

CLUSTAL W (1.83) multiple sequence alignment

AAP36398.1 - - - - DERKKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQIEEL
 NP_001665.1 - - - - DERKKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQIEEL
 1604249C - - - - DERKKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQCEEL
 C34223 - - - - DERKKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQLEEL
 AAP92420.1 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQIEEL
 NP_031524.2 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQIEEL
 BAA09095.1 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQIEEL
 NP_037044.1 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQKESEKLESVNAELKAQIEEL
 BAB84092.1 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQK - - - - - - - -
 AAP93895.1 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQK - - - - - - - -
 AAP93896.1 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQK - - - - - - - -
 NP_004015.2 - - - - DERKRRRERNKIAAA - KCRNKKKEK - - - - TECLQLQY - - - - - - - -
 NP_957258.1 - - - - NDRRKRRRERNKIAAA - KCRNKKKEK - - - - TDNLQKESEKLESINAELKAQIEEL
 AAF21148.1 - - - - EERRKRRREKNVAAA - RCRNKKKER - - - - TEFLQRESERLELMNAELKTQIEEL
 NP_569736.1 - - - - EERRKRRREKNVAAA - RCRNKKKER - - - - TEFLQRESERLELMNAELKTQIEEL
 BAB20088.1 - - - - EERRKRRREKNVAAA - RCRNKKKER - - - - TEFLQRESERLELMNAELKTQIEEL
 NP_446346.1 - - - - EERRKRRREKNVAAA - RCRNKKKER - - - - TEFLQRESERLELMNAELKTQIEEL
 NP_620473.1 - - - - EDRRRRRERNKIAAT - KCRMKKRER - - - - TQNLIKESEVLDTNVELKNQVRQL
 XP_321586.1 - - - - EDRRRRRERNKIAAT - KCRMKKRER - - - - TVNLINESETLDAQNRELKSQVSKL
 1FOSE - - - - KRRIRRERNKMAAA - KSRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 1FOSG - - - - RRIRRERNKMAAA - KSRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 AAG47951.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_CRIGR - - - - EKRRIRRERNKMAAA - KCWNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 XP_234422.2 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 AAA42348.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 NP_877587.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 NP_034364.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 NP_005243.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 CAB40144.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_FELCA - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_MESAU - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_PIG - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_RAT - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 CAA75757.1 - - - - ERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 E34223 - - - - RREKENPKERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_SHEEP - - - - ERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 NP_056890.1 - - - - EVKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 NP_955598.1 - - - - EVKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOSX_MSFR - - - - EVKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 FOS_MSVFB - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDKKSALQTEIANL
 1A02F - - - - MKRRIRRERNKMAAA - KSRNRRREL - - - - TDTLQAETDQLEDEKSALQTEIANL
 AAA66158.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEEEKSALQAEIANL
 AAN03532.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEEEKSALQAEIANL
 NP_990839.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEEEKSALQAEIANL
 FOS_AVINK - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEEEKSALQAEIANL
 AAO11836.1 - - - - EKRRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEEEKSALQTEIANL
 CAD56866.1 - - - - EKKRIRRERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEEEKAALEMEIANL
 BAB39769.2 - - - - EKKRVRERERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQNDIANL
 NP_991132.1 - - - - EKKRVRERERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQNDIANL
 BAC77043.1 - - - - EKKRVRERERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQNDITNL
 FOS_CYPKA - - - - EKKRVRERERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQNDIANL
 AAK58088.1 - - - - EKKRVRERERNKMAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSALQNDIASL
 FOS_FUGRU - - - - EKKRIRRERNKQAAA - KCRNRRREL - - - - TDTLQAETDQLEDEKSSLQNDIANL
 FOS_TETFL - - - - EKKRIRRERNKQAAA - KCRNRRREL - - - - TDSLQAETDQLEAEKSSLQNDIANL

BAC77045.1 - - - EKKRVRERNKQAAA - KCRNRRKEL - - - TDTLQGETDELEDEKSALQNDIANL
BAC77046.1 - - - EKKRVRERNKQAAA - KCRNRRKEL - - - TDTLQGETDELEDEKSALQNDIANL
A60089 - - - EKKRVRERNKMAAA - KCRNRRREL - - - TDTLQAETDDLEDQKSDLQAEIASL
AAC59780.1 - - - EEKRRIRRNKIAAA - KCRNRRREL - - - IDTLQAETDQEDEKSALQAEIDEL
CAD56865.1 - - - EEKRRIRRNKIAAA - KCRNRRREL - - - IDTLQAETDQEDEKSALQAEIDEL
AAC52888.1 - - - EERRRVRRERNKLAAA - KCRNRRKEL - - - TDFLQAETDKLEDEKSGLQREIEEL
AAH52917.1 - - - EERRRVRRERNKLAAA - KCRNRRKEL - - - TDFLQAETDKLEDEKSGLQREIEEL
AAP36227.1 - - - EERRRVRRERNKLAAA - KCRNRRKEL - - - TDFLQAETDKLEDEKSGLQREIEEL
NP_034365.1 - - - EERRRVRRERNKLAAA - KCRNRRKEL - - - TDFLQAETDKLEDEKSGLQREIEEL
NP_005429.1 - - - EERRRVRRERNKLAAA - KCRNRRKEL - - - TDFLQAETDKLEDEKSGLQREIEEL
NP_037085.1 - - - EERRRVRRERNKLAAA - KCRNRRKEL - - - TDFLQAETDKLEDEKSGLQREIEEL
CAD56862.1 - - - LERRRIRRNKMAAA - KCRNRRREL - - - TETLQNETDQEDEKSRLQKEIAGL
NP_005244.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
NP_032063.2 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
AAA61951.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
FRA2_MOUSE - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
AAC08718.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
AAC08724.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
AAC08727.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
AAC08730.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
NP_037086.1 - - - EEKRRIRRNKLA - - - TEKLQTETEELEEEEKSGLQKEIAEL
AAC08715.1 - - - EEKRRIRRNKLA - - - TEKLQAETEELEEEEKSGLQKEIAEL
FRA2_CHICK - - - EEKRRIRRNKLA - - - TEKLQAETEVLEEEEKSVLQKEIAEL
AAC59866.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDQLQAETEKELEQEKSGLQKEIADL
CAD56863.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TEMLQGETEKLEEEEKAELSEIAEL
AAF01350.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDRLQAETDQELEEKAELSEIAEL
XP_218419.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDRLQAETDQELEEKAELSEIAEL
NP_032062.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDRLQAETDQELEEKAELSEIAEL
FOSB_HUMAN - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDRLQAETDQELEEKAELSEIAEL
NP_006723.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDRLQAETDQELEEKAELSEIAEL
CAD56864.1 - - - EEKRRVRRERNKLAAA - KCRNRRREL - - - TDRLQTETDILEEEEKAELSEIAEL
A35847 - - - EQKRAVRRERNKQAAA - RCRKRRVDQ - - - TNELTEEEVQLEKRGESMRKEIEVL
NP_733306.1 - - - EQKRAVRRERNKQAAA - RCRKRRVDQ - - - TNELTEEEVQLEKRGESMRKEIEVL
NP_476587.1 - - - EQKRAVRRERNKQAAA - RCRKRRVDQ - - - TNELTEEEVQLEKRGESMRKEIEVL
XP_318333.1 - - - EEKRRIRRNKQAAA - RCRRRREDH - - - TNELVDETDLQLEKKRQSLAQEIQQL
NP_504557.1 - - - DDKRLKRRQRNKEAAA - RCRQRRIIDL - - - MKELQDQVNDFKNSNDKMAECNNI
T31799 - - - DDKRLKRRQRNKEAAA - RCRQRRIIDL - - - MKELQDQVNDFKNSNDKMAECNNI
CAE64529.1 - - - DDKKLKRRQRNKEAAA - RCRQRRIIDL - - - MKELQDQVNGFKHLNDKKTSDINDL
1GD2 - - - QEPSSKRKAQNRAAQR - AFRKRKEDH - - - LKALETQVVTLKELHSSTTLENDQL
BAA87082.1 - - - QEPSSKRKAQNRAAQR - AFRKRKEDH - - - LKALETQVVTLKELHSSTTLENDQL
NP_593662.1 - - - QEPSSKRKAQNRAAQR - AFRKRKEDH - - - LKALETQVVTLKELHSSTTLENDQL
S15664 - - - QEPSSKRKAQNRAAQR - AFRKRKEDH - - - LKALETQVVTLKELHSSTTLENDQL
CAB91681.2 - - - TEPSSKRKAQNRAAQR - AFRERKEKH - - - LKDLETKVEELKKISETANHENEIL
XP_323224.1 - - - TEPSSKRKAQNRAAQR - AFRERKEKH - - - LKDLETKVEELKKISETANHENEIL
EAA62093.1 - - - SEPTSKRKAQNRAAQR - AFRERKEKH - - - LKDLEAKVEELQKASADSANQENGLL
XP_388976.1 - - - SEPSSKRKAQNRAAQR - AFRERKEKH - - - LKDLETKVDELEKASQAANHENSML
EAA47389.1 - - - KRKAQNRAAQR - AFRERKERH - - - VKDLEAKLADLEAAQQQAATENEKL
XP_329184.1 - - - TPAQSRRKAQNRAAQR - AFRERKERH - - - VKELENRLQLEEEAQVTRSENEKL
EAA60905.1 - - - TPAQSRRKAQNRAAQR - AFRERKERH - - - VRDLEEKVSNLQQESSNLADNERL
EAK95559.1 - - - EELQMKRKAQNRAAQR - AFRERKESK - - - LKELEAKLLASEEERQKLLDELEQI
EAK95697.1 - - - EELQMKRKAQNRAAQR - AFRERKESK - - - LKELEAKLLASEEERQKLLDELEQI
FCR3_CANAL - - - EELQMKRKAQNRAAQR - AFRERKESK - - - LKELEAKLLASEEERQKLLDELEQI
NP_011854.1 - - - DDSKAKKKAQNRAAQR - AFRERKEAR - - - MKELQDKLLESERNRQSLKEIEEL
NP_982964.1 - - - EKKKAQNRAAQR - AFRERKEAR - - - LRELEQKLNKESEQNRDALFREVEQL
AAB29937.1 - - - SEAKSRRTAQNRAAQR - AFRDRKEAK - - - MKSLQERVELLEQKDAQNKTTFDNL
NP_010711.1 - - - SEAKSRRTAQNRAAQR - AFRDRKEAK - - - MKSLQERVELLEQKDAQNKTTFDNL
AAA34463.1 - - - SEAKSRRTAQNRAAQR - AFRDRKEAK - - - MKSLQERVELLEQKDAQNKTTFDNL

