20
AAAJ03000006	6.80E-01	279	55	19
AAAJ03000006	8.90E-01	319	59	18
AAAJ03000006	1.50E+00	324	59	18
NZ_AAAP01003482	8.10E-02	278	63	22
AAAP01003482	8.10E-02	278	63	22
AADW01000010	8.10E-02	317	71	22
NZ_AADW01000010	8.10E-02	317	71	22
NC_004461	8.10E-02	169	43	25
NC_004461	1.20E+00	302	60	19
contig:370:s_epidermidis	8.10E-02	169	43	25
contig:370:s_epidermidis	1.20E+00	302	60	19
AAED01000003	1.40E-01	183	41	22
NZ_AAED01000003	1.40E-01	183	41	22
NZ_AAAN02000003	2.30E-01	260	53	20
AAAN02000003	2.30E-01	260	53	20
AADW01000069	2.30E-01	285	51	17
NZ_AADW01000069	2.30E-01	285	51	17
NZ_AABH02000010	2.30E-01	298	58	19
AABH02000010	2.30E-01	298	58	19
Bcep1157h02.p1c	3.10E-01	300	58	19
NZ_AABG03000015	4.00E-01	181	39	21
NZ_AAAN02000029	4.00E-01	89	26	29
AAAN02000029	4.00E-01	89	26	29
AABG03000015	4.00E-01	181	39	21
NZ_AABQ07000001	4.00E-01	201	49	24
AABQ07000001	4.00E-01	201	49	24
NC_006300	4.00E-01	273	58	21
NC_006300	4.00E-01	273	58	21
NC_006300	5.20E-01	274	61	22
NC_003272	5.20E-01	286	59	20
NC_004829	5.20E-01	183	40	21
NZ_AAAN02000076	6.80E-01	294	56	19
AAAN02000076	6.80E-01	294	56	19
NZ_AAFG01000003	8.90E-01	62	20	32
AAFG01000003	8.90E-01	62	20	32
NZ_AABM02000032	8.90E-01	165	39	23
AABM02000032	8.90E-01	165	39	23
NC_004663	8.90E-01	150	44	29
contig:3563:m_smegmatis	8.90E-01	102	30	29
AAEI01000026	1.20E+00	130	38	29
NZ_AAEI01000026	1.20E+00	130	38	29
NC_005125	1.20E+00	73	24	32
NC_003366	1.20E+00	232	49	21
NC_000951	1.20E+00	114	30	26
Bcep1115d11.q1k	1.20E+00	130	37	28
contig:4304:c_perfringens	1.20E+00	232	49	21
NZ_AAEV01000005	1.50E+00	187	41	21
AAEV01000005	1.50E+00	187	41	21
NZ_AABP02000001	1.50E+00	254	46	18
AABP02000001	1.50E+00	254	46	18
NC_003552	1.50E+00	257	49	19
NC_005362	2.00E+00	125	28	22
AAAY02000105	2.60E+00	112	29	25
AAEH01000017	2.60E+00	238	54	22
NZ_AAEH01000017	2.60E+00	238	54	22
NZ_AAAY02000105	2.60E+00	112	29	25
Eagg385b08.q1ka	2.60E+00	185	42	22

Hit_ID	Expected	Length	#Ident	%S

Fig. 26

Accession	Source	Amino % Identity	Carboxy % Identity	Length
Q53970	Phase-1 flagellin [fliC1] [Salmonella dublin]	100	100	505
P72151	B-type flagellin [fliC] [Pseudomonas aeruginosa]	50	58	488
Q5X5M6	Flagelline [flaA] [Legionella pneumophila str. Paris]	46	61	475
Q6VMV6	Flagellin [fliC] [Escherichia coli]	74	84	488
P13713	Flagellin [fliC] [Serratia marcescens]	65	75	351
Q93RK8	Flagellin [hag] [Bacillus subtilis]	50	49	333
Q02551	Flagellin [flaA] [Listeria monocytogenes]	39	38	287
Q09012	Flagellin [fliC-SS(a)] [Shigella sonnei]	72	84	524
Q8GNT8	Flagellin [Edwardsiella tarda]	65	77	416
Q9FAE7	Flagellin [H8301-fla1] [Acidovorax avenae subsp. avenae]	61	56	492
Q8ZF76	Thermoregulated motility protein (Putative flagellin) [fliC] [Yersinia pestis]	82	80	369
Q7N5J4	Flagellin [fliC] [Photorhabdus luminescens (subsp. laumondii)]	63	77	355
O33578	Flagellar filament protein [fliC] [Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides)]	46	55	493
Q56826	Flagellin [fliC] [Xenorhabdus nematophilus]	76	75	313
P42273	Flagellin 2 [fliC2] [Proteus mirabilis]	63	78	367
O31059	Flagellin A protein [flaA] [Butyrivibrio fibrisolvens]	53	56	472
Q7VZC2	Flagellin [flaA] [Bordetella pertussis]	74	77	391
Q9F4A4	Flagellin protein FliA(C) [fliC] [Clostridium chauvoei]	51	48	413
Q8P9C4	Flagellar protein [fliC] [Xanthomonas campestris (pv. campestris)]	48	55	399
Q82UA3	Hag; flagellin [hag] [Nitrosomonas europaea]	58	57	275
Q84IC5	Flagellin (Fragment) [flaA] [Campylobacter lari]	32	45	490

Fig. 27

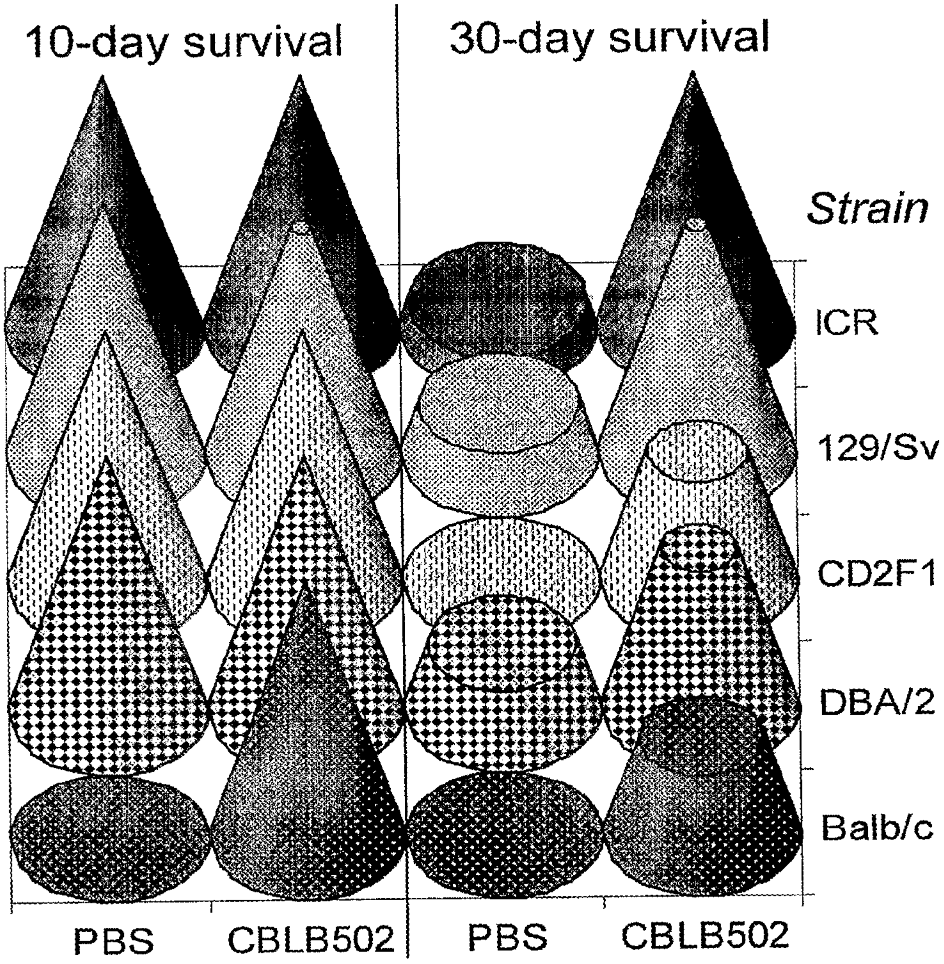
10-day survival
30-day survival
Strain
ICR
129/Sv
CD2F1
DBA/2
Balb/c
PBS
CBLB502
PBS
CBLB502

Fig. 28

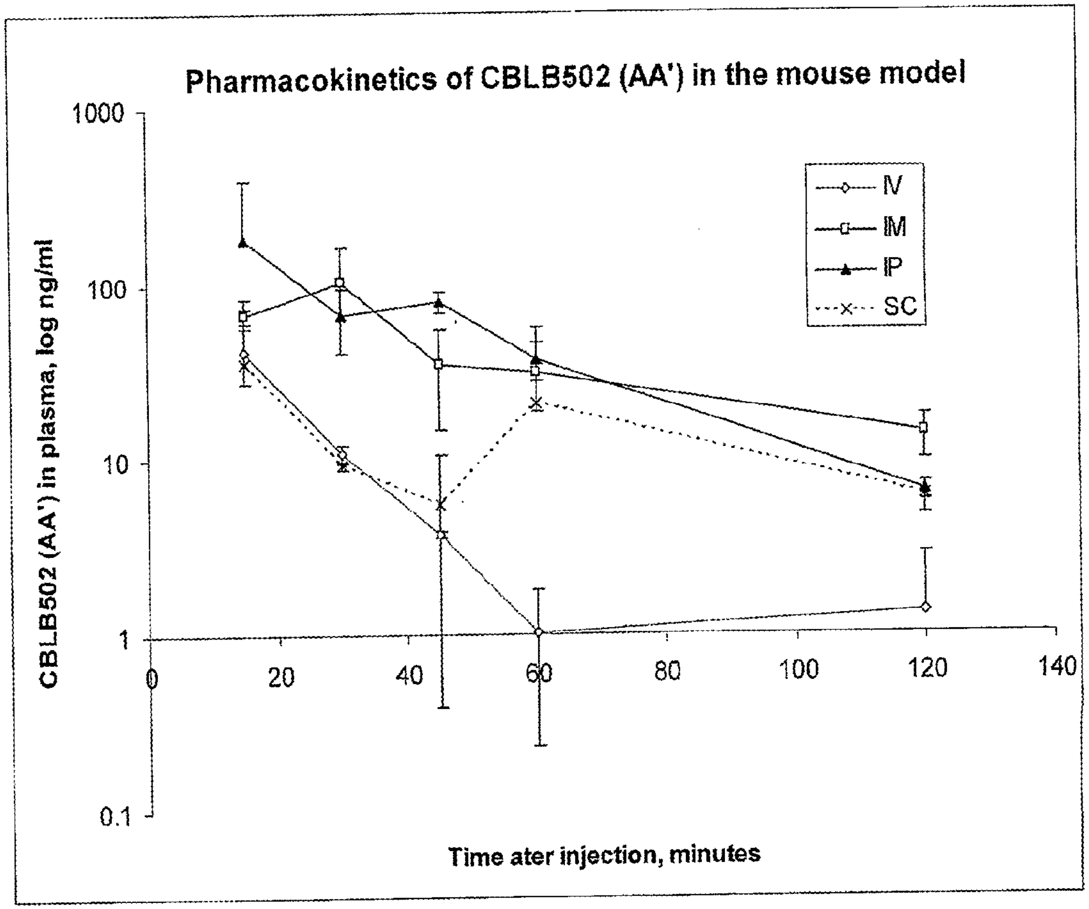
Pharmacokinetics of CBLB502 (AA') in the mouse model
CBLB502 (AA') in plasma, log ng/ml
1000
100
10
1
0.1
0
20
40
60
80
100
120
140
Time ater injection, minutes
IV
IM
IP
SC

Fig. 29

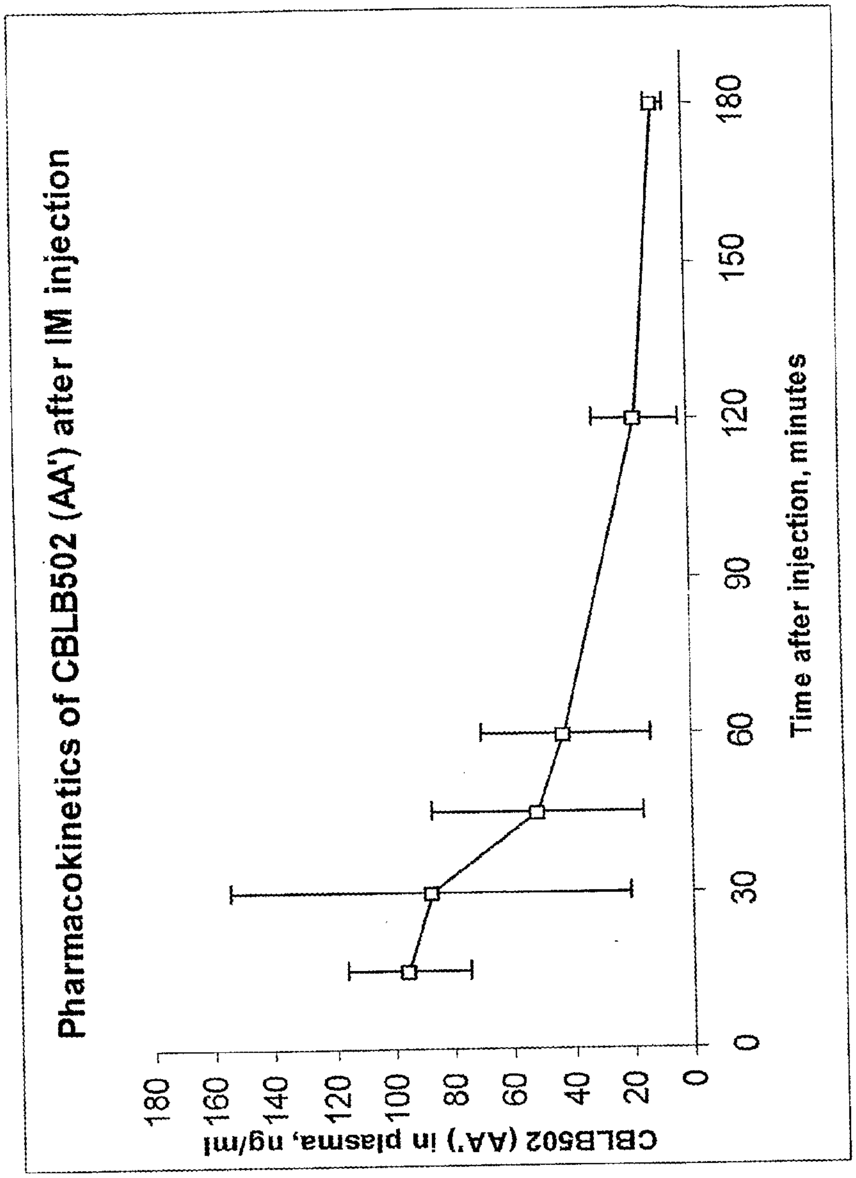
Pharmacokinetics of CBLB502 (AA') after IM injection
CBLB502 (AA') in plasma, ng/ml
180
160
140
120
100
80
60
40
20
0
0
30
60
90
120
150
180
Time after injection, minutes

Fig. 30

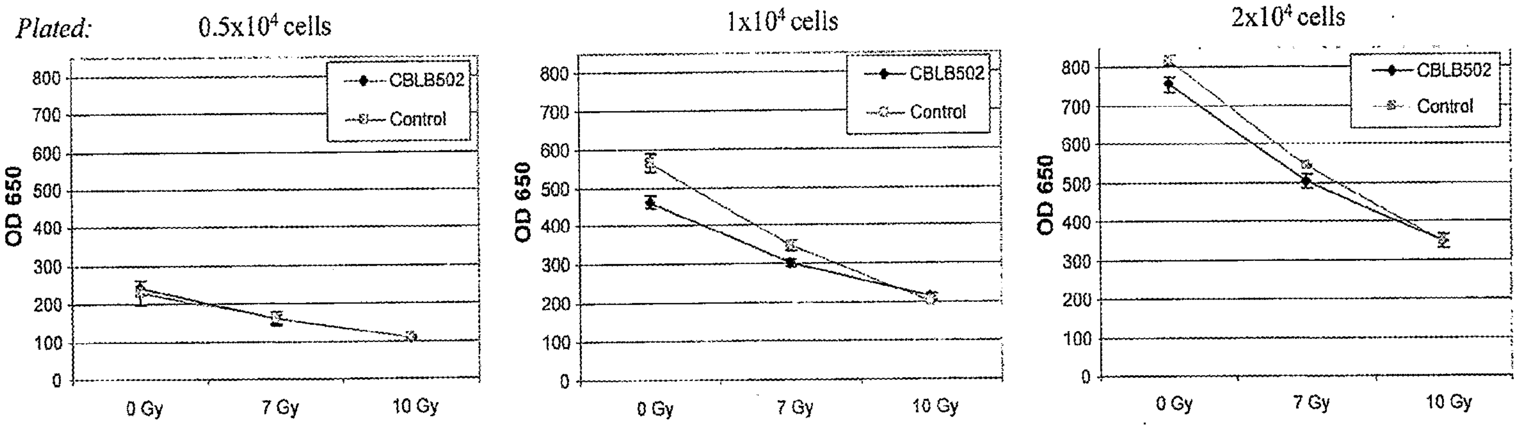
Plated:
0.5x10^4 cells
1x10^4 cells
2x10^4 cells
OD 650
800
700
600
500
400
300
200
100
0
0 Gy
7 Gy
10 Gy
CBLB502
Control

Fig. 31

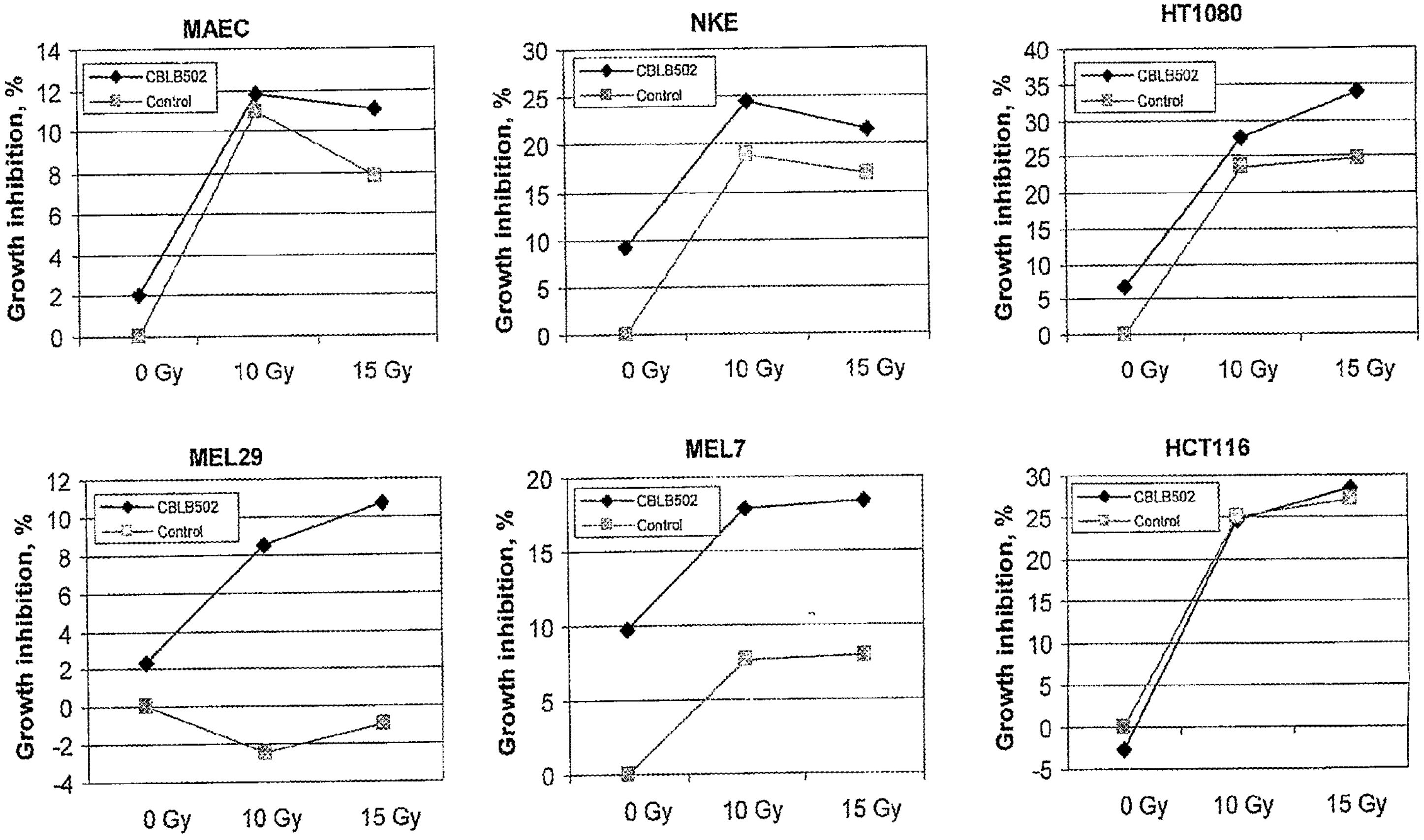
MAEC
NKE
HT1080
MEL29
MEL7
HCT116
Growth inhibition, %
CBLB502
Control
0 Gy
10 Gy
15 Gy
14
12
10
8
6
4
2
0
30
25
20
15
10
5
0
40
35
-2
-4
-5

Fig. 32

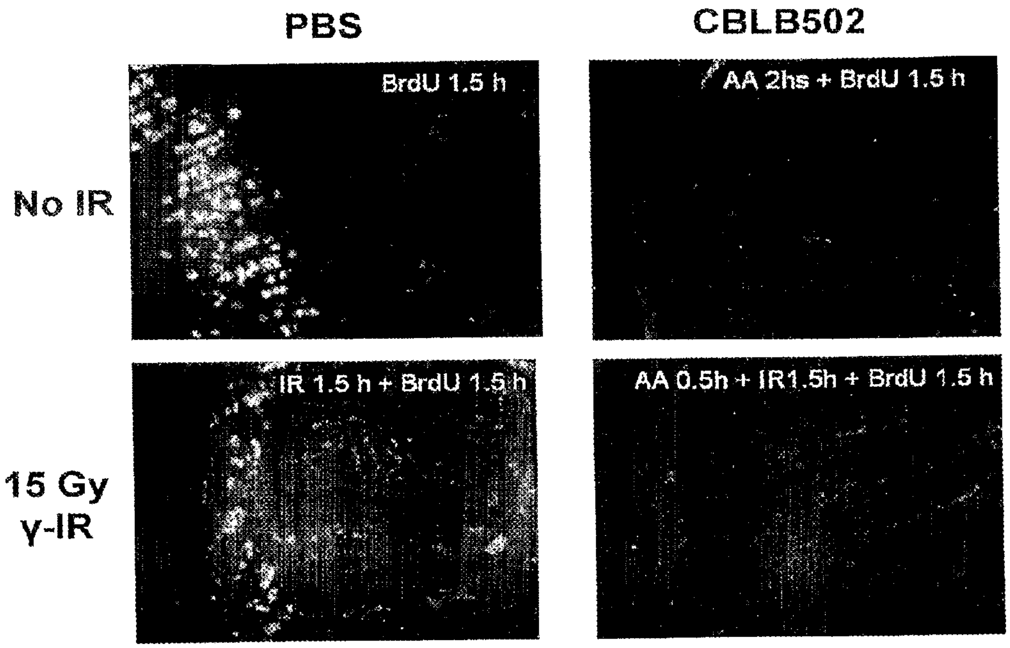
PBS
CBLB502
No IR
15 Gy
γ-IR
BrdU 1.5 h
AA 2hs + BrdU 1.5 h
IR 1.5 h + BrdU 1.5 h
AA 0.5h + IR1.5h + BrdU 1.5 h

