Title:

Interleukin-34 orchestrates bone formation through its binding to Bone Morphogenic Proteins

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Abstract

Rationale: During development, the contribution of IL34, a ligand of macrophage colony stimulating factor receptor (MCSFR), has not been fully defined. Together with its twin cytokine MCSF, they display an essential role in macrophage differentiation and activation, including tissue specialized macrophages. The mechanism of action of each molecule involves the phosphorylation of MCSFR in varying intensity and kinetics. Furthermore, IL34 can interact with other receptors and cofactors, opening a wide range of modulations during development. The aim of this work was to investigate these effects through the suppression of IL34 in different animal models and study molecular interactions, with a particular focus on osteoclast / osteoblast regulation.

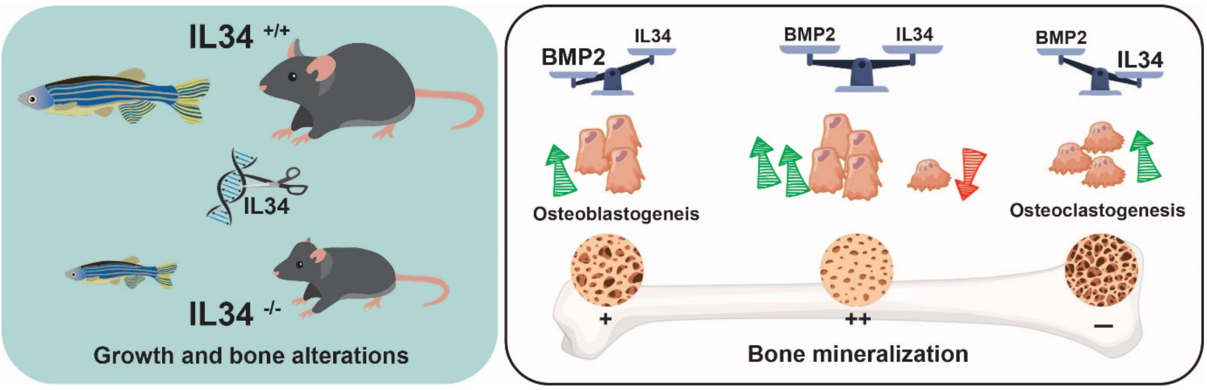
Methods: Two different and unique models of *IL34*$^{-/-}$ were generated in zebrafish and mouse. The skeleton of both species was analyzed and compared by histological and morphometric (Micro-CT) approaches. The role of IL34 and new partners in osteoclast and osteoblast differentiation was analyzed by multiple techniques including mineralization assays, tartrate resistant acid phosphatase (TRAP) staining, receptor phosphorylation and activation assays, and gene expression (real-time quantitative PCR) studies. Furthermore, protein interactions were studied by surface plasmon resonance approach and protein-protein docking ClusPro analysis.

Results: Significant growth delay and hypo-mineralization of skeletal elements were observed in both *IL34*$^{-/-}$ models, as well as craniofacial dysmorphoses in mice. With regard to bone cells, an unexpected increase in the number of osteoclasts and an accumulation of pre-osteoblasts were observed in mice lacking IL34. For the first time, *in vitro* analyses complemented by protein binding and molecular docking studies established that IL34 interacts directly with certain Bone Morphogenetic Proteins (BMPs), modulating their various activities such as the stimulation of osteoblast differentiation.

Conclusions: A new mechanism of action for IL34 through BMPs has been characterized. IL34 interactions with MCSFR and BMPs appear crucial for both osteoclastogenesis and osteoblastogenesis, impacting bone tissue homeostasis and development. The potential interaction of IL34 with different members of the BMP family and their functional impact, including pathological situations such as cancer, should be further explored, opening new therapeutic perspectives.

Keywords: development, bone homeostasis, osteoclastogenesis, osteoblastogenesis, protein docking.

Graphical Abstract



Introduction

Interleukin-34 (IL34) is a soluble cytokine discovered in 2008 by its ability to bind to macrophage colony-stimulating factor receptor (MCSFR), also known as c-FMS/CSF1R/CD115 [1]. This work has rekindled interest in the MCSFR signaling pathway and in the roles of the twin cytokines MCSF/IL34 in the differentiation and activation of myeloid cell lineage, such as macrophages, Langerhans cells, microglia cells and osteoclasts [2–5]. IL34 binding to MCSFR can occur as a homodimer or heterodimer with MCSF/CSF1, depending on the relative amounts of the two cytokines [6]. The twin cytokines induce similar patterns of phosphorylation of MCSFR but with variable intensity and kinetics, raising the question of their functional redundancy and specific functions. Their functional redundancy is confirmed by the greater severity of the bone phenotype associated with *MCSFR* versus *MCSF* invalidation in mice [7,8]. As far as the implications of IL34 during bone development are concerned, the data currently available are scarce, and focus mainly on its pro-osteoclastic action via its binding to the M-CSFR receptor (the binding that led to its identification [1]). Similarly to MCSF, IL34, by binding to MCSFR on the surface of osteoclastic precursors of myeloid origin, induces their engagement in the osteoclastic differentiation pathway which will then be completed by RANKL stimulation [2,9–14]. Regarding the source of IL34, osteoblastic expression [15,16] and chondroblastic expression [17] have been reported, suggesting that IL34 may be involved in communications between bone forming cells and osteoclasts. In the absence of a detailed description of the skeletal phenotype associated with IL34 invalidation during growth, the roles of IL34 in this growth process are still unclear. Additional receptors of IL34 have been identified and include Protein-Tyrosine Phosphatase β/ζ receptor (PTPβ/ζ) [18], Triggering Receptor Expressed on Myeloid cells-2 (TREM2) [19] and syndecan-1 [20]. PTPβ/ζ is mainly expressed by neuronal progenitors and glial cells and known as pleiotrophin/heparin-binding growth-associated molecule receptor [21]. TREM2 is a lipid-binding receptor [22], carried by myeloid lineage cells, whose differentiation and migratory capacities it modulates [23]. Finally, IL34 binds to Syndecan-1 (CD138) and this binding modulates IL34-mediated activation of MCSFR [20]. The diversity of IL34 receptors and co-ligands suggests that this cytokine plays an important role in the differentiation and activation of myeloid, neural and glial cells. In this context, the existence of other partners for IL34 must not be excluded. To analyze these functions, IL34 was suppressed in zebrafish and mouse and the phenotypes of these mutants was fully deciphered during development. New partners have been identified and their functional and biological implications have been analyzed.

Results

Zebrafish and mouse IL34 null models show significant alterations of the skeleton during development

IL34 invalidation was genetically achieved in zebrafish and mouse using respectively CrispR/Cas9 technology on one-cell stage embryos and conventional homologous recombination in embryonic stem cells.

Two zebrafish loss of function lines were generated for the single *Il34* allele, corresponding to a 23 bp deletion (mutant #1) and a 50 bp deletion with a 6 bp insertion (mutant 2) in exon 3 (**Figure 1A**; **Figure S1B-E**). In both zebrafish mutant lines, individuals at homozygous (-/-) status presented a severe growth alteration as shown in adult fish (**Figure 1B**). At 5 days post fertilization, both null mutations resulted in a poorer craniofacial skeletal mineralization (Von Kossa and alcian blue staining) comparatively to the control (+/+) but no evident dysmorphosis (**Figure 1C**, showed example for mutation #1).

The IL34 invalidated mouse line was obtained by CRE-recombinase activation on genetically modified *Il34* gene (**Figure 1D** and **Figure S2**) with LoxP sites in introns 2 and 5 enabling to remove exons 3 to 5 while maintaining a lacZ reporter sequence located in the 5' part of intron 2 ($Il34^{LacZ}$ allele in **Figure S2**). The functionality of the generated $Il34^{LacZ}$ allele was validated in the skin (**Figure S3**), a well-known site of IL34 expression (for instance [24,25]), with in mice homozygous for this allele (thereafter called $Il34^{-/-}$ mice), the expected absence of IL34 expression (**Figure S3A**) associated to a significant reduction of CD207^{+} Langerhans cells (**Figures S3B-D**). The LacZ reporter was also functional as attested by the ß-galactosidase staining on skin section of mice heterozygous for the $Il34^{LacZ}$ allele (**Figure S3E**). $Il34^{-/-}$ mice were phenotypically altered. Indeed, 15 days-old IL34 invalidated mice exhibited a severe growth delay and dysmorphoses in whole skeleton elements, specifically in the craniofacial skeleton associated with hydrocephaly (**Figure 1E**). MicroCT scan 3D reconstructions of skull and tibia enabled visualization of these growth defects in $Il34^{-/-}$ mice (**Figure 1F,** red arrowheads). Morphometric analysis evidenced significant reduction in the skull growth in all planes (sagittal, vertical and transversal) and of the long bone growth in the length and width dimensions in $Il34^{-/-}$ mice compared to wild type (WT) (red vs black values in **Figure 1H** and **Figure S4A**). However, a significant augmentation was observed for the middle cranial vault and no impact was reported on the cranial vault length and the inter-zygomatic root width. Interestingly, the use of a murine IL34 blocking antibody (Sheff.5 clone) during the first post-natal week in WT mouse pups (protocol described in **Figure S4B**) similarly induced skull growth alterations in all planes but to a lower extent when compared to WT mice (brown vs black values in **Figure 1H**). MicroCT scans were also used to determine bone structure parameters and bone mineral density (BMD) in various anatomical sites, namely the mandibular, the vertebral, the cranial and the tibial bones. No significant difference in the trabecular thickness (Tb.Th), the trabecular space (Tr. Sp) or the percentage of bone volume (BV/TV) was observed between $Il34^{+/+}$ and $Il34^{-/-}$ mice whichever bone was considered (**Figure S4C** and **Figure 2C**, red vs black values). On the contrary, the trabecular number (Tb.N) was significantly increased only for the vertebral bone in $Il34^{-/-}$ (**Figure S4C**). Injections of the Sheff.5 blocking antibody had no impact on the bone structure parameters (**Figure S5**). Regarding the bone mineral density, a significant reduction in bone mineralization was observed in the cranial and the tibial bones of $Il34^{-/-}$ mice compared to $Il34^{+/+}$ mice (**Figures 2A-B and D**). The Sheff.5 antibody transitory treatment was insufficient to induce a similar bone mineral reduction in WT mice (**Figure 2A**, **Figure S5**).

Taken together, all those data demonstrated that IL34-invalidaton during development induces important bone modifications.

The absence of IL34 alters the osteoclast-osteoblast balance and bone homeostasis.

Histological analyses on tibia sections performed at the level of the proximal epiphysis (Safranin-O staining **Figure 2E**; Masson's trichrome staining **Figure S6**) revealed an important reduction in the growth plate hypertrophic chondrocytes area (*Il34*$^{+/+}$ 0.277 ± 0.021 mm^2 and *Il34*$^{-/-}$ 0.146 ± 0.094 mm^2). Tartrate resistant acid phosphatase (TRAP) and Osterix (Osx/SP7) dual staining carried out by histoenzymology and immunohistochemistry respectively (**Figure 2F** and top panel **Figure S7** for higher magnification) outlined an increase of both staining corresponding to osteoclastic (red stain) and pre-osteoblastic cells (brown stain) in the null mutant comparatively to the wild-type (*Il34*$^{+/+}$) littermate (**Figure 2F**). Interestingly, the RUNX2 immunohistochemistry staining, which enables identification of cells of the osteoblastic lineage (**Figure S8,** top panels), showed no difference in the number of stained cells between *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice, suggesting a slowdown of the osteoblast differentiation process with an accumulation of Osterix-positive pre-osteoblasts in the null mutant and without reduction of the total number of cells committed in this process.

To identify the part of the *Il34*$^{-/-}$ mouse skeleton phenotype linked to the increased number of osteoclastic cells, a RANKL blocking antibody (IK22.5) was injected during the first postnatal week to totally block the osteoclastogenesis (protocol described in **Figure S4B**). Such blockade had no consequence on the morphometric parameters in the null mutant (green vs red in **Figure 1G**) but impacted the trabecular parameters, the BV/TV and the BMD with significant differences for cranial and tibial bones (green vs red in **Figure S4C** and **Figures 2C-D**). Histological analyses on tibia sections performed at the level of the proximal epiphysis enabled visualization in the null mutant treated with the IK22.5 blocking antibody of a massive reduction of the TRAP positive cells (**Figure 2F** and bottom panels in **Figure S7**) associated with an apparent normalization of the growth plate hypertrophic chondrocytes area from 0.146 ± 0.094 mm^2 to 0.250 ± 0.033 mm^2 (**Figure 2E**) whereas no impact was noticed on the number of Osterix-positive (**Figure 2F** and **Figure S7**) and RUNX2-positive (**Figure S8**) cells.
Overall, these results suggested that IL34 may directly impact osteoblastic differentiation during development.

IL34 improves BMP2 activity in osteoblastic differentiation

BMPs and TGFβs proteins are direct involved in skeletal development and bone homeostasis (nicely reviewed in [26]). Interestingly, Interestingly, conditional knockout BMP2 and BMP4 mice described in the literature have a phenotype similar to our *Il34*$^{-/-}$ mouse model, with small body size and cranial and growth plate defects [27]. BMPs and TGFβs signaling pathways are crucial for proper osteoclast and osteoblast differentiation and maturation by regulating key transcriptional factors as NF-kβ in bone marrow monocytes and RUNX2 in mesenchymal stem cells. In order to see if those phenotypic and histological defects observed in *Il34*$^{-/-}$ models could be due to unknown interactions between IL34 and BMPs / TGFβs members we performed *in vitro* studies to evaluate the impact of IL34 in BMPs / TGFβs signaling during osteoblastogenesis and osteoclastogenesis.

In vitro human mesenchymal stem cell differentiation into osteoblasts was induced by a standard osteoblastic differentiation medium (composition described in the Methods section). This differentiation, quantified by the phosphocalcic mineral deposition (alizarin red staining). and the expression levels of differentiation markers (*RUNX2*, *ALP* and *OCN*), was accelerated by addition of the bone morphogenic protein 2 (BMP2) at 10 ng/mL as shown in **Figure 3A-B**, **Figure S9** and **Figure S10**. The addition of IL34 alone (20 ng/mL) to the differentiation medium had no impact on the rate of osteoblastic differentiation, but interestingly it was able to potentiate the effect of BMP2 when added in combination with an optimal IL34/BMP2 concentration ratio (ng/mL) of two (**Figure 3A**). This concentration ratio corresponded to an equal amount in molarity of the two cytokines (**Figure S11A**). The combination of both molecules resulted in an earlier formation of calcium phosphate crystals (identifiable by alizarin red staining) (**Figure 3A** and **Figure S9**). No mineralization was observed in osteoblasts cultured in basic culture medium (CT-) neither in the presence alone or in combination of BMP2 and IL34 (data not shown). The expression levels of osteoblast differentiation markers were in agreement with the alizarin red staining. Indeed, the combination of both molecules impacted the expression of early (*RUNX2*) and late (*ALP* and *OCN*) markers of osteoblastogenesis in the way of a more rapid differentiation clearly visible from day 3 for *RUNX2* and at day 14 for *ALP* and *OCN* (**Figure 3B** and **Figure S10**). These data suggest a potentiation of BMP2 functions induced by IL34.

To validate this hypothesis, the canonical BMP signaling pathway was analyzed by Western blots in human mesenchymal stem cells. IL34 treatment resulted in an increased and earlier phosphorylation of the SMAD1/5 proteins observed in the presence of BMP2 compared to each molecule alone (Figure 3C). Due to the amount of human mesenchymal stem cells required for Western blot analysis, we decided to use an osteoblastic human osteosarcoma cell line (MNNG-HOS). This cell line recapitulated the same effect in SMAD1/5 phosphorylation of IL34 treatment in the presence of BMP2 **(Figure 4A**), BMP4 and BMP7 (**Figure S11B-E**), whereas IL34 has no similar impact on the phosphorylation of the SMAD2 protein induced by the TGFβ (**Figure 4A**, **Figure S12**). Interestingly, the potentiation effect of IL34 was blocked by the use of a specific human-IL34 blocking antibody named BT34 (**Figure 4B**, **Figure S12**), and the blocking of BMP2 pro-differentiation signaling with its natural inhibitor NOGGIN was annihilated by the presence of IL34 (**Figure 4C**, **Figure S12**). The potentiation effect of IL34 was moreover rapid (**Figure 4D**, **Figure S12**) and as previously mentioned sensitive to the ratio between the two cytokines (**Figure 4E-G, Figure S12**). The combination of BMP2 at 10 ng/mL to IL34 at 20 or 40 ng/mL induced higher SMAD1/5 phosphorylation than those observed with BMP2 alone, while the combination of BMP2 at 10 ng/mL and IL34 at 80 or 100 ng/mL significantly reduced SMAD1/5 phosphorylation (**Figure 4E**, **Figure S12**). The addition of IL34 at 20 ng/mL to BMP2 at 5, 10 or 20 ng/mL induced higher SMAD1/5 phosphorylation than those observed with BMP2 alone, while the combination of IL34 at 20 ng/mL and BMP2 at 40 or 80 ng/mL decreased SMAD1/5 phosphorylation (**Figure 4G**, **Figure S12**). This observation supported the existence of a physical and strong functional interaction between IL34 and some proteins of the BMP family.

To complete the evidence on a physical interaction between IL34 and members of the BMP protein family, the potential impact of BMP2 addition on the IL34-induced osteoclastogenesis was evaluated *in vitro*. Differentiation of human CD14$^+$ cells into osteoclasts can be achieved by a two-step protocol corresponding to a 3-days culture period in the presence of MCSF (25 ng/mL) or IL34 (100 ng/mL) to the culture medium, followed by an 8-days period in presence of MCSF or IL34 combined to RANKL (100 ng/mL). Osteoclasts were identified in the culture by their expression of the TRAP activity (TRAP histoenzymology: purple staining). As previously shown [28], BMP2 addition to the cell cultures (concentrations from 1 to 50 ng/mL) may replace either MCSF or IL34 during the second period. However, while the combined addition of BMP2 (concentrations from 1 to 50 ng/mL) and MCSF to RANKL had no impact on the osteoclastogenesis, the combined addition of BMP2 and IL34 to RANKL induced a reduction of the number of osteoclasts formed (**Figure 3D-E**). Furthermore, the phosphorylation of MCSFR in response to IL34 was inhibited in presence of BMP2 and this inhibition was reversed by addition of NOGGIN supporting the existence of a functional physical link between IL34 and some members of the BMP protein family (**Figure 4H**, **Figure S12**).

Physical interactions between IL34 and some members of BMPs and receptors

To definitively establish the physical interaction between IL34 and BMPs, surface plasmon resonance experiments were performed and demonstrated effective binding of IL34 to BMP2, BMP4 and BMP7 with KD values of 3.63E-07 M, 4.26E-07 M and 9.22E-07 M respectively (**Figure 5A** and **Figure S13**).

A molecular modelling approach (see Materials and Methods), corresponding to a protein-protein docking study, established that IL34 binding to BMP2 occurred at the "Knuckle" sites of the BMP2 dimers known to correspond to the binding sites of BMP type 1 receptors and did not impinge on the "Wrist" sites that correspond to the binding sites of BMP type 2 receptors (**Figure 5B-D**; **Figure S14**). The amino acids of BMP2 and IL34 involved in binding were identified (**Figure 5E** and **Figure S15**), with BMP2 involving a pocket (formed by F305, W310, W313, Y385 and M388) in which the phenylalanine in position 85 for BMPR1A (F85) or the arginine in position 48 for IL34 (R48) are positioned during their respective interactions (Figure 5F). It is important to note that the amino acids involved are phylogenetically highly conserved in both BMP2 and IL34 and that, in addition, the amino acids of BMP2 implicated are also found conserved in several members of the BMP family (**Figure S16**). It was therefore possible to model the binding to IL34 of certain BMPs for which crystallographic structures were available, such as BMP3, BMP6 and BMP7 (**Figure S17**). The existence of direct physical links between BMP proteins and IL34 having been established, the question of the consequences of these links on the binding of BMPs to their receptors on the one hand and the binding of IL34 to MCSFR on the other was raised. Binding of BMP2 to the type 1 BMP receptor is hindered by IL34, which binds to the same site as shown above. It should be noted that this "Knuckle" site is also the binding site for co-receptor proteins of the RGM family (**Figure S14C**) and that it is partially masked by NOGGIN binding (**Figure S14D**). With regard to the binding of BMP2 to type 2 BMP receptors, modelling shows that binding of the

ACVR2A receptor, for example, is entirely possible on a BMP2 dimer with two IL34 binders (**Figure 6A**), the "Wrist" sites not being masked by the presence of IL34. These different possibilities for binding type 1 and 2 receptors and IL34 to a BMP2 dimer are shown in 3D in **Movie S1**. Concerning the binding of IL34 to MCSFR, the binding of IL34 to BMP2 occurs at a site that overlaps with the binding site of MCSFR to IL34 (**Figure 6B**), preventing the simultaneous binding of MCSFR and BMP2 to IL34.

Discussion

IL34, one of the latest cytokines identified [29], has been shown to bind to a variety of receptors with consequences for the differentiation and activation of myeloid, neural and glial cells (For review [4,5]). Surprisingly, the implications of this cytokine during development and growth had not been addressed in detail, unlike those of its receptor MCSFR (for review [30]), although its ability to stimulate differentiation of osteoclasts, cells important for skeletal growth, had been established via binding and activation of this receptor [13,14,31]. The primary aim of the work presented here was to determine these implications by generating two *in vivo* models of IL34 invalidation, one in zebrafish and the other in mice, and to characterize the associated skeletal phenotypes. Both models showed significant growth retardation, with reductions in cartilage mineralization in zebrafish and bone mineralization in mice. Concerning bone mineral density (BMD), the observation in *Il34*$^{-/-}$ mice of a significant reduction of this parameter only in certain bones raises questions. Interestingly, a dichotomy was observed between bones with endochondral mineralization (mandible, vertebrae, tibia trabecular zone (metaphyseal)) and those with intramembranous mineralization (cranial bone, tibia periosteal zone (diaphyseal)), the latter being the only ones to show a reduction in BMD. To decipher the molecular basis of such a difference, further studies will be required, focusing on the expression of all the factors involved in these two types of mineralization (matrix proteins, nucleation factors, enzymes, etc.).

In mice invalidated for IL34, obtained at an expected frequency (Mendelian inheritance) but with a reduced life expectancy (3 weeks), significant craniofacial dysmorphoses were observed with the presence of hydrocephalus. Such defects in craniofacial development are consistent with the previously established implications of IL34 in neural and microglial cells differentiation and activation [24,32–38]. This model should therefore provide a useful additional tool for deciphering the precise functions of IL34 during normal and pathological development of the central nervous system.

Histological study of bone tissue from *IL34*-invalidated mice revealed a marked increase in the number of osteoclasts in the growth plate, in contrast to the phenotype envisaged for the loss of a factor known to stimulate osteoclastogenesis [10,12,13]. As this increase in osteoclast numbers was associated with an accumulation of pre-osteoblasts (OSX-positive) and a reduction in the hypertrophic zone of the growth plate, the question of a role for IL34 in the differentiation of osteoblasts and chondroblasts was raised. To check whether these two points were simply not secondary to the increase in osteoclastogenesis, the consequences of inhibiting RANKL (a factor essential to osteoclastogenesis) during the first week of life in *Il34*$^{-/-}$ mice were analyzed. No impact was observed on the accumulation of OSX-positive cells, while normalization of the size of the hypertrophic zone was observed. These results suggest that IL34 may directly regulate osteoblastic differentiation and probably indirectly that of chondroblasts via osteoclasts, bearing in mind that in inflammatory situations, both mature osteoblasts and hypertrophic chondrocytes can become important sources of pro-osteoclastic IL34 [16,39,40]. Interestingly, a relationship has already been observed between the level of osteoclastic activity and the size of the hypertrophic zone of the growth plate, and vice versa. Thus, a decrease in the hypertrophic zone goes hand in hand with an increase in osteoclastic activity [41,42] and an increase in this zone with a decrease in osteoclastic activity [43–47]. It should then be noted that the disruption of one or other of the elements in this relationship, over and above the repercussions on the other, induces growth retardation in all cases, as has been reported in patients with disorders of osteoclastogenesis (for example, in patients suffering from juvenile osteoporosis [48] or osteopetrosis [49]) as well as in those with chondrodysplasia (for review [50]). The increase in osteoclasts observed in *Il34*$^{-/-}$ mice, appropriately associated with a reduction in the hypertrophic zone of the growth plate, could therefore explain the growth retardation. Establishing the origin of the increase in osteoclasts in relation to the absence of IL34 was not immediately obvious. Osterix expression marks pre-osteoblasts, which are known as an important source of RANKL during growth [51,52]. The accumulation of OSX-positive cells at the subchondral level in *Il34*$^{-/-}$ mice could explain the increased number of osteoclasts, taking into account that an analysis of the number CD11b-positive cells (osteoclast precursors) in the bone marrow and spleen of *Il34*$^{-/-}$ mice reveled a marked increase (**Figure S18**). The question then arose as to the origin of the accumulation of these OSX-positive pre-osteoblasts in *Il34*$^{-/-}$ mice, given that the total number of cells committed to osteoblastic lineage according to RUNX2 labeling did not appear to be affected. An impact of IL34 absence on osteoblastogenesis was therefore strongly suspected.

Members of the TGFβ-BMP family, in particular BMP2, are major stimulators of osteoblastogenesis (for review [26]). The co-addition of IL34 with BMP2 in the culture medium of mesenchymal stem cells undergoing osteoblastic differentiation has shown, for certain ratios, a potentiation of the effect of BMP2 on this differentiation. Protein binding studies showed that IL34 could bind directly to BMP2, and 3D modeling identified the amino acids involved in this binding in the sequences of IL34 and BMP2. With regard to the BMP family, the amino acids involved in IL34 binding were found to be highly conserved, and the veracity of the direct binding of BMP4 and BMP7 to IL34 was established, suggesting that IL34 may potentiate the effects of several family members. IL34 binds to the "Knuckle" site of BMP2, which is also the binding site for type 1 receptors to BMPs, without obscuring the "Wrist" binding site for type 2 receptors. Protein binding studies have also shown that IL34 can directly bind type 2 receptors to BMPs (**Figure S19**), enabling it to occupy the "Knuckle" site of a BMP and transform it into a "Wrist"-like site. A biphasic mechanism of action associated with IL34 binding to BMP dimers can then be proposed (**Figure 6C-D**), corresponding to the progressive modification of the ratio between type 1 and 2 BMP receptors. Thus, in the absence of IL34, basal activity is observed with a receptor ratio of 2/2. Then with an amount of IL34 equivalent to that of BMP2, maximum activity is observed corresponding to a receptor ratio of 1/3. Finally, with an excess of IL34, zero activity is observed with a receptor ratio of 0/4. Interestingly, several studies have reported that in an inflammatory context, BMP2 could inhibit IL34 expression [53–55], suggesting the possible existence of a feedback loop of IL34 potentiation of BMP2 activity. The ratio of IL34 to BMP2 has also been shown to impact IL34 binding to the MCSFR so the osteoclastogenesis in bone. IL34 thus appears to play a key role in bone formation, modulating both osteoclastogenesis via its direct binding to the MCSFR and osteoblastogenesis via its binding to BMPs.

In a more general context, IL34's ability to directly control MCSF receptor activation and indirectly BMP receptors activation defines it as a major player in the development, growth, homeostasis and function of most organs. Further studies will obviously be needed to determine which members of the BMP family are IL34 partners in each organ, in normal physiology and pathological situations (for review [56]) including cancers for which IL34 is already presented as a therapeutic target of major interest [57–59].

Materials and Methods

***In vivo* experiments**

All zebrafish (*Danio rerio*) used for this project were located in the aquaria at the Bateson Centre, at the University of Sheffield (UK). Zebrafish were present in tanks at a density of no more than four zebrafish per liter, with 14 hours light and 10 hours dark cycle, at a temperature of 28 °C. All experimental procedures were carried out in accordance with the UK Home Office Project License PPL70/8178 and personal license IO6008638. All transgenic mice (*Mus Musculus*) used for this project were housed under pathogen-free conditions at the Experimental Therapy Unit at the Faculty of Medicine of the University of Nantes, France (Agreement D44015 and DUO 6781). All protocols applied in the present study were first validated by the French ethical committee of the “Pays de la Loire” (CEEA-PdL-06) and authorized by the French ministry of agriculture and fisheries (authorization # 18415-201901101823350 v2).

Generation of IL34 mutant zebrafish

The zebrafish *Il34* gene (ENSDARG00000091003.2 or ZDB-GENE-050419-150) contains seven exons as human and mouse genes (**Figure 1**). IL34 mutant zebrafish was generated using the CRISPR-Cas9 technology as previously described [60,61]. Exon 3 was targeted using the sequence shown in **Figure S1A** and the corresponding 20 bp spacer region was placed into a guide RNA template for in *vitro* transcription. The gRNA was then transcribed using the MEGAshortscript T7 kit (Life Technologies, UK) and microinjected with Cas9 protein (NEB, UK) into the yolk of zebrafish embryos the one cell stage. F0 adult fish were crossed with wild-type fish to identify founder with germline transmission. Primers used for genotyping were (Fw 5’-TCA GCC AAT AAA TAT CAG ATC CA-3’ and Rv 5’-CGT CTC CTG GTT GCA TTT-3’) which amplify a 300 bp fragment of the WT sequence of zebrafish IL34 exon3 covering the chosen CRISPR target sequence. Obtained fragments of shorter sizes were sequenced to identify mutations induced in the different founders. Two mutations corresponding to a 23 bp deletion (mutant #1 in **Figure 1**) and a 50 bp deletion combined to a 6bp insertion (mutant #2 in **Figure 1**) were obtained. Phenotypes of zebrafishes homozygous for each of these mutations (*Il34*$^{-/-}$ from F3 or following generations) were compared to ensure for link to *Il34* deficiency and not from potential background mutations. Genotyping was performed on DNA extracted from the caudal fins by PCR using same primers as those used to identify founders. Fragments of 300 bp, 277 bp and 256 bp were amplified respectively for *Il34* exon 3 WT, mutant #1 and mutant #2 sequences. Animal were studied at 5 days post fertilization or at 3 months after birth.

Van Kossa and Acian Blue staining of zebrafish skeleton

For Von Kossa staining, samples were fixed in 4% PFA for 2 h at room temperature, rinsed in water containing 0.01% tween 20, and left to incubate in a solution of silver nitrate under a 60 W light bulb for 1 h. After rinsing with water containing 0.01% tween 20, samples were fixed in 2.5% sodium-thiosulfate for 10 min, rinsed and again fixed in 4% PFA for 30 min at room temperature. Preservation was done in glycerol, and samples were kept at room temperature in dark until images were taken.

For Alcian Blue Staining, samples were fixed overnight in 4% PFA at 4 ºC. After several washes in a phosphate buffer solution containing 0.1% tween 20 (PBS-T) and dehydration using methanol, samples were transferred into Alcian blue staining solution (0.1% Alcian Blue, 70% ethanol, 1% concentrated hydrochloric acid) and left to stain overnight at room temperature. Samples where then rinsed in PBS-T and bleached in 30% hydrogen peroxide for 10 min at 37 ºC. A 30% saturated borate solution was then used to eliminate all residues of bleaching solution before putting the samples into a trypsin digestion solution for 30 min at 37 ºC until brains and eyes appeared translucent. A rehydration was performed, and samples were put in glycerol for preservation until images were taken.

Zebrafish were imaged for both stains using the SMZ1500 stereomicroscope, with a DS-Fi1 camera (both Nikon, Japan), at 20 X magnification and Nikon Elements software.

Generation of *Il34* mutant mouse

The *Il34* mutant mouse was generated at the Mouse Clinical Institute (IGBMC, Illkirch, France; Project IR00004258 / K4258) by classical embryonic stem cells (ES) injection in blastocyst stage embryo. Three JM8.N4 ES cell clones carrying the targeted Il34$^{\mathrm{tm1a(EUCOMM)Wtsi}}$ allele were purchased at the European Conditional Mouse Mutagenesis Consortium (EUCOMM) and the clone EPD0146_4_F02 (embryonic stem line JM8.N4; C57BL/6) that was confirmed by PCR and Sanger sequencing (**Figure S2**) as being correctly targeted was used to generate the *Il34* conditional mutant mouse line. Breeding with ERT2-Cre mice (B6.Cg-Tg(UBC-cre/ERT2)1Ejb/J, JR#8085, Jackson Laboratory, Bar Harbor, Maine, USA) enabled to (Tamoxifen dependently) delete exons 3–5 of *Il34* and the neomycin-resistance cassette generating the Il34$^{+/\mathrm{LacZ}}$ mice (**Figure S2**). Breeding with CAG-FLPe mice (C57BL/6-Tg(CAG-flpe)16Ito, RBRC10707, RIKEN BRC, Tsukuba, Ibaraki 305-0074, Japan) allowed to delete the whole LacZ–NeoR cassette and generate mice carrying a loxP-flanked *Il34* allele (*Il34*$^{+/f}$). Homozygous *Il34*$^{LacZ/LacZ}$ mice (called *Il34*$^{-/-}$ in the manuscript) were used for analysis. Mice were genotyped by PCR (**Figure S2**) with the primers Il34-S2: 5’-GTC AGT ATC GGC GGA ATT-3’, Il34-S3: 5’-GTT TGG CCG ATG CTG GCA AAG G-3’ and Il34-AS2: 5’-CTG

TCT TAT GAA GAT GGC ATG CC-3'. Il34-S2 and Il34-AS2 primers enable to amplify a 440 bp fragment in presence of *Il34*^{LacZ} allele, and Il34-S3 and Il34-AS2 primers fragments of 240 bp and 290 bp respectively in presence of wild type (WT) and *Il34*^{f} alleles (**Figure S2**).

Alizarin Red and Alcian Blue double staining of mouse skeleton

The whole-mount skeletal staining protocol used is derived from the protocol of Rigueur and Lyons [62]. Briefly, after euthanasia, all skin, internal organs, adipose tissue and as much as possible muscle were removed before fixation in a PBS 1X pH 7.4 solution containing 2% of paraformaldehyde and 0.2% glutaraldehyde. Skeletons were then dehydrated in ethanol and placed in acetone for permeabilization. Cartilage staining was then realized by submerging the skeletons in the Alcian blue stain (Alcian blue 8GX 0.03% (w/v), 80% EtOH, 20% glacial acetic acid). After washes in 70% and 95% ethanol, a pre-clear of the tissue was realized in a 1% KOH solution. Bone staining was then carried out in Alizarin red stain (Alizarin red 0.005% (w/v) in 1% (w/v) KOH). The Alizarin red solution was then replaced with a v/v mix of glycerol and 1% KOH to remove the excess red color. Skeleton were transferred to 100% glycerol for long-term storage and imaging.

New-born mice treatment with blocking antibodies

The protocol used to treat newborn mice with blocking antibodies was previously described [46]. Briefly, newborn C57BL/6 mice from naïve and transgenic *IL34*$^{+/LacZ}$ mothers received four subcutaneous injections (25 mg/kg of body weight) of respectively Sheff-5 (rat anti-mouse IL34 blocking IgG1 antibody, Diaclone, Besançon, France) and IK22-5 rat anti- mouse RANKL blocking IgG2a antibody [63] or isotopic corresponding control every 2 days beginning at day 1 after birth (**Figure S4B**). The mice were finally sacrificed at postnatal day 15 for phenotyping.

Micro-CT analysis

A Skyscan 1076 micro-CT scanner (Skyscan, Kontich, Belgium) was used to analyze and compare between the different groups of mice (at 15 days postnatal and n=8 for each group except for *Il34*$^{-/-}$ + IK22, n=4) the bone morphometric, structural and mineral parameters at different anatomical sites namely the tibia, the mandible, the vertebra and the cranium. All samples were scanned using the same parameters (pixel size 9 µm, 50 kV, 0.5 mm Aluminum filter, 20 min of scanning). The scanner reconstruction was carried out using the NRecon software and the analyses were performed using CTAn, CTVox, and DataViewer software (Skyscan). In order to obtain the different measurements, the IMAGE-J software (National Institutes of Health, Bethesda, MD, USA) was used. In this way, the acquisition of the image in CTVox was systematically calibrated with a phantom of 5 mm (known size) and all measurements were finally sized using the analysis scale in the IMAGE-J software.

Bone morphometric parameters including tibia total length and width were sized using specific reference marks (**Figure 1C** and **Figure S4A**), and for the cranium measurements were made using the method previously described [64]. Briefly, seven measurements regarding the sagittal, vertical and transversal planes of craniofacial growth were made (**Figure 1C** and **Figure S4A**).

Bone mineral and structural parameters including the bone mineral density (BMD), the percentage of bone volume (BV/TV), the trabecula thickness (Tb.Th), the trabecula separation (Tb.Sp) and the trabecula number (Tb.N) were analyzed for each bone at different anatomical sites using a volume of interest (VOI) measuring 2.0 mm x 1.1 mm × 1.1 mm. The VOI was sectioned using the Data Viewer software and analyzed using the CTAn software. The different points chosen for the analysis are presented in **Figure S4**. To facilitate the identification of changes in the different structures, a "color density range" was used in the CTAn software that made it possible to adjust the correspondence of color and brightness values using image gray scales. For tibia and head images, a brightness level of -32 and a contrast level of 6 from the color density range of the CTAn software were systematically used.

Histology, histoenzymology and immunohistochemistry

Histology, histoenzymology and immunohistochemistry were performed on 3 μm thickness paraffin embedded sections of the different samples prepared as previously described [65]. Masson's trichrome and Safranin-O stains were performed following classical protocols and tartrate-resistant acid phosphatase (TRAP) histoenzymology was carried out as previously described [66]. Immunohistochemistry was performed by using the protocol as previously described [67] and the following antibodies: rabbit monoclonal anti-RUNX2 (Abcam, ref#ab192256, 1/1000), rabbit polyclonal anti- osterix (OSX) (Abcam ref#ab22552, 1/1000), anti-CD207 (eBioscience, ref# 14-2073-80, 1/100).

LacZ staining

Sections (12μm) of *IL34*$^{+/LacZ}$ mice epidermis embedded in OCT were cut using Cryostat Leica CM3050S. Slices were fixed with PFA 1% 5 min, rinsed with PBS 1x and incubated in Xgal (5-bromo-4-chloro-3-indolyl-beta-D-galactopyranoside) solution overnight at 37 °C. Sections were rinsed with PBS 1X, left to dry and mounted with EUKITT® medium.

In vitro experiments

Reagents

Recombinant human Macrophage-Colony Stimulating Factor (MCSF), human interleukin-34 (IL34), human M-CSF receptor (MCSFR/CD115), human TGF-β1, human bone morphogenetic protein 2 (BMP2), human bone morphogenetic protein 4 (BMP4), human bone morphogenetic protein 7 (BMP7), human Noggin, Activin RIIA receptor (ActRIIA), human Activin RIIB receptor (ActRIIB), human TRANCE (RANKL) and antibody anti-human M-CSFR, Anti-Phosho-M-CSFR (Y723) were obtained from R&D Systems (Abingdon, UK). Anti-human IL34 (BT-34) mouse IgG1 monoclonal antibody was produced by Diaclone (Besançon, France) under patent (Heymann D, Ségaliny A, Brion R. University of Nantes /Nantes Hospital/INSERM, "Anti-IL-34 antibodies". WO/2016/097420 A1, 2016). Antibodies directed against human Smad1 (D59D7), human Smad2 (D43B4), anti Phospho-Smad1/5 (ser463/465) (41D10), anti-phospho-Smad2 (Ser465/467) (138D), β-Actin (8H10D10) and HRP-conjugated secondary antibodies were purchased from Cell Signalling (Ozyme, Saint Quentin Yvelines, France). AlphaLISA® SureFire® Ultra Total SMAD1 and p-SMAD1 (Ser463/465) Assay kits were purchase from PerkinElmer (Villebon-sur-Yvette, France).

Cell cultures

The cell lines used in the present study were purchased from the American Tissue Cell Collection (ATCC, Molsheim, France). HEK293 (HEK) transfected with the pCDNA3 empty plasmid or the pCDNA3 plasmid containing the MCSFR gene as described by Segaliny et al., [6]. Human Mesenchymal Stem Cells-Bone Marrow (HMSC-BM) (CLS catalog number 300665, Lot.071222P2) and human MNNG/HOS osteosarcoma cell line (ATCC, catalog number CRL-1547) were cultured in Dulbecco's Modified Eagle's Medium (DMEM, Lonza, Levallois-Perret, France) supplemented with 10% fetal bovine serum (FBS; Hyclone Perbio, Bezons, France) and 2 mmol/L of L-glutamine. All the experiments using HMSC-BM cells were done at passage 2. For the Human MNNG/HOS osteosarcoma cell line experiments were performed between passage 2 and 4. All cell lines were regularly tested for the absence of mycoplasma.

Human osteoclast differentiation

$CD14^+$ monocytes were isolated from peripheral blood of 3 healthy donors $CD14^+$ cells were initially isolated from human peripheral blood donors provided by the French blood bank institute (Etablissement Français du Sang, Nantes, France, authorization number: NTS 2000-24), by using MACS microbeads (MiltenyiBiotec, Bergisch Gladbach, Germany) as previously described [68]. For osteoclast differentiation, $CD14^+$ cells were cultured in alpha-MEM (Lonza) supplemented with 10% human serum (Invitrogen, France) and in the presence of human MCSF (25 ng/mL) or human IL34 (100 ng/mL) +/- human BMP2 (40 or 100 ng/mL) for 3 days. Then cells were treated with same molecules in the presence of human RANKL (100 ng/mL) for 11 days. Medium was renewed every 3 days. After 11 days of treatment, osteoclasts were analyzed by Acid Phosphatase (TRAP) staining kits (Sigma Aldrich, Saint-Quentin Fallavier, France). $TRAP^+$ multinucleated cells with 3 nuclei and more were considered as osteoclasts and were manually enumerated.

Human osteoblastic differentiation

Human Mesenchymal Stem Cells-Bone Marrow (HMSC-BM) (CLS catalog number 300665) were purchased from CLS (Germany). Osteoblast differentiation assays were performed as previously described [67,69]. Briefly, HMSC-BM were cultured in DMEM was supplemented 10% of FBS, vitamin D3 (10^{-8} M; Sigma) and dexamethasone (10^{-7} M; Sigma). After 3 days, ascorbic acid (50 ng/mL; Sigma) and β-glycerophosphate (10 mM; Sigma) were added to allow mineralization detected by alizarin red-S staining for three weeks. Images were captured using a stereomicroscope (Nikon), and mineralized surfaces were quantified using Image J software. Mineralization process was carried out in the presence or absence of human cytokine IL34 (25 ng/mL), BMP2 (10 ng/mL) or combination of both molecules for 3 weeks. RNA samples were collected at days 3, 4, 14 and 21 after the induction of differentiation.

Flow cytometry

FACS analysis of CD11b monocytic bone marrow and spleen cells were performed as previously described [70]. Briefly, after red blood cell lysis (Sigma-Aldrich), bone marrow and spleen cells were labelled with anti-CD11b (clone M1/70; BD Bioscience, Le Pont de Claix, France). Data were acquired using a FACS Canto-II (BD Biosciences).

Western blot

The cells were collected in a RIPA buffer (10 mM Tris pH 8, 1 mM EDTA, 150 mM NaCl, 1% NP40, 0.1% SDS containing a cocktail of protease and phosphatase inhibitors Halt™ (Thermo Fisher, Waltham, MA, USA). The protein concentration was determined using a BCA (bicinchoninic acid) method by BC Assay Protein Quantitation Kit (Interchim, Montluçon, France). 50 µg of protein extracts were prepared in a Laëmmli buffer (62.5 mM Tris–HCl, pH 6.8, 2% SDS, 10% glycerol, 5% 2-mercaptoethanol, 0.001% bromophenol blue) and then separated by SDS-polyacrylamide gel electrophoresis. After electrophoretic transfer, the immobilon-P membranes (Millipore, Molsheim, France) were blotted with the antibodies referenced in the "Reagents" section. The membranes were then probed with secondary antibodies coupled with horseradish peroxidase. Antibody binding was visualized with an enhanced chemiluminescence (ECL) kit Clarity™ Western ECL Substrate (Bio-Rad, Marnes-la-Coquette, France). The luminescence was detected with a ChemiDoc MP Imaging System (Bio-Rad). Blots images and semi-quantitative analysis were done using ImageJ software (USA). Each experiment was repeated at least 3 times.

SMAD1/5 signaling measured by Alpha SureFire® Technology

Direct quantification analysis of cell signaling was performed by using Alpha SureFire® Technology from PerkinElmer in a Victor® Nivo™ multimode microplate reader (ALSU-PSM1; PerkinElmer, Villebon-sur-Yvette, France).

RNA isolation and real-time PCR

Total RNA was extracted using NucleoSpin® RNA Plus (Macherey-Nagel, Duren, Germany). 1 µg of total RNA was used for first strand cDNA synthesis using the OneScript® RT Mix (Ozyme). Real-time PCR was performed on 20 ng of reverse transcribed total RNA (cDNA), 300 nM of primers (QuantiTect Primer® Assays, Qiagen) and PowerUp™ SYBR™ Master Mix from Applied Biosystems™ (Thermo Fisher) in a CFX96 Touch Deep Well Real-Time PCR Detection system from Bio-Rad. Thermal cycle conditions were perform by following manufacture protocol. The analysis was performed with CFX Manager Software (Bio-Rad) using human glyceraldehyde 3-phosphate dehydrogenase (GAPDH), Hypoxanthine Phosphoribosyl transferase 1 (HPRT1) and TATA box binding protein (TBP) as invariant controls (QuantiTect Primer® Assays, Qiagen). Oligonucleotides were designed with Primer-Blast software (NCBI) and purchased from Eurogentec (Eurogentec, Angers, France). The $2^{-\Delta\Delta Ct}$ (cycle threshold) method was used to calculate expression levels. List of primers and gene name symbols with corresponding full names are indicated in Tables S1 and S2 below.

Table S1 Qiagen q-PCR murine primers

Official full name; Alias	**Official symbol**	**Gene Globe Id**
Alkaline phosphatase, liver/bone/kidney	ALPL	QT00012957
Osteocalcin or bone gamma-carboxyglutamate protein	BGLAP	QT00232771
Runt-related transcription factor 2; *CBFA1*	RUNX2	QT00020517

Tumor necrosis factor receptor superfamily, member 11b	TNFRSF11B	QT00014294
Macrophage Colony Stimulating Factor	MCSF	QT00035224
Macrophage Colony Stimulating Factor Receptor	MCSFR	QT00073276
Bone Morphogenetic Protein Receptor 1A	BMPR1A	QT00085358
Bone Morphogenetic Protein Receptor 2	BMPR2	QT00226065
Activin Receptor 2A	ACVR2A	QT00077749

Table S2: Eurogentec q-PCR murine primers

Official full name; Alias	**Official symbol**	**Gene Globe Id**
Interleukin-34	IL-34	Fwd 5’-GGA CAC ACT TCT GGG GAC A-3’ Rev 5’-CCA AAG CCA CGT CAA GTA GG-3’
Langerin	CD207	Fwd 5’-TCA CCT CCA TTG TGC TTC AG-3’ Rev 5’-ATC GTC CAC ACG ACC TCT TT-3’
Glyceraldehyde-3-phosphate dehydrogenase	GAPDH	Fwd 5’-TGC GAC TTC AAC AGC AAC TC-3’ Rev 5’-CTT GCT CAG TGT CCT TGC TG-3’

Surface plasmon resonance (SPR) assays

All SPR experiments were performed on a T200 apparatus (Cytiva) at 25 °C in PBS pH 7.4 containing 0.05% of surfactant P20. Human recombinant BMP2, BMP4 and BMP7 proteins were immobilized (1500- 2300 RU) at pH 4.5 on CM5-S sensor chip by amine coupling following the manufacturer’s instructions (Cytiva, Velizy-Villacoublay, France). IL34 kinetics were measured using one cycle titration, for these five increasing concentrations of recombinant human IL34 (12.5, 25, 50, 100, 200 nM) were injected during 60 s at 100 µL/min on coated BMPs. The last injection was followed by a 600 s dissociation time in running buffer. The KD values were evaluated using a bivalent fitting model (T200 Evaluation software 3.2.1, Cytiva). All sensorgrams were corrected by subtracting the low signal from the control reference surface (without any immobilized protein) and blank buffer injections before fitting. For KD evaluation of IL34 on human recombinant receptors BMPRIIA, Act RIIA and Act RIIB, these receptors were captured on immobilized anti-human Fc (Cytiva), four increasing concentrations of IL34 (18.75, 37.5, 75, 150, 300 nM) were injected. The KD values were evaluated by using a steady-state fitting model. The binding responses of IL34 (50 nM) alone, Nogging (50 nM) alone and a mixing of IL34 and Noggin were measured by 180 s injection on different coated BMP proteins (BMP2, BMP4, BMP7) at a flow rate of 30 µL/min followed by a dissociation time of 400 s in running buffer.

Protein-Protein docking and analysis

Structures of M-CSFR, BMPR1 and IL-34 were extracted from their bound crystallographic forms (1REW for BMPR1A + BMP2 [71], 4WRL for M-CSF:M-CSFR1 [72] and 4DKD for

IL-34:M-CSFR1 [73]). Docking experiments were performed using either BMP-2 fixed and the partner protein mobile, or the reverse, as previously published [71]. ClusPro analysis [74] was performed in balanced mode, only the first 10 binding modes clusters were considered for analysis, the best modes were selected by visual inspection. Interface analysis was performed using the PISA web server [75]. Visualization and superimposition of docking poses and crystallographic structures were done using PyMOL (The PyMOL Molecular Graphics System, Version 2.5 Schrödinger, LLC; Schrödinger, LLC 2015).

Statistical analysis

All experiments were repeated at least three times in independent experiments. The differences between the experimental conditions were assessed with Student's t test or a one-way ANOVA followed by the Mann–Whitney test or Kruskal-Wallis test (in the case of more than two independent samples of equal or different sample size). The results are given as a mean ± SD. Results were considered significant at p-values of ≤ 0.05, p-values of ≤ 0.01 and p-values of ≤ 0.001. GraphPad Prism 6 software (GraphPad Software, San Diego, CA, USA) and Real Statistics Resource Pack Software (Release 8.91), copyright (2013-2023) Charles Zaiontz (www.real-statistics.com) were used for statistical analyses.

Supplementary Material

Supplementary information is available in Supplementary File.

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Data sharing

The authors of this investigation declare that all the data, analytical methods, and study materials are available to the researchers. All the details information is available in Supplemental Data.

Conflict of interests

Authors declare that they have no competing interests.

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Figure 1

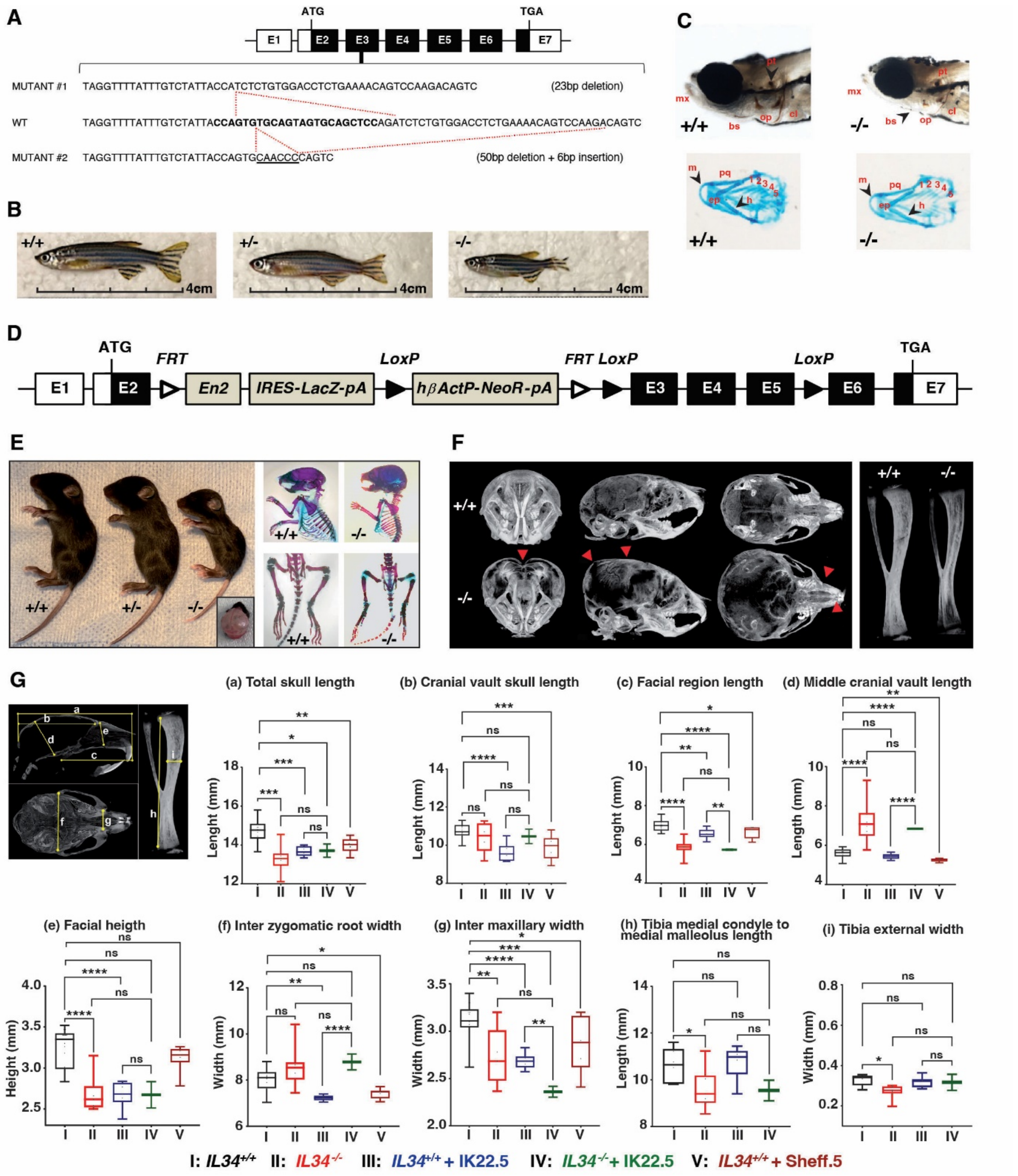


Figure 1. Growth alterations associated with *IL34* genetic invalidations in zebrafish and mouse. (**A**) Scheme of IL34 Exon3 genetic alterations induced by CrispR/Cas9 technology in zebrafish. (**B**) Images of zebrafish mutants compared to the control at age of 3 months. (**C**) Mineralization of craniofacial skeleton by Von Kossa and Acian Blue staining of embryos at 5 days post fecundation. Abbreviations: mx - branchio maxilla, bs - branchistegal ray, op - opercle, cl - cleithrum, pt - pharyngeal teeth, m - Meckel's cartilage, pq - palatoquadrate, ch - ceratohyal, ep - ethmoid plate, marked 1-5 - different arches. (**D**) Scheme of *Il34* floxed allele used to obtain constitutive invalidation of *IL34* in mouse by removing exons 3 to 5 under CRE recombinase activity. (**E**) Images at 15 days after birth of consequences of the constitutive invalidation of *IL34* with detail of hydrocephaly in *Il34*$^{-/-}$ mouse (left panel). And comparative of skeletons at 15 postnatal days visualized by Alizarin red / Alcian blue double staining (right panel). (**F**) MicroCT scan 3D reconstructions of skull and tibia enable to visualize growth

defects (red arrowheads). (**G**) Quantification of growth defects in the different morphometric planes (a to i) in wile type (black box) *vs.* *Il34*$^{-/-}$ mice (red box), both treated with IK22.5 RANKL blocking antibody (blue and green boxes), or wile type mice with Sheff.5 IL34 blocking antibody (brown box). *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001**.** The differences between the experimental conditions were assessed one-way ANOVA test. n=8 except for *Il34*$^{-/-}$ + IK22.5 (n=4).

Figure 2

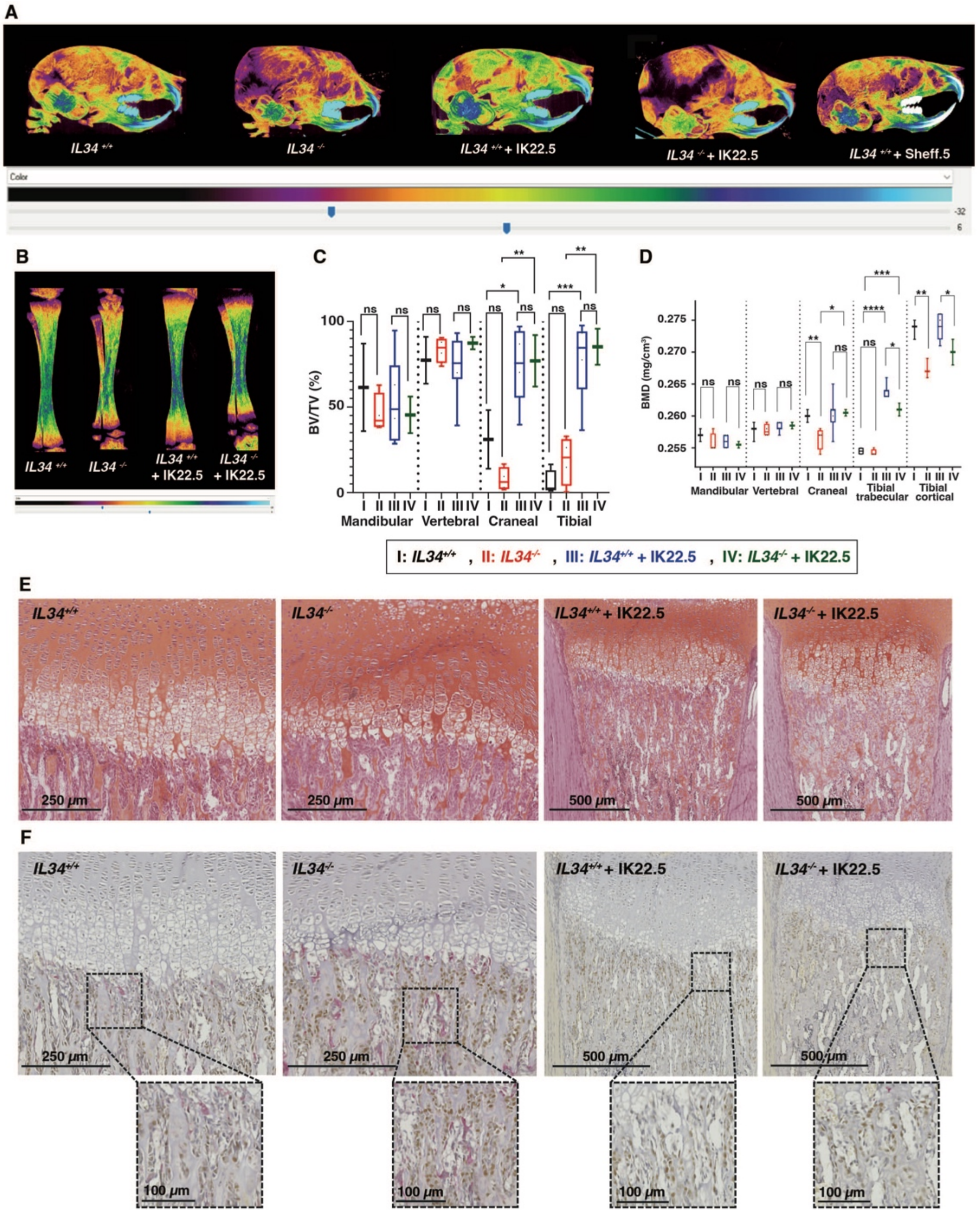


Figure 2. Bone mineral and histologic alterations associated with *IL34* genetic invalidation in mouse. (**A**) Comparative analyses of skull bones mineralization levels between *Il34*$^{+/+}$, *Il34*$^{-/-}$, *Il34*$^{+/+}$ injected with IK22.5 antibody, *Il34*$^{-/-}$ injected with IK22.5 antibody and *Il34*$^{+/+}$ injected with Sheff.5 antibody mice at age of 15 days, using profile views of the microCT scan 3D reconstructions. The color density ranges from black (lower mineralization) to clear blue (higher mineralization). (**B**) Comparative analyses of tibias mineralization levels between *Il34*$^{+/+}$, *Il34*$^{-/-}$, *Il34*$^{+/+}$ treated with IK22.5 antibody and *Il34*$^{-/-}$ treated with IK22.5 antibody mice at age of 15 days, using longitudinal views of the microCT scan 3D reconstructions. (**C**) Comparative analysis of the bone volume (BV)/total volume (TV) ratio between *Il34*$^{+/+}$, *Il34*$^{-/-}$, *Il34*$^{+/+}$ treated with IK22.5 antibody and *Il34*$^{-/-}$ treated with IK22.5 antibody in bone of different anatomical sites: the mandible, the vertebra, the skull and the tibia. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001, ns: not significant. n=8 except for *Il34*$^{-/-}$ + IK22.5 (n=4).

