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CLUSTAL W (1.83) multiple sequence alignment


FTF1_BOMMO       CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN--------KKVYT-CVAERACHIDKTQRK
NP_524143.2      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN--------KKVYT-CVAERSCHIDKTQRK
NP_004950.2      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN--------NKHYT-CTESQSCKIDKTQRK
STF1_MOUSE       CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN--------NKHYT-CTESQSCKIDKTQRK
NP_445796.1      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN--------NKHYT-CTESQSCKIDKTQRK
NP_776828.1      CPVCGDKVSGYHYGLLTCESCKGFFKRTVQN--------NKHYT-CTESQSCKIDKTQRK
STF1_PIG         CPVCGDKVSGYHYGLLTCETCKGFFKRTVQN--------NKHYT-CTESQSCKIDKTQRK
AAA28543.1       CPICGDKISGFHYGIFSCESCKGFFKRTVQN--------RKNYV-CVRGGPCQVSISTRK
7UP2_DROME       CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLTYS-CRGSRNCPIDQHHRN
NP_524325.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLTYS-CRGSRNCPIDQHHRN
NP_066285.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLSYT-CRANRNCPIDQHHRN
NP_542956.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLSYT-CRANRNCPIDQHHRN
NP_989752.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLSYT-CRANRNCPIDQHHRN
CAA54096.1       CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLSYT-CRANRNCPIDQHHRN
NP_005645.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLTYT-CRANRNCPIDQHHRN
NP_034281.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLTYT-CRANRNCPIDQHHRN
NP_786998.1      CVVCGDKSSGKHYGQFTCEGCKSFFKRSVRR--------NLTYT-CRANRNCPIDQHHRN
CAA54248.1       CAICGDRATGKHYGASSCDGCKGFFRRSVRK--------NHMYS-CRFSRQCVVDKDKRN
NP_032287.1      CAICGDRATGKHYGASSCDGCKGFFRRSVRK--------NHMYS-CRFSRQCVVDKDKRN
NP_071516.1      CAICGDRATGKHYGASSCDGCKGFFRRSVRK--------NHMYS-CRFSRQCVVDKDKRN
HN4A_XENLA       CAICGDRATGKHYGASSCDGCKGFFRRSVRK--------NHMYS-CRFSRQCVVDKDKRN
HN4B_XENLA       CAICGDRATGKHYGASSCDGCKGFFRRSVRK--------NHVYA-CRFSRQCIVDKDKRN
HN4G_HUMAN       CAICGDRATGKHYGASTCDGCKGFFRRSIRK--------SHIYS-CRFSRQCVVDKDKRN
HN4G_MOUSE       CAICGDRATGKHYGASSCDGCKGFFRRSIRK--------SHVYS-CRFSRQCVVDKDKRN
S36218           CAICGDRATGKHYGASSCDGCKGFFRRSVRK--------NHQYT-CRFARNCVVDKDKRN
NP_035435.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTVRK--------DLTYT-CRDNKDCLIDKRQRN
NP_036937.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTVRK--------DLTYT-CRDNKDCLIDKRQRN
NP_002948.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTVRK--------DLTYT-CRDNKDCLIDKRQRN
RXRA_XENLA       CAICGDRSSGKHYGVYSCEGCKGFFKRTVRK--------DLTYT-CRDSKDCMIDKRQRN
RXRA_BRARE       CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLTYT-CRDNKDCQIDKRQRN
NP_008848.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLIYT-CRDNKDCLIDKRQRN
NP_033133.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLIYT-CRDNKDCLIDKRQRN
NP_990625.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLIYT-CRDNKDCLIDKRQRN
RXRG_XENLA       CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLVYT-CRDSKDCLIDKRQRN
NP_035436.1      CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLTYS-CRDNKDCTVDKRQRN
RXRB_RAT         CAICGDRSSGKHYGVYSCEGCKGFFKRTIRK--------DLTYS-CRDNKDCTVDKRQRN
USP_BOMMO        CSICGDRASGKHYGVYSCEGCKGFFKRTVRK--------DLTYA-CREDKNCIIDKRQRN
USP_MANSE        CSICGDRASGKHYGVYSCEGCKGFFKRTVRK--------DLTYA-CREDRNCIIDKRQRN
USP_CHOFU        CSICGDRASGKHYGVYSCEGCKGFFKRTVRK--------DLSYA-CREERNCIIDKRQRN
NP_476781.1      CSICGDRASGKHYGVYSCEGCKGFFKRTVRK--------DLTYA-CRENRNCIIDKRQRN
THA_APTPA        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDGCCVIDKITRN
THA_CAIMO        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDGCCVIDKITRN
NP_990644.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDGCCVIDKITRN
THA_PYGAD        CVVCGDKATGYHYRCITCAGCKGFFRRTIQKNL------HPTYS-CKYDGCCVIDKITRN
THA_MOUSE        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDSCCVIDKITRN
THA_PIG          CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDSCCVIDKITRN
THA1_SHEEP       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDSCCVIDKITRN
CAA68539.1       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYDSCCVIDKITRN
THAA_XENLA       CVVCSDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYDGCCIIDKITRN
THAB_XENLA       CVVCSDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYDGCCIIDKITRN
THA_RANCA        CVVCSDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYDGCCIIDKITRN
NP_571471.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYDSCCIIDKITRN
THA_SALSA        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPAYS-CKYDGCCIIDKITRN
THAB_PAROL       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYDCCCIIDKITRN
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THAA_PAROL       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGCCIIDKITRN
THA_HIPHI        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPAYS-CKYEGCCIIDKITRN
NP_000452.2      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGKCVIDKVTRN
THB2_HUMAN       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGKCVIDKVTRN
NP_033406.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSL------HPSYS-CKYEGKCIIDKVTRN
THB1_RAT         CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSL------HPSYS-CKYEGKCIIDKVTRN
THB1_MOUSE       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSL------HPSYS-CKYEGKCIIDKVTRN
THB2_RAT         CVVCGDKATGYHYRCITCEGCKGFFRRTIQKSL------HPSYS-CKYEGKCIIDKVTRN
THB1_SHEEP       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGKCVIDKVTRN
THB_CHICK        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPTYS-CKYEGKCVIDKVTRN
NP_571415.1      CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------NPTYA-CKYEGKCVIDKVTRN
