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CLUSTAL W (1.83) multiple sequence alignment


AP1_CHICK        RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
NP_068607.1      RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
AP1_PIG          RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
AP1_SERCA        RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
1404381A         RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
AP1_COTJA        RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
CAA31252.1       RIKAERKRMRNRIAASKCRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
TJUN_AVIS1       RIKAERKRMRNRIAASKSRKRKLERIARLEEKVKTLKAQNSELASTANMLREQVAQLKQK
NP_034722.1      RIKAERKRLRNRIAASKCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQK
NP_620230.1      RIKAERKRLRNRIAASKCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQK
NP_005345.2      RIKAERKRLRNRIAASKCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQK
JUND_CHICK       RIKAERKRLRNRIAASKCRKRKLERISRLEEKVKSLKSQNTELASTASLLREQVAQLKQK
AAH09465.1       RIKVERKRLRNRLAATKCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQK
NP_068608.2      RIKVERKRLRNRLAATKCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQK
AAA74916.1       RIKVERKRLRNRLAATKCRKRKLERIARLEDKVKTLKAENAGLSSAAGLLREQVAQLKQK
JUNB_CYPCA       RIKAERKRLRNRLAATKCRKRKLERISRLEEKVKVLKNDNAGLSNTASVLRDQVAQLKQK
NP_476586.1      KIKLERKRQRNRVAASKCRKRKLERISKLEDRVKVLKGENVDLASIVKNLKDHVAQLKQQ
CAE52206.1       ------KRARNTEAARRSRARKLQRMKQLEDKVEELLSKNYHLEN-------EVARLKK-
AAH05174.1       GDRKQKKRDQNKSAALRYRQRKRAEGEALEGECQGLEARNRELKERAESVEREIQYVKDL
NP_109618.1      GDRKQKKRDQNKSAALRYRQRKRAEGEALEGECQGLEARNRELRERAESVEREIQYVKDL
ATF4_HUMAN       LDKKLKKMEQNKTAATRYRQKKRAEQEALTGECKELEKKNEALKERADSLAKEIQYLKDL
ATF4_MOUSE       LDKKLKKMEQNKTAATRYRQKKRAEQEALTGECKELEKKNEALKEKADSLAKEIQYLKDL
CYS3_NEUCR       ----EDKRKRNTAASARFRIKKKQREQALEKSAKEMSEKVTQLEGRIQALETENKWLKGL
NP_037044.1      DERKRRRRERNKIAAAKCRNKKKEKTECLQKESEKLESVNAELKAQIEELKNEKQHLIYM
NP_031524.2      DERKRRRRERNKIAAAKCRNKKKEKTECLQKESEKLESVNAELKAQIEELKNEKQHLIYM
NP_001665.1      DERKKRRRERNKIAAAKCRNKKKEKTECLQKESEKLESVNAELKAQIEELKNEKQHLIYM
NP_034365.1      EERRRVRRERNKLAAAKCRNRRKELTDFLQAETDKLEDEKSGLQREIEELQKQKERLELV
NP_005429.1      EERRRVRRERNKLAAAKCRNRRKELTDFLQAETDKLEDEKSGLQREIEELQKQKERLELV
NP_037085.1      EERRRVRRERNKLAAAKCRNRRKELTDFLQAETDKLEDEKSGLQREIEELQKQKERLELV
FOS_MESAU        EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFI
FOS_CRIGR        EEKRRIRRERNKMAAAKCWNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFI
NP_005243.1      EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFI
NP_034364.1      EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFI
AAG47951.1       EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDEKSALQTEIANLLKEKEKLEFI
FOS_MSVFB        EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEDKKSALQTEIANLLKEKEKLEFI
FOS_AVINK        EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEEEKSALQAEIANLLKEKEKLEFI
