

## 1. INFORMATION STORAGE AND PROCESSING

### 1.1. DNA metabolism

#### 1.1.1. Basic replication machinery (13 Results ordered by gene name)

Gene name <sup>a</sup>	Product <sup>b</sup>	Locus_tag <sup>c</sup>	Ref Gene name <sup>d</sup>	Ref Product <sup>e</sup>	RefSeq CG & WGS Best hit <sup>g</sup>	Clade Best hit <sup>h</sup>	Mode Best hit <sup>i</sup>	%id <sup>j</sup>
dnaB	replicative DNA helicase	Cloam1089	dnaB	replicative DNA helicase	Clostridium beijerincki NCIMB 8052	Firmicutes		44,4
dnaE	DNA polymerase III, subunit	Cloam1746	dnaE	DNA polymerase III, alpha subunit	Salinibacter ruber DSM 13855	Bacteroidetes/Chlorobi	anaero.	43,3
dnaG	DNA primase	Cloam1825	dnaG	DNA primase	Halothermothrix orenii H 168	Firmicutes	anaero.	33,6
dnaN	DNA polymerase III, subunit	Cloam1536		putative DNA polymerase III, beta chain (dnaN-like)	Bdellovibrio bacteriovorus HD100	Deltaproteobacteria	aero.	29,2
dnaQ	DNA polymerase III, subunit	Cloam1545		putative DNA polymerase III, epsilon subunit: DnaQ exonuclease (dnaQ-like) (DinG-like helicase)	Symbiobacterium thermophilum IAM 14863	Actinobacteria	micro.	33,5
dnaX	DNA polymerase III, and subunits	Cloam1210		putative DNA polymerase III, gamma/tau subunits	Pelobacter propionicus DSM 2379	Deltaproteobacteria	anaero.	48,5
gyrA	DNA gyrase, A subunit	Cloam1331	gyrA	DNA gyrase, A subunit	Chlorobium limicola DSM 245	Bacteroidetes/Chlorobi	anaero.	53,8
gyrB	DNA gyrase, B subunit	Cloam1332	gyrB	DNA gyrase (topoisomerase II) B subunit	Thermoanaerobacter ethanolicus ATCC 33223	Firmicutes	anaero.	62,6
hoIA	DNA polymerase III, subunit	Cloam1040		putative DNA polymerase III, delta subunit (hoIA-like)	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	21,1
hoIB*	DNA polymerase III, ' subunit	Cloam0793		DNA polymerase III, ' subunit (hoIB-like)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	29,1
hupA	DNA-binding protein	Cloam0973	hupA	DNA-binding protein HU-alpha (HU-2), plays a role in DNA replication and in rpo translation	Symbiobacterium thermophilum IAM 14863	Actinobacteria	micro.	53,9
lig	DNA ligase (NAD-dependent)	Cloam0968	ligA	DNA ligase, NAD-dependent	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	44,7
ssb	single-strand DNA-binding protein	Cloam1609		putative single-strand binding protein (ssb-like)	Desulfuromonas acetoxidans DSM 684	Deltaproteobacteria	anaero.	41,4

## 1. INFORMATION STORAGE AND PROCESSING

### 1.1. DNA metabolism

#### 1.1.2. DNA repair, restriction, and modification (3 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
nth	endonuclease III	Cloam0039		putative endonuclease III (nth-like)	Desulfotalea psychrophila Lsv54	Deltaproteobacteria	anaero.	56,7
poIA	5'-3' exonuclease domain of DNA polymerase I	Cloam1364	poIA	DNA polymerase I	Thermotoga maritima MSB8	Thermotogae	anaero.	42,6
ung*	uracil-DNA glycosylase	Cloam0287	ung	uracil-DNA glycosylase	Chlorobium limicola DSM 245	Bacteroidetes/Chlorobi	anaero.	48,8

**1. INFORMATION STORAGE AND PROCESSING**  
**1.2. RNA metabolism**  
**1.2.1. Basic transcription machinery (8 Results ordered by gene name)**

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
deaD	ATP-dependent RNA helicase	Cloam1879		putative helicase yprA (modular protein)	Symbiobacterium thermophilum IAM 14863	Actinobacteria	micro.	43,9
greA	transcription elongation factor	Cloam0049		putative transcription elongation factor (GreA)	Syntrophobacter fumaroxidans MPOB	Deltaproteobacteria	anaero.	39,6
nusA	transcription translation coupling	Cloam0263	nusA	N utilization substance protein A	Carboxydotherrnus hydrogenoformans Z-2901	Firmicutes	anaero.	36,6
nusG	transcription antitermination protein	Cloam0461	nusG	transcription antitermination protein NusG	Flavobacterium johnsoniae UW101	Bacteroidetes/Chlorobi	aero.	43,5
rpoA	RNA polymerase, a subunit	Cloam1113	rpoA	DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)	Desulfuromonas acetoxidans DSM 684	Deltaproteobacteria	anaero.	45,9
rpoB	RNA polymerase, b subunit	Cloam0456	rpoB	RNA polymerase, beta subunit	Salinibacter ruber DSM 13855	Bacteroidetes/Chlorobi	aero.	49,6
rpoC	RNA polymerase, b' subunit	Cloam0455	rpoC	RNA polymerase, beta' subunit; binds Zn(II)	Geobacter metallireducens			51,1
rpoD	RNA polymerase major factor	Cloam1826	rpoD	RNA polymerase sigma factor	Desulfuromonas acetoxidans DSM 684	Deltaproteobacteria	anaero.	43,9

**1. INFORMATION STORAGE AND PROCESSING**  
**1.2. RNA metabolism**  
**1.2.2. Translation**  
**1.2.2.1. Aminoacyl-tRNA synthesis (21 Results ordered by gene name)**

