

Supplemental file 3

>BminOR2a [gene=OR2a] [protein=odorant receptor 2a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi006479] [locus=Contig1933:2179906:2186009:-
len:1191 odorant receptor 2a]

MSLKINSWDAFKYHWCVWDLSGFRGPQKQSTWYIPYKLYTIAITLLFPIYYPTCFTVESLL
ADNLNDFCEVIYIAMADVTLNIKFLTLFIVRQQLELRPILKHLDAARARTEEEIGVLQDGID
SAKKCFLIILRLFYSAFVTSQLMVIFSVEARLMYPAWYPFDYQASRTKFWIAYGYQTIGFLV
QCTQACSVDTYPQAYMRVLTAHIRALSLRVERIGRKNFSYASSELMCLTKDEMKNRYDEL
VSSIKDHKTIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVGFNISIMLNMAVFFVSV
TMETLILCYYGDLFCQECEGLSKAIYN CNWTVQSTEFKNALSFFLLRSQRVNILMAGNWI
PVKLPFTFVMLIIIEVMSLLIDDYNKIE*

>BminOR7a1 [gene=OR7a1] [protein=odorant receptor 7a1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi005185] [locus=Contig1665:830963:832327:+
len:1191 odorant receptor 7a1]

MFELITGRGIGIASSKDAFIYFFKGCTIVGLSPPKNSGLLYMWSFSVNAICIIISPITGPVGF
VIKYLQNTITTQFLSGLQAALNLIGLPVKCSTVTHALKRLRGIEPTLTIMDARYTRPEDVA
LIRKAALMGNRLVFFFGTSYFMYMLFTVIPPLINGKAPLSVWIPFFDEHQSRHICVQIVYD
LFTMFFVLFHQSLYDSYGSVYIYVISTHLQLLVRRVGRLGTDATKSQDDNMKELVDCVVT
HQQILELLATIEPISTTMFTQFLIISSILCVTMVNMFFFADRSTQLASTLYFLCVLLQTSPCC
YFATELKADSEQLPLAIFHCNWVEQDQHFRKVILYFMHHAQLSIELMAMQLFPINVATNIS
LAKFSFTLFTFIKEMGIGQNAKN*

>BminOR7a2 [gene=OR7a2] [protein=odorant receptor 7a2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi008156] [locus=Contig2615:374025:384926:-
len:1194 odorant receptor 7a2]

MFDLIKGRRRTVFASRDAVIYLFNSFRYVGFNPPAKYRLPYFLYSAIITFFAVLFSPVIFNVG
WLRDRNKL SVMEILTCVQASLNVMAVPLKCIALAMAMNRLRGIEPMVTELDERYTTPED
RAKIKQCAVTGNRLVFGFAVSIFYETLTVISALVGGHAPLSLWIPNVDWHRSTWEYWLQ
VSFDAAVLFFILYHQVLNDSYPAVYIYIIRTQIQLLTSRVEKLGYYDDQKSADENYQELSECIV
IHQKILKIVKIVESVVSITVFTQFLVAAAILGVTMINIFIFADLTTKIASVTYFFCVLLQTSPTC
YHASYLLADCDLRIAIFQC NWIAQNKRFNNLLIYFLHRSQDSIPFFALKLPINLATNLSTS
FREGY*

>BminOR10a [gene=OR10a] [protein=odorant receptor 10a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi009555] [locus=Contig5068:234314:237294:-
len:1065 odorant receptor 10a]

MNFRFLSRTFSLHDYYFYVPKLCLGALGFWPLDTSEPNASNVWAWMNLIILTIGVFTEIHA
GCSALRTDLELALDTLCPAGTSAVTLLKMALIIYYRKDLAWVLKRMRGFMYTRDVSINT
VKEHIVRAHAVMAARLNFIPFVMGFITCTSYNLKPLLMTLILYVQGQPEPMWKL PFMNTAS
ALFHYSMP SFLQAPYFPLTYIFTSYTG YITIFMYGGCDAFYFEFCSNIAALLELLQNDL KSI
ISFGEGLIKTFKFPSQSVQLATVAFGCDWLACNPRLRRYVLMILRSHRAINMAVPFFAPSLV
TFTSILQTSVDHDLPLGSKKSERCSNEQVEAKDGEEVEKEKKRKKVEN*

>BminOR22c [gene=OR22c] [protein=odorant receptor 22c] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi009742] [locus=Contig5835:1170:16990:+ len:1236
odorant receptor 22c]

MRRLLGSEVPIERSFFRIPRFSARIAGFWPLSFDRPLSWLTALRFCVNTFAVAVGGFGEVSY

GFVYLHDLFGALEAFCPGITKVISLLKMTVFFVRRKRWIHVINSMRQLLLLDISAEKRRIVE
PLASFASLLSFVLLLSGSVTNTFFNTLPLLKMGYWKQSLEAELLFPFNVLPEMLPIAILPS
HIPGADALRRHDCFSLLVRSMVSSSALARLSRLAVCFLLVFCCQWSTQRCAKYADTASL
WRWLVERHNKIIDLCSDFALEFYSSDAFLFRHRWCCASQHFGLMLNSASVGVLTIFYYSI
AALTQLFLYCIGGTIVSESSLKVAEVIYDIDWYKCDVRTRRMLLMMICRAQKAKTIQVPF
FTPSLPAFRSARKSIIDQISPKRCERNQSTLIRAKHEEEEEAVE*

>BminOR24a [gene=OR24a] [protein=odorant receptor 24a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi010522] [locus=Contig7932:8746:10806:+ len:1179
odorant receptor 24a]

MLLKFLTQSYPTKNIPLRLALRIIGFYPEESSRRRQAFLIFNWVILVYGCYAEFMFGIQN
LSIDVVRALDALCPVASSIMSVVKVTFWLWYHRAELNRLIKRVTELNAAQDSPKLSAYKHR
YFATATRLSASLLFFGFITATLYGTRAGMINYLSYLRKDEIPFETPFKMIIPKSLLSMPLFPLTF
ILSLWHGYITIAGFAGTDGLFLCFCMYIGTLLKALQYDMKDLLSDVHSGVCKSSAEYEIKE
SLKMIIARHNEIIDLVKRFSAVMSGVILGHFVTSSAIIGTGVLDMLLFSYGVFVYLLHTMT
VTTELYLYCIGGTVVIECSSQLATAAYDSHWYTHSVEVQKMVLLIILRAQRSLVIKVPFFAP
SLSVLTSVSKQLRLCTVF*

>BminOR33ab1-1 [gene=OR33ab1-1] [protein=odorant receptor 33ab1-1] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi000272] [locus=Contig1018:631231:632461:-
len:1170 odorant receptor 33ab1-1]

MGKKLLVVKSSVNTPVDTVACFDIFWMCWKLMSGISINSNKWYVTLYDIVVNIFVTIFYPIH
LTVGLFLVPVLSDFKNLAIITDVACSTKHLYLFRYKLSKIREIQRLLKELDDRVAQDERD
YFNKSIRSAVRRMMLIFCVSYAGDTLASALEVLAKKDRELMYPAWFPFDWSANRYTYA
AVIYQIVGVSLQITQNLAHDTFAPVSLCVMMSGQVRLAMRVSKVGYDESKTLAEHEEELN
ECIEDHKKLLRIFDLLQDVFWYTQLVQFSSVGLNICLTVVFLQFADNIFAYLYYTAYFISM
ALELLPACYYGSKMQEEFQDLPYAIFKSNWIAQRKSFQQNLRIFTELSKKQLTPTAGGIINI
HLTSFVATCKMAYSLYTVLMNMK*

>BminOR33ab1-2 [gene=OR33ab1-2] [protein=odorant receptor 33ab1-2] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi000270] [locus=Contig1018:624095:625322:-
len:1155 odorant receptor 33ab1-2]

MAGSNQVLQSVDSVVLYRAFWLCWHAVGISTAYNKYFCGLYNLLINVLVTIFYPIHLFLGL
FLNPTPADLFQNLISITITCFICSIKHILLRRKLPIHTVQVLLAELDKRVEGADEHAYFQQQ
LVVGAKNVVKLFSIAYGGANMAAISATLLSKERRLLYPAWLPFRWEASTFNYCAAVIYQIA
GVTIQIVQNLANDIYPPMSLCIIAGHVHLLALRVAKVGEDAKKSMKQHNQALIRCIEDHK
KLVRIFELTQDTLSQAELAQFISSGLNMCIVLFYLIIFYVDNVFAYIYYAVYFVSMAIELLPSC
FYGSMLIYEFQQLPSAIFKCSWLQGSREFYQNRIFVQVSLKKIVPLAGGVIGIQLNSFLGT
CKMAYSLYTVCNRMK*

