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CLUSTAL W (1.83) multiple sequence alignment


XP_133376.1       SNEYRVRRERNNIAVR-KSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRG
CEBA_BOVIN        SNEYRVRRERNNIAVR-KSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRG
NP_036656.1       SNEYRVRRERNNIAVR-KSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRG
CEBA_HUMAN        SNEYRVRRERNNIAVR-KSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRG
NP_034013.1       SDEYKMRRERNNIAVR-KSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRN
CAA43179.1        SDEYKMRRERNNIAVR-KSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRN
NP_990584.1       SDEYKLRRERNNIAVR-KSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRN
NP_005185.2       SDEYKIRRERNNIAVR-KSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRN
NP_789745.1       SDEYKIRRERNNIAVR-KSRDKAKMRNLETQHKVLELTGENERLQKKVEQLSREVSTLRN
CEBE_HUMAN        SLEYRLRRERNNIAVR-KSRDKAKRRILETQQKVLEYMAENERLRSRVEQLTQELDTLRN
NP_058791.1       SLEYRLRRERNNIAVR-KSRDKAKRRIMETQQKVLEYMAENERLRSRVDQLTQELDTLRN
NP_031705.2       SPEYRQRRERNNIAVR-KSRDKAKRRNQEMQQKLVELSAENEKLHQRVEQLTRDLAGLRQ
CEBD_HUMAN        SPEYRQRRERNNIAVR-KSRDKAKRRNQEMQQKLVELSAENEKLHQRVEQLTRDLAGLRQ
NP_037286.1       SPEYRQRRERNNIAVR-KSRDKAKRRNQEMQQKLVELSAENEKLHQRVEQLTRDLASLRQ
NP_001797.1       SDEYRQRRERNNMAVK-KSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKD
CEBG_RAT          SDEYRQRRERNNMAVK-KSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKD
CEBG_MOUSE        SDEYRQRRERNNMAVK-KSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKD
A43481            TDEYRRRRERNNIAVR-KSREKAKVRSREVEERVKSLLKEKDALIRQLGEMTNELQLHKQ
CEB_DROVI         TEEYRRRRERNNIAVR-KSREKAKVRSKEVEERVKSLLKEKDALLRQLSEMTNELSLHKQ
AAH18323.1        DEKYWSRRYKNNEAAK-RSRDARRLKENQISVRAAFLEKENALLRQEVVAVRQELSHYRA
BAA05833.1        DEKYWSRRYKNNEAAK-RSRDARRLKENQISVRAAFLEKENALLRQEVVAVRQELSHYRA
AAR99622.1        DEKYWSRRYKNNEAAK-RSRDARRLKENQISVRAAFLEKENALLRQEVVAVRQELSHYRA
NP_059072.1       DEKYWTRRKKNNVAAK-RSRDARRLKENQITIRAAFLEKENTALRTEVAELRKEVGKCKT
NP_062067.1       DEKYWTRRKKNNVAAK-RSRDARRLKENQITIRAAFLEKENTALRTEVAELRKEVGKCKT
NP_003207.1       DEKYWTRRKKNNVAAK-RSRDARRLKENQITIRAAFLEKENTALRTEVAELRKEVGKCKT
A41524            DEKYWTRRKKNNVAAK-RSRDARRLKENQITIRAAFLEKENTALRTEVAELRKEVGRCKN
TEF_PHOSU         DEKYWTRRKKNNVAAK-RSRDARRLKENQITIRAAFLEKENTALRTEVAD----------
NP_766151.1       DDKYWARRRKNNMAAK-RSRDARRLKENQIAIRASFLEKENSALRQEVADLRKELGKCKN
HLF_RAT           DDKYWARRRKNNMAAK-RSRDARRLKENQIAIRASFLEKENSALRQEVADLRKELGKCKN