NP_068608.2 RIKVERKRLRNRLAAT - KCRKRKLER - - - IARLEDKVCTLKAENAGLSSTAGLL
AAH09465.1 RIKVERKRLRNRLAAT - KCRKRKLER - - - IARLEDKVCTLKAENAGLSSTAGLL
AAF75552.1 RIKVERKRLRNRLAAT - KCRKRKLER - - - IARLEDKVCTLKAENAGL - - -
AAH53154.1 RIKAERKRLRNLLAAT - KCRRRKLER - - - IARLEEKVKVLKSDNAGLSNTASVL
JUNB_CYPCA RIKAERKRLRNRLAAT - KCRKRKLER - - - ISRLEEKVKVLKNDNAGLSNTASVL
AAH53234.1 RIKAERKRLRNRLAAT - KCRRRKLER - - - ISRLEDKVVLKSDNAGLSSTASLL
CAD56858.1 RIKAERKRLRNRIAAS - KCRRRKLER - - - ISRLEDKVVLKTDNAGLSNTASLL
CAD56857.1 RIKAERKMRMRNRVAAS - KCRKRKLER - - - IARLEDRVKNLKSQNTELVSSANVL
NP_476586.1 KIKLERKRQRNRVAAS - KCRKRKLER - - - ISKLEDRVVKVLKGENVDLASIVKNL
TVFJJD KIKLERKRQRNRVAAS - KCRKRKLER - - - ISKLEDRVVKVLKGENVDLASIVKNL
XP_316420.1 RIKLERKRRLRNRAAS - KCRKRKLER - - - ISKLEDRVKELKAQNAELGGVVCNL
CAE59807.1 KKLERKRARNRQAAS - KCRQKKMDR - - - IKELEDQVLHEKHRGQRQLDAELVEL
NP_495947.1 KKLERKRARNRQAAT - KCRQKKMDR - - - IKELEEQVLHEKHRGQRQLDAELVEL
A34785 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
AAA40394.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
AAH42210.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
B42026 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
A39429 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
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AAB64016.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
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ATF2_HUMAN DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
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C42026 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
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AAA35951.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
NP_001871.2 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
NP_033845.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
NP_112280.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
BAC29065.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQ - - -
NP_990235.1 DEKRRKFLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQNEVTLL
1604249B DEKRRKVLERNRAAAS - RCRQKRKVW - - - VQSLEKKAEDLSSLNGQLQSEVTLL
JC4028 DEKRSKIIQRNRAAAS - RCRQKRKVW - - - VQSLEKKADELISLNGYLQNEVTLL
ATF7_HUMAN DERRQRFLERNRAAAS - RCRQKRKLW - - - VSSLEKKAEEELTSQNIQLSNEVTLL
NP_006847.1 DERRQRFLERNRAAAS - RCRQKRKLW - - - VSSLEKKAEEELTSQNIQLSNEVTLL
NP_666177.1 DERRQRFLERNRAAAS - RCRQKRKLW - - - VSSLEKKAEEELTSQNIQLSNEVTLL
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XP_235694.2 DERRQRFLERNRAAAS - RCRQKRKLW - - - VSSLEKKAEEELTSQNIQLSNEVTLL
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I78877 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
NP_004895.1 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
NP_878901.1 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
NP_878902.1 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
AAH29022.1 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
NP_766316.1 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
AAH59400.1 DERRRKFLERNRAAAT - RCRQKRKVW - - - VMSLEKKAEEELTQTNMQLQNEVSML
NP_594500.1 DEKRRRILERNRIAAS - KFRQKKKEW - - - IKELEQTANAAFEQSKRLQLLSQL
NP_595707.1 DMKRRRFLERNRIAAS - KCRQKKKLW - - - TQNLEKTAHIACEQSKALRILVSQL
XP_327898.1 DHKRNFLERNRLAAS - KCREKKKLY - - - TQELEGTKINLEARNVSLQREYSIL
EAA58248.1 DDKQEKRTRARNRLAAS - KCRQKKKEQ - - - NHMLETRYEQEKMKNELRTTVNSL
XP_389177.1 SAKREKFLKRNRIAAS - KCRQKKQQ - - - NEALE - - - EHLCR - - -
CAC18235.2 EEKRKNFLERNRVAAL - KCRQRKKQW - - - LANLQQKVEMFSSENDALTATITQL
XP_326838.1 - - - - - RVAAL - KCRQRKKQW - - - LANLQQKVEMFSSENDALTATITQL
XP_390318.1 EEKRKNFLERNRVAAL - KCRQRKKQW - - - LANLQTKVEMFSTENDALTQAQITQL
CAD1519.1 EEKRKNFLERNRVAAL - KCRQRKKQW - - - LANLQNKVEMYSSENDALTQAQITQL
EAA57243.1 EEKRKNFLERNRVAAL - KCRQRKKQW - - - LANLQSKVEMYGAENENLTAQIGQL