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
alaS	alanyl-tRNA synthase	Cloam1696	alaS	alanyl-tRNA synthetase	Chlorobium tepidum TLS	Bacteroidetes/Chlorobi	anaero.	48,3
argS	arginyl-tRNA synthase	Cloam0359		Arginyl-tRNA synthetase 1 (EC 6.1.1.19) (Arginine--tRNA ligase 1) (ArgRS 1)	Bacillus halodurans C-125	Firmicutes	fac.	43
asnS	asparaginylyl-tRNA synthase	Cloam0728		Asparaginylyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase) (AsnRS)	Desulfotomaculum reducens MI-1	Firmicutes	anaero.	52,2
aspS	aspartyl-tRNA synthase	Cloam1540	aspS	aspartyl-tRNA synthetase	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	53,5
cysS	cysteinyl-tRNA synthase	Cloam0734	cysS	cysteinyl-tRNA synthetase	Clostridium thermocellum ATCC 27405	Firmicutes	anaero.	52,3
glnS	glutaminylyl-tRNA synthase	Cloam1207	glnS	glutamine tRNA synthetase	Clostridium thermocellum ATCC 27405	Firmicutes	anaero.	63,8
gltX	glutamyl-tRNA synthase	Cloam0997	gltX	Glutamyl-tRNA synthetase (Glutamate--tRNA ligase) (GluRS)	Prosthecochloris vibrioformis DSM 265	Bacteroidetes/Chlorobi	fac.	47
glyS	glycyl-tRNA synthase, subunit	Cloam0616		putative glycine tRNA synthetase, beta subunit	Clostridium difficile QCD-32g58	Firmicutes	anaero.	37,2
hisS	histidyl-tRNA synthase	Cloam0515	hisS	histidyl-tRNA synthetase	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	50,4
ileS	isoleucyl-tRNA synthase	Cloam0569		Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS)	Alkaliphilus metalliredigenes QYMF	Firmicutes		51,7

leuS	leucyl-tRNA synthase	Cloam1110	leuS	leucyl-tRNA synthetase	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	Deltaproteobacteria	anaero.	51,7
lysS	lysyl-tRNA synthase	Cloam1688	lysS	lysyl-tRNA synthetase	Chlorobium chlorochromatii CaD3	Bacteroidetes/Chlorobi		50,3
metS	methionyl-tRNA synthase	Cloam0440		Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase) (MetRS)	Thermococcus kodakarensis KOD1	Euryarchaeota	anaero.	44,7
pheS	phenylalanyl-tRNA synthase, subunit	Cloam0533	pheS	phenylalanine tRNA synthetase, alpha-subunit	Thermoanaerobacter ethanolicus ATCC 33223	Firmicutes	anaero.	54,3
pheT	phenylalanyl-tRNA synthase, subunit	Cloam0534	pheT	phenylalanyl-tRNA synthetase, beta subunit	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	35,8
proS	prolyl-tRNA synthase	Cloam0426		Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (ProRS)	Blastopirellula marina DSM 3645	Planctomycetes		60
serS	seryl-tRNA synthase	Cloam1669	serS	seryl-tRNA synthetase	Thermoanaerobacter ethanolicus ATCC 33223	Firmicutes	anaero.	51,7
thrS	threonyl-tRNA synthase	Cloam0744	thrS	threonyl-tRNA synthetase	Nitrosococcus oceani ATCC 19707	Gammaproteobacteria		55,4
trpS	tryptophanyl-tRNA synthase	Cloam1432		Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	Francisella tularensis subsp. tularensis Schu 4	Gammaproteobacteria	aero.	53,6
tyrS	tyrosyl-tRNA synthase	Cloam0627	tyrS	tyrosyl-tRNA synthetase	Caldicellulosiruptor saccharolyticus DSM 8903	Firmicutes	anaero.	51
valS	valyl-tRNA synthase	Cloam0259	valS	valyl-tRNA synthetase	Halothermothrix orenii H 168	Firmicutes	anaero.	51,8

## 1. INFORMATION STORAGE AND PROCESSING

### 1.2. RNA metabolism

#### 1.2.2. Translation

##### 1.2.2.2. tRNA maturation and modification (6 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
mnmA	tRNA (5-methylaminomethyl-2-thiouridylate) methyltransferase	Cloam1161	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Clostridium thermocellum ATCC 27405	Firmicutes	anaero.	40,2
mnmE	GTP-binding protein involved in biosynthesis of 5-methylaminomethyl-2-thiouridine	Cloam0156	trmE	tRNA modification GTPase	Aquifex aeolicus VF5	Aquificae	aero.	41,5
mnmG	glucose inhibited division protein A, involved in biosynthesis of 5-methylaminomethyl-2-thiouridine	Cloam1794	gidA	glucose inhibited division protein A	Halothermothrix orenii H 168	Firmicutes	anaero.	49,7
rnpA	protein component of ribonuclease P	Cloam0546		putative RNase P, protein component, involved in tRNA and 4.5S RNA-processing (RnpA)	Pelobacter carbinolicus DSM 2380	Deltaproteobacteria	anaero.	32,9
pth	peptidyl-tRNA hydrolase	Cloam1611	pth	peptidyl-tRNA hydrolase	Bacillus clausii KSM-K16	Firmicutes		42,7
iscS	cysteine desulfurase-NifS homolog	Cloam1691	iscS	Cysteine desulfurase (Thil transpersulfidase) (NifS protein homolog)	Clostridium beijerincki NCIMB 8052	Firmicutes		42,7

**1. INFORMATION STORAGE AND PROCESSING****1.2. RNA metabolism****1.2.2. Translation****1.2.2.3. Ribosomal proteins (50 Results ordered by gene name)**