NP_002117.1       DDKYWARRRKNNMAAK-RSRDARRLKENQIAIRASFLEKENSALRQEVADLRKELGKCKN
NP_493610.1       DSAYFERRRKNNDAAK-RSRDARRQKEEQIASKAHALERENMQLRGKVSSLEQEAAQLR-
NP_525049.1       DAAYYERRRKNNAAAK-KSRDRRRIKEDEIAIRAAYLERQNIELLCQIDALKVQLAAFTS
NP_498426.1       SPKYLEKRMKNNEAAK-KSRASRKHREQKNQTENELLKRKNAALEEELKQAKCELAQMQI
NP_006390.1       DVRRVQRREKNRIAAQ-KSRQRQTQKADTLHLESEDLEKQNAALRKEIKQLTEELKYFTS
NP_058047.1       DVRKVQRREKNRIAAQ-KSRQRQTQKADTLHLESEDLEKQNAALRKEIKQLTEELKYFTS
NP_037044.1       DERKRRRRERNKIAAA-KCRNKKKEKTECLQKESEKLESVNAELKAQIEELKNEKQHLIY
NP_031524.2       DERKRRRRERNKIAAA-KCRNKKKEKTECLQKESEKLESVNAELKAQIEELKNEKQHLIY
NP_001665.1       DERKKRRRERNKIAAA-KCRNKKKEKTECLQKESEKLESVNAELKAQIEELKNEKQHLIY
NP_037085.1       EERRRVRRERNKLAAA-KCRNRRKELTDFLQAETDKLEDEKSGLQREIEELQKQKERLEL
NP_034365.1       EERRRVRRERNKLAAA-KCRNRRKELTDFLQAETDKLEDEKSGLQREIEELQKQKERLEL
NP_005429.1       EERRRVRRERNKLAAA-KCRNRRKELTDFLQAETDKLEDEKSGLQREIEELQKQKERLEL
NP_955598.1       EVKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
FOS_SHEEP         --------ERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
NP_034364.1       EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
AAG47951.1        EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
FOS_CRIGR         EEKRRIRRERNKMAAA-KCWNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
FOS_FELCA         EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
FOS_MESAU         EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
CAB40144.1        EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
NP_005243.1       EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEF
FOS_MSVFB         EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEDKKSALQTEIANLLKEKEKLEF
FOS_AVINK         EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEEEKSALQAEIANLLKEKEKLEF
NP_990839.1       EEKRRIRRERNKMAAA-KCRNRRRELTDTLQAETDQLEEEKSALQAEIANLLKEKEKLEF
FOS_FUGRU         EEKKRIRRERNKQAAA-KCRNRRRELTDTLQAETDQLEDEKSSLQNDIANLLKEKERLEF
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FOS_TETFL        EEKKRIRRERNKQAAA-KCRNRRRELTDSLQAETDQLEAEKSSLQNDIANLLKEKERLEF
FOS_CYPCA        EEKKRVRRERNKMAAA-KCRNRRRELTDTLQAETDELEDEKSALQNDIANLLKEKERLEF
NP_032062.1      EEKRRVRRERNKLAAA-KCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEF
NP_006723.1      EEKRRVRRERNKLAAA-KCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEF
NP_037086.1      EEKRRIRRERNKLAAA-KCRNRRRELTEKLQTETEELEEEKSGLQKEIAELQKEKEKLEF
NP_005244.1      EEKRRIRRERNKLAAA-KCRNRRRELTEKLQAETEELEEEKSGLQKEIAELQKEKEKLEF
FRA2_MOUSE       EEKRRIRRERNKLAAA-KCRNRRRELTEKLQAETEELEEEKSGLQKEIAELQKEKEKLE-
