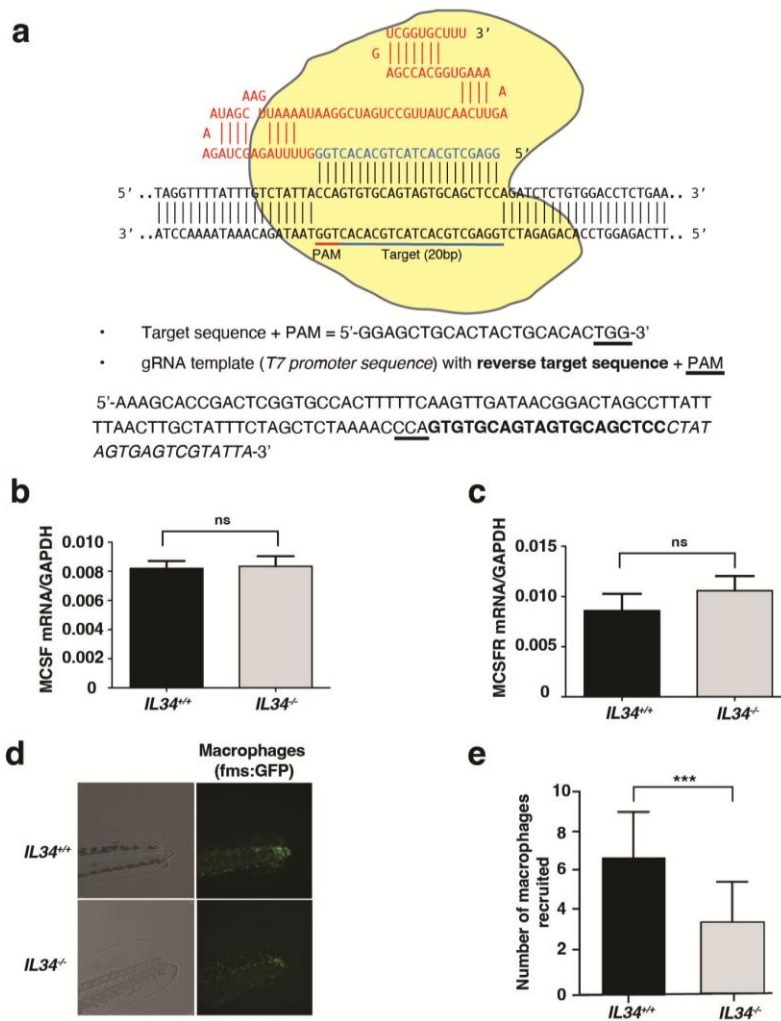


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Supplementary figure 1

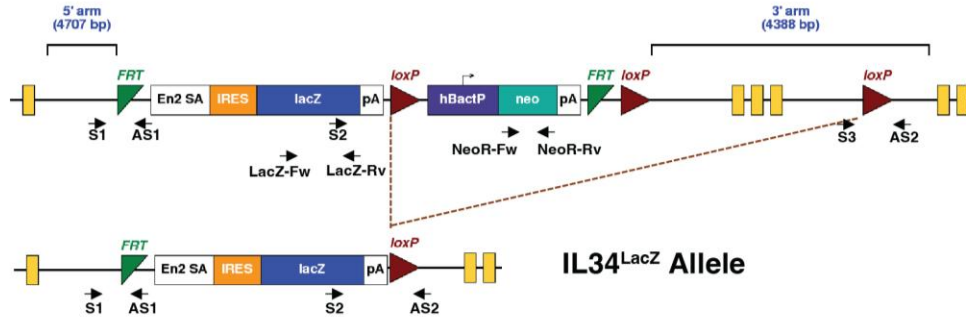


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Figure S1. Tools to *IL34* genetic invalidation in zebrafish using CrispR/Cas9 technology and functional confirmation. (A) Schematic representation of the targeted sequence in *il34* exon 3 including the protospacer adjacent motif (PAM) and the use 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

IL34^{Flox} Allele (GenBank:JN962093.1)



Primer S3

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WT   GTTTGGCCGATGC TGGCAAAGGGCTAAGAAGGGAGAGTCTGC CATGC GCTGACATGTGAG 62
FLOX GTTTGGCCGATGC TGGCAAAGGGCTAAGAAGGGAGAGTCTGC CATGC GCTGACATGTGAG 62
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WT   ACACACGAGGGATGGG GACAGAGAGGATTTGG ACC TTGTTTC AAGCTTAC CTGAGCGCCCC 124
FLOX ACACACGAGGGATGGG GACAGAGAGGATTTGG ACC TTGTTTC AAGCTTAC CTGAGCGCCCC 124
*****

WT   TCTTAAAAAAATTTT TTTTATATGTTGTTGTTT TAAATTTA TAACCCATTGAGTCCAAATTC 186
FLOX TCTTAAAAA----- 133
*****

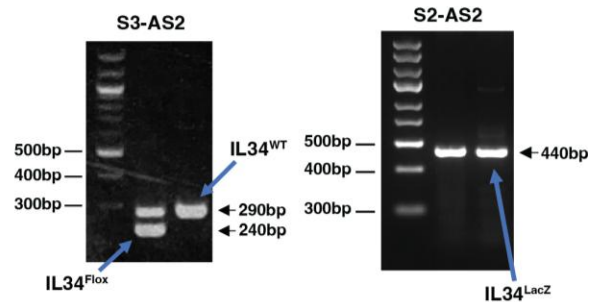
WT   TTCTGCCACTGT TCACTACCCACGCTGGCTAG ACC TTGTA CAGGTGTGTGAGGTTAACAG 248
FLOX ----- 133
*****

WT   TGTACTCATGGGTGC----- 263
FLOX -----GAGATGCGCAACGCAATTAATGATAAC TTCGTATAGCATACATTA 180
*****

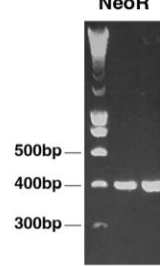
WT   -----ACCGGCA TGCCA TC TTC AT AAGACAG 290
FLOX ACGAAGTTATGGTCTGAGCTCGCATCA GTTCAACCGGCA TGCCA TC TTC AT AAGACAG 240
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Primer AS2

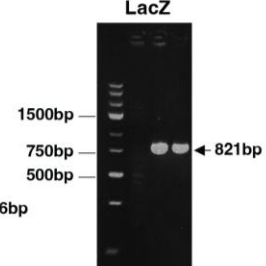
Genotyping



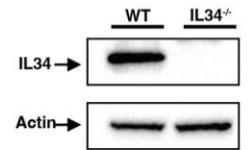
Primers NeoR



Primers LacZ



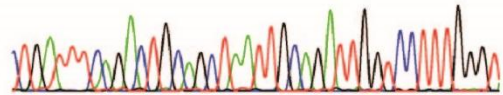
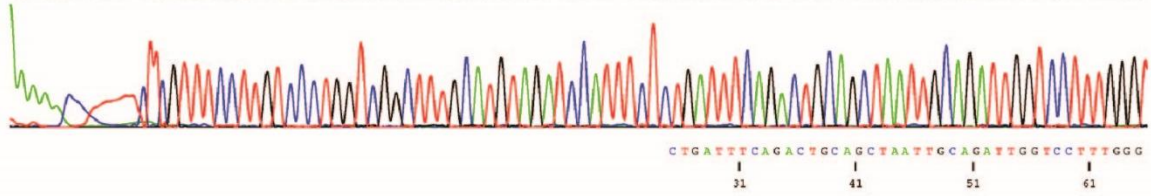
Primers	Sequence	Position in GenBank:JN962093.1
S1	5'-AAAAACCTTCTTCGTTTCC TTGTCCC-3'	14853-14879
S2	5'-GTCAGTATCGGCGGAATT-3'	19807-19825
S3	5'-GTTTGGCCGATGCTGCAAAAGG-3'	23879-23901
AS1	5'-CTCCTACATAGTTGGCAGTG-3'	15202-15222
AS2	5'-CTGTCTTATGAAGATGGCATGCC-3'	24095-24118
LacZ-Fw	5'-CATCGAGCTGGGTAATAAGCGTTGGCAAT-3'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



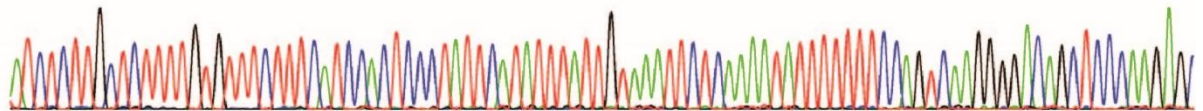
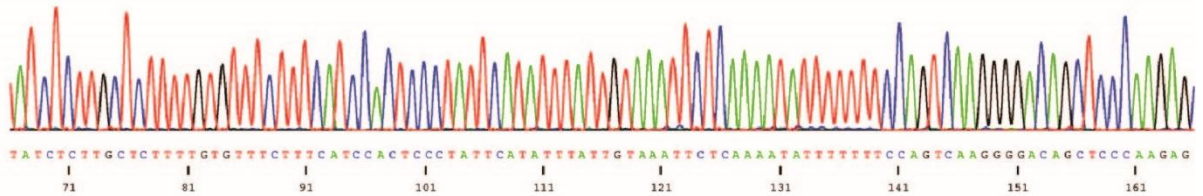
Sanger sequencing of fragment amplified by PCR with S1-AS1 primers on genomic DNA from IL34LacZ/LacZ Mouse

Primer S1

AAAAACCTTCTTCGTTTCCTTGTCCTGGTTCGGCTTGCATGTAGATCCATTTCTCTGATTTTCAGACTGCAGCTAATTGCAGATTGGTCCTTTGGG

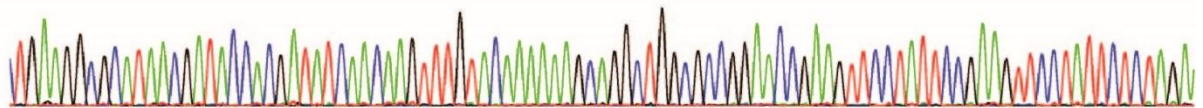
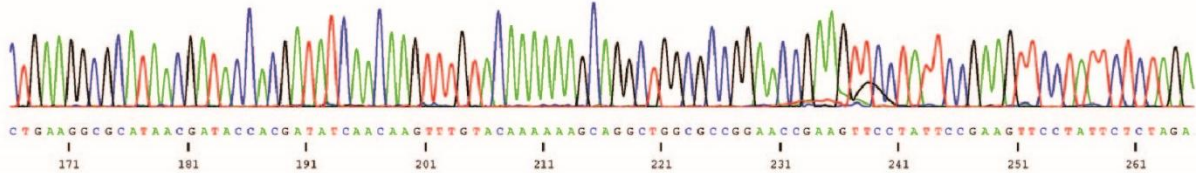


TATCTCTGCTCTTTTGTGTTTCTTTCATCCACTCCCTATTCATATTTATTGTAAATTCTCAAATATTTTTTCCAGTCAAGGGACAGCTCCCAAGAG



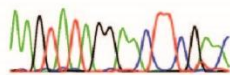
FRT 5'

CTGAAGGCGCATAACGATACCACGATATCAACAAGTTGTACAAAAAGCAGGCTGGCGCCGGAACCGAAGTTCCTATTCCGAAGTTCCTATTTCTCTAGA

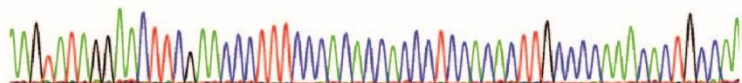


Primer AS1

AAGTATAGGAAC TTCGAACCCTTCCACACCACCCTCCACACTTGCCCCAAA CACTGCCAACTATGTAGGAG



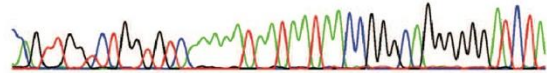
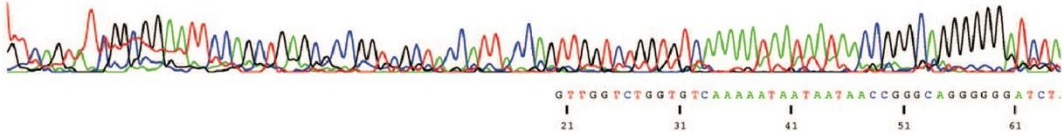
AAGTATAGGAAC TTCGAACCCTTCCACACCACCCTCCACACTTGCCCCAAA CACTGCCA



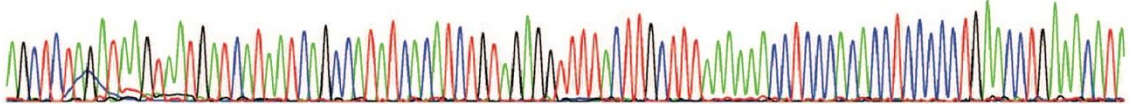
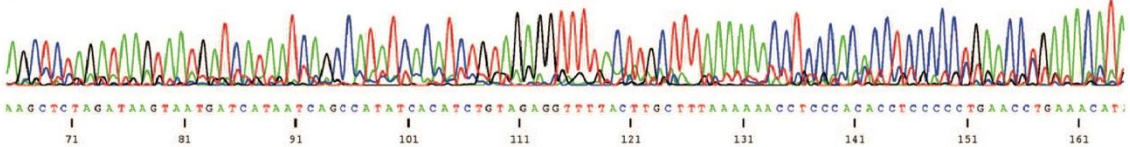
Sanger sequencing of fragment amplified by PCR with S2-AS2 primers on genomic DNA from IL34LacZ/LacZ Mouse

Primer S2

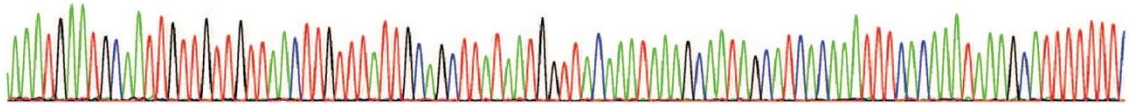
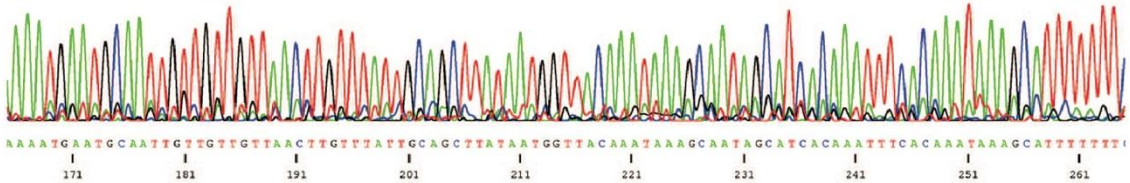
GTCAGTATCGGCGGAATTCAGCTGAGCGCCGGTCGCTACCATACCAGTTGGTCTGGTGTCAAAAATAATAAACCGGGCAGGGGGATCTA



AGCTCTAGATAAGTAATGATCATAATCAGCCATATCACATCTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCTGAACCTGAAACATA

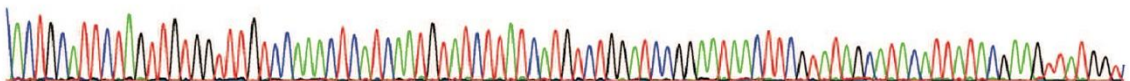
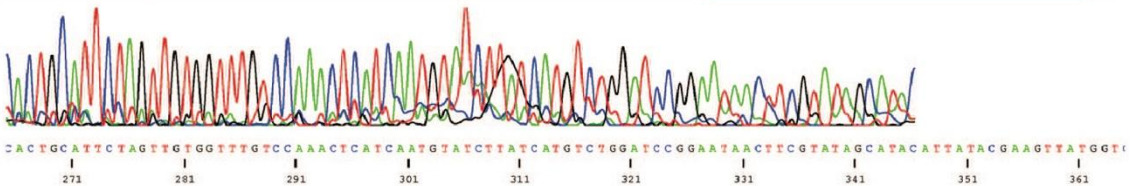


AAATGAATGCAATTGTTGTTGTTAACTTGTATTATGCAGCTTATAATGGTTACAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTT



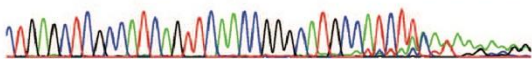
LoxP 3'

CACTGCATTCTAGTTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGGATCCGGAATAAAGTTCGTATAGCATAACATTATACGAAGTTATGGT



Primer AS2

CTGAGCTCGCCATCAGTTCAACCGGCATGCCATCTTCATAAGACAG



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

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Supplementary figure 3

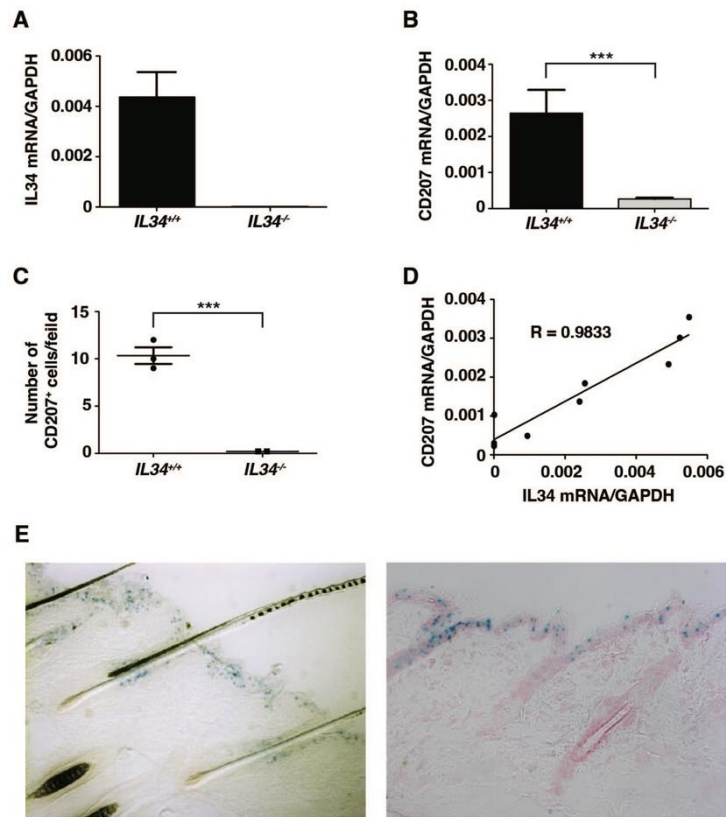
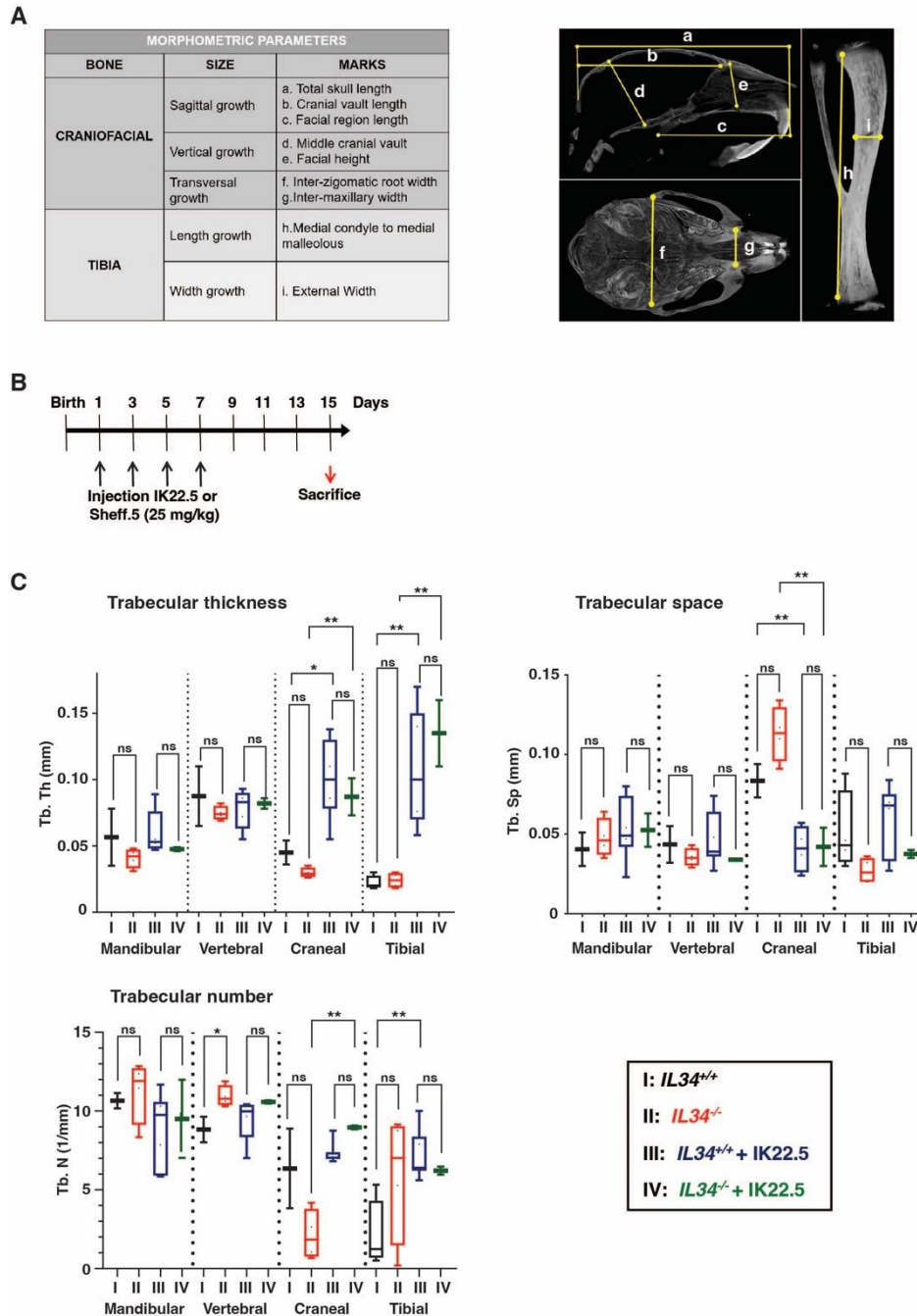


Figure S3. Functional confirmation of *IL34* invalidation and *IL34 LacZ* reporter in mouse. (A-D) In order to confirm the effective loss of IL34 function in *IL34^{-/-}* mouse, skin well-known as an IL34 expression site [16] was used. Correlated to IL34 invalidation, a significant reduction of CD207 expressing cell (Langerhans cells) was observed. (E) β -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.

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Supplementary figure 4



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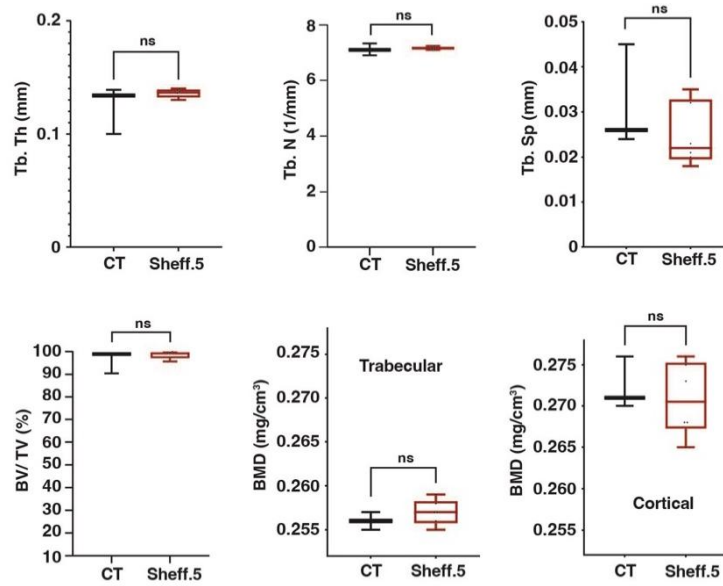
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116 **Figure S4. Graphical representation of morphometric parameters used for mouse head and tibia**117 **analyses, blocking antibodies injections protocol and results of bone trabecular structure analyses at**118 **different anatomical sites. (A)** The seven morphometric parameters (a-g) measured for the head (craniofacial119 **skeleton) and the two parameters (h-i) measured for tibia (appendicular skeleton) are listed and represented on**120 **2D microCT scan views. (B)** The blocking antibodies (IK22.5 and Sheff5) injections protocol was characterized121 **by four subcutaneous injections at postnatal days 1, 3, 5 and 7 of 25 mg/kg of antibody following by a sacrifice**122 **at day 15. (C)** The trabecular thickness (Tb. Th), the trabecular space (Tb. Sp) and the trabecular number (Tb.123 **N) were determined at four anatomical sites, the mandible, the vertebra (C2) the skull and the tibia. $IL34^{+/+}$ are**124 **represented in black, $IL34^{-/-}$ in red, $IL34^{+/+}$ treated with IK22.5 in blue, and $IL34^{-/-}$ treated with IK22.5 in green.**125 *** $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$, ns: not significant. $n = 8$ except for $IL34^{-/-}$ + IK22.5 ($n = 4$).**

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Supplementary figure 5



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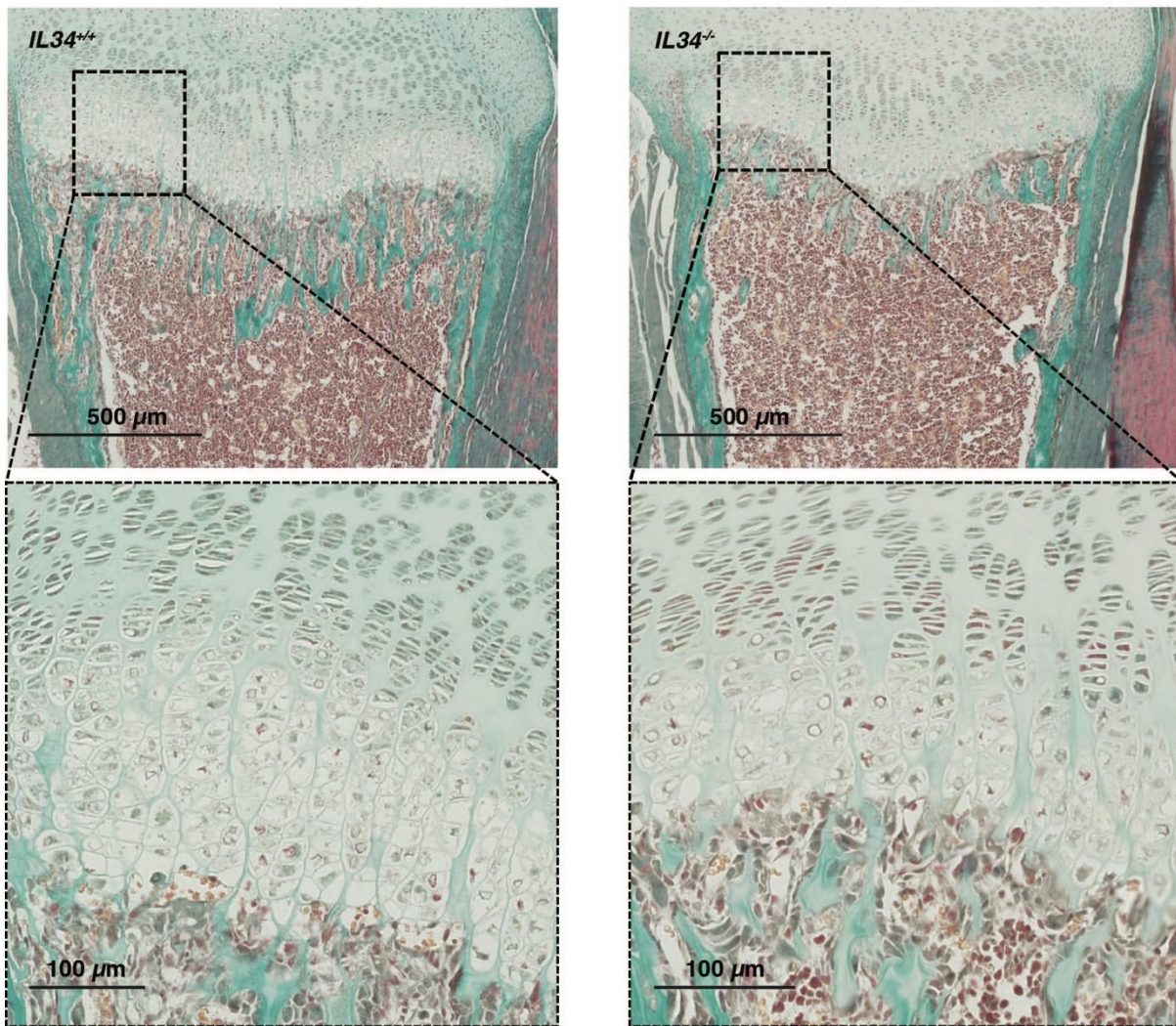
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Figure S5. Analyses of the impact of Sheff.5 antibody injections in WT pups on the bone trabecular structure (Tb. Th, Tb. Sp and Tb. N), the percentage of BV/TV and BMD. No significant variation was observed comparatively to pups injected with a control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



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166 **Figure S6. Histological comparative analysis of the tibia proximal epiphysis area of 15-day-old *IL34^{-/-}* and**167 ***IL34^{+/+}* mice using Masson's trichome stained longitudinal sections. An important reduction of the thickness**168 **of the hypertrophic chondrocytes area was observed in the null mutant. The scales are given as bars with the**169 **corresponding values in the lower part of each histological view.**

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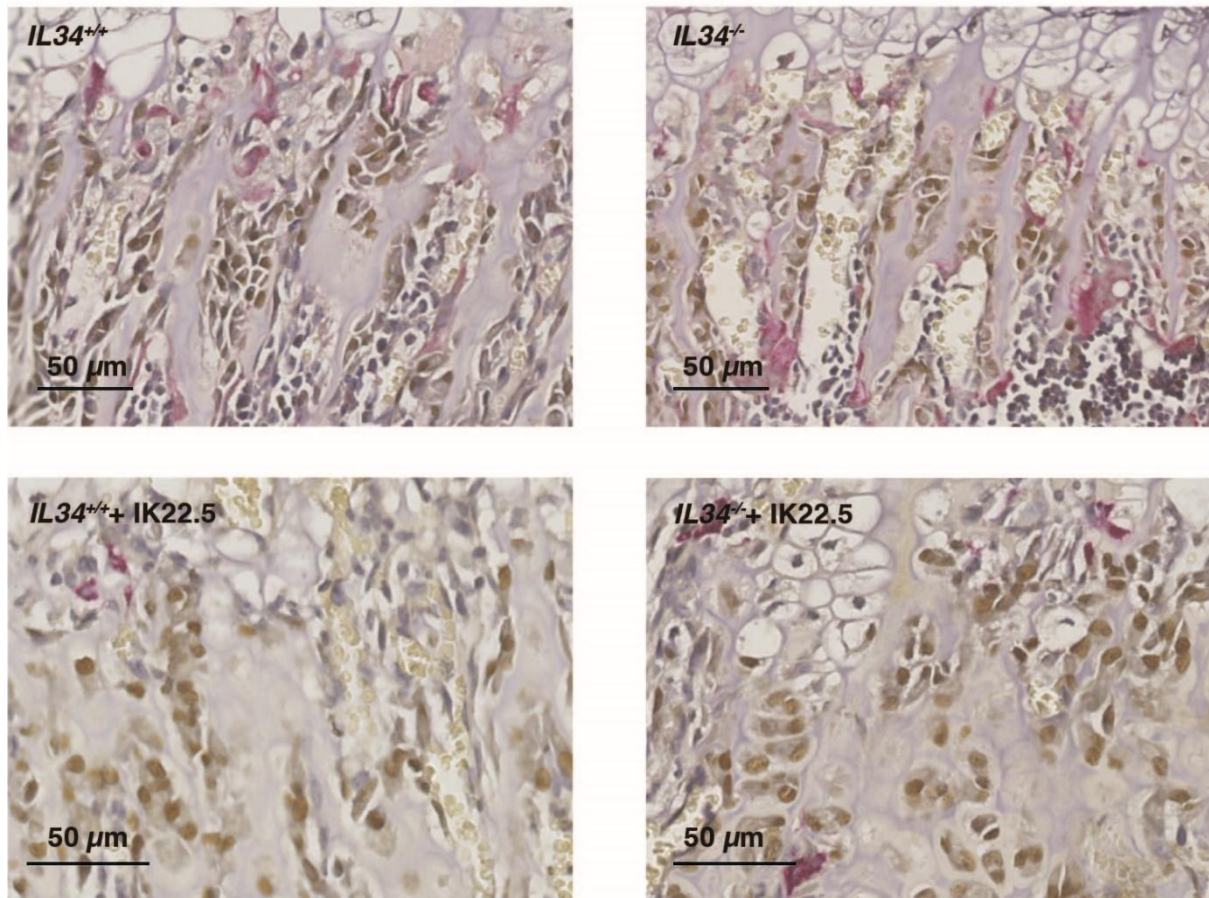
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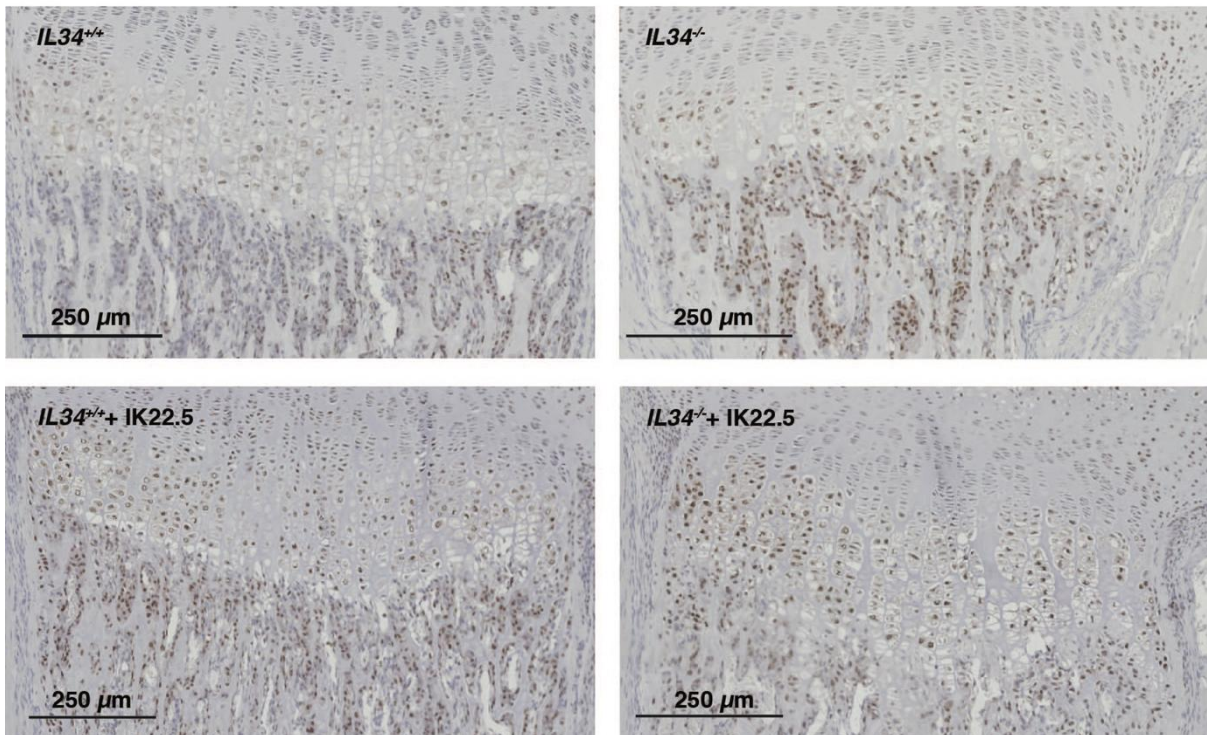
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Figure S7. High magnification views of tartrate resistant acid phosphatase (TRAP) and Osterix dual-staining of tibia longitudinal sections at the level of the proximal epiphysis performed for 15-day-old *Il34*^{-/-} and *Il34*^{+/+} mice treated or 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.



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216 **Figure S8. Comparative analysis of RUNX2 expression in the tibia proximal epiphysis area of 15-day-old**

217 ***Il34*^{-/-} and *Il34*^{+/+} mice treated or not with the IK22.5 antibody using immunohistochemistry applied to**

218 **longitudinal sections. No variation of the number of stained cells was evidenced between *Il34*^{-/-} and *Il34*^{+/+}**

219 **mice as between *Il34*^{-/-} and *Il34*^{+/+} injected with IK22.5 antibody. The scale is given as a bar corresponding to**

220 **250 μm in the lower part of each histological view.**

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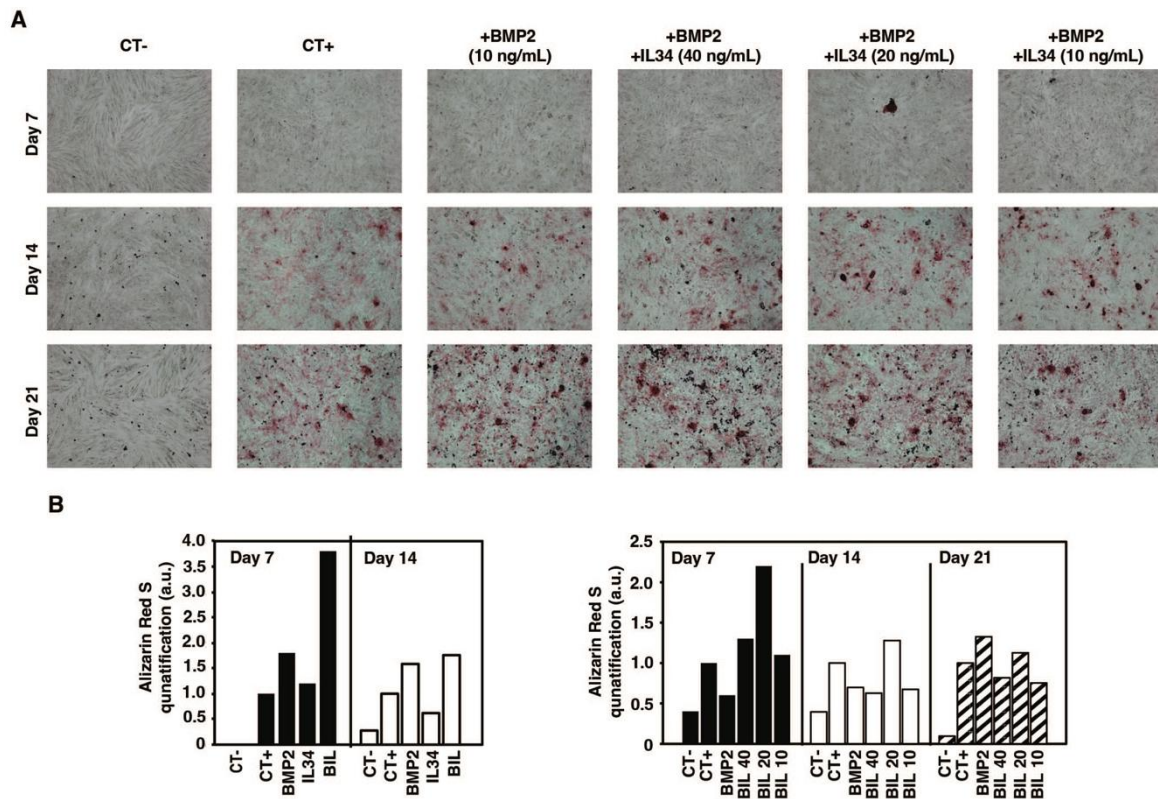
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Supplementary figure 9



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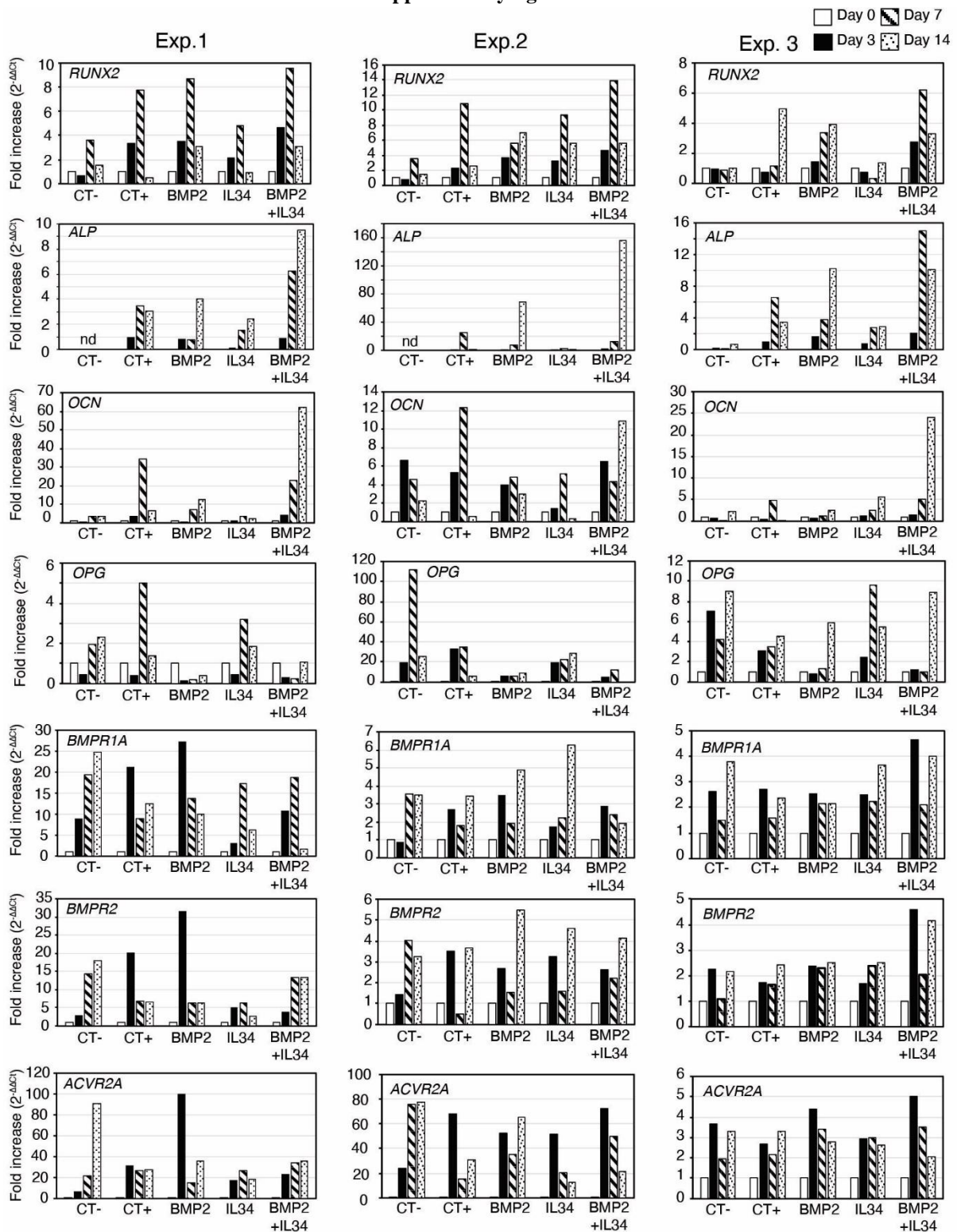
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Figure S9. Functional impact of BMP2, IL34 or combined BMP2+IL34 addition in the culture medium onto osteoblastic differentiations. (A) BMP2 addition (10 ng/mL) to the osteogenic differentiation medium (CT+) induced an acceleration of the differentiation 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 μ m. (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



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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

284 similarly observed in the three experiments. BMP2 addition accelerated the osteoblastic differentiation and the
285 co-addition of IL34 potentialized this effect as evidenced for *RUNX2* expression at days 3 and 7, and for *ALP*
286 and *OCN* at day 14. BMP2 addition alone or in combination with IL34 reduced the *OPG* expression at days 3
287 and 7. Regarding the different receptors of the BMPs, no reproducible effects were observed between
288 experiments, but all three receptors are expressed at all stages (days) of differentiation whatever the culture
289 conditions used. nd: not detected.