THB_PAROL        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------NPTYA-CKYEGKCVIDKVTRN
THBA_XENLA       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGKCVIDKVTRN
THBB_XENLA       CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGKCVIDKVTRN
THB_RANCA        CVVCGDKATGYHYRCITCEGCKGFFRRTIQKNL------HPSYS-CKYEGKCVIDKVTRN
ECR_AEDAE        CLVCGDRESGYHYNALTCEGCKGFFRRSVTK--------NAVYC-CKFGHACEMDMYMRR
ECR_CHITE        CLVCGDRASGYHYNALTCEGCKGFFRRSVTK--------NAVYC-CKFGHECEMDMYMRR
ECR_LUCCU        CLVCGDRASGYHYNALTCEGCKGFFRRSVTK--------NAVYC-CKFGHACEMDMYMRR
NP_724460.1      CLVCGDRASGYHYNALTCEGCKGFFRRSVTK--------SAVYC-CKFGRACEMDMYMRR
ECR_HELVI        CLVCGDRASGYHYNALTCEGCKGFFRRSVTK--------NAVYI-CKFGHACEMDIYMRR
ECR_MANSE        CLVCGDRASGYHYNALTCEGCKGFFRRSVTK--------NAVYI-CKFGHACEMDMYMRR
ECR_BOMMO        CLVCGDRASGYHYNALTCEGCKGFFRRSVTK--------NAVYI-CKFGHACEMDMYMRR
NP_000367.1      CGVCGDRATGFHFNAMTCEGCKGFFRRSMKR--------KALFT-CPFNGDCRITKDNRR
VDR_BOVIN        CGVCGDRATGFHFNAMTCEGCKGFFRRSMKR--------KALFT-CPFNGDCRITKDNRR
NP_058754.1      CGVCGDRATGFHFNAMTCEGCKGFFRRSMKR--------KALFT-CPFNGDCRITKDNRR
VDR_MOUSE        CGVCGDRATGFHFNAMTCEGCKGFFRRSMKR--------KALFT-CPFNGDCRITKDNRR
NP_990429.1      CGVCGDRATGFHFNAMTCEGCKGFFRRSMKR--------KAMFT-CPFNGDCKITKDNRR
VDR_COTJA        CGVCGDRATGFHFNAMTCEGCKGFFRRSMKR--------KAMFT-CPFSGDCKITKDNRR
VDR_XENLA        CGVCGDKATGFHFNAMTCEGCKGFFRRSMKR--------KAMFT-CPFNGDCRITKDNRR
A34714           CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
RRG2_HUMAN       CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
RRG2_MOUSE       CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
NP_000957.1      CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
RRG_NOTVI        CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCQINKVTRN
RRG_XENLA        CFVCNDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCQINKVTRN
NP_571414.1      CFVCQDKSSGYHYGVSSCEGCKGFFRRSIQK--------NMVYT-CHRDKNCQINKVTRN
AAD05222.1       CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
RRA_MOUSE        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
NP_989867.1      CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
RRA_XENLA        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKNCIINKVTRN
RRA_NOTVI        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKTCIINKVTRN
RRB_COTJA        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKNCVINKVTRN
S13512           CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHRDKNCVINKVTRN
RRB_HUMAN        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMIYT-CHRDKNCVINKVTRN
RRB_MOUSE        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMIYT-CHRDKNCVINKVTRN
RRB_NOTVI        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMIYT-CHRDKNCVINKVTRN
RRA_FUGRU        CFVCQDKSSGYHYGVSACEGCKGFFRRSIQK--------NMVYT-CHREKNCIINKVTRN
AAA19972.1       CRVCGDKASGFHYGVHACEGCKGFFRRTIRM--------KLEYEKCDRI--CKIQKKNRN
NP_006229.1      CRVCGDKASGFHYGVHACEGCKGFFRRTIRM--------KLEYEKCERS--CKIQKKNRN
PPAS_XENLA       CKICGDRASGFHYGVHACEGCKGFFRRTIRM--------RLQYEHCDRN--CKIQKKNRN
CAA40856.1       CRICGDKASGYHYGVHACEGCKGFFRRTIRL--------KLVYDKCDRS--CKIQKKNRN
NP_037328.1      CRICGDKASGYHYGVHACEGCKGFFRRTIRL--------KLAYDKCDRS--CKIQKKNRN
CAA68898.1       CRICGDKASGYHYGVHACEGCMGFFRRTIRL--------KLVYDKCDRS--CKIQKKNRN
PPAR_PHACI       CRICGDKASGYHYGVHACEGCKGFFRRTIRL--------KLAYDKCDRS--CKIQKKNRN
PPAR_CANFA       CRICGDRASGYHYGVHACEGCKGFFRRTIRL--------KLAYDKCDRS--CKIQKKNRN
PPAR_CAVPO       CRICGDKASGYHYGVHACEGCKGFFRRTIRL--------KLVYDKCDRS--CKIQKKNRN
PPAR_XENLA       CRVCSDKASGFHYGVHACEGCKGFFRRTIRL--------KLVYDRCERM--CKIQKKNRN
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NP_035276.1      CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
NP_056953.2      CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
CAA73382.2       CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
PPAT_CRIGR       CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
PPAT_MACMU       CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
PPAT_PIG         CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
NP_851367.1      CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
PPAT_RABIT       CRVCSDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYDRCDLN--CRIHKKSRN
PPAT_XENLA       CRVCGDKASGFHYGVHACEGCKGFFRRTIRL--------KLIYERCDLN--CRIHKKSRN
CAB53540.1       CKVCGDVASGFHYGVLACEGCKGFFRRSIQQ--------NIQYKRCLKNENCSIVRINRN
NP_665718.1      CKVCGDVASGFHYGVHACEGCKGFFRRSIQQ--------NIQYKRCLKNENCSIVRINRN
E75_CHOFU        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQ--------KIQYRPCTKNQQCSILRINRN
E75_MANSE        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQ--------KIQYRPCTKNQQCSILRINRN
E75A_DROME       CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQ--------KIQYRPCTKNQQCSILRINRN
E75_GALME        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQ--------KIQYRPCTKNQQCSILRINRN
E75_METEN        CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQ--------KIQYRPCTKNQQCSILRINRN
E75C_DROME       CRVCGDKASGFHYGVHSCEGCKGFFRRSIQQ--------KIQYRPCTKNQQCSILRINRN
NP_038674.1      CKICGDKSSGIHYGVITCEGCKGFFRRSQQS--------NATYS-CPRQKNCLIDRTSRN
NP_599022.1      CKICGDKSSGIHYGVITCEGCKGFFRRSQQS--------NATYS-CPRQKNCLIDRTSRN
RORB_HUMAN       CKICGDKSSGIHYGVITCEGCKGFFRRSQQN--------NASYS-CPRQRNCLIDRTNRN
RORB_RAT         CKICGDKSSGIHYGVITCEGCKGFFRRSQQN--------NASYS-CPRQRNCLIDRTNRN
BAB16893.1       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYV-CPATNQCTIDRNRRK
ESR1_ICTPU       CSVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYV-CPATNQCTIDRNRRK