FRA2_CHICK       EEKRRIRRERNKLAAA-KCRNRRRELTEKLQAETEVLEEEKSVLQKEIAELQKEKEKLEF
A35847           EQKRAVRRERNKQAAA-RCRKRRVDQTNELTEEVEQLEKRGESMRKEIEVLTNSKNQLEY
NP_593039.1      GTKQSMLKARNRQAAQ-KCRIKKKKYLQTLQDQVNYYTSENKELLQSANDLREEIIKLRT
BAA12194.1       EEKRKSFLERNRQAAL-KCRQRKKQWLSNLQAKVEFYGNENEILSAQVSALREEIVSLKT
NP_012228.1      --KRARLLERNRIAAS-KCRQRKKVAQLQLQKEFNEIKDENRILLKKLNYYEKLISKFK-
NP_010964.1      --KRARLLERNRIAAS-KCRQRKKMSQLQLQREFDQISKENTMMKKKIENYEKLVQKMKK
NP_014232.1      ERKRKEFLERNRVAAS-KFRKRKKEYIKKIENDLQFYESEY-------DDLTQVIGKL--
NP_594500.1      DEKRRRILERNRIAAS-KFRQKKKEWIKELEQTANAAFEQSKRLQLLLSQLQQEAFRLKS
NP_595707.1      DMKRRRFLERNRIAAS-KCRQKKKLWTQNLEKTAHIACEQSKALRILVSQLREEVICLKN
ATF2_HUMAN       DEKRRKFLERNRAAAS-RCRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQ
AAH42210.1       DEKRRKFLERNRAAAS-RCRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQ
NP_112280.1      DEKRRKFLERNRAAAS-RCRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQ
NP_990235.1      DEKRRKFLERNRAAAS-RCRQKRKVWVQSLEKKAEDLSSLNGQLQNEVTLLRNEVAQLKQ
ATF7_HUMAN       DERRQRFLERNRAAAS-RCRQKRKLWVSSLEKKAEELTSQNIQLSNEVTLLRNEVAQLKQ
CRB5_MOUSE       DERRRKFLERNRAAAT-RCRQKRKVWVMSLEKKAEELTQTNMQLQNEVSMLKNEVAQLKQ
NP_878901.1      DERRRKFLERNRAAAT-RCRQKRKVWVMSLEKKAEELTQTNMQLQNEVSMLKNEVAQLKQ
NP_112279.1      ARKREVRLMKNREAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD-------
CREB_BOVIN       ARKREVRLMKNREAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD-------
NP_034082.1      ARKREVRLMKNREAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD-------
AAQ24858.1       ARKREVRLMENREAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD-------
BAA83552.1       TRKRELRLMKNREAAR-ECRRKKKEYVKCLENRVAVLESQNKTLIEELKALKD-------
CREM_CANFA       TRKRELRLMKNREAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD-------
CREB_CHLVR       TRKRELRLYKNREAAR-ECRRKKKEYVKCLENRVAVLENQNKALIEELKSLKD-------
NP_996507.1      TRKREIRLQKNREAAR-ECRRKKKEYIKCLENRVAVLENQNKALIEELKSLKELYCQTKN
NP_005162.1      QLKREIRLMKNREAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKTLKD-------
BAB26930.1       QLRREIRLMKNRGAAR-ECRRKKKEYVKCLENRVAVLENQNKTLIEELKTLKD-------
CREM_MOUSE       TRKRELRLMKNREAAK-ECRRRKKEYVKCLESRVAVLEVQNKKLIEELETLKD-------
CREM_HUMAN       TRKRELRLMKNREAAK-ECRRRKKEYVKCLESRVAVLEVQNKKLIEELETLKD-------
NP_776711.1      VLKRVRRKIRNKKSAQ-ESRRKKKVYVGGLESRVLKYTAQNLELQNKVQLLEEQNLSLLD
AAC04325.1       ILKRVRRKIRNKRSAQ-ESRRKKKVYVGGLESRVLKYTAQNMELQNKVQLLEEQNLSLLD
BAB25173.1       VLKRVRRKIRNKRAAQ-ESRKKKKVYVVGLESRVLKYTAQNRELQNKVQRLEEQNLSLLD