(**D**) Comparative analysis of the bone mineral density (BMD) between *Il34*$^{+/+}$, *Il34*$^{-/-}$, *Il34*$^{+/+}$ treated with IK22.5 antibody and *Il34*$^{-/-}$ treated with IK22.5 antibody in bone of different anatomical sites: the mandible, the vertebra, the skull and the tibia. Two areas were considered for the tibia, the trabecular and the cortical. $^*p<0.05$, $^{**}p<0.01$, $^{***}p<0.001$, $^{****}p<0.0001$, ns: not significant. n=8 except for *Il34*$^{-/-}$ + IK22.5 (n=4). (**E**) Chondrocytes stained by safranin-O staining of tibia longitudinal sections at the level of the proximal epiphysis performed for *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice injected or not with the IK22.5 antibody. (**F**) Tartrate resistant acid phosphatase (TRAP) and Osterix (Osx/SP7) dual-staining of tibia longitudinal sections at the level of the proximal epiphysis performed for *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice injected or not with the IK22.5 antibody. TRAP red staining for osteoclast cells. OSX brown staining for pre-osteoblasts cells. The scales are given as bars with the corresponding values in the lower part of each histological view.

Figure 3

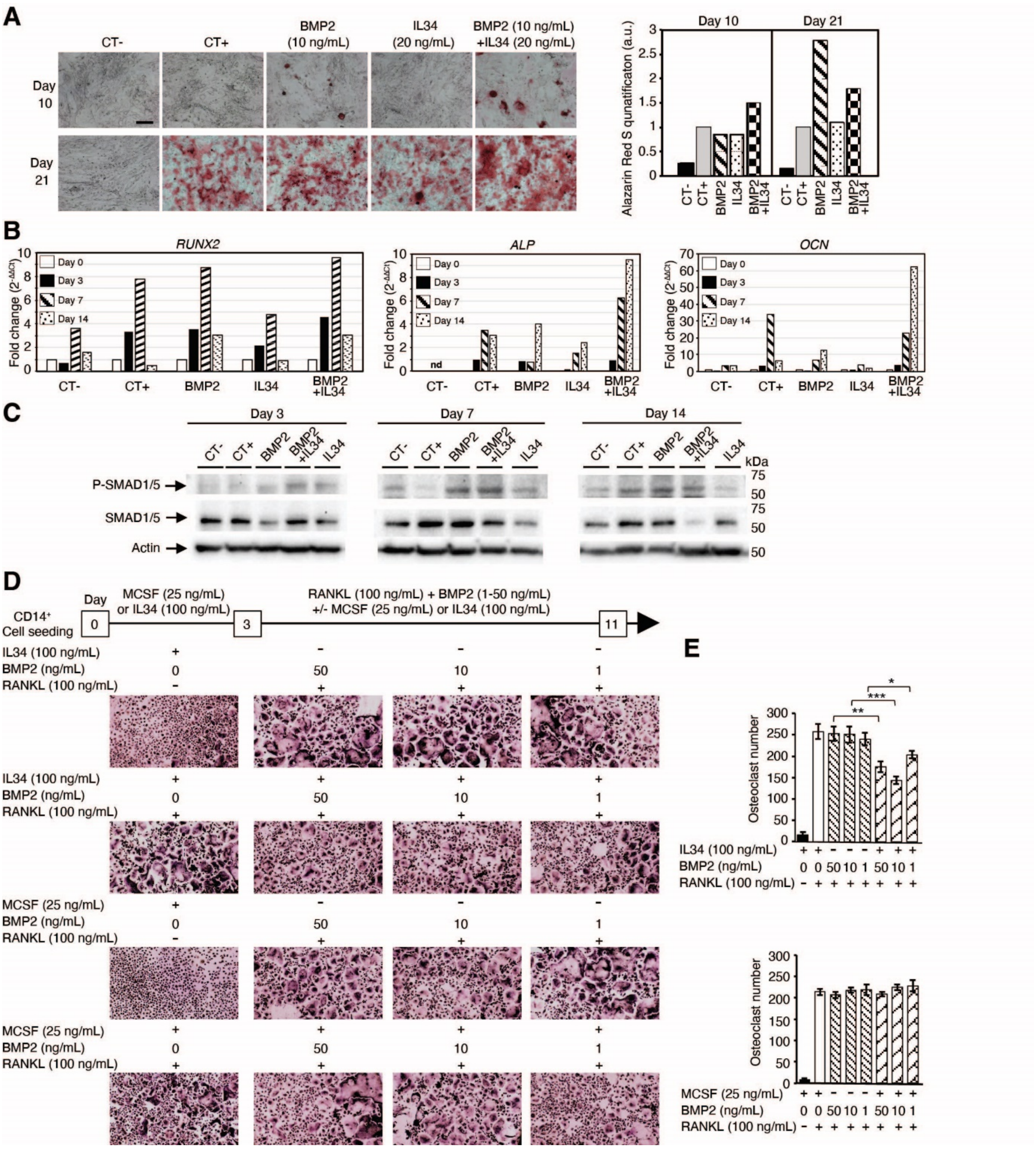


Figure 3. IL34 regulates BMP2-associated osteoblastic and osteoclastic differentiation. (**A**) Images of human mesenchymal stem cells differentiated into osteoblasts cultured in basic culture medium (CT-) or in osteogenic culture medium (CT+) in the absence or presence of BMP2 (10 ng/mL), IL34 (20 ng/mL) or combination of both at 10 and 21 days. Right panel: quantification of alizarin red staining. Magnification was similar for all views and the bar in CT- view at day 10 corresponds to 500 µm. (**B**) Real-time PCR quantification of early (*RUNX2*) and late (*ALP* and *OCN*) markers of osteoblastogenesis at days 0, 3 7 and 14. Data correspond to fold increase by $2^{-\Delta\Delta Ct}$ (cycle threshold) method. A representative experiment is shown. nd: non detected. (**C**) Western blot analysis of SMDA1/5 phosphorylation at different times of human mesenchymal stem cells differentiated into osteoblasts in basic culture medium (CT-) and in osteogenic culture medium (CT+) in the absence or presence of BMP2 (10 ng/mL), IL34 (20 ng/mL) or combination of both. (**D**) Differentiation of human $CD14^+$ cells into osteoclastic cells analyzed by Tartrate Resistant Acid phosphatase activity (TRAP histoenzymology: purple

staining) after 3-day culture period in the presence of MCSF (25 ng/mL) or IL34 (100 ng/mL), followed by an 8-day period of maturation with the addition of RANKL (100 ng/mL) and /or BMP2 addition (concentrations from 1 to 50 ng/mL) (**E**) Quantification of the different experiments repeated in triplicate and presented in **D**. At least two independent experiments have been carried in triplicate. $^{*}p<0.05$, $^{**}p<0.01$, $^{***}p<0.001$.

Figure 4

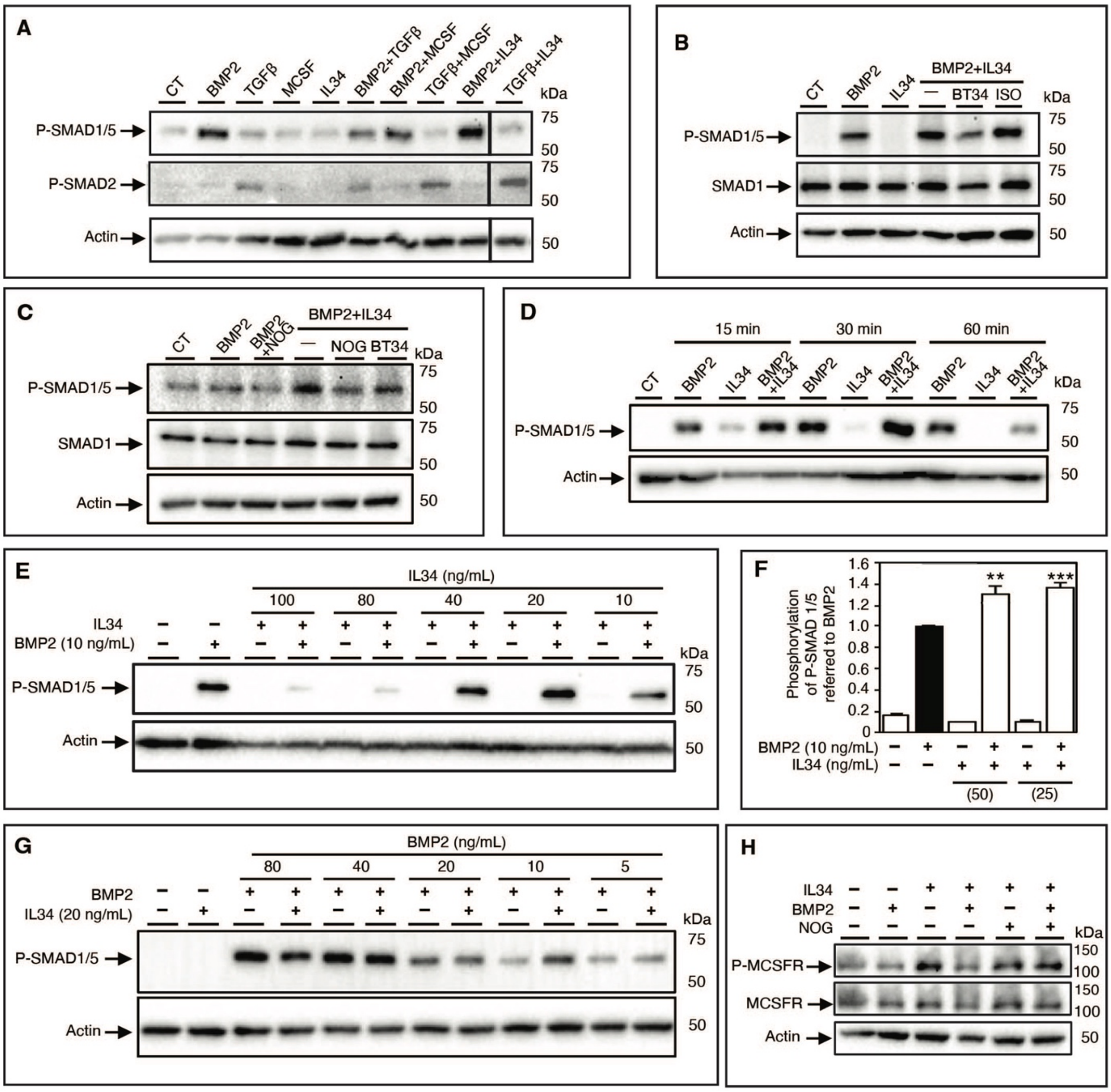


Figure 4. The interaction IL34-BMP2 modulates SMAD1/5 as well as MCSF receptor (MCSFR) phosphorylation and related signaling. (A) Western blot analysis of SMDA1/5 and SMAD2 phosphorylations of human MNNG-HOS osteosarcoma cells in the presence of BMP2 (10 ng/mL), TGFß (10 ng/mL), MCSF (20 ng/mL), IL34 (20 ng/mL) alone or in corresponding combination. A representative experiment is shown. CT: basic culture medium. (B) Western blot analysis of SMDA1/5 phosphorylation of human MNNG-HOS osteosarcoma cells in the presence of BMP2 (10 ng/mL), IL34 (20 ng/mL) alone or in combination (BMP2+IL34, -) plus the human IL34 blocking antibody (BT34) (100 µg/mL) or its irrelevant isotypic control antibody (ISO) (100 µg/mL). CT: basic culture medium. (C) Western blot analysis of SMDA1/5, similar conditions used in B in the presence of the human IL34 blocking antibody (BT34) (100 µg/mL) or the natural inhibitor of BMP2 called NOGGIN (NOG) (200 ng/mL). (D) Kinetic analysis by Western blot of the potentiating effect of IL34 on BMP2-induced SMAD1/5 phosphorylation at 15 min, 30 min and 60 min with similar corresponding molecules concentrations described in B. (E) Western blot analysis of SMDA1/5 as described in B in the presence of a single concentration of BMP2 (10 ng/mL) in combination with gradual quantities of IL34 (10, 20, 40, 80 and 100 ng/mL). (F) The Alpha SureFire technology (Revvity) was used to quantitatively validate the potentiation effect of IL34 on BMP2 activation of SMAD1/5 phosphorylation. Co-additions of 25 or 50 ng/mL of IL34 increased significantly the phosphorylation of SMAD1/5 induced by the addition of BMP2 at 10 ng/mL. **p<0.01, ***p<0.001. (G) Western blot analysis of SMDA1/5 as described in B with a single concentration of IL34 (20

ng/mL) in combination with gradual quantities of IL34 (5, 10, 20, 40 and 80 ng/mL). (H) Western blot analysis of MCSFR phosphorylation expressed in HEK293 transfected cells in the presence or absence of BMP2 (10 ng/mL), IL34 (20 ng/mL) or in combination (BMP2+IL34, -) plus NOGGIN (NOG) (200 ng/mL). Quantifications of all the Western blots presented in this figure are shown in Figure S12. All experiments have done at least three times independently.

Figure 5

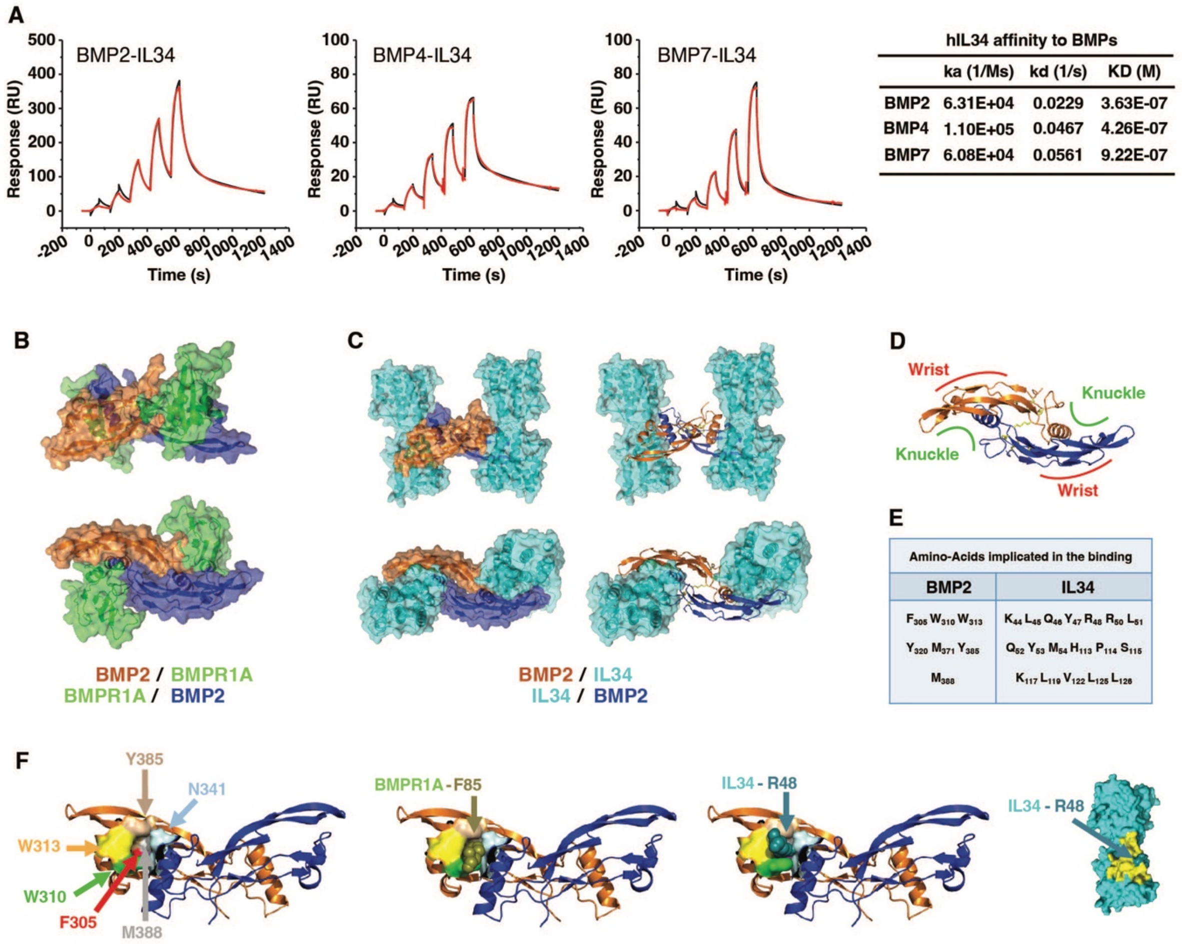


Figure 5. Demonstration and deciphering at the molecular level of the physical interaction between the IL34 protein and proteins of the BMP family. (**A**) Surface plasmon resonance experiments (described in Materials and Methods section) and values of proteins interaction parameters between IL34 and BMPs. ka: association rate constant, kd: dissociation rate constant, KD: affinity constant. (**B**) Molecular modelling of the binding of two BMPR1A receptors (green) to a BMP2 dimer (brown and dark blue) by using PyMOL. (**C**) Molecular modelling of the binding of two IL34 proteins (cyan) to a BMP2 dimer (brown and dark blue) seen in profile (top) and from above (bottom) with a representation of the BMP2 proteins in surface (left) and in structure (right) by using PyMOL. (**D**) Structural representation of a BMP2 dimer seen from above with the location of the "Knuckle" and "Wrist" binding sites to the type 1 and type 2 receptors respectively as described by Sebald and collaborators [76,77]. (**E**) Main amino acid of BMP2 and IL34 identified as being involved in binding. In addition, hydrogen bonds and salt bridges were found between BMP2 and IL34, more specifically between residues K383-D190, D312-K55 and E376-R73. (**F**) Localization on the representation of the BMP2 protein in structure of amino acids important for partner binding: F305 in red, W310 in bright green, W313 in yellow, Y385 in light brown and M388 in grey. These amino acids delineate the pocket in which residues F85 of BMPR1A and R48 of IL34 are positioned during their interaction with BMP2. The amino acid N341 presented in light blue, despite is localization in the most outside part of the pocket, was not identified as important for the binding to IL34. IL34 is displayed in surface representation with the entire binding region colored in yellow, and the important intercalating residue R48 is indicated in duck blue.

Figure 6

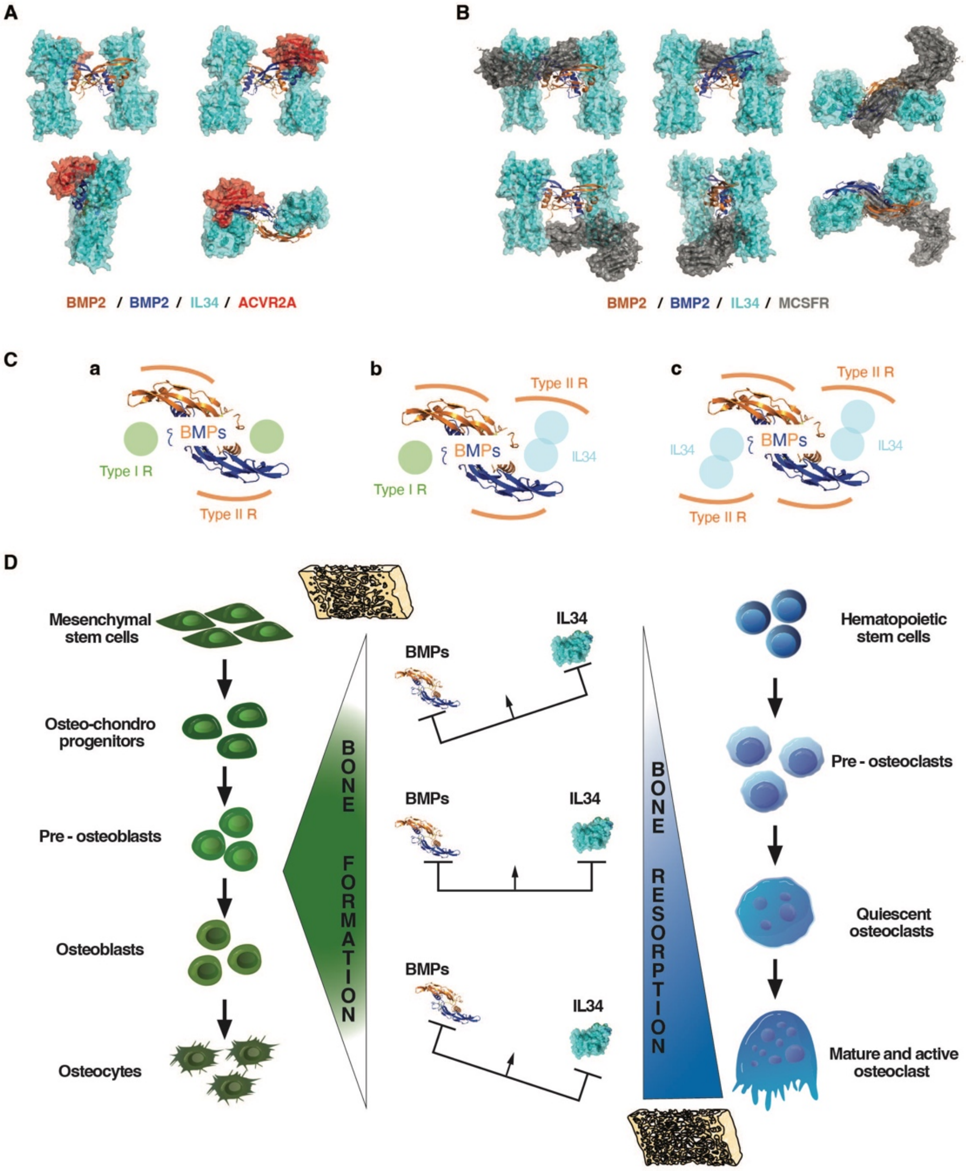


Figure 6. Impacts of the binding between BMP2 and IL34 on the ability of BMP2 and IL34 to bind to ACVR2A and MCSFR receptors respectively: importance of stoichiometry and functional consequences on bone formation and resorption. (**A**) ACVR2A receptor binding to BMP2 ("Wrist" site) does not appear to be affected by IL34 binding to the "Knuckle" sites of a BMP2 dimer. (**B**) MCSFR receptor binding to IL34 occurs at a site overlapping the BMP2 "Knuckle" site binding site. Simultaneous binding of BMP2 and MCSFR to IL34 is therefore impossible. (**C**) BMP receptor binding stoichiometry to a BMP2 dimer. The standard binding of two type 1 and two type 2 receptors per dimer (a), is gradually modified by the amount of IL34 present with potential transformation of a "Knuckle" site into a "Wrist"-like site at intermediate concentrations (b), then a second at high IL34 concentrations (c), bearing in mind that IL34 can bind type 2 BMP receptors. (**D**) Schematic representation of the impact of different ratios of BMPs and IL34 on bone formation and resorption.

Supplementary Figure Legends

Figure S1. Tools to *IL34* genetic invalidation in zebrafish using CrispR/Cas9 technology and functional confirmation. (**A**) Schematic representation of the targeted sequence in *il34* exon 3 including the protospacer adjacent motif (PAM) and the use guide RNA template sequence containing a T7 promoter sequence and the reverse targeted sequence and PAM. (**B-E)** Functional confirmation of *il34* invalidation was achieved showing the loss of the known IL34 effects on the differentiation and survival of monocytes and macrophages, [6,78] using the caudal fin amputations strategy on 3 day embryos from a heterozygous (+/-) in-cross of the double transgenic line *tg*(fms: GFP). This line contained the heterozygous mutant *il34* allele, and GFP expression of macrophages was driven by the *MCSFR* promoter. To visualize these inflammatory cells throughout injury, live images of the amputated caudal fins were taken at 8 hours post fin injuries. The 8 hours-time-point was chosen as this is the optimal time for recruitment of macrophages to the site of injury. At this time, despite no variation of *MCSF* and *MCSFR* transcript expression levels induced by IL34 invalidation **B-C**, an important reduction of the number of macrophages recruited **D-E** was observed in the *il34*$^{-/-}$ comparatively to the control (*il34*$^{+/+}$).

Figure S2. *IL34* genetic invalidation in mouse. *Il34*^{Flox} allele (Genbank: JN962093.1) and the derived *Il34*^{LacZ} allele obtained after recombination between its 5' and 3' LoxP sites are graphically represented. Primers used to genotype the different alleles are given in the table and positioned on the different graphical representations. Primers S3 and AS2 enable to discriminate the *Il34*^{Flox} allele from the WT allele with respectively amplification of 240 bp and 290 bp fragments. Primers S2 and AS2 enable to identify the *Il34*^{LacZ} allele corresponding to the amplification of a 440 bp fragment. LacZ and NeoR primer pairs were used to check the integrity of the *Il34*^{Flox} allele. Fragments amplified with S1-AS1 and S2-AS2 primer pairs from genomic DNA extracted from *Il34*$^{LacZ/LacZ}$ mouse tail were Sanger sequenced to confirm recombination terminals (sequences corresponding to the construct cassette are underlined). The disruption of IL34 has been also analyzed by western blot. Briefly, whole protein extracts were obtained from frozen spleens from WT and IL34 null mice and specific antibody targeting IL34 was used. As showed, IL34 was only detected in WT and not in IL34 null sample.

Figure S3. Functional confirmation of *IL34* invalidation and *IL34 LacZ* reporter in mouse. (**A-D**) In order to confirm the effective loss of IL34 function in *Il34*$^{-/-}$ mouse, skin well-known as an IL34 expression site [25] was used. Correlated to IL34 invalidation, a significant reduction of CD207 expressing cell (Langerhans cells) was observed. (**E**) ß-galactosidase staining (blue) performed on section of *Il34*$^{+/LacZ}$ mouse enable to confirm previously described expression of IL34 [24,25,79] in some keratinocytes and cells from the hair follicle.

Figure S4. Graphical representation of morphometric parameters used for mouse head and tibia analyses, blocking antibodies injections protocol and results of bone trabecular structure analyses at different anatomical sites. (**A**) The seven morphometric parameters (a-g) measured for the head (craniofacial skeleton) and the two parameters (h-i) measured for tibia (appendicular skeleton) are listed and represented on 2D microCT scan views. (**B**) The blocking antibodies (IK22.5 and Sheff5) injections protocol was characterized by four subcutaneous injections at postnatal days 1, 3, 5 and 7 of 25 mg/kg of antibody following by a sacrifice at day 15. (**C**) The trabecular thickness (Tb. Th), the trabecular space (Tb. Sp) and the trabecular number (Tb. N) were determined at four anatomical sites, the mandible, the vertebra (C2) the skull and the tibia. *Il34*$^{+/+}$ are represented in black, *Il34*$^{-/-}$ in red, *Il34*$^{+/+}$ treated with IK22.5 in blue, and *Il34*$^{-/-}$ treated with IK22.5 in green. $^{*}p<0.05$, $^{**}p<0.01$, $^{***}p<0.001$, $^{****}p<0.0001$, ns: not significant. n=8 except for *Il34*$^{-/-}$ + IK22.5 (n=4).

Figure S5. Analyses of the impact of Sheff.5 antibody injections in WT pups on the bone trabecular structure (Tb. Th, Tb. Sp and Tb. N), the percentage of BV/TV and BMD. No significant variation was observed comparatively to pups injected with a control irrelevant antibody from the same idiotype whatever the parameter considered. ns: not significant. CT: control group. n=8.

Figure S6. Histological comparative analysis of the tibia proximal epiphysis area of 15-day-old *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice using Masson's trichome stained longitudinal sections. An important reduction of the thickness of the hypertrophic chondrocytes area was observed in the null mutant. The scales are given as bars with the corresponding values in the lower part of each histological view.

Figure S7. High magnification views of tartrate resistant acid phosphatase (TRAP) and Osterix dual-staining of tibia longitudinal sections at the level of the proximal epiphysis performed for 15-day-old *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice treated or not with the IK22.5 antibody. An important increase of both staining (TRAP in red and OSX in brown) was observed in the null mutant mouse. The IK22.5 injections drastically reduced the number of TRAP-positive cells in both *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice, whereas no evident variation of the number of cells stained for OSX was evidenced. The scale is given as a bar corresponding to 50 μm in the lower part of each histological view.

Figure S8. Comparative analysis of RUNX2 expression in the tibia proximal epiphysis area of 15-day-old *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice treated or not with the IK22.5 antibody using immunohistochemistry applied to longitudinal sections. No variation of the number of stained cells was evidenced between *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice as between *Il34*$^{-/-}$ and *Il34*$^{+/+}$ injected with IK22.5 antibody. The scale is given as a bar corresponding to 250 μm in the lower part of each histological view.

Figure S9. Functional impact of BMP2, IL34 or combined BMP2+IL34 addition in the culture medium onto osteoblastic differentiations. (**A**) BMP2 addition (10 ng/mL) to the osteogenic differentiation medium (CT+) induced an acceleration of the differentiation as evidenced by the higher alizarin red staining corresponding to phosphocalcic crystal deposition at 7, 14 and 21 days. IL34 addition (20 ng/mL) to the osteogenic differentiation medium had no effect on the differentiation (view not shown but the quantification is presented in **B**, right panel). Co-addition of IL34 (10, 20 or 40 ng/mL) with BMP2 (10 ng/mL) potentialized the acceleration of the osteoblastic differentiation observed with BMP2 alone with an optimal concentration ratio (ng/mL) of 2 between BMP2 and IL34. Magnification is similar for all views and the bar in CT- view at day 7 correspond to 500 μm. (**B**) Quantification of the alizarin red staining corresponding to independent experiments from different donors. BIL: BMP2+IL34 addition; Numbers (10, 20 or 40) correspond to the used concentrations of IL34 in ng/mL.

Figure S10. Impacts of the additions of BMP2 (10 ng/mL), IL34 (20 ng/mL) or BMP2+IL34 to the CT+ medium onto the expression of early (*RUNX2*) and late (*ALP* and *OCN*) markers of osteoblast differentiation, onto osteoprotegerin (*OPG*, a major regulatory factor of osteoclastogenesis), and onto type 1 and type 2 receptors of the BMPs (*BMPR1A, BMPR2* and *ACVR2A*). Results of three different experiments (Exp. 1 to 3) carried out with three different batches of mesenchymal stem cells (obtained from different donors) are presented in order to deal with the inter-batches variabilities considering only results similarly observed in the three experiments. BMP2 addition accelerated the osteoblastic differentiation and the co-addition of IL34 potentialized this effect as evidenced for *RUNX2* expression at days 3 and 7, and for *ALP* and *OCN* at day 14. BMP2 addition alone or in combination with IL34 reduced the *OPG* expression at days 3 and 7. Regarding the different receptors of the BMPs, no reproducible effects were observed between experiments, but all three receptors are expressed at all stages (days) of differentiation whatever the culture conditions used. nd: not detected.

Figure S11. Impacts of addition of different combinations of BMP4+IL34 or BMP7+IL34 onto the activation of BMP receptors evidenced by SMAD1-5 phosphorylation in human MNNG-HOS osteosarcoma cell line. (**A**) Correspondence table between concentrations used in ng/mL and in pM or nM for IL34, BMP2, BMP4 and BMP7. (**B**) Joint addition of BMP4 (graded concentrations from 5 to 80 ng/mL) and IL34 (20 ng/mL) induced SMAD1-5 phosphorylation, with greater effects observed with 20 and 80 ng/mL BMP4. (**C**) Joint addition of BMP4 (20 ng/mL) and IL34 (graded concentration from 10 to 80 ng/mL) induced SMAD1-5 phosphorylation, with an optimal effect observed with 20 ng/mL IL34. (**D**) Joint addition of BMP7 (graded concentrations from 5 to 80 ng/mL) and IL34 (20 ng/mL) induced SMAD1-5 phosphorylation, with greater effects observed with 10 and 80 ng/mL BMP7. (**E**) Joint addition of BMP7 (10 ng/mL) and IL34 (graded concentration from 10 to 80 ng/mL) induces SMAD1-5 phosphorylation, with greater effects observed with 20 and 40 ng/mL IL34.

Figure S12. Quantitative analyses of Western blots presented in Figure 4. Histograms corresponding to the control condition, the BMP2-only condition and the IL34-only condition appear in red, black and blue respectively. $^{*}p<0.05$, $^{**}p<0.01$.

Figure S13. Curves obtained during the surface plasmon resonance experiments with immobilization of the BMP proteins (2, 4 and 7) and additions of IL34 and NOGGIN alone or in combination. Whatever the BMP protein considered an effective binding of IL34 as NOGGIN was observed with an additive effect of the two factors.

Figure S14. Representative structures of BMP2 dimer bound proteins resolved experimentally. BMP-2 dimers are displayed in blue and orange surface. (**A**) BMPR1A structure (green) as found in PDB ID 1ES7 [80]. State that binding the knuckle site. (**B**) BMPR1A (green) and Activin Receptor IIA (red) occupy each wrist and knuckle epitopes (PDB ID 2GOO [81]). (**C**) RGMA (yellow) as found in PDB ID 4UHY [82]. State that binding the knuckle site. (**D**) NOGGIN was determined to occupy both epitopes in structure PDB ID 7AG0 [83]. Left: side view of protein complexes, right: top view of protein complexes.

Figure S15. Representative structures of the BMP2 dimer and IL34 in electrostatics surface view with the hydrophobic (white) and hydrophilic sites (red for negative patches, blue for positive patches) and identification of their respective binding sites. (**A**) Representation of the BMP2 dimer with the knuckle site pocket underlined (arrow). (**B**) BMP2 dimer and IL34 position in cartoon representation. (**C**) IL34 with the BMP2 binding site indicated by the arrow. (**D**) IL34 and BMP2 position in cartoon representation.

Figure S16. Analysis in the BMP-TGFß family of the conservation of the amino acids implicated in the binding to IL34 using COBALT alignment tool (NCBI). Alignment of the human protein sequences of the 29 BMP-TGFß family members was first given with amino acids implicated in the binding to IL34 conserved comparatively to BMP2 overlined in green, those changed by another with close physical-chemical proprieties overlined in blue and those changed by another with different physical-chemical proprieties overlined in yellow. Secondly for each BMP-TGFß family members the phylogenic conservation in mammalian (15 species) of the amino acids implicated in the binding to IL34 was analyzed and given. Finally, the phylogenic conservation of the amino acids of IL34 implicated in the binding to BMPs was also analyzed in the same 15 mammalian species and presented.

Figure S17. Representative structures of IL34 binding to different BMP proteins. IL34 is displayed in cyan surface. (**A**) IL34 binding to BMP3 structure (lime color) as found PDB ID 2QCQ [84]. (**B**) IL34 binding to BMP6 structure (wheat color) as found PDB ID 2R52 [85]. (**C**) IL34 binding to BMP7 structure (purple color) as found PDB ID 1BMP [86]. Left: side view of protein complexes, right: top view of protein complexes.

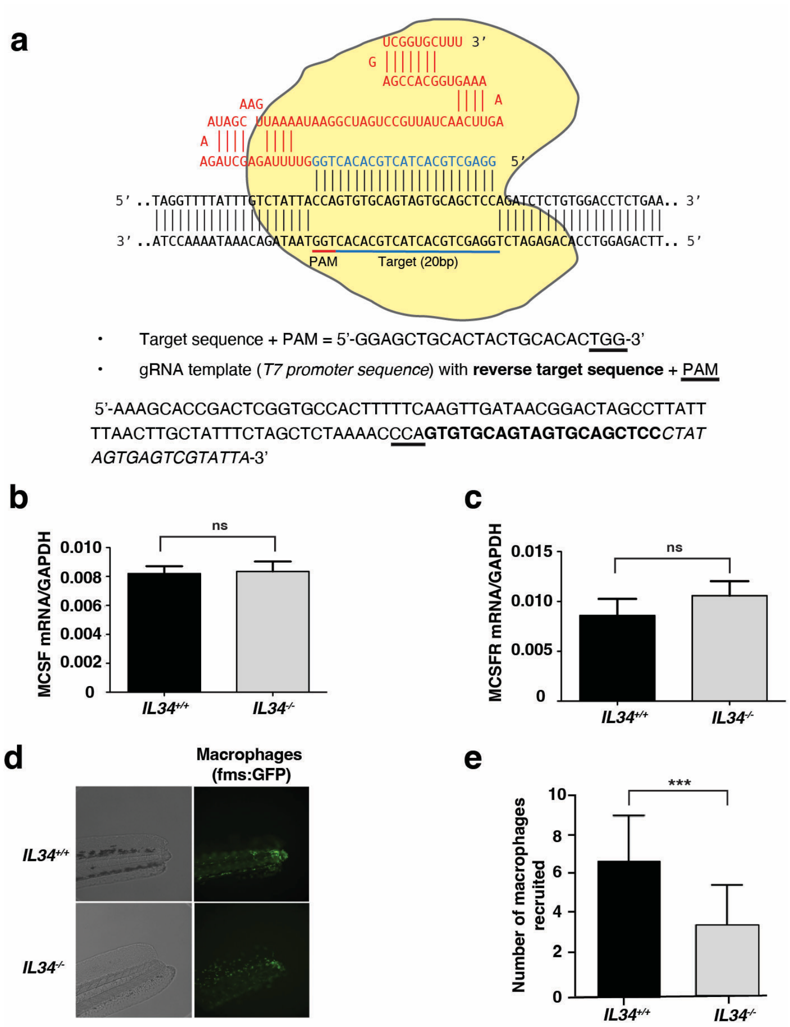
Figure S18. FACS comparative analysis of the populations of CD11b monocytic cells in both the bone marrow and the spleen of *Il34*$^{-/-}$ versus *Il34*$^{+/+}$ mice. In *Il34*$^{-/-}$ (IL34-KO) mice compared with *Il34*$^{+/+}$ (WT) mice, significant increases in the percentage of CD11b-positive cells were observed in both spleen (22.7% vs. 2.54%) and bone marrow (15.2% vs. 9.83%).

Figure S19. Demonstration at the molecular level of the physical interaction between the IL34 protein and proteins of the BMP receptor type II family. The surface plasmon resonance experiments showed that IL34 bound efficiently to BMPRII, ACTRIIA and ACTRIIB with KD values of 1.2E-07 M, 3.6E-07 M and 1.1E-07 M respectively.

Supplementary movie (S1)

Movie S1. Movie evidencing the simultaneous binding of one IL34 monomer (cyan), one BMPR1A monomer (green) and one ACVR2A monomer (red) on a dimer of BMP2 (blue and orange).

Supplementary figure 1

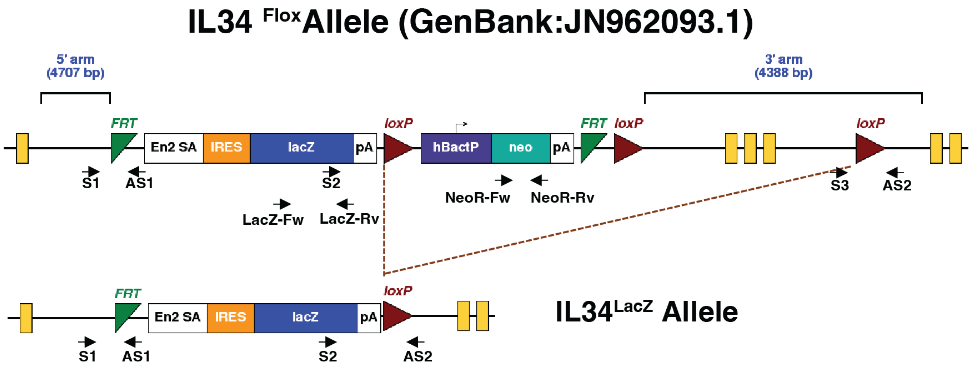


- Target sequence + PAM = 5’-GGAGCTGCACTACTGCACACTGG-3’
- gRNA template (*T7 promoter sequence*) with **reverse target sequence** + PAM

5’-AAAGCACCGACTCGGTGCCACTTTTTCAAGTTGATAACGGACTAGCCTTATT TTAACTTGCTATTTCTAGCTCTAAAACCCA**GTGTGCAGTAGTGCAGCTCC***CTAT AGTGAGTCGTATTA*-3’

Figure S1. Tools to *IL34* genetic invalidation in zebrafish using CrispR/Cas9 technology and functional confirmation. (**A**) Schematic representation of the targeted sequence in *il34* exon 3 including the protospacer adjacent motif (PAM) and the use guide RNA template sequence containing a T7 promoter sequence and the reverse targeted sequence and PAM. (**B-E)** Functional confirmation of *il34* invalidation was achieved showing the loss of the known IL34 effects on the differentiation and survival of monocytes and macrophages, [6,74] using the caudal fin amputations strategy on 3 day embryos from a heterozygous (+/-) in-cross of the double transgenic line *tg*(fms: GFP). This line contained the heterozygous mutant *il34* allele, and GFP expression of macrophages was driven by the *MCSFR* promoter. To visualize these inflammatory cells throughout injury, live images of the amputated caudal fins were taken at 8 hours post fin injuries. The 8 hours-time-point was chosen as this is the optimal time for recruitment of macrophages to the site of injury. At this time, despite no variation of *MCSF* and *MCSFR* transcript expression levels induced by *IL34* invalidation **B-C**, an important reduction of the number of macrophages recruited **D-E** was observed in the *il34*$^{-/-}$ comparatively to the control (*il34*$^{+/+}$).