NP_990839.1      EEKRRIRRERNKMAAAKCRNRRRELTDTLQAETDQLEEEKSALQAEIANLLKEKEKLEFI
FOS_FUGRU        EEKKRIRRERNKQAAAKCRNRRRELTDTLQAETDQLEDEKSSLQNDIANLLKEKERLEFI
FOS_TETFL        EEKKRIRRERNKQAAAKCRNRRRELTDSLQAETDQLEAEKSSLQNDIANLLKEKERLEFI
FOS_CYPCA        EEKKRVRRERNKMAAAKCRNRRRELTDTLQAETDELEDEKSALQNDIANLLKEKERLEFI
NP_032062.1      EEKRRVRRERNKLAAAKCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFV
NP_006723.1      EEKRRVRRERNKLAAAKCRNRRRELTDRLQAETDQLEEEKAELESEIAELQKEKERLEFV
NP_037086.1      EEKRRIRRERNKLAAAKCRNRRRELTEKLQTETEELEEEKSGLQKEIAELQKEKEKLEFM
NP_005244.1      EEKRRIRRERNKLAAAKCRNRRRELTEKLQAETEELEEEKSGLQKEIAELQKEKEKLEFM
FRA2_MOUSE       EEKRRIRRERNKLAAAKCRNRRRELTEKLQAETEELEEEKSGLQKEIAELQKEKEKLE--
FRA2_CHICK       EEKRRIRRERNKLAAAKCRNRRRELTEKLQAETEVLEEEKSVLQKEIAELQKEKEKLEFM
A35847           EQKRAVRRERNKQAAARCRKRRVDQTNELTEEVEQLEKRGESMRKEIEVLTNSKNQLEYL
XP_133376.1      SNEYRVRRERNNIAVRKSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRGI
CEBA_BOVIN       SNEYRVRRERNNIAVRKSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRGI
CEBA_HUMAN       SNEYRVRRERNNIAVRKSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRGI
NP_036656.1      SNEYRVRRERNNIAVRKSRDKAKQRNVETQQKVLELTSDNDRLRKRVEQLSRELDTLRGI
NP_034013.1      SDEYKMRRERNNIAVRKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRNL
CAA43179.1       SDEYKMRRERNNIAVRKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRNL
NP_990584.1      SDEYKLRRERNNIAVRKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRNL
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NP_005185.2       SDEYKIRRERNNIAVRKSRDKAKMRNLETQHKVLELTAENERLQKKVEQLSRELSTLRNL
NP_789745.1       SDEYKIRRERNNIAVRKSRDKAKMRNLETQHKVLELTGENERLQKKVEQLSREVSTLRNL
CEBE_HUMAN        SLEYRLRRERNNIAVRKSRDKAKRRILETQQKVLEYMAENERLRSRVEQLTQELDTLRNL
NP_058791.1       SLEYRLRRERNNIAVRKSRDKAKRRIMETQQKVLEYMAENERLRSRVDQLTQELDTLRNL
NP_031705.2       SPEYRQRRERNNIAVRKSRDKAKRRNQEMQQKLVELSAENEKLHQRVEQLTRDLAGLRQF
CEBD_HUMAN        SPEYRQRRERNNIAVRKSRDKAKRRNQEMQQKLVELSAENEKLHQRVEQLTRDLAGLRQF
NP_037286.1       SPEYRQRRERNNIAVRKSRDKAKRRNQEMQQKLVELSAENEKLHQRVEQLTRDLASLRQF
A43481            TDEYRRRRERNNIAVRKSREKAKVRSREVEERVKSLLKEKDALIRQLGEMTNELQLHKQI
CEB_DROVI         TEEYRRRRERNNIAVRKSREKAKVRSKEVEERVKSLLKEKDALLRQLSEMTNELSLHKQI
CEBG_MOUSE        SDEYRQRRERNNMAVKKSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKDL
CEBG_RAT          SDEYRQRRERNNMAVKKSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKDL
NP_001797.1       SDEYRQRRERNNMAVKKSRLKSKQKAQDTLQRVNQLKEENERLEAKIKLLTKELSVLKDL
AAH18323.1        DEKYWSRRYKNNEAAKRSRDARRLKENQISVRAAFLEKENALLRQEVVAVRQELSHYRAV
AAR99622.1        DEKYWSRRYKNNEAAKRSRDARRLKENQISVRAAFLEKENALLRQEVVAVRQELSHYRAV
BAA05833.1        DEKYWSRRYKNNEAAKRSRDARRLKENQISVRAAFLEKENALLRQEVVAVRQELSHYRAV
NP_062067.1       DEKYWTRRKKNNVAAKRSRDARRLKENQITIRAAFLEKENTALRTEVAELRKEVGKCKTI
NP_003207.1       DEKYWTRRKKNNVAAKRSRDARRLKENQITIRAAFLEKENTALRTEVAELRKEVGKCKTI