A44494           SLKKIRRKIKNKISAQ-ESRRKKKEYMDQLERRVEILVTENHDYKKRLEGLEETNANLLS
CAA66664.1       LLKRHERMIKNRESAC-QSRRKKKEYLQGLEARLQAVLADNQQLRRENAALRRRLEALLA
NP_059102.1      LLKRQQRMIKNRESAC-QSRRKKKEYLQGLEARLQAVLADNQQLRRENAALRRRLEALLA
NP_031374.1      VLRRQQRMIKNRESAC-QSRKKKKEYMLGLEARLKAALSENEQLKKENGTLKRQLDEVVS
NP_196313.1      DQKTLRRLAQNREAAR-KSRLRKKAYVQQLENSRLKLTQLEQELQR--------------
NP_566415.3      DQKTLRRLAQNREAAR-KSRLRKKAYVQQLENSRLKLTQLEQELQR--------------
BAA06486.1       DQKTMRRLAQNREAAR-KSRLRKKAYVQQLENSRLKLTQLEQELQR--------------
TG21_TOBAC       DQKTLRRLAQNREAAR-KSRLRKKAYVQQLENSRLKLSQLEQDLQR--------------
AAF06696.1       DQKTLRRLAQNREAAR-KSRLRKKAYVQQLESSRMKLTQLEQELQR--------------
HBB2_WHEAT       DHKSLRRLAQNREAAR-KSRLRKKAYIQNLESSRLKLTQLEQELQR--------------
AAM64610.1       PDKIQRRLAQNREAAR-KSRLRKKAYVQQLETSRLKLIQLEQEL----------------
S48121           PDKIQRRLAQNREAAR-KSRLRKKAYVQQLETSRLKLIHLEQEL----------------
AAM64781.1       NDKMKRRLAQNREAAR-KSRLRKKAHVQQLEESRLKLSQLEQEL----------------
AAF17682.1       HDKMKRRLAQNREAAR-KSRLRKKAYVQQLEESRLKLSQLEQELEK--------------
TGAB_TOBAC       DEKKRARLVRNRESAQ-LSRQRKKHYVEELEDKVRIMHSTIQDLNAKVAYIIAENATLKT
CAB57979.1       ENKRLKRLLRNRVSAQ-QARERKKAYLIDLEARVKELETKNAELEERLSTLQNENQMLRH
NP_568246.1      ENKRLKRLLRNRVSAQ-QARERKKAYLSELENRVKDLENKNSELEERLSTLQNENQMLRH
NP_850604.1      EYRSLKRLLRNRVSAQ-QARERKKVYVSDLESRANELQNNNDQLEEKISTLTNENTMLRK
NP_850449.1      ELKRERRKQSNRESAR-RSRLRKQAETEELARKVEALTAENMALRSELNQLNEKSDKLRG
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AAM62869.1        EVKREKRKQSNRESAR-RSRLRKQAETEQLSVKVDALVAENMSLRSKLGQLNNESEKLRL
CPR1_PETCR        DLKRERRKQSNRESAR-RSRLRKQAEAEELAIKVDSLTAENMALKAEINRLTLTAEKLTN
TAF1_TOBAC        ELKREKRKQSNRESAR-RSRLRKQAEAEELAIRVQSLTAENMTLKSEINKLMENSEKLKL
EMP1_WHEAT        ELKRERRKQSNRESAR-RSRLRKQQECEELAQKVSELTAANGTLRSELDQLKKDCKTMET
CPR3_PETCR        ELKRQRRKQSNRESAR-RSRLRKQAKSDELQERLDNLSKENRILRKNLQRISEACAEVTS
NP_849510.1       ELKRQKRKQSNRESAR-RSRLRKQAECEQLQQRVESLSNENQSLRDELQRLSSECDKLKS
HBPA_WHEAT        ELKKQKRKLSNRESAR-RSRLRKQAECEELGQRAEALKSENSSLRIELDRIKKEYEELLS
OP2_MAIZE         TEERVRKKESNRESAR-RSRYRKAAHLKELEDQVAQLKAENSCLLRRIAALNQKYN----
CPR2_PETCR        DAKRVRRMLSNRESAR-RSRRRKQAHMTELETQVSQLRVENSSLLKRLTDISQRYN----
OCS1_MAIZE        THRREKRRLSNRESAR-RSRLRKQQHLDELVQEVARLQADNARVAARARDIASQYTRVEQ
AAK19601.1        VERRQKRMIKNRESAA-RSRARKQAYTHELEIKVSRLEEENERLRKQ-------------
NP_172097.1       DPKRAKRIWANRQSAA-RSKERKMRYIAELERKVQTLQTEATSLSAQLTLLQRDTNGLGV
BAB82982.1        EEKALRRKLKNRVAAQ-TARDRKKARMSELEQQVVDLEEENQKLLLENQLLREKTHGLVV