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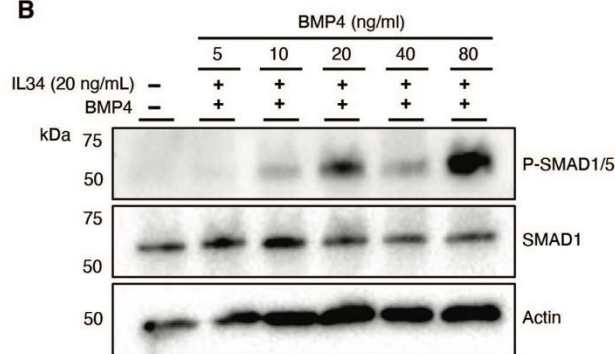
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Supplementary figure 11

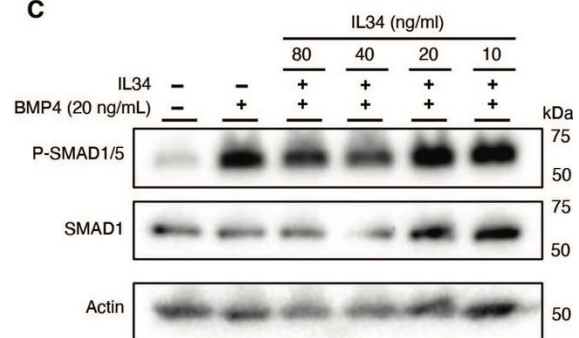
A

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

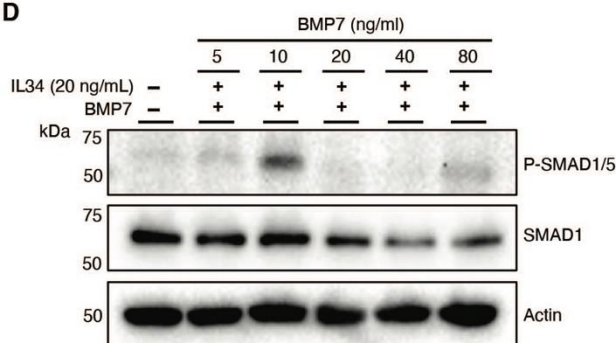
B



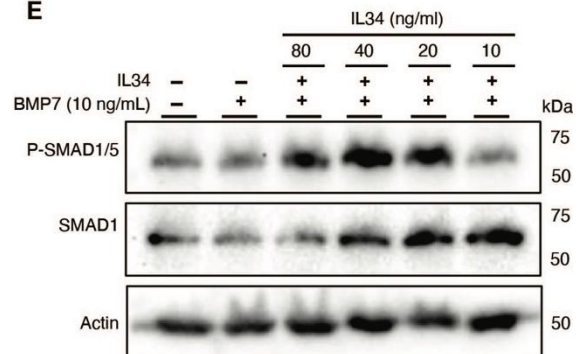
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341 **Figure S11. Impacts of addition of different combinations of BMP4+IL34 or BMP7+IL34 onto the**
 342 **activation of BMP receptors evidenced by SMAD1-5 phosphorylation in human MNNG-HOS**
 343 **osteosarcoma cell line.** (A) Correspondence table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

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Supplementary figure 12

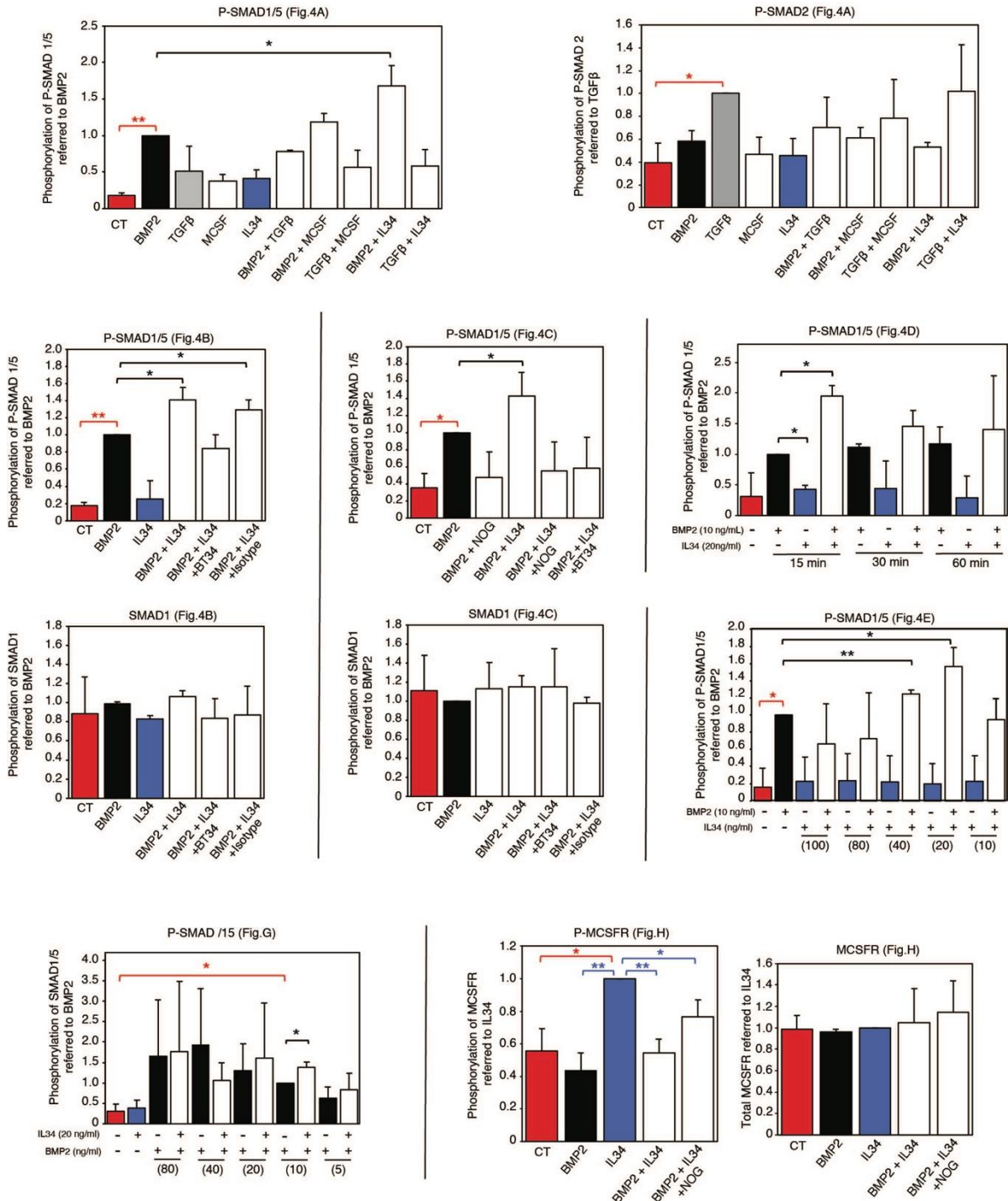
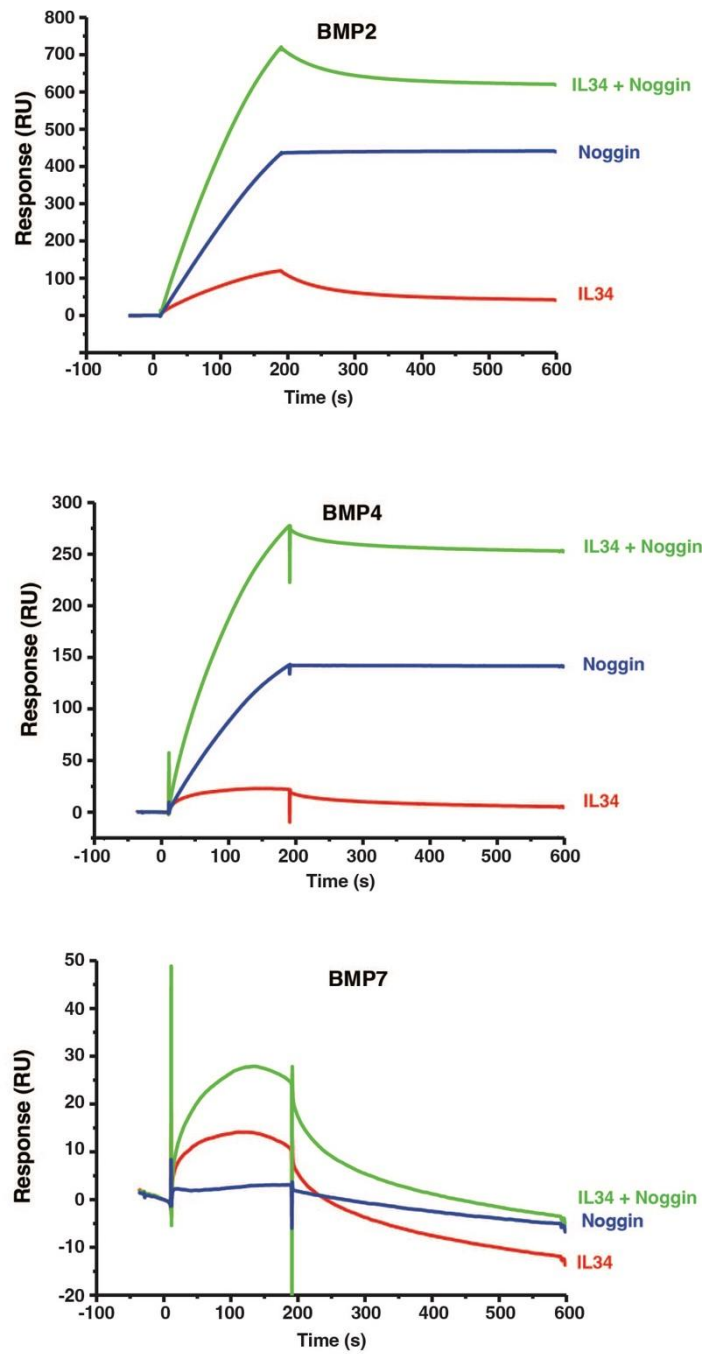


Figure S12. Quantitative analyses of Western blots presented in Figure 4. Histograms corresponding to the control condition, the BMP2-only condition and the IL34-only condition appear in red, black and blue respectively. * $p < 0.05$, ** $p < 0.01$.

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Supplementary figure 13



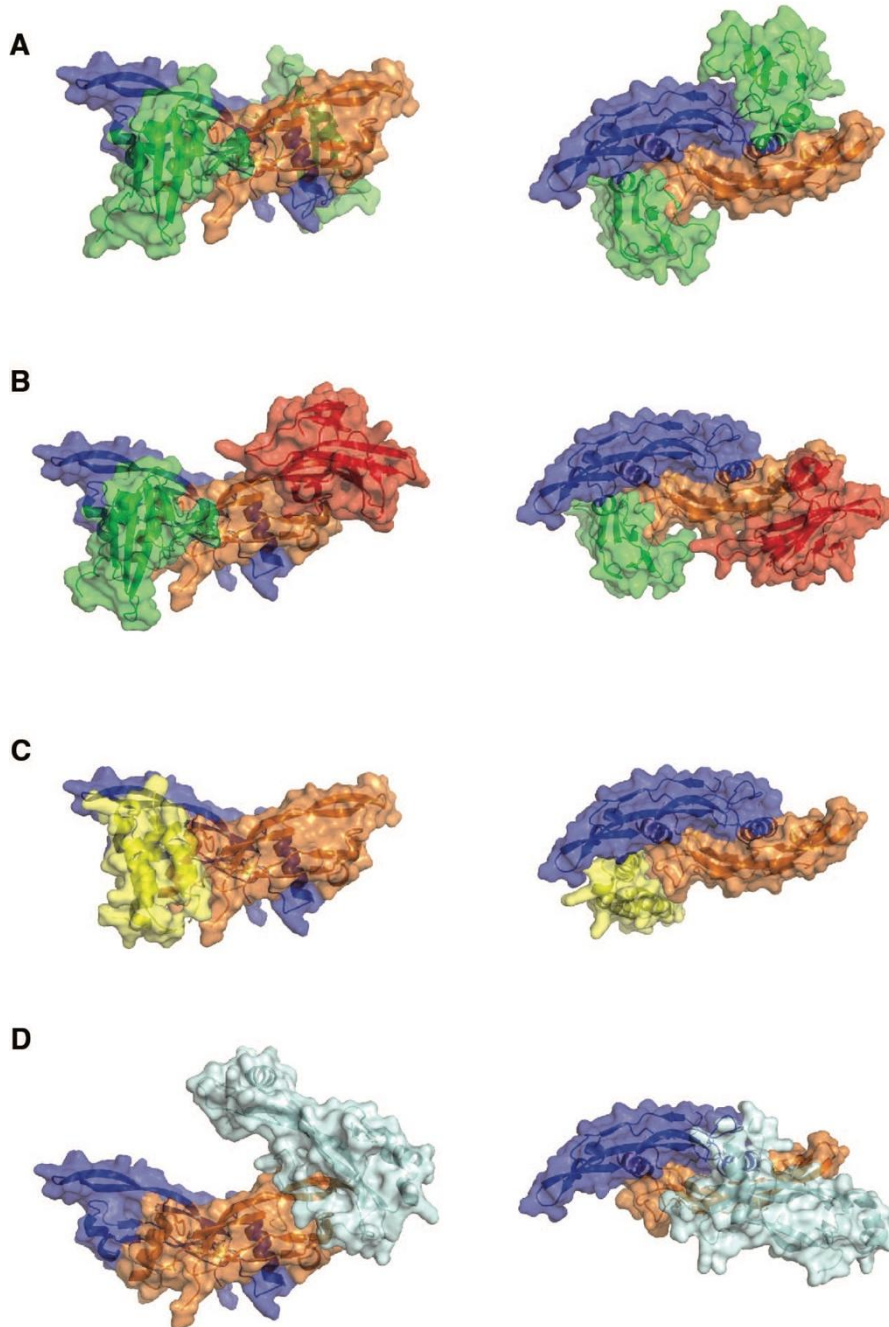
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Figure S13. Curves obtained during the surface plasmon resonance experiments with immobilization of the BMP proteins (2, 4 and 7) and additions of IL34 and NOGGIN alone or in combination. Whatever the BMP protein considered an effective binding of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

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Supplementary figure 14

BMP2 / BMP2 / BMPR1A / ACVR2A / RGMA / NOGGIN

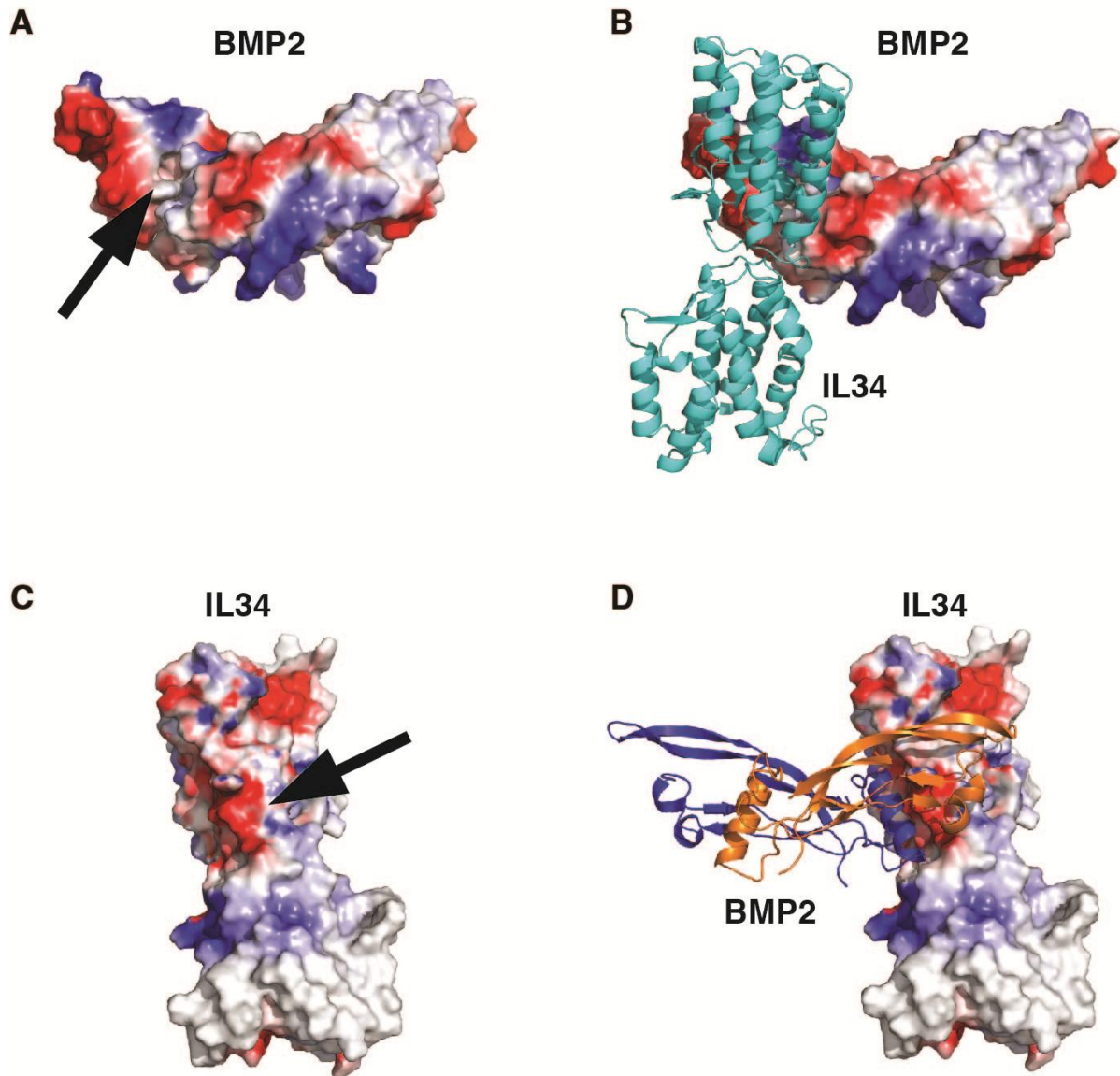


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Figure S14. Representative structures of BMP2 dimer bound proteins resolved experimentally. BMP-2 dimers are displayed in blue and orange surface. (A) BMPR1A structure (green) as found in PDB ID 1ES7 [76]. State that binding the knuckle site. (B) BMPR1A (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.

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Supplementary figure 15



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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.

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Supplementary figure 16

All BMP/TGFβ family members

ALIGN TOTAL

NP_001191.1	BMP2	295	-SCKRRHLYVD	S-DVG	ND	IVAPPG	HAFYCHGEC	PFPLADHLNSTNH	AIVQTLVNSVN	--SKIPKAC	CVPTLSAIS	LYLD	---ENEKVVLRK	SE	VVEGCGCR	396	
NP_001193.2	BMP4	306	KNCRRHSLYVD	S-DVG	ND	IVAPPG	QAFYCHGDC	PFPLADHLNSTNH	AIVQTLVNSVN	--SSIPKAC	CVPTLSAIS	LYLD	---EYDKVVLKR	SE	VVEGCGCR	408	
NP_001710.1	BMP7	328	QACKKHLYVRS	R-DLG	QD	IIAPEG	AAYCEGEC	FPFLNSYMNATNH	AIVQTLVHFINP	-ETVPKPC	CAPTQLNAIS	LYFD	---DSSNVILKR	RN	VVRACGCH	431	
NP_066551.1	BMP5	351	QACKKHLYVRS	R-DLG	QD	IIAPEG	AAYCDGEC	FPFLNAHMNATNH	AIVQTLVHLMFP	-DHVPKPC	CAPTQLNAIS	LYFD	---DSSNVILKR	RN	VVRACGCH	454	
NP_001709.1	BMP6	410	TACKRHLYVRS	R-DLG	QD	IIAPKE	AANYCDGEC	FPFLNAHMNATNH	AIVQTLVHLMNP	-EYVPKPC	CAPTQLNAIS	LYFD	---DSSNVILKR	RN	VVRACGCH	513	
NP_057288.1	GDF2	325	SHCQKTSLRVNS	E-DIG	DS	IIAPKE	EAYCEGEC	FPFLADVTPTKH	AIVQTLVHLKFP	-TKVGKAC	CVPTKLSPLS	LYKD	---dMGVPTLKYH	EG	SVABCGR	429	
NP_005251.1	GDF9	351	NBCELHDFRLS	S-QLK	DN	IVAPHE	NPRYCKGDC	PRAVGHRYGSPV-[1]	TMVQNI IYEKLD	-SSVPRPS	CVPAKYSPLS	LTIE	---PDGSIAYKE	EF	IATKCTCR	454	
NP_000548.2	GDF5	398	ARCSRKALHVN	K-DMG	DD	IIAPLE	EAFHCEGLCE	PFPLRSHLEPTNH	AVIQLMNSMDP	-ESTPPTC	CVPTRLSPIS	LFID	---SANNVYKQ	EF	VVESCGR	501	
NP_001001557.1	GDF6	352	LRCRKRHLHVN	K-ELG	DD	IIAPLE	EAYHCEGVC	DFPLRSHLEPTNH	AIIQLMNSMDP	-GSTPPCC	CVPTKLSPLS	LYID	---AGNNVYKQ	EF	VVESCGR	455	
NP_878248.2	GDF7	347	SRCSRKPLHVN	K-ELG	DD	IIAPLE	EAYHCEGLCDF	PLRSHLEPTNH	AIIQTLNMAP	-DAAPASC	CVPARLSPIS	LYID	---AANNVYKQ	EF	VVESCGR	450	
NP_055297.1	BMP10	321	NYCKRTPLYID	K-EIG	DS	IIAPPG	EAYECRGV	CNYPLAEHLPTKH	AIIQALVHLKNS	-QKASKAC	CVPTKLEPIS	LYLDK	---GVV-TYKFK	EG	AVSCGCR	424	
NP_002183.1	INHBA	319	NICCKQFFVRS	K-DIG	ND	IIAPSG	HANYCEGEC	PSHIAGTSGSSLS[4]	VINHYRMRGHP	-FANLKSC	CVPTKLRPMS	LYYD	---DGQNIKKR	KN	IVIECGCS	426	
NP_002184.2	INHBB	301	NLCCRQFFIID	R-LIG	ND	IIAPTE	YGNYCEGEC	PAYLAGVPGSASS[4]	VVNQYRMRGLNP	--GTVNSC	CIPTKLSMS	LYPD	---DEYNIVKRK	KN	IVIECGCA	407	
NP_005250.1	GDF8	281	--CCRYPLTVS	E-AFG	D	IIAPKE	KANYCSGEC	EFVFLQKYPHTH	----	LVHQANP	-RGSAGP	CCTPTKMSPIN	LYF	---nDRQQIIYKQ	EG	VVDRCGCS	375
NP_005802.1	GDF11	313	--CCRYPLTVS	E-AFG	D	IIAPKE	KANYCSGEC	EYFMQKYPHTH	----	LVQQANP	-RGSAGP	CCTPTKMSPIN	LYF	---nDRQQIIYKQ	EG	VVDRCGCS	407
NP_005529.1	INHBC	245	RMCCRQEFFVD	R-EIG	HD	IIQPEG	AMNFICIGC	PLHIAGMPGIAAS[4]	VLNLLKANTA	AgTTGGGSC	CVPTARRPLS	LYYD	---DSN-IVKTD	EP	VVIECGCS	352	
NP_113667.1	INHBE	245	PLCCRRDHYVD	R-ELG	RD	IIQPEG	QLNYCSGEC	PPHLAGSPGIAAS[4]	VFS-LLKANNP	-WPASTSC	CVPTARRPLS	LYLDh	ngN--VVKTD	EP	VVIECGCS	350	
NP_000651.3	TGFB1	291	KNCCVRQLYID	RKDLG	R	IHEPKG	HANFCLGCP	YIWSLD---TQY	SKVLALYNQHP	-GASAAPC	CVQALEPLS	VYVV	---GRK-PKVEQ	SN	IVRSCKCS	390	
NP_001129071.1	TGFB2	343	DNCCLRPLYID	RKDLG	R	IHEPKG	HANFAGAC	PYLWSSD---TQH	SRVLSLYNTINP	-EASASPC	CVQDLEPLS	LYYI	---GRT-PKIEQ	SN	IVRSCKCS	442	
NP_003230.1	TGFB3	313	ENCCVRPLYID	RqDLG	R	IHEPKG	HANFCSGPC	PYLRASD---TTH	STVLGLYNTLNP	-EASASPC	CVQDLEPLS	LYYV	---GRT-PKVEQ	SN	IVRSCKCS	412	
NP_861525.2	BMP8A	299	QVCRRHLYVRS	R-DLG	LD	IIAPQG	SAYCEGEC	FPFLDSCMNATNH	AIIQLVHLMKP	-NAVPKAC	CAPTCLSATS	LYYD	---SSNNVILKR	RN	VVRACGCH	402	
NP_001711.2	BMP8B	299	QVCRRHLYVRS	R-DLG	LD	IIAPQG	SAYCEGEC	FPFLDSCMNATNH	AIIQLVHLMMP	-DAVPKAC	CAPTCLSATS	LYYD	---SSNNVILKR	RN	VVRACGCH	402	
NP_060525.3	NODAL	245	QLCRKVKFQVDS	N-LIG	GS	IIYPKG	NAYRCEGEC	PNVGEHPHTNH	AYIQSLKRYQP	-HRVPSTC	CAPVTKPLS	LYVD	---nGR--VLLDH	EP	IVIECGCL	347	
NP_004953.1	GDF10	374	RVCSRRYLKVD	R-DIG	NE	IIAPKS	DAYCAGACE	FPMPKIVRPS--[2]	ATIQSIVRAVGI	IPGIPEP	CCVPEKMSLS	LFLD	---ENRNVVLRK	KN	SVDTACR	478	
NP_065685.1	GDF3	262	NLCHRHQLFIN	R-DLG	HK	IIAPKE	MANYCHGEC	PFSLTISLNS--[2]	AFMQALMHAVDP	--EIPQAVCI	PTKLSPLS	LYQD	---NNDNVILRH	EP	VVDECGG	364	
NP_001483.3	GDF1	265	GACRARRLYVRS	R-EVG	HF	IIAPRG	LANYCQC	ALPVALS	GGGPP[4]	AVLRALMHAAAP	-GAADLPC	CVPARLSPIS	LFPD	---NSDNVILRH	EP	VVDECGCR	372
NP_001192.4	BMP3	368	RNCARRYLKVD	R-DIG	SE	IIAPKS	DAYCAGAC	QFPMPKSLKPS--[2]	ATIQSIVRAVGV	vPGIPEP	CCVPEKMSLS	LFPD	---ENKNVILKR	KN	IVTESACR	472	
NP_066277.1	LEFTY1	261	TRCCRQEMYID	Q-GMK	EN	VLEPPG	LAYECVGT	CRQPPEALAFKWP[3]	-----	RQCIASE	TDLSL	IVSI	kegGRT	FPQVVS	EN	RVQKCSCA[12]	366
NP_003231.2	LEFTY2	261	TRCCRQEMYID	Q-GMK	EN	VLEPPG	LAYECVGT	CQPPEALAFNWP[3]	-----	RQCIASE	TASL	IVSI	kegGRT	FPQVVS	EN	RVQKCSCA[12]	366

BMP2

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NP_001191.1 bone morphogenetic protein 2 preproprotein [Homo sapiens]
NP_031579.2 bone morphogenetic protein 2 preproprotein [Mus musculus]
NP_058874.2 bone morphogenetic protein 2 precursor [Rattus norvegicus]
NP_001092611.1 bone morphogenetic protein 2 precursor [Bos taurus]
NP_001182328.1 bone morphogenetic protein 2 precursor [Sus scrofa]
XP_038289102.1 bone morphogenetic protein 2 isoform X1 [Canis lupus familiaris]
XP_023481904.1 bone morphogenetic protein 2 isoform X1 [Equus caballus]
XP_004014402.1 bone morphogenetic protein 2 [Ovis aries]
XP_514508.2 bone morphogenetic protein 2 [Pan troglodytes]
XP_001115987.1 bone morphogenetic protein 2 [Macaca mulatta]
XP_003983818.1 bone morphogenetic protein 2 isoform X2 [Felis catus]
NP_001274493.1 bone morphogenetic protein 2 precursor [Capra hircus]
XP_004061840.1 bone morphogenetic protein 2 [Gorilla gorilla gorilla]
XP_002829993.1 bone morphogenetic protein 2 [Pongo abelii]
XP_031998602.1 bone morphogenetic protein 2 [Hylobates moloch]

NP_001191.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLVPELGRRKFAAAS--SGRPS	42
NP_031579.2	1	-----MVAGTRCLLVLLLPQVLLGGGAAGLIPELGRKKFAAAS---SRPL	41
NP_058874.2	1	-----MVAGTRCLLVLLLPQVLLGGGAAGLIPELGRKKFAGAS---GRPL	41
NP_001092611.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLIPELGRRKFAAS---AGRSS	41
NP_001182328.1	1	-----MVAGTRCLLALLLPQVLLGGGAADLIPELGRRKFAAS---TGLSS	41
XP_038289102.1	1	mclglfsdpggvrpsggfprfparavsasvteerstMVAGTRCLLALLLPQVLLGGGAAGLITELGRKKFAAS---PGRSP	77
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XP_004014402.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLIPELGRRKFAAS---AGRSS	41
XP_514508.2	1	-----MVAGTRCLLALLLPQVLLGGGAAGLVPELGRRKFAAAsaSGRPS	44
XP_001115987.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLVPELGRRKFAAS--SGRPS	42
XP_003983818.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLIPELGRKKFAAS---TGRSS	41
NP_001274493.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLIPELGRKKFAAS---AGRSS	41
XP_004061840.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLVPELGRRKFAAAS--SGRPS	42
XP_002829993.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLVPELGRRKFAAS--SGRPS	42
XP_031998602.1	1	-----MVAGTRCLLALLLPQVLLGGGAAGLVPELGRRKFAAAS--SGRPS	42
NP_001191.1	43	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGSPADHRLERAASRANTVRSFHHEESLEELP	122
NP_031579.2	42	SRPSEDEVLSEFELRLLSMFGLKQRPTPSKDVVPPYMLDLYRRHSQPGAPADHRLERAASRANTVRSFHHEEAVVEELP	121
NP_058874.2	42	SRPSDDVSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGAPADHRLERAASRANTVRSFHHEEALEELP	121
NP_001092611.1	42	SQPSDDVSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRQHSQPGAPADHRLERAASLANTVRSFHHEESLEELP	121
NP_001182328.1	42	SQPSDDVSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGAPADHRLERAASLANTVRSFHHEESLEELP	121
XP_038289102.1	78	SQPSDEVLSEFELRLLSMFGLKRRPTPSRDVAVPPYMLDLYRRHSQPGAPADHRLERAASLANTVRSFHHEESLEELP	157
XP_023481904.1	42	SQPSDDVSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPDAPADHRLERAASLANTVRSFHHEESLEELP	121
XP_004014402.1	42	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRQHSQPGAPADHRLERAASLANTVRSFHHEESLEELP	121
XP_514508.2	45	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGSPADHRLERAASRANTVRSFHHEESLEELP	124
XP_001115987.1	43	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGSPADHRLERAASRANTVRSFHHEESLEELP	122
XP_003983818.1	42	SQPSDEVLSEFELRLLSMFGLKRRPTPSRDVAVPPYMLDLYRRHSQPGAPADHRLERAASLANTVRSFHHEESVEELP	121
NP_001274493.1	42	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRQHSQPGAPADHRLERAASLANTVRSFHHEESLEELP	121
XP_004061840.1	43	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGSPADHRLERAASRANTVRSFHHEESLEELP	122
XP_002829993.1	43	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLDLYRRHSQPGSPADHRLERAASRANTVRSFHHEESLEELP	122
XP_031998602.1	43	SQPSDEVLSEFELRLLSMFGLKQRPTPSRDVAVPPYMLELYRRHSQPGSPADHRLERAASRANTVRSFHHEESLEELP	122
NP_001191.1	123	ETSGKTRRRFFNLSIPTTEEFITSAELQVFREQMQUALGNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	202
NP_031579.2	122	EMSGKTARRFFNLSVPSDEFILTSAEQLIFREQIQEALGN--SSFQHRINIYEI IKPAAANLKFVTRLLDTRLVNQNTS	200
NP_058874.2	122	EMSGKTSRRFFNLSVPTDEFILTSAEQLIFREQMQUALGN--SSFQHRINIYEI IKPATASSKFPVTRLLDTRLVNTQNS	200
NP_001092611.1	122	EMSGKTRRRFFNLSIPTTEEFITSAELQVFRKHMPEALENNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNTQNAS	201
NP_001182328.1	122	EMSGKTRRRFFNLSVPTTEEFITSAELQVFREQTQETLDNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVTPNAS	201
XP_038289102.1	158	EMSGKTRRRFFNLSIPTDEFITSAELQVFREQMQLPNDNSSFHHRINIYEI IKPAAANLKFVTRLLDTRLVNQNAS	237
XP_023481904.1	122	EMSGKTRRRFFNLSIPTTEEFITSAELQVFREQMQLPNDNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	201
XP_004014402.1	122	EMSGKTRRRFFNLSIPTTEEFITSAELQVFRKHMPEALENNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	201
XP_514508.2	125	ETSGKTRRRFFNLSIPTTEESITSAELQVFREQMRDALGNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	204
XP_001115987.1	123	EMSGKTRRRFFNLSIPTTEEFVTSAEQLQVFREQMQUALGDNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	202
XP_003983818.1	122	EMSGKTRRRFFNLSIPTDEFITSAELQVFREQMQLPNDNSSFHHRINIYEI IKPATANLKFVTRLLDTRLVNQNTS	201
NP_001274493.1	122	EMSGKTRRRFFNLSIPTTEEFITSAELQVFRKHMPEALENNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNTQNAS	201
XP_004061840.1	123	ETSGKTRRRFFNLSIPTTEEFITSAELQVFREQMQUALGNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	202
XP_002829993.1	123	ETSGKTRRRFFNLSIPTTEEFITSAELQVFREQMQUALGNSSFHHRINIYEI IKPATANSKFPVTRLLDTRLVNQNAS	202
XP_031998602.1	123	ETSGKTRRRFFNLSIPTTEEFITSAELQVFREQMQUALGNSSFHHRINIYEI IKPATANLKFVTRLLDTRLVNQNAS	202
NP_001191.1	203	RWESFDVTPAVMRWTAQGHANHGFFVEVAHLEEKQGVSKRHVRSRSLHQDEHSWSQIRPLLVTFGHGDKGPHLHKREKR	282
NP_031579.2	201	QWESFDVTPAVMRWTAQGHANHGFFVEVAHLEENPGVSKRHVRSRSLHQDEHSWSQIRPLLVTFGHGDKGPHLHKREKR	280
NP_058874.2	201	QWESFDVTPAVMRWTAQGHANHGFFVEVAHLEEKPGVSKRHVRSRSLHQDEHSWSQVIRPLLVTFGHGDKGPHLHKREKR	280
NP_001092611.1	202	RWESFDVTPAVMRWTAQGLTNHGFFVEVAHLEENQGVSKRHVRSRSLHQDEHSWSQIRPLLVTFGHGDKGPHLHKREKR	281
NP_001182328.1	202	RWESFDVTPAVMRWTAQGVANHGFFVEVAHPEDSPEVSKRHVRSRSLHQDEHSWSQIRPLLVTFGHGDKGPHLHKREKR	281
XP_038289102.1	238	RWESFDVTPAVMRWTAQGLANHGFFVEVAHLEENQGVSKRHVRSRSLHQDEHSWSQIRPLLVTFGHGDKGPHLHKREKR	317
XP_023481904.1	202	RWERFDVTPAVMRWTAQGLANHGFFVEVAHLEENRGASKRHVRSRSLHQDEHSWSQIRPLLVTFGHGDKGPHLHKREKR	281

534	XP_004014402.1	202	RWESFDVTPAVMRWTAQGLTNHGFVVEVAHPEDSHGASKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	281
535	XP_514508.2	205	RWESFDVTPAVMRWTAQGHANHGFFVEVAHLEEKQGVSKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	284
536	XP_001115987.1	203	RWESFDVTPAVMRWTAQGHANHGFFVEVTHLEEKQGVSKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	282
537	XP_003983818.1	202	RWESFDVTPAVMRWTAQGLTNHGFVVEVTHLEENQGVSKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	281
538	NP_001274493.1	202	RWESFDVTPAVMRWTAQGLTNHGFVVEVAHPEDSHGASKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	281
539	XP_004061840.1	203	RWESFDVTPAVMRWTAQGHANHGFFVEVTHLEEKQGVSKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	282
540	XP_002829993.1	203	RWESFDVTPAVMRWTAQGHANHGFFVEVTHLEEKQGVSKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	282
541	XP_031998602.1	203	RWESFDVTPAVMRWTAQGHANHGFFVEVTHLEEKQGVSKRHRVRSRSLHQDEHSWSQIRPLLVTFGHDGKGHPHREKR	282
542				
543	NP_001191.1	283	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	362
544	NP_031579.2	281	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	360
545	NP_058874.2	281	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	360
546	NP_001092611.1	282	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	361
547	NP_001182328.1	282	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	361
548	XP_038289102.1	318	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	397
549	XP_023481904.1	282	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	361
550	XP_004014402.1	282	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	361
551	XP_514508.2	285	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	364
552	XP_001115987.1	283	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	362
553	XP_003983818.1	282	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	361
554	NP_001274493.1	282	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	361
555	XP_004061840.1	283	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	362
556	XP_002829993.1	283	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	362
557	XP_031998602.1	283	QAKHKQRKRLKSSCKRHPLYVDSVGGNDIVAPPGHAFYCHGECPPFLADHLNSTNHAIQTLVNSVNSKIPKACCV	362
558				
559	NP_001191.1	363	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	396
560	NP_031579.2	361	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	394
561	NP_058874.2	361	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	394
562	NP_001092611.1	362	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	395
563	NP_001182328.1	362	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	395
564	XP_038289102.1	398	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	431
565	XP_023481904.1	362	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	395
566	XP_004014402.1	362	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	395
567	XP_514508.2	365	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	398
568	XP_001115987.1	363	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	396
569	XP_003983818.1	362	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	395
570	NP_001274493.1	362	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	395
571	XP_004061840.1	363	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	396
572	XP_002829993.1	363	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	396
573	XP_031998602.1	363	PTELSAISLYLDENEKVVLNQDQVVEGCGCR	396
574				

BMP4

576 NP_001193.2 bone morphogenetic protein 4 isoform a preproprotein [Homo sapiens]
 577 NP_031580.2 bone morphogenetic protein 4 preproprotein [Mus musculus]
 578 NP_036959.2 bone morphogenetic protein 4 precursor [Rattus norvegicus]
 579 XP_024853077.1 bone morphogenetic protein 4 isoform X2 [Bos taurus]
 580 XP_020925510.1 bone morphogenetic protein 4 isoform X2 [Sus scrofa]
 581 XP_038528824.1 bone morphogenetic protein 4 isoform X1 [Canis lupus familiaris]
 582 XP_023483474.1 bone morphogenetic protein 4 isoform X2 [Equus caballus]
 583 NP_001103747.1 bone morphogenetic protein 4 precursor [Ovis aries]
 584 XP_024204496.1 bone morphogenetic protein 4 isoform X2 [Pan troglodytes]
 585 XP_028707390.1 bone morphogenetic protein 4 isoform X2 [Macaca mulatta]
 586 XP_019688586.1 bone morphogenetic protein 4 isoform X1 [Felis catus]
 587 NP_001272575.1 bone morphogenetic protein 4 precursor [Capra hircus]
 588 XP_030857866.1 bone morphogenetic protein 4 isoform X2 [Gorilla gorilla gorilla]
 589 XP_024087813.1 bone morphogenetic protein 4 isoform X3 [Pongo abelii]
 590 XP_032036116.1 bone morphogenetic protein 4 isoform X2 [Hylobates moloch]

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NP_001193.2 1 MIPG-----NRMLMVLLCQVLLGGASHASLI PETGKK 33
 NP_031580.2 1 MIPG-----NRMLMVLLCQVLLGGASHASLI PETGKK 33
 NP_036959.2 1 MIPG-----NRMLMVLLCQVLLGGASHASLI PETGKK 33
 XP_024853077.1 1 MQEGRGGRRGETGAELGPEARSHSVVPSRATHCRSSSEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 XP_020925510.1 1 MQEGRGGGREGVKGVELCPEARSHSVVPSRATHCRSSSEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 XP_038528824.1 1 MHEGRGGGREGRRAEPCPEARSHSVVPSRATHCRSSSEPFQVCSRLAVKNHGLLLYALFSVILLGGSSHASLI PETGKK 80
 XP_023483474.1 1 MQEGRGGGREGRRAEPCPEARSHSVVPSRATHCRSSSEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 NP_001103747.1 1 MIPG-----NRMLMVLLCQVLLGGASHASLI PETGKK 33
 XP_024204496.1 1 MREGRGGGREGRSAEPCPEARSHSVVPSRATHCCSFPEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 XP_028707390.1 1 MREGRGGGREGRSAEPCPEARSHSVVPSRATHCCSFPEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 XP_019688586.1 1 MHEGRGGGREGRRAEPCPEARSHSVVPSRATHCRSSSEPFQVCSRLAVKNHGLLLYALFSVILLGGSSHASLI PETGKK 80
 NP_001272575.1 1 MIPG-----NRMLMVLLCQVLLGGASHASLI PETGKK 33
 XP_030857866.1 1 MREGRGGGREGRSAEPCPEARSHSVVPSRATHCCSFPEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 XP_024087813.1 1 MREGRGGGREGRSAEPCPEARSHSVVPSRATHCCSFPEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80
 XP_032036116.1 1 MREGRGGGREGRSAEPCPEARSHSVVPSRATHCCSFPEPFQVCSRLAVKNHGLLLYALFSVILLGGASHASLI PETGKK 80

NP_001193.2 34 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEE-QIHSTGLEYPERPAS 112
 NP_031580.2 34 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQSQGTGLEYPERPAS 113
 NP_036959.2 34 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQSQGTGLEYPERPAS 113
 XP_024853077.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIQIGLEYPERPAS 160
 XP_020925510.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQTHSVGLEYPERPAS 160
 XP_038528824.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIHSIGLEYPERPAS 160
 XP_023483474.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIHSVGLYPERPAS 160
 NP_001103747.1 34 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIQIGLEYPERPAS 113
 XP_024204496.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEE-QIHSTGLEYPERPAS 159
 XP_028707390.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEE-QIHSAGLEYPERPAS 159
 XP_019688586.1 34 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQTHSVGLEYPERPAS 160
 NP_001272575.1 34 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEEQIQIGLEYPERPAS 113
 XP_030857866.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEE-QIHSTGLEYPERPAS 159
 XP_024087813.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEE-QIHSTGLEYPERPAS 159
 XP_032036116.1 81 KVAEIQQHAGGRRSGQSHELLLRD FEATLLQMFGLRRRPQPSKSAVIPDYMRDLYRLQSGEEEEEE-QIHSTGLEYPERPAS 159

NP_001193.2 113 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 192
 NP_031580.2 114 RANTVRSFHHEEHLENIPTGSESSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEMVP 193
 NP_036959.2 114 RANTVRSFHHEEHLENIPTGSESSAFRFFLNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEMVP 193
 XP_024853077.1 161 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 240
 XP_020925510.1 161 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 240
 XP_038528824.1 161 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 240
 XP_023483474.1 161 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 240
 NP_001103747.1 114 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 193
 XP_024204496.1 160 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 239
 XP_028707390.1 160 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 239
 XP_019688586.1 161 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 240
 NP_001272575.1 114 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 193
 XP_030857866.1 160 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 239
 XP_024087813.1 160 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 239
 XP_032036116.1 160 RANTVRSFHHEEHLENIPTGSENSAFRFLFNLSSIPENEVISSAELRRLFREQVDQGPDWERGFHFRINIYEVMKPPAEVVP 239

NP_001193.2 193 GHLITRLLDTRLVHNNVTRWETF DVSPAVLRWTRERKQPNYGLAIEVTHLHQTRTHQGQHVIRISRLPQSGGNWAQLRPLL 272
 NP_031580.2 194 GHLITRLLDTRLVHNNVTRWETF DVSPAVLRWTRERKQPNYGLAIEVTHLHQTRTHQGQHVIRISRLPQSGGDWAQLRPLL 273
 NP_036959.2 194 GHLITRLLDTRLVHNNVTRWETF DVSPAVLRWTRERKQPNYGLAIEVTHLHQTRTHQGQHVIRISRLPQSGGNWAQLRPLL 273
 XP_024853077.1 241 GHLITRLLDTRLVHNNVTRWETF DVSPAVLRWTRERKQPNYGLAIEVTHLHQTRTHQGQHVIRISRLPQSGGDWAQLRPLL 320
 XP_020925510.1 241 GHLITRLLDTRLVHNNVTRWETF DVSPAVLRWTRERKQPNYGLAIEVTHLHQTRTHQGQHVIRISRLPQSGGDWAQLRPLL 320

649	XP_038528824.1	241	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	320
650	XP_023483474.1	241	GRLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRALPQGSQDWAQLRPLL	320
651	NP_001103747.1	194	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	273
652	XP_024204496.1	240	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	319
653	XP_028707390.1	240	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	319
654	XP_019688586.1	241	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	320
655	NP_001272575.1	194	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	273
656	XP_030857866.1	240	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	319
657	XP_024087813.1	240	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	319
658	XP_032036116.1	240	GHLITRLLDTRLVHHNVTRWETFDFVSPAVLRWTREREKQPNYGLAIEVTHLHQTRTHQGQHVIRISRSLPQGSQDWAQLRPLL	319
659				
660	NP_001193.2	273	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	352
661	NP_031580.2	274	VTFGHDGRGHTLTRRR-AKRSKPKHPQRSRKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	352
662	NP_036959.2	274	VTFGHDGRGHTLTRRR-AKRSKPKHPQRSRKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	352
663	XP_024853077.1	321	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	400
664	XP_020925510.1	321	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	400
665	XP_038528824.1	321	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	400
666	XP_023483474.1	321	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	400
667	NP_001103747.1	274	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	353
668	XP_024204496.1	320	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	399
669	XP_028707390.1	320	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	399
670	XP_019688586.1	321	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	400
671	NP_001272575.1	274	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	353
672	XP_030857866.1	320	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	399
673	XP_024087813.1	320	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	399
674	XP_032036116.1	320	VTFGHDGRGHALTRRRRAKRSPKHHSPQRARKKNKNCRRHSYLVDSVGNNDIIVAPPGQAFYCHGDCPFPLADHLNST	399
675				
676	NP_001193.2	353	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	408
677	NP_031580.2	353	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	408
678	NP_036959.2	353	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	408
679	XP_024853077.1	401	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	456
680	XP_020925510.1	401	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	456
681	XP_038528824.1	401	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	456
682	XP_023483474.1	401	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	456
683	NP_001103747.1	354	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	409
684	XP_024204496.1	400	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	455
685	XP_028707390.1	400	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	455
686	XP_019688586.1	401	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	456
687	NP_001272575.1	354	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	409
688	XP_030857866.1	400	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	455
689	XP_024087813.1	400	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	455
690	XP_032036116.1	400	NHAIVQTLVNSVNSSIPKACCVTELSAISLYLDEYDKVVLKNQEVVVEGCGCR	455
691				
692				
693				

BMP7

695	NP_001710.1	bone morphogenetic protein 7 preproprotein [Homo sapiens]
696	NP_031583.2	bone morphogenetic protein 7 preproprotein [Mus musculus]
697	NP_001178785.1	bone morphogenetic protein 7 precursor [Rattus norvegicus]
698	NP_001192944.1	bone morphogenetic protein 7 precursor [Bos taurus]
699	XP_005673101.1	bone morphogenetic protein 7 isoform X1 [Sus scrofa]
700	NP_001183981.1	bone morphogenetic protein 7 precursor [Canis lupus familiaris]
701	NP_001182087.1	bone morphogenetic protein 7 precursor [Equus caballus]
702	NP_001295493.1	bone morphogenetic protein 7 precursor [Ovis aries]
703	XP_001170064.1	bone morphogenetic protein 7 [Pan troglodytes]
704	XP_001089245.1	bone morphogenetic protein 7 [Macaca mulatta]
705	XP_011279062.2	LOW QUALITY PROTEIN: bone morphogenetic protein 7 [Felis catus]
706	XP_017913119.1	PREDICTED: bone morphogenetic protein 7 [Capra hircus]
707	XP_030860862.1	bone morphogenetic protein 7 [Gorilla gorilla gorilla]
708	XP_024094889.1	bone morphogenetic protein 7 [Pongo abelii]
709	XP_031998385.1	bone morphogenetic protein 7 [Hylobates moloch]
710		
711	NP_001710.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
712	NP_031583.2	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
713	NP_001178785.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
714	NP_001192944.1	1 MHMRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
715	XP_005673101.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
716	NP_001183981.1	1 MHVRSPCAAPRSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
717	NP_001182087.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
718	NP_001295493.1	1 MHMRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
719	XP_001170064.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
720	XP_001089245.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
721	XP_011279062.2	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
722	XP_017913119.1	1 MHMRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
723	XP_030860862.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
724	XP_024094889.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
725	XP_031998385.1	1 MHVRSLRRAAPHSFVALWAPLFLRSALADFSLDNEVHSSFIHRRLSQREREMQREILSILGLPHRPRPHLQGGKHSAP 80
726		
727	NP_001710.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
728	NP_031583.2	81 MFMLDLYNAMAVEESG-PDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 159
729	NP_001178785.1	81 MFMLDLYNAMAVEESG-PDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 159
730	NP_001192944.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
731	XP_005673101.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
732	NP_001183981.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
733	NP_001182087.1	81 MFMLDLYNAMAVEESGPGDGGQFSYPYKAVSSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
734	NP_001295493.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
735	XP_001170064.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
736	XP_001089245.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
737	XP_011279062.2	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSRFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
738	XP_017913119.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
739	XP_030860862.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
740	XP_024094889.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
741	XP_031998385.1	81 MFMLDLYNAMAVEEGGPGDGGQFSYPYKAVFSTQGPPPLASLQDSHFLTDADMVMSFVNLEVDKKEFFHPRYHHREFRFDL 160
742		
743	NP_001710.1	161 SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
744	NP_031583.2	160 SKIPEGEAVTAAEFRIYKDYIRERFDNETFQITVYQVLQEHSGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 238
745	NP_001178785.1	160 SKIPEGEAVTAAEFRIYKDYIRERFDNETFQITVYQVLQEHSGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 238
746	NP_001192944.1	161 SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
747	XP_005673101.1	161 SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
748	NP_001183981.1	161 SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVPLAQDSSLDyLFLDSRTLWASEEGWLVFDITATSNHWVVNP 240
749	NP_001182087.1	161 SKIPEGEAVTAAEFRIYKDYVREDFNETFRISVYQVLQEHLAGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
750	NP_001295493.1	161 SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
751	XP_001170064.1	161 SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
752	XP_001089245.1	161 SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
753	XP_011279062.2	161 SKIPEGKPWTAAEFRIYKDYIRKXLLNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
754	XP_017913119.1	161 SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
755	XP_030860862.1	161 SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
756	XP_024094889.1	161 SKIPEGEAVTAAEFRIYKDYIREHFHNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
757	XP_031998385.1	161 SKIPEGEAVTAAEFRIYKDYIRERFDNETFRISVYQVLQEHLGRES-DLFLDSRTLWASEEGWLVFDITATSNHWVVNP 239
758		
759	NP_001710.1	240 RHNGLQLSVETLDGQSIINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRMANV- 318
760	NP_031583.2	239 RHNGLQLSVETLDGQSIINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRMANV- 317
761	NP_001178785.1	239 RHNGLQLSVETLDGQSIINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRMANV- 317
762	NP_001192944.1	240 RHNGLQLSVETLDGQSIINPKLAGLIGRGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRVANV- 318
763	XP_005673101.1	240 RHNGLQLSVETLDGQSIINPKLAGLIGRGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRVANV- 318
764	NP_001183981.1	241 RHNGLQLCVETLDGQSIINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGAKQRSQNRSKTPKNQAEALRVANv 320
765	NP_001182087.1	240 RHNGLQLSVETLDGQSVINPKLAGLIGRHGPQTKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRVANV- 318
766	NP_001295493.1	240 RHNGLQLSVETLDGQSIINPKLAGLIGRGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRVANV- 318
767	XP_001170064.1	240 RHNGLQLSVETLDGQSIINPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGGKQRSQNRSKTPKNQAEALRMANV- 318