ESR1_HORSE       CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_PIG         CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
NP_031982.1      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
NP_036821.1      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_MESAU       CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_HUMAN       CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_XENLA       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_POEGU       CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
NP_990514.1      CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_SHEEP       CAVCNDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_OREAU       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_ORENI       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDKNRRK
ESR1_PAGMA       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDRNRRK
ESR1_SPAAU       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDRNRRK
ESR1_ORYLA       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTIDRNRRK
ESR1_ONCMY       CAVCSDFASGYHYGVWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTMDRNRRK
ESR1_SALSA       CAVCSDFASGYHYGFWSCEGCKAFFKRSIQG--------HNDYM-CPATNQCTMDRNRRK
ESR2_ANGJA       CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG--------HNGYI-CPATNQCTIDKNRRK
ESR2_MICUN       CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_BOVIN       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_SHEEP       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_MOUSE       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_RAT         CPVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_CALJA       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
NP_001428.1      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_PIG         CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_COTJA       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
NP_990125.1      CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_STUVU       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_ICTPU       CVVCHDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_SPAAU       CAVCHDYASGYHYGVWSCEGCKAFFKRSIQR--------HNDYI-CPATNQCTIDKNRRK
ESR3_MICUN       CAVCHDYASGYHYGVWSCEGCKAFFKRSIQR--------DNEYI-CPATNECTIDKNRRK
ESR2_ORENI       CAVCHDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
ESR2_ONCMY       CAVCSDYASGYHYGVWSCEGCKAFFKRSIQG--------HNDYI-CPATNQCTIDKNRRK
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ERR1_HUMAN       CLVCGDVASGYHYGVASCEACKAFFKRTIQG--------SIEYS-CPASNECEITKRRRK
ERR1_MOUSE       CLVCGDVASGYHYGVASCEACKAFFKRTIQG--------SIEYS-CPASNECEITKRRRK
ERR2_RAT         CLVCGDIASGYHYGVASCEACKAFFKRTIQG--------NIEYS-CPATNECEITKRRRK
NP_004443.2      CLVCGDIASGYHYGVASCEACKAFFKRTIQG--------NIEYS-CPATNECEITKRRRK
ERR2_MOUSE       CLVCGDIASGYHYGVASCEACKAFFKRTIQG--------NIEYN-CPATNECEITKRRRK
NP_036065.1      CLVCGDIASGYHYGVASCEACKAFFKRTIQG--------NIEYS-CPATNECEITKRRRK
ANDR_HUMAN       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
ANDR_PANTR       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
ANDR_MACFA       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
ANDR_PAPHA       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
ANDR_EULFC       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
ANDR_CANFA       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
ANDR_RABIT       CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
NP_036634.1      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
NP_038504.1      CLICGDEASGCHYGALTCGSCKVFFKRAAEG---------KQKYLCASRNDCTIDKFRRK
GCR_SAGOE        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_SAIBB        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_AOTNA        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
NP_000167.1      CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_PIG          CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_SAISC        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_TUPGB        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_RABIT        CLVCSDEASGCHYGVLTCGSCKVFFKRAVKG---------QHNYLCAGRNDCIIDKIRRK
GCR_RAT          CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
NP_032199.1      CLVCSDEASVCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_CAVPO        CLVCSDELSGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRE
GCR_XENLA        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
GCR_ONCMY        CLVCSDEASGCHYGVLTCGSCKVFFKRAVEGWRARQNTDGQHNYLCAGRNDCIIDKIRRK
GCR_PAROL        CLVCSDEASGCHYGVVTCGSCKVFFKRAVEGWRARQNTDGQHNYLCAGRNDCIIDKIRRK
MCR_MOUSE        CLVCGDEASGCHYGVVTCGSCKVFFKRAVE-----------HNYLCAGRNDCIIDKIRRK
NP_037263.1      CLVCGDEASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
MCR_TUPGB        CLVCGDGASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
MCR_SAISC        CLVCGDEASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
NP_000892.1      CLVCGDEASGCHYGVVTCGSCKVFFKRAVEG---------QHNYLCAGRNDCIIDKIRRK
MCR_XENLA        CLVCGDEASGCHYGVVTCGSCKVFFKRAVEGKCSR-----QHSYLCAGRNDCIIDKIRRK
NP_032855.1      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAGRNDCIVDKIRRK
NP_074038.1      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAGRNDCIVDKIRRK
PRGR_RABIT       CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAGRNDCIVDKIRRK
PRGR_SHEEP       CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAGRNDCIVDKIRRK
PRGR_HUMAN       CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAGRNDCIVDKIRRK
NP_990593.1      CLICGDEASGCHYGVLTCGSCKVFFKRAMEG---------QHNYLCAGRNDCIVDKIRRK
                 * :* *  :  *:   :*  *  **:*:                 *     * :    *.