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
rplA	50S ribosomal protein L1	Cloam0459	rplA	50S ribosomal subunit protein L1, regulates synthesis of L1 and L11	Moorella thermoacetica ATCC 39073	Firmicutes	anaero.	60,8
rplB	50S ribosomal protein L2	Cloam1137	rplB	50S ribosomal subunit protein L2	Halothermothrix orenii H 168	Firmicutes	anaero.	68
rplC	50S ribosomal protein L3	Cloam1140	rplC	50S ribosomal subunit protein L3	Croceibacter atlanticus HTCC2559	Bacteroidetes/Chlorobi	aero.	53,3
rplD	50S ribosomal protein L4	Cloam1139	rplD	ribosomal protein L4	Carboxydotherrnus hydrogenoformans Z-2901	Firmicutes	anaero.	44,3
rplE	50S ribosomal protein L5	Cloam1128	rplE	50S ribosomal subunit protein L5	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	67,7
rplF	50S ribosomal protein L6	Cloam1125	rplF	50S ribosomal subunit protein L6	Syntrophomonas wolfei str. Goettingen	Firmicutes	anaero.	52,3
rplI	50S ribosomal protein L9	Cloam1606	rplI	ribosomal protein L9	Syntrophobacter fumaroxidans MPOB	Deltaproteobacteria	anaero.	42,6
rplJ	50S ribosomal protein L10	Cloam0458	rplJ	ribosomal protein L10	Carboxydotherrnus hydrogenoformans Z-2901	Firmicutes	anaero.	45,3
rplK	50S ribosomal protein L11	Cloam0460	rplK	50S ribosomal subunit protein L11, N-terminal believed to regulate RelA	Clostridium acetobutylicum ATCC 824	Firmicutes	anaero.	66,9
rplL	50S ribosomal protein L12	Cloam0457	rplL	50S ribosomal subunit protein L7/L12	Moorella thermoacetica ATCC 39073	Firmicutes	anaero.	69,4
rplM	50S ribosomal protein L13	Cloam1894	rplM	50S ribosomal subunit protein L13	Desulfitobacterium hafniense Y51	Firmicutes	anaero.	28,7
rplN	50S ribosomal protein L14	Cloam1130	rplN	50S ribosomal subunit protein L14	Clostridium acetobutylicum ATCC 824	Firmicutes	anaero.	72,9
rplO	50S ribosomal protein L15	Cloam1121	rplO	50S ribosomal subunit protein L15	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	50
rplP	50S ribosomal protein L16	Cloam1133	rplP	50S ribosomal subunit protein L16	Syntrophobacter fumaroxidans MPOB	Deltaproteobacteria	anaero.	70,1
rplQ	50S ribosomal protein L17	Cloam1112	rplQ	50S ribosomal subunit protein L17	Alteromonas macleodii 'Deep ecotype'	Gammaproteobacteria	aero.	49,2
rplR	50S ribosomal protein L18	Cloam1124	rplR	50S ribosomal subunit protein L18	Thermobifida fusca YX	Actinobacteria	aero.	64,9
rplS	50S ribosomal protein L19	Cloam1462	rplS	50S ribosomal subunit protein L19	Bacillus licheniformis ATCC 14580	Firmicutes	fac.	62,5
rplT	50S ribosomal protein L20	Cloam0531	rplT	50S ribosomal subunit protein L20, also posttranslational autoregulator	Alteromonas macleodii 'Deep ecotype'	Gammaproteobacteria	aero.	58,3
rplU	50S ribosomal protein L21	Cloam0293	rplU	50S ribosomal subunit protein L21	Bacteroides thetaiotaomicron VPI-5482	Bacteroidetes/Chlorobi	anaero.	47,6
rplV	50S ribosomal protein L22	Cloam1135	rplV	50S ribosomal subunit protein L22	Desulfuromonas acetoxidans DSM 684	Deltaproteobacteria	anaero.	54,1
rplW	50S ribosomal protein L23	Cloam1138	rplW	50S ribosomal subunit protein L23	Halothermothrix orenii H 168	Firmicutes	anaero.	59,6
rplX	50S ribosomal protein L24	Cloam1129	rplX	ribosomal protein L24	Desulfitobacterium hafniense DCB-2	Firmicutes	anaero.	51
rpmA	50S ribosomal protein L27	Cloam0292	rpmA	50S ribosomal subunit protein L27	Deinococcus geothermalis DSM 11300	Unknown		63,4
rpmB	50S ribosomal protein L28	Cloam1411	rpmB	ribosomal protein L28	Pelobacter carbinolicus DSM 2380	Deltaproteobacteria	anaero.	49,2
rpmC	50S ribosomal protein L29	Cloam1132	rpmC	ribosomal protein L29	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	65,6
rpmE	50S ribosomal protein L31	Cloam0173	rpmE	50S ribosomal subunit protein L31	Geobacter metallireducens GS-15	Deltaproteobacteria	anaero.	69,7
rpmF	50S ribosomal protein L32	Cloam0257	rpmF	ribosomal protein L32	Geobacter uraniumreducens Rf4	Deltaproteobacteria	micro.	54,2