768	XP_001089245.1	240	RHNLGLQLSVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-	318
769	XP_011279062.2	240	RHNLGLQLCVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVTVN-	318
770	XP_017913119.1	240	RHNLGLQLSVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFFKATEVHLRSTRSTGGKQRSQNRSKTPKNQEALRVANV-	318
771	XP_030860862.1	240	RHNLGLQLSVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-	318
772	XP_024094889.1	240	RHNLGLQLSVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-	318
773	XP_031998385.1	240	RHNLGLQLSVETLDGQSI NPKLAGLIGRHGPQNKQPFMVAFFKATEVHFRSIRSTGSKQRSQNRSKTPKNQEALRMANV-	318
774				
775	NP_001710.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
776	NP_031583.2	318	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPDTVPKPCCAP	397
777	NP_001178785.1	318	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPDTVPKPCCAP	397
778	NP_001192944.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
779	XP_005673101.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
780	NP_001183981.1	321	AKNSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	400
781	NP_001182087.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
782	NP_001295493.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
783	XP_001170064.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
784	XP_001089245.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
785	XP_011279062.2	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
786	XP_017913119.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
787	XP_030860862.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
788	XP_024094889.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
789	XP_031998385.1	319	AENSSDQRQACKKHELYVSRDLGQDDIIIAPEGAAAYCEGECAPPLNSYMNATNHAIVQTLVHFINPETVPKPCCAP	398
790				
791	NP_001710.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
792	NP_031583.2	398	TQLNAISLYFDSSNVILKKRNIVVRACGCH	430
793	NP_001178785.1	398	TQLNAISLYFDSSNVILKKRNIVVRACGCH	430
794	NP_001192944.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
795	XP_005673101.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
796	NP_001183981.1	401	TQLNAISLYFDSSNVILKKRNIVVRACGCH	433
797	NP_001182087.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
798	NP_001295493.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
799	XP_001170064.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
800	XP_001089245.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
801	XP_011279062.2	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
802	XP_017913119.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
803	XP_030860862.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
804	XP_024094889.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
805	XP_031998385.1	399	TQLNAISLYFDSSNVILKKRNIVVRACGCH	431
806				
807				
808				

BMP5

810	NP_066551.1	bone morphogenetic protein 5 isoform 1 preproprotein [Homo sapiens]	
811	NP_031581.2	bone morphogenetic protein 5 preproprotein [Mus musculus]	
812	NP_001101638.1	bone morphogenetic protein 5 precursor [Rattus norvegicus]	
813	NP_001291945.1	bone morphogenetic protein 5 precursor [Bos taurus]	
814	NP_001191830.1	bone morphogenetic protein 5 [Sus scrofa]	
815	XP_532179.2	bone morphogenetic protein 5 [Canis lupus familiaris]	
816	XP_001503274.1	bone morphogenetic protein 5 [Equus caballus]	
817	XP_004018779.1	bone morphogenetic protein 5 [Ovis aries]	
818	XP_518553.2	bone morphogenetic protein 5 isoform X1 [Pan troglodytes]	
819	XP_001109809.1	bone morphogenetic protein 5 [Macaca mulatta]	
820	XP_003986323.1	bone morphogenetic protein 5 [Felis catus]	
821	XP_005696245.1	PREDICTED: bone morphogenetic protein 5 [Capra hircus]	
822	XP_030868477.1	bone morphogenetic protein 5 isoform X1 [Gorilla gorilla gorilla]	
823	XP_002817070.2	bone morphogenetic protein 5 isoform X1 [Pongo abelii]	
824	XP_031996280.1	bone morphogenetic protein 5 isoform X1 [Hylobates moloch]	
825			
826	NP_066551.1	1	MHLTVFLLKGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
827	NP_031581.2	1	MHWTVFLLRGI V GFLWWSGQVQVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
828	NP_001101638.1	1	MHWTVFLLRGI V GFLWSSVQVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
829	NP_001291945.1	1	MHLTVFLLRGI V GFLWSCVWLVGSAGKSLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
830	NP_001191830.1	1	MHLTVFLLRGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
831	XP_532179.2	1	MHLTVFLLRSI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
832	XP_001503274.1	1	MHLTVFLLRGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
833	XP_004018779.1	1	MHLTVFLLRGI V GFLWSCVWLVGSAGKSLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
834	XP_518553.2	1	MHLTVFLLKGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
835	XP_001109809.1	1	MHLTVFLLKGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
836	XP_003986323.1	1	MHLTVFLLRSI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
837	XP_005696245.1	1	MHLTVFLLRGI V GFLWSCVWLVGSAGKSLGDNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
838	XP_030868477.1	1	MHLTVFLLKGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
839	XP_002817070.2	1	MHLTVFLLKGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
840	XP_031996280.1	1	MHLTVFLLKGI V GFLWSCVWLVGYAKGGLDGNHVHSSFIYRRLRNHERREIQREILSILGLPHRPRPFSPGKQASSAPLF 80
841			
842	NP_066551.1	81	MLDLYNAMTNEENPEESEYSVRASLAEETRGA R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
843	NP_031581.2	81	MLDLYNAMASEDNPEESEYLVRVSLAGEAKETR K GYPASPNGYAHLRHLPPRTPLTTQSPPLASLHD T NFLNDADMVMSF 160
844	NP_001101638.1	81	MLDLYNAMASEENPEESEYLVRVSLAGEAKETR K GYPASPNGYAHLRHLPPRTPLTTQSPPLASLHD T NFLNDADMVMSF 160
845	NP_001291945.1	81	MLDLYNAMASEENPEELEYSVRAPLAADSRGARK S PASPNGYPRRIQLSRASPLTTQSPPLASLHD A NFLNDADMVMSF 160
846	NP_001191830.1	81	MLDLYNAMASEENPEEYSVRASLAEETRGA R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD A NFLNDADMVMSF 160
847	XP_532179.2	81	MLDLYNAMANEENPEESEYSVRASLAGE T RGT R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
848	XP_001503274.1	81	MLDLYNAMANEENPEETEYSVRASLAGE T RGR K GYPASPNGYPRGIQLSRTAPLTTQSPPLASLHD T NFLNDADMVMSF 160
849	XP_004018779.1	81	MLDLYNAMASEENPEELEYSVTAPLAADSRG S RKGS P ASPNGYPRRIQLSRASPLTTQSPPLASLHD A NFLNDADMVMSF 160
850	XP_518553.2	81	MLDLYNAMTNEENPEESEYSVRASLAEETRGA R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
851	XP_001109809.1	81	MLDLYNAMTNEENPEESEYSVRASLAEETRGA R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
852	XP_003986323.1	81	MLDLYNAMANEENPEESEYSVRASLAGEARGARK G YPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
853	XP_005696245.1	81	MLDLYNAMASEENPEELEYSVTAPLAADSRG S RKGS P ASPNGYPRRIQLSRASPLTTQSPPLASLHD A NFLNDADMVMSF 160
854	XP_030868477.1	81	MLDLYNAMTNEENPEESEYSVRASLAEETRGA R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
855	XP_002817070.2	81	MLDLYNAMTNEENPEESEYSVRASLAEETRGA R KGYPASPNGYPRRIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
856	XP_031996280.1	81	MLDLYNAMTNEENPEESEYSVRASLAEETRGA R RGYPASPNGYPRGIQLSRTTPLTTQSPPLASLHD T NFLNDADMVMSF 160
857			
858	NP_066551.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
859	NP_031581.2	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDKGNH R RFENETIKISYQI I KEYTNRDADFLLDTRKT 240
860	NP_001101638.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDKS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
861	NP_001291945.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPQGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYANRDADFLLDTRKT 240
862	NP_001191830.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKV 240
863	XP_532179.2	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKQ S NSRFENETIKISYQI I KEYTNRDADFLLDTRKA 240
864	XP_001503274.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
865	XP_004018779.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPQGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKT 240
866	XP_518553.2	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
867	XP_001109809.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
868	XP_003986323.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKQ S NSRFENETIKISYQI I KEYTNRDADFLLDTRKT 240
869	XP_005696245.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPQGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKT 240
870	XP_030868477.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
871	XP_002817070.2	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
872	XP_031996280.1	161	VNLVERDKDFSHQRRHYKEFRFDLTQIPHGEAVTAAEFRIYKDRS N RFENETIKISYQI I KEYTNRDADFLLDTRKA 240
873			
874	NP_066551.1	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRS I NVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK 320
875	NP_031581.2	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRS I NVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAASK 320
876	NP_001101638.1	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRS I NVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAASK 320
877	NP_001291945.1	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHS I NVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK 320
878	NP_001191830.1	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHS I SVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK 320
879	XP_532179.2	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRS I NVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK 320
880	XP_001503274.1	241	EALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRS I NVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK 320
881	XP_004018779.1	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGHS I NVKSAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK 320
882	XP_518553.2	241	QALDVGWLVFDITVTSNHWVINPQNNLGLQLCAETGDGRS I NVKSAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK 320

883	XP_001109809.1	241	QALDVGWLVFDITVTSNHVWVNPQNNLGLQLCAETGDGRSINVKASAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK	320
884	XP_003986323.1	241	QALDVGWLVFDITVTSNHVWVNPQNNLGLQLCAETGDGRSINVKASAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK	320
885	XP_005696245.1	241	QALDVGWLVFDITVTSNHVWVNPQNNLGLQLCAETGDGHSINVKASAGLVGRHGPQSKQPFMVAFFKASEVLLRSVRAANK	320
886	XP_030868477.1	241	QALDVGWLVFDITVTSNHVWVNPQNNLGLQLCAETGDGRSINVKASAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK	320
887	XP_002817070.2	241	QALDVGWLVFDITVTSNHVWVNPQNNLGLQLCAETGDGRSINVKASAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK	320
888	XP_031996280.1	241	QALDVGWLVFDITVTSNHVWVNPQNNLGLQLCAETGDGRSINVKASAGLVGRQGPQSKQPFMVAFFKASEVLLRSVRAANK	320
889				
890	NP_066551.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
891	NP_031581.2	321	RKNQNRNKSNSHQDPSRMPSAGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
892	NP_001101638.1	321	RKNQNRNKSSSHQDPSRIPSAAGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
893	NP_001291945.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
894	NP_001191830.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
895	XP_532179.2	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
896	XP_001503274.1	321	RKNQNRNKSSSHQDSRVSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
897	XP_004018779.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
898	XP_518553.2	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
899	XP_001109809.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
900	XP_003986323.1	321	RKNQNRNKSNSHQDPSRMPSAGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
901	XP_005696245.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
902	XP_030868477.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
903	XP_002817070.2	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
904	XP_031996280.1	321	RKNQNRNKSSSHQDSRMSSVGDYNTSEQKQACKKHELYVSERDLGQDNIIAPEGAAAFYCDGECSPFLNAHMNATNHA	400
905				
906	NP_066551.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
907	NP_031581.2	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
908	NP_001101638.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
909	NP_001291945.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
910	NP_001191830.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
911	XP_532179.2	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
912	XP_001503274.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
913	XP_004018779.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
914	XP_518553.2	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
915	XP_001109809.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
916	XP_003986323.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
917	XP_005696245.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
918	XP_030868477.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
919	XP_002817070.2	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
920	XP_031996280.1	401	IVQTLVHLMFPDHPKPCCAPTKLNAISLYFDDSSNVILKKRNIVVRSCGCH	454
921				

BMP6

924	NP_001709.1	bone morphogenetic protein 6 preproprotein [Homo sapiens]
925	NP_031582.1	bone morphogenetic protein 6 preproprotein [Mus musculus]
926	XP_038951315.1	bone morphogenetic protein 6 isoform X1 [Rattus norvegicus]
927	XP_002697666.2	bone morphogenetic protein 6 isoform X1 [Bos taurus]
928	NP_001161473.1	bone morphogenetic protein 6 precursor [Sus scrofa]
929	XP_038302254.1	LOW QUALITY PROTEIN: bone morphogenetic protein 6 [Canis lupus familiaris]
930	XP_023480199.1	bone morphogenetic protein 6 [Equus caballus]
931	XP_027814245.1	bone morphogenetic protein 6 isoform X1 [Ovis aries]
932	XP_003950760.2	bone morphogenetic protein 6 [Pan troglodytes]
933	XP_001085364.1	bone morphogenetic protein 6 [Macaca mulatta]
934	XP_023109461.1	bone morphogenetic protein 6 [Felis catus]
935	XP_017894411.1	PREDICTED: bone morphogenetic protein 6 isoform X1 [Capra hircus]
936	XP_030868423.1	bone morphogenetic protein 6 [Gorilla gorilla gorilla]
937	XP_024104721.1	bone morphogenetic protein 6 [Pongo abelii]
938	XP_031997037.1	bone morphogenetic protein 6 [Hylobates moloch]
939		
940	NP_001709.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-AaGGQLLDGGSPGRTEQPPSP QSSS-GFLYRRLKTQ 74
941	NP_031582.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-A-GGQLLDGGSPVRAEQPPQ- SSSS-GFLYRRLKTH 71
942	XP_038951315.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-A-GGQLLDGGSPVRAEQPPQ- SSSS-GFLYRRLKTH 71
943	XP_002697666.2	1 M--LGRTAQWLCWWWGLLCSFCGPPPL----PAAAAA--GGALLDGGSPGHAERPPPQ TSSS-GFLYRRLKTH 66
944	NP_001161473.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPSLRPPLPAAAAA-A-GGALLDGGSPGHAEQPPPPQ TSSS-GFLYRRLKTH 73
945	XP_038302254.1	1 M--LGPRAPWLCWWWGLLCSGCCGPPPL-PPAAAAAaA-GGALLDGGSPGHAEPTPPP [14] SSSS-GFLYRRLKTH 85
946	XP_023480199.1	1 MPGLARRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-G-GGALLDGGSPGHAEQPPPPP QSSSsGFLYRRLKTH 74
947	XP_027814245.1	1 M--LGRTAQWLCWWWGLLCSFCGPPPL----PAAAAA--GGALLDGGSPGHAERPPPQ TSSS-GFLYRRLKTH 66
948	XP_003950760.2	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-AaGGQLLDGGSPGRTEQPPSP QSSS-GFLYRRLKTQ 74
949	XP_001085364.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-AaGGQLLDGGSPGRTEQPPSP QSSS-GFLYRRLKTH 74
950	XP_023109461.1	1 M--LGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAAaG-GGALLDGGSPGHAEQPPPPP QSSS-GFLYRRLKTH 72
951	XP_017894411.1	1 M--LGRTAQWLCWWWGLLCSFCGPPPL----PAAAAA--aGGALLDGGSPGHAERPPPQ TSSS-GFLYRRLKTH 67
952	XP_030868423.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-AaGGQLLDGGSPGRTEQPPSP QSSS-GFLYRRLKTQ 74
953	XP_024104721.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-AaGGQLLDGGSPGRTEQPPSP QSSS-GFLYRRLKTQ 74
954	XP_031997037.1	1 MPGLGRRRAQWLCWWWGLLCSGCCGPPPLRPPLPAAAAA-AaGGQLLDGGSPGRTEQPPSP QSSS-GFLYRRLKTQ 74
955		
956	NP_001709.1	75 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQq--LP-RGEPppGRLKSAPLFLMDLYNALSADN 147
957	NP_031582.1	72 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPVL-PpqqQQQ-QQQQQ---TA-REEPppGRLKSAPLFLMDLYNALSND 145
958	XP_038951315.1	72 EKREMQKEILSVLGLPHRPRPLHGLQQPQSPVL-P----QQ-QQSQQ---TA-REEPppGRLKSAPLFLMDLYNLSKDD 141
959	XP_002697666.2	67 EKREMQKEILSVLGLPHRPRPLHGL--PQPVPF-P---QQQ-----Q---PaRGEPppGRLKSAPLFLMDLYNALSADD 131
960	NP_001161473.1	74 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-P---QQQ-----GEPppGRLKSAPLFLMDLYNALSADD 141
961	XP_038302254.1	86 EKREMQKEILSVLGLPHRPRPLHGLPPPQAAF-P---QQQ-----P-RGEPppGRLKSAPLFLMDLYNALSAAAD 150
962	XP_023480199.1	75 EKREMQKEILSVLGLPHRPRPLHGLQQLQPPAL-P---QQQ-----P-RGEPppGRLKSAPLFLMDLYNALSAAAD 139
963	XP_027814245.1	67 EKREMQRTEILSVLGLPHRPRPLHGL--PQPVPF-P---QQQ-----PaRGEPppGRLKSAPLFLMDLYNALSADD 130
964	XP_003950760.2	75 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQq--LP-RGEPppGRLKSAPLFLMDLYNALSADN 146
965	XP_001085364.1	75 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-P---QQQ-QQQQQ---PP-RGEPppGRLKSAPLFLMDLYNALSADD 145
966	XP_023109461.1	73 EKREMQKEILSVLGLPHRPRPLHGLQQPQPAAL-P---QE-----P-RGEPppGRLKSAPLFLMDLYNALSADD 137
967	XP_017894411.1	68 EKREMQRTEILSVLGLPHRPRPLHGL--PQPVPF-P---QQQ-----PaRGEPppGRLKSAPLFLMDLYNALSADD 131
968	XP_030868423.1	75 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQq--LP-RGEPppGRLKSAPLFLMDLYNALSADN 149
969	XP_024104721.1	75 EKREMQKEILSVLGLPHRPRPLHGLQQPQPPAL-R---QQEeQQQQQq--LP-RGEPppGRLKSAPLFLMDLYNALSADN 146
970	XP_031997037.1	75 EKREMQKEILSVLGLPHRPRPLHGLQEPQPPALpQ---QQQqQQQQq--LP-RGEPppGRLKSAPLFLMDLYNALSADD 147
971		
972	NP_001709.1	148 DEDGASEGERQQSWPHEAASSQRRQPPPGAHAHPLNRKSLAPGSGGGA S-PLTSAQDSAFNLNADDMVMSFVNIVE 223
973	NP_031582.1	146 EEDGASEGVGQEPGSHGGASSQLRQPSPGAHAHSLNRKSLAPGGG-GGA S-PLTSAQDSAFNLNADDMVMSFVNIVE 220
974	XP_038951315.1	142 EEDGVSEGEGLPEPESHGRASSQLRQPSPGAHAHSLNRKSLAPGGG-GSA S-PLTSAQDSAFNLNADDMVMSFVNIVE 216
975	XP_002697666.2	132 EEDGASDEERRQPGQGGADASQPRSPSSGAHPLGSGSLATGPGGG-- AsPLTSAQDSAFNLNADDMVMSFVNIVE 206
976	NP_001161473.1	142 EEDLASDKEMQPGPLRGDTSSPPRQPPRAAHLPLGSRSLAAGPG-GSA S-PLTSAQDSAFNLNADDMVMSFVNIVE 216
977	XP_038302254.1	151 DEGWAGEQRRRPRGPRGASSPFRPPGAAPLVGGRSLVAAGPGGGG [4] AsALPASAQDSAFNLNADDMVMSFVNIVE 231
978	XP_023480199.1	140 DEDGSPDEERRPPAPRGAGSPQPGQPPPGAHAHPLNRKSLAPGPGGGGA AtPLTSAQDSAFNLNADDMVMSFVNIVE 216
979	XP_027814245.1	131 EEDGASDEERRQPGPRGAGASQPRSPSPGAHPLGSGSLATGPGGG-- AsPLTSAQDSAFNLNADDMVMSFVNIVE 205
980	XP_003950760.2	147 DEDGASEGERQQSWPHEAASSQRRQPPPGAHAHPLNRKSLAPGSGGGA S-PLTSAQDSAFNLNADDMVMSFVNIVE 222
981	XP_001085364.1	146 EEDGASEGERQQSWPHEAASSQRRQPPPGAHAHPLNRKSLAPGPGSGGA S-PLTSAQDSAFNLNADDMVMSFVNIVE 221
982	XP_023109461.1	138 DEDWASDEERRQPGPRGAGASSQPRQPPPGAHPVNGKSLASGPGGG-- TsPLTSAQDSAFNLNADDMVMSFVNIVE 212
983	XP_017894411.1	132 EEDGASDEERRQPGPRGAGASQSRSPSPGAHPLGSGSLATGPGGG-- AsPLTSAQDSAFNLNADDMVMSFVNIVE 206
984	XP_030868423.1	150 DEDGASEGERQQSWPHEAASSQRRQPPPGAHAHPLNRKSLAPGSGGGA S-PLTSAQDSAFNLNADDMVMSFVNIVE 225
985	XP_024104721.1	147 DEDGASEGERQQSWPHEAASSQRRQPPPGAHAHPLNRKSLAPGPGSGGA S-PLASAQDSAFNLNADDMVMSFVNIVE 222
986	XP_031997037.1	148 DEDGASEEKKQSWPREAASSQRRQPPGVAHPLNRKSLAPGPGSGGA S-PLTSAQDSAFNLNADDMVMSFVNIVE 223
987		
988	NP_001709.1	224 YDKEFSRQRHHKEFKFNLSQIPEGEVAVTAAEFRIYKDCVMGSFKNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 303
989	NP_031582.1	221 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 300
990	XP_038951315.1	217 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 296
991	XP_002697666.2	207 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 286
992	NP_001161473.1	217 YDKEFSRQRHHKEFKFNLSQVPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 296
993	XP_038302254.1	232 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 311
994	XP_023480199.1	217 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 296
995	XP_027814245.1	206 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 285
996	XP_003950760.2	223 YDKEFSRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLLISYQVLQEQHQRSDFLFLDTRVWASEE 302

997	XP_001085364.1	222	YDKFESPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLISIQVLQEHQHRSDSLFLLDTRVWVASEE	301
998	XP_023109461.1	213	HEKEFSPGQRYHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLISIQVLQEHQHRSDSLFLLDTRVWVASEE	292
999	XP_017894411.1	207	YDKFESPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVVGSGFNQTFLISIQVLQEHQHRSDSLFLLGTRAVWASEA	286
1000	XP_030868423.1	226	YDKFESPRQHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSGFNQTFLISIQVLQEHQHRSDSLFLLDTRVWVASEE	305
1001	XP_024104721.1	223	YDKFESPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSGFNQTFLISIQVLQEHQHRSDSLFLLDTRVWVASEE	302
1002	XP_031997037.1	224	YDKFESPRQRHHKEFKFNLSQIPEGEAVTAAEFRIYKDCVMGSGFNQTFLISIQVLQEHQHRSDSLCLLDTRVWVASEE	303
1003				
1004	NP_001709.1	304	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLVHVPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	383
1005	NP_031582.1	301	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLVHVPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	380
1006	XP_038951315.1	297	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLHINPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	376
1007	XP_002697666.2	287	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	366
1008	NP_001161473.1	297	GWLEFDITATSNLWVVTTPQHNLGLQLGVVTDGLSISPGAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	376
1009	XP_038302254.1	312	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLPINPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	391
1010	XP_023480199.1	297	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLSINPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	376
1011	XP_027814245.1	286	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	365
1012	XP_003950760.2	303	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	382
1013	XP_001085364.1	302	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLVHVPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	381
1014	XP_023109461.1	293	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLNINPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	372
1015	XP_017894411.1	287	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLSISPGAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	366
1016	XP_030868423.1	306	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLVHVPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	385
1017	XP_024104721.1	303	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLVHVPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	382
1018	XP_031997037.1	304	GWLEFDITATSNLWVVTTPQHNMGLQLSVVTRDGLVHVPRAAGLVGRDGPYDKQPFMVAFKQSEVHVTRTRSASSRRRQQ	383
1019				
1020	NP_001709.1	384	SRNRSTQSQDVARVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	462
1021	NP_031582.1	381	SRNRSTQSQDVSRRGSS-DYNGSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	459
1022	XP_038951315.1	377	SRNRSTQSQDVSRRGSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	455
1023	XP_002697666.2	367	ARNRSTPAQDVSRRASASaDYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	446
1024	NP_001161473.1	377	SRNRSTQAQDVSRRASAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	455
1025	XP_038302254.1	392	SRNRSTQSQDVSRRVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	470
1026	XP_023480199.1	377	SRNRSTQSQDVSRRVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	455
1027	XP_027814245.1	366	ARNRSTPAQDVSRRASASaDYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	445
1028	XP_003950760.2	383	SRNRSTQSQDVARVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	461
1029	XP_001085364.1	382	SRNRSTQSQDVARVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	460
1030	XP_023109461.1	373	SRNRSTQSQDVSRRVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	451
1031	XP_017894411.1	367	ARNRSTPAQDVSRRASASaDYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	446
1032	XP_030868423.1	386	SRNRSTQSQDVARVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	464
1033	XP_024104721.1	383	SRNRSTQSQDVARVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	461
1034	XP_031997037.1	384	SRNRSTQSQDVARVSSAS-DYNSELKTACKKHELYVSDDLGQDII IAPKGAANYCDGECSPFLNAHMNATNHAIVQ	462
1035				
1036	NP_001709.1	463	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	513
1037	NP_031582.1	460	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	510
1038	XP_038951315.1	456	TLV [29] HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	535
1039	XP_002697666.2	447	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	497
1040	NP_001161473.1	456	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	506
1041	XP_038302254.1	471	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	521
1042	XP_023480199.1	456	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	506
1043	XP_027814245.1	446	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	496
1044	XP_003950760.2	462	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	512
1045	XP_001085364.1	461	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	511
1046	XP_023109461.1	452	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	502
1047	XP_017894411.1	447	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	497
1048	XP_030868423.1	465	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	515
1049	XP_024104721.1	462	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	512
1050	XP_031997037.1	463	TLV HLMNPEYVPKPCCAPTKLNAISLYFDDNSNVILKKRNIVVRACGCH	513
1051				
1052				
1053				
1054				

GDF2 / BMP9

1056	NP_057288.1	growth/differentiation factor 2 preproprotein [Homo sapiens]	
1057	NP_062379.3	growth/differentiation factor 2 preproprotein [Mus musculus]	
1058	NP_001099566.1	growth/differentiation factor 2 precursor [Rattus norvegicus]	
1059	NP_001179349.1	growth/differentiation factor 2 precursor [Bos taurus]	
1060	XP_003133152.2	growth/differentiation factor 2 [Sus scrofa]	
1061	XP_853886.2	growth/differentiation factor 2 isoform X1 [Canis lupus familiaris]	
1062	XP_001500704.1	growth/differentiation factor 2 [Equus caballus]	
1063	XP_004021599.3	growth/differentiation factor 2 [Ovis aries]	
1064	XP_507775.4	growth/differentiation factor 2 [Pan troglodytes]	
1065	XP_001109523.2	growth/differentiation factor 2 [Macaca mulatta]	
1066	XP_003994191.1	growth/differentiation factor 2 [Felis catus]	
1067	XP_005699391.1	PREDICTED: growth/differentiation factor 2 [Capra hircus]	
1068	XP_004049419.1	growth/differentiation factor 2 [Gorilla gorilla gorilla]	
1069	XP_002820746.1	growth/differentiation factor 2 [Pongo abelii]	
1070	XP_032026853.1	growth/differentiation factor 2 [Hylobates moloch]	
1071	NP_057288.1	1 MCPGALWVALPL-LS ---LLAGSLQGKPLQSWGRGSAGGNAHSP LGVPGGGLPEHTFNLKMFLENVKVDFLRSNLNSGVP	76
1072	NP_062379.3	1 MSPGAFRVAL ---LP-lfLLVCVTQKQKPLQNWQEASPGENAHSSSLGSGAGEE-GVFDLQMFLENMKVDFLRSNLNSGIP	75
1073	NP_001099566.1	1 MSPGAFRVVL ---LT-llLLVCPTQKQKPLQSWGQASPGGNARSSSLGSGSRE-GVFDLQMFLENMKVDFLRSNLNSGIP	75
1074	NP_001179349.1	1 MGRGALWVALPV-LC ---LLACSAALGKPLENRRPSTGADAHGLLGGPGGEQEGVTFDLRMFLENMKVDFLRNLNSGVP	76
1075	XP_003133152.2	1 MCRGALWVALPvLS ---LLVCSTQKQKPLDSVRASAGGDAHRLGGAGGEQERGTDFLRMFLENMKVDFLRSNLNSGVP	77
1076	XP_853886.2	1 MCGGAVGGALRA-LC alwLLGCGARGRPLEGRRRPGS-----QGAPGGPR-----DLRALPQAVQRDLRLRNLNSGVP	67
1077	XP_001500704.1	1 MCRGALRVAL ---LA---LLACSAQKPLESRGAAAGGDAHRPRGGPGGEQEGATFDLRMFLENMKVDFLRSNLNSGVP	74
1078	XP_004021599.3	1 MGRGALRMALPV-LS ---LLACSAALGKPLENRRPSTGGDAHRLLRGGPGGEQEGATFDLRMFLENMKVDFLRNLNSGVP	76
1079	XP_507775.4	1 MCPGALWVALPL-LS ---LLAGSLQKPLQSWGRGSAGGNAHSP LGVPGGGLPEHTFNLKMFLENVKVDFLRSNLNSGVP	76
1080	XP_001109523.2	1 MCPGALWVALPL-LS ---LLAGSLQKPLQSWGRGSAGGTAHNPLGVPGGELPEHTFNLKMFLENMKVDFLRSNLNSGVP	76
1081	XP_003994191.1	1 MCCGALWVALPV-LS ---LLACSAQKPLESRGRAPAGGDAHRLLRGGPGGEREGGTFDLRMFLENMKVDFLRSNLNSGVP	76
1082	XP_005699391.1	1 MGRGALRMALPV-LS ---LLACSAALGKPLGNRRPSTGGDAHRLLRGGPGGEQEGVTFDLRMFLENMKVDFLRNLNSGVP	76
1083	XP_004049419.1	1 MCPGALWVALPL-LS ---LLAGSLQKPLQSWGRGSAGGNAHSP LGVPGGGLPEHTFNLKMFLENVKVDFLRSNLNSGVP	76
1084	XP_002820746.1	1 MCLGALWVALPL-LS ---LLAGSLQKPLQSWGRGSAGGNAHSP LGVPGGGLPEHTFNLKMFLENVKVDFLRSNLNSGVP	76
1085	XP_032026853.1	1 MCPGALWVALPL-LS ---LLAGSLQKPLQSWGRGSAGGNAHSP LGVPGGGLPEHTFNLKMFLENMKVDFLRSNLNSGVP	76
1086			
1087	NP_057288.1	77 SQDKTRVEPPQYMI DLNRYTSDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1088	NP_062379.3	76 SQDKTRA EPPQYMI DLNRYTTDKSSTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	155
1089	NP_001099566.1	76 SQDKTRA EPPQYMI DLNRYTTDKSSTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	155
1090	NP_001179349.1	77 SQDRT RAEPPQYMI DLNRYTTDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYLSC	156
1091	XP_003133152.2	78 SQDKTRA EPPQYMI DLNRYTTDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYLSC	157
1092	XP_853886.2	68 AQP RAEPPQYMI DLNRYTSDKAAPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	147
1093	XP_001500704.1	75 SQDKTRA EPPQYMI DLNRYTTDKSSTPTSNIVRSFSDMEDAISITATEDLSFQKHILLFNISIPRHEQITRAELRLHISC	154
1094	XP_004021599.3	77 SQDRT RAEPPQYMI DLNRYTTDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1095	XP_507775.4	77 SQDKTR VEPPQYMI DLNRYTSDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1096	XP_001109523.2	77 SQDKTR VEPPQYMI DLNRYTSDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1097	XP_003994191.1	77 SQDKTRA EPPQYMI DLNRYTTDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYASC	156
1098	XP_005699391.1	77 SQDRT RAEPPQYMI DLNRYTTDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1099	XP_004049419.1	77 SQDKTR VEPPQYMI DLNRYTSDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1100	XP_002820746.1	77 SQDKTR VEPPQYMI DLNRYTSDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1101	XP_032026853.1	77 SQDKTR VEPPQYMI DLNRYTSDKSTTPASNI VRSFSDMEDAISITATEDFPFQKHILLFNISIPRHEQITRAELRLYVSC	156
1102			
1103	NP_057288.1	157 QNHVDP SHDLKGSVVIYDVLDTDAWDSATETKTFLVSDIQDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVESHRKG	236
1104	NP_062379.3	156 QNDVDS THGLEGSMVVYDVLDESETWDQATGKTKTFLVSDIRDEGWETLEVSSAVKRWVRADSTTNKNKLEVTVQSHRES	235
1105	NP_001099566.1	156 QNHVDS THGLEGNMVIYDVLVDVDETDWDSASGKTKTFLVSDIQDEGWETLEVSSAVKRWVRADSTTNKNKLEVTVQRHREG	235
1106	NP_001179349.1	157 QSHMDS PHELKGNMVIYDVLGDGAEVDAPAGTKTFLVSDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG	236
1107	XP_003133152.2	158 QSHVD SHELKGNMIYDVLGDG-----SEGKTKTFLVSDIRDEGWETFEVSSAVKRWVQADSTKSKNKLEVTVESHRKG	232
1108	XP_853886.2	148 QGHGA SRELKGNMAIYDVLGDADAWDASAGTKTFLVSDISDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG	227
1109	XP_001500704.1	155 QSHVDS SHELKGNMVIYDVLGDADAWDASMTKTKTFLVSDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG	234
1110	XP_004021599.3	157 QSHVDS SHELKGNMVIYDVLGDGAEVDAPGGTKTFLVSDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG	236
1111	XP_507775.4	157 QNHVDP SHDLKGSVVIYDVLDTDAWDSATETKTFLVSDIQDEGWETLEVSSAVKRWVRSDSISKSKNKLEVTVESHRKG	236
1112	XP_001109523.2	157 QNHMD SHDLKGSVVIYDVLDTDAWDSAAETKTKTFLVSDIRDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVESHRKG	236
1113	XP_003994191.1	157 QNHGDS SHELKGNMAIYDVLGDADAWDASATGKTKTFLVSDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESHRKG	236
1114	XP_005699391.1	157 QSHVDS SHELKGNMVIYDVLGDGAEVDAPGGTKTFLVSDIRDEGWETFEVSSAVKRWVRADSTKSKNKLEVTVESRRKG	236
1115	XP_004049419.1	157 QNHVDP SHDLKGSVVIYDVLDTDAWDSATETKTFLVSDIQDEGWETLEVSSAVKRWVRSDSISKSKNKLEVTVESHRKG	236
1116	XP_002820746.1	157 QNHVDP SHDLKGSVVIYDVLDTDAWDSAAETKTKTFLVSDIQDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVESHRKG	236
1117	XP_032026853.1	157 QNHVDP SHDLKGNVVIYDVLDTDAWDSATETKTFLVSDIQDEGWETLEVSSAVKRWVRSDSTKSKNKLEVTVENHRKG	236
1118			
1119	NP_057288.1	237 CDTLDI SVPPGSRNLPFFVVFVSNDRSSGKTKETRLRELEMISHEQESVLKLSKDGSTEAGESH--EEDTDGHVAAGSTL	314
1120	NP_062379.3	236 CDTLDI SVPPGSKNLPFFVVFVSNDRSNGTKETRLRELEMIGHEQETMLVK TAKNAYQVAGES-Q-eEGLDGYTAVGPLL	313
1121	NP_001099566.1	236 CSTLDI SVPPGQNLPFFVVFVSNDRSNGTKETRLRELEMIGHEQETVVLVKTKSNAYQEAGESRE-eEERIDGYTAVGPLL	314
1122	NP_001179349.1	237 CDKLDI SVPPGSKNLPFFVVFVSNDRSNGTKETRLRELEMIGHEQESVLRKLSKNTVVEAGENKDeeEEDVRSHTPTSSL	316
1123	XP_003133152.2	233 CDKLDI SVPPGSKNLPFFVVFVSNDRSNGTKETRLRELEMISHEQESVLKLSRNSLLEAGEDKDeeEGMEGHVAMGSSL	312
1124	XP_853886.2	228 CDKLDI SVPPGSKNLPFFVVFVSNDRSNGTKETRLRELEMISHEQESVLTKWSKNSPAGADRKA--EGGEGHMATGSSL	305
1125	XP_001500704.1	235 CDRLDI SVPPGSKNLPFFVVFVSNDRSNGTKETRLRELEMIGHEQESVLRKLSKDGLAEDENRKA--EEDVGEHMATGSSL	312
1126	XP_004021599.3	237 CDKLDI SVPPGSKNLPFFVVFVSNDRSNGTKETRLRELEMISHEQESVIKLSRNTVVEAGENKDeeQ-DVQGHVPTAASL	315
1127	XP_507775.4	237 CDTLDI SVPPGSRNLPFFVVFVSNDRSSGKTKETRLRELEMISHEQESVLKLSKDGSTEAGESH--EEDTDGHVAAGSTL	314
1128	XP_001109523.2	237 CDKLDI SVPPGSRNLPFFVVFVSNDRSSGKTKETRLRELEMISHEQESVLKLSKDGSTEAGESH--EEDADGHVAVGSTL	314

1129	XP_003994191.1	237	CDKLDISVPPGPQNLFFFVFSNDRSNGTKETRLELREMIGHEQESVLKLSKNGPAEAGDNKD--E-DGEGRKATGSSL	313
1130	XP_005699391.1	237	CDKLDISVPPGSKNLFFFVFSNDRSNGTKETRLELREMISHEQESVLKLSRNTVVEAGENKDeeQ-DAQGPVPTAASL	315
1131	XP_004049419.1	237	CDTLDISVPPGSRNLFFFVFSNDHSSGTKETRLELREMISHEQESVLKLSKDGSTEAGESSH--EEDTDGHVAAGSTL	314
1132	XP_002820746.1	237	CDTLDISVPPGSRNLFFFVFSNDHSSGTKETRLELREMISHEQESVLKLSKDGSTEAGESSH--EEDTDGHVAAGSTL	314
1133	XP_032026853.1	237	CDTLDISVPPGSRNLFFFVFSNDHSSGTKETRLELREMISHEQESVLKLSKDGSTEQGESHS--EEDADGHVAAGSTL	314
1134				
1135	NP_057288.1	315	ARRKRSAG-AGSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	393
1136	NP_062379.3	314	ARRKRSTG-ASSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	392
1137	NP_001099566.1	315	ARRKRSTGaASSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	394
1138	NP_001179349.1	317	VRRKRSTG-ANNHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	395
1139	XP_003133152.2	313	ARRKRSAG-ANNHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	391
1140	XP_853886.2	306	ARRKRSAG-ANNHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	384
1141	XP_001500704.1	313	ARRKRSAG-AGNHHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	391
1142	XP_004021599.3	316	VRRKRSTG-ANSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	394
1143	XP_507775.4	315	ARRKRSAG-AGSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	393
1144	XP_001109523.2	315	SRRKRSTG-AGSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	393
1145	XP_003994191.1	314	ARRKRSAG-ANNHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	392
1146	XP_005699391.1	316	VRRKRSTG-ANSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	394
1147	XP_004049419.1	315	ARRKRSAG-AGSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	393
1148	XP_002820746.1	315	ARRKRSAG-AGSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	393
1149	XP_032026853.1	315	ARRKRSTG-AGSHCQKTSLRVNEEDIGDSDSIIAPKEEAYECKGGCFFPLADDVTPTKHAIQTLVHLKFPKVGKACC	393
1150				
1151	NP_057288.1	394	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	429
1152	NP_062379.3	393	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	428
1153	NP_001099566.1	395	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	430
1154	NP_001179349.1	396	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	431
1155	XP_003133152.2	392	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	427
1156	XP_853886.2	385	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	420
1157	XP_001500704.1	392	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	427
1158	XP_004021599.3	395	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	430
1159	XP_507775.4	394	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	429
1160	XP_001109523.2	394	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	429
1161	XP_003994191.1	393	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	428
1162	XP_005699391.1	395	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	430
1163	XP_004049419.1	394	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	429
1164	XP_002820746.1	394	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	429
1165	XP_032026853.1	394	VPTKLSPISVLYKDDMGVPTLKYHEEGSVSVAECGCR	429
1166				
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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]				
NP_005251.1	1	MALPNKFLWFCFAW	LCFPISLGSQASGGEAQIAASAELESGAMPWS	LLQHIDERDRAGLLPALFKVL	69
NP_032136.2	1	MALPSNFLGVCCFAW	LCFLSSLSSQASTESQSGASENSEADPWS	LLLVDGTDTRSGLLPPLFKVL	69
NP_067704.1	1	MAFPSRFLLGCCFAW	LCLLISLSSQASTGESQAGASENSEADPWS	LLLVDGTDTRSGLLPPLFKVL	69
NP_777106.1	1	MALPNKFFLWFCFAW	LCFPISLDSQPSRGEAQIVARTALESEAEETWS	LLKHLDRHRPGLLSPLLNVL	69
NP_001001909.1	1	MALPRKFFLCFCFFAL	FCFPVSCGSQASRREAHFATSVALESEAEFPWS	LLRPPDERHRSGLPSPLFNVL	69
XP_038536812.1	1	[4] LGGLGPTGLWRACACL [25]	AAQPVRPRAAARPRFSSAPAAASGFREAPWA [48]	ALARNRTENSQTCLSFMTLVL	146
XP_001504477.1	1	MALPSKFFLWFCSSAW	LCFPISLGSQASRAAQIAASAELESEAEFPWS	LLQPLNGGNRSGLLPAFLFKVL	69
NP_001136360.2	1	MALPNKFFLWFCFAW	LCFPISLDSLPSRGEAQIVARTALESEAEETWS	LLNHLGGRHRPGLLSPLLEVL	69
XP_527008.1	1	MALPNKFLWFCFAW	LCFPISLGSQASGGEAQIAASAELESGAMPWS	LLQHIDERDRAGLLPALFKVL	69
XP_014996256.1	1	MALPNKFLWFCFAW	LCFPVSLGSQASGGDAQIAASAELESGATPWS	LLQPI DERDRAGLLPPLFKVL	69
NP_001159372.1	1	MALLSNFFLWFLCFSW	LCFPMSLCSRST-EVQIAAGAEWEAKAEPWS	LVQPLDEKDRLGFLPPLFKVL	68
NP_001272637.1	1	MALPNKFFLWFCFAW	LCFPISLDSLPSRGEAQIVARTALESEAEETWS	LLNHLGGRHRPGLLSPLLKVL	69
XP_018883145.1	1	MALPNKFLWFCFAW	LCFPISLGSQASGGEAQIAASAELESGAMPWS	LLQHIDERDRAGLLPPLFKVL	69
XP_002815918.1	1	MALPNKFLWFCFAW	LCFPITLGSQASGGDAQIAASAELESGATPWS	LLQPI DERDRAGLLPPLFKVL	69
XP_032012334.1	1	MALPNKFLWFCIAW	LCFPISLGSQASGGDAQIAASGELESGATPRS	LLQPI DERDRAGLLPPLFKVL	69
NP_005251.1	70	SVGRGGSPRLQPDSSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTRHKQAPGDQVTGILPSVELLFLNDRITT	149		
NP_032136.2	70	SDRRGETPKLQPDSSRALYMKKLYKTYATKEGVKPSRSHLYNTVRLFSFCAQQEQAPSNQVGTGFLPMVDLFLNDRVTA	149		
NP_067704.1	70	SDRRSETPKLQPDSSRALYMKKLYKTYATKEGVKPSRSHLYNTVRLFSFCAQQEQAPSNQMTGFLPMVDLFLNDRVTA	149		
NP_777106.1	70	YDGHREPRLQPDSSRALYMKKLYKTYATKEGTPKSNRSHLYNTVRLFTPCAQHKQAPGDQVAGTFLPSVDLFLNDRVTV	149		
NP_001001909.1	70	YDGHGGLPRLQPDSSRALRYMKKLYKTYATKEGIPKANRSHLYNTVRLFTPCAQHKQAPGDQVGTGFLPSGDLRFLNDRVTA	149		
XP_038536812.1	147	YDQGQGT-----RALRYMKKLYKACATKEGIPKSNRSPLYNTVRLFTSCAQHTQAPGDQATGVSFVVDLFLNDRVPP	220		
XP_001504477.1	70	YDQGQGAPRLQPDSSRALRYMKKLYKAYATKEGIPKSNRSHLYNTVRLFTPCAQHKQAPGDQVAGTFLPSVDLFLNDCVTA	149		
NP_001136360.2	70	YDGHGEPRLQPDSSRALRYMKKLYKAYATKEGTPKSNRSHLYNTVRLFTPCAQHKQAPGDLAGTFLPSVDLFLNDRVTV	149		
XP_527008.1	70	SVGRGGSPRLQPDSSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTRHKQAPGDQVTGILPSVELLFLNDRITT	149		
XP_014996256.1	70	SVGRGGAPRLQPDSSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCQHKQAPGDQVTGILPSVDLFLNDRITT	149		
NP_001159372.1	69	YNGQGDAPRLQPDSSRALRYMKKLYKSFATKEGIPKSNRSPLYNTARLFTSYAQHKQAPGDQVTGTVPSVDLFLHLDVTA	148		
XP_001272637.1	70	YDGHGEPRLQPDSSRALRYMKKLYKAYATKEGIPKSNRSHLYNTVRLFTPCAQHKQAPGDLAGTFLPSVDLFLNDRVTV	149		
XP_018883145.1	70	SVGRGGSPRLQPDSSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCTRHKQAPGDQVTGILPSVELLFLNDRITT	149		
XP_002815918.1	70	SVGRGAPRLQPDSSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCQHKQAPGDQVTGILPSVELLFLNDRITT	149		
XP_032012334.1	70	SVGQGGAPRLQPDSSRALHYMKKLYKTYATKEGIPKSNRSHLYNTVRLFTPCQHKQAPGDQVTGILPSVELLFLNDRITT	149		
NP_005251.1	150	VEHLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPKSSSRTLGRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
NP_032136.2	150	MEHLLKSVLLYTLNNSASSSSTVTCMDLVVKEAMSSGRAPRAYSFTL-----KHRWIEIDVTSLLQPLVTSSE	222		
NP_067704.1	150	MEHLLKSVLLYTLNNSAASSSSTVTCVCDLVVKEPMSSSKATPRAPYSFTL-----RHRWEMDVTSLQPLVASSER	222		
NP_777106.1	150	VEHLPKSVLLYTFNNSISFPFPVKICNLVKEPEFSSKTLPRAPYSFTFNSQFEFRKKYKWEIDVTTAPLEPLVASHKR	229		
NP_001001909.1	150	VEHLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPKSSSRTLGRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
XP_038536812.1	221	VEHLLKSGLLYSFNSISFPFSAVCKCLCHLVKEPEFSSWTPQAPRSLTFLNSQFELKKKYKWEFVDDVTTALRPLVALHKR	300		
XP_001504477.1	150	VEHLLKSVLLYTFNNSVFSFSAVCKVCNLMIKEPE--SKTLPGTPYSFTFNSQFEFRKKYKWEIDVTTAPLEPLVASNKR	227		
NP_001136360.2	150	VEHLPKSVLLYTFNNSISFPFPVKICNLVKEPEFSSKTLPRAPYSFTYNSQFEFRKKYKWEIDVTTAPLEPLVASHKR	229		
XP_527008.1	150	VERLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPKSSSRTLGRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
XP_014996256.1	150	VEHLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPKFSSKTLHRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
NP_001159372.1	149	VEHFKSVLLFTFNSPISFSAVCKVCNLMVKEPESSSGNPHRTLSLTFDSQFEFRKKYRWEIDVTTAPLQPLVASNQR	228		
NP_001272637.1	150	VEHLPKSVLLYTFNNSISFPFPVKICNLVKEPEFSSKTLPRAPYSFTYNSQFEFRKKYKWEIDVTTAPLEPLVASHKR	229		
XP_018883145.1	150	VEHLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPKSSSRTLGRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
XP_002815918.1	150	VEHLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPESSSRTLGRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
XP_032012334.1	150	VEHLLKSVLLYTNINNSVFSFSAVCKVCNLMIKEPKSSSRTLGRAPYSFTFNSQFEFGKKHKWQIDVTSLLQPLVASNKR	229		
NP_005251.1	230	SIHMSINFTCMKDQLEHPSAQNGLFNMTL-VPSLLILYLNDSAQAYHSWYSLHYKRRPSQGPDKRSLASYPVGEAAE	308		
NP_032136.2	223	SIHLSVNFCTCKDQVP---EDGVFSMPLSVPPSLILYLNDSSTQAYHSWQSLQSTWRPLQHPGQA-GVAARPVKEEAIE	297		
NP_067704.1	223	SIHLSVNFCTCRDQAP---ENGTFNMPLSVPPSLILYLNDSSTQAYHSWQSLQSTQRHSQHPGQD-SVTRRVVEEAIE	297		
NP_777106.1	230	NIHMSVNFCTCKDQQLQHPARSDFNMTLLAPSLLLYLNDSAQAFHRWHSLHPKRRPSQGPDKRGLSACPMGEAAE	309		
NP_001001909.1	230	EIHMSIDFTCVKQDLQHPARSDFNMTLLAAPSLLYLNDSSTQAYHRWYSLPWKRRPSQGPDKRGLS-----E	300		
XP_038536812.1	301	SLHMSVNFCTVRNQQQDPVAQDGPWNRTLLVPPSLLLYLNDSAQAHHRWDSLHYKRRSSQRADQKGGLSACPIGEESTE	380		
XP_001504477.1	228	SIHMSVNLTCGKQDLQHPASQDSPLNTLLLPSSLLYLNDSSTQAYHRWHSLHYKRRPSQGPDKRDLASACPEGEAAE	307		
NP_001136360.2	230	NIHMSVNFCAEDQQLQHPARSDFNMTLLVAPSLLYLNDSAQAFHRWHSLHPKRRPSQGPDKRGLSAYPVGEAAE	309		