FTF1_BOMMO       RCPFCRFQKCLDVGMKLEAVRADRMRGGRNKFGPMYKRDRARKLQMMRQRQ------
NP_524143.2      RCPYCRFQKCLEVGMKLEAVRADRMRGGRNKFGPMYKRDRARKLQVMRQRQ------
NP_004950.2      RCPFCRFQKCLTVGMRLEAVRADRMRGGRNKFGPMYKRDRALKQQKKAQIR------
STF1_MOUSE       RCPFCRFQKCLTVGMRLEAVRADRMRGGRNKFGPMYKRDRALKQQKKAQIR------
NP_445796.1      RCPFCRFQKCLTVGMRLEAVRADRMRGGRNKFGPMYKRDRALKQQKKAQIR------
NP_776828.1      RCPFCRFQKCLTVGMRLEAVRADRMRGGRNKFGPMYKRDRALKQQKKAQIR------
STF1_PIG         RCPFCRFQKCLTVGMRLEAVRADGMRGGRNKFGPMYKRDRALKQQKKAQIR------
AAA28543.1       KCPACRFEKCLQKGMKLEAIREDRTRGGRSTYQCSYTLPNSMLSPLLSPDQ------
7UP2_DROME       QCQYCRLKKCLKMGMRREAVQRGRVPPTQPGLAGMHGQYQIANGDPMG----IAG--
NP_524325.1      QCQYCRLKKCLKMGMRREAVQRGRVPPTQPGLAGMHGQYQIANGDPMG----IAG--
NP_066285.1      QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----THGQFALTNGDPLNCHSYLSG--
NP_542956.1      QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----THGQFALTNGDPLNCHSYLSG--
NP_989752.1      QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----THGQFALTNGDPLNCHSYLSG--
CAA54096.1       QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----THGQFALTNGDPLNCHSYLSG--
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NP_005645.1      QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----NPGQYALTNGDPLNGHCYLSG--
NP_034281.1      QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----NPGQYALTNGDPLNGHCYLSG--
NP_786998.1      QCQYCRLKKCLKVGMRREAVQRGRMPPTQP----NPGQYALTNGDPLNGHCYLSG--
CAA54248.1       QCRYCRLKKCFRAGMKKEAVQNERDRISTRR-SSYEDSSL-PSINALLQAEVL----
NP_032287.1      QCRYCRLKKCFRAGMKKEAVQNERDRISTRR-SSYEDSSL-PSINALLQAEVL----
NP_071516.1      QCRYCRLKKCFRAGMKKEAVQNERDRISTRR-SSYEDSSL-PSINALLQAEVL----
HN4A_XENLA       QCRYCRLKKCFRAGMKKEAVQNERDRISTRR-SSYEDSSL-PSINVLIQAEVL----
HN4B_XENLA       QCRYCRLRKCFRAGMKKEAVQNERDRISMRR-SSYEDNGS-LSINVLTQAEAM----
HN4G_HUMAN       QCRYCRLRKCFRAGMKKEAVQNERDRISTRR-STFDGSNI-PSINTLAQAEVR----
HN4G_MOUSE       QCRYCRLRKCFRAGMKKEAVQNERDRISTRR-STYEGSNI-PSINTLAQAEVR----
S36218           QCRYCRLRKCFKAGMKKEAVQNERDRISCRR-TSNDDPDPGNGLSVISLVKA-----
NP_035435.1      RCQYCRYQKCLAMGMKREAVQEERQRGKDRN-ENEVESTSSA-NEDMPVEKIL----
NP_036937.1      RCQYCRYQKCLAMGMKREAVQEERQRGKDRN-ENEVESTSSA-NEDMPVEKIL----
NP_002948.1      RCQYCRYQKCLAMGMKREAVQEERQRGKDRN-ENEVESTSSA-NEDMPVERIL----
RXRA_XENLA       RCQYCRYQKCLAMGMKREAVQEERQRGKERN-ENEVESSNSA-NEDMPVEKIL----
RXRA_BRARE       RCQYCRYQKCLAMGMKREAVQEERQRGRERS-DNEVDSSSSF-NEEMPVEKIL----
NP_008848.1      RCQYCRYQKCLVMGMKREAVQEERQRSRERA-ESEAECATSG-HEDMPVERIL----
NP_033133.1      RCQYCRYQKCLVMGMKREAVQEERQRSRERA-ESEAECASSS-HEDMPVERIL----
NP_990625.1      RCQYCRYQKCLAMGMKREAVQEERQGSRERS-ENEAESTSGG-SEDMPVERIL----
RXRG_XENLA       RCQYCRYQKCLAMGMKREAVQEERQRSREKS-DTEAESTSST-SEEMPVERIL----
NP_035436.1      RCQYCRYQKCLATGMKREAVQEERQRGKDK--DGDGDGAGGA-PEEMPVDRILE---
RXRB_RAT         RCQYCRYQKCLATGMKREAVQEERQRGKDK--DGDGDGAGGA-PEEMPVDRILE---
USP_BOMMO        RCQYCRYQKCLACGMKREAVQEERQRAARRT-EDAHPSSSVQ---ELSIERLLEL--
USP_MANSE        RCQYCRYQKCLACGMKREAVQEERQRAARGT-EDAHPSSSVQ---ELSIERLLEI--
USP_CHOFU        RCQYCRYQKCLACGMKREAVQEERQRNARGA-EDAHPSSSVQVSDELSIERL-----
NP_476781.1      RCQYCRYQKCLTCGMKREAVQEERQRGARNA-AGRLSASGGGSSGPGSVGGS-----
THA_APTPA        QCQLCRFKKCISVGMAMDLVLDDSKRVAKRKLIEENRERRR----KEEMIKSL----
THA_CAIMO        QCQLCRFKKCISVGMAMDLVLDDSKRVAKRKLIEENRERRR----KEEMIKSL----