AAH67956.1 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
NP_989781.1 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
S20955 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
S22298 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
A35663 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
A40120 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
AAB64015.1 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
NP_604392.1 - - - - ARKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLKNQNKTLIEELKAL
NP_957203.1 - - - - TRKREVRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
BAC20140.1 - - - - SRKRELRLLNKREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKAL
NP_031523.2 - - - - QLRREIRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKTL
XP_204339.1 - - - - QLRREIQLMKNREAAR - ECRRKKKEY - - - VKCLKNRVAVLENQNKTLIEELKTL
ATF1_MOUSE - - - - QLRREIRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKTL
BAB26930.1 - - - - QLRREIRLMKNRGAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKTL
CAC15058.1 - - - - QLKREIRLMKNREAAR - ECRRKKKEY - - - VKCLENRV - - - -
NP_005162.1 - - - - QLKREIRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKTL
XP_235657.1 - - - - QLKREIRLMKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKTL
NP_956017.1 - - - - QMKREIRLAKNREAAR - ECRRKKKEY - - - VKCLENRVAVLENQNKTLIEELKTL
B37944 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
C37944 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
JC5602 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
JC6135 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
BAA03564.1 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
BAA03565.1 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
CREM_HUMAN - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
CREM_MOUSE - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
NP_059030.1 - - - - TRKRELRLMKNREAAK - ECRRRKKEY - - - VKCLESRVAVLEVQNKKLIEELET
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- - - - EDKVKKRKESENRESAR - RSRSRKAAR - - - LKDLLEEVSLLRVENSSLRRLADA
- - - - AEKVNKRKESENRESAR - RSRSRKAH - - - TKELEEVSVSLLRVANNSLMRHLADV
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- - - - DDRKRKRMESENRESAK - RSRMRKQRH - - - IDNLKDEANRLGLENRELANRL--
- - - - DERKRKRMESENRESAK - RSRMRKQSH - - - IDNLREQNRDLENRELGNRLRV
- - - - ERRQRKRVSNRLSAR - RSRARKQQR - - - LEELRGESARLRAENRELAHLHAV
- - - - RRRRLRRKISNRESAR - RSRARRRQR - - - VEELERAADELRAERRALASRLDAT
- - - - DERRLRRKISNRESAR - RSRARKQRH - - - LDELARAERLRCNRELAAR--
- - - - DERKRKRMLSNRESAR - RSRARKQQR - - - LEELIAEAARLQAENARVEAQIGAY
- - - - DERKRKRMLSNRESAR - RSRARKQQR - - - LEELIAEAARLQAENARVEAQIGAY
- - - - DERKRKRMLSNRESAR - RSRARKQQR - - - LEELVAEVARLQAENAATQARTAAL
- - - - THRREKRLSNRESAR - RSRLRKQKH - - - LDELVQEVARLQADNARVAAR--
- - - - THRREKRLSNRESAR - RSRLRKQKH - - - LDELVQEVARLQADNARVAARARDI
- - - - DNRREKRLSNRESAR - RSRLRKQKH - - - LDELVQEVARLKAENARVLARANDI
- - - - EERKRKRKESNRLSAQ - RSRARKQQ - - - LDELAGQVAALRARGAL-----
- - - - DERKHRMISNRESAR - RSRMRKQKH - - - LDELWSQVVRRLRTENHNLIDKLNHM
- - - - DERKHRMISNRESAR - RSRMRKQKH - - - LDELWSQVVRRLRTENHNLIDKLNHM
- - - - DERKQRRMISNRESAR - RSRMRKQRH - - - LDELWSQVIRLRTDNHCLMDKLN
- - - - DERKQRRMISNRESAR - RSRMRKQRH - - - LDELWSQVIRLRTDNHCLMDKLN
- - - - NERKQRRMISNRESAR - RSRMRKQRH - - - LDELWSQVMWLRIENHQLLDKLN
- - - - NERKQRRMISNRESAR - RSRMRKQRH - - - LDELLSQVAWLSENHQLLDKLN
- - - - NERKQKRKISNRESAR - RSRMRKQRQ - - - VDELWSQVMWLRDENHQLLRKLN
- - - - NERKQKRKISNRESAR - RSRMRKQRQ - - - VDELWSQVMWLRDENHQLLRKLN
- - - - NERKRRKVSNRESAR - RSRMRKQRH - - - MEELWSMLVQLINKNSLVDLSQA