Fig. 33

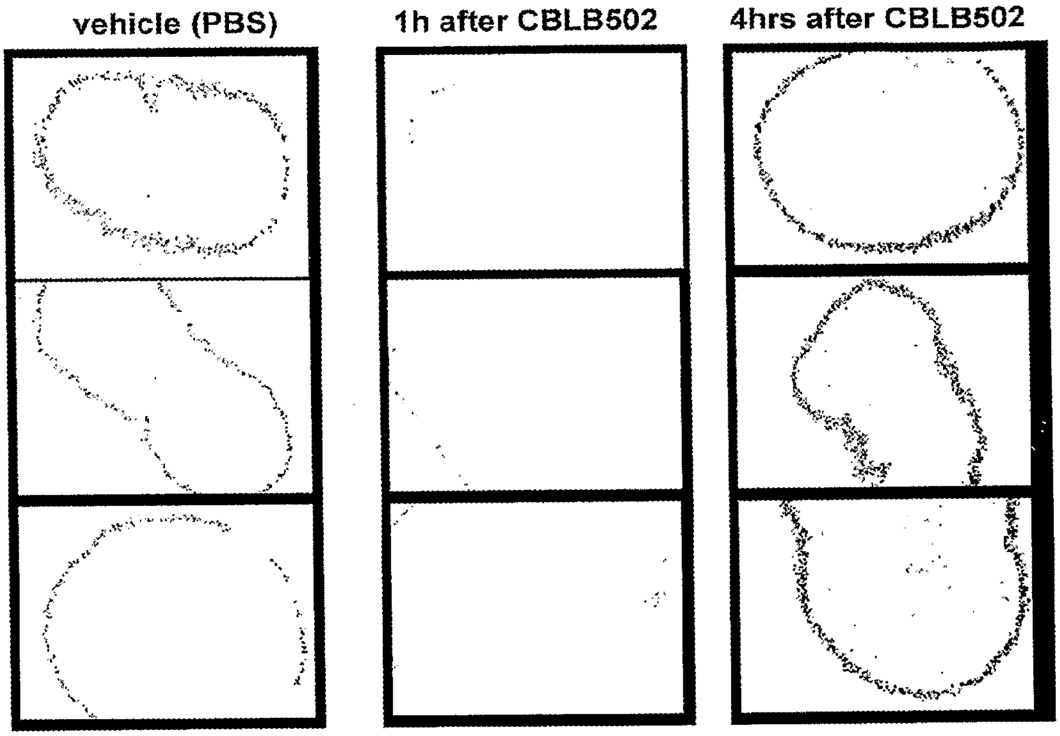

Fig. 34

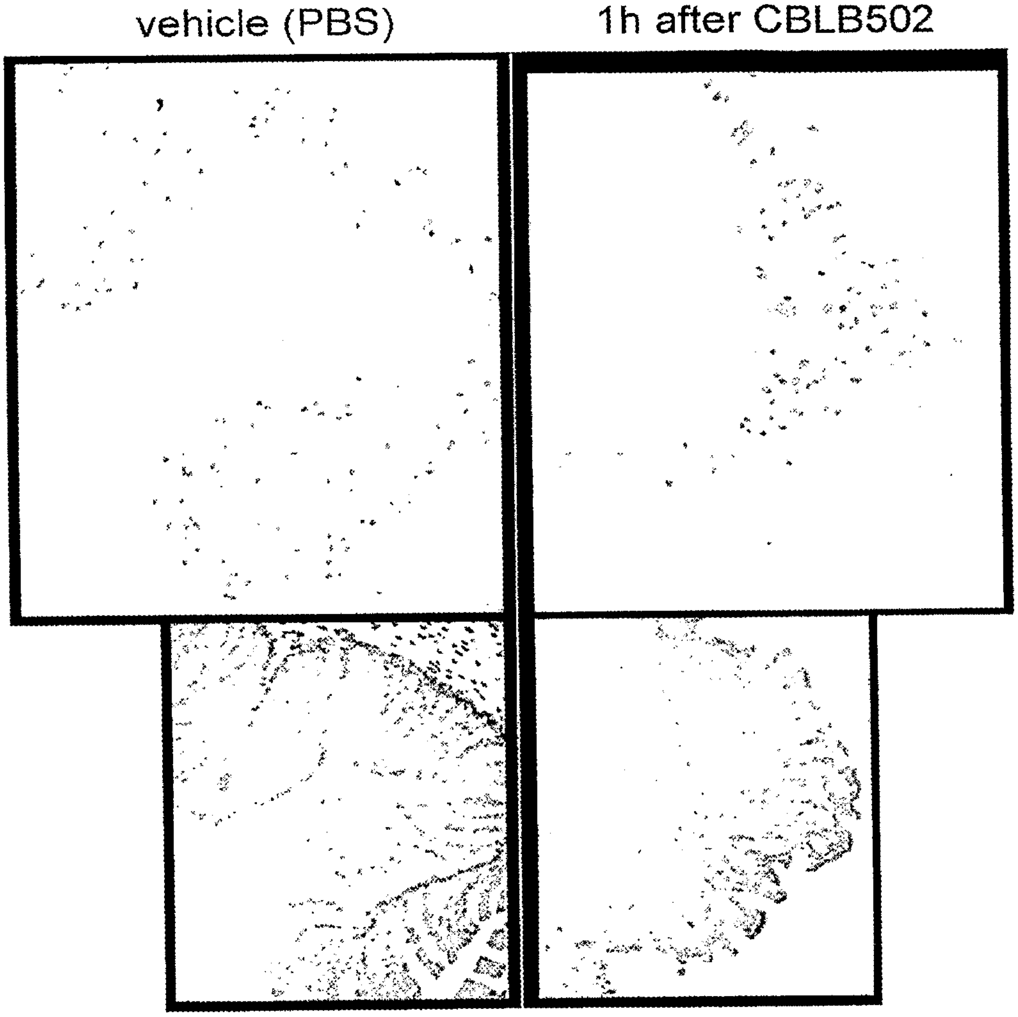

Fig. 35

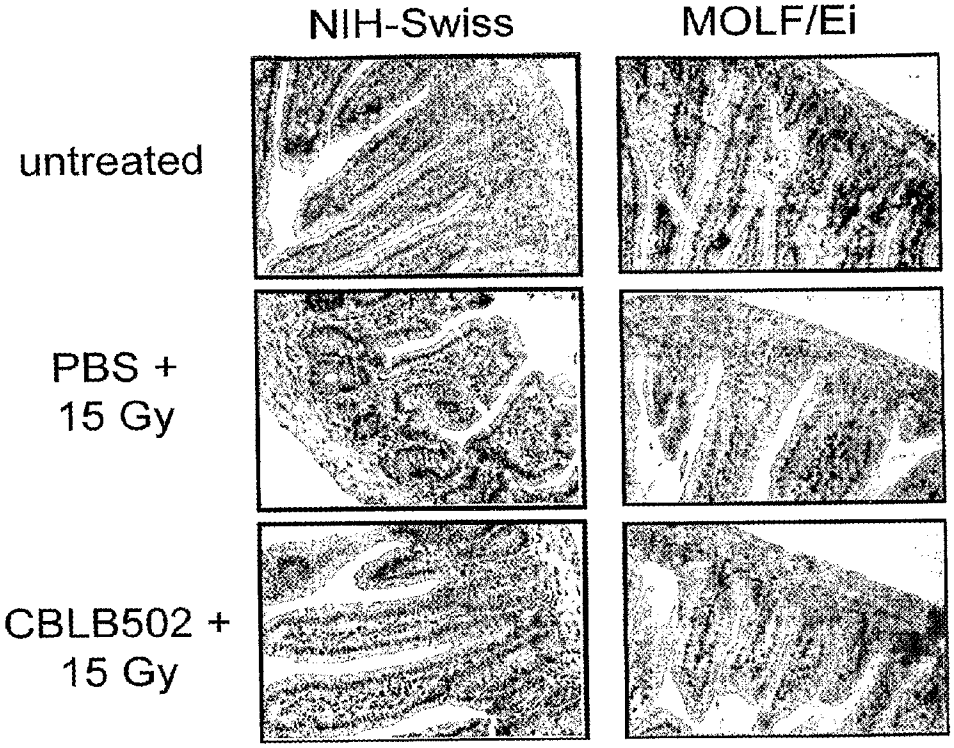

Fig. 36

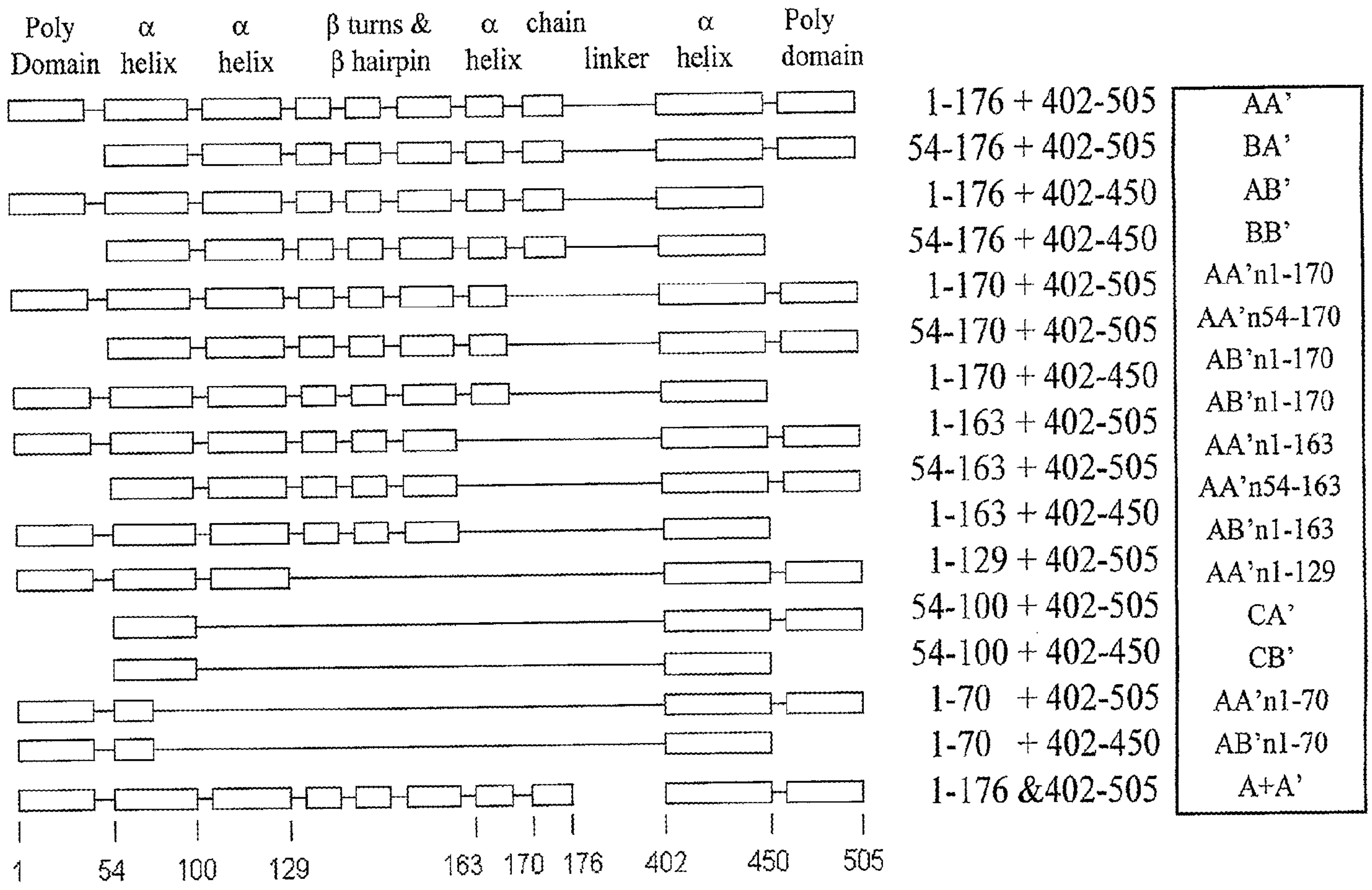
Poly Domain
α helix
α helix
β turns & β hairpin
α helix
chain linker
α helix
Poly domain
1-176 + 402-505
AA'
54-176 + 402-505
BA'
1-176 + 402-450
AB'
54-176 + 402-450
BB'
1-170 + 402-505
AA'n1-170
54-170 + 402-505
AA'n54-170
1-170 + 402-450
AB'n1-170
1-163 + 402-505
AB'n1-170
54-163 + 402-505
AA'n1-163
1-163 + 402-450
AA'n54-163
1-129 + 402-505
AB'n1-163
54-100 + 402-505
AA'n1-129
54-100 + 402-450
CA'
1-70 + 402-505
CB'
1-70 + 402-450
AA'n1-70
1-176 &402-505
AB'n1-70
A+A'
1
54
100
129
163
170
176
402
450
505

Fig. 37

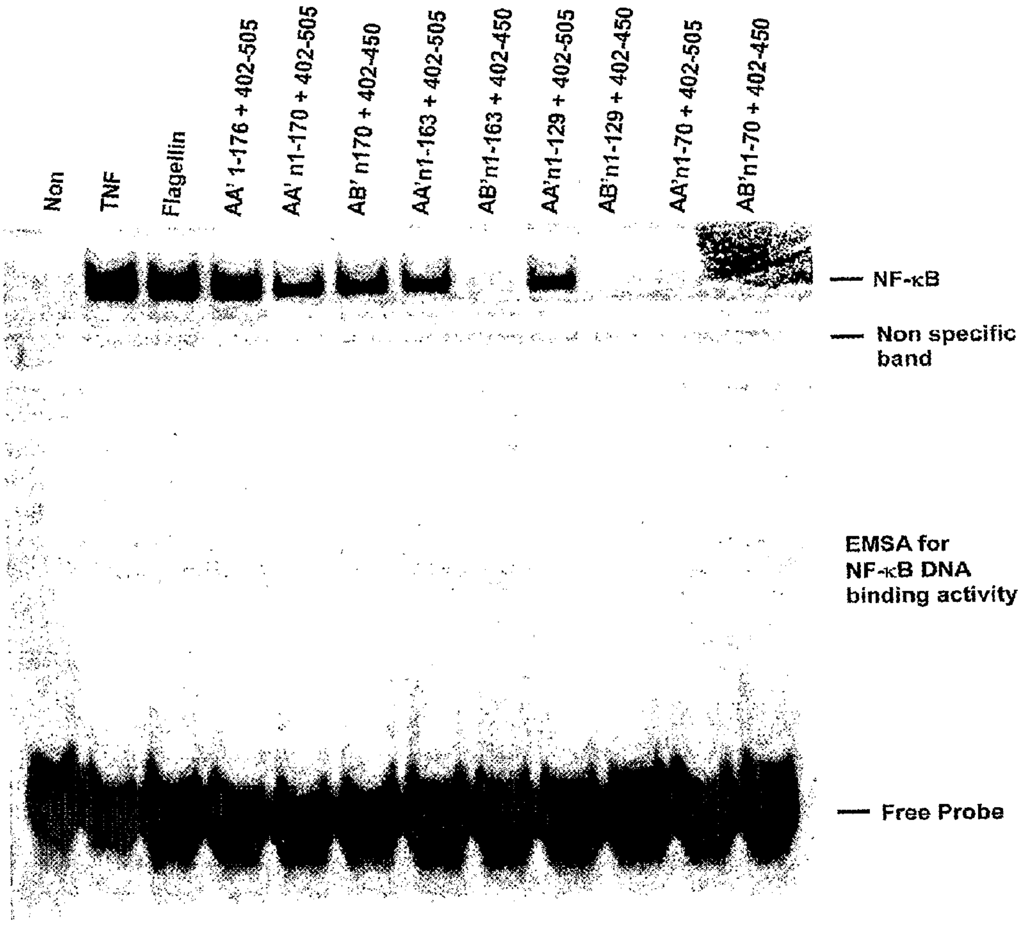
Non
TNF
Flagellin
AA' 1-176 + 402-505
AA' n1-170 + 402-505
AB' n170 + 402-450
AA'n1-163 + 402-505
AB'n1-163 + 402-450
AA'n1-129 + 402-505
AB'n1-129 + 402-450
AA'n1-70 + 402-505
AB'n1-70 + 402-450
NF-κB
Non specific band
EMSA for NF-κB DNA binding activity
Free Probe

Fig. 38

AA'

Nucleotide sequence (990 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTGATGGGTTCAATGTTAATT**CCCCGGGAATTTCCGGTGGTGGTGGTGGAATT**
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGCGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAAT
CTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATG
TCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTT
CCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (329 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLDGFNVN**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFD
SAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AB'

Nucleotide sequence (825 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATT**
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (274 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLDGFNVN**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFD
SAITNL

Fig. 38 - Continued

BA'
Nucleotide sequence (831 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTGAAAAGCCTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTAT
GCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTT
CTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG
Protein sequence (276 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGLDGFNVN**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVD
AVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVP
QNVLSLLR

BB'
Nucleotide sequence (666 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTGAAAAGCCTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTTAG
Protein sequence (221 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGLDGFNVN**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVD
AVRSSLGAIQNRFDSAITNL

CA'
Nucleotide sequence (603 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT

Fig. 38 - Continued

GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAAT
GAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCA
TTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCA
GCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAA
GATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCT
GGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGT
TAG
Protein sequence (200 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQAT**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAI
QNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

CB'
Nucleotide sequence (438 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
TCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAAT
GAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCA
TTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCA
GCCATTACCAACCTTTAG
Protein sequence (145 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQAT**SPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAI
QNRFDSAITNL

A
Nucleotide sequence (639 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGAT*GGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGTCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTGTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTGATGGGTTCAATGTTAAT**TCCCCGGGA**TGA
Protein sequence (212 AA), last three amino acids are derived from primer and pRSETb polylinker:
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GLDGFNVN**SPG**

Fig. 38 - Continued

B
Nucleotide sequence (480 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGT
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTGTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTGAAAAGCCTTGGCCTTGATGGTTCAATGTTAAT**TCCCCGGGATGA**
Protein sequence (159 AA), last three amino acids are derived from primer and pRSETb polylinker:
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGLDGFNVN**SPG**

C
Nucleotide sequence (252 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGT
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
TCCCCGGGATGA
Protein sequence (83 AA), last three amino acids are derived from primer and pRSETb polylinker:
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQAT**SPG**

GST-A'
Nucleotide sequence (1038 bp), GST highlighted:

ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTT
TTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAA
TGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGAT
GGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC
ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG
GATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTT
GATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAA
ACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAA
AAACGTATTGAAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA
TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGAT
CTGGTTCCGCGTGGATCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATG
GGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCT
TCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAA
AACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCG
CGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAG
ATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTC
CTCTCTTTACTGCGTTAG
Protein sequence (345 AA):

Fig. 38 - Continued

MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFE
DRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAW
PLQGWQATFGGGDHPPKSDLVPRGSPGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSK
VDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQ
VPQNVLSLLR

GST-B'

Nucleotide sequence (873 bp), GST highlighted:
ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCCACTCGACTTCTT
TTGGAATATCTTGAAGAAAAATATGAAGAGCATTTGTATGAGCGCGATGAAGGTGATAAA
TGGCGAAACAAAAAGTTTGAATTGGGTTTGGAGTTTCCCAATCTTCCTTATTATATTGAT
GGTGATGTTAAATTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC
ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAAGGAGCGGTTTTG
GATATTAGATACGGTGTTTCGAGAATTGCATATAGTAAAGACTTTGAAACTCTCAAAGTT
GATTTTCTTAGCAAGCTACCTGAAATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAA
ACATATTTAAATGGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTAGTTTGTTTTAAA
AAACGTATTGAAGCTATCCCACAAATTGATAAGTACTTGAAATCCAGCAAGTATATAGCA
TGGCCTTTGCAGGGCTGGCAAGCCACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGAT
CTGGTTCCGCGTGGATCCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATG
GGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCT
TCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAA
AACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (290 AA):
MSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFE
DRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAW
PLQGWQATFGGGDHPPKSDLVPRGSPGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSK
VDAVRSSLGAIQNRFDSAITNL

AA'n1-170

Nucleotide sequence (972 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCC*GATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTTATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGC
CGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTG
CAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCT

Fig. 38 - Continued

TTACTGCGTTAG
Protein sequence (323 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GL**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL
GNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AA'n1-163
Nucleotide sequence (951 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATT**ATCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTAT
GCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTT
CTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG
Protein sequence (316 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKI**IPGIS**
GGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNL
NSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AA'n54-170
Nucleotide sequence (813 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATTGATGTGAAAAGCCTTGGCCTT**ATCCCGGGAATTTCCGGTGGTGGTGGTGGA**
ATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACC
GCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCT
CTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACC
AATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAAT
ATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAG
GTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG

Fig. 38 - Continued

Protein sequence (270 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKIDVKSLGL**IPGISGGGGG**ILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSL
GAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSL
LR

AA'n54-163
Nucleotide sequence (792 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAG
GACAACCAGATGAAAATCCAGGTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTG
CAAAAAATT**ATCCCGGGAATTTCCGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGC
CGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTG
CAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCT
TTACTGCGTTAG
Protein sequence (263 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGE
TITIDLQKI**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRF
DSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AB'n1-170 (or AA'n1-170c402-450)
Nucleotide sequence (807 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*ATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATTGATGTGAAAAGC
CTTGGCCTT**ATCCCGGGAATTTCCGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTTAG
Protein sequence (268 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*MAQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN

Fig. 38 - Continued

GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKIDVKSL
GL**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

AB'n1-163 (or AA'n1-163c402-450)
Nucleotide sequence (786 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAGACTCAATTTAACGGTGTTAAAGTCCTCTCTCAGGACAACCAGATGAAAATCCAG
GTTGGTGCTAACGATGGTGAAACCATTACCATCGATCTGCAAAAAATT**ATCCCGGGAATT**
TCCGGTGGTGGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCC
GCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTG
GACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAAC
CTTTAG
Protein sequence (261 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQTQFNGVKVLSQDNQMKIQVGANDGETITIDLQKI**IPGIS**
GGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

AA'n1-129
Nucleotide sequence (849 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACATTA
ATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGAT
TCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTT
GATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGCCGT
ATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTGCAG
CAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCTTTA
CTGCGTTAG
Protein sequence (282 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDS
ALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLA
QANQVPQNVLSLLR

Fig. 38 - Continued

AA'n54-129
Nucleotide sequence (690 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT
AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATT**
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAAT
CTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATG
TCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTT
CCGCAAAACGTCCTCTCTTTACTGCGTTAG
Protein sequence (229 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAA
AKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMS
KAQILQQAGTSVLAQANQVPQNVLSLLR

AB'n1-129
Nucleotide sequence (684 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACTAACGGGACTAACTCTGATTCC
GATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTGGAAGAAATCGATCGCGTTTCT
AATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACATTA
ATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATTGAT
TCTGCATTGTCAAAACTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGTTTT
GATTCAGCCATTACCAACCTTTAG
Protein sequence (227 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQATN
GTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAAAKKSTANPLASIDS
ALSKVDAVRSSLGAIQNRFDSAITNL

AB'n54-129
Nucleotide sequence (525 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*TTCACTTCTAATATCAAAGGC
CTGACTCAGGCTTCCCGTAACGCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGT
GCGCTGAATGAAATCAACAACAACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT

Fig. 38 - Continued

AACGGGACTAACTCTGATTCCGATCTGAAATCTATCCAGGATGAAATTCAGCAACGTCTG
GAAGAAATCGATCGCGTTTCTAATCAG**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATT**
CTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCT
AACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTG
GGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (174 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDP*FTSNIKGLTQASRNANDGISIAQTTEGALNEINN
NLQRVRELSVQATNGTNSDSDLKSIQDEIQQRLEEIDRVSNQ**IPGISGGGGGILDSMG**TLINEDAAA
AKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

AA'n1-100
Nucleotide sequence (762 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*ATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT**ATCCCGGGAATTTCCGGTGGT**
GGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAG
AAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTT
CGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTGGCAAT
ACGGTAACCAATCTGAACTCCGCGCGTAGCCGTATCGAAGATGCTGACTATGCAACGGAA
GTTTCTAATATGTCTAAAGCGCAGATTCTGCAGCAGGCTGGTACTTCCGTTCTGGCGCAG
GCTAACCAGGTTCCGCAAAACGTCCTCTCTTTACTGCGTTAG

Protein sequence (253 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQAT**I**
PGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNT
VTNLNSARSRIEDADYATEVSNMSKAQILQQAGTSVLAQANQVPQNVLSLLR

AB'n1-100
Nucleotide sequence (597 bp):
ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCG*ATGGCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGACGGCATTTCTATTGCGCAGACCACTGAAGGTGCGCTGAATGAAATCAACAAC
AACCTGCAGCGTGTGCGTGAGTTGTCTGTTCAGGCCACT**ATCCCGGGAATTTCCGGTGGT**
GGTGGTGGAATTCTAGACTCCATGGGTACATTAATCAATGAAGACGCTGCCGCAGCCAAG
AAAAGTACCGCTAACCCACTGGCTTCAATTGATTCTGCATTGTCAAAAGTGGACGCAGTT
CGTTCTTCTCTGGGGGCAATTCAAAACCGTTTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (198 AA):
*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELSVQAT**I**
PGISGGGGGILDSMGTLINEDAAAAKKSTANPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

Fig. 38 - Continued

AA'n1-70

Nucleotide sequence (672 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGAC**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTGGCAATACGGTAACCAATCTGAACTCCGCGCGTAGC
CGTATCGAAGATGCTGACTATGCAACGGAAGTTTCTAATATGTCTAAAGCGCAGATTCTG
CAGCAGGCTGGTACTTCCGTTCTGGCGCAGGCTAACCAGGTTCCGCAAAACGTCCTCTCT
TTACTGCGTTAG

Protein sequence (223 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNAND**IPGISGGGGGILDSMG**TLINEDAAAAKKSTA
NPLASIDSALSKVDAVRSSLGAIQNRFDSAITNLGNTVTNLNSARSRIEDADYATEVSNMSKAQILQ
QAGTSVLAQANQVPQNVLSLLR

AB'n1-70

Nucleotide sequence (507 bp):

ATGCGGGGTTCTCATCATCATCATCATCATGGTATGGCTAGCATGACTGGTGGACAGCAA
*ATGGGTCGGGATCTGTACGACGATGACGATAAGGATCCGATG*GCACAAGTCATTAATACA
AACAGCCTGTCGCTGTTGACCCAGAATAACCTGAACAAATCTCAGTCCTCACTGAGTTCC
GCTATTGAGCGTCTGTCCTCTGGTCTGCGTATCAACAGCGCGAAAGACGATGCGGCAGGC
CAGGCGATTGCTAACCGCTTCACTTCTAATATCAAAGGCCTGACTCAGGCTTCCCGTAAC
GCTAACGAC**ATCCCGGGAATTTCCGGTGGTGGTGGTGGAATTCTAGACTCCATGG**GTACA
TTAATCAATGAAGACGCTGCCGCAGCCAAGAAAAGTACCGCTAACCCACTGGCTTCAATT
GATTCTGCATTGTCAAAAGTGGACGCAGTTCGTTCTTCTCTGGGGGCAATTCAAAACCGT
TTTGATTCAGCCATTACCAACCTTTAG

Protein sequence (168 AA):

*MRGSHHHHHHGMASMTGGQQMGRDLYDDDDKDPM*AQVINTNSLSLLTQNNLNKSQSSLSSAIERLSS
GLRINSAKDDAAGQAIANRFTSNIKGLTQASRNAND**IPGISGGGGGILDSMG**TLINEDAAAAKKSTA
NPLASIDSALSKVDAVRSSLGAIQNRFDSAITNL

FLAGELLIN RELATED POLYPEPTIDES AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. patent application Ser. No. 14/559,669, filed on Dec. 3, 2014, which is a continuation of U.S. patent application Ser. No. 13/110,704, filed on May 18, 2011, now U.S. Pat. No. 8,932,609, which is a divisional of U.S. patent application Ser. No. 11/722,682, filed on May 2, 2008, now U.S. Pat. No. 8,007,812, which is the national stage of International Application No. PCT/US2005/046485, filed on Dec. 22, 2005, which claims the benefit of U.S. Provisional Patent Application No. 60/639,826, filed Dec. 22, 2004, the contents of all of which are incorporated herein by reference.

FIELD OF THE INVENTION

[0002] This invention relates to the use of flagellin related polypeptides to protect mammals from the effects of apoptosis. More specifically, this invention relates to the use of flagellin related polypeptides to protect mammals from exposure to stress, such as radiation and cancer treatments.

REFERENCE TO THE SEQUENCE LISTING

[0003] Reference is made to the sequence listing submitted via EFS-Web, which consists of a file named, "CLE-003D5-SequenceListing.txt" (135 KB), created on Aug. 17, 2015, the contents of which are incorporated herein by reference.

BACKGROUND OF THE INVENTION

[0004] The progression from normal cells to tumor cells involves a loss of negative mechanisms of growth regulation, including resistance to growth inhibitory stimuli and a lack of dependence on growth factors and hormones. Traditional cancer treatments that are based on radiation or cytotoxic drugs rely on the differences in growth control of normal and malignant cells. Traditional cancer treatments subject cells to severe genotoxic stress. Under these conditions, the majority of normal cells become arrested and therefore saved, while tumor cells continue to divide and die.

[0005] However, the nature of conventional cancer treatment strategy is such that normal rapidly dividing or apoptosis-prone tissues are at risk. Damage to these normal rapidly dividing cells causes the well-known side effects of cancer treatment (sensitive tissues: hematopoiesis, small intestine, hair follicles). The natural sensitivity of such tissues is complicated by the fact that cancer cells frequently acquire defects in suicidal (apoptotic) machinery and those therapeutic procedures that cause death in normal sensitive tissues may not be that damaging to cancer cells. Conventional attempts to minimize the side effects of cancer therapies are based on (a) making tumor cells more susceptible to treatment, (b) making cancer therapies more specific for tumor cells, or (c) promoting regeneration of normal tissue after treatment (e.g., erythropoietin, GM-CSF, and KGF).

[0006] There continues to be a need for therapeutic agents to mitigate the side effects associated with chemotherapy and radiation therapy in the treatment of cancer. This invention fulfills these needs and provides other related advantages.

SUMMARY OF THE INVENTION

[0007] A method of protecting a mammal from one or more treatments or conditions that trigger apoptosis comprising administering to said patient a composition comprising a pharmaceutically effective amount of flagellin. The flagellin may comprise SEQ ID NO: 1 or a fragment, variant, analog, homolog, derivative of SEQ ID NO: 1, or combination thereof. The flagellin may induce TLR-5 mediated activity.

[0008] The flagellin may be at least 30% identical to amino acids 1-174 and 418-505 of SEQ ID NO: 1. The flagellin may comprise at least 10 conserved amino acids at positions selected from the group consisting of 89, 90, 91, 95, 98, 101, 115, 422, 423, 426, 431, 436 and 452. The flagellin may comprise the sequence of SEQ ID NOS: 1, 8, 10, 12, 30, 32, 34, 36, 38, 40, 43, 44, 46, 48, 50 and 52.

[0009] The flagellin may be used to treat a mammal undergoing cancer treatment, which may be chemotherapy or radiation therapy. The flagellin may be used to treat a mammal exposed to radiation. The flagellin may be administered in combination with a radioprotectant. The flagellin may be used to treat a mammal from wounding, poisoning, bacterial infection, viral infection and temperature shock. The flagellin may be used to protect from apoptosis in tissues including the GI tract, lungs, kidneys, liver, cardiovascular system, blood vessel endothelium, central and peripheral neural system, hematopoietic progenitor cells, immune system, and hair follicles. The flagellin may also be used to prevent sepsis in the mammal.

[0010] This invention also relates to a method of treating a mammal suffering from a constitutively active NF-κB cancer comprising administering to the mammal a composition comprising a pharmaceutically acceptable amount of an agent which induces NF-κB. The agent may be flagellin. The agent may be administered prior to, together with, or after a treatment for the cancer. The treatment may be chemotherapy or radiation therapy.

[0011] This invention also relates to a method of treating a mammal suffering from damage to normal tissue attributable to treatment of a cancer comprising administering to the mammal a composition comprising a pharmaceutically acceptable amount of an agent which induces NF-κB. The agent may be flagellin. The agent may be administered prior to, together with, or after a treatment for the cancer. The treatment may be chemotherapy or radiation therapy.

[0012] This invention also relates to a method of treating a mammal suffering from damage to normal tissue attributable to stress, comprising administering to the mammal a composition comprising a pharmaceutically acceptable amount of an agent which induces NF-κB. The agent may be flagellin. The agent may be administered prior to, together with, or after a treatment for a disease suffered by the mammal.

[0013] This invention also relates to a method of modulating cell aging in a mammal, comprising administering to the mammal a composition comprising a pharmaceutically acceptable amount of an agent which induces NF-κB. The agent may be flagellin. The agent may be administered prior to, together with, or after a treatment for a disease suffered by the mammal.

[0014] This invention also relates to a pharmaceutical composition comprising an agent which induces NF-κB activity, a chemotherapeutic drug, and optionally a pharmaceutically acceptable adjuvant, diluent, or carrier. The agent may be flagellin.

[0015] This invention also relates to a method of screening for an inducer of NF-κB comprising adding a suspected inducer to an NF-κB activated expression system, and separately adding a control to an NF-κB activated expression system, whereby an inducer of NF-κB is identified by the ability to increase the level of NF-κB activated expression.

[0016] This invention also relates to a method of protecting a mammal from the effects of radiation comprising administering to said mammal a composition comprising a pharmaceutically effective amount of an agent which induces NF-κB. The agent may be flagellin, which may be derived from a species of *Salmonella*. The composition may be administered in combination with a radioprotectant. The radioprotectant may be an antioxidant, which may be amifostine or vitamine E. The radioprotectant may also be a cytokine, which may be stem cell factor.

[0017] This invention relates to a method of protecting a patient from one or more treatments or conditions that trigger apoptosis comprising administering to said patient a composition comprising a pharmaceutically effective amount of an agent which induces NF-κB. The agent may be flagellin, which may be derived from a species of *Salmonella*. The treatment may be a cancer treatment, which may be chemotherapy or radiation therapy. The condition may be a stress, which may be radiation, wounding, poisoning, infection and temperature shock.

[0018] This invention also relates to a method of screening for a modulator of apoptosis comprising adding a suspected modulator to a cell-based apoptosis system, and separately adding a control to a cell-based apoptosis system, whereby a modulator of apoptosis is identified by the ability to alter the rate of apoptosis, wherein the suspected modulator is derived from a mammalian parasite or symbiont.

[0019] This invention also relates to a method of screening for a modulator of NF-κB comprising adding a suspected modulator to an NF-κB activated expression system, and separately adding a control to an NF-κB activated expression system, whereby a modulator of NF-κB is identified by the ability to alter the rate of NF-κB activated expression, wherein the suspected modulator is derived from a mammalian parasite. The parasite may be of a species including, but not limited to, *Salmonella, Mycoplasma*, and *Chlamydia*.

[0020] This invention also relates to a modulator identified by any of the screening methods described herein. This invention also relates to a composition comprising a modulator described herein. The composition may be a pharmaceutical composition comprising a pharmaceutically acceptable amount of a modulator described herein.

[0021] This invention also relates to a method of treating cancer comprising administering to a subject in need of such treatment a pharmaceutical composition comprising a modulator that enhances apoptosis.

[0022] This invention also relates to a method of protecting a patient from one or more treatments that trigger apoptosis comprising administering to said patient a pharmaceutical composition comprising a modulator that inhibits apoptosis. The one or more treatments may be a cancer treatment. The cancer treatment may be chemotherapy or radiation therapy.