rpmG	50S ribosomal protein L33	Cloam0463	rpmG	ribosomal protein L33	Aquifex aeolicus VF5	Aquificae	aero.	71,7
rpmH	50S ribosomal protein L34	Cloam0547	rpmH	50S ribosomal subunit protein L34	Bacteroides fragilis YCH46	Bacteroidetes/Chlorobi	anaero.	81,8
rpml	50S ribosomal protein L35	Cloam0530	rpml	50S ribosomal protein L35	Desulfotobacterium hafniense Y51	Firmicutes	anaero.	62,9
rpmJ	50S ribosomal protein L36	Cloam1117	rpmJ	50S ribosomal subunit protein X	Alteromonas macleodii 'Deep ecotype'	Gammaproteobacteria	aero.	79,5
rpsB	30S ribosomal protein S2	Cloam1890	rpsB	30S ribosomal subunit protein S2	Geobacter metallireducens GS-15	Deltaproteobacteria	anaero.	57,3
rpsC	30S ribosomal protein S3	Cloam1134	rpsC	30S ribosomal subunit protein S3	Pseudomonas syringae pv. tomato str. DC3000	Gammaproteobacteria	aero.	56,4
rpsD	30S ribosomal protein S4	Cloam1114	rpsD	30S ribosomal subunit protein S4	Desulfuromonas acetoxidans DSM 684	Deltaproteobacteria	anaero.	53,4
rpsE	30S ribosomal protein S5	Cloam1123	rpsE	30S ribosomal subunit protein S5	Moorella thermoacetica ATCC 39073	Firmicutes	anaero.	61
rpsF	30S ribosomal protein S6	Cloam1610	rpsF	Ribosomal protein S6	Carboxythermus hydrogenoformans Z-2901	Firmicutes	anaero.	37,6
rpsG	30S ribosomal protein S7	Cloam0453	rpsG	30S ribosomal subunit protein S7, initiates assembly	Rhodopseudomonas palustris CGA009	Alphaproteobacteria	fac.	63,5
rpsH	30S ribosomal protein S8	Cloam1126	rpsH	30S ribosomal subunit protein S8, and regulator	Chlamydia muridarum Nigg	Chlamydiae/Verrucomicrobia		46,7
rpsI	30S ribosomal protein S9	Cloam1893	rpsI	30S ribosomal subunit protein S9	Clostridium perfringens str. 13	Firmicutes	anaero.	66,1
rpsJ	30S ribosomal protein S10	Cloam1141	rpsJ	30S ribosomal subunit protein S10	Solibacter usitatus Ellin6076	Acidobacteria	aero.	67,7
rpsK	30S ribosomal protein S11	Cloam1115	rpsK	30S ribosomal subunit protein S11	Halothermothrix orenii H 168	Firmicutes	anaero.	62,7
rpsL	30S ribosomal protein S12	Cloam0454	rpsL	30S ribosomal subunit protein S12	Polaribacter irgensii 23-P	Bacteroidetes/Chlorobi	aero.	80,5
rpsM	30S ribosomal protein S13	Cloam1116	rpsM	30S ribosomal subunit protein S13	Thermoanaerobacter ethanolicus ATCC 33223	Firmicutes	anaero.	62,7
rpsN	30S ribosomal protein S14	Cloam1127	rpsN	ribosomal protein S14	Carboxythermus hydrogenoformans Z-2901	Firmicutes	anaero.	73,8
rpsO	30S ribosomal protein S15	Cloam1474	rpsO	30S ribosomal subunit protein S15	Halothermothrix orenii H 168	Firmicutes	anaero.	66,3
rpsP	30S ribosomal protein S16	Cloam1467	rpsP	Ribosomal protein S16	Geobacillus kaustophilus HTA426	Firmicutes	aero.	60,2
rpsQ	30S ribosomal protein S17	Cloam1131	rpsQ	30S ribosomal subunit protein S17	Carboxythermus hydrogenoformans Z-2901	Firmicutes	anaero.	67,7
rpsR	30S ribosomal protein S18	Cloam1608	rpsR	30S ribosomal subunit protein S18	Desulfotalea psychrophila LSv54	Deltaproteobacteria	anaero.	61,4
rpsS	30S ribosomal protein S19	Cloam1136	rpsS	30S ribosomal subunit protein S19	Anaeromyxobacter dehalogenans 2CP-C	Deltaproteobacteria	anaero.	75
rpsT	30S ribosomal protein S20	Cloam0933	rpsT	30S ribosomal protein S20	Symbiobacterium thermophilum IAM 14863	Actinobacteria	micro.	48,5

## 1. INFORMATION STORAGE AND PROCESSING

### 1.2. RNA metabolism

#### 1.2.2. Translation

##### 1.2.2.4. Ribosome function, maturation and modification (7 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
ksgA	dimethyladenosine transferase	Cloam1814	ksgA	Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) (16S rRNA dimethylase) (High level kasugamycin resistance protein ksgA) (Kasugamycin dimethyltransferase)	Lactobacillus salivarius subsp. salivarius UCC118	Firmicutes	fac.	43

rbfA	ribosome-binding factor A	Cloam0267		putative ribosome-binding factor A (rbfA-like)	Halothermothrix orenii H 168	Firmicutes	anaero.	30,6
engA	GTP-binding protein	Cloam0371	engA	GTP-binding protein	Thermoanaerobacter ethanolicus ATCC 33223	Firmicutes	anaero.	49,2
obg	GTP-binding protein	Cloam0122	obg	GTP-binding protein, GTP1/OBG family	Carboxythermus hydrogenoformans Z-2901	Firmicutes	anaero.	51
ychF	GTP-binding protein	Cloam0346		putative GTP-binding protein with nucleoside triP hydrolase domain	Syntrophomonas wolfei str. Goettingen	Firmicutes	anaero.	42,6
era	GTP-binding protein	Cloam1148	era	GTP-binding protein	Bacteroides fragilis NCTC 9343	Bacteroidetes/Chlorobi	anaero.	43,1
cspR*	ribosomal methyltransferase	Cloam1178		putative tRNA/rRNA methyltransferase	Bdellovibrio bacteriovorus HD100	Deltaproteobacteria	aero.	33,5