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- - - - EERRRRMVSNRESAR - RSRMRKQRQ - - - LSELWAQVEHLRGANRRLDELNR
- - - - DERKKRRLVSNRESAR - RSRVRKQR - - - LDELSSQVSELRTDNQRLLVELNH
- - - - EERRARRMVSNRESAR - RSRMRKKQ - - - IEELQQQEQLMMNLHSEKVINL
- - - - EERRARRMVSNRESAR - RSRMRKKQ - - - IEELQQQEQLMMNLHSEKVINL
- - - - EKRLRRMASNRESAR - RTRMRERMM - - - KEGLQMVKQLMAYNQFLYNKYISL
- - - - EKRLRRMASNRESAR - RTRMRERMM - - - KEGLQMVKQLMAYNQFLYNKYISL
- - - - NVKRVKRMLSNRESAR - RSRRRKQAH - - - LSELETQVSQRLVENSKLMKGTDV
- - - - NVKRVKRMLSNRESAR - RSRRRKQAH - - - LSELETQVSQRLVENSKLMKGTDV
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- - - - NVKRVKRMLSNRESAR - RSRRRKQAH - - - LSELETQVSQRLVENSKLMKGTDV
- - - - DAKRVRRMLSRESAR - RSRRRKQAH - - - LTELETQVSQRLVENSSLKRLTDI
- - - - DAKRVRRMLSRESAR - RSRRRKQAH - - - LTELETQVSQRLVENSSLKRLTDI
- - - - DAKRVRRMLSRESAR - RSRRRKQAH - - - MTELETQVSQRLVENSSLKRLTDI
- - - - DAKRVRRMLSRESAR - RSRRRKQAH - - - MTELETQVSQRLVENSSLKRLTDI
- - - - VSNRESAR - RSRKRKQAH - - - LADLESQVDQLRGENASLFQQLTDA
- - - - DVKRVRRMVSNRESAR - RSRKRKQAH - - - LADLESQVDQLRGENASLFQQLTDA
- - - - DVKRVRRMVSNRESAR - RSRKRKQAH - - - LADLESQVDQLRGENASLFQQLTDA
- - - - DVKRMRRMVSNRESAR - RSRKRKQAH - - - LADLETQVDQLRGENASLFQQLTDA
- - - - DVKRMRRMVSNRESAR - RSRKRKQAH - - - LADLETQVDQLRGENASLFQQLTDA
- - - - ETKRIRRMVSNRESAR - RSRRRKQAO - - - LSELESQVEQLKGENSSLFKQLTES
- - - - DVKRARRMLSRESAK - RSRRRKQEQ - - - MNEFDTQVGQLRAEHSTLINRLSDM
- - - - DVKRARRMLSRESAR - RSRRRKQEQ - - - MNEFDTQVGQLRAEHSTLINRLSDM
- - - - DVKRARRMLSRESAR - RSRRRKQEQ - - - MNEFDTQAN - - -
- - - - DVKKSRRMLSRESAR - RSRRRKQEQ - - - TSDLETQVNDLKGEHSSLKQLSNM
- - - - DVKKSRRMLSRESAR - RSRRRKQEQ - - - TSDLETQVNDLKGEHSSLKQLSNM
- - - - DVKKSRRMLSRESAR - RSRRRKQEQ - - - TSDLETQVNDLKGEHSSLKQLSNM
- - - - DLKRIRRMNSNRESAK - RSRRRKQEY - - - LVDLETQVDSLKDNSTLYKQL - -
- - - - AMQRQKRMINKRESAA - RSRERKQAY - - - IAELESVTQLEEEAKMFKEQEEQ
- - - - AMQRQKRMINKRESAA - RSRERKQAY - - - IAELESVTQLEEEAKMFKEQEEQ
- - - - AMQRQKRMINKRESAA - RSRERKQAY - - - IAELESVTQLEEEAKMFKEQEE -
- - - - AMQRQKRMINKRESAA - RSRERKQAY - - - IAELEAQVALEEEEHAQLLREQEE -
- - - - AAQRQRMIKNRESAA - RSRERKQAY - - - QVELEALAAKLEEEENELLSKEIEDK
- - - - AAQRQRMIKNRESAA - RSRERKQAY - - - QVELEALAAKLEEEENELLSKEIEDK
- - - - AAQRQRMIKNRESAA - RSRERKQAY - - - QVELETAAKLEEEENEQLLKEIEES
- - - - MERRQRMIKNRESAA - RSRARRQAY - - - TVELELELNLTTEENTKLKEIVEEN
- - - - MERRQRMIKNRESAA - RSRARRQAY - - - TVELELELNLTTEENTKLKEIVEEN
- - - - MERRQRMIKNRESAA - RSRARRQAY - - - TVELELELNLTTEENTKLKE - - -
- - - - IERRHRRMIKNRESAA - RSRARKQAY - - - TVELEAEHLKEENARLKAЕ - - -
- - - - IERRHRRMIKNRESAA - RSRARKQAY - - - TVELEAEHLKEENARLKAЕ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - TVELEAEQLKEENAQLKHALAEI
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - TVELEAEQLKEENAQLKHALAEI
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - TVELEAEQLKEENAQLKHALAEI
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- - - - VERRQRMIKNRESAA - RSRARKQAY - - - TVELEAEQLKEENAQLKHALAEI
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELEIKVSRLEEENERLRKQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELEIKVSRLEEENERLRKQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELEIKVSRLEEENERLRKQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELEIKVSRLEEENERLRKQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELEIKVSRLEEENERLRKQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELENKISRLEEENELLKRQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELENKISRLEEENQRLRE - - -
- - - - MERRQRMIKNRESAA - RSRARKQAY - - - TNELENKVSRLLEEENVRLKRQKE - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - THELENKISRLEEENELLKRQ - - -
- - - - VERRQRMIKNRESAA - RSRARKQAY - - - TNELENKISRLEEENQRLRE - - -
- - - - GNRRHKRMIKNRESAA - RSRARKQAY - - - TNELELEV AHLQAENARLKRQQDQL
- - - - GNRRHKRMIKNRESAA - RSRARKQAY - - - TNELELEV AHLQAENARLKRQQDQL
- - - - GNRRHKRMIKNRESAA - RSRARKQAY - - - TNELELEV AHLQAENARLKRQQDQL

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- - - - - GNRRHKRMIKNRESAA - RSRARKQAY - - - TNELELEV AHLQAENARLKRQQDQL
- - - - - GDRRYKRMKKNRESAA - RSRARKQAY - - - TNELELEIAHLQTENARLKIQQEQL
- - - - - IERRQRRIKKNRESAA - RSRARKQAY - - - TMELEAEVAKLKEENQGLQKKQAEI
- - - - - IERRQRRIKKNRESAA - RSRARKQAY - - - TMELEAEVAKLKEKNEELEKKQAEI
- - - - - VERRQRRIKKNRESAA - RSRARKQAY - - - TMELEAEVQKLKEQNMELQKKQEEI
- - - - - VERRQRRIKKNRESAA - RSRARKQAY - - - TMELEAEVQKLKEQNMELQKKQEEI
- - - - - VERRQRRIKKNRESAA - RSRARKQAY - - - TMELEAEVAKLKEENDELQKKQEEI
- - - - - VERRQRRIKKNRESAA - RSRARKQAY - - - TVELEAEVAKLKEENDELQRKQARI
- - - - - VERRQRRIKKNRESAA - RSRARKQAY - - - TMELEAEVQKLKDNEELVKKQTEI
- - - - - IERRQRRIKKNRESAA - RSRARKQAY - - - TLELEAEIEKLKTKTNQELQKK - - -
- - - - - IERRQRRIKKNRESAA - RSRARKQAY - - - TLELEAEIEKLKTKTNQELQKKQAEI
- - - - - VERRQKRMKKNRESAA - RSRARKQAY - - - TLELEAEIESLKLVNQDLQKKQAEI
- - - - - IERRQKRMKKNRESAA - RSRARKQAY - - - TMELEAEIAQLKELNEELQKK - - -
- - - - - IERRQKRMKKNRESAA - RSRARKQAY - - - TMELEAEIAQLKELNEELQKKQVCL
- - - - - VERRRKRMKKNRESAA - RSRDRKQAY - - - TLELETEVAKLKEIKQELQKK - - -
- - - - - GDRRKRMKKNRESAA - RSRARKQAR - - - VNNLETEVEQLQKENKMLRVKYEQ -
- - - - - VDKKLRRKIKKNRESAA - RSRARKQAO - - - TMEVEVELENLKKDYEELLQHVEL
- - - - - DDRRTIRMMRNRESAL - RSRARKRAY - - - VEELEKEVRRLVDDNLNLKKQ - - -
- - - - - VERRKRRAMKNRESAE - RSRARKQAY - - - LQELEQEVRLLRAENAALRHQCHQL
- - - - - ELKRERRKQSNRESAR - RSRLRKQQE - - - CEELAQKVSELTAAANGTLRSELDQL
- - - - - ELKRERRKQSNRESAR - RSRLRKQQE - - - CEELAQKVSELTAAANGTLRSELDQL
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- - - - - ELKRERRKQSNRESAR - RSRLRKQQE - - - CEELARKVAELTTENSALRSELDQL
- - - - - ELKRERRKQSNRESAR - RSRLRKQQE - - - CEELARKVAELTTENSALRSELDQL
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- - - - - EIKRERRKQSNRESAR - RSRLRKQQE - - - CEELSRKVAELTTENNARTELDQL
- - - - - EIKRERRKQSNRESAR - RSRLRKQQE - - - CEELSRKVAELTTENNARTELDQL
- - - - - ELKRERRKQSNRESAR - RSRLRKQAE - - - TEELARKVEALTAENMALRSELNQL
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- - - - - ELKRERRKQSNRESAR - RSRLRKQAE - - - TEELARKVEMLTAENVSLKSEITRL
- - - - - ESKRERRKQSNRESAR - RSRLRKQAE - - - TEELARKVELLTAENTSLRREISRL
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- - - - - ELKREKRKQSNRESAR - RSRLRKQAE - - - TEELATQVESLAAENTSLRSEIGRL
- - - - - ELKRERRKQSNRESAR - RSRLRKQAE - - - TEELARKVEMLTAENVSLKSEITRL
- - - - - ELKRERRKQSNRESAR - RSRLRKQAE - - - TEELARKVEMLTAENVSLKSEITRL
- - - - - ELKRERRKQSNRESAR - RSRLRKQAE - - - TEELARKVEMLTAENVSLKSEITQL
- - - - - ELKREKRKQSNRESAR - RSRLRKQAE - - - AEELAIRVQSLTAENMTLKSEINKL
- - - - - ELKREKRKQSNRESAR - RSRLRKQAE - - - AEELAIRVQSLTAENMTLKSEINKL
- - - - - ELKREKRKQSNRESAR - RSRLRKQAE - - - AEELAIRVQSLTGENMTLKSEINKL
- - - - - EMKREKRKQSNRESAR - RSRLRKQGE - - - AEELAIRVQSLTSENGLKSEINNF
- - - - - DLKRERRKQSNRESAR - RSRLRKQAE - - - AEELAIKVDSLTAENMALKAEINRL
- - - - - DLKRERRKQSNRESAR - RSRLRKQAE - - - AEELAIKVDSLTAENMALKAEINRL
- - - - - EVKREKRKQSNRESAR - RSRLRKQAE - - - TEQLSVKVDALVAENMSLRSKLGQL
- - - - - EVKREKRKQSNRESAR - RSRLRKQAE - - - TEQLSVKVDALVAENMSLRSKLGQL
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NP_173381.1 - - - - EERRIRRILANRESAR - QTIRRRQAM - - - CEELSKKAADLTYENENLRREKDWA
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AAM62924.1 - - - - DPKRAKRIWANSQSAA - RSKERKMRY - - - IAEELERKVQTLQTEATSLSAQLTLL
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AAF37279.4 - - - - DPKRAKRILANRQSA - RSKERKTRY - - - TGELERKVQTLQNEATTLSAQVTML
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AAM63070.1 - - - - DPKRAKRILANRQSA - RSKERKTRY - - - TGELERKVQTLQNEATTLSAQVTML
AAL87314.1 - - - - DPKRVKRILANRQSA - RSKERKMRY - - - IVELEHKVQTLQTEATTLSAQITLL

