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CLUSTAL W (1.83) multiple sequence alignment


KNIR_DROVI       CKVCGEPAAGFHFGAFTCEGCKSFFGRSYNNIST--------ISECKN-----DGKCIID
NP_524187.1      CKVCGEPAAGFHFGAFTCEGCKSFFGRSYNNIST--------ISECKN-----EGKCIID
NP_788552.1      CKVCGEPAAGFHFGAFTCEGCKSFFGRSYNNLSS--------ISDCKN-----NGECIIN
EGON_DROME       CKVCGEPAAGFHFGAFTCEGCKSFFGRTYNNIAA--------IAGCKH-----NGDCVIN
1411299B         CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----SCCVID
CAA68539.1       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----SCCVID
THA1_SHEEP       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----SCCVID
THA_MOUSE        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----SCCVID
THA_PIG          CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----SCCVID
NP_990644.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----GCCVID
THA_CAIMO        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----GCCVID
THA_APTPA        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYD-----GCCVID
ERBA_AVIER       CVVCGDKATGYHYRCITCEGCKSFFRRTIQKNLH-------PTYSCTYD-----GCCVID
THA_PYGAD        CVVCGDKATGYHYRCITCAGCKGFFRRTIQKNLH-------PTYSCKYD-----GCCVID
THAB_XENLA       CVVCSDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYD-----GCCIID
THA_RANCA        CVVCSDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYD-----GCCIID
THAA_XENLA       CVVCSDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYD-----GCCIID
NP_571471.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYD-----SCCIID
THAB_PAROL       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYD-----CCCIID
THA_SALSA        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PAYSCKYD-----GCCIID
THAA_PAROL       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GCCIID
THA_HIPHI        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PAYSCKYE-----GCCIID
NP_000452.2      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GKCVID
THB2_HUMAN       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GKCVID
NP_033406.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSLH-------PSYSCKYE-----GKCIID
THB2_RAT         CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSLH-------PSYSCKYE-----GKCIID
THB1_MOUSE       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSLH-------PSYSCKYE-----GKCIID
THB1_RAT         CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSLH-------PSYSCKYE-----GKCIID
THB1_SHEEP       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GKCVID
THB_CHICK        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PTYSCKYE-----GKCVID
THBA_XENLA       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GKCVID
THB_RANCA        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GKCVID
THBB_XENLA       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLH-------PSYSCKYE-----GKCVID
NP_571415.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLN-------PTYACKYE-----GKCVID
THB_PAROL        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLN-------PTYACKYE-----GKCVID
NHR1_ONCVO       CVVCGDDATGLHYRAITCEGCKGFFRRTVQQKI---------VYKCKSI-----ERCEIS
NP_000367.1      CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------LFTCPFN-----GDCRIT
VDR_BOVIN        CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------LFTCPFN-----GDCRIT
AAK48863.1       CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------LFTCPFN-----GDCRIT
NP_058754.1      CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------LFTCPFN-----GDCRIT
VDR_MOUSE        CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------LFTCPFN-----GDCRIT
NP_990429.1      CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------MFTCPFN-----GDCKIT
VDR_COTJA        CGVCGDRATGFHFNAMTCEGCKGFFRRSMKRKA---------MFTCPFS-----GDCKIT
VDR_XENLA        CGVCGDKATGFHFNAMTCEGCKGFFRRSMKRKA---------MFTCPFN-----GDCRIT
NP_035066.1      CRVCGDKANGYHFNVMTCEGCKGFFRRAMKRNV---------RLRCPFRK----GTCEIT
NP_443212.1      CRVCGDKANGYHFNVMTCEGCKGFFRRAMKRNV---------RLRCPFRK----GTCEIT
CAB55489.1       CRVCGDKATGYHFNVMTCEGCKGFFRRAMKRNA---------RLRCPFRK----GACEIT
AAM76230.1       CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSI---------GPTCPFA-----GSCEVS
NP_005113.1      CVVCGDQATGYHFNALTCEGCKGFFRRTVSKSI---------GPTCPFA-----GSCEVS
NP_033933.1      CVVCGDRATGYHFHALTCEGCKGFFRRTVSKTI---------GPICPFA-----GRCEVS
NP_075230.1      CVVCGDRATGYHFHALTCEGCKGFFRRTVSKTI---------GPICPFA-----GRCEVS
BAD00038.1       CMVCGDRATGYHFHALTCEGCKGFFRRTVSKNT---------GLTCPFA-----GSCKVN
BAD00039.1       CMVCGDRATGYHFHALTCEGCKGFFRRTVSKNT---------GLTCPFA-----GNCKVN
NH48_CAEEL       CRVCGDKAFSYNFNVITCESCKAFFRRNANKEK---------EIRCPFN-----EQCEIN
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NP_524493.1     CAVCGDKALGYNFNAVTCESCKAFFRRNALAKK---------QFTCPFN-----QNCDIT
NP_741445.1     CTVCSDRANGYNFGVLTCESCKAFFRRNASKHK---------EIKCPFS-----DSCQIT
AAD16050.1      CSVCGDKASGFHYNVLSCEGCKGFFRRSVIKG---------ARYVCHSG-----GHCPMD
NP_113815.1     CSVCGDKASAFHYNVLSCEGCKGFFRRSVIKG---------ARYICHSG-----GHCPMD
NRH3_HUMAN      CSVCGDKASGFHYNVLSCEGCKGFFRRSVIKG---------AHYICHSG-----GHCPMD
NP_033499.1     CRVCGDKASGFHYNVLSCEGCKGFFRRSVVHGGA-------GRYACRGS-----GTCQMD
NRH2_RAT        CRVCGDKASGFHYNVLSCEGCKGFFRRSVVHGGA-------GRYACRGS-----GTCQMD
NP_009052.1     CRVCGDKASGFHYNVLSCEGCKGFFRRSVVRGGA-------RRYACRGG-----GTCQMD
ECR_AEDAE       CLVCGDRESGYHYNALTCEGCKGFFRRSVTKN---------AVYCCKFG-----HACEMD
ECR_CHITE       CLVCGDRASGYHYNALTCEGCKGFFRRSVTKN---------AVYCCKFG-----HECEMD
ECR_LUCCU       CLVCGDRASGYHYNALTCEGCKGFFRRSVTKN---------AVYCCKFG-----HACEMD
NP_724460.1     CLVCGDRASGYHYNALTCEGCKGFFRRSVTKS---------AVYCCKFG-----RACEMD
ECR_HELVI       CLVCGDRASGYHYNALTCEGCKGFFRRSVTKN---------AVYICKFG-----HACEMD
ECR_MANSE       CLVCGDRASGYHYNALTCEGCKGFFRRSVTKN---------AVYICKFG-----HACEMD
ECR_BOMMO       CLVCGDRASGYHYNALTCEGCKGFFRRSVTKN---------AVYICKFG-----HACEMD
NRH4_HUMAN      CVVCGDRASGYHYNALTCEGCKGFFRRSITKN---------AVYKCKNG-----GNCVMD
NRH4_MOUSE      CVVCGDRASGYHYNALTCEGCKGFFRRSITKN---------AVYKCKNG-----GNCVMD
NP_068513.1     CVVCGDRASGYHYNALTCEGCKGFFRRSITKN---------AVYKCKNG-----GNCVMD
NP_004950.2     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKHYTCTE-----SQSCKID
NP_776828.1     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKHYTCTE-----SQSCKID
NP_445796.1     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKHYTCTE-----SQSCKID
STF1_MOUSE      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKHYTCTE-----SQSCKID
AAG35648.1      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKHYTCTE-----SQSCKID
STF1_PIG        CPVCGDKVSGYHYGLLTCETCKGFFKRTVQN---------NKHYTCTE-----SQSCKID
AAK94918.1      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKHYTCTE-----SQNCKID
NP_990409.1     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKRYTCIE-----NQNCQID
NP_995582.1     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------NKRYTCIE-----NQNCQID
NP_109601.1     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------QKRYTCIE-----NQNCQID
FTF1_BOMMO      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------KKVYTCVA-----ERACHID
NP_524143.2     CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN---------KKVYTCVA-----ERSCHID
NH25_CAEEL      CPVCGDRVSGYHYGLLTCESCKGFFKRTVQN---------KKQYQCSA-----EANCHVD
AAA28543.1      CPICGDKISGFHYGIFSCESCKGFFKRTVQN---------RKNYVCVR-----GGPCQVS
NP_034394.1     CLICGDRATGLHYGIISCEGCKGFFKRSICN---------KRVYRCSR-----DKNCVMS
NR61_HUMAN      CLICGDRATGLHYGIISCEGCKGFFKRSICN---------KRVYRCSR-----DKNCVMS
AAG09282.1      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
PRGR_SHEEP      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
PRGR_RABIT      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
PRGR_HUMAN      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
NP_032855.1     CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
NP_074038.1     CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
NP_990593.1     CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAG-----RNDCIVD
AAN63590.1      CLICSDEASGCHYGALTCGSCKVFFKRAIEG---------QHNYLCAG-----RNDCIGD
GCR_SAGOE       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_SAIBB       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_AOTNA       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_SAISC       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
NP_000167.1     CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_PIG         CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_TUPGB       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_RABIT       CLVCSDEASGCHYGVLTCGSCKVFFKRAVKG---------QHNYLCAG-----RNDCIID
