

>sctr_Oryctolagus_cuniculus [EMBL: O46502]
PDLACGVSMNDSSHERQHAYLLKLVKMYTVGYSSSLVMLLVALGILCAFRRLHCTRNYIHMHLFLSFILRALS NFIKDAVLF S
SDDAIHCDAHR-----
VGCKLVMVFFQY CIMANYAWLLVEGLYLHSLLVVSFFSERKC-----
LQGFVVLGWGSPAMFVTSWAVTRHFLED-----
SGCWDINANAAIWWVIRGPVILSILINIFILFINILRILTRKLRTOETRGQD-----
-----MNHYKRLARSTLLLIPLFGVHYIVFVFSPE-GAMEIQL-----
FFELALGSFQGLVVAVLYCFLNGEVQLEEVQKKW-----
>ccapr_Drosophila_melanogaster [GenBank: JC7952]
-----LNSFYFYETE QFAVLWILFTVIVLGN SAVL FVMFINK-----
NRKSRMNYFIKQLALADLCVGLLNVLTDI IWRIT---ISWRAGN-----
LACKAIRFSQVCVTSSTYVLVAMSIDRYDAITHPMNFSKSWK--
RARHLVAGAWLISALFSLPILVLYEEKLIQGH-----PQCWIEL-----GSPIAWQVYM--
SLVSATLFAIPALII SACYAIVKTIWAKGSIFVPTER--AGFGAAPARRASS-----
RGIIPRAKVKTVMKMTLTIVFVFIICWSPYIIFDLLQVFGQIP-H-
SQTNIAIATFIQSLAPLNSAANPLIYCLFSSQVFR T LSRFPFPKWF T-
>caccr_Drosophila_melanogaster [GenBank: Q868T3]
-----LNSFYFYETE QFAVLWILFTVIVLGN SAVL FVMFINK-----
NRKSRMNYFIKQLALADLCVGLLNVLTDI IWRIT---ISWRAGN-----
LACKAIRFSQVCVTSSTYVLVAMSIDRYDAITHPMNFSKSWK--
RARHLVAGAWLISALFSLPILVLYEEKLIQGH-----PQCWIEL-----GSPIAWQVYM--
SLVSATLFAIPALII SACYAIVKTIWAKGSIFVPTER--AGFGAAPARRASS-----
RGIIPRAKVKTVMKMTLTIVFVFIICWSPYIIFDLLQVFGQIP-H-
SQTNIAIATFIQSLAPLNSAANPLIYCLFSSQVFR T LSRFPFPKWF T-
>ccapr_receptor_Anopheles_gambiae [GenBank: NP_996297]
-TRGEEIN SFYFYETE QFAVLWILFTVIVLGN SAVL VTLMLNR-----
TRKSRMNFYFIKQLAIADLCVGLLNVLTDI IWRIT---VWRAGN-----
AACKAIRFVQVCVTSSTYVLVALSIDRYDAITHPMNFSGCWS--
RARKLVA AAW SFSILFSLPITYFYEERLIQ GK-----MQCWIDL-----VEAWRWQLYM--
CWVSGSLFVVPALII SACYAVIVRTIWAKGTILGPIDRTHNGMADLATRRASS-----
RGIIPRAKVKTVMKMTIVIVIVFVLCWSPYIIFDLLQVFGQIP-A-
TQTNVAIATFIQSLAPLNSAANPLIYCLFSTQVCRM IKRLPPFRWLWS
>oxyr_Homo_sapiens [GenBank: NP_000907]
-----LARVEVAVLCLILLLLALSGNACVLLALRTR-----
QKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDIT---FRFYGPD-----
LLCRLVKYLQVVG MFASTY LLLLMSLDRCLAICQPLRSLR---
RTDRLAVLATWLGCLIVASAPQVHIFSLREVADG-----VFDCWAVE-----IQPWGPKAYI--
TWITLAVYIVPVIVLAACYGLISFKIWQNRLRKTAAAAAAEAP--EGAAAAG--DGGRVA-----
LARVSSVKLISKAKIRTVKMTFIVLAFIVCWTPFFFVQMWSVWDAN-----
APKEASAFIIVMLLASLNSCCNPWIYMLFTGHLFH ELVQRF-----
>oxyr_Bos_taurus [GenBank: NP_776559]
-----LARVEVAVLCLILFLALSGNACVLLALRTR-----
HKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDIT---FRFYGPD-----
LLCRLVKYLQVVG MFASTY LLLLMSLDRCLAICQPLRSLR---
RTDRLAVLVTLWLGCLIVASAPQVHIFSLREVADG-----VFDCWAVE-----IQPWGPKAYI--
TWITLAVYIVPVIVLATCYGLISFKIWQNRLRKTAAAAAAEAAAGAEGEAAD--WAGRAI-----
LARVSNVKLISKAKIRTVKMTFIVVLA FIVCWTPFFFVQMWSVWDAD-----
APKEASPFIIAMLLASLNSCCNPWIYMLFTGHLFQELVQRF-----
>oxyr_Gallus_gallus [GenBank: NP_001026740]
-----MAKVEVTVLCILFLALSGNLCVLLAIHTTR-----