NP_038870.2       EEKALRRKLKNRVAAQ-TARDRKKARMSELEQQVVDLEEENHKLQLENQLLREKTHGLVV
XP_214067.1       EEKALRRKLKNRVAAQ-TARDRKKARMSELEQQVVDLEEENQKLQLENQLLREKTHGLVI
MAF_MOUSE         RLKQKRRTLKNRGYAQ-SCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKE
NP_062191.1       RLKQKRRTLKNRGYAQ-SCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKE
NP_005351.2       RLKQKRRTLKNRGYAQ-SCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKE
TMAF_AVIS4        RLKQKRRTLKNRGYAQ-SCRFKRVQQRHVLESEKNQLLQQVEHLKQEISRLVRERDAYKE
NP_034788.1       RLKQKRRTLKNRGYAQ-SCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARERDAYKV
NP_062189.1       RLKQKRRTLKNRGYAQ-SCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARERDAYKV
NP_005452.2       RLKQKRRTLKNRGYAQ-SCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARERDAYKV
NP_032762.1       RLKQRRRTLKNRGYAQ-ACRSKRLQQRRGLEAERARLAAQLDALRAEVARLARERDLYKA
NP_006168.1       RLKQRRRTLKNRGYAQ-ACRSKRLQQRRGLEAERARLAAQLDALRAEVARLARERDLYKA
NP_034885.1       RLKQRRRTLKNRGYAA-SCRVKRVCQKEELQKQKSELEREVDKLARENAAMRLELDALRG
NP_036455.1       RLKQRRRTLKNRGYAA-SCRVKRVCQKEELQKQKSELEREVDKLARENAAMRLELDALRG
NP_990088.1       RLKQRRRTLKNRGYAA-SCRVKRVCQKEELQKQKMELEWEVDKLARENAAMRLELDTLRG
NP_034886.1       QLKQRRRTLKNRGYAA-SCRVKRVTQKEELEKQKAELQQEVEKLASENASMKLELDALRS
NP_002350.1       QLKQRRRTLKNRGYAA-SCRVKRVTQKEELEKQKAELQQEVEKLASENASMKLELDALRS
MAFG_CHICK        QLKQRRRTLKNRGYAA-SCRVKRVTQKEELEKQKAELQQEVEKLASENASMKMELDALRS
NP_002351.1       RLKQRRRTLKNRGYAA-SCRIKRVTQKEELERQRVELQQEVEKLARENSSMRLELDALRS
NP_034887.1       RLKQRRRTLKNRGYAA-SCRIKRVTQKEELERQRVELQQEVEKLARENSSMRLELDALRS
NP_990087.1       RLKQRRRTLKNRGYAA-SCRIKRVTQKEELERQRVELQQEVEKLARENSSMKLELDALRS
NP_035032.1       LIRDIRRRGKNKVAAQ-NCRKRKLENIVELEQDLGHLKDEREKLLREKGENDRNLHLLKR
NP_113977.1       LIRDIRRRGKNKVAAQ-NCRKRKLENIVELEQDLGHLKDEREKLLREKGENDRNLHLLKR
NP_006155.2       LIRDIRRRGKNKVAAQ-NCRKRKLENIVELEQDLDHLKDEKEKLLKEKGENDKSLHLLKK
AAA35612.1        LVRDIRRRGKNKVAAQ-NCRKRKLETIVQLERELERLTNERERLLRARGEADRTLEVMRQ
NP_003195.1       LIRDIRRRGKNKMAAQ-NCRKRKLDTILNLERDVEDLQRDKARLLREKVEFLRSLRQMKQ
NP_032712.2       LIRDIRRRGKNKMAAQ-NCRKRKLDTILNLERDVEDLQRDKARLLREKVEFLRSLRQMKQ
NP_035033.1       LIRDIRRRGKNKVAAQ-NCRKRKLDIILNLEDDICNLQAKKEALKNEQTQCSKAIDIMRQ
NP_004280.4       LIRDIRRRGKNKVAAQ-NCRKRKLDIILNLEDDVCNLQAKKETLKREQAQCNKAINIMKQ
NP_732833.1       LIRDIRRRGKNKVAAQ-NCRKRKLDQILTLEDEVNAVVKRKTQLNQDRDHLESERKRISN
BAA95505.1        -----RRRSKNRIAAQ-RCRKRKLDCIQNLESEIEKLQSEKESLLKERDHILSTLGETKQ
NP_031546.1       -----RRRSKNRIAAQ-RCRKRKLDCIQNLESEIEKLQSEKESLLKERDHILSTLGETKQ
NP_031547.1       -----RRRSKNRIAAQ-RCRKRKLDCIQNLECEIRKLVCEKEKLLSERNHLK--------