>BminOR33ab2 [gene=OR33ab2] [protein=odorant receptor 33ab2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi000271] [locus=Contig1018:628126:630717:+
len:1959 odorant receptor 33ab2]

MAIGISVACTAKHMLRPKLHKIIFVNDILHKLDRRVQTDEDMRYYLKKMRDNCIFMIH
FFTVVYFVSVAIMAVLSALWTGNILYPAYVVDWHGSTWKYLLVMLFQIYGLNMQIVQNLT
NDTYGPMILCLLSGHVHLLSRRILRIGHDSETDLDRNYEELVLCIDDYKVLMRIVERIISCS
YVVQFTAVGVNVVGLIYLLFFADNLFAYCYVVFHILAIMIEIFCCYYGSMVQAEFHALS
YAFRSNWLSQSRTFRRTAVTFTELSLKDVTWVAGGMMKIHLDSFFKTCKMGYSIFTGKH

TKHLRLIYDILMNTYITFGFPAHLVLGIIFSTNQEQQFINLVIGIASVSCVFKHLLLRFRMRE
MQSVNEIFAQLDDRVRTNEDYDYYKRLIERPCNFMVNFFTRCYFAVSITALTMALVTGELL
YPAYIPLQWRTSVFKYAVGILFQFAGVTLQIVQNIANDAYGPVVICMLSGHVHLLANRVSR
VGHNNAESVEDSYRELSCIEDHKLLMSTTTKVERIVSASYLVQFVGVGINICIGLIYLLFF
ADNYFAYVYYTIHIIAIMIELFPCCYYGSMLECEFHDLSSYAIFSSNWPTQPRLFRRNIVNFTE
FTLREVTMYAGGMIRINLDSFFATCKMGYSFFTQVISMK*

>BminOR35a [gene=OR35a] [protein=odorant receptor 35a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi002525] [locus=Contig1301:1915483:1918074:-
len:1254 odorant receptor 35a]

MDYFVPLQFDNRPVKLPIQVTGYKFNFLWPLKEDANILSRLVHNICLSVSVLCYIGTILGES
TFISENISNIPAVAECLCTSMGVQYIIRIFVLLRRQRPLRKLLQNFYRDIYFTYADDAALCK
EINTVIRFMKMFTQFYVPMMLILILYVYDVASIGLASPHKPFYRMSFRWYDAQAPQQFII
TAIYSGWLTISTVTLTWTAEDYTLCLVLCHASFRYKKLRLDLQQLLEMARADLKSGETRCT
NRNLHTAFRRRLCEIFQRQQLLNGFVAEAKAHFTYQIFYVMFFGVLLLCVVSFQFQNAIPIT
VDSSKYISWLISQTAQFLIGYFGQMLMDETTELNRNSFYCCRWEDLLVHGDPHSNKLLLS
DVKFAIMNSQEPIVLDGMKFFPLTYSTVSVALSASVSYFMFLNTMNGEN*

>BminOR43a [gene=OR43a] [protein=odorant receptor 43a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi005218] [locus=Contig1679:27013:31484:+ len:1146
odorant receptor 43a]

MSTAVEDNPLLSVNVRLWKFLSVLFARDWRRCVAFVAPVGLMNAMQFVYLYQQWGDLA
TFILNTFFAVSVFNALLRTCFIKNRDKFEALMRELVTLYDIIQDSGDDYAKSVLAAATKSAR
NISIFNLSASFSDLVVAMAYPLFRQQRVHPFGVALPGIDVTHSPLYEIIYIGQLSFPFTLSSMY
MPYVSLFATFAMFGKATLQILQNDLKNLCDNMKSKTEEELFELLRTNIAHARIARYVSDF
NELVTYLVLIEFLLFSCVICSLFCINIVSKTTSTAEKISIVMYIGTMLYVLFTYYWQANGVL
EMSLLVSDAAYEMQWYKCSRRFKRTLIFIGRTQKPLQIRVGQMYPMTMEVFQSLNNTSY
SYFTLLHNLYND*

>BminOR45a1 [gene=OR45a1] [protein=odorant receptor 45a1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi003431] [locus=Contig1360:740860:742322:+
len:1173 odorant receptor 45a1]

MFKSGLNIKGYFHLQKFTFHRLGIDITTRSAHVTRIYLLILQIVALATILISMASYSWQHIQDI
GEVTNAMTPFMQATITLWKIWLVIYRRREMAEIVENIYLISAKASTKELTHLIQENNRERL
MNTAYYYSVLNTGMLALTAPVLVSFIQYLRLGEFSYILVLKATYPIDYARPLNYFLIWLWS
AVSIYGVYIGSVSVDLSYSWYIHNLVGNFKILQSKLVSAESTADLSERRTHIYYCIAHQRII
AMTEQLNLIYQPIVFVQFSLNALQICFLAYQIGSGVVATVDLPFLFLFMISVGIQLMIYSYG
GQHLQNESVNVSKSIYQTINSSAWPIDLRKVLLISMRAQKPSKLTGIFFDVDLPLFLWVW
RTAGSYVTLLRSVDQKNL*

>BminOR45a3 [gene=OR45a3] [protein=odorant receptor 45a3] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi003430] [locus=Contig1360:734108:735637:-
len:1167 odorant receptor 45a3]

MYKYLRIPYFSFRVIGINLWAQQDQRITSAPCRYYSWTLATAIIILMGFYIYTSDDQDKAIQV
LTVFLQGVLCIIKSGMFVAKGRRFIKLIRNLDALADAATVKEWSEWRHENDWQQCIVRVY
YICCTSTGTLYCTVPAVILLYSQCFREHTVFILPFDAAPLDTGHLFFYTVSYLWCISFIIYAIH
AITAMDSLFCWFIFNISAHFRTLQHELQNVAKTSADVEDSACLHSKITETLHYHRRRIELSA
EFDELYAPIVFIEISVSYLKLCFSAYNLINLGDISGLPVIAVGLVTITFQLCNYCFSGEKLKSVS

KVVS DRIYLA FSWERVPPPLRRL LILPLMRAQRATNLTGFLFVVDHSLLVWIFKTTGSIIGFL
SATKSENTTS*

>BminOR46a [gene=OR46a] [protein=odorant receptor 46a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi004385] [locus=Contig1553:1964416:1965652:+
len:1236 odorant receptor 46a]

MVSPQQSTTPEIDEYLLGLFGLPKHYSSFWHYMYKLYFWHVAIFWMLIFDISMWIKIIGNIS
NLNEIHKVFYLC SMAIAVMAKFMRIHLKNNSYVEIFARMHDDDLLPVNVSELEKLAQSSH
LSCRVRNYYTYLSLTSLTLIFVTKLISEPDELPLSIYIPISVESFWRYLIAYL FQFIGLSLCCLL
NISFDSL SASFFIY LKGQLDILAYRLENIGTNLDVDDNMINLQLRYCIQHYVKVRKITENME
DLLSIPMFVQMISSVLVLVANFYAMTFLTDTSDYVTFIKFLVYQLSMLSQIFMLCYLANEVS
LRS AELSYSLYSSEWTRCSKMNQRLMLLMAAQFGVPIRIKTVNRCYSFNLPAFTSKKKPK
ESSSKEQEDSTEHQSRNVINSTELETRKICSSDLTGIEFVK

>BminOR47b [gene=OR47b] [protein=odorant receptor 47b] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi004946] [locus=Contig1639:505520:508387:-
len:1281 odorant receptor 47b]

MISLSSKATIDNSISSHNSYLTNKS YTHLKHTASKLQ TILAPYRVLKEMLR YGEAVHPPHTC
LFYFRAYIRLLGLWPTERTAENPLY YFYNV LIMILFSFFMLYLIFFKMALFRMRNGETDIIISE
FDALHVQHANLLRDGPRNQ RILQWQRRFFFGEICFFSGFYILSLFLFAAMSLQPLLSQQTL P
FRCKFPFGLDDPDEHPMAFACVYFFQCCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCEN
IRHLGESAAAGTAGACSITSELV VWRELREAVEFHQKIIGLMNRINQTFYWNYSQMGASTF
MICLTAFEALLAQDKPMVAMKFQTYMFSAFMQLLYWCWMGNRTTYDSMEVATAAYDV
HAWYEHSPLLQRQIMFIIKRAQKPLEFRAKPLFGFTFASFTSILSTSYSYFALLRTMSD*

>BminOR49a [gene=OR49a] [protein=odorant receptor 49a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi002639] [locus=Contig1310:104546:106156:-
len:1185 odorant receptor 49a]