QKHSRMYFFMKHLSIADLVVAVFQVLPQLIWDIT---FRFYGPD-----
FLCRLIKYLQVVG MFASTYMLLLLMSLDRCLAICQPLRSLHR---
RADRVSVLLTWLCLLVSIPQIHIFSLRDVGN G-----VYDCWADF-----IQPWGPKAYV--
TWITLMVYIIPVLMLSVCYGLISFKIWQNVKLT AHGPP-----GGQSST--ARGGAA-----
FARVSSTR LISKAKIRTVKMTFIVLAFIVCWTPFFFVQMWSVWDTN-----
APQEASPFIIAMLLASLNSCCNPWIYMLYTGHLFHDL MRRF-----
>vasr1a_Homo_sapiens [GenBank: NP_000697]
-----LAKLEIAVLAVTF AVAVLGNSSVLLALHRTP-----
RKTSRMHLFIRHLSLADLAVAFFQVLPQMCWDIT---YRFRGPD-----

WLCRVVKHLQVFGMFASAYMLVVMVTADRYIAVCHPLKTLQQPA-
RRSRLMIAAAWVLSFVLSTPQYFVFSMIEVNNVT-----KARDCWATF-----IQPWGSRAYV--
TWMTGGIFVAPVVILGTCYGFICYNIWCNVRGKTAS-RQSKGAE--QAGVA-FQKGFL--
APCVSSVKSISRKIRTVKMTFVIVTAYIVCWAPFFIIQMWSVWDPMSVW-
TESENPTITITALLGSLNSCCNPWIYMFSSGHLQDCVQSF-----
>vasr1a_Tribolium_castaneum [GenBank: XP_967376]
-----LARVEVATLAIIFLVTVIGNSTVLLALWTRRRYAG--
RKKLSRMYFFILHLSIADLITAFLSVLPQLAWDIT---YRFYGGF-----
LLCKVVKYGQTLGPLYLSSYVLMATAIDRHQAICYPLTYCSWTS-
RRSKVMVYLAWVASLAFQPLTIFTYTSVGED-----EYDCWATF-----QEPWKGKRAYV--
TWYSISVFMVPLVVLIFTYTSICIEIWQSSSESLRPRSS-----QKSAP---GKR-----
TPLISRAKINTVKQTIIVIVMYIACSTPFILAQWLWATWDPQ-----
SPFIDVEFKKVAQEDYIP-----
>vasr2_Homo_sapiens [GenBank: NP_000045]
-----LARAELALLSIVFVAVALSNGLVLAALARRGR-----
RGHWAPIHVFIGHLCLADLAVALFQVLPQLAWKAT---DRFRGPD-----
ALCRAVKYLQVMGYASSYMLAMTLDRHRAICRPLAYRHGSGAHWNRPVLVAVAFSLLLSLPQLFIFAQRNVEGGS-----
-----GVTDCWACF-----AEPWGRRTYV--
TWIALMVVAPTGLGIAACQVLIFREIHASLVPGPSPSERPGRRR---GRRTGSPGEG-----
AHVSAAVAKTVRMTLVIVVVYVLCWAPFFLVQLWAAWDPE----
APLEGAPFVLLMLLASLNSCTNPWIYASFSSSVSSELRSLL-----
>gnrhr2_Homo_sapiens [GenBank: Q96P88]
-VEGSELPTFSAAAKVRVGVTVLTVFVSSAGGNLAVLWSVTRREPSQ----
LRPSPVRRFLIHLAAADLLVTFVVMPLDATWNIT---VQWLAVD-----
IACRTLMFLKLMATYSAAFLPVVIIGLDRQAAVLNPLGSRSGV--RK---
LLGAAWGLSFLLAFFPQLFHTVHXAGPV-----PFTQCCTTKG---SFKAQWQETTYN--
LFTFCCLFLLPLTAMAIKYSRIVLSVSRPQTRKG---SHAPAGEFALPRSFDN-----
CPRVRLRALRLALLILLTFILCWTPYLLGMWYWFSPTMLT--
EVPPSLSHILFLLGLLNAPLDPLLYGAFTLGCR-----
>gnrhr2_Sus_scrofa [GenBank: AAS68622]
-VESSELPTFSVAAKVRVGVTVVLFVSSAGGNLAVLWSVTRPQPSQ----
LRPSPVRRFLFAHLAAADLLVTFVVMPLDASWNIT---VQWLAGD-----
IACRTLMFLKLMAMYAAAFLPVVIIGLDRQAAVLHPLGPRSGG--RK---
LLGAAWLLSFLALPQLFHTVRRAGPV-----PFTQCCTTKG---SFKAQWQETTYN--
LFTFCCLFLLPLTVMTCYSRIVLSVSSPRTRKG---NDAPAGEFTLRRSLDN-----
RPRVRLRALRLALLVLLTFVLCWTPYLLGLWYWFSPTMLS--
EVPPSLSHILFLLGLLNAPLDPLLYGAFTLGCR-----
>gnrhr1_Rana [GenBank: AA050198]
-HTHFQLPTFSAAKARVIITFVIFTLSATCNLAALWSAARTS--R----
KKRSHVRILILNLTADLLVTFIVMPLDAIWNIT---VQWHAGD-----
IACRILMFLKLLSMYSAFVTVVISVDRQSAIILNPLAINDAK--
KKNKIMLSVAWLMSAVLSLPQLFHTVTITTEPH-----NFTQCTTRG---SFQQHWQETVYN--
MVSFVCLFLLPLLIMICCYSRILLEISKRMK-----GTLSSKEVYLRCSKNN-----