Supplementary figure 2



Primer S3

```
WT     GTTTGGCCGATGCTGGCAAAGGGCTAAGAAGGAGAGTTCTGCCATGCGCTGAGCATGTGAG  62
FLOX   GTTTGGCCGATGCTGGCAAAGGGCTAAGAAGGAGAGTTCTGCCATGCGCTGAGCATGTGAG  62
       *************************************************************

WT     ACACACGAGGGATGGGGACAGAGAGGATTTGGACCTTGTTTCAAGCTTACCTGAGCGCCCC  124
FLOX   ACACACGAGGGATGGGGACAGAGAGGATTTGGACCTTGTTTCAAGCTTACCTGAGCGCCCC  124
       *************************************************************

WT     TCTTAAAAAAATTTTTTTTATTATTGTTGTTTTTAATTTTATAACCCATTGAGTCCAATTAC  186
FLOX   TCTTAAAAA-----------------------------------------------------  133
       *********

WT     TTCTGCCCACTGTTCACTACCCACGCTGGCTAGACCTTGTACAGGTGTTGTGAGGTAACCAG  248
FLOX   --------------------------------------------------------------  133

WT     TGTACTCATGGGTGC-----------------------------------------------  263
FLOX   ---------------GAGATGGCGCAACGCAATTAATGATAACTTCGTATAGCATACATTAT  180

WT     ---------------------------------ACCGGGCATGCCATCTTCATAAGACAG  290
FLOX   ACGAAGTTATGGTCTGAGCTCGCCATCAGTTCAACCGGGCATGCCATCTTCATAAGACAG  240
                                        ***************************
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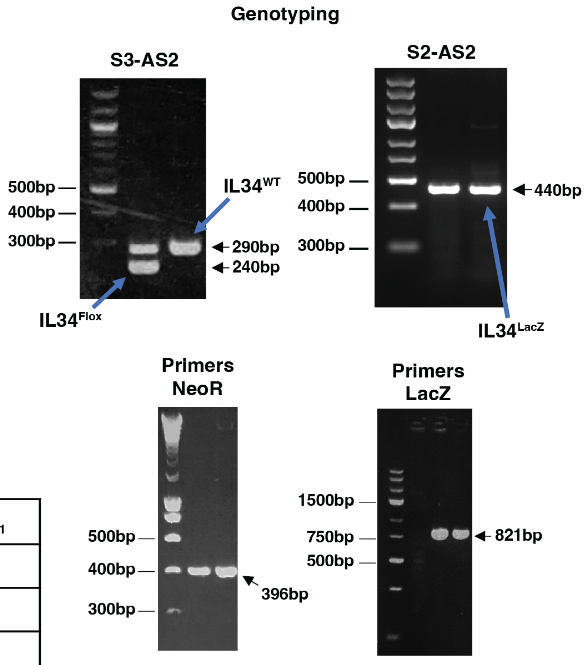
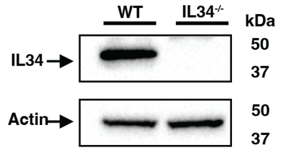
Primer AS2



Primers	Sequence	Position in GenBank:JN962093.1
S1	5'-AAAAACCTTCTTCGTTTCCTTGTCCC-3'	14853-14879
S2	5'-GTCAGTATCGGCGGAATT-3'	19807-19825
S3	5'-GTTTGGCCGATGCTGGCAAAGG-3'	23879-23901
AS1	5'-CTCCTACATAGTTGGCAGTG-3'	15202-15222
AS2	5'-CTGTCTTATGAAGATGGCATGCC-3'	24095-24118
LacZ-Fw	5'-CATCGAGCTGGGTAATAAGCGTTGGCAAT-3'	19048-19076
LacZ-Rv	5'-GTCGCTACCATTACCAGTTGGTCTGGTGTC-3'	19839-19868
NeoR-Fw	5'-ATCTCCTGTCATCTCACCTTGC-3'	21069-21090
NeoR-Rv	5'-CAAGCTCTTCAGCAATATCACG-3'	21443-21464

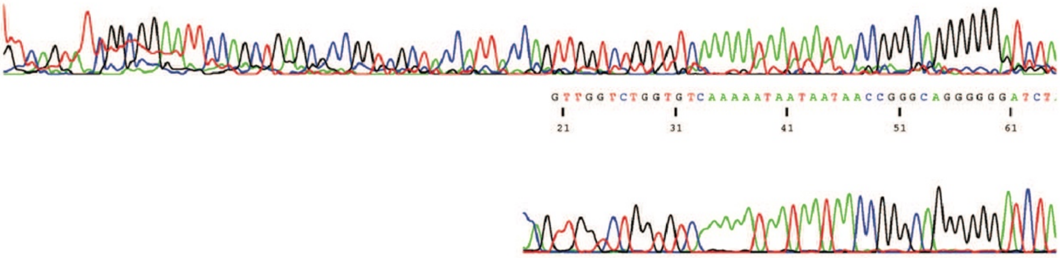


Sanger sequencing of fragment amplified by PCR with S1-AS1 primers on genomic DNA from IL34LacZ/LacZ Mouse

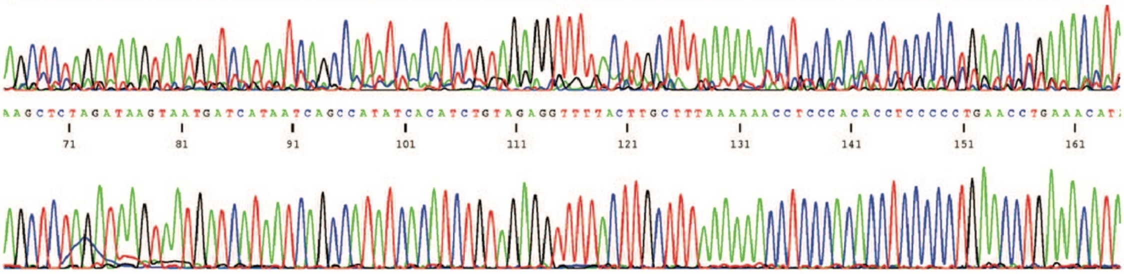
Sanger sequencing of fragment amplified by PCR with S2-AS2 primers on genomic DNA from IL34LacZ/LacZ Mouse

Primer S2

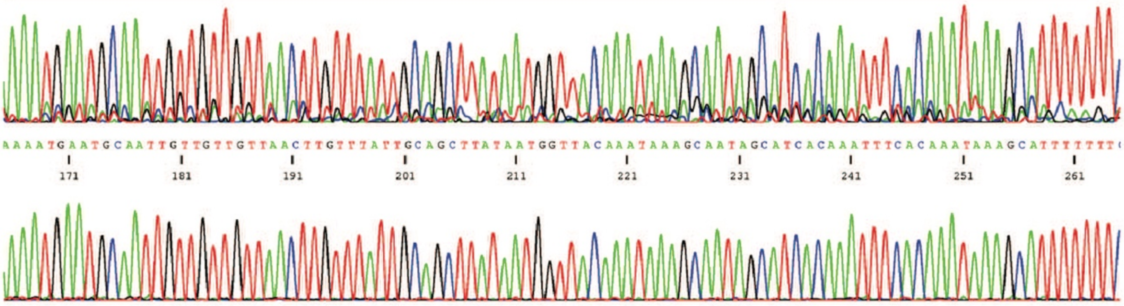
GTCAGTATCGGCGGAATTCCAGCTGAGCGCCGGTCGCTACCATTACCAGTTGGTCTGGTGTCAAAAATAATAATAACCGGGCAGGGGGGATCTA



AGCTCTAGATAAGTAATGATCATAATCAGCCATATCACATCTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATA

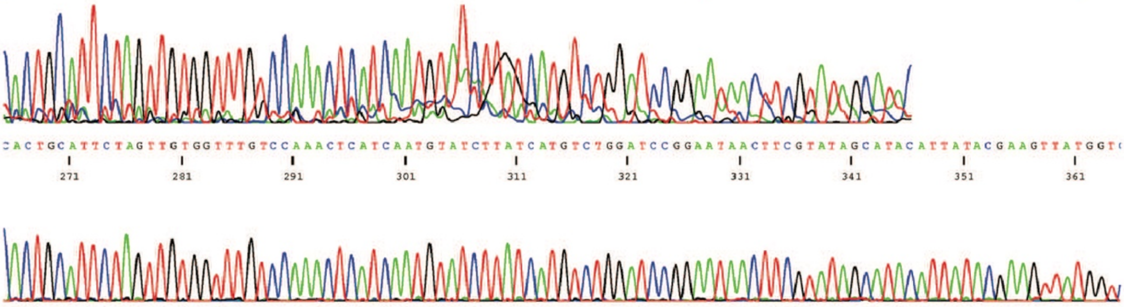


AAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTT



LoxP 3′

CACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGATCCGGAATAACTTCGTATAGCATACATTATACGAAGTTATGGT



Primer AS2

CTGAGCTCGCCATCAGTTCAACCGGGCATGCCATCTTCATAAGACAG

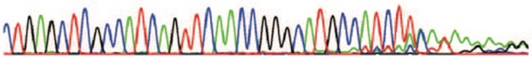


Figure S2. ***IL34* genetic invalidation in mouse.** *Il34*^{Flox} allele (Genbank: JN962093.1) and the derived *Il34*^{LacZ} allele obtained after recombination between its 5' and 3' LoxP sites are graphically represented. Primers used to genotype the different alleles are given in the table and positioned on the different graphical representations. Primers S3 and AS2 enable to discriminate the *Il34*^{Flox} allele from the WT allele with respectively amplification of 240 bp and 290 bp fragments. Primers S2 and AS2 enable to identify the *Il34*^{LacZ} allele corresponding to the amplification of a 440 bp fragment. LacZ and NeoR primer pairs were used to check the integrity of the *Il34*^{Flox} allele. Fragments amplified with S1-AS1 and S2-AS2 primer pairs from genomic DNA extracted from *Il34*$^{LacZ/LacZ}$ mouse tail were Sanger sequenced to confirm recombination terminals (sequences corresponding to the construct cassette are underlined). The disruption of IL34 has been also analyzed by western blot. Briefly, whole protein extracts were obtained from frozen spleens from WT and IL34 null mice and specific antibody targeting IL34 was used. As showed, IL34 was only detected in WT and not in IL34 null sample.

Supplementary figure 3

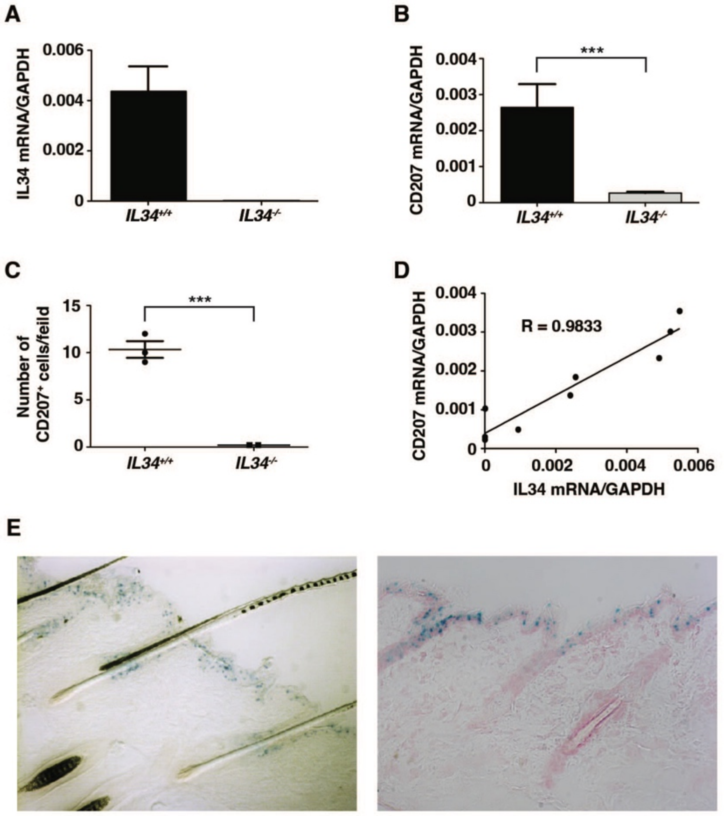
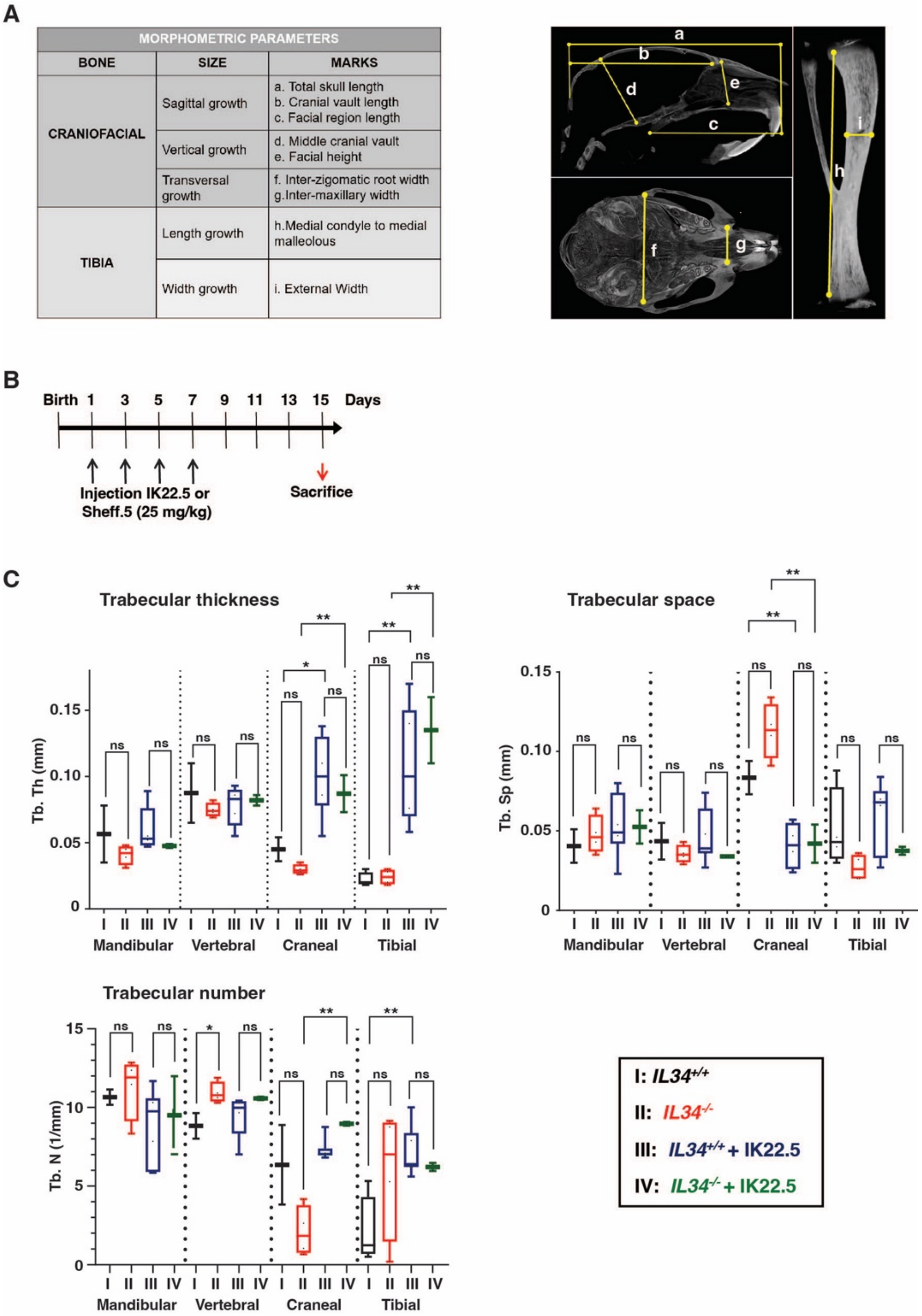


Figure S3. Functional confirmation of *IL34* invalidation and *IL34 LacZ* reporter in mouse. (**A-D**) In order to confirm the effective loss of IL34 function in *Il34*$^{-/-}$ mouse, skin well-known as an IL34 expression site [16] was used. Correlated to IL34 invalidation, a significant reduction of CD207 expressing cell (Langerhans cells) was observed. (**E**) ß-galactosidase staining (blue) performed on section of *Il34*$^{+/LacZ}$ mouse enable to confirm previously described expression of IL34 [15,16,75] in some keratinocytes and cells from the hair follicle.

Supplementary figure 4



MORPHOMETRIC PARAMETERS		
BONE	SIZE	MARKS
CRANIOFACIAL	Sagittal growth	a. Total skull length b. Cranial vault length c. Facial region length
	Vertical growth	d. Middle cranial vault e. Facial height
	Transversal growth	f. Inter-zigomatic root width g.Inter-maxillary width
TIBIA	Length growth	h.Medial condyle to medial malleolous
	Width growth	i. External Width

Figure S4. Graphical representation of morphometric parameters used for mouse head and tibia analyses, blocking antibodies injections protocol and results of bone trabecular structure analyses at different anatomical sites. (**A**) The seven morphometric parameters (a-g) measured for the head (craniofacial skeleton) and the two parameters (h-i) measured for tibia (appendicular skeleton) are listed and represented on 2D microCT scan views. (**B**) The blocking antibodies (IK22.5 and Sheff5) injections protocol was characterized by four subcutaneous injections at postnatal days 1, 3, 5 and 7 of 25 mg/kg of antibody following by a sacrifice at day 15. (**C**) The trabecular thickness (Tb. Th), the trabecular space (Tb. Sp) and the trabecular number (Tb. N) were determined at four anatomical sites, the mandible, the vertebra (C2) the skull and the tibia. *Il34*$^{+/+}$ are represented in black, *Il34*$^{-/-}$ in red, *Il34*$^{+/+}$ treated with IK22.5 in blue, and *Il34*$^{-/-}$ treated with IK22.5 in green. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001, ns: not significant. n=8 except for *Il34*$^{-/-}$ + IK22.5 (n=4).

Supplementary figure 5

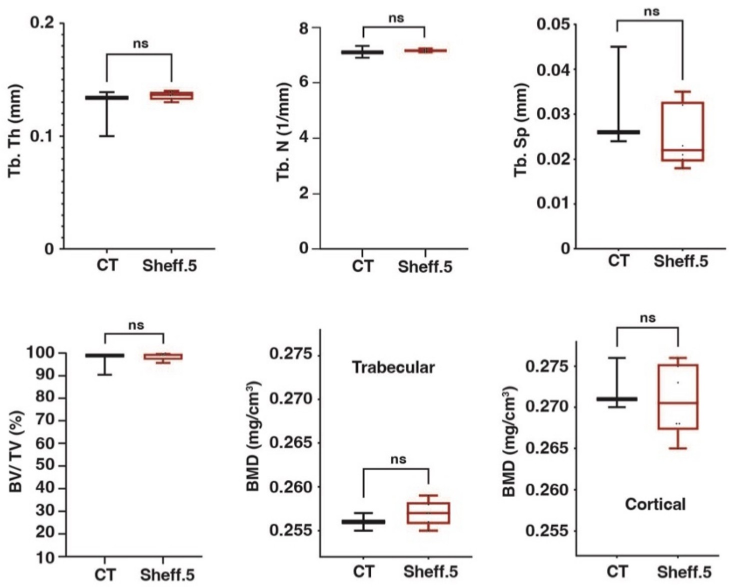


Figure S5. Analyses of the impact of Sheff.5 antibody injections in WT pups on the bone trabecular structure (Tb. Th, Tb. Sp and Tb. N), the percentage of BV/TV and BMD. No significant variation was observed comparatively to pups injected with a control irrelevant antibody from the same idiotype whatever the parameter considered. ns: not significant. CT: control group. n=8.

Supplementary figure 6

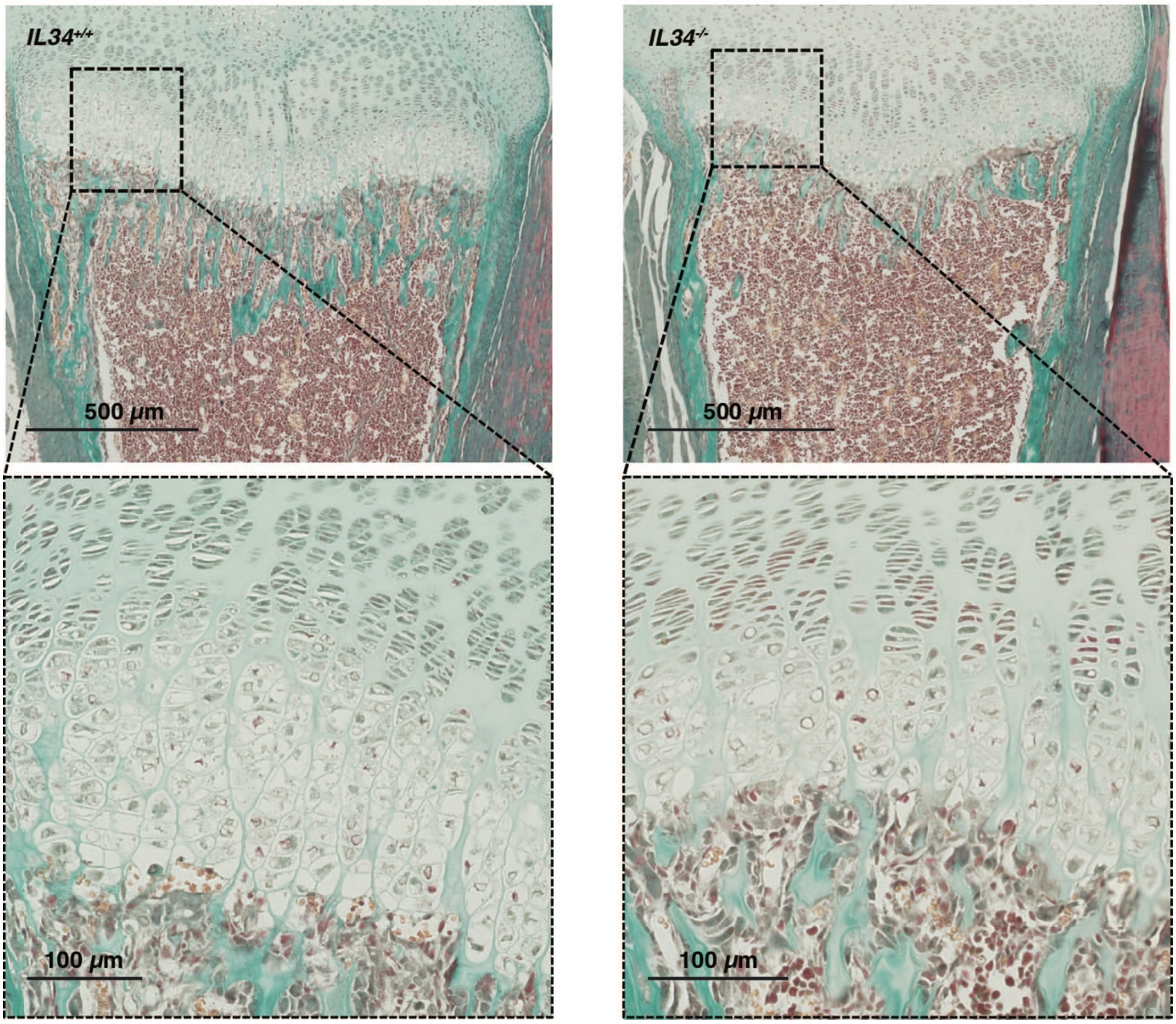


Figure S6. Histological comparative analysis of the tibia proximal epiphysis area of 15-day-old *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice using Masson's trichome stained longitudinal sections. An important reduction of the thickness of the hypertrophic chondrocytes area was observed in the null mutant. The scales are given as bars with the corresponding values in the lower part of each histological view.

Supplementary figure 7

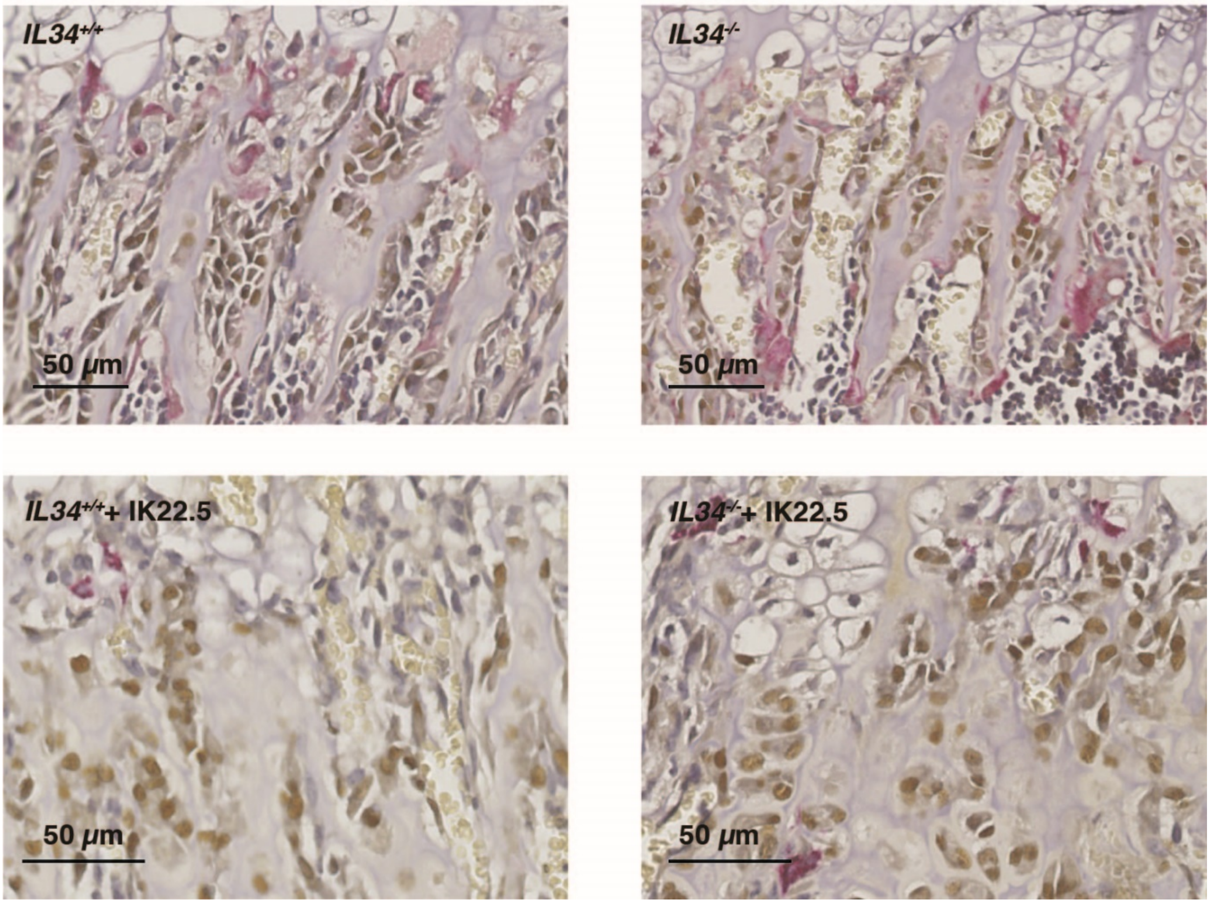


Figure S7. High magnification views of tartrate resistant acid phosphatase (TRAP) and Osterix dual-staining of tibia longitudinal sections at the level of the proximal epiphysis performed for 15-day-old *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice treated or not with the IK22.5 antibody. An important increase of both staining (TRAP in red and OSX in brown) was observed in the null mutant mouse. The IK22.5 injections drastically reduced the number of TRAP-positive cells in both *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice, whereas no evident variation of the number of cells stained for OSX was evidenced. The scale is given as a bar corresponding to 50 µm in the lower part of each histological view.

Supplementary figure 8

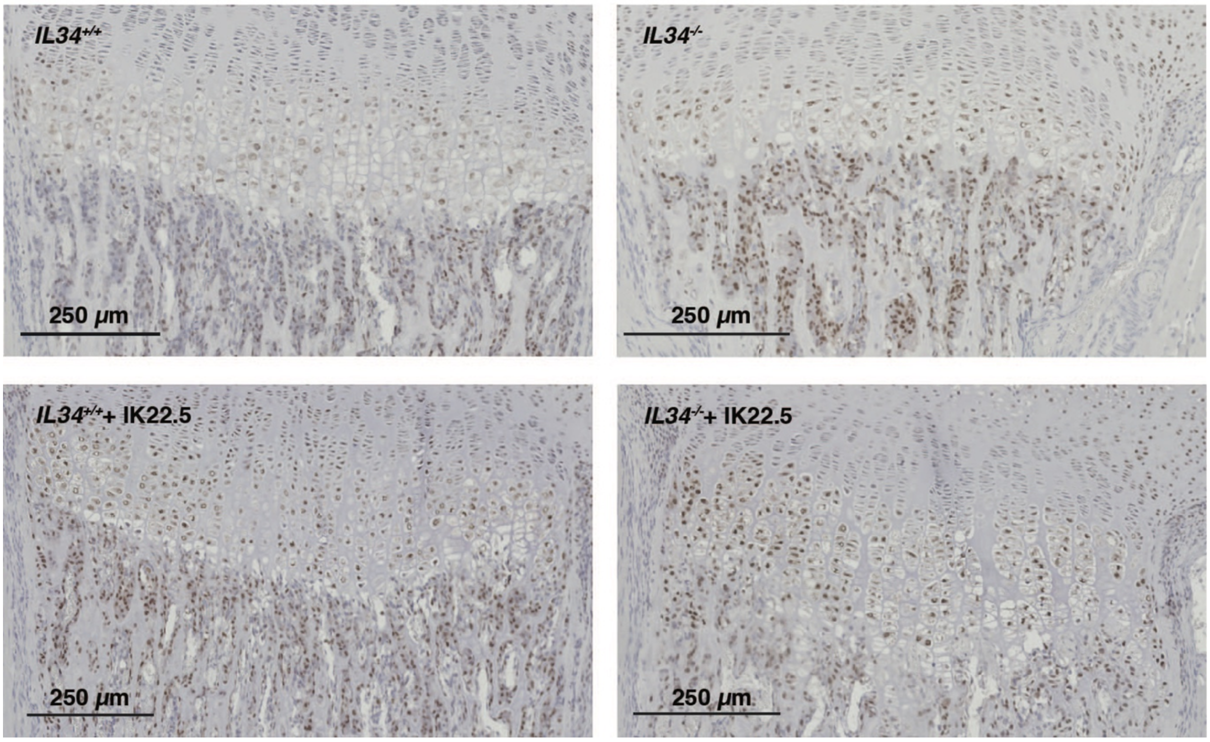


Figure S8. Comparative analysis of RUNX2 expression in the tibia proximal epiphysis area of 15-day-old *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice treated or not with the IK22.5 antibody using immunohistochemistry applied to longitudinal sections. No variation of the number of stained cells was evidenced between *Il34*$^{-/-}$ and *Il34*$^{+/+}$ mice as between *Il34*$^{-/-}$ and *Il34*$^{+/+}$ injected with IK22.5 antibody. The scale is given as a bar corresponding to 250 μm in the lower part of each histological view.

Supplementary figure 9

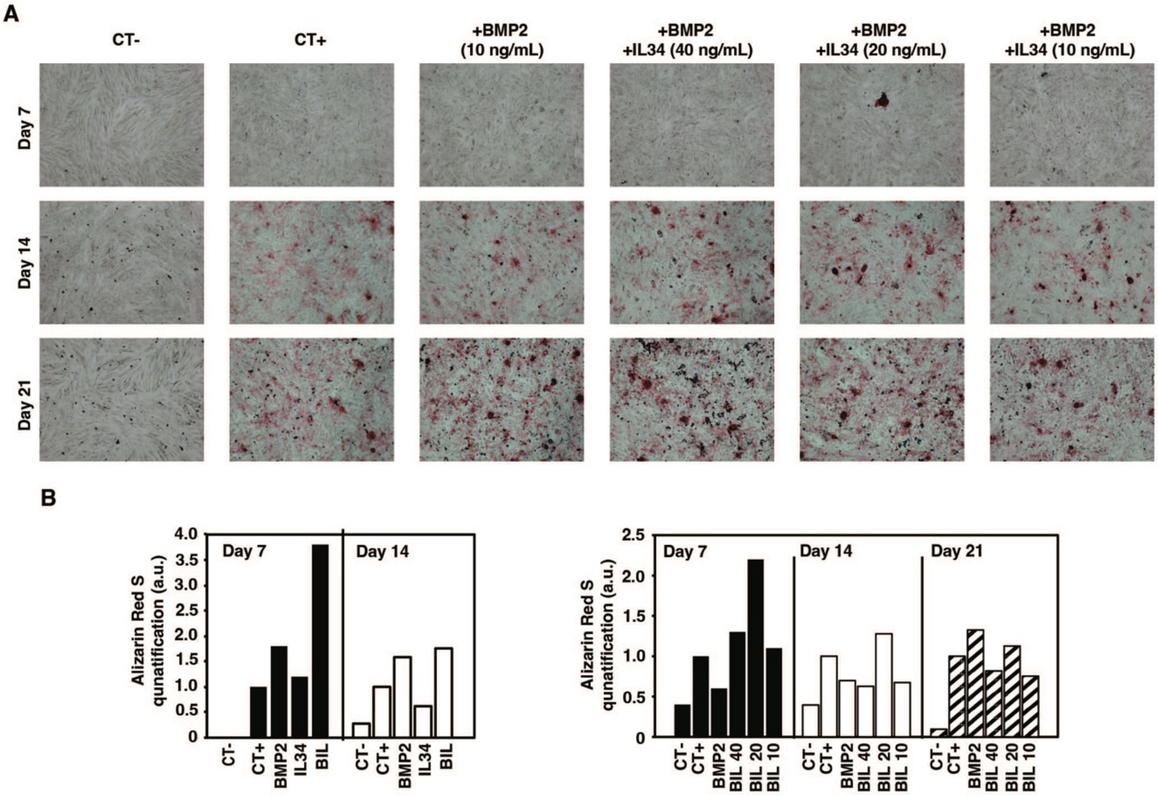


Figure S9. Functional impact of BMP2, IL34 or combined BMP2+IL34 addition in the culture medium onto osteoblastic differentiations. (**A**) BMP2 addition (10 ng/mL) to the osteogenic differentiation medium (CT+) induced an acceleration of the differentiation as evidenced by the higher alizarin red staining corresponding to phosphocalcic crystal deposition at 7, 14 and 21 days. IL34 addition (20 ng/mL) to the osteogenic differentiation medium had no effect on the differentiation (view not shown but the quantification is presented in **B**, right panel). Co-addition of IL34 (10, 20 or 40 ng/mL) with BMP2 (10 ng/mL) potentialized the acceleration of the osteoblastic differentiation observed with BMP2 alone with an optimal concentration ratio (ng/mL) of 2 between BMP2 and IL34. Magnification is similar for all views and the bar in CT- view at day 7 correspond to 500 µm. (**B**) Quantification of the alizarin red staining corresponding to independent experiments from different donors. BIL: BMP2+IL34 addition; Numbers (10, 20 or 40) correspond to the used concentrations of IL34 in ng/mL.

Supplementary figure 10

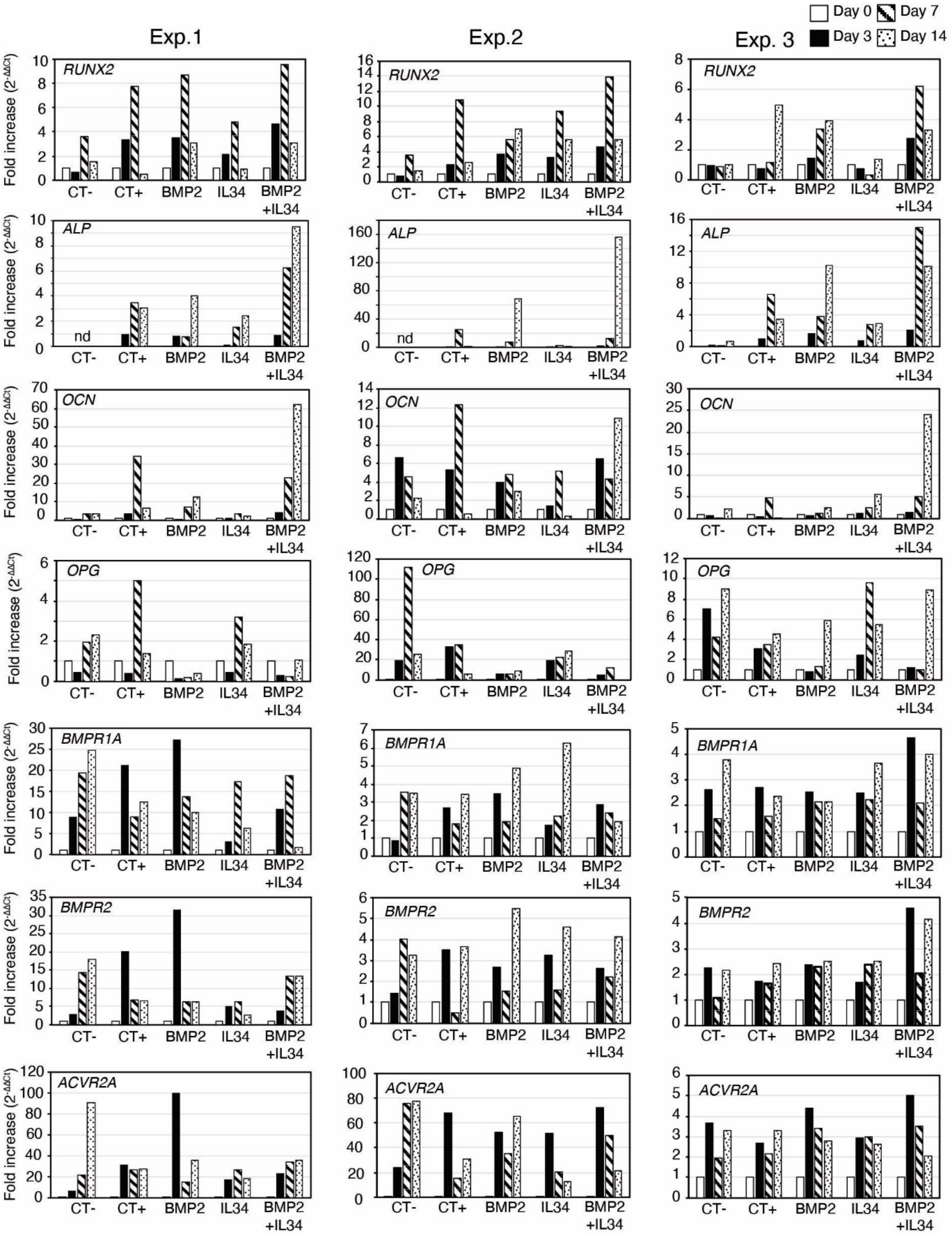


Figure S10. Impacts of the additions of BMP2 (10 ng/mL), IL34 (20 ng/mL) or BMP2+IL34 to the CT+ medium onto the expression of early (*RUNX2*) and late (*ALP* and *OCN*) markers of osteoblast differentiation, onto osteoprotegerin (*OPG*, a major regulatory factor of osteoclastogenesis), and onto type 1 and type 2 receptors of the BMPs (*BMPR1A, BMPR2* and *ACVR2A*). Results of three different experiments (Exp. 1 to 3) carried out with three different batches of mesenchymal stem cells (obtained from different donors) are presented in order to deal with the inter-batches variabilities considering only results similarly observed in the three experiments. BMP2 addition accelerated the osteoblastic differentiation and the co-addition of IL34 potentialized this effect as evidenced for *RUNX2* expression at days 3 and 7, and for *ALP* and *OCN* at day 14. BMP2 addition alone or in combination with IL34 reduced the *OPG* expression at days 3 and 7. Regarding the different receptors of the BMPs, no reproducible effects were observed between experiments, but all three receptors are expressed at all stages (days) of differentiation whatever the culture conditions used. nd: not detected.

Supplementary figure 11

A

IL34 (36 KDa)		BMP2 (26 KDa)		BMP4 (21 KDa)		BMP7 (19 KDa)	
10 ng/mL	277.78 pM	10 ng/mL	384.62 pM	10 ng/mL	476.19 pM	10 ng/mL	526.32 pM
20 ng/mL	555.56 pM	20 ng/mL	769.23 pM	20 ng/mL	952.38 pM	20 ng/mL	1.05 nM
40 ng/mL	1.11 nM	40 ng/mL	1.54 nM	40 ng/mL	1.90 nM	40 ng/mL	2.11 nM
80 ng/mL	2.22 nM	80 ng/mL	3.08 nM	80 ng/mL	3.80 nM	80 ng/mL	4.21 nM

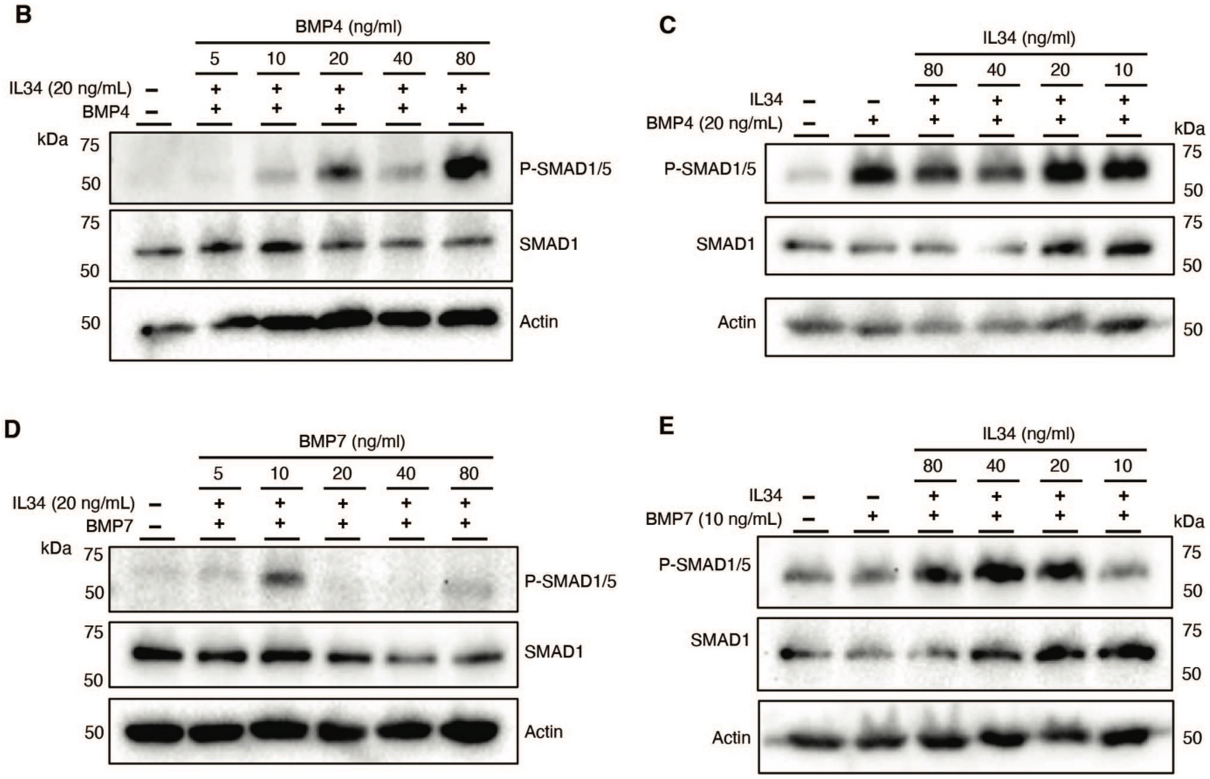


Figure S11. Impacts of addition of different combinations of BMP4+IL34 or BMP7+IL34 onto the activation of BMP receptors evidenced by SMAD1-5 phosphorylation in human MNNG-HOS osteosarcoma cell line. (**A**) Correspondence table between csoncentrations used in ng/mL and in pM or nM for IL34, BMP2, BMP4 and BMP7. (**B**) Joint addition of BMP4 (graded concentrations from 5 to 80 ng/mL) and IL34 (20 ng/mL) induced SMAD1-5 phosphorylation, with greater effects observed with 20 and 80 ng/mL BMP4. (**C**) Joint addition of BMP4 (20 ng/mL) and IL34 (graded concentration from 10 to 80 ng/mL) induced SMAD1-5 phosphorylation, with an optimal effect observed with 20 ng/mL IL34. (**D**) Joint addition of BMP7 (graded concentrations from 5 to 80 ng/mL) and IL34 (20 ng/mL) induced SMAD1-5 phosphorylation, with greater effects observed with 10 and 80 ng/mL BMP7. (**E**) Joint addition of BMP7 (10 ng/mL) and IL34 (graded concentration from 10 to 80 ng/mL) induces SMAD1-5 phosphorylation, with greater effects observed with 20 and 40 ng/mL IL34.

Supplementary figure 12

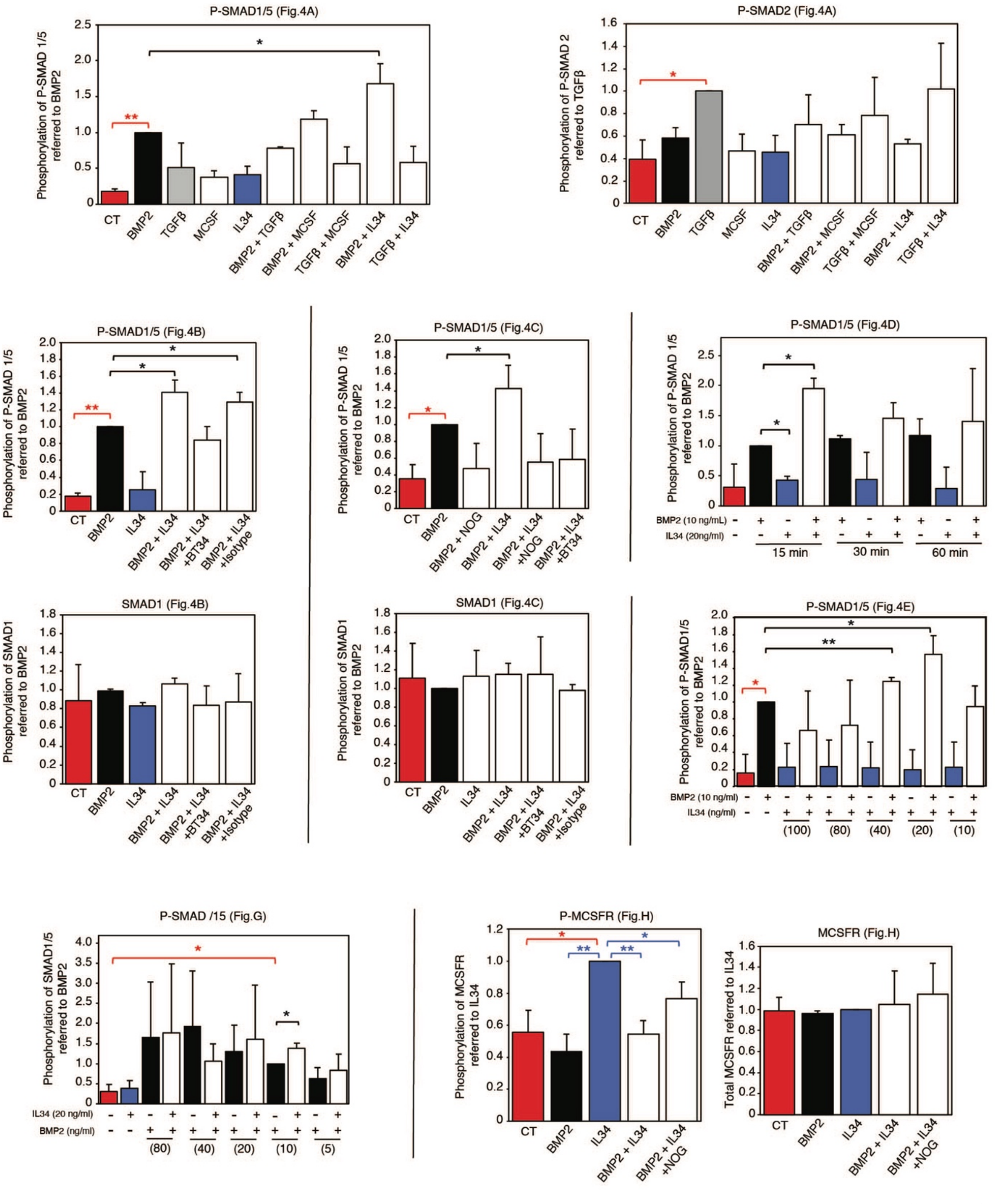


Figure S12. Quantitative analyses of Western blots presented in Figure 4. Histograms corresponding to the control condition, the BMP2-only condition and the IL34-only condition appear in red, black and blue respectively. *p<0.05, **p<0.01.

Supplementary figure 13

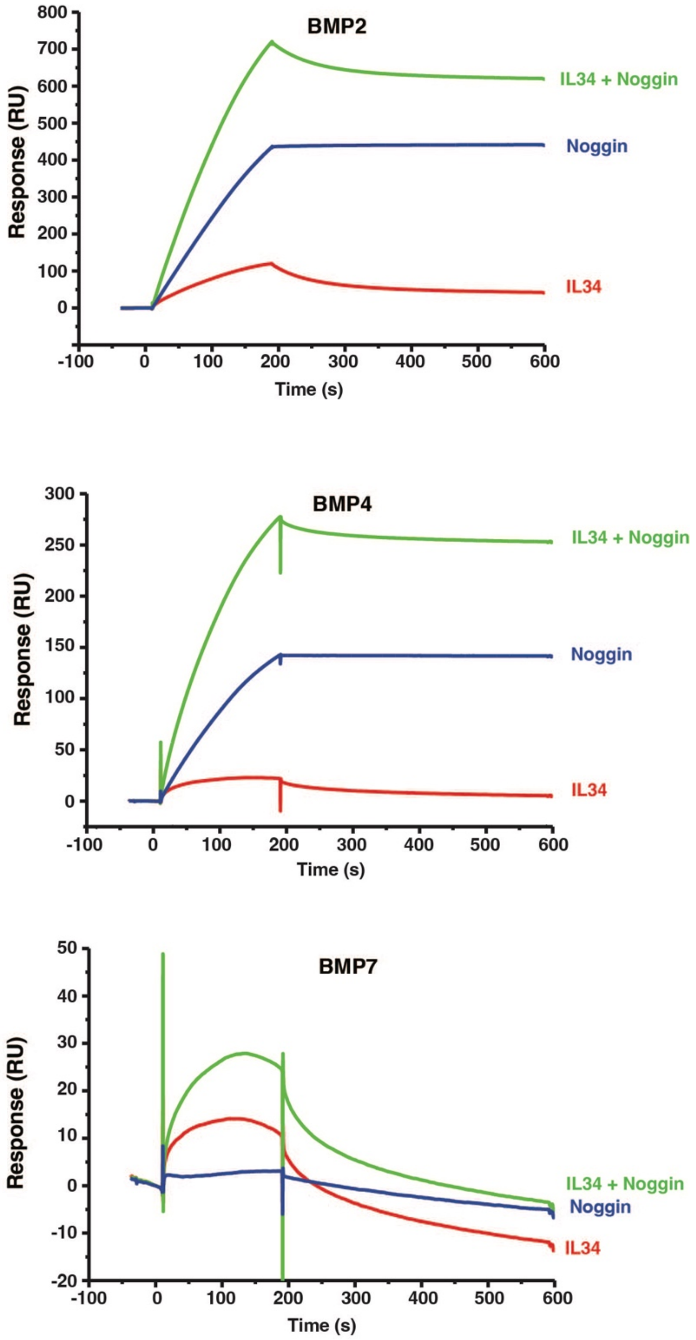


Figure S13. Curves obtained during the surface plasmon resonance experiments with immobilization of the BMP proteins (2, 4 and 7) and additions of IL34 and NOGGIN alone or in combination. Whatever the BMP protein considered an effective binding of IL34 as NOGGIN was observed with an additive effect of the two factors.

Supplementary figure 14

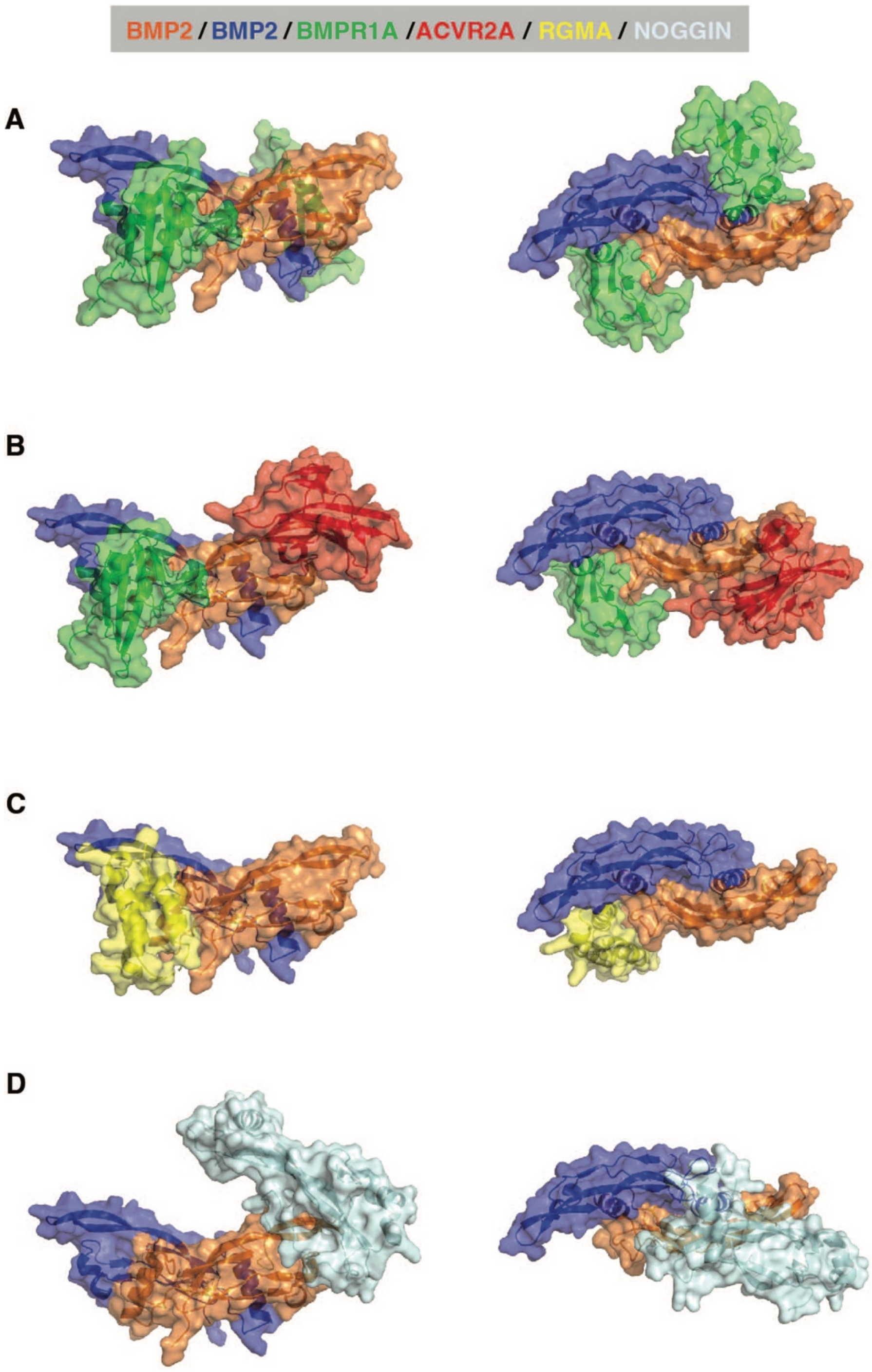


Figure S14. Representative structures of BMP2 dimer bound proteins resolved experimentally. BMP-2 dimers are displayed in blue and orange surface. (**A**) BMPR1A structure (green) as found in PDB ID 1ES7 [76]. State that binding the knuckle site. (**B**) BMPR1A (green) and Activin Receptor IIA (red) occupy each wrist and knuckle epitopes (PDB ID 2GOO [77]). (**C**) RGMA (yellow) as found in PDB ID 4UHY [78]. State that binding the knuckle site. (**D**) NOGGIN was determined to occupy both epitopes in structure PDB ID 7AG0 [79]. Left: side view of protein complexes, right: top view of protein complexes.

Supplementary figure 15

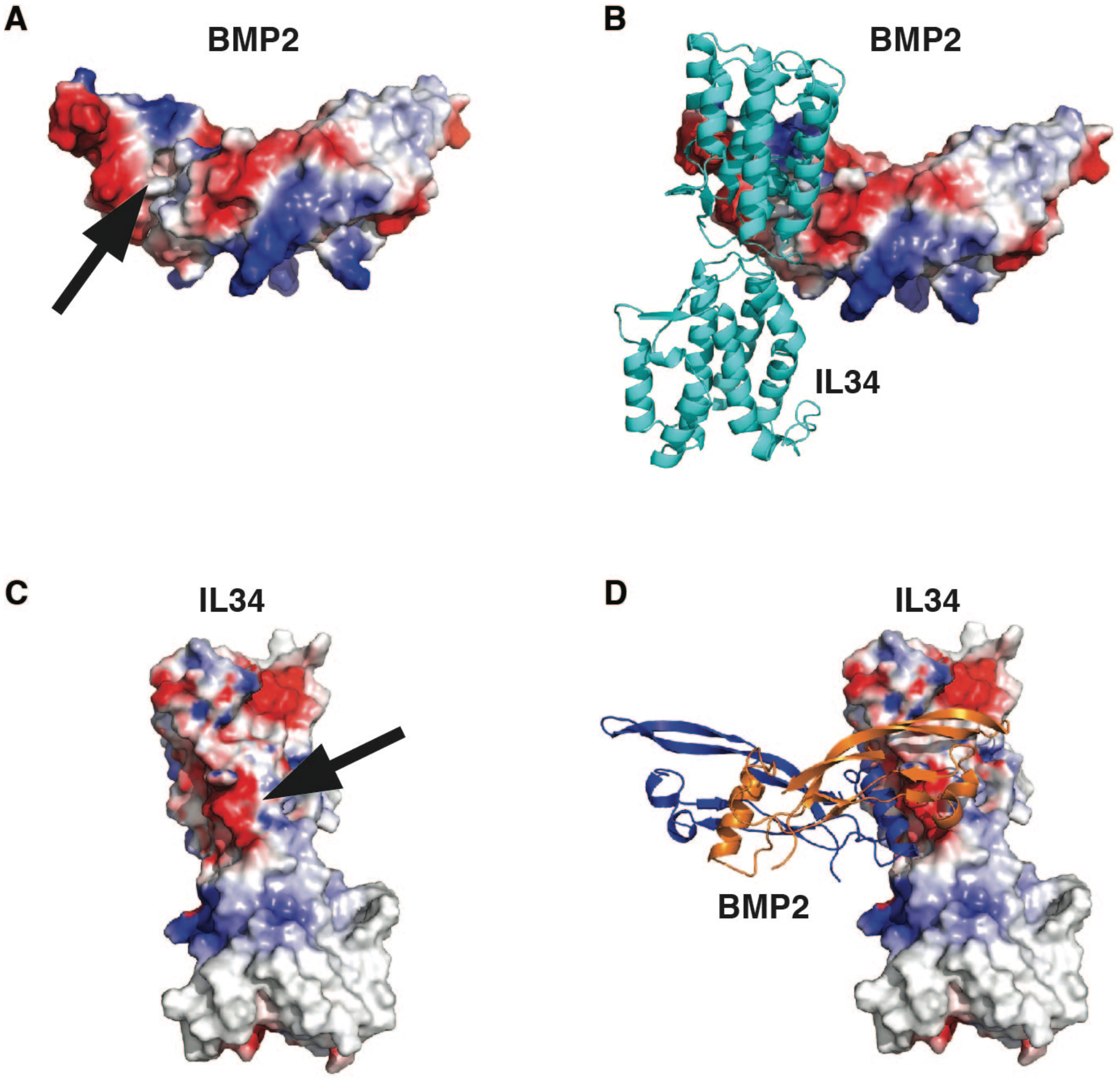
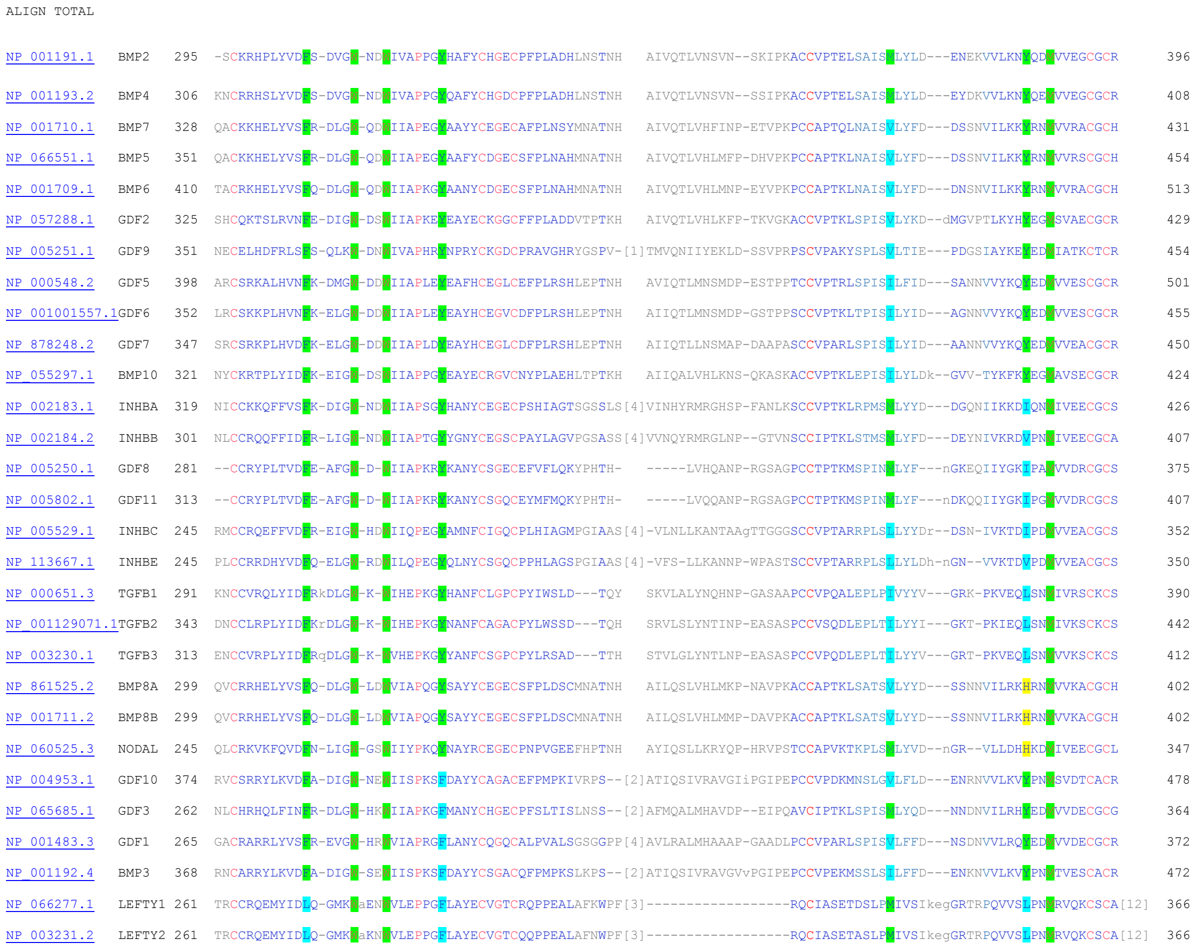


Figure S15. Representative structures of the BMP2 dimer and IL34 in electrostatics surface view with the hydrophobic (white) and hydrophilic sites (red for negative patches, blue for positive patches) and identification of their respective binding sites. (**A**) Representation of the BMP2 dimer with the knuckle site pocket underlined (arrow). (**B**) BMP2 dimer and IL34 position in cartoon representation. (**C**) IL34 with the BMP2 binding site indicated by the arrow. (**D**) IL34 and BMP2 position in cartoon representation.

Supplementary figure 16

All BMP/TGFß family members



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BMP4

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NP_031580.2 bone morphogenetic protein 4 preproprotein [Mus musculus]
NP_036959.2 bone morphogenetic protein 4 precursor [Rattus norvegicus]
XP_024853077.1 bone morphogenetic protein 4 isoform X2 [Bos taurus]
XP_020925510.1 bone morphogenetic protein 4 isoform X2 [Sus scrofa]
XP_038528824.1 bone morphogenetic protein 4 isoform X1 [Canis lupus familiaris]
XP_023483474.1 bone morphogenetic protein 4 isoform X2 [Equus caballus]
NP_001103747.1 bone morphogenetic protein 4 precursor [Ovis aries]
XP_024204496.1 bone morphogenetic protein 4 isoform X2 [Pan troglodytes]
XP_028707390.1 bone morphogenetic protein 4 isoform X2 [Macaca mulatta]
XP_019688586.1 bone morphogenetic protein 4 isoform X1 [Felis catus]
NP_001272575.1 bone morphogenetic protein 4 precursor [Capra hircus]
XP_030857866.1 bone morphogenetic protein 4 isoform X2 [Gorilla gorilla gorilla]
XP_024087813.1 bone morphogenetic protein 4 isoform X3 [Pongo abelii]
XP_032036116.1 bone morphogenetic protein 4 isoform X2 [Hylobates moloch]

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NP_001193.2     1    MIPG-----------------------------------------------NRMLMVVLLCQVLLGGASHASLIPETGKK  33
NP_031580.2     1    MIPG-----------------------------------------------NRMLMVVLLCQVLLGGASHASLIPETGKK  33
NP_036959.2     1    MIPG-----------------------------------------------NRMLMVVLLCQVLLGGASHASLIPETGKK  33
XP_024853077.1  1    MQEGRGGRRGETGAELGPEARSHSVVPSRATHCRSSSEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
XP_020925510.1  1    MQEGRGGGREVKGVELCPEARSHSVVPSRATHCRSSSEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
XP_038528824.1  1    MHEGRGGGREGRRAEPCPEARSHSVVPSRATHCRSSSEPFQQVCSRLAVKNHGLLLYALFSVILLGGSSHASLIPETGKK  80
XP_023483474.1  1    MQEGRGGGREGRRAEPGPEARSHSVVPSRATHCRSSSEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
NP_001103747.1  1    MIPG-----------------------------------------------NRMLMVVLLCQVLLGGASHASLIPETGKK  33
XP_024204496.1  1    MREGRGGGREGRSAEPGPEARSHSVVPSRATHCCSFPEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
XP_028707390.1  1    MREGRGGGREGRSAEPGPEARSHSVVPSRATHCCSFPEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
XP_019688586.1  1    MHEGRGGGREGRRAEPCPEARSHSVVPSRATHCRSSSEPFQQVCSRLAVKNHGLLLYALFSVILLGGSSHASLIPETGKK  80
NP_001272575.1  1    MIPG-----------------------------------------------NRMLMVVLLCQVLLGGASHASLIPETGKK  33
XP_030857866.1  1    MREGRGGGREGRSAEPGPEARSHSVVPSRATHCCSFPEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
XP_024087813.1  1    MREGRGGGREERSAEPGPEARSHSVVPPRATHCCSFPEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80
XP_032036116.1  1    MREGRGGGREGRSAEPGPEARSHSVVPSRATHCCSFPEPFQQVCSRLAVKNHGLLLYALFSVILLGGASHASLIPETGKK  80

NP_001193.2     34   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEE-QIHSTGLEYPERPAS  112
NP_031580.2     34   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQSQGTGLEYPERPAS  113
NP_036959.2     34   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQSQGTGLEYPERPAS  113
XP_024853077.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIQGIGLEYPERPAS  160
XP_020925510.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQTHSVGLEYPERPAS  160
XP_038528824.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIHSIGLEYPERPAS  160
XP_023483474.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKNAVVPDYMRDLYRLQSGEEEEEEQIHSVGLEYPERPAS  160
NP_001103747.1  34   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIQGIGLEYPERPAS  113
XP_024204496.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEE-QIHSTGLEYPERPAS  159
XP_028707390.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEE-QIHSAGLEYPERPAS  159
XP_019688586.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQTHSVGLEYPERPAS  160
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XP_030857866.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEE-QIHSTGLEYPERPAS  159
XP_024087813.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEE-QIHSTGLEYPERPAS  159
XP_032036116.1  81   KVAEIQGHAGGRRSGQSHELLRDFEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEE-QIHSTGLEYPERPAS  159

NP_001193.2     113  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWERGFHRINIYEVMKPPAEVVP  192
NP_031580.2     114  RANTVRSFHHEEHLENIPGTSESSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEMVP  193
NP_036959.2     114  RANTVRSFHHEEHLENIPGTSESSAFRFFFNLSSIPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEMVP  193
XP_024853077.1  161  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWDQGFHRINIYEVMKPPAEVVP  240
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XP_023483474.1  161  RANTVRSFHHEEHLESIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWEQGFHRINVYEVMKPPAEVVP  240
NP_001103747.1  114  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEVVP  193
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XP_028707390.1  160  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWERGFHRINIYEVMKPPAEVVP  239
XP_019688586.1  161  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVVSSAELRLFREQVNQGPDWEQGFHRINIYEVMKPPAEVVP  240
NP_001272575.1  114  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEVVP  193
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XP_024087813.1  160  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWERGFHRINIYEVMKPPAEVVP  239
XP_032036116.1  160  RANTVRSFHHEEHLENIPGTSENSAFRFLFNLSSIPENEVISSAELRLFREQVDQGPDWEQGFHRINIYEVMKPPAEVVP  239

NP_001193.2     193  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  272
NP_031580.2     194  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGDWAQLRPLL  273
NP_036959.2     194  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  273
XP_024853077.1  241  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGDWAQLRPLL  320
XP_020925510.1  241  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGDWAQLRPLL  320
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XP_023483474.1  241  GRLITRLLDTRLVHHSVTRWETFDVSPAVLRWTREKQPNYGLAIEVTPLHQTRTHQGQHVRISRALPQGSGDWAQLRPLL  320
NP_001103747.1  194  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGDWAQLRPLL  273
XP_024204496.1  240  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  319
XP_028707390.1  240  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  319
XP_019688586.1  241  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGDWAQLRPLL  320
NP_001272575.1  194  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQDQHVRISRSLPQGSGDWAQLRPLL  273
XP_030857866.1  240  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  319
XP_024087813.1  240  GHLITRLLDTRLIHHNVTRWETFDVSPAVLRWTREKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  319
XP_032036116.1  240  GHLITRLLDTRLVHHNVTRWETFDVSPAVLRWTGEKQPNYGLAIEVTHLHQTRTHQGQHVRISRSLPQGSGNWAQLRPLL  319

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NP_031580.2     274  VTFGHDGRGHTLTRRR-AKRSPKHHPQRSRKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  352
NP_036959.2     274  VTFGHDGRGHTLTRRR-AKRSPKHHPQRSRKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  352
XP_024853077.1  321  VTFGHDGRGHALTRRRRAKRSPKHHPQRARKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  400
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XP_023483474.1  321  VTFGHDGRGHALTRRRRAKRSPKHHPQRARKKTKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  400
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XP_019688586.1  321  VTFGHDGRGHALTRRQRAKRSPKHHPQRARKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  400
NP_001272575.1  274  VTFGHDGRGHALTRRRRAKRSPKHHPQRARKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  353
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XP_032036116.1  320  VTFGHDGRGHALTRRRRAKRSPKHHPQRARKKNKNCRRHSLYVDFSDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNST  399

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NP_031580.2     353  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  408
NP_036959.2     353  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  408
XP_024853077.1  401  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  456
XP_020925510.1  401  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  456
XP_038528824.1  401  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  456
XP_023483474.1  401  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  456
NP_001103747.1  354  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVALKNYQEMVVEGCGCR  409
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XP_024087813.1  400  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  455
XP_032036116.1  400  NHAIVQTLVNSVNSSIPKACCVPTELSAISMLYLDEYDKVVLKNYQEMVVEGCGCR  455
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BMP7

NP_001710.1 bone morphogenetic protein 7 preproprotein [Homo sapiens]
NP_031583.2 bone morphogenetic protein 7 preproprotein [Mus musculus]
NP_001178785.1 bone morphogenetic protein 7 precursor [Rattus norvegicus]
NP_001192944.1 bone morphogenetic protein 7 precursor [Bos taurus]
XP_005673101.1 bone morphogenetic protein 7 isoform X1 [Sus scrofa]
NP_001183981.1 bone morphogenetic protein 7 precursor [Canis lupus familiaris]
NP_001182087.1 bone morphogenetic protein 7 precursor [Equus caballus]
NP_001295493.1 bone morphogenetic protein 7 precursor [Ovis aries]
XP_001170064.1 bone morphogenetic protein 7 [Pan troglodytes]
XP_001089245.1 bone morphogenetic protein 7 [Macaca mulatta]
XP_011279062.2 LOW QUALITY PROTEIN: bone morphogenetic protein 7 [Felis catus]
XP_017913119.1 PREDICTED: bone morphogenetic protein 7 [Capra hircus]
XP_030860862.1 bone morphogenetic protein 7 [Gorilla gorilla gorilla]
XP_024094889.1 bone morphogenetic protein 7 [Pongo abelii]
XP_031998385.1 bone morphogenetic protein 7 [Hylobates moloch]

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NP_001178785.1  1    MHVRSLRAAAPHSFVALWAPLFLLRSALADFSLDNEVHSSFIHRRLRSQERREMQREILSILGLPHRPRPHLQGKHNSAP  80
NP_001192944.1  1    MHMRSLRAAAPHSFVALWAPLFLLRSALADFSLDNEVHSSFIHRRLRSQERREMQREILSILGLPHRPRPHLQGKHNSAP  80
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XP_024094889.1  1    MHVRSLRAAAPHSFVALWAPLFLLRSALADFSLDNEVHSSFIHRRLRSQERREMQREILSILGLPHRPRPHLQGKHNSAP  80
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XP_031998385.1  81   MFMLDLYNAMAVEEGGGPGGQGFSYPYKAVFSTQGPPLASLQDSHFLTDADMVMSFVNLVEHDKEFFHPRYHHREFRFDL  160

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NP_031583.2     160  SKIPEGEAVTAAEFRIYKDYIRERFDNETFQITVYQVLQEHSGRESD-LFLLDSRTIWASEEGWLVFDITATSNHWVVNP  238
NP_001178785.1  160  SKIPEGEAVTAAEFRIYKDYIRERFDNETFQITVYQVLQEHSGRESD-LFLLDSRTIWASEEGWLVFDITATSNHWVVNP  238
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NP_001295493.1  161  SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_001170064.1  161  SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_001089245.1  161  SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_011279062.2  161  SKIPEGKPWTAAEFRIYKDYIRKXLNNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_017913119.1  161  SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_030860862.1  161  SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_024094889.1  161  SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239
XP_031998385.1  161  SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVFQVLQEHLGRESD-LFLLDSRTLWASEEGWLVFDITATSNHWVVNP  239

NP_001710.1     240  RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-  318
NP_031583.2     239  RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHLRSIRSTGGKQRSQNRSKTPKNQEALRMASV-  317
NP_001178785.1  239  RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHLRSIRSTGGKQRSQNRSKTPKNQEALRMASV-  317
NP_001192944.1  240  RHNLGLQLSVETLDGQSINPKLAGLIGRQGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVANV-  318
XP_005673101.1  240  RHNLGLQLSVETLDGQSINPKLAGLIGRQGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVANV-  318
NP_001183981.1  241  RHNLGLQLCVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHLRSTRSTGAKQRSQNRSKTPKNQEALRVANVa  320
NP_001182087.1  240  RHNLGLQLSVETLDGQSVNPKLAGLIGRHGPQTKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVANV-  318
NP_001295493.1  240  RHNLGLQLSVETLDGQSINPKLAGLIGRQGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVANV-  318
XP_001170064.1  240  RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-  318
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XP_001089245.1   240   RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-   318
XP_011279062.2   240   RHNLGLQLCVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPXNQEALRVTNV-   318
XP_017913119.1   240   RHNLGLQLSVETLDGQSINPKLAGLIGRQGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVANV-   318
XP_030860862.1   240   RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-   318
XP_024094889.1   240   RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-   318
XP_031998385.1   240   RHNLGLQLSVETLDGQSINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-   318

NP_001710.1      319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
NP_031583.2      318   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPDTVPKPCCAP   397
NP_001178785.1   318   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPDTVPKPCCAP   397
NP_001192944.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_005673101.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
NP_001183981.1   321   AKNSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   400
NP_001182087.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
NP_001295493.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_001170064.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_001089245.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_011279062.2   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_017913119.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_030860862.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_024094889.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398
XP_031998385.1   319   AENSSSDQRQACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP   398

NP_001710.1      399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
NP_031583.2      398   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   430
NP_001178785.1   398   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   430
NP_001192944.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_005673101.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
NP_001183981.1   401   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   433
NP_001182087.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
NP_001295493.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_001170064.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_001089245.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_011279062.2   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_017913119.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_030860862.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_024094889.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
XP_031998385.1   399   TQLNAISVLYFDDSSNVILKKYRNMVVRACGCH   431
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BMP5

NP_066551.1 bone morphogenetic protein 5 isoform 1 preproprotein [Homo sapiens]
NP_031581.2 bone morphogenetic protein 5 preproprotein [Mus musculus]
NP_001101638.1 bone morphogenetic protein 5 precursor [Rattus norvegicus]
NP_001291945.1 bone morphogenetic protein 5 precursor [Bos taurus]
NP_001191830.1 bone morphogenetic protein 5 [Sus scrofa]
XP_532179.2 bone morphogenetic protein 5 [Canis lupus familiaris]
XP_001503274.1 bone morphogenetic protein 5 [Equus caballus]
XP_004018779.1 bone morphogenetic protein 5 [Ovis aries]
XP_518553.2 bone morphogenetic protein 5 isoform X1 [Pan troglodytes]
XP_001109809.1 bone morphogenetic protein 5 [Macaca mulatta]
XP_003986323.1 bone morphogenetic protein 5 [Felis catus]
XP_005696245.1 PREDICTED: bone morphogenetic protein 5 [Capra hircus]
XP_030868477.1 bone morphogenetic protein 5 isoform X1 [Gorilla gorilla gorilla]
XP_002817070.2 bone morphogenetic protein 5 isoform X1 [Pongo abelii]
XP_031996280.1 bone morphogenetic protein 5 isoform X1 [Hylobates moloch]

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NP_066551.1     1    MHLTVFLLKGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
NP_031581.2     1    MHWTVFLLRGIVGFLWSGWVQVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
NP_001101638.1  1    MHWTVFLLRGIVGFLWSSWVQVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
NP_001291945.1  1    MHLTVFLLRGIVGFLWSCWVLVGSAKGSLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
NP_001191830.1  1    MHLTVFLLRGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_532179.2     1    MHLTVFLLRSIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_001503274.1  1    MHLTVFLLRGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_004018779.1  1    MHLTVFLLRGIVGFLWSCWVLVGSAKGSLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_518553.2     1    MHLTVFLLKGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_001109809.1  1    MHLTVFLLKGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_003986323.1  1    MHLTVFLLRSIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_005696245.1  1    MHLTVFLLRGIVGFLWSCWVLVGSAKGSLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_030868477.1  1    MHLTVFLLKGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_002817070.2  1    MHLTVFLLKGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80
XP_031996280.1  1    MHLTVFLLKGIVGFLWSCWVLVGYAKGGLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF  80

NP_066551.1     81   MLDLYNAMTNEENPEESEYSVRASLAEETRGARKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
NP_031581.2     81   MLDLYNAMASEDNPEESEYLVRVSLAGEAKETRKGYPASPNGYAHRLHLPPRTPLTTQSPPLASLHDTNFLNDADMVMSF  160
NP_001101638.1  81   MLDLYNAMASEENPEESEYLVRVSLAGEAKETRKGYPASPNGYAHRLHLPPRIPLTTQSPPLASLHDTNFLNDADMVMSF  160
NP_001291945.1  81   MLDLYNAMASEENPEELEYSVRAPLAADSRGARKGSPASPNGYPRRIQLSRASPLTTQSPPLASLHDANFLNDADMVMSF  160
NP_001191830.1  81   MLDLYNAMASEENPEEPEYSVRASLAGETRGARKGSPASPNGYPRRIQLSRTTPLTTQSPPLASLHDANFLNDADMVMSF  160
XP_532179.2     81   MLDLYNAMANEENPEESEYSVRASLAGETRGTRKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_001503274.1  81   MLDLYNAMANEENPDETEYSVRASLAGETRGGRKGYPASPNGYPRGIQLSRTAPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_004018779.1  81   MLDLYNAMASEENPEELEYSVTAPLAADSRGSRKGSPASPNGYPRRIQLSRASPLTTQSPPLASLHDANFLNDADMVMSF  160
XP_518553.2     81   MLDLYNAMTNEENPEESEYSVRASLAEETRGARKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_001109809.1  81   MLDLYNAMTNEENPEESEYSVRASLAEETRGARKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_003986323.1  81   MLDLYNAMANEENPEESEYSVRASLAGEARGARKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_005696245.1  81   MLDLYNAMASEENPEELEYSVTAPLAADSRGSRKGSPASPNGYPRRIQLSRASPLTTQSPPLASLHDANFLNDADMVMSF  160
XP_030868477.1  81   MLDLYNAMTNEENPEESEYSVRASLAEETRGARKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_002817070.2  81   MLDLYNAMTNEENPEESEYSVRASLAEETRGARKGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160
XP_031996280.1  81   MLDLYNAMTNEENPEESEYSVRASLAEETRGARRGYPASPNGYPRGIQLSRTTPLTTQSPPLASLHDTNFLNDADMVMSF  160

NP_066551.1     161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
NP_031581.2     161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDKGNHRFENETIKISIYQIIKEYTNRDADLFLLDTRKT  240
NP_001101638.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDKSNHRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
NP_001291945.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPQGEAVTAAEFRIYKDRSNGRFENETIKISIYQIIKEYANRDADLFLLDTRKT  240
NP_001191830.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNSRFENETIKISIYQIIKEYTNRDADLFLLDTRKV  240
XP_532179.2     161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDQSNSRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
XP_001503274.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNSRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
XP_004018779.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPQGEAVTAAEFRIYKDRSNGRFENETIKISIYQIIKEYTNRDADLFLLDTRKT  240
XP_518553.2     161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
XP_001109809.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
XP_003986323.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDQSNSRFENETIKISIYQIIKEYTNRDADLFLLDTRKT  240
XP_005696245.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPQGEAVTAAEFRIYKDRSNGRFENETIKISIYQIIKEYTNRDADLFLLDTRKT  240
XP_030868477.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
XP_002817070.2  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240
XP_031996280.1  161  VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRSNNRFENETIKISIYQIIKEYTNRDADLFLLDTRKA  240

NP_066551.1     241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK  320
NP_031581.2     241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAASK  320
NP_001101638.1  241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAASK  320
NP_001291945.1  241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
NP_001191830.1  241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHSISVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_532179.2     241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_001503274.1  241  EALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_004018779.1  241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_518553.2     241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK  320
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XP_001109809.1   241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_003986323.1   241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_005696245.1   241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHSINVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_030868477.1   241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_002817070.2   241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK  320
XP_031996280.1   241  QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRSINVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK  320

NP_066551.1      321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
NP_031581.2      321  RKNQNRNKSNSHQDPSRMPSAGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
NP_001101638.1   321  RKNQNRNKSSSHQDPSRIPSAGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
NP_001291945.1   321  RKNQNRNKSGSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
NP_001191830.1   321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_532179.2      321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_001503274.1   321  RKNQNRNKSSSHQDSSRVSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_004018779.1   321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_518553.2      321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_001109809.1   321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_003986323.1   321  RKNQNRNKSNSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_005696245.1   321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_030868477.1   321  RKNQNRNKSSSHQDSSRMSNVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_002817070.2   321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400
XP_031996280.1   321  RKNQNRNKSSSHQDSSRMSSVGDYNTSEQKQACKKHELYVSFRDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNATNHA  400

NP_066551.1      401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
NP_031581.2      401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
NP_001101638.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
NP_001291945.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
NP_001191830.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_532179.2      401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_001503274.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_004018779.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_518553.2      401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_001109809.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_003986323.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_005696245.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_030868477.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_002817070.2   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
XP_031996280.1   401  IVQTLVHLMFPDHVPKPCCAPTKLNAISVLYFDDSSNVILKKYRNMVVRSCGCH   454
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BMP6

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NP_001709.1 bone morphogenetic protein 6 preproprotein [Homo sapiens]
NP_031582.1 bone morphogenetic protein 6 preproprotein [Mus musculus]
XP_038951315.1 bone morphogenetic protein 6 isoform X1 [Rattus norvegicus]
XP_002697666.2 bone morphogenetic protein 6 isoform X1 [Bos taurus]
NP_001161473.1 bone morphogenetic protein 6 precursor [Sus scrofa]
XP_038302254.1 LOW QUALITY PROTEIN: bone morphogenetic protein 6 [Canis lupus familiaris]
XP_023480199.1 bone morphogenetic protein 6 [Equus caballus]
XP_027814245.1 bone morphogenetic protein 6 isoform X1 [Ovis aries]
XP_003950760.2 bone morphogenetic protein 6 [Pan troglodytes]
XP_001085364.1 bone morphogenetic protein 6 [Macaca mulatta]
XP_023109461.1 bone morphogenetic protein 6 [Felis catus]
XP_017894411.1 PREDICTED: bone morphogenetic protein 6 isoform X1 [Capra hircus]
XP_030868423.1 bone morphogenetic protein 6 [Gorilla gorilla gorilla]
XP_024104721.1 bone morphogenetic protein 6 [Pongo abelii]
XP_031997037.1 bone morphogenetic protein 6 [Hylobates moloch]

NP_001709.1     1    MPGLGRRAQWLCWWWGLLCSCCGPPPLRPPLPAAAAA-AaGGQLLGDGGSPGRTEQPPPSP    QSSS-GFLYRRLKTQ  74
NP_031582.1     1    MPGLGRRAQWLCWWWGLLCSC-GPPPLRPPLPVAAAA-A-GGQLLGAGGSPVRAEQPPPQ-    SSSS-GFLYRRLKTH  71
XP_038951315.1  1    MPGLGRRAQWLCWWWGLLCSC-GPPPLRPPLPVAAAA-A-GGQLLGAGGSPVRAEQPPPQ-    SSSS-GFLYRRLKTH  71
XP_002697666.2  1    M--LGRTAQWLCWWWGLLCSFCGPPPL----PAAAAA---GGALLGDGGSPGHAERPPPPQ    TSSS-GFLYRRLKTH  66
NP_001161473.1  1    MPGLGRRAQWLCWWWGLLCSCCGPPSLRPPLPAAAAA-A-GGALLGDGGSPGHAEQPPPPQ    TSSS-GFLYRRLKTH  73
XP_038302254.1  1    M--LGPRAPWLCWWWGLLCSCCGPPPL-PPAAAAAAAaA-GGALLGDGGSPGHAEPTPPPP[14]SSSS-GFLYRRLKTH  85
XP_023480199.1  1    MPGLARRAQWLCWWWGLLCSCCGPPPLRPSLPAAAAT-G-GGALLGDGGSPGHAEQPPPPP    QSSSsGFLYRRLKTH  74
XP_027814245.1  1    M--LGRTAQWLCWWWGLLCSFCGPPPL----PAAAAA---GGALLGDGGSPGHAERPPPPQ    TSSS-GFLYRRLKTH  66
XP_003950760.2  1    MPGLGRRAQWLCWWWGLLCSCCGPPPLRPPLPAAAAA-AaGGQLLGDGGSPGRTEQPPPSP    QSSS-GFLYRRLKTQ  74
XP_001085364.1  1    MPGLGRRAQWLCWWWGLLCSCCGPPPLRPPLPAAAAA-AaGGQLLGDGGSPGRTEQPPPSP    QSSS-GFLYRRLKTH  74
XP_023109461.1  1    M--LGRRAQWLCWWWGLLCSCCGPPPLRPPLPAAAAAaG-GGALLGDGGSPGHAEQPPPPP    QSSS-GFLYRRLKTH  72
XP_017894411.1  1    M--LGRTAQWLCWWWGLLCSFCGPPPL----PAAAAA--aGGALLGDGGSPGHAERPPPPQ    TSSS-GFLYRRLKTH  67
XP_030868423.1  1    MPGLGRRAQWLCWWWGLLCSCCGPPPLRPPLPATAAA-AaGGQLLGDGGSPGRTEQPSPSP    QSSS-GFLYRRLKTQ  74
XP_024104721.1  1    MPGLGRRAQWLCWWWGLLCSCCGPPPLRPPLPAAAAA-AaGGQLLGDGGSPGQTEQPPPSP    QSSS-GFLYRRLKTQ  74
XP_031997037.1  1    MPGLGRRAQWLCWWWGLLCSCCGPPPLRPPLPAAAAA-AaGGQLLGDGGSPGRTEQPPPSP    QSSS-GFLYRRLKTQ  74

NP_001709.1     75   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQq--LP-RGEPPPGRLKSAPLFMLDLYNALSADN  147
NP_031582.1     72   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPVL-PpqqQQQ-QQQQQ---TA-REEPPPGRLKSAPLFMLDLYNALSNDD  145
XP_038951315.1  72   EKREMQKEILSVLGLPHRPRPLHGLQQPQSPVL-P----QQ-QQSQQ---TA-REEPPPGRLKSAPLFMLDLYNSLSKDD  141
XP_002697666.2  67   EKREMQKEILSVLGLPHRPRPLHGL--PQPPVF-P---QQQ-----Q----PaRGEPPPGRLKSAPLFMLDLYNALSADD  131
NP_001161473.1  74   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-P---QQQ-QQQTH-------GEPPPGRLKSAPLFMLDLYNALSADD  141
XP_038302254.1  86   EKREMQKEILSVLGLPHRPRPLHGLPPPQPAAF-P---QQQ----------P-RGEPPPGRLKSAPLFMLDLYNALAAAD  150
XP_023480199.1  75   EKREMQKEILSVLGLPHRPRPLHGLQQLQPPAL-P---QQQ----------P-RGEPPPGRLKSAPLFMLDLYNALAAAD  139
XP_027814245.1  67   EKREMQREILSVLGLPHRPRPLHGL--PQPPVF-P---QQQ----------PaRGEPPPGRLKSAPLFMLDLYNALSADD  130
XP_003950760.2  75   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQ---LP-RGEPPPGRLKSAPLFMLDLYNALSADN  146
XP_001085364.1  75   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-P---QQQ-QQQQQ---PP-RGEPPPGQLKSAPLFMLDLYNALSADD  145
XP_023109461.1  73   EKREMQKEILSVLGLPHRPRPLHGLQQPQPAAL-P---QEQ----------P-RGEPPPGRLKSAPLFMLDLYNALAADD  137
XP_017894411.1  68   EKREMQREILSVLGLPHRPRPLHGL--PQPPVF-P---QQQ----------PaRGEPPPGRLKSAPLFMLDLYNALSADD  131
XP_030868423.1  75   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQqqqLP-RGEPPPGRLKSAPLFMLDLYNALSADN  149
XP_024104721.1  75   EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQ---LP-RGEPPPGRLKSAPLFMLDLYNALSADN  146
XP_031997037.1  75   EKREMQKEILSVLGLPHRPRPLHGLQEPQPPALpQ---QQQqQQQQQ---LP-RGEPPPGRLKSAPLFMLDLYNALSTDD  147

NP_001709.1     148  DEDGASEGERQQSWPHEAASSSQRRQPPPGAAHPLNRKSLLAPGSGSGGA   S-PLTSAQDSAFLNDADMVMSFVNLVE  223
NP_031582.1     146  EEDGASEGVGQEPGSHGGASSSQLRQPSPGAAHSLNRKSLLAPGPG-GGA   S-PLTSAQDSAFLNDADMVMSFVNLVE  220
XP_038951315.1  142  EEDGVSEGEGLEPESHGRASSSQLKQPSPGAAHSLNRKSLLAPGPG-GSA   S-PLTSAQDSAFLNDADMVMSFVNLVE  216
XP_002697666.2  132  EEDGASDEERRQPGQRGGADASQPRSPSSGAAHPLGSGSLLATGPGGG--   AsPLTSAQDSAFLNDADMVMSFVNLVE  206
NP_001161473.1  142  EEDLASDKEMGQPGLRGGTDSSPPRQPPPRAAHPLGSRSLLAAGPG-GSA   S-PLTSAQESAFLNDADMVMSFVNLVE  216
XP_038302254.1  151  DEGWEAGEQRRPRGPRGGAGSSPPRRPPPGAAPPVGGRSLVAAGPGGGGG[4]AsALTSAQDSAFLNDADMVMSFVNLVE  231
XP_023480199.1  140  DEDGPSDEERRPPAPRGGAGSPQPGQPPPGAAHPLNRKSLLAPGPGGGGA   AtPLTSAQDSAFLNDADMVMSFVNLVE  216
XP_027814245.1  131  EEDGASDEERRQPGPRGGAGASQPRSPSPGAAHPLGSGSLLATGPGGG--   AsPLTSAQDSAFLNDADMVMSFVNLVE  205
XP_003950760.2  147  DEDGASEGERQQSWPHEAASSSQRRQPPPGAAHPLNRKSLLAPGSGSGGA   S-PLTSAQDSAFLNDADMVMSFVNLVE  222
XP_001085364.1  146  EEDGASEGERQQPWPHEGASSSQPRQPAPGAAHPLNRKSLLAPGPGSGGA   S-PLTSAQDSAFLNDADMVMSFVNLVE  221
XP_023109461.1  138  DEDWASDEERRQPGPRGGAGSSQPRQPPPGAAHPVNGKSLLASGPGGG--   TsPLTSAQDSAFLNDADMVMSFVNLVE  212
XP_017894411.1  132  EEDGASDEERRQPGPRGGAGASQSRSPSPGAAHPLGSGSLLATGPGGG--   AsPLTSAQDSAFLNDADMVMSFVNLVE  206
XP_030868423.1  150  DEDGASEGERQQSWPHEAASSSQRRQPPPGAAHPLNRKSLLAPGSGSGGA   S-PLTSAQDSAFLSDADMVMSFVNLVE  225
XP_024104721.1  147  DEDGASEGERQQSWPHEAASSSQRRQPPPGAAHPLNRKSLLAPGPGSGGA   S-PLASAQDSAFLNDADMVMSFVNLVE  222
XP_031997037.1  148  DEDGASEEKKQQSWPREAASSSQRRQPPPGAVHPLNRKSLLAPGPGSGGA   S-PLTSAQDSAFLNDADMVMSFVNLVE  223