GCR_RAT         CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
NP_032199.1     CLVCSDEASVCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_CAVPO       CLVCSDELSGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_XENLA       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
GCR_SHEEP       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QH------------------
GCR_ONCMY       CLVCSDEASGCHYGVLTCGSCKVFFKRAVEGWRARQNTDGQHNYLCAG-----RNDCIID
GCR_PAROL       CLVCSDEASGCHYGVVTCGSCKVFFKRAVEGWRARQNTDGQHNYLCAG-----RNDCIID
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MCR_MOUSE       CLVCGDEASGCHYGVVTCGSCKVFFKRAVE-----------HNYLCAG-----RNDCIID
NP_037263.1     CLVCGDEASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
MCR_TUPGB       CLVCGDGASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
MCR_SAISC       CLVCGDEASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
NP_000892.1     CLVCGDEASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAG-----RNDCIID
MCR_XENLA       CLVCGDEASGCHYGVVTCGSCKVFFKRAVEGKCSR-----QHSYLCAG-----RNDCIID
AAG37994.1      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_EULFC      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_CANFA      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
AAS19691.1      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_PAPHA      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_MACFA      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_HUMAN      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_PANTR      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
AAM96904.1      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
ANDR_RABIT      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
NP_036634.1     CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
NP_038504.1     CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCAS-----RNDCTID
AAP85538.1      CLSCEDEASGCHYEALTCGSCKVFFKRAAEG---------NQKYLCAS-----RNDCTID
AAQ93376.1      CLVCGDIASGYHYGVASCEACKAFFKRTIQG---------NIEYSCPA-----TNECEIT
NP_036065.1     CLVCGDIASGYHYGVASCEACKAFFKRTIQG---------NIEYSCPA-----TNECEIT
ERR2_RAT        CLVCGDIASGYHYGVASCEACKAFFKRTIQG---------NIEYSCPA-----TNECEIT
NP_004443.2     CLVCGDIASGYHYGVASCEACKAFFKRTIQG---------NIEYSCPA-----TNECEIT
ERR2_MOUSE      CLVCGDIASGYHYGVASCEACKAFFKRTIQG---------NIEYNCPA-----TNECEIT
ERR1_HUMAN      CLVCGDVASGYHYGVASCEACKAFFKRTIQG---------SIEYSCPA-----SNECEIT
ERR1_MOUSE      CLVCGDVASGYHYGVASCEACKAFFKRTIQG---------SIEYSCPA-----SNECEIT
AAS46251.1      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_PIG        CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_HORSE      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
NP_031982.1     CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
NP_036821.1     CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_MESAU      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_HUMAN      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_XENLA      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_POEGU      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
NP_990514.1     CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_SHEEP      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_OREAU      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_ORENI      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_ONCMY      CAVCSDFASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTMD
ESR1_SALSA      CAVCSDFASGYHYGFWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTMD
ESR1_PAGMA      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_SPAAU      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
ESR1_ORYLA      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYMCPA-----TNQCTID
BAB16893.1      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYVCPA-----TNQCTID
ESR1_ICTPU      CSVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYVCPA-----TNQCTID
ERB1_CARAU      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_ONCMY      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_SPAAU      CAVCHDYASGYHYGVWSCEGCKAFFKRSIQR---------HNDYICPA-----TNQCTID
ESR3_MICUN      CAVCHDYASGYHYGVWSCEGCKAFFKRSIQR---------DNEYICPA-----TNECTID
ESR2_ORENI      CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ERB2_CARAU      CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_ANGJA      CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG---------HNGYICPA-----TNQCTID
ESR2_MICUN      CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_ICTPU      CVVCHDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_BOVIN      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_SHEEP      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
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ESR2_MOUSE          CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_RAT            CPVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_CALJA          CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
NP_001428.1         CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_PIG            CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_COTJA          CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
NP_990125.1         CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
ESR2_STUVU          CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG---------HNDYICPA-----TNQCTID
CAA42718.1          CAVCGDNASCQHYGVRTCEGCKGFFKRTVQK---------SAKYICLA-----NKDCPVD
NR41_RAT            CAVCGDNASCQHYGVRTCEGCKGFFKRTVQK---------SAKYICLA-----NKDCPVD
NP_002126.2         CAVCGDNASCQHYGVRTCEGCKGFFKRTVQK---------NAKYICLA-----NKDCPVD
NR41_CANFA          CAVCGDNASCQHYGVRTCEGCKGFFKRTVQK---------NAKYICLA-----NKDCPVD
NR42_XENLA          CAVCGDNASCQHYGVRTCEGCKGFFKRTVQK---------NAKYICLA-----NKDCPVD
HR38_BOMMO          CAVCGDTAACQHYGVRTCEGCKGFFKRTVQK---------GSKYVCLA-----EKSCPVD
HR38_DROME          CAVCGDTAACQHYGVRTCEGCKGFFKRTVQK---------GSKYVCLA-----DKNCPVD
NP_038641.1         CAVCGDNAACQHYGVRTCEGCKGFFKRTVQK---------NAKYVCLA-----NKNCPVD
NR42_RAT            CAVCGDNAACQHYGVRTCEGCKGFFKRTVQK---------NAKYVCLA-----NKNCPVD
NP_006177.1         CAVCGDNAACQHYGVRTCEGCKGFFKRTVQK---------NAKYVCLA-----NKNCPVD
NP_008912.2         CAVCGDNAACQHYGVRTCEGCKGFFKRTVQK---------NAKYVCLA-----NKNCPVD
NP_113816.1         CAVCGDNAACQHYGVRTCEGCKGFFKRTVQK---------NAKYVCLA-----NKNCPVD
NP_056558.1         CAVCGDNAACQHYGVRTCEGCKGFFKRTVQK---------NAKYVCLA-----NKNCPVD
NP_497731.1         CAVCNDRAVCLHYGARTCEGCKGFFKRTVQK---------NSKYTCAG-----NKTCPID
7UP2_DROME          CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLT---------YSCR-----GSRNCPID
NP_524325.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLT---------YSCR-----GSRNCPID
NP_066285.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLS---------YTCR-----ANRNCPID
NP_989752.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLS---------YTCR-----ANRNCPID
NP_542956.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLS---------YTCR-----ANRNCPID
CAA54096.1          CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLS---------YTCR-----ANRNCPID
NP_776827.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLS---------YTCR-----ANRNCPID
NP_005645.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLT---------YTCR-----ANRNCPID
NP_034281.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLT---------YTCR-----ANRNCPID
NP_786998.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLT---------YTCR-----ANRNCPID
NP_571255.1         CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLT---------YTCR-----ANRNCPID
NP_571261.1         CMVCGDKSSGKHYGQFTCEGCKSFFKRSVRRNLS---------YTCR-----GNRDCPID
EAR2_MOUSE          CVVCGDKSSGKHYGVFTCEGCKSFFKRTIRRNLS---------YTCR-----SNRDCQID
NP_620813.1         CVVCGDKSSGKHYGVFTCEGCKSFFKRTIRRNLS---------YTCR-----SNRDCQID
NP_005225.2         CVVCGDKSSGKHYGVFTCEGCKSFFKRSIRRNLS---------YTCR-----SNRDCQID
AAH54649.1          CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLS---------YTCR-----DNKDCLVD
NP_571313.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLS---------YTCR-----DNKECLVD
NP_035435.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLT---------YTCR-----DNKDCLID
NP_036937.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLT---------YTCR-----DNKDCLID
NP_002948.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLT---------YTCR-----DNKDCLID
RXRA_XENLA          CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLT---------YTCR-----DSKDCMID
NP_571228.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLT---------YTCR-----DNKDCMID
RXRA_BRARE          CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLT---------YTCR-----DNKDCQID