MDFVEFFWLPNALYRVVGYDFQQLARAHWRQTIMKAFLIFTTISGICTRIYMLFQLRELIL
SGDILNSFRLGVYISYAIDSNVKFFVFLN AQRLRVYIQSLSNEYPMTSIKRKVYQVDKYTF
KRAHLMIVAYLSVTNSILLGPMLQSIFVYIIDLSHYGYTVAAFSYLHPTPMSYNFN YCTPHY
YILYISEYLN GHFCTTTNLGTDLYVCTFAGQFCMQLEYLGYSLEIYEPSVKNSKTDCEFLI
EWIRKHQLMLNLCSELNEVFGTLLFKLISNCAVFCIIVVQLKLEGFGFGFLNFLSFFFVAVS
QFFMVCQYGQKLITISENLALCAYKNRWYNGSQTYKTLLFNIIARAQKPARLTAKGFQPIS
LATFQIVMTMTYRVFAVLQRALD*

>BminOR63a1-1 [gene=OR63a1-1] [protein=odorant receptor 63a1-1] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi004869] [locus=Contig1630:134511:137029:-
len:1248 odorant receptor 63a1-1]

MMMENAE EYKRN YNYIKVLIRVSFSLGVNLTAPSKIKDALKLISVILSVTSLLSMYGHCC
YLMRHLDRMPLIAEAVFTALQILMAAIKLIYFFFTHRTFYRLLDQTLTHEIIRKMEILQQDFP
INRQLKKEIDDIMNAVWRNIRRILLFYFFCCVGIIANYFFTALFQNL YHHLKQTPNYEFILPV
PSQYPFWEKKGMAFPYYHLQMYVTGSALYVSGLGAVSFEGVFMVLCQHAVGLVKVHNL
LVL RATSAQIPVERRLEYLRYTIFNYQRINKYMHEIQTIFRHISLSQFILSLIVIGFVLFEINYG
LGSNIIIFIRLIMYISASITQITIYCYHGQALTTVNEKIPLAYYNCN WYGENKTFKQLIMMMI
MRTNKEFYLEVSWFTLMNLATLISLIKASVSYYLLLQHFQEN*

>BminOR63a1-2 [gene=OR63a1-2] [protein=odorant receptor 63a1-2] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi004870] [locus=Contig1630:137870:141751:-

len:1260 odorant receptor 63a1-2]

MILENEEEIYKRNYNSSKVLFRVSFALGVNLTAPSKAKNTLKIVHVILIVSSILSLYAHWCYL
MRHFDSIPLIAEAVFTALQILMAAIKLIYFFFTHRTFYRLDQTLTHEIIRKIEILQQDFPINRQ
LKKEIDDIMNAVWRNIRRIFLFYFFCCVGIANYFFFTALFQONLYHHLKQTPNYEFILPVPALY
PFWEKKGMAFPYYHLQMYMTGSALYVSGLGAVSFEGVFMVLCQHAGLVKVHNLLVLR
ATSAQIPVERRLEYLRYTIFTYQRINKYMQEIQTIFRHISLSQFLLSLIVLGFVLFEINYGLQIF
KGSNIHIFIRLIMYISASITQITIYCYHGQALTTVNEKIPLAYYNCNWWYGENKTFKQLIMMMI
MRTNKEFYLEVSWFTLMNLATLISLIRASVSYLLQLQNFQEN*

>BminOR63a2 [gene=OR63a2] [protein=odorant receptor 63a2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi004730] [locus=Contig1608:3254925:3260579:++
len:1200 odorant receptor 63a2]

MYSIHERKELRVHNIWRIRELKRISYIIGINLNAQTKLKRSLRIINVLIIIFSCIALYPHWLMIK
QAQGDIPLIAETSTTALQTTTALIKMAYMLFNQHKFHKLLQKVETHDLLQRIEFLTGMPIK
PNLKREINAIMETNWKQTRRQLLFTIGTCICIMCNFFYALFKNLYNHLQGTPNYVYILPFT
GYPMFLDKGMASPYAMDMFFGACSLFAAGMSALSFGSFMVLCKHSCGLVQVVCLLL
LRSTSAMVPKPQRVEYLRVCIVQHQRTEFINDVNRLYRHICLSQFLHSLAIYGFVLFEMNF
GLESNKVTFIRMIMYLCAALTCDCQLQHVNGQFLANELEKIPLACYNCEWYHETDDFKKT
LKMIIMRSNKKFCFQISWFTVMSLATLMGVS*

>BminOR67c [gene=OR67c] [protein=odorant receptor 67c] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi008170] [locus=Contig2615:487416:491445:++
len:1215 odorant receptor 67c]

MLPEARTFSEFIYPIKVYQTIGEDIYHRSPGRVRRLLLKSLLYIGFFNFNHLHVLGEIVYFVK
ALNSFATILEATGVAPCIGFSFVADFKQIALTIHRGTLRKHLDQMEELFPKTAMQQVEYKLR
EHERAMRRVMYIFTLLCLAYTTTFSLYPALKASVQYWLLGAPVFERNFGEFAWYPYNATE
KTWVYWLTYMGQVHGAYLAGVAFLSADLILVASVTQLCMHFDNISRCLEEFSGASQKTS
AQEDLQYLQALVVKHAKCLELSEHVNSIFSLSLLNFLTASLTICFIGFQVTASSIEDIVKYII
FLTASLVQVFVVCYYGDELMTASMRIGDAAYNQNWFGCDRQYKWLLTIMIMRSQKPA
RAPTFPPISFRTYMKVISMSYQFFALLRTTYSKGKN*

>BminOR67d1 [gene=OR67d1] [protein=odorant receptor 67d1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi000893] [locus=Contig1067:243913:245328:++
len:1167 odorant receptor 67d1]

MTVKQIRPSDSFAKLIKMARLVSSLVGADVSTENYRVNIVTIIIVFCIIYFIFTATTVASVFSE
DWTYLLLEASCMVGSVLQGITKLISGIGRTTDVSGMRLELEDLYRRYESKGETYCRVLNER
CDRVWQVIKMGVGHYIGASVVGILLTTILVIKTNEKIYVMHFFIPGVDVETSFGYLLTTAVH
TVVFLAGAFGLFAGDLFFLIYLGQPELFRDILILKIKELNEAAQKDNKTEHLLINIIQWHQ
YYTDYNERCNEVFYIITMQIMTSVSICTMYIILMGDWPAYLYILIALCGLYLYCIHTN
IQTCNAAFFDELYNINWYELDVKRQKMMILMKSQNPSEIKIGGVLPVSVQTALQITKTIY
GIFTMMLGFLDEEQ*

>BminOR67d2 [gene=OR67d2] [protein=odorant receptor 67d2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi000894] [locus=Contig1067:247755:249223:-
len:1167 odorant receptor 67d2]

MAVKRVRPSESFAKIIKFFHLISSLVGADVSDENYRVNIVTIIIFCIVYFIFTGTTVASVFSEN
WTYLLLEASCMVGSVLQGITKLISAFAPAKEICGTRMELENLYREYEAKGDDYSEVLNKSC
ERVWQVIKMGVQMYLIAGAGIILITVVLIFASTEKVFLMHFLIPGIDVHTQAGYLITLAVHT

VCFLFGAFLFAGDLFFLLFLGQPMFLDLLALKVKSLNEAAAQKSKTAKRLLIDIIEWHQ
YYTDYNLRCNHMFYYINSMQIVTSGISIICTLYILLMGDWPGAYLYILIAFSGLYLYCIMGT
KIQTCNTAFCQELCNINFYDLEVKNQKMIVPILMKAQNPSEIKIGGFLPLSVQTALQITKTIY
GIFTMMLGFLEENQ*

>BminOR67d3 [gene=OR67d3] [protein=odorant receptor 67d3] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi001522] [locus=Contig1141:1873563:1874918:1874918:
len:1161 odorant receptor 67d3]

MQTETRPSDNFHKLLRIIRLSSSLIGVDIIDENYKFNYVVAFVLLAIAWNMCSIYTICKDLT
TDWTVLLDVFSPISCATQGVVKMCSLILYPKLYRELALDLEIYKKYQVVGPNYEAKLFE
WNKSMKKILIIGGLVYFVSALLALVTPLFLYIYKGERHLIIMCQMPYVDVATDHGYFITIGY
NVLCVFVAAFGLYGADLYVFLFLTHSIFFYDIFALKVGDHLHKILHENNKDKRIKSLINDITE
WHQYYLEFNDKCNVIFFWSTITAHVLCCTTLGILSTLLIIMLKYPGAYPYIFVCFVWLYMYC
ILGTRVEICIDQFCDGIYDINWYDLVDSDQKTVSLMLMESQVPRVITIAGIEPLSVNTALKIT
RSIYSLVMMVMQFNE*

>BminOR71a [gene=OR71a] [protein=odorant receptor 71a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi004512] [locus=Contig1553:5022464:5028175:5028175:
len:1047 odorant receptor 71a]