1243 [XP_527008.1](#) 230 SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGGPDQERSLSAYPVGEEAAE 309
1244 [XP_014996256.1](#) 230 SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHRWYSLYYKRRPSQGGPDQERSLSAYPVGEDAAE 309
1245 [NP_001159372.1](#) 229 NIHMSVNLTCVKAQLQPPSARDGPFNVTLLVPPSLILYLNDTSAQAHHRWYSLHYKRRPSQGGAGQKRGLSACQGEESAE 308
1246 [NP_001272637.1](#) 230 NIHMSVNFCAKDKLQHPASARDSLNFMTLLVAPSLILYLNDTSAQAFHRWHSLSLHPKRRKPSQGGPDQRELSAYPVGEEAAE 309
1247 [XP_018883145.1](#) 230 SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGGPDQERSLSAYPVGEEAAE 309
1248 [XP_002815918.1](#) 230 SIHMSINFTCMKDQLEHPSAQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLNYKRRPSQGGPDQERSLSAYPVGEEAAE 309
1249 [XP_032012334.1](#) 230 SIHMSINFTCMKDQLEHLSVQNGLFNMTLLVSPSLILYLNDTSAQAYHSWYSLHYKRRPSQGGPDQERSLSAYPVGEEAAE 309
1250
1251 [NP_005251.1](#) 309 DGRSShhRHRRGQETVSSLELKKPLGPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 388
1252 [NP_032136.2](#) 298 VERSP--RHRRGQKAIRSEAKGPLLTASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 375
1253 [NP_067704.1](#) 298 VERSP--RHRRGQKTLSSETKKPL-TASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 374
1254 [NP_777106.1](#) 310 GVRLS--RHRRDQESVSSLELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 387
1255 [NP_001001909.1](#) 301 GVPSS--RHRRAQDVTSSLELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 378
1256 [XP_038536812.1](#) 381 GGRSS--RHRRGQDVTSSLHKLPLAPASFNLSEYFKHFLFPQHECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 458
1257 [XP_001504477.1](#) 308 GITSS--RHRRSQEAIVSSLELKKPLVPASVNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 385
1258 [NP_001136360.2](#) 310 GVRSS--RHRRDQESASSLELKKPLVPASVNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 387
1259 [XP_527008.1](#) 310 DGRSShhRHRRGQETVSSLELKKPLGPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 389
1260 [XP_014996256.1](#) 310 DGRSShhRHRRGQETVSSLELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 389
1261 [NP_001159372.1](#) 309 AVRPS--RHRRGQETIGLEPQKPLVPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 386
1262 [NP_001272637.1](#) 310 GVRSS--RHRRDQESVSSLELKKPLVPASVNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 387
1263 [XP_018883145.1](#) 310 DGRSShhRHRRGQETVSSLELKKPLGPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 389
1264 [XP_002815918.1](#) 310 DGRSShhRHRRGQETVSSLELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 389
1265 [XP_032012334.1](#) 310 DGRSShhRHRRGQETVSSLELKKPLVPASFNLSEYFKQFLFPQNECELHDFRLSSQLKNDNIVAPHRNPRYCKGDCPR 389
1266
1267 [NP_005251.1](#) 389 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 454
1268 [NP_032136.2](#) 376 AVRHRRYGSPVHTMVQNIIEKLDPSVPRPSCVPGKYSPLSLTIEPDGSIAYKEEDDIATRCTCR 441
1269 [NP_067704.1](#) 375 AVRHRRYGSPVHTMVQNIIEKLDPSVPRPSCVPGKYSPLSLTIEPDGSIAYKEEDDIATRCTCR 440
1270 [NP_777106.1](#) 388 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLAIEPDGSIAYKEEDDIATKCTCR 453
1271 [NP_001001909.1](#) 379 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLAIEPDGSIAYKEEDDIATKCTCR 444
1272 [XP_038536812.1](#) 459 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 524
1273 [XP_001504477.1](#) 386 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIESDGSITYKEEDDIATKCTCR 451
1274 [NP_001136360.2](#) 388 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLAIEPDGSIAYKEEDDIATKCTCR 453
1275 [XP_527008.1](#) 390 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 455
1276 [XP_014996256.1](#) 390 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 455
1277 [NP_001159372.1](#) 387 ALGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIESDGSIAAYKEEDDIATKCTCR 452
1278 [NP_001272637.1](#) 388 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLAIEPDGSIAYKEEDDIATKCTCR 453
1279 [XP_018883145.1](#) 390 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 455
1280 [XP_002815918.1](#) 390 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 455
1281 [XP_032012334.1](#) 390 AVGHRYGSPVHTMVQNIIEKLDSSVPRPSCVPAKYSPLSLTIEPDGSIAYKEEDDIATKCTCR 455
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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]
NP_000548.2	1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAtnANARAKGGT 80
NP_032135.2	1 MRLPKLLTLLLWHLAWLDLELICTVLGAPDLGQRTPGAKPGLTKAEAKERPPLARNVFRPGGHIYGVGA--TNARAKGSS 78
XP_003749648.1	1 MRLPKLLTLLLWHLAWLDLGLVCTVLGAPDLGQRPPGARFGLAKAEAKERPPLTRNI FRPGGHSYGVGA--TSARAKGSS 78
NP_001179202.1	1 MRLPKLLTLLLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLAQNI FRPGGHSYGGGA--TNARAKGGT 78
NP_001231226.1	1 MRLPKLLTFLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLAQNI FRPGGHSYGGGA--TNARAKGGT 78
XP_542974.1	1 MRLPKLLTFLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLARSVFRPGGHSYGGGA--ANARAKGGT 78
NP_001296325.1	1 MRLPKLLTFLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLARNI FRPGGHSYGGGA--ANARAKGGT 78
XP_004014573.2	1 MRLPKLLTLLLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLAQNI FRPGGHSYGGGA--TNARAKGGT 78
XP_530287.4	1 MRLPKLLTLLLWYLAWLDFEICTVLGAPDLGQRPGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAtnANARAKGGT 80
XP_001099806.2	1 MRLPKLLTFLWYLAWLDFEICTVLGAPDWGQKAQGTFRPGLAKAEAKERPPLARNVFRPGGHSYGGGA--ANARAKGGT 78
XP_003983628.1	1 MRLPKLLTFLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLARSIFRPGGHSYGGGA--TNARAKGGT 78
XP_017913249.1	1 MRLPKLLTLLLWHLAWLDLEFICTVLGAPDLGQRPGARFGLAKAEAKERPPLAQNI FRPGGHSYGGGA--TNARAKGGT 78
XP_018872428.1	1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAtnANARAKGGT 80
XP_003779391.1	1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPGTRPGLAKAEAKERPPLARNI FRPGGHSYGGGAsnANARAKGGT 80
XP_031998077.1	1 MRLPKLLTFLWYLAWLDFEICTVLGAPDLGQRPGTRPGLAKAEAKERPPLARNVFRPGGHSYGGGAsnANARAKGGT 80
NP_000548.2	81 GQTGGLTQPKKDEPKKLPRPGGPEPKPGHPPTQRTARTVTPKGQLPGGKAPPKAGSVSSFLLLKKAREPGPPREPKE 160
NP_032135.2	79 GQ----TQAKKDEPRKMPRSGGPETKPGPSSQTRQAAARTVTPKGQLPGGKASSKAGSAPSSFLLLKKTREPGTPREPKE 154
XP_003749648.1	79 GQ----TQAKKDEPRKMPRASGSETKPGPSPQTRQAAARTVTPKGQLSGGKASAKAGSAPSSFLLLKKTREPGTPREPKE 154
NP_001179202.1	79 GQTGGLTQPKKDEPKKLPRSGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPSKAGSVPSFLLKKAREPGSPREPKE 158
NP_001231226.1	79 GQTGGLTQPKKDEPKKLPRSGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVSPFLLKKAREPGSPREPKE 158
XP_542974.1	79 GQTGGLTQPKKDEPKKLPRSGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVPSFLLKKAREPGSPREPKE 158
NP_001296325.1	79 GQTGGLTQPKKDEPKKLPRSGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVSPFLLKKAREPGPPREPKE 158
XP_004014573.2	79 GQTGGLTQPKKDEPKKLPRSGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPSKAGSVPSFLLKKAREPGSPREPKE 158
XP_530287.4	81 GQKGGTQPKKDEPKKLPRPGGPEPKPGHPPQTRQTTARTVTPKGQLPGGKAPPKAGSVSSFLLLKKAREPGPPREPKE 160
XP_001099806.2	79 GHTGGLTQPKKDEPKKLPRPGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVSSFLLLKKAREPGSPREPKE 158
XP_003983628.1	79 GQTAGLTQPKKDEPKKLPRSGGPEPKPGHPSQTRQARTVTPKGQLPGGKAPPKAGSVSPFLLKKARETGPPEPKE 158
XP_017913249.1	79 GQTGGLTQPKKDEPKKLPRSGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPSKAGSVPSFLLKKAREPGSPREPKE 158
XP_018872428.1	81 GQTGGLTQPKKDEPKKLPRPGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVSSFLLLKKAREPGPPREPKE 160
XP_003779391.1	81 GQTGGLTQPKKDEPKKLSRPGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVSSFLLLKKAREPGPPREPKE 160
XP_031998077.1	81 GQTGGLTQPKKDEPKK--PRPGGPEPKPGHPPQTRQARTVTPKGQLPGGKAPPKAGSVSSFLLLKKAREPGPPREPKE 159
NP_000548.2	161 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 240
NP_032135.2	155 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 234
XP_003749648.1	155 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 234
NP_001179202.1	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
NP_001231226.1	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
XP_542974.1	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
NP_001296325.1	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
XP_004014573.2	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
XP_530287.4	161 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 240
XP_001099806.2	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
XP_003983628.1	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
XP_017913249.1	159 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 238
XP_018872428.1	161 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 240
XP_003779391.1	161 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 240
XP_031998077.1	160 PFRPPPI TPHEYMLSlyRTLSADRRKGGNSVKLEAGLANTITSFIDKGQDDRGPVVRKQRYVFDISALEKDGLLGAELR 239
NP_000548.2	241 ILRKKPSDTAKPAAPGGGAAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 320
NP_032135.2	235 ILRKKPLDVAKPAVPSGGRVAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 314
XP_003749648.1	235 ILRKKPLDVAKPAVPSGGRVAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 314
NP_001179202.1	239 ILRKKPLDAKPAVPGSRAAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 318
NP_001231226.1	239 ILRKKPSDTAKPAVPGIGRAAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 318
XP_542974.1	239 ILRKKPSDTAKPAVPSIGRAAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 318
NP_001296325.1	239 ILRKKSSDTAKPGAPSSRAAQLKLSLSSCPGSRQPAALLDVRVSPGLDGSWEVFDIWKLFERNFKNSAQLCLELEAWERGR 318
XP_004014573.2	239 ILRKKPLDVAKPAVPGSRAAQLKLSLSSCPGSRQPAALLDVRVSPGLDSSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR 318

1358	XP 530287.4	241	ILRKKPSDTAKPAAPGGGAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	320
1359	XP 001099806.2	239	ILRKKPSDTAKSAAPVGGRAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	318
1360	XP 003983628.1	239	ILRKKPSDAAKPVAPGIRRAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	318
1361	XP 017913249.1	239	ILRKKPLDAAKPVAPSSGRAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	318
1362	XP 018872428.1	241	ILRKKPSDTAKPAAPGGGAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	320
1363	XP 003779391.1	241	ILRKKPSDTAKPVAPGGGAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	320
1364	XP 031998077.1	240	ILRKKPSDTAKPAAPGGGAAQLKLSSCPSGRQPAALLDVRVSVPLDGGSGWEVFDIWKLFERNFKNSAQLCLELEAWERGR	319
1365				
1366	NP 000548.2	321	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNLKARC	400
1367	NP 032135.2	315	AVDLRGLGFERTARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLANRQGKRPSKNLKARC	394
1368	XP 003749648.1	315	AVDLRGLGFERAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLANRQGKRPSKNLKARC	394
1369	NP 001179202.1	319	AMDRLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNPKARC	398
1370	NP 001231226.1	319	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNPKARC	398
1371	XP 542974.1	319	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNPKARC	398
1372	NP 001296325.1	319	AVDLRGLGFDRTARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPTKNPKARC	398
1373	XP 004014573.2	319	AMDRLRSLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNPKARC	398
1374	XP 530287.4	321	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNLKARC	400
1375	XP 001099806.2	319	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNLKARC	398
1376	XP 003983628.1	319	AMDRLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNPKARC	398
1377	XP 003749648.1	319	AMDRLRSLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNPKARC	398
1378	XP 018872428.1	321	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNLKARC	400
1379	XP 003779391.1	321	TVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNLKARC	400
1380	XP 031998077.1	320	AVDLRGLGFDRAARQVHEKALFLVFGRTKKRDLFFNEIKARSGDDDKTVYEYLFSSQRRKRRAPLATRQGKRPSKNLKARC	399
1381				
1382	NP 000548.2	401	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	480
1383	NP 032135.2	395	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	474
1384	XP 003749648.1	395	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	474
1385	NP 001179202.1	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1386	NP 001231226.1	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1387	XP 542974.1	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1388	NP 001296325.1	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1389	XP 004014573.2	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1390	XP 530287.4	401	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	480
1391	XP 001099806.2	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1392	XP 003983628.1	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1393	XP 017913249.1	399	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	478
1394	XP 018872428.1	401	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	480
1395	XP 003779391.1	401	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	480
1396	XP 031998077.1	400	SRKALHVNKDMGDDMI IAPLE EAFHCEGLCEFFLRSHLEPTNHAVIQTLMNSMDPESTPPTCCVPTRLSPISLFID	479
1397				
1398	NP 000548.2	481	SANNVVKQEDV VVESCGR	501
1399	NP 032135.2	475	SANNVVKQEDV VVESCGR	495
1400	XP 003749648.1	475	SANNVVKQEDV VVESCGR	495
1401	NP 001179202.1	479	SANNVVKQEDV VVESCGR	499
1402	NP 001231226.1	479	SANNVVKQEDV VVESCGR	499
1403	XP 542974.1	479	SANNVVKQEDV VVESCGR	499
1404	NP 001296325.1	479	SANNVVKQEDV VVESCGR	499
1405	XP 004014573.2	479	SANNVVKQEDV VVESCGR	499
1406	XP 530287.4	481	SANNVVKQEDV VVESCGR	501
1407	XP 001099806.2	479	SANNVVKQEDV VVESCGR	499
1408	XP 003983628.1	479	SANNVVKQEDV VVESCGR	499
1409	XP 017913249.1	479	SANNVVKQEDV VVESCGR	499
1410	XP 018872428.1	481	SANNVVKQEDV VVESCGR	501
1411	XP 003779391.1	481	SANNVVKQEDV VVESCGR	501
1412	XP 031998077.1	480	SANNVVKQEDV VVESCGR	500
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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]		
NP_001001557.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRDS DAGREG---QEPQRPQDEPR	76
NP_038554.1	1	MDTPRVLLWAI FLISFLWDLPGFQQASISSSSSStELDSTKDVGNRKEGKMQRTPQESAEGRTPEHGLRQKDLRR	77
NP_001013056.1	1	MDTPRVLLWAI FLISFLWDLPGFQQASISSSSS--tELDSTKDVENRKGKMQRT PQESAEGRTPEHGLRQKDLRR	75
NP_001001140.1	1	MDTSRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSAKGMRSRKEGRMPRAPRENATAREPldrQEPFPPRPQDEEPQ	79
XP_020944737.1	1	MDTPKVVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSAKGMRSRKEGKMQRAPRESATAQAPperQEPQRPQDEEPR	79
XP_038297057.1	1	MDAPRVLLSAVFLVGFWDLPFGFQQASIPSSPSA-QPAAAKGTRSRRDG---RAPRDRAP-REP1---EPEP-----PE	67
XP_023504500.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSAKGIRSRREGKMPRAPQESATAQAPlerQEHQPRQDEEPR	78
XP_027829270.1	1	MDTSRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSAKGMRSRKEGKMQRAPRENATAREPldrQEPFPPRPQDEEPQ	79
XP_016815191.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRDS DAGREG---QEPQRPQDEPR	76
XP_001090825.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSSA-ELGSTKGMRSRKEGKMQRAPRDS DAGREG---QEPQRPQDEPR	76
XP_023104260.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSAKGMRSRKEGKIIPRAPRDSATAGEPqqrHEPQRPQDEPR	79
XP_017913739.1	1	MDTSRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSAKGMRSRKEGKMQRAPRENATAREPldrQEPFPPRPQDEEPQ	78
XP_004047376.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSTKGMRSRKEGKMQRAPRDS DAGREG---QEPQRPQDEPR	76
XP_002819344.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSTKGMRSRKEGKMQRAPRDS DAGREG---QEPQRPQDEPR	76
XP_032614364.1	1	MDTPRVLLSAVFLISFLWDLPGFQQASISSSSSA-ELGSTKGMRSRKEGKMQRAPRDS DAAREG---QQPQPDPDKPR	76
NP_001001557.1	77	A----QQPRAQEPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	152
NP_038554.1	78	R--PPGQHQQEPGRGLRVVPHEYMYSIYKTYIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	155
NP_001013056.1	76	R--LPGQSLGQEPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	153
NP_001001140.1	80	R-rPPQPEAREPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	158
XP_020944737.1	80	R-rPPQPEAREPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	158
XP_038297057.1	68	P-----QPGGAAAVPHDYMYSYRTHSIAEKLGINASLFQSSGAANTITSFVDRGLDLSHTPLRRQKYLFDV	137
XP_023504500.1	79	R-rPPQHQQAQESPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	158
XP_027829270.1	80	R-rPPERREAREPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	158
XP_016815191.1	77	A----QQPRAQEPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANMITSFVDRGLDLSHTPLRRQKYLFDV	152
XP_001090825.1	77	A----QQPRAQEPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	152
XP_023104260.1	80	R-rPPQPEAREPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	158
XP_017913739.1	79	R-rPPERREAREPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	157
XP_004047376.1	77	A----QQPRAQEPGRGLRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	152
XP_002819344.1	77	A----QQPRAQEPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	152
XP_032614364.1	77	A----QQPRAQEPGRGRVVPHEYMYSIYRTYSIAEKLGINASFFQSSKSANTITSFVDRGLDLSHTPLRRQKYLFDV	152
NP_001001557.1	153	SMSDKKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE	232
NP_038554.1	156	STLSDKEELVGAELRLYRQAPPTPWGLPARPLHLQLFPCLSPLLLDARTLDPQGPTQAGWEVFDVWQGLRPQWPKQLCLE	235
NP_001013056.1	154	STLSDKEELVGAELRLYRQAPPTPWGPQTRPLHLQLFPCLSPLLLDARTLDPQGPTQAGWEVFDVWQGLRPQWPKQLCLE	233
NP_001001140.1	159	STLSDKEELVGAELRLFRQAPAAPWGPAGPLRLQLFACQSPLLLEARS LDPQGAPRPGWEVFDVWRGLRPQWPKQLCLE	238
XP_020944737.1	159	STLSDKEELVGAELRLFRQAPAAPWGPAGPLRLQLFACQSPLLLDARTLDPQGAPRAGWEVFDVWQGLRHQPWKQLCLE	238
XP_038297057.1	138	SALPEREELVGAELRLFRAPPPRGRPP-RPLRLQLSPCLSPRLGARTLSPQGP PRAGWEVFDVVRGLRPPRGRPLCLE	216
XP_023504500.1	159	STLSDKEELVGAELRLFRQAPAVPWGPAGPLHVQLFPCLSPQLDARTLDPQGAPRAGWEVFDVWQGLRHQPWKQLCLE	238
XP_027829270.1	159	STLSDKEELVGAELRLFRQAPAVPWGPAGPLHLQLFACQSPLLLEARS LDPQGAPRPGWEVFDVWRGLRPQWPKQLCLE	238
XP_016815191.1	153	SMSDKKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE	232
XP_001090825.1	153	SMSDKKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE	232
XP_023104260.1	159	STLSDKEELVGAELRLFRQAPATPWGPAGPLHVQLFPCLSPQLDARTLDPQGAPRAGWEVFDVWQGLRQPWKQLCLE	238
XP_017913739.1	158	STLSDKEELVGAELRLFRQAPAAPWGPAGPLHLQLFACQSPLLLEARS LDPQGAPRPGWEVFDVWRGLRPQWPKQLCLE	237
XP_004047376.1	153	SMSDKKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE	232
XP_002819344.1	153	SMSDKKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSSLLLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE	232
XP_032614364.1	153	SMSDKKEELVGAELRLFRQAPSAPWGPPAGPLHVQLFPCLSPQLDARTLDPQGAPPAGWEVFDVWQGLRHQPWKQLCLE	232
NP_001001557.1	233	LRAAW-GELDAGE AEARARGPQQ-PPPLDLRSLGFGRVRVPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGP	305
NP_038554.1	236	LRAAW-GELDAGD TGARARGPQQ-PPPLDLRSLGFGRVRVPQERALLVVFTRSQRKNLFTMHEQLGSA-EAA--	306
NP_001013056.1	234	LRAAV-GELDARD SGARPRGPQQ-SPPLDLRSLGFGRVRVPQERALLVVFTRSQRKNLFTMHEQLGSA-EAA--	304
NP_001001140.1	239	LRAAWgGEPGAAE DEARAPGPQQ-PPPLDLRSLGFGRVRVPQERALLVVFTRSQRKTLFAEMREQLGSAteVVG	313
XP_020944737.1	239	LRAAW-GEPGAGE AEARVGPQQ-PPPLDLRSLGFGRVRVPQERALLVVFTRSQRKNLFAEMREQLGSA-EVAGP	311
XP_038297057.1	217	LRAAW-AGAGAGA [11] AGAGARGPQQ---GPDRLRSLGFGRGARRQERALLVVFTRSRRRSLAEARGPQQG-----	293
XP_023504500.1	239	LRAAW-GELGAGE DEARAPGPQQ-PPPLDLRSLGFGRVRVPQERALLVVFTRSQRKNLFAEMREQLGSA-EVAGP	311
XP_027829270.1	239	LRAAWgGEPGGEE AEAPARGPQQ-PPPLDLRSLGFGRVRVPQERALLVVFTRSQRKTLFAEMREQLGSAteVVG	313

1490 [XP_016815191.1](#) 233 LRAAW-GELDAGE AEARARGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGP 305
1491 [XP_001090825.1](#) 233 LRAAW-GEPDARE AETHARGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGP 305
1492 [XP_023104260.1](#) 239 LRAAW-GEPEGAGE AEARAPGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EVAGP 312
1493 [XP_017913739.1](#) 238 LRAAW-GEPEGAGE AEARARGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EVVG 312
1494 [XP_004047376.1](#) 233 LRAAW-GELDAGE AEARARGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGP 305
1495 [XP_002819344.1](#) 233 LRAAW-GEPDAGE AETRARGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EAADL 305
1496 [XP_032614364.1](#) 233 LRAAW-GEPEAGE AEARARGPQQ-PPPPDLRSLGFGRVRPQERALLVVFTRSQRKNLFAEMREQLGSA-EAAGP 305
1497
1498 [NP_001001557.1](#) 306 GAGAEBSW PPPSGAPDARWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 382
1499 [NP_038554.1](#) 307 --GAEBSW PAPSGPDAGSWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSRKPLHVNFKELGDDTIAPLEEAYH 381
1500 [NP_001013056.1](#) 305 --GAEBSW PAPSGPDAGSWLPSPGRRRRRTALSSRHGKRHGKKSRLRCSRKPLHVNFKELGDDTIAPLEEAYH 379
1501 [NP_001001140.1](#) 314 GAGAEBSG [7] PPPSGTPDAGLWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 397
1502 [XP_020944737.1](#) 312 GA--EGSW PPPSGTPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 386
1503 [XP_038297057.1](#) 294 ----- [1] APAPGTPLAAPWPPGRRRRR-TALASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAFH 362
1504 [XP_023504500.1](#) 312 SGGAEBSW PPPSGPDVGPWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 388
1505 [XP_027829270.1](#) 314 GAGAEBSG [1] PPPSGIPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 391
1506 [XP_016815191.1](#) 306 GAGAEBSW PPPSGAPDARWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 382
1507 [XP_001090825.1](#) 306 GVGAEBSW PPPSGAPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 382
1508 [XP_023104260.1](#) 313 GAGADBSW PPPSGAPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 389
1509 [XP_017913739.1](#) 313 GAGAEBSG [1] PPPSGIPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 390
1510 [XP_004047376.1](#) 306 GAGAEBSW PPPSGAPDARWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 382
1511 [XP_002819344.1](#) 306 GTGAEBSW PPLSGAPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 382
1512 [XP_032614364.1](#) 306 GAGAEBSW PPPSGAPDAGWLPSPGRRRRRTAFASRHGKRHGKKSRLRCSKKPLHVNFKELGDDTIAPLEEAYH 382
1513
1514 [NP_001001557.1](#) 383 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 455
1515 [NP_038554.1](#) 382 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 454
1516 [NP_001013056.1](#) 380 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 452
1517 [NP_001001140.1](#) 398 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 470
1518 [XP_020944737.1](#) 387 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 459
1519 [XP_038297057.1](#) 363 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 435
1520 [XP_023504500.1](#) 389 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 461
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1522 [XP_016815191.1](#) 383 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 455
1523 [XP_001090825.1](#) 383 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 455
1524 [XP_023104260.1](#) 390 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 462
1525 [XP_017913739.1](#) 391 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 463
1526 [XP_004047376.1](#) 383 CEGVCDPFLRSHLEPTNHAIQTLNMSMDPGSTPPSCCVPTKLTPISELYIDAGNNVVYKQEDVVVESCGR 455
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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]

NP_878248.2	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--GGggRTLAQAAGAAAVPAAAVPRARAAR	74
NP_001299805.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAWSPGG--GGGG-----RTLARAPGPSALQAAAVFGPRAVR	70
XP_006239940.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAWSPGG--GGGG-----RTLAPAPGPSALQAAAVFGPRAVR	70
NP_001193030.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAESPGG--GGGG--SG--TTLAAAEGETSAALAAASFGPRGAR	72
XP_003354958.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAGSPGG--GGGG--R---RTLAAAAGASAAAPAAAVPRAARAAR	71
XP_038309370.1	1	MDLSAAAAALCLWLLSACRPRDGLgLEAAAVLRAAGAGX-GPGGRggGGGG--GG--RALAPAGVSAAPAAAVPGARAAR	75
XP_023475218.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAGSPGG--GGGG--GG--RTLAAAAGASTGPAAPAAVPGARAAR	72
XP_027824132.2	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAESPGG--GGGGggGG--TTLAAAAGASAAALAAASFPERGAR	74
XP_003308955.2	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--G---RTLAAAAGAAAVPAAAVPRARAAR	71
XP_001096970.2	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--GGggRTLAQAAGAAAVPAAAVSRARAPR	74
XP_023107842.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGGdgGSGS--GG--RTLAPAGVSAAPAAAVPGVRAAR	74
XP_017910266.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPAESPGG--GGGG--GG--TTLAAAAGASAAAPAAASFGPRGAR	72
XP_004028950.1	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--G---RTLAAAAGAAAVPAAAVPRARAAR	71
XP_002812295.2	1	MDLSAAAAALCLWLLSACRPRDGL--EAAAVLRAAGAGPVRSPGG--GGGG--G---RTLAAAAGASAVPAAAVPRARAAR	71
XP_032028233.1	1	MDLNAALCLWLLSACRPRDGL--EAAAVLRAAGVGPVRSPGG--GGGG--E---RTLAAAAGAAAVPAAAVPRARAAR	71
NP_878248.2	75	RAAGSG FRNGSVVPHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFDFVSS	147
NP_001299805.1	71	RAAGSG FRNGSVVPHFMMSLYRSLAGRAP---VAAASG---HGRVDTITGFTDQATQDETAaEPGQSFDFVSS	140
XP_006239940.1	71	RAAGSG FRNGSVVPHFMMSLYRSLAGRAP---AAATSG---HGRVDTITGFTDQATQDESAA-EPGQSFDFVSS	139
NP_001193030.1	73	RATGSG FRNGSVVPHQFMMSLYRSLTGRTPAGPVAVSTSGsgRGRADTITGTFADQAIQDESAA-QTGLNFLDFVSS	148
XP_003354958.1	72	RAAGSG FRNGSVVPHQFMMSLYRSLAGRAPTGAAVSTSGsgRGRADTITGTFADQATQDESAA-ETGQSFDFVSS	147
XP_038309370.1	76	RAAGSG[8]FGNGSVVPHQFMMSLYRNLAGRAPAGGAAASTSGsgRGRADTITGTFADQANQDDPPA-ETGQSFDFVSS	159
XP_023475218.1	73	RAASG FRNGSVVPHQFMMSLYRSLAGRAPAGAAAASTSGsgRGRADTITGTFADQATQDESAA-ETGQSFDFVSS	148
XP_027824132.2	75	RATGSG FRNGSVVPHQFMMSLYRSLAGRTPAGPVAASTSGsgRGRADTITGTFADQATQDESAA-ETGLNFLDFVSS	150
XP_003308955.2	72	RAAGSG FRNGSVVPHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFDFVSS	144
XP_001096970.2	75	RAAGSG FRNGSVVPHFMMSLYRSLAGRAPARAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFDFVSS	147
XP_023107842.1	75	RAAGSG FRNGSVVPHQFMMSLYRNLAGRAPAGAAAASTSGsgRGRADTITGTFADQANQDESAA-ETGQSFDFVSS	150
XP_017910266.1	73	RATGSG FRNGSVVPHQFMMSLYRSLAGRTPAGPVAASTSGsgRGRADTITGTFADQATQDESAA-ETGLNFLDFVSS	148
XP_004028950.1	72	RAVSG FRNGSVVPHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFDFVSS	144
XP_002812295.2	72	RAAGSG FRNGSVVPHFMMSLYRSLAGRAPAGAAVTSASG---HGRADTITGFTDQATQDESAA-ETGQSFDFVSS	144
XP_032028233.1	72	RAAGSG FRNGSVVPHFMMSLYRSLAGRAPAGAAAVSASG---HGRADTITGFTDQATQDESAA-ETGQSFDFVSS	144
NP_878248.2	148	LNDADDEVVGAELRVLRRGSPESGPGSWSPPPLLLL-STCFGAARAPRLLYSRAAEPLVGQRWEAFVDVADAMRRHRREPRP	226
NP_001299805.1	141	LSEADDEVVNAELRVLRRRSPEDRDSATLPLPLLLL-STCFDEAGTAHLLHSRAAEPLGGARWEAFVDVAVQSHRRWPRA	219
XP_006239940.1	140	LSDSDEVVNAELRVLRRRSPEDRDSATLPLPLLLL-STCFDEAGTAHLLHSRAAEPLDSARWEAFVDVAVQSHRRWPRT	218
NP_001193030.1	149	LPDADEVLGAELRVLRRREGSARGPGSASP--LLLSTCFSAASAPRLLHSRAAEFLDARWEVFDVADALRRHRREPRP	226
XP_003354958.1	148	LPDADEVVGAELRVLRRRESPEPGGRATSP--LLLSTCFGAARAPRLLHSRAAEHLEGARWEVFDVVDVAVRRHRREPRP	225
XP_038309370.1	160	LNDADDEVVAAELRVLRRSPGPGGAAAPPLLLL-STCFGAARAPRLLHSRAAEPLARARWEVFDVADVAVRRHRREPRP	238
XP_023475218.1	149	LSADDEVVGAELRVLRRREFPEPSSGSAIQPPLLLLSTCFGAASAPRLLHSRAAEPLDARWEVFDVADVAVRRHRREPRP	228
XP_027824132.2	145	LPDADEVLGAELRVLRRREGSARGPGSASLA--LLLSTCFNAAARAPRLLHSRAAEPLDARWEVFDVADALRRHRREPRP	228
XP_003308955.2	145	LNDADDEVVGAELRVLRRGSPESGPGSWSPPPLLQL-STCFGAARAPRLLYSRAAEPLVGQRWEAFVDVADAMRRHRREPRP	223
XP_001096970.2	148	LNDADDEVVGAELRVLRRGSPGPGSWSPPPLLLL-STCFGAARAPRLLYSRAAEPLVGQRWEAFVDVADAMRRHRREPRP	226
XP_023107842.1	151	LPDADEVVGAELRVLRRRESPELPGSATPLPLLLL-STCFGAARAPRLLHSRAAEPLAGARWEVFDVADVAVRRHRQEPHA	229
XP_017910266.1	149	LPDADEVLGAELRVLRRREGSARGPGSASLP--LLLSTCFNAAARAPRLLHSRAAEPLDARWEVFDVADALRRHRREPRP	226
XP_004028950.1	145	LNDADDEVVGAELRVLRRGSPESGPGSWSPPPLLLL-STCFGAARAPRLLYSRAAEPLVGQRWEAFVDVADAMRRHRREPRP	223
XP_002812295.2	145	LNDADDEVVGAELRVLRRGSPGPGSWSPPPLLLL-STCFGAARAPRLLYSRAAEPLVGQRWEAFVDVADAMRRHRREPRH	223
XP_032028233.1	145	LNDADDEVVGAELRVLRRGSPGPGSWSPPPLLLL-STCFGAARAPRLLYSRAAEPLVGQRWEAFVDVADAMRRHRREPRP	223
NP_878248.2	227	PRAFCLLLRAVAGVPVPSPLALRRLGFGWPGGGG SAAEERAVLVSSRTQRKESLFREIRAQARALGAALASEPLPDP	303

1608 NP_001299805.1 220 SRKFCLVLRVAVTAESESPALALRRLGFGWPGGGG [3] TAAEERALLVSSRTQRKESLFREIRAQARALRA--AAEPPDDP 297

1609 XP_006239940.1 219 SRKFCLVLRVAVTAESESPALALRRLGFGWPGGGG [3] TAAEERALLVSSRTHRKESLFREIRAQARALRA--AAELPDDP 296

1610 NP_001193030.1 227 SRAFCLSLRGVVGARSVPALALRPLGFGLRGGGG AAEEERALLVSSRTQRKESLFREIRSQARALGAALAVESRPDS 303

1611 XP_003354958.1 226 TSAFCLLLRGVVGPRDPLALRRLGFGSSGGDG AAEEERALLVSSRTQRKESLFREIRAQARAFGAALAAEPPDDP 302

1612 XP_038309370.1 239 ARAFCLLRSVAGPSREPLALRGLGFGSRGARG AGAEERALLVSSRAHRKGSLEFRE---ARALGAALAAEPPDDP 311

1613 XP_023475218.1 229 TRVFCLLLRAAAGPARGPLALQLLGFSGRGGGG AAEEERALLVSSRTQRKESLFREIRAQARALGAPLAAEPPDDP 305

1614 XP_027824132.2 229 SRAFCLSLRGVVGARSVPALALRRLGFGLRGGGG [5] AAEEERALLVSSRTQRKESLFREIRSQARALGAALAAESRPDD 310

1615 XP_003308955.2 224 PRAFCLLLRAVAGVPVSPALALRRLGFGWPGGGG SAAEERALLVSSRTQRKESLFREIRAQARALGAALASEPLDDP 300

1616 XP_001096970.2 227 PRAFCLLLRAVTGPVRSPLALRRLGFRWPGGGG SAPEERALLVSSRTQRKESLFREMRQAARALGAALAAQPPDDP 303

1617 XP_023107842.1 230 TRAFCLLLRSVAGPSQGPLALRRLGFGSRGRDG AAEEERALLVSSRTQRKGSLEFREIRAQARALGAALAAEPPDDP 306

1618 XP_003308955.2 227 SRAFCLSLRGVVGARSVPALALRRLGFGLRGGGG [1] AAEEERALLVSSRTQRKESLFREIRSQARALGAALAAESRPDD 304

1619 XP_004028950.1 224 PRAFCLLLRAVAGVPVSPALALRRLGFGWPGGGG SAAEERSLLVSSRTQRKESLFREIRAQARALGAALAAEPLDDP 300

1620 XP_002812295.2 224 PRAFCLLLRAVAGVPVRSPLALRRLGFGWPGGGG SAAEERALLVSSRTQRKESLFREIRAQARALGAALASEPPDDP 300

1621 XP_032028233.1 224 PRAFCLLLRAVAGVPVRSPLALRRLGFGWPGGGG SAAEERALLVSSRTQRKESLFREIRAQARALGAALASEQPPDDP 300

1622

1623 NP_878248.2 304 GTGTASPRAVIGRRRRRTALAGTRTAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 376

1624 NP_001299805.1 298 GPGAGSRKANLGGRRRRRTALAGTRGAQGS [4] GGG [13] AGRGHGRRGRSRCSRKSLHVD[KELG]DDI[IIAPLD]EAY 387

1625 XP_006239940.1 297 GLGAGSRKATPGRRRRRTALAGTRGAQGS GGG [13] AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 382

1626 NP_001193030.1 304 RPGVGSPTAVIGRRRRRTALAGARAAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 376

1627 XP_003354958.1 303 GPAIGSSTAVIGRRRRRTALAGARAAQDS GAG GGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 375

1628 XP_038309370.1 312 GPGPRSPAAVTGRRRRRTALAGARPAQGG GGG AGRGHGRRGRSRCSRRPLHVD[KELG]DDI[IIAPLD]EAY 384

1629 XP_023475218.1 306 GPGTGSPTAVIGRRRRRTALAGTRAAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 378

1630 XP_027824132.2 311 GPGVGSPTAVIGRRRRRTALAGARAAQGS GGG AGRGQRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 383

1631 XP_003308955.2 301 GTRTASPRAVIGRRRRRTALAGTRTAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 373

1632 XP_001096970.2 304 GTGTGSPRAVTAGRRRRRTALAGTRTAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 376

1633 XP_023107842.1 307 GPGTGSPTAVISGRRRRRTALTGARATQGS [2] GGG AGRGHGRRGRTRCSRRPLHVD[KELG]DDI[IIAPLD]EAY 381

1634 XP_017910266.1 305 GPGVGSPTAVIGRRRRRTALAGARAAQGS GGG AGRGHGRRVRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 377

1635 XP_004028950.1 301 GTGTGSPRAVIGRRRRRTALAGTRTAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 373

1636 XP_002812295.2 301 GTGTGSPRAVIGRRRRRTALAGTRTAQGS SGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 373

1637 XP_032028233.1 301 GTGTGSPRAVIGRRRRRTALAGTRTAQGS GGG AGRGHGRRGRSRCSRKPLHVD[KELG]DDI[IIAPLD]EAY 373

1638

1639 NP_878248.2 377 HCEGLCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 450

1640 NP_001299805.1 388 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 461

1641 XP_006239940.1 383 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 456

1642 NP_001193030.1 377 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 450

1643 XP_003354958.1 376 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 449

1644 XP_038309370.1 385 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 458

1645 XP_023475218.1 379 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 452

1646 XP_027824132.2 384 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 457

1647 XP_003308955.2 374 HCEGLCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 447

1648 XP_001096970.2 377 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 450

1649 XP_023107842.1 382 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 455

1650 XP_017910266.1 378 HCEGVCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 451

1651 XP_004028950.1 374 HCEGLCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 447

1652 XP_002812295.2 374 HCEGLCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 447

1653 XP_032028233.1 374 HCEGLCDFPLRSHLEPTNHAI IQTLNLSMAPDAAPASCCVPARLSPIS [LYIDAANNVYKQ]ED[VVEACGCR] 447

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BMP10

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]

NP_055297.1	1	MGSLVLTLCALFCLAAYLVSGSPIMNLEQSPLEEDMSLFGDVFSEQDGVDFNTLLQSMKDEFLKTNLNSDIPTQDSAKVD	80
NP_033886.2	1	MGSLVLP LSAVFCLVAHSASGSPIMGLEQSPLEEDMPFFDDIFTEQDGI DFNTLLQSMKNEFLKTNLNSDIPVQDTGRVD	80
NP_001026994.1	1	MGSLVLP LSAVFCLVARLASGSPIMGLEQSPLEEDMPFFDDIFTEQDGI DFNTLLQSMKDEFLKTNLNSDIPVQDTGRVD	80
NP_001179047.1	1	MGSVVLQLCTLSCLLVHVSNGPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTNLNSDIPM QDSAKVD	80
XP_003125118.1	1	MGFLALQLCALSCLVAPVWSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNSLLQSMKNEFLKTNLNSDIPM QDSAKVD	80
XP_538528.2	1	MGSLALQLCAVFGFLVAHSVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQTMKNEFLKTNLNSDIPVQDSAKVD	80
XP_001491666.1	1	MGSLALELCAVFLVAHVSNGPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTNLNSDIPM QDSAKVD	80
XP_004005868.2	1	MGSVVLQLCTLSCLLLHAVSGN PIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTNLNSDIPM QDSAKVD	80
XP_525772.1	1	MGSLVLTLCALFCLAAYLVSGSPIMNLEQSPLEEDMSLFGDVFSEQDGVDFNTLLQSMKDEFLKTNLNSDIPTQDSAKVD	80
XP_001096299.1	1	MGSLGLTLCALFCLAHSVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKDEFLKTNLNSDIPVQDSAKVD	80
XP_023107498.1	1	MGSLALQLCALVCLVHVSNGPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTNLNSDIPVQDSAKVD	80
XP_005686884.1	1	MGSVVLQLCTLSCLLLHAVSGN PIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKNEFLKTNLNSDIPM QDSAKVD	80
XP_004029400.1	1	MGSLVLTLCALFCLAAYLVSGSPIMNLEQSPLEEDMSLFGDVFSEQDGVDFNTLLQSMKDEFLKTNLNSDIPTQDSAKVD	80
XP_024098418.1	1	MGSLVLTLCALFCLAAYLVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKDEFLKTNLNSDIPVQDSAKVD	80
XP_032033811.1	1	MGSLVLTLCAFCLAAYLVSGSPIMSLEQSPLEEDMPLFDDVFSEQDGVDFNTLLQSMKDEFLKTNLNSDIPTQESAKVD	80
NP_055297.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
NP_033886.2	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVTFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
NP_001026994.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
NP_001179047.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEIVMAELRLYTLVQRDRMIYDG	160
XP_003125118.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVTMAELRLYTLVQRDRMIYDG	160
XP_538528.2	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_001491666.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_004005868.2	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEIVMAELRLYTLVQRDRMIYDG	160
XP_525772.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_001096299.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_023107498.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_005686884.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPASFNGLRKYPLLFNVSIPHHEEIVMAELRLYTLVQRDRMIYDG	160
XP_004029400.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_024098418.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYHLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
XP_032033811.1	81	PPEYMLELYNKFATDRTSMPSANIIRSFKNEDLFSQPVSFNGLRKYPLLFNVSIPHHEEVVMAELRLYTLVQRDRMIYDG	160
NP_055297.1	161	VDRKTIIFEVLESKGDNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE	240
NP_033886.2	161	VDRKTIIFEVLESADGSEERSMLVLVST EITYGTNSEWETFDVTDATRRWQKSGPSTHQLEIHIESRQNAEDTGRGQLE	240
NP_001026994.1	161	VDRKTIIFEVLESADGSEERSMLVLVST EITYGTNSEWETFDVTDATRRWQKSGPSTHQLEIHIESRQNAEDTGRGQLE	240
NP_001179047.1	161	VDRKTIIFEVLESKEDHEGERNMLVLVSGEITYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHEDTGRGQLE	240
XP_003125118.1	161	VDRKTIIFEVLESQGDHEGERSLLVLVSGEITYGTNSEWETFDVTDAIRRWQNSGSGSTHQLEVHIESRQGM-EDAGRQLE	239
XP_538528.2	161	VDRKTIIFEVLESRGDTEGERSMLVLVSGEITYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESRHGDTEDAGRQLE	240
XP_001491666.1	161	VDRKTIIFEVLESKGDNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESRQDEAEDAGRQLE	240
XP_004005868.2	161	VDRKTIIFEVLESKEDHEGERSMLVLVSGEITYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHEDTGRGQLE	240
XP_525772.1	161	VDRKTIIFEVLESKGDNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE	240
XP_001096299.1	161	VDRKTIIFEVLESKGDNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHDEAEDASSGRLE	240
XP_023107498.1	161	VDRKTIIFEVLESRGDTEGERSMLVLVSGEITYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESRQDEAEDAGRQLE	240
XP_005686884.1	161	VDRKTIIFEVLESKEDHEGERSMLVLVSGEITYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHEDTGRGQLE	240
XP_004029400.1	161	VDRKTIIFEVLESKGDNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRHWQKSGSSTHQLEVHIESKHDEAEDASSGRLE	240
XP_024098418.1	161	VDRKTIIFEVLESKGDNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE	240
XP_032033811.1	161	VDRKTIIFEVLESKGGNEGERNMLVLVSGEITYGTNSEWETFDVTDAIRRWQKSGSSTHQLEVHIESKHDEAEDASSGRLE	240
NP_055297.1	241	IDTSAQNKHNP LLIIVFSDQSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGEALLQMRNIIYDSTARIRRNKAG	320
NP_033886.2	241	IDMSAQNKHDP LLLVVFSDQSSDNKQKEELNELITHEQ--DLD-LDSDAFFSGPDEEALLQMRNMIIDDSARIRRNKAG	317