NP_008848.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLI---------YTCR-----DNKDCLID
NP_033133.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLI---------YTCR-----DNKDCLID
NP_990625.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLI---------YTCR-----DNKDCLID
RXRG_XENLA          CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLV---------YTCR-----DSKDCLID
NP_035436.1         CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLT---------YSCR-----DNKDCTVD
RXRB_RAT            CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLT---------YSCR-----DNKDCTVD
S37781              CAICGDRSSGKHYGVYSCEGCKGFFKRTIRKDLT---------YSCR-----DNKDCTVD
USP_BOMMO           CSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLT---------YACR-----EDKNCIID
USP_MANSE           CSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLT---------YACR-----EDRNCIID
USP_CHOFU           CSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLS---------YACR-----EERNCIID
NP_476781.1         CSICGDRASGKHYGVYSCEGCKGFFKRTVRKDLT---------YACR-----ENRNCIID
NP_059019.1         CVVCGDKASGRHYGAVSCEGCKGFFKRSVRKNLT---------YSCR-----SSQDCIIN
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TR4_MOUSE          CVVCGDKASGRHYGAVSCEGCKGFFKRSVRKNLT---------YSCR-----SSQDCIIN
TR4_HUMAN          CVVCGDKASGRHYGAVSCEGCKGFFKRSVRKNLT---------YSCR-----SNQDCIIN
TR2_HUMAN          CVVCGDKASGRHYGAVTCEGCKGFFKRSIRKNLV---------YSCR-----GSKDCIIN
HR78_DROME         CLVCGDRASGRHYGAISCEGCKGFFKRSIRKQLG---------YQCR-----GAMNCEVT
NH41_CAEEL         CVVCGDKASGRHYGAVSCEGCKGFFKRSIRKRIG---------YVCR-----SQKDCPVT
NP_003260.1        CKVCGDRSSGKHYGVYACDGCSGFFKRSIRRNRT---------YVCK---SGNQGGCPVD
NP_689415.1        CKVCGDRSSGKHYGVYACDGCSGFFKRSIRRNRT---------YVCK---SGNQGGCPVD
NP_990501.1        CKVCGDRSSGKHYGVYACDGCSGFFKRSIRRNRT---------YVCK---SGNQGGCPVD
NR21_ORYLA         CKVCGDRSSGKHYGVYACDGCSGFFKRSIRRNRI---------YLCK---SGSQGGCPVD
NR21_XENLA         CKVCGDRSSGKHYGVYACDGCSGFFKRSIRRNRS---------YVCK---SGNQGGCPVD
NP_524596.1        CKVCRDHSSGKHYGIYACDGCAGFFKRSIRRSRQ---------YVCK---SQKQGLCVVD
TLL_DROVI          CKVCRDHSSGKHYGIYACDGCAGFFKRSIRRSRQ---------YVCK---SQKQGLCVVD
NP_502094.1        CRVCEDHSSGKHYSIFSCDGCAGFFKRSIRRHRQ---------YVCKNKGSPSEGQCKVD
NP_038736.1        CRVCGDSSSGKHYGIYACNGCSGFFKRSVRRRLI---------YRCQ----VGAGMCPVD
NP_055064.1        CRVCGDSSSGKHYGIYACNGCSGFFKRSVRRRLI---------YRCQ----VGAGMCPVD
NP_497074.1        CAVCGDVALGKHYGVNACNGCKGFFRRSIWKNRT---------YACR-----HGGKCLVA
NP_501775.1        CDVCGDVAFGKHYGINACNGCKGFFRRSVWSRRQ---------YSCR-----FGGDCPVV
CAA54248.1         CAICGDRATGKHYGASSCDGCKGFFRRSVRKNHM---------YSCRF-----SRQCVVD
NP_032287.1        CAICGDRATGKHYGASSCDGCKGFFRRSVRKNHM---------YSCRF-----SRQCVVD
NP_071516.1        CAICGDRATGKHYGASSCDGCKGFFRRSVRKNHM---------YSCRF-----SRQCVVD
HN4A_XENLA         CAICGDRATGKHYGASSCDGCKGFFRRSVRKNHM---------YSCRF-----SRQCVVD
HN4B_XENLA         CAICGDRATGKHYGASSCDGCKGFFRRSVRKNHV---------YACRF-----SRQCIVD
HN4G_HUMAN         CAICGDRATGKHYGASTCDGCKGFFRRSIRKSHI---------YSCRF-----SRQCVVD
HN4G_MOUSE         CAICGDRATGKHYGASSCDGCKGFFRRSIRKSHV---------YSCRF-----SRQCVVD
S36218             CAICGDRATGKHYGASSCDGCKGFFRRSVRKNHQ---------YTCRF-----ARNCVVD
NP_492615.2        CHICNDKSTGKHYGAISCDGCKGFFRRSIRKRYH---------YQCRF-----EQNCDVT
NP_491103.1        CAICGDRATGKHYGAMSCDGCKGFFRRTIRKRHS---------YVCRF-----GEKCQVD
NH35_CAEEL         CHICSDVATGRHYGAIACNGCKGFFRRTVRRNYE---------YHCRF-----ESKCEID
NP_496066.2        CLICGEPSTGKHYGIVACLGCKTFFRRAVVQRQD---------TECKR-----EKPCDVT
NH14_CAEEL         CVVCGDKAIGKHYGAVACNGCKGFFRRSVWQNLQ---------YTCRF-----NKQCNID
NP_492612.1        CAVCGDKSTGTHYGVISCNGCKGFFRRTVLRDQK---------FTCRF-----NKRCVID
NHR1_CAEEL         CAVCSDLATGYHYGVASCNGCKTFFRRTIVSEQT---------FICQY-----NGNCDVN
NP_498554.1        CLVCSDISTGYHYGVPSCNGCKTFFRRTIMKNQT---------FSCQF-----QGKCPVD
NP_504455.1        CAVCDDIATGKHYSVASCNGCKTFFRRALVNNRE---------FVCQG-----NKDCPVN
NH40_CAEEL         CVVCSDFASGIHYSVASCNGCKTFFRRALVNKQT---------FTCQF-----SGDCVVG
NP_502117.2        CAVCGDTPAKIHYGVLACFGCKGFFRRAVKDGRNK--------YVCRF-----EKNCEVT
NP_741456.1        CAVCGDGIAKLHYGVLACYGCKGFFRRTLT-GKYR--------YACRF-----SNNCIVD
NP_510423.1        CSVCCDEASGRHYGVVACFGCKGFFRRTVRAGKN---------YVCRY-----SKKCRID
NP_000957.1        CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
RRG2_HUMAN         CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
RRG2_MOUSE         CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
A34714             CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
RRG_NOTVI          CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCQIN
RRG_XENLA          CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCQIN
AAB59953.1         CFVCQDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCQIN
NP_571414.1        CFVCQDKSSGYHYGVSSCEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCQIN
AAD05222.1         CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
RRA_MOUSE          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
NP_989867.1        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
RRA_XENLA          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCIIN
RRA_NOTVI          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKTCIIN
RRB_COTJA          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCVIN
S13512             CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----DKNCVIN
RRB_HUMAN          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MIYT-CHR-----DKNCVIN
RRB_MOUSE          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MIYT-CHR-----DKNCVIN
RRB_NOTVI          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MIYT-CHR-----DKNCVIN
RRA_FUGRU          CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKN--------MVYT-CHR-----EKNCIIN
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AAA19972.1       CRVCGDKASGFHYGVHACEGCKGFFRRTIRMK--------LEYEKCDR-----I--CKIQ
NP_006229.1      CRVCGDKASGFHYGVHACEGCKGFFRRTIRMK--------LEYEKCER-----S--CKIQ
CAA40856.1       CRICGDKASGYHYGVHACEGCKGFFRRTIRLK--------LVYDKCDR-----S--CKIQ
NP_037328.1      CRICGDKASGYHYGVHACEGCKGFFRRTIRLK--------LAYDKCDR-----S--CKIQ
CAA68898.1       CRICGDKASGYHYGVHACEGCMGFFRRTIRLK--------LVYDKCDR-----S--CKIQ
PPAR_PHACI       CRICGDKASGYHYGVHACEGCKGFFRRTIRLK--------LAYDKCDR-----S--CKIQ
PPAR_CANFA       CRICGDRASGYHYGVHACEGCKGFFRRTIRLK--------LAYDKCDR-----S--CKIQ
PPAR_CAVPO       CRICGDKASGYHYGVHACEGCKGFFRRTIRLK--------LVYDKCDR-----S--CKIQ
PPAR_XENLA       CRVCSDKASGFHYGVHACEGCKGFFRRTIRLK--------LVYDRCER-----M--CKIQ
PPAS_XENLA       CKICGDRASGFHYGVHACEGCKGFFRRTIRMR--------LQYEHCDR-----N--CKIQ
NP_851367.1      CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
PPAT_PIG         CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
PPAT_CRIGR       CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
PPAT_MACMU       CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
CAA73382.2       CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
NP_056953.2      CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
NP_035276.1      CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
PPAT_RABIT       CRVCSDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYDRCDL-----N--CRIH
PPAT_XENLA       CRVCGDKASGFHYGVHACEGCKGFFRRTIRLK--------LIYERCDL-----N--CRIH
CAB53540.1       CKVCGDVASGFHYGVLACEGCKGFFRRSIQQN--------IQYKRCLK-----NENCSIV
NP_665718.1      CKVCGDVASGFHYGVHACEGCKGFFRRSIQQN--------IQYKRCLK-----NENCSIV
NP_035714.2      CKVCGDVASGFHYGVHACEGCKGFFRRSIQQN--------IQYKKCLK-----NENCSIM
NRD2_HUMAN       CKVCGDVASGFHYGVHACEGCKGFFRRSIQQN--------IQYKKCLK-----NENCSIM
NRD2_RAT         CKVCGDVASGFHYGVHACEGCKGFFRRSIQQN--------IQYKKCLK-----NENCSIM
E75_CHOFU        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQK--------IQYRPCTK-----NQQCSIL
E75_MANSE        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQK--------IQYRPCTK-----NQQCSIL
E75A_DROME       CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQK--------IQYRPCTK-----NQQCSIL
E75_GALME        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQK--------IQYRPCTK-----NQQCSIL
E75_METEN        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQK--------IQYRPCTK-----NQQCSIL
E75C_DROME       CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQK--------IQYRPCTK-----NQQCSIL
NP_493284.1      CQVCSDKASGFHYGVFACEGCKGFFRRSIQQK--------ITYRACTR-----AEDCLIL
AAH14804.1       CKICGDKSSGIHYGVITCEGCKGFFRRSQQCN--------VAYS-CTR-----QQNCPID
RORG_HUMAN       CKICGDKSSGIHYGVITCEGCKGFFRRSQRCN--------AAYS-CTR-----QQNCPID
AAH58269.1       CKICGDKSSGIHYGVITCEGCKGFFRRSQQNN--------ASYS-CPR-----QRNCLID