MAFDSMANFRTLTRLIILGLWHGGNGSWFERHYRYYQLFLHTTLTFTFTLLMCLEVIYSE
SLNYAIDVLKYMLCEMALVFKVLNAWYYARKISELMNEWQVSEIFALRTSDEKQMWQKT
QKNFHKLTMTYICTGFNSAMCALIGVLLMGASELPYALWMPKNWRETYFWGMYCYEFL
AMPFTCVCNITIDLFQAYLLLHLTLCYRVISMRLERLDNAGTDEAITKEFLNNIKMQQRVK
DENPVHCLAMLQYVLIVSLQMFLPCYYANELTVESEKLGHIHLYSCDWTGFLVDFSPAAPN
RSTAPSQRRSTFAIQRSAFEVQHAVGQIVHTTYNHMNFQFQDLWSLQY*

>BminOR74a1 [gene=OR74a1] [protein=odorant receptor 74a1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi008540] [locus=Contig3074:406405:440169:440169:
len:1461 odorant receptor 74a1]

MLYRPRLENGKLISLSWPIAAYRLLNNICWPLQDDATQLERLFDRLWAFGLIFMQHNDAL
ELRYIILNNNNLDEMLICGPTYLILVEIHLRAFQLGLKKNFAKRFQKQFYAEIYIDEVSHPKL
HGNMRKRLRPIWFYSFLYFGTLSSYVIMPLINYLNKVKAPLYKMYYPIDIMPNIYVAVVL
SNIWVGFTVITMVSGEDNVLSEVMIHLNGRFLLLQKLRQDAERLLHAADDRNIADLR
RIVEAIKENVRLYKFAEDFKLEFSFRLFVNLSFSAGLICVLGFKVYTTNEMSSTFYESNWEL
VILRSRDTKANVRLMKTLLLAISTNQKPFVLTGFNYFSVSLTAVLKQQLASTNNNIPMADL
VMAFSCDSFGNKCYIFSRELGLSTAIFNKVIARVANEVSIAEYNIRMEISNNIVRGINTFLIEE
SPHFADKFRPPYTHTHVHTVHSVQGTCHSFGAMKLSWRFTSDASSGIAAALAC*

>BminOR74a2 [gene=OR74a2] [protein=odorant receptor 74a2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi006486] [locus=Contig1934:70696:73794:73794:
len:1107 odorant receptor 74a2]

MRYLPISYHKPLLPNGRHPIDWQLYGFFCSNGWPLAAHITKTRYIVDILVTMMQFMSES
MVLIGEAVVMYDNLDNISFVCTVLAPNLILFEMMLRAYNIIYKRNSFRTHVEEFYKKIYIQ
RTWNPSELFEEKIRRHLPKYSTFTYIITLVTVYVYVPISGLVKNERLLPFPIKFGFDYTPWPR
YVVFLLAMSIWTGFAVVGPLIGEANMLAMQILHLNGRYSLLLQDLRKISRDSIAEHERCKD
KDNMLVTQRFRCRLFIIIRRNVELNDFAKSLQEYQYSFRVFMMAVSATLLCVLGLTATTD
ELSTSYCCDWEEVIFHSRDAEENKKIMKLIALAIHLNSKPFRLTGLNFSVVNYETVVS
LAFC*

>BminOR82a [gene=OR82a] [protein=odorant receptor 82a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi006911] [locus=Contig2103:127264:129844:-
len:879 odorant receptor 82a]

MMDYIIYHIDDLALATASLSIVFTNVLTVIKTSTFLTYKREFKSLMAEFERMYDESGAKRCL
VTNLVGA KR FVKLYFYSVSCTGLYFTIKPLVSMIWAKFQNKPLLELPMPMRFPDFESTP
GYQFAYVYTIFITIMVVMHAASVDGLFVLFTTNLRGHFVALQYFIETNTFDKSDALLQREL
RFYVQYHVRLLDLSQSVQHIFKPIIFGQFLMTSLQVIWALSCSAVGTA VQMSQWYNLPPRH
RHLRLMMLRSQREIIISAGFYEASLANFMSILKAAMSYITFIQSIE*

>BminOR83a1 [gene=OR83a1] [protein=odorant receptor 83a1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi011217] [locus=Contig900:6114563:6116706:+
len:1233 odorant receptor 83a1]

MSSNEEKKKSDYLTTVQQGCPLYGQRPDMFRLMRWNL CFAAMYRLPLERYFPACLRLLA
ITLDWTYELCLYSTMLHIDILFMYTLYLNKDKDDLELIVSCMIQTVIYTWAIVIKVFFKRVK
PKRVEELMRYLNEECQTRSAPGFTYVTMKESADLANKCSAVFLIWCYAGVICWLFVPIFN
QDRSLPLACWYPIDYKVPVVYEIVYFLQTVGQLQVASAFGCSSAFYLQVSVLFSGQFDVL
NCSLKNILATTYLILRKPESELILLREKQNIANYELNQQYNAKEHNSDFDCIAHLVDVKT PK
PKKFYEAFKIAFSPCVTQHLYILNGLKMLEELYSFLWFLKTIQVTMLICLVAFACVKRSPWY
LHSSEIKQDVLFFILNAQRPFRLTG GKMYNLNVEKFRSMDLRQPQ*

>BminOR83a2 [gene=OR83a2] [protein=odorant receptor 83a2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi011218] [locus=Contig900:6118081:6121777:+
len:999 odorant receptor 83a2]

MIPPSKRNIDTTERCANPNGCITNEKRCDLFVYVRWLLFSFAVRPIPFDKVLPPSMHGYSAL
INVVLEIFLHFSVIHIFVLFICTIYFN YDNGDLEFLISSGIQVLLYFWAIVIKVAFRHIYPELVD
GILDFVNEEYVLHSAVELRDKERIPDEYTNEFFVAKELPFDLDCLP HLLNTADTMRTSRFRE
AFKYAIEPCVKHHIFILNALRKLESLYNKIWLLKTIEVTFAMCMCAFHLVKSSNDTQFLQV
LCLGQYTVLGLLEIFMICYAGEIHYVNSQRCDEALLRSSWYPHLREVRADFLFLIHAQRSE
ELTAGKFNPLRLDKFRGVSS*

>BminOR85bc2 [gene=OR85bc2] [protein=odorant receptor 85bc2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi001695] [locus=Contig1207:1634762:1636675:+
len:993 odorant receptor 85bc2]

MENLEKFVRLANFFGNHIGMKPWGRLDGFQRRFLFYFSSINLLITFIAESSYIIVTITSDFILA
VMTLSYVTFIVVAYAKWYYLYTYQTERTAFFQRLETLPCTKSQQEAIKLSEYIRMNKLSTI
SYTISFLMCISTYTFYTIARQFIYTNLLHVPGTERNLPYQAVYPWDWRDNWYVVCYVSQ
GFAGWHSTCAQMAFDLMLCTLSTHLIMHYDHISRSLEGYQTKFAEIHGKNGLTQQARAA
MELKAVKDDIKFISSIVAYHTELLRFDW SHADIRFQKMTILVAERAQDPAALKATKLITISR
DTMTVIMQMSYKFFT VLR TMYGD*

>BminOR85d1 [gene=OR85d1] [protein=odorant receptor 85d1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi001692] [locus=Contig1207:1504148:1505546:-
len:975 odorant receptor 85d1]

MSNQPIHFESFNYLANIFYTSIGLYAYEQAGERTKDRAAYIRRQLLSIFSIIIVNMNIALLSQ
LMYIFLAFANNNNFVETTMLSSFVVFVIVSDFKIYNICRQRARISAMMQALHALYPQTLAE
QTKYKVQWQLQRYNRLAYAFV FYEMLVWGYNLFPLLNYLIYEVWLALRVVEKTL PYN
CWTPFDWHNNDWIYYHMYLMLSASGQACISGQLANDLLLSALAVQLIMHYRELARRIEA
HVAGRETSSDDSEYIRHAVYNHNWFDADMSYRKMLIFIMARAQKPSKLQATT FMTV SMS

TMTDVSNSKYIVSYNIFHMYSKI*

>BminOR85d2 [gene=OR85d2] [protein=odorant receptor 85d2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi001691] [locus=Contig1207:1498210:1500581:-
len:1263 odorant receptor 85d2]

MSTQIVEFDRFIKTANFWYSFNGIVAYDDIYRQPGDEPKRRSVQTRLATVLRQIFS FVSLAN
LTWVLIETLTFVVVNFVENADFLEAARNFTFMGFVIVAIKYLNLKQRSRLSVLMQKLYEI
YPKQSTDQRPYDLQSHLRHYRRIGFIYAFLYAFTVWAYNSLPMVNYLLAPLLQQT VYER
VLPYSCWVPFEWRDNWLYYPLYVSQALAGHEALAAAYLASDLLLCAAMVQLIMHFRKLA
RDIQAYQAGSSCTKQDVMAQQAQRDLSFLSTAVYYHNRTLALCQLINEIFGLPVLINFISTS
FVMCFLAFQFTVGVSFDDLIMLVFYMICSLVQIYMICSYGQELVTASENIGHVVYNHNWL
VTDIRYKLLIMIIERAQKPAILRATSFLNVSMGTITDLLQLSYKFYALIRTM YAR*

