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Pp_CPRc -----MTTTTGMALIS-----FMPPFFSIFEVWACLLLVGTVAFFVWRQ-----
Pp_CPRd -----MATSAMALIS-----FMPPFFSIFEVWACLLLVGTIVFFFWRPY-----
Pp_CPRa -----MTSVKMALIS-----FMPPAFSIFEVWASVLLVTAVAFFLWRQ-----
Pp_CPRb -----MALIAVSI-----VMPPFFSIFEIWACVLLFATVGFLLYRQ-----
Ca_CPR1 --MESSS--ELVR-----SIESAIGVSLG-----SDAVLMLTTTSFAVIVG--LVVFFLKRS--SD-----
Ph_CPR1 --MESSSSELFK-----SIESAFGVSL-----TDTLIVLLTTTSFALIVG--LIVFLLKRS--SD-----
Ce_CPR1 --METKL--ELVR-----SIESALGVSLGED-----GDKVILVLTTSFAVIVG--LVVFLWKRS--SD-----
Op_CPR1 --MDTKL--ELIR-----SIESALGVSLGDD-----VN-QILLVLTTSFAVIVG--LLMFLWKRS--GD-----
Gm_CPR1 --MANSSELVRT-----VVESVLGVS-----VSDSVMVIAATSVLIVG--LLVFWWRKS--SD-----
Vr_CPR1 --MANSNDLVR-----AVESFLGVSLGDS-----VSDSLLIATTSAAVVG--LLVFLWKKS--SD-----
Vs_CPR1 --MTSSNSDLVR-----TIESALGISLGD-----VSDSVVIAATTSAAVIG--LLVFLWRKS--PD-----
Pt_CPR1 --MSSSGSNLAR-----FVQSVLGISFGDS-----LSDSVVVIITTSFAALVG--LVVFLWKRS--SD-----
Rc_CPR1 --MSFSGDLVR-----YIESVLGVELGGSP-----MSDSVVVIITTSFAVIG--LLVFLWKRS--SD-----
Gh_CPR1 --MSS--SDLVG-----FVESVLGVSLGEGS-----VTDSMIVIAATTSFAVILG--LLVFFWKKSGSE-----
At_ATR1 MTSALYASDLFK-----QLKSIMGTDLSLSD-----DVVLVIAATTSALVAG--FVVLWKKTTAD-----
Ha_CPR1 --MSSGSEWVE-----WALGVG-----TDSVLVITTSLVAVIGVVALFLWKRS--SD-----
Pso_CPR1 --MGSNNLAN-----SIESMLGISIGSEY-----ISDPFIMVTTVASMIG--FGFFACMK-----
Am_CPR2 --MAGESL-----ATS--LP-----ATLLENRDLLMLTTTSIAVLIGCAVLLWRRSS-----
Pc_CPR2a --MGGESL-----ATS--LP-----ATLLENRDLLMLTTTSIAVLIGCAVLLWRRSS-----
Pc_CPR2b --MQSESM-----EVS PFDL L A S I L-----KIDSVESMTLLLENRDVLMMLTTTSFAVLIGLGLVMMWRRSSTTM-----
Aa_CPR2 --MQSTTSV-----KLS PFDL M T A L L N-----G-----KVSFDTSNTSDTNIPLAVFMENRELLMLTTTSIAVLIGCVVLLWRRSS--S-----
Ht_CPR2b -----MQSDSV-----KVS PFDL V S A A M N-----GKAMEKLNASESEDPTTLPALKMLVENRELLTLTTTSFAVLIGCLVFLMWRSS--S-----
Ht_CPR2a -----MDSSE-----KLS PFDL M S A I L K-----GAKLDGSNSSDSGVAVSPAVMAMLLENKELVMI TTTSIAVLIGCVVLLWRRSS-----
Cb_CPR2 --MESTIE-----KLS PLD L M T A I L K-----GVKLDNSNGSAG--VEHPAVVAMLMENKDLMMM TTTSIAVLIGLVVYLWRRGA-----
Ph_CPR2 --MDSTAE-----KLS AFD F M S A I L N K G-----GKIFDQLNTSSGDSTSPDSVATLLMDNKELMMI TTTSIAVLIGCAVLLWRRSS-----
Gh_CPR2 --MDS S S S S S-----GPS PLD L M S A L V K A K-----MDPSNASSDS--AAQVTVL FENREFVMI TTTSIAVLIGCVVLLWRRSASQ-----
Rc_CPR2 --MQP S S S S A G S I-----MKV S PFDL I S A V I K G N-----LDPSNVSESS--AVEVATMLYENREFVMI TTTSIAVLIGCVVLLWRRSGSQ-----
Pt_CPR2b --MSS S S S-----IKV S PLD L M Q A I I K G K-----VDPANVSSESGGSVAEVATLILENREFVMI TTTSIAVLIGCVVLLWRRSSGY-----
Pt_CPR2a --MQ S S S S-----MKV S P L E M Q A I I K G K-----VDPTNVSESGGSAAEMATLIRENREFVMI TTTSIAVLIGYVVLLWRRSSGY-----
Vv_CPR2 --MQ S S V K-----V S PFDL M S A I I K G S-----MDQSNVSESG--GAAAMVLENREFIMI TTTSIAVLIGCVVLLWRRS--GQ-----
Lj_CPR2 --ME S S S M-----K I S PLD L M S A M I K G T-----LDPSNVSTSG--AGSVFLENREFVMI TTTSIAVLIGCVVFLWRRSTGN-----
Psa_CPR2 --MQ D S T M-----K F S PLD L M T A I I K G K-----FNPSNDSSQAP--A-SIIFENREFVMI TTTSIAVLIGCVVLLWRRSNSN-----
At_ATR2 --MSS S S S-----S T S M I D L M A A I I K G E P V I V S D P A N A S A Y E S-----VAAELSSMLIENRFAMIV TTTSIAVLIGCIVMLWRRSGSG-----
Ec_CPR2 --MEQTAV-----KV S L F D L F S S I L N G K-----LDPSNFSSDS--AAILIENREILMILTTAIAVFIGCGFLYWRSS-----
Os_CPR2a --MDSGGGGGGGGG-----AALRPSALDLVAALLTGRGR-----PEEEGWPPSLAENRHLLVLTTSIAVLIGCGVALLVRRSSIS-----
Sb_CPR2a --MDSAS-----A-----AALKPSALDILLAALLTGRED-----PEGG--AHWAENRHLLLTTSIAVLIGCGVALLVRRSSAP-----
Ta_CPR2a --MDSAA-----AGMRDSALDILLAALLTGRAP-----PAAA--DGDQNRRLALLATSIAVLIGCGVALLFRSS-----
Sb_CPR2b --MDSATT-----SGAMELVAALLRGRVP-----PELMGG--DGAEGR--ALVATLAAAVLGAALFVLWRRAAAGKRRKRE-----
Zm_CPR2b1 --MDSAT-----SGAMELVAALLRGRVP-----PELGG--DGAEGR--ALVATLAAAVLGAALFVLWRRAAAGKRRKRE-----
Zm_CPR2b2 --MDSAT-----SGAMELVAALLRGRVP-----PELGG--EGAEGR--AVVATLAAAVLGAALFVLRRRAAGNKRKTE-----
Os_CPR2b --MESSA-----GPMELVAALLRGLTPR-AEQLLQLSSGGGEEAAG--GAEAR--AAVATVAAALLGCAFLVLRVRSAGRKRKRE-----
Sb_CPR2c -----MAALEAARSWAGSVIP-----PELAA--AAGGDPLAALAAATAALVAGLLILAVWFRSGGG-----
Zm_CPR2c -----MAALEAVRSWAVSVIP-----PELAA--AAGGDPLAALAAATAALVAGLLILAVWFRSGGG-----
Os_CPR2c -----MALALEAARSWAASVLP-----PELAA--AAGGDPLAALAAATAALVAGVILAVWFRSGGG-----
Ta_CPR2c -----MTSHARVRKLG-----SRAAALLAGLLVLAFLWRSGGS-----
    
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Tch_CPR  --MQANSNTVEGASQ--GKSLLDISRLDHFAL1LNGKGG-----DLGAMTGSALILTENSQNLMI2TTIALAVLVACVFFFVWRRGGSD-----
Tcu_CPR  --MQANSNTVEGASQ--GKSLLDISRLDHFAL1LNGKGG-----DLGAMTGSALILTENSQNLMI2TTIALAVLVACVFFFVWRRGGSD-----
Pm_CPR   --MQSNSNTVESGTQGLGKSLLEISRLDHVFS1LVNGKG-----DLGGMMESAVVLRENSELLMV2TTSLAVLIACVLLFWRRGGSA-----
Sm_CPRb  -----MESSVDLVLA1IGIKG-----MASATIPPYL2FLLGLALIFASAALFLWRRADSS-----
Sm_CPRC  -----MESSLDFVLAL1GVKG-----MASTNISPL2TLLSALLLVAGALFLWKAADAG-----
Sm_CPRa  -----
Cre_CPR  -----MDLNVA2IACVFLVIAALALLSIRRKSSG-----
consensus 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....