1733	NP_001026994.1	241	IDMSAQNKHDP LLVVFSD DQSGDKEQKEELNELISHEQ--DLD-LGTDGFFG GPDEEALLQMRSNMIDDSTARIRRNAKG	317
1734	NP_001179047.1	241	IDTSA RNKHD P LLVVFSD DQSSSEKERKEELDEMI AHEQFP EMDNL DLDGY SNGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1735	XP_003125118.1	240	IDTSA RNKHE P LLVVFSD DQSSSEKERKEELSEMI AHEQFP ELDNL GLGYS SGPGE EALLQMR SNI IYDSTARIRRNAKG	319
1736	XP_538528.2	241	IDTSA RNKHV P LLVVFSD DQSSSEKERKEELNEMIAHEQLLELDNLGLGYS SGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1737	XP_001491666.1	241	IDTSA ENKHD P LLVVFSD DQSSSEKERKEELTEMI AHEQLLELDNLGLGYS SGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1738	XP_004005868.2	241	IDTSA QNKHE P LLVVFSD DQSSSEKERKEELDEMI AHEQFP EMDNL DLDGY SNGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1739	XP_525772.1	241	IDTSA QNKHN P LLVVFSD DQSSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1740	XP_001096299.1	241	IDTSA QNKHN P LLVVFSD DQSSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1741	XP_023107498.1	241	IDTSA RNKHV P LLVVFSD DQSSSEKERTEELNEMIAHEQLLEFDNLGMDYS SGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1742	XP_005686884.1	241	IDTSA RNKHE P LLVVFSD DQSSSEKERKEELDEMI AHEQFP EMDNL DLDGY SNGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1743	XP_004029400.1	241	IDTSA QNKHN P LLVVFSD DQSSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1744	XP_024098418.1	241	IDTSA QNKHN P LLVVFSD DQSSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPGE EALLQMR SNI IYDSTARIRRNAKG	320
1745	XP_032033811.1	241	IDTSA QNKHN P LLVVFSD DQSSSDKERKEELNEMISHEQLPELDNLGLDSFSSGPAE EALLQMR SNI IYDSTARIRRNAKG	320
1746				
1747	NP_055297.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1748	NP_033886.2	318	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L D P I S L	397
1749	NP_001026994.1	318	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L D P I S L	397
1750	NP_001179047.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1751	XP_003125118.1	320	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	399
1752	XP_538528.2	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1753	XP_001491666.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1754	XP_004005868.2	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1755	XP_525772.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1756	XP_001096299.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1757	XP_023107498.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1758	XP_005686884.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1759	XP_004029400.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1760	XP_024098418.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1761	XP_032033811.1	321	NYCKRTPLYID KEIG DS II IAPPG EAY ECR GC NY PLA EHL TP TK HAI I Q A L V H L K N S Q R A S K A C C V P T K L E P I S L	400
1762				
1763	NP_055297.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1764	NP_033886.2	398	YLDKGVVTYKFK EG AV SEC GC R	421
1765	NP_001026994.1	398	YLDKGVVTYKFK EG AV SEC GC R	421
1766	NP_001179047.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1767	XP_003125118.1	400	YLDKGVVTYKFK EG AV SEC GC R	423
1768	XP_538528.2	401	YLDKGVVTYKFK EG AV SEC GC R	424
1769	XP_001491666.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1770	XP_004005868.2	401	YLDKGVVTYKFK EG AV SEC GC R	424
1771	XP_525772.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1772	XP_001096299.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1773	XP_023107498.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1774	XP_005686884.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1775	XP_004029400.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1776	XP_024098418.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1777	XP_032033811.1	401	YLDKGVVTYKFK EG AV SEC GC R	424
1778				
1779				
1780				
1781				
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1784

INHBA

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1789 NP_002183.1 inhibin beta A chain preproprotein [Homo sapiens]
 1790 NP_032406.1 inhibin beta A chain preproprotein [Mus musculus]
 1791 NP_058824.1 inhibin beta A chain preproprotein [Rattus norvegicus]
 1792 NP_776788.1 inhibin beta A chain precursor [Bos taurus]
 1793 NP_999193.1 inhibin beta A chain precursor [Sus scrofa]
 1794 XP_540364.2 inhibin beta A chain [Canis lupus familiaris]
 1795 NP_001075378.1 inhibin beta A chain precursor [Equus caballus]
 1796 NP_001009458.1 inhibin beta A chain precursor [Ovis aries]
 1797 XP_519063.2 inhibin beta A chain [Pan troglodytes]
 1798 XP_028701686.1 inhibin beta A chain [Macaca mulatta]
 1799 NP_001009856.1 inhibin beta A chain precursor [Felis catus]
 1800 NP_001272510.1 inhibin beta A chain precursor [Capra hircus]
 1801 XP_004045385.1 inhibin beta A chain [Gorilla gorilla gorilla]
 1802 XP_002818070.1 inhibin beta A chain [Pongo abelii]
 1803 XP_032614156.1 inhibin beta A chain [Hylobates moloch]

1804
1805
1806
1807

1808 [NP_002183.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALALPKDVPNSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1809 [NP_032406.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDGPN SQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1810 [NP_058824.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDGPN SQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1811 [NP_776788.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDV P NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1812 [NP_999193.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSGGHSAAFDPCSCALATLPKDV P NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1813 [XP_540364.2](#) 1 MPLLWLRGFLVASCWIIVRSSPTPGPEGGAAPACALALPRDAPNSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1814 [NP_001075378.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDV P NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1815 [NP_001009458.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDV P NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1816 [XP_519063.2](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALALPKDVP NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1817 [XP_028701686.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALALPKDVP NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1818 [NP_001009856.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEPGAAPDCPSCALATLPKDV P NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1819 [NP_001272510.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALATLPKDV P NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1820 [XP_004045385.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALALPKDVP NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1821 [XP_002818070.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALALPKDVP NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80
 1822 [XP_032614156.1](#) 1 MPLLWLRGFLFLASCWIIVRSSPTPGSEGHSAAPDCPSCALALPKDVP NSQPEMVEAVKKHILNMLHLKKRPDVTQVPVK 80

1823
 1824 [NP_002183.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1825 [NP_032406.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1826 [NP_058824.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1827 [NP_776788.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEIWLFLK 160
 1828 [NP_999193.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAEAGTARKTLRFEISKEGSDLSVVERAEIWLFLK 160
 1829 [XP_540364.2](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1830 [NP_001075378.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1831 [NP_001009458.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEIWLFLK 160
 1832 [XP_519063.2](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1833 [XP_028701686.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1834 [NP_001009856.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1835 [NP_001272510.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEIWLFLK 160
 1836 [XP_004045385.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1837 [XP_002818070.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160
 1838 [XP_032614156.1](#) 81 AALLNAIRKLVHGKVGENG YVEIEDDIGRAEMNELMEQTSEIITFAESGTARKTLHFEISKEGSDLSVVERAEVWFLK 160

1839
 1840 [NP_002183.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1841 [NP_032406.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1842 [NP_058824.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDMGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1843 [NP_776788.1](#) 161 VPKANRTRSKVTIRLFQQQKHLQGS LDAGEEAEVGLKGEKSEMLISEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDI 240
 1844 [NP_999193.1](#) 161 VPKANRTRTKVSIIRLFQQQRRPQGS ADAGEEAEVGFPEEKSEVLISEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDI 240
 1845 [XP_540364.2](#) 161 VPKANRTRTKVTIRLLQ--KHPQGS LDAGEEADMDFPEERNEVLISEKVV DARKSTWHVFPVSSSIQRLLDQGRSSLDV 238
 1846 [NP_001075378.1](#) 161 VPKANRTRSKVTIRLLQKQ--PQGS DTRGEEAEADLMEERSEQLISEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDI 240
 1847 [NP_001009458.1](#) 161 VPKANRTRSKVTIRLFQQQKHLQGS LDAGEEAEVGLKGEKSEMLISEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDI 240
 1848 [XP_519063.2](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1849 [XP_028701686.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1850 [NP_001009856.1](#) 161 VPKANRTRTKVTIRLLQKQ--PQGS DTRGEEAEADLMEERSEQLISEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 238
 1851 [NP_001272510.1](#) 161 VPKANRTRSKVTIRLFQQQKHLQGS LDAGEEAEVGLKGEKSEMLISEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDI 240
 1852 [XP_004045385.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1853 [XP_002818070.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240
 1854 [XP_032614156.1](#) 161 VPKANRTRTKVTIRLFQQQKHPQGS LDTGEEAEVGLKGERSELLSEKVV DARKSTWHVFPVSSSIQRLLDQGKSSLDV 240

1855
 1856 [NP_002183.1](#) 241 RIACEQCQESGASLVLLGKKKKKEE EGEKGGGEGGAGADEEKEQSHRPFMLQARQSEDPHRRRRRRGLECDGKVN I 320
 1857 [NP_032406.1](#) 241 RIACEQCQESGASLVLLGKKKKKEE VGDGKGGGSDGL--EEKEQSHRPFMLQARQSEDPHRRRRRRGLECDGKVN I 318

1858	NP_058824.1	241	RIACEQCQESGASLVLLGKKKKKEVDGDGKKKDGSDGGL--EEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	318
1859	NP_776788.1	241	RIACEQCQETGASLVLLGKKKKKEEEEGEGKKRD-GEAGGDEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	319
1860	NP_999193.1	241	RIACEQCCHETGASLVLLGKKKKKEEAEGRKRDRG--EGAGVDEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	318
1861	XP_540364.2	239	RIACEQCCHETGASLVLLGKKKKKEEEEGEGKKKDGAGAGGDEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	318
1862	NP_001075378.1	241	RIACEQCCHETGASLVLLGKKKKKEEEEGEGKKKDGAGAGVDEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	320
1863	NP_001009458.1	241	RIACEQCQETGASLVLLGKKKKKEEEEGEGKKRD-GEAGGDEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	319
1864	XP_519063.2	241	RIACEQCQESGASLVLLGKKKKKEEEEGEGKKKGGGEGAGADEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	320
1865	XP_028701686.1	241	RIACEQCQESGASLVLLGKKKKKEEEEGEGKKKGGGEGAGADEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	320
1866	NP_001009856.1	239	RIACEQCCHETGASLVLLGKKKKKEEEEGEGKKKDGAGAGADEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	318
1867	NP_001272510.1	241	RIACEQCQETGASLVLLGKKKKKEEEEGEGKKRD-GEAGGDEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	319
1868	XP_004045385.1	241	RIACEQCQESGASLVLLGKKKKKEEEEGEGKKKGGGEGAGADEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	320
1869	XP_002818070.1	241	RIACEQCQESGASLVLLGKKKKKEEEEGEGKKKGGGEGAGADEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	320
1870	XP_032614156.1	241	RIACEQCQESGASLVLLGKKKKKEEEEGEGKKKGGGEGAGADEEKEQSHRPFMLQARQSEDPHRRRRRGLCEDGKVNI	320
1871				
1872	NP_002183.1	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	400
1873	NP_032406.1	319	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	398
1874	NP_058824.1	319	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	398
1875	NP_776788.1	320	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	399
1876	NP_999193.1	319	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	398
1877	XP_540364.2	319	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	398
1878	NP_001075378.1	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINQYRLRGNPFANLKSCCVPTKLRPMS	400
1879	NP_001009458.1	320	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	399
1880	XP_519063.2	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	400
1881	XP_028701686.1	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	400
1882	NP_001009856.1	319	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	398
1883	NP_001272510.1	320	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	399
1884	XP_004045385.1	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	400
1885	XP_002818070.1	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	400
1886	XP_032614156.1	321	CCKKQFFVSKDIGNDI IAPSGHANYCEGECPSHIAGTSGSSLSFHSTVINHYRMRGHS PFANLKSCCVPTKLRPMS	400
1887				
1888	NP_002183.1	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1889	NP_032406.1	399	LYYDDGQNI IKKDNQNIIVEECGCS	424
1890	NP_058824.1	399	LYYDDGQNI IKKDNQNIIVEECGCS	424
1891	NP_776788.1	400	LYYDDGQNI IKKDNQNIIVEECGCS	425
1892	NP_999193.1	399	LYYDDGQNI IKKDNQNIIVEECGCS	424
1893	XP_540364.2	399	LYYDDGQNI IKKDNQNIIVEECGCS	424
1894	NP_001075378.1	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1895	NP_001009458.1	400	LYYDDGQNI IKKDNQNIIVEECGCS	425
1896	XP_519063.2	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1897	XP_028701686.1	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1898	NP_001009856.1	399	LYYDDGQNI IKKDNQNIIVEECGCS	424
1899	NP_001272510.1	400	LYYDDGQNI IKKDNQNIIVEECGCS	425
1900	XP_004045385.1	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1901	XP_002818070.1	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1902	XP_032614156.1	401	LYYDDGQNI IKKDNQNIIVEECGCS	426
1903				

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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]

NP_002184.2	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPTPAAP-PPPPPGSPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
NP_032407.1	1	MDGLPGRALGAACLLLLVAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG[4]	FRRPEELGRVDGFLE	80
NP_542949.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG[4]	FRRPEELGRVDGFLE	80
NP_789822.2	1	MDGLPGRALGAACLLMLAVGSLGPGVWGSPTPPPLPAAPqPPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	77
NP_001158314.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGALGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_038281949.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_023478506.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_027820847.1	1	MDGLPGRALGAACVMLAVGSLGPGVWGSPTPPPSPAAPqPPPPPGAPGGAQDTCTSCGG	FRRPEELGRVDGFLE	77
XP_016805107.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_001090729.4	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_003990762.4	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_017917150.1	1	MDGLPGRALGAACVMLAVGSLGPGVWGSPTPPPSPAAPqPPPPPGAPGGAQDTCTSCGG	FRRPEELGRVDGFLE	77
XP_004031753.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_024099269.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
XP_032001809.1	1	MDGLPGRALGAACLLLLAAGWLGPEAWGSPTPPPSPAAP-PPPPPGAPGGSQDTCTSCGG	FRRPEELGRVDGFLE	76
NP_002184.2	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
NP_032407.1	81	AVKRHILSRQLRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	160	
NP_542949.1	81	AVKRHILSRQLRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	160	
NP_789822.2	78	AVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	157	
NP_001158314.1	77	AVKRHILNRLQMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_038281949.1	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGSDGQERVSEI ISFAETDGLASSR	156	
XP_023478506.1	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_027820847.1	78	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGPERVSEI ISFAETDGLASSR	157	
XP_016805107.1	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_001090729.4	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_003990762.4	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_017917150.1	78	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGPERVSEI ISFAETDGLASSR	157	
XP_004031753.1	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_024099269.1	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPGADGQERVSEI ISFAETDGLASSR	156	
XP_032001809.1	77	AVKRHILSRQLMRGRPNITHAVPKAAMVTALRKLHAGKVREDGRVEI PHLDGHASPAADGQERVSEI ISFAETDGLASSR	156	
NP_002184.2	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNMVEKRVDLKRSWHTFPLTEAIIQ	236	
NP_032407.1	161	VRLYFFVSNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNVVEKRVDLKRSWHTFPIITEAIIQ	240	
NP_542949.1	161	VRLYFFVSNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNVVEKRVDLKRSWHTFPIITEAIIQ	240	
NP_789822.2	158	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGPGDRWA AVEKRVDLKRSWHTFPLTEPIIQ	237	
NP_001158314.1	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQPGHGDWRV DVEKRVDLKRSWHTFPLTEAIIQ	236	
XP_038281949.1	157	VRLYFFVSNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQQGDRWNA VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_023478506.1	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNV VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_027820847.1	158	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGPGDRWA AVEKRVDLKRSWHTFPLTEPIIQ	237	
XP_016805107.1	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNM VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_001090729.4	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNM VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_003990762.4	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNV VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_017917150.1	158	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGPGDRWA AVEKRVDLKRSWHTFPLTEPIIQ	237	
XP_004031753.1	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNM VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_024099269.1	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNM VEKRVDLKRSWHTFPLTEAIIQ	236	
XP_032001809.1	157	VRLYFFISNEGNQNLFFVQASLWLYLKLPLPYVLEKGSRRKVRVKVYFQEQGHGDRWNM VEKRVDLKRSWHTFPLTEAIIQ	236	
NP_002184.2	237	ALFERGERRLNLDVQCDSQELAVVPVFDVDPGEESHRRPFVVVQARLGD SRHRIRKRGLECDGRNTLCCRQQFFIDRLIG	316	
NP_032407.1	241	ALFERGERRLNLDVQCDSQELAVVPVFDVDPGEESHRRPFVVVQARLGD SRHRIRKRGLECDGRNTLCCRQQFFIDRLIG	320	

1978	NP 542949.1	241	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTSLCCRQFFIDRLIG	320
1979	NP 789822.2	238	ALFSRGERRLSLDVQCDSQRELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	317
1980	NP 001158314.1	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLVDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1981	XP 038281949.1	237	ALFERGERRLSLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1982	XP 023478506.1	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1983	XP 027820847.1	238	ALFSRGERRLSLDVQCDSQRELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTSLCCRQFFIDRLIG	317
1984	XP 016805107.1	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1985	XP 001090729.4	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1986	XP 003990762.4	237	SLFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1987	XP 017917150.1	238	ALFSRGERRLSLDVQCDSQRELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	317
1988	XP 004031753.1	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1989	XP 024099269.1	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1990	XP 032001809.1	237	ALFERGERRLNLDVQCDSQELAVVPFVDPGEESHPRFVVVQARLGDSRHRIRKRGLECDGRTNLCCRQFFIDRLIG	316
1991				
1992	NP 002184.2	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
1993	NP 032407.1	321	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G P V N S C C I P T K L S S M S L Y F D D E Y N I V K R D	400
1994	NP 542949.1	321	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G P V N S C C I P T K L S S M S L Y F D D E Y N I V K R D	400
1995	NP 789822.2	318	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	397
1996	NP 001158314.1	317	S D I I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
1997	XP 038281949.1	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
1998	XP 023478506.1	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
1999	XP 027820847.1	318	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	397
2000	XP 016805107.1	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
2001	XP 001090729.4	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G A V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
2002	XP 003990762.4	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
2003	XP 017917150.1	318	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	397
2004	XP 004031753.1	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
2005	XP 024099269.1	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
2006	XP 032001809.1	317	NDI I I A P T G Y G N Y C E G S C P A Y L A G V P G S A S S F H T A V N Q Y R M R G L N P G T V N S C C I P T K L S T M S L Y F D D E Y N I V K R D	396
2007				
2008	NP 002184.2	397	P N I V E E C G C A	407
2009	NP 032407.1	401	P N I V E E C G C A	411
2010	NP 542949.1	401	P N I V E E C G C A	411
2011	NP 789822.2	398	P N I V E E C G C A	408
2012	NP 001158314.1	397	P N I V E E C G C A	407
2013	XP 038281949.1	397	P N I V E E C G C A	407
2014	XP 023478506.1	397	P N I V E E C G C A	407
2015	XP 027820847.1	398	P N I V E E C G C A	408
2016	XP 016805107.1	397	P N I V E E C G C A	407
2017	XP 001090729.4	397	P N I V E E C G C A	407
2018	XP 003990762.4	397	P N I V E E C G C A	407
2019	XP 017917150.1	398	P N I V E E C G C A	408
2020	XP 004031753.1	397	P N I V E E C G C A	407
2021	XP 024099269.1	397	P N I V E E C G C A	407
2022	XP 032001809.1	397	P N I V E E C G C A	407
2023				
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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_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]	
NP_005250.1	1	-MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDVIRQ	79
NP_034964.1	1	mMQKLQMYVYIYLFMLIAAGPVDLNEGSERENVEKEGLCNACAWRQNTYRSRIEAIKIQILSKLRLETAPNISKDAIRQ	80
NP_062024.1	1	mTQKPQMYVYIYLFVLIAGPVDLNEDESEANVEKEGLCNACAWRQNTYRSRIEAIKIQILSKLRLETAPNISKDAIRQ	80
NP_001001525.1	1	-MQKLQISVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACLWRENTTSSRLEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_999600.2	1	-MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACMWRQNTKSSRLEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_001002959.1	1	-MQRLQICVYIYLFVLIAGPVDLSENSEQKENVEKEGLCNACMWRQNTKSSRIEAIKIQILSKLRLETAPNISRDVAVRQ	79
NP_001075286.1	1	-MQKLQISVYIYLFVLIAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_001009428.1	1	-MQKLQIFVYIYLFMLIVAGPVDLNENSEQKENVEKGLCNACLRQNNKSSRLEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_001073388.1	1	-MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_001073588.1	1	-MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
XP_003991021.1	1	-MQKLQIYVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_001272666.1	1	-MQKLQIFVYIYLFMLIVAGPVDLNENSEQKENVEKGLCNACLRQNNKSSRLEAIKIQILSKLRLETAPNISKDAIRQ	79
XP_018877573.1	1	-MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
XP_002812720.1	1	-MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
XP_032609257.1	1	-MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTKSSRIEAIKIQILSKLRLETAPNISKDAIRQ	79
NP_005250.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQVQDGPKKCCFFKFSKIQYNKVVKAQLWIY	159
NP_034964.1	81	LLPRAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQADGPKKCCFFKFSKIQYNKVVKAQLWIY	160
NP_062024.1	81	LLPRAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQADGPKKCCFFKFSKIQYNKVVKAQLWIY	160
NP_001001525.1	80	LLPKAPPLLELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDLLTQVEGPKKCCFFKFSKIQYNKLVKAQLWIY	159
NP_999600.2	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDLLMQVEGPKKCCFFKFSKIQYNKVVKAQLWIY	159
NP_001075286.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDLLMQVEGPKKCCFFKFSKIQYNKVVKAQLWIY	159
NP_001009428.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDLLEAVQEKPKCCFFKFSKIQHNVKVVKAQLWIY	159
NP_001073388.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQVQDGPKKCCFFKFSKIQYNKVVKAQLWIY	159
NP_001073588.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQVQDGPKKCCFFKFSKIQYNKVVKAQLWIY	159
XP_003991021.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDLLMQVEGPKKCCFFKFSKIQYNKVVKAQLWIY	159
NP_001272666.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDLLEAVQEKPKCCFFKFSKIQHNVKVVKAQLWIY	159
XP_018877573.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQVQDGPKKCCFFKFSKIQYNKVVKAQLWIY	159
XP_002812720.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQVQDGPKKCCFFKFSKIQYNKVVKAQLWIY	159
XP_032609257.1	80	LLPKAPPLRELIDQYDVQRDSSDGSLEDDDYHATTETIITMPTESDFLMQVQDGPKKCCFFKFSKIQYNKVVKAQLWIY	159
NP_005250.1	160	LRPVETPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_034964.1	161	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	240
NP_062024.1	161	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	240
NP_001001525.1	160	LRPVKTPATVFVQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_999600.2	160	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_001002959.1	160	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_001075286.1	160	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_001009428.1	160	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_001073388.1	160	LRPVETPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_001073588.1	160	LRPVETPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_003991021.1	160	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_001272666.1	160	LRPVKTPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
XP_018877573.1	160	LRPVETPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
XP_002812720.1	160	LRPVETPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
XP_032609257.1	160	LRPVETPTTFVFQILRLIKPMKDGTRYTGIRSLKLDMPGTGIWQSIDVKTVLQNLKQPESNLGIEIKALDENGHDLAV	239
NP_005250.1	240	TFFPGGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDLEAFGLDII IAPKRKANYCSGCECFVFLQ	319
NP_034964.1	241	TFFPGGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDLEAFGLDII IAPKRKANYCSGCECFVFLQ	320

2099	NP_062024.1	241	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	320
2100	NP_001001525.1	240	TFPEPGEDGLTFFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2101	NP_999600.2	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKASYCSGECEFFVFLQ	319
2102	NP_001002959.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2103	NP_001075286.1	240	TFPRPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2104	NP_001009428.1	240	TFPEPGEEGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFLFLQ	319
2105	NP_001073388.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2106	NP_001073588.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2107	XP_003991021.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2108	NP_001272666.1	240	TFPEPGEEGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFLFLQ	319
2109	XP_018877573.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2110	XP_002812720.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2111	XP_032609257.1	240	TFPGPGEDGLNPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDEAFGDDIIAPKRRKANYCSGECEFFVFLQ	319
2112				
2113	NP_005250.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2114	NP_034964.1	321	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	376
2115	NP_062024.1	321	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	376
2116	NP_001001525.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGEGQIIYGKTPAVVDRCGCS	375
2117	NP_999600.2	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2118	NP_001002959.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2119	NP_001075286.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2120	NP_001009428.1	320	KYPHTHLVHQANPKGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPGVVDRCGCS	375
2121	NP_001073388.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2122	NP_001073588.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2123	XP_003991021.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2124	NP_001272666.1	320	KYPHTHLVHQANPKGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPGVVDRCGCS	375
2125	XP_018877573.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2126	XP_002812720.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2127	XP_032609257.1	320	KYPHTHLVHQANPRGSAGPCCTPTKMSPINLYFNGKEQIIYGKTPAVVDRCGCS	375
2128				

2129

2130

GDF11

2131

2132

NP_005802.1 growth/differentiation factor 11 preproprotein [Homo sapiens]

2133

NP_034402.1 growth/differentiation factor 11 preproprotein [Mus musculus]

2134

NP_058899.1 growth/differentiation factor 11 precursor [Rattus norvegicus]

2135

XP_002687467.2 growth/differentiation factor 11 [Bos taurus]

2136

NP_001231239.1 growth/differentiation factor 11 precursor [Sus scrofa]

2137

XP_038534852.1 growth/differentiation factor 11 [Canis lupus familiaris]

2138

XP_023499520.1 growth/differentiation factor 11 [Equus caballus]

2139

XP_012031460.3 growth/differentiation factor 11 [Ovis aries]

2140

XP_016778746.2 growth/differentiation factor 11 [Pan troglodytes]

2141

XP_015007410.2 growth/differentiation factor 11 [Macaca mulatta]

2142

XP_003988905.1 growth/differentiation factor 11 [Felis catus]

2143

XP_017903600.1 PREDICTED: growth/differentiation factor 11 [Capra hircus]

2144

XP_018894140.2 growth/differentiation factor 11 [Gorilla gorilla gorilla]

2145

XP_024112308.1 growth/differentiation factor 11 [Pongo abelii]

2146

XP_032029354.1 growth/differentiation factor 11 [Hylobates moloch]

2147

2148

2149

2150

2151

2152

2153

[NP_005802.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 78

[NP_034402.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 76

[NP_058899.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GVGGERSRPAPSAAPEPDGCPVCVWRQHSRELRLES](#) 76

[XP_002687467.2](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 77

[NP_001231239.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSAAPEPDGCPVCVWRQHSRELRLES](#) 75

[XP_023499520.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSAAPEPDGCPVCVWRQHSRELRLES](#) 76

[XP_012031460.3](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 75

[XP_016778746.2](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 78

[XP_015007410.2](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 76

[XP_003988905.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 79

[XP_017903600.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GAGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 75

[XP_018894140.2](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 77

[XP_024112308.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAAa-GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 78

[XP_032029354.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 80

[XP_032029354.1](#) 1 [MVLAAPLLLGFLLLALELRPRGEAAEGP-AAAAAAAAAAAA---GVGGERSRPAPSVAPEPDGCPVCVWRQHSRELRLES](#) 77

[NP_005802.1](#) 79 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 158

[NP_034402.1](#) 77 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 156

[NP_058899.1](#) 77 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 156

[XP_002687467.2](#) 78 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 157

[NP_001231239.1](#) 76 [VKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 155

[XP_038534852.1](#) 77 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 156

[XP_023499520.1](#) 76 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 155

[XP_012031460.3](#) 79 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 158

[XP_016778746.2](#) 77 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 156

[XP_015007410.2](#) 80 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 159

[XP_003988905.1](#) 76 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 155

[XP_017903600.1](#) 78 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 157

[XP_018894140.2](#) 79 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 158

[XP_024112308.1](#) 81 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 160

[XP_032029354.1](#) 78 [IKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQIILDLHDFQGDALQPEDFLEEDEYHATTETVISMASETDPAVQTDGS](#) 157

[NP_005802.1](#) 159 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 238

[NP_034402.1](#) 157 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 236

[NP_058899.1](#) 157 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 236

[XP_002687467.2](#) 158 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIDLHRSRSGHWQSI](#) 237

[NP_001231239.1](#) 156 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIDLHRSRSGHWQSI](#) 235

[XP_038534852.1](#) 157 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 236

[XP_023499520.1](#) 156 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIDLHRSRSGHWQSI](#) 235

[XP_012031460.3](#) 159 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIDLHRSRSGHWQSI](#) 238

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[XP_015007410.2](#) 160 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 239

[XP_003988905.1](#) 156 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 235

[XP_017903600.1](#) 158 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIDLHRSRSGHWQSI](#) 237

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[XP_024112308.1](#) 161 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 240

[XP_032029354.1](#) 158 [PLCCHFHFSPKVMFTKVLKAQLWVYLRVPRPATVYLQILRLKPLTGEGTAGGGGGRRHIRIRSLKIELHRSRSGHWQSI](#) 237

2201

2202

[NP_005802.1](#) 239 [DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAELHPFMELRVLENTKRSRRNLGLDCDEHSSESRCRYPL](#) 318

2203

[NP_034402.1](#) 237 [DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAELHPFMELRVLENTKRSRRNLGLDCDEHSSESRCRYPL](#) 316

2204	NP_058899.1	237	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	316
2205	XP_002687467.2	238	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	317
2206	NP_001231239.1	236	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	315
2207	XP_038534852.1	237	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	316
2208	XP_023499520.1	236	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	315
2209	XP_012031460.3	239	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	318
2210	XP_016778746.2	237	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	316
2211	XP_015007410.2	240	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	319
2212	XP_003988905.1	236	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	315
2213	XP_017903600.1	238	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	317
2214	XP_018894140.2	239	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	318
2215	XP_024112308.1	241	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	320
2216	XP_032029354.1	238	DFKQVLHSWFRQPQSNWGIEINAFDPSGTDLAVTSLGPGAEGLHHPFME	LRVLENTKRSRRNLGLDCDEHSSESRC	RYPL	317
2217						
2218	NP_005802.1	319	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	398
2219	NP_034402.1	317	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	396
2220	NP_058899.1	317	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	396
2221	XP_002687467.2	318	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	397
2222	NP_001231239.1	316	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	395
2223	XP_038534852.1	317	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	396
2224	XP_023499520.1	316	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	395
2225	XP_012031460.3	319	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	398
2226	XP_016778746.2	317	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	396
2227	XP_015007410.2	320	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	399
2228	XP_003988905.1	316	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	395
2229	XP_017903600.1	318	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	397
2230	XP_018894140.2	319	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	398
2231	XP_024112308.1	321	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	400
2232	XP_032029354.1	318	TVDLEAFGDDII IAPKREKANYCSGQCEYMFMQKYPHTHLVQQANPRGS	AGPCCTPTKMSPINLYFN	DKQQIIYGKIPG	397
2233						
2234	NP_005802.1	399	VVDRCGCS		407	
2235	NP_034402.1	397	VVDRCGCS		405	
2236	NP_058899.1	397	VVDRCGCS		405	
2237	XP_002687467.2	398	VVDRCGCS		406	
2238	NP_001231239.1	396	VVDRCGCS		404	
2239	XP_038534852.1	397	VVDRCGCS		405	
2240	XP_023499520.1	396	VVDRCGCS		404	
2241	XP_012031460.3	399	VVDRCGCS		407	
2242	XP_016778746.2	397	VVDRCGCS		405	
2243	XP_015007410.2	400	VVDRCGCS		408	
2244	XP_003988905.1	396	VVDRCGCS		404	
2245	XP_017903600.1	398	VVDRCGCS		406	
2246	XP_018894140.2	399	VVDRCGCS		407	
2247	XP_024112308.1	401	VVDRCGCS		409	
2248	XP_032029354.1	398	VVDRCGCS		406	
2249						

2250

INHBC

2252	NP_005529.1	inhinin beta C chain preproprotein [Homo sapiens]		
2253	NP_034695.1	inhinin beta C chain preproprotein [Mus musculus]		
2254	NP_072136.1	inhinin beta C chain precursor [Rattus norvegicus]		
2255	NP_001192912.1	inhinin beta C chain precursor [Bos taurus]		
2256	XP_003355541.3	inhinin beta C chain [Sus scrofa]		
2257	XP_849169.2	inhinin beta C chain [Canis lupus familiaris]		
2258	XP_001488633.1	inhinin beta C chain [Equus caballus]		
2259	XP_004006594.3	inhinin beta C chain [Ovis aries]		
2260	XP_522443.1	inhinin beta C chain [Pan troglodytes]		
2261	XP_001115940.1	inhinin beta C chain [Macaca mulatta]		
2262	XP_023112929.1	inhinin beta C chain [Felis catus]		
2263	XP_005680345.1	PREDICTED: inhinin beta C chain [Capra hircus]		
2264	XP_004053482.1	inhinin beta C chain [Gorilla gorilla gorilla]		
2265	XP_002823468.3	inhinin beta C chain [Pongo abelii]		
2266	XP_032028142.1	inhinin beta C chain [Hylobates moloch]		
2267				
2268	NP_005529.1	1	--MTSSLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTALQH	78
2269	NP_034695.1	1	--MASSLLLALLFLPTTIVVNPKEGTEGPCACWGAIQFDLESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRGALKTALQR	78
2270	NP_072136.1	1	--MASSLLLALLFLTLATVVNLTGDGCPACWGATFDLESHRELLLDLAKRSILDKLHLTQRPTLNRPVSRGALKTALQR	78
2271	NP_001192912.1	1	--MICSFLAFVLVLAAMVATPRADRQCPACGEPALDVESHRELLLNLAKRSLDKLHLTQRPTLGRPVSGVALRAALRR	78
2272	XP_003355541.3	1	maMISLLAFVFLAPATVATPQADSQCACGGPTLDLESQRDLNLAKRSLDKLHLTQRPTLNRPVSRRAALRTALQG	80
2273	XP_849169.2	1	--MISPLLAFLFLAPATVAIPRADSQCACGGPAVDVSRQRELLLDLAKRSILEKLHLTQRPTLNRPVSGAALRAALQR	78
2274	XP_001488633.1	1	--MISMLLAFLFLAPATVATSRADQCPACAGPTLDLESQRELLLDLAKRSLDKLHLTQRPTLNRPVSRRAALRTVLQR	78
2275	XP_004006594.3	1	--MICSFLAFVLVLAAMVATPRADRQCPACGEPALDVESHRELLLNLAKRSLDKLHLTQRPTLGRPVSRVALRAALQR	78
2276	XP_522443.1	1	--MTSSLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTALQH	78
2277	XP_001115940.1	1	--MTSSLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTALQR	78
2278	XP_023112929.1	1	--MISLLAFLLLAPAPAAIPRADSQCACGGPALDLDLRQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTVLQH	78
2279	XP_005680345.1	1	--MICSFLAFVLVLAAMVATPRADRQCPACGEPALDVESHRELLLNLAKRSLDKLHLTQRPTLGRPVSRVALRAALQR	78
2280	XP_004053482.1	1	--MTSSLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTALQH	78
2281	XP_002823468.3	1	--MTSLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTALQR	78
2282	XP_032028142.1	1	--MTSSLLAFLLLAPTTVATPRAGGQCPACGGPTLELESQRELLLDLAKRSILDKLHLTQRPTLNRPVSRRAALRTALQR	78
2283				
2284	NP_005529.1	79	LHGVPPQGALLEDNREQE-CEIISFAETGLSTINQTRLDHFHSSDRTAGDREVQQAASLMFFVQLPSNT-TWTLKVRVVLVVG	156
2285	NP_034695.1	79	LRGPRRETLEHDQRQE-YEIIISFADTDLSSINQTRLEFHFH-SGRMASGMEVRQTRFMFFVQFPHNA-TQTMNIRVVLVLR	156
2286	NP_072136.1	79	LRGTRAETLEHDQRQE-YEIIISFADTGLSNINQTRLEFHFH-SDRTTGGVEVLQTRFMFFMQLPPTNT-TQTMNIRVVLVLR	155
2287	NP_001192912.1	79	LHGPPQGALPEADGQE-YEIIISFAETGLCNTTQTRLDHFHSSDSSAGGLEVQQAASLMFFVQLPNT-TCPLKVRVLELS	156
2288	XP_003355541.3	81	LHGPPQGVLPEDRQE-YEIIISFAETGLSNINQTRLDHFHSSDRTAGDREVQQAASLMFFVQLPNT-TWTLKVRVLELG	158
2289	XP_849169.2	79	LHGPPQGMPEADGQE-YEIIISFADTGLSDINQTRLDHFHSS-DRTAGSMEIQQAASLMFFVQIPNT-TQTLKLVILVLS	155
2290	XP_001488633.1	79	LHGPPQGVLPEDRQE-YEIIISFAETGLSNINQTRLDHFH-SDRTAGSMEIQQAASLMFFVQLPNT-TQTMKVRILVPG	155
2291	XP_004006594.3	79	LHGPPQGVLPEDGQE-YEIIISFAETGLCNTTQTRLDHFHSSDSSAGGLEVQQAASLMFFVQLPNT-TCPLKVRVLELS	156
2292	XP_522443.1	79	LHGVPQGALLEDNREQE-CEIISFAETGLSTINQTRLDHFHSSNRTAGDREVQQAASLMFFVQLPSNT-TWTLKVRVVLVVG	156
2293	XP_001115940.1	79	LHGVPPQGALPEDNREQE-CEIISFAETGLSTINQTRLDHFHSSDRTAGDREVQQAASLMFFVQLPSNT-TWTLKVRVVLVVG	156
2294	XP_023112929.1	79	LHGPPQGTLEADREQE-YEIIISFADTGFSNINQTRLDHFHSSDRTAGSMEIQQAASVMFFVQLPNT-TLPLKLRILVPG	157
2295	XP_005680345.1	79	LHGPPQGVLPEDGQE-YEIIISFAETGLCNTTQTRLDHFHSSDSSASGLEVQQAASLMFFVQLPNT-TCPLKVRVLELS	156
2296	XP_004053482.1	79	LHGVPPQGALLEDNREQE-CEIISFAETGLSTINQTRLDHFHSSDRTAGDREVQQAASLMFFVQLPSNT-TWTLKVRVVLVVG	156
2297	XP_002823468.3	79	LHGVPPQGALLEDNREQE-CEIISFAETGLSTINQTRLDHFHSSDRTAGDREVQQAASLMFFVQLPSNT-TWTLKMRVVLVVG	156
2298	XP_032028142.1	79	LRGVPQGALPEDNQE-CEIISFAETGLSTINQTRLDHFHSSDRTAGDREVQQAASLVFVQLPSNT-TWTLKVRVVLVVG	156
2299				
2300	NP_005529.1	157	PHNTNLTATQYLLVVDASGWHQLLGPPEAQAACSQGHLTLELVLEGQVAQSSVILGGAHRPFVAAARVRVGGKHIHRR	236
2301	NP_034695.1	157	PYDTNLTLSQYVVQVNASGWYQLLGPPEAQAACSQGHLTLELVPEQVAHSSLIIDGVSHPFVAAQVRVEGKHRVRRR	236
2302	NP_072136.1	156	PYDTNLTLSQYMLQVDASGWHQLLGPPEAQAACSQGHLTLELVPEQVAHSSLIIDGVSHPFVAAQVRVEGKHRVRRR	235
2303	NP_001192912.1	157	PRDTNLTLSATQHLLQVDDTGWHLQLLGPPEAQAAYSQGHIALELAPEEQVDWSVVLARAHRPFVTAARVRVGGQHRVRRR	236
2304	XP_003355541.3	159	PHGTNLTATQHPLEVNNSGWHQLLGPPEAQAAYSQGHILELVPEEQVAWNSVILDGAHRPFVTAARVRVGGKHRVRRR	238
2305	XP_849169.2	156	SRDTNLTLSATQHLLVDASGWHQLLGPPEAQAACSQGHITLELVPEEQVAWSVILGGAHRPFVAAKVRVGGKHRVRRR	235
2306	XP_001488633.1	156	PHDTNLTATQHLLVVDASGWHQLLGPPEAQAACSQRHITLELVPEEQVAQSSVILGGAHRPFVAAARVRVGGKHRVRRR	235
2307	XP_004006594.3	157	PRDTNLTLSATQHLLVVDNSGWHQLLGPPEAQAAYSQGHITLELAPEEQVAWSVILAGAHRPFVTAARVRVGGKHLRLLRR	236
2308	XP_522443.1	157	PHNTNLTATQYLLVVDASGWHQLLGPPEAQAACSQGHLTLELVLEGQVAQSSVILGGAHRPFVAAARVRVGGKHIHRR	236
2309	XP_001115940.1	157	PHNTNLTATQYLLVVDASGWHQLLGPPEAQAAYSQGHITLELVPEEQVAQSSVILGGAHRPFVAAARVRVGGKHIHRR	236
2310	XP_023112929.1	158	SHDTNLTWATQQLVVDASGWHRLFLGPPEAQAAFSQGHITLELVLEGQVAQSSVILGGAHRPFVAAKVRVGGKHLRLLRR	237
2311	XP_005680345.1	157	PRDTNLTLSATQHLLVVDNSGWHQLLGPPEAQAAYSQGHIALELAPEEQVAWSVILAGAHRPFVTAARVRVGGKHLRLLRR	236
2312	XP_004053482.1	157	PHNTNLTATQYLLVVDASGWHQLLGPPEAQAACSQGHITLELVLEGQVAQSSVILGGAHRPFVAAARVRVGGKHIHRR	236
2313	XP_002823468.3	157	PHNTNLTATQYLLVVDASGWHQLLGPPEAQAACSQGHITLELVLEGQVAQSSVILGGAHRPFVAAARVRVGGKHIHRR	236
2314	XP_032028142.1	157	PHNTNLSLATQYLLVVDASGWHQLLGPPEAQAACSQGHITLELVLEGQVAQSSVILGGAHRPFVAAARVRVGGKHIHRR	236
2315				
2316	NP_005529.1	237	GIDCQGGSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC	316
2317	NP_034695.1	237	GIDCQGASRMCCRQEYFVDFREIGLNDI IQPEG AMNFCIGQCPHLVAGMPGISASFHTAVLNLLKANAAGTTGRGSC	316
2318	NP_072136.1	236	GINCQGLSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLVAGMPGISASFHTAVLNLLKANTAAGTTGRGSC	315
2319	NP_001192912.1	237	GIDCQGRSKMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLVAGMPGIAASFHTAVLNLLKANTAAGTTGRGSC	316
2320	XP_003355541.3	239	GIDCQGRSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGHCPHLVAGVPGIAASFHTAVLNLLKANTAAGTTGGGSC	318
2321	XP_849169.2	236	GINCQGGSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLVAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC	315
2322	XP_001488633.1	236	GINCQGGSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLVAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC	315
2323	XP_004006594.3	237	GIDCQGRSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLVAGMPGIAASFHTAVLNLLKANTAAGTTGRGSC	316
2324	XP_522443.1	237	GIDCQGGSRMCCRQEYFVDFREIGLHDI IQPEG AMNFCIGQCPHLIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC	316

2325 [XP_001115940.1](#) 237 GIDCQEGSRMCCRQEFFVDREIGHDHIIQPEGAMNFCIGQCPLHVAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC 316
 2326 [XP_023112929.1](#) 238 GIDCQGGSRMCCRQEFFVDREIGHDHIIQPEGAMNFCIGQCPLHVAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC 317
 2327 [XP_005680345.1](#) 237 GIDCQGRSRMCCRQEFFVDREIGHDHIIQPEGAMNFCIGQCPLHVAGMPGIAASFYTSVLNLLKVNNTAAGTTGGSSC 316
 2328 [XP_004053482.1](#) 237 GIDCQGGSRMCCRQEFFVDREIGHDHIIQPEGAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC 316
 2329 [XP_002823468.3](#) 237 GIDCQGGSRMCCRQEFFVDREIGHDHIIQPEGAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC 316
 2330 [XP_032028142.1](#) 237 GIDCQGGSRMCCRQEFFVDREIGHDHIIQPEGAMNFCIGQCPLHIAGMPGIAASFHTAVLNLLKANTAAGTTGGGSC 316
 2331
 2332
 2333 [NP_005529.1](#) 317 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2334 [NP_034695.1](#) 317 CVPTSRRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2335 [NP_072136.1](#) 316 CVPTSRRPLSLYYDRDSNIVKTDIPDVVEACGCS 351
 2336 [NP_001192912.1](#) 317 CVPTVRRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2337 [XP_003355541.3](#) 319 CVPTARRPLSLYYDKDSNIVKTDIPDVVEACGCS 354
 2338 [XP_849169.2](#) 316 CVPTARRPLSLYYDRDSNVVKTDPDVVEACGCS 351
 2339 [XP_001488633.1](#) 316 CVPTTTRPLSLYYDRDSNIVKTDIPDVVEACGCS 351
 2340 [XP_004006594.3](#) 317 CVPTIRRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2341 [XP_522443.1](#) 317 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2342 [XP_001115940.1](#) 317 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2343 [XP_023112929.1](#) 318 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 353
 2344 [XP_005680345.1](#) 317 CVPTIRRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2345 [XP_004053482.1](#) 317 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2346 [XP_002823468.3](#) 317 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 352
 2347 [XP_032028142.1](#) 317 CVPTARRPLSLYYDRDSNIVKTDIPDVVEACGCS 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]		
NP_113667.1	1	MRLPDVQLWLVL LL WALVRAQGTGSCVPCSCGGSKLAPQAERALVLELAKQQIILDGLHLTSRPRITHPPQAALTRAL	76
NP_032408.2	1	MKLPKALWLL LL WALVWVQSTRSACPCSCGGPTLAPQGERALVLELAKQQIILEGLHLTSRPRITRPLPQAALTRAL	76
NP_114003.2	1	MGLSNVQLWTL LL WALAWVQSTRSACPCSCGAPTLPQGERALVLELAKQQIILEGLHLTSRPRITRPLPQAALTRAL	76
NP_001192771.1	1	MGLLVQQLVLL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAVLTRAL	76
XP_003126368.2	1	MGLPDVQLWLVL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAALTRAL	76
XP_005625596.1	1	MGLPDVQLWLVL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAALTRAL	76
XP_001488840.1	1	MELPDVQLVLL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAALTRAL	76
XP_004006593.1	1	MGLHKVQLVLL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAVLTRAL	76
XP_509161.2	1	MRLPDVQLWLVL LL WALVRAQGTGSCVPCSCGGSKLAPQAERALVLELAKQQIILDGLHLTSRPRITHPPQAALTRAL	76
XP_001115958.2	1	MGLPVVQLWLVL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAALTRAL	76
XP_003988987.1	1	MGLPDGQRQLVLL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAALTRAL	76
XP_005680344.1	1	[32]MGLHKVQLVLL LL WALVWAQVAGSACPCSCGGPTLAPQAERALVLELAKQQIILEGLHLTSRPRITHPPQAVLTRAL	108
XP_004053483.1	1	MQLPDVQLWLVL LL WALVRAQGTGSCVPCSCGGSKLAPQAERALVLELAKQQIILDGLHLTSRPRITHPPQAALTRAL	76
XP_002823469.1	1	MGLPDVQLWLVL LL WALVWAQVAGSACPCSCGGSKLAPQAERALVLELAKQQIILDGLHLTSRPRITHPPQAALTRAL	76
XP_032029168.1	1	MGLPDVQLWLVL LL WALVRAQGTGSCVPCSCGGSKLAPQAERALVLELAKQQIILDGLHLTSRPRITHPPQAALTRAL	76
NP_113667.1	77	RRLLQPGSVAPGN EE VISFATVTD-STSA YS SL LT FHLS TP SRSH LY HARL WL HVLP TL PG TL CL RI FRWG PR RR RR Q GS R	155
NP_032408.2	77	RRLLQPKSMVPGN RE KVISFATII DK ST ST YR SM LT FL Q LS PLW SH LY HAR L WL HV PS FP GT LY LR IF RC GT TR CR-G FR	155
NP_114003.2	77	RRLLQPRSMVPGN RE KVISFATSID K ST ST YR SV LT FL Q LS PLW SH LY HAR L WL HV PS FP AT LY LR IF GC GT TR CR-G SR	155
NP_001192771.1	77	RRLLQGRVVPAN GE VISFAVLT DS STAT CS ST LT FL HL ST PR SH LY HARL WL QVLP TL PG PL SL RI FRWG GR RR GR GS R	156
XP_003126368.2	77	RRLLQGRVVPAN GE VISFAAIT DS ST ST CG ST LT FL HL ST PR SH LY HAR L WL HAL PT LP GT LS LR IF FR GR PR RR RR GS R	156
XP_005625596.1	77	RRLLQPRSMPIAD GD EVISFATVAD-ST S AC SV LT FL DL ST AQ PH QL SR ARL WL HAR P AP GS LY LR V FR GR PG GG Q RG AR	155
XP_001488840.1	77	RRLLQPGSAAPAN GE VISFATIT DS ST ST CS SV LT FL HL SA PR SH LE HAR L WL HAL PT LP GA LY LR IF QC GR PR RR RR Q GS R	156
XP_004006593.1	77	RRLLQGRVVPAN GE VISFAVLT DS STAT CS ST LT FL HL ST PR SH LY HARL WL HVLP TL PG PL SL RI FRWG GR RR GR GS R	156
XP_509161.2	77	RRLLQPGSVAPGN EE VISFATVTD-STSA YS SL LT FHLS TP SRSH LY HARL WL HVLP TL PG TL CL RI FRWG PR RR RR Q GS R	155
XP_001115958.2	77	RRLLQPGSVAPGN EE VISFATVTD-STSA YS SL LT FHLS TP FR HH LY HAR L WL HML PT LP GT CL RI FRWG PR RR RR H Q RS R	155
XP_003988987.1	77	RRLLQPGSVAPGN EE VISFATIT EP ST S AC SV LT FL HL ST AQ SR HL Y HARL WL RVLP TF PG TL SL RT FRWN PG RR RR RES R	156
XP_005680344.1	109	RRLLQGRRAAPAN GE VISFAVLT DS STAT CS ST LT FL HL ST PR SH LY HARL WL HVLP TL PG PL SL RI FRWG GR RR GR GS R	188
XP_004053483.1	77	RRLLQPGSVAPGN EE VISFATVTD-STSVH SS LT FL HL ST PR SH LY HAR L WL HVLP TL PG TL CL RI FRWG PR RR RR Q GS R	155
XP_002823469.1	77	RRLLQPGSVAPGN EE VISFATVTD-STSA YS SL LT FHLS TP SRSH LY HARL WL HVLP TL PG TL CL RI FRWG PR RR RR PF GS R	155
XP_032029168.1	77	RRLLQPGSVASGN EE VISFATVTD-STSA YS SL LT FHLS TP SRSH LY HARL WL HVLP TL PG TL CL RI FRWG PR RR RR Q GS R	155
NP_113667.1	156	TLLAEHHITNLG WH LTLPSSGLR GE KS GV LK LQ LD CR PLEG-NST VT GQ-PRRL LD TAG HQ Q PF LE LK IRAN EP GAG RA	233
NP_032408.2	156	TFLAEHQTTSSG WH ALTLPSSGLR SE DS GV VK LQ LE FR PLDL-NST AG L-PRRL LD TAG Q Q RP FLE LK IRAN EP GAG RA	233
NP_114003.2	156	TFLADYQTTSSG WH ALTLPSSGLR GE ES AV TK LQ LE FR PLDL-NST TA RL-PRRL LD TAG Q Q RP FLE LK IRAN EP GAG RA	233
NP_001192771.1	157	VFLAEHQLTTPG WH ALTLPSSGLK RE ES GV LK LR LD CS PLEG-NRT VT TPQ---L LD TAG E Q R PFLE LK TRPK LP GAG RA	231
XP_003126368.2	157	VLLAEHQMTTPG WH ALTLPSSGLR RE ES GV LK LQ LD CR ALEG-NG TA LQ-PCQL LD TAG E Q R PFLE LK TRPK EP GAG RA	234
XP_005625596.1	156	TLLAEQHLPAAG WH ALALPSSGLR AE SAV LQ LK CR LLPG-NRT SA Q Q 1GRRL LD TAG DR RF FL Q L QI WP REP AG RA	234
XP_001488840.1	157	ALLAEHQMTTPG WH ALTLPSSGLR GE ES GV LK LQ LD CR PLEG-NST AA RQ-PRQL LD DMV GD RR PF LE LK IR PS EP AG RA	234
XP_004006593.1	157	VFLAEHQLTTPG WH ALTLPSSGLK RE ES GV LK LR LD CS SLEG-NRT VA PQ---L LD SAGE Q R PF LE LK TRPK WP GAG RA	231
XP_509161.2	156	TLLAEHHITNLG WH ALTLPSSGLR GE KS GV LK LQ LD CR PLEG-NST IT GQ-PRRL LD TAG HQ Q PF LE LK IRAN EP GAG RA	233
XP_001115958.2	156	TLLAEHHITNLG WH ALTLPSSGLR GE KS GV LK LQ LD CR PLEGn ST VT G Q-PRRL LD TAG HQ Q PF LE LK IRAN EP GAG RA	234
XP_003988987.1	157	TLLAEHQMTTPG WH ALTLPSSGLR GE ES GV LK LQ LD CR PLEG-NAT AA ---PQ WL VD TAG DR RF LE LK IR PS EP AG RT	232
XP_005680344.1	189	VFLAEHQLTTPG WH ALTLPSSGLK RE ES GV LK LR LD CS SLEG-NRT VA PQ---L LD SAGE Q R PF LE LK TRPK WP GAG RA	263
XP_004053483.1	156	TLLAEHHITNLG WH ALTLPSSGLR AE KS GV LK LQ LD CR PLEG-NST VT GQ-PRQL LD TAG HQ Q PF LE LK IQAN EP GAG RA	233
XP_002823469.1	156	TLLAEHHITNLG WH ALTLPSSGLR GE KS GV LK LQ LD CR PLEG-NST VT GQ-PRRL VD TAG HQ Q PF LE LK IRAN EP GAG RA	233
XP_032029168.1	156	TLLAEHHITNLG WH ALTLPSSGLR GE KS GV LK LQ LD CR PLEG-NST VT GQ-PRRL LD TAG HQ Q PF LE LK IRAN EP GAG RA	233
NP_113667.1	234	RRRTPTCEPAT PL CCRRDHYV LE QELG RD ILQPEG QL NYCSG QC PPHLAGSPGIAASFHSAVFSLLKANNPWPASTS	313
NP_032408.2	234	RRRTPTCEPET PL CCRRDHYV LE QELG RD ILQPEG QL NYCSG QC PPHLAGSPGIAASFHSAVFSLLKANNPWPAGSS	313