>BminOR85e [gene=OR85e] [protein=odorant receptor 85e] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi007558] [locus=Contig2333:492873:496795:+
len:984 odorant receptor 85e]

MDFSEQVESTLLYSHEDKPRIANLFVAQVTSFKVTGQIPFNVGYRLGYIYCFFVILQTLHM
GVLFLKTSYDMLLSGKLEQITDALMSIMFWSGVYATCYWFLRSQRLLAFLQRINEHYWH
HSLPGLSFVSWHRTFVLTKRLTTVWVLTCVVSTVSYGLAPLVMGVHALPLKCWYPFDPL
NEQATLPETDDDELNQYMYCREHLTNLSTLQHLYSQQPAVTFPEALHLAIGERSMVRILN
LVQYLTLTLIELLMFTYFGELLRRHSVRSGEAFWRSQWWTHAVAIRQDIFILLENSKRAVR
LTAGKFYAMDVDRLRSLISQQPIVG*

>BminOR88a [gene=OR88a] [protein=odorant receptor 88a] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi007186] [locus=Contig2177:57657:59015:+ len:1206
odorant receptor 88a]

MALQQERNGAAKVCAIDDLCAILHPAQRYLGLNYLNFRRVNGREFAIPRSKLLNIALFLAV
VDCTGNVIKCGKAINARDVTKAQEIFAVFGMGLVMTMRGLQLALNRDKLSKFYNDIDRIF
PRSENLQQHMEVEKVHNYIKRRFLLHTTLTVTVSAFLTMPAMKFLLFYDFESNDIVADEF
HVNPSWLPFGVKDKVTTYPIYIYEVILASAAVNMIVTWDEVFVVLISQLCMYYEYLGKL
LEEMKVQDAMDAKKINAFYKQLHDYIYMHQYLNNLAVDLNDLFNFSILFSDAGIAISICF
NLVLITDATDYLQMITYASPLFVEVWLIYDAAKWGTLLETVTARINEILYEQKWYDSSARF
GKYTMMWIQSTNEPFRLTAFNMFYVNMKHFQDVCSKCFL*

>BminOR94ab [gene=OR94ab] [protein=odorant receptor 94ab] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi011849] [locus=Contig953:283315:284727:+
len:1143 odorant receptor 94ab]

MRETSASVLGTRIGIARVLMRLLQILGLWPMWQARQSSSTSTRCRIWLTRYRYRYLLHAPL
TFTYNTLMWIEALTRWERADHILYISITEVGMMALTLNFWRLDKRAWHFMHELSDRL
ALRNKAERQWWRKQQRFFARVVVCYIGGGAGVLVTAFGATLHMSGYYLPYDYWLPFE
WHNAQNYWYAYGYEVIAMSLTCISNVTMDMILCYLFFHVALLYKLIGMRLMALQQLHEP
LAVQQLMNIIELHKRVKRLTAQCESLSVPILVQIVLSAFILCLCAYRLQSMQISENPGQFLA
MLQFASVLTQLIFLPCYFANEITINSDALTTCVYNSSWEEFSPSTRKQMNLYMELLKRPAHI
KAGNFFLVGLPVFTKVAAMI*

>BminORCO [gene=ORCO] [protein=odorant receptor coreceptor] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi011214] [locus=Contig900:6030904:6047567:+
len:1554 odorant receptor coreceptor]

MQPSKYVGLVADLMPNIRLMKYSGLFMHNFTGGSGLFKKIYSSIHLVLVLVQFLLILVNLA

MNAEEVNELSGNTITVLFFTHCITKFVYLAVSQKNFYRTLNIWNQANSHPLFAESDARYH
AIALAKMRKLFTLVMLTTVASAVAWTTITFFGESVKFALDKETNSTITVEIPRLPIKSFYPWN
AGAGMFYMFISFVFQCYLLFSMVHSNLCDFVFCSWLIFACEQLQHLKGIMKPLMELSASL
DTYRPNSAALFRSLSANSKSELINNEEKEHTDLDISGVYSSKADWGAQFRAPSTLQTFNG
MNGMNGTNPNGLTRKQEMMVRSIAIKYWVERHKHVRLVAAIGDITYGGALLHMLTSTI
MLTLLAYQATKITGVNVYAFTTVGYLGYALAQVFHFCIFGNRLIESSSVMEAAYSCHWY
DGSEEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASFAIEVCGFALFVAIMSGEGCARR
VAIWLWVSVHSGHSPLSQNLFFVAFALIYITNTVLL*

>BminOR1-1 [gene=OR1-1] [protein=odorant receptor OR1-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi010399] [locus=Contig760:1261200:1262805:-
len:957 odorant receptor OR1-1]

MGKLVSSRIFPSDPSKGKIGSIQYNVWLAQLFGVPVVLKAESPCLKIVLGIYGILITLV
VTFIYTGFEIYDMILCWPNLDSLTONICLSLTHIAGVLKLMAFYHGEFENKIPLTIYASLVGS
TGVLGIMYLLHSQIFPYRVKLPDWMLGTQLAYMGISVLVFALQIVADYLNVTMINQIRF
QLKILNLAFEELKLDCVNKKEHINLNKRLQTIVEHHCLLRDLRNDVEDLFRPLVLIQFFTS
LVIFAMTGFQAIVKAENSNGAALIYCYCGCIFCELFVYCWFGNEVSEQSKTLTSSGYSSH
LNRERLSQQA*

>BminOR2-1 [gene=OR2-1] [protein=odorant receptor OR2-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi012274] [locus=Contig982:348766:357197:+
len:1101 odorant receptor OR2-1]

MHPTRRHRWPYYIYSACINISLGIFLPATMIAKLFFIENLSQLIGLLYLGVTLTMATTKQWSL
WLHRSQLLAVHYLGLKDARCMRHAVDRQHILTAIRICHLYYAAYMFLYELSSSGFAYIGF
KLRQLVYDGWFPQFYADAAQNLTVTLIYQNFVMTFFVLQNVNNDMYPQCYLAILGHL
RALTARISRIGKDGVLNVDENIEELTNCVEDHKNLLGYFNCIRPVISRTIFIQAITAFVLC
AVNYVAFERDAAQKLIATYIFAVLIEALPCCWYVNSLMEECGELTTALYNQWYDQNRK
FRKMLIIFMQRSQHTMVL MAGDLVPITLQTFNLFLCLCVQSIYALCSDIYSIIYLILLVA

>BminOR3-1 [gene=OR3-1] [protein=odorant receptor OR3-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi001029] [locus=Contig1067:2655921:2657619:+
len:858 odorant receptor OR3-1]

MKRVGYFDQHRLASCLLTVPIFICVSSAYRTYIIRNDFDEVITISLFKISGAYVTTARSLIVMY
KAQEFLNFFDGIDRWYQELQCDGNEITLKKVHEFMRIVKKASKTILILTALTFYITVIQLL
ATADYEHKSISFGTFLIKDLQYKLESTTDMTELEALKCIKKCVKDHVMIKYHNDLEVLFS
SGSSVSVSIFGITPCVIIVFSTMVSSNRNLFLCYIFKFKFTIHLHLQDHMSLLIADIQLSLV
MISTFIFFWVANDFCCEVIWDYFPHIYNICYNL*

>BminOR3-2 [gene=OR3-2] [protein=odorant receptor OR3-2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi003768] [locus=Contig1403:591622:609321:+
len:1128 odorant receptor OR3-2]

MTSYQNMPLYSVNIKIFLKLGLIGSGARTMRVLLGLVLILTYSGQLINFCKTWNEDIGESG
MNFHVVALIMHSVVRFFVVLKKAKKFERFFQRTEQWFTDIEQNSDPGVVRMLQDVITHA
RKVTRIGFYTSIIGALCAYIYPFSFEERKFILDIDYFFFDKQTPFYEFFLLQALILVPVFIFV
YLPFANFLLMSLKFGVILMDLCTKLRNLSNQDEATQLRELKECISYHEKIIFRNDLEYLV
SIDGFFHIALFSLMLCMLLFFLSLVHDIRLILTALAFISFHIYIIGITYYYADNFSNESLKVAYA
AYDTPWYEGNSELRKCVQVMIARSHRPLEIKSGGLYPMTLENFQAILRISYSYFMSMLQG
FNQQ*

>BminOR4-1 [gene=OR4-1] [protein=odorant receptor OR4-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi006901] [locus=Contig2083:263072:268337:-
len:1068 odorant receptor OR4-1]