IPKARMRTLKMSVVIVSSFIICWTPYFLLGLWYWFYPEIME-
EKVSQSTHILFIFGLVNACLDPIYGLFTIHFRRKSLQRYC-----
>gnrhr_Typhlonectes_natans [GenBank: AAD49750]
-----PTFSTAACKVRVTITFVLFISSACFNIIALWTITQK---Y----
KKRSHVRILISNLAVADLLVTFIVMPLDAIWNIT---VQWYAGD-----
LVCRVLMFLKLVAMYASAFVTVVISLDRQSAIILNPLGIGDAK--
KKNKIMLCVAVVLSVLLAVPQLFVHAVSPSQSE-----YFIQCATVG---SFQGHWQETLYN--
MFTFSCFLFLLPLLIMVLCYSRILIEISRKMKK-----ACVSSKEVHLRRSSNN-----
IPKARLRTLKMSIVIVLTFIVCWTPYLLGIWYWFSPPEMLTRERVPPLSHILFLLGFLNACLDPLIYGLFTI-----

>gnrhr3_Oryzias_latipes [GenBank: BAC97833]
--DALQLPTFSTAACKVRVIITFTLCAVSAVCNLLVLAAGKG---G----
KKRSHVRILIMNLTVADLLVTFIVMPVDAAWNIT---VQWQAGD-----
LACRLLMFMKLVAMYSAFVTVVISLDRQSAIILNPLGISEAK--
RKSIMLTVAWTTSVILSLPQMFIFHNVTISVPE-----NFTQCTTHG---SFVQRWQETLYN--
MFTFVCLFLLPLVIMIFCYTRILVEISSRIAR-----TNMVSARDIHLRRSHNN-----

IPKARMRTLKMSIVIVTSFIIICWTPYYLLGLWYWLFPKME-
ETVSHSLTHMLFIFGLFNACLDPIITYGLFTIHLRQGAKR-----
>gnrhr_Ciona_intestinalis [GenBank: NP_001027765]
-VLIQTWFQFDTLHLVRLVLTWLLFCLSMAGNMFVLSLRGS-----
KSRHFIMFHLALSNLVYTFVMPSPDAVWNTT---MEWLAGD-----
VMCRLCQMMKQFGMYASSFMVVVIGADRVTGILSPLPCHSQR--
KRGYYMVATAWISSLICCLPAGFIFSVASIPTCEG-----IPIYQCIDFN---VLQDVSLLRPYY--
FFTMCMSFLLPLICTLVSYSLIVCEISNMKER-----DRVLMGRRHSVNTAS-----
IQRAKNRTILMRTLITLTLFLVCWGPYYGKGIYDWFIRYEDH--
TPPDAWDTVMYVVMYLNPNVLPVLPVIVFVGLKEIRGKFKQRLN-----
>akhr_Tribolium_castaneum [GenBank: ABE0225]
--KLPISMRFNEGHQLSIIIVYSILMVFSIAIANTTVLVLIVKRRR-----
KTPSRINTMLMHLAIADLLVTFMMPLEIGWAST---VSWYAGD-----
AMCRIMMFFRMFGLYLSSFILVCISVDRFYAVLKLPLYLRALD--
RRDKFMLLGAWLGATLCSIPQMVVFHVESHVFNIT-----WYQQCVTYN---VFPTYAHELTLYL--
LFGMVMYALPLAVIIFSASILLEIRRRTR-----NPYGDSVTRSSLAF-----
LGKAKVRTLKMTIIIVLVFFVCWTPYYVMCIWYWLDR--
ESAKNVQRIQKALFLFACTNSCMNPVYGVFNIRA-----
>akhr_Anopheles_gambiae [GenBank: ABD60146]
-YEMPIDMRFNSGHILSIMVYTTLMVFSATGNLTVLSILAQRKV-----
RASSRINIMLAHLAIADLLVTFMMPLEIGWAYT---VRWTAGD-----
LMCRVMAFFRTFGLYLSSFILICISVDRYFAVLKP--LKVHE--
HRAVLMIAAAWIMSGLCSLPQAFIFHLEGHVFNIT-----GYQQCVTYH---YFEEIYQIIYN--
VLVMCLMYTFPLIVILYCYGSIYYEIFSRTN-----PRNLESFRRSSIDV-----
LGRAKRKTLRMTIMIVIVFVVCWTPYYVMSLWYWLDR--
ESTKNVDQRIQKGLFLFASTNSCMNPVYGVFNVRK-----
>akhr_Periplaneta_americana [GenBank: ABB20590]
---MTDDMKFNDGHRMSIITYSILMVSVAGNSTVLITILKRGR-----
TLRYGNNYMFHMLAIADLLVTFMMPLEIAWNIT---VSWKGGD-----
LMCRIMLFFRTFGLFLSSFVIVCISLDRCAVAILRPMKSKLLNVARRGKMLMTVAWILATLCSLPQAVIFHVEPHVFNVT-----
-----WYEQCVSN---FFSTKMHEFTYR--VLGMVMYGLPLIVIVISYACILGEIIRRYQ-----
LSPDDSFRRSSLVF-----LNRARNRTLKMAIIFVVFVICWTPYYVMCLWYWIDE--
RSAETVDHRVQKALFLFASTNSCMNPVYGVFNRLGRGSGYGATGGRVQG
>akhr_Bombyx_mori [GenBank: NP_001037049]
--ELPLEMRFNYSHMVSMTVYVSLMVISATGNLTVLYQLVRRRR--A---