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Pp_CPRc  -----GAKPVKPVVVAKPVAPIEDEVEENSSVKKRVTVFFGTQTGTAEGFAKATVEEAKSRYEG-SAVFKVLDLDDYAADDEQYAAARLKKKEKFFALFMVAT
Pp_CPRd  -----APKP-----VVVVKPAMVVEEDVEEDSRVKRVMVFFGTQTGTAEGFAKATAEEAKSRYEG-TAVFKVMDPDDYGADNERYAARLKKKEKFFALFMVAT
Pp_CPRa  -----GEKKAVETKPVVAKPVQLDEEFE--DSSVKRVTVFFGTQTGTAEGFAKATAEEAKSRYDSSSVFKVVDLDDYGADDEQYAAARLKKKESLALFMVAT
Pp_CPRb  -----GSKGAEP-QPLQAKKVEEIEELPEDITIONHVSFFGTQTGTAEGFAKALAEAAQSRYGD-SVEFKVLDLEFYGADDDOYAAAKLKRERIAFFAVAT
Ca_CPR1  ---RSKEVKPVVFPK--SLNVEPEEIEVEPVGKVKVTVFFGTQTGTAEGFAKALSEETIKARYE--KAVFKVMDDDYAADDDLVEEKLKKETIAFFMVAT
Ph_CPR1  ---RSKEVKPVVFTK--SLNTEPEEIELEPVGKVKVTVFFGTQTGTAEGFAKALSTAEETIKARYE--KAVFKVMDDDYAADDDLVEEKLKKETIAFFMVAT
Ce_CPR1  ---RSRETKSVVVKLVLTALQEEEEIEVDLDPSSVKVTVFFGTQTGTAEGFAKALAEETIKTRYE--KAVFKVLDLDDYAADDDOYEEKLKKETIAFFMVAT
Op_CPR1  ---RGKEIKPVGCSQGCALLVEEEKE--EVDPTKVKVTVFFGTQTGTAEGFAKALSEETIKARYE--KAVFKVFDLDDYAADDDOYEEKLKKETIAFFMLAT
Gm_CPR1  ---RSKEQKPLAVPKLLVKEDDEE--VDAGSGKTRVAVFFGTQTGTAEGFAKALAEETIKARYE--KAAVKVADLDDYAMDDDOYEEKLKKESLAFVFLAT
Vr_CPR1  ---RSKEVKPVVPRDLME--EEE--VDVAAGKTKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAAVKVLDLDDYAADDDLVEEKLKKESLVFFMLAT
Vs_CPR1  ---RSRELRPVIVPKFTVKH--EDDE--VEVDRGKTKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVMDDDYATDDDOYEEKLKKETLVFFMLAT
Pt_CPR1  ---RSKDVKPLVVPKSLSVKDEEDE--SEALGGKTKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAAVKVFDLDDYAMDDDOYEEKLKKETLALFMVAT
Rc_CPR1  ---RSKEVTPLVVPKSLSVKDEEDE--AETLAGKTKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAAVKVLDLDDYAMDDDOYEEKLKKETLVFFMVAT
Gh_CPR1  ---RSRDVKPLVAPKPVSLKDEEDDDAVIAAGKTKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAAVKVLDLDDYAMDDDOYEEKLKKETIAFFMVAT
At_ATR1  ---RSGELKPLMIPKSLMAKDEDDD--LDLGSKTRVSVFFGTQTGTAEGFAKALSEETIKARYE--KAAVKVLDLDDYAADDDOYEEKLKKETIAFFCVAT
Ha_CPR1  ---RGKDPKTLVVPKPLSLKEEEE--EDEAEGKTKVCFVFFGTQTGTAEGFAKALAEETIKVRYE--KAVFKVLDLDDYALDDDOYEEKLKKETIAFFMVAT
Pso_CPR1 ---SSSQKPIETYKPP--IIDKEEEIEIIVDPGKIKLTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAAEDDOYEEKLKKESLVFFMVAT
Am_CPR2  -----LRSVKSVPEPKLIVPKVEIE--DEVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAKFRVLDLDDYAAEDDEYEEKFKKESFAFFFLAT
Pc_CPR2a -----LRSVKSVPEPKLIVPKVEIE--DEVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAKFRVLDLDDYAAEDDEYEEKFKKESFAFFFLAT
Pc_CPR2b -----TKSAKKLEPAKIVIPKFEME--EVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--DAIFKTVLDLDDYAGDDDEYETIKLKKESMVFFFLAT
Aa_CPR2  -----A-AKKAESPVIIVPKVTE--DEVDGGRKKVTVFFGTQTGTAEGFAKALVEEAKARYE--KAVFKVLDLDDYAAEDDEYEEKLKKESLAFVFLAT
Ht_CPR2b -----KLVQDPVPVQIVVKKKEKE--SEVDGKKKVSIFVGTQTGTAEGFAKALVEEAKVRYE--KTSFKVLDLDDYAAEDDEYEEKLKKESLAFVFLAT
Ht_CPR2a -----KLVQDPVPVQIVVKKKEKE--SEVDGKKKVSIFVGTQTGTAEGFAKALVEEAKVRYE--KTSFKVLDLDDYAAEDDEYEEKLKKESLAFVFLAT
Cro_CPR2 -----GSGKKVVEPKLIVPKSVMEPEEIDEGKKKFTVFFGTQTGTAEGFAKALAEETIKARYE--KAVIKVLDLDDYAADDEYEEKFRKETIAFFLILAT
Cb_CPR2  -----GSAKKVVPEPKLIVPKGPEVEEVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--QANFKVMDDDYAADDEYEEKMKKETIAFFFLAT
Ph_CPR2  -----TSAKKVVDPKLVVPKSVMEPEEIDEGKKKFTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAADDEYEEKLKKETIAFFFLAT
Gh_CPR2  -----KPKQIQLP-LKPSIIEKEP--E--LEVDGKKKVTVFFGTQTGTAEGFAKALVEEAKARYE--KATFNTVLDLDDYAADDEYEEKMKKDNLAFVFLAT
Rc_CPR2  -----KSKSVAIEPLKPLVVKEP--E--PEPDDGKIKLTVFFGTQTGTAEGFAKALSEEAARYE--KATFKVLDLDDYAADDDYEYETIKLKKESLALFFVAT
Pt_CPR2b -----QRPKVPVP-PKPLIVKDL--E--PEVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKTVLDLDDYAGDDDEYEEKLKKEDLVIFFLAT
Pt_CPR2a -----QKPKVPVP-PKPLIVKDL--E--PEVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKTVLDLDDYAADDDYEYEEKLKKESLALFFLAT
Vv_CPR2  -----KQSKTPEP-PKPLIVKDL--E--VEVDGKQKVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKVLDLDDYAGDDDEYEEKLKKETIAFFFLAT
Lj_CPR2  -----KAKSIEPP--KRVVEKLSDE--AEVDGGRKKVTVFFGTQTGTAEGFAKATAEEAKVRYE--KAKFKTVLDLDDYAQDDDEYEEKLKKETLALFFLAT
Psa_CPR2 -----KSKQIEVP--KLVIKKLP--E--LDVDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--KAKFRVMDDDYAADDDYEYEEKLKRETMALFFLAT
At_ATR2  -----NSKRVEPL--KPLVIKPR--E--EIDGGRKKVTVFFGTQTGTAEGFAKALGEEAKARYE--KTRFKTVLDLDDYAADDDYEYEEKLKKEDVAFVFLAT
Ec_CPR2  -----NKSSKIVETQKLIVEKEPEP--E--VDGKKKVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKVLDLDDYAGDDDEYEEKLKKETIALFFLAT
Os_CPR2a --APAARAQEPQPRAPAPAKRKQEAEPDPPDGRQRVAVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDEYAAADDEYEEKQKKEKIALFFVAT
Sb_CPR2a --RAAAAAASQAPPRSLAAKPKD--EPDPPDGRPRVTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAAEDDEYEEKLKKESIALFFLAT
Ta_CPR2a --GAAPLAHKSAAKPLAAKDDQ--EPDPPDGRQRVAVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAAEDDEYEEKLKKENIAFFFLAT
Sb_CPR2b AAAAAVAEATEVKARAAG--GEDEKAADDGRRKVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKVLDLDDYAAEDDEYEEKLKKELALFFVAT
Zm_CPR2b1 --AAVAAEATQAKARGGKA--AE--EKPADDGRRKVTVFFGTQTGTAEGFAKALAEETIKARYE--KASFKVLDLDDYAAEDDEYEEKLKKEKALFFVAT
Zm_CPR2b2 --GAAATEATRAKARGVKVSAEEIE--EKPADDGRRKVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKVLDLDDYAAEDDEYEEKLKKEKALFFVAT
Os_CPR2b EAERSAAAAGVGGKGNASAAAG--EAGGADGRKRVTVFFGTQTGTAEGFAKALAEETIKARYE--KATFKVLDLDEYAMEDEYEEERLKKEKISLFFVAT
Sb_CPR2c -----APSKPVAAVPRPPPVK--VDADADVDDGRRKRVTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAQEDDEYEEKLKKETVVALFFLAT
Zm_CPR2c -----APSKPVATPLRPPPVK--VDADADVDDGRRKRVTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAQEDDEYEEKLKKETVVALFFLAT
Os_CPR2c -----APPKAAAAPPRPPPVK--I--EADADADVDDGRRKRVTVFFGTQTGTAEGFAKALAEETIKARYE--KAVFKVLDLDDYAAEDDEYEEKLKREKIVLFFLAT
Ta_CPR2c -----APPKPPASFRPPPVK--VDAD--DADDGRRKRVTVFFGTQTGTAEGFAKALAEETIKARYE--KVLFKVLDLDDYAAEDDEYEEKLKKETFALFFLAT
    
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Tch_CPR  -----TQKPAVKPTPLVK-EED EEEEDDSAKKKVTIFFGTRTGTAEQFAKALAEAAKARYE--KAVFKVVDLDNYAADDEQYEEKLKKKELAFFMLAT
Tcu_CPR  -----TQKPAVRPTPLVK-EED EEEEDDSAKKKVTIFFGTQTGTAEQFAKALAEAAKARYE--KAVFKVVDLDNYAADDEQYEEKLKKKELAFFMLAT
Pm_CPR   -----PSKLPEKPTPLGRVEEE EEEEDDSGKKKVTVFFGTQTGTAEQFAKALVEAAKARYD--KAVFKVVDLDDYAADDEQYEEKLKKKELAFFMLAT
Sm_CPRb  -----KRESEPVKVVKPVVEIEEE-GDELDGFSNKVTVFFGTQTGTAEQFAKALAEAAKARYE--KVLFKIVDLNDAADDETYQLKLNKFAIFMLAT
Sm_CPRc  -----KRVAEPPTVVTPIVEAEE EADDLAGYTSKVTVFFGTQTGTAEQFAKALVEAAKARYD--RVLFKAVDLNDAADDDHYRLRLKKEKLAIFMLAT
Sm_CPRa  -----MFKKPTIEVEPE-DDDPD--KKKVSVFFGTQTGTAEQFAKALVEAAKARYD--KVLFKIVDLNDAADDETYQLKLNKFAIFMLAT
Cre_CPR  -----NATAVSTAPPITRTSISAE---DPSKPCVRIYGTQTGTAEQFAKALAEAAKARYE--KAVFKVVDLDNYAADDEQYEEKLKKKELAFFMLAT
consensus 101.....110.....120.....130.....140.....150.....160.....170.....180.....190.....