MMLFIVYDNLETLLDITEFILFWGFTLNAMMKGSTMILMRCEIESILKGLIVRHPKTEEERV
AFQLVPYFKTINASNKYLSMWHLSTISIFALHPMLASIYGYISREDENESFEFTLPFMMGY
YDTNRPLPYVITYFTQCCGAFYMSLLFLSGDLLVSLVHLVNMHFGYLIYRIESFQPTGTD
ADMKVLGPLMEYHNEILDYAERIDSTFSLATLLNYVGTCLVLCLIGLQIALGSEILNVFKFL
AFLISTIVQVFFVSYFGNNLKDLSTGISDAFYNHPWHDANYKYMRMLVIPIARAQRYAHLT
AFKFFEISMDSFKSYKELFGIEESGTSIATEDKTQNRKMFSFTMVNT*

>BminOR5-1 [gene=OR5-1] [protein=odorant receptor OR5-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi005394] [locus=Contig1697:2592421:2593658:++
len:1158 odorant receptor OR5-1]

MSFEEKPPGVKELFRTHWTVWKWLGQVTHPEYPKLHIAYTILLNISFSIGYPLHLLLGQLN
LKTMQDVLLNLTISVPVAVCTLKYFNIWRNLAKVRHLEQMFTLYARIDHPEEWIYYRKVI
IPYALKVLHLFYFICVGTAITSELTLLIMGFAYEWRLMYPAYFPFDPYATKAGYVTAHVQII
GLMVQLAENLVSDTYGGMCLTLLAGHANLLGQRVASIGYDERKTQEENNRELVDCCIHDHN
VLFDCHRTLGDIIIGFLFVQITSASLIMGVVIYVIFVGNAFEVYALFLFACIMEVFPTC
YYATYFEIEFEKLTYQMFCSCNWMDQNREFKRNLIVCVEQSLKTRYFRVGGMFRINLQIFFA
TCKGAYSVLAVALRLK*

>BminOR5-2 [gene=OR5-2] [protein=odorant receptor OR5-2] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi007381] [locus=Contig2236:327376:328608:-
len:1173 odorant receptor OR5-2]

MPATETTISGVSVFHFHDVTLQYLGLMPPTKKLYRYLYYVYSLVLNIIITVGYPTMLMIGLI
KSEKSDVFKNMSINFCSACSIKIFAFWWRLAEVQKIYAIISKLDKHIVRSTDYELYKIYAL
RRAQHVLYFILVIGLGAAISSEVATIIGGFLGEWRLMYPAYFPFDIERSLWGYPIAHYQCFG
VTAQIFQNLINDTLPPMALAMLGHVRLNLNVRVARIGHDTSVSVVRKQACNTEFLLCVED
YKALLEFRVAIQRLCSLGTFFVQILVTAINMGVVIFYLFFVNGIFTYIYYVFLIAMPLEIFPL
CYYGTSVQMEFEELTYGIFSCNWMDQNAAFKNLRIFAEQSLRTQIVIAGGMFAVNLDTF
FGTLKGAYSLFTVVVQMK*

>BminOR6-1 [gene=OR6-1] [protein=odorant receptor OR6-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi007806] [locus=Contig2464:168072:169281:-
len:1098 odorant receptor OR6-1]

MPERRKWLYALYSLIPNVLVTIWLPVSFVFSYATMTTEDLVPSSLLTSIQVAINVIGCSVKIV
VMAFLLPKLRTANVFMDRDLARCRAEEEEIAELRKIVQQGNRFVVLFAMSYSYASSTFLG
SVIFGRPPYALYNPFIDWRKSRLEFIAASLMEFALMDVACFQQVVDSDYAVIYVCILRTHM
NILLMRLGRLATNTETKLEENLEELKLCIIDHKNLLGLYDIVAPIISVTIFIQFMITASILSATLI
NIFIFADQLSAQIACCFYILAVVVEIFPLCYAQCLMDDSERLSQQIFHSNWIAQDVRFRKM
LVFFMQRTQRMELNAGKIFPITLGSFLNIAKFSFSLYTLIKKM GIRERLGL*

>BminOR7-1 [gene=OR7-1] [protein=odorant receptor OR7-1] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi011393] [locus=Contig914:106338:107659:-
len:1152 odorant receptor OR7-1]

MSKILRVSRAKIYKSRDAVSYLENIFTFLGTNPLEHRSRRYYFLYYFYSFTLNFISLLYCPLSF
HIGYIKLTHVLTNSQLLTAIQNAIQVSGIPIKVVAITWYMKRLQHAVEILDELVDNYTQRED
LAKIRECVRRRCRKVILLFCLPYYSFGISTIALGVLQNPAPLTVWVPFLDGKRAAWEWYWTIV

LWDTLVMFILLCHQLGNDTYPPIFIKVISTHMQLLVTRVNRLGRPGALTADKHYEELLASKI
VAPVISVTLFTQFATTATLLNWFGDMEYPENIISLAFFCCQLVQILPCCLSASQLIADCERL
PDAIFHCNWMDQDRRFRRAILFFLQRTQTPIRFSCCLKLFDANLETSVAIGKFAFSLYTLIHEA
EDGGKTDN*

>BminOR8-1-1 [gene=OR8-1-1] [protein=odorant receptor OR8-1-1] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi002251]
[locus=Contig1291:3119669:3122246:+ len:1038 odorant receptor OR8-1-1]

MFQDQVRLPLQRRITSPENTRNMRKLTDLLYGRGA AKFESNESFQLIFQCWSLFGIKPLKQ
YRSGRLLHMCFCWFCLILCPFSFYMGYLQTLQTAPVMVQLSLLQATVNVLGLPLKAIVITI
FQTHLRS AEPIFVRLDERYQSTESREQIKNCVALSTRLFTIVGFMYHLYGGITYFQALVTNN
YPLRTWLPFTDYIPQPTIRYWAHFMFEVFHMAFLLSVQFTMDVFPAYIRNLRTHLNLTER
VSQLGGNP DFTDEQNYDELVDCIIMPTCYQASMIEEYSTKLPDAIFHCNWLAMDKRCRKL
TIYFMHRAQENVTFVALKLFKINLTNLSVSKSCCKEQQ*

>BminOR8-1-2 [gene=OR8-1-2] [protein=odorant receptor OR8-1-2] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi001974] [locus=Contig1263:54980:56532:-
len:978 odorant receptor OR8-1-2]

MTVILTTLQATLNVQALPLKATVASIYLNRLRSVESIFKSLDARYQSPQGRFAIKDSVMKSA
HLFFIVSVSYFTYGTISWLSSVFTHQTPLNIWLPFVDWIPQPTIRFWMHFIFEVLYVHFLLI
QFTNDVYSVIYLKALRTHITLLAERVSKLGENPEFNDDDDNYEELIDCVRSHQELLHLVGSV
LSLTIFLQFTVA AVILCVCMLNIFIFADASHQAITIVYYVCVMLQTL PACYQASMLKADSTN
LPNAIFHCNWLAFDKRSRRLLIYFLHRAQEEISFLAAKLFEINLGTNLSRKGIIPAKRPYISM
GYSQVIIFEMLRSV*

>BminOR8-1-3 [gene=OR8-1-3] [protein=odorant receptor OR8-1-3] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi012276] [locus=Contig982:386075:389553:+
len:1167 odorant receptor OR8-1-3]

MQKFSDVLYGRVESDCDTNKPFKTLLHLYGLIGIKPKPKGFLPTLHMVIVWMAFGFTPLLS
IVGFIRFQKTATITESLTRLQAVINAIFIVVKS LVVLVNLKRL ENVEPVMKSLDERYNTTQER
QQISDCVA ACTRLYASMGCLYYSYGTLSILSALISHKQPFVWYPFLDLISNPTIYFYTCLLL
EACYGYFLLAAQYLHDIYPTLYMRTLRTQIQLLRARISRLGEDPDMSDKENHKELVECIDT
HQKILQVVD MVGSVCSP TIFIQFSVVAIVHCICMVNLFIFADTINKVITILYYATVGMQILPT
CYEASTLEMESKLPDSIFHCNWLALDKRGRRLITFFIQRAQVEVSFVAIQMF EINLRTYVA
IFEEAFTYGKSFTVH*

>BminOR8-2-1 [gene=OR8-2-1] [protein=odorant receptor OR8-2-1] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi009485] [locus=Contig4893:4740:6866:-
len:1188 odorant receptor OR8-2-1]