NP_001709.1     224  YDKEFSPRQRHHKEFKFNLSQIPEGEVVTAAEFRIYKDCVMGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE  303
NP_031582.1     221  YDKEFSPHQRHHKEFKFNLSQIPEGEAVTAAEFRVYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE  300
XP_038951315.1  217  YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRVYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE  296
XP_002697666.2  207  YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLGTRAVWASEA  286
NP_001161473.1  217  YDKELSPRQRHHKEFKFNLSQVPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQQRQHRDSDLFLLDTRVVWASEE  296
XP_038302254.1  232  YEKEFSPGQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE  311
XP_023480199.1  217  YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRMVWASEE  296
XP_027814245.1  206  YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLGTRAVWASEA  285
XP_003950760.2  223  YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE  302
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XP_001085364.1   222   YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE   301
XP_023109461.1   213   HEKEFSPGQRYHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE   292
XP_017894411.1   207   YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSFKNQTFLISIYQVLQEHQHRDSDLFLLGTRAVWASEA   286
XP_030868423.1   226   YDKEFSPRQQHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE   305
XP_024104721.1   223   YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSFKNQTFLISIYQVLQEHQHRDSDLFLLDTRVVWASEE   302
XP_031997037.1   224   YDKEFSPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSFKNQTFLISIYQVLQEHQHRDSDLCLLDTRVVWASEE   303

NP_001709.1      304   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGVHVHPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASSRRRQQ   383
NP_031582.1      301   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGLHVNPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASSRRRQQ   380
XP_038951315.1   297   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGLHINPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASSRRRQQ   376
XP_002697666.2   287   GWLEFDITATSNLWVLTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFFKASEVHVRSARSAPGRRRQQ   366
NP_001161473.1   297   GWLEFDITATSNLWVLTPQHNLGLQLGVVTQDGLSISPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTARSATGRRRQQ   376
XP_038302254.1   312   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGLPINPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSAPGRRRQQ   391
XP_023480199.1   297   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGLSINPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSATGRRRQQ   376
XP_027814245.1   286   GWLEFDITATSNLWVLTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFFKASEVHVRSARSAPGRRRQQ   365
XP_003950760.2   303   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGVHVHPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASSRRRQQ   382
XP_001085364.1   302   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGVHIHPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASGRRRQQ   381
XP_023109461.1   293   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGLNINPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSAPGRRRQQ   372
XP_017894411.1   287   GWLEFDITATSNLWVLTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFFKASEVHVRSARSAPGRRRQQ   366
XP_030868423.1   306   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGVHVHPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASSRRRQQ   385
XP_024104721.1   303   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRDGVHIHPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRTTRSASSRRRQQ   382
XP_031997037.1   304   GWLEFDITATSNLWVVTPQHNMGLQLSVVTRNGVHVHPRAAGLVGRDGPYDKQPFMVAFFKVSEVHVRATRSASSRRRQQ   383

NP_001709.1      384   SRNRSTQSQDVARVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   462
NP_031582.1      381   SRNRSTQSQDVSRGSGSS-DYNGSELKTACKKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   459
XP_038951315.1   377   SRNRSTQSQDVSRGSSAS-DYNSSELKTACKKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   455
XP_002697666.2   367   ARNRSTPAQDVSRASSASaDYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   446
NP_001161473.1   377   SRNRSTQAQDVSRASSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   455
XP_038302254.1   392   SRNRSTQSQDVSRVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   470
XP_023480199.1   377   SRNRSTQSQDVSRVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   455
XP_027814245.1   366   ARNRSTPAQDVSRASSASaDYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   445
XP_003950760.2   383   SRNRSTQSQDVARVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   461
XP_001085364.1   382   SRNRSTQSQDVARVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   460
XP_023109461.1   373   SRNRSTQSQDVSRVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   451
XP_017894411.1   367   ARNRSTPAQDVSRASSASaDYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   446
XP_030868423.1   386   SRNRSTQSQDVARVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   464
XP_024104721.1   383   SRNRSTQSQDVARVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   461
XP_031997037.1   384   SRNRSTQSQDVARVSSAS-DYNSSELKTACRKHELYVSFQDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNATNHAIVQ   462

NP_001709.1      463   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   513
NP_031582.1      460   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   510
XP_038951315.1   456   TLV[29] HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   535
XP_002697666.2   447   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   497
NP_001161473.1   456   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   506
XP_038302254.1   471   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   521
XP_023480199.1   456   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   506
XP_027814245.1   446   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   496
XP_003950760.2   462   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   512
XP_001085364.1   461   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   511
XP_023109461.1   452   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   502
XP_017894411.1   447   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   497
XP_030868423.1   465   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   515
XP_024104721.1   462   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   512
XP_031997037.1   463   TLV     HLMNPEYVPKPCCAPTKLNAISVLYFDDNSNVILKKYRNMVVRACGCH   513
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GDF2/BMP9

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NP_057288.1 growth/differentiation factor 2 preproprotein [Homo sapiens]
NP_062379.3 growth/differentiation factor 2 preproprotein [Mus musculus]
NP_001099566.1 growth/differentiation factor 2 precursor [Rattus norvegicus]
NP_001179349.1 growth/differentiation factor 2 precursor [Bos taurus]
XP_003133152.2 growth/differentiation factor 2 [Sus scrofa]
XP_853886.2 growth/differentiation factor 2 isoform X1 [Canis lupus familiaris]
XP_001500704.1 growth/differentiation factor 2 [Equus caballus]
XP_004021599.3 growth/differentiation factor 2 [Ovis aries]
XP_507775.4 growth/differentiation factor 2 [Pan troglodytes]
XP_001109523.2 growth/differentiation factor 2 [Macaca mulatta]
XP_003994191.1 growth/differentiation factor 2 [Felis catus]
XP_005699391.1 PREDICTED: growth/differentiation factor 2 [Capra hircus]
XP_004049419.1 growth/differentiation factor 2 [Gorilla gorilla gorilla]
XP_002820746.1 growth/differentiation factor 2 [Pongo abelii]
XP_032026853.1 growth/differentiation factor 2 [Hylobates moloch]
NP_057288.1     1    MCPGALWVALPL-LS---LLAGSLQGKPLQSWGRGSAGGNAHSPLGVPGGGLPEHTFNLKMFLENVKVDFLRSLNLSGVP  76
NP_062379.3     1    MSPGAFRVAL---LP-lfLLVCVTQQKPLQNWEQASPGENAHSSLGLSGAGEE-GVFDLQMFLENMKVDFLRSLNLSGIP  75
NP_001099566.1  1    MSPGAFRVVL---LT-llLLVCPTQQKPLQSWGQASPGGNARSSLGLSGSREE-GVFDLKMFLENMKVDFLRSLNLSGIP  75
NP_001179349.1  1    MGRGALWVALPV-LC---LLACSALGKPLENRGRPSTGADAHGLLGGPGGEQEGVTFDLRMFLENMKVDFLRNLNLSGVP  76
XP_003133152.2  1    MCRGVLWVALPVaLS---LLVCSTQGKPLDSRVRASAGGDAHRLLGGAGGEQERGTFDLRMFLENMKVDFLRSLNLSGVP  77
XP_853886.2     1    MCGGAVGGALRA-LCalwLLGCGARGRPLEGRRRPGS-------QGAPGGPR-----DLRALPQAVQRDLLRGLNLSGVP  67
XP_001500704.1  1    MCRGALRVAL---LA---LLACSAQGKPLESRGRAAGGDAHRPRGGPGGEQEAGTFDLRMFLENMKVDFLRSLNLSGVP  74
XP_004021599.3  1    MGRGALRMALPV-LS---LLACSALGKPLENRGRPSTGGDAHRLLRGPGGEQEGATFDLRMFLENMKVDFLRNLNLSGVP  76
XP_507775.4     1    MCPGALWVALPL-LS---LLAGSLQGKPLQSWGRGSAGGNAHSPLGVPGGGLPEHTFNLKMFLENVKVDFLRSLNLSGVP  76
XP_001109523.2  1    MCPGALWVALPL-LS---LLAGSLQGKPLQSWGRGSAGGTAHNPLGVPGGELPEHTFNLKMFLENMKVDFLRSLNLSGVP  76
XP_003994191.1  1    MCCGALWVALPV-LS---LLACSAQGKPLESRGRAPAGGDAHRLLGGPGGEREGGTFDLRMFLENMKVDFLRSLNLSGVP  76
XP_005699391.1  1    MGRGALRMALPV-LS---LLACSALGKPLGNRGRPSTGGDAHRLLGGPGGEQEGVTFDLRMFLENMKVDFLRNLNLSGVP  76
XP_004049419.1  1    MCPGALWVALPL-LS---LLAGSLQGKPLQSWGRGSAGGNAHSPLGVPGGGLPEHTFNLKMFLENVKVDFLRSLNLSGVP  76
XP_002820746.1  1    MCLGALWVALPL-LS---LLAGSLQGKPLQSWGRGSAGGNAHSPLGVPGGGLPEHTFNLKMFLENVKVDFLRSLNLSGVP  76
XP_032026853.1  1    MCPGALWVALPL-LS---LLAGSLQGKPLQSWGRGSAGGNAHSPLGVPGGGLPEHTFNLKMFLENMKVDFLRSLNLSGVP  76

NP_057288.1     77   SQDKTRVEPPQYMIDLYNRYTSDKSTTPASNIVRSFSMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156
NP_062379.3     76   SQDKTRAEPPQYMIDLYNRYTTDKSSTPASNIVRSFSVEDAISTAATEDFPFQKHILIFNISIPRHEQITRAELRLYVSC  155
NP_001099566.1  76   SQDKTRAEPPQYMIDLYNRYTTDKSSTPASNIVRSFSVEDAISTAATEDFPFQKHILIFNISIPRHEQITRAELRLYVSC  155
NP_001179349.1  77   SQDRTRAEPPQYMIDLYNRYTTDKTSTPASNIVRSFSVEDAVSIATTEDFPFQKHILLFNISIPRHEQITRAELRLYLSC  156
XP_003133152.2  78   SQDKTRAEPPQYMIDLYNRYTTDKTSTPASNIVRSFSVEDAVSVSATEDFPFQKHILLFNISVPRHEQITRAELRLYLSC  157
XP_853886.2     68   AQPRARAEPPQYMLDLYHRYASDKAAAPASNVVRSFSVEDAVSIMATEDFPFQKHILLFNVSIPRHEQITRAELRLYVSC  147
XP_001500704.1  75   SQDKTRAEPPQYMIDLYNRYTTDKSSTPTSNIVRSFSVEDAVSVMATEDLSFQKHILFFNISIPRHEQITRAELRLHISC  154
XP_004021599.3  77   SQDRTRAEPPQYMIDLYNRYTTDKTSTPASNIVRSFSVEDAVSLATTEDFPFQKHFLLFNISIPRHEQITRAELRLYVSC  156
XP_507775.4     77   SQDKTRVEPPQYMIDLYNRYTSDKSTTPASNIVRSFSMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156
XP_001109523.2  77   SQDKTRVEPPQYMIDLYNRYTSDKSTTPASNIVRSFSMEDAISMTATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156
XP_003994191.1  77   SQDKTRAEPPQYMIDLYNRYTTDKSTTPASNIVRSFSVEDAVSLAATEEFPFQKHILLFNISIPRHEQITRAELRLYASC  156
XP_005699391.1  77   SQDRTRAEPPQYMIDLYNRYTTDKTSTPASNIVRSFSVEDAVSLATTEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156
XP_004049419.1  77   SQDKTRVEPPQYMIDLYNRYTSDKSTTPASNIVRSFSMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156
XP_002820746.1  77   SQDKTRVEPPQYMIDLYNRYTSDKSTTPASNIVRSFSMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156
XP_032026853.1  77   SQDKTRVEPPQYMIDLYNRYTSDKSTTPASNIVRSFSMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC  156

NP_057288.1     157  QNHVDPSHDLKGSVVIYDVLDGTDAWDSATETKTFLVSQDIQDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVESHRKG  236
NP_062379.3     156  QNDVDSTHGLEGSMVVYDVLEDSETWDQATGTKTFLVSQDIRDEGWETLEVSSAVKRWVRADSTTNKNKLEVTVQSHRES  235
NP_001099566.1  156  QNHVDSTHGLEGNMVVYDVLDVDETWDSASGTKTFLVSQDIQDEGWETLEVSSAVKRWVRADSTTNKNKLEVTVQRHREG  235
NP_001179349.1  157  QSHMDSPHELKGNMVIYDVLDGAEVWDAPAGTKTFLVSQDIRDEGWETFEVSSAVKRWIRADSTKSKNKLEVTVESHRKG  236
XP_003133152.2  158  QSHVDASHELKGNMIIYDVLDGA-----SEGTKTFLVSQDIRDEGWETFEVSSAVKRWAQADSTKSKNKLEVTVESHRKG  232
XP_853886.2     148  QGHGAASRELRGNMAIYDVLDGADAWDASAGTKTFLVSQDISDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG  227
XP_001500704.1  155  QSHVDSSHELKGNMVIYDVLDGADAWDTSMGTKTFLVSQDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG  234
XP_004021599.3  157  QSHVDSSHELKGNMVIYDVLDGAEVWDAPGGTKTFLVSQDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG  236
XP_507775.4     157  QNHVDPSHDLKGSVVIYDVLDGTDAWDSATETKTFLVSQDIQDEGWETLEVSSAVKRWVRSDSIKSKNKLEVTVESHRKG  236
XP_001109523.2  157  QNHMDHSHDLKGSMVIYDVLDGTDAWDSAAETKTFLVSQDIRDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVESHRKG  236
XP_003994191.1  157  QNHGDSSHELKGNMAIYDVLDGADAWDASTGTKTFLVSQDIRDEGWETFEVSSAVKRWARADSTKSKNKLEVTVESHRKG  236
XP_005699391.1  157  QSHVDSSHELKGNMVIYDVLDGAEVWDAPGGTKTFLVSQDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESRRKG  236
XP_004049419.1  157  QNHVDPSHDLKGSVVIYDVLDGTDAWDSATETKTFLVSQDIQDEGWETLEVSSAVKRWVRSDSIKSKNKLEVTVESHRKG  236
XP_002820746.1  157  QNHVDPSHDLKGSVVIYDVLDGTDAWDSAAETKTFLVSQDIQDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVESHRKG  236
XP_032026853.1  157  QNHVDPSHDLKGNVVIYDVLDGTDAWDSATETKTFLVSQDIQDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVENHRKG  236

NP_057288.1     237  CDTLDISVPPGSRNLPFFVVFSNDHSSGTKETRLELREMISHEQESVLKKLSKDGSTEAGESSH--EEDTDGHVAAGSTL  314
NP_062379.3     236  CDTLDISVPPGSKNLPFFVVFSNDRSNGTKETRLELKEMIGHEQETMLVKTAKNAYQVAGES-Q-eEEGLDGYTAVGPLL  313
NP_001099566.1  236  CSTLDISVPPGSQNLPFFVVFSNDRSNGTKETRLELKEMIGHEQETVLVKTSKNAYQEAGESRE-eEERIDGYTAVGPLL  314
NP_001179349.1  237  CDKLDISVPPGSKNLPFFVVFSNDRSNGTKETRLELREMIGHEQESVLRKLSKNTVVEAGENKDeeEEDVRSHTPTESSL  316
XP_003133152.2  233  CDKLDISVPPGSKNLPFFVVFSNDRSNGTKETTLELREMISHEQESVLKKLSRNSLLEAGEDKDgeEEGMEGHVAMGSSL  312
XP_853886.2     228  CDKLDISVPPGSKNLPFFVVFSNDRSNGTKETRLELREMISHEQDSVLTKWSKNSPAGAGDRKA--EGGGEGHMATGSSL  305
XP_001500704.1  235  CDRLDISVPPGSKNLPFFVVFSNDRSNGTKETRLELREMIGHEQESVLRKLSKDGLAEADENKD--EEDVEGSMAAGSSL  312
XP_004021599.3  237  CDKLDISVPPGSKNLPFFVVFSNDRSNGTKETRLELREMISHEQESVIKKLSRNTVVEAGENKDeeQ-DVQGHVPTAASL  315
XP_507775.4     237  CDTLDISVPPGSRNLPFFVVFSNDHSSGTKETRLELREMISHEQESVLKKLSKDGSTEAGESSH--EEDTDGHVAAGSTL  314
XP_001109523.2  237  CDKLDISVPPGSRNLPFFVVFSNDHSSGTKETRLELREMISHEQESVLKKLSKEGSTEAGESSH--EEDADGHVAVGSTL  314
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XP_003994191.1   237   CDKLDISVPPGPQNLPFFVVFSNDRSNGTKETRLELREMIGHEQESVLKKLSKNGPAEAGDNKD--E-DGEGRKATGSSL  313
XP_005699391.1   237   CDKLDISVPPGSKNLPFFVVFSNDRSNGTKETRLELREMISHEQESVLKKLSRNTVVEAGENKDeeQ-DAQGPVPTAASL  315
XP_004049419.1   237   CDTLDISVPPGSRNLPFFVVFSNDHSSGTKETRLELREMISHEQESVLKKLSKDGSTEAGESSH--EEDTDGHVAAGSTL  314
XP_002820746.1   237   CDTLDINVPPGSRNLPFFVVFSNDHSSGTKETRLELREMISHEQESVLKKLSKDGSTEAGESSH--EEDTDGHVAAGSTL  314
XP_032026853.1   237   CDTLDISVPPGSRNLPFFVVFSNDHSSGTKETRLELREMISHEQESVLKKLSKDGSTEQGESSH--EEDADGHVAAGSTL  314

NP_057288.1      315   ARRKRSAG-AGSHCQKTSLRVNFEDIGWDSWIIAPKEYEAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  393
NP_062379.3      314   ARRKRSTG-ASSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  392
NP_001099566.1   315   ARRKRSTGaASSHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  394
NP_001179349.1   317   VRRKRSTG-ANNHCQKTSLRVNFEDIGWDSWIIAPKEYDAFECKGGCFFPLADDVTPTKHAIVKTLVHLKFPMKVGKACC  395
XP_003133152.2   313   ARRKRSAG-ANNHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPMKVGKACC  391
XP_853886.2      306   ARRKRSAG-ANNHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGGCFFPLADDMTPTKHAIVQTLVHLKFPMKVGKACC  384
XP_001500704.1   313   ARRKRSAG-AGNHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPMKVGKACC  391
XP_004021599.3   316   VRRKRSAG-ANSHCQKTSLRVNFEDIGWDSWIIAPKEYDAFECKGGCFFPLADDVTPTKHAIVKTLVHLKFPMKVGKACC  394
XP_507775.4      315   ARRKRSAG-AGSHCQKTSLRVNFEDIGWDSWIIAPKEYEAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  393
XP_001109523.2   315   SRRKRSTG-AGSHCQKTSLRVNFEDIGWNSWIIAPKEYEAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  393
XP_003994191.1   314   ARRKRSAG-ANNHCQKTSLRVNFEDIGWDSWIIAPKEYDAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPMKVGKACC  392
XP_005699391.1   316   VRRKRSAG-ANSHCQKTSLRVNFEDIGWDSWIIAPKEYDAFECKGGCFFPLADDVTPTKHAIVKTLVHLKFPMKVGKACC  394
XP_004049419.1   315   ARRKRSAG-AGSHCQKTSLRVNFEDIGWDSWIIAPKEYEAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  393
XP_002820746.1   315   ARRKRSAG-AGSHCQKTSLRVNFEDIGWDSWIIAPKEYEAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  393
XP_032026853.1   315   ARRKRSTG-AGSHCQKTSLRVNFEDIGWDSWIIAPKEYEAYECKGGCFFPLADDVTPTKHAIVQTLVHLKFPTKVGKACC  393

NP_057288.1      394   VPTKLSPISVLYKDDMGVPTLKYHYEGMSVAECGCR  429
NP_062379.3      393   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  428
NP_001099566.1   395   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  430
NP_001179349.1   396   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  431
XP_003133152.2   392   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  427
XP_853886.2      385   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  420
XP_001500704.1   392   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  427
XP_004021599.3   395   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  430
XP_507775.4      394   VPTKLSPISVLYKDDMGVPTLKYHYEGMSVAECGCR  429
XP_001109523.2   394   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  429
XP_003994191.1   393   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  428
XP_005699391.1   395   VPTKLSPISILYKDDMGVPTLKYHYEGMSVAECGCR  430
XP_004049419.1   394   VPTKLSPISVLYKDDMGVPTLKYHYEGMSVAECGCR  429
XP_002820746.1   394   VPTKLSPISVLYKDDMGVPTLKYHYEGMSVAECGCR  429
XP_032026853.1   394   VPTKLSPISVLYKDDMGVPTLKYHYEGMSVAECGCR  429
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GDF9

NP_005251.1 growth/differentiation factor 9 isoform 1 preproprotein [Homo sapiens]
NP_032136.2 growth/differentiation factor 9 precursor [Mus musculus]
NP_067704.1 growth/differentiation factor 9 precursor [Rattus norvegicus]
NP_777106.1 growth/differentiation factor 9 precursor [Bos taurus]
NP_001001909.1 growth/differentiation factor 9 precursor [Sus scrofa]
XP_038536812.1 growth/differentiation factor 9 isoform X1 [Canis lupus familiaris]
XP_001504477.1 growth/differentiation factor 9 [Equus caballus]
NP_001136360.2 growth/differentiation factor 9 precursor [Ovis aries]
XP_527008.1 growth/differentiation factor 9 isoform X1 [Pan troglodytes]
XP_014996256.1 growth/differentiation factor 9 [Macaca mulatta]
NP_001159372.1 growth/differentiation factor 9 precursor [Felis catus]
NP_001272637.1 growth/differentiation factor 9 precursor [Capra hircus]
XP_018883145.1 growth/differentiation factor 9 [Gorilla gorilla gorilla]
XP_002815918.1 growth/differentiation factor 9 isoform X1 [Pongo abelii]
XP_032012334.1 growth/differentiation factor 9 isoform X1 [Hylobates moloch]

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NP_005251.1      1       MARPNKFLLWFCCFAW    LCFPISLGSQASGGEAQIAASAELESGAMPWS    LLQHIDERDRAGLLPALFKVL  69
NP_032136.2      1       MALPSNFLLGVCCFAW    LCFLSSLSSQASTEESQSGASENVESEADPWS    LLLPVDGTDRSGLLPPLFKVL  69
NP_067704.1      1       MAFPSRFLLGVCCFAW    LCLLISLSSQASTGESQAGASENLESEADPWS    LLLPVDGTDRSGLLPPLFKVL  69
NP_777106.1      1       MALPNKFFLWFCCFAW    LCFPISLDSQPSRGEAQIVARTALESEAETWS    LLKHLDGRHRPGLLSPLLNVL  69
NP_001001909.1   1       MALPRKFFLCFCCFAL    FCFPVSCGSQASRREAHFATSAVLESEAEPWS    LLRPPDERHRSGLPSPLFNVL  69
XP_038536812.1   1    [4]LGGLGPTGLWRACACL[25]AAQPVRPRRAAVRPRFSSAPAAASGFREAPWA[48]ALARNRTENSQTCLSFMTLVL 146
XP_001504477.1   1       MALPSKFFLWFCCSAW    LCFPISLGSQASREAAQIAASAELESEAEPWS    LLQPLNGGNRSGLLPALFKVL  69
NP_001136360.2   1       MALPNKFFLWFCCFAW    LCFPISLDSLPSRGEAQIVARTALESEAETWS    LLNHLGGRHRPGLLSPLLEVL  69
XP_527008.1      1       MALPNKFLLWFCCFAW    LCFPISLGSQASGGEAQIAASAELESGAMPWS    LLQHIDERDRAGLLPALFKVL  69
XP_014996256.1   1       MALPNKFLLWFYCFAW    LCFPVSLGSQASGGDAQIAASAELESGATPWS    LLQPIDERDRAGLLPPLFKVL  69
NP_001159372.1   1       MALLSNFFLWFLCFSW    LCFPMSLCSRAST-EVQIAAGAEWEAKAEPWS    LVQPLDEKDRLGFLPPLFKVL  68
NP_001272637.1   1       MALPNKFFLWFCCFAW    LCFPISLDSLPSRGEAQIVARTALESEAETWS    LLNHLGGRHRPGLLSPLLKVL  69
XP_018883145.1   1       MALPNKFLLWFCCFAW    LCFPISLGSQASGGEAQIAASAELESGAMPWS    LLQHIDERDRAGLLPPLFKVL  69
XP_002815918.1   1       MALPNKFLLWFCCFAW    LCFPITLGSQASGGDAQIAASAELESGATPWS    LLQPIDERDRAGLLPPLFKVL  69
XP_032012334.1   1       MALPNKFLLWFCCIAW    LCFPISLGSQASGGDAQIAASGELESGATPRS    LLQPIDERDRAGLLPPLFKVL  69

NP_005251.1      70   SVGRGGSPRLQPDSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTRHKQAPGDQVTGILPSVELLFNLDRITT  149
NP_032136.2      70   SDRRGETPKLQPDSRALYYMKKLYKTYATKEGVPKPSRSHLYNTVRLFSPCAQQEQAPSNQVTGPLPMVDLLFNLDRVTA  149
NP_067704.1      70   SDRRSETPKLQPDSRALYYMKKLYKTYATKEGVPKPSRSHLYNTVRLFSPCAQQEQAPSNQMTGPLPMVDLLFNLDRVTA  149
NP_777106.1      70   YDGHREPPRLQPDDRALSYMKRLYKAYATKEGTPKSNRSHLYNTVRLFTPCAQHKQAPGDQAAGTLPSVDLLFNLDRVTV  149
NP_001001909.1   70   YDGHGGLPRLQPDSRALRYMKRLYKTYATKEGIPKANRSHLYNTVRLFTPCAQHKQAPGDQVTGTLPSGDLRFNLDRVTA  149
XP_038536812.1   147  YDGQGGTP------RALRYMKRLYKACATKEGIPKSNRSPLYNTVRLFTSCAQHTQAPGDQATGSVPPVDLLFNLDRVPP  220
XP_001504477.1   70   YDGQGGAPRLQPDSRALRYMKRLYKAYATKEGIPKSNRGHLYNTVRLFTPCAQHKQAPGDQVAGTLPSVDLLFNLDCVTA  149
NP_001136360.2   70   YDGHGEPPRLQPDDRALRYMKRLYKAYATKEGTPKSNRRHLYNTVRLFTPCAQHKQAPGDLAAGTFPSVDLLFNLDRVTV  149
XP_527008.1      70   SVGRGGSPRLQPDSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTRHKQAPGDQVTGILPSVELLFNLDRITT  149
XP_014996256.1   70   SVGRGGAPRLQPDSRALHYMKNLYKTYATKEGIPKSNRSHLYNTVRLFTPCTQHKQVPGDQVTGILPSVDLLFNLDRITT  149
NP_001159372.1   69   YNGQGDAPRLQPDSRALRYMKRLYKSFATKEGIPKSNRSPLYNTARLFTSYAQHKQAPGDQVTGTVPSVDLLFHLDRVTA  148
NP_001272637.1   70   YDGHGEPPRLQPDDRALRYMKRLYKAYATKEGTPKSNRRHLYNTVRLFTPCAQHKQAPGDLAAGTFPSVDLLFNLDRVTV  149
XP_018883145.1   70   SVGRGGSPRLQPDSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTRHKQAPGDQVTGILPSVELLFNLDRITT  149
XP_002815918.1   70   SVGRGRAPRLQPDSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTQHKQAPGDQVTGILPSVELLFNLDRITT  149
XP_032012334.1   70   SVGQGGAPRLQPDSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTQHKQAPGDQVTGILPSVELLFNLDRITT  149

NP_005251.1      150  VEHLLKSVLLYNINNSVSFSSAVKCVCNLMIKEPKSSSRTLGRAPYSFTFNSQFEFGKKHKWIQIDVTSLLQPLVASNKR  229
NP_032136.2      150  MEHLLKSVLLYTLNNSASSSSTVTCMCDLVVKEAMSSGRAPPRAPYSFTL-------KKHRWIEIDVTSLLQPLVTSSER  222
NP_067704.1      150  MEHLLKSVLLYTLNNSAASSSTVTCVCDLVVKEPMSSSKATPRAPYSFTL-------RKHRWIEMDVTSLLQPLVASSER  222
NP_777106.1      150  VEHLFKSVLLYTFNNSISFPFPVKCICNLVIKEPEFSSKTLPRAPYSFTFNSQFEFRKKYKWIEIDVTAPLEPLVASHKR  229
NP_001001909.1   150  VEHLLKSVLLYTWNNSISFPSPVKCECSLVVKEPELSNKTLPKAPYSFTLNSPFTFQKKHKWIEIDVTAILQPLVVSNKR  229
XP_038536812.1   221  VEHLLKSGLLYSFSNSISFPSAVKCLCHLVIKEPEFSSWTPQRAPSLLTFNSQFELKKKYKWFEVDVTTALRPLVALHKR  300
XP_001504477.1   150  VEHLLKSVLLYTFNNSVSFPSAVKCVCNLVIKEPE--SKTLPGTPYSFTFNSQFEFRKKYKWIEMDVTPLLQPLVASNKK  227
NP_001136360.2   150  VEHLFKSVLLYTFNNSISFPFPVKCICNLVIKEPEFSSKTLPRAPYSFTYNSQFEFRKKYKWMEIDVTAPLEPLVASHKR  229
XP_527008.1      150  VERLLKSVLLYNINNSVSFSSAVKCVCNLMIKESKSSSRTLGRAPYSFTFNSQFEFGKKHKWIQIDVTSLLQPLVASNKR  229
XP_014996256.1   150  VEHLLKSVLLYTINNSVSFSSAVKCVCNLMIKEPKFSSKTLHRAPYSFTFNSQFEFGKKHKWIEIDVTSLLQPLVASNKR  229
NP_001159372.1   149  VEHFIKSVLLFTFSNPISFSSAVKCVCNLVMKEPESSSGNPHRTLSSLTFDSQFEFRKKYRWIEVDVTAPLQPLVASNQR  228
NP_001272637.1   150  VEHLFKSVLLYTFNNSISFPFPVKCICNLVIKEPEFSSKTLPRAPYSFTYNSQFEFRKKYKWMEIDVTAPLEPLVASHKR  229
XP_018883145.1   150  VEHLLKSVLLYNINNSVSFSSAVRCVCNLMIKEPKSSSRTLCRAPYSFTFNSQFEFGKKHKWIQIDVTSLLQPLVASNKR  229
XP_002815918.1   150  VEHLLKSVLLYTINNSVSFSSAVKCVCNLMIKEPESSSRTLCRAPYSFTFNSQFEFGKKHKWIQIDVTSLLQPLVASNKR  229
XP_032012334.1   150  VEHLLKSVLLYTINNSVSFSSAVKCVCNLMIKEPKSSSRTLCRAPYSFTFNSQFEFGKKHKWIQIDVTSLLQPLVASNKR  229

NP_005251.1      230  SIHMSINFTCMKDQLEHPSAQNGLFNMTL-VSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGPDQERSLSAYPVGEEAAE  308
NP_032136.2      223  SIHLSVNFTCTKDQVP----EDGVFSMPLSVPPSLILYLNDTSTQAYHSWQSLQSTWRPLQHPGQA-GVAARPVKEEAIE  297
NP_067704.1      223  SIHLSVNFTCTRDQAP----ENGTFNMPLSVPPSLILYLNDTSTQAYHSWQSLQSTQRHSQHPGQD-SVTTRPVEEEATE  297
NP_777106.1      230  NIHMSVNFTCVKDQLQHPSARDSLFNMTLLLAPSLLLYLNDTSAQAFHRWHSLHPKRKPSQDPDQKRGLSACPMGEEAAE  309
NP_001001909.1   230  EIHMSIDFTCVKDQLQHLSAQESPCNMTLLAAPSLLLYLNDTSTQAYHRWYSLPWKRRPSQGPDQKRGLS---------E  300
XP_038536812.1   301  SLHMSVNFTCVRNQQQDPVAQDGPWNRTLLVPPSLLLYLNDTSAQAHHRWDSLHYKRRSSQRADQKGGLSACPIGEESTE  380
XP_001504477.1   228  SIHMSVNLTCGKDQLQHPSAQDSPLNTTLLLFPSLLLYLNDTSAQAYHRWHSLHYKRRPSQGPDQKRDLSACPEGEGAAE  307
NP_001136360.2   230  NIHMSVNFTCAEDQLQHPSARDSLFNMTLLVAPSLLLYLNDTSAQAFHRWHSLHPKRKPSQGPDQKRGLSAYPVGEEAAE  309
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XP_527008.1      230  SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGPDQERSLSAYPVGEEAAE  309
XP_014996256.1   230  SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVPPSLILYLNDTSAQAYHRWYSLYYKRRPSQGPDQERSLSAYPVGEDAAE  309
NP_001159372.1   229  NIHMSVNLTCVKAQLQPPSARDGPFNVTLLVPPSLLLYLNDTSAQAHHRWYSLHYKRRPSQGAGQKRGLSACPQGEESAE  308
NP_001272637.1   230  NIHMSVNFTCAKDQLQHPSARDSLFNMTLLVAPSLLLYLNDTSAQAFHRWHSLHPKRKPSQGPDQRRELSAYPVGEEAAE  309
XP_018883145.1   230  SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGPDQERSLSAYPVGEEAAE  309
XP_002815918.1   230  SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLNYKRRPSQGPDQERSLSAYPVGEEAAE  309
XP_032012334.1   230  SIHMSINFTCMKDQLEHLSVQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGPDQERSLSAYPVGKEAAE  309

NP_005251.1      309  DGRSShhRHRRGQETVSSELKKPLGPASFNLSEYFRQFLLPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  388
NP_032136.2      298  VERSP--RRRRGQKAIRSEAKGPLLTASFNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  375
NP_067704.1      298  VERSP--RHRRGQKTLSSETKKPL-TASFNLSEYFRQFLFPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  374
NP_777106.1      310  GVRLS--RHRRDQESVSSELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHKYNPRYCKGDCPR  387
NP_001001909.1   301  GVPSS--RHRRAQDTVSSELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHKYNPRYCKGDCPR  378
XP_038536812.1   381  GGRSS--RHRRGQDTVSLELHKPLAPASFNLSEYLKHFLFPQHECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  458
XP_001504477.1   308  GITSS--RHRRSQEAVSSELKKPLVPASLNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPQRYNPRYCKGDCPR  385
NP_001136360.2   310  GVRSS--RHRRDQESASSELKKPLVPASVNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHKYNPRYCKGDCPR  387
XP_527008.1      310  DGRSShhRHRRGQETVSSELKKPLGPASFNLSEYFKQFLLPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  389
XP_014996256.1   310  DGRSShhRHRRGQETVSSELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  389
NP_001159372.1   309  AVRPS--RHRRGQETIGLEPQKPLVPASFNLSEYFKQFLFPQNECELHDFRLSFSQLKWDSWIVAPHRYNPRYCKGDCPR  386
NP_001272637.1   310  GVRSS--RHRRDQESVSSELKKPLVPASVNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHKYNPRYCKGDCPR  387
XP_018883145.1   310  DGRSShhRHRRGQETVSSELKKPLGPASFNLSEYFKQFLLPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  389
XP_002815918.1   310  DGRSShrRHRRGQETVSSELKKPLVPASFNLSEYFKQFIFPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  389
XP_032012334.1   310  DGRSShhRHRRGQETVSSELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSFSQLKWDNWIVAPHRYNPRYCKGDCPR  389

NP_005251.1      389  AVGHRYGSPVHTMVQNIIYEKLDSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  454
NP_032136.2      376  AVRHRYGSPVHTMVQNIIYEKLDPSVPRPSCVPGKYSPLSVLTIEPDGSIAYKEYEDMIATRCTCR  441
NP_067704.1      375  AVRHRYGSPVHTMVQNIIYEKLDPSVPRPSCVPGKYSPLSVLTIEPDGSIAYKEYEDMIATRCTCR  440
NP_777106.1      388  AVGHRYGSPVHTMVMNIIHEKLDSSVPRPSCVPAKYSPLSVLAIEPDGSIAYKEYEDMIATKCTCR  453
NP_001001909.1   379  AVGHRYGSPVHTMVQNIIHEKLDSSVPRPSCVPAKYSPLSVLAIEPDGSIAYKEYEDMIATKCTCR  444
XP_038536812.1   459  AVGHRYGSPVHTMVQNIIHEKLNSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  524
XP_001504477.1   386  AVGHRYGSPVHTMVQNIIHEKLDSSVPRPSCVPAKYSPLSVLTIESDGSITYKEYEDMIATKCTCR  451
NP_001136360.2   388  AVGHRYGSPVHTMVQNIIHEKLDSSVPRPSCVPAKYSPLSVLAIEPDGSIAYKEYEDMIATKCTCR  453
XP_527008.1      390  AVGHRYGSPVHTMVQNIIYEKLDSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  455
XP_014996256.1   390  AVGHRYGSPVHTMVQNIIYEKLDSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  455
NP_001159372.1   387  ALGHRYGSPVHTMVQNIIHEKLDSSVPRPSCVPAKYSPLSVLTIESDGSIAYKEYEDMIATKCTCR  452
NP_001272637.1   388  AVGHRYGSPVHTMVQNIIHEKLDSSVPRPSCVPAKYSPLSVLAIEPDGSIAYKEYEDMIATKCTCR  453
XP_018883145.1   390  AVGHRYGSPVHTMVQNIIYEKLDSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  455
XP_002815918.1   390  AVGHRYGSPVHTMVQNIIYEKLDSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  455
XP_032012334.1   390  AVGHRYGSPVHTMVQNIIYEKLDSSVPRPSCVPAKYSPLSVLTIEPDGSIAYKEYEDMIATKCTCR  455
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GDF5

NP_000548.2 growth/differentiation factor 5 preproprotein [Homo sapiens]
NP_032135.2 growth/differentiation factor 5 preproprotein [Mus musculus]
XP_003749648.1 growth/differentiation factor 5 [Rattus norvegicus]
NP_001179202.1 growth/differentiation factor 5 precursor [Bos taurus]
NP_001231226.1 growth/differentiation factor 5 precursor [Sus scrofa]
XP_542974.1 growth/differentiation factor 5 [Canis lupus familiaris]
NP_001296325.1 growth/differentiation factor 5 precursor [Equus caballus]
XP_004014573.2 growth/differentiation factor 5 [Ovis aries]
XP_530287.4 growth/differentiation factor 5 [Pan troglodytes]
XP_001099806.2 growth/differentiation factor 5 [Macaca mulatta]
XP_003983628.1 growth/differentiation factor 5 [Felis catus]
XP_017913249.1 PREDICTED: growth/differentiation factor 5 [Capra hircus]
XP_018872428.1 PREDICTED: growth/differentiation factor 5 [Gorilla gorilla gorilla]
XP_003779391.1 growth/differentiation factor 5 [Pongo abelii]
XP_031998077.1 growth/differentiation factor 5 [Hylobates moloch]

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NP_000548.2     1    MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAtnANARAKGGT  80
NP_032135.2     1    MRLPKLLTLLLWHLAWLDLELICTVLGAPDLGQRTPGAKPGLTKAEAKERPPLARNVFRPGGHIYGVGA--TNARAKGSS  78
XP_003749648.1  1    MRLPKLLTLLLWHLAWLDLGLVCTVLGAPDLGQRPPGARPGLAKAEAKERPPLTRNIFRPGGHSYGVGA--TSARAKGSS  78
NP_001179202.1  1    MRLPKLLTLLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLAQNIFRPGGHSYGGGA--TNARAKGGT  78
NP_001231226.1  1    MRLPKLLTFLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLAQNIFRPGGHSYGGGA--TNARAKGGT  78
XP_542974.1     1    MRLPKLLTFLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLARSVFRPGGHSYGGGA--ANARAKGGT  78
NP_001296325.1  1    MRLPKLLTFLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLARNIFRPGGHSYGGGA--TSARAKGGT  78
XP_004014573.2  1    MRLPKLLTLLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLAQNIFRPGGHSYGGGA--TNARAKGGT  78
XP_530287.4     1    MRLPKLLTLLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAtnANARAKGGT  80
XP_001099806.2  1    MRLPKLLTFLLWYLAWLDLEFICTVLGAPDWGQKAQGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGA--ANARAKGGT  78
XP_003983628.1  1    MRLPKLLTFLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLARSIFRPGGHSYGGGA--TNARAKGGT  78
XP_017913249.1  1    MRLPKLLTLLLWHLAWLDLEFICTVLGAPDLGQRPQGARPGLAKAEAKERPPLAQNIFRPGGHSYGGGA--TNARAKGGT  78
XP_018872428.1  1    MRLPKLLTFFLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAtnANARAKGGT  80
XP_003779391.1  1    MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNIFRPGGHSYGGGAanANARAKGGT  80
XP_031998077.1  1    MRLPKLLTFLLWYLAWLDLEFICTVLGAPDLGQRPQGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAsnANARAKGGT  80

NP_000548.2     81   GQTGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQATARTVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKE  160
NP_032135.2     79   GQ----TQAKKDEPRKMPPRSGGPETKPGPSSQTRQAAARTVTPKGQLPGGKASSKAGSAPSSFLLKKTREPGTPREPKE  154
XP_003749648.1  79   GQ----TQAKKDEPRKVPPRASGSETKPGPSPQTRQAAARTVTPKGQLSGGKASAKAGSAPSSFLLKKTREPGTPREPKE  154
NP_001179202.1  79   GQTGGLTQPKKDEPKKLPPRSGGPEPKPGHPPQTRQGATRTVTPKGQLPGGKAPSKAGSVPSPFLLKKAREPGSPREPKE  158
NP_001231226.1  79   GQTGGLTQPKKDEPKKLPPRSGGLEPKPGHPPQTRQAATRTVTPKGQLPGGKAPQKAGSVPSPFLLKKAREPGSPREPKE  158
XP_542974.1     79   GQTGGLTQPKKDEPKKLPPRPGSPEPKPGHPTQTRQAAPRTVTPKGQLPGGKAPPKAGSVPGPFLLKKARETGPPPEPKE  158
NP_001296325.1  79   GQTGGPTQPKKDEPKKLPPRPGGSEPKPGHPPQTRQAATRTVTPKGQLPGGKAPPKAGSVPSPFLLKKAREPGPPREPKE  158
XP_004014573.2  79   GQTGGLTQPKKDEPKKLPSRSGGPESKPGHPPQTRQGATRTVTPKGQLPGGKAPSKAGSVPSPFLLKKAREPGSPREPKE  158
XP_530287.4     81   GQKGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQTTARTVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKE  160
XP_001099806.2  79   GHTGGLTQPKKDEPKKLPPRPGGPEPKPGHPPQTRQATARTVTPKGQLPGGKVPPKAGSVPSSFLLKKAREPGSPREPKE  158
XP_003983628.1  79   GQTAGLTQPKKDEPKKLPPRSGGPEPKPGHPSQTRQAATRTVTPKGQLPGGKSPPKAGSVPSPFLLKKARETGPPQEPKE  158
XP_017913249.1  79   GQTGGLTQPKKDEPKKLPSRSGGPEPKPGHPPQTRQGATRTVTPKGQLPGGKAPSKAGSVPSPFLLKKAREPGSPREPKE  158
XP_018872428.1  81   GQTGGLTQPRKDEPKKLPPRPGGPEPKPGHPPQTRQATARTVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKE  160
XP_003779391.1  81   GQTGGLTQPKKDEPKKLSPRPGGPEPKPGHPPQTRQATARTVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKE  160
XP_031998077.1  81   GQTGGLTQPKKDEPKK-PPRPGGPEPKPGHPPQTRQATARTVTPKGQLPGGKAPPKAGSVPSSFLLKKAREPGPPREPKE  159

NP_000548.2     161  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  240
NP_032135.2     155  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLGAELR  234
XP_003749648.1  155  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  234
NP_001179202.1  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLGAELR  238
NP_001231226.1  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLAAELR  238
XP_542974.1     159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  238
NP_001296325.1  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  238
XP_004014573.2  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLGAELR  238
XP_530287.4     161  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKNGLLGAELR  240
XP_001099806.2  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  238
XP_003983628.1  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  238
XP_017913249.1  159  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPAVRKQRYVFDISALEKDGLLGAELR  238
XP_018872428.1  161  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  240
XP_003779391.1  161  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  240
XP_031998077.1  160  PFRPPPITPHEYMLSLYRTLSDADRKGGNSSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR  239

NP_000548.2     241  ILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  320
NP_032135.2     235  ILRKKPLDVAKPAVPSSGRVAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  314
XP_003749648.1  235  ILRKKPLDVAKPAVPSSGRVAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  314
NP_001179202.1  239  ILRKKPLDAAKPVAPGSGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  318
NP_001231226.1  239  ILRKKPSDTAKPVAPGIGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  318
XP_542974.1     239  ILRKKPSDTAKPVAPSIGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  318
NP_001296325.1  239  ILRKKSSDTAKPGAPSSRRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  318
XP_004014573.2  239  ILRKKPLDVAKPVAPGSGRAAQLKLSSCPSGRQPAALLDVRSVPGLDSSGWEVFDIWKLFRSFKNSAQLCLELEAWERGR  318
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XP_530287.4       241  ILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  320
XP_001099806.2    239  ILRKKPSDTAKSAAPVGGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  318
XP_003983628.1    239  ILRKKPSDAAKPVAPGIRRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  318
XP_017913249.1    239  ILRKKPLDAAKPVAPSSGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRSFKNSAQLCLELEAWERGR  318
XP_018872428.1    241  ILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  320
XP_003779391.1    241  ILRKKPSDTAKPVAPGGGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  320
XP_031998077.1    240  ILRKKPSDTAKPAAPGGGRAAQLKLSSCPSGRQPAALLDVRSVPGLDGSGWEVFDIWKLFRNFKNSAQLCLELEAWERGR  319

NP_000548.2       321  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARC  400
NP_032135.2       315  AVDLRGLGFERTARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLANRQGKRPSKNLKARC  394
XP_003749648.1    315  AVDLRGLGFERAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLANRQGKRPSKNLKARC  394
NP_001179202.1    319  AMDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNPKARC  398
NP_001231226.1    319  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNPKARC  398
XP_542974.1       319  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNPKARC  398
NP_001296325.1    319  AVDLRGLGFDRTARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPTKNPKARC  398
XP_004014573.2    319  AMDLRSLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNPKARC  398
XP_530287.4       321  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARC  400
XP_001099806.2    319  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKTRC  398
XP_003983628.1    319  AMDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATGQGKRPSKNPKARC  398
XP_017913249.1    319  AMDLRSLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNPKARC  398
XP_018872428.1    321  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARC  400
XP_003779391.1    321  TVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARC  400
XP_031998077.1    320  AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGQDDKTVYEYLFSQRRKRRAPLATRQGKRPSKNLKARC  399

NP_000548.2       401  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  480
NP_032135.2       395  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  474
XP_003749648.1    395  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  474
NP_001179202.1    399  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  478
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XP_542974.1       399  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  478
NP_001296325.1    399  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  478
XP_004014573.2    399  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  478
XP_530287.4       401  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  480
XP_001099806.2    399  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  478
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XP_017913249.1    399  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  478
XP_018872428.1    401  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  480
XP_003779391.1    401  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  480
XP_031998077.1    400  SRKALHVNFKDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISILFID  479

NP_000548.2       481  SANNVVYKQYEDMVVESCGCR  501
NP_032135.2       475  SANNVVYKQYEDMVVESCGCR  495
XP_003749648.1    475  SANNVVYKQYEDMVVESCGCR  495
NP_001179202.1    479  SANNVVYKQYEDMVVESCGCR  499
NP_001231226.1    479  SANNVVYKQYEDMVVESCGCR  499
XP_542974.1       479  SANNVVYKQYEDMVVESCGCR  499
NP_001296325.1    479  SANNVVYKQYEDMVVESCGCR  499
XP_004014573.2    479  SANNVVYKQYEDMVVESCGCR  499
XP_530287.4       481  SANNVVYKQYEDMVVESCGCR  501
XP_001099806.2    479  SANNVVYKQYEDMVVESCGCR  499
XP_003983628.1    479  SANNVVYKQYEDMVVESCGCR  499
XP_017913249.1    479  SANNVVYKQYEDMVVESCGCR  499
XP_018872428.1    481  SANNVVYKQYEDMVVESCGCR  501
XP_003779391.1    481  SANNVVYKQYEDMVVESCGCR  501
XP_031998077.1    480  SANNVVYKQYEDMVVESCGCR  500
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GDF6

NP_001001557.1 growth/differentiation factor 6 preproprotein [Homo sapiens]
NP_038554.1 growth/differentiation factor 6 preproprotein [Mus musculus]
NP_001013056.1 growth/differentiation factor 6 precursor [Rattus norvegicus]
NP_001001140.1 growth/differentiation factor 6 precursor [Bos taurus]
XP_020944737.1 growth/differentiation factor 6 [Sus scrofa]
XP_038297057.1 growth/differentiation factor 6 isoform X1 [Canis lupus familiaris]
XP_023504500.1 growth/differentiation factor 6 [Equus caballus]
XP_027829270.1 growth/differentiation factor 6 isoform X1 [Ovis aries]
XP_016815191.1 growth/differentiation factor 6 [Pan troglodytes]
XP_001090825.1 growth/differentiation factor 6 [Macaca mulatta]
XP_023104260.1 growth/differentiation factor 6 [Felis catus]
XP_017913739.1 PREDICTED: growth/differentiation factor 6 [Capra hircus]
XP_004047376.1 growth/differentiation factor 6 [Gorilla gorilla gorilla]
XP_002819344.1 growth/differentiation factor 6 [Pongo abelii]
XP_032614364.1 growth/differentiation factor 6 [Hylobates moloch]

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NP_038554.1     1    MDTPRVLLWAIFLISFLWDLPGFQQASISSSSSSStELDSTKDVGNRKEGKMQRTPQESAEGRTP---PEHGLRQKDLRR  77
NP_001013056.1  1    MDTPRVLLWAIFLISFLWDLPGFQQASISSSSS--tELDSTKDVENRKGGKMQRTPQESAEGRTP---KEHRPRPNELRR  75
NP_001001140.1  1    MDTSRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSAKGMRSRKEGRMPRAPRENATAREPldrQEPPPRPQEEPQ  79
XP_020944737.1  1    MDTPKVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELDSAKGMRSRKEGKMPRAPRESATAQAPperQEPQPRPQEEPR  79
XP_038297057.1  1    MDAPRVLLSAVFLVGFLWDLPGFQQASIPSSSPSA-QPAAAKGTRSRRDG---RAPRDRAP-REPl---EPEP-----PE  67
XP_023504500.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSS-A-ELGSAKGIRSRREGKMPRAPQESATAQAPlerQEHQPQRQDEPR  78
XP_027829270.1  1    MDTSRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSAKGMRSRKEGKMPRAPRENATARAPldrQEPPPRPQEEPQ  79
XP_016815191.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRDSDAGREG---QEPQPRPQDEPR  76
XP_001090825.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRESDAGREG---QEPQRRPQDEPQ  76
XP_023104260.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSAKGMRSRKEGKIPRAPRDSATAGEPqqrHEPQPRPQDEPR  79
XP_017913739.1  1    MDTSRVLLSAVFLISFLWDLPGFQQASISSSSS-A-ELGSAKGMRSRKEGKMPRAPRENATARAPldrQEPPPRPQEEPQ  78
XP_004047376.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRESDAGREG---QEPQPRPQDEPR  76
XP_002819344.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRESDAGREG---QEPQPRPQDEPR  76
XP_032614364.1  1    MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRESDAAREG---QQPQPPPQDKPR  76

NP_001001557.1  77   A----QQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  152
NP_038554.1     78   R--PPGQHQGQEPPGRGLRVVPHEYMLSIYKTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  155
NP_001013056.1  76   R--LPGQSLGQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  153
NP_001001140.1  80   R-rPPQQPEAREPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  158
XP_020944737.1  80   R-rPPQQPEAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  158
XP_038297057.1  68   P---------QPPGGAARAVPHDYMLSVYRTHSIAEKLGINASLFQSSGAANTITSFVDRGRDAAARAPLRRQEYVFDV  137
XP_023504500.1  79   RrrPPKQHQAQESPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  158
XP_027829270.1  80   R-rPPERREAREPPGRGPRVVPHEYMLSIYRTYSIAETLGINASFSQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  158
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XP_001090825.1  77   A----QQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  152
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XP_017913739.1  79   R-rPPERREAREPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  157
XP_004047376.1  77   A----QQPRAQEPPGRGLRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  152
XP_002819344.1  77   A----QQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  152
XP_032614364.1  77   A----QQPRAQEPPGRGPRVVPHEYMLSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDDLSHTPLRRQKYLFDV  152

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NP_038554.1     156  STLSDKEELVGAELRLYRQAPPTPWGLPARPLHLQLFPCLSPLLLDARTLDPQGPTQAGWEVFDVWQGLRPQPWKQLCLE  235
NP_001013056.1  154  STLSDKEELVGAELRLYRQAPPTPWGPQTRPLHLQLFPCLSPLLLDSRTLDPQGPTEAGWEVFDVWQVLRPQPWKQLCLE  233
NP_001001140.1  159  STLSDKEELVGAELRLFRQAPAAPWGPPAGPLRLQLFACQSPLLLEARSLDPQGAPRPGWEVFDVWRGLRPQPWKQLCLE  238
XP_020944737.1  159  STLSDKEELVGAELRLFRQAPAAPGGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPRAGWEVFDVWQGLRHQPRKQLCLE  238
XP_038297057.1  138  SALPEREELVGAELRLFRRAPPPPRGPP-RPLRLQLSPCLSPRLLGARTLSPQGPPRAGWEVFDVRPGLRPPPRGPLCLE  216
XP_023504500.1  159  STLSDKEELVGAELRLFRQAPAVPWGPPAGPLHVQLFPCLSPLQLDARTLDPQGAPRAGWEVFDVWQGLRHQPWKQLCLE  238
XP_027829270.1  159  STLSDKEELVGAELRLFRQAPAVPWGPPAGPLHLQLFACQSPLLLEARSLDPQGAPRPGWEVFDVWRGLRPQPWKQLCLE  238
XP_016815191.1  153  SMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE  232
XP_001090825.1  153  SMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE  232
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XP_017913739.1  158  STLSDKEELVGAELRLFRQAPAAPWGPPAGPLHLQLFACQSPLLLEARSLDPQGAPRPGWEVFDVWRGLRPQPWKQLCLE  237
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XP_002819344.1  153  SMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSSLLLDARTLDPQGAPPAGWEVFDVWQGLRRQPWKQLCLE  232
XP_032614364.1  153  SMLSDKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPQLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE  232

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NP_001013056.1  234  LRAVW-GELDARD    SGARPRGPQQ-SPPLDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFTEMHEQLGSA-EAA--  304
NP_001001140.1  239  LRAAWgGEPGAAE    DEARAPGPQQ-PPPPDLRSLGFGRRVRTPQERALLVVFSRSQRKTLFAEMREQLGSAtEVVGP  313