KRASRLDILLMHLAVADLMVTFMMPLEIAWAGT---VQWFAGD-----
LMCRVMMFTRTFGLYLSSFVLICIAVDRYAAILKPLNVTWIATVRRR--
IIVAWVCAGLASLPQSFIFHVEEHPEVK-----GYNQCVSYG---SLPTEKHEFAYF--
LVNMILMYVIPLVSTLYCSCAALFEIIRAN-----TAN-DKMRRSIGL-----
LGRARARTLKMTVTIVLVFFTCWSPYCYCLWYWIDK--
ESIKNLDPALQKAMWLFSCNTSCANPIVYGVFNRRNRWNWRAGKFNQGRCRS
>gnrhr_Crassostrea_gigas [GenBank: CAI64587]
-----LKFSNDYAHSIISLGVVFLIGALGNIASFVTLCSKN-----
RKSPTNFLLHLSSADLLVMFVIVPVGEMIHVFNAT---IAWLGN-----
FLCKLYHFLWNFGQYVATFLLCCISIDRYLAFVFLRSLTQS-
PRTRSFMAATAWVLSAILSAPESVIFHVETHPKYR-----TFRQCVTFN---FFPSHNHELAYN--
LFNLTLYALPLLIITTSYSLILWEISKTKQCKEETKCLSTRSRLRRSSVGN-----
MERARIRTLKMTLVIVSVFVICWTPYFVLSAWWWVFD--
DSASQLDPKVQRGLFLFAVNSCMDPIVYGMFTT-----
>gnrhr1_Caenorhabditis_briggsae [GenBank: CAE60355]
-----IAIKSSVISIVLTYLALFILAFIGNVTMFMILCRNQL-----
VKVRRVHSLLLHMNIAHLLVTLVVMPEILHNYM---VAWFAGD-----
IMCRVCKFFDVFGLSLSMNVLICITLDRFYSIFFPLYAMRAR--
KSVQRMVSIWIVSLITSAPQLYLFKTAEHPCFA-----WYTQCVSLN---
FIGELSNVVFYFSIINI IQVYIAPLIVTVICYSLILWKISRKTKLVGEKESEKSSELLLRNGQNN-----
-----LEKARSRTLKMTFVIVLAFVISCWTPYVILMFLHFLR-----
RTDWIPKDIRKFIYAFVLSAISPYLYGYFSF-----
>gnrhr1_Caenorhabditis_elegans [GenBank: NP_491453]
-----VTVNDSVLSIVFTYLAFLAFVGNVTMFLILCRNQL-----

VKVRVHSLLLHMNIAHLLVTLVMPKEILHNYM---VAWFAGD-----
VMCRICKFFDVFAISLSMNLICITLDRFYISIFFPLYAMRAR--
KSVQRMVSAFWTISFVTSAPQLYLKFTATHPCFD-----WYTQCVSKN---
FIGELSNADVFFFISVNI IQVYIAPL FVTVCYSLILWRISRKSKLVGEKESEKSSSELLLRNGQNN-----
-----LEKAKSRTLKMTFVIVLAFIFCWPYPYSILMFLHFLR-----
HTDWIPKDIRKFIYAFVLSAISPYLYGYFSF-----
>corr_Anopheles [GenBank: AAQ67361]
LSCYEHAPTLKSGVIRVIVLSAMAIVSLLGNVATMWNIQNRKSRRVTRHNWSAIYSLIFHLSIADVLVTGFCLIGEAAWY
T---VDWVAGN-----
LFCKLFKLCQMFSLYLSTYVVLVGVDRWVAVKYPKMSLNTA--
RRCHRFLFVAYLLSFLSTPQWMI FRVAKGPFVE-----DFYQCVTHG---FYTDRWQEQLYT--
TFTLVFMFI IPLLILIGTYLSTFMTISSSEKIFRIDTSAVDRTTYRRSDTNRQ-----
RLIHKAKMKSRLRISVVIVVAFVVCWTPYYIMMLIFMFLN---
PTERFGE DLQSGIFFFGMSNSLINPLIYGAFHLVPIRQRNQNQHVRG
>corr_Manduca sexta [GenBank: AAR14318]
-SCLEHAPILTKSTVIRASVLSAMA ILSFFGNLATIISIQRGKRGRGRARPSWTAIYSLIFQLSIADLLVTIFCIAGEAAWSF
T---VQWYAGN-----
IACKIFKFLQMFALYQSTFIIVLVIGVDRWLAVKYPKMSMATA--
TRSGRLVVI AWVLSVLSIPQTVVFRVAKGPFVE-----EFYQCVTHG---FYTERWQEQAYT--
TLSLVFMFVLPVLVILISTYVSTVRTIARSEKVFKP---EVRREQEYFTPDMMNR-----
RLIDRAKMKSLRMSVVIVAAFLVWVAPYYMMI IFTFLN---
PDKDQSEELLSGIFFFGMSNSLVNPIYIYAFHLWPKKRSRHSRHS DRESGG
>corr_Drosophila melanogaster [GenBank: JC7896]
EHVMDHAPQLSRSGLLKVYVLA VMALFSLGNNLLTIWNIYKTRISRNSRHTWSAIYSLMFHLSIADVLVTWFCIIGEAAWCY
T---VQWLANE-----
LTCKLVKLFQMFSLY LSTYVVLVIGVDRWIAVKYPKMSLNMA--
KRCHRLGGTYILSLVLSLPQFFIFHVARGPFVE-----EFYQCVTHG---FYTADWQEQMYA--