BRIEF DESCRIPTION OF THE DRAWINGS

[0023] FIG. **1** demonstrates that p53 deficiency accelerated development of GI syndrome in mice. Panel A: I.P. injection of PFTα (10 mg/kg) protects C57Bl/6J mice (if not indicated otherwise, here and below 6-8 weeks old males were used) from a single 9 Gy dose of gamma radiation and a fractioned cumulative radiation dose 12.5 Gy (5×2.5 Gy). PFTα has no effect on survival of mice treated with single 12.5 and 25 Gy doses of IR: (results of representative experiments are shown; Shepherd 4000 Ci Cesium 137 source at a dose rate of 4 Gy per minute was used). Panel B: Wild-type and p53-null C57Bl/6J mice differ in their relative sensitivity to low (10 Gy) and high (15Gy) doses of gamma radiation: wild-type mice were more sensitive to 10 Gy but more resistant to 15 Gy as compared to p53-null mice. Panel C: Mice treated with 11 Gy of total body gamma irradiation were injected 12 h later with 1.5×10^7 bone marrow cells from wild type or p53-null syngeneic C57Bl/6J mice. (This dose causes 100% lethality in nonreconstituted controls group of mice). Two months later, after complete recovery of hematopoiesis, animals were treated with 15 Gy of total body gamma radiation and showed no difference in death rates between the two groups differing in the p53 status of their bone marrow. Panel D: Comparison of dynamics of injury to small intestines of wild-type and p53-null mice at the indicated time points after 15 Gy of gamma radiation indicates accelerated damage in p53-null mice (haematoxylin-eosin stained paraffin sections; magnification ×125). 24 h panels include images of TUNEL staining if sections of crypts: massive apoptosis is evident in wild type but not in p53-deficient epithelium.

[0024] FIG. **2** demonstrates the dynamics of cell proliferation and survival in small intestine of wild type and p53-null mice. Panel A: Comparison of proliferation rates in intestines of wild-type and p53 null mice after treatment with IR. (Left) Autoradiographs of whole-body sections (1.7× magnification) of 4-week-old wild-type and p53 null mice injected intraperitoneally with ^{14}C-thymidine (10 μCi per animal) treated or untreated with 15 Gy of gamma radiation. Arrows point at intestines. (Right) Comparison of BrdU incorporation in small intestine of wild-type and p53-null mice at different time points after 15 Gy of gamma radiation. BrdU (50 mg/kg) was injected 2 h before sacrificing mice followed by immunostaining. Fragments of 96 h panels are shown at higher magnification (×400). Panel B: Comparison of the number of BrdU positive cells/crypt in small intestine of wild-type and p53-null mice at different time points after 15 Gy of gamma radiation. Three animals were analyzed for each time point, five ileum cross sections were prepared from each animal and analyzed microscopically to estimate the number of crypts and villi. Numbers of BrdU-positive cells in the crypts were counted in 5 random fields under 200× magnification (100-30 crypts) and the average number of BrdU-positive cells was plotted. Panel C: Tracing the number and position of BrdU-labeled cells in small intestine of wild type and p53-null mice during different time points after 15 Gy of gamma radiation. BrdU was injected 30 min. before irradiation and mice were sacrificed at the indicated time points. Accelerated migration from crypts to villi followed by rapid elimination of labeled cells was observed in p53-null mice.

[0025] FIG. **3** demonstrates that recombinant flagellin is capable of NF-κB activation.

[0026] FIG. **4** shows a representative experiment testing the ability of flagellin to protect mice from radiation. C56BL6 mice (6 week old males, 10 animals per group) were injected i.v. with 2.0 μg (0.1 mg/kg) or 5 μg (0.25 mg/kg) of flagellin in PBS. Four hours later, mice were irradiated with 15 Gy and mouse survival was monitored daily.

[0027] FIG. **5** shows histological sections (HE stained) of small intestinal epithelium of mice that were treated with 15

Gy of gamma radiation with or without i.v. injection of 0.25 mg/kg of flagellin. Complete destruction of crypts and villi in control mouse contrasts with close to normal morphology of tissue from flagellin-treated animal.

[0028] FIG. **6** shows the effect of flagellin on mouse sensitivity to 10Gy of total body gamma radiation.

[0029] FIG. **7** shows the effect of flagellin injected i.v. at indicated times before irradiation on mouse sensitivity to 13Gy (left) and 10Gy (right) of total body gamma radiation.

[0030] FIG. **8** shows the effect of flagellin on mouse sensitivity to 10, 13 and 15 Gy of total body gamma radiation.

[0031] FIG. **9** shows the domain structure of bacterial flagellin. The Ca backbone trace, hydrophobic core distribution and structural information of F41. Four distinct hydrophobic cores that define domains D1, D2a, D2b and D3. All the hydrophobic side-chain atoms are displayed with the Ca backbone. Side-chain atoms are color coded: Ala, yellow; Leu, Ile or Val, orange; Phe and Tyr, purple (carbon atoms) and red (oxygen atoms). c, Position and region of various structural features in the amino-acid sequence of flagellin. Shown are, from top to bottom: the F41 fragment in blue; three b-folium folds in brown; the secondary structure distribution with a-helix in yellow, b-structure in green, and b-turn in purple; tic mark at every 50th residue in blue; domains D0, D1, D2 and D3; the axial subunit contact region within the proto-element in cyan; the well-conserved amino-acid sequence in red and variable region in violet; point mutations in F41 that produce the elements of different supercoils. Letters at the bottom indicate the morphology of mutant elements: L (D107E, R124A, R124S, G426A), L-type straight; R (A449V), R-type straight; C (D313Y, A414V, A427V, N433D), curly33.

[0032] FIG. **10** shows a schematic of *Salmonella* flagellin domains, its fragments, and its interaction with TLR5. Dark bars denote regions of the flagellin gene used to construct fragments comprising A, B, C, A' and B'.

[0033] FIG. **11** shows soluble flagellin (FliC), and two fragments (AA' and BB') after fractionation by SDS-PAGE, with molecular weight markers listed to the left.

[0034] FIG. **12** shows induction of NF-κB nuclear translocation by *Salmonella* flagellin (FliC) and flagellin fragments.

[0035] FIG. **13** shows activation of NF-κB-regulated luciferase reporter construct by flagellin and flagellin fragments in H116 cells. Concentrations of proteins are given in μg/ml.

[0036] FIG. **14** shows NF-κB DNA binding in HT29 human colon cancer cells induced by flagellin and flagellin fragments.

[0037] FIG. **15** shows the activation of a NF-κB reporter in HCT116 reporter cells by full-length flagellin and flagellin fragments.

[0038] FIG. **16** shows a comparison of the radioprotective properties of flagellin (FliC) and fragments AA' and BB'.

[0039] FIG. **17** shows that the AA' fragment protects intestinal epithelium from degeneration caused by radiation. A: Histological sections (hematoxylin and eosin-stained) of small intestinal epithelium of mice 5 days after 14 Gy irradiation are shown. B: Treatment with the AA' fragment prevents apoptosis ongoing 5 hours after irradiation in endothelial cells of villi (detected by immunostaining for endothelial marker CD31 and marked by arrows), as determined by TUNEL assay. C: Histological sections of skin of mice 5 days after 14Gy of gamma irradiation demonstrate the protective effect of the AA' fragment for sebaceous glands (red arrows).

[0040] FIG. **18** shows that the AA' fragment provides partial protection and delays death of mice after supralethal irradiation with 17 and 20 Gy total-body gamma radiation.

[0041] FIG. **19** shows anti-flagellin antibody titers induced in mice after 21 and 28 days by flagellin and AA'. For individual mice, the averages of two measurements are shown. Mice were injected with: Fl: flagellin; or AA'. 21 d and 28 ds—mice injected with first dose 21 and 28 days before second, respectively. PBS: saline buffer (no serum) control; blank: empty well reading control.

[0042] FIG. **20** shows anti-flagellin antibody titers induced in mice after 21 and 28 days by flagellin and AA'. For individual mice, the averages of two measurements are shown. Mice were injected with: Fl: flagellin; or AA'. 21 d and 28 ds—mice injected with first dose 21 and 28 days before second, respectively. PBS: saline buffer (no serum) control; blank: empty well reading control.

[0043] FIG. **21** shows that flagellin fragment AA' protects mice from multiple successive doses of gamma-irradiation. Arrows denote radiation treatments (days 1-4).

[0044] FIG. **22** shows the effect of AA' on tumor sensitivity to radiation treatment. Left Panel: NIH3T3-derived sarcoma cells were injected s.c. in NIH-Swiss mice. When tumors reached 7-10 mm in diameter, mice received three 4.3 Gy doses of total body irradiation, with or without pretreatment with AA'. The dynamics of tumor growth after radiation treatment is displayed. U/t: untreated; AA': AA' with no irradiation; 3×4Gy: irradiation only; 3×4Gy+AA': AA' and irradiation. (The shape of curves reflects slow growth of tumors that is a characteristic of this model). Results are displayed as relative tumor volumes normalized to tumor volume measured at day 7 after last irradiation. Right Panel: The experiment was done in the same way with another syngeneic mouse tumor model: B16 melanoma (C57BL6 background). Treatment was applied when tumors reached 4-5 mm in diameter and involved three subsequent 4 Gy doses of total body gamma radiation applied with or without pretreatment with AA' (30 min. before irradiation, 5 μg/mouse).

[0045] FIG. **23** shows the influence of NS398 on the radioprotection of LPS and AA' in mice after 13 Gy of total-body gamma irradiation.

[0046] FIGS. **24**A and **24**B show a comparison of amino acid sequences of the conserved amino (FIG. **24**A) and carboxy (FIG. **24**B) terminus from 21 species of bacteria. The 13 conserved amino acids important for TLR5 activity are shown with shading. The amino acid sequences are identified by their accession numbers from TrEMBL (first letter=Q) or Swiss-Prot (first letter=P). The amino terminus sequences have SEQ ID NOs: 1-21, respectively, for each of the 21 bacterial species, and the carboxy terminus sequences have SEQ ID NOs: 22-42, respectively.

[0047] FIGS. **25**A-D show results of a BLAST search using SEQ ID NO: 1 as the query sequence. The parameters used in all searches was as follows: expected value cutoff=lO, matrix=BLOSUM62, gap penalties of existence=11 and extension=1, filtering=none. FIG. **25**A: NR_Bacteria (Protein-Protein); FIG. **25**B: NR_Bacteria (Protein-DNA); FIG. **25**C: Bacterial Genomes (Protein-Protein); FIG. **25**D: Bacterial Genomes (Protein-DNA).

[0048] FIG. **26** shows the percentage identities of the amino- and carboxy-terminus of the homologs shown in FIG. **24** compared to SEQ ID NO: 1, as shown in BLAST results using the same search parameters as listed for FIGS. **25**A-D.

[0049] FIG. **27** demonstrates that AA' mediates rescue of multiple mouse strains after 10 Gy total-body γ-IR. Cone heights represent fractions of survivors.

[0050] FIG. **28** demonstrates the pharmacokinetics of AA' after intravenous (i.v.), subcutaneous (s.c.), intraperitoneal (i.p.) or intramuscular (i.m.) injection.

[0051] FIG. **29** demonstrates the extended pharmacokinetics of AA' after intramuscular (i.m.) injection.

[0052] FIG. **30** demonstrates the influence of AA' on gamma-irradiation induced cell death and growth inhibition in A549 cells.

[0053] FIG. **31** demonstrates the influence of AA' on gamma-irradiation induced cell death and growth inhibition in multiple cell lines.

[0054] FIG. **32** demonstrates the influence of irradiation and AA' on BrdU incorporation in small intestinal crypts of NIH-Swiss mice. A comparison of BrdU incorporation in small intestine of control and AA' treated NIH-Swiss mice, with and without 15 Gy of gamma radiation is shown. BrdU (50 mg/kg) was injected 1.5 h before sacrificing mice and immunostaining was done as previously described (Watson A J & Pritchard D M., *Am J Physiol Gastrointest Liver Physiol.* 2000 January; 278(1):G 1-5). Red channel of the image is shown (positive signal is bright white on the dark background).

[0055] FIG. **33** demonstrates the duration of AA'-mediated growth arrest and reduced BrdU incorporation in small intestine of mice. BrdU (50 mg/kg) was injected in Balb/c mice i.p., 1 or 4 hrs after CBLB502 (AA') injection. Samples of small intestine were obtained 1.5 hrs after BrdU injection. Immunostaining was done as previously described (Watson A J & Pritchard D M., *Am J Physiol Gastrointest Liver Physiol.* 2000 January; 278(1):G 1-5). Inverted image is shown (positive signal is dark on the light background).

[0056] FIG. **34** demonstrates the influence of AA' on BrdU incorporation in colonic crypts of NIH-Swiss mice. BrdU (50 mg/kg) was injected in NIH-Swiss mice i.p., 1 hr after CBLB502 (AA') injection, Samples of colon were obtained 1.5 hrs after BrdU injection. Immunostaining was done as previously described (Watson A J & Pritchard D M., *Am J Physiol Gastrointest Liver Physiol.* 2000 January; 278(1): G1-5). Inverted image is shown (positive signal is dark on the light background). Bottom panel shows smaller magnification/larger area of the sample.

[0057] FIG. **35** demonstrates the morphology of small intestine in TLR5 deficient MOLF/Ei and TLR5 wt NIH-Swiss mice after treatment with AA'.

[0058] FIG. **36** depicts flagellin derivatives. The domain structure and approximate boundaries (amino acid coordinates) of selected flagellin derivatives (listed on the right). FliC flagellin of *Salmonella dublin* is encoded within 505 amino acids (aa).

[0059] FIG. **37** shows the testing of additional flagellin derivatives tested for NF-κB stimulating activity.

[0060] FIG. **38** shows the nucleotide and amino acid sequence for the following flagellin variants: AA' (SEQ ID NO: 7-8), AB' (SEQ ID NO: 9-10), BA' (SEQ ID NO: 11-12), BB' (SEQ ID NO: 13-14), CA' (SEQ ID NO: 15-16), CB' (SEQ ID NO: 17-18), A (SEQ ID NO: 19-20), B (SEQ ID NO: 21-22), C (SEQ ID NO: 23-24), GST-A' (SEQ ID NO: 25-26), GST-B' (SEQ ID NO: 27-28), AA'n1-170 (SEQ ID NO: 29-30), AA'n1-163 (SEQ ID NO: 33-34), AA'n54-170 (SEQ ID NO: 31-32), AA'n54-163 (SEQ ID NO: 335-36), AB'n1-170 (SEQ ID NO: 37-38), AB'n1-163 (SEQ ID NO: 39-40), AA'n1-129 (SEQ ID NO: 41-42), AA'n54-129 (SEQ ID NO: 43-44), AB'n1-129 (SEQ ID NO: 45-46), AB'n54-129 (SEQ ID NO: 47-48), AA'n1-100 (SEQ ID NO: 49-50), AB'n1-100 (SEQ ID NO: 51-52), AA'n1-70 (SEQ ID NO: 53-54) and AB'n1-70 (SEQ ID NO: 55-56). The pRSETb leader sequence is shown in Italic (leader includes Met, which is also amino acid 1 of FliC). The N terminal constant domain is underlined. The amino acid linker sequence is in Bold. The C terminal constant domain is underlined. GST, if present, is highlighted.

DETAILED DESCRIPTION

[0061] This invention is related to protecting normal cells and tissues from apoptosis caused by stresses including, but not limited to, chemotherapy, radiation therapy and radiation. There are two major mechanisms controlling apoptosis in the cell: the p53 pathway (pro-apoptotic) and the NF-κB pathway (anti-apoptotic). Both pathways are frequently deregulated in tumors: p53 is usually lost, while NF-κB becomes constitutively active. Hence, inhibition of p53 and activation of NF-κB in normal cells may protect them from death caused by stresses, such as cancer treatment, but would not make tumor cells more resistant to treatment because they have these control mechanisms deregulated. This contradicts the conventional view on p53 and NF-κB, which are considered as targets for activation and repression, respectively.

[0062] This invention relates to inducing NF-κB activity to protect normal cells from apoptosis. By inducing NF-κB activity in a mammal, normal cells may be protected from apoptosis attributable to cellular stress, which occurs in cancer treatments and hyperthermia; exposure to harmful doses of radiation, for example, workers in nuclear power plants, the defense industry or radiopharmaceutical production, and soldiers; and cell aging. Since NF-κB is constitutively active in many tumor cells, the induction of NF-κB activity may protect normal cells from apoptosis without providing a beneficial effect to tumor cells. Once the normal cells are repaired, NF-κB activity may be restored to normal levels. NF-κB activity may be induced to protect such radiation- and chemotherapy-sensitive tissues as the hematopoietic system (including immune system), the epithelium of the gut, and hair follicles.

[0063] Inducers of NF-κB activity may also be used for several other applications. Pathological consequences and death caused by exposure of mammals to a variety of severe conditions including, but not limited to, radiation, wounding, poisoning, infection, aging, and temperature shock, may result from the activity of normal physiological mechanisms of stress response, such as induction of programmed cell death (apoptosis) or release of bioactive proteins, cytokines.

[0064] Apoptosis normally functions to "clean" tissues from wounded and genetically damaged cells, while cytokines serve to mobilize the defense system of the organism against the pathogen. However, under conditions of severe injury both stress response mechanisms can by themselves act as causes of death. For example, lethality from radiation may result from massive p53-mediated apoptosis occurring in hematopoietic, immune and digestive systems. Rational pharmacological regulation of NF-κB may increase survival under conditions of severe stress. Control over these factors may allow control of both inflammatory response and the life-death decision of cells from the injured organs. Tissues that may be protected from apoptosis by administering NF-κB inducers include, but are not limited to, the GI tract, lungs, kidneys, liver, cardiovascular system, blood vessel endothelium, central and peripheral neural system, hematopoietic progenitor cells, immune system, and hair follicles.

[0065] The protective role of NF-κB is mediated by transcriptional activation of multiple genes coding for: a) anti-apoptotic proteins that block both major apoptotic pathways, b) cytokines and growth factors that induce proliferation and survival of HP and other stem cells, and c) potent ROS-scavenging antioxidant proteins, such as MnSOD (SOD-2). Thus, by temporal activation of NF-κB for radioprotection, it may be possible to achieve not only suppression of apoptosis in cancer patients, but also the ability to reduce the rate of secondary cancer incidence because of simultaneous immunostimulatory effect, which, may be achieved if activation of NF-κB is reached via activation of Toll-like receptors.

[0066] Another attractive property of the NF-κB pathway as a target is its activation by numerous natural factors that can be considered as candidate radioprotectants. Among these, are multiple pathogen-associated molecular patterns (PAMPs). PAMPs are molecules that are not found in the host organism, are characteristic for large groups of pathogens, and cannot be easily mutated. They are recognized by Toll-like receptors (TLRs), the key sensor elements of innate immunity. TLRs act as a first warning mechanism of immune system by inducing migration and activation of immune cells directly or through cytokine release. TLRs are type I membrane proteins, known to work as homo- and heterodimers. Upon ligand binding, TLRs recruit MyD88 protein, an indispensable signaling adaptor for most TLRs. The signaling cascade that follows leads to effects including (i) activation of NF-κB pathway, and (ii) activation of MAPKs, including Jun N-terminal kinease (JNK). The activation of the NF-κB pathway by Toll-like receptor ligands makes the ligands attractive as potential radioprotectors. Unlike cytokines, many PAMPs have little effect besides activating TLRs and thus are unlikely to produce side effects. Moreover, many PAMPs are present in humans.

[0067] Consistently with their function of immunocyte activation, all TLRs are expressed in spleen and peripheral blood leukocytes, with more TLR-specific patterns of expression in other lymphoid organs and subsets of leukocytes. However, TLRs are also expressed in other tissues and organs of the body, e.g., TLR1 is expressed ubiquitously, TLR5 is also found in GI epithelium and endothelium, while TLRs 2, 6, 7 and 8 are known to be expressed in lung.

1. DEFINITIONS

[0068] It is to be understood that the terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting. It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.

[0069] As used herein, the terms "administer" when used to describe the dosage of an agent that induces NF-κB activity, means a single dose or multiple doses of the agent.

[0070] As used herein, the term "analog", when used in the context of a peptide or polypeptide, means a peptide or polypeptide comprising one or more non-standard amino acids or other structural variations from the conventional set of amino acids.

[0071] As used herein, the term "antibody" means an antibody of classes IgG, IgM, IgA, IgD or IgE, or fragments, fragments or derivatives thereof, including Fab, $F(ab')_2$, Fd, and single chain antibodies, diabodies, bispecific antibodies, bifunctional antibodies and derivatives thereof. The antibody may be a monoclonal antibody, polyclonal antibody, affinity purified antibody, or mixtures thereof which exhibits sufficient binding specificity to a desired epitope or a sequence derived therefrom. The antibody may also be a chimeric antibody. The antibody may be derivatized by the attachment of one or more chemical, peptide, or polypeptide moieties known in the art. The antibody may be conjugated with a chemical moiety.

[0072] As used herein, "apoptosis" refers to a form of cell death that includes progressive contraction of cell volume with the preservation of the integrity of cytoplasmic organelles; condensation of chromatin (i.e., nuclear condensation), as viewed by light or electron microscopy; and/or DNA cleavage into nucleosome-sized fragments, as determined by centrifuged sedimentation assays. Cell death occurs when the membrane integrity of the cell is lost (e.g., membrane blebbing) with engulfment of intact cell fragments ("apoptotic bodies") by phagocytic cells.

[0073] As used herein, the term "cancer" means any malignant growth or tumor caused by abnormal and uncontrolled cell division; it may spread to other parts of the body through the lymphatic system or the blood stream.

[0074] As used herein, the term "cancer treatment" means any treatment for cancer known in the art including, but not limited to, chemotherapy and radiation therapy.

[0075] As used herein, the term "combination with" when used to describe administration of an agent that induces NF-κB activity and an additional treatment means that the agent may be administered prior to, together with, after, or metronomically with the additional treatment. The term "together with," "simultaneous" or "simultaneously" as used herein, means that the additional treatment and the agent of this invention are administered within 48 hours, preferably 24 hours, more preferably 12 hours, yet more preferably 6 hours, and most preferably 3 hours or less, of each other. The term "metronomically" as used herein means the administration of the agent at times different from the additional treatment and at certain frequency relative to repeat administration and/or the additional treatment.

[0076] The agent may be administered at any point prior to the additional treatment including, but not limited to, about 48 hr, 46 hr, 44 hr, 42 hr, 40 hr, 38 hr, 36 hr, 34 hr, 32 hr, 30 hr, 28 hr, 26 hr, 24 hr, 22 hr, 20 hr, 18 hr, 16 hr, 14 hr, 12 hr, 10 hr, 8 hr, 6 hr, 4 hr, 3 hr, 2 hr, or 1 hr prior to the additional treatment. The agent may be administered at any point after the additional treatment including, but not limited to, about 1 hr, 2 hr, 3 hr, 4 hr, 6 hr, 8 hr, 10 hr, 12 hr, 14 hr, 16 hr, 18 hr, 20 hr, 22 hr, 24 hr, 26 hr, 28 hr, 30 hr, 32 hr, 34 hr, 36 hr, 38 hr, 40 hr, 42 hr, 44 hr, 46 hr, or 48 hr after exposure.

[0077] As used herein, the term "derivative", when used in the context of a peptide or polypeptide, means a peptide or polypeptide different other than in primary structure (amino acids and amino acid analogs). By way of illustration, derivatives may differ by being glycosylated, one form of post-translational modification. For example, peptides or polypeptides may exhibit glycosylation patterns due to expression in heterologous systems. If at least one biological activity is retained, then these peptides or polypeptides are derivatives according to the invention. Other derivatives include, but are not limited to, fusion peptides or fusion polypeptides having a covalently modified N- or C-terminus, PEGylated peptides or polypeptides, peptides or polypeptides associated with lipid moieties, alkylated peptides or polypeptides, peptides or polypeptides linked via an amino acid side-chain functional group to other peptides, polypeptides or chemicals, and additional modifications as would be understood in the art.

[0078] As used herein, the term "fragment", when used in the context of a peptide or polypeptide, means a portion of a reference peptide or polypeptide.

[0079] As used herein, the term "homolog", when used in the context of a peptide or polypeptide, means a peptide or polypeptide sharing a common evolutionary ancestor.

[0080] As used herein, the term "treat" or "treating" when referring to protection of a mammal from a condition, means preventing, suppressing, repressing, or eliminating the condition. Preventing the condition involves administering a composition of this invention to a mammal prior to onset of the condition. Suppressing the condition involves administering a composition of this invention to a mammal after induction of the condition but before its clinical appearance. Repressing the condition involves administering a composition of this invention to a mammal after clinical appearance of the condition such that the condition is reduced or maintained. Elimination the condition involves administering a composition of this invention to a mammal after clinical appearance of the condition such that the mammal no longer suffers the condition.

[0081] As used herein, the term "tumor cell" means any cell associated with a cancer.

[0082] As used herein, the term "variant", when used in the context of a peptide or polypeptide, means a peptide or polypeptide that differs in amino acid sequence by the insertion, deletion, or conservative substitution of amino acids, but retain at least one biological activity. Representative examples of "biological activity" include, but are not limited to, the ability to bind to TLR5 and to be bound by a specific antibody. A conservative substitution of an amino acid, i.e., replacing an amino acid with a different amino acid of similar properties (e.g., hydrophilicity, degree and distribution of charged regions) is recognized in the art as typically involving a minor change. These minor changes can be identified, in part, by considering the hydropathic index of amino acids, as understood in the art. Kyte et al., *J. Mol. Biol.* 157:105-132 (1982). The hydropathic index of an amino acid is based on a consideration of its hydrophobicity and charge. It is known in the art that amino acids of similar hydropathic indexes can be substituted and still retain protein function. In one aspect, amino acids having hydropathic indexes of ±2 are substituted. The hydrophilicity of amino acids can also be used to reveal substitutions that would result in proteins retaining biological function. A consideration of the hydrophilicity of amino acids in the context of a peptide permits calculation of the greatest local average hydrophilicity of that peptide, a useful measure that has been reported to correlate well with antigenicity and immunogenicity. U.S. Pat. No. 4,554,101, incorporated herein by reference. Substitution of amino acids having similar hydrophilicity values can result in peptides retaining biological activity, for example immunogenicity, as is understood in the art. In one aspect, substitutions are performed with amino acids having hydrophilicity values within ±2 of each other. Both the hyrophobicity index and the hydrophilicity value of amino acids are influenced by the particular side chain of that amino acid. Consistent with that observation, amino acid substitutions that are compatible with biological function are understood to depend on the relative similarity of the amino acids, and particularly the side chains of those amino acids, as revealed by the hydrophobicity, hydrophilicity, charge, size, and other properties.

2. METHODS OF TREATMENT

[0083] a. Constitutively Active NF-κB Tumor

[0084] This invention relates to a method of treating a mammal suffering from a constitutively active NF-κB cancer comprising administering to the mammal a composition comprising a therapeutically effective amount of an agent that induces NF-κB activity. The agent that induces NF-κB activity may be administered in combination with a cancer treatment, such as chemotherapy and radiation therapy.

[0085] The cancer treatment may comprise administration of a cytotoxic agent or cytostatic agent, or combination thereof. Cytotoxic agents prevent cancer cells from multiplying by: (1) interfering with the cell's ability to replicate DNA and (2) inducing cell death and/or apoptosis in the cancer cells. Cytostatic agents act via modulating, interfering or inhibiting the processes of cellular signal transduction which regulate cell proliferation and sometimes at low continuous levels.

[0086] Classes of compounds that may be used as cytotoxic agents include, but are not limited to, the following: alkylating agents (including, without limitation, nitrogen mustards, ethylenimine derivatives, alkyl sulfonates, nitrosoureas and triazenes): uracil mustard, chlormethine, cyclophosphamide (Cytoxan®), ifosfamide, melphalan, chlorambucil, pipobroman, triethylene-melamine, triethylenethiophosphoramine, busulfan, carmustine, lomustine, streptozocin, dacarbazine, and temozolomide; antimetabolites (including, without limitation, folic acid antagonists, pyrimidine analogs, purine analogs and adenosine deaminase inhibitors): methotrexate, 5-fluorouracil, floxuridine, cytarabine, 6-mercaptopurine, 6-thioguanine, fludarabine phosphate, pentostatine, and gemcitabine; natural products and their derivatives (for example, vinca alkaloids, antitumor antibiotics, enzymes, lymphokines and epipodophyllotoxins): vinblastine, vincristine, vindesine, bleomycin, dactinomycin, daunorubicin, doxorubicin, epirubicin, idarubicin, ara-c, paclitaxel (paclitaxel is commercially available as Taxol®), mithramycin, deoxycoformycin, mitomycin-c, 1-asparaginase, interferons (preferably IFN-α), etoposide, and teniposide. Other proliferative cytotoxic agents are navelbene, CPT-11, anastrazole, letrazole, capecitabine, reloxafine, cyclophosphamide, ifosamide, and droloxafine.

[0087] Microtubule affecting agents interfere with cellular mitosis and are well known in the art for their cytotoxic activity. Microtubule affecting agents useful in the invention include, but are not limited to, allocolchicine (NSC 406042), halichondrin B (NSC 609395), colchicine (NSC 757), colchicine derivatives (e.g., NSC 33410), dolastatin 10 (NSC 376128), maytansine (NSC 153858), rhizoxin (NSC 332598), paclitaxel (Taxol®, NSC 125973), Taxol® derivatives (e.g., derivatives (e.g., NSC 608832), thiocolchicine (NSC 361792), trityl cysteine (NSC 83265), vinblastine sulfate (NSC 49842), vincristine sulfate (NSC 67574), natural and synthetic epothilones including but not limited to epothilone A, epothilone B, and discodermolide (see Service, (1996) Science, 274:2009) estramustine, nocodazole, MAP4, and the like. Examples of such agents are also described in Bulinski (1997) J. Cell Sci. 110:3055 3064; Panda (1997) Proc. Natl. Acad. Sci. USA 94:10560-10564; Muhlradt (1997) Cancer Res. 57:3344-3346; Nicolaou (1997) Nature

387:268-272; Vasquez (1997) Mol. Biol. Cell. 8:973-985; and Panda (1996) J. Biol. Chem 271:29807-29812.

[0088] Also suitable are cytotoxic agents such as epidophyllotoxin; an antineoplastic enzyme; a topoisomerase inhibitor; procarbazine; mitoxantrone; platinum coordination complexes such as cis-platin and carboplatin; biological response modifiers; growth inhibitors; antihormonal therapeutic agents; leucovorin; tegafur; and haematopoietic growth factors.