AAK48898.1        -----RRRSKNRIAAQ-RCRKRKLDCIQNLECEIRKLVCEKEKLLSERNQLK--------
CAA31252.1        RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
AP1_COTJA         RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
1404381A          RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
AP1_CHICK         RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
AP1_PIG           RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
NP_068607.1       RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
AP1_SERCA         RIKAERKRMRNRIAAS-KCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
TJUN_AVIS1        RIKAERKRMRNRIAAS-KSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQ
NP_034722.1       RIKAERKRLRNRIAAS-KCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQ
NP_005345.2       RIKAERKRLRNRIAAS-KCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQ
NP_620230.1       RIKAERKRLRNRIAAS-KCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQ
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JUND_CHICK       RIKAERKRLRNRIAAS-KCRKRKLERISRLEEKVKSLKSQNTELASTASLLREQVAQLKQ
AAH09465.1       RIKVERKRLRNRLAAT-KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQ
NP_068608.2      RIKVERKRLRNRLAAT-KCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQ
AAA74916.1       RIKVERKRLRNRLAAT-KCRKRKLERIARLEDKVKTLKAENAGLSSAAGLLREQVAQLKQ
JUNB_CYPCA       RIKAERKRLRNRLAAT-KCRKRKLERISRLEEKVKVLKNDNAGLSNTASVLRDQVAQLKQ
NP_476586.1      KIKLERKRQRNRVAAS-KCRKRKLERISKLEDRVKVLKGENVDLASIVKNLKDHVAQLKQ
A30208           ------KRARNTLAAR-KSRERKAQRLEELEAKIEELIAERDR-----------------
CPC1_CRYPA       ------KRAKNTLAAR-KSRARKAERMDELERQVRELEAEKEKLAA-------ELA----
CAE52206.1       ------KRARNTEAAR-RSRARKLQRMKQLEDKVEELLSKNYHLEN-------EVARLKK
NP_013707.1      PETKQKRTAQNRAAQR-AFRERKERKMKELEKKVQSLESIQQQNEVEATFLRDQLITLVN
AP1_KLULA        TEAKDKRTAQNRAAQR-AFRERRERKMKELEDKVSQLESLNKQSELETKFLRNQVTNLLS
AAB29937.1       SEAKSRRTAQNRAAQR-AFRDRKEAKMKSLQERVELLEQKDAQNKTTTDFLLCSLKSLLS
NP_593662.1      QEPSSKRKAQNRAAQR-AFRKRKEDHLKALETQVVTLKELHSSTTLENDQLRQKVRQLEE
NP_011854.1      DDSKAKKKAQNRAAQK-AFRERKEARMKELQDKLLESERNRQSLLKEIEELRKANTEINA
NP_012283.1      DEELQKKKRQNRDAQR-AYRERKNNKLQVLEETIESLSKVVKNYETKLNRLQNELQAKES
NP_594523.1      TAAEEDKRRRNTAASA-RFRIKKKLKEQQLERTAKELTEKVAILETRVRELEMENNWLKG
CYS3_NEUCR       ----EDKRKRNTAASA-RFRIKKKQREQALEKSAKEMSEKVTQLEGRIQALETENKWLKG
NP_012282.1      DKIKQERRRKNTEASQ-RFRIRKKQKNFENMNKLQNLNTQINKLRDRIEQLNKENEFWKA
AAH05174.1       GDRKQKKRDQNKSAAL-RYRQRKRAEGEALEGECQGLEARNRELKERAESVEREIQYVKD