TFTLVFTFLLPLCILFGTYMSTFRTISSSEKMFQG-SKLANYSTAKLPTQTNRQ-----
RLIHKAKMKSRLRISVVI IIAFLICWTPYYMMIMFMFLN---
PDKRIGDDLQDAIFFFGMSNSLVNPLIYGAFHLCPGKGGKSSGGGNNNA
>gnrhr2_Caenorhabditis briggsae [GenBank: CAE60908]
-----LGYITSDYAQMLIYGIFVLIGLPVNISTLIYMLKRYR-----
HAKSFLLLLHINLNISDILVGLYVPLIGLWLVLT---LEWRGGE-----
YLCKFMRFVDAFVFAISSNIMVCI ALYRLSALRYPLWVNAVG-
HSRVPRMLVLAWSLAVVTMLPQMFVWNEVQFNHITQCVT-----VWTEI INKEHALSESELRNMKLYS--
IQNAII IFYVPLMILVACYVLILKDIYKTLNTDTECSSAAYLSEMSSSKTGKATAHKKEQESFVTLTTRTV---RG--
QEKFRRAKVRSLRITLLLLILTYAVTWL PYNLLS WWMVLHFD S---
YKENLDSNYILNSLVVLSVINPFIYGRGCG-----
>gnrhr2_Caenorhabditis elegans [GenBank: CAB02736]
-----LGHVPSDYAQM LLYGIFALIGLPVNISTLIYMLKRYR-----
HAKSFLLLLHINLNISDILVGLYVPLIGLWLVLT---LEWRGGA-----
YLCKFMRFVDAFVFAISSNIMVCI ALYRLSALRYPLWVNAVG-
HSRVPRMLILAWALAVVTMLPQMLVWNEVQFSNITQCVT-----VWTEI INKREKLSESELRNMKLYS--
IQNATI IFYIPLMILVACYVLILKDIYKTLNTDTECSSAAYLSEMSSSKTGKKAALHKKDQESFVTLTTRTV---RG--
QEKFRRAKVRSLRITLLLLILTYAVTWL PYNLLS WWMVLHWDS---
YRENLDSNYILNSLVVLSVINPFIYGRGCG-----
>rhodlk_Anopheles gambiae [GenBank: EAA01405]
----QFPPMNPLWHSILGFAIFMLGMISMTGNGCVMI FTNTKS-----
LRTPSNLLVVNLA FSDFFMMFTMGPPMVINCWH---ETWTFGP-----
FACELYAMLGSLFGCASIWMTMIAFD RYNVIVKGLAGKPMTN-
NGALLRILGVVWFALFWTLAPLFGWNRYP EGNMT-----ACGTDY--LTQT--WLSRSYI--
I IYAI FVYWLPLLTIIYSYTFILKAVSAHEKNMREQAKKMNVASLRTQEAQNT-----
-
STEMKLAKVALVTISLWF-----

>rhodlk_Culex pipens [GenBank: AAP56248]
----QFPPMNPLWHSILGFAIFCLGMVSMIGNGCVISIFTSTPS-----
LKAPS NLLVVNLA FSDFLMMFTMGPPMVINCWH---QTWVFGP-----
FACELYACLGSLFGCTS IWMTMLIAFD RYNVIMKGLAAKPMTN-

SGAKIKILGVWAFSLFWTLAPFFGWNRYVPEGNMT-----ACGTDY--LTQT--WLSRSYI--
LIYAI FVYWLPLLLTI IYSYTFILKAVSAHEEQMREQAQKKNVASLRSSSEAQQT-----
-SAEIKLAKVALVTISLWFMARTPYLVINFTGIFKAAP-----
ISPLATIWGS LFAKANAVYNP IYVYGIGHPKYRA-----
>rhodlk_Rana_castesbeiana [GenBank: BAA76864]
----QSHLGT PGMFMSAFMLFTIIFGFPLNVLTVICTIKY-----KKLRSHLNYILVNLAVANLIVICFGS-
TTAFYSFSQ--MYFALGT-----
LACKIEGFTATLGGMVS LWSLAVVAFERFLVICKPMGSFTFR-
ENHAILGCI FTWVIGLVAAS PPLLGWSRYIPEGLQCS-----CGPDW--YTVNNKWNNESYV--
IFIFCFCFGFPLAVIVFSYGRLLLT LHAVAKQ-----QEQSAST-----
QKAEREVTRMVIMMIAGFLVCWLPYASFALWAVTHRG----
ETFDLRMASIPSVFSKASTVYNPFIYIFMNRQFRS-----
>rhodlk_Homo_sapiens [GenBank: AAX37093]
-----AFLPLGLKVTIVGLYLAVCVGGLLGNCLVMYVILRHTK-----
MKTATNIYIFNLALADTLVLLTLPFQGTDILLG----FWPFGN-----
ALCKTVIAIDYNNMFTSTFTLTAMSVDRYVAICHPIRALDVRTSSKAQAVNVAIWALASVVGVPVAIMGSAQVEDEEI-----
-----ECLVEIP---TPQDYWGPVFA--ICIFLFSFIVPVLVIVSVCYSLMIRRLR-----
GVRLLSGSREK-----DRNLRRI TRLVLVVAVFVGCWTFVQVFLAQGLGVQ--
PSSETAVAILR FCTALGYVNSCLNP ILYAFLDENFKACFR-----
>vasr1a_Rattus_norvegicus [EMBL: Q5M8D1]