MRNVNLNFYRRGKDDFETNESFVLLFRSWSSVGFIPKKPKRIADIIHQLICWTCVIICPYIYF
SGVIETMSYLPITIVLANLGA AINCIAFPLKAFYIKANIDRLHDVGTIFKDL DGRYQRPQDQ
MQIRDLVTNSRRIFAVSFILCWFYATLSGLVALFAHEYPHGNNLPFIDWLPESNFKFWLHFT
FEVMFLQYLVQVNLTNDSFPAIYIRAIRTHVSLTDRVSRLG SNPDLNDQENFEELVDCIVS
HQKLLQISDTVGTILSLTFFQFTIYAAIICVCMLNMFIFGNATTKVVTVVYLVIPVFWQTIPT
CYQASMLEGDCAKLPLAIFHSNWLALDKRCHKLIIFMQRTQKEISFTA IKL FQINLRTNLS
IAKFSFTLYTFINAMDFGKTR*

>BminOR9 [gene=OR9] [protein=odorant receptor OR9] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi007416] [locus=Contig2256:29896:32987:+ len:1212]

odorant receptor OR9]

MVHREHDNISGGRGVITVLKLLGLWHYEGAMRIPYILFSGLLHSICTIPYTIMMCLDVLQA
TDLKKFTNTMYMTLTELCLVVKLVNVWCYSRLLVDFFAAFEHDKLYQLQDVEERLNWR
RPQRNFARVVFIYITVSFSAMVSAFIGVLYREDYELPYPYAPPFDWRTPRGYWYAYFYELL
AMPITGLSNCAFDMIQSYMMLQLSLCFKLISARLACMGALQEDGASSGFCEVKFHREFVDI
VNLIMTLQIFLPCYCGNEIIQHSGSLNNAIYSTEWFRCSPRMRKYLIHYMEMLQRPVCVRA
GNFFEISLDTVAIYPACVVRAGTEVRNVQRVACATNHGQTIKATMTYELPGFPCIFAQPLLT
DHLMTVLARDRVGPLRLHTGANVLHSRHHGIINALRKVIN*

```

      10      20      30      40      50      60      70      80      90     100     110
BminOR2a : -----MSLKINSWDAFKYHWCVDLSGFRGPKQSTWYIPYKLYTIAITLLFFIYYTCTFTVESLLADNLNDFCEVIYIYAMADVTLNKIFLTFLFIVRQQLLEL : 98
BcucOR2a : -----MIVITLLFFIYYTCTFTVESLLADNLNDFCEVIYIYAMADVTLNKIFLTFLFIVRQQLLEL : 59
BdorOR2a : -----MTLKINSWDAFKYHWRVWDLGFRGPKQSQSVWYIPYKLYTIAITLLFFIYYTCTFTVESFLADNLNDFCEVIYIYAMADMTLNKIFLTFLFIVRQQLLEL : 98
BlatOR2a : -----MTLKINSWDAFKYHWRVWDLGFRGPKQSQSVWYIPYKLYTIAITLLFFIYYTCTFTVESFLADNLNDFCEVIYIYAMADMTLNKIFLTFLFIVRQQLLEL : 98
BoleOR2a : -----MSLKINSWDAFKYHWRVWDLGFRGPKQSQSAWYIPYKLYTIAITLLFFIYYTCTFTVESLLADNLNDFCEVIYIYAMADVTLNKIFLTFLFIVRQQLLEL : 98
CcaphOR2aX1 : -----
CcaphOR2aX2 : -----
RzepOR2a : MIVYIYVSNCITVLVMAARVNSWDAFKYHWRVWDLGFRGPKTSSPYIPYKVVTIVITLLFFIYYTCTFTVKSMADNLNDFCEVIYIYAMSVVTLNVKFLTFLFIVRQQLLEL : 112
DmelOR2a : -----MEKQEDFKLNTHSVAVYHWRVWELTGLMRPPGVSS---LLYVVSIVTNVLVTVLFLSLARLLFTTNMAGLCENLITITTDIVANLKEANYVMYKQLHEI : 100
                                     i           p           n       ce       i           n       kf       vr       l       e

      120     130     140     150     160     170     180     190     200     210     220
BminOR2a : RPIIKHLDAKARTE---EEIGVLODGIDSAKKCELIILRLFYSAFVTSQLMVIFSVEARLMYPAWYFPDYQASRTKEFWIAYGYQTIGFLVQCTQACSVDTYQAYMRVLTAH : 207
BcucOR2a : RPIIKRLDARAKTE---EEIGVLODGIDSAKKCELIILRLFYSAFVTSQLMVIFSGEARLMYPAWYFPDYQASRTKEFWIAYGYQTIGFLVQCTQACSVDTYQAYMRVLTAH : 168
BdorOR2a : RPIIKRLDARAKTE---EEMNVLOEGIDSAKKCELIILRLFYSAFVTSQFMVIFSAEARLMYPAWYFPDYQASRTKEFWIAYGYQTIGFLVQCTQACSVDTYQAYMRVLTAH : 207
BlatOR2a : RPIIKRLDARAKTE---EEMNVLOEGIDSAKKCELIILRLFYSAFVTSQLMVIFSAEARLMYPAWYFPDYQASRTKEFWIAYGYQTIGFLVQCTQACSVDTYQAYMRVLTAH : 207
BoleOR2a : RPIIKRLDARAKSE---KEIIVLODGIDSAKKCELIILRLFYSAFVTSQLMVIFSSETRLMYPAWYFPDYQASRTKEFWIAYGYQTIGFLVQCTQACSVDTYQAYMRVLTAH : 207
CcaphOR2aX1 : -----MYPAWYFPDYKASRINFWIAIYGYQSVGFLVQCTQACSVDTYQAYMRVLTAH : 52
CcaphOR2aX2 : -----MYPAWYFPDYKASRINFWIAIYGYQSVGFLVQCTQACSVDTYQAYMRVLTAH : 52
RzepOR2a : GPIIKQLDARAKSD---EEINVLQKIDSAKKCELTIVLQLFYSAFVTSQLMVIFSAEARLMYPAWYFPDYKASRTKEFWIAYGYQTIGFLVQCTQACSVDTYQAYMRVLTAH : 221
DmelOR2a : RSLRLMLDARARLVGDPEEISALRKEVNIAGQTERTFASIEVFQTTLSQVRNVVRPDRLELLYPANFGVDNMHSTRNYVLINIQLFLHLIVQAIGNQASISYEPHFLCLLTCH : 212
          l      data      e      l      a      f      f      s      v      lmYPAWyfpdy as      fwiaygYQ      GfIVQctQaCsvDcYpQaymr LtaH

      230     240     250     260     270     280     290     300     310     320     330
BminOR2a : TRALSLRVERIGRNKFSYASSELMLCLTKDEMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNISIMLNMAVFFISVMTETLILCY : 317
BcucOR2a : TRALSLRIEAI GRKSNFNCDSSEFIPLTKDEMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNISIMLNMAVFFISVMTETLILCY : 278
BdorOR2a : TRALSLRIERI GRGNFSGVSSELMSCKENEMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNISIMLNMAVFFISVMTETLILCY : 317
BlatOR2a : TRALSLRIERI GRGNFSGASSELTSCKEDMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNISIMLNMAVFFISVMTETLILCY : 317
BoleOR2a : TRALSLRIERI GRKNFSSASSEFMCLKKEEMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNISIMLNMAVFFISVMTETLILCY : 317
CcaphOR2aX1 : MQALSLRIERI GLNANDNTSTSLKYLTKDEMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNLSIMLNMAVFFISVMTETLILCY : 162
CcaphOR2aX2 : MQALSLRIERI GLNANDNTSTSLKYLTKDEMKNRYVELVSCI KDHKTIIELFSTIQKPSI SGTSMAGQFVCTGVAQCTIGVYMLVYG--FNLSIMLNMAVFFISVMTETLILCY : 162
RzepOR2a : MRALSLRIERI GFGTKSCDSPDTSHLTKAEMKHNYVELVSCI KDHKTIIELFSTIQKPSI SGTSLAQFICTGLAQCTIGVYMLVYG--FNLSIMLNMAVFFIAVMTETLILCY : 331
DmelOR2a : MRALSLRVRRI GCRTEKSNKQTYEAWREIV---YOEIEICIRLARVHRREIIRQLVLSVPCMAQFVCSAAVQCTVAMHFLYVADDDHDHTANIIISIVFESSAVILEVFVIVCY : 321
          rAlslRierIG      s      Emk nY ELvscIkDhktieIlfstIQkpiSgtsmAQFvCtgvaQCTigvymLYVg      fn siMlnmaVFF sVtmEtlilCY

      340     350     360     370     380     390     400     410
BminOR2a : YGDLFCQCECHLSKAIYNCNWTQSTEFKNALISFFLLRSQRVNVLMAGNWIIPVKLPFTFVMLIIIEVMSLLIDDYKNKIE : 396
BcucOR2a : YGDMFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 354
BdorOR2a : YGDLFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 393
BlatOR2a : YGDLFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 393
BoleOR2a : YGDLFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 393
CcaphOR2aX1 : YGDLFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 238
CcaphOR2aX2 : YGDLFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 238
RzepOR2a : YGDLFCQCECHLSKAIYNCNWTQSTSEFKKALCFLLRSQRVNVLMAGNWIIPVKLPFTFVMVVKSSYSIFTLSSFK--- : 391
DmelOR2a : FQDRMRTQSBAICAFNDCNNIEQLPKKRELFLLANTQSPSLIYAGNYIALSDEFEQVMRFTYSIFTLILRAK--- : 397
          yGdlfcqecE Ls AiYnCNwt Qs eFK Lc fL RsQRvnlvmlAGNwItpv LpTfVmv      ys fttl k
```