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Pp_CPRc YGDGEPTDNaARFYHWFTEEN-GELELEL----HILSELRFGVFGLGNRQYEHFNKVAKVIDTAFAKHGAKRIVEVGLGDDDSIETEDDFAAWKEKLWPELDV-
Pp_CPRd YGDGEPTDNaSRFHNFTEEN-EELELEL----GLNELNFGVFGNGNRQYEHFNKVAKEIDKALAKQGAKRILECGLGDDDDQCIEDDFTAWKEKLWPELDA-
Pp_CPRa YGDGEPTDNaARFYKWFVES-GEDDQI----GLDGLKYAVFGLGNRQYEHFNKVAKVIDEALTOQGAQRIVEVGLGDDDDQSIEDDFTAWKEKLWPELDG-
Pp_CPRb YGDGEPTDNaARFYHKLVDSD-EDNDF----KLGKMGKFGVFGNGNRQYEHFNKVAVIDEALKEYGGERLVOVGLGDDNDCIEDDFAAWKLLWLPALDE-
Ca_CPR1 YGDGEPTDNaARFYKWFTEG-QERGV----WLQHLTYGVFGLGNRQYEHFNKIGKVIDEQLSEQGAKRLVPVGLGDDDDQCIEDDFAAWREQLWPELDQ-
Ph_CPR1 YGDGEPTDNaARFYKWFTEG-QERGV----WLQHLTYGVFGLGNRQYEHFNKIGKVIDEQLSEQGAKRLVPVGLGDDDDQCIEDDFAAWREQLWPELDQ-
Ce_CPR1 YGDGEPTDNaARFYKWFSEV-KEREP----WLQQLTYGVFGLGNRQYEHFNKIGKVIDDOLIEQGAKRITVPLGLGDDDDQCIEDDFAAWRDQLWPELDK-
Op_CPR1 YGDGEPTDNaARFYKWFTEG-KEREP----WLQQLTYGVFGLGNRQYEHFNKIGNVIHEQLSEQGAKRITVPVGLGDDDDQCIEDDFAAWREQLWPELDQ-
Gm_CPR1 YGDGEPTDNaARFYKWFTEGKDERGI----WLQQLTYGVFGLGNRQYEHFNKIGKVIDEELSEQGAKRLVPLGLGDDDDQSIEDDFAAWKESLWSELDDQ-
Vr_CPR1 YGDGEPTDNaARFYKWFTEGKDERGI----WLQQLTYGVFGLGNRQYEHFNKIGKVIDEELAEQGAKRILVAVGLGDDDDQSIEDDFAAWKESLWSELDDQ-
Vs_CPR1 YGDGEPTDNaARFYKWFTEGKERGT----WLQQLTYGVFGLGNRQYEHFNKIGKVIDEDLIEQGAKRILVPVGLGDDDDQSIEDDFAAWKETLWPELDQ-
Pt_CPR1 YGDGEPTDNaARFYKWFTEG-NERGI----WLQQLSYGVFGLGNRQYEHFNKIGKVIDDLIEQGGKRLVPVGLGDDDDQCIEDDFAAWKEFLWPELDQ-
Rc_CPR1 YGDGEPTDNaARFYKWFTEE-HERGV----WLQQLTYGTFGLGNRQYEHFNKIGKVIDEOLNEQGAKRITVPVGLGDDDDQCIEDDFTAWRELWPELDN-
Gh_CPR1 YGDGEPTDNaARFYKWFTEG-NERLP----WLQQLTYGVFGLGNRQYEHFNKIGKVIDEQLSEQGAKRITVAVGLGDDDDQCIEDDFTAWRELWPELDQ-
At_ATR1 YGDGEPTDNaARFYKWFTEE-NERDI----KLQQLAYGVFALGNRQYEHFNKIGTIVDEELCKKGAKRILIEVGLGDDDDQSIEDDFAAWKESLWSELDDK-
Ha_CPR1 YGDGEPTDNaARFYKWFTEE-HERGV----WLQQLKFGVFGNGNRQYEHFNKIGKVIDEQLFCEQGAKRITVPVGLGDDDDQCIEDDFTAWRELWPELDP-
Pso_CPR1 YGDGEPTDNaARFYKWFTEQE-HERGE----WLQQLTYGVFGLGNRQYEHFNKIGKVIDEQLGKQGAKRITVAVGLGDDDDQCIEDDFTAWRELWPELDQ-
Am_CPR2 YGDGEPTDNaARFYKWFSEGE-EEKGE----WLNKLOYGVFGLGNRQYEHFNKIGKVIDDGLADQGAKRITVEVGMGDDDDQCIEDDFTAWRESVWPELDK-
Pc_CPR2a YGDGEPTDNaARFYKWFSEGE-EEKGD----WLNKLOYGVFGLGNRQYEHFNKIGKVIDDGLADQGAKRITVEVGMGDDDDQCIEDDFTAWRELWPELDK-
Pc_CPR2b YGDGEPTDNaARFYKWFCEG-KERGE----WLNKLOYGVFGLGNRQYEHFNKIGKVIDDGLVEQGAKRILVPVGMGDDDDQCIEDDFTAWRELWPELDQ-
Aa_CPR2 YGDGEPTDNaARFYKWFTEG-EEKGE----WLEKLOYAVFGLGNRQYEHFNKIGKVIDEKLVEQGAKRILVPVGMGDDDDQCIEDDFTAWKELWPELDQ-
Ht_CPR2b YGDGEPTDNaARFYKWFTEG-EPKGE----WLNKLOYGVFGLGNRQYEHFNKIGKVIDDGLVEQGAKRILVPVGLGDDDDQCIEDDFTAWKELWPELDQ-
Sr_CPR2 YGDGEPTDNaARFYKWFTEG-DDKGE----WLNKLOYGVFGLGNRQYEHFNKIGKVIDDGLVEQGAKRILVPVGLGDDDDQCIEDDFTAWKELWPELDQ-
Ht_CPR2a YGDGEPTDNaARFYKWFTEG-DDKGV----WLEKLOYGVFGLGNRQYEHFNKIGKVIDEGLTEQGAKRILVPVGLGDDDDQSIEDDFAAWKELWPELDQ-
Cro_CPR2 YGDGEPTDNaARFYKWFVEG-NDRGD----WLNKLOYGVFGLGNRQYEHFNKIGKVIDEKVAEQGGKRITVPLVGLGDDDDQCIEDDFAAWRENWPELDN-
Cb_CPR2 YGDGEPTDNaARFYKWFSEGE-KDRGD----MFKNLHYGVFGLGNRQYEHFNKIGKVIDDGLFEQGGKRLVPVGLGDDDDQCIEDDFAARRDNWPELDN-
Ph_CPR2 YGDGEPTDNaARFYKWFVEG-KERGD----YFKNLOYGVFGLGNRQYEHFNKIGKVIDEELAEQGGKRLVPVGLGDDDDQCIEDDFAAWRDWLWPELDK-
Gh_CPR2 YGDGEPTDNaARFYKWFTEG-KERGE----WLNQMKYGTIFGLGNRQYEHFNKIGKVIDEELTEQGAKRITVPLGLGDDDDQCIEDDFTAWRELWPELDQ-
Rc_CPR2 YGDGEPTDNaARFYKWFTEG-KERGE----WLQDLKFGVFGNGNRQYEHFNKIGKVIDEELIEQGAKRILVPVGLGDDDDQCIEDDFTAWKESLWPELDQ-
Pt_CPR2b YGDGEPTDNaARFYKWFTEG-NERGE----WLKDLPYAVFGLGNRQYEHFNKIGKVIDDKIFADQGGKRLVPVGLGDDDDQCIEDDFAAWRELWPELDQ-
Pt_CPR2a YGDGEPTDNaARFYKWFTEG-NERGE----WLKDLPYAVFGLGNRQYEHFNKIGKVIDKILGNQGGKQLVPVGLGDDDDQCIEDDFAAWRELWPELDQ-
Vv_CPR2 YGDGEPTDNaARFYKWFVEG-KERGE----WLQNLKYGVFGLGNRQYEHFNKVAKVDDIIEQGGKRLVPVGLGDDDDQCIEDDFAAWRELWPELDQ-
Lj_CPR2 YGDGEPTDNaARFYKWFVEG-DEKEEG----WLRNLEYAVFGLGNRQYEHFNKVAIVDDKILADFGGKRLVPVGLGDDDDQCIEDDFTAWKEELWLPALDE-
Psa_CPR2 YGDGEPTDNaARFYKWFTEE-YEGEED----SFKNLSYGVFGLGNRQYEHFNKVAKVDDKILIEQGGKRLVPVGLGDDDDQCIEDDFTAWKEELWLPALDE-
At_ATR2 YGDGEPTDNaARFYKWFTEG-NDRGE----WLNKLNKYGVFGLGNRQYEHFNKVAKVDDIIEQGAQRILVOVGLGDDDDQCIEDDFTAWREALWPELDT-
Ec_CPR2 YGDGEPTDNaARFYKWFTEG-KEREM----WLQNLQFGVFGNGNRQYEHFNKVAKEVDEILIEQGGKRLVPVGLGDDDDQCIEDDFTAWRELWPELDQ-
Os_CPR2a YGDGEPTDNaARFYKWFGE-NERGE----WLSNLRFGVFGNGNRQYEHFNKVGKVDQLAEQGGKRITVPLGLGDDDDQCIEDDFAAWKELWPELDK-
Sb_CPR2a YGDGEPTDNaARFYKWFVEG-NERGE----WLNKLNRFVFGNGNRQYEHFNKVGKVDQLAEQGGKRITVPVGLGDDDDQCIEDDFAAWKELWPELDK-
Ta_CPR2a YGDGEPTDNaARFYKWFSEGE-NERGE----WLSNLRFGVFGNGNRQYEHFNKVGKVDQLAEQGGKRITVPVGLGDDDDQCIEDDFAAWKELWPELDK-
Sb_CPR2b YGDGEPTDNaARFYKWFTEG-NERGV----WLNDFEYAVFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFAAWKEALWPELDR-
Zm_CPR2b1 YGDGEPTDNaARFYKWFTEG-NERGV----WLNDFEYAVFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFAAWKEALWPELDR-
Zm_CPR2b2 YGDGEPTDNaARFYKWFTEG-NERGI----WLHDFEYAVFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFTWKTWPELDR-
Os_CPR2b YGDGEPTDNaARFYKWFTEG-NERGV----WLNDFOYATIFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFAAWKETLWPELDQ-
Sb_CPR2c YGDGEPTDNaARFYKWFTEG-KEKEV----WLKALIKYGTIFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFTAWKELWPELDQ-
Zm_CPR2c YGDGEPTDNaARFYKWFTEG-KEKEV----WLKDLIKYGTIFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFTAWKELWPELDQ-
Os_CPR2c YGDGEPTDNaARFYKWFTEG-KEKEV----WLKDLIKYAVFGLGNRQYEHFNKVAKVDEILIEQGGKRLVPVGLGDDDDQCIEDDFTAWKEQWPELDQ-
Ta_CPR2c YGDGEPTDNaARFYKWFTEG-KEKEV----WLKDFNLYAVFGLGNRQYEHFNKVAKEVDEILIEQGGKRLVPVGLGDDDDQCIEDDFTAWKELWPELDQ-