NP_195601.1 ----- RILANRQSAA - RSKERKMRY - - - IVELEHKVQLQTEATTLSAQLTLL
NP_849520.1 ----- DPKRVKRILANRQSAA - RSKERKMRY - - - IVELEHKVQLQTEATTLSAQLTLL
BAAT6425.1 ----- DPKRAKRILANRQSAA - RSKERKMRY - - - ISELEHKVQLQTEATTLSAQLTLL
NP_179719.1 ----- DPKRVKRILANRVSAA - RSKERKTRY - - - MAELEHKVQLQTEATTLSAQLTHL
NP_973502.1 ----- DPKRVKRILANRVSAA - RSKERKTRY - - - MAELEHKVQLQTEATTLSAQLTHL
NP_912474.1 ----- DPKRVKRVLANRQSAA - RSKERKMRY - - - IAELEQKVQILQSEATNLSAQLTMM
NP_922490.1 ----- DPKRVKRVLANRQSAA - RSKERRMRY - - - IAELEQKVQILQTEATTLSAQLTLL
BAD09726.1 ----- DPKRVKRILANRQSAA - RSKERKMRY - - - IQELEHKVQVLQTEATTLSAQLTML
AAL78371.1 ----- DPKRVKRILANRQSAA - RSKERKMRY - - - IQKLEHKVQVLQTEASTLSHSLKCL
CAA05898.1 ----- DPKRAKRILANRLSAA - RSKERKTRY - - - ISELEHKVQKLQTTTLSTQVTIL
S52203 ----- DPKRAKRILANRLSAA - RSKERKTRY - - - ISELEHKVQKLQTTTLSTQVTIL
CAA52015.1 ----- DPKRAKRILANRLSAA - RSKERKTRY - - - ISELEHKVQKLQTTTLSTQVTIL
CAD39525.2 ----- DPRRVKRILNNRASAT - KSKEKKMKH - - - VGELOQRKLQVLQSETTTLGAQVTVM
AAL69473.1 ----- DPKRVKRILANRQSAQ - RSRVRKLQY - - - ISELERSVTSLQAEVSVLSPRVAFL
NP_850369.1 ----- DPKRVKRILANRQSAQ - RSRVRKLQY - - - ISELERSVTSLQAEVSVLSPRVAFL
NP_191371.1 ----- DPKRVKRILANRQSAQ - RSRVRKLQY - - - ISELERSVTSLQTEVSVLSPRVAFL
NP_913295.1 ----- DPKRVKRILANRQSAQ - RSRVRKLQY - - - ISELERSVTSLQTEVSALSPLSPRVAFL
NP_178948.1 ----- DPKEVRRILKNRESAA - HLKQKKLQY - - - MINLEHRINFVENENASIFEKIKLL
NP_178956.1 ----- DPKEVRRILKNQESAA - RSKQKKLQY - - - MINLELKINFLENKNASIFEKIKLL
NP_565355.1 ----- DPKVRRILKNRELAA - SSKQRKLKY - - - MIDLEHRIKFLENKNALIFEKIKLL
NP_850010.1 ----- DAKKYKRMLANRASAA - RSKENREKK - - - IRDMELRVETLENTQASLFGTMULL
NP_199756.1 ----- DEKKRKRLKLSNRESAR - RSRLKKQKL - - - MEDTIHEISSLERRIKENSERCRAV
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NP_913739.1 ----- EAKRRARLVRNRESAH - QSRQRKKQY - - - VEELEGKVKVMQATIADLTARISCV
AA051139.1 ----- ELKKQRRLVKNREYAS - QSRSRRKIY - - - VENIETKLQTKTNQDCASIQLNSV
NP_174998.1 ----- VAKKRRRRVRNRDAAV - RSRERKKEY - - - VQDLEKKSKYLERECLRLGRMLECF
AAO22523.1 ----- ETKRLKRLRNRVSAQ - QARERKKAY - - - LGELENRVKDLENRNSELEERLSTL
NP_568246.1 ----- ENKRLKRLRNRVSAQ - QARERKKAY - - - LSELENRVKDLENKNSELEERLSTL
CAB57979.1 ----- ENKRLKRLRNRVSAQ - QARERKKAY - - - LIDLEARVKELETKNAELEERLSTL
T08591 ----- ESKRLKRLRNRVSAQ - QARERKKAY - - - LIDLETTRVKDLEKKNSELEERLSTL
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NP_916476.1 ----- EQNRLKRLRNRVSAQ - QARERKKAY - - - MTELEAKAKDLELRNAELEQRVSTL
NP_850604.1 ----- EYRSLKRLRNRVSAQ - QARERKKVY - - - VSDLESRANELQNNNDQLEEKISTL
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CAC88375.1 ----- EQRRIERVLNRRAAAQ - TSRERKRLE - - - MEKLESEKIDMEQQNQFLLQRLAQM
EAA66464.1 ----- EQRRIERVLNRRAAAQ - TSRERKRLE - - - MEKLESEKIDMEQQNQFLLQRLAQM
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CAC88374.1 ----- EQRRVERVLNRRAAQ - SSRERKRLE - - - VEALE - - - KRNKELETLLINV
XP_329046.1 ----- EQRRVERVLNRRAAQ - SSRERKRLE - - - VEGLE - - - RRNKELE - - -
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EAA47880.1 ----- EQRRVERVLNRRAAQ - SSRERKRQE - - - VEALE - - - QRNAALEQQLLHF
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----- DSSNKKRLCGNREAVR - KYREKKKAR ----- TAYLEDEVMRLQSLNEQFLRKLQSQ
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----- DSSNKKRLCGNREAVR - KYREKKKAR ----- TAYLEDEVMRLQSLNEQFLRKLQSQ
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----- ELRNRRRLQNRRYAR - KCASKKQSEVEKLADEVEEVVEIQLRSQLSRTNLAT
----- IEKVLRLAQNREAAR - KSRLRKKAY ----- VQQLENSKLKLIQLEQEL -----
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CAE64642.1 VSEDEKKRLRNTEAAR - RCREKIKRK - - - TDDLEQQLTGLTAQNDLMNQHRI
NP_506292.1 VSEDEKKRLRNTEAAR - RCREKIKRK - - - TDDLETTELTRLTARNEVMNQHRI
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AAQ72476.1 RRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
AAA9274.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
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CEBB_RAT SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
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1HJB SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
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NP_005185.2 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
1H89 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
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BAB40971.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
AAD19576.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
BAA09637.1 S66246 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
NP_789745.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
CAA76309.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
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NP_571959.2 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
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AAS93421.1 CAA72289.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
XP_133376.1 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL
NP_036656.1 JC4311 SDEYKMRERNNIA - KSRDKAKMR - - - NLETQHKVLELTAEENERLQKKVEQL