[0089] Cytostatic agents that may be used include, but are not limited to, hormones and steroids (including synthetic analogs): 17α-ethinylestradiol, diethylstilbestrol, testosterone, prednisone, fluoxymesterone, dromostanolone propionate, testolactone, megestrolacetate, methylprednisolone, methyl-testosterone, prednisolone, triamcinolone, hlorotrianisene, hydroxyprogesterone, aminoglutethimide, estramustine, medroxyprogesteroneacetate, leuprolide, flutamide, toremifene, zoladex.

[0090] Other cytostatic agents are antiangiogenics such as matrix metalloproteinase inhibitors, and other VEGF inhibitors, such as anti-VEGF antibodies and small molecules such as ZD6474 and SU6668 are also included. Anti-Her2 antibodies from Genetech may also be utilized. A suitable EGFR inhibitor is EKB-569 (an irreversible inhibitor). Also included are Imclone antibody C225 immunospecific for the EGFR, and src inhibitors.

[0091] Also suitable for use as an cytostatic agent is Casodex® (bicalutamide, Astra Zeneca) which renders androgen-dependent carcinomas non-proliferative. Yet another example of a cytostatic agent is the antiestrogen Tamoxifen® which inhibits the proliferation or growth of estrogen dependent breast cancer. Inhibitors of the transduction of cellular proliferative signals are cytostatic agents. Representative examples include epidermal growth factor inhibitors, Her-2 inhibitors, MEK-1 kinase inhibitors, MAPK kinase inhibitors, PI3 inhibitors, Src kinase inhibitors, and PDGF inhibitors.

[0092] A variety of cancers may be treated according to this invention including, but not limited to, the following: carcinoma including that of the bladder (including accelerated and metastatic bladder cancer), breast, colon (including colorectal cancer), kidney, liver, lung (including small and non-small cell lung cancer and lung adenocarcinoma), ovary, prostate, testes, genitourinary tract, lymphatic system, rectum, larynx, pancreas (including exocrine pancreatic carcinoma), esophagus, stomach, gall bladder, cervix, thyroid, and skin (including squamous cell carcinoma); hematopoietic tumors of lymphoid lineage including leukemia, acute lymphocytic leukemia, acute lymphoblastic leukemia, B-cell lymphoma, T-cell lymphoma, Hodgkins lymphoma, non-Hodgkins lymphoma, hairy cell lymphoma, histiocytic lymphoma, and Burketts lymphoma; hematopoietic tumors of myeloid lineage including acute and chronic myelogenous leukemias, myelodysplastic syndrome, myeloid leukemia, and promyelocytic leukemia; tumors of the central and peripheral nervous system including astrocytoma, neuroblastoma, glioma, and schwannomas; tumors of mesenchymal origin including fibrosarcoma, rhabdomyoscarcoma, and osteosarcoma; and other tumors including melanoma, xenoderma pigmentosum, keratoactanthoma, seminoma, thyroid follicular cancer, teratocarcinoma, and cancers of the gastrointestinal tract or the abdominopelvic cavity.

[0093] b. Treatment of Side Effects from Cancer Treatment

[0094] This invention also relates to a method of treating a mammal suffering from damage to normal tissue attributable to treatment of a constitutively active NF-κB cancer, comprising administering to the mammal a composition comprising a therapeutically effective amount of an agent that induces NF-κB activity. The agent that induces NF-κB activity may be administered in combination with a cancer treatment described above.

[0095] c. Modulation of Cell Aging

[0096] This invention also relates to a method of modulating cell aging in a mammal, comprising administering to the mammal a therapeutically effective amount of an agent that induces NF-κB activity. The agent that induces NF-κB activity may be administered in combination with other treatments.

[0097] d. Treatment of Stress

[0098] This invention also relates to a method of treating a mammal suffering from damage to normal tissue attributable to stress, comprising administering to the mammal a composition comprising a therapeutically effective amount of an agent that induces NF-κB activity. The agent that induces NF-κB activity may be administered in combination with other treatments. The stress may be attributable to any source including, but not limited to, radiation, wounding, poisoning, infection, and temperature shock.

[0099] e. Radiation

[0100] This invention is also related to the protection of cells from the effects of exposure to radiation. Injury and death of normal cells from ionizing radiation is a combination of direct radiation-induced damage to the exposed cells and an active genetically programmed cell reaction to radiation-induced stress resulting in suicidal death or apoptosis. Apoptosis plays a key role in massive cell loss occurring in several radiosensitive organs (i.e., hematopoietic and immune systems, epithelium of digestive tract, etc.), the failure of which determines general radiosensitivity of the organism.

[0101] Exposure to ionizing radiation (IR) may be short- or long-term, it may be applied as a single or multiple doses, to the whole body or locally. Thus, nuclear accidents or military attacks may involve exposure to a single high dose of whole body irradiation (sometimes followed by a long-term poisoning with radioactive isotopes). The same is true (with strict control of the applied dose) for pretreatment of patients for bone marrow transplantation when it is necessary to prepare hematopoietic organs for donor's bone marrow by "cleaning" them from the host blood precursors. Cancer treatment may involve multiple doses of local irradiation that greatly exceeds lethal dose if it were applied as a total body irradiation. Poisoning or treatment with radioactive isotopes results in a long-term local exposure to radiation of targeted organs (e.g., thyroid gland in the case of inhalation of 125I). Finally, there are many physical forms of ionizing radiation differing significantly in the severity of biological effects.

[0102] At the molecular and cellular level, radiation particles are able to produce breakage and cross-linking in the DNA, proteins, cell membranes and other macromolecular structures. Ionizing radiation also induces the secondary damage to the cellular components by giving rise to the free radicals and reactive oxygen species (ROS). Multiple repair systems counteract this damage, such as several DNA repair pathways that restore the integrity and fidelity of the DNA, and antioxidant chemicals and enzymes that scavenge the free radicals and ROS and reduce the oxidized proteins and lipids.

Cellular checkpoint systems detect the DNA defects and delay cell cycle progression until damage is repaired or decision to commit cell to growth arrest or programmed cell death (apoptosis) is reached

[0103] Radiation can cause damage to mammalian organism ranging from mild mutagenic and carcinogenic effects of low doses to almost instant killing by high doses. Overall radiosensitivity of the organism is determined by pathological alterations developed in several sensitive tissues that include hematopoietic system, reproductive system and different epithelia with high rate of cell turnover.

[0104] The acute pathological outcome of gamma irradiation leading to death is different for different doses and is determined by the failure of certain organs that define the threshold of the organism's sensitivity to each particular dose. Thus, lethality at lower doses occurs from bone marrow aplasia, while moderate doses kill faster by inducing gastrointestinal (GI) syndrome. Very high doses of radiation can cause almost instant death eliciting neuronal degeneration.

[0105] Organisms that survive a period of acute toxicity of radiation can suffer from long-term remote consequences that include radiation-induced carcinogenesis and fibrosis developing in exposed organs (e.g., kidney, liver or lungs) months and years after irradiation.

[0106] Cellular DNA is the major target of IR causing a variety of types of DNA damage (genotoxic stress) by direct and indirect (free radical-based) mechanisms. All organisms maintain DNA repair system capable of effective recovery of radiation-damaged DNA; however, errors in the DNA repair process may lead to mutations.

[0107] Tumors are generally more sensitive to gamma radiation and can be treated with multiple local doses that cause relatively low damage to normal tissue. Nevertheless, in some instances, damage of normal tissues is a limiting factor in application of gamma radiation for cancer treatment. The use of gamma-irradiation during cancer therapy by conventional, three-dimensional conformal or even more focused BeamCath delivery has also dose-limiting toxicities caused by cumulative effect of irradiation and inducing the damage of the stem cells of rapidly renewing normal tissues, such as bone marrow and gastrointestinal (GI) tract.

[0108] At high doses, radiation-induced lethality is associated with so-called hematopoietic and gastrointestinal radiation syndromes. Hematopoietic syndrome is characterized by loss of hematopoietic cells and their progenitors making it impossible to regenerate blood and lymphoid system. The death usually occurs as a consequence of infection (result of immunosuppression), hemorrhage and/or anemia. GI syndrome is caused by massive cell death in the intestinal epithelium, predominantly in the small intestine, followed by disintegration of intestinal wall and death from bacteriemia and sepsis. Hematopoietic syndrome usually prevails at the lower doses of radiation and leads to a more delayed death than GI syndrome.

[0109] In the past, radioprotectants were typically antioxidants—both synthetic and natural. More recently, cytokines and growth factors have been added to the list of radioprotectants. The mechanism of their radioprotection is considered to be a result of a facilitating effect on regeneration of sensitive tissues. There is no clear functional distinction between both groups of radioprotectants, however, since some cytokines induce the expression of cellular antioxidant proteins, such as manganese superoxide dismutase (MnSOD) and metallothionein.

[0110] The measure of protection for a particular agent is expressed by dose modification factor (DMF or DRF). DMF is determined by irradiating the radioprotector treated subject and untreated control subjects with a range of radiation doses and then comparing the survival or some other endpoints. DMF is commonly calculated for 30-day survival (LD50/30 drug-treated divided by LD50/30 vehicle-treated) and quantifies the protection of the hematopoietic system. In order to estimate gastrointestinal system protection, LD50 and DMF are calculated for 6- or 7-day survival. DMF values provided herein are 30-day unless indicated otherwise.

[0111] As shown below, inducers of NF-κB possess strong pro-survival activity at the cellular level and on the organism as a whole. In response to super-lethal doses of radiation, inducers of NF-κB inhibit both gastrointestinal and hematopoietic syndromes, which are the major causes of death from acute radiation exposure. As a result of these properties, inducers of NF-κB may be used to treat the effects of natural radiation events and nuclear accidents. Moreover, since inducers of NF-κB acts through mechanisms different from all presently known radioprotectants, they can be used in combination with other radioprotectants, thereby, dramatically increasing the scale of protection from ionizing radiation.

[0112] As opposed to conventional radioprotective agents (e.g., scavengers of free radicals), inducers of NF-κB activity may not reduce primary radiation-mediated damage but may act against secondary events involving active cell reaction to primary damage, therefore complementing the existing lines of defense. Pifithrin-alpha, a pharmacological inhibitor of p53 (a key mediator of radiation response in mammalian cells), is an example of this new class of radioprotectants. However, the activity of p53 inhibitors is limited to protection of the hematopoietic system and has no protective effect in digestive tract (gastrointestinal syndrome), therefore, reducing therapeutic value of these compounds. Anti-apoptotic pharmaceuticals with broader range of activity are desperately needed.

[0113] Inducers of NF-κB may be used as a radioprotective agent to extend the range of tolerable radiation doses by increasing radioresistance beyond the levels achievable by currently available measures (shielding and application of existing bioprotective agents) and drastically increase the chances of survival, for example, in case of onboard nuclear accidents or large-scale solar particle events. With an approximate DMF (30-day survival) greater than 1.5, the NF-κB inducer flagellin is more effective than any currently reported natural compound.

[0114] Inducers of NF-κB may be also useful for treating irreplaceable cell loss caused by low-dose irradiation, for example, in the central nervous system and reproductive organs. Inducers of NF-κB may also be used during cancer chemotherapy to treat the side effects associated with chemotherapy, including alopecia.

[0115] In one embodiment, a mammal is treated for exposure to radiation, comprising administering to the mammal a composition comprising a therapeutically effective amount of a composition comprising an inducer of NF-κB. The composition comprising an inducer of NF-κB may be administered in combination with one or more radioprotectants. The one or more radioprotectants may be any agent that treats the effects of radiation exposure including, but not limited to, antioxidants, free radical scavengers and cytokines.

[0116] Inducers of NF-κB may inhibit radiation-induced programmed cell death in response to damage in DNA and other cellular structures; however, inducers of NF-κB may not deal with damage at the cellular level and may not prevent mutations. Free radicals and reactive oxygen species (ROS) are the major cause of mutations and other intracellular damage. Antioxidants and free radical scavengers are effective at preventing damage by free radicals. The combination of an inducer of NF-κB and an antioxidant or free radical scavenger may result in less extensive injury, higher survival, and improved health for exposure. Antioxidants and free radical scavengers that may be used in the practice of the invention include, but are not limited to, thiols, such as cysteine, cysteamine, glutathione and bilirubin; amifostine (WR-2721); vitamin A; vitamin C; vitamin E; and flavonoids such as orientin and vicenin derived from Indian holy basil (*Ocimum sanctum*).

[0117] Inducers of NF-κB may also be administered in combination with a number of cytokines and growth factors that confer radioprotection by replenishing and/or protecting the radiosensitive stem cell populations. Radioprotection with minimal side effects may be achieved by the use of stem cell factor (SCF, c-kit ligand), Flt-3 ligand, and interleukin-1 fragment IL-1b-rd. Protection may be achieved through induction of proliferation of stem cells (all mentioned cytokines), and prevention of their apoptosis (SCF). The treatment allows accumulation of leukocytes and their precursors prior to irradiation thus enabling quicker reconstitution of the immune system after irradiation. SCF efficiently rescues lethally irradiated mice with DMF in the range of 1.3-1.35 and is also effective against gastrointestinal syndrome. Flt-3 ligand also provides strong protection in mice (70-80% 30-day survival at LD100/30, equivalent to DMF>1.2) and rabbits.

[0118] In addition, combinations of cytokines may provide enhanced radioprotection, such as: TPO combined with interleukin 4 (IL-4) and/or interleukin 11 (IL-11); GM-CSF combined with IL-3; G-CSF combined with Flt-3 ligand; 4F combination: SCF, Flt-3 ligand, TPO and IL-3; and 5F combination: 4F with addition of SDF-1.

[0119] In addition, gastrointestinal radioprotectors may be used, including transforming growth factor beta3 (TGFb3), interleukin 11 (IL-11), and mentioned keratinocyte growth factor (KGF). While these radioprotectors also protect the intestine, they are likely to synergize with flagellin or flagellin related polypeptides since the results below show that flagellin and flagellin related polypeptides protect endothelium, while these gastrointestinal radioprotectors protect epithelium of GI tract.

[0120] Several factors, while not cytokines by nature, stimulate the proliferation of immunocytes and may be used in combination with inducers of NF-κB. For example, 5-AED (5-androstenediol) is a steroid that stimulates the expression of cytokines and increases resistance to bacterial and viral infections. A subcutaneous injection of 5-AED in mice 24 h before irradiation improved survival with DMF=1.26. Synthetic compounds, such as ammonium tri-chloro(dioxoethylene-O,O'—) tellurate (AS-101), may also be used to induce secretion of numerous cytokines and for combination with inducers of NF-κB. Additional radioprotectors include, growth hormone (GH), thrombopoietin (TPO), interleukin 3 (IL-3), granulocyte-macrophage colony-stimulating factor (GM-CSF), granulocyte colony-stimulating factor (G-CSF), and stromal derived factor-1 (SDF-1).

[0121] Growth factors and cytokines may also be used to provide protection against gastrointestinal syndrome. Keratinocyte growth factor (KGF) promotes proliferation and differentiation in the intestinal mucosa, and increases the post-irradiation cell survival in the intestinal crypts. Hematopoietic cytokine and radioprotectant SCF may also increase intestinal stem cell survival and associated short-term organism survival.

[0122] Inducers of NF-κB may offer protection against both gastrointestinal (GI) and hematopoietic syndromes. Since mice exposed to 15 Gy of whole-body lethal irradiation die mostly from GI syndrome, a composition comprising an inducer of NF-κB and one or more inhibitors of GI syndrome may be more effective. Inhibitors of GI syndrome that may be used in the practice of the invention include, but are not limited to, cytokines such as SCF and KGF.

[0123] The composition comprising an inducer of NF-κB may be administered at any point prior to exposure to radiation including, but not limited to, about 48 hr, 46 hr, 44 hr, 42 hr, 40 hr, 38 hr, 36 hr, 34 hr, 32 hr, 30 hr, 28 hr, 26 hr, 24 hr, 22 hr, 20 hr, 18 hr, 16 hr, 14 hr, 12 hr, 10 hr, 8 hr, 6 hr, 4 hr, 3 hr, 2 hr, or 1 hr prior to exposure. The composition comprising an inducer of NF-κB may be administered at any point after exposure to radiation including, but not limited to, about 1 hr, 2 hr, 3 hr, 4 hr, 6 hr, 8 hr, 10 hr, 12 hr, 14 hr, 16 hr, 18 hr, 20 hr, 22 hr, 24 hr, 26 hr, 28 hr, 30 hr, 32 hr, 34 hr, 36 hr, 38 hr, 40 hr, 42 hr, 44 hr, 46 hr, or 48 hr after exposure to radiation.

[0124] f. Sepsis

[0125] This invention also relates to a method of preventing sepsis in a mammal comprising administering to the mammal a composition comprising a therapeutically effective amount of an agent that induces NF-κB activity. The agent that induces NF-κB activity may be administered in combination with other treatments.

[0126] Viral or bacterial infections may stimulate the innate immune system through Toll-like receptor (TLR) ligands. Macrophages may be protected and/or stimulated by flagellin and flagellin related polypeptides due to the presence of TLR5 on their surface. For example, a crucial step in the development of an anthrax infection is death of macrophages killed from within by *B. anthracis*. Protection of intestinal endothelium against various stresses using flagellin and flagellin related polypeptides may prevent GI cell death and also may prevent penetration of the GI wall by infectious agent, thereby preventing GI bleeding caused by infections such as Ebola. Other hemorrhagic viral infections may also be prevented by rescue of endothelium and gastrointestinal epithelium.

3. AGENT

[0127] This invention also relates to an agent that induces NF-κB activity. The agent may be an artificially synthesized compound or a naturally occurring compound. The agent may be a low molecular weight compound, polypeptide or peptide, or a fragment, analog, homolog, variant or derivative thereof.

[0128] The agent may also be an NF-κB inducing cytokine including, but not limited to, IL2, IL6, TNF and TGFβ. The agent may also be a prostaglandin. The agent may also be a growth factor including, but not limited to, KGF and PDGF. The agent may also be an antibody that induces NF-κB activity.

[0129] a. Flagellin

[0130] In one embodiment, the agent that induces NF-κB activity is flagellin. As shown in the Examples below, flagellin and flagellin related polypeptides possess strong pro-survival activity at the cellular level and for the organism as a whole. Interestingly, flagellin also stimulates natural killer (NK) cells and T-lymphocytes, which are the major components of anti-tumor immunity (Tsujimoto H, et. al., *J Leukoc Biol.* 2005 October; 78(4):888-97; Caron G., et. al., *J Immunol.* 2005 Aug. 1; 175(3):1551-7; Honko A N & Mizel S B, *Immunol Res.* 2005; 33(1):83-101). As a result, flagellin may be used as a radioprotectant in cancer treatments.

[0131] The present invention is also related to flagellin related polypeptides, such as those polypetpides described herein. As used herein, the term "flagellin" is intended to mean a flagellin or flagellin-related polypeptide from any source, including a variety of Gram-positive and Gram-negative bacterial species. The amino acid sequences of flagellin from 23 bacterial species are depicted in FIG. 7 of U.S. Patent Publication No. 2003/0044429, the contents of which are incorporated herein by reference. The nucleotide sequences encoding the flagellin polypeptides listed in FIG. 7 of U.S. 2003/0044429 are publically available at sources including the NCBI Genbank database.

[0132] Flagellin is the major component of bacterial flagellum. Flagellin is composed of three domains (FIG. **9**). Domain 1 (D1) and domain 2 (D2) are discontinuous and are formed when residues in the amino terminus and carboxy terminus are juxtaposed by the formation of a hairpin structure. The amino and carboxy terminus comprising the D1 and D2 domains is most conserved, whereas the middle hypervariable domain (D3) is highly variable. Studies with a recombinant protein containing the amino D1 and D2 and carboxyl D1 and D2 separated by an *Escherichia coli* hinge (ND1-2/ECH/CD2) indicate that D1 and D2 are bioactive when coupled to an ECH element. This chimera, but not the hinge alone, induced $I_{\kappa}B_{\alpha}$ degradation, NF-κB activation, and NO and IL-8 production in two intestinal epithelial cell lines. The non-conserved D3 domain is on the surface of the flagellar filament and contains the major antigenic epitopes. The potent proinflammatory activity of flagellin may reside in the highly conserved N and C D1 and D2 regions.

[0133] Flagellin induces NF-κB activity by binding to Toll-like receptor 5 (TLR5). The TLR family is composed of at least 10 members and is essential in innate immune defense against pathogens. The innate immune system recognizes pathogen-associated molecular patterns (PAMPs) that are conserved on microbial pathogens. TLR may recognize a conserved structure that is particular to bacterial flagellin. The conserved structure may be comprised of a large group of residues that are somewhat permissive to variation in amino acid content. Smith et al., Nat Immunol. 4:1247-53 (2003) have identified 13 conserved amino acids in flagellin that are part of the conserved structure recognized by TLR5. The 13 conserved amino acids of flagellin important for TLR5 activity are shown in FIG. **24**.

[0134] In a preferred embodiment, the flagellin is from a species of *Salmonella*, a representative example of which is *S.dublin* (encoded by GenBank Accession Number M84972) (SEQ ID NO: 1). In another preferred embodiment, the flagellin related-polypeptide is a fragment, variant, analog, homolog, or derivative of SEQ ID NO: 1, or combination thereof, that binds to TLR5 and induces TLR5-mediated activity, such as activation of NF-κB activity. A fragment, variant, analog, homolog, or derivative of flagellin may be obtained by rational-based design based on the domain structure of Flagellin and the conserved structure recognized by TLR5.

[0135] In a more preferred embodiment, the fragment, variant, analog, homolog, or derivative of SEQ ID NO: 1, or combination thereof, comprises at least 10, 11, 12, or 13 of the 13 conserved amino acids shown in FIG. **24** (positions 89, 90, 91, 95, 98, 101, 115, 422, 423, 426, 431, 436 and 452). In another more preferred embodiment, the amino- and carboxy-terminus of the fragment, variant, analog, homolog, or derivative of SEQ ID NO: 1, or combination thereof, is at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identical to amino acids 1-174 and 418-505 of SEQ ID NO: 1. FIG. **26** lists the percentage identity of the amino- and carboxy-terminus of flagellin with known TLR-5 stimulating activity, as compared to SEQ ID NO: 1.

[0136] Flagellin homologs may be a flagellin polypeptide from any Gram-positive or Gram-negative bacterial species including, but not limited to, the flagellin polypeptides disclosed in U.S. Pat. Pub. 2003/000044429, the contents of which are incorporated herein, and the flagellin peptides corresponding to the Accession numbers listed in the BLAST results shown in FIGS. **25**A-D. Also contemplated, are fragments, variants, analogs and derivatives of flagellin homologs.

[0137] Flagellin fragments may be portions of a flagellin polypeptide that stimulate TLR5 activity. Numerous deletional mutants of flagellin have been made that retain at least some TLR5 stimulating activity. In addition to the deletional mutants disclosed in the Examples herein, representative deletional mutants include translation of GenBank Accession number D13689 missing amino acids 185-306 or 444-492, and translation of GenBank Accession number M84973 missing amino acids 179-415. Also contemplated, are homologs, variants, analogs and derivatives of flagellin fragments.

[0138] Flagellin variants include flagellin polypeptides with transposon insertions and changes to the variable D3 domain. The D3 domain may be substituted in part, or in whole, with a hinge or linker polypeptide that allows the D1 and D2 domains to properly fold such that the variant stimulates TLR5 activity. Representative examples of variant hinge elements may be found in the *E. coli* MukB protein and SEQ ID NOS: 3 and 4. Also contemplated, are fragments, homologs, analogs and derivatives of flagellin variants.

4. COMPOSITION

[0139] This invention also relates to a composition comprising a therapeutically effective amount of an inducer of NF-κB. The composition may be a pharmaceutical composition, which may be produced using methods well known in the art. As described above, the composition comprising an inducer of NF-κB may be administered to a mammal for the treatment of conditions associated with apoptosis including, but not limited to, exposure to radiation, side effect from cancer treatments, stress and cell aging. The composition may also comprise additional agents including, but not limited to, a radioprotectant or a chemotherapeutic drug.

[0140] a. Administration

[0141] Compositions of this invention may be administered in any manner including, but not limited to, orally, parenterally, sublingually, transdermally, rectally, transmucosally, topically, via inhalation, via buccal administration, intrapleurally, or combinations thereof. Parenteral administration includes, but is not limited to, intravenous, intraarterial, intraperitoneal, subcutaneous, intramuscular, intrathecal, and intraarticular. Transmucosally administration includes, but is not limited to intranasal. For veterinary use, the composition may be administered as a suitably acceptable formulation in accordance with normal veterinary practice. The veterinarian can readily determine the dosing regimen and route of administration that is most appropriate for a particular animal.

[0142] The composition may be administered prior to, after or simultaneously with a stress that triggers apoptosis, or a combination thereof. The composition may be administered from about 1 hour to about 48 hours prior to or after exposure to a stress that triggers apoptosis.

[0143] b. Formulation

[0144] Compositions of this invention may be in the form of tablets or lozenges formulated in a conventional manner. For example, tablets and capsules for oral administration may contain conventional excipients including, but not limited to, binding agents, fillers, lubricants, disintegrants and wetting agents. Binding agents include, but are not limited to, syrup, accacia, gelatin, sorbitol, tragacanth, mucilage of starch and polyvinylpyrrolidone. Fillers include, but are not limited to, lactose, sugar, microcrystalline cellulose, maizestarch, calcium phosphate, and sorbitol. Lubricants include, but are not limited to, magnesium stearate, stearic acid, talc, polyethylene glycol, and silica. Disintegrants include, but are not limited to, potato starch and sodium starch glycollate. Wetting agents include, but are not limited to, sodium lauryl sulfate). Tablets may be coated according to methods well known in the art.

[0145] Compositions of this invention may also be liquid formulations including, but not limited to, aqueous or oily suspensions, solutions, emulsions, syrups, and elixirs. The compositions may also be formulated as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations may contain additives including, but not limited to, suspending agents, emulsifying agents, nonaqueous vehicles and preservatives. Suspending agent include, but are not limited to, sorbitol syrup, methyl cellulose, glucose/sugar syrup, gelatin, hydroxyethylcellulose, carboxymethyl cellulose, aluminum stearate gel, and hydrogenated edible fats. Emulsifying agents include, but are not limited to, lecithin, sorbitan monooleate, and acacia. Nonaqueous vehicles include, but are not limited to, edible oils, almond oil, fractionated coconut oil, oily esters, propylene glycol, and ethyl alcohol. Preservatives include, but are not limited to, methyl or propyl p-hydroxybenzoate and sorbic acid.

[0146] Compositions of this invention may also be formulated as suppositories, which may contain suppository bases including, but not limited to, cocoa butter or glycerides. Compositions of this invention may also be formulated for inhalation, which may be in a form including, but not limited to, a solution, suspension, or emulsion that may be administered as a dry powder or in the form of an aerosol using a propellant, such as dichlorodifluoromethane or trichlorofluoromethane. Compositions of this invention may also be formulated transdermal formulations comprising aqueous or nonaqueous vehicles including, but not limited to, creams, ointments, lotions, pastes, medicated plaster, patch, or membrane.

[0147] Compositions of this invention may also be formulated for parenteral administration including, but not limited to, by injection or continuous infusion. Formulations for injection may be in the form of suspensions, solutions, or emulsions in oily or aqueous vehicles, and may contain formulation agents including, but not limited to, suspending, stabilizing, and dispersing agents. The composition may also be provided in a powder form for reconstitution with a suitable vehicle including, but not limited to, sterile, pyrogen-free water.

[0148] Compositions of this invention may also be formulated as a depot preparation, which may be administered by implantation or by intramuscular injection. The compositions may be formulated with suitable polymeric or hydrophobic materials (as an emulsion in an acceptable oil, for example), ion exchange resins, or as sparingly soluble derivatives (as a sparingly soluble salt, for example).

[0149] c. Dosage

[0150] A therapeutically effective amount of the agent required for use in therapy varies with the nature of the condition being treated, the length of time that induction of NF-κB activity is desired, and the age and the condition of the patient, and is ultimately determined by the attendant physician. In general, however, doses employed for adult human treatment typically are in the range of 0.001 mg/kg to about 200 mg/kg per day. The dose may be about 1 μg/kg to about 100 μg/kg per day. The desired dose may be conveniently administered in a single dose, or as multiple doses administered at appropriate intervals, for example as two, three, four or more subdoses per day. Multiple doses often are desired, or required, because NF-κB activity in normal cells may be decreased once the agent is no longer administered.

[0151] The dosage of an inducer of NF-κB may be at any dosage including, but not limited to, about 1 μg/kg, 25 μg/kg, 50 μg/kg, 75 μg/kg, 100 μg/kg, 125 μg/kg, 150 μg/kg, 175 μg/kg, 200 μg/kg, 225 μg/kg, 250 μg/kg, 275 μg/kg, 300 μg/kg, 325 μg/kg, 350 μg/kg, 375 μg/kg, 400 μg/kg, 425 μg/kg, 450 μg/kg, 475 μg/kg, 500 μg/kg, 525 μg/kg, 550 μg/kg, 575 μg/kg, 600 μg/kg, 625 μg/kg, 650 μg/kg, 675 μg/kg, 700 μg/kg, 725 μg/kg, 750 μg/kg, 775 μg/kg, 800 μg/kg, 825 μg/kg, 850 μg/kg, 875 μg/kg, 900 μg/kg, 925 μg/kg, 950 μg/kg, 975 μg/kg or 1 mg/kg.

[0152] This invention has multiple aspects, illustrated by the following non-limiting examples.