XP_020944737.1  239  LRAAW-GEPGAGE    AEARVPGPQQ-PPSPDLRSLGFGRRVRTPQERALLVVFTRSQRKNLFAEMREQLGSA-EVAGP  311
XP_038297057.1  217  LRAAW-AGAGAGA[11]AGAGARGPGP---GPDLRSLGFGRGARRPQERALLVVFSRSRRRSLLAEARGRPGGG------  293
XP_023504500.1  239  LRASW-GELGAGE    DEARAPGPQQ-PPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EVAGP  311
XP_027829270.1  239  LRAAWgGEPGGEE    AEAPAPGPQQ-PPPPDLRSLGFGRRVRTPQERALLVVFSRSQRKTLFAEMREQLGSAtEVVGP  313
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XP_023104260.1  239  LRAAW-GEPGAGE    AEARAPGPQQqPPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EVAGP  312
XP_017913739.1  238  LRAAWgGEPGAEE    AEARAPGPQQ-PPPPDLRSLGFGRRVRTPQERALLVVFSRSQRKTLFAEMREQLGSAtEVVGP  312
XP_004047376.1  233  LRAAW-GELDAGE    AEARARGPQQ-PPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEVREQLGSA-EAAGP  305
XP_002819344.1  233  LRAAW-GEPDAGE    AETRARGPQQ-PPPPDLRSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAADL  305
XP_032614364.1  233  LRAAW-GEPEAGE    AEARARGPQQ-PPPPDLWSLGFGRRVRPPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGP  305

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NP_038554.1     307  --GAEGSW   PAPSGSPDAGSWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYH  381
NP_001013056.1  305  --GAEGSW   PAPSGAPDAGSWLPSPGRRRRRTALSSRHGKRHGKKSRLRCSRKPLHVNFKELGWDDWIIAPLEYEAYH  379
NP_001001140.1  314  GAGAEGSG[7]PPPSGTPDAGLWSPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  397
XP_020944737.1  312  GA--EGSW   PPPSGTPDAGPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  386
XP_038297057.1  294  --------[1]APAPGTPLAAPWPPPPGRRRR-TALASRHGKRHGKKSRLRCGKKPLHVNFKELGWDDWIIAPLEYEAFH  362
XP_023504500.1  312  SGGAEGSW   PPPSGSPDVGPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  388
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XP_016815191.1  306  GAGAEGSW   PPPSGAPDARPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  382
XP_001090825.1  306  GVGAEGSW   PPPSGAPDAGPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  382
XP_023104260.1  313  GAGADGSW   PPPSGAPDAGPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  389
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XP_002819344.1  306  GTGAEGSW   PPLSGAPDAGPWVPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  382
XP_032614364.1  306  GAGAEGSW   PPPSGAPDAGPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGWDDWIIAPLEYEAYH  382

NP_001001557.1  383  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  455
NP_038554.1     382  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  454
NP_001013056.1  380  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  452
NP_001001140.1  398  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEEMVVESCGCR  470
XP_020944737.1  387  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  459
XP_038297057.1  363  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTRLTPISILYIDAGNNVVYKQYEDMVVESCGCR  435
XP_023504500.1  389  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  461
XP_027829270.1  392  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEEMVVESCGCR  464
XP_016815191.1  383  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  455
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XP_023104260.1  390  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  462
XP_017913739.1  391  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEEMVVESCGCR  463
XP_004047376.1  383  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  455
XP_002819344.1  383  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  455
XP_032614364.1  383  CEGVCDFPLRSHLEPTNHAIIQTLMNSMDPGSTPPSCCVPTKLTPISILYIDAGNNVVYKQYEDMVVESCGCR  455
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GDF7

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NP_878248.2 growth/differentiation factor 7 preproprotein [Homo sapiens]
NP_001299805.1 growth/differentiation factor 7 isoform 1 preproprotein [Mus musculus]
XP_006239940.1 growth/differentiation factor 7 isoform X1 [Rattus norvegicus]
NP_001193030.1 growth/differentiation factor 7 precursor [Bos taurus]
XP_003354958.1 growth/differentiation factor 7 isoform X1 [Sus scrofa]
XP_038309370.1 LOW QUALITY PROTEIN: growth/differentiation factor 7 [Canis lupus familiaris]
XP_023475218.1 growth/differentiation factor 7 [Equus caballus]
XP_027824132.2 growth/differentiation factor 7 [Ovis aries]
XP_003308955.2 growth/differentiation factor 7 [Pan troglodytes]
XP_001096970.2 growth/differentiation factor 7 [Macaca mulatta]
XP_023107842.1 growth/differentiation factor 7 [Felis catus]
XP_017910266.1 PREDICTED: growth/differentiation factor 7 [Capra hircus]
XP_004028950.1 growth/differentiation factor 7 [Gorilla gorilla gorilla]
XP_002812295.2 growth/differentiation factor 7 [Pongo abelii]
XP_032028233.1 growth/differentiation factor 7 [Hylobates moloch]
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NP_878248.2      1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--GGggRTLAQAAGAAAVPAAAVPRARAAR  74
NP_001299805.1   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAWSPGG--GGGG------RTLARAPGPSALQAAAVPGPRAVR  70
XP_006239940.1   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAWSPGG--GGGG------RTLAPAPGPSALQAAAVPGPRAVR  70
NP_001193030.1   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAESPGG--GGGG--SG--TTLAAAEGTSAALAAASPGPRGAR  72
XP_003354958.1   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAGSPGG--GGGG--R---RTLAAAAGASAAPAAAAPGPRAAR  71
XP_038309370.1   1    MDLSAAAALCLWLLSACRPRDGLglEAAAVLRAAGAGX-GPGGRggGGGG--GG--RALAPAAGVSAAPAAAAPGARAAR  75
XP_023475218.1   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAGSPGG--GGGG--GG--RTLAAAAGASTGPAAAAPGARAAR  72
XP_027824132.2   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAESPGG--GGGGggGG--TTLAAAAGASAALAAASPEPRGAR  74
XP_003308955.2   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--G---RTLAQAAGAAAVPAAAVPRARAAR  71
XP_001096970.2   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--GGggRTLAQAAGAAAVPAAAVSRARAPR  74
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XP_017910266.1   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAESPGG--GGGG--GG--TTLAAAAGASAAPAAASPGPRGAR  72
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XP_002812295.2   1    MDLSAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--G---RTLAQAAGASAVPAAAIPRARAAR  71
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NP_001299805.1   71   RAAGSG   FRNGSVVPHHFMMSLYRSLAGRAP----VAAASG---HGRVDTITGFTDQATQDETAAaEPGQSFLFDVSS  140
XP_006239940.1   71   RAAGSG   FRNGSVVPHHFMMSLYRSLAGRAP----AAATSG---HGRVDTITGFTDQATQEESAA-EPGQSFLFDVSS  139
NP_001193030.1   73   RATGSG   FRNGSVVPHQFMMSLYRSLTGRTPAGPVAVSTSGsgrHGRADTVTGFADQAIPDESAA-QTGLNFLFDVSS  148
XP_003354958.1   72   RAAGSG   FRNGSVVPHQFMMSLYRSLAGRAPTGAVAASTSGagrHGRADTITGFADQATQDESAA-ETGQRFLFDVSS  147
XP_038309370.1   76   RAAGSG[8]FGNGSVVPHQFMMSLYRNLAGRAPAGGAAASTSGsgrRGRADTITGFADQANQDDPPA-ETGQSFLFDVSS  159
XP_023475218.1   73   RAASSG   FRNGSVVPHQFMMSLYRSLAGRAPAGAAAASTSGsgrHGRADTITGFADQATQDESAA-ETGQSFLFDVSS  148
XP_027824132.2   75   RATGSG   FRNGSVVPHQFMMSLYRSLAGRTPAGPVAASTSGsgrHGRADTVTGFADQATPDESAA-ETGLNFLFDVSS  150
XP_003308955.2   72   RAAGSG   FRNGSVVPHHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTIIGFTDQATQDESAA-ETGQSFLFDVSS  144
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XP_004028950.1   72   RAAVSG   FRNGSVVPHHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFLFDVSS  144
XP_002812295.2   72   RAAGSG   FRNGSVVPHHFMMSLYRSLAGRAPAGAATVSASG---HGRADTITGFTDQATQDESAA-ETGQSFLFDVSS  144
XP_032028233.1   72   RAAGSG   FRNGSVVPHHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFLFDVSS  144

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NP_001299805.1   141  LSEADEVVNAELRVLRRRSPEPDRDSATLLPRLLL-STCPDEAGTAHLLHSRAAEPLGGARWEAFDVTDAVQSHRRWPRA  219
XP_006239940.1   140  LSDSDEVVNAELRVLRRRSPEPDRDSATLPPLLLL-STCPDEAGTAHLLHSRAAEPLDSARWEAFDVTDAVQSHRRWPRT  218
NP_001193030.1   149  LPDADEVLGAELRVLRRESGARGPGSASPP--LLLlSTCPSAASAPRLLHSRAAEFLDAARWEVFDVADALRRHRREPRT  226
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XP_023475218.1   149  LSDADEVVGAELRVLRREFPEPSSGSAIPQPLLLLlSTCPGAASAPLLLHSRAAEPLDGARWEVFDVADAVRRHRREPRA  228
XP_027824132.2   151  LPDADEVLGAELRVLRRESGARGPGSASLA--LLLlSTCPNAARAPRLLHSRAAESLDTARWEVFDVADALRRHRREPRP  228
XP_003308955.2   145  LNDADEVVGAELRVLRRGSPESGPGSWTSPPLLQL-STCPGAARAPRLLYSRAAEPLVGQRWEAFDVADAMRRHHREPRP  223
XP_001096970.2   148  LNDADEVVGAELRVLRRGSPEPGPGSSTSPPLLLL-STCPGAARAPRLLYSRAAEPLVGQRWEVFDVADAMRRHRREPRP  226
XP_023107842.1   151  LPDADEVVGAELRVLRRESPELGPGSATPLPLLLL-STCPGAARAPRLLHSRAAEPLAGARWEVFDVADAVRRHRQEPHA  229
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XP_004028950.1   145  LNDADEVVGAELRVLRRGSPESGPGSWTSPPLLLL-STCPGAARAPRLLYSRAAEPLVGQRWEAFDVADAMRRHRREPRP  223
XP_002812295.2   145  LNDADEVVGAELRVLRRGSPEPGPGSWTSPPVLLL-STCPGAARAPRLLYSRAAEPLVGQRWEAFDVADAMRRHRREPRH  223
XP_032028233.1   145  LNDADEVVGAELRVLRRGSPEPGPGSWTSPPLLLL-STCPGAARAPRLLYSRAAEPVVGQRWEAFDVADAMRRHRREPRP  223

NP_878248.2      227  PRAFCLLLRAVAGPVPSPLALRRLGFGWPGGGG   SAAEERAVLVVSSRTQRKESLFREIRAQARALGAALASEPLPDP  303
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NP_001299805.1  220  SRKFCLVLRAVTASESSPLALRRLGFGWPGGGD[3]TAAEERALLVISSRTQRKESLFREIRAQARALRA--AAEPPPDP  297
XP_006239940.1  219  SRKFCLVLRAVTGAESSPLALRRLGFGWPGGGD[3]TAAEERALLVISSRTHRKESLFREIRAQARALRA--AAELPPDP  296
NP_001193030.1  227  SRAFCLSLSGVVGSARVPLALRPLGFGLRGGGG   AAAEERALLVVSSRTQRKESLFREIRSQARALGAALAVESRPDS  303
XP_003354958.1  226  TSAFCLLLRGVVGPGRDPLALRLLGFGSSGGDG   AAEEERALLVVSSRTQRKESLFREIRAQARAFGAALAAEPPPDP  302
XP_038309370.1  239  ARAFCLRLRSVAGPSREPLALRGLGFGSRGARG   AGAEERALLVVSSRAHRKGSLFRE----ARALGAALAAEPPPDP  311
XP_023475218.1  229  TRVFCLLLRAAAGPARGPLALQLLGFGSRGGGG   AAAEERALLVVSSRTQRKESLFREIRAQARALGAPLAAEPPPDP  305
XP_027824132.2  229  SRAFCLSLRGVVGSARVPLALRLLGFGLRGGGG[5]AAAEERALLVVSSRTQRKESLFREIRSQARALGAALAAESRPDP  310
XP_003308955.2  224  PRAFCLLLRAVAGPVPSPLALRRLGFGWPGGGG   SAAEERALLVVSSRTQRKESLFREIRAQARALGAALASEPLPDP  300
XP_001096970.2  227  PRAFCLLLRAVTGPVRSPLALRRLGFRWPGGGG   SAPEERALLVVSSRTQRKESLFREMRAQARALGAALAAQPPPDP  303
XP_023107842.1  230  TRAFCLLLRSVAGPSQGPLALRLLGFGSRGRDG   AAAEERALLVVSSRTQRKGSLFREIRAQARALGAALAAEPPRDP  306
XP_017910266.1  227  SRAFCLSLRGVVGSARVPLALRLLGFGLRGGGG[1]AAAEERALLVVSSRTQRKESLFREIRSQARALGAARAAESRPDP  304
XP_004028950.1  224  PRAFCLLLRAVAGPVPSPLALRRLGFGWPGGGG   SAAEERSLLVVSSRTQRKESLFREIRAQARALGAAVASEPLPDP  300
XP_002812295.2  224  PRAFCLLLRAVAGPVRSPLALRRLGFGWSGGGG   SAAEERALLVVSSRTQRKESLFREIRAQARALGAALASEPPPDP  300
XP_032028233.1  224  PRAFCLLLRAVAGPVRSPLALRRLGFGWPGGGG   SAAEERALLVVSSRTQRKESLFREIRAQARALGAALASEQPPDP  300

NP_878248.2     304  GTGTASPRAVIGGRRRRRTALAGTRTAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  376
NP_001299805.1  298  GPGAGSRKANLGGRRRRRTALAGTRGAQGS[4]GGG[13]AGRGHGRRGRSRCSRKSLHVDFKELGWDDWIIAPLDYEAY  387
XP_006239940.1  297  GLGAGSRKATPGGRRRRRTALAGTRGAQGS   GGG[13]AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  382
NP_001193030.1  304  RPGVGSPTAVIGGRRRRRTALAGARAAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  376
XP_003354958.1  303  GPAIGSSTAVIGGRRRRRTALAGARAAQDS   GAG    GGRGHGRRSRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  375
XP_038309370.1  312  GPGPRSPAAVTGGRRRRRTALAGARPAQGG   GGG    AGRGHGRRGRSRCSRRPLHVDFKELGWDDWIIAPLDYEAY  384
XP_023475218.1  306  GPGTGSPTAVIGGRRRRRTALAGTRAAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  378
XP_027824132.2  311  GPGVGSPTAVIGGRRRRRTALAGARAAQGS   GGG    AGRGQGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  383
XP_003308955.2  301  GTRTASPRAVIGGRRRRRTALAGTRTAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  373
XP_001096970.2  304  GTGTGSPRAVTAGRRRRRTALAGTRTAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  376
XP_023107842.1  307  GPGTGSPTAVISGRRRRRTALTGARATQGS[2]GGG    AGRGHGRRGRTRCSRRPLHVDFKELGWDDWIIAPLDYEAY  381
XP_017910266.1  305  GPGVGSPTAVIGGRRRRRTALAGARAAQGS   GGG    AGRGHGRRVRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  377
XP_004028950.1  301  GTGTGSPRAVIGGRRRRRTALAGTRTAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  373
XP_002812295.2  301  GTGTGSPRAVIGGRRRRRTALAGTRTAQGS   SGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  373
XP_032028233.1  301  GTGTGSPRAVIGGRRRRRTALAGTRTAQGS   GGG    AGRGHGRRGRSRCSRKPLHVDFKELGWDDWIIAPLDYEAY  373

NP_878248.2     377  HCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  450
NP_001299805.1  388  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  461
XP_006239940.1  383  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  456
NP_001193030.1  377  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  450
XP_003354958.1  376  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  449
XP_038309370.1  385  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  458
XP_023475218.1  379  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  452
XP_027824132.2  384  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  457
XP_003308955.2  374  HCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  447
XP_001096970.2  377  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  450
XP_023107842.1  382  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  455
XP_017910266.1  378  HCEGVCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  451
XP_004028950.1  374  HCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  447
XP_002812295.2  374  HCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  447
XP_032028233.1  374  HCEGLCDFPLRSHLEPTNHAIIQTLLNSMAPDAAPASCCVPARLSPISILYIDAANNVVYKQYEDMVVEACGCR  447
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BMP10

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NP_055297.1 bone morphogenetic protein 10 preproprotein [Homo sapiens]
NP_033886.2 bone morphogenetic protein 10 preproprotein [Mus musculus]
NP_001026994.1 bone morphogenetic protein 10 precursor [Rattus norvegicus]
NP_001179047.1 bone morphogenetic protein 10 precursor [Bos taurus]
XP_003125118.1 bone morphogenetic protein 10 [Sus scrofa]
XP_538528.2 bone morphogenetic protein 10 [Canis lupus familiaris]
XP_001491666.1 bone morphogenetic protein 10 [Equus caballus]
XP_004005868.2 bone morphogenetic protein 10 [Ovis aries]
XP_525772.1 bone morphogenetic protein 10 [Pan troglodytes]
XP_001096299.1 bone morphogenetic protein 10 [Macaca mulatta]
XP_023107498.1 bone morphogenetic protein 10 [Felis catus]
XP_005686884.1 PREDICTED: bone morphogenetic protein 10 [Capra hircus]
XP_004029400.1 bone morphogenetic protein 10 [Gorilla gorilla gorilla]
XP_024098418.1 bone morphogenetic protein 10 [Pongo abelii]
XP_032033811.1 bone morphogenetic protein 10 [Hylobates moloch]
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NP_055297.1     1    MGSLVLTLCALFCLAAYLVSGSPIMNLEQSPLEEDMSLFGDVFSEQDGVDFNTLLQSMKDEFLKTLNLSDIPTQDSAKVD  80
NP_033886.2     1    MGSLVLPLSAVFCLVAHSASGSPIMGLEQSPLEEDMPFFDDIFTEQDGIDFNTLLQSMKNEFLKTLNLSDIPVQDTGRVD  80
NP_001026994.1  1    MGSLVLPLSAVFCLVARLASGSPIMGLEQSPLEEDMPFFDDIFTEQDGIDFNTLLQSMKDEFLKTLNLSDIPPQDTGRVD  80
NP_001179047.1  1    MGSVVLQLCTLSCLLVHSVSGNPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTLNLSDIPMQDSAKVD  80
XP_003125118.1  1    MGFLALQLCALSCLVAPWVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNSLLQSMKNEFLKTLNLSDIPMQDSAKVD  80
XP_538528.2     1    MGSLALQLCAVFGLVAHSVSGSPIMSLEQSPLEEDMPLFDDVFSEQDSVDFNTLLQTMKNEFLKTLNLSDIPPQDSAKVD  80
XP_001491666.1  1    MGSLALELCALFCLVAHLVSGSPIMSLERSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTLNLSDIPMQDSAKVD  80
XP_004005868.2  1    MGSVVLQLCTLSCLLLHAVSGNPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTLNLSDIPMQDSAKVD  80
XP_525772.1     1    MGSLVLTLCALFCLAAYLVSGSPIMNLEQSPLEEDMSLFGDVFSEQDGVDFNTLLQSMKDEFLKTLNLSDIPTQDSAKVD  80
XP_001096299.1  1    MGSLGLTLCALFCLAAHSVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKDEFLKTLNLSDIPTQDSAKVD  80
XP_023107498.1  1    MGSLALQLCALVCLVVHSVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTLNLSDIPSQDSAKVD  80
XP_005686884.1  1    MGSVVLQLCTLSCLLLHAVSGNPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTLNLSDIPMQDSAKVD  80
XP_004029400.1  1    MGSLVLTLCALFCLAAYLVSGSPIMNLEQSPLEEDMSLFGDVFSEQDGVDFNTLLQSMKDEFLKTLNLSDIPTQDSAKVD  80
XP_024098418.1  1    MGSLVLTLCALFCLAAYLVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKDEFLKTLNLSDIPTQDSAKVD  80
XP_032033811.1  1    MGSLVLTLCAFFCLAAYLVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKDEFLKTLNLSDIPTQESAKVD  80

NP_055297.1     81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVIMAELRLYTLVQRDRMIYDG  160
NP_033886.2     81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVTFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMMYDG  160
NP_001026994.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGIRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRLMYDG  160
NP_001179047.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEDIIMAELRLYTLVQRDRLIYEG  160
XP_003125118.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLYSQPVSFNGLRKYPLLFNVSIPHHEEVTMAELRLYTLVQRDRLMYEG  160
XP_538528.2     81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEVIMAELRLYTLVQRDRLIYDG  160
XP_001491666.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLFFNVSIPHHEEVIMAELRLYTLVQRDRIIYDG  160
XP_004005868.2  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEDIIMAELRLYTLVQRDRLIYEG  160
XP_525772.1     81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVMMAELRLYTLVQRDRMIYDG  160
XP_001096299.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVIMAELRLYTLVQRDRMIYDG  160
XP_023107498.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEVIMAELRLYTLVQRDRMIYDG  160
XP_005686884.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNRLRKYPLLFNVSIPHHEDIIMAELRLYTLVQRDRLIYEG  160
XP_004029400.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVIMAELRLYTLVQRDRMIYDG  160
XP_024098418.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYHLLFNVSVPHHEEVIMAELRLYTLVQRDRMIYDG  160
XP_032033811.1  81   PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVIMAELRLYTLVQRDRMIYDG  160

NP_055297.1     161  VDRKITIFEVLESKGDNEGERNMLVLVSGEIYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE  240
NP_033886.2     161  VDRKITIFEVLESADGSEEERSMLVLVSTEIYGTNSEWETFDVTDATRRWQKSGPSTHQLEIHIESRQNQAEDTGRGQLE  240
NP_001026994.1  161  VDRKIIIFEVLESADGSEDERSMLVLVSTEIYGTNSEWETFDITDATRRWQKSGPSTHQLEIHIESRQNQAEDTGRGQLE  240
NP_001179047.1  161  VDRKITIFEVLESKEDHEGERNMLVLVSGEIYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHEMEDTLGRGQLE  240
XP_003125118.1  161  VDRKITIFEVLESQGDHEGERSLLVLVSGEIYGTNSEWETFDVTDAIRRWQNSGSSTHQLEVHIESRQGM-EDAGRGQLE  239
XP_538528.2     161  VDRKITIFEVLESRGDTEGERSMLVLVSGEIYGTNSEWETFDVTDAIRRWQRSGSSTHQLEVHIESRHDGTEDAGRGHLE  240
XP_001491666.1  161  VDRKITIYEVLESKGDNEGERTMLVLVSGEIYGTNSEWETFDVTNAIRHWQKSGLSTHQLEVHIESRQDEAEDAGRGQLE  240
XP_004005868.2  161  VDRKITIFEVLESKEDHEGERSMLVLVSGEIYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHETEDTLGKGQLE  240
XP_525772.1     161  VDRKITIFEVLESKGDNEGERNMLVLVSGEIYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE  240
XP_001096299.1  161  VDRKITIFEVLESKGDNEGERNMLVLVSGEIYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHDEAEDASSGRLE  240
XP_023107498.1  161  VDRKITIFEVLESRGDSEGERSMLVLVSGEIYGTNSEWETFDVTEAIRRWQKSGSSTHQLEVHIESRHDGVEDAGRGQLE  240
XP_005686884.1  161  VDRKITIFEVLESKEDHEGERSMLVLVSGEIYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHETEDTLGRGQLE  240
XP_004029400.1  161  VDRKITIFEVLESKGDNEGERNMLVLVSGEIYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHDEAEDASSGRLE  240
XP_024098418.1  161  VDRKITIFEVLESKGDNEGERNMLVLVSGEIYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE  240
XP_032033811.1  161  VDRKITIFEVLESKGGNEGERNMLVLVSGEIYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEADDASSGRLE  240

NP_055297.1     241  IDTSAQNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
NP_033886.2     241  IDMSAQNKHDPLLVVFSDDQSNDKEQKEELNELITHEQ--DLD-LDSDAFFSGPDEEALLQMRSNMIDDSSARIRRNAKG  317
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NP_001026994.1  241  IDMSAQNKHDPLLVVFSDDQSGDKEQKEELNELISHEQ--DLD-LGTDGFFGGPDEEALLQMRSNMIDDSTARIRRNAKG  317
NP_001179047.1  241  IDTSARNKHDPLLVVFSDDQSSEKERKEELDEMIAHEQFPEMDNLDLDGYSNGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_003125118.1  240  IDISARNKHEPLLVVFSDDQSSEKERKEELSEMIAHEQFPELDNLGLGGYSSGPGEEALLQMRSNIIYDSTARIRRNAKG  319
XP_538528.2     241  IDTSARNKHVPLLVVFSDDQSSEKERKEELNEMIAHEQLLELDNLGLEGYSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_001491666.1  241  IDTSAENKHDPLLVVFSDDQSSEKEGKEELTEMIAHEQLLELDNLGLEGFSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_004005868.2  241  IDTSAQNKHEPLLVVFSDDQSSEKERKEELDEMIAHEQFPEMDNLDLDGYSNGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_525772.1     241  IDTSAQNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_001096299.1  241  IDTSAQNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDNLGLDGFSGGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_023107498.1  241  IDTSARNKHVPLLVVFSDDQSSEKERTEELNEMIAHEQLLEFDNLGMDSYSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_005686884.1  241  IDTSARNKHEPLLVVFSDDQSSEKERKEELDEMIAHEQFPEMDNLDLDGYSNGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_004029400.1  241  IDTSAQNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDSLGLDSFSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_024098418.1  241  IDTSAQNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDSLGLDSFSSGPGEEALLQMRSNIIYDSTARIRRNAKG  320
XP_032033811.1  241  IDTSAQNKHNPLLIVFSDDQSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPAEEALLQMRSNIIYDSTARIRRNAKG  320

NP_055297.1     321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
NP_033886.2     318  NYCKKTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLDPISIL  397
NP_001026994.1  318  NYCKKTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLDPISIL  397
NP_001179047.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_003125118.1  320  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  399
XP_538528.2     321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKVCCVPTKLEPISIL  400
XP_001491666.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_004005868.2  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_525772.1     321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_001096299.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_023107498.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_005686884.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_004029400.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_024098418.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400
XP_032033811.1  321  NYCKRTPLYIDFKEIGWDSWIIAPPGYEAYECRGVCNYPLAEHLTPTKHAIIQALVHLKNSQKASKACCVPTKLEPISIL  400

NP_055297.1     401  YLDKGVVTYKFKYEGMAVSECGCR  424
NP_033886.2     398  YLDKGVVTYKFKYEGMAVSECGCR  421
NP_001026994.1  398  YLDKGVVTYKFKYEGMAVSECGCR  421
NP_001179047.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_003125118.1  400  YLDKGVVTYKFKYEGMAVSECGCR  423
XP_538528.2     401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_001491666.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_004005868.2  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_525772.1     401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_001096299.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_023107498.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_005686884.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_004029400.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_024098418.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
XP_032033811.1  401  YLDKGVVTYKFKYEGMAVSECGCR  424
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INHBA

NP_002183.1 inhibin beta A chain preproprotein [Homo sapiens]
NP_032406.1 inhibin beta A chain preproprotein [Mus musculus]
NP_058824.1 inhibin beta A chain preproprotein [Rattus norvegicus]
NP_776788.1 inhibin beta A chain precursor [Bos taurus]
NP_999193.1 inhibin beta A chain precursor [Sus scrofa]
XP_540364.2 inhibin beta A chain [Canis lupus familiaris]
NP_001075378.1 inhibin beta A chain precursor [Equus caballus]
NP_001009458.1 inhibin beta A chain precursor [Ovis aries]
XP_519063.2 inhibin beta A chain [Pan troglodytes]
XP_028701686.1 inhibin beta A chain [Macaca mulatta]
NP_001009856.1 inhibin beta A chain precursor [Felis catus]
NP_001272510.1 inhibin beta A chain precursor [Capra hircus]
XP_004045385.1 inhibin beta A chain [Gorilla gorilla gorilla]
XP_002818070.1 inhibin beta A chain [Pongo abelii]
XP_032614156.1 inhibin beta A chain [Hylobates moloch]

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NP_002183.1     1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
NP_032406.1     1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHGSAPDCPSCALATLPKDGPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
NP_058824.1     1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHGAAPDCPSCALATLPKDGPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
NP_776788.1     1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
NP_999193.1     1    MPLLWLRGFLLASCWIIVRSSPTPGSGGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
XP_540364.2     1    MPLLWLRGFLVASCWIIVRSSPTPGPEGPGAAPACPACALTALPRDAPNSQPEMVEAVKKHILNMLHLKKRPEVTQPVPK  80
NP_001075378.1  1    MPLLWLRGFLLASCWIIVKSSPTPGSEGHSAAPNCPSCALATLPKDVPNAQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
NP_001009458.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
XP_519063.2     1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
XP_028701686.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
NP_001009856.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGPGAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLKKRPEVTQPVPK  80
NP_001272510.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
XP_004045385.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
XP_002818070.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80
XP_032614156.1  1    MPLLWLRGFLLASCWIIVRSSPTPGSEGHSAAPDCPSCALAALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQPVPK  80

NP_002183.1     81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_032406.1     81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_058824.1     81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_776788.1     81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEIWLFLK  160
NP_999193.1     81   AALLNAIRKLHVGKVGENGYVELEDDIGRRAEMNELMEQTSEIITFAEAGTARKTLRFEISKEGSDLSVVERAEIWLFLK  160
XP_540364.2     81   AALLNAIRKLHVGKVGENGFVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_001075378.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_001009458.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISQEGSDLSVVERAEIWLFLK  160
XP_519063.2     81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
XP_028701686.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTTRKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_001009856.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
NP_001272510.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEIWLFLK  160
XP_004045385.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
XP_002818070.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160
XP_032614156.1  81   AALLNAIRKLHVGKVGENGYVEIEDDIGRRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWLFLK  160

NP_002183.1     161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDV  240
NP_032406.1     161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGDEAEEMGLKGERSELLLSEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDV  240
NP_058824.1     161  VPKANRTRTKVTIRLFQQQKHPQGSLDMGDEAEEMGLKGERSELLLSEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDV  240
NP_776788.1     161  VPKANRTRSKVTIRLFQQQKHLQGSLDAGEEAEEVGLKGEKSEMLISEKVVDARKSTWHIFPVSSCIQRLLDQGKSSLDI  240
NP_999193.1     161  VPKANRTRTKVSIRLFQQQRRPQGSADAGEEAEDVGFPEEKSEVLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSALDI  240
XP_540364.2     161  VPKANRTRTKVTIRLLQ--KHPQGSLDAGEEAEDMGFPEERNEVLISEKVVDARKSTWHIFPVSSSIQRLLDQGRSSLDV  238
NP_001075378.1  161  VPKANRTRSKVTIRLLQQQKHPQGSSDTREEAEEADLMEERSEQLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDI  240
NP_001009458.1  161  VPKANRTRSKVTIRLFQQQKHLQGSLDAGEEAEEVGLKGEKSEMLISEKVVDARKSTWHIFPVSSCIQRLLDQGKSSLDI  240
XP_519063.2     161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDV  240
XP_028701686.1  161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDV  240
NP_001009856.1  161  VPKANRTRTKVTIQLLQKQ--PQGGVDAGEEAEEMGLMEERNEVLISEKVVDARKSTWHIFPVSSSIQRLLDQGKSSLDV  238
NP_001272510.1  161  VPKANRTRSKVTIRLFQQQKHLQGSLDAGEEAEEVGLKGEKSEMLISEKVVDARKSTWHIFPVSSCIQRLLDQGKSSLDI  240
XP_004045385.1  161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDV  240
XP_002818070.1  161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDV  240
XP_032614156.1  161  VPKANRTRTKVTIRLFQQQKHPQGSLDTGEEAEEVGLKGERSELLLSEKVVDARKSTWHVFPVSSSIQRLLDQGKSSLDV  240

NP_002183.1     241  RIACEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320
NP_032406.1     241  RIACEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGL--EEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  318
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NP_058824.1      241  RIACEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGL--EEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  318
NP_776788.1      241  RIACEQCQETGASLVLLGKKKKKEEEGEGKKRD-GEGGAGGDEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  319
NP_999193.1      241  RTACEQCHETGASLVLLGKKKKKEEEAEGRKRDG--EGAGVDEEKEQSHRPFLMLQARQSEEHPHRRRRRGLECDGKVNI  318
XP_540364.2      239  RIACEQCHETGASLVLLGKKKKKEEEGEGKKKDGGDAGAGGDEDKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  318
NP_001075378.1   241  RIACDQCHETGASLVLLGKKKKKEEEGEGKKKDGGEAGAGVDEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320
NP_001009458.1   241  RIACEQCQETGASLVLLGKKKRKEEEGEGKKRD-GEGGAGGDEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  319
XP_519063.2      241  RIACEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320
XP_028701686.1   241  RIACEQCQESGASLVLLGKKKKKEEEGDGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320
NP_001009856.1   239  RIACEQCHETGASLVLLGKKKKKEEEGEGKKKDGGDGGAGADEDKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  318
NP_001272510.1   241  RIACEQCQETGASLVLLGKKKRKEEEGEGKKRD-GEGGAGGDEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  319
XP_004045385.1   241  RIACEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320
XP_002818070.1   241  RIACEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320
XP_032614156.1   241  RIACEQCQESGASLVLLGKKKKKEEEGEGKKKGGGEGGAGADEEKEQSHRPFLMLQARQSEDHPHRRRRRGLECDGKVNI  320

NP_002183.1      321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  400
NP_032406.1      319  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  398
NP_058824.1      319  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  398
NP_776788.1      320  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  399
NP_999193.1      319  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  398
XP_540364.2      319  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGGCPSHIAGTSGSSLSFHSTVINHYRLRGHSPFTNLKSCCVPTKLRPMS  398
NP_001075378.1   321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINQYRLRGHNPFANLKSCCVPTKLRPMS  400
NP_001009458.1   320  CCKKQFYVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  399
XP_519063.2      321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  400
XP_028701686.1   321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  400
NP_001009856.1   319  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  398
NP_001272510.1   320  CCKKQFYVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  399
XP_004045385.1   321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  400
XP_002818070.1   321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  400
XP_032614156.1   321  CCKKQFFVSFKDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHSPFANLKSCCVPTKLRPMS  400

NP_002183.1      401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
NP_032406.1      399  MLYYDDGQNIIKKDIQNMIVEECGCS  424
NP_058824.1      399  MLYYDDGQNIIKKDIQNMIVEECGCS  424
NP_776788.1      400  MLYYDDGQNIIKKDIQNMIVEECGCS  425
NP_999193.1      399  MLYYDDGQNIIKKDIQNMIVEECGCS  424
XP_540364.2      399  MLYYDDGQNIIKKDIQNMIVEECGCS  424
NP_001075378.1   401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
NP_001009458.1   400  MLYYDDGQNIIKKDIQNMIVEECGCS  425
XP_519063.2      401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
XP_028701686.1   401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
NP_001009856.1   399  MLYYDDGQNIIKKDIQNMIVEECGCS  424
NP_001272510.1   400  MLYYDDGQNIIKKDIQNMIVEECGCS  425
XP_004045385.1   401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
XP_002818070.1   401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
XP_032614156.1   401  MLYYDDGQNIIKKDIQNMIVEECGCS  426
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INHBB

NP_002184.2 inhibin beta B chain preproprotein [Homo sapiens]
NP_032407.1 inhibin beta B chain preproprotein [Mus musculus]
NP_542949.1 inhibin beta B chain precursor [Rattus norvegicus]
NP_789822.2 inhibin beta B chain precursor [Bos taurus]
NP_001158314.1 inhibin beta B chain precursor [Sus scrofa]
XP_038281949.1 inhibin beta B chain [Canis lupus familiaris]
XP_023478506.1 inhibin beta B chain [Equus caballus]
XP_027820847.1 inhibin beta B chain [Ovis aries]
XP_016805107.1 inhibin beta B chain [Pan troglodytes]
XP_001090729.4 inhibin beta B chain [Macaca mulatta]
XP_003990762.4 inhibin beta B chain [Felis catus]
XP_017917150.1 PREDICTED: inhibin beta B chain [Capra hircus]
XP_004031753.1 inhibin beta B chain [Gorilla gorilla gorilla]
XP_024099269.1 inhibin beta B chain [Pongo abelii]
XP_032001809.1 inhibin beta B chain [Hylobates moloch]

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NP_002184.2      1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPTPAAP-PPPPPPGSPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
NP_032407.1      1    MDGLPGRALGAACLLLVAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG[4]FRRPEELGRVDGDFLE  80
NP_542949.1      1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG[4]FRRPEELGRVDGDFLE  80
NP_789822.2      1    MDGLPGRALGAACLLMLAVGSLGPGVWGSPTPPPLPAAPqPPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  77
NP_001158314.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGALGGSQDTCTSCGG   FRRPEELGRLDGDFLE  76
XP_038281949.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
XP_023478506.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDRDFLE  76
XP_027820847.1   1    MDGLPGRALGAACLVMLAVGWLGPGVWGSPTPPPSPAAPqPPPPPPGAPGGAQDTCTSCGG   FRRPEELGRVDGDFLE  77
XP_016805107.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
XP_001090729.4   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
XP_003990762.4   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
XP_017917150.1   1    MDGLPGRALGAACLVMLAVGWLGPGVWGSPTPPPSPAAPqPPPPPPGAPGGAQDTCTSCGG   FRRPEELGRVDGDFLE  77
XP_004031753.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
XP_024099269.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76
XP_032001809.1   1    MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPPGAPGGSQDTCTSCGG   FRRPEELGRVDGDFLE  76

NP_002184.2      77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
NP_032407.1      81   AVKRHILSRLQLRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  160
NP_542949.1      81   AVKRHILSRLQLRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  160
NP_789822.2      78   AVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  157
NP_001158314.1   77   AVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_038281949.1   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGSDGQERVSEIISFAETDGLASSR  156
XP_023478506.1   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_027820847.1   78   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGPERVSEIISFAETDGLASSR  157
XP_016805107.1   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_001090729.4   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_003990762.4   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_017917150.1   78   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGPERVSEIISFAETDGLASSR  157
XP_004031753.1   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_024099269.1   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPGADGQERVSEIISFAETDGLASSR  156
XP_032001809.1   77   AVKRHILSRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEIPHLDGHASPAADGQERVSEIISFAETDGLASSR  156

NP_002184.2      157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQ  236
NP_032407.1      161  VRLYFFVSNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNVVEKKVDLKRSGWHTFPITEAIQ  240
NP_542949.1      161  VRLYFFVSNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNVVEKKVDLKRSGWHTFPITEAIQ  240
NP_789822.2      158  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGGRRKVRVKVYFQEQGPGDRWAAVEKRVDLKRSGWHTFPLTEPIQ  237
NP_001158314.1   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEPGHGDRWDVVEKRVDLKRSGWHTLPLTEAIQ  236
XP_038281949.1   157  VRLYFFVSNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGQGDRWNAVEKKVDLKRSGWHTFPLTEAIQ  236
XP_023478506.1   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNVVEKKVDLKRSGWHTFPLTEAIQ  236
XP_027820847.1   158  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGGRRKVRVKVYFQEQGPGDRWAAVEKRVDLKRSGWHTFPLTEPIQ  237
XP_016805107.1   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQ  236
XP_001090729.4   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQ  236
XP_003990762.4   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNVVEKKVDLKRSGWHTFPLTEAIQ  236
XP_017917150.1   158  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGGRRKVRVKVYFQEQGPGDRWAAVEKRVDLKRSGWHTFPLTEPIQ  237
XP_004031753.1   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQ  236
XP_024099269.1   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQ  236
XP_032001809.1   157  VRLYFFISNEGNQNLFVVQASLWLYLKLLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSGWHTFPLTEAIQ  236

NP_002184.2      237  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
NP_032407.1      241  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTSLCCRQQFFIDFRLIG  320
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NP_542949.1     241  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTSLCCRQQFFIDFRLIG  320
NP_789822.2     238  ALFSRGERRLSLDVQCDSCRELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  317
NP_001158314.1  237  ALFERGERRLNLDVQCDGCQELAVVPVFVDPGEESHRPFVVVQARLVDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_038281949.1  237  ALFERGERRLSLDVQCDGCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_023478506.1  237  ALFERGERRLNLDVQCDGCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_027820847.1  238  ALFSRGERRLSLDVQCDGCRELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTSLCCRQQFFIDFRLIG  317
XP_016805107.1  237  ALFERGERRLNLDVQCDSCQELAVVPVFVDPAEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_001090729.4  237  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_003990762.4  237  SLFERGERRLNLDVQCDGCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_017917150.1  238  ALFSRGERRLSLDVQCDGCRELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  317
XP_004031753.1  237  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_024099269.1  237  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316
XP_032001809.1  237  ALFERGERRLNLDVQCDSCQELAVVPVFVDPGEESHRPFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQQFFIDFRLIG  316

NP_002184.2     317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
NP_032407.1     321  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV  400
NP_542949.1     321  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGPVNSCCIPTKLSSMSMLYFDDEYNIVKRDV  400
NP_789822.2     318  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  397
NP_001158314.1  317  WSDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_038281949.1  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_023478506.1  317  WNDWIIAPIGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_027820847.1  318  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  397
XP_016805107.1  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_001090729.4  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGAVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_003990762.4  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_017917150.1  318  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  397
XP_004031753.1  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_024099269.1  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396
XP_032001809.1  317  WNDWIIAPTGYYGNYCEGSCPAYLAGVPGSASSFHTAVVNQYRMRGLNPGTVNSCCIPTKLSTMSMLYFDDEYNIVKRDV  396

NP_002184.2     397  PNMIVEECGCA  407
NP_032407.1     401  PNMIVEECGCA  411
NP_542949.1     401  PNMIVEECGCA  411
NP_789822.2     398  PNMIVEECGCA  408
NP_001158314.1  397  PNMIVEECGCA  407
XP_038281949.1  397  PNMIVEECGCA  407
XP_023478506.1  397  PNMIVEECGCA  407
XP_027820847.1  398  PNMIVEECGCA  408
XP_016805107.1  397  PNMIVEECGCA  407
XP_001090729.4  397  PNMIVEECGCA  407
XP_003990762.4  397  PNMIVEECGCA  407
XP_017917150.1  398  PNMIVEECGCA  408
XP_004031753.1  397  PNMIVEECGCA  407
XP_024099269.1  397  PNMIVEECGCA  407
XP_032001809.1  397  PNMIVEECGCA  407
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GDF8

NP_005250.1 growth/differentiation factor 8 preproprotein [Homo sapiens]
NP_034964.1 growth/differentiation factor 8 preproprotein [Mus musculus]
NP_062024.1 growth/differentiation factor 8 precursor [Rattus norvegicus]
NP_001001525.1 growth/differentiation factor 8 precursor [Bos taurus]
NP_999600.2 growth/differentiation factor 8 precursor [Sus scrofa]
NP_001002959.1 growth/differentiation factor 8 precursor [Canis lupus familiaris]
NP_001075286.1 growth/differentiation factor 8 precursor [Equus caballus]
NP_001009428.1 growth/differentiation factor 8 precursor [Ovis aries]
NP_001073388.1 growth/differentiation factor 8 precursor [Pan troglodytes]
NP_001073588.1 growth/differentiation factor 8 precursor [Macaca mulatta]
XP_003991021.1 growth/differentiation factor 8 [Felis catus]
NP_001272666.1 growth/differentiation factor 8 precursor [Capra hircus]
XP_018877573.1 growth/differentiation factor 8 [Gorilla gorilla gorilla]
XP_002812720.1 growth/differentiation factor 8 [Pongo abelii]
XP_032609257.1 growth/differentiation factor 8 [Hylobates moloch]

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NP_005250.1     1    -MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDVIRQ  79
NP_034964.1     1    mMQKLQMYVYIYLFMLIAAGPVDLNEGSEREENVEKEGLCNACAWRQNTRYSRIEAIKIQILSKLRLETAPNISKDAIRQ  80
NP_062024.1     1    mIQKPQMYVYIYLFVLIAAGPVDLNEDSEREANVEKEGLCNACAWRQNTRYSRIEAIKIQILSKLRLETAPNISKDAIRQ  80
NP_001001525.1  1    -MQKLQISVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACLWRENTTSSRLEAIKIQILSKLRLETAPNISKDAIRQ  79
NP_999600.2     1    -MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACMWRQNTKSSRLEAIKIQILSKLRLETAPNISKDAIRQ  79
NP_001002959.1  1    -MQRLQICVYIYLFVLIVAGPVDLSENSEQKENVEKEGLCNACMWRQNTKSSRIEAIKIQILSKLRLETAPNISRDAVRQ  79
NP_001075286.1  1    -MQKLQISVYIYLFVLILAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79
NP_001009428.1  1    -MQKLQIFVYIYLFMLLVAGPVDLNENSEQKENVEKKGLCNACLWRQNNKSSRLEAIKIQILSKLRLETAPNISKDAIRQ  79
NP_001073388.1  1    -MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79
NP_001073588.1  1    -MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79
XP_003991021.1  1    -MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79
NP_001272666.1  1    -MQKLQIFVYIYLFMLLVAGPVDLNENSEQKENVEKKGLCNACLWRQNNKSSRLEAIKIQILSKLRLETAPNISKDAIRQ  79
XP_018877573.1  1    -MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79
XP_002812720.1  1    -MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79
XP_032609257.1  1    -MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ  79

NP_005250.1     80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
NP_034964.1     81   LLPRAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQADGKPKCCFFKFSSKIQYNKVVKAQLWIY  160
NP_062024.1     81   LLPRAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQADGKPKCCFFKFSSKIQYNKVVKAQLWIY  160
NP_001001525.1  80   LLPKAPPLLELIDQFDVQRDASSDGSLEDDDYHARTETVITMPTESDLLTQVEGKPKCCFFKFSSKIQYNKLVKAQLWIY  159
NP_999600.2     80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDLLMQVEGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
NP_001002959.1  80   LLPRAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETVIAMPAETDLLMQVEGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
NP_001075286.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDLLMQVEGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
NP_001009428.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHVTTETVITMPTESDLLAEVQEKPKCCFFKFSSKIQHNKVVKAQLWIY  159