NP_002117.1       DDKYWARRRKNNMAAKRSRDARRLKENQIAIRASFLEKENSALRQEVADLRKELGKCKNI
HLF_RAT           DDKYWARRRKNNMAAKRSRDARRLKENQIAIRASFLEKENSALRQEVADLRKELGKCKNI
NP_493610.1       DSAYFERRRKNNDAAKRSRDARRQKEEQIASKAHALERENMQLRGKVSSLEQEAAQLR--
NP_525049.1       DAAYYERRRKNNAAAKKSRDRRRIKEDEIAIRAAYLERQNIELLCQIDALKVQLAAFTS-
NP_006390.1       DVRRVQRREKNRIAAQKSRQRQTQKADTLHLESEDLEKQNAALRKEIKQLTEELKYFTSV
NP_058047.1       DVRKVQRREKNRIAAQKSRQRQTQKADTLHLESEDLEKQNAALRKEIKQLTEELKYFTSV
NP_594500.1       DEKRRRILERNRIAASKFRQKKKEWIKELEQTANAAFEQSKRLQLLLSQLQQEAFRLKSQ
NP_014232.1       ERKRKEFLERNRVAASKFRKRKKEYIKKIEN--DLQFYESE-----YDDLTQVIGKL---
NP_112280.1       DEKRRKFLERNRAAASRCRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQL
AAH42210.1        DEKRRKFLERNRAAASRCRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQL
ATF2_HUMAN        DEKRRKFLERNRAAASRCRQKRKVWVQSLEKKAEDLSSLNGQLQSEVTLLRNEVAQLKQL
NP_990235.1       DEKRRKFLERNRAAASRCRQKRKVWVQSLEKKAEDLSSLNGQLQNEVTLLRNEVAQLKQL
ATF7_HUMAN        DERRQRFLERNRAAASRCRQKRKLWVSSLEKKAEELTSQNIQLSNEVTLLRNEVAQLKQL
BAA12194.1        EEKRKSFLERNRQAALKCRQRKKQWLSNLQAKVEFYGNENEILSAQVSALREEIVSLKTL
NP_012228.1       --KRARLLERNRIAASKCRQRKKVAQLQLQKEFNEIKDENRILLKKLNYYEKLISKFK--
NP_034082.1       ARKREVRLMKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD--------
NP_112279.1       ARKREVRLMKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD--------
CREB_BOVIN        ARKREVRLMKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD--------
AAQ24858.1        ARKREVRLMENREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD--------
BAA83552.1        TRKRELRLMKNREAARECRRKKKEYVKCLENRVAVLESQNKTLIEELKALKD--------
CREM_CANFA        TRKRELRLMKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKD--------
CREB_CHLVR        TRKRELRLYKNREAARECRRKKKEYVKCLENRVAVLENQNKALIEELKSLKD--------
NP_005162.1       QLKREIRLMKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKTLKD--------
BAB26930.1        QLRREIRLMKNRGAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKTLKD--------
CREM_MOUSE        TRKRELRLMKNREAAKECRRRKKEYVKCLESRVAVLEVQNKKLIEELETLKD--------
CREM_HUMAN        TRKRELRLMKNREAAKECRRRKKEYVKCLESRVAVLEVQNKKLIEELETLKD--------
NP_568246.1       ENKRLKRLLRNRVSAQQARERKKAYLSELENRVKDLENKNSELEERLSTLQNENQMLRHI
BAA06486.1        DQKTMRRLAQNREAARKSRLRKKAYVQQLENSRLKLT----QLEQELQR-----------
TG21_TOBAC        DQKTLRRLAQNREAARKSRLRKKAYVQQLENSRLKLS----QLEQDLQR-----------
AAF06696.1        DQKTLRRLAQNREAARKSRLRKKAYVQQLESSRMKLT----QLEQELQR-----------
CPR1_PETCR        DLKRERRKQSNRESARRSRLRKQAEAEELAIKVDSLTAENMALKAEINRLTLTAEKLTND
TAF1_TOBAC        ELKREKRKQSNRESARRSRLRKQAEAEELAIRVQSLTAENMTLKSEINKLMENSEKLKLE
NP_850449.1       ELKRERRKQSNRESARRSRLRKQAETEELARKVEALTAENMALRSELNQLNEKSDKLRGA
AAM62869.1        EVKREKRKQSNRESARRSRLRKQAETEQLSVKVDALVAENMSLRSKLGQLNNESEKLRLE
EMP1_WHEAT        ELKRERRKQSNRESARRSRLRKQQECEELAQKVSELTAANGTLRSELDQLKKDCKTMETE
NP_849510.1       ELKRQKRKQSNRESARRSRLRKQAECEQLQQRVESLSNENQSLRDELQRLSSECDKLKSE