## 1. INFORMATION STORAGE AND PROCESSING

### 1.2. RNA metabolism

#### 1.2.2. Translation

##### 1.2.2.5. Translation factors (12 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
efp	elongation factor P	Cloam0572	efp	translation initiation factor eIF-5A	Moorella thermoacetica ATCC 39073	Firmicutes	anaero.	49,7
fusA	elongation factor G	Cloam1619	fusA	translation elongation factor G	Moorella thermoacetica ATCC 39073	Firmicutes	anaero.	52,7
frr	ribosome recycling factor	Cloam1887	frr	ribosome releasing factor	Geobacillus kaustophilus HTA426	Firmicutes	anaero.	53,6
hemK	N5-glutamine methyltransferase, modulation of release factors activity	Cloam1616	hemK	modification methylase, HemK family	Clostridium difficile QCD-32g58	Firmicutes	anaero.	40
infA	initiation factor IF-1	Cloam1118	infA	protein chain initiation factor IF-1	Rubrobacter xylanophilus DSM 9941	Actinobacteria	aero.	82
infB	initiation factor IF-2	Cloam0266	infB	translation initiation factor IF-2	Carboxythermus hydrogenoformans Z-2901	Firmicutes	anaero.	42
infC	initiation factor IF-3	Cloam0529	infC	protein chain initiation factor IF-3	Buchnera aphidicola str. Sg (Schizaphis graminum)	Gammaproteobacteria		55,4
lepA	GTP-binding elongation factor	Cloam0113	lepA	GTP-binding elongation factor	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	57
prfA	peptide chain release factor 1 (RF1)	Cloam0175	prfA	peptide chain release factor RF-1	Treponema denticola ATCC 35405	Spirochaetes	anaero.	58,9
smpB	tmRNA-binding protein	Cloam1778	smpB	SsrA-binding protein	Thermus thermophilus HB27	Deinococcus-Thermus	aero.	58
tsf	elongation factor Ts	Cloam1889	tsf	translation elongation factor Ts	Thermoanaerobacter ethanolicus ATCC 33223	Firmicutes	anaero.	57,2
tufA	elongation factor Tu	Cloam0464	tufB	putative protein chain elongation factor EF-Tu; GTP-binding factor (duplicate of tufA)	Halothermothrix orenii H 168	Firmicutes	anaero.	77,1

## 1. INFORMATION STORAGE AND PROCESSING

### 1.2. RNA metabolism

#### 1.2.3. RNA degradation (2 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
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pnp	polyribonucleotide nucleotidyltransferase	Cloam1473	pnp	polynucleotide phosphorylase, has polyadenylase activity	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Fusobacteria	anaero.	53
rnc	ribonuclease III	Cloam0250	rnc	dsRNA-specific ribonuclease	Solibacter usitatus Ellin6076	Acidobacteria	aero.	42,6

## 2. PROTEIN PROCESSING, FOLDING, AND SECRETION

### 2.1. Protein post-translational modification (2 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
map	methionine aminopeptidase	Cloam1119	map	methionine aminopeptidase (MAP) (peptidase M)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	54,6
pepA	aminopeptidase A/I	Cloam0131	pepA	cytosol aminopeptidase (leucine aminopeptidase) (LAP) (leucyl aminopeptidase) (aminopeptidase A/I)	Clostridium perfringens str. 13	Firmicutes	anaero.	46,4

## 2. PROTEIN PROCESSING, FOLDING, AND SECRETION

### 2.2. Protein folding (5 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
dnaJ	Hsp70 co-chaperone	Cloam0758	dnaJ	Chaperone protein DnaJ (Heat shock protein 40) (HSP40)	Pelodictyon luteolum DSM 273	Bacteroidetes/Chlorobi	anaero.	47,1
dnaK	chaperone Hsp70	Cloam0757	dnaK	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	Borrelia burgdorferi B31	Spirochaetes	aero.	63,4
groEL	class I heat-shock protein	Cloam1649	groL	chaperone Hsp60 (GroEL), part of GroE chaperone system	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	64,7
groES	class I heat-shock protein	Cloam0817	groES	chaperonin, 10 kDa	Porphyromonas gingivalis W83	Bacteroidetes/Chlorobi	anaero.	58,9
grpE	Hsp70 co-chaperone	Cloam0756	grpE	GrpE protein	Chloroflexus aurantiacus J-10-fl	Chloroflexi	anaero.	37,8

## 2. PROTEIN PROCESSING, FOLDING, AND SECRETION

### 2.3. Protein translocation and secretion (5 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
ffh	protein component of signal recognition particle (SRP)	Cloam1602	ffh	4.5S-RNP protein, GTP-binding export factor, part of signal recognition particle with 4.5 RNA	Carboxydotherrmus hydrogenoformans Z-2901	Firmicutes	anaero.	56,9
ftsY	signal recognition particle receptor	Cloam0799	ftsY	Cell division protein FtsY	Porphyromonas gingivalis W83	Bacteroidetes/Chlorobi	anaero.	48,2
secA	preprotein translocase subunit (ATPase)	Cloam1732	secA	preprotein translocase secA subunit, essential ATPase protein	Chlorobium tepidum TLS	Bacteroidetes/Chlorobi	anaero.	48,8

secE	membrane-embeded preprotein translocase subunit	Cloam0462	secE	Preprotein translocase subunit SecE	Listeria monocytogenes str. 4b F2365	Firmicutes	fac.	47,3
secY	membrane-embeded preprotein translocase subunit	Cloam1120	secY	preprotein translocase secY subunit, essential membrane protein	Syntrophobacter fumaroxidans MPOB	Deltaproteobacteria	anaero.	52

## 2. PROTEIN PROCESSING, FOLDING, AND SECRETION

### 2.4. Protein turnover (3 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
gcp	probable O-sialoglycoprotein endopeptidase	Cloam0874		putative metalloendopeptidase, glycoprotease family	Clostridium perfringens str. 13	Firmicutes	anaero.	48,3
hflB	ATP-dependent protease	Cloam0831	ftsH	Cell division protein FtsH, ATP-dependent zinc protease	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	57,3
lon	ATP-dependent protease La	Cloam1447	lon	DNA-binding ATP-dependent protease La; heat shock K-protein	Geobacter uraniumreducens Rf4	Deltaproteobacteria	micro.	49,1

## 3. CELLULAR PROCESSES

### 3.1. Cell division (1 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
ftsZ	cytoskeletal cell division protein	Cloam0778	ftsZ	Cell division protein FtsZ, tubulin-like GTP-binding protein and GTPase	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	51,7