NP_031704.1 - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
CEBA_BOVIN - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
CEBA_HUMAN - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
CEBA_MOUSE - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
NP_004355.2 - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
AAD19575.1 - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
AAH63874.1 - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
1NWQ - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
AAR24284.1 - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQLKVLELTSDNDRLRKVEQL
S26295 - - - - SNEYRVRRERNNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRKVEQL
CAA60698.1 - - - - NNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRNGVEQL
S54834 - - - - NNIAVR - KSRDKAKQR - - - NVETQQKVLELTSDNDRLRNGVEQL
A56554 - - - - SNEYRVRRERNNIAVR - KSRDKAKMR - - - NVETQQKVFELOSSDNDKLRKVEQL
I51171 - - - - STEYRVRRERNNIAVR - KSRDKAKMR - - - NVETQQKVVELSNDNEKLRKVEQL
NP_571960.1 - - - - STEYRLRERNNIAVR - KSRDKAKMR - - - NVETQQKVIELSADNDRLRKVEHL
A37280 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - IMETQQKVLEYMAENERLRSRVDQL
NP_058791.1 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - IMETQQKVLEYMAENERLRSRVDQL
XP_139135.2 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - IMETQQKVLEYMAENERLRNRVDQL
AAC50709.1 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - ILETQQKVLEYMAENERLRSRVEQL
NP_001796.2 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - ILETQQKVLEYMAENERLRSRVEQL
CEBE_HUMAN - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - ILETQQKVLEYMAENERLRSRVEQL
CAA10944.1 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - ILETQQKVLEYMAENERLRSRVEQL
AAC51130.1 - - - - SLEYRLRERNNIAVR - KSRDKAKRR - - - ILETQQKVLEYMAENERLRSRVEEL
CEBD_HUMAN - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLHQRVEQL
NP_005186.2 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLHQRVEQL
AAA59927.1 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLHQRVEQL
CEBD_MOUSE - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLHQRVEQL
NP_031705.2 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLHQRVEQL
NP_037286.1 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLHQRVEQL
JC7264 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLQQRVEQL
NP_776692.1 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NQEMQQKLVELSAENEKLQQRVEQL
AAH45282.1 - - - - SPEYQRERNNIAVR - KSRDKAKQR - - - NLDMQQKMIELGAENERLHKTIDQL
AAH56512.1 - - - - SPEYQRERNNIAVR - KSRDKAKQR - - - NLDMQQKMIELGAENERLHKTIDQL
AAH62522.1 - - - - SPEYQRERNNIAVR - KSRDKAKQR - - - NLDMQQKMIELGAENERLHKTIDQL
NP_571962.1 - - - - SPEYQRERNNIAVR - KSRDKAKQR - - - NLDMQQKMIELGAENERLHKTIDQL
BAC92757.1 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NVDMQQRLLSSENELHKKIELL
BAC92758.1 - - - - SPEYQRERNNIAVR - KSRDKAKRR - - - NTDMQQKMLELSSENELHKKIELL
I51172 - - - - SPEYQRERNNIAVR - KSRDKAKKR - - - NMDMQQKLLLELSSENELHKRIDML
BAB40972.1 - - - - SVEYQRERNNIAVR - KSRDKARRR - - - ILLTQQRAMQLQEENQKLQLRIGQL
NP_571912.1 - - - - SAEYQRERNNIAVR - KSRDKARRR - - - IQMTQQRALQLQDENHRLQVHIQRL
A43481 - - - - TDEYRRRERNNIAVR - KSREKAKVR - - - SREVEERVKSLLKEKDALIRQLGEM
NP_523843.1 - - - - TDEYRRRERNNIAVR - KSREKAKVR - - - SREVEERVKSLLKEKDALIRQLGEM
CEB_DROME - - - - TDEYRRRERNNIAVR - KSREKAKVR - - - SREVEERVKSLLKEKDALIRQLGEM
CEB_DROVI - - - - TEEYRRRERNNIAVR - KSREKAKVR - - - SKEVEERVKSLLKEKDALLRQLSEM
XP_309553.1 - - - - TDEYRRRERNNIAVR - KSREKAKVR - - - SREVEEKVKTLLKEKDVLIRKIEEK
S26300 - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVNQLKEENERLEAKIKLL
XP_341843.1 - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVNQLKEENERLEAKIKLL
CEBG_MOUSE - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVNQLKEENERLEAKIKLL
CEBG_RAT - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVNQLKEENERLEAKIKLL
NP_001797.1 - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVNQLKEENERLEAKIKLL
A36673 - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVNQLKEENERLEAKIKLL
AAC60217.1 - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVTQLKEENERLEAKIKLL
I50223 - - - - SDEYQRERNNMAVK - KSRLKSKQK - - - AQDTLQRVTQLKEENERLEAKIKLL
NP_571961.1 - - - - SDEYQRERNNLAVK - KSRMRSKQK - - - AQDTQQRVNELKEENERLEAKIKLL
XP_315443.1 - - - - DDEYRRKRDRNNQAVK - RSRVKSCKM - - - TEETQQRVNDLRLKNQLLEDKIDNQ
A53066 - - - - TQEYVDKRARNNVAVR - KSRAKAKEK - - - QRETEGRVKSLLDQNDQLQKKV DLL
AAG61258.1 - - - - TQEYVDKRARNNVAVR - KSRAKAKEK - - - QRETEGRVKNLLDQNDQLQKKV DLL