NP_109618.1      GDRKQKKRDQNKSAAL-RYRQRKRAEGEALEGECQGLEARNRELRERAESVEREIQYVKD
ATF4_HUMAN       LDKKLKKMEQNKTAAT-RYRQKKRAEQEALTGECKELEKKNEALKERADSLAKEIQYLKD
ATF4_MOUSE       LDKKLKKMEQNKTAAT-RYRQKKRAEQEALTGECKELEKKNEALKEKADSLAKEIQYLKD
GA15_MOUSE       QGRTRKRKQSGQCPAR-PGKQRMKEKEQENERKVAQLAEENERLKQEIERLTREVETTRR
GA15_CRILO       ----RKRKQSGQCPARGTGKQRMKEKEQENERKVAQLAEENERLKQEIERLTREVEATR-
AAB27103.1       QGRTRKRKQSGHSPAR-AGKQRMKEKEQENERKVAQLAEENERLKQEIERLTREVEATRR
                           .

XP_133376.1      IFRQL
CEBA_BOVIN       IFRQL
NP_036656.1      IFRQL
CEBA_HUMAN       IFRQL
NP_034013.1      LFKQL
CAA43179.1       LFKQL
NP_990584.1      LFKQL
NP_005185.2      LFKQL
NP_789745.1      LFKTL
CEBE_HUMAN       LFRQI
NP_058791.1      LFRQI
NP_031705.2      FFKKL
CEBD_HUMAN       FFKQL
NP_037286.1      FFKEL
NP_001797.1      LFLEH
CEBG_RAT         LFLEH
CEBG_MOUSE       LFLEH
A43481           IYMQL
CEB_DROVI        IYMQL
AAH18323.1       VLSRY
BAA05833.1       VLSRY
AAR99622.1       VLSRY
NP_059072.1      IVSKY
NP_062067.1      IVSKY
NP_003207.1      IVSKY
A41524           IVSKY
TEF_PHOSU        -----
NP_766151.1      ILAKY
HLF_RAT          ILAKY
NP_002117.1      ILAKY
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NP_525049.1      -----
NP_498426.1      TIRDM
NP_006390.1      VLNSH
NP_058047.1      VLSSH
NP_037044.1      MLNLH
NP_031524.2      MLNLH
NP_001665.1      MLNLH
NP_037085.1      VLEAH
NP_034365.1      VLEAH
NP_005429.1      VLEAH
NP_955598.1      ILAAH
FOS_SHEEP        ILAAH
NP_034364.1      ILAAH
AAG47951.1       ILAAH
FOS_CRIGR        ILAAH
FOS_FELCA        ILAAH
FOS_MESAU        ILAAH
CAB40144.1       ILAAH
NP_005243.1      ILAAH
FOS_MSVFB        ILAAH
FOS_AVINK        ILAAH
NP_990839.1      ILAAH
FOS_FUGRU        ILAAH
FOS_TETFL        ILAAH
FOS_CYPCA        ILAAH
NP_032062.1      VLVAH
NP_006723.1      VLVAH
NP_037086.1      MLVAH
NP_005244.1      MLVAH
FRA2_MOUSE       -----
FRA2_CHICK       MLVAH
A35847           LLATH
NP_593039.1      LVFAH
BAA12194.1       LLIAH
NP_012228.1      -----
NP_010964.1      ISRLH
NP_014232.1      -----
NP_594500.1      QLLAH
NP_595707.1      QLLAH
ATF2_HUMAN       LLLAH
AAH42210.1       LLLAH
NP_112280.1      LLLAH
NP_990235.1      LLLAH
ATF7_HUMAN       LLLAH
CRB5_MOUSE       LLLTH
NP_878901.1      LLLTH
NP_112279.1      -----
CREB_BOVIN       -----
NP_034082.1      -----
AAQ24858.1       -----
BAA83552.1       -----
CREM_CANFA       -----
CREB_CHLVR       -----
NP_996507.1      D----
NP_005162.1      -----
BAB26930.1       -----
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CREM_MOUSE        -----