NP_990644.1      QCQLCRFKKCISVGMAMDLVLDDSKRVAKRKLIEENRERRR----KEEMIKSL----
THA_PYGAD        QCQLCRFKKCISVGMAMDLVLYDSKRVAKRKLIEENRERRR----KEEMIKSL----
THA_MOUSE        QCQLCRFKKCIAVGMAMDLVLDDSKRVAKRKLIEQNRERRR----KEEMIRSL----
THA_PIG          QCQLCRFKKCIAVGMAMDLVLDDSKRVAKRKLIEQNRERRR----KEEMIRSL----
THA1_SHEEP       QCQLCRFKKCIAVGMAMDLVLDDSKRVAKRKLIEQNRERRR----KEEMIRSL----
CAA68539.1       QCQLCRFKKCIAVAMAMDLVLDDSKRVAKRKLIEQNRERRR----KEEMIRSL----
THAA_XENLA       QCQLCRFKKCIAVGMAMDLVLDDGKRVAKRKLIEENRQRRR----KEEMIKTL----
THAB_XENLA       QCQLCRFKKCIAVGMAMDLVLDDSKRVAKRKLIEENRVRRR----KEEMIKTL----
THA_RANCA        QCQLCRFKKCIAVGMAMDLVLDDSKRVAKRKLIEENRERRR----KEEMIKTL----
NP_571471.1      QCQLCRFRKCISVGMAMDLVLDDSKRVAKRRLIEENREKRK----KEEIVKTL----
THA_SALSA        QCQLCRFRKCIAVCMAMDLVLDDSKRVAKRRLIEENREKRK----KDEIVKTL----
THAB_PAROL       QCQLCRFKKCIAVGMAMDLVLDDSKRVAKRRLIEENRERRK----KEEIVKTL----
THAA_PAROL       QCQLCRFKKCISVGMAMDLVLDDSKRVAKRRLIEENREKRK----REEMVRTL----
THA_HIPHI        QCQLCRFKKCISVGMAMDLVLDDSKRVAKRRLIEENREKRK----REEMVRTL----
NP_000452.2      QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKSI----
THB2_HUMAN       QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKSI----
NP_033406.1      QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKSI----
THB1_RAT         QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKSI----
THB1_MOUSE       QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKSI----
THB2_RAT         QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKSI----
THB1_SHEEP       QCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQRSM----
THB_CHICK        QCQECRFKKCIFVGMATDLVLDDSKRLAKRKLIEENREKRR----REELQKTI----
NP_571415.1      QCQECRFKKCIAVGMATDLVLDDSKRLAKRKLIEENRERRR----REELQKTV----
THB_PAROL        QCQECRFKKCIAVGMATDLVLDDSKRLAKRKLIEENRERRR----KEELQKTV----
THBA_XENLA       QCQECRFKKCIAVGMATDLVLDDNKRLAKRKLIEENREKRR----KDEIQKSL----
THBB_XENLA       QCQECRFKKCKTVGMATDLVLDDSKRLAKRKLIEENREKRR----KDEIQKSI----
THB_RANCA        QCQECRFKKCIAVGMATDLVLDDSKRLAKRKLIEENREKRR----KDELQKTL----
ECR_AEDAE        KCQECRLKKCLAVGMRPECVVPENQCAIKRKEKKAQKEKDK---VQTNATVSTT---
ECR_CHITE        KCQECRLKKCLAVGMRPECVVPENQCAIKRKEKKAQKEKDK---VPGIVGSNTS---
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ECR_LUCCU        KCQECRLKKCLAVGMRPECVVPENQCAMKRREKKAQKEKDK---IQTSVCATEI---
NP_724460.1      KCQECRLKKCLAVGMRPECVVPENQCAMKRREKKAQKEKDK---MTTSPSSQHG---
ECR_HELVI        KCQECRLKKCLAVGMRPECVVPENQCAMKRKEKKAQREKDK---LPVSTTTVDD---
ECR_MANSE        KCQECRLKKCLAVGMRPECVVPESTCKNKRREKEAQREKDK---LPVSTTTVDD---
ECR_BOMMO        KCQECRLKKCLAVGMRPECVIQE---PSKNKDRQRQK-KDKGILLPVSTTTVEDH--
NP_000367.1      HCQACRLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEEA---LKDSLRPKLS---
VDR_BOVIN        HCQACRLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEEA---LKDSLRPKLS---
NP_058754.1      HCQACRLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEA---LKDSLRPKLS---
VDR_MOUSE        HCQACRLKRCVDIGMMKEFILTDEEVQRKREMIMKRKEEEA---LKDSLRPKLS---
NP_990429.1      HCQACRLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEEA---LKESLKPKLS---
VDR_COTJA        HCQACRLKRCVDIGMMKEFILTDEEVQRKREMILKRKEEEA---LKESLKPKLS---
VDR_XENLA        HCQSCRLKRCVDIGMMKEFILTDEEVQRKRQMINKRKSEEA---LKESMRPKIS---
A34714           RCQYCRLQKCFEVGMSKEAVRNDRN-KKKK-EVKEEGSP-DSYELSPQLEELIT---
RRG2_HUMAN       RCQYCRLQKCFEVGMSKEAVRNDRN-KKKK-EVKEEGSP-DSYELSPQLEELIT---