BAD16556.1 - - - TMEYVEKRARNNAVR - KSRAKAKEK - - - QRETEGRVKGLMDQNHQLQKKVDM
NP_871835.1 - - - EDDYSTKRKRNNNEAVN - RTRQKKRQE - - - ENDTAEKDELKENETLERKVEQL
T15174 - - - EDDYSTKRKRNNNEAVN - RTRQKKRQE - - - ENDTAEKDELKENETLERKVEQL
CAE67150.1 - - - EDDYTSKRKRNNNEAVN - RTRQKKRQE - - - ENDTAEKDELKKENEALERKVEQL
AAB06796.1 - - - DEEYRKKRERNNSVR - ESREKKRQN - - - ALIVEQKVQDLTKENSLLEERVSLL
NP_497269.1 - - - SSDYRHKRDKNNLASQ - KSRQKRQAK - - - IRESKEERERLEKRKVQLQAMVLTL
T16528 - - - SSDYRHKRDKNNLASQ - KSRQKRQAK - - - IRESKEERERLEKRKVQLQAMVLTL
CAE69150.1 - - - SSDYRLKRDKNNLASQ - KSRQKRQAK - - - IREAKEEKEQLERRQVQLKAMVTTL
CAE58077.1 - - - SYDYRTMRDKNNLASQ - RSRQKRQDK - - - IRETREEKGRLEARNLKAQILGL
NP_648434.1 - - - DPAYKEKRKKNNNEAVQ - RTREKTKKS - - - AEERKKRIDLKQNDALKVQIETS
A41524 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
NP_990713.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
TEF_PHOSU - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
CAD97856.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
NP_003207.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
NP_059072.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
NP_062067.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
CAB62497.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
AAA81373.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
AAS45600.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
NP_705617.1 - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
TEF_HUMAN - - - DEKYWTRRKKNNAAK - RSRDARRLK - - - ENQITIRAAFLEKENTALRTEVAEL
AAH54981.1 - - - DEKYWNRRKKNNAAK - RSRDARRLK - - - ENQITVRAAFLEKENTALRSEVADL
AAA58445.1 - - - DDKYWARRRKKNMAAK - RSRDARRLK - - - ENQIAIRASFLEKENSALRQEVAL
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BAC37522.1 - - - DDKYWARRRKKNMAAK - RSRDARRLK - - - ENQIAIRASFLEKENSALRQEVAL
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HLF_RAT - - - DDKYWARRRKKNMAAK - RSRDARRLK - - - ENQIAIRASFLEKENSALRQEVAL
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NP_571475.1 - - - DDKYWARRRKKNMAAK - RSRDARRLK - - - ENQITVRAAFLERENSALRQEVAEL
NP_001343.2 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
NP_058670.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
NP_036675.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
AAH18323.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
A55558 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
AAR99621.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
AAR99622.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
BAA05833.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
AAP36478.1 - - - DEKYWSRRYKNNEAAK - RSRDARRLK - - - ENQISVRAAFLEKENALLRQEVVAV
AAF04508.1 - - - DDKYWARRRKNNIAAK - RSRDARRQK - - - ENQIAMRARYLEKENATLHQEVQL
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NP_524832.2 - - - DDKYWARRRKNNIAAK - RSRDARRQK - - - ENQIAMRARYLEKENATLHQEVQL
AAF15511.1 - - - DDKYWARRRKNNIAAK - RSRDARRQK - - - ENQIAMRARYLEKENATLHQEVQL
AAO25043.1 - - - DDKYWARRRKNNIAAK - RSRDARRQK - - - ENQIAMRARYLEKENATLHQEVQL
AAS93764.1 - - - DDKYWARRRKNNIAAK - RSRDARRQK - - - ENQIAMRARYLEKENATLHQEVQL
NP_729297.1 - - - DDKYWARRRKNNIAAK - RSRDARRQK - - - ENQIAMRARYLEKENATLHQEVQL
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XP_316411.1 - - - DDKYWARRRKNNMAAK - RSRDARRMK - - - ENQIALRAGYLEKENMNHLREVEQL
BAC06840.1 - - - DQKYWSRRKKNNAAK - RSREARRIK - - - ENQIALRAAYLEKENSTLKDDELKNL
AAQ22473.1 - - - DAAYYERRRKNNAAAK - KSRDRRIK - - - EDEIAIRAAYLERQNIELLCQIDAL
NP_525049.1 - - - DAAYYERRRKNNAAAK - KSRDRRIK - - - EDEIAIRAAYLERQNIELLCQIDAL
S17370 - - - DAAYYERRRKNNAAAK - KSRDRRIK - - - EDEIAIRAAYLERQNIELLCQIDAL

NP_572367.1 - - - - DTAYYERRKNNAAK - KSRDRRIK - - - EDEIAIRAAAYLERQNIELLCRIDAL
XP_321187.1 - - - - DSAYYERRKNNAAK - KSRDRRIK - - - EDEIAIRAAFLERENIELKFELAAA
CAE55183.1 - - - - DPSYWEKRRKNNEAAK - RSRDARRAK - - - EDEIAIRCAFLERENCHLKFTVDTL
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NP_723075.1 - - - - DESYWDRRRRNNEAAK - RSREKRRYN - - - DMVLEQRVIELTKENHVLKAQLDIAI
CAA72535.1 - - - - DESYWDRRRRNNEAAK - RSREKRRYN - - - DMVLEQRVIELTKENHVLKAQLDIAI
NP_477191.1 - - - - DESYWDRRRRNNEAAK - RSREKRRYN - - - DMVLEQRVIELTKENHVLKAQLDIAI
XP_317705.1 - - - - DDSYWDRRRRNNEAAK - RSREKRRFN - - - DMVLEQRVVELTKENHVLKAQLDIAI
CAE68044.1 - - - - DESYYERRARRNNKAAQ - KSREARKKI - - - DAENSHRVNQLEMENNHLKAYIYKL
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CYS3_NEUCR - - - - EDKRKRNTAASA - RFRIKKKQR - - - EQALEKSAKEMSEKVTQLEGRIQAL
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1DGC - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
1YSAD - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
1LD4 - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
1YSAC - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
2DGC - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
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CAE52208.1 - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
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CAE52217.1 - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
CAE52220.1 - - - - KRARNTEAAR - RSRARKLQR - - - MKQLEDKVEELLSKNYHLENEVARL
NP_984085.1 - - - - DDPVALKRARNTEAAR - RSRARKLER - - - MNQLEERVEQLLQKNSELEAEVARL
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EAK95477.1 - - - - KRAKNTEAAR - RSRARKMER - - - MSQLEDKVENLINEKQALQDQVERL
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XP_323369.1 - - - - KRARNTLAAR - KSRERKAQR - - - LEELEAKIEELIAERDR - - - -
EAA48944.1 - - - - KRARNTLAAR - KSRERKAMR - - - FEELEDKLEKLTAERDHFKN - - - -
XP_389462.1 - - - - KRARNTLAAR - KSRERKAMK - - - MDELEDKIAKLEEERD - - - -
EAK83968.1 - - - - KDPRVAKRLSNTLAAR - RSRHRKAEE - - - LRLLNKEKIEALTSEVESWKRCEQA
AAL09315.1 - - - - KRARNTEAAR - KSRARKLER - - - QGDMERRIAELSKELEETRQMVE - -