Example 1

P53 Deficiency Accelerated Development of GI Syndrome in Mice

[0153] The primary cause of death from ionizing radiation (IR) of mammals depends on the radiation dose. At doses of up to 9-10 Gy, mice die 12-20 days later, primarily from lethal bone marrow depletion-hematopoietic (HP) syndrome. At this dose, irradiated mice can be rescued from lethality by bone marrow transplantation. Animals that receive >15 Gy die between 7-12 days after treatment (before hematopoietic syndrome can kill them) from complications of damage to the small intestine-gastrointestinal (GI) syndrome. In both cases of HP and GI syndromes, lethal damage of tissues starts from massive p53-dependent apoptosis. This observation allowed us earlier to suggest that p53 could be a determinant of radiation-induced death. Consistently, p53-deficient mice were resistant to doses of radiation that kill through HP syndrome, and lethality of wild type animals receiving 6-11 Gy of gamma radiation could be reduced by temporary pharmacological inhibition of p53 by the small molecule p53 inhibitor pifithrin-alpha (PFT) (Komarov et al 1999). Identification of p53 as a factor sensitizing tissues to genotoxic stress was further strengthened by demonstrating the p53 dependence of hair loss (alopecia) occurring as a result of experimental chemotherapy or radiation. Hence, based on previous observations, one would expect that p53 continues to play an important role in development of lethal GI syndrome after higher doses of IR. Surprisingly, p53-deficiency sensitizes mice to higher doses of IR causing lethal gastro-intestinal syndrome (FIG. **1**). Continuous cell proliferation in the crypts of p53-deficient epithelium after IR correlates with accelerated death of damaged cells of crypt and rapid destruction of villi. p53 prolongs survival by inducing growth arrest in the crypts of small intestine thereby preserving integrity of the guts (FIG. **2**). Thus, proapoptotic function of p53 promotes hematopoietic syndrome while its growth arrest function delays development of gastro-intestinal syndrome.

[0154] The dynamics of cell population in the small intestine have been analyzed in great detail. Cell proliferation in the epithelia of the gut is limited to the crypts where stem cells and early proliferating progenitors are located. After a couple of cell divisions, already differentiated descendants of crypt stem cells move up the villi to be shed at the villar tip. In the small intestine of the mouse, the entire "trip" of the cell (the proliferative compartment to the tip of the villus) normally takes between 3 and 5 days. Although reaction of the small intestine to gamma radiation has been well examined at a pathomorphological level, it still remains unclear what is the exact cause of GI lethality, including the primary event. Death may occur as a direct consequence of the damage of epithelial crypt cells and followed denudation of villi leading to fluid and electrolyte imbalance, bacteremia and endotoxemia. Besides inflammation and stromal responses, endothelial dysfunctions seem to be the important factors contributing to lethality. In summary, pharmacological suppression of p53 that was shown to be so effective as a method of protection from IR-induced HP syndrome, is useless (if not detrimental) against GI syndrome. Therefore, it is necessary to develop alternative approaches to radioprotection of epithelium of small intestine that will rely on another mechanism, such as, for example, activation of NF-κB and subsequent inhibition of cell death.

Example 2

Flagellin Delays Mouse Death Caused by IR-Induced GI Syndrome

[0155] Whole body irradiation of mice with 15 Gy gamma radiation caused death within 8 days from GI syndrome providing a conventional model of radiation induced damage of GI tract. To test whether flagellin was capable of protecting GI epithelium from IR, we tested the effect of i.v.-injected flagellin on the dynamics of mouse lethality after 15 Gy of radiation. We used a range of flagellin doses, all of which were significantly lower than the highest tolerable dose known from literature (300 μg/mouse). Irradiation was done 4 hours post treatment. The results of a representative experiment are shown in FIG. **4**. As expected, control irradiated mice (that received PBS i.v.) died between 5 and 8 days post-treatment. Animals that received flagellin lived significantly longer; the extension of animal survival correlated with the dose of flagellin. Pathomorphological analysis of the small intestine on day 7 after irradiation revealed dramatic differences between flagellin-treated and control groups (FIG. **5**). Intravenous, intraperitoneal and subcutaneous delivery of 0.2 mg/kg of flagellin followed by 13 Gy irradiation afforded similar degree of protection, leading to 85-90% 30-day survival of mice (data not shown). While not being bound by theory, flagellin may be a radioprotectant due to its activation of NF-κB, which presumably acts as an inhibitor of apoptotic death.

Example 3

Flagellin Rescues Mice from Lethal IR-Induced Hematopoietic Syndrome

[0156] We next tested whether flagellin had an effect on mouse IR-induced death from HP syndrome that was experimentally induced by lower radiation doses (usually up to 11 Gy) that are incapable of causing lethal GI toxicity. The experiments were done similarly to the above-described ones (FIGS. **14** and **15**), however, instead of 15Gy, mice received 10Gy, the dose that caused 100% killing in control group by day 13 (FIG. **6**). Flagellin-treated group (5 μg/mouse) showed complete protection from this dose of IR surprisingly indicating that flagellin-mediated radioprotection acts not only against GI but also against HP IR-induced syndromes.

Example 4

Time Dependence on the Protective Effect of Flagellin

[0157] Mice were next administered flagellin at different times prior to 13Gy of gamma irradiation. The results of one of such experiments is shown in FIG. **7**. The obtained results show that flagellin is effective as a radioprotectant from 13Gy if injected 1-4 h before treatment.

[0158] In order to further estimate the dependence of radioprotective activity of flagellin on the time of treatment, mice were injected at several time points relative to the moment of gamma-irradiation. Experiments were performed essentially as explained above, using intraperitoneal injection of 5 μg/mouse (0.2 mg/kg) of full-length flagellin or, for control mice, 5 μg/mouse (0.2 mg/kg) of bacterial RNA polymerase. The experiments were performed using the NIH-Swiss mouse strain. The results show that flagellin provides ~90% survival after 13 Gy irradiation if injected at 1 or 2 hours before treatment (FIG. **7**). Only −1 h graph is shown for clarity, however, both timepoints (−1 and −2 h) provide similar degree and dynamics of survival. The 4 h timepoint shows somewhat lower protection. Flagellin injected 24 hours before irradiation had no protective effect against 13 Gy induced death.

[0159] Interestingly, administration of flagellin 24 hours before 10 Gy gamma-irradiation provided 100% protection. While 13 Gy irradiation in mice primarily induces death from GI syndrome, 10 Gy-induced death is mostly mediated by hematopoietic syndrome. Accordingly, such long-term protection from 10 Gy irradiation may be mediated by enhanced proliferation or survival of hematopoietic stem cell induced by flagellin and/or long-living secondary cytokines.

Example 5

Determination of $LD_{50/30}$, $LD_{50/7}$ and DMF for Flagellin

[0160] We next obtained an estimate of radiation dose-dependent protection for flagellin. As shown above (FIG. **7**), treatment with flagellin was sufficient for 100% protection against 10 Gy gamma-irradiation (this dose causes death from hematopoietic syndrome) and 90% 30-day survival at 13 Gy (both hematopoietic and GI syndromes). Experiments were performed as described above, using flagellin 5 μg/mouse (0.2 mg/kg), intraperitoneally injected 1 h before irradiation.

[0161] At 15 Gy, however, 100% 7-day survival was followed by delayed death after 13 days (0% 30-day survival), while control group had fully succumbed to GI syndrome by day 7 (FIG. **8**). The kinetics of the flagellin-treated group mortality after 15 Gy irradiation is reminiscent of such of control group at 10 Gy, hinting at death caused by hematopoietic syndrome. The results provide an estimate of flagellin $LD_{50/30}$ around 13.5-14 Gy and DMF_{30} of about 1.75-1.8. This degree of radioprotection is significantly higher than any reported for a natural compound.

Example 6

Rational Design and Cloning of Flagellin Fragments

[0162] *Salmonella* flagellin, encoded by the FliC gene (SEQ ID NO: 2), is a strong activator of pro-survival NF-κB pathway. This is the most likely mechanism of its radioprotective action. Previous studies have shown that binding of flagellin to Toll-like receptor 5 (TLR5) on the cell surface is a necessary step that triggers activation of NF-κB. The domain structure of *Salmonella* flagellin is described in sufficient detail in the literature (FIG. **9**). Moreover, previous structural studies of flagellin-TLR5 complex (FIG. **10**) provide the ability to distinguish between domains that are essential or dispensable for binding and thus NF-κB activation. Protein minimization may provide reduced immune response after repeated administration of flagellin-related polypeptides. This may be achieved, in part, due to lower immunogenicity of low molecular weight proteins and smaller number of immunogenic epitopes available.

[0163] The domains needed for TLR5 binding may be located exclusively in the evolutionary conserved N- and C-terminal domains of bacterial flagellins. The hypervariable domain (amino acids 178-402) does not come into close contact with TLR5. As was demonstrated previously, replacement of this domain with a flexible linker peptide did not disrupt binding to TLR5. In addition, N-terminal and C-terminal coiled-coil polymerization domains (amino acids 1-55, 456-505) do not bind to TLR5 and likely are dispensable (see modified N and C termini B and B', respectively, as shown herein). Also, another fragment N-terminus lacking all domains but major N-terminal α-helix that actually binds TLR5 (amino acids 56-100) may be sufficient for binding.

[0164] Accordingly, three types of N-termini (A, B, C) and two types of C-termini (A',B'), connected with a flexible linker (SEQ ID NOS: 3 and 4) taken from pGEX-KG cloning vector (SEQ ID NOS: 5 and 6) were combined into expression constructs to produce several possible flagellin fragments (Table 1). In addition, constructs representing separate N-termini (A, B, C) and glutathione-S-transferase (GST)-fusions of C-termini (GST-A', GST-B') were prepared. All constructs were cloned in the pRSETb bacterial expression vector and 6×His-tagged proteins were produced and purified for further experiments (FIG. **11**).

TABLE 1

Name	Structure	DNA	Protein
AA'	(1-177)-Linker-(402-505)	SEQ ID NO: 7	SEQ ID NO: 8
AB'	(1-177)-Linker-(402-450)	SEQ ID NO: 9	SEQ ID NO: 10
BA'	(56-177)-Linker-(402-505)	SEQ ID NO: 11	SEQ ID NO: 12
BB'	(56-177)-Linker-(402-450)	SEQ ID NO: 13	SEQ ID NO: 14
CA'	(56-100)-Linker-(402-505)	SEQ ID NO: 15	SEQ ID NO: 16
CB'	(56-100)-Linker-(402-450)	SEQ ID NO: 17	SEQ ID NO: 18
A	(1-177)	SEQ ID NO: 19	SEQ ID NO: 20
B	(56-177)	SEQ ID NO: 21	SEQ ID NO: 22
C	(56-100)	SEQ ID NO: 23	SEQ ID NO: 24
GST-A'	GST-Linker-(402-505)	SEQ ID NO: 25	SEQ ID NO: 26
GST-B'	GST-Linker-(402-450)	SEQ ID NO: 27	SEQ ID NO: 28

Example 7

Selection of Biologically Active Flagellin Fragments

[0165] Since the radioprotective activities of flagellin appear to be NF-κB dependent, we tested the ability of the flagellin fragments to induce NF-κB translocation to the nucleus and binding to its target sites in DNA. This was tested by electrophoretic mobility shift assay (EMSA) using nuclear extracts from flagellin- and fragment-treated A549 lung cancer cells and labeled synthetic NF-κB binding kB oligonucleotide.

[0166] Only flagellin itself and fragments AA', AB', and BA' were capable of inducing NF-κB translocation (FIG. **12**). The level of translocation is comparable for flagellin and fragments AA', AB', and BA'. The hypervariable domain does not appear to be necessary for NF-κB translocation, while the presence of at least one polymerization domain, N- or C-terminal, is required. Mixtures of the N- and C-terminal fragments (A+A', A+B') were inactive.

[0167] While translocation of NF-κB to the nucleus is a crucial step in induction of NF-κB-regulated inhibitors of apoptosis, it is not sufficient in itself. To directly test the ability of selected fragments to induce expression of NF-κB-regulated genes, we performed reporter assay experiments. Flagellin and the AA', BB', A' and B' fragments were used for treatment of H116 human colon cancer cells carrying luciferase gene under a NF-κB-responsive promoter. The reporter construct contained three NF-κB-binding sites from the E-selectin promoter combined with a Hsp70 minimal promoter that is routinely used for the detection of NF-κB status of cells. Luciferase activity was measured in cell lysates six hours after addition of flagellin or its truncated fragments into the medium. TNF was used as positive control. The results of a representative experiment are shown in FIG. **13** and indicates that flagellin and fragment AA' are capable of NF-κB activation, whereas fragments BB', GST-A' and GST-B' are not.

Example 8

Further Optimization of Flagellin Fragments

[0168] We further minimized the AA' flagellin fragment by producing additional fragments through stepwise removal of peptide fragments from its N-terminal half (Table 2). Electrophoretic mobility shift assays were performed as described above using nuclear extracts from flagellin- and fragment-treated HT29 human colon cancer cells and labeled synthetic NF-κB binding κB oligonucleotide. NF-κB binding activity in HT29 cells was stimulated with TNFa (10 ng/ml), or flagellin fragments (1 mg/ml) for 15 min. As shown in FIG. **14**, fragments AA'n1-170, AA'n54-170, AA'n1-163 and AA'n54-163 each induce NF-κB translocation, with levels comparable to that of flagellin for AA'n1-170, AA'n54-170 and AA'n1-163.

TABLE 2

Name	Structure	DNA	Protein
AA'n54-177	(54-177)-Linker-(402-505)	SEQ ID NO: 11	SEQ ID NO: 12
AA'n1-170	(1-170)-Linker-(402-505)	SEQ ID NO: 29	SEQ ID NO: 30
AA'n54-170	(54-170)-Linker-(402-505)	SEQ ID NO: 31	SEQ ID NO: 32
AA'n1-163	(1-163)-Linker-(402-505)	SEQ ID NO: 33	SEQ ID NO: 34
AA'n54-163	(54-163)-Linker-(402-505)	SEQ ID NO: 35	SEQ ID NO: 36

[0169] In order to study the ability of the AA' fragments to directly activate NF-κB-regulated transcription, we performed reporter assay experiments as described above for a wide range of concentrations of flagellin, original AA' and AA'-derived fragments. As shown above, AA' and AA'n1-170 induce NF-κB-regulated transcription at the level comparable to such of flagellin over the studied range of concentrations (FIG. **15**, left). AA' and AA'n1-170 are more active than flagellin in the very low concentration range (FIG. **15**, right), possibly due to their reduced molecular weight. The results with fragment AA'n1-170 show that AA'-derived flagellin fragments may be made with a portion of the N-terminal domain removed without significant loss of activity and may be used as effective radioprotectors.

[0170] The above experiments (EMSA and reporter activation assay) were repeated with flagellin and AA' fragments subjected to 30 minutes boiling and renaturation before being applied to cells. The results were comparable to those obtained without boiling (data not shown). This shows that the observed differences in flagellin fragment activity may not be caused by changes in protein stability.

Example 9

In Vivo Comparison of Radioprotective Properties of Flagellin and Flagellin Fragments

[0171] As shown above, full-length flagellin provides protection from both hematopoietic and gastrointestinal syndromes. The radioprotective potential of flagellin fragments was similarly tested after gamma-irradiation with 11 Gy (dose that induces hematopoietic syndrome-associated mortality in mice) or 14 Gy (dose that causes death from GI syndrome). Mice (10 animals per group) were injected subcutaneously with 5.0 μg/mouse (0.2 mg/kg) of flagellin or its fragments, AA' or BB', and gamma-irradiated 1 hour later.

[0172] The degree of radioprotection displayed by the AA' fragment is at least comparable to full-length flagellin (FIG. **16**). Both the AA' fragment and full-length flagellin showed 100% 30-day survival for mice irradiated with 11 Gy and 14 Gy. Meanwhile, 0% of mice injected with the BB' fragment survived to 30 days. This is expected since the BB' fragment is incapable of inducing NF-κB in vitro. These results show that significant reduction in the size of flagellin (about 40% removed) may be achieved without a decrease in the degree of radioprotection. In addition, the ability to predict radioprotective potential from results of in vitro NF-κB activation is confirmed.

Example 10

Identification of Cellular Targets of Flagellin-Mediated Radioprotection

[0173] Tissue samples of intestinal mucosa were taken 5 days after 14 Gy irradiation from mice pretreated with flagellin and control mice. Control animals were treated with 5.0 μg/mouse (0.2 mg/kg) bacterial RNA-polymerase. Pathomorphological analysis of the small intestine reveals reduction of the size of crypts and villi and a number of the cells with condensed apoptotic nuclei in control mouse and near-normal morphology in the treated mouse (data not shown). Tissue samples (small intestine and skin from the back) were also obtained from mice treated with the AA' fragment. The results shown in FIG. **17** are areas of typical morphology observed over a set of at least 3 mice. After treatment with flagellin and the AA' fragment, mice demonstrated near-normal intestinal morphology with preservation of the villi/crypt structure (FIG. **17**A).

[0174] In addition to purely histological observation of cell death and survival, we performed more specialized tests of apoptotic cell death in intestinal tissue using a TUNEL assay, which detects apoptosis-associated DNA fragmentation. These experiments allowed us to define with a high degree of probability cellular populations that are depleted by radiation and rescued by flagellin fragment treatment. The earliest radiation-induced alterations detectable in the small intestine after treatment with IR is apoptosis occurring in vascular endothelial cells of villi, which is seen as early as 5 hours post treatment (FIG. **17**B). This apoptosis, which is believed to be critical for radiosensitivity of the small intestine, was almost completely blocked in the mice pretreated with the AA' fragment (FIG. **17**B, bottom panel). Degeneration of villi and crypts, occurring within the next several days post treatment and greatly suppressed in AA' fragment-treated animals, comes as a consequence of injury of blood vessels. Effective protection of endothelial cells of the small intestine by the flagellin fragment may be due to expression of TLR5 in these cells.

[0175] Remarkably, the AA' fragment and flagellin also prevented the radiation-induced disappearance of sebaceous glands located at the base of skin hair follicles (FIG. **27**C). These results further confirm the suitability of AA' fragment for radioprotection and for the prevention of radiation-induced hair loss.

Example 11

Protection from Supralethal Radiation

[0176] In order to explore the limits of radioprotection provided by the AA' fragment, we irradiated mice with 17 Gy and 20 Gy single doses of total body gamma-radiation. The experiment was performed as described above using inactive flagellin fragment (CB) as a negative control.

[0177] As expected, we observed a 100% mortality in both groups at 17 and 20 Gy (FIG. **18**). However, death was significantly delayed in both cases by administration of the AA' fragment. Most remarkably, the kinetics of death at 17 Gy in control mice conform to GI syndrome (6-7 day mortality), while death of mice treated with the AA' fragment appear to be mediated by hematopoietic syndrome (10-15 day mortality). This shows that flagellin and flagellin fragments may protect against the GI syndrome at doses as high as 17 Gy. In addition, this shows that even further radioprotection may be obtained by flagellin and flagellin fragments combined with hematopoietic radioprotectors.

Example 12

Immunogenicity and Repetitive Administration Studies

[0178] Overall immunogenicity of a protein may determines its suitability for repeated use. Antibodies generated by immune system are capable of reducing the therapeutic activity of the protein and also may induce anaphylactic reaction upon second exposure if IgE antibodies are produced against the protein. Thus, any reduction in the amount and variety of antibodies compared to full-length flagellin is an improvement. Accordingly, after repeated introduction of flagellin or its fragments we monitored; a) efficiency of radioprotection afforded at second exposure; b) local and general allergic reactions; and c) antibody titer.

[0179] We tested the ability of AA' to protect mice that were exposed to it. A group of 20 NIH-Swiss mice were subcutaneously injected with 5 μg/mouse (0.2 mg/kg) of AA'. A second injection of a equal dose of AA' was administered after 21 (10 mice) and 28 days (another 10 mice), with the time elapsed being sufficient for formation of antibodies. The second injection of AA' was followed by 13 Gy of whole-body gamma irradiation (1 h post-injection). 100% 30-day survival was observed in both groups, as it was observed with mice that had no previous exposure to AA' (data not shown). These results show that activity of AA' is not diminished over long-term repeated administration and reaffirm its potential for multiple-use applications. Also, no local allergic reaction or anaphylaxis was observed either with flagellin or AA'.

[0180] We also performed an ELISA determination of antibody titers in order to quantify the effect that AA' has on the immune status of the organism. 96-well plates were coated with flagellin or AA', 20 mg/ml, 50 ml/well, and incubated overnight at +4° C. Blood serum samples collected from mice were added to the wells in several dilutions and incubated overnight followed by 6 hrs reaction with secondary goat anti-mouse IgG HPO-conjugate antibodies. Measurements were performed using a spectrophotometer with a 414 nm filter. The antibody titers determined for individual mice and average titers are shown in FIG. **19** and FIG. **20**.

[0181] AA' induces far lower antibody levels in mice (FIG. **19**), on the order of 0.8 mg/ml serum at 21 day and about 10% more at 28 days. Flagellin, on another hand (FIG. **20**), induces a high titer of antibodies, around 20 mg/ml, at both 21 and 28 days. Overall, this shows that removal of the hypervariable domain sharply reduces the immunogenicity of AA' compared to the original protein (approximately 25×). FIG. **19** also shows that the majority of AA'-specific antibodies are capable of recognizing flagellin. This confirms that the rational design of AA' does not produce a sizable number of new immunogenic epitopes while removing >95% of the immunogenicity of the original protein.

Example 13

Acute Toxicity Studies of Flagellin and AA'

[0182] The lethal dose of *Salmonella* flagellin is between 1 mg/kg (systemic inflammation) and 10 mg/kg (100% lethality). We subcutaneously administered increasing doses of AA' to mice (4 mice per dose group) at 0.5, 1, 2, 4 and 8 mg/kg. Due to the lower (~60%) molecular weight, 8 mg/kg of AA' correspond to a molar-equivalent dose of 13.3 mg/kg of flagellin. Several days after administration at all doses, no visible detrimental effects were observed, such as mortality, morbidity or signs of systemic inflammation such as reduced activity and fever. This shows that the pro-inflammatory effect of AA' is negligible compared to full-length flagellin, especially considering that AA' provides an efficient radioprotection at 0.2 mg/kg. The reduced toxicity may be sue to the absence of the central pro-inflammatory domain in the AA' fragment.

Example 14

Protection from Fractioned Irradiation by AA'

[0183] Repetitive irradiation within a short period of time may be common, for example, in space radiation events and in clinical radiotherapy regimens. We tested the ability of the AA' flagellin fragment to protect mice from sub-lethal (4 treatments of 3 Gy) and 100% lethal (4 treatments of 4 Gy) regimens of fractionated gamma-irradiation. Fragment AA' or saline buffer was given to NIH-Swiss female mice before every irradiation (once a day for 4 days). AA' was administered as described above for single-dose irradiation (5 μg/mouse, given subcutaneously 1 h before irradiation).

[0184] The results in FIG. **21** show that AA' provides significant protection against repetitive doses of radiation received within a short timeframe. The cumulative dose of fractionated radiation that is still compatible with 100% 30-day survival after AA' treatment is comparable to such obtained in single-dose irradiation scenarios.

Example 15

AA' Protects Normal Tissues without Compromising the Anti-Tumor Therapeutic Effect of Radiation

[0185] The ultimate test of a potential radioprotective agent in cancer treatment is tumor selectivity, its ability to protect normal tissues while providing no or little protection to the tumor. We injected 10 NIH-Swiss mice subcutaneously, in both flanks (20 tumors total), with 2×10^6 cells of syngeneic sarcoma cell line model (NIH3T3-derived and spontaneously transformed sarcoma with p53 inactivated by dominant negative inhibitor GSE56). When tumors reached the size of 5-7 mm in diameter (day 5), the mice were injected subcutaneously with 0.2 mg/kg of AA' or saline vehicle and irradiated 1 hours later with 4 Gy of total-body γ-irradiation (3×4.3 Gy=12.9 Gy total dose). Injections and irradiations were done at days 5, 6 and 7.

[0186] As the results show in FIG. **11**, AA' enhanced the radiation-induced shrinkage of tumors. By day 18, all the irradiated tumor-bearing mice died from acute radiation toxicity whereas 100% of mice that obtained both radiotherapy and AA' were both cured and survived the treatment. Similar result was obtained with another syngeneic tumor model—B16 melanoma cells (FIG. **11**, right panel). Surprisingly, even in unirradiated mice, AA' administration caused a decrease in the growth rate of tumors. This may be due to AA'-induced immunostimulating, which is known to be caused by other ligands of Toll-like receptors. These results indicate that AA' increases the tolerance of mice to radiation with no effect on the radiosensitivity of two types of tumors, thus opening the possibility of combining radiotherapy with AA' to improve treatment outcome.

Example 16

Radioprotective Mechanisms of AA' and LPS are Different

[0187] Lipopolysaccharide of gram-negative bacteria (LPS) is a ligand of another Toll-like receptor, TLR4. LPS is a strong inducer of NF-κB and a subsequent cascade of cytokines. LPS is known as a radioprotective compound, but its high toxicity makes its use unfeasible (radioprotective dose is very close to the lethal dose). One of the major mechanisms underlying the radioprotection by LPS is the activation of cyclooxygenase 2 (COX-2) that, in turn, drives the synthesis of GI-protective prostaglandins. The possibility that radioprotection by TLR5 also relies on COX-2 activity was tested by administering s.c. LPS (2 mg/kg), AA' (0.2 mg/kg') or vehicle 1 hr before irradiation of NIH-Swiss mice in combination with i.p injection of 1 mg/kg of NS398, a synthetic COX-2 inhibitor, or the corresponding vehicle. The mice were then treated with 13 Gy of total-body γ-irradiation. NS398 completely abolished LPS-mediated radioprotection but not the radioprotection of AA' (FIG. **12**). This result shows that AA' does not significantly rely on COX-2 for its activity and induces radioprotection by a mechanism different from the mechanism of LPS-mediated protection.

Example 17

AA' Protects Multiple Mouse Strains

[0188] We have extensively confirmed that AA' protects NIH-Swiss and ICR mice from radiation. To confirm that the radioprotection activity of AA' is not confined to a few mouse strains, several additional strains of mice with dissimilar origins were tested for protection by AA': 129/Sv, DBA/2 (relatively radioresistant), Balb/c (relatively radiosensitive) and Balb/c×DBA/2 F1 hybrid CD2F1. Experimental groups were injected with 0.2 mg/kg AA' 30 minutes before irradiation, while control groups were injected with vehicle (PBS).

[0189] All groups of mice (8-10 mice each, 8-12 week old females) were exposed to 10 Gy of single-dose, whole-body gamma-irradiation. Survival of mice at days 10 and 30 is shown. The results are shown in FIG. **27** as a cone graph. At 10 days, only Balb/c mice display mortality, which is drastically reduced by AA' administration (0% vs. 100% survival). At day 30, all tested strains display improved survival (0-25% vs. 50-100%) after AA' administration.

Example 18

Pharmacokinetics of AA'

[0190] Pharmacokinetic parameters (effective concentration and the duration of drug the presence in the organism) may be important for route, dose and time of drug administration. The pharmacokinetics of CBLB502 (AA') were thus tested for four common routes of injection: intravenous (i.v.), subcutaneous (s.c.), intraperitoneal (i.p.) or intramuscular (i.m.). A radioprotective dose of CBLB502 (AA'), 0.2 mg/kg, was injected in 12-15 week old ICR mice and plasma samples were collected at the specified times after injection (at least 3 mice/point). The levels of CBLB502 in plasma were measured by sandwich ELISA using known concentrations of CBLB502 spiked in the control ICR plasma for calibration. The results are shown in FIG. **28** and FIG. **29**.

[0191] The results show that the highest levels and longest persistence of CBLB502 in plasma are provided by intramuscular or intraperitoneal injection. After intramuscular injection, significant (>5 ng/ml) levels of CBLB502 are observed in mouse plasma >3 hours. Intravenous injection leads to a more rapid disappearance of CBLB502 from the bloodstream.

Example 19

Influence of AA' on Gamma-Irradiation Induced Cell Death and Growth Inhibition in A549 Cells

[0192] The A549 human lung adenocarcinoma cell line is reported to respond to flagellin by activation of NF-κB DNA-binding activity (Tallant T., et. al., *BMC Microbiol.* 2004 Aug. 23; 4:33). We decided to check whether this activation translates in the protection of cells from γ-IR in cell growth inhibition assay.

[0193] Tumor cells were seeded in wells of three 96-well plates in 3 different densities (0.5×10^4, 1×10^4 and 2×10^4 cells/well, producing single-cell, spare or semi-contact layer). After cells had attached to plastic, CBLB502 (2 μg/ml) was added to the wells of non-irradiated cells, or 15 min prior to 7 Gy or 10 Gy of gamma-irradiation. Control wells received equal volume of vehicle (PBS). All points were done in quadruplicate. 72 hours after irradiation, medium was replaced with methylene blue in 50%-methanol and the relative numbers of viable cells in wells were measured using spectrophotometer at 650 nm. The results are shown in FIG. **30**. This experiment was also repeated with fixed dose of 1×10^4 A549 cells/well, CBLB502 was added 1 hour before 5, 10 or 15 Gy of gamma-irradiation (data not shown). We observed a similar effect of flagellin in all tested experiment conditions.

[0194] Gamma-irradiation induced a dose-dependent reduction in the number of A549 cells plated at all three densities (up to 60% as compared to non-irradiated control wells). CBLB502 had no or slight effect on cell numbers, with or without gamma-irradiation. This indicates that tumor cells are not significantly protected by CBLB502 (AA') from radiation. This effect may be due to tumor cells having constitutively active NF-κB pathway or some other mechanism.

Example 20

Influence Of AA' On Gamma-Irradiation Induced Cell Death And Growth Inhibition In Multiple Cell Lines

[0195] Based on the results using A549 cells, several additional tumor cell lines (human melanoma Mel-7 and Mel-29, colon cancer HCT116, lung cancer HT1080), immortalized kidney epithelial cells (NKE) and normal mouse aortal endothelial cells (MAEC)) were tested in growth inhibition assay after 10 and 15 Gy of gamma-irradiation, as compared with intact control, with or without pretreatment with CBLB502. Cells were seeded in 96-well plates night before the treatments. CBLB502 (2 μg/ml) was added to the wells 4 hrs, 1 hr or 10 min before irradiation (all points were done in quadruplicate). 48 hours later, methylene blue staining was performed to determine the relative amount of the viable cells in the wells. All three time-points had shown the same effect (results for CBLB502 added 1 hr before irradiation are shown in FIG. **31**). The percent of growth inhibition was calculated from the OD650 in control non-irradiated wells, taken as 0% inhibition.