AAB29937.1        SEAKSRRTAQNRAAQRAFRDRKEAKMKSLQERVELLEQKDAQNKTTTDFLLCSLKSLLSE
AP1_KLULA         TEAKDKRTAQNRAAQRAFRERRERKMKELEDKVSQLESLNKQSELETKFLRNQVTNLLSE
NP_593662.1       QEPSSKRKAQNRAAQRAFRKRKEDHLKALETQVVTLKELHSSTTLENDQLRQKVRQLEEE
MAF_MOUSE         RLKQKRRTLKNRGYAQSCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKEK
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NP_062191.1      RLKQKRRTLKNRGYAQSCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKEK
NP_005351.2      RLKQKRRTLKNRGYAQSCRFKRVQQRHVLESEKNQLLQQVDHLKQEISRLVRERDAYKEK
TMAF_AVIS4       RLKQKRRTLKNRGYAQSCRFKRVQQRHVLESEKNQLLQQVEHLKQEISRLVRERDAYKEK
NP_034788.1      RLKQKRRTLKNRGYAQSCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARERDAYKVK
NP_062189.1      RLKQKRRTLKNRGYAQSCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARERDAYKVK
NP_005452.2      RLKQKRRTLKNRGYAQSCRYKRVQQKHHLENEKTQLIQQVEQLKQEVSRLARERDAYKVK
NP_032762.1      RLKQRRRTLKNRGYAQACRSKRLQQRRGLEAERARLAAQLDALRAEVARLARERDLYKAR
NP_006168.1      RLKQRRRTLKNRGYAQACRSKRLQQRRGLEAERARLAAQLDALRAEVARLARERDLYKAR
NP_034885.1      RLKQRRRTLKNRGYAASCRVKRVCQKEELQKQKSELEREVDKLARENAAMRLELDALRGK
NP_036455.1      RLKQRRRTLKNRGYAASCRVKRVCQKEELQKQKSELEREVDKLARENAAMRLELDALRGK
NP_990088.1      RLKQRRRTLKNRGYAASCRVKRVCQKEELQKQKMELEWEVDKLARENAAMRLELDTLRGK
NP_034886.1      QLKQRRRTLKNRGYAASCRVKRVTQKEELEKQKAELQQEVEKLASENASMKLELDALRSK
NP_002350.1      QLKQRRRTLKNRGYAASCRVKRVTQKEELEKQKAELQQEVEKLASENASMKLELDALRSK
MAFG_CHICK       QLKQRRRTLKNRGYAASCRVKRVTQKEELEKQKAELQQEVEKLASENASMKMELDALRSK
NP_002351.1      RLKQRRRTLKNRGYAASCRIKRVTQKEELERQRVELQQEVEKLARENSSMRLELDALRSK
NP_034887.1      RLKQRRRTLKNRGYAASCRIKRVTQKEELERQRVELQQEVEKLARENSSMRLELDALRSK
NP_990087.1      RLKQRRRTLKNRGYAASCRIKRVTQKEELERQRVELQQEVEKLARENSSMKLELDALRSK
NP_035032.1      LIRDIRRRGKNKVAAQNCRKRKLENIVELEQDLGHLKDEREKLLREKGENDRNLHLLKRR
NP_113977.1      LIRDIRRRGKNKVAAQNCRKRKLENIVELEQDLGHLKDEREKLLREKGENDRNLHLLKRK
NP_006155.2      LIRDIRRRGKNKVAAQNCRKRKLENIVELEQDLDHLKDEKEKLLKEKGENDKSLHLLKKQ
AAA35612.1       LVRDIRRRGKNKVAAQNCRKRKLETIVQLERELERLTNERERLLRARGEADRTLEVMRQQ
NP_003195.1      LIRDIRRRGKNKMAAQNCRKRKLDTILNLERDVEDLQRDKARLLREKVEFLRSLRQMKQK
NP_032712.2      LIRDIRRRGKNKMAAQNCRKRKLDTILNLERDVEDLQRDKARLLREKVEFLRSLRQMKQK
NP_732833.1      LIRDIRRRGKNKVAAQNCRKRKLDQILTLEDEVNAVVKRKTQLNQDRDHLESERKRISNK
BAA95505.1       -----RRRSKNRIAAQRCRKRKLDCIQNLESEIEKLQSEKESLLKERDHILSTLGETKQN
NP_031546.1      -----RRRSKNRIAAQRCRKRKLDCIQNLESEIEKLQSEKESLLKERDHILSTLGETKQN
NP_031547.1      -----RRRSKNRIAAQRCRKRKLDCIQNLECEIRKLVCEKEKLLSERNHLK---------
AAK48898.1       -----RRRSKNRIAAQRCRKRKLDCIQNLECEIRKLVCEKEKLLSERNQLK---------
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AP1_CHICK        VMNH
NP_068607.1      VMNH
AP1_PIG          VMNH
AP1_SERCA        VMNH
1404381A         VMNH
AP1_COTJA        VMNH
CAA31252.1       VMNH
TJUN_AVIS1       VMNH
NP_034722.1      VLSH
NP_620230.1      VLSH
NP_005345.2      VLSH
JUND_CHICK       VLSH
AAH09465.1       VMTH
NP_068608.2      VMTH