2425	NP_114003.2	234	RRRTP T CE S ETPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P AG S S 313	
2426	NP_001192771.1	232	RRRTP S CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y RLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG T S 311	
2427	XP_003126368.2	235	RRRTP T CE P ET X CCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG T S 314	
2428	XP_005625596.1	235	RRRTP T CE P ETPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG T S 314	
2429	XP_001488840.1	235	RRRTP T CE P ETPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG N S 314	
2430	XP_004006593.1	232	RRRTP S CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y RLN F CSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG T S 311	
2431	XP_509161.2	234	RRRTP T CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P AG S T 313	
2432	XP_001115958.2	235	RRRTP T CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P AG S T 314	
2433	XP_003988987.1	233	RRRTP T CE P ETPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG T S 312	
2434	XP_005680344.1	264	RRRTP S CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y RLN F CSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P LG T S 343	
2435	XP_004053483.1	234	RRRTP T CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P AG S T 313	
2436	XP_002823469.1	234	RRRTP T CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P AG S T 313	
2437	XP_032029168.1	234	RRRTP T CE P ATPLCCRRDHYVDF Q ELG R RD I LQPEG Y QLNYCSGQC P PHLAGSPGIAASFHS A VF S LLKANN P W P AG S T 313	
2438				
2439				
2440	NP_113667.1	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2441	NP_032408.2	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2442	NP_114003.2	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2443	NP_001192771.1	312	CCVPTARR P LS L YLD R DGNVV K TD P DI V VEAC G CS 348	
2444	XP_003126368.2	315	CCVPTARR S LS L YLD R DGNVV K TD P DI V VEAC G CS 351	
2445	XP_005625596.1	315	CCVPTARR P LS L YLD R DGNVV K TD P DI V VEAC G CS 351	
2446	XP_001488840.1	315	CCVPTARR P LS L YLD R DGNVV K TD P DI V VEAC G CS 351	
2447	XP_004006593.1	312	CCVPTARR P LS L YLD R DGNVV K TD P DI V VEAC G CS 348	
2448	XP_509161.2	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2449	XP_001115958.2	315	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 351	
2450	XP_003988987.1	313	CCVPTARR P LS L YLD R DGNVV K TD P DI V VEAC G CS 349	
2451	XP_005680344.1	344	CCVPTARR P LS L YLD R DGNVV K TD P DI V VEAC G CS 380	
2452	XP_004053483.1	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2453	XP_002823469.1	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2454	XP_032029168.1	314	CCVPTARR P LS L YLDHNGNVV K TD P DI V VEAC G CS 350	
2455				
2456				
2457				

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TGFB1

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2462

NP_000651.3 transforming growth factor beta-1 proprotein preproprotein [Homo sapiens]

2463 NP_035707.1 transforming growth factor beta-1 proprotein preproprotein [Mus musculus]

2464 NP_067589.1 transforming growth factor beta-1 proprotein precursor [Rattus norvegicus]

2465 NP_001159540.1 transforming growth factor beta-1 proprotein precursor [Bos taurus]

2466 XP_020949162.1 transforming growth factor beta-1 isoform X1 [Sus scrofa]

2467 XP_038300925.1 transforming growth factor beta-1 proprotein isoform X1 [Canis lupus familiaris]

2468 XP_005596143.1 transforming growth factor beta-1 isoform X1 [Equus caballus]

2469 XP_027833173.1 transforming growth factor beta-1 proprotein isoform X3 [Ovis aries]

2470 XP_009433930.1 transforming growth factor beta-1 isoform X2 [Pan troglodytes]

2471 XP_028695614.1 transforming growth factor beta-1 proprotein isoform X1 [Macaca mulatta]

2472 XP_006941294.1 transforming growth factor beta-1 proprotein isoform X1 [Felis catus]

2473 XP_017917139.1 PREDICTED: transforming growth factor beta-1 isoform X1 [Capra hircus]

2474 XP_018870688.1 transforming growth factor beta-1 proprotein isoform X1 [Gorilla gorilla gorilla]

2475 XP_009230906.2 transforming growth factor beta-1 [Pongo abelii]

2476 XP_032028718.1 transforming growth factor beta-1 proprotein [Hylobates moloch]

2477

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2479

2480

2481

2482

[NP_000651.3](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2483

[NP_035707.1](#) 1 MPPSGRLRLPLLLPLPWLVLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2484

[NP_067589.1](#) 1 MPPSGRLRLPLLLPLPWLVLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2485

[NP_001159540.1](#) 1 MPPSGRLRLPLLLPLLWLLMLTGRFVAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGDVPPGPLEAILAL 80

2486

[XP_020949162.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGDVPPGPLEAVLAL 80

2487

[XP_038300925.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2488

[XP_005596143.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2489

[XP_027833173.1](#) 1 MPPSGRLRLPLLLPLLWLLMLTGRFVAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGDVPPGPLEAILAL 80

2490

[XP_009433930.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2491

[XP_028695614.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2492

[XP_006941294.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2493

[XP_017917139.1](#) 1 MPPSGRLRLPLLLPLLWLLMLTGRFVAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGDVPPGPLEAILAL 80

2494

[XP_018870688.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2495

[XP_009230906.2](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2496

[XP_032028718.1](#) 1 MPPSGRLRLPLLLPLLWLLVLTGRPAAGLSTCKTIDMELVKKRRIEAIARGQILSKLRLASPPSQGEVPPGPLEAVLAL 80

2497

2498

[NP_000651.3](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVETHNEIYDKFKQSTHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2499

[NP_035707.1](#) 81 YNSTRDRVAGESADPEPEPEADYAKEVTRVLMVDRNNAIYEKTKDISHSIYFFNTSDIREAVPEPPLLSRAELRLQL 160

2500

[NP_067589.1](#) 81 YNSTRDRVAGESADPEPEPEADYAKEVTRVLMVDRNNAIYDKTKDITHSIYFFNTSDIREAVPEPPLLSRAELRLQRF 160

2501

[NP_001159540.1](#) 81 YNSTRDRVAGESAETEPEPEADYAKEVTRVLMVEYGNKIYDKMKSSSHSIYFFNTSELREAVPEFVLLSRADVRLRL 160

2502

[XP_020949162.1](#) 81 YNSTRDRVAGESVPEPEPEADYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEFVLLSRAELRLRL 160

2503

[XP_038300925.1](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVENTNKIYEKVKSPHSIYMLFNTSELREAVPEFVLLSRAELRLRL 160

2504

[XP_005596143.1](#) 81 YNSTRAQVAGESAETEPEPEADYAKEVTRVLMVEKENEIYKTVETGSHSIYFFNTSELRAAVDPMLLSRAELRLRL 160

2505

[XP_027833173.1](#) 81 YNSTRDRVAGESAETEPEPEADYAKEVTRVLMVEYGNKIYDKMKSSSHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2506

[XP_009433930.1](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVETHNEIYDKFKQSTHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2507

[XP_028695614.1](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVETHNEIYDKFKQSTHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2508

[XP_006941294.1](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVENTNKIYEKVQRTPHSIYMLFNTSELREAVPEFVLLSRAELRLRL 160

2509

[XP_017917139.1](#) 81 YNSTRDRVAGESAETEPEPEADYAKEVTRVLMVEYGNKIYDKMKSSSHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2510

[XP_018870688.1](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVETHNEIYDKFKQSTHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2511

[XP_009230906.2](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVETHNEIYDKFKQSTHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2512

[XP_032028718.1](#) 81 YNSTRDRVAGESAEPPEPEADYAKEVTRVLMVETHNEIYDKFKQSTHSIYFFNTSELREAVPEFVLLSRAELRLRL 160

2513

2514

[NP_000651.3](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSRGGEIEGFRLSAHSCSDSKDNTLQVDIN-GF 239

2515

[NP_035707.1](#) 161 KSSVEQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVRQWLNQGDGIQGFRLSAHSCSDSKDNKLHVEIN-GI 239

2516

[NP_067589.1](#) 161 KSTVEQHVELYQKYSNNSWRYLGNRLLPDTPPEWLSFDVTVGVRQWLNQGDGIQGFRLSAHSCSDSKDNVLHVEIN-GI 239

2517

[NP_001159540.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLTREIEIEGFRLSAHSCSDSKDNTLQVDIN-GF 239

2518

[XP_020949162.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLTREIEIEGFRLSAHSCSDSKDNTLHVEINAGF 240

2519

[XP_038300925.1](#) 161 KLKAEQHVELYQKYSNNSWRYLSNRLLPDTPPEWLSFDVTVGVRQWLSHGGEVEGFRLSAHSCSDSKDNTLQVDINAGF 240

2520

[XP_005596143.1](#) 161 KLKAEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSHGGEVEGFRLSAHSCSDSKDNTLRVGINVGF 240

2521

[XP_027833173.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLTREIEIEGFRLSAHSCSDSKDNTLQVDINAGF 240

2522

[XP_009433930.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSRGGEIEGFRLSAHSCSDSKDNTLQVDINAGF 240

2523

[XP_028695614.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSRGGEIEGFRLSAHSCSDSKDNTLQVDINAGF 240

2524

[XP_006941294.1](#) 161 KLKAEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSHGGEVEGFRLSAHSCSDSKDNTLRVGINVGF 240

2525

[XP_017917139.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLTREIEIEGFRLSAHSCSDSKDNTLQVDINAGF 240

2526

[XP_018870688.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSRGGEIEGFRLSAHSCSDSKDNTLQVDINAGF 240

2527

[XP_009230906.2](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSRGGEIEGFRLSAHSCSDSKDNTLQVDIN-GF 239

2528

[XP_032028718.1](#) 161 KLKVEQHVELYQKYSNNSWRYLSNRLLPSPDSPEWLSFDVTVGVRQWLSHGGEIEGFRLSAHSCSDSKDNTLQVDIN-GF 239

2529

2530

[NP_000651.3](#) 240 TTGRRGDLATIHGMNRPFLMLMATPLERAQHLQSSRHRRALDTNYCFSSTTEKNCCVRQLYIDRKDLGKRIIHEPKGIIHA 319

2531

[NP_035707.1](#) 240 SPKRRGDLGTIHDMNRPFLMLMATPLERAQHLHSSRHRRALDTNYCFSSTTEKNCCVRQLYIDRKDLGKRIIHEPKGIIHA 319

2532 [NP_067589.1](#) 240 SPKRRGDLGTIHDMNRPFLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 319
 2533 [NP_001159540.1](#) 240 SSGRRGDLATIHGMNRPFLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 319
 2534 [XP_020949162.1](#) 241 NSGRRGDLATIHGMNRPFLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2535 [XP_038300925.1](#) 241 SSSRRGDLATIHGMNRPFLLMATPLERAQHLHSSRQRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2536 [XP_005596143.1](#) 241 SSSRRGDLATIDGMNRPFLLMATPLERAQQLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
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 2538 [XP_009433930.1](#) 241 TTGRRGDLATIHGMNRPFLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2539 [XP_028695614.1](#) 241 TTGRRGDLATIHGMNRPFLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2540 [XP_006941294.1](#) 241 SSSRRGDLATIHGMNRPFLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2541 [XP_017917139.1](#) 241 SSGRRGDLATIHGMNRPFLLMATPLERAQHLHSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2542 [XP_018870688.1](#) 241 TTGRRGDLATIHGMNRPFLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 320
 2543 [XP_009230906.2](#) 240 TTGRRGDLATIHGMNRPFLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 319
 2544 [XP_032028718.1](#) 240 TTGRRGDLATIHGMNRPFLLMATPLERAQHLQSSRHRRALDTNYCFSSTEKNCCVRQLYIDRKDLGKRIHEPKGHA 319
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 2546 [NP_000651.3](#) 320 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 390
 2547 [NP_035707.1](#) 320 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASASPCCVPALEPLFVYYVGRKPKVECSNIVRSCKCS 390
 2548 [NP_067589.1](#) 320 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASASPCCVPALEPLFVYYVGRKPKVECSNIVRSCKCS 390
 2549 [NP_001159540.1](#) 320 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 390
 2550 [XP_020949162.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2551 [XP_038300925.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2552 [XP_005596143.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2553 [XP_027833173.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2554 [XP_009433930.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2555 [XP_028695614.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2556 [XP_006941294.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2557 [XP_017917139.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2558 [XP_018870688.1](#) 321 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 391
 2559 [XP_009230906.2](#) 320 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 390
 2560 [XP_032028718.1](#) 320 NFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLFVYYVGRKPKVECSNIVRSCKCS 390
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TGFB2

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2568 NP_003229.1 transforming growth factor beta-2 proprotein isoform 2 preproprotein [Homo sapiens]
 2569 NP_033393.2 transforming growth factor beta-2 proprotein isoform 1 preproprotein [Mus musculus]
 2570 NP_112393.2 transforming growth factor beta-2 proprotein precursor [Rattus norvegicus]
 2571 XP_005216841.1 transforming growth factor beta-2 isoform X1 [Bos taurus]
 2572 XP_020919952.1 transforming growth factor beta-2 isoform X1 [Sus scrofa]
 2573 XP_545713.2 transforming growth factor beta-2 proprotein isoform X1 [Canis lupus familiaris]
 2574 XP_014970470.1 transforming growth factor beta-2 proprotein isoform X1 [Macaca mulatta]
 2575 XP_001172158.1 transforming growth factor beta-2 isoform X1 [Pan troglodytes]
 2576 XP_004013651.1 transforming growth factor beta-2 proprotein isoform X1 [Ovis aries]
 2577 XP_003364612.1 transforming growth factor beta-2 isoform X1 [Equus caballus]
 2578 XP_003999556.1 transforming growth factor beta-2 proprotein isoform X1 [Felis catus]
 2579 XP_017915648.1 PREDICTED: transforming growth factor beta-2 isoform X1 [Capra hircus]
 2580 XP_004028464.2 transforming growth factor beta-2 proprotein isoform X1 [Gorilla gorilla gorilla]
 2581 XP_002809490.1 transforming growth factor beta-2 isoform X1 [Pongo abelii]
 2582 XP_031992675.1 transforming growth factor beta-2 proprotein isoform X2 [Hylobates moloch]

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2588 [NP_003229.1](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2589 [NP_033393.2](#) 1 MHYCVLSTFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2590 [NP_112393.2](#) 1 MHYCVLRTFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2591 [XP_005216841.1](#) 1 MHYCVLSAFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2592 [XP_020919952.1](#) 1 MHYCVLSAFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2593 [XP_545713.2](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2594 [XP_014970470.1](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2595 [XP_001172158.1](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2596 [XP_004013651.1](#) 1 MHYCVLSAFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2597 [XP_003364612.1](#) 1 MHYCVLSAFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2598 [XP_003999556.1](#) 1 MHYCVLSAFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2599 [XP_017915648.1](#) 1 MHYCVLSAFLLLHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2600 [XP_004028464.2](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2601 [XP_002809490.1](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLNSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80
 2602 [XP_031992675.1](#) 1 MHYCVLSAFLILHLVTVALSSTCSTLDMQFMRKRIEAIHQILSKLKLTSPPEDYPEPEEVPPEVISIYNSTRDLLQE 80

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2604 [NP_003229.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPFFPSE-----NAIPPTFYRPFYFRIVRF 132
 2605 [NP_033393.2](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSHLPSE-----NAIPPTFYRPFYFRIVRF 132
 2606 [NP_112393.2](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSHPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2607 [XP_005216841.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVFCGYLDAIPPTFYRPFYFRIVRF 160
 2608 [XP_020919952.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2609 [XP_545713.2](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2610 [XP_014970470.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2611 [XP_001172158.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2612 [XP_004013651.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVFCGYLDAIPPTFYRPFYFRIVRF 160
 2613 [XP_003364612.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2614 [XP_003999556.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2615 [XP_017915648.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFLPSETVCPVVTTPSGSVGSLCSRQSQVFCGYLDAIPPTFYRPFYFRIVRF 160
 2616 [XP_004028464.2](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2617 [XP_002809490.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160
 2618 [XP_031992675.1](#) 81 KASRRAAACERERSDEEYAKEVYKIDMPSFFPSETVCPVVTTPSGSVGSLCSRQSQVLCGYLDAIPPTFYRPFYFRIVRF 160

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2620 [NP_003229.1](#) 133 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 212
 2621 [NP_033393.2](#) 133 DVSTMEKNASNLVKA EFRVFR LQNPKARV AEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 212
 2622 [NP_112393.2](#) 161 DVSTMEKNASNLVKA EFRVFR LQNPKARV AEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2623 [XP_005216841.1](#) 161 DVSSMEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2624 [XP_020919952.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV AEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2625 [XP_545713.2](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2626 [XP_014970470.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2627 [XP_001172158.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2628 [XP_004013651.1](#) 161 DVSSMEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2629 [XP_003364612.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2630 [XP_003999556.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2631 [XP_017915648.1](#) 161 DVSSMEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2632 [XP_004028464.2](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2633 [XP_002809490.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240
 2634 [XP_031992675.1](#) 161 DVSA MEKNASNLVKA EFRVFR LQNPKARV PEQRI ELYQ I LKSKDLTSPTQRY IDSKVVKTRAE GEWLSFDVTD AVHEWLH 240

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2636 [NP_003229.1](#) 213 HKDRNLGFKI SLHCPCTFVPSNNYI IPNKSELEARFAGIDGTSTYTSGDQTIKSTRKKN SGKTPHLLMLLPSYRLE 292

2637	NP_033393.2	213	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKTSGKTPHLLMLLPSYRLE	292
2638	NP_112393.2	241	HKDRNLGFKISLHCPCTFIPSNYYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKS	320
2639	XP_005216841.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2640	XP_020919952.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2641	XP_545713.2	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2642	XP_014970470.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2643	XP_001172158.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2644	XP_004013651.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2645	XP_003364612.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2646	XP_003999556.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2647	XP_001172158.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2648	XP_004028464.2	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2649	XP_002809490.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2650	XP_031992675.1	241	HKDRNLGFKISLHCPCTFVPSNNYIIPNKSEELERFAGIDGTSTYASGDQTIKSTRKKN	320
2651				
2652	NP_003229.1	293	SQQTNRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	372
2653	NP_033393.2	293	SQSSRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHTKVLVSLYNTINP	372
2654	NP_112393.2	321	SQSSRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHTKVLVSLYNTINP	400
2655	XP_005216841.1	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2656	XP_020919952.1	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2657	XP_545713.2	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2658	XP_014970470.1	321	SQQTNRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2659	XP_001172158.1	321	SQQTNRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2660	XP_004013651.1	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2661	XP_003364612.1	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2662	XP_003999556.1	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2663	XP_017915648.1	321	SQSNRRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2664	XP_004028464.2	321	SQQTNRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2665	XP_002809490.1	321	SQQTNRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2666	XP_031992675.1	321	SQQTNRKKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGKTIHEPKGNANFCAGACPYLWSSDTQHSRVLSLYNTINP	400
2667				
2668	NP_003229.1	373	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	414
2669	NP_033393.2	373	EASASPCCVSQDLEPLTLYYIGNTPKIEQSNIVKSKCS	414
2670	NP_112393.2	401	EASASPCCVSQDLEPLTLYYIGNTPKIEQSNIVKSKCS	442
2671	XP_005216841.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2672	XP_020919952.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2673	XP_545713.2	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2674	XP_014970470.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2675	XP_001172158.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2676	XP_004013651.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2677	XP_003364612.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2678	XP_003999556.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2679	XP_017915648.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2680	XP_004028464.2	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2681	XP_002809490.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2682	XP_031992675.1	401	EASASPCCVSQDLEPLTLYYIGKTPKIEQSNIVKSKCS	442
2683				
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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]		
NP_003230.1	1	MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLAALYNS	76
NP_033394.2	1	MKMHLQRALVVLALLNLATIISLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLAALYNS	76
NP_037306.1	1	MKMHLQRALVVLALLNLATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLAALYNS	76
NP_001094653.1	1	[42] LKMHLQRALVVLALLNFATVLSLSMSTCTTLDLDFNHKRRKVEAIRGQILSKLRLTSPDPGSLASVPIQVLDLYNS	118
XP_005666412.1	1	[45] MKMHLQRALVVLALLNFATVLSLSMSTCTTLDLDFDHKRRKVEAIRGQILSKLRLTSPDPMSLANIPTQVLDLYNS	121
XP_854119.2	1	[45] MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLAALYNS	121
XP_001492737.1	1	MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLAALYNS	76
XP_004010851.1	1	[42] LKMHLQRALVVLALLNFATVLSLSMSTCTTLDLDFNHKRRKVEAIRGQILSKLRLTSPDPGSLASVPIQVLDLYNS	118
XP_001161669.1	1	MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLAALYNS	76
NP_001244404.1	1	MKMHLQRALVVLALLNFASVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLAALYNS	76
XP_003987900.1	1	MKMHLRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPSVMTHVPYQVLAALYNS	76
XP_005686198.1	1	[42] LKMHLQRALVVLALLNFATVLSLSMSTCTTLDLDFNHKRRKVEAIRGQILSKLRLTSPDPGSLASVPIQVLDLYNS	118
XP_004055526.1	1	MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLAALYNS	76
XP_002825003.1	1	MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLAALYNS	76
XP_031990693.1	1	MKMHLQRALVVLALLNFATVLSLSLSTCTTLDLDFGHIKKKRVEAIRGQILSKLRLTSPPEPTVMTHVPYQVLAALYNS	76
NP_003230.1	77	RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNTNLFRAEFVRLV	156
NP_033394.2	77	RELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNGTNLFRAEFVRLV	156
NP_037306.1	77	RELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNGTNLFRAEFVRLV	156
NP_001094653.1	119	RELLEEVHGERGDVCTQANTESEYYAKEIYKFDMIQGLEEHNDLTVCPKGITSKI FRFNVSSEKNETNLFRAEFVRFM	198
XP_005666412.1	122	RELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKGITSKI FRFNVSSEKNETNLFRAEFVRLM	201
XP_854119.2	122	RELLEEMQGEREDSCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNGTNLFRAEFVRLV	201
XP_001492737.1	77	RELLEEMHGEREDGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNGTNLFRAEFVRLV	156
XP_004010851.1	119	RELLEEVHGERGDVCTQANTESEYYAKEIYKFDMIQGLEEHNDLTVCPKGITSKI FRFNVSSEKNETNLFRAEFVRFM	198
XP_001161669.1	77	RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNTNLFRAEFVRLV	156
NP_001244404.1	77	RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNTNLFRAEFVRLV	156
XP_003987900.1	77	RELLEEMQGEREDSCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNGTNLFRAEFVRLV	156
XP_005686198.1	119	RELLEEVHGERGDVCTQANTESEYYAKEIYKFDMIQGLEEHNDLTVCPKGITSKI FRFNVSSEKNETNLFRAEFVRFM	198
XP_004055526.1	77	RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNTNLFRAEFVRLV	156
XP_002825003.1	77	RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNTNLFRAEFVRLV	156
XP_031990693.1	77	RELLEEMHGEREEGCTQENTESEYYAKEIHKFDMIQGLAEHNELAVCPKGITSKVFRFNVSSEKNTNLFRAEFVRLV	156
NP_003230.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
NP_033394.2	157	PNPSSKRTEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
NP_037306.1	157	PNPSSKRTEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
NP_001094653.1	199	PNPASKRSEQRLELFQILQPEGHEIAKQRYIDGKNLPTRTGTEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	278
XP_005666412.1	202	PNPSSKRSEQRLELFQILQPEGHEIAKQRYIDGKNLPTRTGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	281
XP_854119.2	202	PNPSSKRSEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	281
XP_001492737.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
XP_004010851.1	199	PNPASKRSEQRLELFQILQPEGHEIAKQRYIDGKNLPTRTGTEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	278
XP_001161669.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
NP_001244404.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
XP_003987900.1	157	PNPSSKRSEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
XP_005686198.1	199	PNPASKRSEQRLELFQILQPEGHEIAKQRYIDGKNLPTRTGTEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	278
XP_004055526.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
XP_002825003.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
XP_031990693.1	157	PNPSSKRNEQRLELFQILRPDEHIAKQRYIGGKNLPTRTGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNG	236
NP_003230.1	237	DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKQKDHHPHLILMMIPPHRLDNPGGQQRKRALDNTNYCFRNLEENCC	316
NP_033394.2	237	DILENVHEVMEIKFKGVDNEDDHGRGDLGRLKQKDHHPHLILMMIPPHRLDSPGQGSQRKRALDNTNYCFRNLEENCC	316

2759	NP_037306.1	237	DILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDSPGQGGQRKKRALDTNYCFRNLEENCC	316
2760	NP_001094653.1	279	DILENIQELMEIKFKGVSDDDPGRGDLGRLKKKE-HI PHLILMMIPPNRLDSPG-HSQRKKRALDTNYCFRNLEENCC	356
2761	XP_005666412.1	282	DILENIQEVMEIKFKGVSDDDPGRGDLGRLKKKE-HSPHLILMMIPDRLDNPGLAGQRKKRALDTNYCFRNLEENCC	360
2762	XP_854119.2	282	DILENIHEVMEIKFKGVDSEEDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	361
2763	XP_001492737.1	237	DILENIHEVMEIKFKGVSDDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2764	XP_004010851.1	279	DILENIQELMEIKFKGVSDDDPGRGDLGRLKKKE-HI PHLILMMIPPNRLDSPG-HSQRKKRALDTNYCFRNLEENCC	356
2765	XP_001161669.1	237	DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2766	NP_001244404.1	237	DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2767	XP_003987900.1	237	DILENIHEVMEIKFKGVSDDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2768	XP_005686198.1	279	DILENIQELMEIKFKGVSDDDPGRGDLGRLKKKE-HI PHLILMMIPPNRLDSPG-HSQRKKRALDTNYCFRNLEENCC	356
2769	XP_002825003.1	237	DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2770	XP_002825003.1	237	DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2771	XP_031990693.1	237	DILENIHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLILMMIPPHRLDNPQGGQRKKRALDTNYCFRNLEENCC	316
2772				
2773	NP_003230.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2774	NP_033394.2	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2775	NP_037306.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSSDTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2776	NP_001094653.1	357	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSSDTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	436
2777	XP_005666412.1	361	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	440
2778	XP_854119.2	362	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	441
2779	XP_001492737.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2780	XP_004010851.1	357	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSSDTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	436
2781	XP_001161669.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2782	NP_001244404.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2783	XP_003987900.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2784	XP_005686198.1	357	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSSDTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	436
2785	XP_004055526.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2786	XP_002825003.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2787	XP_031990693.1	317	VRPLYIDRQDLGKRWVHEPKGYANFCSGPCPYLRSADTTHTSVLGLYNTLNPEASASPCCVPQDLEPLTLYYVGRTP	396
2788				
2789	NP_003230.1	397	KVEQSNVVKSCCKS	412
2790	NP_033394.2	397	KVEQSNVVKSCCKS	412
2791	NP_037306.1	397	KVEQSNVVKSCCKS	412
2792	NP_001094653.1	437	KVEQSNVVKSCCKS	452
2793	XP_005666412.1	441	KVEQSNVVKSCCKS	456
2794	XP_854119.2	442	KVEQSNVVKSCCKS	457
2795	XP_001492737.1	397	KVEQSNVVKSCCKS	412
2796	XP_004010851.1	437	KVEQSNVVKSCCKS	452
2797	XP_001161669.1	397	KVEQSNVVKSCCKS	412
2798	NP_001244404.1	397	KVEQSNVVKSCCKS	412
2799	XP_003987900.1	397	KVEQSNVVKSCCKS	412
2800	XP_005686198.1	437	KVEQSNVVKSCCKS	452
2801	XP_004055526.1	397	KVEQSNVVKSCCKS	412
2802	XP_002825003.1	397	KVEQSNVVKSCCKS	412
2803	XP_031990693.1	397	KVEQSNVVKSCCKS	412
2804				
2805				
2806				
2807				
2808				

2809

BMP8A/B

2810

2811

2812

2813

NP_861525.2 bone morphogenetic protein 8A preproprotein [Homo sapiens]

2814

NP_001711.2 bone morphogenetic protein 8B preproprotein [Homo sapiens]

2815

NP_031584.1 bone morphogenetic protein 8A isoform 2 preproprotein [Mus musculus]

2816

NP_031585.2 bone morphogenetic protein 8B preproprotein [Mus musculus]

2817

NP_001102902.1 bone morphogenetic protein 8A precursor [Rattus norvegicus]

2818

XP_002729572.1 bone morphogenetic protein 8B isoform X1 [Rattus norvegicus]

2819

XP_024845991.1 bone morphogenetic protein 8A [Bos taurus]

2820

XP_020953264.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8A [Sus scrofa]

2821

XP_003356374.4 LOW QUALITY PROTEIN: bone morphogenetic protein 8B [Sus scrofa]

2822

XP_038477617.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8B isoform X1 [Canis lupus familiaris]

2823

XP_038543221.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8B isoform X1 [Canis lupus familiaris]

2824

XP_023488611.1 bone morphogenetic protein 8B [Equus caballus]

2825

XP_023488599.1 bone morphogenetic protein 8B [Equus caballus]

2826

XP_014947141.3 bone morphogenetic protein 8B [Ovis aries]

2827

XP_027824135.1 bone morphogenetic protein 8B [Ovis aries]

2828

XP_024213824.1 bone morphogenetic protein 8A [Pan troglodytes]

2829

XP_016815266.2 bone morphogenetic protein 8B [Pan troglodytes]

2830

XP_028691411.1 bone morphogenetic protein 8B isoform X2 [Macaca mulatta]

2831

XP_028691408.1 bone morphogenetic protein 8B isoform X1 [Macaca mulatta]

2832

XP_014991435.2 bone morphogenetic protein 8B [Macaca mulatta]

2833

XP_023113593.1 LOW QUALITY PROTEIN: bone morphogenetic protein 8A [Felis catus]

2834

XP_017897638.1 PREDICTED: bone morphogenetic protein 8A [Capra hircus]

2835

XP_017897686.1 PREDICTED: bone morphogenetic protein 8B [Capra hircus]

2836

XP_004025569.3 bone morphogenetic protein 8A [Gorilla gorilla gorilla]

2837

XP_030864436.1 bone morphogenetic protein 8B [Gorilla gorilla gorilla]

2838

XP_024103873.1 bone morphogenetic protein 8B-like [Pongo abelii]

2839

XP_009250410.2 bone morphogenetic protein 8B [Pongo abelii]

2840

XP_032016255.1 bone morphogenetic protein 8A [Hylobates moloch]

2841

NP_861525.2 1 MA AR PGPLWLLGLT LCAALGGGG-PGLRPPPGPCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2843

NP_001711.2 1 MT AL PGPLWLLGLA LCAALGGGG-PGLRPPPGPCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2844

NP_031584.1 1 MA MR PGPLWLLGLA LCAALGGGH--GPRPPTHCTPQRRRLGARERRDMQREILAVLGLPGRPRPR A 61

2845

NP_031585.2 1 MA AR PGLLWLLGLA LCVLGGGH--LSHPPHVFPQRRRLGVREPRDMQREIREVLGLPGRPRSR A 61

2846

NP_001102902.1 1 MA VR PGPLWLLGLA LCAALGGGH--GPRPPTHCTPQRRRLGARERRDMQREILAVLGLPGRPRPR A 61

2847

XP_002729572.1 1 MA AG PGLLWLLGLA LCVLGGSS--LPRSHPVFPQRRRLGVREPRDMQREIREVLGLPGRPRSR A 61

2848

XP_024845991.1 1 MA AR PGPLWLLGLA LCAALSGGGvPGPRPPLGCPQRRRLGPRERRDLQREILAVLGLPGRPRPR A 63

2849

XP_020953264.1 1 MA TC PAAVRLAT-- -----PPGCPQSRRLGPRERRDLQREILAVLGLPGRPXPR A 47

2850

XP_003356374.4 1 MA AR PGPLWLLGLV LCTLISGCG-PGPRPPGCPQSRRLGPRERRDLQREILEVLGLPGRPRPR A 62

2851

XP_038477617.1 1 MA AR PGPLWLVGLA LCAALSGGG-PGPRPPAGCPARRLGPERRDMQREILAVLGLPGRPRPR A 62

2852

XP_038543221.1 1 MA[14]AR[27] PGPLWLVGLA LCAALSGGG-PGPRPFRGPRPPWAAARERRDMQREILAVLGLPGRPRPR A 103

2853

XP_023488611.1 1 MA AR PPSLWLLGLA LCAALGGGG-PGPRPPPGCPPRRLGPRERRDLQREILAVLGLPGRPRPR T 62

2854

XP_023488599.1 1 MA AR PPSLWLLGLA LCAALGGGG-PGPRPPPGCPPRRLGPRERRDLQREILAVLGLPGRPRPR T 62

2855

XP_014947141.3 1 MA AR PGPLWLLGLA LCAALSGGGvPGPRPPLGCPQRRRLGPRERRDLQREILAVLGLPGRPRPR A 63

2856

XP_027824135.1 1 MA AR PGPLWLLGLA LCAALSGGGvPGPRPPLGCPQRRRLGPRERRDLQREILAVLGLPGRPRPR A 63

2857

XP_024213824.1 1 MA AR PGPLWLLGLT LCAALGGGG-PGLRPPPGPCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2858

XP_016815266.2 1 MT AL PGPLWLLGLA LCAALGGGG-PGLRPPPGPCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2859

XP_028691411.1 1 MA AL PGPLWLLGLA LCAALGGGS-PGLRPPPGPCPQRRRLGARERRDVQREILAVLGLPGRPRLR A 62

2860

XP_028691408.1 1 MA[8]AQ[27]PSVMSVLSLS[31]LCLISGSQ---DQPDREGAQWVFWVSLGVEHQPGAGLRLSLAAGPL S 126

2861

XP_014991435.2 1 MA AL PGPLWLLGLA LCAALGGGG-PGLRPPPGPCPQRRRLGERERRDVQREILSVLGLPGRPRPR V 62

2862

XP_023113593.1 1 MA AR PGSLWLVGLA LCAALSGGG-PGPRAPAGCPARRLGPERRDMQREILAVLGLPGRPRPR[352] A 414

2863

XP_017897638.1 1 MA AR PGPLWLLGLA LCAALSGGGvPGPRPPLGCPQRRRLGPRERRDLQREILAVLGLPGRPRPR A 63

2864

XP_017897686.1 1 MA AR PGPLWLLGLA LCAALSGGGvPGPRPPLGCPQRRRLGPRERRDLQREILAVLGLPGRPRPR A 63

2865

XP_004025569.3 1 MA AR PGPLWLLGLT LCAALGGGG-PGLRPPPGPCPQRRRLGARERRDVQREILAVLGLPGRPRPR P 62

2866

XP_030864436.1 1 MT AL PGPLWLLGLA LCAALGGGG-PVLRPPPGCPQRRRLGARERRDVQHEILAVLGLPGRPRPR A 62

2867

XP_024103873.1 1 MA AL PGPLWLLGLA LCAALGGGG-PGPRPQPCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2868

XP_009250410.2 1 MA AL PGPLWLLGLA LCAALGGGG-PGLRPLPGCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2869

XP_032016255.1 1 MA AL PGPLWLLGLA LCAALGGGG-PGPRPQPCPQRRRLGARERRDVQREILAVLGLPGRPRPR A 62

2870

2871

NP_861525.2 63 P PAASRL PASAPFLMFLDLYHAMAGDDDEDGAPAE--QRLGRADLVMSFVNMVVERDRALGHQEPHWKEFRFDLTQ 134

2872

NP_001711.2 63 P PAASRL PASAPFLMFLDLYHAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVVERDRALGHQEPHWKEFRFDLTQ 134

2873

NP_031584.1 62 Q PAAARQ PASAPFLMFLDLYHAMT--DDDDGGPPQ--AHLGRADLVMSFVNMVVERDRTLGYQEPHWKEFFHFDLTQ 131

2874

NP_031585.2 62 P[1]-GAAQQ PASAPFLMFLDLYRAMT--DDSGGGTPQp--HLDRADLIMS FVNIVEHRTDLGYQEPHWKEFFHFDLTQ 131

2875

NP_001102902.1 62 P PAAARQ PASAPFLMFLDLYHAMT--DDDDGGPPQ--AHLGRADLVMSFVNMVVERDRALGHQEPHWKEFFHFDLTQ 131

2876

XP_002729572.1 62 P[1]-ATAQQ PASAPFLMFLNLYHAMT--DDSGNGPPQp--HLHRADLIMS FVNIVEHRTDLGYQEPHWKEFFHFDLTQ 131

2877

XP_024845991.1 64 P PAAALL PASAPFLMFLDLYRAVADDDDEDGAPAE--RRLGRADLVMSFVNMVVERDPALGHQEPHWKEFFHFDLTQ 135

2878

XP_020953264.1 48 P PAGAGL PASAPFLMFLDLYRAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVVERDRALGHQEPHWKEFRFDLTQ 119

2879

XP_003356374.4 63 P PAGAGL PASAPFLMFLDLYRAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVVERDRALGHQEPHWKEFFHFDLTQ 134

2880

XP_038477617.1 63 P PAAARL PASAPFLMFLGLYRAMARDHDEDGGPPXA--RRPGRADLVMSFVNNVVERDRTLGHQEPHWKEFFHFDLTQ 134

2881

XP_038543221.1 104 P PAAARL PASAPFLMFLGLYRAMSSD--EQCCPPC--LCGGRATMVCS--ISLVERDRTLGHQEPHWKEFFHFDLTQ 172

2882

XP_023488611.1 63 P PAAARP PASAPFLMFLDLYHAMAGDDAEDGGPPE--RRLGHADLVMSFVNMVVELDRTLGHQEPHWKEFRFDLTQ 134

2883	XP_023483599.1	63	P	PAAARP	PASAPLFMLDLYHAMAGDDAEDGGPPE--RRLGHADLVMSFVNMGERGPGRRRPAVTPDLRLARVR	134					
2884	XP_014947141.3	64	P	PAAALL	PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERHPALGHQEPHWKEFFHFDLTQ	135					
2885	XP_027824135.1	64	P	PAAALL	PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFFHFDLTQ	135					
2886	XP_024213824.1	63	P	PAASRL	PASAPLFMLDLYHAMAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2887	XP_016815266.2	63	P	PAASRL	PASAPLFMLDLYHAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2888	XP_028691411.1	63	P	PAASRL	PASAPLFMLDLYHAMAGDDDEDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2889	XP_028691408.1	127	P[5]	PSLEQT[7]	PARPPVWPSTLSGGWLVGAVATSSAHSkvrAIPASPALLCL-LVERDHALGHREPHWKEFFHFDLTQ	211					
2890	XP_014991435.2	63	A	PAASQL	PASAPLFMLDLYHAMAGDDDKDDAPAE--RRLGRADLVMSFVNMVERDHALGHQEPHWKEFFHFDLTQ	134					
2891	XP_023113593.1	415	P	SAAARL	PASAPLFMLDLYHAMARDDEDGGPPE--RRPGRADLVMSFVNMVERDRTLGHQEPHWKEFFHFDLTQ	486					
2892	XP_017897638.1	64	P	PAAALL	PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFFHFDLTQ	135					
2893	XP_017897686.1	64	P	PAAALL	PASAPLFMLDLYRAVAGDDDEDGGAPE--RRLGRADLVMSFVNMVERDPALGHQEPHWKEFFHFDLTQ	135					
2894	XP_004025569.3	63	P	PAASRL	PASAPLFMLDLYHAMAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2895	XP_030864436.1	63	P	PAASRL	PASAPLFMLDLYHAVAGDDDEDGAPAE--QRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2896	XP_024103873.1	63	P	PVASRL	PASAPLFMLDLYHAMAGDDDDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2897	XP_009250410.2	63	P	PAASRL	PASAPLFMLDLYHAMAGDDNEDGAPAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2898	XP_032016255.1	63	P	PAASRL	PASAPLFMLDLYHAMAGDDDEDGALAE--RRLGRADLVMSFVNMVERDRALGHQEPHWKEFFHFDLTQ	134					
2899											
2900	NP_861525.2	135	I	PAGEAVTAAEFRIYKVP	SIHLLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2901	NP_001711.2	135	I	PAGEAVTAAEFRIYKVP	SIHLLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2902	NP_031584.1	132	I	PAGEAVTAAEFRIYK	EPSTHPLNNTLHISMFEVVQEHSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHH	208					
2903	NP_031585.2	132	I	PAGEAVTAAEFRIYK	EPSTHPLNNTLHISMFEVVQEHSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHH	208					
2904	NP_001102902.1	132	I	PAGEAVTAAEFRIYK	EPSTHPPNTLHISMFEVVQERSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHN	208					
2905	XP_002729572.1	132	I	PAGEAVTAAEFRIYK	EPSTHPPNTLHISMFEVVQERSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLNHN	208					
2906	XP_024845991.1	136	I	PAGEAVTAAEFRIYK	LPSTHPLNQTLHISMFEVVQEHSNRESDLFFLDLQTLRSGDEGWLVLDITAASDRWLLSRN	212					
2907	XP_020953264.1	120	I	PAGEAVTAAEFRIYK	LPSTHPLNQTLHISMFEVVPEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRS	196					
2908	XP_003356374.4	135	I	PAGEAVTAAEFRIYK	LPSTHQLNQTLHVSMFEVVPEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRS	211					
2909	XP_038477617.1	135	I	PEGEAVTAAEFQIYK	LASTHLLNRTLHVSTFEVVREQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASGRWLLGRN	211					
2910	XP_028543221.1	173	I	PEGEAVTAAEFRIYK	LASTHLLNRTLHVSTFEVVREQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASGRWLLGRN	249					
2911	XP_023488611.1	135	I	PAGEAVTAAEFRIYK	LPSTHPLNRTLHVSMFEVVRERANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLNRN	211					
2912	XP_023483599.1	135	D[9]	PGGGTRAAGE	LRPLKSSASMLLG-----PPRPRQRGPCCVHVQGHHP-----QVTALSP-----	193					
2913	XP_014947141.3	136	I	PAGEAVTAAEFRIYK	LPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRN	212					
2914	XP_027824135.1	136	I	PAGEAVTAAEFRIYK	LPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRN	212					
2915	XP_024213824.1	135	I	PAGEVVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2916	XP_016815266.2	135	I	PAGEVVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2917	XP_028691411.1	135	I	PDGEAVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRRH	211					
2918	XP_028691408.1	212	I	PDGEAVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRRH	288					
2919	XP_014991435.2	135	I	PDGEAVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRRH	211					
2920	XP_023113593.1	487	I	PEGEAVTAAEFRIYK	MASTHLLNGTLHVSMFEVVRERANRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLSRN	563					
2921	XP_017897638.1	136	I	PAREAVTAAEFRIYK	LPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRN	212					
2922	XP_017897686.1	136	I	PAGEAVTAAEFRIYK	LPSTHPLNQTLHISMFEVVLEQSNRESDLFFLDLQTLRSGDEGWLVLDVTAASDRWLLNRN	212					
2923	XP_004025569.3	135	I	PAGEVVTAAEFRIYK	VPSIYLLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2924	XP_030864436.1	135	I	PAGEVVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2925	XP_024103873.1	135	I	PAGEAVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRRH	211					
2926	XP_009250410.2	135	I	PAGEAVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDCWLLKRRH	211					
2927	XP_032016255.1	135	I	PAGEAVTAAEFRIYK	VPSIHLNRTLHVSMFQVQVEQSNRESDLFFLDLQTLRAGDEGWLVLDVTAASDRWLLKRRH	211					
2928											
2929	NP_861525.2	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKSNE	LPQANRLPGIF	289			
2930	NP_001711.2	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKSNE	LPQANRLPGIF	289			
2931	NP_031584.1	209	KDLGLRLY	VETADGHSMDPGLAGLLG	QRAPRSQQPFVVTFFRAS--QSPV	RAPRAARPLRRRQPKKTNE	LPHNKLPGIF	286			
2932	NP_031585.2	209	KDLGLRLY	VETEDGHSIDPGLAGLLG	QRAPRSQQPFVVTFFRAS--QSPV	RAPRTARPLKKKQLNQINQLPHSNKHLGIL		286			
2933	NP_001102902.1	209	KDLGLRLY	VETEDGHSIDPGLAGLLG	QTAPRSRQPFVVTFFRAS--SSPVRT	PRAVRPLRRRQPKKTNE	LPHNKLPGIF	286			
2934	XP_002729572.1	209	KDLGLRLY	VETEDGHSIDPGLAGLLG	QTAPRSRQPFVVTFFRAS--QSPV	RAPRTARPLKKKLNQVNLPHSNKHLGIF		286			
2935	XP_024845991.1	213	KDLGLRLY	VETDDGHSVDPGLAGLLG	QRAPRSQPFVVTFFRASpg	GPAPARAARPLRRRQPKKTNE	LPHNKLPGIF	292			
2936	XP_020953264.1	197	KDLGLRLY	VETDDGRSVDPSLAGLLG	QRAPRSQPFVVTFFRAS--LGPV	RAPRAVRPLRRRPPKRSNE	LPPNKLPGIF	274			
2937	XP_003356374.4	212	KDLGLRLY	VETDDGRSVDPSLAGLLG	QRAPRSQPFVVTFFRAS--XPV	RAPRAVRPLRRRPPKRSNE	LPPNKLPGIF	289			
2938	XP_038477617.1	212	KDLGLRLY	VETEDGRSVDPSLAGLLG	RAPRSQPFVVTFFRAS--PGV	RAPRAARPLRRRPPKKSNE	LPHNKLPGIF	289			
2939	XP_038543221.1	250	KDLGLRLY	VETEDGRSVDPSLAGLLG	RAPRSQPFVVTFFRAS--PGV	RAPRAARPLRRRPPKKSNE	LPHNKLPGIF	327			
2940	XP_023488611.1	212	KDLGLRLY	VETEDGLSVDPSLAGLLG	QRAPRSQPFVVTFFRAS--SRP	VAPRAVRPLRRRPLKKTNE	LPHNKLPGIF	289			
2941	XP_023483599.1	194	-----	LSVS---	GLSVDPSLAGLLG	QRAPRSQPFVVTFFRAS--PRP	VAPRAVRPLRRRPPKKTNE	LPHNKLPGIF	262		
2942	XP_014947141.3	213	KDLGLRLY	VETDDGRSVDPSLAGLLG	QRAPRSQPFVVTFFRASpc	GPAPARAARPLRRRPPKKTNE	LPPNRLPGIF	292			
2943	XP_027824135.1	213	KDLGLRLY	VETDDGRSVDPSLAGLLG	QRAPRSQPFVVTFFRASpg	GPAPARAARPLRRRPPKKTNE	LPPNRLPGIF	292			
2944	XP_024213824.1	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2945	XP_016815266.2	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2946	XP_028691411.1	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2947	XP_028691408.1	289	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	366			
2948	XP_014991435.2	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2949	XP_023113593.1	564	KDLGLRLY	VETDDGHSVDPGLAGLLG	RAPRSQPFVVTFFRAS--PGV	RAPRAARPLRRRPPKKTNE	LPHNKLPGIF	641			
2950	XP_017897638.1	213	KDLGLRLY	VETDDGRSVDPSLAGLLG	QRAPRSQPFVVTFFRASpg	LGPAPARAARPLRRRPPKKTNE	LPPNRLPGIF	292			
2951	XP_017897686.1	213	KDLGLRLY	VETDDGRSVDPSLAGLLG	QRAPRSQPFVVTFFRASpg	LGPAPARAARPLRRRPPKKTNE	LPPNRLPGIF	292			
2952	XP_004025569.3	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QQAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2953	XP_030864436.1	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2954	XP_024103873.1	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2955	XP_009250410.2	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	SRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2956	XP_032016255.1	212	KDLGLRLY	VETEDGHSVDPGLAGLLG	QRAPRSQQPFVVTFFRAS--PSPIRT	PRAVRPLRRRQPKKTNE	LPQANRLPGIF	289			
2957											
2958	NP_861525.2	290	DDVRGSHGRQV	CRRHELIVS	QDLG	LD	VIAPQ	CSAYYCEGEC	SFPLDSCMNATNHAILQSLVHLMK	NAVPAKACAP	369