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Tch_CPR  YGDGEPTDNaARFYKWFLEg-KEREP-----WLSdLTyGvFGLGnrQyEHfNkVAKAVdEVLIEQgAKRLVPVGLGDDdQCIEdDFTAWREQvWPELDQ-
Tcu_CPR  YGDGEPTDNaARFYKWFLEg-KEREP-----WLSdLTyGvFGLGnrQyEHfNkVAKAVdEVLIEQgAKRLVPVGLGDDdQCIEdDFTAWREQvWPELDQ-
Pm_CPR   YGDGEPTDNaARFYKWFSEtEKERGP-----WLSnLpYgVfGLGnrQyEHfNkVACTvDEALnEQgGkRLVPVGLGDDdQCIEdDFTAWREQvWPELDQ-
Sm_CPRb  YGDGEPTDNaARFYKfLTeGGERGS-----WlSemTyGtFGLGnrQyEHfNkVAMvVDEELeKQgAKRLVPCgAGDDdQCIEdDFTAWREQLWPELDT-
Sm_CPRc  YGDGEPTDNaARFYKfLTeGGDERGL-----WlNemTyAvfGLGnrQyEYfNkVgKdVDEELeKQgAKRLVPCgVgDDdQCIEdDfSAwREQLWPELDA-
Sm_CPRa  YGDGEPTDNaARFYKWFVEg-EEKEP-----WlGnLSyAvfGLGnrQyEHfNkVAVeVDEALeKQgAKRLlKcGLGDDdQCIEdDFTAWREQLWPELDV-
Cre_CPR  YGDGEPTDNaAVfYSWllKEAEAVENGdKEPFLoGVSyAvfGLGnKQyEHfNSVgKkVfKAMKACGATAlCRRgDgDDdGVIddDFEKwCTELyEALDKS
consensus ***** ** * ..... * ** * * * ..... * ..... * ..... * ..... * ..... * ..... * ..... * .....
201.....210.....220.....230.....240.....250.....260.....270.....280.....290.....
    
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Pp_CPRc  --LLKDPEDSQATTPKTAVLAAVA EYRTVITYEPGTKLHVE---EYSGKKIGQAAVDVHPC--KAEVAFVKELHSPESGRSCTHLEFDIANTGLSYETGD
Pp_CPRd  --LLKDPEDITASTPKTPYHAAVA EYRTVITYEAGTKLHVE---EYAAKKTGQAGYDTLHPC--KSEVAFVKELHTSESDRSCTHSEFDIANTGLSYETGD
Pp_CPRa  --LLTT--EDAPTTPHAPYQAAVA EYRLVITYEPGTKLYVE---EYAAKKNGQAVYDALHPC--RADVAFVKELHKPLSDRSCTHLEFGIANTGLSYETGD
Pp_CPRb  --ILGT---GQTTPTATVYAAVA EYRLVITYEAGTEVHEE---SYEARKNGQGVFVSHPC--KAEVAFVKELHTALSDRSCTHFEFDIANTGITYETGD
Ca_CPR1  --ILRDEDDASSASTP---YTAATLE YRVLVTHDITMS-LED---KHASMANGNTTYDIHPC--KVNNAVQRELHTPESDRSCTHLEFDISGTGIFYETGD
Ph_CPR1  --ILRDEDDANSAATP---YTAATPE YRVLVTHDHTAAN-PED---KHAMVNGTTAYDIHPC--KVNNAVQRELHTPESDRSCTHLEFDISGTGIFYETGD
Ce_CPR1  --ILRDEDDSSAAVATP---YTAATHE YRVVTHDSSADSIEH---KQLNMMNGNTSYDIQHPC--LVNAVQRELHTPESDRSCTHLEFDIAGTGIKYETGD
Op_CPR1  --ILRDEDDATSATP---YTAATLE YRVVTHNSEAASYED---KQFSMANGNSSYDIHPC--IVNAVQRELHKPESDRSCTHLEFDISGTGINYETGD
Gm_CPR1  --LLRDEDDVNTVSTP---YKAATPE YRVVTHDSTVTSKND---NHLNVANGNAVFDIHPHPC--RVNVAQRELHKPESDRSCTHLEFDISGTGIIYETGD
Vr_CPR1  --LLRDEDDANTVSTP---YTAATLE YRVVTHDPTAASTYD---NHSTVANGNTEFDIHPHPC--RVNAVQRELHKPESDRSCTHLEFDISGTGIIYETGD
Vs_CPR1  --LLRDEDDVNTASTP---YTAATSE YRVVTHDPTVSPSYE---NHFNVANGGVAFDIHPHPC--RVNAVRRRELHKPQSDRSCTHLEFDISGTGIIYETGD
Pt_CPR1  --LLRDEDDVNAPSTP---YTAATPE YRVLVTHDPSIISVED---KFSNLANGNVSFDIHPHPC--RVNAVQRELHKAESDRSCTHLEFDITGTGITYETGD
Rc_CPR1  --LLRDEDDVNGASTP---YTAATPE YRVVTHDASATSCED---K-SVLENGNTSIDIHPHPC--RVNAVQRELHKPESDRSCTHLEFDISGTGIIYETGD
Gh_CPR1  --LLRDEDDENATSTP---YTAATPE YRVVTHDPAVMHVEE---NYSNKANGNATYDLHPHPC--RVNAVQRELHKPESDRSCTHLEFDISGTGITYETGD
At_ATR1  --LLKDEDD-KSVAATP---YTAATPE YRVVTHDPRFTTQKS---MESNVANGNTTIDIHPHPC--RVDVAVQRELHTHESDRSCTHLEFDISRTGITYETGD
Ha_CPR1  --LLRDEDDNANAASTP---YTAATLE YRVVTHDPTTSLVED---KFNLANGNATFDAQHPHPC--RVNAVQRELHKPESDRSCTHLEFDISGTGIRYEAGD
Pso_CPR1 --LLRDEDDAAPSVAATP---YTAATVPE YRVVTHETTVAALDD---KHINTANGDVAFDIHPHPC--RTIVAQRELHKPKSDRSCTHLEFDISGSSLT YETGD
Am_CPR2  --LLLD-EDDTSAAATP---YTAAVLE YRVVYDQPDAT--LDQSLSTONGHTVHDAQHPC--RSNVAVKRELHKPASDRSCTHLEFDISHTGLAYETGD
Pc_CPR2a --LLLD-EDDTSAAATP---YTAAVLE YRVVYDQL-DTAT--LDRSLSTONGHTVHDAQHPC--RSSVAAKRELHKPASDRSCTHLEFDISHTGLAYETGD
Pc_CPR2b --LLLD-EESKAAATP---YTAAVLE YRVVQFYNQD-TSSP-LVRSMSKLNHAVYDAQHPC--RANVAVRRELHTPASDRSCTHLEFDISSTGLAYETGD
Aa_CPR2  --LLRD-EDDTSVATP---YTAAVA EYRVVFHDKP-ETYD----QDQ-LTNGHAVHDAQHPC--RSNVAVKRELHSPLSDRSCTHLEFDISNTGLSYETGD
Ht_CPR2b --LLRD-DDDTSVATP---YTAAVA EYRVVFHEKP-DMYD----ENS-QTNGHAVHDAQHPC--RANVAVKRELHSSSESDRSCTHLEFDISHTGLSYETGD
Sr_CPR2  --LLRD-EDDTSVITP---YTAAVLE YRVVYHDKPADSYA---EQDHTNGHVHDAQHPS--RSNVAVKRELHTSQSDRSCTHLEFDISHTGLSYETGD
Ht_CPR2a --LLLD-EDDKTAATP---YTAATPE YRVVVFHDKP-DTFS----ENHSQTNGHTVHDAQHPC--RSNVAVKRELHTPESDRSCTHLEFDISHTGLSYETGD
Cro_CPR2 --LLRD-EDDITVSTT---YTAATPE YRVVFPDKSDSLISEANGHANGYANGNTVYDAQHPC--RSNVAVKRELHTPASDRSCTHLEFDIAGTGLSYGTGD
Cb_CPR2  --LLRD-EDYPPVSTP---YTAAVLE YRVVVFHDQSDLPSE-NLANGRANGHASYDAQHPC--KVNNAVKRELHTPLSDRSCTHLEFDISGTGLEYETGD
Ph_CPR2  --LLMDGDDATTVAATP---YTAAVLE YRVVTHEKSN--LDNELSNANGHANGHAVIDAQHPC--SANVAVKRELHTPASDRSCTHLEFDISGTGLVYETGD
Gh_CPR2  --LLRDEDD-ATVSTP---YTAAVLE YRVVVFYDPAAPLED---KNWSNANGHATYDAQHPC--RSNVAVKRELHAPESDRSCTHLEFDIAGTGLSYETGD
Rc_CPR2  --VLRGEDDAATVSTP---YTAAVLE YRVVVFYDPEDAPIED---KRWSNANGHAVHDAQHPC--RANVAVKRELHTPASDRSCTHLEFDIAGTGLSYETGD
Pt_CPR2b --LLLDGDDPTAVSTP---YTAATVSE YRVVVFHSPEDAPLED---DNWSNANGHAYDAQHPC--RANVAVRRELHTPASDRSCTHLEFDISGTGLAYGTGD
Pt_CPR2a --LLLDGDDPTGVSTP---YTAAVA EYRVVTHDPEDAPIED---DNWSNANGHATYDAQHPC--RANVAVRRELHTPASDRSCTHLEFDISGTGLVYGTGD
Vv_CPR2  --LLRDEDDATTVSTP---YTAAVLE YRVVVFHDPEGASLQD---KSWGANGHTVHDAQHPC--RANVAVKRELHTPASDRSCTHLEFDISGTGLTYETGD
Lj_CPR2  --LLRGDD-ITVSTP---YTAAVLE YRVVTHDPLDASVDE---KKWHNVNGHATVDAQHPV--RSNVAVKRELHTPVSDRSCTHLEFDISGTGVAYETGD
Psa_CPR2 --LLRDEDD-TPVATP---YTAAVSE YRVVTHDPLDATVDE---KKRHNVNGHAVDAQHPV--RANVAVRRELHTPASDRSCTHLEFDISGTGLVYETGD
At_ATR2  --ILREEDG-TAVATP---YTAAVLE YRVVTHDSEDAKFND---INMANGNGYTVFDAQHPY--KANVAVKRELHTPESDRSCTHLEFDIAGSGLTYETGD
Ec_CPR2  --LLRDESDKTSVSTP---YTAATVPE YRVVVFHDATDASLQD---KNWSNANGYTVVDVQHPHPC--RANVAVKRELHTPVSDRSCTHLEFDISGTGLTYETGD
Os_CPR2a --LLRVEDDKSAAPT---YTAATPE YRVVVLKPEEAMHIN---KSFSLSNGHAVYDIQHPC--RANVAVRRELHTPASDRSCTHLEFDISGTGLTYETGD
Sb_CPR2a --LLROEDDSSTAPT---YTAATPE YRVVVFVKPEDAMHIN---KSFTLSNGHAVYDIQHPC--RANVAVRRELHTPASDRSCTHLEFDITGTGLKYETGD
Ta_CPR2a --LLRVEDNNSSTAQSP---YTAATPQ YRVVLTKPEDATHIN---KSFSLSNGHVVYDSQHPHPC--RANVAVRRELHTPASDRSCTHLEFDIAGTSLTYETGD
Sb_CPR2b --LLRDEDDASTGTT---YTAATPE YRVVFEFIKPEEAAHLE---RNFLSANGHAVHDAQHPC--QANVAVRRELHTPASDRSCTHLEFDIAGTGLTYETGD
Zm_CPR2b1 --LLRDEDDASPGTT---YTAATPE YRVVFEFIKPEEAAHLE---RNFLSANGHAVHDAQHPC--QANVAVRRELHTPASDRSCTHLEFDIAGTGLTYETGD
Zm_CPR2b2 --LLGDGNDISTGTT---YTAATPE YRVVFEFMGPEEAAHLE---RNSSLANGHAVHDAQHPC--KFRADVAVRRELHTPASDRSCTHLEFDIAGTGLTYETGD
Os_CPR2b --LLRDEDDVSTGTT---YTAATPE YRVVFEFVKPEEAAHLE---RNFLSANGYAVHDAQHPC--RANVAVRRELHTPASDRSCTHLEFDIAGTGLTYETGD
Sb_CPR2c --LLRDEDDITGASTP---YTAATPE YRVVVFIDKSDLFQD---RSWTLANGTGVIDIHPHPC--RANVAVKRELHKPASDRSCTHLEFDISGTGLVYETGD
Zm_CPR2c --LLRDEDDTNGASTP---YTAATPE YRVVVFIDKSDLFQD---RSWTLANGTGVIDIHPHPC--RANVAVKRELHKPASDRSCTHLEFDISGTGLVYETGD
Os_CPR2c --LLRDEDDITGASTP---YTAATPE YRVVVFIDKSDVSFQD---KSWSLANGSGVIDIHPHPC--RSNVAVKRELHKPASDRSCTHLEFDISGTGLVYETGD
Ta_CPR2c --LLRDEDDITGATTP---YTAATPE YRVVVFIDKSDLEFED---KSWTLANGNGVIDIHPHPC--RANVAVKRELHKPASDRSCTHLEFDISGTGLVYETGD