CREM_HUMAN        -----
NP_776711.1       QLRRL
AAC04325.1        QLRKL
BAB25173.1        QLRKL
A44494            QLHKL
CAA66664.1        ENSEL
NP_059102.1       ENSGL
NP_031374.1       ENQRL
NP_196313.1       -----
NP_566415.3       -----
BAA06486.1        -----
TG21_TOBAC        -----
AAF06696.1        -----
HBB2_WHEAT        -----
AAM64610.1        -----
S48121            -----
AAM64781.1        -----
AAF17682.1        -----
TGAB_TOBAC        Q----
CAB57979.1        ILKNT
NP_568246.1       ILKNT
NP_850604.1       MLINT
NP_850449.1       ANATL
AAM62869.1        ENEAI
CPR1_PETCR        DNSRL
TAF1_TOBAC        ENAAL
EMP1_WHEAT        ENKKL
CPR3_PETCR        ENHSI
NP_849510.1       ENNSI
HBPA_WHEAT        KNTSL
OP2_MAIZE         -----
CPR2_PETCR        -----
OCS1_MAIZE        ENTVL
AAK19601.1        -----
NP_172097.1       ENNEL
BAB82982.1        ENQEL
NP_038870.2       ENQEL
XP_214067.1       ENQEL
MAF_MOUSE         KYEKL
NP_062191.1       KYEKL
NP_005351.2       KYEKL
TMAF_AVIS4        KYEKL
NP_034788.1       KCEKL
NP_062189.1       KCEKL
NP_005452.2       KCEKL
NP_032762.1       RCDRL
NP_006168.1       RCDRL
NP_034885.1       KCEAL
NP_036455.1       KCEAL
NP_990088.1       KYEAL
NP_034886.1       KYEAL
NP_002350.1       KYEAL
MAFG_CHICK        KYEAL
NP_002351.1       KYEAL
NP_034887.1       KYEAL
NP_990087.1       KYEAL
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NP_035032.1      RLSTL
NP_113977.1      KLSTL
NP_006155.2      QLSTL
AAA35612.1       QLTEL
NP_003195.1      KVQSL
NP_032712.2      KVQSL
NP_035033.1      KLHGL
NP_004280.4      KLHDL
NP_732833.1      KFAML
BAA95505.1       NLTGL
NP_031546.1      NLTGL
NP_031547.1      -----
AAK48898.1       -----
CAA31252.1       KVMNH
AP1_COTJA        KVMNH
1404381A         KVMNH
AP1_CHICK        KVMNH
AP1_PIG          KVMNH
NP_068607.1      KVMNH
AP1_SERCA        KVMNH
TJUN_AVIS1       KVMNH
NP_034722.1      KVLSH
NP_005345.2      KVLSH
NP_620230.1      KVLSH
JUND_CHICK       KVLSH
AAH09465.1       KVMTH
NP_068608.2      KVMTH
AAA74916.1       KVMTH
JUNB_CYPCA       KVLRH
NP_476586.1      QVMEH
A30208           -----
CPC1_CRYPA       -----
CAE52206.1       -----
NP_013707.1      ELKKY
AP1_KLULA        ELKRY
AAB29937.1       EITKY
NP_593662.1      ELRIL
NP_011854.1      ENRLL
NP_012283.1      ENHAL
NP_594523.1      LIRPT
CYS3_NEUCR       LVTEK
NP_012282.1      KLNDI
AAH05174.1       LLIEV
NP_109618.1      LLIEV
ATF4_HUMAN       LIEEV
ATF4_MOUSE       LIEEV
GA15_MOUSE       ALIDR
GA15_CRILO       -----
AAB27103.1       ALIDR
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