RRG2_MOUSE       RCQYCRLQKCFEVGMSKEAVRNDRN-KKKK-EVKEEGSP-DSYELSPQLEELIT---
NP_000957.1      RCQYCRLQKCFEVGMSKEAVRNDRN-KKKK-EVKEEGSP-DSYELSPQLEELIT---
RRG_NOTVI        RCQYCRLQKCFEVGMSKEAVRNDRN-KKKK-EIKEEVVT-DSYEMPPEMEALIQ---
RRG_XENLA        RCQFCRLQKCFQVGMSKEAVRNDRN-KKKK-EIKEEVVLPDSYEMPPEMEELI----
NP_571414.1      RCQYCRLQKCFEVGMSKEAVRNDRN-KKKK-DVKDEVIPPESYELSGELEELV----
AAD05222.1       RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-EVPKPECS-ESYTLTPEVGELIE---
RRA_MOUSE        RCQYCRLQKCFDVGMSKESVRNDRN-KKKK-EAPKPECS-ESYTLTPEVGELIE---
NP_989867.1      RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-DVPKTECS-ESYIVTPEVEELIE---
RRA_XENLA        RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-ESPKPEAI-ESYILSPETQDLIE---
RRA_NOTVI        RCQYCRLQKCFEVGMSKESVRNDRN-KKKKQEAPKQECT-ESYIITPEVEDLV----
RRB_COTJA        RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-EPTKQEST-ENYEMTAELDDLTE---
S13512           RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-EPTKQEST-ENYEMTAELDDLTE---
RRB_HUMAN        RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-ETSKQECT-ESYEMTAELDDLTE---
RRB_MOUSE        RCQYCRLQKCFEVGMSKESVRNDRN-KKKK-EPSKQECT-ESYEMTAELDDLTE---
RRB_NOTVI        RCQYCRLQRCFEVGMSKESVRNDRN-KKKK-EPIKQECI-ESLEMTAELDDLTE---
RRA_FUGRU        RCQYCRLQKCLEVGMSKESVRNDRN-KKKK-DEKKPECI-ENYVLSPDTEQMIN---
AAA19972.1       KCQYCRFQKCLALGMSHNAIRFGRMPDGEKRKLVAGLTASEGCQHNPQLADL-----
NP_006229.1      KCQYCRFQKCLALGMSHNAIRFGRMPEAEKRKLVAGLTANEGSQYNPQVADL-----
PPAS_XENLA       KCQYCRFNKCLSLGMSHNAIRFGRMPESEKRKLVQAPVSDSAAPDSP-VSDLD----
CAA40856.1       KCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEHDLKDSETADL-----
NP_037328.1      KCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEHDLKDSETADL-----
CAA68898.1       KCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEHDIEDSETADL-----
PPAR_PHACI       KCQYCRFQKCLSDGMSHNAIRFGRMPRSEKAKLKAEILTCEHDLEDSEVADL-----
PPAR_CANFA       KCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEILTCEQDPEDAETADL-----
PPAR_CAVPO       KCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAEVLTCDRDSEGAETADL-----
PPAR_XENLA       KCQYCRFEKCLNVGMSHNAIRFGRMPRSEKAKLKAEVLMCDQDVKDSQMADL-----
NP_035276.1      KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
NP_056953.2      KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
CAA73382.2       KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
PPAT_CRIGR       KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
PPAT_MACMU       KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
PPAT_PIG         KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
NP_851367.1      KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
PPAT_RABIT       KCQYCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADLR----
PPAT_XENLA       KCQFCRFQKCLAVGMSHNAIRFGRMPQAEKEKLLAEISS-DIDQLNPESADQR----
CAB53540.1       RCQQCRFKKCLSVGMSRDAVRFGRIPKREKQRMLAEMQSAMNLANNQLSS-------
NP_665718.1      RCQQCRFKKCLSVGMSRDAVRFGRIPKREKQRMLAEMQNAMNLANNQLSS-------
E75_CHOFU        RCQYCRLKKCIAVGMSRDAVRFGRVPKREKARILAAMQQSSSSRAHEQAA-------
E75_MANSE        RCQYCRLKKCIAVGMSRDAVRFGRVPKREKARILAAMQQSSTSRAHEQAA-------
E75A_DROME       RCQYCRLKKCIAVGMSRDAVRFGRVPKREKARILAAMQQSTQNRGQQRAL-------
E75_GALME        RCQYCRLKKCIAVGMSRDAVRFGRVPKREKARILAAMQ-SSTTRAHEQAAA------
E75_METEN        RCQYCRLKKCIAVGMSRDAVRFGRVPKREKAKILAAMQ-SVNAKSQERAVL------