## 3. CELLULAR PROCESSES

### 3.2. Transport (4 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
pitA*	low-affinity inorganic phosphate transporter	Cloam0136		putative low-affinity inorganic phosphate transporter (pitA-like)	Synechococcus sp. WH 5701	Cyanobacteria		44,4
ptsG	phosphotransferase system (PTS) glucose-specific enzyme II	-						
ptsH	histidine-containing phosphocarrier protein of the phosphotransferase system (PTS)	Cloam1753	ptsH	phosphocarrier protein HPr	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	58
ptsI	phosphotransferase system (PTS) enzyme I	Cloam1752		putative PTS family enzyme I and Hpr components, PEP-protein phosphotransferase	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	39,8



		Cloam0618		putative Sugar phosphotransferase system IIA component (EC 2.7.1.69)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	40,8
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#### 4. ENERGETIC AND INTERMEDIARY METABOLISM

##### 4.1. Glycolysis (10 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
eno	enolase	Cloam1651	eno	enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	66,6
fbaA	fructose-1,6-bisphosphate aldolase	Cloam1837	fbaA	fructose-bisphosphate aldolase	Halothermothrix orenii H 168	Firmicutes	anaero.	32,9
gapA	glyceraldehyde 3-phosphate dehydrogenase	Cloam1840	gapA	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)	Thermotoga maritima MSB8	Thermotogae	anaero.	67,1
gpmA	phosphoglycerate mutase	Cloam0341	gpmA	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (Phosphoglyceromutase) (PGAM) (BPG-dependent PGAM) (dPGM)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	67,3
ldh	L-lactate dehydrogenase	_						
pfkA	6-phosphofructokinase	Cloam0626	pfk	6-phosphofructokinase (ATP-dependent phosphofructokinase) (ATP-PFK)	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	48,5
pgi	glucose-6-phosphate isomerase	Cloam1751	pgi	Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)	Halothermothrix orenii H 168	Firmicutes	anaero.	47,3
pgk	phosphoglycerate kinase	Cloam0802	pgk	3-phosphoglycerate kinase	Chlamydia trachomatis D/UW-3/CX	Chlamydiae/Verrucomicrobia		33,6
pykA*	pyruvate kinase	Cloam0519	ppdK	pyruvate phosphate dikinase	Bacteroides fragilis NCTC 9343	Bacteroidetes/Chlorobi	anaero.	72,9
tpiA	triose phosphate isomerase	Cloam1668	tpiA	Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)	Tenacibaculum sp. MED152	Bacteroidetes/Chlorobi	aero.	47,2
		Cloam1211	pfp	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase (PPi-PFK) - anaero.	Rhodospirillum rubrum ATCC 11170	Alphaproteobacteria	fac.	70,8

#### 4. ENERGETIC AND INTERMEDIARY METABOLISM

##### 4.2. Proton-motive force generation (9 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
atpA	ATP synthase chain	Cloam1053		V-type ATP synthase beta chain 1 (EC 3.6.3.14) (V-type ATPase subunit B 1)	Porphyromonas gingivalis W83	Bacteroidetes/Chlorobi	anaero.	80,9
atpB	ATP synthase A chain	_						
atpC	ATP synthase chain	_						

atpD	ATP synthase chain	Cloam1052		V-type ATP synthase alpha chain 1 (EC 3.6.3.14) (V-type ATPase subunit A 1)	Bacteroides fragilis YCH46	Bacteroidetes/Chlorobi	anaero.	68,8
atpE	ATP synthase C chain	Cloam1056		putative V(Vacuolar)-type Na <sup>+</sup> -ATP synthase subunit K	Bacteroides fragilis YCH46	Bacteroidetes/Chlorobi	anaero.	54,4
atpF	ATP synthase B chain	Cloam1050		putative V-type ATPase, subunit E	Porphyromonas gingivalis W83	Bacteroidetes/Chlorobi	anaero.	36,7
atpG	ATP synthase chain	–						
atpH	ATP synthase chain	–						
yidC	essential for proper integration of ATPase into the membrane	Cloam0544		hypothetical protein; putative membrane protein	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	27,9
		Cloam1054		putative V(Vacuolar)-type ATP synthase subunit D	Bacteroides fragilis YCH46	Bacteroidetes/Chlorobi	anaero.	54,6
		Cloam1055		putative V(Vacuolar)-type Na <sup>+</sup> ATP synthase subunit I	Bacteroides fragilis NCTC 934	Bacteroidetes/Chlorobi	anaero.	36,9

#### 4. ENERGETIC AND INTERMEDIARY METABOLISM

##### 4.3. Pentose phosphate pathway (3 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
rpe	ribulose-phosphate 3-epimerase	Cloam1603	rpe	D-ribulose-5-phosphate 3-epimerase	Campylobacter fetus subsp. fetus 82-40	Epsilonproteobacteria	micro.	47,6
rpiA	ribose 5-phosphate isomerase	Cloam0751	rpiB	ribose 5-phosphate isomerase B, also acts as allose 6-phosphate isomerase	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	55,6
tkk	transketolase	Cloam1259		putative Transketolase	Thermotoga maritima MSB8	Thermotogae	anaero.	45,8