-----LAKLEIAVLAVIFVAVLGNSSVLLALHRTP-----
RKT SRMHLFIRHLSLADLAVAFFQVLPQLCWDIT---YRFRGPD-----
WLCRVVKHLQVFAMFASAYMLVVM TADRYIAVCHPLKTLQQPA-
RRSRLMIATSWVLSFILSTPQYFIFSVIEIEVNNG-----TKTQDCWATF-----IQPWGTRAYV--
TWMTSGVFVAPVVVLGTCYGFICYHIWRNIRGKTASSRHSKDGKSGEAVGPFHKGLLV-----
TPCVSSVKISIRAKIRTVKMTFVIVSAYILCWAPFFIVQMWSVWDDNFIV-
T DSENPSITITALLASLNSCCNPWIYMFSGHLLQDCVQSF-----
>akhr_Apis_mellifera [GenBank: NP_001035354]
---LPIDMRFNEGHI VSI VFSVLMII SAIGNTTVLILITCRKR-----
VSKSRIHIMLMLAIADLLVTF LMMPLEIGWAIT--VSWKAGD-----
VMCRIMAFFRMFGLYLSSFVLCISMDRYYAVIKPLQLWDVD--
KRGKIMLSFAWIGSVVCSLPQTI VFHLETHPNVT-----WYSQCVTFN---AFPTYTHEITYS--
LFGMIMMYWFLPVVII YTYT SILL EIRRRSK-----KSEDDKIRRSSIGF-----
LTRAKIRTLKMTVII IAVFFICWTPYVMSLWYWIDR--
NSAYKIDQRIQKGLFLFACTNSCMNP IYVYGA FNIRD-----
>vasr1a_Microtus_ochrogaster [GenBank: AAD02821]
-----LAKLEIAVLAVIFVAVLGNSSVLLALHRTP-----
RKT SRMHLFIRHLSLADLAVAFFQVLPQLCWDIT---YRFRGPD-----
WLCRVVKHLQVFAMFASAYMLVVM TADRYIAVCHPLKTLQQPT-
RRSRLMIAASWVLSFLLSTPQYFIFSMIEIEVNNG-----TKTQDCWATF-----IQPWGTRAYV--
TWMTSGVFVVPVILGTCYGFICYHIWRNVRGKTAS-RQSKG---SGEDVAPFHKGLLV-----
TPCVSSVKTISR AKIRTVKMTFVIVTAYILCWAPFFIVQMWSVWDDNFIV-
T DSENPSITITALLASLNSCCNPWIYMFSGHLLQDCVQSF-----
>ghrhr_homosapiens [EMBL: Q02643]
YPVACPVPLELLAEE--
ESYFSTVKI IYTVGHSISIVALFVAITILVALRRLHCP RNYVHTQLFTTFILKAGAVFLKDAALFHSDDDTDHCSFST-----
-----VLCKVSVAAASHFATMTNF SWLLAEAVYLNCLLASTSPSSRRA----
FWWLVLGAWGLPVLF TGTWV SCKLAFED-----
IACWDLDDTSPYWWII KGP I VLSVGVNFGFLNI IRI LRKLEPAQGS LHT-----
-----QSQYWRLSKSTLFLIPLFGIHYIIFNFLPDNAGLGIRL-----
PLELGLGSFQGFIVAILYCFLNQEV RTEISR-----
>ghrhr_Gallus_gallus [EMBL: Q309X7]
YHIACPVEDEI PLEE--
QSYFSTIKI IYTVGYSLSITS LIIAVTVLMAFRRLRCPRNYIHIQLFFTFILKAI AIFIKDSVLFQEEDIDHCSFST-----
-----TECKISVVFCHYFMMTNFIWLLVEALYLNCLLLSSLSHGRRY----
FWWLVLFGWGFPTLFTFIWILAKFYFED-----
TACWDINQDSPYWWII KGP I IISVGVNFVLFINI IRI LKLDPRQINFNN-----
-----SSQYRRLSRSTLLLIPLFGTHYIVFNFLPEYTS LGIRL-----
YLELCIGSFQGFIVAILYCFLNQEVQTEIGR-----

>sctr_Homo_sapiens [EMBL: Q53T00]
PNLACGVNVNDSSNEKRHSYLLKLVKMYTVGYSSSLVMLLVALGILCAFRRLHCTRNYIHMHLFVVSFILRALS NFIKDAVLF S
SDDVTYCDAHR-----
AGCKLVMVLFQYICIMANYSWLLVEGLYLHTLLAISFFSERKY----
LQGFVAFGWGSPAIFVALWAIARHFLED-----
VGCWDINANASIIWIRGPVILSILINFIILFINILRILMRKLRTQETRGNE-----
-----VSHYKRLARSTLLLIPLFGIHYIVFAFSPE-DAMEIQL-----
FFELALGSFQGLVVAVLYCFLNGEVQLEEVQKKW-----
>calcr_Cavia_porcellus [EMBL: O08893]
NRTWSNYTLCNAFTPEKLNAYVLYLAIIVGHSSMSIITLVVSLGIFVYFRSLGCQRVTLHKNMFLTYILNSMIIIIHLVEVVP
NGELVRKDP-----
VSKILHFFHQYMMACNYFWMLCEGIYLTIVVSVFNEAKH----
LRWYLLGWGFPLVPTTIHAITRALYFN-----DNCW-
ISVDTHLLYIIHGPMVALVNVFFFLNIVRVLVTKMR--
ETHEAE-----