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Tch_CPR  --LLRDEDEDEPTSAIP--YTAATPEYRVETIYDSVSVSYEE---THALKONGQAVYDIHHPCL--RSNVAVRRELHTPLSDRSCIHLEFDISDTGLIYETGD
Tcu_CPR  --LLRDEDEDEPTSAIP--YTAATPEYRVETIYDSVSVSYEE---THALKONGQAVYDIHHPCL--RSNVAVRRELHTPLSDRSCIHLEFDISDTGLIYETGD
Pm_CPR   --LLRDEDDQPSSAIP--YTAATPQYRVETIHDPPVPLYEE---TYAT-QNGQAFIDIHHPCL--RANVAVQRELHTPLSDRSCIHLEFDISGTGLIYETGD
Sm_CPRb  --LLRNEDDVVLAIP--YTAAVSEYRVVIFHENPVKLLLEGSF--SATMENGGSVVDMMHPC--RAIVAVQRELHTPLSDRSCIHLEFDVAGTGLSYETGD
Sm_CPRc  --LLRNEDDVVAIPSTTT--YTAAVSEYRVVIFHEKLAKLVEGSF--LP-VENGGPVVIDMMHPC--RAIVAAARKELHTPLSDRSCIHLEFDIAATGLSYETGD
Sm_CPRa  --LLRSED--ETGSATP--YMAATPEYRVVIFHEGGTKAYEK-----VANGESLCDISHPI--RSPVAVRRELHTPLSDRSCIHLEFDISYTGILYLTGD
Cre_CPR  SDLVGKRADQNGVHAAP--PARVAAYEVEVLRGSGGEAPA-----FPSGTG-KDVHSPF--WAKITTVRELHTPLASDRSCVHVEVDVSGSGITYEAGD
consensus  .....310.....320.....330.....340.....350.....360.....370.....380.....390.....
                *                *      *      *      *      *      *      *      *      *      *      *