2959	NP 001711.2	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMMPDAVPKACCAP	369
2960	NP 031584.1	287	DDGHGSRGREVCRRELYVSRDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	366
2961	NP 031585.2	287	DDGHGSHGREVCRRELYVSRDLGLDVIAPQGSAYYCEGECIYPLNSCMNSTNHATMQALVHLMKPDIIIPKVCVCP	366
2962	NP 001102902.1	287	DDGHGSRGREVCRRELYVSRDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	366
2963	XP 002729572.1	287	DDGHGSLDREVCRRELYVSRDLGLDVIAPQGSAYYCEGECIYPLNSCMNSTNHATMQALVHLMKPDIVPKVCVCP	366
2964	XP 024845991.1	293	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLLKPHAVPKACCAP	372
2965	XP 020953264.1	275	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	354
2966	XP 003356374.4	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2967	XP 038477617.1	290	DDVHGTDRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2968	XP 038543221.1	328	DDVHGTDRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	407
2969	XP 023488611.1	290	DDVHGSDGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2970	XP 023483599.1	263	DDVHGSDGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	342
2971	XP 014947141.3	293	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLLKPDVVPKACCAP	372
2972	XP 027824135.1	293	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLLKPDVVPKACCAP	372
2973	XP 024213824.1	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2974	XP 016815266.2	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMMPDAVPKACCAP	369
2975	XP 028691411.1	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2976	XP 028691408.1	367	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	446
2977	XP 014991435.2	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLGSCMNATNHAILQSLVHLMTPDAVPKACCAP	369
2978	XP 023113593.1	642	DDVHGTDRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	721
2979	XP 017897638.1	293	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLLKPDVVPKACCAP	372
2980	XP 017897686.1	293	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLLKPDVVPKACCAP	372
2981	XP 004025569.3	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2982	XP 030864436.1	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2983	XP 024103873.1	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2984	XP 009250410.2	290	DDVHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMTPDAVPKACCAP	369
2985	XP 032016255.1	290	DDIHGSHGRQVCRRELYVSDLGLDVIAPQGSAYYCEGECFPLDSCMNATNHAILQSLVHLMKPDVVPKACCAP	369
2986				
2987	NP 861525.2	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
2988	NP 001711.2	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
2989	NP 031584.1	367	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	399
2990	NP 031585.2	367	TELSAISLLYYDRNNNVILRRERNVQVQACGCH	399
2991	NP 001102902.1	367	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	399
2992	XP 002729572.1	367	TKLSAISLLYYDRNNNVILRRERNVQVQACGCH	399
2993	XP 024845991.1	373	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	405
2994	XP 020953264.1	355	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	387
2995	XP 003356374.4	370	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	402
2996	XP 038477617.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	402
2997	XP 038543221.1	408	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	440
2998	XP 023488611.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	402
2999	XP 023483599.1	343	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	375
3000	XP 014947141.3	373	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	405
3001	XP 027824135.1	373	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	405
3002	XP 024213824.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3003	XP 016815266.2	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3004	XP 028691411.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3005	XP 028691408.1	447	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	479
3006	XP 014991435.2	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3007	XP 023113593.1	722	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	754
3008	XP 017897638.1	373	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	405
3009	XP 017897686.1	373	TKLSATSLLYYDSSNNVILRKHNRNVVRCGCH	405
3010	XP 004025569.3	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3011	XP 030864436.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3012	XP 024103873.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3013	XP 009250410.2	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3014	XP 032016255.1	370	TKLSATSLLYYDSSNNVILRKHNRNVVKACGCH	402
3015				
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NP_060525.3 nodal homolog isoform 1 preproprotein [Homo sapiens]
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_060525.3	1	MHAHCLPFLL-HAWWALLQAGAATVATALLRTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAEDVAVDQGNWTF	AFDF	79	
NP_038639.2	1	MSAHSRLRILLQACWALLHPRAPTAALPLWTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAQVDVDTGQNWTF	TFDF	80	
NP_001099864.1	1	MSVHCLPVLQLQTCWTLHPRVATAALPLWTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAQVDVDTGQNWTF	TFDF	80	
NP_001192911.1	1	MHAQCLWFLHAWWALLQAGAAMVAPVPLRPWGQSSPSPLAYMLSLYREPLPRADII	IRSLQAQMQVDGQNWTF	AFDF	80	
XP_004049593.2	1	MHAHCLPFLL-HAWWALLQAGAATVATALLRTRGQSSPSPLAYMLGLYRDPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	79	
XP_546146.2	1	MHAPRLPLFLLHACWALLQAGAATVAPVPLRARVQSSSPAPLAYMLSLYRDPLPRADII	IRSLQAQDVEVDGHNWTF	AFDF	80	
XP_001503787.1	1	MHARLPFLLHAGWALLQAGAATVAPVPLRTRGEPSSPSPLAYMLSLYRDPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	80	
XP_004021483.4	1	MDAHLWLFLHAWWALLQAGAAMVAPVPLRPWGQSSPSPLAYMLSLYREPLTRADII	IRSLQAQMQVDGQNWTF	AFDF	80	
XP_521502.2	1	MHAHCLPFLL-HAWWALLQAGAATVATALLRTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	79	
XP_001108137.1	1	MHAHCLPFLL-HAWWALLQAGDATATAHLRTRGQSSPSPLAYMLSLYRNPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	79	
XP_019668767.3	1	MQAPRLPWFFLHAWWALLQAGAETVAPVPLRTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAQDVHADGQNWTF	AFDF	80	
XP_005699204.2	1	MHAHRLWLFLHAWWALLQAGAAMVAPVPLRPWGQSSPSPLAYMLSLYREPLTRADII	IRSLQAQMQVDGQNWTF	AFDF	80	
XP_004049593.2	1	MHAHCLPFLL-HAWWALLQAGAATVATALLRTRGQSSPSPLAYMLGLYRDPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	79	
XP_002820901.1	1	MHAHCLPFLL-HAWWALLQAGAATVATALLRTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	79	
XP_031995113.1	1	MHAHCLPFLL-HACWALLQVGAATVATALLRTRGQSSPSPLAYMLSLYRDPLPRADII	IRSLQAQDVEVDGQNWTF	AFDF	79	
NP_060525.3	80	SFLSQEEDLAWAELRLQLSSPVDLPTEGSLAIEIFHQPKPDT	EQASDSCLERFQMDLFTV	TVLSQVTFSLGSMVLEVRPL	159	
NP_038639.2	81	SFLSQEEDLVWAEELRLQLPGPMDIPT	TEGLTIDIFHQAKGDP	PERDPADCLERIMWETFTV	VIPISQVTFASGSTVLEVKPL	160
NP_001099864.1	81	SFLSQEEDLVWAEELRLQLSSPMDSPK	TKGPLTIDIFHQAKPDP	EQADPACLERVWMERITV	TPSQVTFASDSTVLEVKPL	160
NP_001192911.1	81	SFLSQEEDLEWAEELRLQLSSPVALP	PNIPLSIEIFHQPKL--	DKNPPDCLERFRMDLFTV	TVLSQVTFSSGSMVLEVRPL	158
XP_004049593.2	80	SFLSQEEDLAWAELRLQLSSPVDLPT	EGSLAIEIFHQPKPDT	EQASDSCLERFQMDLFTV	TVLSQVTFSLGSMVLEVRPL	159
XP_546146.2	81	SFLSQVEDLVWAEELRLQLSSPVALP	PGVLLSIEIFHQKPD	EAQDLAACQERLRMDLFTV	PLSHVTFSSGSMVLEVRPL	160
XP_001503787.1	81	SFLSQEEDLVSAELRLQLSSPLDL	PLDVPLSIEIFHQKPLEAD	QDPAYCLERLRMDLFTV	TQSQVTFSSGSMVLEVRPL	160
XP_004021483.4	81	SFLSQEEDLEWAEELRLQLSSPVALP	PNIPLSIEIFHQPKL--	DKNPPDCLERFRMDLFTV	TVLSQVTFSLGSMVLEVRPL	158
XP_521502.2	80	SFLSQEEDLAWAELRLQLSSPVDLPT	EGSLAIEIFHQKPNTE	EQASDSCLERFQMDLFTV	TVLSQVTFSLGSMVLEVRPL	159
XP_001108137.1	80	SFLSQEEDLAWAELRLQLSSPMDLPT	EGSLAIEIFHQKPDTE	EQASACFERFQMDLFTV	TVLSQVTFSSGSMVLEVRPL	159
XP_019668767.3	81	SFLSQAEEDLVWAEELRLQLASPL	LDLPGVLPVSEILHQKLP	DAEQDPADCLERLRMDSFTV	PLSQMFTSSGSMVLEVRPL	160
XP_005699204.2	81	SFLSQEEDLEWAEELRLQLSSPVALP	PNIPLSIEIFHQPKL--	DKNPPDCLERFRMDLFTV	TVLSQVTFSLGSMVLEVRPL	158
XP_004049593.2	80	SFLSQEEDLAWAELRLQLSSPVDLPT	EGSLAIEIFHQKPKPDT	EQASDSCLERFQMDLFTV	TVLSQVTFSLGSMVLEVRPL	159
XP_002820901.1	80	SFLSQEEDLAWAELRLQLSSPVDLPT	EGSLAIEIFHQKPKPDT	EQASDSCLERFQMDLFTV	TVLSQVTFSLGSMVLEVRPL	159
XP_031995113.1	80	SFLSQEEDLAWAELRLQLSSPVDLPT	EGSVAIKIFHQKPKPDT	EQASVSCLERFQMDLFTV	TVLSQVTFSLGSMVLEVRPL	159
NP_060525.3	160	SKWLKHPGALEKQMSRVAGECWRP	PTTP ATNVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
NP_038639.2	161	SKWLKDPRALEKQVSSRAEK	CWHQPYTPP [4] STNVL	-MLYSNRPEQRLGGATLLWEA	ESSWRAQEGQLSVERggWGR	240
NP_001099864.1	161	SKWLKDPRALEKQVSSQAGC	WHQSHQTP [4] STSVL	-MLYSNRPEQRLGGATLLWEA	ESSWRAQEGQLSVERsgWGR	240
NP_001192911.1	159	SKWLKHPGGLREQTS	SLAGECWRPPTTP VTDV	LLLLYSNLSPEQRLGGSTLLWEA	ESSWRAQEGQLSRE---RGT	232
XP_004049593.2	160	SKWLKHPGALEKQMSRVAGEC	WPQPTTP ATNVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
XP_546146.2	161	SKWLKHPGELEAQMSMAG	GCQRPPTTP VTSVLLV	LYSNLSPEQRLGGSTLLWEA	ESSWRAQEGQLSSE---RRR	234
XP_001503787.1	161	SKWLKHPGELEAQMS	SLAGECWPQPTTP VADVLLM	LYSNLSPEQRLGGSTLLWEA	ESSWRAQEGQLSRE---RDR	234
XP_004021483.4	159	SKWLKHPGGLRERMS	SLAGECWRPTTP VTDV	LLLLYSNLSPEQRLGGSTLLWEA	ESSWRAQEGQLSRE---RGT	232
XP_521502.2	160	SKWLKHPGALEKQMSRVAGEC	WRPPTTP ATNVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
XP_001108137.1	160	SKWLKHPGTLEKQMSRVAGEC	WRPPTTP ATDVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
XP_019668767.3	161	SKWLKHPGELEAQMS	SLAGECWPQPTTP VASALLV	LYSNLSPEQRLGGSTLLWEA	ESSWRAQEGQLSRE---RGR	234
XP_005699204.2	159	SKWLKHPGGLREQMS	SLAGECWRQAPTTP VTDV	LLLLYSNLSPEQRLGGSTLLWEA	ESSWRAQEGQLSRE---RGT	232
XP_004049593.2	160	SKWLKHPGALEKQMSRVAGEC	WPQPTTP ATNVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
XP_002820901.1	160	SKWLKHPGALEKQMSRVAGEC	WRPPTTP ATNVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
XP_031995113.1	160	SKWLKHPGALEKQMSRVAGEC	WLRPPTTP ATNVLLM	LYSNLSQEQRLGGSTLLWEA	ESSWRAQEGQLSWE---WGK	233
NP_060525.3	234	RHRRHHLPRDRS	QLCRVKFQVDFNLIG	SGSIIYPKQINAYRCE	GECPNPVGGEEFHPTNHAYIQSLLKRYQPHRVPSTCC	313
NP_038639.2	241	RQRRHHLPRDRS	QLCRVKFQVDFNLIG	SGSIIYPKQINAYRCE	GECPNPVGGEEFHPTNHAYIQSLLKRYQPHRVPSTCC	320

3092	NP_001099864.1	241	RQRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	320
3093	NP_001192911.1	233	RHRRYHV Q DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP A TCC	312
3094	XP_004049593.2	234	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	313
3095	XP_546146.2	235	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	314
3096	XP_001503787.1	235	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	314
3097	XP_004021483.4	233	RHRRYHV Q DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP A TCC	312
3098	XP_521502.2	234	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	313
3099	XP_001108137.1	234	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	313
3100	XP_019668767.3	235	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	314
3101	XP_005699204.2	233	RHRRYHV Q DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP A TCC	312
3102	XP_004049593.2	234	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	313
3103	XP_002820901.1	234	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	313
3104	XP_031995113.1	234	RHRRHHL P DRS Q LCR K V K F Q V D ENLIG S IIYPKQ N AYRCEGEC P NPVGE E F F HPTNHAYIQSLLKRYQPHRVP S TCC	313
3105				
3106				
3107	NP_060525.3	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3108	NP_038639.2	321	APVKT K PLS S LYVDN G RVLLE H HK D I V E E CGCL	354
3109	NP_001099864.1	321	APVKT K PLS S LYVDN G RVLLE H HK D I V E E CGCL	354
3110	NP_001192911.1	313	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	346
3111	XP_004049593.2	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3112	XP_546146.2	315	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	348
3113	XP_001503787.1	315	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	348
3114	XP_004021483.4	313	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	346
3115	XP_521502.2	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3116	XP_001108137.1	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3117	XP_019668767.3	315	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	348
3118	XP_005699204.2	313	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	346
3119	XP_004049593.2	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3120	XP_002820901.1	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3121	XP_031995113.1	314	APVKT K PLS S LYVDN G RVLLD H HK D I V E E CGCL	347
3122				
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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]

[NP_004953.1](#) 1 MAHVPARTS--PGP GPQLLLLL-PLFLLLRDVGSHRAPAWSALFAAADGLQGDRDLQRHPGDAATLGPQAQDM 74
[NP_665684.2](#) 1 MAPGPARTS--LGS --QLLFMV--PLLLLL-RGAGCGHRGWSLFAAAAGLQGDRLDQSPGDAAGALGPQAQDM 70
[NP_077351.1](#) 1 MAPGLARIS--LRS --QLLPLV--PLLLLL-RGAGCGHRVPSWSSLFAADSVDQRDLQSPGDAAGALGPQAQDI 70
[NP_001069635.1](#) 1 MARGPARTS--LGP GSQQLPLLLs1LLLLL--RDAGSHTAAARPFAAADGLAGDKNPQRSPGDVAAAQSPGAQDM 74
[XP_003133153.1](#) 1 MALGPATR--PEP GSL---LL1PLLLLL--RDAGSHTAPAWSAFPMAADSLAGDKDPQRSPGDTAATVGPQAQDM 71
[XP_853904.2](#) 1 MGRCPARTSqtPGR[7]RPLLL--LL--PLLLLLLRGAGDPPPEPA---PAPAARPAARTPRPRGALGDAASALGLGARD 78
[XP_001494823.3](#) 1 MARGPARTS--PGP GPQLLPLL--PLLLLLRDAGSHTVPARSALFAAADGLVGHKDAQWPLGDAAGALGPQAQDM 73
[XP_004021600.2](#) 1 MARGPARTS--LGP RSQQLPLLLs1LLLLL--RDAGSHTAAARPFAAADGLAGDKNPQRSPGDVAAAQSPGAQDM 74
[XP_001135281.2](#) 1 MAHVPARTS--PGP GPQLLLLL--PLFLLLRDVGSHRAPAWSALFAAADGLQGDRLDQHPGDAATLGPQAQDM 73
[XP_015002444.2](#) 1 MARVPTRTS--QGP GPQLLPLL--PLFLLLRDAGSHPAPAWSALFAAADGLQGDRLDQHPGDAATLGPQAQDM 73
[XP_003994192.2](#) 1 MARGPARTS--PGR RPQLLPLL--PLLLLLRDAGSHPAPAWSALFAAADGLAGIKDPPWRLGDAATLGPQAQDM 73
[XP_005699392.3](#) 1 MARGPARTS--LGP GSQQLPLLLs1LLLLL--RDAGSHTAAARPFAAADGLAGDKNPQRSPGDVAAAQSPGAQDM 74
[XP_004049420.1](#) 1 MAHVPARTS--PGP GPQLLLLL--PLFLLLRDVGSHRAPAWSALFAAADGLQGDRLDQHPGDAATLGPQAQDM 73
[XP_002820747.1](#) 1 MARVPARTS--PGP GFQLLLLL--PLFLLLRDVGSHRAPAWSALFAAADGLQGDRLDQHPGDAATLGPQAQDM 73
[XP_032026867.1](#) 1 MAHVPARTS--PGP GPQLLLLL--PLFLLLRDVGSHRAPAWSALFAAADGLQGDRLDQHPGDAATLGPQAQDM 73

[NP_004953.1](#) 75 VAVHMLRLEYEKYSRQGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRALEVLCCKPRA 154
[NP_665684.2](#) 71 VAIHMLRLEYEKYRRGAPPGGNTVRSFRARLEMDQKPVYFFNLQSMQDSEMLTAAFPHYSEPPRWRPRAREVFCCKPRA 150
[NP_077351.1](#) 71 VAVHMLRLEYEKYRRGAPPGGNTVRSFRARLDVIDQKPVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRAREVFCCKPRA 150
[NP_001069635.1](#) 75 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRAREVFCCKPRA 153
[XP_003133153.1](#) 72 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRAREVFCCKPRA 150
[XP_853904.2](#) 79 AAHMLRLEYEKYRRGAPPGGNTVRSFRARLDVTDQKAVYFFNLQSMQDSEMLTAAFPHYSEPPRWRPRAREVFCCKPRA 157
[XP_001494823.3](#) 74 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRAREVFCCKPRA 152
[XP_004021600.2](#) 75 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRAREVFCCKPRA 153
[XP_001135281.2](#) 74 VAVHMLRLEYEKYSRQGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRALEVLCCKPRA 153
[XP_015002444.2](#) 74 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRALEVLCCKPRA 153
[XP_003994192.2](#) 74 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTAAFPHYSEPPRWRPRAREVFCCKPRA 152
[XP_005699392.3](#) 75 VAVHMLRLEYEKYSRRGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRAREVFCCKPRA 153
[XP_004049420.1](#) 74 VAVHMLRLEYEKYSRQGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRALEVLCCKPRA 153
[XP_002820747.1](#) 74 VAVHMLRLEYEKYSRQGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRALEVLCCKPRA 153
[XP_032026867.1](#) 74 VAVHMLRLEYEKYSRQGARPGGNTVRSFRARLEVVDQKAVYFFNLQSMQDSEMLTATFHFYSEPPRWRPRALEVLCCKPRA 153

[NP_004953.1](#) 155 KNASGRPLPLGPPTRQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEERDPGV 234
[NP_665684.2](#) 151 KNASCRLLPGLPARLHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDGEKDPGV 230
[NP_077351.1](#) 151 KNASCRLLPGLPARLHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDGEKDLGV 230
[NP_001069635.1](#) 154 KNASCRLPPGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEKDTGV 233
[XP_003133153.1](#) 151 KNASCRLLPGLPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEKDPGV 230
[XP_853904.2](#) 158 RSASCRLPPGPPTRRHLLFRSLSQNTAAQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLWQALDPAGGAPGA 237
[XP_001494823.3](#) 153 KNASCRLLPGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDGEKDPGV 232
[XP_004021600.2](#) 154 KNASCRLPPGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEKDTGV 233
[XP_001135281.2](#) 154 KNASGRPLPLGPPTRQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEERDPGV 233
[XP_015002444.2](#) 154 KNASGRPLPLGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEERDPGV 233
[XP_003994192.2](#) 153 KNASCRLLPGLPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDGEKDPGV 232
[XP_005699392.3](#) 154 KNASCRLPPGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEKDTGV 233
[XP_004049420.1](#) 154 KNASGRPLPLGPPTRQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEERDPV 233
[XP_002820747.1](#) 154 KNASGRPLPLGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEERDPGV 233
[XP_032026867.1](#) 154 KNASGRPLPLGPPARQHLLFRSLSQNTATQGLLRGAMALAPPRLGLWQAKDISPIVKAARRDGEELLSAQLDSEERDPGV 233

[NP_004953.1](#) 235 PRPSYPYILVYANDLAISEPNSVAVTLQRYDPPFAGDFEPAAPNNSADPRVRRAAQATGPLQDNELPGLDERPPRA- 313
[NP_665684.2](#) 231 PRPSSHMPYILVYANDLAISEPNSVAVSLQRYDPPFAGDFEPGAAPNNSADPRVRRAAQVSKPLQDNELPGLDERPPAPAL 310

3198	NP 077351.1	231	PRPSSHMPYILVYANDLAISEPNSAVTLQRYDPPFAGDFEPGAAPNSSADPRVRRAAQVSKPLQDNELPGLDERPAPAL	310
3199	NP 001069635.1	234	PRLGPHAPYILYANDLAISEPNSAVTLQRYDPPFQAGDPEPGAAPNSSADPRVRRATQATGPLQNNELPGLDERPAQAP	313
3200	XP 003133153.1	231	PRPSPHAPYILYANDLAISEPNSAVTLQRYDPPFQAGDPEPGAAPNSSADPRVRRATQATGPLQDNELPGLDERPAHTP	310
3201	XP 853904.2	238	AGPSAPLPYLLVYADDLAIAEPNSVAGTLQRYDPLPAADPEPRAADNGSADPRVRRASQAPGPLQDNELPGLHERPGRMP	317
3202	XP 001494823.3	233	PRPSPHAPYILVYANDLAISEPNSAVTLQRYDPPFQAGDPEPGAAPNSSADPRVRRATQVTGPLQDNELPGLDERPAHGP	312
3203	XP 004021600.2	234	PRLGPHAPYILYANDLAISEPNSVAVTLQRYDPPFQAGDPEPGAAPNISADPRVRRATQAPGPLQNNELPGLDERPAHTP	313
3204	XP 001135281.2	234	PQPSPYAPYILVYANDLAISEPNSAVTLQRYDPPFQAGDPEPRGAPNNSADPRVRRAAQATGPLQDNELPGLDERPPRA-	312
3205	XP 015002444.2	234	PRPSPYAPYILVYANDLAISEPNSAVTLQRYDPPFQAGDPEPHAAPNSSADPRVRRAAQATGPLQDNELPGLDERPPRA-	312
3206	XP 003994192.2	233	SRPSPHAPYILVYADDLAISEPNSAVTLQRYDPPFQAGDPEPGAAPNSSADPRVRRATQATGPLQDNELPGLDERPAHAS	312
3207	XP 005699392.3	234	PRLGPHAPYILYANDLAISEPNSVAVTLQRYDPPFQAGDPEPGAAPNSSADPRVRRATQAPGPLQNNELPGLDERPAHTP	313
3208	XP 002820747.1	234	PRPSPYAPYILVYANDLAISEPNSAVTLQRYDPPFQAGDPEPRAAPNNSADPRVRRAAQATGPLQDNELPGLDERPPRA-	312
3209	XP 002820747.1	234	PRPSPYAPYILVYANDLAISEPNSAVTLQRYDPPFQAGDPEPRAAPNSSADPRVRRAAQATGPLQDNELPGLDERPPRA-	312
3210	XP 032026867.1	234	PRPSPYAPYILVYANDLAISEPNSAVTLQRYDPPFQAGDPEPRAAPNSSADPRVRRATQATGPLQDNELPGLDERPSRA-	312
3211				
3212	NP 004953.1	314	HAQH--FHKHQLWPSFFRALKPRGRKDRRKKQVEVFM-AASQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	390
3213	NP 665684.2	311	HAQN--FHKHEFWSSFFRALKPRGRKDRRKKQDQFTTaASSQVLDFFEKTMQKARRRQWDEPRVCSRRYLKVDADIG	388
3214	NP 077351.1	311	HAQH--FHKHEFWSSFFRALKPRGRKDRRKKQDQFTTpSSSQVLDFFEKTMQKARRRQWDEPRVCSRRYLKVDADIG	388
3215	NP 001069635.1	314	HAQH--YHKHELWPNPLRALKPRGRKDRRKKQDQVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	390
3216	XP 003133153.1	311	HTQH--YHKHELWPNPLRALKPRGRKDRRKKQDQVFM-TSSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	387
3217	XP 853904.2	318	PARQppRPRHELWRGFLRALKPRGRKDRRKKQDQVFM--pAASRVLDFFEKTMQKARRRQWDEPRVCSRRYLKVDADIG	395
3218	XP 001494823.3	313	HAQP--YHKHELWPSFFRALKSRGRKDRRKKQDQVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	389
3219	XP 004021600.2	314	HGQH--YHKHELWPSFFRALKPRGRKDRRKKQDQVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	390
3220	XP 001135281.2	313	HAQH--FHKHQLWPSFFRALKPRGRKDRRKKQVEVFM-AASQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	389
3221	XP 015002444.2	313	HAQH--FHKHQLWPSFFRALKPRGRKDRRKKQVEVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	389
3222	XP 003994192.2	313	HAQH--YHKHELWPGFFRALKPRGRKDRRKKQDQVFM-GSSRVLDFFEKTMQKARRKQWAEPRVCSRRYLKVDADIG	389
3223	XP 005699392.3	314	HGQH--YHKHELWPSFFRALKPRGRKDRRKKQDQVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	390
3224	XP 004049420.1	313	HAQH--FHKHQLWPSFFRALKPRGRKDRRKKQVEVFM-AASQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	389
3225	XP 002820747.1	313	PAQH--FHKHQLWPSFFRALKPRGRKDRRKKQVEVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	389
3226	XP 032026867.1	313	HAQH--FHKHQLWPSFFRALKPRGRKDRRKKQDQVFM-ASSQVLDFFEKTMQKARRKQWDEPRVCSRRYLKVDADIG	389
3227				
3228	NP 004953.1	391	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	470
3229	NP 665684.2	389	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	468
3230	NP 077351.1	389	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	468
3231	NP 001069635.1	391	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	470
3232	XP 003133153.1	388	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	467
3233	XP 853904.2	396	NEIIVLPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	475
3234	XP 001494823.3	390	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3235	XP 004021600.2	391	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGVPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	470
3236	XP 001135281.2	390	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3237	XP 015002444.2	390	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3238	XP 003994192.2	390	NEIILPKSFDAYYCAGVCEFFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3239	XP 005699392.3	391	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGVPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	470
3240	XP 004049420.1	390	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3241	XP 002820747.1	390	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3242	XP 032026867.1	390	NEIISPKSFDAYYCAGACEFMPMKIVRPSNHATIQSIVRAVGIVPGIPEPCCVDPKMNSLGLFLDENRNVVLKVPNN	469
3243				
3244	NP 004953.1	471	SVETCACR	478
3245	NP 665684.2	469	SVETCACR	476
3246	NP 077351.1	469	SVETCACR	476
3247	NP 001069635.1	471	SVETCACR	478
3248	XP 003133153.1	468	SVETCACR	475
3249	XP 853904.2	476	SVETCACR	483
3250	XP 001494823.3	470	SVETCACR	477
3251	XP 004021600.2	471	SVETCACR	478
3252	XP 001135281.2	470	SVETCACR	477
3253	XP 015002444.2	470	SVETCACR	477
3254	XP 003994192.2	470	SVETCACR	477
3255	XP 005699392.3	471	SVETCACR	478
3256	XP 004049420.1	470	SVETCACR	477
3257	XP 002820747.1	470	SVETCACR	477
3258	XP 032026867.1	470	SVETCACR	477
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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]		
NP_065685.1	1	MLRFLPDLAFSFL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFPVPIILKKIFQDREAAATTGVSRLDCYVKE	75
NP_032134.2	1	MQPYQRLLALGFLLLITLPWGTQSEFQDSDLQFLGLEKAPSPHRFPVPRVLRKIIRAREAAAASGASQDLCYVKE	76
NP_001103141.1	1	MQPSQRLLTLGFLLLITLARGQTSEFQDYDFLQFLGLKAPSPHRFPVPRVLRKIIRAREAAAASGASQDLCYVKE	76
XP_002687893.2	1	MLPSLAAIALCLLF-TLAFGQTLQFHEHVFLRFLGLDKVPSPKKFPVPSILKRIFQAQEEAASTGISKDLCYVKE	75
XP_003126560.2	1	[10]MLPSLPGALAFLL-TLTVGQTFPFQEHVFLQFLGLDKVPSPKKFPVPSILKRIFQDHEAAATSGLSQDLCYVKE	85
XP_534896.1	1	MIPSRVIALRLLL-TVALAQTFQFQEHVFLQFLGLDKVPSPKKFPVPSILKRIFQDQEEAAINGDSQDVCYIKD	75
XP_001493186.1	1	MIPSLPALALGLLL-TLALGQTFQFQENVFLQFLGLDKVPSPKKFPVPSILKRIFQDREAAATSGSGLDCSIKN	75
XP_004006951.3	1	MLPSLAAIALCLLY-TLALGQTLQFHEHVFLRFLGLDKVPSPKKFPVPSILKRIFQAQEEAASTGISKDLCYVKE	75
XP_508988.2	1	MLRFLPDLAFSFL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFPVPIILKKIFQDREAAATTGVSRLDCYVKE	75
XP_001112644.1	1	MLRFLPDLAFSFL-TLAFGQAVQFQEYVFLQFMGLDKAPSPQKFPVPIILKKIFQDREAAATTGVSRLDCYVKE	75
XP_003988425.1	1	MIPSLPALALGLLL-TVALAQTFQFQENVFLQFLGLDKVPSPKKFPVPSILKRIFQDREAAATSVDSRDFCYIKD	75
XP_005680965.2	1	MLPSLAAIALCLLY-TLALGQTLQFHEHVFLRFLGLDKVPSPKKFPVPSILKRIFQAQEEAASTGISKDLCYVKE	75
XP_004052681.2	1	MLRFLPDLAFSFL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFPVPIILKKIFQDREAAATTGVSRLDCYVKE	75
XP_002822896.1	1	MLRFLPDLAFSFL-ILALGQAVQFQEYVFLQFLGLDKAPSPQKFPVPIILKKIFQDREAAATTGVSRLDCYVKE	75
XP_032015430.1	1	MLRFLPDLAFSFL-ILALGHAVRFQEYVFLQFLGLDKAPSPQKFPVPIILKKIFQDREAAATTGVSRLDCYIK	75
NP_065685.1	76	LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSSYINLGPPELELALFLVQ-EPH	154
NP_032134.2	77	LGVRGNLLQLLPDQGFFLNTQKPFQDGSCLQKVLVFNLSAIKEKAKLTMQLTLDLGPSSYINLRPELVVALSVVQ-DRG	155
NP_001103141.1	77	LGVRGNLRLRLPDQGFFLYKSDLPQAS-CLQKLLYFNLSAIRDKEQLTMQLGLDLGPNSSYINLRPELELALSVLQ-EPR	155
XP_002687893.2	76	LGVRGNLRLRLPDQGSFLYSELSHAS-CLQKLLSFNLSAIGDEEQLTMQLGLDLGPNSSYINLRPELELALSVLQ-EPH	154
XP_003126560.2	86	LGVRGDVLRRLPDQGFFLYKSNHPQAASCLQKLLYFNLSAIVIKD-EQLTMQLALDLGPNSSYINLRPELELALSVLQ-EPH	163
XP_534896.1	76	LGISGNLRLRLDLKGLFLYKSKRPQASSCLQKFLYFNLSAIKDKELLTMQLGLDLGPNSSYINLRPELELALSVLQ-EPH	154
XP_001493186.1	76	LGVRGNVLRRLPDQGFFLYKSDLPQAS-CLQKLLYFNLSAIRDKEQLTMQLGLDLGPNSSYINLRPELELALSVLQ-EPR	153
XP_004006951.3	76	LGVRGNLRLRLPDQGSFFYSENLSHAP-CLQKLLSFNLSAIGDEEQLTMQLGLDLGPNSSYINLRPELELALSVLQ-EPH	154
XP_508988.2	76	LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSSYINLGPPELELALFLVQ-EPH	154
XP_001112644.1	76	LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSSYINLGPPELELALFLVQ-EPP	154
XP_003988425.1	76	FGVRGNVLRRLPDQGLFLYKSRKLSQASSCLQKFLYFNLSAIRKEQLTMQLGLDLGPNSSYINLRPELELALFLVQ-EPO	154
XP_005680965.2	76	LGVRGNLRLRLPDQGSFLYSENLSHAP-CLQKLLSFNLSAIGDEEQLTMQLGLDLGPNSSYINLRPELELALSVLQ-EPH	154
XP_004052681.2	76	LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSSYINLGPPELELALFLVQ-EPH	154
XP_002822896.1	76	LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSSYINLGPPELELALFLVQ-EPH	154
XP_032015430.1	76	LGVRGNVLRFLPDQGFFLYPKKISQASSCLQKLLYFNLSAIKEREQLTLAQLGLDLGPNSSYINLGPPELELALFLVQ-EPH	154
NP_065685.1	155	VWGQTPPKPGKMFVLRVSPWPQGVAVHFNLLDVAKDNDNPNRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRSLHASLL	234
NP_032134.2	156	VWGRSHPKVGRLLFLRSPVPGQGLQFNLQAGLKWSSNRLKNDLHLEILVKEDRYSRVTVQENPCDRLLRSLHASLL	235
NP_001103141.1	156	VWGRSHPKLGRLLVQKSVLPGQGLQFNLQGVVQDWNRRHQLKNDLHLEILVKEDRYSRVNAQLDNPCNLMHSLHASLL	235
XP_002687893.2	155	VIDQATPKMGKMTLQSVLPWPQGVVHFNLLDVAKR-NDNPHKNLGLFLEILVKGGRALGENFQLEGTCARLRSLHTSLL	233
XP_003126560.2	164	VWGQATPKGTGMFVLQSVWPQGVILRFLNLEAVKR-NNSSWKNLAFLEILVKGDALGENFQLEDTCARLRSLHASLL	242
XP_534896.1	155	GWGQSIKPKPKMLVLQSVWPQGVVHFNLLDVAKDNDNPNRKNLGLLLEILVKGNRDFVNFQLEDTCARLRSLHASLL	234
XP_001493186.1	154	VWGQSIKPKPKMFALQSVWPQGVVHFNLLDVAKDNDNPNRKNLGLFLEILVKGDRDFGVNFQLEDTCARLRSLHASLL	233
XP_004006951.3	155	GTDQSTLKMGRMFTLQSVLPWPQGVVHFNLLDVAKR-NDNPHKNLGLFLEILVKGGRASGENFQLEGTCARLRSLHTSLL	233
XP_508988.2	155	VWGQTPPKPGKMFVLRVSPWPQGVAVHFNLLDVAKDNDNPNRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRSLHASLL	234
XP_001112644.1	155	VWGQTPPKPGKMFVLRVSPWPQGVAVHFNLLDVAKDNDNPNRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRSLHASLL	234
XP_003988425.1	155	EGDQIPKPKGRMLVLQSVPRPQGVVHFNLLDVAKDNDNPNRKNLGLLLEILVKGNRDGVNFQLEDTCARLRSLHASLL	234
XP_005680965.2	155	VTDQSTPKMGRMFTLQSVLPWPQGVVHFNLLDVAKR-NDNPHKNLGLFLEILVKGGRASGENFQLEGTCARLRSLHTSLL	233
XP_004052681.2	155	VWGQTPPKPGKMFVLRVSPWPQGVAVHFNLLDVAKDNDNPNRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRSLHASLL	234
XP_002822896.1	155	VWGQTPPKPGKMFVLRVSPWPQGVAVHFNLLDVAKDNDNPNRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRSLHASLL	234
XP_032015430.1	155	VWGQTPPKPGKMFVLRVSPWPQGVAVHFNLLDVAKDNDNPNRKNFGLFLEILVKEDRDSGVNFQPEDTCARLRSLHASLL	234
NP_065685.1	235	VVTLNPDQC-HP-SRKRRAAIPVPLKSCKNLCHRHLQFVNRDLGHHKVIAPKGMANYCHGCEPFSLTISLNSSNYAF	312
NP_032134.2	236	VVTLNPKHChPS-SRKRRAAIVPKGFCRNFCHRHLQFVNRDLGHHKVIAPKGMANYCHGCEPFSMTTYLNSSNYAF	314
NP_001103141.1	236	VVTLNPKHChPS-SRKRRAAIPKGLCRNLCHRHLQFVNRDLGHHKVIAPKGMANYCHGDCPFTMTTYLNSSNYAF	314

3338	XP_002687893.2	234	VVTLHPEQC-RSpSRKRRRAAVSTSKASCKSLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3339	XP_003126560.2	243	VATLNPEQC-HPaSRKRRRAAFPAKVPCKNLCHRHQLFINRDLGHHKIIAPKGMANYCHGDCPPFLTISLNSSNYAF	321
3340	XP_534896.1	235	VVTLNPEQC-HPsSRKRRRAILFPKASCQNLCHRHQLFINRDLGHHKIIAPKGMANYCHGDCPPFLTISLNSSNYAF	313
3341	XP_001493186.1	234	VVTLNPEQC-HPsSRKRRRAIPAPNASCKNLCHRHQLFINRDLGHHKIIAPKGMANYCHGDCPPFLTISLNSSNYAF	312
3342	XP_004006951.3	234	VVTLHPEQC-QSpSRKRRRAAVSTSKAACKSLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3343	XP_508988.2	235	VVTLNPDQC-HS-SRKRRRAIPVPKVSCKNLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3344	XP_001112644.1	235	VVALNPDEC-PP-SRKRRRAIPVPKVSCKNLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3345	XP_003988425.1	235	VVTLHPEQC-HPsSRKRRRAIPAPKAPCRNLCHRHQLFINRDLGHHKIIAPKGMANYCHGDCPPFLTISLNSSNYAF	313
3346	XP_005680965.2	234	VVTLHPEQC-RSpSRKRRRAAVSTSKAACKSLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3347	XP_004052681.2	235	VVTLNPDQC-HP-SRKRRRAIPVPKVSCKSLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3348	XP_002822896.1	235	VVTLNPDHC-HP-SRKRRRAIPVPKVSCKNLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3349	XP_032015430.1	235	VVTLNPDQC-HP-SRKRRRAIPVPKVSCKNLCHRHQLFINRDLGHHKIIAPKGMANYCHGECPPFLTISLNSSNYAF	312
3350				
3351	NP_065685.1	313	MQALMHAVDPEIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3352	NP_032134.2	315	MQALMHMADPKVPKAVCVPTKLSPISELYQSDKNVILRHEDVVVDECGCG	366
3353	NP_001103141.1	315	MQALMHMADPRVPKAVCIPTKLSPISELYQDNEKNVILRHEDVVVDECGCG	366
3354	XP_002687893.2	313	MQALMHAVDPEVPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3355	XP_003126560.2	322	MQALMHAVDPQVPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	373
3356	XP_534896.1	314	MQALMHAVDPEIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	365
3357	XP_001493186.1	313	MQALMHAVDPQIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3358	XP_004006951.3	313	MQALMHAVDPEVPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3359	XP_508988.2	313	MQALMHAVDPKIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3360	XP_001112644.1	313	MQALMHAVDPEIPQAVCVPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3361	XP_003988425.1	314	MQALMHAVDPEIPQAVCVPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	365
3362	XP_005680965.2	313	MQALMHAVDPEVPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3363	XP_004052681.2	313	MQALMHAVDPEIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3364	XP_002822896.1	313	MQALMHAVDPEIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
3365	XP_032015430.1	313	MQALMHAVDSEIPQAVCIPTKLSPISELYQDNDNDNVILRHEDVVVDECGCG	364
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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]

NP_001483.3 1 MPPPQQPCGHLLLLL-ALLPSLPLTRAPVPPGPAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR 79
 NP_001156754.1 1 MLPVCHRFCDH---LLL-LLLLPSTTLAPAPASMGPAALLQVLGLPEAPRSVPTLRPVPVPMWRLFRRRDPQEARVGR- 75
 NP_001037705.1 1 MLPVCHRFCDH---LLL-LLLLPSTTLAPASLGPAAALLQVLGLPETPRSVPTLRPVPVPMWRLFRRRDPQEARVGR- 75
 XP_010804844.1 1 MPPLCRRPSRRVLLLLL-ALLPSSPPACAPAPPGPAALLQALGLPDVPRGAPESRPVPPVMWRLFRRRDHQPARDPR 79
 XP_013846750.2 1 MPSPCRR---ALLLLL-ALLPSSPLARAPAAPGPAALLRALGLSDAPRDAPTSRPVPPVMWRLFRRRDHQPARDPR 75
 XP_038284034.1 1 MPALRRPPGRRVLFLLL-ALLPSSPPARAPAPPGPAALLQALGLPDVHRGAPKRPVPPVMWRLFRRRDPQEARVGR 79
 XP_023481294.1 1 MPPRRPGRRVLFLLL-ALLPSSPPARAPAPPGPAALLQALGLRDAPRDAPTRPVPVPMWRLFRRRDPQESRNLN 79
 XP_027825180.1 1 MPPLCRRPGRQVLLLLL-ALLPSSPPACAPAPSGPAALLQALGLPDVPRGAPKSRPVPVPMWRLFRRRDHQPARDPR 78
 XP_016791031.1 1 MPPPQQPCGHLLLLL-ALLPSLPPTRAPVPPGPAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR 79
 XP_001115596.2 1 MLPPRQPGGQHLLLL-VLLPSSLPTTRAPVPPGPAALLQALGLRDAPQAGAPRLRPVPPVMWRLFRRRDPQETRSGSR 79
 XP_023103436.1 1 MPSPCRRPGRVLFLLL-ALLPSSPPARAPAPPGPAALLQALGLPDHRGAPTRPVPVPMWRLFRRRDPQEARVGR 79
 XP_017906949.1 1 MPPLCRRPGRQVLLLLL-ALLPSSPPACAPAPPGPAALLQALGLPDVPRGAPKSRPVPVPMWRLFRRRDHQPARDPR 78
 XP_030860111.1 1 MPPPQQPCGHLLLLL-ALLPSLPTTRAPVPPGPAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR 79
 XP_024094156.1 1 MPPPQQPCGHLLLLL-ALLPSSLPTTRAPVPPGPAALLQALGLRDEPQGAPRLRPVPPVMWRLFRRRDPQETRSGSR 79
 XP_032026077.1 1 MPPPQQPCGHLLLLL-ALLPSLPTTRAPVPPGPAALLQALGLRDAPQAGAPRLRPVPPVMWRLFRRRDPQETRSGSR 80