NP_001073388.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
NP_001073588.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
XP_003991021.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDLLMQVEGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
NP_001272666.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHVTTETVITMPTESDLLAEVQEKPKCCFFKFSSKIQHNKVVKAQLWIY  159
XP_018877573.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
XP_002812720.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY  159
XP_032609257.1  80   LLPKAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYNKVVKAQLWIY  159

NP_005250.1     160  LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_034964.1     161  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  240
NP_062024.1     161  LRAVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  240
NP_001001525.1  160  LRPVKTPATVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_999600.2     160  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_001002959.1  160  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_001075286.1  160  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGAGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_001009428.1  160  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_001073388.1  160  LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_001073588.1  160  LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
XP_003991021.1  160  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
NP_001272666.1  160  LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
XP_018877573.1  160  LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
XP_002812720.1  160  LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239
XP_032609257.1  160  LRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV  239

NP_005250.1     240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
NP_034964.1     241  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  320
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NP_062024.1      241  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  320
NP_001001525.1   240  TFPEPGEDGLTPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
NP_999600.2      240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKASYCSGECEFVFLQ  319
NP_001002959.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
NP_001075286.1   240  TFPRPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
NP_001009428.1   240  TFPEPGEEGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQ  319
NP_001073388.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
NP_001073588.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
XP_003991021.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
NP_001272666.1   240  TFPEPGEEGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFLFLQ  319
XP_018877573.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
XP_002812720.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319
XP_032609257.1   240  TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVFLQ  319

NP_005250.1      320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
NP_034964.1      321  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  376
NP_062024.1      321  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  376
NP_001001525.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGEGQIIYGKIPAMVVDRCGCS  375
NP_999600.2      320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
NP_001002959.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
NP_001075286.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
NP_001009428.1   320  KYPHTHLVHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCGCS  375
NP_001073388.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
NP_001073588.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
XP_003991021.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
NP_001272666.1   320  KYPHTHLVHQANPKGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPGMVVDRCGCS  375
XP_018877573.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
XP_002812720.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
XP_032609257.1   320  KYPHTHLVHQANPRGSAGPCCTPTKMSPINMLYFNGKEQIIYGKIPAMVVDRCGCS  375
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GDF11

NP_005802.1 growth/differentiation factor 11 preproprotein [Homo sapiens]
NP_034402.1 growth/differentiation factor 11 preproprotein [Mus musculus]
NP_058899.1 growth/differentiation factor 11 precursor [Rattus norvegicus]
XP_002687467.2 growth/differentiation factor 11 [Bos taurus]
NP_001231239.1 growth/differentiation factor 11 precursor [Sus scrofa]
XP_038534852.1 growth/differentiation factor 11 [Canis lupus familiaris]
XP_023499520.1 growth/differentiation factor 11 [Equus caballus]
XP_012031460.3 growth/differentiation factor 11 [Ovis aries]
XP_016778746.2 growth/differentiation factor 11 [Pan troglodytes]
XP_015007410.2 growth/differentiation factor 11 [Macaca mulatta]
XP_003988905.1 growth/differentiation factor 11 [Felis catus]
XP_017903600.1 PREDICTED: growth/differentiation factor 11 [Capra hircus]
XP_018894140.2 growth/differentiation factor 11 [Gorilla gorilla gorilla]
XP_024112308.1 growth/differentiation factor 11 [Pongo abelii]
XP_032029354.1 growth/differentiation factor 11 [Hylobates moloch]

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NP_005802.1     1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GVGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  78
NP_034402.1     1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAA---GVGGERSSRPAPSAPPEPDGCPVCVWRQHSRELRLES  76
NP_058899.1     1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAA---GVGGERSSRPAPSAAPEPDGCPVCVWRQHSRELRLES  76
XP_002687467.2  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA--GAGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  77
NP_001231239.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAA----GAGGERSSRPAASVAPEPDGCPVCLWRQHSRELRLES  75
XP_038534852.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAA---GAGGERSSRPAPSAAPEPDGCPVCVWRQHSRELRLES  76
XP_023499520.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAA----GAGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  75
XP_012031460.3  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GAGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  78
XP_016778746.2  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAA---GVGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  76
XP_015007410.2  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAaaGVGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  79
XP_003988905.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAA----GAGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  75
XP_017903600.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA--GAGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  77
XP_018894140.2  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GVGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  78
XP_024112308.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGPvAAAAAAAAAAAAaaGVGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  80
XP_032029354.1  1    MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA--GVGGERSSRPAPSVAPEPDGCPVCVWRQHSRELRLES  77

NP_005802.1     79   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  158
NP_034402.1     77   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  156
NP_058899.1     77   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  156
XP_002687467.2  78   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  157
NP_001231239.1  76   VKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  155
XP_038534852.1  77   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  156
XP_023499520.1  76   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  155
XP_012031460.3  79   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  158
XP_016778746.2  77   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  156
XP_015007410.2  80   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  159
XP_003988905.1  76   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  155
XP_017903600.1  78   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  157
XP_018894140.2  79   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  158
XP_024112308.1  81   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  160
XP_032029354.1  78   IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQGDALQPEDFLEEDEYHATTETVISMAQETDPAVQTDGS  157

NP_005802.1     159  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  238
NP_034402.1     157  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  236
NP_058899.1     157  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  236
XP_002687467.2  158  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIDLHSRSGHWQSI  237
NP_001231239.1  156  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIDLHSRSGHWQSI  235
XP_038534852.1  157  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  236
XP_023499520.1  156  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  235
XP_012031460.3  159  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIDLHSRSGHWQSI  238
XP_016778746.2  157  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  236
XP_015007410.2  160  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  239
XP_003988905.1  156  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  235
XP_017903600.1  158  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIDLHSRSGHWQSI  237
XP_018894140.2  159  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  238
XP_024112308.1  161  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  240
XP_032029354.1  158  PLCCHFHFSPKVMFTKVLKAQLWVYLRPVPRPATVYLQILRLKPLTGEGTAGGGGGGRRHIRIRSLKIELHSRSGHWQSI  237

NP_005802.1     239  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  318
NP_034402.1     237  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  316
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NP_058899.1     237  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  316
XP_002687467.2  238  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  317
NP_001231239.1  236  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  315
XP_038534852.1  237  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  316
XP_023499520.1  236  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  315
XP_012031460.3  239  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  318
XP_016778746.2  237  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  316
XP_015007410.2  240  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  319
XP_003988905.1  236  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  315
XP_017903600.1  238  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  317
XP_018894140.2  239  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  318
XP_024112308.1  241  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  320
XP_032029354.1  238  DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHPFMELRVLENTKRSRRNLGLDCDEHSSESRCCRYPL  317

NP_005802.1     319  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  398
NP_034402.1     317  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  396
NP_058899.1     317  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  396
XP_002687467.2  318  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  397
NP_001231239.1  316  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  395
XP_038534852.1  317  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  396
XP_023499520.1  316  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  395
XP_012031460.3  319  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  398
XP_016778746.2  317  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  396
XP_015007410.2  320  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  399
XP_003988905.1  316  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  395
XP_017903600.1  318  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  397
XP_018894140.2  319  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  398
XP_024112308.1  321  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  400
XP_032029354.1  318  TVDFEAFGWDWIIAPKRYKANYCSGQCEYMFMQKYPHTHLVQQANPRGSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPG  397

NP_005802.1     399  MVVDRCGCS  407
NP_034402.1     397  MVVDRCGCS  405
NP_058899.1     397  MVVDRCGCS  405
XP_002687467.2  398  MVVDRCGCS  406
NP_001231239.1  396  MVVDRCGCS  404
XP_038534852.1  397  MVVDRCGCS  405
XP_023499520.1  396  MVVDRCGCS  404
XP_012031460.3  399  MVVDRCGCS  407
XP_016778746.2  397  MVVDRCGCS  405
XP_015007410.2  400  MVVDRCGCS  408
XP_003988905.1  396  MVVDRCGCS  404
XP_017903600.1  398  MVVDRCGCS  406
XP_018894140.2  399  MVVDRCGCS  407
XP_024112308.1  401  MVVDRCGCS  409
XP_032029354.1  398  MVVDRCGCS  406
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INHBC

NP_005529.1 inhibin beta C chain preproprotein [Homo sapiens]
NP_034695.1 inhibin beta C chain preproprotein [Mus musculus]
NP_072136.1 inhibin beta C chain precursor [Rattus norvegicus]
NP_001192912.1 inhibin beta C chain precursor [Bos taurus]
XP_003355541.3 inhibin beta C chain [Sus scrofa]
XP_849169.2 inhibin beta C chain [Canis lupus familiaris]
XP_001488633.1 inhibin beta C chain [Equus caballus]
XP_004006594.3 inhibin beta C chain [Ovis aries]
XP_522443.1 inhibin beta C chain [Pan troglodytes]
XP_001115940.1 inhibin beta C chain [Macaca mulatta]
XP_023112929.1 inhibin beta C chain [Felis catus]
XP_005680345.1 PREDICTED: inhibin beta C chain [Capra hircus]
XP_004053482.1 inhibin beta C chain [Gorilla gorilla gorilla]
XP_002823468.3 inhibin beta C chain [Pongo abelii]
XP_032028142.1 inhibin beta C chain [Hylobates moloch]

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NP_005529.1     1    --MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQH  78
NP_034695.1     1    --MASSLLLALLFLTPTTVVNPKTEGPCPACWGAIFDLESQRELLLDLAKKSILDKLHLSQRPILSRPVSRGALKTALQR  78
NP_072136.1     1    --MASSLLLALLFLTLATVVNLKTDGPCPACWGATFDLESHRELLLDLAKKSILDKLHLSQRPILSRPVSREALKTALRR  78
NP_001192912.1  1    --MICSLFLAFLVLAAAMVATPRADRQCPACGEPALDVESHRELLLNLAKRSILDKLHLSQRPTLGRPVSGVALRAALHR  78
XP_003355541.3  1    maMISSLLLAFLFLAPATVATPQADSQCLACGGPTLDLESQRDLLLNLAKRSILDKLHLTQRPTLSRPVSRAALRTALQG  80
XP_849169.2     1    --MISPLLLAFLFLAPATVAIPRADSQCLACGGPAVDVERQRELLLDLAKRSILEKLHLSQRPTLSRPVSGAALRAALQR  78
XP_001488633.1  1    --MISSMLLAFLFLAPATVATSRADGQCLACAGPTLDLESQRELLLDLAKRNILDKLHLSQRPTLSRPVSRAALRTVLQR  78
XP_004006594.3  1    --MICSLFLAFLVLPAAMVATPRADRQCPACGEPALDVESHRELLLNLAKRSILDKLHLSQRPTLGRPVSRVALRAALQR  78
XP_522443.1     1    --MTSSLLLAFLLLAPTTVATPRSGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQH  78
XP_001115940.1  1    --MTSSLLLAFFLLAPTTVATPRAGGQCPACGGPTLELESQRELLLHLAKRSILDKLHLSQRPTLNRPVSRAALRTALQR  78
XP_023112929.1  1    --MISSLLLAFLLLAPAPAAIPRADSQCLACGGPALDLDRQRELLLDLAKRSILDKLRLSQRPTLSRPVSRAALRTVLQH  78
XP_005680345.1  1    --MICSLFLAFLVLPAAMVATPRADRQCPACGEPALDVESHRELLLNLAKRSILDKLHLSQRPTLGRPVSRVALRAALQR  78
XP_004053482.1  1    --MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQH  78
XP_002823468.3  1    --MTTSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQR  78
XP_032028142.1  1    --MTSSLLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRAALRTALQR  78

NP_005529.1     79   LHGVPQGALLEDNREQE-CEIISFAETGLSTINQTRLDFHFSSDRTAGDREVQQASLMFFVQLPSNT-TWTLKVRVLVLG  156
NP_034695.1     79   LRGPRRETLLEHDQRQEeYEIISFADTDLSSINQTRLEFHF-SGRMASGMEVRQTRFMFFVQFPHNA-TQTMNIRVLVLR  156
NP_072136.1     79   LRGTRAETLLEHDQRQE-YEIISFADTGLSNINQTRLEFHF-SDRTTGGVEVLQTRFMFFMQLPPNT-TQTMNIRVLVLR  155
NP_001192912.1  79   LHGPPQGALPEADEGQE-YEIISFAETGLCNTTQTRLDFHFSSDSSAGGLEVQQASLMFFVQLPPNT-TCPLKVRVLELS  156
XP_003355541.3  81   LHGPPQGVLPEADRAQE-YEIISFAETGLSNIDQTRLDFHFPSDRTSGSLEVQQASLMFFVQLPPNA-TWTLKVRVLELG  158
XP_849169.2     79   LHGPPQGMLPEADGEQE-YEIISFADTGLSDINQTRLDFHFS-DRTASGMEIQQASLMFFVQIPPNT-TQTLKLKILVLS  155
XP_001488633.1  79   LHGPPQGVLPEADRGQE-YEIISFAQTGLSNVNQTRLDFYF-SDRTAGGMEIQQASLMFFVQLPPNT-TQTMKVRILVPG  155
XP_004006594.3  79   LHGPPQGVLPEADGGQE-YEIITFAETGLCNTTQTRLDFHFSSDSSAGGLEVQQASLMFFVQLPPNT-TCPLKVRVLELS  156
XP_522443.1     79   LHGVPQGALLEDNREQE-CEIISFAETGLSTINQTRLDFHFSSNRTAGDREVQQASLMFFVQLSSNT-TWTLKVRVLVLG  156
XP_001115940.1  79   LHGVPQGALPEDNREQE-CEIISFAETGLSTINKTRLDFHFSSDRTAGDREVQQASLMFFVQLPSNT-TWTLKVRVLVLG  156
XP_023112929.1  79   LHGPPQGTLLEADREQE-YEIISFADTGFSNINQTRLDFHFSSDRTASAMEIQQASVMFFVQLPPNTiTLPLKLRILVPG  157
XP_005680345.1  79   LHGPPQGVLPEADGGQE-YEIITFAETGLCNTTQTRLDFHFSSDSSASGLEVQQASLMFFVQLPPNT-TCPLKVRVLELS  156
XP_004053482.1  79   LHGVPQGALLEDNREQE-CEIISFAETGLSTINQTRLDFHFSSDRTAGDREVQQASLMFFVQLPSNT-TWTLKVRVLVLG  156
XP_002823468.3  79   LHGVPQGALLEDNREQE-CEIISFAETGLSTINQTRLDFHFSSDRTAGDREVQQASLMFFVQLPSNT-TWTLKMRVLVLG  156
XP_032028142.1  79   LRGVPQGALPEDNGEQE-CEIISFAETGLSTINQTRLDFHFSSDRTAGDREVQQASLVFFVQLPSNT-TWTLKVRVLVLG  156

NP_005529.1     157  PHNTNLTLATQYLLEVDASGWHQLPLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHQIHRR  236
NP_034695.1     157  PYDTNLTLTSQYVVQVNASGWYQLLLGPEAQAACSQGHLTLELVPESQVAHSSLILGWFSHRPFVAAQVRVEGKHRVRRR  236
NP_072136.1     156  PYDTNLTLTSQYMLQVDASGWYQLLLGPEAQAACSQGHLTLELVPESQLAHSSLILDGVSHRPFVAAQVRVEGKHRVRRR  235
NP_001192912.1  157  PRDTNLTSATQHLLQVDDTGWHQLLLGPEAQTAYSQGHLALELAPEEQVDWSPVVLARAAHRPFVTARVRVGGQHRVRRR  236
XP_003355541.3  159  PHGTNLTLATQHPLEVNNSGWHQLLLGPEAEAAYSQGHLILELVPEGQVAWNSVILDGAAHRPFVTARVRVGGKHRVRRR  238
XP_849169.2     156  SRDTNLTSATQHLLDVDASGWHQLFLGREAQAACNQGHLTLELVPEGQGAWSSVILGGAAHRPFVSAKVKAGGKHRVHRR  235
XP_001488633.1  156  PHDTNLTLATQHLLEVDASGWHQLLLGPEAQAACSQRHLTLELVPEGQVAQSSVILGGAAHRPFVAARVRVGGKHRVRRR  235
XP_004006594.3  157  PRDTNLTSATQHLLEVNDSGWHQLLLGPEAQTAYSQGHLTLELAPEGQVAWSPVILAGAAHRPFVTARVRVGGKHRLRRR  236
XP_522443.1     157  PHNTNLTLATQYLLEVDASGWHQLLLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHRIHRR  236
XP_001115940.1  157  PHNTNLTLATQYLLEVDASGWHQLLLGPEAQAAYSQGHLTLELVPEGQVAQSSVILGGAAHRPFVAARVRVGGKHRIHRR  236
XP_023112929.1  158  SHDTNLTWATQQLLEVDASGWHRLFLGPEAQAAFSQGHLTLELVLEGQGAQSSVILGGAAHRPFVAAKVKVGGKHRLHRR  237
XP_005680345.1  157  PRDTNLTSATQHLLEVNDSGWHQLLLGPEAQTAYSQGHLALELAPEGQEAWSPVILAGAAHRPFVTARVRVGGKHRLRRR  236
XP_004053482.1  157  PHNTNLTLATQYLLEVDASGWHQLLLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHRIHRR  236
XP_002823468.3  157  PHNTNLTLATQYLLEVDASGWHQLLLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHRIHRR  236
XP_032028142.1  157  PHNTNLSLATQYLLEVDASGWHQLLLGPEAQAACSQGHLTLELVLEGQVAQSSVILGGAAHRPFVAARVRVGGKHRIHRR  236

NP_005529.1     237  GIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC  316
NP_034695.1     237  GIDCQGASRMCCRQEFFVDFREIGWNDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANAAAGTTGRGSC  316
NP_072136.1     236  GINCQGLSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGISASFHTAVLNLLKANTDAGTARRGSC  315
NP_001192912.1  237  GIDCQGRSKMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIAASFYTSVLNLLKVNTAAGTTRGSSC  316
XP_003355541.3  239  GIDCQGRSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGHCPLHVAGVPGIAASFHTAVLNLLKANTAAGTTGGGSC  318
XP_849169.2     236  GINCQGGSRMCCRQEFFVDFRDIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIAASFHTAVLNLLKANTAAGTAGGGSC  315
XP_001488633.1  236  GINCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIAASFHTTVFNLLKANTAAGATGGGSC  315
XP_004006594.3  237  GIDCQGRSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIAASFYTSVLNLLKVNTAAGTTRGSSC  316
XP_522443.1     237  GIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC  316
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XP_001115940.1   237   GIDCQEGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHVAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC   316
XP_023112929.1   238   GIDCQGGSRMCCRREFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIAASFHTAVLNLLKANTAAGTAGGGSC   317
XP_005680345.1   237   GIDCQGRSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCTGQCPLHVAGMPGIAASFYTSVLNLLKVNTAAGTTRGSSC   316
XP_004053482.1   237   GIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC   316
XP_002823468.3   237   GIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC   316
XP_032028142.1   237   GIDCQGGSRMCCRQEFFVDFREIGWHDWIIQPEGYAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC   316


NP_005529.1      317   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
NP_034695.1      317   CVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
NP_072136.1      316   CVPTSRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   351
NP_001192912.1   317   CVPTVRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_003355541.3   319   CVPTARRPLSLLYYDKDSNIVKTDIPDMVVEACGCS   354
XP_849169.2      316   CVPTARRPLSLLYYDRDSNVVKTDIPDMVVEACGCS   351
XP_001488633.1   316   CVPTTRRPLSLLYYDRDSNIVKTDIPDMVVETCGCS   351
XP_004006594.3   317   CVPTIRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_522443.1      317   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_001115940.1   317   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_023112929.1   318   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   353
XP_005680345.1   317   CVPTIRRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_004053482.1   317   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_002823468.3   317   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
XP_032028142.1   317   CVPTARRPLSLLYYDRDSNIVKTDIPDMVVEACGCS   352
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INHBE

NP_113667.1 inhibin beta E chain preproprotein [Homo sapiens]
NP_032408.2 inhibin beta E chain preproprotein [Mus musculus]
NP_114003.2 inhibin beta E chain precursor [Rattus norvegicus]
NP_001192771.1 inhibin beta E chain precursor [Bos taurus]
XP_003126368.2 LOW QUALITY PROTEIN: inhibin beta E chain [Sus scrofa]
XP_005625596.1 inhibin beta E chain isoform X1 [Canis lupus familiaris]
XP_001488840.1 inhibin beta E chain [Equus caballus]
XP_004006593.1 inhibin beta E chain [Ovis aries]
XP_509161.2 inhibin beta E chain [Pan troglodytes]
XP_001115958.2 inhibin beta E chain [Macaca mulatta]
XP_003988987.1 inhibin beta E chain [Felis catus]
XP_005680344.1 PREDICTED: inhibin beta E chain [Capra hircus]
XP_004053483.1 inhibin beta E chain [Gorilla gorilla gorilla]
XP_002823469.1 inhibin beta E chain [Pongo abelii]
XP_032029168.1 inhibin beta E chain [Hylobates moloch]

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NP_113667.1     1        MRLPDVQLWLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRAL  76
NP_032408.2     1        MKLPKAQLWLILLWALVWVQSTRSACPSCGGPTLAPQGERALVLELAKQQILEGLHLTSRPRITRPLPQAALTRAL  76
NP_114003.2     1        MGLSNVQLWTILLWALAWVQSTRSACPSCGAPTLTPQGERALVLELAKQQILEGLHLTSRPRITRPLPQAALTRAL  76
NP_001192771.1  1        MGLLKVQLQLVLLWALVWAQVAGSACPSCGGPTLAPQAERALVLKLAKQQILEGLQLTSRPRLTHPPPKAVLTRAL  76
XP_003126368.2  1        MGLPDVQLWLVLLWALVWAQGEGSVCPSCGGPTLAPQAERALVLELAKQQILQGLHLSSRPRITHPPPQAALTRAL  76
XP_005625596.1  1        MGLPDVQPQLVLLWALVWAQGAGSGCPSCGGPTLAPQAERALVLELAKQQILEGLHLTSRPRITHPPPQAALARAL  76
XP_001488840.1  1        MELPDVQLQLVLLWALVWAQGAGSVCPSCGGPTLAPQAERALVLELAKQQILEGLHLTSRPRITHPPSQAALTRAL  76
XP_004006593.1  1        MGLHKVQLQLVLLWALVWAQVAGSACPSCGGPTLAPQAERALVLKLAKQQILEGLQLTSRPRMTHPPPPAVLTRAL  76
XP_509161.2     1        MRLPDVQLWLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRAL  76
XP_001115958.2  1        MGLPVVQLWLVLLWTLVRAQGTGSVCPSCGDSKLAPQAERALVLELAKQQILEGLHLTSRPRITHPPPQAALTRAL  76
XP_003988987.1  1        MGLPDGQRQLVLLWALVWAQGAGSVCPSCGGPTLEPQAERALVLELAKQQILEGLHLTSRPRITHPPPQAALTRAL  76
XP_005680344.1  1    [32]MGLHKVQLQLVLLWALVWAQVAGSACPSCGGPTLAPQAERALVLKLAKQQILEGLQLTSRPRMTHPPPQAVLTRAL  108
XP_004053483.1  1        MQLPDVQLWLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRAL  76
XP_002823469.1  1        MGLPDVQLWLVLLWALVRAQGTGSVCPSCGGSKLAPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRAL  76
XP_032029168.1  1        MGLPDVQLWLVLLWALVRAQGTGSVCPSCGGSKLTPQAERALVLELAKQQILDGLHLTSRPRITHPPPQAALTRAL  76

NP_113667.1     77   RRLQPGSVAPGNGEEVISFATVTD-STSAYSSLLTFHLSTPRSHHLYHARLWLHVLPTLPGTLCLRIFRWGPRRRRQGSR  155
NP_032408.2     77   RRLQPKSMVPGNREKVISFATIIDKSTSTYRSMLTFQLSPLWSHHLYHARLWLHVPPSFPGTLYLRIFRCGTTRCR-GFR  155
NP_114003.2     77   RRLQPRSMVPGNREKVISFATSIDKSTSTYRSVLTFQLSPLWSHHLYHARLWLHVPPSFPATLYLRIFGCGTTRCR-GSR  155
NP_001192771.1  77   RRLQRGRVVPANGEQVISFAVLTDSSTATCSSTLTFHLSTPRSHHLYHARLWLQVLPTLPGPLSLRIFRWGGRRRGRGSR  156
XP_003126368.2  77   RRLQRGSVGPAHGEEVISFAAITDSSTSTCGSTLTFHLSTPRSHHLYHARLWVHALPTLPGTLSLRIFRRGPRRRRRGSR  156
XP_005625596.1  77   RRLQPRSMPIADGDEVISFATVAD-STSACSSVLTFDLSTAQPHQLSRARLWLHARPAPPGSLYLRVFGRRPGGGQRGAR  155
XP_001488840.1  77   RRLQPGSAAPANGEEVISFATITDSSTSTCSSVLTFHLSAPRSHHLEHARLWLHALPTLPGALYLRIFQCGPRRRRQGSR  156
XP_004006593.1  77   RRLQRGRVAPANGEQVISFAVLTDSSTATCSSTLTFHLSTPRSHHLYHARLWLHVLPTLPGPLSLRIFRWGGRRRGRGSR  156
XP_509161.2     77   RRLQPGSVAPGNGEEVISFATVTD-STSAYSSLLTFHLSTPRSHHLYHARLWLHVLPTLPGTLCLRIFRWGPRRRRQGSR  155
XP_001115958.2  77   RRLQPGSVAPGNGEEVISFATVTD-STSAYSSLLTFHLSTPRFHHLYHARLWLHMLPTLPGTLCLRIFRWGPRRRHQRSR  155
XP_003988987.1  77   RRLQPGSVAPVNGEEVISFATITEPSTSACSSVLTFHLSTAQSRHLYHARLWLRVLPTFPGTLSLRTFRWNPGRRRRESR  156
XP_005680344.1  109  RRLQRGRAAPANGEQVISFAVLTDSSTATCSSTLTFHLSTPRSHHLYHARLWLHVLPTLPGPLSLRIFRWGGRRRGRGSR  188
XP_004053483.1  77   RRLQPGSVAPGNGEEVISFATVTD-STSVHSSLLTFHLSTPRSHHLYHARLWLHVLPTLPGTLCLRIFRWGPRRRRQGSR  155
XP_002823469.1  77   RRLQPGSVAPGNGEEVISFATVTD-STSAYSSLLTFHLSTPRSHHLYHARLWLHVLPTLPGTLCLRIFRWGPRRRRPGSR  155
XP_032029168.1  77   RRLQPGSVASGNGEEVISFATVTD-STSAYSSLLTFHLSTPRSHHLYHARLWLHVLPTLPGTLCLRIFRWGPRRRRQGSR  155

NP_113667.1     156  TLLAEHHITNLGWHTLTLPSSGLRGEKSGVLKLQLDCRPLEG-NSTVTGQ-PRRLLDTAGHQQPFLELKIRANEPGAGRA  233
NP_032408.2     156  TFLAEHQTTSSGWHALTLPSSGLRSEDSGVVKLQLEFRPLDL-NSTAAGL-PRLLLDTAGQQRPFLELKIRANEPGAGRA  233
NP_114003.2     156  TFLADYQTTSSGWHALTLPSSGLRSEESGVTKLQLEFRPLDL-NSTTARL-PRLLLDTAGQQRPFLELKIRANEPGAGRA  233
NP_001192771.1  157  VFLAEHQLTTPGWHALTLPSSGLKREESGVLKLRLDCSPLEG-NRTVTPQ----LLDTAGEQRPFLELKTRPKLPGAGRA  231
XP_003126368.2  157  VLLAEHQMTTPGWHALTLPSSGLRREESGVLKLQLDCRALEG-NGTAALQ-PCQLLDTAGEQRPFLELKTRPKEPGAGRA  234
XP_005625596.1  156  TLLAEQHLPAAGWHALALPSGGLRAEESAVLQLQLKCRLLPG-NRTSAQQlGRRLLDTAGDRRPFLQLQIWPREPGAGRA  234
XP_001488840.1  157  ALLAEHQMKTPGWHALTLPSSGLRGEESGVLKLQLDCRPLED-NSTAARQ-PRQLLDMVGDRRPFLELKIRPSEPGAGRA  234
XP_004006593.1  157  VFLAEHQLTTPGWHALTLPSSGLKREESGVLKLRLDCSSLEG-NRTVAPQ----LLDSAGEQRPFLELKTRPKWPGAARA  231
XP_509161.2     156  TLLAEHHITNLGWHALTLPSSGLRGEKSGVLKLQLDCRPLEG-NSTITGQ-PRRLLDTAGHQHPFLELKIRANEPGAGRA  233
XP_001115958.2  156  TLLAEHHITNLGWHALTLPSSGLRGEKSGVLKLQLDCRPLEGnNSTVTGQ-PRRLLDTAGHQQPFLELKIRANEPGAGRA  234
XP_003988987.1  157  TLLAEHQMTTPGWHALTLPSSGLRGEASAVLKLQLDCRLPGG-NATAA---PQWLVDTAGDERPFLELKIWPKGPGAGRT  232
XP_005680344.1  189  VFLAEHQLTTPGWHALTLPSSGLKREESGVLKLRLDCSSLEG-NRTVAPQ----LLDSAGEQRPFLELKTRPKWPGAARA  263
XP_004053483.1  156  TLLAEHHITNLGWHALTLPSSGLRAEKSGVLKLQLDCRPLEG-NSTVTGQ-PRQLLDTAGHQQPFLELKIQANEPGAGRA  233
XP_002823469.1  156  TLLAEHHITNLGWHALTLPSSGLRGEKSGVLKLQLDCRPLEG-NSTVTGQ-PRRLVDTAGHQQPFLELKIRANEPGAGRA  233
XP_032029168.1  156  TLLAEHHITNLGWHALTLPSSGLRGEKSGVLKLQLDCRPLEG-NSTVTGQ-PRRLLDTAGHQQPFLELKIRANEPGAGRA  233

NP_113667.1     234  RRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPASTS  313
NP_032408.2     234  RRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPAGSS  313
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NP_114003.2     234  RRRTPTCESETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPAGSS  313
NP_001192771.1  232  RRRTPSCEPATPLCCRRDHYVDFQELGWRDWILQPEGYRLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPLGTS  311
XP_003126368.2  235  RRRTPTCEPETPXCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVLSLLKANNPWPLGTS  314
XP_005625596.1  235  RRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPLGTS  314
XP_001488840.1  235  RRRTPTCEPETPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPLGNS  314
XP_004006593.1  232  RRRTPSCEPATPLCCRRDHYVDFQELGWRDWILQPEGYRLNFCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPLGTS  311
XP_509161.2     234  RRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPASTS  313
XP_001115958.2  235  RRRTPTCEPATPLCCRRDHYVDFQELGWQDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPASTS  314
XP_003988987.1  233  RRRTPTCEPETPLCCRRDHYVDFRELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPLGTS  312
XP_005680344.1  264  RRRTPSCEPATPLCCRRDHYVDFQELGWRDWILQPEGYRLNFCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPLGTS  343
XP_004053483.1  234  RRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPASTS  313
XP_002823469.1  234  RRRTPTCEPATPLCCRRDHYVDFQELGWRDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPASTS  313
XP_032029168.1  234  RRRTPTCEPATPLCCRRDRYVDFQELGWQDWILQPEGYQLNYCSGQCPPHLAGSPGIAASFHSAVFSLLKANNPWPASTS  313


NP_113667.1     314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
NP_032408.2     314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
NP_114003.2     314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
NP_001192771.1  312  CCVPTARRPLSLLYLDRDGNVVKTDVPDMVVEACGCS  348
XP_003126368.2  315  CCVPTARRSLSLLYLDRDGNVVKTDVPDMVVEACGCS  351
XP_005625596.1  315  CCVPTARRPLSLLYLDRDGNVVKTDVPDMVVEACGCS  351
XP_001488840.1  315  CCVPTARRPLSLLYLDRDGNVVKTDVPDMVVEACGCS  351
XP_004006593.1  312  CCVPTARRPLSLLYLDRDGNVVKTDVPDMVVEACGCS  348
XP_509161.2     314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
XP_001115958.2  315  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  351
XP_003988987.1  313  CCVPTARRPLSLLYLDRDGNVVKTDVPDMVVEACGCS  349
XP_005680344.1  344  CCVPTARRPLSLLYLDRDGNVVKTDVPDMVVEACGCS  380
XP_004053483.1  314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
XP_002823469.1  314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
XP_032029168.1  314  CCVPTARRPLSLLYLDHNGNVVKTDVPDMVVEACGCS  350
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TGFB1

NP_000651.3 transforming growth factor beta-1 proprotein preproprotein [Homo sapiens]
NP_035707.1 transforming growth factor beta-1 proprotein preproprotein [Mus musculus]
NP_067589.1 transforming growth factor beta-1 proprotein precursor [Rattus norvegicus]
NP_001159540.1 transforming growth factor beta-1 proprotein precursor [Bos taurus]
XP_020949162.1 transforming growth factor beta-1 isoform X1 [Sus scrofa]
XP_038300925.1 transforming growth factor beta-1 proprotein isoform X1 [Canis lupus familiaris]
XP_005596143.1 transforming growth factor beta-1 isoform X1 [Equus caballus]
XP_027833173.1 transforming growth factor beta-1 proprotein isoform X3 [Ovis aries]
XP_009433930.1 transforming growth factor beta-1 isoform X2 [Pan troglodytes]
XP_028695614.1 transforming growth factor beta-1 proprotein isoform X1 [Macaca mulatta]
XP_006941294.1 transforming growth factor beta-1 proprotein isoform X1 [Felis catus]
XP_017917139.1 PREDICTED: transforming growth factor beta-1 isoform X1 [Capra hircus]
XP_018870688.1 transforming growth factor beta-1 proprotein isoform X1 [Gorilla gorilla gorilla]
XP_009230906.2 transforming growth factor beta-1 [Pongo abelii]
XP_032028718.1 transforming growth factor beta-1 proprotein [Hylobates moloch]

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NP_000651.3     1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
NP_035707.1     1    MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
NP_067589.1     1    MPPSGLRLLPLLLPLPWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
NP_001159540.1  1    MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAILAL  80
XP_020949162.1  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAVLAL  80
XP_038300925.1  1    MPPSGLRLLPLLLPLLRLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_005596143.1  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_027833173.1  1    MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAILAL  80
XP_009433930.1  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_028695614.1  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_006941294.1  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_017917139.1  1    MPPSGLRLLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGPLPEAILAL  80
XP_018870688.1  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_009230906.2  1    MPPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80
XP_032028718.1  1    MPPSGLRLLPLLLPLLWLLVLTLGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGPLPEAVLAL  80

NP_000651.3     81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
NP_035707.1     81   YNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYEKTKDISHSIYMFFNTSDIREAVPEPPLLSRAELRLQRL  160
NP_067589.1     81   YNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYDKTKDITHSIYMFFNTSDIREAVPEPPLLSRAELRLQRF  160
NP_001159540.1  81   YNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLLRL  160
XP_020949162.1  81   YNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL  160
XP_038300925.1  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKIYEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRL  160
XP_005596143.1  81   YNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEIYKTVETGSHSIYMFFNTSELRAAVPDPMLLSRAELRLLRL  160
XP_027833173.1  81   YNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
XP_009433930.1  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
XP_028695614.1  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
XP_006941294.1  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVENTNKIYEKVQRTPHSIYMLFNTSELREAVPEPVLLSRAELRLLRL  160
XP_017917139.1  81   YNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
XP_018870688.1  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
XP_009230906.2  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160
XP_032028718.1  81   YNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL  160

NP_000651.3     161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDIN-GF  239
NP_035707.1     161  KSSVEQHVELYQKYSNNSWRYLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEIN-GI  239
NP_067589.1     161  KSTVEQHVELYQKYSNNSWRYLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEIN-GI  239
NP_001159540.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREEIEGFRLSAHCSCDSKDNTLQVDIN-GF  239
XP_020949162.1  161  KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINAGF  240
XP_038300925.1  161  KLKAEQHVELYQKYSNDSWRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINAGF  240
XP_005596143.1  161  KLSVEQHVELYQKYSNNSWRYLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGFRLSAHCSCDSKDNTLRVGINVGF  240
XP_027833173.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREEIEGFRLSAHCSCDSKDNTLQVDINAGF  240
XP_009433930.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINAGF  240
XP_028695614.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINAGF  240
XP_006941294.1  161  KLKAEQHVELYQKYSNNSWRYLSNRLLAPSDTPEWLSFDVTGVVRQWLSHGGEVEGFRLSAHCSCDSKDNTLQVDINAGF  240
XP_017917139.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTHREEIEGFRLSAHCSCDSKDNTLQVDINAGF  240
XP_018870688.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINAGF  240
XP_009230906.2  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDIN-GF  239
XP_032028718.1  161  KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSHGGEIEGFRLSAHCSCDSKDNTLQVDIN-GF  239

NP_000651.3     240  TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  319
NP_035707.1     240  SPKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  319
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NP_067589.1      240  SPKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  319
NP_001159540.1   240  SSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  319
XP_020949162.1   241  NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_038300925.1   241  SSSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRQRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_005596143.1   241  SSSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_027833173.1   241  SSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_009433930.1   241  TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_028695614.1   241  TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_006941294.1   241  SSSRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_017917139.1   241  SSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_018870688.1   241  TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  320
XP_009230906.2   240  TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  319
XP_032028718.1   240  TTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHA  319

NP_000651.3      320  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  390
NP_035707.1      320  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  390
NP_067589.1      320  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  390
NP_001159540.1   320  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  390
XP_020949162.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_038300925.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_005596143.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_027833173.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_009433930.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_028695614.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_006941294.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_017917139.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_018870688.1   321  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  391
XP_009230906.2   320  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  390
XP_032028718.1   320  NFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS  390
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TGFB2

NP_003229.1 transforming growth factor beta-2 proprotein isoform 2 preproprotein [Homo sapiens]
NP_033393.2 transforming growth factor beta-2 proprotein isoform 1 preproprotein [Mus musculus]
NP_112393.2 transforming growth factor beta-2 proprotein precursor [Rattus norvegicus]
XP_005216841.1 transforming growth factor beta-2 isoform X1 [Bos taurus]
XP_020919952.1 transforming growth factor beta-2 isoform X1 [Sus scrofa]
XP_545713.2 transforming growth factor beta-2 proprotein isoform X1 [Canis lupus familiaris]
XP_014970470.1 transforming growth factor beta-2 proprotein isoform X1 [Macaca mulatta]
XP_001172158.1 transforming growth factor beta-2 isoform X1 [Pan troglodytes]
XP_004013651.1 transforming growth factor beta-2 proprotein isoform X1 [Ovis aries]
XP_003364612.1 transforming growth factor beta-2 isoform X1 [Equus caballus]
XP_003999556.1 transforming growth factor beta-2 proprotein isoform X1 [Felis catus]
XP_017915648.1 PREDICTED: transforming growth factor beta-2 isoform X1 [Capra hircus]
XP_004028464.2 transforming growth factor beta-2 proprotein isoform X1 [Gorilla gorilla gorilla]
XP_002809490.1 transforming growth factor beta-2 isoform X1 [Pongo abelii]
XP_031992675.1 transforming growth factor beta-2 proprotein isoform X2 [Hylobates moloch]

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NP_003229.1     1    MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
NP_033393.2     1    MHYCVLSTFLLLHLVPVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPDEVPPEVISIYNSTRDLLQE  80
NP_112393.2     1    MHYCVLRTFLLLHLVPVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPDEVPPEVISIYNSTRDLLQE  80
XP_005216841.1  1    MHYCVLSAFLLLHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_020919952.1  1    MHYCVLSAFLLLHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_545713.2     1    MHYCVLSAFLILHLVTAALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_014970470.1  1    MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_001172158.1  1    MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_004013651.1  1    MHYCVLSAFLLLHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_003364612.1  1    MHYCVLSAFLLLHLVAVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_003999556.1  1    MHYCVLSAFLLLHLVTAALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_017915648.1  1    MHYCVLSAFLLLHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_004028464.2  1    MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_002809490.1  1    MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLNSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80
XP_031992675.1  1    MHYCVLSAFLILHLVTVALSLSTCSTLDMDQFMRKRIEAIRGQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE  80

NP_003229.1     81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSE----------------------------NAIPPTFYRPYFRIVRF  132
NP_033393.2     81   KASRRAAACERERSDEEYYAKEVYKIDMPSHLPSE----------------------------NAIPPTFYRPYFRIVRF  132
NP_112393.2     81   KASRRAAACERERSDEEYYAKEVYKIDMPSHFPSETVCPVVTTSSGSVGSFCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_005216841.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVFCGYLDAIPPTFYRPYFRIVRF  160
XP_020919952.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_545713.2     81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSFCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_014970470.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_001172158.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_004013651.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVFCGYLDAIPPTFYRPYFRIVRF  160
XP_003364612.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_003999556.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRHSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_017915648.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVFCGYLDAIPPTFYRPYFRIVRF  160
XP_004028464.2  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_002809490.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160
XP_031992675.1  81   KASRRAAACERERSDEEYYAKEVYKIDMPPFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPYFRIVRF  160

NP_003229.1     133  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  212
NP_033393.2     133  DVSTMEKNASNLVKAEFRVFRLQNPKARVAEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVQEWLH  212
NP_112393.2     161  DVSTMEKNASNLVKAEFRVFRLQNPKARVAEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_005216841.1  161  DVSSMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_020919952.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVAEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_545713.2     161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_014970470.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_001172158.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_004013651.1  161  DVSSMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_003364612.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_003999556.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_017915648.1  161  DVSSMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_004028464.2  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_002809490.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240
XP_031992675.1  161  DVSAMEKNASNLVKAEFRVFRLQNPKARVPEQRIELYQILKSKDLTSPTQRYIDSKVVKTRAEGEWLSFDVTDAVHEWLH  240

NP_003229.1     213  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  292
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NP_033393.2     213  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHLLLMLLPSYRLE  292
NP_112393.2     241  HKDRNLGFKISLHCPCCTFIPSNNYIIPNKSQELEARFAGIDGTSTYASGDQKTIKSTRKKSSGKTPHLLLMLLPSYRLE  320
XP_005216841.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKSPHLLLMLLPSYRLE  320
XP_020919952.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_545713.2     241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_014970470.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_001172158.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_004013651.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKSPHLLLMLLPSYRLE  320
XP_003364612.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_003999556.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_017915648.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKSPHLLLMLLPSYRLE  320
XP_004028464.2  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_002809490.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320
XP_031992675.1  241  HKDRNLGFKISLHCPCCTFVPSNNYIIPNKSEELEARFAGIDGTSTYTSGDQKTIKSTRKKNSGKTPHLLLMLLPSYRLE  320

NP_003229.1     293  SQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  372
NP_033393.2     293  SQQSSRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHTKVLSLYNTINP  372
NP_112393.2     321  SQQSSRRRKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHTKVLSLYNTINP  400