RORB_RAT         CKICGDKSSGIHYGVITCEGCKGFFRRSQQNN--------ASYS-CPR-----QRNCLID
RORB_HUMAN       CKICGDKSSGIHYGVITCEGCKGFFRRSQQNN--------ASYS-CPR-----QRNCLID
NP_038674.1      CKICGDKSSGIHYGVITCEGCKGFFRRSQQSN--------ATYS-CPR-----QKNCLID
NP_599022.1      CKICGDKSSGIHYGVITCEGCKGFFRRSQQSN--------ATYS-CPR-----QKNCLID
HR3_GALME        CKVCGDKSSGVHYGVITCEGCKGFFRRSQSTV--------VNYQ-CPR-----NKACVVD
HR3_MANSE        CKVCGDKSSGVHYGVITCEGCKGFFRRSQSTV--------VNYQ-CPR-----NKACVVD
NP_788303.1      CKVCGDKSSGVHYGVITCEGCKGFFRRSQSSV--------VNYQ-CPR-----NKQCVVD
NP_740887.1      CKVCGDKSSGVHYGVITCEGCKGFFRRSQSSI--------VNYQ-CPR-----QKNCVVD
E78A_DROME       CKVCGDKASGYHYGVTSCEGCKGFFRRSIQKQ--------IEYR-CLR-----DGKCLVI
NP_509713.2      CKVCGDKASGYHYGVTSCEGCKGFFRRSIQRK--------IDYR-CLK-----QQVCEIK
NHR2_CAEEL       CMVCGDNSTGYHYGVQSCEGCKGFFRRSVHKN--------IAYV-CTK-----GENCTFS
NP_494785.1      CAICQESAEGFHFGAEACRACAAFFRRTVSNR---------KTYSCQG-----NNDCDVT
NP_503561.2      CSICREDGDGYHFGAEACRACAAFFRRSVSLD---------KTYLCRG-----NNDCEIT
NP_505589.1      CAVCNEVGDGLHFGAEACRACTAFFRRSVALS---------KKYECRA-----GRNCEVS
NP_510659.1      CSVCGEAGDGAHFGAEACRACAAFFRRSVALN---------KAYVCRA-----MGTCVIQ
NP_741644.1      CLICCEVADGHHFGAAACRACAAFFRRTVQLN---------KVHDCPK-----NGQCFIL
NP_504771.1      CLICGDSADSLHFGALSCRACAAFFRRKVAGR---------RNIFRRC-----DRQCKVD
NP_503608.2      CEVCGDKTSGRHFGVMSCRACAAFFRRAATWN---------LEKRICP-----NGTCHTS
NP_507680.1      CKVCGDTGNGMHFGAFTCRACAAFFRRAASRK---------FLR----------KCENH
                 *  * :     ::   :*  *  ** *

KNIR_DROVI       KKN-------RTTCKACRLRKCYNVGMSKGG-----------------SRYGRRSNWFK
NP_524187.1      KKN-------RTTCKACRLRKCYNVGMSKGG-----------------SRYGRRSNWFK
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NP_788552.1      KKN-------RTACKACRLKKCLMVGMSKSG------------------SRYGRRSNWFK
EGON_DROME       KKN-------RTACKACRLRKCLLVGMSKSG------------------SRYGRRSNWFK
1411299B         KIT-------RNQCQLCRFKKCIAVAMAMDL----VLDDS---------KRV-AKRKLIE
CAA68539.1       KIT-------RNQCQLCRFKKCIAVAMAMDL----VLDDS---------KRV-AKRKLIE
THA1_SHEEP       KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDS---------KRV-AKRKLIE
THA_MOUSE        KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDS---------KRV-AKRKLIE
THA_PIG          KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDS---------KRV-AKRKLIE
NP_990644.1      KIT-------RNQCQLCRFKKCISVGMAMDL----VLDDS---------KRV-AKRKLIE
THA_CAIMO        KIT-------RNQCQLCRFKKCISVGMAMDL----VLDDS---------KRV-AKRKLIE
THA_APTPA        KIT-------RNQCQLCRFKKCISVGMAMDL----VLDDS---------KRV-AKRKLIE
ERBA_AVIER       KIT-------RNQCQLCRFKKCISVGMAMDL----VLDDS---------KRV-AKRKLIE
THA_PYGAD        KIT-------RNQCQLCRFKKCISVGMAMDL----VLYDS---------KRV-AKRKLIE
THAB_XENLA       KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDS---------KRV-AKRKLIE
THA_RANCA        KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDS---------KRV-AKRKLIE
THAA_XENLA       KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDG---------KRV-AKRKLIE
NP_571471.1      KIT-------RNQCQLCRFRKCISVGMAMDL----VLDDS---------KRV-AKRRLIE
THAB_PAROL       KIT-------RNQCQLCRFKKCIAVGMAMDL----VLDDS---------KRV-AKRRLIE
THA_SALSA        KIT-------RNQCQLCRFRKCIAVCMAMDL----VLDDS---------KRV-AKRRLIE
THAA_PAROL       KIT-------RNQCQLCRFKKCISVGMAMDL----VLDDS---------KRV-AKRRLIE
THA_HIPHI        KIT-------RNQCQLCRFKKCISVGMAMDL----VLDDS---------KRV-AKRRLIE
NP_000452.2      KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
THB2_HUMAN       KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
NP_033406.1      KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
THB2_RAT         KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
THB1_MOUSE       KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
THB1_RAT         KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
THB1_SHEEP       KVT-------RNQCQECRFKKCIYVGMATDL----VLDDS---------KRL-AKRKLIE
THB_CHICK        KVT-------RNQCQECRFKKCIFVGMATDL----VLDDS---------KRL-AKRKLIE
THBA_XENLA       KVT-------RNQCQECRFKKCIAVGMATDL----VLDDN---------KRL-AKRKLIE
THB_RANCA        KVT-------RNQCQECRFKKCIAVGMATDL----VLDDS---------KRL-AKRKLIE
THBB_XENLA       KVT-------RNQCQECRFKKCKTVGMATDL----VLDDS---------KRL-AKRKLIE
NP_571415.1      KVT-------RNQCQECRFKKCIAVGMATDL----VLDDS---------KRL-AKRKLIE
THB_PAROL        KVT-------RNQCQECRFKKCIAVGMATDL----VLDDS---------KRL-AKRKLIE
NHR1_ONCVO       KIS-------RNICQFCRFQKCLRNGMTKSL----VLNET---------ERI-AKRKMII
NP_000367.1      KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIL
VDR_BOVIN        KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIL
AAK48863.1       KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIL
NP_058754.1      KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIM
VDR_MOUSE        KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIM
NP_990429.1      KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIL
VDR_COTJA        KDN-------RRHCQACRLKRCVDIGMMKEF----ILTDE---------EVQ-RKREMIL
VDR_XENLA        KDN-------RRHCQSCRLKRCVDIGMMKEF----ILTDE---------EVQ-RKRQMIN
NP_035066.1      RKT-------RRQCQACRLRKCLESGMKKEM----IMSDA---------AVE-QRRALIK
NP_443212.1      RKT-------RRQCQACRLRKCLESGMKKEM----IMSDA---------AVE-QRRALIK
CAB55489.1       RKT-------RRQCQACRLRKCLESGMKNEM----IMSDE---------AVE-ERRALIK
AAM76230.1       KIQ-------RRHCPACRLQKCLDAGMRKDM----ILSAE---------ALA-LRRAKQA
NP_005113.1      KTQ-------RRHCPACRLQKCLDAGMRKDM----ILSAE---------ALA-LRRAKQA
NP_033933.1      KAQ-------RRHCPACRLQKCLNVGMRKDM----ILSAE---------ALA-LRRARQA
NP_075230.1      KAQ-------RRHCPACRLQKCLNVGMRKDM----ILSAE---------ALA-LRRARQA
BAD00038.1       KAQ-------RRHCPACRLQKCLDAGMKKEM----ILSAE---------ALA-QRRAKQA
BAD00039.1       KAQ-------RRHCPACRLQKCLDAGMKKEM----ILSAE---------ALV-QRRAKQA
NH48_CAEEL       MVS-------RRFCQRCRLTKCFAVSLAEKS----HRLEE---------LFVGMKKEWIM
NP_524493.1      VVT-------RRFCQKCRLRKCLDIGMKSEN----IMSEE---------DKL-IKRRKIE
NP_741445.1      SAS-------RKFCQACRLNKCFAVGMNSEW----LNDLK---------PKSSIVSGKFK
AAD16050.1       TYM-------RRKCQECRLRKCRQAGMREEC----VLSEE---------QIRLKKLKRQE
NP_113815.1      TYM-------RRKCQECRLRKCRHAGMREEC----VLSEE---------QIRLKKLKRQE
NRH3_HUMAN       TYM-------RRKCQECRLRKCRQAGMREEC----VLSEE---------QIRLKKLKRQE
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NP_033499.1      AFM-------RRKCQLCRLRKCKEAGMREQC----VLSEE---------QIRKKRIQKQQ
NRH2_RAT         AFM-------RRKCQLCRLRKCKEAGMREQC----VLSEE---------QIRKKKIQKQQ
NP_009052.1      AFM-------RRKCQQCRLRKCKEAGMREQC----VLSEE---------QIRKKKIRKQQ
ECR_AEDAE        MYM-------RRKCQECRLKKCLAVGMRPEC----VVPEN---------QCAIKRKEKKA
ECR_CHITE        MYM-------RRKCQECRLKKCLAVGMRPEC----VVPEN---------QCAIKRKEKKA
ECR_LUCCU        MYM-------RRKCQECRLKKCLAVGMRPEC----VVPEN---------QCAMKRREKKA
NP_724460.1      MYM-------RRKCQECRLKKCLAVGMRPEC----VVPEN---------QCAMKRREKKA
ECR_HELVI        IYM-------RRKCQECRLKKCLAVGMRPEC----VVPEN---------QCAMKRKEKKA
ECR_MANSE        MYM-------RRKCQECRLKKCLAVGMRPEC----VVPES---------TCKNKRREKEA
ECR_BOMMO        MYM-------RRKCQECRLKKCLAVGMRPEC----VIQE------------PSKNKDRQR
NRH4_HUMAN       MYM-------RRKCQECRLRKCKEMGMLAECMYTGLLTEI---------QCKSKRLRKNV
NRH4_MOUSE       MYM-------RRKCQECRLRKCREMGMLAECMYTGLLTEI---------QCKSKRLRKNV
NP_068513.1      MYM-------RRKCQDCRLRKCREMGMLAEC----LLTEI---------QCKSKRLRKNV
NP_004950.2      KTQ-------RKRCPFCRFQKCLTVGMRLE-----AVR----------ADRMRGGRNK-F
NP_776828.1      KTQ-------RKRCPFCRFQKCLTVGMRLE-----AVR----------ADRMRGGRNK-F
NP_445796.1      KTQ-------RKRCPFCRFQKCLTVGMRLE-----AVR----------ADRMRGGRNK-F
STF1_MOUSE       KTQ-------RKRCPFCRFQKCLTVGMRLE-----AVR----------ADRMRGGRNK-F
AAG35648.1       KTL-------RKRCPFCRFQKCLTVGMRLE-----AVR----------ADRMRGGRNK-F
STF1_PIG         KTQ-------RKRCPFCRFQKCLTVGMRLE-----AVR----------ADGMRGGRNK-F
AAK94918.1       KTQ-------RKRCPYCRFQKCLTVGMRLE-----AVR----------ADRMRGGRNK-F
NP_990409.1      KTQ-------RKRCPYCRFQKCLSVGMKLE-----AVR----------ADRMRGGRNK-F
NP_995582.1      KTQ-------RKRCPYCRFQKCLSVGMKLE-----AVR----------ADRMRGGRNK-F
NP_109601.1      KTQ-------RKRCPYCRFKKCIDVGMKLE-----AVR----------ADRMRGGRNK-F
FTF1_BOMMO       KTQ-------RKRCPFCRFQKCLDVGMKLE-----AVR----------ADRMRGGRNK-F
NP_524143.2      KTQ-------RKRCPYCRFQKCLEVGMKLE-----AVR----------ADRMRGGRNK-F
NH25_CAEEL       RTC-------RKRCPSCRFQKCLTMGMKME-----AVR----------ADRMRGGRNK-F
AAA28543.1       IST-------RKKCPACRFEKCLQKGMKLE-----AIR----------EDRTRGGRST-Y
NP_034394.1      RKQ-------RNRCQYCRLLKCLQMGMNRK-----AIR----------EDGMPGGRNKSI
NR61_HUMAN       RKQ-------RNRCQYCRLLKCLQMGMNRK-----AIR----------EDGMPGGRNKSI
AAG09282.1       KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKFNKVRVMRT
PRGR_SHEEP       KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKFNKVRVMRT
PRGR_RABIT       KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKFNKVRVMRA
PRGR_HUMAN       KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKFNKVRVVRA
NP_032855.1      KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKFNKVRVMRT
NP_074038.1      KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKFNKVRVMRA
NP_990593.1      KIR-------RKNCPACRLRKCCQAGMVLG-----GRK----------FKKLNKMKVVRT
AAN63590.1       KIR-------RKNCPSCRLKKCCQAGMVLG-----GRK----------FKKYNRLKPGRE
GCR_SAGOE        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_SAIBB        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_AOTNA        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_SAISC        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKKI-IKGIQQ
NP_000167.1      KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_PIG          KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_TUPGB        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_RABIT        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_RAT          KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
NP_032199.1      KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_CAVPO        KIR-------RENCPACRYRKCLQAGMNLQ-----ARK----------TKKK--IKGIQQ
GCR_XENLA        KIR-------RKNCPACRYRKCLQAGMNLE-----ARK----------TKKK--IKGIQQ
GCR_SHEEP        ------------------------------------------------------------
GCR_ONCMY        KIR-------RKNCPACRFRKCLQAGMNLE-----ARK----------NKKL--IRLKGQ
GCR_PAROL        KIR-------RKNCPACRFRKCLQAGMNLE-----ARK----------NKKL--IKMKVH
MCR_MOUSE        KIR-------RKNCPACRLQKCLQAGMNLG-----ARK----------SKKLGKLKGLHE
NP_037263.1      KIR-------RKNCPACRLQKCLQAGMNLG-----ARK----------SKKLGKLKGLHE
MCR_TUPGB        KIR-------RKNCPACRLQKCLQAGMNLG-----ARK----------SKKLGKLKGLHE
MCR_SAISC        KIR-------RKNCPACRLQKCLQAGMNLG-----ARR----------SKKLGKLKGIHE
NP_000892.1      KIR-------RKNCPACRLQKCLQAGMNLG-----ARK----------SKKLGKLKGIHE
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MCR_XENLA       KIR-------RKNCPACRLQKCLQAGMNLG-----ARK----------SKKLGKLKGVHE
AAG37994.1      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
ANDR_EULFC      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
ANDR_CANFA      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
AAS19691.1      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
ANDR_PAPHA      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
ANDR_MACFA      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
ANDR_HUMAN      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
ANDR_PANTR      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
AAM96904.1      KFR-------RKNCPPCRLRKCYEAGMTLG-----ARR----------LKKLGNLKLQEE
ANDR_RABIT      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
NP_036634.1     KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
NP_038504.1     KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKLQEE
AAP85538.1      KFR-------RKNCPSCRLRKCYEAGMTLG-----ARK----------LKKLGNLKAQEE
AAQ93376.1      KRR-------RKSCQACRFMKCLKVGMLKE-----GVR----------LDRVRGGRQKYK
NP_036065.1     KRR-------RKSCQACRFMKCLKVGMLKE-----GVR----------LDRVRGGRQKYK
ERR2_RAT        KRR-------RKSCQACRFMKCLKVGMLKE-----GVR----------LDRVRGGRQKYK
NP_004443.2     KRR-------RKSCQACRFMKCLKVGMLKE-----GVR----------LDRVRGGRQKYK
ERR2_MOUSE      KRR-------RKSCQACRFMKCLKVGMLKE-----GVR----------LDRVRGGRQKYK
ERR1_HUMAN      KRR-------RKACQACRFTKCLRVGMLKE-----GVR----------LDRVRGGRQKYK
ERR1_MOUSE      KRR-------RKACQACRFTKCLRVGMLKE-----GVR----------LDRVRGGRQKYK
AAS46251.1      KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
ESR1_PIG        KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
ESR1_HORSE      KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
NP_031982.1     KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
NP_036821.1     KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
ESR1_MESAU      KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
ESR1_HUMAN      KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRMLKHK
ESR1_XENLA      KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRLLKHK
ESR1_POEGU      KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGRVMKQK
NP_990514.1     KNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDRRGGEMMKQK
ESR1_SHEEP      KNR-------RKSCQACRLRKCY-------------------------------------
ESR1_OREAU      KNR-------RKSCQACRLRKCYEVGMMKG-----GMR----------KDR--GRVLRRE
ESR1_ORENI      KNR-------RKSCQACRLRKCYEVGMMKG-----GMR----------KDR--GRVLRRE
ESR1_ONCMY      RNR-------RKSCQACRLRKCYEVGMVKG-----GLR----------KDR-GGRVLRKD
ESR1_SALSA      RNR-------RKSCQACRLRKCYEVGMVKG-----GLR----------KDR-GGRVLRKD
ESR1_PAGMA      RNR-------RKSCQACRLRKCYEVGMMKG-----GMR----------KDR-G-RVLRRD
ESR1_SPAAU      RNR-------RKSCQACRLRKCYEVGMMKG-----GVR----------KDR-G-RVLRRD
ESR1_ORYLA      RNR-------RKSCQACRLRKCYEVGMMKG-----GVR----------KDR-I-RILRRD
BAB16893.1      RNR-------RKSCQACRLRKCYEVGMMKG-----GIR----------KDR-GGRSVRRE
ESR1_ICTPU      RNR-------RKSCQACRLRKCYEVGMMKG-----GFR----------KER-GGRIIKHN
ERB1_CARAU      KNR-------RKSCQACRLRKCYEVGMMKC-----GLR----------RDRSSYQQRGAQ
ESR2_ONCMY      KNR-------RKSCQACRLRKCYEVGMMKC-----GLR----------RDRGSYQQRGAQ
ESR2_SPAAU      KNR-------RKSCQACRLHKCYNVGMTKC-----GMR----------KERGNF--RDPQ
ESR3_MICUN      KNR-------RKSCQACRLRKCYEVGMTKC-----GMR----------KERGNY--RSPQ
ESR2_ORENI      KNR-------RKSCQACRLRKCYEVGMTKC-----GIR----------KERGNY--RNSQ
ERB2_CARAU      KSR-------RKSCQACRLRKCYEVGMMKC-----GVR----------RERCSYRGGRHR
ESR2_ANGJA      KNR-------RKSCQACRLRKCYEVGMMKC-----GVR----------RERCTYRGARHR
ESR2_MICUN      KNR-------RKSCQACRLRKCYEVGMMKC-----GVR----------RERCSYRGARHR
ESR2_ICTPU      KNR-------RKSCQACRLRKCYEMGMMKC-----GAR----------RERCGYRAS--R
ESR2_BOVIN      KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRIVRRQ
ESR2_SHEEP      KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRIVRRQ
ESR2_MOUSE      KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRIVRRQ
ESR2_RAT        KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRIVRRQ
ESR2_CALJA      KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRLVRRQ
NP_001428.1     KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRLVRRQ
ESR2_PIG        KNR-------RKSCQACRLRKCYEVGMVKC-----GSR----------RERCGYRIVRKQ
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ESR2_COTJA       KNR-------RKSCQACRLRKCYEVGMMKC-----GSR----------RERCGYRILRRH
NP_990125.1      KNR-------RKSCQACRLRKCYEVGMMKC-----GSR----------RERCGYRILRRH
ESR2_STUVU       KNR-------RKSCQACRLRKCYEVGMMKC-----GSR----------RERCGYRILRSH
CAA42718.1       KRR-------RNRCQFCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NR41_RAT         KRR-------RNRCQFCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NP_002126.2      KRR-------RNRCQFCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NR41_CANFA       KRR-------RNRCQFCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NR42_XENLA       KRR-------RNRCQFCRFQKCLVVGMVKE-----VVR----------TDSLKGRRGRLP
HR38_BOMMO       KRR-------RNRCQFCWFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
HR38_DROME       KRR-------RNRCQFCRFQKCLVVGMVKE-----VVR----------TDSLKGRRGRLP
NP_038641.1      KRR-------RNRCQYCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NR42_RAT         KRR-------RNRCQYCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NP_006177.1      KRR-------RNRCQYCRFQKCLAVGMVKE-----VVR----------TDSLKGRRGRLP
NP_008912.2      KRR-------RNRCQYCRFQKCLSVGMVKE-----VVR----------TDSLKGRRGRLP
NP_113816.1      KRR-------RNRCQYCRFQKCLSVGMVKE-----VVR----------TDSLKGRRGRLP
NP_056558.1      KRR-------RNRCQYCRFQKCLSVGMVKE-----VVR----------TDSLKGRRGRLP
NP_497731.1      KRY-------RSRCQYCRYQKCLEVGMVKE-----IVR----------HGSLSGRRGRLS
7UP2_DROME       QHH-------RNQCQYCRLKKCLKMGMRRE-----AVQ----------RGRVPPTQPGLA
NP_524325.1      QHH-------RNQCQYCRLKKCLKMGMRRE-----AVQ----------RGRVPPTQPGLA
NP_066285.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_989752.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_542956.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
CAA54096.1       QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_776827.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_005645.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_034281.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_786998.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_571255.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMPPTQP---
NP_571261.1      QHH-------RNQCQYCRLKKCLKVGMRRE-----AVQ----------RGRMSNSQS---
EAR2_MOUSE       QHH-------RNQCQYCRLKKCFRVGMRKE-----AVQ----------RGRIPHALP---