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Pp_CPRc HVGVYVENSRRDVEEAAYKLGMPDLDTIFSLHVDAAEEGQLLAGS--LPPFPFGPLLLETALRRYTDLLNPPRKAVLMALAAFASDPPEEAERLTYLASLKGK
Pp_CPRd HVGVYVENNOEDVEEAARHLGMPDLDTIFSLHVDAAEEGQLLAGS--LPPFPFGPLLLETALRRYADLLNPPRKAVLNVLAVFASDPPEEVERLKYMASLQGG
Pp_CPRa HVGVYVENSQEDVEEAAKHLGYPDLDTIFSLHVDAAEEGQLLAGS--LPPFPFGPLLLETALRRYADLLSPPRKSVLSVLAAFASDPPEEAERLKHLSASLLGK
Pp_CPRb HVGVYVENSSEEDVEEAARLLGVDRDMIFSLHVDAAE---AASN--LPQFPFGPLTVDTALRRYADLLNPPRKATLSILAAYAQDPPEEAERLKFLASVDGK
Ca_CPR1 HVGVYFAENSEEDTVEEAARLLGQSLDLVFSIHADKEDGTALGGS--LPPFPFGPCTLRALARYADLLNPPRKATLVALAAHATEPSEAEKLFKLASPOGK
Ph_CPR1 HVGVYAENCEETVEEAARLLGQSLDLVFSITLTDKEDGTALGGS--LPPFPFGPCTLRALARYADLLNPPRKATLIALAAHAAEPSEAEERLKFLASPOGK
Ce_CPR1 HVGVYAENCEENVEEAARLLGQSLDLVFSIHADKEDGTPLGGS--LAPPFPGPCTLRALARYADLLTPPKKATLIALAAHSSSEPSEAEERLKFLSSQOGK
Op_CPR1 HVGVYAENCDGTVEQAAYKLGQPLDLVFSIHADKEDGTSLGG--LPPFPFGPCTLRALARYADLLNPPRKAAALVALAAHASEPSEAEERLKFLSSPOGK
Gm_CPR1 HVGVYFAENGDETVEEAAGLLGQPLDLVFSIHTNNEEDGTPLGGS--LPPFPFGPCTLRALARYADLLNPPRKASLVALAAHTSEPSEADRITFLSSPOGK
Vr_CPR1 HVGVYAENCNETVEETGKLLGQNLDLVFSIHTDKDDGTSLGG--LPPFPFGPCTLRALARYADLLNPPRKAALLALATHASEPS-DEERLKFLSSPOGK
Vs_CPR1 HVGVYAENCDETVEEAAGLLGQSLDLVFSIHTDKEDGTSLGG--LPPFPFGPCTLRALARYADLLNPPRKAATVALAAHASEPSEAEERLKFLSSPOGK
Pt_CPR1 HLGVYAENSDETVEEAAGLLDKPLDLLFSIHADNEDGTALGGS--LPPFPFGPCTLRALARYADLLSPPKKAALLALAAHASEPSEADRILKFLSSPOGK
Rc_CPR1 HVGVYAENFEENVEEAAGLLGQPLDLLFSIHADNEDGAPLGG--LAPPFPGPCTLRALARYADLLNPPRKAALLALAAHASEPSEAEERLYLSSPEGK
Gh_CPR1 HVGVYADNCVETVEEAARLLGQPLDLLFSIHTDNEDGTSAGS--LPPFPASPCTLRMALARYADLLNPPRKAALLALAAHATEPSEAEKLFKLSSPOGK
At_ATR1 HVGVYAENHVEETVEEAAGLLGHSLDLVFSIHADKEDGSPLESA--VPPFPFGPCTLRGLARYADLLNPPRKSALVALAAAYATEPSEAEKLLKHLITSPDGK
Ha_CPR1 HVGVYENCAENVEEAAGLLGQPLDLVFSVYTEKEDGTPLGG--LPPFPFGPCTLRQTSARYADLLNPPRKAALLALAAHASEPSEAEERLKFLSSPOGK
Pso_CPR1 HVGVYAENCDETVEEAAGLLGQSLDLLFSIHTDKEDGSPQGS--LPPFPFGPCTLRALARYADLLNPPRKSALIALAAHASEPSEAEERLFLSSPLGK
Am_CPR2 HVGVYCNLVEITVEEAEEKLLGMPNNTYFSVHTDNEDGTPITGG--SLPPFP-PCTVRSALARYADLLSSPKKSALLALAAHASDPTTEADRRLFLASPAGK
Pc_CPR2a HVGVYCNLVEITVEEAEEKLLGMPNNTYFSVHIDDEDGTPITGG--SLPPFP-PCTVRSALARYADLLSSPKKSALLALAAHASDPTTEADRRLFLASPAGK
Pc_CPR2b HVGVYCNLVEITVEEAERLLDITSPDITYFSIHTENEDGTPISGG--SLPPFP-PCSFRTALTRYADLLSTPKKSALLALAAHASDPTSEADRRLFLASPVGK
Aa_CPR2 HVGVYCNLSEVVEEAERLLGLPPTYFSVHADNEDGTPISGG--SLPPFP-PCTLRKALARYADLLSSPKKSALLALAAHATDSTEADRILKFLASPAGK
Ht_CPR2b HVGVYCNLSEVVEEAERLLGLPPTYFSIHTDKEDGTPISGG--SLAPPFP-PCTLRKALARYADLLSSPKKSALLALAAHATDPAEADRILKFLASPDGK
Sr_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSVHADKEDGTPISGG--SLPPFP-PCTLRDALARYADLLSSPKKSALLALAAHASDPTTEADRILKFLASPAGK
Ht_CPR2a HVGVYCNLSEVVEEAERLLGLPADTYFSIHTDNEDGTPISGG--TLQPPFP-PCTLRKALARYADLLSSPKKSALLALAAHASDPTTEADRILQFLASREGK
Cro_CPR2 HVGVYCNLSEVVEEAERLLNLPPTYFSIHADKEDGTPISGG--SLPPFP-PCTLRALARYADLLNTPPKKSALLALAAHASDPTNEADRILKYLASPAGK
Cb_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSVHTDKEDGTPISGG--ALPPFP-PCTLRALARYADLLSAPKKAALLALAAHASDPTVEADRILHVLSPAGK
Ph_CPR2 HVGVYCNLSEVVEEAERLLNISPDTFFSIHTDKEDGTPISGG--SLPSFP-PCTLRALARYADLLSSPKKSALLALAAHASDPTKEADRILRYLSPAGK
Gh_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSVHTDKEDGTPISGG--SLPSFP-PCTLRALARYADLLSSPKKAALLALAAHASDPTTEADRILRHLSPAGK
RC_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSIHTDKEDGTPISGG--SLPAPPFP-PCTLRALARYADLLSSPKKSALLALAAHATDPTTEADRILRHLSPAGK
Pt_CPR2b HVGVYCNLSEVVEEAERLLGLSPDITYFSIHTDNEDGTPISGG--ALPPFP-PSTLRALARYADLLSPPKKSALLALAAHATDPTTEADRILRHLSPAGK
Pt_CPR2a HVGVYCNLSEVVEEAERLLGLSPDITYFSIHTDNEDGTPISGG--ALPPFP-SSTLRALARYADLLSSPKKSALLALAAHATNPTTEADRILRHLSPAGK
Vv_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSIHTEREDGTPISGG--SLSPFP-PCTLRALARYADLLSSPKKSALLALAAHASDPTSEADRILKYLASPSGK
Lj_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSVHTDDEDGKPLSGS--SLPPTFP-PCTLRALARYADLLSSPKKSALLALAAHASNPSEADRILRHLSPAGK
Psa_CPR2 HVGVYCNLSDTVEEAERLLGLSPDITYFSIHTDDEDGKPLSGS--SLPPFP-PCTLRALARYADLLSSPKKSALLALAAHASDPTSEADRILRHLSPAGK
At_ATR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSIHTDDEDGTPIS-S--SLPPFP-PCNLRALARYADLLSSPKKSALLALAAHASDPTTEADRILKHLSPAGK
Ec_CPR2 HVGVYCNLSEVVEEAERLLGLSPDITYFSIHTDDEDGKPLSGS--ALAPPFP-PCTLRALARYADLLNSPKKAALLALAAHASDPTKEADRILRYLSPAGK
Os_CPR2a HVGVYAENCTETVEEVENLLGYSPDITYFSIHADDEDGTPIFGG--SLPPFP-SPCTVRLARYADLLSFPKKSALLALASHASDPTKEADRILRHLSPAGK
Sb_CPR2a HVGVYAENCTETVEEAEKLLGYSPDITYFSIHADDEDGTPHCGG--SLPPFP-SPCTVRLARYADLLNSPKKSALLALAAHASDPTKEADRILRHLSPAGK
Ta_CPR2a HVGVYAENSIETVEEAEKLLDYSPTDITYFSIYADDEDGTPIFGG--SLPPFP-SPCTVRLARYADLLNSPKKSALLALAAHASDPTKEADRILRHLSPAGK
Sb_CPR2b HVGVYENCPETVEEAEKLLGYSPDITYFSIHTADKEDGTPISGG--SLAPPFP-SPITVRLARYADLLNSPKKTSVALATYASDPTTEADRILRFLASAAGK
Zm_CPR2b1 HVGVYENCPETVEEAEKLLGYSPDITYFSIHTADKEDGTPISGG--SLAPPFP-SPITVRLARYADLLNSPKKSALLALATYASDPTTEADRILRFLASAAGK
Zm_CPR2b2 HVGVYENCPETVEEAEKLLGYSPDITYFSIHTADKEDGTPISGG--PPFP-SPITVRLARYADLLNSPKKSALLALATYASDPTTEADRILRFLASAAGK
Os_CPR2b HVGVYENCLEVVEEAERLLGYSPDITYFSIHTADKEDGTPISGG--SLAPPFP-SPITVRLARYADLLNSPKKSALLALATYASDPTTEADRILRFLASPAGK
Sb_CPR2c HVGVYAENSVETVEEAEKLLDLSPTDITYFSIHADDEDGSPRKGGS--LAPPFP-SPCTLRALARYADLLNPPKKAALLALASHASDPTTEADRILRFLASPAGK
Zm_CPR2c HVGVYAENSVETVEEAEKLLDLSPTDITYFSIHADDEDGSPRKGGS--LAPPFP-SPCTLRALARYADLLNPPKKAALLALASHASDPTTEADRILRFLASPAGK
Os_CPR2c HVGVYSENATETVEEAEKLLDLSPTDITYFSIHADDEDGSPRKGGS--LAPPFP-SPCTLRALARYADLLNPPKKAALLALAAHASDPTTEADRILRFLASPAGK
Ta_CPR2c HVGVYSENATETVEEAEKLLDLSPTDITYFSIHADDEDGSPRKGGS--LAPPFP-SPCTLRALARYADLLNPPKKAALLALAAHASDPTTEADRILRFLASPAGK

| | | | | |
|-----------|---|-------------------|--------------|--|
| Tch_CPR | HVGVHTENSIETVEEAAKLLGYQLDTIFSVHGDKEDGTPLGGS-SLPPFPFPGPCTLR | TALARYADLLNPPRKA | FLAALAAHASDP | AEAERLKFLSSPAGK |
| Tcu_CPR | HVGVHTENSIETVEEAAKLLGYQLDTIFSVHGDKEDGTPLGGS-SLPPFPFPGPCTLR | TALARYADLLNPPRKA | FLAALAAHASDP | AEAERLKFLSSPAGK |
| Pm_CPR | HVGVYAENLSDTVEEAAKLLGYPLDTIISVHSDKEDGTPLGGS-SLPPFPFPGPCTLQ | TALARYADLLNPPRKA | ALVALASHASDP | AEAERLKFLSSPAGK |
| Sm_CPRb | HVGVYAENCHDVVEEAQQLLGHSLDTVFSLHIES | EDGSSLAGN--LLPPFP | TPCTLR | TALARYADLQTPPRKAVLGVLAAYASDP |
| Sm_CPRC | HVGVYAENCHDVVEEAANLLDYTLDTVFSLHITD | EDGTPLPGS--LLPPFP | TPCTLR | TALARYADLQTPPRKAVLAVLAAYTSETSHADR |
| Sm_CPRa | HVGVFAENQDDVVEEAAKVLGYSLDTIFTLHGDN | EDGSPVSG---VPPPF | MGPIITMKAAL | QQHTDLQNP |
| Cre_CPR | HTATYARNGEAVVSQVAELLGFDLEARIKLLALPADADAASG---- | LPPFPF | GPVTVRTAL | SYFADVLSSPHREALNALASFAADREEAARLALLGSPAGK |
| consensus | * * | * * | * * | * * |
| | 401 410 420 430 440 450 460 470 480 490 | | | |