XP_005216841.1  321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_020919952.1  321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_545713.2     321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_014970470.1  321  SQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_001172158.1  321  SQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_004013651.1  321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_003364612.1  321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_003999556.1  321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_017915648.1  321  SQQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSADTQHSRVLSLYNTINP  400
XP_004028464.2  321  SQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_002809490.1  321  SQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400
XP_031992675.1  321  SQQTNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINP  400

NP_003229.1     373  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  414
NP_033393.2     373  EASASPCCVSQDLEPLTILYYIGNTPKIEQLSNMIVKSCKCS  414
NP_112393.2     401  EASASPCCVSQDLEPLTILYYIGNTPKIEQLSNMIVKSCKCS  442
XP_005216841.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_020919952.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_545713.2     401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_014970470.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_001172158.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_004013651.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_003364612.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_003999556.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_017915648.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_004028464.2  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_002809490.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
XP_031992675.1  401  EASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS  442
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TGFB3

NP_003230.1 transforming growth factor beta-3 proprotein isoform 1 preproprotein [Homo sapiens]
NP_033394.2 transforming growth factor beta-3 proprotein precursor [Mus musculus]
NP_037306.1 transforming growth factor beta-3 proprotein preproprotein [Rattus norvegicus]
NP_001094653.1 transforming growth factor beta-3 proprotein [Bos taurus]
XP_005666412.1 transforming growth factor beta-3 isoform X1 [Sus scrofa]
XP_854119.2 transforming growth factor beta-3 proprotein [Canis lupus familiaris]
XP_001492737.1 transforming growth factor beta-3 [Equus caballus]
XP_004010851.1 transforming growth factor beta-3 proprotein [Ovis aries]
XP_001161669.1 transforming growth factor beta-3 isoform X1 [Pan troglodytes]
NP_001244404.1 transforming growth factor beta-3 proprotein precursor [Macaca mulatta]
XP_003987900.1 transforming growth factor beta-3 proprotein [Felis catus]
XP_005686198.1 PREDICTED: transforming growth factor beta-3 [Capra hircus]
XP_004055526.1 transforming growth factor beta-3 proprotein [Gorilla gorilla gorilla]
XP_002825003.1 transforming growth factor beta-3 [Pongo abelii]
XP_031990693.1 transforming growth factor beta-3 proprotein [Hylobates moloch]

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NP_003230.1     1        MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLALYNST  76
NP_033394.2     1        MKMHLQRALVVLALLNLATISLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLALYNST  76
NP_037306.1     1        MKMHLQRALVVLALLNLATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLALYNST  76
NP_001094653.1  1    [42]LKMHLQRALVVLALLNFATVSLSMSTCTTLDFNHIKRKRVEAIRGQILSKLRLTSPPDPSGLASVPIQVLDLYNST  118
XP_005666412.1  1    [45]MKMHLQRALVVLALLNFATVSLSMSTCTTLDFDHIKRKRVEAIRGQILSKLRLTSPPDPSMLANIPTQVLDLYNST  121
XP_854119.2     1    [45]MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLALYNST  121
XP_001492737.1  1        MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLALYNST  76
XP_004010851.1  1    [42]LKMHLQRALVVLALLNFATVSLSMSTCTTLDFNHIKRKRVEAIRGQILSKLRLTSPPDPSGLASIPIQVLDLYNST  118
XP_001161669.1  1        MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLALYNST  76
NP_001244404.1  1        MKMHLQRALVVLALLNFASVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLALYNST  76
XP_003987900.1  1        MKMHLHRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLALYNST  76
XP_005686198.1  1    [42]LKMHLQRALVVLALLNFATVSLSMSTCTTLDFNHIKRKRVEAIRGQILSKLRLTSPPDPSGLASIPIQVLDLYNST  118
XP_004055526.1  1        MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLALYNST  76
XP_002825003.1  1        MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLALYNST  76
XP_031990693.1  1        MKMHLQRALVVLALLNFATVSLSLSTCTTLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLALYNST  76

NP_003230.1     77   RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRV  156
NP_033394.2     77   RELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNGTNLFRAEFRVLRV  156
NP_037306.1     77   RELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNGTNLFRAEFRVLRV  156
NP_001094653.1  119  RELLEEVHGERGDVCTQANTESEYYAKEIYKFDMIQGLEEHNDLTVCPKGITSKIFRFNVSSVEKNETNLFRAEFRVFRM  198
XP_005666412.1  122  RELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKGITSKIFRFNVSSVEKNETNLFRAEFRVLRM  201
XP_854119.2     122  RELLEEMQGEREDSCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNGTNLFRAEFRVLRV  201
XP_001492737.1  77   RELLEEMHGEREDGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNGTNLFRAEFRVLRV  156
XP_004010851.1  119  RELLEEVHGERGDVCTQANTESEYYAKEIYKFDMIQGLEEHNDLTVCPKGITSKIFRFNVSSVEKNETNLFRAEFRVFRM  198
XP_001161669.1  77   RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRV  156
NP_001244404.1  77   RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRV  156
XP_003987900.1  77   RELLEEMQGEREDSCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNGTNLFRAEFRVLRV  156
XP_005686198.1  119  RELLEEVHGERGDVCTQANTESEYYAKEIYKFDMIQGLEEHNDLTVCPKGITSKIFRFNVSSVEKNETNLFRAEFRVFRM  198
XP_004055526.1  77   RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRV  156
XP_002825003.1  77   RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRV  156
XP_031990693.1  77   RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSVEKNRTNLFRAEFRVLRV  156

NP_003230.1     157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
NP_033394.2     157  PNPSSKRTEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
NP_037306.1     157  PNPSSKRTEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
NP_001094653.1  199  PNPASKRSEQRIELFQILQPGEHIAKQRYIDGKNLPTRGTGEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  278
XP_005666412.1  202  PNPSSKRSEQRIELFQILQPDEHIAKQRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  281
XP_854119.2     202  PNPSSKRSEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  281
XP_001492737.1  157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
XP_004010851.1  199  PNPASKRSEQRIELFQILQPGEHIAKQRYIDGKNLPTRGTGEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  278
XP_001161669.1  157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
NP_001244404.1  157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
XP_003987900.1  157  PNPSSKRSEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
XP_005686198.1  199  PNPASKRSEQRIELFQILQPGEHIAKQRYIDGKNLPTRGTGEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  278
XP_004055526.1  157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
XP_002825003.1  157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236
XP_031990693.1  157  PNPSSKRNEQRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG  236

NP_003230.1     237  DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
NP_033394.2     237  DILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGSQRKKRALDTNYCFRNLEENCC  316
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NP_037306.1      237  DILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDSPGQGGQRKKRALDTNYCFRNLEENCC  316
NP_001094653.1   279  DILENIQELMEIKFKGVDSDDDPGRGDLGRLKKKKE-HIPHLILMMIPPNRLDSPG-HSQRKKRALDTNYCFRNLEENCC  356
XP_005666412.1   282  DILENIQEVMEIKFKGVDSEDDPGRGDLGRLKKKKE-HSPHLILMMIPPDRLDNPGLGAQRKKRALDTNYCFRNLEENCC  360
XP_854119.2      282  DILENIHEVMEIKFKGVDSEEDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  361
XP_001492737.1   237  DILENIHEVMEIKFKGVDSEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
XP_004010851.1   279  DILENIQELMEIKFKGVDSDDDPGRGDLGRLKKKKE-HIPHLILMMIPPNRLDSPG-HSQRKKRALDTNYCFRNLEENCC  356
XP_001161669.1   237  DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
NP_001244404.1   237  DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
XP_003987900.1   237  DILENIHEVMEIKFKGVDSEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
XP_005686198.1   279  DILENIQELMEIKFKGVDSDDDPGRGDLGRLKKKKE-HIPHLILMMIPPNRLDSPG-HSQRKKRALDTNYCFRNLEENCC  356
XP_004055526.1   237  DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
XP_002825003.1   237  DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316
XP_031990693.1   237  DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPPHRLDNPGQGGQRKKRALDTNYCFRNLEENCC  316

NP_003230.1      317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
NP_033394.2      317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
NP_037306.1      317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSSDTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
NP_001094653.1   357  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSSDTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  436
XP_005666412.1   361  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTA  440
XP_854119.2      362  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  441
XP_001492737.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
XP_004010851.1   357  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSSDTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  436
XP_001161669.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
NP_001244404.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
XP_003987900.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
XP_005686198.1   357  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSSDTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  436
XP_004055526.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
XP_002825003.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396
XP_031990693.1   317  VRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTP  396

NP_003230.1      397  KVEQLSNMVVKSCKCS  412
NP_033394.2      397  KVEQLSNMVVKSCKCS  412
NP_037306.1      397  KVEQLSNMVVKSCKCS  412
NP_001094653.1   437  KVEQLSNMVVKSCKCS  452
XP_005666412.1   441  KVEQLSNMVVKSCKCS  456
XP_854119.2      442  KVEQLSNMVVKSCKCS  457
XP_001492737.1   397  KVEQLSNMVVKSCKCS  412
XP_004010851.1   437  KVEQLSNMVVKSCKCS  452
XP_001161669.1   397  KVEQLSNMVVKSCKCS  412
NP_001244404.1   397  KVEQLSNMVVKSCKCS  412
XP_003987900.1   397  KVEQLSNMVVKSCKCS  412
XP_005686198.1   437  KVEQLSNMVVKSCKCS  452
XP_004055526.1   397  KVEQLSNMVVKSCKCS  412
XP_002825003.1   397  KVEQLSNMVVKSCKCS  412
XP_031990693.1   397  KVEQLSNMVVKSCKCS  412
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BMP8A/B

NP_861525.2 bone morphogenetic protein 8A preproprotein [Homo sapiens]
NP_001711.2 bone morphogenetic protein 8B preproprotein [Homo sapiens]
NP_031584.1 bone morphogenetic protein 8A isoform 2 preproprotein [Mus musculus]
NP_031585.2 bone morphogenetic protein 8B preproprotein [Mus musculus]
NP_001102902.1 bone morphogenetic protein 8A precursor [Rattus norvegicus]
XP_002729572.1 bone morphogenetic protein 8B isoform X1 [Rattus norvegicus]
XP_024845991.1 bone morphogenetic protein 8A [Bos taurus]
XP_020953264.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8A [Sus scrofa]
XP_003356374.4 LOW QUALITY PROTEIN: bone morphogenetic protein 8B [Sus scrofa]
XP_038477617.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8B isoform X1 [Canis lupus familiaris]
XP_038543221.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8B isoform X1 [Canis lupus familiaris]
XP_023488611.1 bone morphogenetic protein 8B [Equus caballus]
XP_023483599.1 bone morphogenetic protein 8B [Equus caballus]
XP_014947141.3 bone morphogenetic protein 8B [Ovis aries]
XP_027824135.1 bone morphogenetic protein 8B [Ovis aries]
XP_024213824.1 bone morphogenetic protein 8A [Pan troglodytes]
XP_016815266.2 bone morphogenetic protein 8B [Pan troglodytes]
XP_028691411.1 bone morphogenetic protein 8B isoform X2 [Macaca mulatta]
XP_028691408.1 bone morphogenetic protein 8B isoform X1 [Macaca mulatta]
XP_014991435.2 bone morphogenetic protein 8B [Macaca mulatta]
XP_023113593.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8A [Felis catus]
XP_017897638.1 PREDICTED: bone morphogenetic protein 8A [Capra hircus]
XP_017897686.1 PREDICTED: bone morphogenetic protein 8B [Capra hircus]
XP_004025569.3 bone morphogenetic protein 8A [Gorilla gorilla gorilla]
XP_030864436.1 bone morphogenetic protein 8B [Gorilla gorilla gorilla]
XP_024103873.1 bone morphogenetic protein 8B-like [Pongo abelii]
XP_009250410.2 bone morphogenetic protein 8B [Pongo abelii]
XP_032016255.1 bone morphogenetic protein 8A [Hylobates moloch]

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NP_861525.2     1   MA    AR    PGPLWLLGLT    LCALGGGG-PGLRPPPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62
NP_001711.2     1   MT    AL    PGPLWLLGLA    LCALGGGG-PGLRPPPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62
NP_031584.1     1   MA    MR    PGPLWLLGLA    LCALGGGH--GPRPPHTCPQRRLGARERRDMQREILAVLGLPGRPRPR      A  61
NP_031585.2     1   MA    AR    PGLLWLLGLA    LCVLGGGH--LSHPPHVFPQRRLGVREPRDMQREIREVLGLPGRPRSR      A  61
NP_001102902.1  1   MA    VR    PGPLWLLGLA    LCALGGGH--GPRPPHTCPQRRLGARERRDMQREILAVLGLPGRPRPR      A  61
XP_002729572.1  1   MA    AG    PGLLWLLGLA    LCVLGSSH--LPRSPHVFPQHRLGVREPRDMQREIREVLGLPGRPRSR      A  61
XP_024845991.1  1   MA    AR    PGPLWLLGLA    LCALSGGGvPGPRPPLGCPQRRLGPRERRDLQREILAVLGLPGRPRPR      A  63
XP_020953264.1  1   MA    TC    PAAVRLAT--    --------------PPGCPQSRLGPRERRDLQREILAVLGLPGRPXPR      A  47
XP_003356374.4  1   MA    AR    PGTLWLLGLV    LCTLSGCG-PGPRPPPGCPQSRLGPRERRDLQREILAVLGLPGRPRPR      A  62
XP_038477617.1  1   MA    AR    PGPLWLVGLA    LCALSGGG-PGPRPPAGCPARRLGPRERRDMQREILAVLGLPGRPRPR      A  62
XP_038543221.1  1   MA[14]AR[27]PGPLWLVGLA    LCALSGGG-PGPRPRPGRPPPWAAARERRDMQREILAVLGLPGRPRPR      A  103
XP_023488611.1  1   MA    AR    PSPLWLLGLA    LCALGGGG-PGPRPPPGCPPRRLGPRERRDLQREILAVLGLPGRPRPR      T  62
XP_023483599.1  1   MA    AR    PSPLWLLGLA    LCALGGGG-PGPRPPPGCPPRRLGPRERRDLQREILEVLGLPGRPRPR      T  62
XP_014947141.3  1   MA    AR    PGPLWLLGLA    LCALSGGGvPGPRPPLGCPQRRLGPRERRDLQREILAVLGLPGRPRPR      A  63
XP_027824135.1  1   MA    AR    PGPLWLLGLA    LCALSGGGvPGPRPPLGCPQRRLGPRERRDLQREILAVLGLPGRPRPR      A  63
XP_024213824.1  1   MA    AR    PGPLWLLGLT    LCALGGGG-PGLRPQPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62
XP_016815266.2  1   MT    AL    PGPLWLLGLA    LCALGGGG-PGLRPPPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62
XP_028691411.1  1   MA    AL    PGPLWLLGLA    LCALGGGS-PGLRPQPGCPQRRLGARERRDVQREILAVLGLPGRPRLR      A  62
XP_028691408.1  1   MA[ 8]AQ[27]PSVMSVLSLS[31]LCLISGSQ---DQPDREGAQWEFGVWSLGSVEHQPGAGLRLSLAAGPL      S  126
XP_014991435.2  1   MA    AL    PGPLWLLGLA    LCALGGGG-PGLRPPPGCPQRRLGERERRDVQREILSVLGLPGRPRPR      V  62
XP_023113593.1  1   MA    AR    PGSLWLVGLA    LCALSGGG-PGPRAPAGCPARRLGPRERRDMQREILAVLGLPGRPRPR[352]A  414
XP_017897638.1  1   MA    AR    PGPLWLLGLA    LCALSGGGvPGPRPQLGCPQRRLGPRERRDLQREILAVLGLPGRPRPR      A  63
XP_017897686.1  1   MA    AR    PGPLWLLGLA    LCALSGGGvPGPRPPLGCPQRRLGPRERRDLQREILAVLGLPGRPRPR      A  63
XP_004025569.3  1   MA    AR    PGPLWLLGLT    LCALGGGG-PGLRPQPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      P  62
XP_030864436.1  1   MT    AL    PGPLWLLGLA    LCALGGGG-PVLRPPPGCPQRRLGARERRDVQHEILAVLGLPGRPRPR      A  62
XP_024103873.1  1   MA    AL    PGPLWLLGLA    LCALGGGG-PGPRPQPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62
XP_009250410.2  1   MA    AL    PGPLWLLGLA    LCALGGGG-PGLRPLPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62
XP_032016255.1  1   MA    AL    PGPLWLLGLA    LCALGGGG-PGPRPQPGCPQRRLGARERRDVQREILAVLGLPGRPRPR      A  62

NP_861525.2     63  P   PAASRL    PASAPLFMLDLYHAMAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
NP_001711.2     63  P   PAASRL    PASAPLFMLDLYHAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
NP_031584.1     62  Q   PAAARQ    PASAPLFMLDLYHAMT--DDDDGGPPQ--AHLGRADLVMSFVNMVERDRTLGYQEPHWKEFHFDLTQ  131
NP_031585.2     62  P[1]-GAAQQ    PASAPLFMLDLYRAMT--DDSGGGTPQp--HLDRADLIMSFVNIVERDRTLGYQEPHWKEFHFDLTQ  131
NP_001102902.1  62  P   PAAARQ    PASAPLFMLDLYHAMT--DDDDGGPPQ--AHLGRADLVMSFVNMVERDRTLGYQEPHWKEFHFDLTQ  131
XP_002729572.1  62  P[1]-ATAQQ    PASAPLFMLNLYHAMT--DDSGNGPPQp--HLHRADLIMSFVNIVEHDRTLGYQEPHWKEFHFDLTQ  131
XP_024845991.1  64  P   PAAALL    PASAPLFMLDLYRAVADDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFHFDLTQ  135
XP_020953264.1  48  P   PAGAGL    PASAPLFMLDLYRAMAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  119
XP_003356374.4  63  P   PAGAGL    PASAPLFMLDLYRAMAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFHFDLTQ  134
XP_038477617.1  63  P   PAAARL    PASAPLFMLGLYRAMARDDHEDGGPXA--RRPGRADLVMSFVNVVERDRTLGHQEPHWKEFHFDLTQ  134
XP_038543221.1  104 P   PAAARL    PASAPLFMLGLYRAMSSD--EQGCPPC--LCGGRATMVCS-ISLVERDRTLGHQEPHWKEFHFDLTQ  172
XP_023488611.1  63  P   PAAARP    PASAPLFMLDLYHAMAGDDAEDGGPPE--RRLGHADLVMSFVNMVELDRTLGHQEPHWKEFRFDLTQ  134
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XP_023483599.1  63   P    PAAARP    PASAPLFMLDLYHAMAGDDAEDGGPPE--RRLGHADLVMSFVNMGERGPGGRRGPAVTPDLRLARVR  134
XP_014947141.3  64   P    PAAALL    PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERHPALGHQEPHWKEFHFDLTQ  135
XP_027824135.1  64   P    PAAALL    PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFHFDLTQ  135
XP_024213824.1  63   P    PAASRL    PASAPLFMLDLYHAMAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
XP_016815266.2  63   P    PAASRL    PASAPLFMLDLYHAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
XP_028691411.1  63   P    PAASRL    PASAPLFMLDLYHAMADDDDEDGAPAE--RRLGRADLIMSFVNMVERDHALGHREPHWKEFRFDLTQ  134
XP_028691408.1  127  P[5]PSLEQT[7]PARPPWVPSTLSGGWLGAVAHTSSAHSkvRAIPSASPALLCL-LVERDHALGHREPHWKEFRFDLTQ  211
XP_014991435.2  63   A    PAASQL    PASAPLFMLDLYHAMAGDDDKDDAPAE--RRLGRADLVMSFVNMVERDHALGHWEPHWKEFRFDLTQ  134
XP_023113593.1  415  P    SAAARL    PASAPLFMLDLYHAMARDDDEDGGPPE--RRPGRADLVMSFVNMVERDRTLGHQEPHWKEFRFDLTQ  486
XP_017897638.1  64   P    PAAALL    PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFHFDLTQ  135
XP_017897686.1  64   P    PAAALL    PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFHFDLTQ  135
XP_004025569.3  63   P    PAASRL    PASAPLFMLDLYHAMAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
XP_030864436.1  63   P    PAASRL    PASAPLFMLDLYHAVAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
XP_024103873.1  63   P    PVASRL    PASAPLFMLDLYHAMAGDDDDDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFCFDLTQ  134
XP_009250410.2  63   P    PAASRL    PASAPLFMLDLYHAMAGDDNEDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFRFDLTQ  134
XP_032016255.1  63   P    PAASRL    PASAPLFMLDLYHAMAGDDDEDGALAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFHFDLTQ  134

NP_861525.2     135  I    PAGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRH  211
NP_001711.2     135  I    PAGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRH  211
NP_031584.1     132  I    PAGEAVTAAEFRIYKEPSTHPLNTTLHISMFEVVQEHSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHH  208
NP_031585.2     132  I    PAGEAVTAAEFRIYKEPSTHPLNTTLHISMFEVVQEHSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHH  208
NP_001102902.1  132  I    PAGEAVTAAEFRIYKEPSTHPPNTTLHISMFEVVQERSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHN  208
XP_002729572.1  132  I    PAGEAVTAAEFRIYKEPSTHPPNTTLHISMFEVVQERSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHN  208
XP_024845991.1  136  I    PAGEAVTAAEFRIYKLPSTHPLNQTLHISMFEVVPEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLSRN  212
XP_020953264.1  120  I    PAGEAVTAAEFRIYKLPSTHPLNQTLHISMFEVVPEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRS  196
XP_003356374.4  135  I    PAGEAVTAAEFRIYKLPSTHQLNQTLHVSMFEVVPEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRS  211
XP_038477617.1  135  I    PEGEAVTAAEFQIYKLASTHLLNRTLHVSTFEVVREQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASGRWLLGRN  211
XP_038543221.1  173  I    PEGEAVTAAEFRIYKLASTHLLNRTLHVSTFEVVREQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASGRWLLGRN  249
XP_023488611.1  135  I    PAGEAVTAAEFRIYKLPSTHPLNRTLHVSMFEVVRERANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLNRN  211
XP_023483599.1  135  D[9]PGGGTRAAGELRPLKSSASMLLG------------PPRPRQRGPCCVHVQGHHP--------QVTALSP-------  193
XP_014947141.3  136  I    PAGEAVTAAEFRIYKLPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLQSGDEGWLVLDVTAASDRWLLNRN  212
XP_027824135.1  136  I    PAGEAVTAAEFRIYKLPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRN  212
XP_024213824.1  135  I    PAGEVVTAVEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRH  211
XP_016815266.2  135  I    PAGEVVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQSNRESDLFFLDLQTLRDGDEGWLVLDVTAASDCWLLKHH  211
XP_028691411.1  135  I    PDGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRH  211
XP_028691408.1  212  I    PDGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRH  288
XP_014991435.2  135  I    PDGEAVTAAEFRIYKVPSIHLLNRTLHVSMFQVVQEQANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRH  211
XP_023113593.1  487  I    PEGEMVTAAEFRIYKMASTHLLNGTLHVSMFEVVREQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLSRN  563
XP_017897638.1  136  I    PAREAVTAAEFRIYKLPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRN  212
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NP_861525.2     290  DDVRGSHGRQVCRRHELYVSFQDLGWLDWVIAPQGYSAYYCEGECSFPLDSCMNATNHAILQSLVHLMKPNAVPKACCAP  369
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NP_031584.1      287  DDGHGSRGREVCRRHELYVSFRDLGWLDWVIAPQGYSAYYCEGECAFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP  366
NP_031585.2      287  DDGHGSHGREVCRRHELYVSFRDLGWLDSVIAPQGYSAYYCAGECIYPLNSCMNSTNHATMQALVHLMKPDIIPKVCCVP  366
NP_001102902.1   287  DDGHGSRGREVCRRHELYVSFRDLGWLDWVIAPQGYSAYYCEGECAFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP  366
XP_002729572.1   287  DDGHGSLDREVCRRHELYVSFRDLGWLDSVIAPQGYSAYYCAGECIYPLNSCMNSTNHATMQALVHLMKPDIVPKVCCVP  366
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NODAL

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NP_038639.2 nodal preproprotein [Mus musculus]
NP_001099864.1 nodal homolog precursor [Rattus norvegicus]
NP_001192911.1 nodal homolog precursor [Bos taurus]
XP_004049593.2 nodal homolog isoform X1 [Gorilla gorilla gorilla]
XP_546146.2 nodal homolog isoform X1 [Canis lupus familiaris]
XP_001503787.1 nodal homolog [Equus caballus]
XP_004021483.4 nodal homolog [Ovis aries]
XP_521502.2 PREDICTED: nodal homolog isoform X1 [Pan troglodytes]
XP_001108137.1 PREDICTED: nodal homolog isoform 2 [Macaca mulatta]
XP_019668767.3 nodal homolog [Felis catus]
XP_005699204.2 PREDICTED: nodal homolog [Capra hircus]
XP_004049593.2 nodal homolog isoform X1 [Gorilla gorilla gorilla]
XP_002820901.1 nodal homolog isoform X1 [Pongo abelii]
XP_031995113.1 nodal homolog isoform X1 [Hylobates moloch]
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NP_001099864.1  1    MSVHCLPVLLLQTCWTLLHPRVATAAALPLWTRGQPSSPSPLAYMLSLYRDPLPRADIIRSLQAQDVDVTGQNWTFTFDF  80
NP_001192911.1  1    MHAQCLWLFLLHAWWALLQAGAAMVAPVPLRPWGQPSSPSPLAYMLSLYREPLPRADIIRSLQAQDMQVDGQNWTFAFDF  80
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XP_546146.2     1    MHAPRLPLFLLHACWALLQAGAATVAPVPLRARVQPSSPAPLAYMLSLYRDPLPRADIIRSLQAQDVEVDGHNWTFAFDF  80
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XP_004021483.4  1    MDAHRLWLFLLHAWWALLQAGAAMVAPVPLRPWGQPSSPSPLAYMLSLYREPLTRADIIRSLQAQDMQVDGQNWTFAFDF  80
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XP_004021483.4  159  SKWLKHPGGLRERMSSLAGECWRRTPTPP   VTDVLLLLYSNLSPEQRRLGGSTLLWEAESSWRAQEGQLSRE---RGT  232
XP_521502.2     160  SKWLKRPGALEKQMSRVAGECWPRPPTPP   ATNVLLMLYSNLSQEQRWLGGSTLLWEAESSWRAQEGQLSWE---WGK  233
XP_001108137.1  160  SKWLKHPGTLEKQMSRVAGECWQRPPTPP   ATDVLLMLYSNLSQEQRQLGGSTLLWEAESSWRAQEGQLSWE---WGK  233
XP_019668767.3  161  SKWLKHPGELAEQASSLARECPQRPPVPP   VASALLVLYSNLSPEQRRLGGSTLLWEAESSWRAREGQLSQE---RGR  234
XP_005699204.2  159  SKWLKHPGGLREQMSSLAGECWRQAPTPP   VTDVLLLLYSNLSPEQRRLGGSTLLWEAESSWRAQEGQLSRE---RGT  232
XP_004049593.2  160  SKWLKRPGALEKQMSRVAGECWPQPPTPP   ATNVLLMLYSNLSQEQRRLGGSTLLWEAESSWRAQEGQLSWE---WGK  233
XP_002820901.1  160  SKWLKRPGALEKQMSRVAGECWPRPTTPP   ATNVLLMLYSNLSQEQRRLGGSTLLWEAESSWRAQEGQLSWE---WGK  233
XP_031995113.1  160  SKWLKRPGALEKQMSRVAGECWLRPPTPP   ATNVLLMLYSNLSQEQRQLGGSTLLWEAESSWRAQEGQLSWE---WGK  233

NP_060525.3     234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313
NP_038639.2     241  RQRRHHLPDRSQLCRRVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  320
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NP_001099864.1  241  RQRRHHLPDRSQLCRRVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  320
NP_001192911.1  233  RHRRYHVQDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPATCC  312
XP_004049593.2  234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313
XP_546146.2     235  RHRRHHVPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  314
XP_001503787.1  235  RHRRHHLPDRSQLCRKVKFQVDFNVIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  314
XP_004021483.4  233  RHRRYHVQDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPATCC  312
XP_521502.2     234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313
XP_001108137.1  234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313
XP_019668767.3  235  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  314
XP_005699204.2  233  RHRRYHVQDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPATCC  312
XP_004049593.2  234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313
XP_002820901.1  234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313
XP_031995113.1  234  RHRRHHLPDRSQLCRKVKFQVDFNLIGWGSWIIYPKQYNAYRCEGECPNPVGEEFHPTNHAYIQSLLKRYQPHRVPSTCC  313


NP_060525.3     314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
NP_038639.2     321  APVKTKPLSMLYVDNGRVLLEHHKDMIVEECGCL  354
NP_001099864.1  321  APVKTKPLSMLYVDNGRVLLEHHKDMIVEECGCL  354
NP_001192911.1  313  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  346
XP_004049593.2  314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
XP_546146.2     315  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  348
XP_001503787.1  315  APVKTKPLSMLYVDNGRVLLDHHRDMIVEECGCL  348
XP_004021483.4  313  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  346
XP_521502.2     314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
XP_001108137.1  314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
XP_019668767.3  315  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  348
XP_005699204.2  313  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  346
XP_004049593.2  314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
XP_002820901.1  314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
XP_031995113.1  314  APVKTKPLSMLYVDNGRVLLDHHKDMIVEECGCL  347
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GDF10

NP_004953.1 growth/differentiation factor 10 preproprotein [Homo sapiens]
NP_665684.2 growth/differentiation factor 10 preproprotein [Mus musculus]
NP_077351.1 growth/differentiation factor 10 precursor [Rattus norvegicus]
NP_001069635.1 growth/differentiation factor 10 precursor [Bos taurus]
XP_003133153.1 growth/differentiation factor 10 [Sus scrofa]
XP_853904.2 growth/differentiation factor 10 [Canis lupus familiaris]
XP_001494823.3 growth/differentiation factor 10 [Equus caballus]
XP_004021600.2 growth/differentiation factor 10 [Ovis aries]
XP_001135281.2 growth/differentiation factor 10 [Pan troglodytes]
XP_015002444.2 growth/differentiation factor 10 [Macaca mulatta]
XP_003994192.2 growth/differentiation factor 10 isoform X2 [Felis catus]
XP_005699392.3 PREDICTED: growth/differentiation factor 10 isoform X1 [Capra hircus]
XP_004049420.1 growth/differentiation factor 10 [Gorilla gorilla gorilla]
XP_002820747.1 growth/differentiation factor 10 isoform X1 [Pongo abelii]
XP_032026867.1 growth/differentiation factor 10 [Hylobates moloch]

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NP_004953.1      1    MAHVPARTS--PGP   GPQLLLLLl-PLFLLLLRDVAGSHRAPAWSALPAAADGLQGDRDLQRHPGDAAATLGPSAQDM  74
NP_665684.2      1    MAPGPARIS--LGS   --QLLPMV--PLLLLL-RGAGCGHRGPSWSSLPSAAAGLQGDRDSQQSPGDAAAALGPGAQDM  70
NP_077351.1      1    MAPGLARIS--LRS   --QLLPLV--PLLLLL-RGAGCGHRVPSWSSLPSAADSVQRDRDLQQSPGDAAAALGPGAQDI  70
NP_001069635.1   1    MARGPARTS--LGP   GSQQLPLLslLLLLLL-RDADGSHTAAARPPPPAAADGLAGDKNPQRSPGDVAAAQSPGAQDM  74
XP_003133153.1   1    MALGPAWTR--PEP   GSL---LLllPLLLLL-RDAGGSHTAPAWSAAPMAADSLAGDKDPQRSPGDTAATVGPGAQDM  71
XP_853904.2      1    MGRCPARTSqtPGR[7]RPLLL-LL--PLLLLLLRGAGGDPPEPA---PPAPAARPAAARTPRGALGDAASALGLGARDA  78
XP_001494823.3   1    MARGPARTS--PGP   GPQLLPLL--PLLLLLLRDAGGSHTVPARSALPAAADGLVGHKDAQWPLGDAAAALGPGARDM  73
XP_004021600.2   1    MARGPARTS--LGP   RSQQLPLLslLLLLLL-RDADGSHTAAARPAPPAAADGLAGDKNPQRSPGDVAAAQSPGAQDM  74
XP_001135281.2   1    MAHVPARTS--PGP   GPQLLLLL--PLFLLLLRDVAGSHRAPAWSALPAAADGLQGDRDPQRHPGDAAATLGPSAQDM  73
XP_015002444.2   1    MARVPTRTS--QGP   GPQLLPLL--PLFLLLLRDAAGSHRAPAWSALPAAADGLQGDRDPQRAPGDAAATLGPGAQDM  73
XP_003994192.2   1    MARGPAGTS--PGR   RPQLLPLL--PLLLLLLRDAGGSHPAPAWSASPAASDGLAGIKDPWRSLGDAATTLGPGAQDM  73
XP_005699392.3   1    MARGPARTS--LGP   GSQQLPLLslLLLLLL-RDADGSHTAAARPAPPAAADGLAGDKNPQRSPGDVAAAQSPGAQDM  74
XP_004049420.1   1    MAHVPARTS--PGP   GPQLLLLL--PLFMLLLRDVAGSHRAPAWSALPAAADGLQGDRDPQRHPGDAAATLGPSAQDM  73
XP_002820747.1   1    MARVPARTS--PGP   GPQLLLLL--PLFLLLLRDVAGSHRAPAWSALPAAADGLQGDRDPQRPPGDAAATLGPSAQDM  73
XP_032026867.1   1    MAHVPARTS--PGP   GPQLLLLL--PLFLLLLQDVAGSHRAPAWSALPSAADGLQGDRDPQRPPGDAAATLSPGAQDM  73

NP_004953.1      75   VAVHMHRLYEKYSRQGARPGGGNTVRSFRARLEVVDQKAVYFFNLTSMQDSEMILTATFHFYSEPPRWPRALEVLCKPRA  154
NP_665684.2      71   VAIHMLRLYEKYNRRGAPPGGGNTVRSFRARLEMIDQKPVYFFNLTSMQDSEMILTAAFHFYSEPPRWPRAREVFCKPRA  150
NP_077351.1      71   VAVHMLRLYEKYNRRGAPPGGGNTVRSFRARLDVIDQKPVYFFNLTSMQDSEMILTATFHFYSEPPRWPRAREVFCKPRA  150
NP_001069635.1   75   VAVHMLRLYEKYSRRGARPGGGNTVRSFRARLEVVNQKAVYFFNLTSMQDSEMILTATFHFYSEP-QWPPAREVPCKQRA  153
XP_003133153.1   72   VAVHMLRLYEKYSRRGARPGGGNTVRSFRARLEVVNQKAVYFFNLTSMQDSEMILTATFHFYSEP-RLPRAREIPCKQRA  150
XP_853904.2      79   AAAHMLRLYDKYGRRGARPGGGNTVRSFRARLDTVDQRQAYVFNLTSLQDSEVILSATFHLYMEP-RWPRAREEPCRQRA  157
XP_001494823.3   74   VAVHMLRLYEKYSRRGARPGGGNTVRSFRARLEVVNQKAVYFFNLTSMQDSEMILTATFHFYSEP-RWPQAREVPCKQRA  152
XP_004021600.2   75   VAVHMLRLYEKYSRRGARPGGGNTVRSFRARLEVVNQKAVYFFNLTSMQDSEMILTATFHFYAEP-QWPPAREVPCKQRA  153
XP_001135281.2   74   VAVHMHRLYEKYSRQGARPGGGNTVRSFRARLEVVDQKAVYFFNLTSMQDSEMILTATFHFYSEPPRWPRALEVLCKPRA  153
XP_015002444.2   74   VAVHMHRLYEKYSRRGARPGGGNTVRSFRARLEVVDQKAVYFFNLTSMQDSETILMATFHFYSEPPRWPRALEVLCKPRA  153
XP_003994192.2   74   VAVHMLRLYEKYSRRGARPGGGNTVRSFRARLEVVDQKAVYFFNLTSMQDSEMILAATFHFYAEP-RWPRAREAPCKQRA  152
XP_005699392.3   75   VAVHMLRLYEKYSRRGARPGGGNTVRSFRARLEVVNQKAVYFFNLTSMQDSEMILTATFHFYAEP-QWPPAREVPCKQRA  153
XP_004049420.1   74   VAVHMHRLYEKYSRQGARPGGGNTVRSFRARLEVVDQKAVYFFNLTSMQDSEMILTATFHFYSEPPRWPRALEVLCKPRA  153
XP_002820747.1   74   VAVHMHRLYEKYSRQGARPGGGNTVRSFRARLEVVDQKAVYFFNLTSMQDSEMILTATFHFYSEPPRWPRALEVLCKPRA  153
XP_032026867.1   74   VAVHMHRLYEKYSRQGARPGGGNTVRSFRARLEVVDQKSVYFFNLTSMQDSEMILTATFHFYSEPPRWPRALEVLCKPRA  153

NP_004953.1      155  KNASGRPLPLGPPTRQHLLFRSLSQNTATQGLLRGAMALAPPPRGLWQAKDISPIVKAARRDGELLLSAQLDSEERDPGV  234
NP_665684.2      151  KNASCRLLTPGLPARLHLIFRSLSQNTATQGLLRGAMALTPPPRGLWQAKDISSIIKAARRDGELLLSAQLDTGEKDPGV  230
NP_077351.1      151  KNASCRLLTPGLPARLHLIFRSLSQNTATQGLLRGAMALTPPPRGLWQAKDISSIIKAARRDGELLLSAQLDSGEKDLGV  230
NP_001069635.1   154  KNASCRLLPPGPPARQHLLFRSLSQNTATQGLLRGAMALPPPPRGLWQAKDISLIVKAARRDGELLLSAQLDSGEKDTGV  233
XP_003133153.1   151  KNASCRLLPLGPPARQHLLFRSLSQNTATQGLLRGAMTLPPPPRGLWQVKDISPIVKAARRDGELLLSAQLDSGDKDPGV  230
XP_853904.2      158  RSASCRLPPPGPPTRRHLLFRSVAQNTAAQGLLRGALALAPPPRGLWQARDISPIVRAARQAGELLLWAQLDPAGGAPGA  237
XP_001494823.3   153  KNASCRLLPPGPPARQHLLFRSLSQNTATQGLLRGAMALAPPPRGLWQAKDISPIVKAARRDGELLLSAQLDAGEKDPGV  232
XP_004021600.2   154  KNASCRLLPPGPPARQHLLFRSLSQNTATQGLLRGAMALPPPPRGLWQAKDISLIVKAARRDGELLLSAQLDSGEKDTGV  233
XP_001135281.2   154  KNASGRPLPLGPPTRQHLLFRSLSQNTATQGLLRGAMALAPPPRGLWQAKDISPIVKAARRDGELLLSAQLDSEERDPGV  233
XP_015002444.2   154  KNASGRSLPLGPPARQHLLFRSLSQNTATQGLLRGAMALSPPPRGLWQAKDISPIVKAARRDGELLLSAQLDSEERDPGV  233
XP_003994192.2   153  KNVSCRLLPLGLPARQHLLFRSLSQNTATQGLLRGAMALAPPPRGLWQAKDISPIVKAARQDGELILSAQLDPGEKAPGG  232
XP_005699392.3   154  KNASCRLLPPGPPARQHLLFRSLSQNTATQGLLRGAMALPPPPRGLWQAKDISLIVKAARRDGELLLSAQLDSGEKETGV  233
XP_004049420.1   154  KNASGRPLPLGPPTRQHLLFRSLSQNTATQGLLRGAMALAPPPRGLWQAKDISPIVKAARRDGELLLSAQLDSEERDPAV  233
XP_002820747.1   154  KNASGRPLPLGPPARQHLLFRSLSQNKATQGLLRGAMALAPPPRGLWQAKDISPIVKAARRDGELLLSAQLDSEERDPGV  233
XP_032026867.1   154  KNASGRPLPLGPPARQHLLFRSLSQNTATQGLLRGAMALAPPTRGLWQAKDISPIVKAARRDDELLLSAQLDSEERDPGV  233

NP_004953.1      235  PRPSPYAPYILVYANDLAISEPNSVAVTLQRYDPFPAGDPEPRAAPNNSADPRVRRAAQATGPLQDNELPGLDERPPRA-  313
NP_665684.2      231  PRPSSHMPYILVYANDLAISEPNSVAVSLQRYDPFPAGDFEPGAAPNSSADPRVRRAAQVSKPLQDNELPGLDERPAPAL  310
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NP_077351.1      231  PRPSSHMPYILVYANDLAISEPNSVAVTLQRYDPFPAGDFEPGAAPNSSADPRVRRAAQVSKPLQDNELPGLDERPAPAL  310
NP_001069635.1   234  PRLGPHAPYILIYANDLAISEPNSVAVTLQRYDPFQAGDPEPGAAPNSSADPRVRRATQATGPLQNNELPGLDERPAQAP  313
XP_003133153.1   231  PRPSPHAPYILIYANDLAISEPNSVAVTLQRYDPFQAGDPEPGASPNSSADPRVRRATQATGPLQDNELPGLDERPAHTP  310
XP_853904.2      238  AGPSAPLPYLLVYADDLAIAEPNSVAGTLQRYDPLPAADPEPRAADNGSADPRVRRASQAPGPLQDNELPGLHERPGRMP  317
XP_001494823.3   233  PRPSPHAPYILVYANDLAISEPNSVAVTLQRYDPFQTGDPEPGAAPNSSADPRVRRATQVTGPLQDNELPGLDERPAHGP  312
XP_004021600.2   234  PRLGPHAPYILIYANDLAISEPNSVSVTLQRYDPFQAGDPEPGAAPNISADPRVRRATQAPGPLQNNELPGLDERPAHTP  313
XP_001135281.2   234  PQPSPYAPYILVYANDLAISEPNSVAVTLQRYDPFPAGDPEPRGAPNNSADPRVRRAAQATGPLQDNELPGLDERPPRA-  312
XP_015002444.2   234  PRPSPYAPYILVYANDLAISEPNSVAVTLQRYDPFPAGDPEPHAAPNSSADPRVRRAAQATGPLQDNELPGLDERPPRA-  312
XP_003994192.2   233  SRPSPHAPYILVYADDLAISEPNSVAVTLQRYDPFQAGDPEPGAAPNSSADPRVRRATQATGPLQDNELPGLDERPAHAS  312
XP_005699392.3   234  PRLGPHAPYILIYANDLAVSEPNSVSVTLQRYDPFQAGDPEPGAAPNSSADPRVRRATQAPGPLQNNELPGLDERPAHTP  313
XP_004049420.1   234  PRPSPYAPYILVYANDLAISEPNSVAVTLQRYDPFPAGDPEPRAAPNNSADPRVRRAAQATGPLQDNELPGLDERPPRA-  312
XP_002820747.1   234  PRPSPYAPYILVYANDLAISEPNSVAVTLQRYDPFPAGDPEPRAAPNSSADPRVRRAAQATGPLQDNELPGLDERPPRA-  312
XP_032026867.1   234  PRPSPYAPYILVYANDLAISEPNSVAVTLQRYDPFPAGDPDPRAAPNSSADPRVRRATQATGPLQDNELPGLDERPSRA-  312

NP_004953.1      314  HAQH--FHKHQLWPSPFRALKPRPGRKDRRKKGQEVFM-AASQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  390
NP_665684.2      311  HAQN--FHKHEFWSSPFRALKPRTGRKDRKKKDQDTFTaASSQVLDFDEKTMQKARRRQWDEPRVCSRRYLKVDFADIGW  388
NP_077351.1      311  HAQH--FHKHEFWSSPFRALKPRTGRKDRKKKDQDTFTpSSSQVLDFDEKTMQKARRRQWDEPRVCSRRYLKVDFADIGW  388
NP_001069635.1   314  HAQH--YHKHELWPNPLRALKPRPGRKDRRKKGQDVFM-ASSQVLDFDEKTMQKARKKQWDEPRVCSRRYLKVDFADIGW  390
XP_003133153.1   311  HTQH--YHKHELWPNPFRALKPRPGRKDRRKKDQDVFM-TSSQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  387
XP_853904.2      318  PARQppRPRHELWRGPLGALKPRPGRRERRRKGPDA--pAASRVLDFDEQTMRKARRRQWAEPRVCSRRYLRVDFADIGW  395
XP_001494823.3   313  HAQP--YHKHELWPSPFRALKSRPGRKDRRRKGQDAFA-ASSQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  389
XP_004021600.2   314  HGQH--YHKHELWPSPFRALKPRPGRKDRRKKGQDVFM-ASSQVLDFDEKTMQKARKKQWDEPRVCSRRYLKVDFADIGW  390
XP_001135281.2   313  HAQH--FHKHQLWPSPFRALKPRPGRKDRRKKGQEVFM-AASQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  389
XP_015002444.2   313  HAQH--FHKHQLWPSPFRALKPRPGRKDRRKKGQEVFM-ASSQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  389
XP_003994192.2   313  HAQH--YHKHELWPGPFRALKPRPGRKDRRKKGPDVFV-GSSRVLDFDEKTMQKARRKQWAEPRVCSRRYLKVDFADIGW  389
XP_005699392.3   314  HGQH--YHKHELWPSPFRALKPRPGRKDRRKKGQDVFM-ASSQVLDFDEKTMQKARKKQWDEPRVCSRRYLRVDFADIGW  390
XP_004049420.1   313  HAQH--FHKHQLWPSPFRALKPRPGRKDRRKKGQEVFM-AASQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  389
XP_002820747.1   313  PAQH--FHKHQLWPSPFRALKPRPGRKDRRKKGQEVFM-ASSQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFTDIGW  389
XP_032026867.1   313  HAQH--FHKHQLWPSPFRALKPRPGRKDRRKKGQDVFM-ASSQVLDFDEKTMQKARRKQWDEPRVCSRRYLKVDFADIGW  389

NP_004953.1      391  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIIPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  470
NP_665684.2      389  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNAVLKVYPNM  468
NP_077351.1      389  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  468
NP_001069635.1   391  NEWIISPKSFDAYYCSGACEFPMPKMVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMSSLGVLFLDENRNVVLKVYPNM  470
XP_003133153.1   388  NEWIISPKSFDAYYCSGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  467
XP_853904.2      396  NEWIVLPKSFDAYYCAGECEFPMPKVVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRDVVLKVYPNM  475
XP_001494823.3   390  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  469
XP_004021600.2   391  NEWVISPKSFDAYYCSGACEFPMPKMVRPSNHATIQSIVRAVGIVPGVPEPCCVPDKMSSLGVLFLDENRNVVLKVYPNM  470
XP_001135281.2   390  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIIPGIPEPCCVPDKMNSLGVLFLDESRNVVLKVYPNM  469
XP_015002444.2   390  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  469
XP_003994192.2   390  NEWIILPKSFDAYYCAGVCEFPMPKMVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  469
XP_005699392.3   391  NEWVISPKSFDAYYCSGACEFPMPKMVRPSNHATIQSIVRAVGIVPGVPEPCCVPDKMSSLGVLFLDENRNVVLKVYPNM  470
XP_004049420.1   390  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIIPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  469
XP_002820747.1   390  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  469
XP_032026867.1   390  NEWIISPKSFDAYYCAGACEFPMPKIVRPSNHATIQSIVRAVGIVPGIPEPCCVPDKMNSLGVLFLDENRNVVLKVYPNM  469

NP_004953.1      471  SVDTCACR   478
NP_665684.2      469  SVETCACR   476
NP_077351.1      469  SVETCACR   476
NP_001069635.1   471  SVETCACR   478
XP_003133153.1   468  SVETCACR   475
XP_853904.2      476  SVETCACR   483
XP_001494823.3   470  SVETCACR   477
XP_004021600.2   471  SVETCACR   478
XP_001135281.2   470  SVDTCACR   477
XP_015002444.2   470  SVDTCACR   477
XP_003994192.2   470  SVETCACR   477
XP_005699392.3   471  SVETCACR   478
XP_004049420.1   470  SVDTCACR   477
XP_002820747.1   470  SVDTCACR   477
XP_032026867.1   470  SVDTCACR   477
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GDF3

NP_065685.1 growth/differentiation factor 3 preproprotein [Homo sapiens]
NP_032134.2 growth/differentiation factor 3 preproprotein [Mus musculus]
NP_001103141.1 growth/differentiation factor 3 precursor [Rattus norvegicus]
XP_002687893.2 growth/differentiation factor 3 [Bos taurus]
XP_003126560.2 growth/differentiation factor 3 [Sus scrofa]
XP_534896.1 growth/differentiation factor 3 [Canis lupus familiaris]
XP_001493186.1 growth/differentiation factor 3 [Equus caballus]
XP_004006951.3 growth/differentiation factor 3 [Ovis aries]
XP_508988.2 growth/differentiation factor 3 [Pan troglodytes]
XP_001112644.1 growth/differentiation factor 3 [Macaca mulatta]
XP_003988425.1 growth/differentiation factor 3 [Felis catus]
XP_005680965.2 PREDICTED: growth/differentiation factor 3 [Capra hircus]
XP_004052681.2 growth/differentiation factor 3 [Gorilla gorilla gorilla]
XP_002822896.1 growth/differentiation factor 3 [Pongo abelii]
XP_032015430.1 growth/differentiation factor 3 [Hylobates moloch]

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NP_065685.1     1        MLRFLPDLAFSFLL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPYILKKIFQDREAAATTGVSRDLCYVKE  75
NP_032134.2     1        MQPYQRLLALGFLLlTLPWGQTSEFQDSDLLQFLGLEKAPSPHRFQPVPRVLRKIIRAREAAAASGASQDLCYVKE  76
NP_001103141.1  1        MQPSQRLLTLGFLLlTLARGQTSEFQDYDFLQFLGLKKAPSPHRFQPVPRILRKIIRARETAAASGASQDLCYVKE  76
XP_002687893.2  1        MLPSLAALALCLLF-TLAFGQTLQFHEHVFLRFLGLDKVPSPKKFQPVPSILKRIFQAQEEAASTGISKDLCYVKE  75
XP_003126560.2  1    [10]MLPSLPGLALAFLL-TLTVGQTFPFQEHVFLQFLGLDKVPSPKKFQPVPYILKRIFQDHEAAATSGLSQDLCYVKE  85
XP_534896.1     1        MIPSRTVLALRLLL-TVALAQTFQFQEHVFLQFLGLDKVPSPQKFQPVPSILKKIFQDQEAAAINGDSQDVCYIKD  75
XP_001493186.1  1        MIPSLPALALGLLL-TLALGQTFQFQENVFLQFLGLDKVPSPQKFQPVPYILKKIFQDREAAATTGGSQDLCSIKN  75
XP_004006951.3  1        MLPSLAALALCLLY-TLALGQTLQFHEHVFLRFLGLDKVPSPKKFQPAPSILKRIFQAQEAAASTGISKDLCYVKE  75
XP_508988.2     1        MLRFLPDLAFSFLL-ILASGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPYILKKIFQDREAAATTGVSRDLCYVKE  75
XP_001112644.1  1        MLRFLPDLAFSFLL-TLAFGQAVQFQEYVFLQFMGLDKAPSPQKFQPVPYILKKIFQDREAAATTGVSRDLCYVKE  75
XP_003988425.1  1        MIPSLPFLAVGLLL-TVALAQTVQFQEYVFLQFLGLDKVPSPQRFQPVPYILKKIFQDREAAATSVDSRDFCYIKD  75
XP_005680965.2  1        MLPSLAALALCLLY-TLALGQTLQFHEHVFLRFLGLDKVPSPKKFQPVPSILKRIFQAQEAAASTGISKDLCYVKE  75
XP_004052681.2  1        MLRFLPDLAFSFLL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPYILKKIFQDREAAATTGVSRDLCYVKE  75
XP_002822896.1  1        MLRFLPDLAFSFLL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFQPVPYILKKIFQDREAAATTGVSRDLCYVKE  75
XP_032015430.1  1        MLRFLPDLAFSFLL-ILALGHAVRFQEYVFLQFLGLDKAPSPQKFQPVPYILKKIFQDREAAATTGVSQDLCYIKE  75

NP_065685.1     76   LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELELALFLVQ-EPH  154
NP_032134.2     77   LGVRGNLLQLLPDQGFFLNTQKPFQDGSCLQKVLYFNLSAIKEKAKLTMAQLTLDLGPRSYYNLRPELVVALSVVQ-DRG  155
NP_001103141.1  77   LGVRGNLLRLLPDQGFFLNTQKPSQDGSCLQKVLSFNLSAVKEKGKLTMAQLILHLGPRSYHYLQLELVVAVSVVQ-DRG  155
XP_002687893.2  76   LGVRGNILRLLPDQGSFLYSESLSHAS-CLQKLLSFNLSAIGDEEQLTMAQLGLDLGPNTYYNLGPELELSLSLVQtEPH  154
XP_003126560.2  86   LGVRGDVLRLLPDQGFFLYSKNHPQAASCLQKLLYFNLSVIKD-EQLTMAQLALDLGPNTYYNLGPELELTLSLVQ-EPH  163
XP_534896.1     76   LGISGNILRLLLDKGLFLYSKKRPQASSCLQKFLYFNLSAIKDKELLTMAQLGLDLGPNTYYKPGPELELALSLVQ-EPH  154
XP_001493186.1  76   LGVRGNVLRLLPDQGFYLYSKDLPQAS-CLQKLLYFNLAAIRDKEQLTMAQLGLDLGSNTYYNLGPELELALSLVQ-EPR  153
XP_004006951.3  76   LGVRGNILRLLPDQGSFFYSENLSHAP-CLQKLLSFNLSAIGDEEQLTMAQLGLDLGPSTYYNLGPELELSLSLVQtEPH  154
XP_508988.2     76   LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELELALFLVQ-EPH  154
XP_001112644.1  76   LGVRGNVLRFLPDQGFFLYPKKFSQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELELALFLVQ-EPP  154
XP_003988425.1  76   FGVRGNVLRLLPDQGLFLYSRKLSQASSCLQKFLYFNLSAIKEKEQLTMAQLGLDLGPNTYYKLGPELELALFLVQ-EPQ  154
XP_005680965.2  76   LGVRGNILRLLPDQGSFLYSENLSHAP-CLQKLLSFNLSAIGDEEQLTMAQLGLDLGPSTYYNLGPELELSLSLVQtEPH  154
XP_004052681.2  76   LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELELALFLVQ-EPH  154
XP_002822896.1  76   LGVRGNVLRFLPDQGFFLYPKKFSQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELELALFLVQ-EPH  154
XP_032015430.1  76   LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSYYNLGPELELALFLVQ-EPH  154

NP_065685.1     155  VWGQTTPKPGKMFVLRSVPWPQGAVHFNLLDVAKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLL  234
NP_032134.2     156  VWGRSHPKVGRLLFLRSVPGPQGQLQFNLQGALKDWSSNRLKNLDLHLEILVKEDRYSRVTVQPENPCDRLLRSLHASLL  235
NP_001103141.1  156  VWGRSHPKLGRLLVQKSVLGPQGSLQFNLQGVVKDWNRHQLKNLDLYLEILVKEDRYSRVNAQLDNPCNQLMHSLHASLL  235
XP_002687893.2  155  VIDQATPKMGKMFTLQSVPWPQGVLHFNLLDVAKR-NNDPHKNLGLFLEIVVKGGRALGENFQLEGTCARLRRSLHTSLL  233
XP_003126560.2  164  VWGQATPKTGTMFVLQSVPWPQGILRFNLLEVAKR-NNSSWKNLAFFLEILVKGDRALGENFQLEDTCARLRRSLHASLL  242
XP_534896.1     155  GWGQSIPKPGKMLVLQSVPWPRGVVHFNLLDVAKDWNNNPRKNLGLLLEILVKGNRDFVVNFQLQDTCARLRQSLHASLL  234
XP_001493186.1  154  VWGQSISTPGKPFALQSVPWPQGVLRFNLLDVAKDWNNNPQKNLGLFLEILVKGDRDFGVNFQLEDTCARLRHSLHASLL  233
XP_004006951.3  155  GTDQSTLKMRKMFTLQSVPWPQGVLHFNLLDAAKR-NNDPRKNLALFLEIVVKGGRASGENFQLEGTCARLRRSLHTSLL  233
XP_508988.2     155  VWGQTTPKPGKMFVLRSVPWPQGAVHFNLLDVAKDWNDNPRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLL  234
XP_001112644.1  155  VWGQTTPKPGKMFVLRSVPWPQGAVHFNLLDVAKDWNDNPQKNFGLFLEILVKEDRDSGVNFQPEDTCARLRRSLHASLL  234
XP_003988425.1  155  EGDQPIPKPGRMLVLQSVPRPQGVVHFNLLDVAKDWNNDSQKNLGLLLEILVKGNRDIGVTFQLQDACARLRQSLRASLL  234
XP_005680965.2  155  VTDQSTPKMGKMITLQSVPWPQGVLHFNLLDVAKR-NNDPHKNLALFLEIVVKGGRASGENFQLEGTCARLRRSLHASLL  233
XP_004052681.2  155  VWGQTTPKPGKMFVLRSVPWPQGAVHFNLLDVAKDWNDNPWKNFGLFLEILVKEDRDSGVNFQPEDTCARLRCSLHASLL  234
XP_002822896.1  155  VWGQTTPKPGKIFVLRSVPWPQGAVHFNLLDVAKDWNDNPQKNFGLFLEILVKEDRDSGVNFQPEDTCARLRRSLHASLL  234
XP_032015430.1  155  VWGQTTPKPGKMSVLRSVPWPQGAVHFNLLDVAKDWNDNPQKNFGLFLEILVKEDRDSGVNFQPEDTCARLRRSLHASLL  234

NP_065685.1     235  VVTLNPDQC-HP-SRKRRAAIPVPKLSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF  312