[0196] Both human melanoma cell lines and MAEC cells were rather resistant to gamma-irradiation and showed only slight (<20%) growth inhibition after both 10 and 15 Gy comparing with intact cells (0 Gy). NKE, HT1080 and HCT116 cells showed up to 40% of growth inhibition after gamma-irradiation. Remarkably, CBLB502 had no or only a slight inhibitory effect on tumor cell growth, irradiated or not. The experiment was repeated twice. In addition, similar results were obtained on tested lung adenocarcinoma H1299 and prostate cancer CWR22 (data not shown). This indicates that there is no significant protection provided by CBLB502 to the tumor cell lines against radiation-induced cell death.

Example 21

Influence of Irradiation and AA' on BrdU Incorporation in Small Intestinal Crypts

[0197] Besides a direct inhibition of apoptosis, temporary halt of proliferation followed by repair may be an alternative mechanism of radioprotection, and has been described for other radioprotectors such as TGF-β3 (Booth D., et. al., *Int J Cancer.* 2000 Apr. 1; 86(1):53-9). Accordingly, we decided to examine the possible influence of CBLB502 (AA') on the proliferative activity of the cells in small intestine (with and without irradiation) during the first hours after its administration (FIG. **32**). CBLB502 or PBS was injected i.p. in mice, followed after 30 min by 15 Gy irradiation (if used). 2 hr after injection (1.5 hr after irradiation if it was applied), BrdU was injected intraperitoneally. Samples of small intestine were obtained after additional 1.5 hours.

[0198] Without irradiation, BrdU was incorporated at high levels in the nuclei of cells in the intestinal crypts of untreated NIH-Swiss mice (FIG. **32**, top left), whereas DNA synthesis (as measured by BrdU incorporation) was nearly undetectable in the crypts of CBLB502-treated mice (FIG. **32**, top right). In vehicle-treated irradiated mice, the incorporation of BrdU was lower than in control mice. Importantly, the level of BrdU incorporation was strongly reduced by CBLB502, possibly indicating quick (S phase) growth arrest, as opposed to later (G2 phase) irradiation-induced growth arrest. Therefore, cytostatic activity of CBLB502 or flagellin may be an additional mechanism of radioprotection of small intestine.

Example 22

Duration of AA'-Mediated Growth Arrest and Reduced BrdU Incorporation

[0199] We next determined the duration of the CBLB502-induced growth arrest in small intestine. CBLB502 or PBS was injected i.p. in mice, BrdU was injected 1 or 4 hours later and samples of small intestine were obtained after additional 1.5 hours from several mice (samples from three mice are shown) (FIG. **33**).

[0200] Incorporation of BrdU in intestine was reduced as compared to control if BrdU was injected after 1 hour (as it was shown in the previous experiment where BrdU was injected after 2 hr). NIH-Swiss, ICR and Balb/c mice displayed a similar degree of CBLB502-mediated block of BrdU incorporation (Balb/c samples are shown in FIG. **33**). If BrdU was injected 4 hr after injection of CBLB502, the levels of incorporation/DNA synthesis were even higher than in control. This indicates that inhibition of intestinal stem cell proliferation by CBLB502 may be temporary and may be quickly resolved (by 4 hours), followed by a period of increased proliferation (possibly due to the partial synchronization of cells).

Example 23

Influence of AA' on BrdU Incorporation in Colonic Crypts

[0201] The colon is much less radiosensitive than small intestine. To further examine the relationship between reduced proliferation in the small intestine and radioprotection, we determined the effect of CBLB502 on BrdU incorporation in the colon. CBLB502 or PBS was injected i.p. in mice, BrdU was injected 1 hour later and samples of small intestine were obtained after additional 1.5 hours (FIG. **34**).

[0202] Unlike in the small intestine, CBLB502 has no effect on BrdU incorporation in colon. This is surprising since TLR5 is plentiful in both organs. The difference in effects may be due to the higher amount of symbiotic bacteria in the colon, which may mask the effect of additional TLR5 signaling induced by CBLB502.

Example 24

Comparison of Radioprotective Potential by Route of Administration

[0203] We next tested radioprotection provided by FliC flagellin administered via several routes: intravenous (i.v.), intraperitoneal (i.p.), intramuscular (i.m.), subcutaneous (s.c.) and gavage. For parenteral (non-gavage) routes, mice were injected with 0.2 mg/kg of FliC flagellin dissolved in PBS or vehicle, followed 1 hr later by 13 Gy irradiation. In gavage delivery experiment, 5 mice were given to swallow an increased dose (50 μg) of FliC in 50 μl of PBS 1 h before 13 Gy gamma-irradiation. Both experiments were done in 8-10 week old female NIH-Swiss mice, 5-10 mice/group.

[0204] All tested routes besides gavage afforded similar degree of protection, leading to 85-90% 30-day survival of mice (data not shown). No protection against radiation was provided by gavage delivery, which may be due to digestion of the protein by the gastrointestinal environment. In addition, flagellin receptor, TLR5, is absent on the luminal side of intestinal epithelium that is exposed to intestinal contents (Gewirtz A T., et. al., *J Immunol.* 2001 Aug. 15; 167(4):1882-5)

Example 25

Effect of AA' on the Morphology of Small Intestine

[0205] Flagellin (and CBLB502) may induce NF-κB activity via binding to TLR5. Accordingly, CBLB502-mediated radioprotection may be dependent on the presence and activity of TLR5. MOLF/Ei mice are a known natural model of TLR5 deficiency (Sebastiani G., et. al., *Genomics*. 2000 Mar. 15; 64(3):230-40). To verify that CBLB502-mediated radioprotection is indeed TLR5-dependent, we tested the protection of small intestine from radiation by CBLB502 in MOLF/Ei and NIH-Swiss mice (FIG. **35**). Both strains of mice were given 0.2 mg/kg CBLB502 (AA') or PBS 0.5 hr before 15 Gy of gamma-irradiation. The samples of small intestine were obtained 4 days after irradiation, stained by hematoxylin-eosin and subjected to pathomorphological analysis.

[0206] In NIH-Swiss (TLR5 wild type) mice, CBLB502 pretreatment led to preservation of intestinal morphology (long villae, normal crypts) as compared to short villae and disappearance of normal crypt structure in PBS-treated mice. Meanwhile, in TLR5-deficient MOLF/Ei mice the administration of CBLB502 had no improving effect on intestinal morphology after 15 Gy of gamma-irradiation: short villae and destruction of the normal crypt structure was observed, with or without CBLB502. This indicates that the presence of TLR5 may be necessary for CBLB502-mediated radioprotection in the small intestine.

Example 26

Flagellin Derivatives

[0207] Additional flagellin variants were produced based on the domain structure shown in FIG. **36**. The flagellin variants were then tested along with some of the variants discussed above for NF-κB stimulating activity (Table 3). A549 cells were left unstimulated or stimulated with TNF (10 ng/ml) as indicated or 1 μg/ml of purified flagellin or the various indicated flagellin derivatives for 45 min and whole cell extracts prepared as described in Example 7. EMSA assays were preformed and the NF-κB DNA-protein complex detected as described in Example 7.

TABLE 3

Name	N-terminal	C-terminal	DNA	Protein	NF-κB Stimulation
AA'	1-176	402-505	SEQ ID NO: 7	SEQ ID NO: 8	Yes
AB'	1-176	402-450	SEQ ID NO: 9	SEQ ID NO: 10	Yes
BA'	54-176	402-505	SEQ ID NO: 11	SEQ ID NO: 12	Yes
BB'	54-176	402-450	SEQ ID NO: 13	SEQ ID NO: 14	No
CA'	54-100	402-505	SEQ ID NO: 15	SEQ ID NO: 16	No
CB'	54-100	402-450	SEQ ID NO: 17	SEQ ID NO: 18	No
AA'n1-170	1-170	402-505	SEQ ID NO: 29	SEQ ID NO: 30	Yes
AA'n54-170	54-170	402-505	SEQ ID NO: 31	SEQ ID NO: 32	Yes
AB'n1-170	1-170	402-450	SEQ ID NO: 37	SEQ ID NO: 38	Yes
AA'n1-163	1-163	402-505	SEQ ID NO: 33	SEQ ID NO: 34	Yes
AA'n54-163	54-163	402-505	SEQ ID NO: 35	SEQ ID NO: 36	Yes
AB'n1-163	1-163	402-450	SEQ ID NO: 39	SEQ ID NO: 40	Yes
AA'n1-129	1-129	402-505	SEQ ID NO: 41	SEQ ID NO: 42	Yes
AA'n54-129	54-129	402-505	SEQ ID NO: 43	SEQ ID NO: 44	Yes
AB'n1-129	1-129	402-450	SEQ ID NO: 45	SEQ ID NO: 46	untested
AB'n54-129	54-129	402-450	SEQ ID NO: 47	SEQ ID NO: 48	Untested
AA'n1-100	1-100	402-505	SEQ ID NO: 49	SEQ ID NO: 50	untested
AB'n1-100	1-100	402-450	SEQ ID NO: 51	SEQ ID NO: 52	untested
AA'n1-70	1-70	402-505	SEQ ID NO: 53	SEQ ID NO: 54	No
AB'n1-70	1-70	402-450	SEQ ID NO: 55	SEQ ID NO: 56	No
A	1-176		SEQ ID NO: 19	SEQ ID NO: 20	No
B	54-176		SEQ ID NO: 21	SEQ ID NO: 22	No
C	54-100		SEQ ID NO: 23	SEQ ID NO: 24	No
GST-A'		402-505	SEQ ID NO: 25	SEQ ID NO: 26	No
GST-B'		402-450	SEQ ID NO: 27	SEQ ID NO: 28	No

[0208] The results in Table 3 indicate that flagellin variants with at least one polymerization domain (aa1-50 or aa 450-505) that linked to domains contained within the amino-terminal region (aa 1-176) and those of the carboxy terminus (aa 402-505) are capable of stimulating NF-κB and would thus be expected to be radioprotectors. Physical linkage of the recognition domains may be required for activity as domains supplied unlinked in trans fail to activate NF-κB. As an alternative to the linking of the domains in a single polypeptide, the domains may be linked using a linker, which is a molecule that is used to join two molecules. The linker may be capable of forming covalent bonds or high-affinity non-covalent bonds to both molecules. Suitable linkers are well known to those of ordinary skill in the art and include, but are not limited to, straight or branched-chain carbon linkers, heterocyclic carbon linkers, or peptide linkers. The linkers may be joined to the constituent amino acids through their side groups (e.g., through a disulfide linkage to cysteine).

[0209] The region between amino acids 163 and 176 may be required for activity when the carboxyl polymerization domain (aa 450-505) is absent. Since this region is dispensable for activity when the carboxyl polymerization domain is present it may be involved in stabilizing the derivative. The region between amino acids 70 and 129 may be important for activation and may be involved in derivative recognition. The region between amino acids 402 and 450 may also be required for activity. The domains identified above are located within three large α-helices (located within amino acids 54-129 and 402-450) and, to produce an active derivative, may need to form a ring-like structure (with or without polymerization domain).

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Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

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                85                  90                  95

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        195                 200                 205

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    210                 215                 220

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225                 230                 235                 240

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                245                 250                 255

Thr Ala Glu Ala Lys Ala Ile Ala Gly Ala Ile Lys Gly Gly Lys Glu
            260                 265                 270

Gly Asp Thr Phe Asp Tyr Lys Gly Val Thr Phe Thr Ile Asp Thr Lys
        275                 280                 285

Thr Gly Asp Asp Gly Asn Gly Lys Val Ser Thr Thr Ile Asn Gly Glu
    290                 295                 300

Lys Val Thr Leu Thr Val Ala Asp Ile Ala Thr Gly Ala Ala Asp Val
305                 310                 315                 320

Asn Ala Ala Thr Leu Gln Ser Ser Lys Asn Val Tyr Thr Ser Val Val
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Asn Gly Gln Phe Thr Phe Asp Asp Lys Thr Lys Asn Glu Ser Ala Lys
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Ser Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala
405 410 415

Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val
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Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr
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Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile
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ctagactcca tgggtacatt aatcaatgaa gacgctgccg cagccaagaa aagtaccgct 720

aacccactgg cttcaattga ttctgcattg tcaaaagtgg acgcagttcg ttcttctctg 780

ggggcaattc aaaaccgttt tgattcagcc attaccaacc ttggcaatac ggtaaccaat 840

ctgaactccg cgcgtagccg tatcgaagat gctgactatg caacggaagt ttctaatatg 900

tctaaagcgc agattctgca gcaggctggt acttccgttc tggcgcaggc taaccaggtt 960

ccgcaaaacg tcctctcttt actgcgttag 990

<210> SEQ ID NO 8
<211> LENGTH: 329
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 8

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val
        195                 200                 205
```

-continued

```
Asn Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met
    210                 215                 220

Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala
225                 230                 235                 240

Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val
                245                 250                 255

Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr
            260                 265                 270

Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile
        275                 280                 285

Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln
    290                 295                 300

Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val
305                 310                 315                 320

Pro Gln Asn Val Leu Ser Leu Leu Arg
                325


<210> SEQ ID NO 9
<211> LENGTH: 825
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 9

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac     360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc     420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct     480

aatcagactc aatttaacgg tgttaaagtc ctctctcagg acaaccagat gaaaatccag     540

gttggtgcta acgatggtga aaccattacc atcgatctgc aaaaaattga tgtgaaaagc     600

cttggccttg atgggttcaa tgttaattcc ccgggaattt ccggtggtgg tggtggaatt     660

ctagactcca tgggtacatt aatcaatgaa gacgctgccg cagccaagaa aagtaccgct     720

aacccactgg cttcaattga ttctgcattg tcaaaagtgg acgcagttcg ttcttctctg     780

ggggcaattc aaaaccgttt tgattcagcc attaccaacc tttag                     825


<210> SEQ ID NO 10
<211> LENGTH: 274
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 10

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
```

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```
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val
        195                 200                 205

Asn Ser Pro Gly Ile Ser Gly Gly Gly Gly Ile Leu Asp Ser Met
    210                 215                 220

Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala
225                 230                 235                 240

Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val
                245                 250                 255

Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr
            260                 265                 270

Asn Leu


<210> SEQ ID NO 11
<211> LENGTH: 831
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 11

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg     300

gaagaaatcg atcgcgtttc taatcagact caatttaacg gtgttaaagt cctctctcag     360

gacaaccaga tgaaaatcca ggttggtgct aacgatggtg aaaccattac catcgatctg     420

caaaaaattg atgtgaaaag ccttggcctt gatgggttca atgttaattc cccgggaatt     480

tccggtggtg gtggtggaat tctagactcc atgggtacat taatcaatga agacgctgcc     540

gcagccaaga aaagtaccgc taacccactg gcttcaattg attctgcatt gtcaaaagtg     600

gacgcagttc gttcttctct gggggcaatt caaaaccgtt ttgattcagc cattaccaac     660
```

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```
cttggcaata cggtaaccaa tctgaactcc gcgcgtagcc gtatcgaaga tgctgactat    720

gcaacggaag tttctaatat gtctaaagcg cagattctgc agcaggctgg tacttccgtt    780

ctggcgcagg ctaaccaggt tccgcaaaac gtcctctctt tactgcgtta g            831
```

<210> SEQ ID NO 12
<211> LENGTH: 276
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 12

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
                85                  90                  95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Thr Gln Phe
            100                 105                 110

Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln Met Lys Ile Gln Val
        115                 120                 125

Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp Leu Gln Lys Ile Asp
    130                 135                 140

Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val Asn Ser Pro Gly Ile
145                 150                 155                 160

Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn
                165                 170                 175

Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser
            180                 185                 190

Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser Ser Leu Gly
        195                 200                 205

Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu Gly Asn Thr
    210                 215                 220

Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu Asp Ala Asp Tyr
225                 230                 235                 240

Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln Ile Leu Gln Gln Ala
                245                 250                 255

Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro Gln Asn Val Leu
            260                 265                 270

Ser Leu Leu Arg
        275
```

<210> SEQ ID NO 13
<211> LENGTH: 666
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 13

-continued

```
atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg     300

gaagaaatcg atcgcgtttc taatcagact caatttaacg gtgttaaagt cctctctcag     360

gacaaccaga tgaaaatcca ggttggtgct aacgatggtg aaaccattac catcgatctg     420

caaaaaattg atgtgaaaag ccttggcctt gatgggttca atgttaattc cccgggaatt     480

tccggtggtg gtggtggaat tctagactcc atgggtacat taatcaatga agacgctgcc     540

gcagccaaga aaagtaccgc taacccactg gcttcaattg attctgcatt gtcaaaagtg     600

gacgcagttc gttcttctct gggggcaatt caaaaccgtt ttgattcagc cattaccaac     660

ctttag                                                                666
```

```
<210> SEQ ID NO 14
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 14

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
                85                  90                  95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Thr Gln Phe
            100                 105                 110

Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln Met Lys Ile Gln Val
        115                 120                 125

Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp Leu Gln Lys Ile Asp
    130                 135                 140

Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val Asn Ser Pro Gly Ile
145                 150                 155                 160

Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn
                165                 170                 175

Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser
            180                 185                 190

Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser Ser Leu Gly
        195                 200                 205

Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu
    210                 215                 220

<210> SEQ ID NO 15
```

-continued

```
<211> LENGTH: 603
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 15

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

tccccgggaa tttccggtgg tggtggtgga attctagact ccatgggtac attaatcaat     300

gaagacgctg ccgcagccaa gaaaagtacc gctaacccac tggcttcaat tgattctgca     360

ttgtcaaaag tggacgcagt tcgttcttct ctgggggcaa ttcaaaaccg ttttgattca     420

gccattacca accttggcaa tacggtaacc aatctgaact ccgcgcgtag ccgtatcgaa     480

gatgctgact atgcaacgga agtttctaat atgtctaaag cgcagattct gcagcaggct     540

ggtacttccg ttctggcgca ggctaaccag gttccgcaaa acgtcctctc tttactgcgt     600

tag                                                                   603


<210> SEQ ID NO 16
<211> LENGTH: 200
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 16

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly
                85                  90                  95

Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn
            100                 105                 110

Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg
        115                 120                 125

Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn
    130                 135                 140

Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu
145                 150                 155                 160

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln Ile
                165                 170                 175

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro
            180                 185                 190

Gln Asn Val Leu Ser Leu Leu Arg
        195                 200
```

-continued

```
<210> SEQ ID NO 17
<211> LENGTH: 438
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 17

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

tccccgggaa tttccggtgg tggtggtgga attctagact ccatgggtac attaatcaat     300

gaagacgctg ccgcagccaa gaaaagtacc gctaacccac tggcttcaat tgattctgca     360

ttgtcaaaag tggacgcagt tcgttcttct ctgggggcaa ttcaaaaccg ttttgattca     420

gccattacca acctttag                                                   438


<210> SEQ ID NO 18
<211> LENGTH: 145
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 18

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly
                85                  90                  95

Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn
            100                 105                 110

Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg
        115                 120                 125

Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn
    130                 135                 140

Leu
145


<210> SEQ ID NO 19
<211> LENGTH: 639
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 19

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240
```

-continued

```
caggcgattg ctaaccgctt cacttctaat atcaaaggtc tgactcaggc ttcccgtaac    300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac    360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc    420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct    480

aatcagactc aatttaacgg tgttaaagtc ctgtctcagg acaaccagat gaaaatccag    540

gttggtgcta acgatggtga aaccattacc atcgatctgc aaaaaattga tgtgaaaagc    600

cttggccttg atgggttcaa tgttaattcc ccgggatga                           639


<210> SEQ ID NO 20
<211> LENGTH: 212
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 20

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val
        195                 200                 205

Asn Ser Pro Gly
    210


<210> SEQ ID NO 21
<211> LENGTH: 480
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 21

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa     60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggt    120
```

-continued

```
ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt    180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact    240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg    300

gaagaaatcg atcgcgtttc taatcagact caatttaacg gtgttaaagt cctgtctcag    360

gacaaccaga tgaaaatcca ggttggtgct aacgatggtg aaaccattac catcgatctg    420

caaaaaattg atgtgaaaag ccttggcctt gatgggttca atgttaattc cccgggatga    480
```

<210> SEQ ID NO 22
<211> LENGTH: 159
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 22

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
                85                  90                  95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Thr Gln Phe
            100                 105                 110

Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln Met Lys Ile Gln Val
        115                 120                 125

Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp Leu Gln Lys Ile Asp
    130                 135                 140

Val Lys Ser Leu Gly Leu Asp Gly Phe Asn Val Asn Ser Pro Gly
145                 150                 155
```

<210> SEQ ID NO 23
<211> LENGTH: 252
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 23

```
atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa     60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggt    120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt    180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact    240

tccccgggat ga                                                        252
```

<210> SEQ ID NO 24
<211> LENGTH: 83
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 24

-continued

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Ser Pro Gly


<210> SEQ ID NO 25
<211> LENGTH: 1038
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 25

atgtccccta tactaggtta ttggaaaatt aagggccttg tgcaacccac tcgacttctt      60

ttggaatatc ttgaagaaaa atatgaagag catttgtatg agcgcgatga aggtgataaa     120

tggcgaaaca aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat     180

ggtgatgtta aattaacaca gtctatggcc atcatacgtt atatagctga caagcacaac     240

atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg     300

gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt     360

gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa     420

acatatttaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat     480

gttgttttat acatggaccc aatgtgcctg gatgcgttcc caaaattagt ttgttttaaa     540

aaacgtattg aagctatccc acaaattgat aagtacttga aatccagcaa gtatatagca     600

tggcctttgc agggctggca agccacgttt ggtggtggcg accatcctcc aaaatcggat     660

ctggttccgc gtggatcccc gggaatttcc ggtggtggtg gtggaattct agactccatg     720

ggtacattaa tcaatgaaga cgctgccgca gccaagaaaa gtaccgctaa cccactggct     780

tcaattgatt ctgcattgtc aaaagtggac gcagttcgtt cttctctggg ggcaattcaa     840

aaccgttttg attcagccat taccaacctt ggcaatacgg taaccaatct gaactccgcg     900

cgtagccgta tcgaagatgc tgactatgca acggaagttt ctaatatgtc taaagcgcag     960

attctgcagc aggctggtac ttccgttctg gcgcaggcta accaggttcc gcaaaacgtc    1020

ctctctttac tgcgttag                                                  1038


<210> SEQ ID NO 26
<211> LENGTH: 345
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 26

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30
```

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```
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

Gly Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met
225                 230                 235                 240

Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala
                245                 250                 255

Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val
            260                 265                 270

Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr
        275                 280                 285

Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile
    290                 295                 300

Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln
305                 310                 315                 320

Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val
                325                 330                 335

Pro Gln Asn Val Leu Ser Leu Leu Arg
            340                 345


<210> SEQ ID NO 27
<211> LENGTH: 873
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 27

atgtccccta tactaggtta ttggaaaatt aagggccttg tgcaacccac tcgacttctt      60

ttggaatatc ttgaagaaaa atatgaagag catttgtatg agcgcgatga aggtgataaa     120

tggcgaaaca aaaagtttga attgggtttg gagtttccca atcttcctta ttatattgat     180

ggtgatgtta aattaacaca gtctatggcc atcatacgtt atatagctga caagcacaac     240
```

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```
atgttgggtg gttgtccaaa agagcgtgca gagatttcaa tgcttgaagg agcggttttg    300

gatattagat acggtgtttc gagaattgca tatagtaaag actttgaaac tctcaaagtt    360

gattttctta gcaagctacc tgaaatgctg aaaatgttcg aagatcgttt atgtcataaa    420

acatatttaa atggtgatca tgtaacccat cctgacttca tgttgtatga cgctcttgat    480

gttgttttat acatggaccc aatgtgcctg gatgcgttcc caaaattagt ttgttttaaa    540

aaacgtattg aagctatccc acaaattgat aagtacttga aatccagcaa gtatatagca    600

tggcctttgc agggctggca agccacgttt ggtggtggcg accatcctcc aaaatcggat    660

ctggttccgc gtggatcccc gggaatttcc ggtggtggtg gtggaattct agactccatg    720

ggtacattaa tcaatgaaga cgctgccgca gccaagaaaa gtaccgctaa cccactggct    780

tcaattgatt ctgcattgtc aaaagtggac gcagttcgtt cttctctggg ggcaattcaa    840

aaccgttttg attcagccat taccaacctt tag                                 873
```

```
<210> SEQ ID NO 28
<211> LENGTH: 290
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 28

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1               5                   10                  15

Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
            20                  25                  30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
        35                  40                  45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
    50                  55                  60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65                  70                  75                  80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
                85                  90                  95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
            100                 105                 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
        115                 120                 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
    130                 135                 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145                 150                 155                 160

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
                165                 170                 175

Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
            180                 185                 190

Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
        195                 200                 205

Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
    210                 215                 220

Gly Ser Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met
225                 230                 235                 240

Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala
```

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                245                 250                 255

Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val
            260                 265                 270

Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr
        275                 280                 285

Asn Leu
    290


<210> SEQ ID NO 29
<211> LENGTH: 972
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 29

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac     360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc     420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct     480

aatcagactc aatttaacgg tgttaaagtc ctctctcagg acaaccagat gaaaatccag     540

gttggtgcta acgatggtga aaccattacc atcgatctgc aaaaaattga tgtgaaaagc     600

cttggcctta tcccgggaat ttccggtggt ggtggtggaa ttctagactc catgggtaca     660

ttaatcaatg aagacgctgc cgcagccaag aaaagtaccg ctaacccact ggcttcaatt     720

gattctgcat tgtcaaaagt ggacgcagtt cgttcttctc tgggggcaat tcaaaaccgt     780

tttgattcag ccattaccaa ccttggcaat acggtaacca atctgaactc cgcgcgtagc     840

cgtatcgaag atgctgacta tgcaacggaa gtttctaata tgtctaaagc gcagattctg     900

cagcaggctg gtacttccgt tctggcgcag gctaaccagg ttccgcaaaa cgtcctctct     960

ttactgcgtt ag                                                         972


<210> SEQ ID NO 30
<211> LENGTH: 323
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 30

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80
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```
Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Ile Pro Gly Ile Ser
        195                 200                 205

Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn Glu
    210                 215                 220

Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile
225                 230                 235                 240

Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser Ser Leu Gly Ala
                245                 250                 255

Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu Gly Asn Thr Val
            260                 265                 270

Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu Asp Ala Asp Tyr Ala
        275                 280                 285

Thr Glu Val Ser Asn Met Ser Lys Ala Gln Ile Leu Gln Gln Ala Gly
    290                 295                 300

Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro Gln Asn Val Leu Ser
305                 310                 315                 320

Leu Leu Arg


<210> SEQ ID NO 31
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 31

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg     300

gaagaaatcg atcgcgtttc taatcagact caatttaacg gtgttaaagt cctctctcag     360

gacaaccaga tgaaaatcca ggttggtgct aacgatggtg aaaccattac catcgatctg     420

caaaaaattg atgtgaaaag ccttggcctt atcccgggaa tttccggtgg tggtggtgga     480

attctagact ccatgggtac attaatcaat gaagacgctg ccgcagccaa gaaaagtacc     540

gctaacccac tggcttcaat tgattctgca ttgtcaaaag tggacgcagt tcgttcttct     600

ctgggggcaa ttcaaaaccg ttttgattca gccattacca accttggcaa tacggtaacc     660
```

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```
aatctgaact ccgcgcgtag ccgtatcgaa gatgctgact atgcaacgga agtttctaat    720

atgtctaaag cgcagattct gcagcaggct ggtacttccg ttctggcgca ggctaaccag    780

gttccgcaaa acgtcctctc tttactgcgt tag                                 813
```

<210> SEQ ID NO 32
<211> LENGTH: 270
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 32

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
                85                  90                  95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Thr Gln Phe
            100                 105                 110

Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln Met Lys Ile Gln Val
        115                 120                 125

Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp Leu Gln Lys Ile Asp
    130                 135                 140

Val Lys Ser Leu Gly Leu Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly
145                 150                 155                 160

Ile Leu Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala
                165                 170                 175

Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser
            180                 185                 190

Lys Val Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe
        195                 200                 205

Asp Ser Ala Ile Thr Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser
    210                 215                 220

Ala Arg Ser Arg Ile Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn
225                 230                 235                 240

Met Ser Lys Ala Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala
                245                 250                 255

Gln Ala Asn Gln Val Pro Gln Asn Val Leu Ser Leu Leu Arg
            260                 265                 270
```

<210> SEQ ID NO 33
<211> LENGTH: 951
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 33

```
atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa     60
```

-continued

```
atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca    120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc    180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc    240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac    300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac    360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc    420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct    480

aatcagactc aatttaacgg tgttaaagtc ctctctcagg acaaccagat gaaaatccag    540

gttggtgcta acgatggtga aaccattacc atcgatctgc aaaaaattat cccgggaatt    600

tccggtggtg gtggtggaat tctagactcc atgggtacat taatcaatga agacgctgcc    660

gcagccaaga aaagtaccgc taacccactg gcttcaattg attctgcatt gtcaaaagtg    720

gacgcagttc gttcttctct gggggcaatt caaaaccgtt ttgattcagc cattaccaac    780

cttggcaata cggtaaccaa tctgaactcc gcgcgtagcc gtatcgaaga tgctgactat    840

gcaacggaag tttctaatat gtctaaagcg cagattctgc agcaggctgg tacttccgtt    900

ctggcgcagg ctaaccaggt tccgcaaaac gtcctctctt tactgcgtta g             951


<210> SEQ ID NO 34
<211> LENGTH: 316
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 34