NP_001483.3 80 RTSPGVTLQPCHVEELGVAGNIVRHIIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA 157
 NP_001156754.1 76 -----PLRPCHVEELGVAGNIVRHIIPDSGLSSRPAPARTSGLCPEWTVVFDLSNVEPTERTRARLELRLEAeSE-DT 148
 NP_001037705.1 76 -----PLKPCHEVEELGVAGNIVRHIIPDSGLSSRIIPARTSGLCPEWTVVFDLSNVEPTERTRARLELRLEAeSE-DT 148
 XP_010804844.1 80 RMPPGATLRPCHVEELGVAGNIVRHIIPDRGAAARPEPASAAGQCPEWTVVFDLSAVEPAERPSQARLELRFEA-AE-AT 157
 XP_013846750.2 76 RTPPAAALRPCHVEELGVAGNIVRHIIPDRGAAARPEPASAAGQCPEWTVVFDLSTVEPAERPSQVRLERLFAA-EE-AS 153
 XP_038284034.1 80 RTPQGTTLRPCHVEELGVAGNIVRHIIPDRGAPTRPEPASAAGQCPEWTVVFDLSAVEPAERPSRARLELRFAA-AE-TA 157
 XP_023481294.1 80 RTPPGATLRPCHVEELGVAGNIVRHIIPDRGAPARPEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AE-TA 158
 XP_027825180.1 79 RMPPRATLRPCHVEELGVAGNIVRHIIPDRGAAARPEPASAAGQCPEWTVVFDLSAVEPAERPSQARLEVRFAA-AE-AT 156
 XP_016791031.1 80 RTSPGVTLQPCHVEELGVAGNIVRHIIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA 157
 XP_001115596.2 80 RMPSPGVTLQPCHVEELGVAGNIVRHIIPDRGAPTRASDPAASAVGHCPWTVVFDLSAVEPAERPSRARLELRFAA-AA-A- 156
 XP_023103436.1 80 RTPQGTTLRPCHVEELGVAGNIVRHIIPDRGAPTRPEPASAAGQCPEWTVVFDLSAVEPAERPSRARLEMRFAA-AA-AA 157
 XP_017906949.1 79 RMSPRATLRPCHVEELGVAGNIVRHIIPDRGAAARPEPASAAGQCPEWTVVFDLSAVEPAERPSQARLEVRFAA-AE-AT 156
 XP_030860111.1 80 RTSPGVTLQPCHVEELGVAGNIVRHIIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA 157
 XP_024094156.1 80 RTFPGVTLQPCHVEELGVAGNIVRHIIPDRGAPTRASEPASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA 157
 XP_032026077.1 81 RTSPGVTLQPCHVEELGVAGNIVRHIIPDRGAPTRASELASAAGHCPEWTVVFDLSAVEPAERPSRARLELRFAA-AA-AA 158

NP_001483.3 158 A--PEGGWELSAQAGQGAGADPGVLLRQLVLPALGPPVRAELLLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL 235
 NP_001156754.1 149 ----GGWELSVALLWADAHEH--PGPELLRVPAFP-GVLLRADLLGTAVANASVPTVRLALSLHPGATAACGRLEASL 220
 NP_001037705.1 149 ----RGWELSVALLAEAHEH--PGPELLRVPAFP-GLPLRADLLGTAVANASVPTVRLALSLHPGATAACGRLEASL 220
 XP_010804844.1 158 Ag-TTGGWELSVAPAGAGLG---PVGLRQVVTTLGQPVRAELLLGSIWARNASAPRSLRLTLALRHRTPAACARLAEASL 232
 XP_013846750.2 154 Ag-MAGSWELSVARAGSG-----PVLLRQAVTALGTPVRAELLLGAAWARNASAPRSLRLTLALRPRAPTVCARLAEASL 226
 XP_038284034.1 158 ----AGWELSLARAAGEGAGARPVLLRQAVTALGTPVRAELLLGAAWARNASAPRSLRLALALRPRAPAACARLAEASL 232
 XP_023481294.1 159 ----GGWELSVARAAGEAGVAG--PVLLRQAVTALGTPVRAELLLGAAWARNASAPRSLRLALALRPRAPPARAXAEASL 231
 XP_027825180.1 157 Ag-TTGGWELSVAPAGAGLG---RVGLRQVVTTLGQPVRAELLLGSIWARNASAPRSLRLTLALRHRTLAACARLAEASL 231
 XP_016791031.1 158 A--PEGGWELSAQAGQGAGADPGVLLRQLVLPALGPPVRAELLLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL 235
 XP_001115596.2 157 ---PEGGWELSVSAQAGQGAGADPGVLLRQLVLPALGPPVRAELLLGTAWARNASWPRSLRLALALRPRAPAACARLAEASL 233
 XP_023103436.1 158 Ee--PAGWELSVTQAAGEAVAG--PVLLRQAVTALGTPVRAELLLGAAWARNASAPRSLRLALALRPRAPPARAXAEASL 233
 XP_017906949.1 157 Ag-TTGGWELSVAPAGAGLG---RVGLRQVVTTLGQPVRAELLLGSIWARNASAPRSLRLTLALRHRTLAACARLAEASL 231
 XP_030860111.1 158 A--PEGGWELSAQAGQGAGADPGVLLRQLVLPALGPPVRAELLLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL 235
 XP_024094156.1 158 ---PEGGWELSAQAGQGAGADPGVLLRQLVLPALGPPVRAELLLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL 234
 XP_032026077.1 159 AaaPEGGWELSAQAVQAGADPGVLLRQLVLPALGPPVRAELLLGAAWARNASWPRSLRLALALRPRAPAACARLAEASL 238

NP_001483.3 236 LLVTLDPRLCHPLARPRRDAEPLVGGGPGGACRARRLYVS[REVG][HR][VIAPRG][LAN]YCQGCALPVALSGGGPPAL 315
 NP_001156754.1 221 LLVTLDPRLC-PLPRLRRHTEPRVEVGPVGTCTRRLHVS[REVG][HR][VIAPRG][LAN]FCQGCALPETLRGPGGPPAL 299

3442	NP_001037705.1	221	LLVTLDPRLC-PLPRSRHTEPRVGGGPVGTCTRRRLHVS	REVGHRRVIAPRG	LANFCQGTALPETLRGPGGPPAL	299
3443	XP_010804844.1	233	LLVTLDQRLCHPLARPRREAEPPVGGGSGGSCRARRLYVS	REVGHRRVIAPRG	LANYCQKCALPAVLSEPGGTPAL	312
3444	XP_013846750.2	227	LLVTLDPRLCHPLARPRREAEPAVGGGSGGACRTRRLYVS	REVGHRRVIAPRG	LANYCQKCALPAALSEPGGTPAL	306
3445	XP_038284034.1	233	LLVTLDPRLCHPLARPRREAEPAVGSPGGACRTRRLYVS	REVGHRRVIAPRG	LANYCQGCCLPATLSGPGGTPPL	312
3446	XP_023481294.1	232	LLATLDPRLCXPLARPRREAEPAVGGAPXGACRARRLYVS	REVGHRRVIAPRG	LANYCQGCALPAALSGPGGPPAL	311
3447	XP_027825180.1	232	LLVTLDQRLCHSLARPRREAEPPVGGGSGDSCRARRLYVS	REVGHRRVIAPRG	LANYCQKCALPAVLSEAGGAPAL	311
3448	XP_016791031.1	236	LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVS	REVGHRRVIAPRG	LANYCQGCALPVALSGSGGPPAL	315
3449	XP_001115596.2	234	LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVS	REVGHRRVIAPRG	LANYCQGCALPVTLSGSGGPPAL	313
3450	XP_023103436.1	234	LLVTLDPRLCHPLARPRREAEPSVGGSPGGACRTRRLYVS	REVGHRRVIAPRG	LANYCQGCCLPAALSGPGGTPPL	313
3451	XP_017906949.1	232	LLVTLDQRLCHSLARPRREAEPPVGGGSGDSCRARRLYVS	REVGHRRVIAPRG	LANYCQKCALPAVLSEAGGAPAL	311
3452	XP_030860111.1	236	LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVS	REVGHRRVIAPRG	LANYCQGCALPVALSGSGGPPAL	315
3453	XP_024094156.1	235	LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVS	REVGHRRVIAPRG	LANYCQGCALPVALSGSGGPPAL	314
3454	XP_032026077.1	239	LLVTLDPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVS	REVGHRRVIAPRG	LANYCQGCALPVALSGSGGPPAL	318
3455						
3456	NP_001483.3	316	NHAVLRALMHAAAP-GAADLPCCVPARLSPIS	LFFDNSDNVVLRC	EDVVDECGCR	372
3457	NP_001156754.1	300	NHAVLRALMHAAAPtPGAGSPCCVPERLSPIS	LFFDNSDNVVLRH	EDVVDECGCR	357
3458	NP_001037705.1	300	NHAVLRALMHAAAPtPGVGSPPCCVPERLSPIS	LFFDNSDNVVLRH	EDVVDECGCR	357
3459	XP_010804844.1	313	NHAVLRLTMHAAAP-GAAGLPCCVPARLSPIS	LFFDNSDNVVLRH	EDVVDECGCR	369
3460	XP_013846750.2	307	NHAVLRALMHSAAAP-GAAGLPCCVPARLSPIS	LFFDNDNVVLRH	EDVVDECGCR	363
3461	XP_038284034.1	313	NHAVLRALMHAAAP-GAAGLPCCVPARLSPIS	LFFDNSDNVVLRH	EDVVDECGCR	369
3462	XP_023481294.1	312	NHAVLRALMHAAAP-GAAGLPCCVPARLSPIS	LFFDNSDNVVLRH	EDVVDECGCR	368
3463	XP_027825180.1	312	NHAVLRLTMHAAAP-GAAGLPCCVPARLSPIS	LFFDNSDNVVLRH	EDVVAVDECGCR	368
3464	XP_016791031.1	316	NHAVLRALMHAAAP-GAADLPCCVPARLSPIS	LFFDNSDNVVLRC	EDVVDECGCR	372
3465	XP_001115596.2	314	NHAVLRALMHATTP-GAADLPCCVPARLSPIS	LFFDNSDNVVLRC	EDVVDECGCR	370
3466	XP_023103436.1	314	NHAVLRALMHAAAP-GAAGLPCCVPARLSPIS	LFFDNSDNVVLRH	EDVVDECGCR	370
3467	XP_017906949.1	312	NHAVLRLTMHAAAP-GAAGLPCCVPARLSPIS	LFFDNSDNVVLRH	EDVVAVDECGCR	368
3468	XP_030860111.1	316	NHAVLRALMHAAAP-GAADLPCCVPARLSPIS	LFFDNSDNVVLRC	EDVVDECGCR	372
3469	XP_024094156.1	315	NHAVLRALMHAAAP-GAADLPCCVPARLSPIS	LFFDNSDNVVLRC	EDVVDECGCR	371
3470	XP_032026077.1	319	NHAVLRALMHAAAP-GATDLPCCVPARLSPIS	LFFDNSDNVVLRC	EDVVDECGCR	375
3471						
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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]		
NP_001192.4	1	M--AGASRLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDELQPDQKDVSEHMLRLYDRYS---TVQAA-R	74
NP_775580.1	1	M--AGARGLLCLWLGYFCLNLAQGQRPNLHPLGLRETEPSDRATGGSPSPDLRPHDKVSEHMLWLYDRYSGSSRVQAT-R	77
NP_058801.1	1	M--AGARGLLCLWLGCFCVSLAQGQRPNLHPLGLRTESSDRMTGGGSPDLRPHDKVSEHMLWLYDRYSGSSNRAQAT-R	77
NP_001179197.1	1	M--AGARGLLHLWLSCVSLAQGQRLRQFPPELRVAVPADRAAGGGPESPLQPLDQVSEHMLRLYDRYSG-GRTEEA-R	76
NP_001193317.1	1	M--AAARALLPLWLGCFCVSLAQGLRRQFPPELRDAVPGHRAAGGGPDPPLQPLDPLSEHMLRLYDRYSYG-GASAEAR	77
XP_038299875.1	1	M--AGARGLLWLWLCFCVSLARAERPKPLQLHGAGSGDRAAGGGSPVLRPLDKVSEHMLRLYDRYSGgGGAERAE-R	77
XP_023493625.1	1	M--AGARRLLWLWLCFCVSLAQGERLKHQFPPELRVAVPADRAAGGGPESPLQPLDQVSEHMLRLYDRYSGSSGRAEAA-R	77
XP_027826928.1	1	M--AGARGLLHLWLSCVSLAQGQRLRQFPPELRVAVPADRAAGGGPESPLQPLDQVSEHMLRLYDRYSG-GGAEEA-R	76
XP_001144027.1	1	M--AGASRLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDELQPDQKDVSEHMLRLYDRYS---TVQAA-W	74
XP_001089525.2	1	MatAGASRLFLWLGCFCVSLAQGERPKPLRELRKAVPGDRTAGGGPDAELQPDQKDVSEHMLRLYDRYS---TVQAA-R	76
XP_006931098.2	1	M--AGALRLLCLWLGCFCVSLARGEGLTRVPEPHRAVPGDRTAGGGPVPVLRPHDKVSEHMLRLYDRYSGgGRAEAE-R	77
XP_005682010.3	1	M--AGARGLLHLWLSCVSLAQGQRLRQFPPELRVAVPADRAAGGGPESPLQPLDQVSEHMLRLYDRYSG-GGAEEA-P	76
XP_004038932.1	1	M--ARASRLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDELQPDQKDVSEHMLRLYDRYS---TVQAA-R	74
XP_002814965.1	1	M--AGASRLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDELQPDQKDVSEHMLRLYDRYS---TVQAA-R	74
XP_032019797.1	1	M--AGASRLFLWLGCFCVSLAQGERPKPPFPELRKAVPGDRTAGGGPDELQPDQKDVSEHMLRLYDRYS---TVQAE-R	74
NP_001192.4	75	TPGSLEGGSQPWRPRLREEGNTVRSFRAAAETLERKGLYIFNLTSLTKSENILSATLYFCIGELGNISLSCPVSQGGCSH	154
NP_775580.1	78	TPGSQPLG-----PQLRGGNTVRSFRAAAAGTPOKGLHTFNLTSLTKSENILSATLYFYVVELVNIISLSCPESQGGCSH	152
NP_058801.1	78	TPGSQPLG-----PQLRGGNTVRSFRAAAAGTLQRKGLHTFNLTSLTKSENILSATLYFYIGELVNTSVNCPESQGGCSH	152
NP_001179197.1	77	TPGNSERGSPSLRPQPLREEGNTVRSFRAGAAGMLENKELHI FNLTSLTKSENILSATLYFYIRELINISLSCPVSQECCH	156
NP_001193317.1	78	TPGSPEPGSPPLRPQPRREEGNTVRSFRAGAAGTLENKELHVFNLTSLTKSENILSATLYFYIGELINATLSCPASRGCSH	157
XP_038299875.1	78	ARGASERGSQPARPQPLREEGNTVRSFRGGAAGTGLSKGLHI FNLTSLTKSENILSATLYFYVVELVNIISLSCPESRGCSH	157
XP_023493625.1	78	TPGISERGSQSLRPQPLREEGNTVRSFRAGAAGTLESKGLHI FNLTSLTKSENILSATLYFYIGELINTLSLSCPVSQGGCSH	157
XP_027826928.1	77	TPGNSERGSPSLRPQPLREEGNTVRSFRAGAAGMLENKELHI FNLTSLTKSENILSATLYFYIRELINISLSCPVSQECCH	156
XP_001144027.1	75	TPGSLEGGSQPWRPRLREEGNTVRSFRAAAETLERKGLYIFNLTSLTKSENILSATLYFCIGELGNISLSCPVSQGGCSH	154
XP_001089525.2	77	TPGSLEGGSKPWRPQSLREEGNTVRSFRAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELNSSLSCPVSQGGCSH	156
XP_006931098.2	78	AQRSSERGSQPLRPPLREEGNTVRSFRAGASGTGLSKGLHI FNLTSLTKSENILSATLYFYIGELINISLSCPASRGCSH	157
XP_005682010.3	77	TPGTXBERGSPSLRPQPLREEGNTVRSFRAGAAGMLENKELHI FNLTSLTKSENILSATLYFYIRELINISLSCPVSQECCH	156
XP_004038932.1	75	TPGSLEGGSQPWRPQPLREEGNTVRSFRAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNISLSCPVSQGGCSH	154
XP_002814965.1	75	TPGSPEGGQLPWRPQPLREEGNTVRSFRAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNISLSCPVSQGGCSH	154
XP_032019797.1	75	TPGSLEGGSQPWRPQPRREEGNTVRSFRAAAETLERKGLYIFNLTSLTKSENILSATLYFYIGELGNISLSCPVSQGGCSH	154
NP_001192.4	155	HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSDVMAKSHRDIMSWLSKIDITQLLRKAKENEFLIGFNIITKGRQLPKRRLLP	234
NP_775580.1	153	HTQRQHIQIDLSAWILK--SNQSQLLGHLSDVVVRPYRDSVSWLSKIDITQLLRKAKQNEFLIGFNITRAHELPKRMLP	230
NP_058801.1	153	DSQRKHIQIDLSAWTLQ--SNQSQLLGHLSDVAKPHRDMSWLSKIDITQLLRKAKQDEFLIGFNITRAHELPKRMLL	230
NP_001179197.1	157	HAQRKHIQIDLSAWILKSSGNQSQLLGHLSDVGGKPHRDVFSWLSKIDITQLLRKAKENEFLIGFNIITKGRQLPKKMT	236
NP_001193317.1	158	HAQRKHIQIDLSAWVQLSRNQSQLLGHLSDVAKPHRDMSWLSKIDITQLLRKAKENEFLIGFNIITSRGHQLPKKVIP	237
XP_038299875.1	158	HAQRKHMQIDLSVSIKSDRNQSQLLGHLSDVAKSHRDFGSWLSKIDITQLLRKAKENEFLIGFNITKSGHQLPKKRLP	237
XP_023493625.1	158	HAQRKHIQIDLSAWILKSNRNQSQLLGHLSDVAKPHRDVFSWLSKIDITQLLRKAKENEFLIGFNITKSGHQLPKKMLP	237
XP_027826928.1	157	HAQRKHIQIDLSAWILKSSGNQSQLLGHLSDVGGKPHGDFVSWLSKIDITQLLRKAKENEFLIGFNIITKGRQLPKKMT	236
XP_001144027.1	155	HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSDVMAKSHRDIMSWLSKIDITQFLRKAENEFLIGFNIITKSGHQLPKRRLLP	234
XP_001089525.2	157	HAPRKHIQIDLSAWILKFNRNQSQLLGHLSDVMAKSHRDIMSWLSKIDITQFLRKAENEFLIGFNIITKSGHQLPKRMLP	236
XP_006931098.2	158	HAQRKHVLDLSAWILKSNRNQSQLLGHLSDVAKPHRDVFSWLSKIDITQLLRKAKENEFLIGFNITKSGHQLPKKMLP	237
XP_005682010.3	157	HAQRKHIQIDLSAWILKSSGNQSQLLGHLSDVGGKPHGDFVSWLSKIDITQLLRKAKENEFLIGFNIITKGRQLPKKMT	236
XP_004038932.1	155	HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSDVMAKSHRDIMSWLSKIDITQFLRKAENEFLIGFNIITKSGHQLPKRRLLP	234
XP_002814965.1	155	HAQRKHIQIDLSAWTLKFSRNQSQLLGHLSDVMAKSHRDIMSWLSKIDITQFLRKAENEFLIGFNIITKSGHQLPKRRLLP	234
XP_032019797.1	155	HAHSKHIQIDLSAWTLKFSRNQSQLLSHLSVDMAKSHQDIMSWSKIDITQFLRKAENEFLIGFNIITKSGHQLPKRRLLP	234
NP_001192.4	235	FPEPYILVYANDAAI SEPEVSVSSQLQHRNFPTGTVPKWDSHIRAAALSIERRK-KRSTGVLLPLQNNELPGAIEYQYKDE	313
NP_775580.1	231	FPEPYILVYANDAAI SEPEVSVSSQLQRHDFTAGTGPRLDSHVREALSVERRK-KRSTGILLPLQNNELPGAIEYQYKEE	309

3549	NP_058801.1	231	FPEPYILVYANDAAI CEPESVSVSSLQGRHRDFTAGTVPRLD SHVREALSVERRK-KRSTGILLPLQNNELPGA EYQYKEAG	309
3550	NP_001179197.1	237	SPEPYILVYANDAAI SEPEVSVSSLQGRHRNFPTGAVPKLDSQRSAPS IERRRrKRSTGVLLPLQNNELPGA EYQYKEDE	316
3551	NP_001193317.1	238	FPEPYILVYANDAAI SEPEVSVASLQGRHRNFAGAVPKLDRHLRAALS IERRR-KRSAGLLLPLQNNELPGA EYQYKEDG	316
3552	XP_038299875.1	238	FPEPYILVYANDAAI SEPEVSVSSLQGRHRNFATGTM PKLASHIRAALS IERRR-KRSAGVLLPLQNNELPGA EYQYREDG	316
3553	XP_023493625.1	238	FPEPYILVYANDAAI SEPEVSVSSLQGRHRNFPIGAVPKLDSHIRAALS IERRR-KRSTGVLLPLQNNELPGA EYQYKEEG	316
3554	XP_027826928.1	237	SPEPYILVYANDAAI SEPEVSVSSLQGRHRNFPTGAVPKLDSHRAALS MERRRrKRSTGVLLPLQNNELPGA EYQYKEDR	316
3555	XP_001144027.1	235	FPEPYILVYANDAAI SETESVSVSSLQGRHRNFPTGTVPKWDSHIRAALS IERRR-KRSTGVLLPLQNNELPGA EYQYKDE	313
3556	XP_001089525.2	237	FPEPYILIYANDAAI SEPEVSVSSLQGHQNFPTGTVPKWDSHIRAALS IERRR-KRSTGVLLPLQNNELPGA EYQYKDE	315
3557	XP_006931098.2	238	FPEPYILVYANDAAI SEPEVSVSSLQGRHRNFPIGAVPRPDGHIKAALS IERRR-KRSAGVLLPLQNNELPGA EYQYREDG	316
3558	XP_005682010.3	237	SPEPYILVYANDAAI SEPEVSVSSLQGRHRNFPTGAVPKLDSHRAALS MERRRrKRSTGVLLPLQNNELPGA EYQYKEDR	316
3559	XP_004038932.1	235	FPEPYILVYANDAAI SEPEVSVSSLQGRHRNFPTGTVPKWDSHIRAALS IERRR-KRSTGVLLPLQNNELPGA EYQYKDE	313
3560	XP_002814965.1	235	FPEPYILVYANDAAI SEPEVSVSSLQGHQNFPTGTVPKWDSHIRAALS IERRR-KRSTGVLLPLQNNELPGA EYQYKDE	313
3561	XP_032019797.1	235	FPEPYILVYANDAAI SEPEVSVSNLQGHQNIPTGTVPKWDSHIRAALS IERRR-KRSTGVLLPLQNNELPGA EYQYKDE	313
3562				
3563	NP_001192.4	314	VWEERKPYKTLQQAPEKSKNKKKQKRGPHRKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	393
3564	NP_775580.1	310	AWEERKPYKSLQTQPEKSRNKKKQKRGSHQKQTLQFDEQTLKKARRKQWV EPRNCARRYLKVD ADIGISEN IISPKS	389
3565	NP_058801.1	310	VWEERKPYKSLQTQPEKSRNKKKQKRGPHQKQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	389
3566	NP_001179197.1	317	VWEERKPYKTLQTQPPDKSKNKKKQKRGPPQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3567	NP_001193317.1	317	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3568	XP_0038299875.1	317	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3569	XP_023493625.1	317	VWEERKPYKTLQTQPEKSKNKKKQKRGPPQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3570	XP_027826928.1	317	VWEERKPYKTLQTQPPDKSKS KKKQKRGPPQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3571	XP_001144027.1	314	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	393
3572	XP_001089525.2	316	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	395
3573	XP_006931098.2	317	VWEERKPYKTLQTQAPEKTKNKKKQKRGPPQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3574	XP_005682010.3	317	VWEERKPYKTLQTQPPDKSKS KKKQKRGPPQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	396
3575	XP_004038932.1	314	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	393
3576	XP_002814965.1	314	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	393
3577	XP_032019797.1	314	VWEERKPYKTLQTQPEKSKNKKKQKRGPHQKSQTLQFDEQTLKKARRKQWI EPRNCARRYLKVD ADIGISEN IISPKS	393
3578				
3579	NP_001192.4	394	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	472
3580	NP_775580.1	390	DAFYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVSGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVDSCACR	468
3581	NP_058801.1	390	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVSGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVDSCACR	468
3582	NP_001179197.1	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3583	NP_001193317.1	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3584	XP_038299875.1	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3585	XP_023493625.1	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3586	XP_027826928.1	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3587	XP_001144027.1	394	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	472
3588	XP_001089525.2	396	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	474
3589	XP_006931098.2	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3590	XP_005682010.3	397	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	475
3591	XP_004038932.1	394	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	472
3592	XP_002814965.1	394	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	472
3593	XP_032019797.1	394	DAYYCSGACQFPMPKSLKPSNHATI QSVIRAVGVVPGIPEPCCVPEKMSSLS LFFDENKNVVLKV PNM TVESCACR	472
3594				
3595				

Lefty1/2

3597

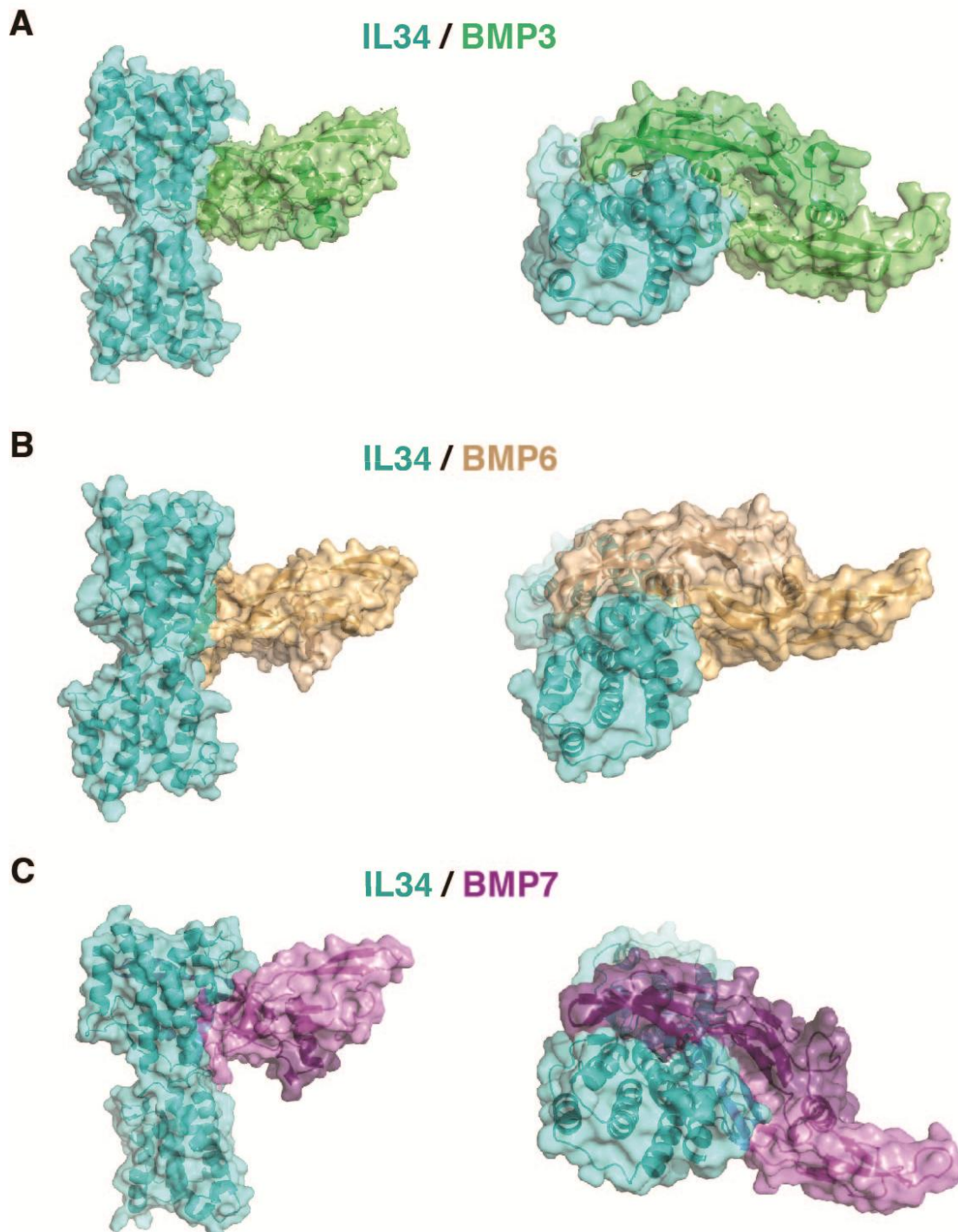
3598	NP_066277.1	left-right determination factor 1 preproprotein [Homo sapiens]
3599	NP_034224.1	left-right determination factor 1 preproprotein [Mus musculus]
3600	NP_001102550.1	left-right determination factor 1 precursor [Rattus norvegicus]
3601	XP_038527596.1	LOW QUALITY PROTEIN: left-right determination factor 1 [Canis lupus familiaris]
3602	XP_023488302.1	left-right determination factor 1 [Equus caballus]
3603	XP_001138066.1	left-right determination factor 1 [Pan troglodytes]
3604	XP_014970690.1	left-right determination factor 1 [Macaca mulatta]
3605	XP_023103692.2	left-right determination factor 1 [Felis catus]
3606	XP_004028529.2	left-right determination factor 1 [Gorilla gorilla gorilla]
3607	XP_002809441.3	left-right determination factor 1 isoform X1 [Pongo abelii]
3608	XP_031992497.1	left-right determination factor 1-like [Hylobates moloch]
3609	NP_003231.2	left-right determination factor 2 isoform 1 preproprotein [Homo sapiens]
3610	NP_796073.1	left-right determination factor 2 preproprotein [Mus musculus]
3611	NP_001007557.1	left-right determination factor 2 precursor [Rattus norvegicus]
3612	NP_001192972.2	left-right determination factor 2 precursor [Bos taurus]
3613	NP_001182275.1	left-right determination factor 2 precursor [Sus scrofa]
3614	XP_004013679.2	left-right determination factor 2 [Ovis aries]
3615	XP_514238.2	left-right determination factor 2 [Pan troglodytes]
3616	XP_028681962.1	left-right determination factor 2 [Macaca mulatta]
3617	XP_017915466.1	PREDICTED: left-right determination factor 2 isoform X1 [Capra hircus]
3618	XP_004028532.1	left-right determination factor 2 isoform X1 [Gorilla gorilla gorilla]
3619	XP_002809438.1	left-right determination factor 2 isoform X1 [Pongo abelii]
3620	XP_031992501.1	left-right determination factor 2 isoform X1 [Hylobates moloch]
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3624	NP_034224.1	1 MPFLWLCWALWALSIVLSREALTGEQILGSLIQQLQLDQPPVLDKADVEGMVIPS HVRTQYVALLQHS HASRSRGKRFSSQ 80
3625	NP_001102550.1	1 MRFLWLCWALWALFQVSPGEALTGEQVLGSLQLQLRDRPVLDKADVEGMVIPS HVRAQYVALLQHS HDRSRGKRFSSQ 80
3626	XP_038527596.1	1 MTPVWLCWALWALPLTGPGAALSGERILGGLRQLHLSQVPLDEGEVEALVTPAHVTAQYVALLRRSHGAHSRGKRFSSQ 80
3627	XP_023488302.1	1 MQPVWLCWALWALPLTGPGAALTEEQILGSLQLQLHLSSEMPALDQGDVGQLVPTHVRAQYVALLQRSHGAHSRGKRFSSQ 80
3628	XP_001138066.1	1 MQPLWLCWTLWVPLASPGAALTGEQLLGSLLRQLQLREVPTLDRADMEELVPTHVRAQYVALLQRSHGDCSRGKRFSSQ 80
3629	XP_014970690.1	1 MRPLWLCWALWVPLAGPGAALTGEQLLGSLLQLQLLSEAPVLDKADVEGMVIPS HVRAQYVALLQRSHGDRSRGKRFSSQ 80
3630	XP_023103692.2	1 MRPLWLCWALWALPLTGPGAALTGEQVRSLLRQLGLREAPVLDQRDVEGLVTPAHVRAQYVALLRRSHGAHSRRKRFSSQ 80
3631	XP_004028529.2	1 MQPLWLCWALWVPLASPGAALTGEQLLGSLLRQLQLREVPTLDRADMEELVPTHVRAQYVALLQRSHGDRSRGKRFSSQ 80
3632	XP_002809441.3	1 MQPLWLCWALWVPLASPGAALTGEQLLGSLLQLQLREVPTLDRAYMEELVPTHVRAQYVALLRRSHGDRSRGKRFSSQ 80
3633	XP_031992497.1	1 MRPLWLCWALWVPLAGPGAALTGEQLLGSLLRQLQLLSEAPVLDKADVEGMVIPS HVRAQYVALLQRSHGDRSRGKRFSSQ 80
3634	NP_003231.2	1 MWPLWLCWALWVPLAGPGAALTEEQLLGSLLRQLQLSEVPVLDKADVEGMVIPS HVRAQYVALLRRSHGDRSRGKRFSSQ 80
3635	NP_796073.1	1 MKSLWLCWALWVPLAGPGAAMTEEQVLSLLQLQLSQAPPLDSADVEEMAIPTHVRSQYVALLQGS HADRSRGKRFSSQ 80
3636	NP_001007557.1	1 MQSLWLCWTLWVPLAGPGAALTTEEQLVLSLLKQLQLSQAPVLDKADVEGMVIPS HVSSQYVALLQGS HADRSRGKRFSSQ 80
3637	NP_001192972.2	1 MRPLWLCWALWVPLAGPGAALTGEQLLGSLLQLQLLSEVPVLDKADVEGMVIPS HVRAQYVALLQRSHGDRSRGKRFSSQ 80
3638	NP_001182275.1	1 MRALWLCWALWALPLAGPGAALTEEQILGSLQLQLHLSSEVPALDKADVDGLVTPAHVRAQYVALLQRSHGARSRGKRFSSQ 80
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3648	NP_034224.1	81 NLREVAGRFLVSETSTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPRALRRQKRLSPHSARARVTIEWLRFREDGNSRT 160
3649	NP_001102550.1	81 NFREVAGRFLVSETSSHLLVVFGEQRLPPNSELVQAVLRLFQEPVPRALRRQKRLSPHSARARVTIEWLRFREDGNSRT 160
3650	XP_038527596.1	81 RFREVAGRWLATEASTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPRALRRRLERLSPHSARARVTIEWLQVRDDGNSRT 160
3651	XP_023488302.1	81 DFREVAGRLLGSDASRHLVVFAMEQRLPPNRELLQAVLRLFQEPVPEALRTHGRSPRSARARVTVEWLRVRDDGNSRT 160
3652	XP_001138066.1	81 SFREVAGRFLASEASTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPKAALHRRHGRSPRSARARVTVEWLRVRDDGNSRT 160
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3662	NP_001182275.1	81 NFREVAGRFLLEASTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPRALRRRERLSPRSARARVTQWLHVRDDGNSRT 160
3663	XP_004013679.2	81 NFREVAGRFLASEASTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPRALRRRERLSPRSARARVTQWLHVRDDGNSRT 160
3664	XP_514238.2	81 SFREVAGRFLASEASTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPKAALHRRHGRSPRSARARVTVEWLRVRDDGNSRT 160
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3669	XP_031992501.1	81 SFREVAGRFLASEASTHLLVVFGEQRLPPNSELVQAVLRLFQEPVPKAALHRRHGRSPRSARARVTVEWLRVRDDGNSRT 160

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3689 XP 028681962.1 161 SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPQPLLLQVSVQREHLGFLASGAHKLVRFAAQQ-AP--AG-LGEPQLE 236
3690 XP 017915466.1 161 ALIDSRLVSIHESGWKAFDVTEAVNFWQQLSRPQPLLLQVSVQREHLGFLASSAHLVRFAAQQ-PS--SGrQGEPQLE 237
3691 XP 004028532.1 161 SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPQPLLLQVSVQREHLGFLASGAHKLVRFAAQQ-AP--AG-LGEPQLE 236
3692 XP 002809438.1 161 SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPQPLLLQVSVQREHLGFLASGAHKLVRFAAQQ-AP--AG-LGEPQLE 236
3693 XP 031992501.1 161 SLIDSRLVSVHESGWKAFDVTEAVNFWQQLSRPQPLLLQVSVQREHLGFLASGAHKLVRFAAQQ-AP--AG-LGEPQLE 236
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3697 NP 001102550.1 239 LHTLDLKDYGAGNCDPEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLTYECVGSCLQLPESLTIKWFPLGPRQC 318
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3699 XP 023488302.1 238 LHSLDLGRYGAQGDCEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFKWFPLGPRQC 317
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3703 XP 004028529.2 237 LHTLDLGDYGAQGDCEAPMTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFKWFPLGPRQC 316
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3705 XP 031992497.1 237 LHTLDLGDYGAQGDCEAPMTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFKWFPLGPRQC 316
3706 NP 003231.2 237 LHTLDLDRYGAQGDCEAPMTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFNWFPLGPRQC 316
3707 NP 796073.1 239 LHTLDLKDYGAGNCDPEPVPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLTYECVGSCLQLPESLTIKWFPLGPRQC 318
3708 NP 001007557.1 237 LHTLDLKDYGAGNCDPEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLTYECVGSCLQLPESLTIKWFPLGPRQC 316
3709 NP 001192972.2 238 LHTLDLDRYGAQGDCEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFKWFPLGPRQC 317
3710 NP 001182275.1 238 LHTLDLDRYGAQGDCEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFKWFPLGPRQC 317
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3712 XP 514238.2 237 LHTLDLDRYGAQGDCEAPMTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFNWFPLGPRQC 316
3713 XP 028681962.1 237 LHTLDLDRYGAQGDCEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAVKWFPLGPRQC 316
3714 XP 017915466.1 238 LHTLDLDRYGAQGDCEAPVTEGTRCCRQETVVDGQMKKAENIVLEPPGLTYECVGTCTROPPEALAFKWFPLGPRQC 317
3715 XP 004028532.1 237 LHTLDLDRYGAQGDCEAPMTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFNWFPLGPRQC 316
3716 XP 002809438.1 237 LHTLDLDRYGAQGDCEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFKWFPLGPRQC 316
3717 XP 031992501.1 237 LHTLDLGDYGAQGDCEAPVTEGTRCCRQEMYIDGQMKKAENIVLEPPGLAYECVGTCTROPPEALAFNWFPLGPRQC 316
3718
3719 NP 066277.1 317 IASETDSLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3720 NP 034224.1 319 VASEMTSLFIIVSVKEGGRTRPQVVSIPNIRVQKCSASD GALIPR RLQP 368
3721 NP 001102550.1 319 VASEMTSLFIIVSIKEDGTRPQVVSIPNIRVQKCSASD GALIPR RLEP 368
3722 XP 038527596.1 319 VPSETSLFIIVTVKEGGRTRPQVVSIPNIRVQKCSASD GALIPR KLEP 368
3723 XP 023488302.1 318 IASETSLFIIVSVKEGGRTRPQVVSIPNIRVQKCSASD GALVPR KLEP 367
3724 XP 001138066.1 317 IASETDSLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3725 XP 014970690.1 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR GLQP 366
3726 XP 023103692.2 318 VASETSLFIIVGVKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLGP 367
3727 XP 004028529.2 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3728 XP 002809441.3 317 IASETASLFIIVGIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
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3730 NP 003231.2 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3731 NP 796073.1 319 VASEMTSLFIIVSVKEGGRTRPQVVSIPNIRVQKCSASD GALIPR GIDL 368
3732 NP 001007557.1 317 VASEMTSLFIIVSIKEDGTRPQVVSIPNIRVQKCSASD GALIPR GIDL 366
3733 NP 001192972.2 318 IASEATSLFIIVSIQEGGRLQPQVVSIPNIRVQKCSASD GALVPR KLEP 367
3734 NP 001182275.1 318 IASETSLFIIVSIQEGGRLQPQVVSIPNIRVQKCSASD GALVPR KLEP 367
3735 XP 004013679.2 318 IASETSLFIIVSIQEGGRLQPQVVSIPNIRVQKCSASD GALVPR KLEP 367
3736 XP 514238.2 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3737 XP 028681962.1 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3738 XP 017915466.1 318 IASETSLFIIVSIQEGGRLQPQVVSIPNIRVQKCSASD GALVPR KLEP 367
3739 XP 004028532.1 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3740 XP 002809438.1 317 IASETASLFIIVGIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3741 XP 031992501.1 317 IASETASLFIIVSIKEGGRTRPQVVSIPNIRVQKCSASD GALVPR RLQP 366
3742

3818	XP_511082.1	225	HSTGSVRPVRAQ[6]	242
3819	NP_001181288.1	225	HSTGLARPVRAQ[6]	242
3820	XP_006941782.1	225	RSPGPKTGPPAQ	236
3821	XP_017917158.1	223	RVLGPSAGPPTQ	234
3822	G3RBA4_GORGO	216	-----	216
3823	XP_002826665.1	225	HSTGSARPVRAQ[6]	242
3824	XP_032013754.1	225	NSTGSVRPVRAQ[6]	242

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Figure S16. Analysis in the BMP-TGFβ 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-TGFβ 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-TGFβ 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.



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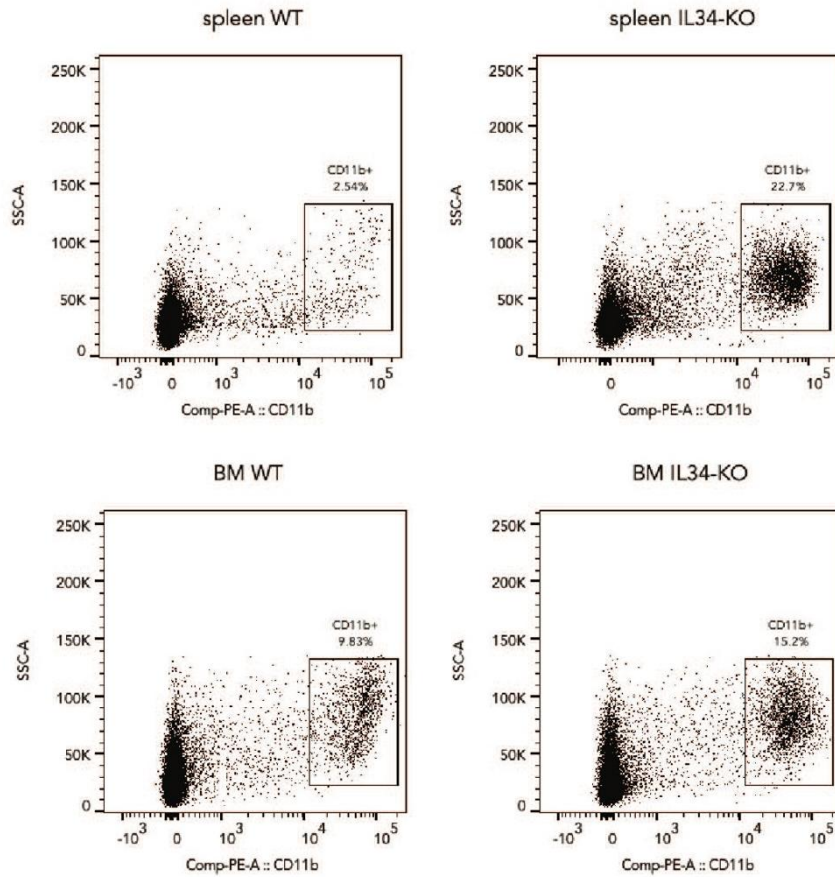
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Figure S17. Representative structures of IL34 binding to different BMP proteins. IL34 is displayed in cyan surface. (A) IL34 binding to BMP3 structure (lime color) as found PDB ID 2QCQ [80]. (B) IL34 binding to BMP6 structure (wheat color) as found 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.

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Supplementary figure 18

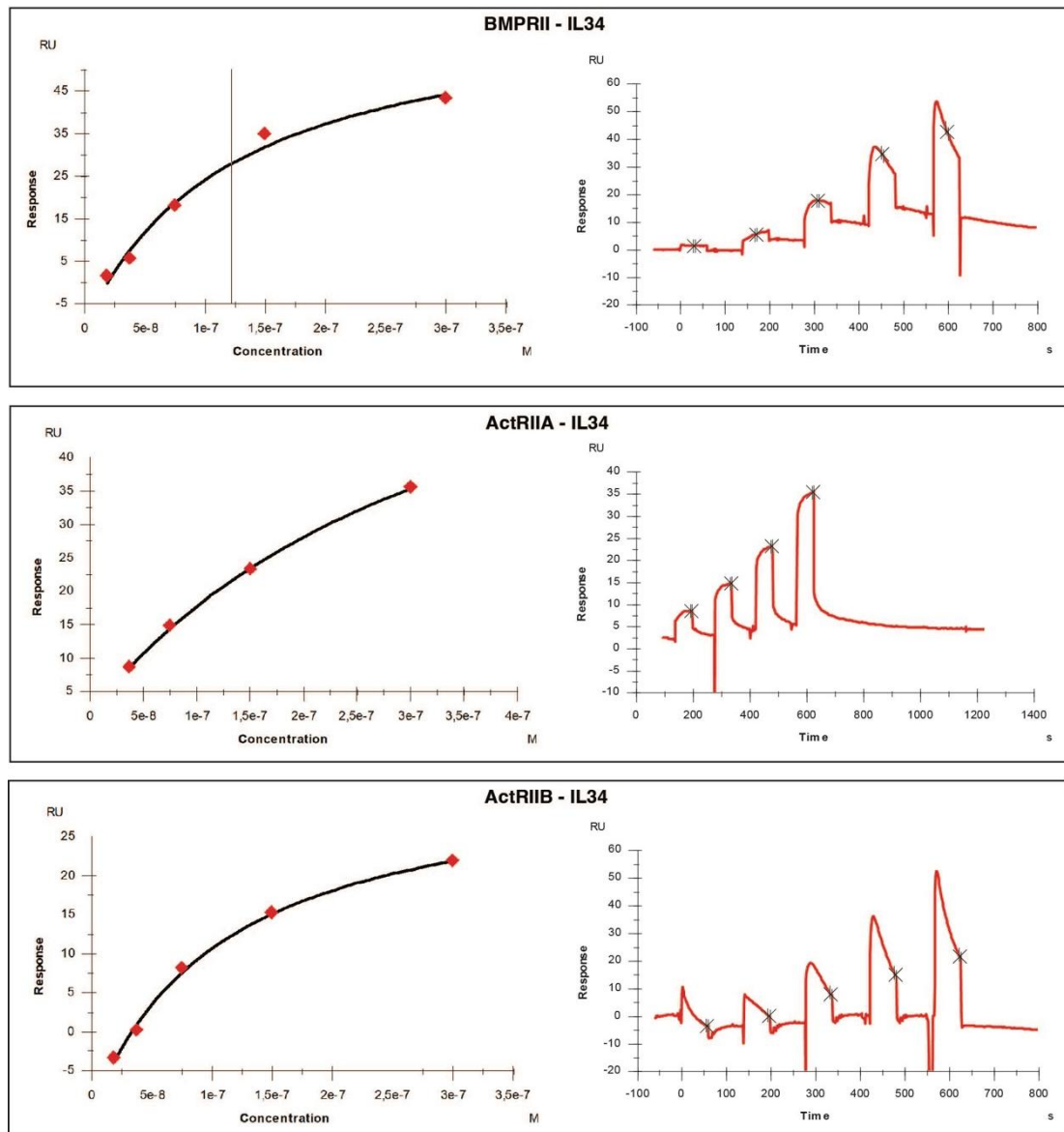


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Figure S18. FACS comparative analysis of the populations of CD11b monocytic cells in both the bone marrow and the spleen of *Il34*^{-/-} versus *Il34*^{+/+} mice. In *Il34*^{-/-} (IL34-KO) mice compared with *Il34*^{+/+} (WT) mice, significant increases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

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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

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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 BMPRI1A monomer (green) and one ACVR2A monomer (red) on a dimer of BMP2 (blue and orange).