NP_620813.1      QHH-------RNQCQYCRLKKCFRVGMRKE-----AVQ----------PGPIPHALP---
NP_005225.2      QHH-------RNQCQYCRLKKCFRVGMRKE-----AVQ----------RGRIPHSLP---
AAH54649.1       KRQ-------RNRCQYCRYQKCLAMGMKRE-----VVQDERQRSVQEERQR-NKER----
NP_571313.1      KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQK-NKER----
NP_035435.1      KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-GKDRN---
NP_036937.1      KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-GKDRN---
NP_002948.1      KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-GKDRN---
RXRA_XENLA       KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-GKERN---
NP_571228.1      KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-AKERS---
RXRA_BRARE       KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-GRERS---
NP_008848.1      KRQ-------RNRCQYCRYQKCLVMGMKRE-----AVQ--------EERQR-SRERA---
NP_033133.1      KRQ-------RNRCQYCRYQKCLVMGMKRE-----AVQ--------EERQR-SRERA---
NP_990625.1      KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQG-SRERS---
RXRG_XENLA       KRQ-------RNRCQYCRYQKCLAMGMKRE-----AVQ--------EERQR-SREKS---
NP_035436.1      KRQ-------RNRCQYCRYQKCLATGMKRE-----AVQ--------EERQR-GKDK----
RXRB_RAT         KRQ-------RNRCQYCRYQKCLATGMKRE-----AVQ--------EERQR-GKDK----
S37781           KRQ-------RNRCQYCRYQKCLATGMKRE-----AVQ--------EERQR-GKDK----
USP_BOMMO        KRQ-------RNRCQYCRYQKCLACGMKRE-----AVQ--------EERQRAARRTE---
USP_MANSE        KRQ-------RNRCQYCRYQKCLACGMKRE-----AVQ--------EERQRAARGTE---
USP_CHOFU        KRQ-------RNRCQYCRYQKCLACGMKRE-----AVQ--------EERQRNARGAE---
NP_476781.1      KRQ-------RNRCQYCRYQKCLTCGMKRE-----AVQ--------EERQRGARNAA---
NP_059019.1      KHH-------RNRCQFCRLKKCLEMGMKME-----SVQ----------SERKPFDVQ---
TR4_MOUSE        KHH-------RNRCQFCRLKKCLEMGMKME-----SVQ----------SERKPFDVQ---
TR4_HUMAN        KHH-------RNRCQFCRLKKCLEMGMKME-----SVQ----------SERKPFDVQ---
TR2_HUMAN        KHH-------RNRCQYCRLQRCIAFGMKQD-----SVQ----------CERKPIEVS---
HR78_DROME       KHH-------RNRCQFCRLQKCLASGMRSD-----SVQ----------HERKPIVDR---
NH41_CAEEL       KFH-------RNRCQYCRLRKCLSMGMRSE-----SVQ----------AERRPVNNS---
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NP_003260.1       KTH-------RNQCRACRLKKCLEVNMNKD-----AVQHE--------RGPRTSTIRK--
NP_689415.1       KTH-------RNQCRACRLKKCLEVNMNKD-----AVQHE--------RGPRTSTIRK--
NP_990501.1       KTH-------RNQCRACRLKKCLEVNMNKD-----AVQHE--------RGPRTSTIRK--
NR21_ORYLA        KTH-------RNQCRACRLKKCLEVNMNKD-----AVQHE--------RGPRTSTIRK--
NR21_XENLA        KTH-------RNQCRACRLKKCLEVNMNKD-----AVQHE--------RGPRTSTIRK--
NP_524596.1       KTH-------RNQCRACRLRKCFEVGMNKD-----AVQHE--------RGPRNSTLRR--
TLL_DROVI         KTH-------RNQCRACRLRKCFEVGMNKD-----AVQHE--------RGPRNSTLRR--
NP_502094.1       KTH-------RNQCRACRLRKCLEIGMNKD-----AVQHE--------RGPRNSSLRR--
NP_038736.1       KAH-------RNQCQACRLKKCLQAGMNQD-----AVQNE--------RQPR-SMAQV--
NP_055064.1       KAH-------RNQCQACRLKKCLQAGMNQD-----AVQNE--------RQPR-STAQV--
NP_497074.1       KEQ-------RNACRSCRLTRCLDVGMNPR-----AVQGDT------VEDPEWDEEAM--
NP_501775.1       KEH-------RNVCRSCRLKKCFEVGMNPD-----SVQNE--------RDRNAKNGGM--
CAA54248.1        KDK-------RNQCRYCRLKKCFRAGMKKE-----AVQNE--------RDRISTRRSSYE
NP_032287.1       KDK-------RNQCRYCRLKKCFRAGMKKE-----AVQNE--------RDRISTRRSSYE
NP_071516.1       KDK-------RNQCRYCRLKKCFRAGMKKE-----AVQNE--------RDRISTRRSSYE
HN4A_XENLA        KDK-------RNQCRYCRLKKCFRAGMKKE-----AVQNE--------RDRISTRRSSYE
HN4B_XENLA        KDK-------RNQCRYCRLRKCFRAGMKKE-----AVQNE--------RDRISMRRSSYE
HN4G_HUMAN        KDK-------RNQCRYCRLRKCFRAGMKKE-----AVQNE--------RDRISTRRSTFD
HN4G_MOUSE        KDK-------RNQCRYCRLRKCFRAGMKKE-----AVQNE--------RDRISTRRSTYE
S36218            KDK-------RNQCRYCRLRKCFKAGMKKE-----AVQNE--------RDRISCRRTSND
NP_492615.2       KNK-------RNACRACRLQKCVKAGMKSN-----AIQNE--------RDAIGKRKKTTG
NP_491103.1       KAK-------RNSCRKCRFDVCLRKGMRRD-----AVQTE--------RDRIRPANPLSN
NH35_CAEEL        KHN-------RAVCRYCRFMKCISSGMRDD-----QVQSE--------RDVIGKREKKDN
NP_496066.2       TMA-------RKACRACRYRKCLESGMSKE-----ALQPR--------RDLIGCRRIRSR
NH14_CAEEL        KDH-------RNACRYCRFQKCLADGMKPE-----AIQNE--------RDRIGSTKRRKR
NP_492612.1       KNF-------RCACRYCRFQKCVQVGMKRE-----AIQFE--------RDPVGSPTSGAS
NHR1_CAEEL        KNI-------RCACRHCRFNKCLLVGMDAKALQIPAIQND--------RDRIGPTKK---
NP_498554.1       KSI-------RCACRHCRFEKCLQVGMDRN-----AIQQN--------RDPIGYTKRTRR
NP_504455.1       KGV-------RCACRYCRLQKCLAVGMDKN-----SIQND--------RDRIGYTKRKRR
NH40_CAEEL        KSV-------RCVCRSCRLKKCFDMGMDPK-----AIQHD--------RDKIRYTKALKK
NP_502117.2       KFE-------RNACRYCRFRKCLLVGMNPD-----YVRPD--------REKSKKGKTVLS
NP_741456.1       KFQ-------RNSCRYCRFQRCIQAGMDPK-----AVRPD--------RDQTGKQKVPRI
NP_510423.1       KAG-------RNVCRSCRFQKCLEVGMEPD-----AIRPD--------RDKTGRQKNPRR
NP_000957.1       KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-EV
RRG2_HUMAN        KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-EV
RRG2_MOUSE        KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-EV
A34714            KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-EV
RRG_NOTVI         KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-EI
RRG_XENLA         KVT-------RNRCQFCRLQKCFQVGMSKE-----AVRN----------DRN-KKKK-EI
AAB59953.1        KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-DV
NP_571414.1       KVT-------RNRCQYCRLQKCFEVGMSKE-----AVRN----------DRN-KKKK-DV
AAD05222.1        KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-EV
RRA_MOUSE         KVT-------RNRCQYCRLQKCFDVGMSKE-----SVRN----------DRN-KKKK-EA
NP_989867.1       KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-DV
RRA_XENLA         KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-ES
RRA_NOTVI         KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKKQEA
RRB_COTJA         KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-EP
S13512            KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-EP
RRB_HUMAN         KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-ET
RRB_MOUSE         KVT-------RNRCQYCRLQKCFEVGMSKE-----SVRN----------DRN-KKKK-EP
RRB_NOTVI         KVT-------RNRCQYCRLQRCFEVGMSKE-----SVRN----------DRN-KKKK-EP
RRA_FUGRU         KVT-------RNRCQYCRLQKCLEVGMSKE-----SVRN----------DRN-KKKK-DE
AAA19972.1        KKN-------RNKCQYCRFQKCLALGMSHN-----AIRF----------GRMPDGEKRKL
NP_006229.1       KKN-------RNKCQYCRFQKCLALGMSHN-----AIRF----------GRMPEAEKRKL
CAA40856.1        KKN-------RNKCQYCRFHKCLSVGMSHN-----AIRF----------GRMPRSEKAKL
NP_037328.1       KKN-------RNKCQYCRFHKCLSVGMSHN-----AIRF----------GRMPRSEKAKL
CAA68898.1        KKN-------RNKCQYCRFHKCLSVGMSHN-----AIRF----------GRMPRSEKAKL
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PPAR_PHACI       KKN-------RNKCQYCRFQKCLSDGMSHN-----AIRF----------GRMPRSEKAKL
PPAR_CANFA       KKN-------RNKCQYCRFHKCLSVGMSHN-----AIRF----------GRMPRSEKAKL
PPAR_CAVPO       KKN-------RNKCQYCRFHKCLSVGMSHN-----AIRF----------GRMPRSEKAKL
PPAR_XENLA       KKN-------RNKCQYCRFEKCLNVGMSHN-----AIRF----------GRMPRSEKAKL
PPAS_XENLA       KKN-------RNKCQYCRFNKCLSLGMSHN-----AIRF----------GRMPESEKRKL
NP_851367.1      KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
PPAT_PIG         KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
PPAT_CRIGR       KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
PPAT_MACMU       KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
CAA73382.2       KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
NP_056953.2      KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
NP_035276.1      KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
PPAT_RABIT       KKS-------RNKCQYCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
PPAT_XENLA       KKS-------RNKCQFCRFQKCLAVGMSHN-----AIRF----------GRMPQAEKEKL
CAB53540.1       RIN-------RNRCQQCRFKKCLSVGMSRD-----AVRF----------GRIPKREKQRM
NP_665718.1      RIN-------RNRCQQCRFKKCLSVGMSRD-----AVRF----------GRIPKREKQRM
NP_035714.2      RMN-------RNRCQQCRFKKCLSVGMSRD-----AVRF----------GRIPKREKQRM
NRD2_HUMAN       RMN-------RNRCQQCRFKKCLSVGMSRD-----AVRF----------GRIPKREKQRM
NRD2_RAT         RMN-------RNRCQQCRFKKCLSVGMSRD-----AVRF----------GRIPKREKQRM
E75_CHOFU        RIN-------RNRCQYCRLKKCIAVGMSRD-----AVRF----------GRVPKREKARI
E75_MANSE        RIN-------RNRCQYCRLKKCIAVGMSRD-----AVRF----------GRVPKREKARI
E75A_DROME       RIN-------RNRCQYCRLKKCIAVGMSRD-----AVRF----------GRVPKREKARI
E75_GALME        RIN-------RNRCQYCRLKKCIAVGMSRD-----AVRF----------GRVPKREKARI
E75_METEN        RIN-------RNRCQYCRLKKCIAVGMSRD-----AVRF----------GRVPKREKAKI
E75C_DROME       RIN-------RNRCQYCRLKKCIAVGMSRD-----AVRF----------GRVPKREKARI