#### 4. ENERGETIC AND INTERMEDIARY METABOLISM

##### 4.4. Lipid metabolism (7 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
cdsA	phosphatidate cytidyltransferase	Cloam1573	cdsA	Phosphatidate cytidyltransferase (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diacylglycerol synthase) (CDS) (CTP:phosphatidate cytidyltransferase) (CDP-DAG synthase) (CDP-DG synthetase)	Vibrio vulnificus CMCP6 chromosome	Gammaproteobacteria	fac.	31,5
fadD	acyl-CoA synthase	–						
gpsA	sn-glycerol-3-phosphate dehydrogenase	Cloam0870	gpsA	glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H- dependent glycerol-3-phosphate dehydrogenase)	Geobacter uraniumreducens Rf4	Deltaproteobacteria	micro.	49,3
plsB	sn-glycerol-3-phosphate acyltransferase	–						

plsC	1-acyl-sn-glycerol-3-phosphate acyltransferase	Cloam1445		putative 1-acyl-sn-glycerol-3-phosphate acyltransferase (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase) (LPAAT) (plsC)	Clostridium acetobutylicum ATCC 824	Firmicutes	anaero.	36,2
psd	phosphatidylserine decarboxylase	-						
pssA	phosphatidylserine synthase	-						
		Cloam0330	pgsA	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (Phosphatidylglycerophosphate synthase) (PGP synthase)	Clostridium difficile QCD-32g58	Firmicutes	anaero.	46
		Cloam0597	cls	cardiolipin synthetase 2 (Cardiolipin synthase 2) (CL synthase 2)	Bacillus anthracis str. Ames	Firmicutes	fac.	43,3
		Cloam0005	pgpA	phosphatidylglycerophosphatase A	Prosthecochloris aestuarii DSM 271	Bacteroidetes/Chlorobi		40
		Cloam0256	plsX	fatty acid/phospholipid synthesis protein, methyltransferase domain	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Fusobacteria	anaero.	47,3
		Cloam1600		putative acyl-CoA synthetase with NAD(P)-binding domain and succinyl-CoA synthetase domain	Moorella thermoacetica ATCC 39073	Firmicutes	anaero.	42,4

#### 4. ENERGETIC AND INTERMEDIARY METABOLISM

##### 4.5. Biosynthesis of nucleotides (15 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
adk	adenylate kinase	Cloam1458	adk	Adenylate kinase (ATP-AMP transphosphorylase)	Frankia sp. EAN1pec	Actinobacteria	aero.	43,5
dcd	dCTP deaminase	-						
gmk	guanylate kinase	Cloam0289	gmk	Guanylate kinase (GMP kinase)	Clostridium beijerincki NCIMB 8052	Firmicutes		45
hpt	hypoxanthine phosphoribosyltransferase	Cloam0832	hpt	Hypoxanthine-guanine phosphoribosyltransferase	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	54,9
ndk	nucleoside diphosphate kinase	Cloam0822	ndk	nucleoside diphosphate kinase (NDK) (NDP kinase) (nucleoside-2-P kinase)	Methanocaldococcus jannaschii DSM 2661	Euryarchaeota	anaero.	43,7
nrdE	ribonucleoside-diphosphate reductase (major subunit)	Cloam0913		putative B12-dependent ribonucleoside diphosphate (1.17.4.1)/triphosphate(1.17.4.2) reductase (nrdJ-like)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	55
nrdF	ribonucleoside-diphosphate reductase (minor subunit)	-						
ppa*	inorganic pyrophosphatase	Cloam1022	hppA	Pyrophosphate-energized proton pump (Pyrophosphate-energized inorganic pyrophosphatase) (H <sup>+</sup> -PPase) (Membrane-bound proton-translocating pyrophosphatase)	Bacteroides fragilis YCH46	Bacteroidetes/Chlorobi	anaero.	58,1

prsA	phosphoribosylpyrophosphate synthase	Cloam1613	prsA	ribose-phosphate pyrophosphokinase (RPPK) (phosphoribosyl pyrophosphate synthetase) (P-Rib-PP synthetase) (PRPP synthetase)	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	55
pyrG	CTP synthase	Cloam0808	pyrG	CTP synthase (UTP-ammonia ligase) (CTP synthetase)	Caldicellulosiruptor saccharolyticus DSM 8903	Firmicutes	anaero.	59,8
thyA*	thymidylate synthase	Cloam1244		putative Thymidylate synthase (FAD) (thyX)	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	37,7
tmk	thymidylate kinase	Cloam0356	tmk	thymidylate kinase	Carboxydotherrmus hydrogenoformans Z-2901	Firmicutes	anaero.	51,7
trxA	thioredoxin	Cloam0816	trx	thioredoxin	Desulfotomaculum reducens MI-1	Firmicutes	anaero.	53,4
trxB	thioredoxin reductase	Cloam1697	trxB	Thioredoxin reductase	Carboxydotherrmus hydrogenoformans Z-2901	Firmicutes	anaero.	53,2
upp*	uracil phosphoribosyltransferase	Cloam1719	pyrR	Bifunctional protein: pyrimidine operon regulatory protein; Uracil phosphoribosyltransferase (UPRTase)	Carboxydotherrmus hydrogenoformans Z-2901	Firmicutes	anaero.	63,1
		Cloam1514	cdd	Cytidine deaminase (3.5.4.5)	Halothermothrix orenii H 168	Firmicutes	anaero.	53,2
		Cloam1777	ssnA	Cytosine deaminase and related metal-dependent hydrolases (3.5.4.3)	Syntrophobacter fumaroxidans MPOB	Deltaproteobacteria	anaero.	41
		Cloam1253	nrdD	Anaero. ribonucleoside-triphosphate reductase (Oxygen-sensitive ribonucleoside-triphosphate reductase)	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	65,3
		Cloam1254		putative anaero. ribonucleotide reductase activating enzyme (NrdG-like)	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	49,5