Pp_CPRc EEYSKMWVQSQRSLTEVLAAFSSVKLPLGVFFASVAPRLQPRFYSSISSPKLSPSRIHVTCALVHGSPSTGRIHRGVCSTWMKNAQSNFACSADGCS-WA
Pp_CPRd ADYSKMWVQSQRSLTEVLSAFPSVKLPLGVFFGSAVAPRLQPRFYSSISSPKVSPSRIHVTCALVYGPSTGRIHRGVCSTWMKNAQSKESHSADECS-WA
Pp_CPRa EEYTKMWVQSQRSLTEVLAAFPSVKLPLGVLFACVAPRLQPRFYSSISSPKFSPTRIHVTCALVYGPSTGRIHRGVCSTWMKNARSKDTYSGADDCS-WA
Pp_CPRb DEYAQWVQSQRSLLETLAAFPKAVPLGVFFAGVAPRLQPRFYSSISSPAIHPTRIHVTCALVYKSPSTGRIHRGVCSTWMKNANSTIKSGPDKCS-SA
Ca_CPR1 DEYSQWVQSQRSLVEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPARVHVTICALVYGPSTGRIHKGVCSTWMKNAVPLEK--SHNCS-SA
Ph_CPR1 DDYSTWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPTRVHVTICALVNGPTPTGRIHKGVCSTWMKNAVPLEK--SHNCS-SA
Ce_CPR1 DDYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFVFNRVHVTICALVYGPSTPTGRIHRGVCSTWMKNAVPSER--SHDSS-QA
Op_CPR1 DEYAQGTVGNQKSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPNRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPSER--SHECS-KA
Gm_CPR1 DEYSKMWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFSPQKVHVTICALVCGPTPTGRIHKGVCSTWMKNAVPLEK--SRDCS-WA
Vr_CPR1 DEYSKMWVQSQRSLVEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPQRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SODCS-SA
Vs_CPR1 DEYSKMWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPQRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SHDCS-RA
Pt_CPR1 NEYSHWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRYTPNRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SYECS-WA
Rc_CPR1 DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFALSRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SHDSS-WA
Gh_CPR1 DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFVAPRVHVTICALVYGPSTPTGRIHRGVCSTWMKNAVPLEK--SNDCS-WA
At_ATR1 DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPSRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SHECS-GA
Ha_CPR1 DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRYAPHRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SSDCS-WA
Pso_CPR1 NEYSKMWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRFAPSRVHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--S--S-WA
Am_CPR2 DEYAQWVQSHRSLLLEVLAEFPSAKPPLGVFFASVAPRLQPRYSSISSPRMPSRIHVTICALVYEKPTPTGRIHKGVCSTWMKNAVPLEK--SHDCS-WA
Pc_CPR2a DEYAQWVQSHRSLLLEVLAEFPSAKPPLGVFFASVAPRLQPRYSSISSPRMPSRIHVTICALVYEKPTPTGRIHKGVCSTWMKNAVPLEK--SHDCS-WA
Pc_CPR2b DEYAQWVQSQRSLLEVLAAFPKAPPLGVFFASVAPRLQPRYSSISSPRMAPSRIHVTICALVHETTPAGRIHKGVCSTWMKNAVPLEK--AHVSS-WA
Aa_CPR2 DEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFASVAPRLQPRYSSISSPRFAPNRVHVTICALVYEQTPSGRVHKGVCSTWMKNAVPMTE--SODCS-WA
Ht_CPR2b DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFASVAPRLQPRYSSISSPRMAPNRVHVTICALVYEKTPAGRIHKGVCSTWMKNAVPMTE--CLDCS-WA
Sr_CPR2 DEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPSRIHVTICALVYETTPAGRIHKGVCSTWMKNAVPLEK--SPDCS-QA
Ht_CPR2a DEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPSRIHVTICALVYEKTPGRIHKGVCSTWMKNAVPLEK--NODCS-SA
Cro_CPR2 DEYAQSLVANQRSLLLEVMAEFPSAKPPLGVFFAAVAPRLQPRFYSSISSPRMAPSRIHVTICALVYEKTPGRIHKGVCSTWMKNAVPLEK--SRDCS-WA
Cb_CPR2 EEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFAGVAPRLQPRFYSSISSPKIAPSRIHVTICALVYEKPTPTGRIHKGVCSTWMKNAVPLEK--SPNCS-SA
Ph_CPR2 EEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFASVAPRLQPRFYSSISSPRMAPSRIHVTICALVHDKLPTGRVHKGVCSTWMKNAVPLEK--SHSCS-TA
Gh_CPR2 DEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMAPSRIHVTICALVYEKPTPTGRIHKGVCSTWMKNAVPLEK--SDDCG-WA
Rc_CPR2 DEYTQWVQSHRSLLLEVMAEFPSAKPPLGVFFAGVAPRLQPRFYSSISSPKIAETRIHVTICALVYEKPTPTGRIHKGVCSTWMKNAVPLEK--SHECS-WA
Pt_CPR2b DEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFASVAPRLQPRYSSISSPRMAPSRIHVTICALVLEKTPAGRIHKGVCSTWMKNAVPLEK--SHDCS-WA
Pt_CPR2a DEYAQWVQSHRSLLLEVMAEFPSAKPPLGVFFASVAPRLQPRYSSISSPRMAPSRIHVTICALVLEKTPAGRIHKGVCSTWMKNAVPLEK--SHDCS-WA
Vv_CPR2 DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPKMPSRIHVTICALVCDKMPGRIHKGVCSTWMKNAVPLEK--SODCS-WA
Lj_CPR2 DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRFYSSISSPRMAPSRIHVTICALVNDKMPGRIHKGVCSTWMKNAVPLEK--SODCS-WA
Psa_CPR2 DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMAPSRIHVTICALVHDKMPGRIHKGVCSTWMKNAVPLEK--NODCS-WA
At_ATR2 DEYSKMWVQSQRSLLEVMAEFPSAKPPLGVFFAGVAPRLQPRFYSSISSPKIAETRIHVTICALVYEKMPGRIHKGVCSTWMKNAVPLEK--SENCSS-SA
Ec_CPR2 DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPSRIHVTICALVHEKTPAGRIHKGVCSTWMKNAVPLEK--NHDCSSWA
Os_CPR2a KEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SQECS-WA
Sb_CPR2a KEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SQECS-WA
Ta_CPR2a KEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SQECS-WA
Sb_CPR2b DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SKDCS-WA
Zm_CPR2b1 DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SKDCS-WA
Zm_CPR2b2 DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SKDCS-WA
Os_CPR2b DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--TKDCS-WA
Sb_CPR2c DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SEESS-WA
Zm_CPR2c DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SEECSS-WA
Os_CPR2c DEYSQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYSSISSPRMPTTRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SEECSS-WA
Ta_CPR2c DEYAQWVQSQRSLLEVMAEFPSAKPPLGVFFAAVAPRLQPRFYSSISSPKIAPSRIHVTICALVYGPSTPTGRIHKGVCSTWMKNAVPLEK--SEECSS-WA

| | |
|-----------|---|
| Tch_CPR | DEYSQWVTASQRSLLLEIMAEFPSAKPPLGVFFAAIAPRLQPRYYSISSSPRFAPSRIHVTCALVYGPSPTGRIHKGVCSNWMKNSLPSEE--THDCS-WA |
| Tcu_CPR | DEYSQWVTASQRSLLLEIMAEFPSAKPPLGVFFAAIAPRLQPRYYSISSSPRFAPSRIHVTCALVYGPSPTGRIHKGVCSNWMKNSLPSEE--THDCS-WA |
| Pm_CPR | DEYSQWITVSQRSLLLEVMAEFPSAKPPLGVFFAAVAPRLQPRYYSISSSPRYASNRIVHVTALVYGPSPTGRIHKGVCSNWMKNSVPSEK--SQYCS-WA |
| Sm_CPRb | DEYSQYIATSQRTLLEVMEDFPSVKVPLGVFFASVSPRLIPRYYSISSSPKYVASRIHVTCALVYGPSLTGRIFKGCSTWMKNARSAEE--AGDECSWA |
| Sm_CPRc | EDYSQYISSCQRTLLEVLADFSSVKLPLGVFFASVAPRLMPRYYSISSSPKFAPIRIHVTCALVHGPSPTGRLFRGVCSTWMKNARSAEE--AGDDCSWA |
| Sm_CPRa | DEYSQYIAASQRSLLLEVLQDFPSVKLPITGVFFAAVGARLQPRYYSISSSPRFSPSRIHVTSALVYGKSPTGRLHRGVCSTWMKHAKSSEE--TGNDCSWS |
| Cre_CPR | AEYADFVIGKPHRSLLLEVLQAFPSAKPTIGAFFGCIAPRLQPRFYYSISSSPKQHPNSVHVTCAVVRDTMPTGRVHEGVASTWLQRHGNGAA-----V |
| consensus | ..*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....*.....* |
| | 501.....510.....520.....530.....540.....550.....560.....570.....580.....590..... |

Pp_CPRc PIFVROSNFRLPADSSTPIIMVGP GTGLAPFRGFLQERAAALQESGSM LGPAKLFFGCRSRTODFIYEDELKSYVEKG-VMELTVAFSREGSKKEYVQDKM
Pp_CPRd PIFVROSNFRLPLNSNTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRTRAHDFIYDNEELKSFVEKG-VTELTVAFSREGPKKEYVQDKM
Pp_CPRa PIFVROSNFRLPADSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRTRTODFIYEELNAFVEKG-ITELTVAFSREGPRKEYVQDKM
Pp_CPRb PIFVROSNFRLPADPATPIIMVGP GTGLAPFRGFLQERDAALQKSGATLGP AKLFFGCRSSDKDFIYEDELNDYKNG-ITELTVAFSRONSQKEYVQDKM
Ca_CPR1 PIFVTRPSNFKLPDPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Ph_CPR1 PIFVTRPSNFKLPADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Ce_CPR1 PVFVTRPSNFKLPADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Op_CPR1 PIFVTRPSNFKLPADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Gm_CPR1 PIFVTRPSNFKLPADHSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPEKEYVQHKM
Vr_CPR1 PIFVTRPSNFKLPVDHSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGAEKEYVQHKM
Vs_CPR1 PIFVTRPSNFKLPADHSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPEKEYVQHKM
Pt_CPR1 PIFVTRPSNFKLPADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Rc_CPR1 PVFVTRPSNFKLPDPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Gh_CPR1 PIFVTRPSNFKLPADPSVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
At_ATR1 PIFVTRPSNFKLPDPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Ha_CPR1 PIVVTRPSNFKLPANPSTSIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPOKEYVQHKM
Pso_CPR1 PIFVTRPSNFKLPADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPEKEYVQHKM
Am_CPR2 PIFVROSNFKLPSDTKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Pc_CPR2a PIFVROSNFKLPSDTKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Pc_CPR2b PIFVROSNFRLPTDSKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPAKEYVQHKM
Aa_CPR2 PIVVTRPSNFRLPSDPKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGATKEYVQHKM
Ht_CPR2b PIVVTRPSNFRLPSDPKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Sr_CPR2 SIVVTRPSNFRLPSDPKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Ht_CPR2a PIFVTRPSNFRLPADPKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGASKEYVQHKM
Cro_CPR2 PIFVROSNFKLPADPKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Cb_CPR2 PVFVTRPSNFRLPADPKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPAKEYVQHKM
Ph_CPR2 PIFVROSNFKLPADNKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPNKEYVQHKM
Gh_CPR2 PIFVROSNFKLPSDTKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Rc_CPR2 PIFVROSNFKLPAADTKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Pt_CPR2b PVFVROSNFKLPAADTKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Pt_CPR2a PIFVROSNFKLPAADTKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Vv_CPR2 PIFVROSNFKLPAASVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Lj_CPR2 PIFVROSNFKLPAADNKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Psa_CPR2 PIFVROSNFRLPADNKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
At_ATR2 PIFVROSNFKLPSDSKVPPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Ec_CPR2 PIFVROSNFKLPAADSTVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGATKEYVQHKM
Os_CPR2a PIFVROSNFKLPTDPTVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPSKEYVQHKM
Sb_CPR2a PIFVROSNFKLPAADPTVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Ta_CPR2a PIFVROSNFKLPAADPTVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Sb_CPR2b PIFVROSNFKLPAADPSVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Zm_CPR2b1 PIFVROSNFKLPAADPSVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Zm_CPR2b2 PIFVROSNFKLPAADPSVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Os_CPR2b PVFVROSNFKLPAADPSVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Sb_CPR2c PIFVROSNFKLPAADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Zm_CPR2c PIFVROSNFKLPAADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM
Os_CPR2c PIVVROSNFKLPAADPTVPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPAKEYVQHKM
Ta_CPR2c PIFVROSNFRLPADPSSTPIIMVGP GTGLAPFRGFLQERAAALQESGFTLGP AKLFFGCRNRMDFIYEELKSFVDQGVISELITAFSREGPTKEYVQHKM