NP_493284.1      RNN-------RNRCQCCRLKKCLAVGMSRD-----AVRF----------GRVPKREKARM
AAH14804.1       RTS-------RNRCQHCRLQKCLALGMSRD-----AVKF----------GRMSKKQRDSL
RORG_HUMAN       RTS-------RNRCQHCRLQKCLALGMSRD-----AVKF----------GRMSKKQRDSL
AAH58269.1       RTN-------RNRCQHCRLQKCLALGMSRD-----AVKF----------GRMSKKQRDSL
RORB_RAT         RTN-------RNRCQHCRLQKCLALGMSRD-----AVKF----------GRMSKKQRDSL
RORB_HUMAN       RTN-------RNRCQHCRLQKCLALGMSRD-----AVKF----------GRMSKKQRDSL
NP_038674.1      RTS-------RNRCQHCRLQKCLAVGMSRD-----AVKF----------GRMSKKQRDSL
NP_599022.1      RTS-------RNRCQHCRLQKCLAVGMSRD-----AVKF----------GRMSKKQRDSL
HR3_GALME        RVN-------RNRCQYCRLQKCLKLGMSRD-----AVKF----------GRMSKKQREKV
HR3_MANSE        RVN-------RNRCQYCRLQKCLKLGMSRD-----AVKF----------GRMSKKQREKV
NP_788303.1      RVN-------RNRCQYCRLQKCLKLGMSRD-----AVKF----------GRMSKKQREKV
NP_740887.1      RVN-------RNRCQYCRLKKCIELGMSRD-----AVKF----------GRMSKKQREKV
E78A_DROME       RLN-------RNRCQYCRFKKCLSAGMSRD-----SVRY----------GRVPKRSRELN
NP_509713.2      RES-------RNRCQYCRFKKCLDSGMSKD-----SVRQ----------MKFRNAMR--D
NHR2_CAEEL       YENCAANRGVRTRCQACRFAKCLAVGMNRD-----NVR--------------VNKETDKD
NP_494785.1      INI-------RCMCRACRYIKCIEVGMNPA-----GVQQR--------LPPS--KTLVEV
NP_503561.2      ANI-------RCMCRSCRFAKCLEVGMNPA-----GVQQR--------RDTIGKREIKPD
NP_505589.1      SNI-------RCMCRSCRYDKCIEVGMNPE-----CVQNR--------RENDTPKADLQF
NP_510659.1      KNV-------RCMCRACRFTKCIAVGMRKS-----AVQRH--------RELFASQETSSE
NP_741644.1      SNV-------RNMCRACRYEKCLEVGMQRS-----SVQQK--------RDQLGRRDGLPT
NP_504771.1      TGM-------RKLCASCRYDKCLKVGMRES-----AVLSR--------LAKKNQNYKKSI
NP_503608.2      VNG-------KFNCKQCRLKKCLDVGMDTR-----RFQTD--------RDLISCS-----
NP_507680.1      LIF-------ALKCKNCRLQRCYEAGMSSE-----NFQFC--------RDLIGAKGAIPK


KNIR_DROVI       IHCLLQEHEQAAAAAAGKAP-------
NP_524187.1      IHCLLQEHEQAAAAAG-KAPP------
NP_788552.1      IHCLLQEQQQQAVAAMAAHH-------
EGON_DROME       IHCLLQEQQTTSGLGGGSSV-------
1411299B         QNRERR----RKEEMIRSL--------
CAA68539.1       QNRERR----RKEEMIRSL--------
THA1_SHEEP       QNRERR----RKEEMIRSL--------
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THA_MOUSE        QNRERR----RKEEMIRSL--------
THA_PIG          QNRERR----RKEEMIRSL--------
NP_990644.1      ENRERR----RKEEMIKSL--------
THA_CAIMO        ENRERR----RKEEMIKSL--------
THA_APTPA        ENRERR----RKEEMIKSL--------
ERBA_AVIER       ENRERR----RKEEMIKSL--------
THA_PYGAD        ENRERR----RKEEMIKSL--------
THAB_XENLA       ENRVRR----RKEEMIKTL--------
THA_RANCA        ENRERR----RKEEMIKTL--------
THAA_XENLA       ENRQRR----RKEEMIKTL--------
NP_571471.1      ENREKR----KKEEIVKTL--------
THAB_PAROL       ENRERR----KKEEIVKTL--------
THA_SALSA        ENREKR----KKDEIVKTL--------
THAA_PAROL       ENREKR----KREEMVRTL--------
THA_HIPHI        ENREKR----KREEMVRTL--------
NP_000452.2      ENREKR----RREELQKSI--------
THB2_HUMAN       ENREKR----RREELQKSI--------
NP_033406.1      ENREKR----RREELQKSI--------
THB2_RAT         ENREKR----RREELQKSI--------
THB1_MOUSE       ENREKR----RREELQKSI--------
THB1_RAT         ENREKR----RREELQKSI--------
THB1_SHEEP       ENREKR----RREELQRSM--------
THB_CHICK        ENREKR----RREELQKTI--------
THBA_XENLA       ENREKR----RKDEIQKSL--------
THB_RANCA        ENREKR----RKDELQKTL--------
THBB_XENLA       ENREKR----RKDEIQKSI--------
NP_571415.1      ENRERR----RREELQKTV--------
THB_PAROL        ENRERR----RKEELQKTV--------
NHR1_ONCVO       DNRERR----KLEHLRTLLKA------
NP_000367.1      KRKEEE----ALKDSLRPKLS------
VDR_BOVIN        KRKEEE----ALKDSLRPKLS------
AAK48863.1       KRKEEE----ALKDSLRPKLS------
NP_058754.1      KRKEEE----ALKDSLRPKLS------
VDR_MOUSE        KRKEEE----ALKDSLRPKLS------
NP_990429.1      KRKEEE----ALKESLKPKLS------
VDR_COTJA        KRKEEE----ALKESLKPKLS------
VDR_XENLA        KRKSEE----ALKESMRPKIS------
NP_035066.1      RKKREK----IEAPPPGGQG-------
NP_443212.1      RKKREK----IEAPPPGGQG-------
CAB55489.1       RKKSER----TGTQPLGVQG-------
AAM76230.1       QRRAQQ----TPMQLSNEQEE------
NP_005113.1      QRRAQQ----TPVQLSKEQEE------
NP_033933.1      QRRAEK----ASLQLNQQQKE------
NP_075230.1      RRRAQK----ASLQLSQQQKE------
BAD00038.1       QRRAQW----AAVQLSKGQQE------
BAD00039.1       QRRAQW----APVQLSKGQQE------
NH48_CAEEL       SEEARL----EKKQRVEENR-------
NP_524493.1      TNRAKR----RLMENGTDACD------
NP_741445.1      RKKPDM----KNNLKVEVDD-------
AAD16050.1       EEQAQA----TSVSPRVSSP-------
NP_113815.1      EEQAQA----TSVSPRVSSP-------
NRH3_HUMAN       EEQAHA----TSLPPRASSP-------
NP_033499.1      QQQPPP----PSEPAASS---------
NRH2_RAT         QQQPPP----PTEPASGS---------
NP_009052.1      QQESQS----QSQSPVGP---------
ECR_AEDAE        QKEKDK---VQTNATVSTT--------
ECR_CHITE        QKEKDK---VPGIVGSNTS--------
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ECR_LUCCU        QKEKDK---IQTSVCATEI--------
NP_724460.1      QKEKDK---MTTSPSSQHG--------
ECR_HELVI        QREKDK---LPVSTTTVDD--------
ECR_MANSE        QREKDK---LPVSTTTVDD--------
ECR_BOMMO        QK-KDKGILLPVSTTTVEDH-------
NRH4_HUMAN       KQHADQ----TVNEDS-----------
NRH4_MOUSE       KQHADQ----TVNEDD-----------
NP_068513.1      KQHADQ----TVNEDSEGRD-------
NP_004950.2      GPMYKRDRALKQQKKAQIR--------
NP_776828.1      GPMYKRDRALKQQKKAQIR--------
NP_445796.1      GPMYKRDRALKQQKKAQIR--------
STF1_MOUSE       GPMYKRDRALKQQKKAQIR--------
AAG35648.1       GPMYKRDRALKQQKKAQIR--------
STF1_PIG         GPMYKRDRALKQQKKAQIR--------
AAK94918.1       GPMYKRDRALKQQKKALIR--------
NP_990409.1      GPMYKRDRALKQQKKALIR--------
NP_995582.1      GPMYKRDRALKQQKKALIR--------
NP_109601.1      GPMYKRDRALKQQKKALIR--------
FTF1_BOMMO       GPMYKRDRARKLQMMRQRQ--------
NP_524143.2      GPMYKRDRARKLQVMRQRQ--------
NH25_CAEEL       GSFYKKDRAHRMQRNAMRV--------
AAA28543.1       QCSYTLPNSMLSPLLSPDQ--------
NP_034394.1      GPVQISEEEIERIMSGQE---------
NR61_HUMAN       GPVQISEEEIERIMSGQE---------
AAG09282.1       LDAVALPQPVGIPNESQA---------
PRGR_SHEEP       LDAVALPQPVGIPNESQA---------
PRGR_RABIT       LDAVALPQPVGIPNESQR---------
PRGR_HUMAN       LDAVALPQPLGVPNESQA---------
NP_032855.1      LDGVALPQSVGLPNESQA---------
NP_074038.1      LDGVALPQSVAFPNESQT---------
NP_990593.1      LD-VALQQPAVLQDETQSL--------
AAN63590.1       LDRIATSSPMECQQALTR---------
GCR_SAGOE        ATTGVSQETSENPANKTIVP-------
GCR_SAIBB        ATTGVSQETSENPANKTIVP-------
GCR_AOTNA        ATTGVSQETSENPANKTIVP-------
GCR_SAISC        ATTGVSQETSENPANKTIV--------
NP_000167.1      ATTGVSQETSENPGNKTIVP-------
GCR_PIG          ATTGVSQETSENSANKTIVP-------
GCR_TUPGB        TTTGISQETPENSANKTIVP-------
GCR_RABIT        TSTGVSQETSENPSNRTVVP-------
GCR_RAT          ATAGVSQDTSENP-NKTIVPA------
NP_032199.1      ATAGVSQDTSENA-NKTIVPA------
GCR_CAVPO        ATTGVSQNTSENP-NKTIVPA------
GCR_XENLA        STTATARESPETSMTRTLVP-------
GCR_SHEEP        ---------------------------
GCR_ONCMY        QTTMEPNPPPP----------------
GCR_PAROL        RPTGSAEPISN----------------
MCR_MOUSE        EQPQQPPPPPPQSPEEGTTY-------
NP_037263.1      EQPQQPPPPPPQSPEEGT---------
MCR_TUPGB        EQPQQPPP--PQSPEEGTTY-------
MCR_SAISC        EQPQQQ-PPPPPPPPQSPE--------
NP_000892.1      EQPQQQQPPPPPPPPQSP---------
MCR_XENLA        EHPQQPLQQTPTAS-------------
AAG37994.1       GEASSATSPTEEPAQKLT---------
ANDR_EULFC       GEASSATSPTEESSQKLT---------
ANDR_CANFA       GEASNVTSPTEEPTQKLT---------
AAS19691.1       GEASSTTSPTEETAQKLT---------
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ANDR_PAPHA        GEASSTTSPTEETAQKLT---------
ANDR_MACFA        GEASSTTSPTEETAQKLT---------
ANDR_HUMAN        GEASSTTSPTEETTQKLT---------
ANDR_PANTR        GEASSTTSPTEETTQKLT---------
AAM96904.1        GEASSTTSPTEETTQKLT---------
ANDR_RABIT        GESSSASSPTEDTTQKLT---------
NP_036634.1       GENSSAGSPTEDPSQKMT---------
NP_038504.1       GENSNAGSPTEDPSQKMT---------
AAP85538.1        LEGSPGQSEGREMPPNMS---------
AAQ93376.1        RRIDAENSPYLNPQLVQP---------
NP_036065.1       RRIDAENSPYLNPQLVQP---------
ERR2_RAT          RRLDSENSPYLSLQISPP---------
NP_004443.2       RRLDSESSPYLSLQISPP---------
ERR2_MOUSE        RRLDSENSPYLNLPISPP---------
ERR1_HUMAN        RRPEVDPLPFPGPFPAGP---------
ERR1_MOUSE        RRPEVDPLPFPGPFPAGP---------
AAS46251.1        RQRDDGEGRNEAVPSGDM---------
ESR1_PIG          RQRDDGEGRNEAVPPGDM---------
ESR1_HORSE        RQRDDGEGRNEAGPSGDR---------
NP_031982.1       RQRDDLEGRNEMGASGDM---------
NP_036821.1       RQRDDLEGRNEMGTSGDM---------
ESR1_MESAU        RQRDDLEGRNDMGPSGDM---------
ESR1_HUMAN        RQRDDGEGRGEVGSAGDM---------
ESR1_XENLA        RQKEEQEQKNDVDPSEIR---------
ESR1_POEGU        RQREEQDSRNGEASSTEL---------
NP_990514.1       RQREEQDSRNGEASSTEL---------
ESR1_SHEEP        ---------------------------