E75C_DROME       RCQYCRLKKCIAVGMSRDAVRFGRVPKREKARIWRPCNRAPRIAASSDPS-------
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NP_038674.1       RCQHCRLQKCLAVGMSRDAVKFGRMSKKQRDSLYAEVQKHRMQQQQRDHQQ------
NP_599022.1       RCQHCRLQKCLAVGMSRDAVKFGRMSKKQRDSLYAEVQKHRMQQQQRDHQQ------
RORB_HUMAN        RCQHCRLQKCLALGMSRDAVKFGRMSKKQRDSLYAEVQKHQQRLQEQRQEQ------
RORB_RAT          RCQHCRLQKCLALGMSRDAVKFGRMSKKQRDSLYAEVQKHQQRLQEQRQQQ------
BAB16893.1        SCQACRLRKCYEVGMMKGGIRKDR-GGRSVRRERRRSSNE-DRDKSSSDQCSR----
ESR1_ICTPU        SCQACRLRKCYEVGMMKGGFRKER-GGRIIKHNRRPSGLK-ERERGYSKAQSG----
ESR1_HORSE        SCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGE-GRNEAGPSGDR-----
ESR1_PIG          SCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGE-GRNEAVPPGDM-----
NP_031982.1       SCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLE-GRNEMGASGDM-----
NP_036821.1       SCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLE-GRNEMGTSGDM-----
ESR1_MESAU        SCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDLE-GRNDMGPSGDM-----
ESR1_HUMAN        SCQACRLRKCYEVGMMKGGIRKDRRGGRMLKHKRQRDDGE-GRGEVGSAGDM-----
ESR1_XENLA        SCQACRLRKCYEVGMMKGGIRKDRRGGRLLKHKRQKEEQE-QKNDVDPSEIR-----
ESR1_POEGU        SCQACRLRKCYEVGMMKGGIRKDRRGGRVMKQKRQREEQD-SRNGEASSTEL-----
NP_990514.1       SCQACRLRKCYEVGMMKGGIRKDRRGGEMMKQKRQREEQD-SRNGEASSTEL-----
ESR1_SHEEP        SCQACRLRKCY----------------------------------------------
ESR1_OREAU        SCQACRLRKCYEVGMMKGGMRKDR--GRVLRREKH--GPA-QR-QTSQNLPTHKASP
ESR1_ORENI        SCQACRLRKCYEVGMMKGGMRKDR--GRVLRREKR--RAC-DRDKPAKDLPHTRAS-
ESR1_PAGMA        SCQACRLRKCYEVGMMKGGMRKDR--GRVLRRDKQRTGTS-DRDKASKGLEHRT---
ESR1_SPAAU        SCQACRLRKCYEVGMMKGGVRKDR--GRVLRRDKRRTGTS-DRDKASKGLEHRT---
ESR1_ORYLA        SCQACRLRKCYEVGMMKGGVRKDR--IRILRRDKRRTGVG-DGDKVVKGQEHKT---
ESR1_ONCMY        SCQACRLRKCYEVGMVKGGLRKDR-GGRVLRKDKRYCGPAGDREKPYGDLEH-----
ESR1_SALSA        SCQACRLRKCYEVGMVKGGLRKDR-GGRVLRKDKRYCGPAGDREKPYGDLEH-----
ESR2_ANGJA        SCQACRLRKCYEVGMMKCGVRRER-CTY--RGARHRR-MPHIRELAGTGGGARTQ--
ESR2_MICUN        SCQACRLRKCYEVGMMKCGVRRER-CSY--RGARHRRGGLQPRDPTGRG-LVRVG--
ESR2_BOVIN        SCQACRLRKCYEVGMVKCGSRRER-CGY--RIVRRQRNSDEQLHCLSKTKRNGG---
ESR2_SHEEP        SCQACRLRKCYEVGMVKCGSRRER-CGY--RIVRRQRNSDEQLHCLSKTKRNGA---
ESR2_MOUSE        SCQACRLRKCYEVGMVKCGSRRER-CGY--RIVRRQRSASEQVHCLNKAKRTSG---
ESR2_RAT          SCQACRLRKCYEVGMVKCGSRRER-CGY--RIVRRQRSSSEQVHCLSKAKRNGG---
ESR2_CALJA        SCQACRLRKCYEVGMVKCGSRRER-CGY--RLVRRQGNAEEQLHCAGKAKRSGG---
NP_001428.1       SCQACRLRKCYEVGMVKCGSRRER-CGY--RLVRRQRSADEQLHCAGKAKRSGG---
ESR2_PIG          SCQACRLRKCYEVGMVKCGSRRER-CGY--RIVRKQRNSEGHLHCLSRAKKNGD---
ESR2_COTJA        SCQACRLRKCYEVGMMKCGSRRER-CGY--RILRRHRNSED---CMGKTKKYNEAAT
NP_990125.1       SCQACRLRKCYEVGMMKCGSRRER-CGY--RILRRHRNSED---CMGKTKKYNEAAT
ESR2_STUVU        SCQACRLRKCYEVGMMKCGSRRER-CGY--RILRSHRGAEERVHCLGRARRYSE---
ESR2_ICTPU        SCQACRLRKCYEMGMMKCGARRER-CGY--RASRRTAPMRDGSARPVGVRGQSQ---
ESR2_SPAAU        SCQACRLHKCYNVGMTKCGMRKER-GNF--RDPQMRRVTRLSSQGRTSGPSVLN---
ESR3_MICUN        SCQACRLRKCYEVGMTKCGMRKER-GNY--RSPQMRRMTRLTSQGRTDSSSVLT---
ESR2_ORENI        SCQACRLRKCYEVGMTKCGIRKER-GNY--RNSQARRLTRLSSQGKTAEPKGIT---
ESR2_ONCMY        SCQACRLRKCYEVGMMKCGLRRDR-GSYQQRGAQQKRLARFSGRMRTSGPRS-----
ERR1_HUMAN        ACQACRFTKCLRVGMLKEGVRLDRVRGG--RQKYKRRPEVDPLPFPGPFPAGP----
ERR1_MOUSE        ACQACRFTKCLRVGMLKEGVRLDRVRGG--RQKYKRRPEVDPLPFPGPFPAGP----