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu
        195                 200                 205
```

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```
Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys
    210                 215                 220

Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val
225                 230                 235                 240

Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser
                245                 250                 255

Ala Ile Thr Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg
            260                 265                 270

Ser Arg Ile Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser
        275                 280                 285

Lys Ala Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala
    290                 295                 300

Asn Gln Val Pro Gln Asn Val Leu Ser Leu Leu Arg
305                 310                 315


<210> SEQ ID NO 35
<211> LENGTH: 792
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 35

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg     300

gaagaaatcg atcgcgtttc taatcagact caatttaacg gtgttaaagt cctctctcag     360

gacaaccaga tgaaaatcca ggttggtgct aacgatggtg aaaccattac catcgatctg     420

caaaaaatta tcccgggaat ttccggtggt ggtggtggaa ttctagactc catgggtaca     480

ttaatcaatg aagacgctgc cgcagccaag aaaagtaccg ctaacccact ggcttcaatt     540

gattctgcat tgtcaaaagt ggacgcagtt cgttcttctc tgggggcaat tcaaaaccgt     600

tttgattcag ccattaccaa ccttggcaat acggtaacca atctgaactc cgcgcgtagc     660

cgtatcgaag atgctgacta tgcaacggaa gtttctaata tgtctaaagc gcagattctg     720

cagcaggctg gtacttccgt tctggcgcag gctaaccagg ttccgcaaaa cgtcctctct     780

ttactgcgtt ag                                                         792


<210> SEQ ID NO 36
<211> LENGTH: 263
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 36

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
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```
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
                85                  90                  95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Thr Gln Phe
            100                 105                 110

Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln Met Lys Ile Gln Val
        115                 120                 125

Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp Leu Gln Lys Ile Ile
    130                 135                 140

Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr
145                 150                 155                 160

Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro
                165                 170                 175

Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser
            180                 185                 190

Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu
        195                 200                 205

Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu Asp
    210                 215                 220

Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln Ile Leu
225                 230                 235                 240

Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro Gln
                245                 250                 255

Asn Val Leu Ser Leu Leu Arg
            260


<210> SEQ ID NO 37
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 37

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac     360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc     420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct     480

aatcagactc aatttaacgg tgttaaagtc ctctctcagg acaaccagat gaaaatccag     540

gttggtgcta acgatggtga aaccattacc atcgatctgc aaaaaattga tgtgaaaagc     600

cttggcctta tcccgggaat ttccggtggt ggtggtggaa ttctagactc catgggtaca     660

ttaatcaatg aagacgctgc cgcagccaag aaaagtaccg ctaacccact ggcttcaatt     720

gattctgcat tgtcaaaagt ggacgcagtt cgttcttctc tgggggcaat tcaaaaccgt     780

tttgattcag ccattaccaa cctttag                                         807
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<210> SEQ ID NO 38
<211> LENGTH: 268
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 38

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Ile Pro Gly Ile Ser
        195                 200                 205

Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn Glu
    210                 215                 220

Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile
225                 230                 235                 240

Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser Ser Leu Gly Ala
                245                 250                 255

Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu
            260                 265


<210> SEQ ID NO 39
<211> LENGTH: 786
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 39

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240
```

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```
caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac    300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac    360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc    420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct    480

aatcagactc aatttaacgg tgttaaagtc ctctctcagg acaaccagat gaaaatccag    540

gttggtgcta acgatggtga aaccattacc atcgatctgc aaaaaattat cccgggaatt    600

tccggtggtg gtggtggaat tctagactcc atgggtacat taatcaatga agacgctgcc    660

gcagccaaga aaagtaccgc taacccactg gcttcaattg attctgcatt gtcaaaagtg    720

gacgcagttc gttcttctct gggggcaatt caaaaccgtt ttgattcagc cattaccaac    780

ctttag                                                               786
```

```
<210> SEQ ID NO 40
<211> LENGTH: 261
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 40

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln
                165                 170                 175

Met Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp
            180                 185                 190

Leu Gln Lys Ile Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu
        195                 200                 205

Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys
    210                 215                 220

Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val
225                 230                 235                 240

Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser
                245                 250                 255
```

-continued

```
Ala Ile Thr Asn Leu
            260


<210> SEQ ID NO 41
<211> LENGTH: 849
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 41

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac     360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc     420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct     480

aatcagatcc cgggaatttc cggtggtggt ggtggaattc tagactccat gggtacatta     540

atcaatgaag acgctgccgc agccaagaaa agtaccgcta acccactggc ttcaattgat     600

tctgcattgt caaaagtgga cgcagttcgt tcttctctgg gggcaattca aaaccgtttt     660

gattcagcca ttaccaacct tggcaatacg gtaaccaatc tgaactccgc gcgtagccgt     720

atcgaagatg ctgactatgc aacggaagtt tctaatatgt ctaaagcgca gattctgcag     780

caggctggta cttccgttct ggcgcaggct aaccaggttc cgcaaaacgt cctctcttta     840

ctgcgttag                                                             849


<210> SEQ ID NO 42
<211> LENGTH: 282
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 42

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140
```

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```
Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser
                165                 170                 175

Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr
            180                 185                 190

Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala
        195                 200                 205

Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile
    210                 215                 220

Thr Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg
225                 230                 235                 240

Ile Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala
                245                 250                 255

Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln
            260                 265                 270

Val Pro Gln Asn Val Leu Ser Leu Leu Arg
        275                 280


<210> SEQ ID NO 43
<211> LENGTH: 690
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 43

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg     300

gaagaaatcg atcgcgtttc taatcagatc ccgggaattt ccggtggtgg tggtggaatt     360

ctagactcca tgggtacatt aatcaatgaa gacgctgccg cagccaagaa aagtaccgct     420

aacccactgg cttcaattga ttctgcattg tcaaaagtgg acgcagttcg ttcttctctg     480

ggggcaattc aaaaccgttt tgattcagcc attaccaacc ttggcaatac ggtaaccaat     540

ctgaactccg cgcgtagccg tatcgaagat gctgactatg caacggaagt ttctaatatg     600

tctaaagcgc agattctgca gcaggctggt acttccgttc tggcgcaggc taaccaggtt     660

ccgcaaaacg tcctctcttt actgcgttag                                      690


<210> SEQ ID NO 44
<211> LENGTH: 229
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 44

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
        35                  40                  45
```

-continued

```
Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
    50                  55                  60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65                  70                  75                  80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
                85                  90                  95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Ile Pro Gly
            100                 105                 110

Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile
        115                 120                 125

Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala
    130                 135                 140

Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser Ser Leu
145                 150                 155                 160

Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu Gly Asn
                165                 170                 175

Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu Asp Ala Asp
            180                 185                 190

Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln Ile Leu Gln Gln
        195                 200                 205

Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro Gln Asn Val
    210                 215                 220

Leu Ser Leu Leu Arg
225
```

<210> SEQ ID NO 45
<211> LENGTH: 684
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 45

```
atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac     360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta acgggactaa ctctgattcc     420

gatctgaaat ctatccagga tgaaattcag caacgtctgg aagaaatcga tcgcgtttct     480

aatcagatcc cgggaatttc cggtggtggt ggtggaattc tagactccat gggtacatta     540

atcaatgaag acgctgccgc agccaagaaa agtaccgcta acccactggc ttcaattgat     600

tctgcattgt caaaagtgga cgcagttcgt tcttctctgg gggcaattca aaaccgtttt     660

gattcagcca ttaccaacct ttag                                            684
```

<210> SEQ ID NO 46
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 46

-continued

```
Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser
    130                 135                 140

Ile Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser
145                 150                 155                 160

Asn Gln Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser
                165                 170                 175

Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr
            180                 185                 190

Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala
        195                 200                 205

Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile
    210                 215                 220

Thr Asn Leu
225
```

<210> SEQ ID NO 47
<211> LENGTH: 525
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 47

```
atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccgt tcacttctaa tatcaaaggc     120

ctgactcagg cttcccgtaa cgctaacgac ggcatttcta ttgcgcagac cactgaaggt     180

gcgctgaatg aaatcaacaa caacctgcag cgtgtgcgtg agttgtctgt tcaggccact     240

aacgggacta actctgattc cgatctgaaa tctatccagg atgaaattca gcaacgtctg     300

gaagaaatcg atcgcgtttc taatcagatc ccgggaattt ccggtggtgg tggtggaatt     360

ctagactcca tgggtacatt aatcaatgaa gacgctgccg cagccaagaa aagtaccgct     420

aacccactgg cttcaattga ttctgcattg tcaaaagtgg acgcagttcg ttcttctctg     480

ggggcaattc aaaaccgttt tgattcagcc attaccaacc tttag                     525
```

<210> SEQ ID NO 48
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

-continued

<400> SEQUENCE: 48

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1 5 10 15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
20 25 30

Pro Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ser Arg Asn Ala
35 40 45

Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ala Leu Asn Glu
50 55 60

Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser Val Gln Ala Thr
65 70 75 80

Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile Gln Asp Glu Ile
85 90 95

Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn Gln Ile Pro Gly
100 105 110

Ile Ser Gly Gly Gly Gly Gly Ile Leu Asp Ser Met Gly Thr Leu Ile
115 120 125

Asn Glu Asp Ala Ala Ala Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala
130 135 140

Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg Ser Ser Leu
145 150 155 160

Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn Leu
165 170

<210> SEQ ID NO 49
<211> LENGTH: 762
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 49

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa 60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca 120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc 180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc 240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac 300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac 360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta tcccgggaat ttccggtggt 420

ggtggtggaa ttctagactc catgggtaca ttaatcaatg aagacgctgc cgcagccaag 480

aaaagtaccg ctaacccact ggcttcaatt gattctgcat tgtcaaaagt ggacgcagtt 540

cgttcttctc tgggggcaat tcaaaaccgt tttgattcag ccattaccaa ccttggcaat 600

acggtaacca atctgaactc cgcgcgtagc cgtatcgaag atgctgacta tgcaacggaa 660

gtttctaata tgtctaaagc gcagattctg cagcaggctg gtacttccgt tctggcgcag 720

gctaaccagg ttccgcaaaa cgtcctctct ttactgcgtt ag 762

<210> SEQ ID NO 50
<211> LENGTH: 253
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