ESR1_OREAU        KHGPAQR-QTSQNLPTHKASP------
ESR1_ORENI        KRRACDRDKPAKDLPHTRAS-------
ESR1_ONCMY        KRYCGPAGDREKPYGDLEH--------
ESR1_SALSA        KRYCGPAGDREKPYGDLEH--------
ESR1_PAGMA        KQRTGTSDRDKASKGLEHRT-------
ESR1_SPAAU        KRRTGTSDRDKASKGLEHRT-------
ESR1_ORYLA        KRRTGVGDGDKVVKGQEHKT-------
BAB16893.1        RRRSSNEDRDKSSSDQCSR--------
ESR1_ICTPU        RRPSGLKERERGYSKAQSG--------
ERB1_CARAU        QNRLTRFSGRMRTSGPRS---------
ESR2_ONCMY        QKRLARFSGRMRTSGPRS---------
ESR2_SPAAU        MRRVTRLSSQGRTSGPSVLN-------
ESR3_MICUN        MRRMTRLTSQGRTDSSSVLT-------
ESR2_ORENI        ARRLTRLSSQGKTAEPKGIT-------
ERB2_CARAU        RN-PPIRDSSGGAIGVRGH--------
ESR2_ANGJA        RM-PHIRELAGTGGGARTQ--------
ESR2_MICUN        RGGLQPRDPTGRGL-VRVG--------
ESR2_ICTPU        RT-APMRDGSARPVGVRGQSQ------
ESR2_BOVIN        RNSDEQLHCLSKTKRNGG---------
ESR2_SHEEP        RNSDEQLHCLSKTKRNGA---------
ESR2_MOUSE        RSASEQVHCLNKAKRTSG---------
ESR2_RAT          RSSSEQVHCLSKAKRNGG---------
ESR2_CALJA        GNAEEQLHCAGKAKRSGG---------
NP_001428.1       RSADEQLHCAGKAKRSGG---------
ESR2_PIG          RNSEGHLHCLSRAKKNGD---------
ESR2_COTJA        RNSED---CMGKTKKYNEAAT------
NP_990125.1       RNSED---CMGKTKKYNEAAT------
ESR2_STUVU        RGAEERVHCLGRARRYSE---------
CAA42718.1        SKPKQP--PDASPTNLLTSL-------
NR41_RAT          SKPKQP--PDASPTNLLTSL-------
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NP_002126.2       SKPKQP--PDASPANLLTSL-------
NR41_CANFA        SKPKQP--PDASPANLLTSL-------
NR42_XENLA        SKPKQI--AESSPVDLINSL-------
HR38_BOMMO        SKPKCP---QESPPSPPISLI------
HR38_DROME        SKPKSP---QESPPSPPISLI------
NP_038641.1       SKPKSP--QDPSPPSPPVSL-------
NR42_RAT          SKPKSP--QDPSPPSPPVSL-------
NP_006177.1       SKPKSP--QEPSPPSPPVSL-------
NP_008912.2       SKPKSPLQQEPSQPSPPS---------
NP_113816.1       SKPKSPLQQEPSQPSPPS---------
NP_056558.1       SKPKSPLQQEPSQPSPPS---------
NP_497731.1       SKTKLA--RSEDQPSPPLPL-------
7UP2_DROME        GMHGQYQIANGDPMG------IAG---
NP_524325.1       GMHGQYQIANGDPMG------IAG---
NP_066285.1       -THGQFALTNGDPLNCH--SYLSG---
NP_989752.1       -THGQFALTNGDPLNCH--SYLSG---
NP_542956.1       -THGQFALTNGDPLNCH--SYLSG---
CAA54096.1        -THGQFALTNGDPLNCH--SYLSG---
NP_776827.1       -SHGQFALTNGDPLNCH--SYLSG---
NP_005645.1       -NPGQYALTNGDPLNGH--CYLSG---
NP_034281.1       -NPGQYALTNGDPLNGH--CYLSG---
NP_786998.1       -NPGQYALTNGDPLNGH--CYLSG---
NP_571255.1       -NPGQYALTNGDPLNGH--CYLSG---
NP_571261.1       -SPGQYLSNGSDPYNGQ--PYLSG---
EAR2_MOUSE        ---GPAACS---PPGATGVEPFTGPPV
NP_620813.1       ---GPAACS---PPGAAGVEPFAGPPV
NP_005225.2       ---GAVAASSGSPPGSALAAVASG---
AAH54649.1        --DGEVESSSAANEE------------
NP_571313.1       --DGDYECSSSANEEMPVEKILE----
NP_035435.1       --ENEVESTSSANEDMPVEKIL-----
NP_036937.1       --ENEVESTSSANEDMPVEKIL-----
NP_002948.1       --ENEVESTSSANEDMPVERIL-----
RXRA_XENLA        --ENEVESSNSANEDMPVEKIL-----
NP_571228.1       --EAEFGG--CANEDMPVEKILEA---
RXRA_BRARE        --DNEVDSSSSFNEEMPVEKIL-----
NP_008848.1       --ESEAECATSGHEDMPVERIL-----
NP_033133.1       --ESEAECASSSHEDMPVERIL-----
NP_990625.1       --ENEAESTSGGSEDMPVERIL-----
RXRG_XENLA        --DTEAESTSSTSEEMPVERIL-----
NP_035436.1       --DGDGDGAGGAPEEMPVDRILE----
RXRB_RAT          --DGDGDGAGGAPEEMPVDRILE----
S37781            --DGDGEGAGGAPEEMPVDRILE----
USP_BOMMO         --DAHPSSSVQ---ELSIERLLEL---
USP_MANSE         --DAHPSSSVQ---ELSIERLLEI---
USP_CHOFU         --DAHPSSSVQVSDELSIERL------
NP_476781.1       --GRLSASGGGSSGPGSVGGS------
NP_059019.1       --REKPSNCAASTEKIYIRKDLR----
TR4_MOUSE         --REKPSNCAASTEKIYIRKDLR----
TR4_HUMAN         --REKPSNCAASTEKIYIRKDLR----
TR2_HUMAN         --REKSSNCAASTEKIYIRKDLR----
HR78_DROME        --KEGIIAAAGGSSTSGGGNGSS----
NH41_CAEEL        --SMLCNNDNNQQNTTPEHLSPN----
NP_003260.1       ---QVALYFRGHKEENGAA--------
NP_689415.1       ---QVALYFRGHKEDNGAA--------
NP_990501.1       ---QVALYFRGHKEESSGA--------
NR21_ORYLA        ---QVALYFRGHKEVNGSS--------
NR21_XENLA        ---QVALYFRGHKEVNGST--------
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NP_524596.1     ---HMAMYKDAMMGAGEMP--------
TLL_DROVI       ---HMAMYKDAMMGAAEMP--------
NP_502094.1     ---QQMMFDHGSSPNS-----------
NP_038736.1     ---HLDAMETGSDPRSEPVVA------
NP_055064.1     ---HLDSMESNTESRPESLVA------
NP_497074.1     ---PETLSISTQTDALKVK--------
NP_501775.1     ---GGPMSSPTQSSLCKELTI------
CAA54248.1      DSSL-PSINALLQAEVL----------
NP_032287.1     DSSL-PSINALLQAEVL----------
NP_071516.1     DSSL-PSINALLQAEVL----------
HN4A_XENLA      DSSL-PSINVLIQAEVL----------
HN4B_XENLA      DNGS-LSINVLTQAEAM----------
HN4G_HUMAN      GSNI-PSINTLAQAEVR----------
HN4G_MOUSE      GSNI-PSINTLAQAEVR----------
S36218          DPDPGNGLSVISLVKA-----------
NP_492615.2     AEKE-DLIDQLVAAETL----------
NP_491103.1     GSNG-GIVPDDPLLDTL----------
NH35_CAEEL      MKTYCQDPTPRTSPEL-----------
NP_496066.2     PSCS-TSTPTPPRPQVE----------
NH14_CAEEL      SGANSENNSDSEGTPS-----------
NP_492612.1     LNGTPFKKDRSPGYEN-----------
NHR1_CAEEL      ---IKMSSGSDDEQATT----------
NP_498554.1     YPPIKKVEASDECSPA-----------
NP_504455.1     HDDNDMEGGVHHSEHI-----------
NH40_CAEEL      KREEEKRLKEMVIKED-----------
NP_502117.2     KKK-SVSRSLSYRLAD-----------
NP_741456.1     KKK-QIDEELLNHMMRL----------
NP_510423.1     NTEGSIKKVSVGSILG-----------
NP_000957.1     KEEGSP-DSYELSPQLEELIT------
RRG2_HUMAN      KEEGSP-DSYELSPQLEELIT------
RRG2_MOUSE      KEEGSP-DSYELSPQLEELIT------
A34714          KEEGSP-DSYELSPQLEELIT------
RRG_NOTVI       KEEVVT-DSYEMPPEMEALIQ------
RRG_XENLA       KEEVVLPDSYEMPPEMEELI-------
AAB59953.1      KDEVIPPESYELSGELEELV-------
NP_571414.1     KDEVIPPESYELSGELEELV-------
AAD05222.1      PKPECS-ESYTLTPEVGELIE------
RRA_MOUSE       PKPECS-ESYTLTPEVGELIE------
NP_989867.1     PKTECS-ESYIVTPEVEELIE------
RRA_XENLA       PKPEAI-ESYILSPETQDLIE------
RRA_NOTVI       PKQECT-ESYIITPEVEDLV-------
RRB_COTJA       TKQEST-ENYEMTAELDDLTE------
S13512          TKQEST-ENYEMTAELDDLTE------
RRB_HUMAN       SKQECT-ESYEMTAELDDLTE------
RRB_MOUSE       SKQECT-ESYEMTAELDDLTE------
RRB_NOTVI       IKQECI-ESLEMTAELDDLTE------
RRA_FUGRU       KKPECI-ENYVLSPDTEQMIN------
AAA19972.1      VAGLTASEGCQHNPQLADL--------
NP_006229.1     VAGLTANEGSQYNPQVADL--------
CAA40856.1      KAEILTCEHDLKDSETADL--------
NP_037328.1     KAEILTCEHDLKDSETADL--------
CAA68898.1      KAEILTCEHDIEDSETADL--------
PPAR_PHACI      KAEILTCEHDLEDSEVADL--------
PPAR_CANFA      KAEILTCEQDPEDAETADL--------
PPAR_CAVPO      KAEVLTCDRDSEGAETADL--------
PPAR_XENLA      KAEVLMCDQDVKDSQMADL--------
PPAS_XENLA      VQAPVS-DSAAPDSPVSDLD-------
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NP_851367.1      LAEISS-DIDQLNPESADLR-------
PPAT_PIG         LAEISS-DIDQLNPESADLR-------
PPAT_CRIGR       LAEISS-DIDQLNPESADLR-------
PPAT_MACMU       LAEISS-DIDQLNPESADLR-------
CAA73382.2       LAEISS-DIDQLNPESADLR-------
NP_056953.2      LAEISS-DIDQLNPESADLR-------
NP_035276.1      LAEISS-DIDQLNPESADLR-------
PPAT_RABIT       LAEISS-DIDQLNPESADLR-------
PPAT_XENLA       LAEISS-DIDQLNPESADQR-------
CAB53540.1       LAEMQSAMN-LANNQLSS---------
NP_665718.1      LAEMQNAMN-LANNQLSS---------
NP_035714.2      LIEMQSAMKTMMNTQFS----------
NRD2_HUMAN       LIEMQSAMKTMMNSQFS----------
NRD2_RAT         LIEMQSAMKTMMSTQFG----------
E75_CHOFU        LAAMQQSSSSRAHEQAA----------
E75_MANSE        LAAMQQSSTSRAHEQAA----------
E75A_DROME       LAAMQQSTQNRGQQRAL----------
E75_GALME        LAAMQ-SSTTRAHEQAAA---------
E75_METEN        LAAMQ-SVNAKSQERAVL---------
E75C_DROME       WRPCNRAPRIAASSDPS----------
NP_493284.1      FEEMQKTNVQSQRDQIA----------
AAH14804.1       HAEVQKQLQQQQQQEQVA---------
RORG_HUMAN       HAEVQKQLQQRQQQQQEP---------
AAH58269.1       YAEVQKHQQRLQEQRQQQ---------
RORB_RAT         YAEVQKHQQRLQEQRQQQ---------
RORB_HUMAN       YAEVQKHQQRLQEQRQEQ---------
NP_038674.1      YAEVQKHRMQQQQRDHQQ---------
NP_599022.1      YAEVQKHRMQQQQRDHQQ---------
HR3_GALME        EDEVRYHRAQMRAQTDAA---------
HR3_MANSE        EDEVRYHKAQMRAQNDAA---------
NP_788303.1      EDEVRFHRAQMRAQSDAA---------
NP_740887.1      EDEVRMHKELAANGLGYQ---------
E78A_DROME       GAAASSAAAGAPASLNVD---------
NP_509713.2      DKSPDSVFVPEISTLERQEE-------
NHR2_CAEEL       VKPSVASPNFEMTSQ------------
NP_494785.1      SMDLPTVSNPSILSFPSP---------
NP_503561.2      STDLMQLLGSVGDGYP-----------
NP_505589.1      DTSKTEIRRP-IPNFNI----------
NP_510659.1      SSSNPRISPT--LSWPMD---------
NP_741644.1      NREEP-VLDTMRRAYEK----------
NP_504771.1      VGSPDAYEPSTSTSDS-----------
NP_503608.2      -AISQSLATFLGRPEFILCCEP-----
NP_507680.1      LKVPKSFEQTVGRPYFVLQCDP-----
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