ERR2_RAT          SCQACRFMKCLKVGMLKEGVRLDRVRGG--RQKYKRRLDSENSPYLSLQISPP----
NP_004443.2       SCQACRFMKCLKVGMLKEGVRLDRVRGG--RQKYKRRLDSESSPYLSLQISPP----
ERR2_MOUSE        SCQACRFMKCLKVGMLKEGVRLDRVRGG--RQKYKRRLDSENSPYLNLPISPP----
NP_036065.1       SCQACRFMKCLKVGMLKEGVRLDRVRGG--RQKYKRRIDAENSPYLNPQLVQP----
ANDR_HUMAN        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETTQKLT------
ANDR_PANTR        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETTQKLT------
ANDR_MACFA        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETAQKLT------
ANDR_PAPHA        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSTTSPTEETAQKLT------
ANDR_EULFC        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASSATSPTEESSQKLT------
ANDR_CANFA        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGEASNVTSPTEEPTQKLT------
ANDR_RABIT        NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGESSSASSPTEDTTQKLT------
NP_036634.1       NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGENSSAGSPTEDPSQKMT------
NP_038504.1       NCPSCRLRKCYEAGMTLGARKLKKLGNLKLQEEGENSNAGSPTEDPSQKMT------
GCR_SAGOE         NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATTGVSQETSENPANKTIVP----
GCR_SAIBB         NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATTGVSQETSENPANKTIVP----
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GCR_AOTNA        NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATTGVSQETSENPANKTIVP----
NP_000167.1      NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATTGVSQETSENPGNKTIVP----
GCR_PIG          NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATTGVSQETSENSANKTIVP----
GCR_SAISC        NCPACRYRKCLQAGMNLEARKTKKKI-IKGIQQATTGVSQETSENPANKTIV-----
GCR_TUPGB        NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQTTTGISQETPENSANKTIVP----
GCR_RABIT        NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQTSTGVSQETSENPSNRTVVP----
GCR_RAT          NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATAGVSQDTSENP-NKTIVPA---
NP_032199.1      NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQATAGVSQDTSENA-NKTIVPA---
GCR_CAVPO        NCPACRYRKCLQAGMNLQARKTKKK--IKGIQQATTGVSQNTSENP-NKTIVPA---
GCR_XENLA        NCPACRYRKCLQAGMNLEARKTKKK--IKGIQQSTTATARESPETSMTRTLVP----
GCR_ONCMY        NCPACRFRKCLQAGMNLEARKNKKL--IRLKGQQTTMEPNPPPP-------------
GCR_PAROL        NCPACRFRKCLQAGMNLEARKNKKL--IKMKVHRPTGSAEPISN-------------
MCR_MOUSE        NCPACRLQKCLQAGMNLGARKSKKLGKLKGLHEEQPQQPPPPPPQSPEEGTTY----
NP_037263.1      NCPACRLQKCLQAGMNLGARKSKKLGKLKGLHEEQPQQPPPPPPQSPEEGT------
MCR_TUPGB        NCPACRLQKCLQAGMNLGARKSKKLGKLKGLHEEQPQQPPP--PQSPEEGTTY----
MCR_SAISC        NCPACRLQKCLQAGMNLGARRSKKLGKLKGIHEEQPQQQ-PPPPPPPPQSPE-----
NP_000892.1      NCPACRLQKCLQAGMNLGARKSKKLGKLKGIHEEQPQQQQPPPPPPPPQSP------
MCR_XENLA        NCPACRLQKCLQAGMNLGARKSKKLGKLKGVHEEHPQQPLQQTPTAS----------
NP_032855.1      NCPACRLRKCCQAGMVLGGRKFKKFNKVRVMR-TLDGVALPQSVGLPNESQA-----
NP_074038.1      NCPACRLRKCCQAGMVLGGRKFKKFNKVRVMR-ALDGVALPQSVAFPNESQT-----
PRGR_RABIT       NCPACRLRKCCQAGMVLGGRKFKKFNKVRVMR-ALDAVALPQPVGIPNESQR-----
PRGR_SHEEP       NCPACRLRKCCQAGMVLGGRKFKKFNKVRVMR-TLDAVALPQPVGIPNESQA-----
PRGR_HUMAN       NCPACRLRKCCQAGMVLGGRKFKKFNKVRVVR-ALDAVALPQPLGVPNESQA-----
NP_990593.1      NCPACRLRKCCQAGMVLGGRKFKKLNKMKVVR-TLD-VALQQPAVLQDETQSL----
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