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Tch_CPR PVFVRSNFKLPADSTTPIVMGPGTGFAFPRGFLQERAKLQEAGEKLGPAVLFFGCRNRMDYIYEDELKGYVEKGVLTDLIVAFSREGATKEYVQHKM
Tcu_CPR PVFVRSNFKLPADSTTPIVMGPGTGFAFPRGFLQERAKLQEAGEKLGPAVLFFGCRNRMDYIYEDELKGYVEKGI LTNLIVAFSREGATKEYVQHKM
Pm_CPR PVFVRSNFKLPADPSVPIVMGPGTGLAPFRGFLQERAAIQKSGEKLGPVAVLFFGCRNRMDYIYEDELKSYVENGVLTDELIVAFSREGATKEYVQHKI
Sm_CPRb PIFVRSNFKLPANSTTPIVMIGPGTGLAPFRGFLQERAAIQASGETLGPVAVLFFGCRNRKODFIYEELKEYVKKETLSSLYVAFSREGSTKEYVQNKM
Sm_CPRc PIFVRSNFKLPADPKIPIVMIGPGTGLAPFRGFLQERAAIQDSGEQLGPSVLFFGCRNRNODFIYERELNEYVSRGTLANLYVAFSREGSTKEYVQHKM
Sm_CPRa RIFVRSNFKLPKSTVPIVMIGPGTGLAPFRGFLQERAAIQESGEQLGTAILYFGCRNRKODYIYEELARYRETGVITDLYVAFSREGPTKEYVQDIM
Cre_CPR PVFVRHSHFRLPKAASTPIVMGPGTGLAPFRGFLQERAAIKNSGAE LGPAHLFFGCRSRGTDYIYQOEL EGYVADGVL SNLHVAFSRDQSSKDYVQHII
consensus .....* * * * * .....* * * * * .....* * * * * .....* * * * * .....* * * * * .....* * * * * .....* * * * * .....* * * * * .....* * * * * .....* * * * *
601.....610.....620.....630.....640.....650.....660.....670.....680.....690.....
    
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Pp_CPRc LEQAGEVWSLIKGGGYYVCGDAKGMARDVHRMLHTTIVQEEGAEGSKAEATVKKQLQVDGRYL RDVW
 Pp_CPRd LEQAGDVWRLIRGGGYYVCGDAKGMARDVHRMLHTTIVQEESEVSSKAEATVKKQLQVDGRYL RDVW
 Pp_CPRa LEQAGEVWKLIRGGGYYVCGDAKGMARDVHRMLHTTIVQEEGVTSSEAEAVVKKLSLDGRYL RDVW
 Pp_CPRb QQHASDIWRLLSADGYLYVCGDAKGMARDVHRVHSHIVQEDGVDSSKAEATVKKQLQVDGRYL RDVW
 Ca_CPR1 MEKASEVWSLISQGGYYVCGDAKGMARDVHRTLHTTIVQEQENANSSKAEATVKKQLQMDGRYL RDVW
 Ph_CPR1 MEKASHVWSLISQEGYLYVCGDAKGMARDVHRTLHTTIVQEQEKADSSKAEATVKKQLQMDGRYL RDVW
 Ce_CPR1 MEKAAETWSSLISQEGYLYVCGDAKGMARDVHRALHTTIVQEQEKT DSSKAEATVKKQLQMDGRYL RDVW
 Op_CPR1 TEKAAQFWSLISQVGYLYVCGDAKGMARDVHRTLHTTIVQEQENV DSSKAEATVKKQLQTDGRYL RDVW
 Gm_CPR1 MDKAAANLWNLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQENV DSSKAEATVKKQLQMDGRYL RDVW
 Vr_CPR1 MDKAAHLWSSLISQGGYLYVCGDAKGMARDVHRTLHSHIVQEQENV DSSKAEATVKKQLQMDGRYL RDVW
 Vs_CPR1 MDKAEYLWSSLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQENADSSKAEATVKKQLQMDGRYL RDVW
 Pt_CPR1 VDRAAETWTLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQGGLDSSKTESMVKKLQMDGRYL RDVW
 Rc_CPR1 MDKAAQIWSLISERGYLYVCGDAKGMARDVHRTLHTTIVQEQGNLDSSKTESMVKKLQMDGRYL RDVW
 Gh_CPR1 MDKAAADIWNLISKGGYLYVCGDAKGMARDVHRTLHTTIVQEQENV DSSKAEATVKKQLQMDGRYL RDVW
 At_ATR1 MEKAAQVWDLIKKEEGYLYVCGDAKGMARDVHRTLHTTIVQEQEGVSSSEAEATVKKQLQTEGRYL RDVW
 Ha_CPR1 MDKAAAYIWEVLSQGAHTYVCGDAKGMARDVHRTLHTTIVQEQGNLDSSKTEL FVKKLQMDGRYL RDVW
 Pso_CPR1 MEKATDVWNLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQGPMSSAAEA AVKKLQVEGRYL RDVW
 Am_CPR2 LQKASEIWNLMISEGAYLYVCGDAKGMARDVHRMLHTTIAEQEQALDSSKAESWVKKLQMTGRYL RDVW
 Pc_CPR2a LQKASEIWNLMISEGAYLYVCGDAKGMARDVHRMLHTTIAEQEQALDSSKAESWVKKLQMTGRYL RDVW
 Pc_CPR2b SQKASEIWDMLSHGAYLYVCGDAKGMARDVHRMLHTTIAEQEQALDSSHAESLVKKNLHMSGRYL RDVW
 Aa_CPR2 TQKASDIWNLLISEGAYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKAE L YVKNLQMAGRYL RDVW
 Ht_CPR2b NEKASDLWKL L ISEGAYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKAE L FVKNLQCRGRYL RDVW
 Sr_CPR2 SQKASDIWKL L ISEGAYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKAE L YVKNLQMSGRYL RDVW
 Ht_CPR2a SQKASDIWNMLISEGAYLYVCGDAKGMARDVHRTLHTTIVQEQGNLDSSKAE L YVKNLQMSGRYL RDVW
 Cro_CPR2 AEKASDIWRMISDGAYLYVCGDAKGMARDVHRTLHTTIAEQEQSMDSIQAE GFVKNLQMTGRYL RDVW
 Cb_CPR2 AOKAWDVWNLISEGGYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKTES FVKNLQMTGAVL RDVW
 Ph_CPR2 TEKAAADIWNMLISQGGYLYVCGDAKGMARDVHRTLHTTIAEQEQGSLDSSKAE G M VKNLQTTGRYL RDVW
 Gh_CPR2 MEKAKDIWDMISQGGYLYVCGDAKGMARDVHRALHTTIVQEQGSLDSSKAE S M VKNLQMSGRYL RDVW
 RC_CPR2 SEKALDIWNMLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQ-----
 Pt_CPR2b MQKASDIWNMLISQGGYLYVCGDAKGMARDVHRALHTTIVQEQGSLDSSKTES FVKS LQMN GRYL RDVW
 Pt_CPR2a MQKASDIWNMLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKTES FVKG LQMN GRYL RDVW
 Vv_CPR2 MEKASDIWNMLISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKAE S M VKNLQMTGRYL RDVW
 Lj_CPR2 MEKASDIWNMLISQGAYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKAE G M VKNLQLN GRYL RDVW
 Psa_CPR2 MEKASDIWNMLISQGAYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSKTES M VKNLQMTGRYL RDVW
 At_ATR2 MDKASDIWNMLISQGAYLYVCGDAKGMARDVHRTLHTTIAEQEQSMDSIQAE GFVKNLQTSGRYL RDVW
 Ec_CPR2 AEKASYIWEMLISQGAYLYVCGDAKGMARDVHRTLHTTIAEQEQGSLDSSKTES L VKNLQMDGRYL RDVW
 Os_CPR2a AEKAPEIWSIISPGGYLYVCGDAKGMARDVHRTLHTTIVQEQGSLDSSNTE S YVKS LQMEGRYL RDVW
 Sb_CPR2a AOKAAELWSIISQGGYLYVCGDAKGMARDVHRTLHTTIVQEQGSMDSN SKTES YVKS LQMEGRYL RDVW
 Ta_CPR2a AEKAAELWSIISQGGYLYVCGDAKGMARDVHRALHTTIVQEQGSLDSSKAE G YVKNLQMEGRYL RDVW
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 Os_CPR2b SQKASEIWDMLISQGGYLYVCGDAKGMARDVHRMLHTTIVQEQGSLDSSKAE S FVKS LQTEGRYL RDVW
 Sb_CPR2c VEKATEIWNMLISHGGYLYVCGDAKGMARDVHRMLHTTIVQEQGSLDSSKTES YVKS LQMEGRYL RDVW
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 Os_CPR2c TEKATEIWNMLISQGGYLYVCGDAKGMARDVHRALHTTIVQEQGSLDSSKTES YVKS LQMDGRYL RDVW
 Ta_CPR2c VDKATEIWNMLISQGGYLYVCGDAKGMARDVHRMLHTTIVQEQGSLDSSKTEL YVKNLQMEGRYL RDVW

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Tch_CPR  LEKASDTWSLIAQGGYLYVCGDAKGMARDVHRTLHTIVQEQESVDSSKAEFLVKKLQMDGRYL RDITW
Tcu_CPR  LEKASDTWSLIAQGGYLYVCGDAKGMARDVHRTLHTIVQEQESVDSSKAEFLVKKLQMDGRYL RDITW
Pm_CPR   TEKGSYIWNLIAQGGYLYVCGDAKGMARDVHRTLHSLIVQEQESVDSTSAEATVKKLQTEGRYL RDVW
Sm_CPRb  MEKAVDMWKLISDGAYLYVCGDAKGMARDVHRTLHTIVKQEG--NVSEPEAFVKQLQNDGRYL RDVW
Sm_CPRc  QDKATDLWRLISNGAYLYVCGDAKGMARDVHKLITIVQTEG--NVKEAFAFVKQLQNDGRYL RDVW
Sm_CPRa  MKKANQLWDITSGDGYLYVCGDAKGMARDVHRTLHTIVQEQQSLDSSKTEAFVKKLQMDGRYL RDVW
Cre_CPR  GREAAALWPIITGGGAHLYVCGDAKYMAKDVHKAFAVALVEKGGKCSGTOAEMFVKELTDAGRYQ RDVW
consensus .....*.....*****..**..***.....
701.....710.....720.....730.....740.....750.....760.....
    
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