SYMYLKAVKATMILVPLLGIQFVVFPWRPSNKVLGKIYD-----
YFMHSLIHFGQFFVATIYCFCNNEVQTLKRQWAQFKIQW
>calcr_Mus_musculus [EMBL: Q60755]
NRTWSNYTLCNAFTSEKLNAYVLYLALVGHSSLSIAALVASMLIFWIFKNLSCQRVTLHKKHMFLTYILNSIIIIHLVEVVP
NGDLVRRDPMHIFHHNTHMWTMQWELSPPLPLCAHEGKMDPHASEVISCKVLHFLHQYMMSCNYFWMLCEGIYLTIVMAVF
TDEQR----LRWYLLGWGFPIVPTTIHAITRALYFN-----DNCW-
LSAETHLLYIIHGPMVALVNVFFFLNIVRVLVTKMR--
QTHEAE-----
SYMYLKAVKATMVLVPLLGIQFVVFPWRPSNKVLGKIYD-----
YLMHSLIHFGQFFVATIYCFCNHEVQTLKRQWTQFKIQW
>rhod_Camponotus_abdominalis [EMBL: Q17292]
----QFPPMNPPLWHALLGFVIGVLGVISVIGNGMVIYIFTTTKS-----
LRTPSNLLVVNLAISDFLMMCLMSPAMVINCYY---ETWVLGP-----
LFCELYGLAGSLFGCASIWMTMIAFDRYNVIVKGLSAKPMTI-
NGALIRILTIWFFTLAWTIAPMFGWNRYPVEGNMT-----ACGTDY--LTKD--LFSRSYI--
LIYSIFVYFTPLFLIIYSYFFIIQAVAAHEKNMREQAKKMNVASLRSANQST-----
-SAECKLAKVALMTISLWFMAWTPYLVINYSGIFETTK-----
ISPLFTIWGSLFAKANAVYNPIVYGISHPKYRA-----
>rhod_Procambarus_clarkii [EMBL: P35356]
----QYPPMNPMMYPLLLIFMLFTGILCLAGNFVTIWFVFMNTKS-----
LRTPANLLVVNLAMSDFLMMFTMFPMMVTCYY---HTWTLGP-----
TFCQVYAFGLNLCGCASIWMTVFITFDRYNVIVKGVAGEPLST-
KKASLWILTIVVLSITWCIAFFFGWNRYPVEGNLT-----GCGTDY--LSED--ILSRSYL--
YDYSTWVYLLPLP-
IYCYVSIKAVAAHEKGMRDQAKKMGIKSLRNEEAQKT-----
SAECLAKIAMTTVALWFIAWTPYLLINWVGMFARSY-----
LSPVYTIWGYVFAKANAVYNPIVYAISHPKYRA-----
>rhod_Alligator_mississippiensis [EMBL: P52202]
----QYLAEPWKYSALAAAYMFMLIILGFPINFLTLYVTVQH-----KKLRSPLNYILLNLAVADLFMV-
LGGFTTTLTYTSMN--GYFVFGV-----
TGCYFEGFFATLGGEEVALWCLVVLAIERYIVVCKPMSNFRFG-
ENHAIMGVVFTWIMALTCAAPPLVGWSRYIPEGMQCS-----CGVDY--YTLKPEVNNESFV--
IYMFVVHFAIPLAVIFFCYGRLVCTVKEAAAQ-----QQESATT-----
QKAEKEVTRMVIIMVVSFLICWVPYASVAFYIFSNQG----
SDFGPVFMTIPAFFAKSSAIYNPVIYIVMKNQFRN-----
>rhod_Astyanax_fasciatus [EMBL: P41590]
----QYLLAPPWAYACLAAYMFLLILVGFVFNFLTLYVTIEH-----KKLRTPLNYILLNLAVADLFMV-
FGGFTTMTYTSLN--GYFVFGV-----
LGCNLEGFFATFGGINSWCLVVLVLSIERWVVVCKPMSNFRFG-
ENHAIMGVVFTWFMALACTVPPPLVGWSRYIPEGMQCS-----CGIDY--YTRAEGFNNESEFV--
IYMFVVHFLTPLFVITFCYGRLVCTVKEAAAQ-----QQESETT-----
QRAEREVTRMVIIMFIAYLVCWLPYASVSWWIFTNQG----
SEFGPIFMTVPAFFAKSSSIYNPVIYICLNKQFRH-----
>rhod_Caluumys_philander [EMBL: Q6W3E1]

---QYYLAEPWQFSCLAAYMFMLIVLGFPINFLTLYVTIQH-----KKLRTPLNYILLNLAIADLFMV-
FGGFTTTTLYTSLH--GYFVFGP-----
TGCDLEGFFATLGGEIALWSLVLAIERYIVVCKPMSNFRFG-
ENHAIMGVAFTWVMALACAAPPLVGSRYIPEGMQCS-----CGIDY--YTLKPEVNNESFV--
IYMFVVHFTIPMVVIFFCYQGLVFTVKEAAAQ-----QQESATT-----
QKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIF'THQG----
SNFGPILMTLPAFFAKTSAVYNPVIYIMLNKQFRT-----
>gnrhr1_Cavia_porcellus [EMBL: Q8CH60]
---QGALPTLTLGKIRVTVTFFLFLVSTTLNASFLLKQKWTQKKEKG-
KKLSRMKVLLKHLTLANLLETIVMPLDGMWNIT---VQWYAGE-----
LLCKILSYLKLFSMYAPAFMMVVISLDRSMAITRPLPVQSNR--