EAA59883.1 - - - - - KRARNTEAAR - KSRARKLER - - - QGDMERRIAELSKELEETRQMVE - -
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FOS_PIG LKEKEKLEFILA AH - - -
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NP_955598.1 LKEKEKLEFILA AH - - -
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FOS_MSVFB LKEKEKLEFILA AH - - -
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AAN03532.1 LKEKEKLEFILA AH - - -
NP_990839.1 LKEKEKLEFILA AH - - -
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NP_037085.1 QKQKERLELVLEAH---
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NP_032063.2 QKEKEKLEFMLVAH---
AAA61951.1 QKEKEKLEFMLVAH---
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AAC08730.1 QKEKEKLE-----
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AAC08715.1 -----
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CAD56863.1 RKEKDKEFMLVAH---
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FOSB_HUMAN QKEKERLEFVLVAH---
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CAD56864.1 HKEKERLEFVLVAH---
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T31799 RNKLNSLKNYLETH---
CAE64529.1 RNKLNSLKSYLENH---
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XP_323224.1 RKKMEKMSNELNEY---
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EAA60905.1 KREIARYSTENEIL---
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FCR3_CANAL KKQ-----
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AAA34463.1	LCSLKSLLSKITKY----
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EAL02912.1	RAQVDVLKNELAKY----
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XP_323551.1	QAEYEALK-----
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AAC72897.1	ESERKRISNKFAML----
A33111	ESERKRISNKFAML----
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NP_732834.1	ESERKRISNKFAML----
NP_732835.1	ESERKRISNKFAML----
T13936	ESERKRISNKFAML----
AAB59246.1	ESERKRISNKFAML----
XP_309091.1	LSEHKKIRDKFMSL----
A49672	LRSLRQMKQKVQSL----
AAA20466.1	LRSLRQMKQKVQSL----
AAC40108.1	LRSLRQMKQKVQSL----
BAC03440.1	LRSLRQMKQKVQSL----
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XP_340887.1	LRSLRQMKQKVQSL----
BAB23483.1	LRSLRQMKQKVQSL----
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NFL1_MOUSE	LRSLRQMKQKVQSL----
NP_003195.1	LRSLRQMKQKVQSL----
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AAH56142.1	NKAINIMKQKLHDL----
BAA76288.1	NKAINIMKQKLHDL----
AAF17228.1	NKAINIMKQKLHDL----
AAF61404.1	NKAINIMKQKLHDL----
NP_004280.4	NKAINIMKQKLHDL----
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XP_231763.2	NKAINTMRQKLYDL----
A54692	DRTLEVMRQQLTEL----
AAA35612.1	DRTLEVMRQQLTEL----
NP_006154.1	DRTLEVMRQQLTEL----
NP_032711.2	DRTLEVMRQQLAEI----
S32537	DRTLEVMRQQLAEI----
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NP_878309.1	SSNLKEMKQQLSTL----
AAH61724.1	DRNLHLLKRKLSTL----

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I49261	DRNLHLLKRRLSTL----
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I59340	DKSLHLLKKQLSTL----
NP_006155.2	DKSLHLLKKQLSTL----
NP_990448.1	DKSLRQMKKQLTTL----
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NP_031546.1	LSTLGETKQNLTGL----
BAA95505.1	LSTLGETKQNLTGL----
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XP_221712.2	LSTLGETKQNLTGL----
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CAD56856.1	REQVAQLKQKVMNH----
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CAD56860.1	REQVAQLKQKVLT-----
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XP_326838.1 REEVVNLTLLAH---

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JX0307	KD-----
CAC34846.1	KD-----
CREM_CANFA	KD-----
S36101	KD-----
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JC6135	KD-----
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CRBA_DROME	EETNANLSQLHKL---
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XP_290732.2	AKEIQYLKDLIEEE----
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AAS57931.1	SREIKYLKDLMEEV----
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CEBA_HUMAN	SRELDTLRGIFRQL---
CEBA_MOUSE	SRELDTLRGIFRQL---
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CAA60698.1	SRELDTLRGIFRQL---
S54834	SRELDTLRGIFRQL---
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NP_058791.1	TQEELDTLRNLFRQI---
XP_139135.2	TQEELDTLRNLFRQI---
AAC50709.1	TQEELDTLRNLFRQI---
NP_001796.2	TQEELDTLRNLFRQI---
CEBE_HUMAN	TQEELDTLRNLFRQI---
CAA10944.1	TQEELDTLRNLFRQI---
AAC51130.1	TQEELDTLRNLFRQI---
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NP_005186.2	TRDLAGLRQFFKQL---
AAA59927.1	TRDLAGLRQFFKQL---
CEBD_MOUSE	TRDLAGLRQFFKQL---
NP_031705.2	TRDLAGLRQFFKQL---
NP_037286.1	TRDLASLRQFFKEL---
JC7264	TRDLAGLRRFFKQL---
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AAH56512.1	TRELSSLRNFFKQM---
AAH62522.1	TRELSSLRNFFKQM---
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BAC92758.1	TRDLSSLRHYFKQL---
I51172	TRDLTSLRHFFKQL---
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CEB_DROVI	TNELSLHKQIYMQL---
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XP_341843.1	TKELSVLKDLFLEH---
CEBG_MOUSE	TKELSVLKDLFLEH---
CEBG_RAT	TKELSVLKDLFLEH---
NP_001797.1	TKELSVLKDLFLEH---
A36673	TKELSVLKDLFLEH---
AAC60217.1	TKELSVLKDLFLEH---
I50223	TKELSVLKDLFLEH---
NP_571961.1	SKELSVLKDLFLEH---

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AAG61258.1	SKELNVLKGLFLNV----
BAD16556.1	TKELTVLKGLFLNV----
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T15174	QKELSFLKEMFMAY----
CAE67150.1	QKELSFLKEMFMAY----
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T16528	ETQVEDYKRLVMMF----
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CAE58077.1	EAQVDDYKRMVMMF----
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TEF_PHOSU	-----
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XP_343957.1	RKELGKCKNILAKY----
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NP_002117.1	RKELGKCKNILAKY----
NP_766151.1	RKELGKCKNILAKY----
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NP_001343.2	RQELSHYRAVLSRY----
NP_058670.1	RQELSHYRAVLSRY----
NP_036675.1	RQELSHYRAVLSRY----
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A55558	RQELSHYRAVLSRY----
AAR99621.1	RQELSHYRAVLSRY----
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AAP36478.1	RQELSHYRAVLSRY----
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AAF04509.1	KQENMDLRARLSKF----
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AAQ22473.1	KVQLAAFTS-----
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S17370	KVQLAAFTS-----
NP_572367.1	EVQLAAITS-----
XP_321187.1	RKQL-----
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NP_504576.1	RAETDKLRALILTT---
T31706	RAETDKLRALILTT---
CAE64514.1	RAETDKLRTLILTT---
CAE72616.1	QQEAAKLR-----
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CAA45597.1	K-----
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NP_446179.1	K-----
NP_059069.1	K-----
NP_005375.1	K-----
AAH60943.1	K-----
XP_372707.1	K-----
AAM29449.1	RDKFN-----
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EAA62399.1	EMENRWLKNLLTEK---
CYS3_NEUCR	ETENKWLKGTVTEK---
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1YSAC	KK-----
2DGC	KK-----
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CAE52206.1	KK-----
CAE52208.1	KK-----
CAE52210.1	KK-----
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XP_389462.1	- - - - -
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