NP_032134.2     236  VVTLNPKHChPS-SRKRRAAISVPKGFCRNFCHRHQLFINFQDLGWHKWVIAPKGFMANYCHGECPFSMTTYLNSSNYAF  314
NP_001103141.1  236  VVTLNLKHChPS-SRKKRAAIPIPKGLCRNLCHRHQLFVNFQDLGWHKWVIAPKGFMANYCHGDCPFTMTTYLNSSNYAF  314
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XP_002687893.2   234   VVTLHPEQC-RSpSRKRRAAVSTSKASCKSLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_003126560.2   243   VATLNPEQC-HPaSRKRRAAFPASKVPCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGDCPFSLTTSLNSSNYAF   321
XP_534896.1      235   VVTLNPEQC-HPsSRKRREAILFPKASCQNLCHRHQLFINFQDLGWHKWIIAPKGFMANYCHGDCPFSLTTSLNSSNYAF   313
XP_001493186.1   234   VVTLNPEQC-HPsSRKRRSAIPAPNASCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGDCPFSLTTSLNSSNYAF   312
XP_004006951.3   234   VVTLHPEQC-QSpSRKRRAAVSTSKAACKSLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_508988.2      235   VVTLNPDQC-HS-SRKRRAAIPVPKVSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_001112644.1   235   VVALNPDEC-PP-SRKRRAAIPVPKVSCKNLCHRHQLFINFQDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_003988425.1   235   VVTLHPEQC-HPsSRKRREAIPAPKAPCRNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGDCPFSLTTSLNSSNYAF   313
XP_005680965.2   234   VVTLHPEQC-RSpSRKRRAAVSTSKAACKSLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_004052681.2   235   VVTLNPDQC-HP-SRKRRAAIPVPKVSCKSLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_002822896.1   235   VVTLNPDHC-HP-SRKRRAAIPVPKVSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312
XP_032015430.1   235   VVTLNPDQC-HP-SRKRRAAIPVPKVSCKNLCHRHQLFINFRDLGWHKWIIAPKGFMANYCHGECPFSLTISLNSSNYAF   312

NP_065685.1      313   MQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG   364
NP_032134.2      315   MQALMHMADPKVPKAVCVPTKLSPISMLYQDSDKNVILRHYEDMVVDECGCG   366
NP_001103141.1   315   MQALMHMADPRVPKAVCIPTKLSPISMLYQDNEKNVILRHYEDMVVDECGCG   366
XP_002687893.2   313   MQALMHAVDPEVPQAVCIPTKLSPISMLYQDNDDNVILRHYEDMIVDECGCG   364
XP_003126560.2   322   MQALMHAVDPQVPQAVCIPTRLSPISMLYQDNNDNVILRHYEDMVVDECGCG   373
XP_534896.1      314   MQALMHAVDPEIPQAVCIPTKLSPISMLYQDNDDNVILRHYEDMVVDECGCG   365
XP_001493186.1   313   MQALMHAVDPQIPQAVCIPTKLSPISMLYQDNDDNVILRHYEDMVVDECGCG   364
XP_004006951.3   313   MQALMHAVDPEVPQAVCIPTKLSPISMLYQDNDDNVILRHYEDMIVDECGCG   364
XP_508988.2      313   MQALMHAVDPKIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG   364
XP_001112644.1   313   MQALMHAVDPEIPQAVCVPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG   364
XP_003988425.1   314   MQALMHAVDPEIPQAVCVPTKLSPISMLYQDNDDNVILRHYEEMVVDECGCG   365
XP_005680965.2   313   MQALMHAVDPEVPQAVCIPTKLSPISMLYQDNDDNVILRHYEDMIVDECGCG   364
XP_004052681.2   313   MQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG   364
XP_002822896.1   313   MQALMHAVDPEIPQAVCIPTKLSPISMLYQDNNDNVILRHYEDMVVDECGCG   364
XP_032015430.1   313   MQALMHAVDSEIPQAVCIPTKLSPISMLYQDNDDNVILRHYEDMVVDECGCG   364
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eGDF1

NP_001483.3 embryonic growth/differentiation factor 1 precursor [Homo sapiens]
NP_001156754.1 embryonic growth/differentiation factor 1 precursor [Mus musculus]
NP_001037705.1 embryonic growth/differentiation factor 1 precursor [Rattus norvegicus]
XP_010804844.1 embryonic growth/differentiation factor 1 [Bos taurus]
XP_013846750.2 embryonic growth/differentiation factor 1 [Sus scrofa]
XP_038284034.1 embryonic growth/differentiation factor 1 [Canis lupus familiaris]
XP_023481294.1 LOW QUALITY PROTEIN: embryonic growth/differentiation factor 1 [Equus caballus]
XP_027825180.1 embryonic growth/differentiation factor 1 [Ovis aries]
XP_016791031.1 embryonic growth/differentiation factor 1 [Pan troglodytes]
XP_001115596.2 embryonic growth/differentiation factor 1 [Macaca mulatta]
XP_023103436.1 embryonic growth/differentiation factor 1 [Felis catus]
XP_017906949.1 PREDICTED: embryonic growth/differentiation factor 1 [Capra hircus]
XP_030860111.1 embryonic growth/differentiation factor 1 [Gorilla gorilla gorilla]
XP_024094156.1 embryonic growth/differentiation factor 1 [Pongo abelii]
XP_032026077.1 embryonic growth/differentiation factor 1 [Hylobates moloch]

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NP_001483.3     1    MPPPQQGPCGHHLLLLL-ALLLPSLPLTRAPVPPGPAAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR  79
NP_001156754.1  1    MLPVCHRFCDH---LLL-LLLLPSTTLAPAPASMGPAAALLQVLGLPEAPRSVPTHRPVPPVMWRLFRRRDPQEARVGR-  75
NP_001037705.1  1    MLPVCHRFCDH---LLL-LLLLPSTTLAHAPASLGPAAALLQVLGLPETPRSVPTLRPVPPVMWRLFRSRNPQEARVGR-  75
XP_010804844.1  1    MPPLCRRPSRRVLLLLL-ALLLPSSPPACAPAPPGPAAALLQALGLPDVPRGAPESRPVPPVMWRLFRRRDHQEARADPR  79
XP_013846750.2  1    MPSPCRR----ALLLLL-ALLLPSPSLARAPAAPGPAASLLRALGLSDAPRDAPTSRPVPPVMWRLFRRRDHQEARAGSR  75
XP_038284034.1  1    MPALRRPPGRRVLFLLL-ALLLPSPPPARAPAPPGPAAALLQALGLPDVHRGAPKPRPVPPVMWRLFRHRDPQEARVGPR  79
XP_023481294.1  1    MPPPRRGPGRRVLFLLL-ALLLPSPPPARAPAPPGPAAALLQALGLRDAPRDAPTPRPVPPVMWHLFRRRDPQESRTNLR  79
XP_027825180.1  1    MPPLCRRPGRQVLLLL--ALLLPSSPPACAPAPSGPAAALLQALGLPDVPRGAPKSRPVPPVMWRLFRRRDHQEARADPR  78
XP_016791031.1  1    MPPPQQGPCGHHLLLLL-ALLLPSLPPTRAPVPPGPAASLLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR  79
XP_001115596.2  1    MLPPRQGPGGQHLLLLL-VLLLPSLSPTRAPVPPGPAAALLQALGLRDAPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR  79
XP_023103436.1  1    MPSPCRRPGRRVLFLLL-ALLLPSPPPARAPAPPGPAATLLQALGLPDAHRGAPTPRPVPPVMWRLFRHRDPQEARVGPR  79
XP_017906949.1  1    MPPLCRRPGRQVLLLL--ALLLPSSPPACAPAPPGPAAALLQALGLPDVPRGAPKSRPVPPVMWRLFRRRDHQEARADPR  78
XP_030860111.1  1    MPPPQQGPCGHHLLLLL-ALLLPSLPPTRAPVPPGPAAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGLR  79
XP_024094156.1  1    MPPPRQGPCGHHLLLLL-ALLLPSLPPTSAPVPPGPAAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR  79
XP_032026077.1  1    MPPPRQGHCGHHLLLLLlALLLPSLSPTRAPVPPGPAAALLQALGLRDAPQGAPRLRPVPPVMWRLFRRRDPQETRPGSR  80

NP_001483.3     80   RTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA  157
NP_001156754.1  76   ------PLRPCHVEELGVAGNIVRHIPDSGLSSRPAQPARTSGLCPEWTVVFDLSNVEPTERPTRARLELRLEAeSE-DT  148
NP_001037705.1  76   ------PLKPCHVEELGVAGNIVRHIPDSGLSSRIIQPARTSGLCPEWTVVFDLSSVEPIERPTRARLELRLEAeSE-DT  148
XP_010804844.1  80   RMPPGATLRPCHVEELGVAGNIVRHVLDRGAAARPPEPASAAGQCPEWTVVFDLSAVEPAERPSQARLELRFEA-AE-AT  157
XP_013846750.2  76   RTPPAAALRPCHVEELGVAGNIVRHVPDRGAAARRPEPASAAGQCPEWTVVFDLSTVEPAERPSQVRLELRFAA-EE-AS  153
XP_038284034.1  80   RTPQGTTLRPCHVEELGVAGNIVRHIPDRGAPTRPPEPAWAAGQCPEWTVVFDLSAVEAAERPSRARLELRFAA-AE-TA  157
XP_023481294.1  80   RTPPGATLRPCHLEELGVAGNIVRHVLDRGAPARPPEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AEaTA  158
XP_027825180.1  79   RMPPRATLRPCHVEELGVAGNIVRHVLDSGAAARSPEPAPAAGQCPEWTVVFDLSAVEPAERPSQARLEVRFAA-AE-AT  156
XP_016791031.1  80   RTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA  157
XP_001115596.2  80   RMSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASDPASAVGHCPEWTVVFDLSAVESAERPSRARLELRFAA-AA-A-  156
XP_023103436.1  80   RTPQGTTLRPCHMEELGVAGNIVRHISDRGAPTRPPEPAWASGQCPEWTVVFDLSAVEPAERPSRARLEMRFAA-AA-AA  157
XP_017906949.1  79   RMSPRATLRPCHVEELGVAGNIVRHVLDSGAAARSPEPASAAGQCPEWTVVFDLSAVEPAERPSQARLEVRFAA-AE-AT  156
XP_030860111.1  80   RTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA  157
XP_024094156.1  80   RTFPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA  157
XP_032026077.1  81   RTSPGVTLQPCHMEELGVAGNIVRHIPDRGAPTRASELASAAGHCPGWTVVFDLSAVEPAERPSRARLELHFAA-AA-AA  158

NP_001483.3     158  A--PEGGWELSVAQAGQGAGADPGPVLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL  235
NP_001156754.1  149  -----GGWELSVALWADAEH--PGPELLRVPAPP-GVLLRADLLGTAVAANASVPCTVRLALSLHPGATAACGRLAEASL  220
NP_001037705.1  149  -----RGWELSVALLAEAEH--PGPELLRVQAPP-GLPLRADLLGTAVAANASVPRTLRLALALHPGAAATCGRLAEASL  220
XP_010804844.1  158  Ag-TTGGWELSVAPAGAGLG----PVGLRQVVPTLGQPVRAELLGSIWARNASAPRSLRLTLALRHRTPAACARLAEASL  232
XP_013846750.2  154  Ag-MAGSWELSVARAGSG------PVLLRQAVTALGTPVRAELLGAAWARNASAPRSLRLTLALRPRAPTVCARLTEASL  226
XP_038284034.1  158  -----AGWELSLARAAEGEAGGARPVLLRQAVPTLGTPVRAELLGAAWARNASAPRSLRLALALRPRAPAACARLAEASL  232
XP_023481294.1  159  -----GGWELSVARAAEGAGPG--PVLLRQAVLALGTPVRAELLGAAWARNASAPRSLRLSLALRPRVPPPARAXAEASL  231
XP_027825180.1  157  Ag-TTGGWELSVAPAGAGLG----RVGLRQVVPTLGQPVRAELLGSIWARNASAPRSLRLTLALRHRTLAACARLAEASL  231
XP_016791031.1  158  A--PEGGWELSVAQAGQGAGADPGPVLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL  235
XP_001115596.2  157  ---PEGGWELSVSQAGQGTGAGPGPVLLRQLVPALGPPVRAELLGTAWARNASWPRSLRLALALRPRTPAACARLAEASL  233
XP_023103436.1  158  Ee--PAGWELSVTQAAEGAVAG--PVLLRQVVPTLTAPVRAELLGAAWAHNASAPRSLRLALALRPRAPAACAHLAEASL  233
XP_017906949.1  157  Ag-TTGGWELSVAPAGAGLG----RVGLRQVVPTLGQPVRAELLGSIWARNASAPRSLRLTLALRHRTLAACARLAEASL  231
XP_030860111.1  158  A--PEGGWELSVAQAGQGAGADPGPVLLRQLVPTLGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL  235
XP_024094156.1  158  ---PEGGWELSVAQAGQGAGADPGPVLLRQLVPALGPPVRAELLGAAWALNASWPRSLRLALALRPRAPAACARLAEASL  234
XP_032026077.1  159  AaaPEGGWELSVAQAVQGAGADPGPVLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL  238

NP_001483.3     236  LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPAL  315
NP_001156754.1  221  LLVTLDPRLC-PLPRLRRHTEPRVEVGPVGTCRTRRLHVSFREVGWHRWVIAPRGFLANFCQGTCALPETLRGPGGPPAL  299
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NP_001037705.1   221   LLVTLDPRLC-PLPRSRRHTEPRVGGGPVGTCRTRRLHVSFREVGWHRWVIAPRGFLANFCQGTCALPETLRGPGGPPAL   299
XP_010804844.1   233   LLVTLDQRLCHPLARPRREAEPPVGGGSGGSCRARRLYVSFREVGWHRWVIAPRGFLANYCQGKCALPAVLSEPGGTPAL   312
XP_013846750.2   227   LLVTLDPRLCHPLARPRREAEPAVGGGSGGACRTRRLYVSFREVGWHRWVIAPRGFLANYCQGKCALPAALSEPGGTPAL   306
XP_038284034.1   233   LLVTLDPRLCHPLARPRREAEPALGGSPGGACRTRRLYVSFREVGWHRWVIAPRGFLANYCQGQCSLPATLSGPGGTPPL   312
XP_023481294.1   232   LLATLDPRLCXPLARPRREAEPAVGGAPXGACRARRLYVSFREVGWHRWVIAPRXFLANYCQGQCALPAALSGPGGPPAL   311
XP_027825180.1   232   LLVTLDQRLCHSLARPRREAEPPVGGGSGDSCRARRLYVSFREVGWHRWVIAPRGFLANYCQGKCALPAVLSEAGGAPAL   311
XP_016791031.1   236   LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPAL   315
XP_001115596.2   234   LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQCALPVTLSGSGGPPAL   313
XP_023103436.1   234   LLVTLDPRLCHPLARPRREAEPSVGGSPGGACRTRRLYVSFREVGWHRWVIAPRGFLANYCQGQCSLPAALSGPGGTPPL   313
XP_017906949.1   232   LLVTLDQRLCHSLARPRREAEPPVGGGSGDSCRARRLYVSFREVGWHRWVIAPRGFLANYCQGKCALPAVLSEAGGAPAL   311
XP_030860111.1   236   LLVTLDPRLCHPLARPRRDAEPVLGGSPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPAL   315
XP_024094156.1   235   LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPAL   314
XP_032026077.1   239   LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPPAL   318

NP_001483.3      316   NHAVLRALMHAAAP-GAADLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGCR   372
NP_001156754.1   300   NHAVLRALMHAAAPtPGAGSPCCVPERLSPISVLFFDNSDNVVLRHYEDMVVDECGCR   357
NP_001037705.1   300   NHAVLRALMHAAAPtPGVGSPCCVPERLSPISVLFFDNSDNVVLRHYEDMVVDECGCR   357
XP_010804844.1   313   NHAVLRTLMHAAAP-GAAGLPCCVPARLSPISVLFFDNSDNVVLRHYEDMVVDECGCR   369
XP_013846750.2   307   NHAVLRALMHSAAP-GAAGLPCCVPARLSPISVLFFDNNDNVVLRHYEDMVVDECGCR   363
XP_038284034.1   313   NHAVLRALMHAAAP-GAAGLPCCVPARLSPISVLFFDNSDNVVLRHYEDMVVDECGCR   369
XP_023481294.1   312   NHAVLRALMHAAAP-GAAGLPCCVPARLSPISVLFFDNSDNVVLRHYEDMVVDECGCR   368
XP_027825180.1   312   NHAVLRTLMHAAAP-GAAGLPCCVPARLSPISVLFFDNSDNVVLRRYEDMAVDECGCR   368
XP_016791031.1   316   NHAVLRALMHAAAP-GAADLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGCR   372
XP_001115596.2   314   NHAVLRALMHATTP-GAADLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGCR   370
XP_023103436.1   314   NHAVLRALMHAAAP-GAAGLPCCVPARLSPISVLFFDNSDNVVLRHYEDMVVDECGCR   370
XP_017906949.1   312   NHAVLRTLMHAAAP-GAAGLPCCVPARLSPISVLFFDNSDNVVLRRYEDMAVDECGCR   368
XP_030860111.1   316   NHAVLRALMHAAAP-GAADLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGCR   372
XP_024094156.1   315   NHAVLRALMHAAAP-GAADLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGCR   371
XP_032026077.1   319   NHAVLRALMHAAAP-GATDLPCCVPARLSPISVLFFDNSDNVVLRQYEDMVVDECGCR   375
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BMP3

NP_001192.4 bone morphogenetic protein 3 preproprotein [Homo sapiens]
NP_775580.1 bone morphogenetic protein 3 isoform 2 preproprotein [Mus musculus]
NP_058801.1 bone morphogenetic protein 3 precursor [Rattus norvegicus]
NP_001179197.1 bone morphogenetic protein 3 precursor [Bos taurus]
NP_001193317.1 bone morphogenetic protein 3 precursor [Sus scrofa]
XP_038299875.1 bone morphogenetic protein 3 [Canis lupus familiaris]
XP_023493625.1 bone morphogenetic protein 3 [Equus caballus]
XP_027826928.1 bone morphogenetic protein 3 [Ovis aries]
XP_001144027.1 bone morphogenetic protein 3 [Pan troglodytes]
XP_001089525.2 bone morphogenetic protein 3 [Macaca mulatta]
XP_006931098.2 bone morphogenetic protein 3 [Felis catus]
XP_005682010.3 PREDICTED: LOW QUALITY PROTEIN: bone morphogenetic protein 3 [Capra hircus]
XP_004038932.1 bone morphogenetic protein 3 [Gorilla gorilla gorilla]
XP_002814965.1 bone morphogenetic protein 3 [Pongo abelii]
XP_032019797.1 bone morphogenetic protein 3 [Hylobates moloch]

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NP_001192.4     1    M--AGASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHMLRLYDRYS---TVQAA-R  74
NP_775580.1     1    M--AGARGLLCLWLGYFCLNLAQGQRPNLHLPGLRETEPSDRATGGSPSPDLRPHDKVSEHMLWLYDRYSGsSRVQAT-R  77
NP_058801.1     1    M--AGARGLLCLWLGCFCLNLAQGQRPNLHLPGLRGTESSDRMTGGGPSPDLRPHDKVSEHMLWLYDRYSGsNRAQAT-R  77
NP_001179197.1  1    M--AGARGLLHLWLSCLCVSLAQGQRLRQPFPELRVAVPADRAAGGGPESPLQPLDQVSEHMLRLYDRYSG-GRTEEA-R  76
NP_001193317.1  1    M--AAARALLPLWLGCLCGSLAQGLRRQQPFPELRDAVPGHRAAGGGPDPPLQPLDPLSEHMLRLYDSYSG-GASAEAaR  77
XP_038299875.1  1    M--AGARGLLWLWLGCFCGSLARAERPKPGLPQLHGAGSGDRAAGGGSGPVLRPLDKVSEHMLRLYDRYSGgGGARAE-R  77
XP_023493625.1  1    M--AGARRLLYLWLGCFCVSLAQGERLKQHFPELPKTVPGDRTAGGGSGPVLRPHDKVSEHMLRLYDRYSGsGRAEAA-R  77
XP_027826928.1  1    M--AGARGLLHLWLSCLCVSLAQGQRLRQPFPELRVAVPADRAAGGGPESPLQPLDQLSEHMLRLYDRYSG-GGAEEA-R  76
XP_001144027.1  1    M--AGASRLLFLWLGCFCVNLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHMLRLYDRYS---TVQAA-W  74
XP_001089525.2  1    MatAGASRLLFLWLGCFCVSLAQGERPKLPLRELRKAVPGDRTAGGGPDAELQPQDKVSEHMLRLYDRYS---TVQAA-R  76
XP_006931098.2  1    M--AGALRLLCLWLGCFCVSLARGEGLTRTVPEPHRAVPGDRTAGGGPGPVLQPHDKVSEHMLRLYDRYSGgGRAEAE-R  77
XP_005682010.3  1    M--AGARGLLHLWLSCLCVSLAQGQRLRQPFPELRVAVPADRAAGGGPESPLQPLDQLSEHMLRLYDRYSG-GGAEEA-P  76
XP_004038932.1  1    M--ARASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHMLRLYDRYS---TVQAA-R  74
XP_002814965.1  1    M--AGASRLLFLWLGCFCVSLAQGERPKPPFSELRKAVPGDRTAGGGPDTELQPQDKVSEHMLRLYDRYS---TVQAA-R  74
XP_032019797.1  1    M--AGASRLLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDSELQPQDKVSEHMLRLYDRYS---TVQAE-R  74

NP_001192.4     75   TPGSLEGGSQPWRPRLLREGNTVRSFRAAAAETLERKGLYIFNLTSLTKSENILSATLYFCIGELGNISLSCPVSGGCSH  154
NP_775580.1     78   TPGSQLPG-----PQPLRGGNTVRSFRAAAAGTPQTKGLHTFNLTSLTKSENILSATLYFYVGELVNISLSCPEPQGCSH  152
NP_058801.1     78   TPGSQLPG-----PQPLRGGNTVRSFRAAAAGTLQRKGLHTFNLTSLTKSENILSATLYFYIGELVNTSVNCPESQGCSH  152
NP_001179197.1  77   TPGNSERGSPSLRPQPLREGNTVRSFRAGAAGMLENKELHIFNLTSLTKSENILSATLYFYIRELINISLSCPVSQECSH  156
NP_001193317.1  78   TPGSPEPGSPPLRPQPRREGNTVRSFRAGAAGTLENKELHVFNLTSLTKSENVLSATLYFYIGELINATLSCPASRGCSH  157
XP_038299875.1  78   ARGASERGSQPARPQPLREGNTVRSFRGGAAGTLGSKGLHIFNLTSLTKSENILSATLYFYVGELINISLSCPESRGCSH  157
XP_023493625.1  78   TPGISERGSQSLRPQPLREGNTVRSFRAGAAGTLESKGLHIFNLTSLTKSENILSATLYFYIGELINTSLSCPVSQGCSH  157
XP_027826928.1  77   TPGNSERGSPSLRPQPLREGNTVRSFRAGAAGMLENKELHIFNLTSLTKSENILSATLYFYIRELINISLSCPVSQECSH  156
XP_001144027.1  75   TPGSLEGGSQPWRPRPLREGNTVRSFRAAAAETLERKGLYIFNLTSLTKSENILSATLYFCIGELGNISLSCPVSGGCSH  154
XP_001089525.2  77   TPGSLEGGSKPWRPQSLREGNTVRSFRAAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNSSLSCPVSGGCSH  156
XP_006931098.2  78   AQRSSERGSQPLRPPPLREGNTVRSFRAGASGTLGSKGLHIFNLTSLTKSENILSATLYFYIGELINISLSCPASRGCSP  157
XP_005682010.3  77   TPGTXERGSPSLRPQPLREGNTVRSFRAGAAGMLENKELHIFNLTSLTKSENILSATLYFYIRELINISLSCPVSQECSH  156
XP_004038932.1  75   TPGSLEGGSQPWRPQPLREGNTVRSFRAAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNISLSCPVSGGCSH  154
XP_002814965.1  75   TPGSPEGGLQPWRPQPLREGNTVRSFRAAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNISLSCPVSGGCSH  154
XP_032019797.1  75   TPGSLEGGSQPWRPQPPREGNTVRSFRAAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNISLSCPVSGGCSH  154

NP_001192.4     155  HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSVDMAKSHRDIMSWLSKDITQLLRKAKENEEFLIGFNITSKGRQLPKRRLP  234
NP_775580.1     153  HTQRQHIQIDLSAWILK--SNQSQLLGHLSVDVVRPYRDSVSWLSKDITQLLRKAKQNEEFLIGFNITSRAHELPKRMLF  230
NP_058801.1     153  DSQRQHIQIDLSAWTLQ--SNQSQLLGHLSVDTAKPYRDSMSWLSKDITQLLRKAKQDEEFLIGFNITSRAHELPKRMLL  230
NP_001179197.1  157  HAQRKHIQIDLSAWILKSSGNQSQLLGHLSVDGGKPHRDFVSWLSKDITQLLRKAKENEEFLIGFNITTKGHQLPKKMTP  236
NP_001193317.1  158  HAQRRHIQISLSAWVLQLSRNQSQLLGHLSVDVAKPHRDMASWLSKDITQLLRKAKENEEFLIGFNITSRGHQLPKKVIP  237
XP_038299875.1  158  HAQRKHMQIDLSVSILKSDRNQSQLFGHLSVDVAKSHRDFGSWLSKDITQLLRKAKENEEFLIGFNITSKGHQLPKKRLP  237
XP_023493625.1  158  HAQRKHIQIDLSAWILKSNRNQSQLLGNLSVDVAKPHRDFVSWLSKDITQFLRKAKENEEFLIGFNITSKGHQLPKKMLP  237
XP_027826928.1  157  HAQRKHIQIDLSAWILKSSGNQSQLLGHLSVDGGKPHGDFVSWLSKDITQLLRKAKENEEFLIGFNITTKGHQLPKKMTP  236
XP_001144027.1  155  HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSVDMAKSHRDIMSWLSKDITQFLRKAKENEEFLIGFNITSKGHQLPKRRLP  234
XP_001089525.2  157  HAPRKHIQIDLSAWILKFNRNQSQLLGHLSVDMAKSHRDIMSWLSKDITQFLRKAKENEEFLIGFNITSKGHQLPKRMLP  236
XP_006931098.2  158  HAQRKHVLIDLSAWILKSDRNQSQHLGHLSVDVAKSHRDLGSWLSKDITQLLRRAKENEEFLIGFNITSKGHQLPKKMLP  237
XP_005682010.3  157  HAQRKHIQIDLSAWILKSSGNQSQLLGHLSVDGGKPHGDFVSWLSKDITQLLRKAKENEEFLIGFNITTKGHQLPKKMTP  236
XP_004038932.1  155  HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSVDMAKSHRDIMSWLSKDITQFLRKAKENEEFLIGFNITSKGHQLPKRRLP  234
XP_002814965.1  155  HAQRKHIQIDLSAWTLKFSRNPSQLLGHLSVDMAKSHRDIMSWLSKDITQFLRKAKGNEAFLIGFNVTSKGHQLPKRRLP  234
XP_032019797.1  155  HAHSKHIQIDLSAWTLKFSRNQSQLLSHLSVDMAKSHQDIMSWLSKDITQFLRKAKENEEFLIGFNITSKGHQLPKRRLP  234

NP_001192.4     235  FPEPYILVYANDAAISEPESVVSSLQGHRNFPTGTVPKWDSHIRAALSIERRK-KRSTGVLLPLQNNELPGAEYQYKKDE  313
NP_775580.1     231  FPEPYILVYANDAAISEPESVVSSLQRHRDFTAGTGPRLDSHVREALSVERRK-KRSTGILLPLQNNELPGAEYQYKEEG  309
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NP_058801.1     231  FPEPYILVYANDAAICEPESVVSSLQRHRDFTAGTVPRLDSHVREALSVERRK-KRSTGILLPLQNNELPGAEYQYKEAG  309
NP_001179197.1  237  SPEPYILVYANDAAISEPESVVSSLQGHRNFPTGAVPKLDSQSRSAPSIERRRrKRSTGVLLPLQNNELPGAEYQYKEDE  316
NP_001193317.1  238  FPEPYILVYANDAAISEPESVVASLQGHRNFPAGAVPKLDRHLRAALSTERRR-KRSAGLLLPLQNNELPGAEYQYKEDG  316
XP_038299875.1  238  FPEPYILVYANDAAISEPESVVSSLQGHRNFATGTMPKLASHIRAALSIERRK-KRSAGVLLPLQNNELPGAEYQYREDG  316
XP_023493625.1  238  FPEPYILVYANDAAISEPENVVSSLQGHRNFPIGAVPKLDSHIRAALSIERRK-KRSTGVLLPLQNNELPGAEYQYKEEG  316
XP_027826928.1  237  SPEPYILVYANDAAISEPESVVSSLQGHRNFPTGAVPKLDSHSRAALSMERRRrKRSTGVLLPLQNNELPGAEYQYKEDR  316
XP_001144027.1  235  FPEPYILVYANDAAISETESVVSSLQGHRNFPTGTVPKWDSHIRAALSIERRK-KRSTGVLLPLQNNELPGAEYQYKKDE  313
XP_001089525.2  237  FPEPYILIYANDAAISEPESVVSSLQGHQNFPTGTVPKWDSHIRAALSIERRK-KRSTGVLLPLQNNELPGAEYQYKKDE  315
XP_006931098.2  238  FPEPYILVYANDAAISEPESVVSSLQRHRNFPIGAVPRPDGHIKAALSTERRR-KRSAGVLLPLQNNELPGAEYQYREDG  316
XP_005682010.3  237  SPEPYILVYANDAAISEPESVVSSLQGHRNFPTGAVPKLDSHSRAALSMERRRrKRSTGVLLPLQNNELPGAEYQYKEDR  316
XP_004038932.1  235  FPEPYILVYANDAAISQPESVVSSLQGHRNFPTGTVPKWDSHIRAALSTERRK-KRSTGVLLPLQNNELPGAEYQYKKDE  313
XP_002814965.1  235  FPEPYILVYANDAAISEPESVVSSLQGHQNFPTGTVPKWDSHIRAALSIERRK-KRSTGVLLPLQNNELPGAEYQYKKDE  313
XP_032019797.1  235  FPEPYILVYANDAAISEPESVVSNLQGHQNIPTGTVPKWDSHIRAALSIERRK-KRSTGVLLPLQNNELPGAEYQYKKDE  313

NP_001192.4     314  VWEERKPYKTLQAQAPEKSKNKKKQRKGPHRKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  393
NP_775580.1     310  AWEERKPYKSLQTQPPEKSRNKKKQRKGSHQKGQTLQFDEQTLKKARRKQWVEPRNCARRYLKVDFADIGWSEWIISPKS  389
NP_058801.1     310  VWEERKPYKSLQTQPPEKSRSKKKQRKGPHQKGQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  389
NP_001179197.1  317  VWEERKPYKTLQTQPPDKSKNKKKQRKGPQQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  396
NP_001193317.1  317  VWEERKPYKTLQTQPPEKSKNKKKQRKGPHQKSQTLQFDEQTLKKARRRQWIEPRNCARRYLKVDFADIGWSEWIISPKS  396
XP_038299875.1  317  VWEEKKPYKTLQTQAPEKTKNKKKQRKGLHQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  396
XP_023493625.1  317  VWEERKPYKTLQTQPPEKSKNKKKQRKGPQQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  396
XP_027826928.1  317  VWEERKPYKTLQTQPPDKSKSKKKQRKGPQQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLRVDFADIGWSEWIISPKS  396
XP_001144027.1  314  VWEERKPYKTLQTQPPEKSKNKKKQRKGPHQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  393
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XP_005682010.3  317  VWEERKPYKTLQTQPPDKSKSKKKQRKGPQQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLRVDFADIGWSEWIISPKS  396
XP_004038932.1  314  VWEERKPYKTLQTQPPEKSKNKKKQRKGPHQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  393
XP_002814965.1  314  VWEERKPYKTLQTQPPEKSKNKKKQRKGPHQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  393
XP_032019797.1  314  VWEERKPYKTLQTQPPEKGKNKKKQRKGPHQKSQTLQFDEQTLKKARRKQWIEPRNCARRYLKVDFADIGWSEWIISPKS  393

NP_001192.4     394  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  472
NP_775580.1     390  FDAFYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVSGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVDSCACR  468
NP_058801.1     390  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVSGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVDSCACR  468
NP_001179197.1  397  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  475
NP_001193317.1  397  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  475
XP_038299875.1  397  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  475
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XP_027826928.1  397  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  475
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XP_001089525.2  396  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  474
XP_006931098.2  397  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  475
XP_005682010.3  397  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  475
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XP_002814965.1  394  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  472
XP_032019797.1  394  FDAYYCSGACQFPMPKSLKPSNHATIQSIVRAVGVVPGIPEPCCVPEKMSSLSILFFDENKNVVLKVYPNMTVESCACR  472
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Lefty1/2

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NP_066277.1 left-right determination factor 1 preproprotein [Homo sapiens]
NP_034224.1 left-right determination factor 1 preproprotein [Mus musculus]
NP_001102550.1 left-right determination factor 1 precursor [Rattus norvegicus]
XP_038527596.1 LOW QUALITY PROTEIN: left-right determination factor 1 [Canis lupus familiaris]
XP_023488302.1 left-right determination factor 1 [Equus caballus]
XP_001138066.1 left-right determination factor 1 [Pan troglodytes]
XP_014970690.1 left-right determination factor 1 [Macaca mulatta]
XP_023103692.2 left-right determination factor 1 [Felis catus]
XP_004028529.2 left-right determination factor 1 [Gorilla gorilla gorilla]
XP_002809441.3 left-right determination factor 1 isoform X1 [Pongo abelii]
XP_031992497.1 left-right determination factor 1-like [Hylobates moloch]
NP_003231.2 left-right determination factor 2 isoform 1 preproprotein [Homo sapiens]
NP_796073.1 left-right determination factor 2 preproprotein [Mus musculus]
NP_001007557.1 left-right determination factor 2 precursor [Rattus norvegicus]
NP_001192972.2 left-right determination factor 2 precursor [Bos taurus]
NP_001182275.1 left-right determination factor 2 precursor [Sus scrofa]
XP_004013679.2 left-right determination factor 2 [Ovis aries]
XP_514238.2 left-right determination factor 2 [Pan troglodytes]
XP_028681962.1 left-right determination factor 2 [Macaca mulatta]
XP_017915466.1 PREDICTED: left-right determination factor 2 isoform X1 [Capra hircus]
XP_004028532.1 left-right determination factor 2 isoform X1 [Gorilla gorilla gorilla]
XP_002809438.1 left-right determination factor 2 isoform X1 [Pongo abelii]
XP_031992501.1 left-right determination factor 2 isoform X1 [Hylobates moloch]
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NP_066277.1      1    MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYVALLQRSHGDRSRGKRFSQ  80
NP_034224.1      1    MPFLWLCWALWALSLVSLREALTGEQILGSLLQQLQLDQPPVLDKADVEGMVIPSHVRTQYVALLQHSHASRSRGKRFSQ  80
NP_001102550.1   1    MRFLWLCWALWALFQVSPGEALTGEQVLGSLLQQLRLDRPPVLDKADVEGMVIPSHVRAQYVALLQHSHDSRSRGKRFSQ  80
XP_038527596.1   1    MTPVWLCWALWALPLTGPGAALSGERILGGLLRQLHLSQVPVLDEGEVEALVTPAHVTAQYVALLRRSHGAHSRGKRFSQ  80
XP_023488302.1   1    MQPVWLCWALWALPLTGPGAALTEEQILGSLLQQLHLSEMPALDQGDVGQLVIPTHVRAQYVALLQRSHGAHSRGKRFSQ  80
XP_001138066.1   1    MQPLWLCWTLWVLPLASPGAALTGEQLLGSLLRQLQLREVPTLDRADMEELVIPTHVRAQYVALLQRSHGDCSRGKRFSQ  80
XP_014970690.1   1    MRPLWLCWALWVLPLAGPGTALTGEQLLGSLLQQLQLSEAPVLDRADMEELVIPAHVRAQYVTLLQRSHGDRSRGKRFSQ  80
XP_023103692.2   1    MRPLWLCWALWALPLTGPGAALTGEQVRASLLRQLGLREAPVLDQRDVEGLVTPAHVRAQYVALLRRSHGAHSRRKRFSQ  80
XP_004028529.2   1    MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLREVPTLDRADMEELVIPTHVRAQYVALLQRSHGDRSRGKRFSQ  80
XP_002809441.3   1    MQPLWLCWALWVLPLASPGAALTGEQLLGSLLQQLQLREVPTLDRAYMEELVIPTHVRAQYVALLRRSHGDRSRGKRFSQ  80
XP_031992497.1   1    MRPLWLCWALWVLPLAGPAVALTGEQLLGSLLRQLQLREAPTLDRADMEELVIPTHVRAQYVALLQRSHGDRSRGKRFSQ  80
NP_003231.2      1    MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQ  80
NP_796073.1      1    MKSLWLCWALWVLPLAGPGAAMTEEQVLSSLLQQLQLSQAPTLDSADVEEMAIPTHVRSQYVALLQGSHADRSRGKRFSQ  80
NP_001007557.1   1    MQSLWLCWTLCVLPLAGPGAAVTEEQVLSSLLKQLQLSQAPVLDRVDVEGMAIPTHVSSQYVALLQGSHADRSRGKRFSQ  80
NP_001192972.2   1    MQPLWLCWALWVLPLAGPGAALTEERILDSLLQQLHLSEVPIVDKATVEGLVIPAHVRAQYVALLQRGHGARSRGKRFSQ  80
NP_001182275.1   1    MRALWLCWALWALPLAGPGAALTEQQILGSLLQQLHLSEVPALDKADVDGLVIPAHVRAQYVALLQRSHGARSRGKRFSQ  80
XP_004013679.2   1    MRPLWLCWALWVLPQAGPGAALTEERILDSLLQQLHLSEVPIMDKAAVEGLVIPAHVRAQYVALLQRGHGARSRGKRFSQ  80
XP_514238.2      1    MWPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQ  80
XP_028681962.1   1    MRPLWLCWALWVLPLAGPGVAMTGEQLLGSLLQQLQLSEVPVPDRVDMEELVIPAHVRAQYVALLRRSHGDRSRGKRFSH  80
XP_017915466.1   1    MRPLWLCWALWVLPLAGPGAALTEERILDSLLQQLHLSEVPIVDKAAVEGLVIPAHVRAQYVALLQRGHGARSRGKRFSQ  80
XP_004028532.1   1    MWPLWLCWALWVLSLAGPGAALTEEQLLGSLLRQLQLSEVPVLNRADMEKLVIPAHVRAQYVVLLRRSHGDRSRGKRFSQ  80
XP_002809438.1   1    MRPLWLCWALWVLPLAGPGAALTEEQLLGSLLRQLQLSEVPTLDRADMEKLVIPAHVRAQYVALLRRSHGDRSRGKRFSQ  80
XP_031992501.1   1    MRPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLSEVPVLDRADMEKLVIPDHVRAQYVALLRRSHGDRSRGKRFSQ  80

NP_066277.1      81   SFREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRT  160
NP_034224.1      81   NLREVAGRFLVSETSTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPRTALRRQKRLSPHSARARVTIEWLRFRDDGSNRT  160
NP_001102550.1   81   NFREVAGRFLVSETSSHLLVFGMEQRLPPNSELVQAVLRLFQEPVPRTALRRQKRLSPHSARARVTIEWLRFREDGSNRT  160
XP_038527596.1   81   RFREVAGRWLATEASTHLLVFGMERRLPPNSELLRAVLRLFQEPVPRAALRRLERLSPHSARARVTIEWLQVRDDGPNRT  160
XP_023488302.1   81   DFREVAGRLLGSDASRHLLVFAMEQRLPPDRELLQAVLRLFQEPVPEAALRTHGRLSPRSHRARVTVEWLHVRDDGSNRT  160
XP_001138066.1   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAWARVTVEWLRVRDDGSNRT  160
XP_014970690.1   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKATLHRHGRLSPRSARARVTVEWLRVRDDGSNRT  160
XP_023103692.2   81   RVREVAGRLLAAEASTHVLVFGMEGRLPPNSELVQAVLRLFQEPVPKAALRRLERLSPHGARVRVTVEWLRIHEDSSNHT  160
XP_004028529.2   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQQPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT  160
XP_002809441.3   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT  160
XP_031992497.1   81   SFREVAGRFLASEASTHLLVFSMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRT  160
NP_003231.2      81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT  160
NP_796073.1      81   NFREVAGRFLMSETSTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPRTALRRFERLSPHSARARVTIEWLRVREDGSNRT  160
NP_001007557.1   81   NFREVAGRFLVSETSSHLLVFGMEQRLPPNSELVQAMLRLFQEPVPRTALRRLERLPPHSAQARVTIEWLRVREDGSNRT  160
NP_001192972.2   81   NFREVVGRFLTSEASSHLLVFDMEQRLPPRSELVQAVLRLFQEPVPRAALRRHERLFPRSDRARVTVQWLHVRDDGSNRT  160
NP_001182275.1   81   NFREVVGRFLLSEASTHLLVFDMEQRLPPHSELVQAVLRLFQEPVPKAALRRHERLFPRSDRARVTVQWLHIREDGSNRT  160
XP_004013679.2   81   NFREVVGRFLASETSSHLLVFHMEQRLPPRSELVQAVLRLFQEPVPRAALRRHERLFPRSDRARVTVQWLHVRDDGSNRT  160
XP_514238.2      81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT  160
XP_028681962.1   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKATLHRHGRLSPRGARARVTVEWLRVRDDGSNRT  160
XP_017915466.1   81   NFREVVGRFLASETSSHLLVFDMEQRLPPRSELVQAVLRLFQEPVPRAALRRHERLFPRSDRARVTVQWLHVRDDGSNRT  160
XP_004028532.1   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT  160
XP_002809438.1   81   SFREVAGRFLASEASTHLLVFGMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSAQARVTVEWLRVRDDGSNRT  160
XP_031992501.1   81   SFREVAGRFLASEASTHLLVFSMEQRLPPNSELVQAVLRLFQEPVPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRT  160
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NP_066277.1      161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
NP_034224.1      161  ALIDSRLVSIHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSSHKLVRFAAQG-TPdgKG-QGEPQLE  238
NP_001102550.1   161  ALIDSRLVSIHESGWKVFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQG-TPdgKG-LGEPQLE  238
XP_038527596.1   161  SLVDSRLVSLHESGWKAFDVTEAVTFWQQLSRPRQPLLLQVSVQREHLGPPASGAHRLVRFASQG-XPraPG-QGEPRLE  238
XP_023488302.1   161  SLIDSRLVSVHESGWKAFDVTEAVNFWRQLGRPRQPLLLQVSVQREQPGPRAASAHRLVRFASQGpAG--GG-RGEPQLE  237
XP_001138066.1   161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_014970690.1   161  SLIDSRLVSVHESGWKVFDVTEAVNFWQQLSRPRQPLLLQVSVQREHPGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_023103692.2   161  YLVDSRLVSLQGSGWKAFDVTEAVNFWRQLGRSGQPLLLQVSVQRAHLGPRASGAHTLLRFASQG--QegTG-QGEPQLE  237
XP_004028529.2   161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLNRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_002809441.3   161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_031992497.1   161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--VG-LGEPQLE  236
NP_003231.2      161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
NP_796073.1      161  ALIDSRLVSIHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQG-TPdgKG-QGEPQLE  238
NP_001007557.1   161  ALIDSRLVSIYESGWKVFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPGTWSAHKLVRFAAQG-TPdgK---GEPQLE  236
NP_001192972.2   161  ALIDSRLVTIHESGWKALDVTEAVNFWQQLRSPRQPLLLQVLVQREHLGPLASSAHRLVRFAPQG-PS--SGwQGEPQLE  237
NP_001182275.1   161  SLIDSRLVSIHESGWQALDVTEAVTFWQQLRRPRQPLLLQVSVQREPPGPRGSDAHRLVRFASQG-PS--GGgQGEPQLE  237
XP_004013679.2   161  ALIDSRLVSIHESGWKALDVTEAVNFWQQLGSPRQPLLLQVLVQREHLGPLASSAHRLVRFAPQG-PS--SGrQGEPQLE  237
XP_514238.2      161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_028681962.1   161  SLIDSRLVSVHESGWKVFDVTEAVNFWQQLSRPRPPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_017915466.1   161  ALIDSRLVSIHESGWKALDVTEAVNFWQQLRSPRQPLLLQVLVQREHLGPLASSAHRLVRFAPQG-PS--SGrQGEPQLE  237
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XP_002809438.1   161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236
XP_031992501.1   161  SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQG-AP--AG-LGEPQLE  236

NP_066277.1      237  LHTLDLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPFLGPRQC  316
NP_034224.1      239  LHTLDLKDYGAQGNCDPEAPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCLQLPESLTSRWPFLGPRQC  318
NP_001102550.1   239  LHTLDLKDYGAQGNCDPETPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCLQPPESLTIRWPFLGPRQC  318
XP_038527596.1   239  LHTLDLGTYGAQGDCDPEVPVTQAARCCRQEVYIDLRGMKWAENWVLEPPGFLAYECVGTCQQPPRPLPFEWPLLGPRQC  318
XP_023488302.1   238  LHSLDLGRYGAQGDCDPEAPVTEGTRCCRREMYIDLEGLKWAENWVLEPPGFLAYECVGTCRQPPEPLSFKWPFLGPRQC  317
XP_001138066.1   237  LHTLDLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPFLGPRQC  316
XP_014970690.1   237  LHTLDLGDYGAQGDCDPEAPVTEGTRCCRQEMYIDLQGMKWADNWVLEPPGFLAYECVGTCQQPPEALAFKWPFLGPRQC  316
XP_023103692.2   238  LHTLDLGVYGAQGDCDPEAPAAEGARCCRQETYVDLRGMRWAENWVLEPPGFLAYECVGACQQPPEPPTFRRPFPGPRQC  317
XP_004028529.2   237  LHTLDLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCQQPPEALAFKWPFLGPRQC  316
XP_002809441.3   237  LHTLDLGDYGAQGDCDPEGPVTEGTRCCRQEMYTDLQGMKWAENWVLEPPGFLAYECVGTCQQPPEALAFKWPFLGPRQC  316
XP_031992497.1   237  LHTLDLGDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCQQPPEALAFKWPFLGPRQC  316
NP_003231.2      237  LHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQC  316
NP_796073.1      239  LHTLDLKDYGAQGNCDPEVPVTEGTRCCRQEMYLDLQGMKWAENWILEPPGFLTYECVGSCLQLPESLTIGWPFLGPRQC  318
NP_001007557.1   237  LHTLDLKDYGAQGNCDPEAPVTEGTRCCRKEMYLDLQGMKWAENWILEPPGFLIYECVGSCRQLPESLTIGWPFLGPRQC  316
NP_001192972.2   238  LHTLDLRDYGAQGNCDPKAPVTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCQQPPESLTFKWPFLGPRQC  317
NP_001182275.1   238  LHTLDLRDYGAQGNCDPKAPVTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCQQPPEPLAFRWPFLGPRQC  317
XP_004013679.2   238  LHTLDLRDYGAQGNCDPKAPVTEGTRCCRQETYIDLQGMKWAENWVLEPPGFLTYECVGTCQQPPESLTFKWPFLGPRQC  317
XP_514238.2      237  LHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQC  316
XP_028681962.1   237  LHTLDLRDYGAQGDCDPEAPVTEGTRCCRQEMYIDLQGMKWADNWVLEPPGFLAYECVGTCQQPPEALAVKWPFLGPRQC  316
XP_017915466.1   238  LHTLDLRDYGAQGNCDPKAPVTEGTRCCRQETYIDLQGMKWAENWVLEPPGFLTYECVGTCQQPPESLTFKWPFLGPRQC  317
XP_004028532.1   237  LHTLDLRDYGAQGDCDPEAPMTEGTRCCRQEMYIDLQGMKWAKNWVLEPPGFLAYECVGTCQQPPEALAFNWPFLGPRQC  316
XP_002809438.1   237  LHTLDLRDYGAQGDCDPEAPVTEGTRCCRQEMYTDLQGMKWAENWVLEPPGFLAYECVGTCQQPPEALAFKWPFLGPRQC  316
XP_031992501.1   237  LHTLDLGDYGAQGDCDPEAPVTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCQQPSEALAFNWPFLGPRQC  316

NP_066277.1      317  IASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
NP_034224.1      319  VASEMTSLPMIVSVKEGGRTRPQVVSLPNMRVQTCSCASDGALIPR   RLQP  368
NP_001102550.1   319  VASEMTSLPLIVSIKEDGRTRPQVVSLPNMRVQRCSCASDGALIPR   RLEP  368
XP_038527596.1   319  VPSETTSLPMIVTVKEGGRPRPRVVSLPNMRVQKCSCSWDGMPVPR   KLEP  368
XP_023488302.1   318  IASETTSLPVIVSVKEGGRPRAQVVSLPDMRVQKCSCASDGAPVPR   KLEP  367
XP_001138066.1   317  IASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
XP_014970690.1   317  IASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   GLQP  366
XP_023103692.2   318  VASETTSLPLIVGVKEGGRPRPQVVSLPNMRVEKCSCAWDGAPVPR   RLGP  367
XP_004028529.2   317  IASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
XP_002809441.3   317  IASETASLPMIVGIKEGGRIRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
XP_031992497.1   317  VASETASLPMIVSIKEGGKTRPQVVSLPNMRVQKCSCASDGALVPR[5]RLV-  370
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NP_001007557.1   317  VASEMTSLPMIVSIKEDGKTRPQVVSLPNMRVQTCSCASDGALIPR   GIDL  366
NP_001192972.2   318  IASEATSLPMIVSIQEGGQLQPQVVSLPNMRVQTCSCAWDGVLVPR   KLEP  367
NP_001182275.1   318  IASETTSLPVIVSIQEGGKPRPQVVSLPNMRVKRCSCAWDGAPVPR   KLEP  367
XP_004013679.2   318  IASETTSLPMIVSIQEGGRLQPQVVSLPNMRVQTCSCAWDGVLVPR   KLEP  367
XP_514238.2      317  IASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
XP_028681962.1   317  IASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
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XP_004028532.1   317  IASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
XP_002809438.1   317  IASETASLPMIVGIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
XP_031992501.1   317  IASETASLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPR   RLQP  366
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IL34

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NP_001128572.1 interleukin-34 isoform 1 precursor [Mus musculus]
XP_008770749.1 interleukin-34 isoform X1 [Rattus norvegicus]
NP_001093794.1 interleukin-34 precursor [Bos taurus]
NP_001272904.1 interleukin-34 precursor [Sus scrofa]
XP_022274925.1 interleukin-34 isoform X1 [Canis lupus familiaris]
XP_023493074.1 interleukin-34 isoform X1 [Equus caballus]
XP_012044914.3 interleukin-34 isoform X1 [Ovis aries]
XP_511082.1 interleukin-34 isoform X1 [Pan troglodytes]
NP_001181288.1 interleukin-34 precursor [Macaca mulatta]
XP_006941782.1 interleukin-34 isoform X1 [Felis catus]
XP_017917158.1 PREDICTED: interleukin-34 isoform X1 [Capra hircus]
UniProtKB G3RBA4_GORGO interleukin-34 [Gorilla gorilla gorilla]
XP_002826665.1 interleukin-34 isoform X1 [Pongo abelii]
XP_032013754.1 interleukin-34 isoform X1 [Hylobates moloch]
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XP_008770749.1  1       MPWG---LAW-LYC    LGILLDVALGNENLEIWTLAQDKECDLTGYLRGKLQYKNRLQYMKHYFPINYRIAVPY  68
NP_001093794.1  1       MPQG---LAW-LRY    LGILLGMALGNEGLEPWPLTRSDECAITGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  68
NP_001272904.1  1       MPRG---LAW-LRY    LGILLGMALGNKGLEVWPVTSSEECAITGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  68
XP_022274925.1  1   [10]LPPQ---MRWgLRL[11]LGLLLGMALGNQGLEMWPLTQNEECAVTGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  90
XP_023493074.1  1   [ 9]-PAEsdtVGWgLAL[20]FGILLGMALGNKGLEVWPLTQSEECAVTGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  100
XP_012044914.3  1       MPQG---LAW-LRY    LGILLGMALGNEGLEPWPLTRSDECAITGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  68
XP_511082.1     1       MPRG---FTW-LRY    LGIFLGVALGNEPLEMWPLTQNEECTVTGFLRDKLQYRSRLQYMKHYFPINYKISVPY  68
NP_001181288.1  1       MPRG---FAW-LRY    IGILLGMACGNEHLEIWPLTQSEECTVTGFLRDKLQYRNRLQYMKHYFPINYKISVPY  68
XP_006941782.1  1       MPRG---FAW-LHY    LGIFLAMALGNEGLEMWPLTQSEECAVTGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  68
XP_017917158.1  1       MPQG---LAW-LRY    LGILLGMALGNEGLEPWPLTRSDECAITGFLRDKLQYRNRLQYMKHYFPINYRVSVPY  68
G3RBA4_GORGO    1       MPRG---FTW-LRY    LGIFLGVALGNEPLEMWPLTQNEECTVTGFLRDKLQYRSRLQYMKHYFPINYKISVPY  68
XP_002826665.1  1       MPRG---FAL-LRY    LGIFLGMALGNEPLEMWPLTQSEECTVTGFLRDKLQYRSRLQYMKHYFPINYKISVPY  68
XP_032013754.1  1       MPRG---FAW-LHD    LGIFLGVALGNEPLEMWPLTQSEECTVTGFLRDKLQYRSRLQYMKHYFPINYKISVPY  68

NP_001380423.1  69   EGVFRIANVTRLQRAQVSERELRYLWVLVSLSATESVQDVLLEGHPSWKYLQEVETLLLNVQQGLT   DVEVSPKVESV  145
NP_001128572.1  69   EGVLRVANITRLQKAHVSERELRYLWVLVSLNATESVMDVLLEGHPSWKYLQEVQTLLENVQRSLM   DVEIGPHVEAV  145
XP_008770749.1  69   EGVLRVANITRLQKAHVSERELRYLWVLVSLNATESVLDVLLEGHPSWKYLQEVQTLLENVQRSLM   DVEIGPHVEAV  145
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NP_001272904.1  69   EGVLRTANVTRLQRARVTQRELQYLWVWVSLSATESVQEVLLEGHPSWKYLEEVHTLLLDVRQGLA   GVEISPQVEAV  145
XP_022274925.1  91   EGVLRMANITRLQRARVSQQELRYLWVWVSLSATESVQEVLLEGHPSWKYLEDVHTLLLDVQQSLT[7]DVEVGPKVEAV  174
XP_023493074.1  101  EGVLRMANVTRLQRARVSQQELRYLWVWVSLSATEWVQEVLLEDHPSWKYLEEVHTLLLDVQQSLR   DVEVSPQVEAV  177
XP_012044914.3  69   EGVLRTANITRLQRARVSQQELRYLWVLVSLSATEWVQEVLLEGHPSRKFLEEVHTLLLDVKQGLR   GMEVSPQVEAV  145
XP_511082.1     69   EGVFRIANVTRLQRAQVSERELRYLWVLVSLSATESVQDVLLEGHPSWKYLQEVQMLLLNVQQGLT   DVEVSPKVESV  145
NP_001181288.1  69   EGVFRIANVTRLQRARVSERELRYLWVLVSLSATESVQDVLLDGHPSWKYLQEVQTLLLNVQKGLM   DVEVSPKVESV  145
XP_006941782.1  69   EGVLRMANITRLQRAQVSQQELRYLWVWVSLSATESVQEVLLEGHPSWKFLEEVHTLLLDVQQGLT   DVEVSPKVEAV  145
XP_017917158.1  69   EGVLRTANITRLQRARVSQQELRYLWVLVSLSATEWVQEVLLEGHPSRKFLEEVHTLLLDVKQGLR   GMEVSPQVEAV  145
G3RBA4_GORGO    69   EGVFRIANVTRLQRAQVSERELRYLWVLVSLSATESVQDVLLEGHPSWKYLQQVQTLLLNVQQGLT   DVEVSPKVESV  145
XP_002826665.1  69   EGVFRIANVTRLQRALVSERELRYLWVLVSLSATESVQDVLLEGHPSWKYLQEVQTLLLNVQQGLM   DVEVSPKVESV  145
XP_032013754.1  69   EGVFRIANVTRLQRAQVSERELRYLWVLVSLSATESVQDVLLEGHPSWKYLQEVQTLLLNVQQGLT   DVEVSPKVESV  145

NP_001380423.1  146  LSLLNAPGPNLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQSCSPE-PSLQYAATQLYPPPPWSPSSPP  224
NP_001128572.1  146  LSLLSTPGLSLKLVRPKALLDNCFRVMELLYCSCCKQSPILKWQDCELPRLHPHSPG-SLMQCTATNVYPLSRQTPTSLP  224
XP_008770749.1  146  LSLLSTPGLSLKLVRPKALLDNCFRVMELLYCSCCKQSPILKWQDCELPRLHPHSPE-SLMQCAATNVYPLPRQPPTSLP  224
NP_001093794.1  146  LNLLSAPG-SLKLVRPKALLDNCFRVMQLLYCPCCKESSVLNWQDCEAPQPQPRSP--ASAQCEAAQLYPLPQPPSTSLP  222
NP_001272904.1  146  LSLLSAPG-SLKLVRPKALLDNCFRVMEQLYCSCCKHSSILNWQDCEVPGPQPHSPE-PSSQCVAAQLYPLPQQPPTSLP  223
XP_022274925.1  175  VSLLSAPRLSLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQHHSPE-PSSQCVAAQLYPLSQSPPISLP  253
XP_023493074.1  178  LSLLSAPGLSLKLVRPKALLDNCFRVMELLYCPCCKHSSVLNWQDCELPSPQPHSPEsSSSQCVAAQLYPWPQQPPTSLP  257
XP_012044914.3  146  LNLLSAPG-SLKLVRPKALLDNCFRVMELLYCPCCKESSVLNWQDCEAPQPQARSP--ASAQCEATQLYPLPQPPSTSLP  222
XP_511082.1     146  LSLLNAPGPNLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQSCSPE-PSLQYAATQLYPPPPWSPSSPP  224
NP_001181288.1  146  LSLLNAPGPNLKPVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQSYCPE-PSLQYAATQLYPPPPWSPSSPP  224
XP_006941782.1  146  VSLLSTPRLSLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQPHSPE-PSSQCVAAPLYPLPQQPPISLP  224
XP_017917158.1  146  LNLLSAPG-SLKLVRPKALLDNCFRVMELLYCPCCKESSVLNWQDCEAPQPQARSP--ASAQCEATQLYPLPQPPSTSLP  222
G3RBA4_GORGO    146  LSLLNAPGPNLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQSCSPE-PSLQYAATQLYPPP--------  216
XP_002826665.1  146  LSVLNAPGPNLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQSCSPE-PSLQYAATQLYPPPPWSPSSPP  224
XP_032013754.1  146  LSLLNAPGPNLKLVRPKALLDNCFRVMELLYCSCCKQSSVLNWQDCEVPSPQSYSPE-PSLQYAATQLYPPPPWSPSSPP  224

NP_001380423.1  225  HSTGSVRPVRAQ[6]  242
NP_001128572.1  225  GSPSSSHGSLP-     235
XP_008770749.1  225  RSPSSNHGPLP-     235
NP_001093794.1  223  RVLGPSAGPPTQ     234
NP_001272904.1  224  RSPGPTAGSLDP     235
XP_022274925.1  254  RSPRSKPGAPAP     265
XP_023493074.1  258  RSPGSEAGVPPQ     269
XP_012044914.3  223  RVLGPSAGPPTQ     234
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XP_511082.1     225  HSTGSVRPVRAQ[6]  242
NP_001181288.1  225  HSTGLARPVRAQ[6]  242
XP_006941782.1  225  RSPGPKTGPPAQ     236
XP_017917158.1  223  RVLGPSAGPPTQ     234
G3RBA4_GORGO    216  ------------     216
XP_002826665.1  225  HSTGSARPVRAQ[6]  242
XP_032013754.1  225  NSTGSVRPVRAQ[6]  242
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Figure S16. Analysis in the BMP-TGFß family of the conservation of the amino acids implicated in the binding to IL34 using COBALT alignment tool (NCBI). Alignment of the human protein sequences of the 29 BMP-TGFß family members was first given with amino acids implicated in the binding to IL34 conserved comparatively to BMP2 overlined in green, those changed by another with close physical-chemical proprieties overlined in blue and those changed by another with different physical-chemical proprieties overlined in yellow. Secondly for each BMP-TGFß family members the phylogenic conservation in mammalian (15 species) of the amino acids implicated in the binding to IL34 was analyzed and given. Finally, the phylogenic conservation of the amino acids of IL34 implicated in the binding to BMPs was also analyzed in the same 15 mammalian species and presented.

Supplementary figure 17

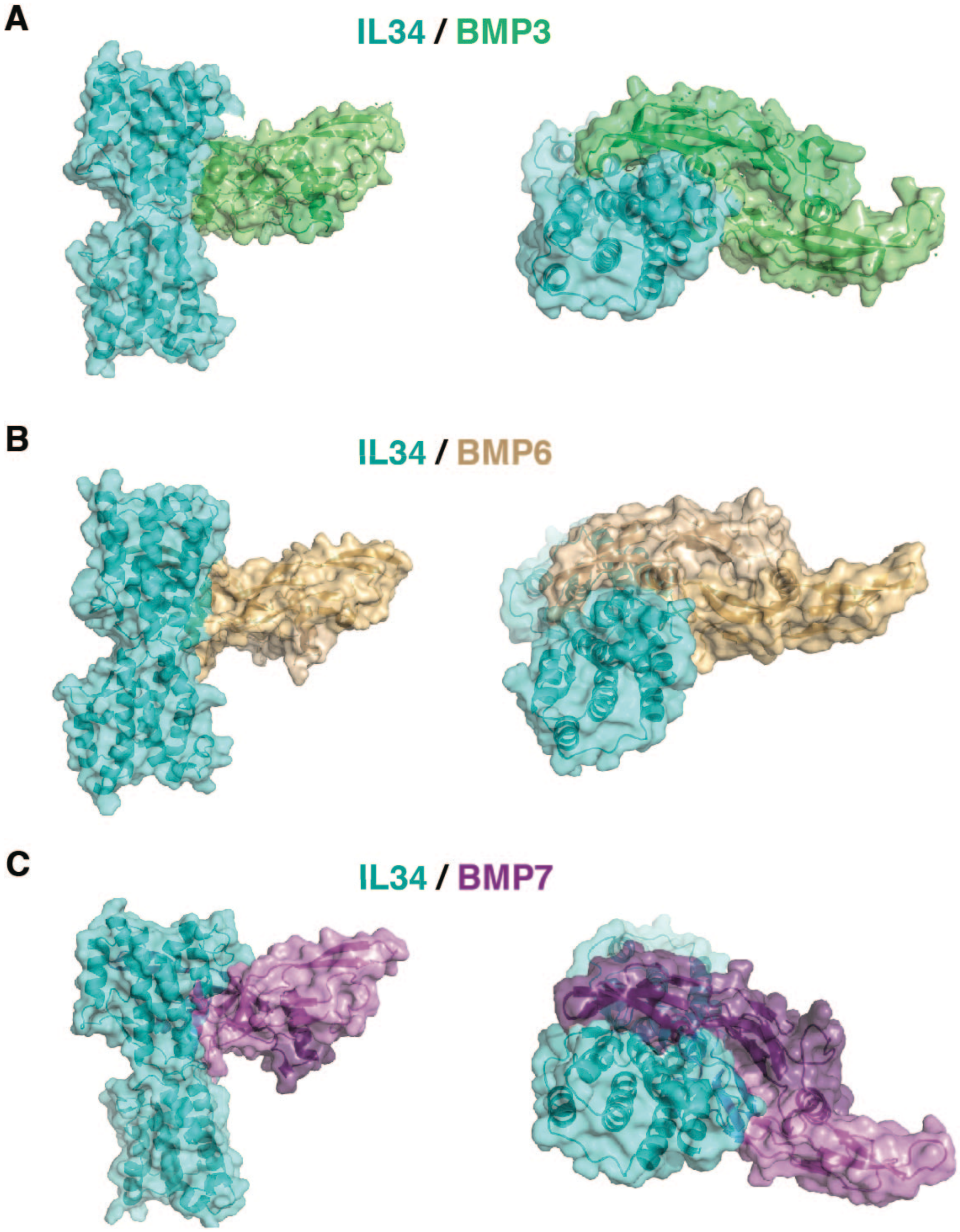


Figure S17. Representative structures of IL34 binding to different BMP proteins. IL34 is displayed in cyan surface. (**A**) IL34 binding to BMP3 structure (lime color) as found PDB ID 2QCQ [80]. (**B**) IL34 binding to BMP6 structure (wheat color) as found PDB ID 2R52 [81]. (**C**) IL34 binding to BMP7 structure (purple color) as found PDB ID 1BMP [82]. Left: side view of protein complexes, right: top view of protein complexes.

Supplementary figure 18

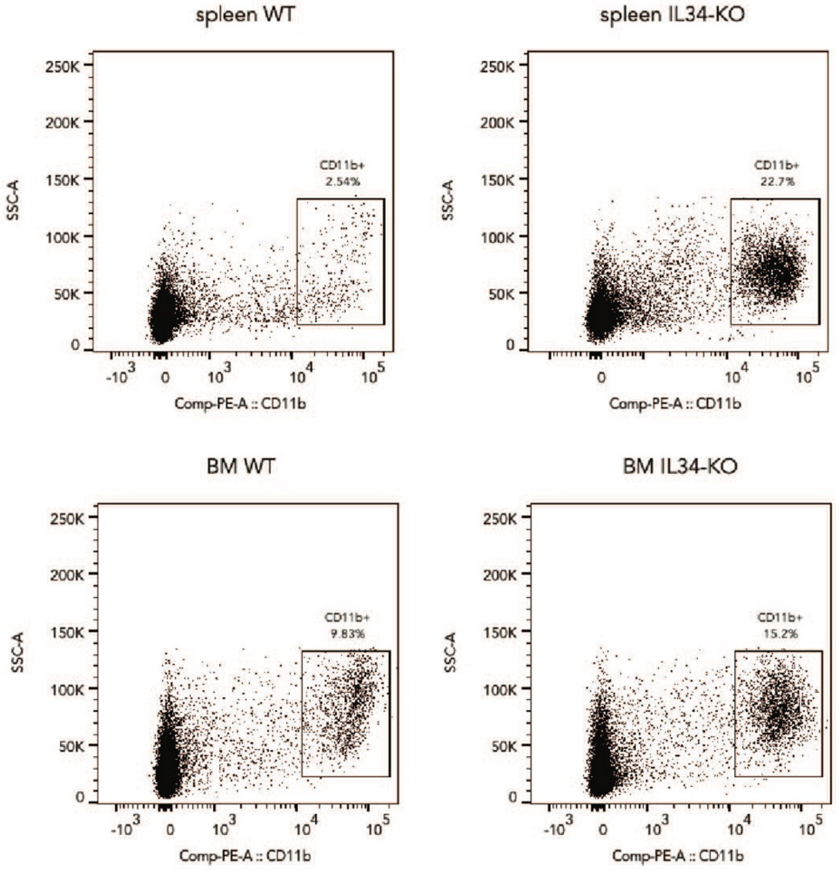
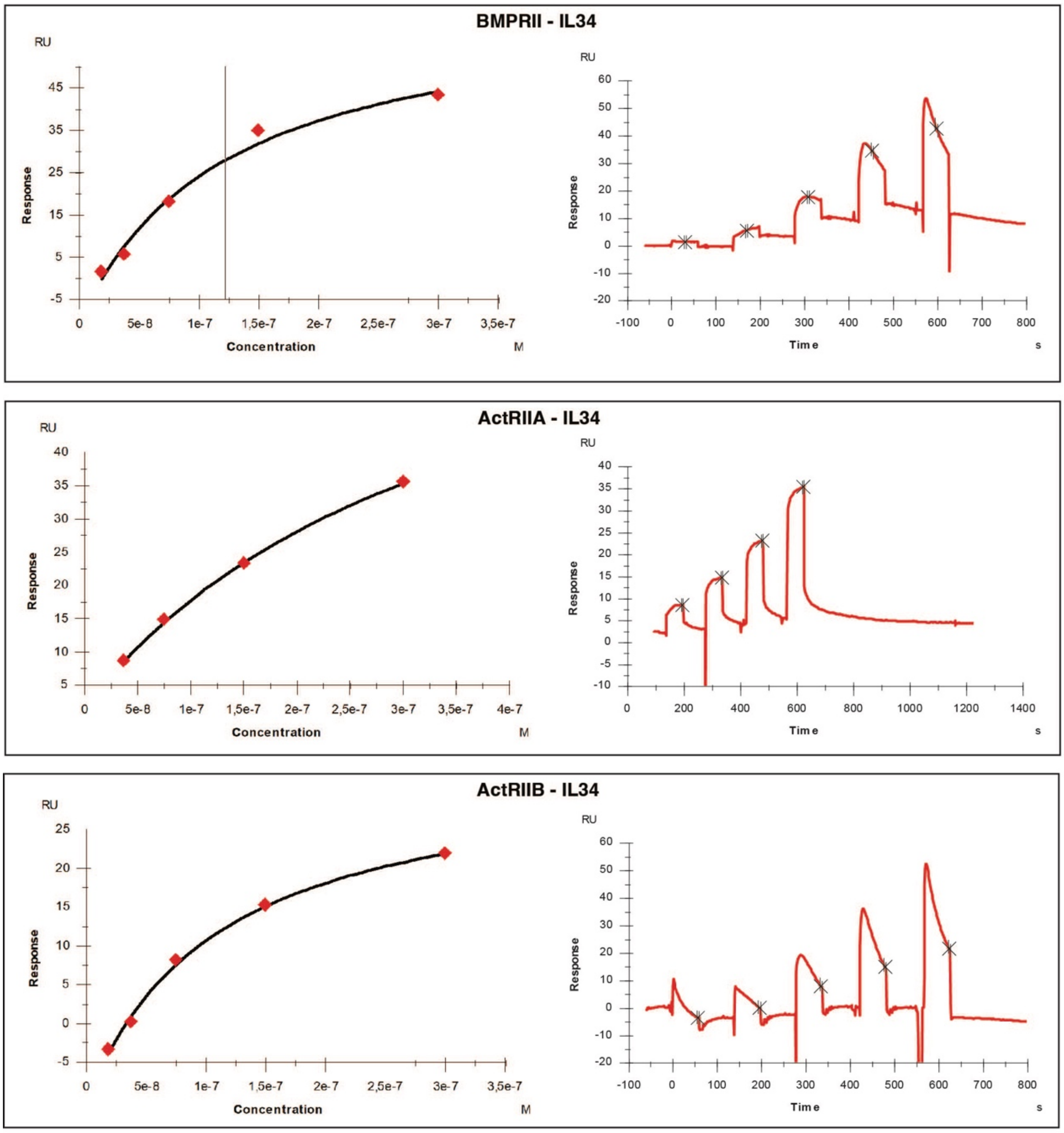


Figure S18. FACS comparative analysis of the populations of CD11b monocytic cells in both the bone marrow and the spleen of *Il34*$^{-/-}$ versus *Il34*$^{+/+}$ mice. In *Il34*$^{-/-}$ (IL34-KO) mice compared with *Il34*$^{+/+}$ (WT) mice, significant increases in the percentage of CD11b-positive cells were observed in both spleen (22.7% vs. 2.54%) and bone marrow (15.2% vs. 9.83%).

Supplementary figure 19



hIL34 affinity to receptors

	KD (M)
BMPRII	1.2 +/- 0,6 E-07
ActRIIA	3.6 +/- 0,7 E-07
ActRIIB	1.1 +/- 0,3 E-07

Figure S19. Demonstration at the molecular level of the physical interaction between the IL34 protein and proteins of the BMP receptor type II family. The surface plasmon resonance experiments showed that IL34 bound efficiently to BMPRII, ACTRIIA and ACTRIIB with KD values of 1.2E-07 M, 3.6E-07 M and 1.1E-07 M respectively.

Supplementary movie (S1)

Movie S1. Movie evidencing the simultaneous binding of one IL34 monomer (cyan), one BMPR1A monomer (green) and one ACVR2A monomer (red) on a dimer of BMP2 (blue and orange).