KLEQSMTGLAWGLSSVLAGPQLYIFKMIHLENGPGQ-----TEVFSQCVTHC---SFPQWWHQAFYN--
FFTFICLFIIPLLIMLICNAKIIFTLTQVLQO-----DSNKLQLNQSKNN-----
IPRARLRTLKMTVAFAASFIVCWTPYYVVLGLWYWFDPGMLH--
RMSEPVNHFFFLFAFLNPCFDPLIYGYFSL-----
>gnrhr1_Mus_musculus [EMBL: Q01776]
---QGKLPRTLTVSGKIRVTVTFFLFLSSTAFNASFLLKQKWTQKRKKG-
KKLSRMKVLLKHLTLANLLETIVMPLDGMWNIT---VQWYAGE-----
FLCKVLSYLKLFSMYAPAFMMVVISLDRSLAITQPLAVQSNS--
KLEQSMISLAWILSIVFAGPQLYIFRMIYLDGSG-----PTVFSQCVTHC---SFPQWWHQAFYN--
FFTFGCLFIIPLLIMLICNAKIIIFALTRVLHQ-----DPRKLQLNQSKNN-----
IPRARLRTLKMTVAFATSFVVCWTPYYVVLGIWYWFDPPEMLN--
RVSEPVNHFFFLFAFLNPCFDPLIYGYFSL-----
>gnrhr1_Trichosurus_vulpecula [EMBL: Q9TTI8]
---HRDLPTLTLGKIRVMVTFFLFLVSTAFNASFLMKLQRQTQKKEEV-
KKLTRMKVLLKHLTLANLLETIVMPLDGIWNVT---VQWYAGE-----
FLCKALSYLKLFSMYAPAFMMVVISLDRFLAITRPLAVKSN--
KVGQSLIAVAWFLSIVLAGPQLYIFRMIYVEDISGQ-----TGNFSQCVTHC---SFPEWWQEAFYN--
LLTFSCFLFIGPLLIMLVCNAKIIFTLTQVLHQ-----DPHELQLNRSKNN-----
IPRARLRTLKMTVAFATLFTICWTPYYVVLGIWYWFDPPEMLN--
RVSDPVNHFFFLFGLLNPCFDPLIYGYFSL-----
>gnrhrII_Callithrix_jacchus [EMBL: Q95MG6]
-VEGSELPTFSTAACKVRVGTIVLTVSSAGGNLAVLWSVTRPQPSQ----
LRPSPVRRFLFAHLAAADLLVTVFVMPLDATWNIT---VQWLAGD-----
IACRTLMFLKLMAMYAAAFPPVIGLDRQAAVLNPLGSRSGV--RK---
LLGAAWGLSFLALPQLFLFHTVHRAGPV-----PFTQCATKG---SFKARWQETTYN--
LFTFCCLFLLPLTAMATCYSRIVLGVSSPRTRKG---SHAPAGEFALRRSFDN-----
RPRVRLRALRLALLVLLTFILCWTPYYLLGLWYWFSPSMLS--
EVPSSLSHILFLFGLLNAPLDPLLYGAFTLGCRR-----
>gnrhr3_Tetraodon_nigroviridis [EMBL: Q3LG36]
--DALQLPTFSTAACKVRVITFSLCAVSVCNLVVLWAAGNG---G----
KRKSHVRILIMNLTVADLLVTFVMPVDAVWNIT---VQWQAGD-----
AACRLLMFLKLVAMYSCAFVTVVISLDRQSAIILNPLGISEAK--
RKSKITLAVAWTMSVLSLPQMFIFHNVTITVPE-----NFTQCTTHG---SFVQHWQETLYN--
MFTFACLFLLPLIIMIFCYTRILVEISSRMAR-----NNLSRDVHLRRSHNN-----
IPKARMRTLKMSIVIVTSFIVCWTPYYLLGLWYWLFPEKME-
ETVSHSLTHMLFIFGLFNACLDPITYGLFTVRLHQGLKR-----
>gnrhr2_Gallus_gallus [EMBL: Q5EFE0]
AEEPLLLPTFSPAAQARVAATFVLFVLSAGCNVAVLRAAGGRR--G----
GGRSHIRVLLRHLAAADLLVTVVMPLDIWNIT---LQWRAGD-----
LACRLLMYLRLLAMYASAFVTVVISLDRQAAIILRPLAIARAR--
CRNRAMLRAAWMLSAALAVPQLFLFHTVTLHAPH-----NFTQCTTHG---SFPQWHETLYN--
MLSFSCFLFLLPLLIMVCCYTRILLEISRRMGS-----SLFSSRDVPLRCSGSN-----
IPRARLRTLKMSLVIVSSFILCWTPYYLLGLWYWFPCPRAMQ-
QKVPPSLSHILFIFGLFNACLDPITYGLFTIPFRRRCGCP-----
>vasr2_Mus_musculus [EMBL: Q3SWS4]
-----LVRAELALLSTIFVAVALSNGLVLGALIRRGR-----
RGRWAPMHVFISHLCLADLAVALFQVLPQLAWDAT---DRFHGPD-----
ALCRAVKYLQVMGYASSYMIAMTLDRHRAICRPMLAYRHGGGARWNRPVLVAVAFSLLLSLPQLFIFAQRDVGNGS-----

-----GVFDCWARF-----AEPWGLRAYV--
TWIALMVFVAPALGIAACQVLIFREIHASLVPGPSEERAGRRRR---GHRTGSPSEG-----
AHVSAAMAKTVRMTLDPPLCCSCCWLALTAVPTPGSMLPS-----
VAVSPRSCVACFAVLRGTPHTAWVLKMSF-----