-continued

```
<400> SEQUENCE: 50

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile
    130                 135                 140

Leu Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys
145                 150                 155                 160

Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys
                165                 170                 175

Val Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp
            180                 185                 190

Ser Ala Ile Thr Asn Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala
        195                 200                 205

Arg Ser Arg Ile Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met
    210                 215                 220

Ser Lys Ala Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln
225                 230                 235                 240

Ala Asn Gln Val Pro Gln Asn Val Leu Ser Leu Leu Arg
                245                 250


<210> SEQ ID NO 51
<211> LENGTH: 597
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 51

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgacg gcatttctat tgcgcagacc actgaaggtg cgctgaatga aatcaacaac     360

aacctgcagc gtgtgcgtga gttgtctgtt caggccacta tcccgggaat ttccggtggt     420

ggtggtggaa ttctagactc catgggtaca ttaatcaatg aagacgctgc cgcagccaag     480

aaaagtaccg ctaacccact ggcttcaatt gattctgcat tgtcaaaagt ggacgcagtt     540
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cgttcttctc tgggggcaat tcaaaaccgt tttgattcag ccattaccaa cctttag       597


<210> SEQ ID NO 52
<211> LENGTH: 198
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 52

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu
            100                 105                 110

Gly Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu
        115                 120                 125

Ser Val Gln Ala Thr Ile Pro Gly Ile Ser Gly Gly Gly Gly Gly Ile
    130                 135                 140

Leu Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala Ala Lys
145                 150                 155                 160

Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys
                165                 170                 175

Val Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp
            180                 185                 190

Ser Ala Ile Thr Asn Leu
        195


<210> SEQ ID NO 53
<211> LENGTH: 672
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 53

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgaca tcccgggaat ttccggtggt ggtggtggaa ttctagactc catgggtaca     360

ttaatcaatg aagacgctgc cgcagccaag aaaagtaccg ctaacccact ggcttcaatt     420

gattctgcat tgtcaaaagt ggacgcagtt cgttcttctc tgggggcaat tcaaaaccgt     480

tttgattcag ccattaccaa ccttggcaat acggtaacca atctgaactc cgcgcgtagc     540

cgtatcgaag atgctgacta tgcaacggaa gtttctaata tgtctaaagc gcagattctg     600
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cagcaggctg gtacttccgt tctggcgcag gctaaccagg ttccgcaaaa cgtcctctct     660

ttactgcgtt ag                                                         672


<210> SEQ ID NO 54
<211> LENGTH: 223
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 54

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Ile Pro Gly Ile Ser Gly Gly Gly Gly
            100                 105                 110

Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala
        115                 120                 125

Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu
    130                 135                 140

Ser Lys Val Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg
145                 150                 155                 160

Phe Asp Ser Ala Ile Thr Asn Leu Gly Asn Thr Val Thr Asn Leu Asn
                165                 170                 175

Ser Ala Arg Ser Arg Ile Glu Asp Ala Asp Tyr Ala Thr Glu Val Ser
            180                 185                 190

Asn Met Ser Lys Ala Gln Ile Leu Gln Gln Ala Gly Thr Ser Val Leu
        195                 200                 205

Ala Gln Ala Asn Gln Val Pro Gln Asn Val Leu Ser Leu Leu Arg
    210                 215                 220


<210> SEQ ID NO 55
<211> LENGTH: 507
<212> TYPE: DNA
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 55

atgcggggtt ctcatcatca tcatcatcat ggtatggcta gcatgactgg tggacagcaa      60

atgggtcggg atctgtacga cgatgacgat aaggatccga tggcacaagt cattaataca     120

aacagcctgt cgctgttgac ccagaataac ctgaacaaat ctcagtcctc actgagttcc     180

gctattgagc gtctgtcctc tggtctgcgt atcaacagcg cgaaagacga tgcggcaggc     240

caggcgattg ctaaccgctt cacttctaat atcaaaggcc tgactcaggc ttcccgtaac     300

gctaacgaca tcccgggaat ttccggtggt ggtggtggaa ttctagactc catgggtaca     360

ttaatcaatg aagacgctgc cgcagccaag aaaagtaccg ctaacccact ggcttcaatt     420
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gattctgcat tgtcaaaagt ggacgcagtt cgttcttctc tgggggcaat tcaaaaccgt    480

tttgattcag ccattaccaa cctttag                                        507


<210> SEQ ID NO 56
<211> LENGTH: 168
<212> TYPE: PRT
<213> ORGANISM: Salmonella dublin

<400> SEQUENCE: 56

Met Arg Gly Ser His His His His His His Gly Met Ala Ser Met Thr
1               5                   10                  15

Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Asp Lys Asp
            20                  25                  30

Pro Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln
        35                  40                  45

Asn Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg
    50                  55                  60

Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly
65                  70                  75                  80

Gln Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln
                85                  90                  95

Ala Ser Arg Asn Ala Asn Asp Ile Pro Gly Ile Ser Gly Gly Gly Gly
            100                 105                 110

Gly Ile Leu Asp Ser Met Gly Thr Leu Ile Asn Glu Asp Ala Ala Ala
        115                 120                 125

Ala Lys Lys Ser Thr Ala Asn Pro Leu Ala Ser Ile Asp Ser Ala Leu
    130                 135                 140

Ser Lys Val Asp Ala Val Arg Ser Ser Leu Gly Ala Ile Gln Asn Arg
145                 150                 155                 160

Phe Asp Ser Ala Ile Thr Asn Leu
                165


<210> SEQ ID NO 57
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 57

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn
1               5                   10                  15

Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Ser
                85                  90                  95

Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Lys Ser Ile
            100                 105                 110

Gln Asp Glu Ile Gln Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Asn
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```
        115                 120                 125

Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gln Asp Asn Gln Met
    130                 135                 140

Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asp Leu
145                 150                 155                 160

Gln Lys Ile Asp Val Lys Ser Leu Gly Leu Asp Gly Phe Asn
                165                 170


<210> SEQ ID NO 58
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 58

Met Ala Leu Thr Val Asn Thr Asn Ile Ala Ser Leu Asn Thr Gln Arg
1               5                   10                  15

Asn Leu Asn Ala Ser Ser Asn Asp Leu Asn Thr Ser Leu Gln Arg Leu
            20                  25                  30

Thr Thr Gly Tyr Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
        35                  40                  45

Gln Ile Ser Asn Arg Leu Ser Asn Gln Ile Ser Gly Leu Asn Val Ala
    50                  55                  60

Thr Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Ala Glu Gly
65                  70                  75                  80

Ala Leu Gln Gln Ser Thr Asn Ile Leu Gln Arg Ile Arg Asp Leu Ala
                85                  90                  95

Leu Gln Ser Ala Asn Gly Ser Asn Ser Asp Ala Asp Arg Ala Ala Leu
            100                 105                 110

Gln Lys Glu Val Ala Ala Gln Gln Ala Glu Leu Thr Arg Ile Ser Asp
        115                 120                 125

Thr Thr Thr Phe Gly Gly Arg Lys Leu Leu Asp Gly Ser Phe Gly Thr
    130                 135                 140

Thr Ser Phe Gln Val Gly Ser Asn Ala Tyr Glu Thr Ile Asp Ile Ser
145                 150                 155                 160

Leu Gln Asn Ala Ser Ala Ser Ala Ile Gly Ser Tyr Gln Val Gly Ser
                165                 170                 175

Asn Gly Ala Gly Thr Val Ala Ser Val Ala Gly Thr Ala
            180                 185


<210> SEQ ID NO 59
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Legionella pneumophila

<400> SEQUENCE: 59

Met Ala Gln Val Ile Asn Thr Asn Val Ala Ser Leu Thr Ala Gln Arg
1               5                   10                  15

Asn Leu Gly Val Ser Gly Asn Met Met Gln Thr Ser Ile Gln Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
        35                  40                  45

Ala Ile Ser Gln Arg Met Thr Ala Gln Ile Arg Gly Met Asn Gln Ala
    50                  55                  60

Val Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Val Ala Glu Gly
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65                  70                  75                  80

Ala Met Gln Glu Thr Thr Asn Ile Leu Gln Arg Met Arg Glu Leu Ser
                85                  90                  95

Val Gln Ala Ala Asn Ser Thr Asn Asn Ser Ser Asp Arg Ala Ser Ile
            100                 105                 110

Gln Ser Glu Ile Ser Gln Leu Lys Ser Glu Leu Glu Arg Ile Ala Gln
        115                 120                 125

Asn Thr Glu Phe Asn Gly Gln Arg Ile Leu Asp Gly Ser Phe Ser Gly
    130                 135                 140

Ala Ser Phe Gln Val Gly Ala Asn Ser Asn Gln Thr Ile Asn Phe Ser
145                 150                 155                 160

Ile Gly Ser Ile Lys Ala Ser Ser Ile Gly Gly Ile Ala Thr Ala Thr
                165                 170                 175

Gly Thr Glu


<210> SEQ ID NO 60
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 60

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn
1               5                   10                  15

Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Ile Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Val Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Thr
                85                  90                  95

Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Ser Ser Ile
            100                 105                 110

Gln Ala Glu Ile Thr Gln Arg Leu Glu Glu Ile Asp Arg Val Ser Glu
        115                 120                 125

Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala Glu Asn Asn Glu Met
    130                 135                 140

Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Thr Ile Asn Leu
145                 150                 155                 160

Ala Lys Ile Asp Ala Lys Thr Leu Gly Leu Asp Gly Phe Asn
                165                 170


<210> SEQ ID NO 61
<211> LENGTH: 173
<212> TYPE: PRT
<213> ORGANISM: Serratia marcescens

<400> SEQUENCE: 61

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Met Ala Gln Asn
1               5                   10                  15

Asn Leu Asn Lys Ser Gln Ser Ser Leu Gly Thr Ala Ile Glu Arg Leu
            20                  25                  30
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Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ser Asn Arg Phe Thr Ala Asn Ile Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Val Asn Asp Asn Leu Gln Asn Ile Arg Arg Leu Thr
                85                  90                  95

Val Gln Ala Gln Asn Gly Ser Asn Ser Thr Ser Asp Leu Lys Ser Ile
            100                 105                 110

Gln Asp Glu Ile Thr Gln Arg Leu Ser Glu Ile Asn Arg Ile Ser Glu
        115                 120                 125

Gln Thr Asp Phe Asn Gly Val Lys Val Leu Ser Ser Asp Gln Lys Leu
    130                 135                 140

Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Thr Asp Ile Asp Leu
145                 150                 155                 160

Lys Lys Ile Asp Ala Lys Gln Leu Gly Met Asp Thr Phe
                165                 170


<210> SEQ ID NO 62
<211> LENGTH: 168
<212> TYPE: PRT
<213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 62

Met Arg Ile Asn His Asn Ile Ala Ala Leu Asn Thr Ser Arg Gln Leu
1               5                   10                  15

Asn Ala Gly Ser Asn Ser Ala Ala Lys Asn Met Glu Lys Leu Ser Ser
            20                  25                  30

Gly Leu Arg Ile Asn Arg Ala Gly Asp Asp Ala Ala Gly Leu Ala Ile
        35                  40                  45

Ser Glu Lys Met Arg Ser Gln Ile Arg Gly Leu Asp Met Ala Ser Lys
    50                  55                  60

Asn Ala Gln Asp Gly Ile Ser Leu Ile Gln Thr Ser Glu Gly Ala Leu
65                  70                  75                  80

Asn Glu Thr His Ser Ile Leu Gln Arg Met Ser Glu Leu Ala Thr Gln
                85                  90                  95

Ala Ala Asn Asp Thr Asn Thr Asp Ser Asp Arg Ser Glu Leu Gln Lys
            100                 105                 110

Glu Met Asp Gln Leu Ala Ser Glu Val Thr Arg Ile Ser Thr Asp Thr
        115                 120                 125

Glu Phe Asn Thr Lys Lys Leu Leu Asp Gly Thr Ala Gln Asn Leu Thr
    130                 135                 140

Phe Gln Ile Gly Ala Asn Glu Gly Gln Thr Met Ser Leu Ser Ile Asn
145                 150                 155                 160

Lys Met Asp Ser Glu Ser Leu Lys
                165


<210> SEQ ID NO 63
<211> LENGTH: 192
<212> TYPE: PRT
<213> ORGANISM: Listeria monocytogenes

<400> SEQUENCE: 63
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Met Lys Val Asn Thr Asn Ile Ile Ser Leu Lys Thr Gln Glu Tyr Leu
1               5                   10                  15

Arg Lys Asn Asn Glu Gly Met Thr Gln Ala Gln Glu Arg Leu Ala Ser
            20                  25                  30

Gly Lys Arg Ile Asn Ser Ser Leu Asp Asp Ala Ala Gly Leu Ala Val
        35                  40                  45

Val Thr Arg Met Asn Val Lys Ser Thr Gly Leu Asp Ala Ala Ser Lys
    50                  55                  60

Asn Ser Ser Met Gly Ile Asp Leu Leu Gln Thr Ala Asp Ser Ala Leu
65                  70                  75                  80

Ser Ser Met Ser Ser Ile Leu Gln Arg Met Arg Gln Leu Ala Val Gln
                85                  90                  95

Ser Ser Asn Gly Ser Phe Ser Asp Glu Asp Arg Lys Gln Tyr Thr Ala
            100                 105                 110

Glu Phe Gly Ser Leu Ile Lys Glu Leu Asp His Val Ala Asp Thr Thr
        115                 120                 125

Asn Tyr Asn Asn Ile Lys Leu Leu Asp Gln Thr Ala Thr Gly Ala Ala
    130                 135                 140

Thr Gln Val Ser Ile Gln Ala Ser Asp Lys Ala Asn Asp Leu Ile Asn
145                 150                 155                 160

Ile Asp Leu Phe Asn Ala Lys Gly Leu Ser Ala Gly Thr Ile Thr Leu
                165                 170                 175

Gly Ser Gly Ser Thr Val Ala Gly Tyr Ser Ala Leu Ser Val Ala Asp
            180                 185                 190


<210> SEQ ID NO 64
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 64

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn
1               5                   10                  15

Asn Leu Asn Lys Ser Gln Ser Ser Leu Ser Ser Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Ile Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Val Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Ser Glu Ile Asn Asn Asn Leu Gln Arg Ile Arg Glu Leu Ser
                85                  90                  95

Val Gln Ala Thr Asn Gly Thr Asn Ser Asp Ser Asp Leu Asn Ser Ile
            100                 105                 110

Gln Asp Glu Ile Thr Gln Arg Leu Ser Glu Ile Asp Arg Val Ser Asn
        115                 120                 125

Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ala Ser Asp Gln Thr Met
    130                 135                 140

Lys Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Glu Ile Ala Leu
145                 150                 155                 160

Asp Lys Ile Asp Ala Lys Thr Leu Gly Leu Asp Asn Phe Ser
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                165                 170


<210> SEQ ID NO 65
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Edwardsiella tarda

<400> SEQUENCE: 65

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Met Ala Gln Asn
1               5                   10                  15

Asn Leu Asn Lys Ser Gln Ser Ala Leu Gly Thr Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ser Asn Arg Phe Thr Ala Asn Ile Asn Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Val Asn Asp Asn Leu Gln Asn Ile Arg Arg Leu Thr
                85                  90                  95

Val Gln Ala Gln Asn Gly Ser Asn Ser Ser Ser Asp Leu Gln Ser Ile
            100                 105                 110

Gln Asp Glu Ile Thr Gln Arg Leu Ser Glu Ile Asp Arg Ile Ser Gln
        115                 120                 125

Gln Thr Asp Phe Asn Gly Val Lys Val Leu Ser Lys Asp Gln Lys Leu
    130                 135                 140

Thr Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Asp Ile Asp Leu
145                 150                 155                 160

Lys Asn Ile Asn Ala Gln Ser Leu Gly Leu Asp Lys Phe Asn
                165                 170


<210> SEQ ID NO 66
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Acidovorax avenae

<400> SEQUENCE: 66

Met Ala Ser Thr Ile Asn Thr Asn Val Ser Ser Leu Thr Ala Gln Arg
1               5                   10                  15

Asn Leu Ser Leu Ser Gln Ser Ser Leu Asn Thr Ser Ile Gln Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
        35                  40                  45

Ala Ile Ser Glu Arg Phe Thr Ser Gln Ile Arg Gly Leu Asn Gln Ala
    50                  55                  60

Val Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Ala Glu Gly
65                  70                  75                  80

Ala Leu Lys Ser Thr Gly Asp Ile Leu Gln Arg Val Arg Glu Leu Ala
                85                  90                  95

Val Gln Ser Ala Asn Ala Thr Asn Ser Ser Gly Asp Arg Lys Ala Ile
            100                 105                 110

Gln Ala Glu Val Gly Gln Leu Leu Ser Glu Met Asp Arg Ile Ala Gly
        115                 120                 125

Asn Thr Glu Phe Asn Gly Gln Lys Leu Leu Asp Gly Ser Phe Gly Ser
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    130                 135                 140

Ala Thr Phe Gln Val Gly Ala Asn Ala Asn Gln Thr Ile Thr Ala Thr
145                 150                 155                 160

Thr Gly Asn Phe Arg Thr Asn Asn Tyr Gly Ala Gln Leu Thr Ala Ser
                165                 170                 175

Ala Ser Gly Ala Ala Thr Ser Gly Ala Ser
            180                 185


<210> SEQ ID NO 67
<211> LENGTH: 173
<212> TYPE: PRT
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 67

Met Ala Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn Asn
1               5                   10                  15

Leu Asn Lys Ser Gln Ser Ser Leu Gly Thr Ala Ile Glu Arg Leu Ser
            20                  25                  30

Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln Ala
        35                  40                  45

Ile Ala Asn Arg Phe Thr Ser Asn Ile Lys Gly Leu Thr Gln Ala Ala
    50                  55                  60

Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly Ser
65                  70                  75                  80

Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Val Arg Glu Leu Thr Val
                85                  90                  95

Gln Ala Gln Asn Gly Ser Asn Ser Ser Ser Asp Leu Asp Ser Ile Gln
            100                 105                 110

Asp Glu Ile Ser Leu Arg Leu Ala Glu Ile Asp Arg Val Ser Asp Gln
        115                 120                 125

Thr Gln Phe Asn Gly Lys Lys Val Leu Ala Glu Asn Thr Thr Met Ser
    130                 135                 140

Ile Gln Val Gly Ala Asn Asp Gly Glu Thr Ile Asp Ile Asn Leu Gln
145                 150                 155                 160

Lys Ile Asp Ser Lys Ser Leu Gly Leu Gly Ser Tyr Ser
                165                 170


<210> SEQ ID NO 68
<211> LENGTH: 174
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 68

Met Ala Gln Val Ile Asn Thr Asn Ser Leu Ser Leu Leu Thr Gln Asn
1               5                   10                  15

Asn Leu Asn Arg Ser Gln Gly Thr Leu Gly Ser Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Val Arg Gly Leu Thr Gln Ala
    50                  55                  60

Ala Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Ile Asn Thr Asn Leu Gln Arg Ile Arg Glu Leu Thr
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                85                  90                  95

Val Gln Ser Gln Asn Gly Ser Asn Ser Glu Ser Asp Ile Lys Ser Ile
            100                 105                 110

Gln Glu Glu Val Thr Gln Arg Leu Lys Glu Ile Asp Arg Ile Ser Glu
        115                 120                 125

Gln Thr Gln Phe Asn Gly Val Arg Val Leu Arg Glu Asp Ser Lys Met
    130                 135                 140

Thr Ile Gln Val Gly Ala Asn Asp Asn Glu Val Ile Asp Ile Asp Leu
145                 150                 155                 160

Lys Lys Ile Asp Lys Glu Ala Leu Asn Leu Gly Lys Phe Thr
                165                 170


<210> SEQ ID NO 69
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 69

Met Thr Thr Ile Asn Thr Asn Ile Gly Ala Ile Ala Ala Gln Ala Asn
1               5                   10                  15

Met Thr Lys Val Asn Asp Gln Phe Asn Thr Ala Met Thr Arg Leu Ser
            20                  25                  30

Thr Gly Leu Arg Ile Asn Ala Ala Lys Asp Asp Ala Ala Gly Met Ala
        35                  40                  45

Ile Gly Glu Lys Met Thr Ala Gln Val Met Gly Leu Asn Gln Ala Ile
    50                  55                  60

Arg Asn Ala Gln Asp Gly Lys Asn Leu Val Asp Thr Thr Glu Gly Ala
65                  70                  75                  80

His Val Glu Val Ser Ser Met Leu Gln Arg Leu Arg Glu Leu Ala Val
                85                  90                  95

Gln Ser Ser Asn Asp Thr Asn Thr Ala Ala Asp Arg Gly Ser Leu Ala
            100                 105                 110

Ala Glu Gly Lys Gln Leu Ile Ala Glu Ile Asn Arg Val Ala Glu Ser
        115                 120                 125

Thr Thr Phe Asn Gly Met Lys Val Leu Asp Gly Ser Phe Thr Gly Lys
    130                 135                 140

Gln Leu Gln Ile Gly Ala Asp Ser Gly Gln Thr Met Ala Ile Asn Val
145                 150                 155                 160

Asp Ser Ala Ala Ala Thr Asp Ile Gly Ala His Lys Ile Ser Ser Ala
                165                 170                 175

Ser Thr Val Val Ala Asp Ala Ala Leu Thr Asp Thr Thr
            180                 185


<210> SEQ ID NO 70
<211> LENGTH: 175
<212> TYPE: PRT
<213> ORGANISM: Xenorhabdus nematophila

<400> SEQUENCE: 70

Met Ala Ser Val Ile Asn Thr Asn Asp Ser Ala Leu Leu Ala Gln Asn
1               5                   10                  15

Asn Leu Thr Lys Ser Lys Gly Ile Leu Gly Ser Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
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```
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Val Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ala Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Ile Arg Glu Leu Thr
                85                  90                  95

Val Gln Ser Glu Asn Gly Ser Asn Ser Lys Ser Asp Leu Asp Ser Ile
            100                 105                 110

Gln Lys Glu Val Thr Gln Arg Leu Glu Glu Ile Asp Arg Ile Ser Thr
        115                 120                 125

Gln Thr Gln Phe Asn Gly Ile Lys Val Leu Asn Gly Asp Val Thr Glu
    130                 135                 140

Met Lys Ile Gln Val Gly Ala Asn Asp Asn Glu Thr Ile Gly Ile Lys
145                 150                 155                 160

Leu Gly Lys Ile Asn Ser Glu Lys Leu Asn Leu Lys Glu Phe Ser
                165                 170                 175


<210> SEQ ID NO 71
<211> LENGTH: 175
<212> TYPE: PRT
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 71

Met Ala Gln Val Ile Asn Thr Asn Tyr Leu Ser Leu Val Thr Gln Asn
1               5                   10                  15

Asn Leu Asn Arg Ser Gln Ser Ala Leu Gly Asn Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Met Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ser Asn Ile Asn Gly Leu Thr Gln Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Val Ser Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Ile Arg Glu Leu Thr
                85                  90                  95

Val Gln Ala Lys Asn Gly Thr Asn Ser Asn Ser Asp Ile Asn Ser Ile
            100                 105                 110

Gln Asn Glu Val Asn Gln Arg Leu Asp Glu Ile Asn Arg Val Ser Glu
        115                 120                 125

Gln Thr Gln Phe Asn Gly Val Lys Val Leu Ser Gly Glu Lys Ser Lys
    130                 135                 140

Met Thr Ile Gln Val Gly Thr Asn Asp Asn Glu Val Ile Glu Phe Asn
145                 150                 155                 160

Leu Asp Lys Ile Asp Asn Asp Thr Leu Gly Val Ala Ser Asp Lys
                165                 170                 175


<210> SEQ ID NO 72
<211> LENGTH: 200
<212> TYPE: PRT
<213> ORGANISM: Butyrivibrio fibrisolvens

<400> SEQUENCE: 72

Met Val Val Gln His Asn Met Gln Ala Ala Asn Ala Ser Arg Met Leu
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1               5                   10                  15

Gly Ile Thr Thr Gly Asp Gln Ser Lys Ser Thr Glu Lys Leu Ser Ser
            20                  25                  30

Gly Phe Lys Ile Asn Arg Ala Ala Asp Asp Ala Ala Gly Leu Ser Ile
        35                  40                  45

Ser Glu Lys Met Arg Lys Gln Ile Arg Gly Leu Asp Gln Ala Ser Thr
    50                  55                  60

Asn Ala Ser Asp Gly Ile Ser Ala Val Gln Thr Ala Glu Gly Ala Leu
65                  70                  75                  80

Thr Glu Val His Ser Met Leu Gln Arg Met Asn Glu Leu Ala Val Gln
                85                  90                  95

Ala Ala Asn Gly Thr Asn Ser Glu Ser Asp Arg Ser Ser Ile Gln Asp
            100                 105                 110

Glu Ile Asn Gln Leu Thr Thr Glu Ile Asp Arg Val Ala Glu Thr Thr
        115                 120                 125

Lys Phe Asn Glu Thr Tyr Leu Leu Lys Gly Gly Asn Gly Asp Arg Thr
    130                 135                 140

Val Arg Val Tyr Ala His Asp Ala Gly Leu Val Gly Ser Leu Ser Gln
145                 150                 155                 160

Asn Thr Thr Lys Ala Thr Phe Gln Met Arg Lys Leu Glu Ile Gly Asp
                165                 170                 175

Ser Tyr Thr Ile Gly Gly Thr Thr Tyr Lys Ile Gly Ala Glu Thr Val
            180                 185                 190

Lys Glu Ala Met Thr Ala Leu Lys
        195                 200


<210> SEQ ID NO 73
<211> LENGTH: 177
<212> TYPE: PRT
<213> ORGANISM: Bordetella pertussis

<400> SEQUENCE: 73

Met Ala Ala Val Ile Asn Thr Asn Tyr Leu Ser Leu Val Ala Gln Asn
1               5                   10                  15

Asn Leu Asn Lys Ser Gln Ser Ala Leu Gly Ser Ala Ile Glu Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Gln
        35                  40                  45

Ala Ile Ala Asn Arg Phe Thr Ala Asn Val Lys Gly Leu Thr Gln Ala
    50                  55                  60

Ala Arg Asn Ala Asn Asp Gly Ile Ser Ile Ala Gln Thr Thr Glu Gly
65                  70                  75                  80

Ala Leu Asn Glu Ile Asn Asn Asn Leu Gln Arg Ile Arg Glu Leu Thr
                85                  90                  95

Val Gln Ala Ser Asn Gly Thr Asn Ser Ala Ser Asp Ile Asp Ser Ile
            100                 105                 110

Gln Gln Glu Val Asn Gln Arg Leu Glu Glu Ile Asn Arg Ile Ala Glu
        115                 120                 125

Gln Thr Asp Phe Asn Gly Ile Lys Val Leu Lys Ser Asn Ala Thr Asp
    130                 135                 140

Met Thr Leu Ser Ile Gln Val Gly Ala Lys Asp Asn Glu Thr Ile Asp
145                 150                 155                 160
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Ile Lys Ile Asp Arg Asn Ser Asn Trp Asn Leu Tyr Asp Ala Val Gly
                165                 170                 175

Thr


<210> SEQ ID NO 74
<211> LENGTH: 167
<212> TYPE: PRT
<213> ORGANISM: Clostridium chauvoei

<400> SEQUENCE: 74

Met Ile Ile Asn His Asn Met Asn Ala Leu Asn Ala His Arg Asn Met
1               5                   10                  15

Met Gly Asn Ile Ala Thr Ala Gly Lys Ser Met Glu Lys Leu Ser Ser
            20                  25                  30

Gly Leu Arg Ile Asn Arg Ala Gly Asp Asp Ala Ala Gly Leu Ala Ile
        35                  40                  45

Ser Glu Lys Met Arg Gly Gln Ile Arg Gly Leu Asp Gln Ala Ser Arg
    50                  55                  60

Asn Ala Gln Asp Gly Ile Ser Leu Ile Gln Thr Ala Glu Gly Ala Leu
65                  70                  75                  80

Ala Glu Thr His Ser Ile Leu Gln Arg Met Arg Glu Leu Ser Val Gln
                85                  90                  95

Ser Ala Asn Asp Thr Asn Val Ala Val Asp Arg Thr Ala Ile Gln Asp
            100                 105                 110

Glu Ile Asn Ser Leu Thr Glu Glu Ile Asn Arg Ile Ser Gly Asp Thr
        115                 120                 125

Glu Phe Asn Thr Gln Lys Leu Leu Asp Gly Gly Phe Lys Gly Glu Phe
    130                 135                 140

Gln Ile Gly Ala Asn Ser Asn Gln Thr Val Lys Leu Asp Ile Gly Asn
145                 150                 155                 160

Met Ser Ala Ala Ser Leu Gly
                165


<210> SEQ ID NO 75
<211> LENGTH: 178
<212> TYPE: PRT
<213> ORGANISM: Xanthomonas campestris

<400> SEQUENCE: 75

Met Ala Gln Val Ile Asn Thr Asn Val Met Ser Leu Asn Ala Gln Arg
1               5                   10                  15

Asn Leu Asn Thr Asn Ser Ser Ser Met Ala Leu Ser Ile Gln Gln Leu
            20                  25                  30

Ser Ser Gly Lys Arg Ile Thr Ser Ala Ser Val Asp Ala Ala Gly Leu
        35                  40                  45

Ala Ile Ser Glu Arg Phe Thr Thr Gln Ile Arg Gly Leu Asp Val Ala
    50                  55                  60

Ser Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Ala Glu Gly
65                  70                  75                  80

Ala Met Val Glu Ile Gly Asn Asn Leu Gln Arg Ile Arg Glu Leu Ser
                85                  90                  95

Val Gln Ser Ala Asn Ala Thr Asn Ser Ala Thr Asp Arg Glu Ala Leu
            100                 105                 110

Asn Ser Glu Val Lys Gln Leu Thr Ser Glu Ile Asp Arg Val Ala Asn
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        115                 120                 125

Gln Thr Ser Phe Asn Gly Thr Lys Leu Leu Asn Gly Asp Phe Ser Gly
    130                 135                 140

Ala Leu Phe Gln Val Gly Ala Asp Ala Gly Gln Thr Ile Gly Ile Asn
145                 150                 155                 160

Ser Ile Val Asp Ala Asn Val Asp Ser Leu Gly Lys Ala Asn Phe Ala
                165                 170                 175

Ala Ser


<210> SEQ ID NO 76
<211> LENGTH: 161
<212> TYPE: PRT
<213> ORGANISM: Nitrosomonas europaea

<400> SEQUENCE: 76

Met Pro Gln Val Ile Asn Thr Asn Ile Ala Ser Leu Asn Ala Gln Arg
1               5                   10                  15

Asn Leu Asn Val Ser Gln Asn Ser Leu Ser Thr Ala Leu Gln Arg Leu
            20                  25                  30

Ser Ser Gly Leu Arg Ile Asn Ser Ala Lys Asp Asp Ala Ala Gly Leu
        35                  40                  45

Ala Ile Ser Glu Arg Met Thr Ser Gln Ile Arg Gly Met Asn Gln Ala
    50                  55                  60

Ala Arg Asn Ala Asn Asp Gly Ile Ser Leu Ala Gln Thr Ala Glu Gly
65                  70                  75                  80

Ala Leu Val Glu Ile Gly Asn Asn Leu Gln Arg Ile Arg Glu Leu Ala
                85                  90                  95

Val Gln Ser Ala Asn Ala Thr Asn Ser Glu Asp Asp Arg Glu Ala Leu
            100                 105                 110

Gln Lys Glu Val Thr Gln Leu Ile Asp Glu Ile Gln Arg Val Gly Glu
        115                 120                 125

Gln Thr Ser Phe Asn Gly Thr Lys Leu Leu Asp Gly Ser Phe Ala Ser
    130                 135                 140

Gln Ile Phe Gln Val Gly Ala Asn Glu Gly Glu Thr Ile Asp Phe Thr
145                 150                 155                 160

Asp


<210> SEQ ID NO 77
<211> LENGTH: 178
<212> TYPE: PRT
<213> ORGANISM: Campylobacter lari

<400> SEQUENCE: 77

Gly Phe Arg Ile Asn Thr Asn Gly Ala Ser Leu Asn Ala Gln Val Asn
1               5                   10                  15

Ala Gly Leu Asn Ser Arg Asn Leu Asp Ser Ser Leu Ala Arg Leu Ser
            20                  25                  30

Ser Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala Ser Gly Leu Ala
        35                  40                  45

Ile Ala Asp Ser Leu Lys Thr Gln Ala Asn Ser Leu Gly Gln Ala Ile
    50                  55                  60

Asn Asn Ala Asn Asp Ala Asn Ser Met Leu Gln Ile Ala Asp Lys Ala
65                  70                  75                  80
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Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Ile Lys Val Lys Ala Thr
                85                  90                  95

Gln Ala Ala Gln Asp Gly Gln Thr Ala Lys Thr Arg Ala Met Ile Gln
            100                 105                 110

Gly Glu Ile Asn Lys Leu Met Glu Glu Leu Asp Asn Ile Ala Asn Thr
        115                 120                 125

Thr Thr Tyr Asn Gly Lys Gln Leu Leu Ser Gly Ser Phe Ser Asn Ala
    130                 135                 140

Gln Phe Gln Ile Gly Asp Lys Ala Asn Gln Thr Val Asn Ala Thr Ile
145                 150                 155                 160

Gly Ser Thr Asn Ser Ala Lys Val Gly Gln Thr Arg Phe Glu Thr Gly
                165                 170                 175

Ala Val


<210> SEQ ID NO 78
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Salmonella enterica

<400> SEQUENCE: 78

Pro Leu Ala Ser Ile Asp Ser Ala Leu Ser Lys Val Asp Ala Val Arg
1               5                   10                  15

Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn
            20                  25                  30

Leu Gly Asn Thr Val Thr Asn Leu Asn Ser Ala Arg Ser Arg Ile Glu
        35                  40                  45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Ala Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Arg
                85


<210> SEQ ID NO 79
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 79

Ala Ile Ala Val Val Asp Asn Ala Leu Ala Ala Ile Asp Ala Gln Arg
1               5                   10                  15

Ala Asp Leu Gly Ala Val Gln Asn Arg Phe Lys Asn Thr Ile Asp Asn
            20                  25                  30

Leu Thr Asn Ile Ser Glu Asn Ala Thr Asn Ala Arg Ser Arg Ile Lys
        35                  40                  45

Asp Thr Asp Phe Ala Ala Glu Thr Ala Ala Leu Ser Lys Asn Gln Val
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ala Ile Leu Ala Gln Ala Asn Gln Leu Pro
65                  70                  75                  80

Gln Ala Val Leu Ser Leu Leu Arg
                85


<210> SEQ ID NO 80
<211> LENGTH: 89
<212> TYPE: PRT
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<213> ORGANISM: Legionella pneumophila

<400> SEQUENCE: 80

Ala Ile Lys Arg Ile Asp Ala Ala Leu Asn Ser Val Asn Ser Asn Arg
1               5                   10                  15

Ala Asn Met Gly Ala Leu Gln Asn Arg Phe Glu Ser Thr Ile Ala Asn
            20                  25                  30

Leu Gln Asn Val Ser Asp Asn Leu Ser Ala Ala Arg Ser Arg Ile Gln
        35                  40                  45

Asp Ala Asp Tyr Ala Ala Glu Met Ala Ser Leu Thr Lys Asn Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ala Met Leu Ala Gln Ala Asn Ser Leu Pro
65                  70                  75                  80

Gln Ser Val Leu Ser Leu Leu Gly Arg
                85


<210> SEQ ID NO 81
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 81

Pro Leu Glu Thr Ile Asp Lys Ala Leu Ala Lys Val Asp Asn Leu Arg
1               5                   10                  15

Ser Asp Leu Gly Ala Val Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn
            20                  25                  30

Leu Gly Asn Thr Val Asn Asn Leu Ser Ser Ala Arg Ser Arg Ile Glu
        35                  40                  45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Ala Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Thr Thr
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Gln Gly
                85


<210> SEQ ID NO 82
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Serratia marcescens

<400> SEQUENCE: 82

Pro Leu Ala Thr Leu Asp Lys Ala Leu Ala Gln Val Asp Gly Leu Arg
1               5                   10                  15

Ser Ser Leu Gly Ala Val Gln Asn Arg Phe Asp Ser Val Ile Asn Asn
            20                  25                  30

Leu Asn Ser Thr Val Asn Asn Leu Ser Ala Ser Gln Ser Arg Ile Gln
        35                  40                  45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Ala Asn Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Ser Thr
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Arg
                85


<210> SEQ ID NO 83
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<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Bacillus subtilis

<400> SEQUENCE: 83

Ala Leu Thr Thr Ile Lys Thr Ala Ile Asp Thr Val Ser Ser Glu Arg
1               5                   10                  15

Ala Lys Leu Gly Ala Val Gln Asn Arg Leu Glu His Thr Ile Asn Asn
            20                  25                  30

Leu Gly Thr Ser Ser Glu Asn Leu Thr Ser Ala Glu Ser Arg Ile Arg
        35                  40                  45

Asp Val Asp Met Ala Ser Glu Met Met Glu Tyr Thr Lys Asn Asn Ile
    50                  55                  60

Leu Thr Gln Ala Ser Gln Ala Met Leu Ala Gln Ala Asn Gln Gln Pro
65                  70                  75                  80

Gln Gln Val Leu Gln Leu Leu Lys Gly
                85


<210> SEQ ID NO 84
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Leptospira interrogans

<400> SEQUENCE: 84

Val Ile Gly Leu Ala Asp Ala Ala Leu Thr Lys Ile Met Lys Gln Arg
1               5                   10                  15

Ala Asp Met Gly Ala Tyr Tyr Asn Arg Leu Glu Tyr Thr Ala Lys Gly
            20                  25                  30

Leu Met Gly Ala Tyr Glu Asn Met Gln Ala Ser Glu Ser Arg Ile Arg
        35                  40                  45

Asp Ala Asp Met Ala Glu Glu Val Val Ser Leu Thr Thr Lys Gln Ile
    50                  55                  60

Leu Val Gln Ser Gly Thr Ala Met Leu Ala Gln Ala Asn Met Lys Pro
65                  70                  75                  80

Asn Ser Val Leu Lys Leu Leu Gln Gln Ile
                85                  90


<210> SEQ ID NO 85
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Shigella sonnei

<400> SEQUENCE: 85

Pro Leu Ser Lys Leu Asp Glu Ala Leu Ala Lys Val Asp Lys Leu Arg
1               5                   10                  15

Ser Ser Leu Gly Ala Val Gln Asn Arg Phe Asp Ser Ala Ile Thr Asn
            20                  25                  30

Leu Gly Asn Thr Val Asn Asp Leu Ser Ser Ala Arg Ser Arg Ile Glu
        35                  40                  45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Ala Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Thr Thr
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Arg
                85
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<210> SEQ ID NO 86
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Edwardsiella tarda

<400> SEQUENCE: 86

Pro Leu Ala Thr Leu Asp Lys Ala Leu Ser Gln Val Asp Asp Leu Arg
1   5   10   15

Ser Gly Leu Gly Ala Val Gln Asn Arg Phe Asp Ser Val Ile Asn Asn
            20   25   30

Leu Asn Ser Thr Val Asn Asn Leu Ser Ala Ser Arg Ser Arg Ile Gln
        35   40   45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Ala Gln Ile
    50   55   60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Ser Thr
65   70   75   80

Gln Asn Val Leu Ser Leu Leu Arg
                85

<210> SEQ ID NO 87
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Acidovorax avenae

<400> SEQUENCE: 87

Ala Leu Lys Ile Ile Asp Ala Ala Leu Ser Ala Val Asn Gly Gln Arg
1   5   10   15

Ala Ser Phe Gly Ala Leu Gln Ser Arg Phe Glu Thr Thr Val Asn Asn
            20   25   30

Leu Gln Ser Thr Ser Glu Asn Met Ser Ala Ser Arg Ser Arg Ile Gln
        35   40   45

Asp Ala Asp Phe Ala Ala Glu Thr Ala Asn Leu Ser Arg Ser Gln Ile
    50   55   60

Leu Gln Gln Ala Gly Thr Ala Met Val Ala Gln Ala Asn Gln Leu Pro
65   70   75   80

Gln Gly Val Leu Ser Leu Leu Lys
                85

<210> SEQ ID NO 88
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Yersinia pestis

<400> SEQUENCE: 88

Pro Leu Glu Thr Leu Asp Asp Ala Ile Lys Gln Val Asp Gly Leu Arg
1   5   10   15

Ser Ser Leu Gly Ala Val Gln Asn Arg Phe Glu Ser Ala Val Thr Asn
            20   25   30

Leu Asn Asn Thr Val Thr Asn Leu Thr Ser Ala Arg Ser Arg Ile Glu
        35   40   45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Ala Gln Ile
    50   55   60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ser Gln Ala Asn Gln Val Pro
65   70   75   80

Gln Thr Val Leu Ser Leu Leu Asn

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                85


<210> SEQ ID NO 89
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Photorhabdus luminescens

<400> SEQUENCE: 89

Pro Leu Glu Thr Leu Asp Ser Ala Leu Ala Gln Val Asp Ser Leu Arg
1               5                   10                  15

Ser Ser Leu Gly Ala Ile Gln Asn Arg Leu Glu Ser Thr Val Asn Asn
            20                  25                  30

Leu Asn Asn Thr Val Asn Asn Leu Ser Ala Ala Arg Ser Arg Ile Glu
        35                  40                  45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Arg Gly Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ala Val Leu Ala Gln Ala Asn Gln Val Pro
65                  70                  75                  80

Gln Asn Val Met Ser Leu Leu Arg
                85


<210> SEQ ID NO 90
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Rhodobacter sphaeroides

<400> SEQUENCE: 90

Ala Ile Gly Val Ile Asp Val Ala Leu Ser Lys Ile Ser Gln Ser Arg
1               5                   10                  15

Ser Glu Leu Gly Ala Val Ser Asn Arg Leu Asp Ser Thr Ile Ser Asn
            20                  25                  30

Leu Thr Asn Ile Ser Thr Ser Val Gln Ala Ala Lys Ser Gln Val Met
        35                  40                  45

Asp Ala Asp Phe Ala Ala Glu Ser Thr Asn Leu Ala Arg Ser Gln Ile
    50                  55                  60

Leu Ser Gln Ala Ser Thr Ala Met Leu Ala Gln Ala Asn Ser Ser Lys
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Arg Gly
                85


<210> SEQ ID NO 91
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Xenorhabdus nematophila

<400> SEQUENCE: 91

Pro Leu Asp Thr Leu Asp Lys Ala Leu Ala Gln Val Asp Asp Met Arg
1               5                   10                  15

Ser Ser Leu Gly Ala Val Gln Asn Arg Leu Glu Ser Thr Val Asn Asn
            20                  25                  30

Leu Asn Asn Thr Val Asn Asn Leu Ser Ala Ala Arg Ser Arg Ile Glu
        35                  40                  45

Asp Ala Asp Tyr Ala Val Glu Val Ser Asn Met Ser Arg Gly Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro
65                  70                  75                  80
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Gln Thr Val Leu Ser Leu Leu Arg
                85


<210> SEQ ID NO 92
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Proteus mirabilis

<400> SEQUENCE: 92

Ala Leu Ala Thr Leu Asp Asn Ala Ile Ser Lys Val Asp Glu Ser Arg
1               5                   10                  15

Ser Lys Leu Gly Ala Ile Gln Asn Arg Phe Gln Ser Thr Ile Asn Asn
            20                  25                  30

Leu Asn Asn Thr Val Asn Asn Leu Ser Ala Ser Arg Ser Arg Ile Leu
        35                  40                  45

Asp Ala Asp Tyr Ala Thr Glu Val Ser Asn Met Ser Lys Asn Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ala Val Leu Ala Gln Ala Asn Gln Val Pro
65                  70                  75                  80

Gln Thr Val Leu Ser Leu Leu Arg
                85


<210> SEQ ID NO 93
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Butyrivibrio fibrisolvens

<400> SEQUENCE: 93

Ala Ile Asp Ala Ile Ser Asp Ala Leu Ala Lys Val Ser Ala Gln Arg
1               5                   10                  15

Ser Ala Leu Gly Ser Ile Gln Asn Arg Leu Glu His Ser Ile Ala Asn
            20                  25                  30

Leu Asp Asn Val Val Glu Asn Thr Asn Ala Ala Glu Ser Arg Ile Arg
        35                  40                  45

Asp Thr Asp Met Ala Asp Glu Met Val Thr Tyr Ser Lys Asn Asn Ile
    50                  55                  60

Leu Met Gln Ala Gly Gln Ser Met Leu Ala Gln Ala Asn Gln Ala Thr
65                  70                  75                  80

Gln Gly Val Leu Ser Ile Leu Gln
                85


<210> SEQ ID NO 94
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Bordetella pertussis

<400> SEQUENCE: 94

Ala Leu Ser Lys Leu Asp Asp Ala Met Lys Ala Val Asp Glu Gln Arg
1               5                   10                  15

Ser Ser Leu Gly Ala Ile Gln Asn Arg Phe Glu Ser Thr Val Ala Asn
            20                  25                  30

Leu Asn Asn Thr Ile Thr Asn Leu Ser Ala Ala Arg Ser Arg Ile Glu
        35                  40                  45

Asp Ser Asp Tyr Ala Thr Glu Val Ser Asn Met Thr Lys Asn Gln Ile
    50                  55                  60
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Leu Gln Gln Ala Gly Thr Ser Val Leu Ala Gln Ala Asn Gln Val Pro
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Arg
                85


<210> SEQ ID NO 95
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Clostridium chauvoei

<400> SEQUENCE: 95

Ser Ile Lys Thr Ile Asn Ser Ala Ile Glu Gln Val Ser Thr Gln Arg
1               5                   10                  15

Ser Lys Leu Gly Ala Val Gln Asn Arg Leu Glu His Thr Ile Asn Asn
            20                  25                  30

Leu Asn Thr Ser Ser Glu Asn Leu Thr Ala Ala Glu Ser Arg Val Arg
        35                  40                  45

Asp Val Asp Met Ala Lys Glu Met Met Ala Phe Ser Lys Asn Asn Ile
    50                  55                  60

Leu Ser Gln Ala Ala Gln Ala Met Leu Gly Gln Ala Asn Gln Gln Pro
65                  70                  75                  80

Gln Gly Val Leu Gln Leu Leu Arg
                85


<210> SEQ ID NO 96
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Xanthomonas campestris

<400> SEQUENCE: 96

Ala Leu Glu Ile Val Asp Lys Ala Leu Thr Ser Val Asn Ser Ser Arg
1               5                   10                  15

Ala Asp Met Gly Ala Val Gln Asn Arg Phe Thr Ser Thr Ile Ala Asn
            20                  25                  30

Leu Ala Ala Thr Ser Glu Asn Leu Thr Ala Ser Arg Ser Arg Ile Ala
        35                  40                  45

Asp Thr Asp Tyr Ala Lys Thr Thr Ala Glu Leu Thr Arg Thr Gln Ile
    50                  55                  60

Leu Gln Gln Ala Gly Thr Ala Met Leu Ala Gln Ala Lys Ser Val Pro
65                  70                  75                  80

Gln Asn Val Leu Ser Leu Leu Gln
                85


<210> SEQ ID NO 97
<211> LENGTH: 84
<212> TYPE: PRT
<213> ORGANISM: Nitrosomonas europaea

<400> SEQUENCE: 97

Ile Asp Asp Ala Leu Lys Ile Val Asn Ser Thr Arg Ala Asp Leu Gly
1               5                   10                  15

Ala Ile Gln Asn Arg Phe Ser Ser Ala Ile Ala Asn Leu Gln Thr Ser
            20                  25                  30

Ala Glu Asn Leu Ser Ala Ser Arg Ser Arg Ile Gln Asp Ala Asp Phe
        35                  40                  45

Ala Ala Glu Thr Ala Ala Leu Thr Arg Ala Gln Ile Leu Gln Gln Ala
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    50                  55                  60

Gly Val Ala Met Leu Ser Gln Ala Asn Ala Leu Pro Asn Asn Val Leu
65                  70                  75                  80

Ser Leu Leu Arg


<210> SEQ ID NO 98
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Campylobacter lari

<400> SEQUENCE: 98

Val Met Asp Ile Ala Asp Thr Ala Ile Ala Asn Leu Asp Thr Ile Arg
1               5                   10                  15

Ala Asn Ile Gly Ala Thr Gln Asn Gln Ile Thr Ser Thr Ile Asn Asn
            20                  25                  30

Ile Ser Val Thr Gln Val Asn Val Lys Ala Ala Glu Ser Gln Ile Arg
        35                  40                  45

Asp Val Asp Phe Ala Ser Glu Ser Ala Asn Tyr Ser Lys Ala Asn Ile
    50                  55                  60

Leu Ala Gln Ser Gly Ser Tyr Ala Met Ala Gln Ala Asn Ala Ala Ser
65                  70                  75                  80

Gln Asn Val Leu Arg Leu Leu Gln
                85
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1.-**13**. (canceled)

14. A composition comprising a *Salmonella* flagellin polypeptide, wherein the polypeptide comprises an amino acid sequence selected from SEQ ID NOs: 12, 30, 32, 34, 36, 38, 40, 42, and 44.

15. The composition of claim **14**, wherein the composition further comprises a radioprotectant.

16. The composition of claim **15**, wherein the radioprotectant is selected from an antioxidant, amifostine, vitamin E, a cytokine, a stem cell factor, a growth factor, keratinocyte growth factor, a steroid, 5-androstenediol, and ammonium trichloro(dioxoethylene-O,O')tellurate.

17. The composition of claim **14**, wherein the polypeptide is capable of inducing NFκB activity.

18. A pharmaceutical composition comprising a *Salmonella* flagellin polypeptide, wherein the polypeptide comprises an amino acid sequence selected from SEQ ID NOs: 12, 30, 32, 34, 36, 38, 40, 42, and 44 and a pharmaceutically acceptable adjuvant diluent, or carrier.

19. The pharmaceutical composition of claim **18**, wherein the composition further comprises a radioprotectant.

20. The pharmaceutical composition of claim **19**, wherein the radioprotectant is selected from an antioxidant, amifostine, vitamin E, a cytokine, a stem cell factor, a growth factor, keratinocyte growth factor, a steroid, 5-androstenediol, and ammonium trichloro(dioxoethylene-O,O')tellurate.

21. The pharmaceutical composition of claim **18**, wherein the polypeptide is capable of inducing NFκB activity.

* * * * *