#### 4. ENERGETIC AND INTERMEDIARY METABOLISM

##### 4.6. Biosynthesis of cofactors (12 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
coaA*	pantothenate kinase	Cloam1150		putative Pantothenate kinase type III (PanK, CoaX)	Syntrophus aciditrophicus SB	Deltaproteobacteria	anaero.	36,6
coaD	4'-phospho-pantetheine adenyltransferase	Cloam1088	coaD	Phosphopantetheine adenyltransferase (Pantetheine- phosphate adenyltransferase) (PPAT) (Dephospho-CoA pyrophosphorylase)	Bacillus halodurans C-125	Firmicutes	fac.	51,9
coaE	dephosphocoenzyme A kinase	Cloam0986	coaE	Dephospho-CoA kinase (Dephosphocoenzyme A kinase)	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Fusobacteria	anaero.	32,7
dfp	phosphopantothenate cysteine ligase, 4'-phospho-pantothenyl-L-cysteine decarboxylase	Cloam1437	dfp	Coenzyme A biosynthesis bifunctional protein coaBC (DNA/pantothenate metabolism flavoprotein) [Includes: Phosphopantothenoylcysteine decarboxylase (PPCDC) (CoaC); Phosphopantothenate--cysteine ligase (Phosphopantothenoylcysteine synthase) (PPC synthetase) (PPCS) (CoaB)]	Desulfotomaculum reducens MI-1	Firmicutes	anaero.	44,9
folA	dihydrofolate reductase	Cloam1093	folA	Dihydrofolate reductase	Bacillus sp. NRRL B-14911	Firmicutes		45,5
glyA	glycine hydroxymethyltransferase	Cloam0752	glyA	serine hydroxymethyltransferase (serine methylase) (SHMT)	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	62,9

metK	methionine adenosyltransferase	Cloam1766	metK	S-adenosylmethionine synthetase (Methionine adenosyltransferase) (AdoMet synthetase) (MAT)	Nitrosomonas eutropha C71	Betaproteobacteria		51,6
nadR	adenyl transferase	-						
nadV	nicotinamide phosphoribosyltransferase	-						
pdxY*	pyridoxal kinase	Cloam0285	pdxK	pyridoxine kinase (Pyridoxal kinase) (Vitamin B6 kinase) (Pyridoxamine kinase) (PN/PL/PM kinase)	Clostridium acetobutylicum ATCC 824	Firmicutes	anaero.	39,6
ribF	riboflavin kinase, FMN adenylyltransferase	Cloam0270	ribF	Riboflavin biosynthesis protein [Includes: Riboflavin kinase (Flavokinase); FMN adenylyltransferase (FAD pyrophosphorylase) (FAD synthetase)]	Bdellovibrio bacteriovorus HD100	Deltaproteobacteria	aero.	39,4
yloS	thiamine pyrophosphokinase	Cloam0118		putative Thiamine pyrophosphokinase (TPK) (Thiamine diphosphokinase) (thiN-like)	Clostridium thermocellum ATCC 27405	Firmicutes	anaero.	34,7
		Cloam1821	nadE	NH(3)-dependent NAD(+) synthetase (6.3.1.5)	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	56
		Cloam0053		putative nicotinate (nicotinamide) nucleotide adenylyltransferase (nadD)	Clostridium tetani E88	Firmicutes	anaero.	33,3
		Cloam1857	nadC	Nicotinate-nucleotide pyrophosphorylase (EC 2.4.2.19)	Halothermothrix orenii H 168	Firmicutes	anaero.	52
		Cloam0328	nadA	quinolinate synthetase complex, subunit A (6.3.1.5)	Clostridium thermocellum ATCC 27405	Firmicutes	anaero.	53
		Cloam0357	nadB	Best similarity : L-aspartate oxidase (EC 1.4.3.16) (LASPO) (Quinolinate synthetase B) Annotation : putative NADH-dependent fumarate reductase (1.3.1.6) (frd)	Geobacter sulfurreducens PCA	Deltaproteobacteria	anaero.	49,1

## 5. POORLY CHARACTERIZED (7 Results ordered by gene name)

Gene name	Product	Locus_tag	Ref Gene name	Ref Product	RefSeq CG & WGS Best hit	Clade Best hit	Mode Best hit	%id
mesJ	conserved hypothetical protein	Cloam0833		putative tRNA(Ile)-lysidine synthase (mesJ-like)	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	32,5
mraW	methyltransferase	Cloam0789	mraW	S-adenosyl-methyltransferase MraW	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	48,9
ybeY	conserved hypothetical protein	Cloam1232		hypothetical protein	Exiguobacterium sibiricum 255-15	Firmicutes	fac.	32,6
ycfF	HIT family	Cloam0303		HIT family hydrolase	Halothermothrix orenii H 168	Firmicutes	anaero.	45,4
ycfH	putative deoxyribonuclease, tatD family	Cloam1263	tatD	Mg-dependent DNase	Clostridium thermocellum ATCC 27405	Firmicutes	anaero.	43,5
yoaE	conserved hypothetical protein	Cloam1233		putative Hemolysin-related protein	Thermotoga maritima MSB8	Thermotogae	anaero.	36,8
yqgF	conserved hypothetical protein	Cloam1509		putative Holliday junction resolvase (EC 3.1.-.-)	Crocospaera watsonii WH 8501 (Synechocystis sp. WH 8501)	Cyanobacteria		36,7

yraL	conserved hypothetical protein	Cloam0961	predicted methyltransferases	Thermoanaerobacter tengcongensis MB4	Firmicutes	anaero.	41,7
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### Supplementary Table 3 : Essential gene set identification

<sup>a</sup> gene name as in the available *C. acidaminovorans* annotation.

<sup>b</sup> gene product as in the available *C. acidaminovorans* annotation.

<sup>c</sup> Cloam naming reference.

<sup>d</sup> gene name as in the RefSeq best hit corresponding entry.

<sup>e</sup> gene product as in the RefSeq best hit corresponding entry.

<sup>f</sup> RefSeq best hit (in Complete Genomes of in Whole Genome Shotgun sections).

<sup>g</sup> RefSeq best hit clade.

<sup>h</sup> RefSeq mode ( aero. = aerobic, anaero. = anaerobic, fac. = facultative aerobic, micro. = microaerophilic)

<sup>i</sup> percentage identity

Lines highlighted in yellow indicates *C. acidaminovorans* genes that might supplement absent essential genes.

Lines highlighted in orange indicates essential genes not identified in the *C. acidaminovorans* genome annotation.

The essential gene set used is as previously reported (13).