AAA74916.1       VMTH
JUNB_CYPCA       VLRH
NP_476586.1      VMEH
CAE52206.1       ----
AAH05174.1       LIEV
NP_109618.1      LIEV
ATF4_HUMAN       IEEV
ATF4_MOUSE       IEEV
CYS3_NEUCR       VTEK
NP_037044.1      LNLH
NP_031524.2      LNLH
NP_001665.1      LNLH
NP_034365.1      LEAH
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NP_005429.1      LEAH
NP_037085.1      LEAH
FOS_MESAU        LAAH
FOS_CRIGR        LAAH
NP_005243.1      LAAH
NP_034364.1      LAAH
AAG47951.1       LAAH
FOS_MSVFB        LAAH
FOS_AVINK        LAAH
NP_990839.1      LAAH
FOS_FUGRU        LAAH
FOS_TETFL        LAAH
FOS_CYPCA        LAAH
NP_032062.1      LVAH
NP_006723.1      LVAH
NP_037086.1      LVAH
NP_005244.1      LVAH
FRA2_MOUSE       ----
FRA2_CHICK       LVAH
A35847           LATH
XP_133376.1      FRQL
CEBA_BOVIN       FRQL
CEBA_HUMAN       FRQL
NP_036656.1      FRQL
NP_034013.1      FKQL
CAA43179.1       FKQL
NP_990584.1      FKQL
NP_005185.2      FKQL
NP_789745.1      FKTL
CEBE_HUMAN       FRQI
NP_058791.1      FRQI
NP_031705.2      FKKL
CEBD_HUMAN       FKQL
NP_037286.1      FKEL
A43481           YMQL
CEB_DROVI        YMQL
CEBG_MOUSE       FLEH
CEBG_RAT         FLEH
NP_001797.1      FLEH
AAH18323.1       LSRY
AAR99622.1       LSRY
BAA05833.1       LSRY
NP_062067.1      VSKY
NP_003207.1      VSKY
NP_002117.1      LAKY
HLF_RAT          LAKY
NP_493610.1      ----
NP_525049.1      ----
NP_006390.1      LNSH
NP_058047.1      LSSH
NP_594500.1      LLAH
NP_014232.1      ----
NP_112280.1      LLAH
AAH42210.1       LLAH
ATF2_HUMAN       LLAH
NP_990235.1      LLAH
ATF7_HUMAN       LLAH
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BAA12194.1        LIAH
NP_012228.1       ----
NP_034082.1       ----
NP_112279.1       ----
CREB_BOVIN        ----
AAQ24858.1        ----
BAA83552.1        ----
CREM_CANFA        ----
CREB_CHLVR        ----
NP_005162.1       ----
BAB26930.1        ----
CREM_MOUSE        ----
CREM_HUMAN        ----
NP_568246.1       LKNT
BAA06486.1        ----
TG21_TOBAC        ----
AAF06696.1        ----
CPR1_PETCR        NSRL
TAF1_TOBAC        NAAL
NP_850449.1       NATL
AAM62869.1        NEAI
EMP1_WHEAT        NKKL
NP_849510.1       NNSI
AAB29937.1        ITKY
AP1_KLULA         LKRY
NP_593662.1       LRIL
MAF_MOUSE         YEKL
NP_062191.1       YEKL
NP_005351.2       YEKL
TMAF_AVIS4        YEKL
NP_034788.1       CEKL
NP_062189.1       CEKL
NP_005452.2       CEKL
NP_032762.1       CDRL
NP_006168.1       CDRL
NP_034885.1       CEAL
NP_036455.1       CEAL
NP_990088.1       YEAL
NP_034886.1       YEAL
NP_002350.1       YEAL
MAFG_CHICK        YEAL
NP_002351.1       YEAL
NP_034887.1       YEAL
NP_990087.1       YEAL
NP_035032.1       LSTL
NP_113977.1       LSTL
NP_006155.2       LSTL
AAA35612.1        LTEL
NP_003195.1       VQSL
NP_032712.2       VQSL
NP_732833.1       FAML
BAA95505.1        LTGL
NP_031546.1       LTGL
NP_031547.1       ----
AAK48898.1        ----
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