Supplemental figure 3-1 The alignment of OR2a


```

10      20      30      40      50      60      70      80      90      100     110     120
ElatCR10a : --MNERFLSRTFFELDVFYVVFCLGALGFNPLDTSAFNANNUAWNLIITIGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 121
CcapCR10a : --MNERFLSRTFFELDVFYVVFCLGSMGFNPMDCRQCANUGAWNLIITAGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 121
EucCR10a : --MNERFLSRTFFELDVFYVVFCLGALGFNPLDCEFGAFNUAWNLIITIGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 122
EoleCR10a : --MNERFLSRTFFELDVFYVVFCLGALGFNPLDSAFNANNUAWNLIITIGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 121
EminCR10a : --MNERFLSRTFFELDVFYVVFCLGALGFNPLDSAFNANNUAWNLIITIGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 121
RcapCR10a : --MNERFLSRTFFELDVFYVVFCLGSMGFNPMDCRQCANUGAWNLIITAGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 122
DmelCR10a : MSEKIRFLSRTFFELDVFYVVFCLGALGFNPLDTSAFNANNUAWNLIITIGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 121
EborCR10a : --MNERFLSRTFFELDVFYVVFCLGALGFNPLDTSAFNANNUAWNLIITIGVFTFTHAGGCAVLRTDLELALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE--VSINTV : 121
          mxfzFLSRTffpL dVYfYVfKfclG  GfNF dT  a nv aw nliil IGV TFIHAGC I tdlLALDILCPAGTSAVTLLKMLIYVYFQDLAWULRMSRLVVERE in

130     140     150     160     170     180     190     200     210     220     230     240     250
ElatCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--I : 237
CcapCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--I : 234
EucCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--I : 236
EoleCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--I : 235
EminCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMTASALFHYG--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--I : 242
RcapCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--I : 237
DmelCR10a : CRCHIRLHSAVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--M : 237
EborCR10a : EKHIVRAHVAHVAARLNFIFVVGFTICTSYNLRPLIMLILYVQG--GEEMKRLPFNMT--MFSELHAFVYFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS--E : 235
          k hi xahvvaARLNFIFVVGFTICTSYNLRPLIMLILYVQG  qepmKkLPFNMT  MF ELL aFyFELTYFTAYTGVIITFMVGGCAFYFEECSNTAALLLCLNDRS dks

260     270     280     290     300     310     320     330     340     350     360     370     380
ElatCR10a : FALEENRSLITTESSTVLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 361
CcapCR10a : IVSFEQCVTFACESTVLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 358
EucCR10a : LSGGDFRTITAEESTVLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 360
EoleCR10a : VYHFSKFIITTESSTVLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 359
EminCR10a : VYHFSKFIITTESSTVLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 359
RcapCR10a : VGVGCGMLSLIAEELTLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 361
DmelCR10a : FRYEYDHLIEFSQVYIIECRNRSVIRHNAIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 363
EborCR10a : VYTFSDCLITTESSTVLENRLVCFIRHNDIELTRFECRYTVITLAHFVSAGLVIGASIFEDMTFTGFGI--VVIIGVTIAVLGQFIYCYGGSVAESVQCATVAFGCDHACNRLR--I : 359
          l t e t lewrlv fi xhndIleltxff krys itlahfvsaaglvigasifedmtftgfgi  viyi ytiavlgqlfiycygs vaesvqcattvafgcdhacnrlr 1RRYv

80      390     400     410     420     430     440
ElatCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 404
CcapCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 401
EucCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 403
EoleCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 402
EminCR10a : LMIILRSHRAINNVVFESFSLVTFSTILQTSVCHDFGSEFSEPCSNQVEAKGEEFEVEKRRRFEVEN : 354
RcapCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 404
DmelCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 402
EborCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 402
          lmiI RScRAisNVVFESFSLVTFSTILQTSgsiiaa sstk

80      390     400     410     420     430     440
ElatCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 404
CcapCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 401
EucCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 403
EoleCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 402
EminCR10a : LMIILRSHRAINNVVFESFSLVTFSTILQTSVCHDFGSEFSEPCSNQVEAKGEEFEVEKRRRFEVEN : 354
RcapCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 404
DmelCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 402
EborCR10a : LMIILRSCRAISNVVFESFSLVTFSTILQTSGSIIAASSEN----- : 402
          lmiI RScRAisNVVFESFSLVTFSTILQTSgsiiaa sstk

```

Supplemental figure 3-3 The alignment of OR10a

```

10      20      30      40      50      60      70      80      90      100     110
EborCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-FKVGEEFEKYRLLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 116
ElatCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-FKVGEEFEKYRLLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 116
EoleCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-LNVGEEFEKYRLLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 116
EucCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-FQSGEEFEKYRLLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 116
CcapCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-SKTSSEFEKYRLLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 116
RcapCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-RIFSNAEENFFGLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 116
DmelCR13a : MLENPFRLEKDEKNERFFLQCINLKLNGSNPIK-RIFSNAEENFFGLVYTTAAVYVAMVGITIGFQSAFLIKSFGNIMVTENGCTTFMGVLNFVRILHLRLHQRFCQLLACFVED : 113
          mlfnpk kdp f FP QCINLKLNGSNPI  f  LY TAAVYVAMVGITIGFQ AFL  f g I vTEngCTTFMGVLNFVRILHLRLHQR F Ql a Fvkd

120     130     140     150     160     170     180     190     200     210     220     230
EborCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 232
ElatCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 232
EucCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 232
EoleCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 232
CcapCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 232
RcapCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 231
DmelCR13a : INIISSSSHETVEPACARNRVFQVIVSQCSSLITMYCILPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR-YALTVLTAAAGVCVVITLFAEDSLPGFFVYTCQQR : 224
          INIt Ss p Ve CAr Mvrfqvis I LIeMYC IPLVLYMYLTINVEFDVDSMPKFFPYRMLFPYDANHGWR YalTY FTAAAGVCVVITLFAEDSLPGFF YTCQQR

240     250     260     270     280     290     300     310     320     330     340     350
EborCR13a : ILHQIDNNIFDSYATATRAGG-TEAVFQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 348
ElatCR13a : ILHQIDNNIFDSYATATRAGG-TEAVFQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 348
EucCR13a : ILHQIDNNIFDSYATATRAGG-TEAVFQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 348
EoleCR13a : ILHQIDNNIFDSYATATRAGG-TEADYQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 348
CcapCR13a : ILHQIDNNIFDSYATATRAGG-TEADYQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 348
RcapCR13a : ILHQIDNNIFDSYATATRAGG-TEADYQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 316
DmelCR13a : ILHQIDNNIFDSYATATRAGG-TEADYQRECRIRLDIAAKHCVLFNVSRMEFFSFLVWFLISVLCMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN : 321
          iLH idni syA x g g te qre xRld Ia KH lf F E FFaFI LvNf IS vLICMVGFQLVIGQNMFIQGYVKEIIVHLSLSQLVLCWNGDNITQN

360     370     380     390     400     410     420     430     440     450     460
EborCR13a : SLEMANHLYACNWSVRFVAA-----DEETRESFPIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 441
ElatCR13a : SLEMANHLYACNWSVRFVAA-----DEEKESFPIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 441
EucCR13a : SLEMANHLYACNWSVRFVAA-----ADEQVMAAPFIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 446
EoleCR13a : SLEMANHLYACNWSVRFVAA-----ADEQVMAAPFIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 446
CcapCR13a : SLEMANHLYACNWSVRFVAA-----ADEQVMAAPFIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 446
RcapCR13a : SLEMANHLYACNWSVRFVAA-----ADEQVMAAPFIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 416
DmelCR13a : SLEMANHLYACNWSVRFVAA-----ADEQVMAAPFIVSYSTSAAFKKNIQFMIMRSQRCTCITAMKFSILSNFSGLISSSMSYFALLQSFYNEEN-- : 418
          SlenA hLYACnKE  y T fR lqFMIRxQR tCITA RFS LSL SFpgl S SsSYfAlLQsfYe eEn

```

Supplemental figure 3-4 The alignment of OR13a

```

100      100      100      100      100      100      100      100      100      100
BcorOR22c:  --NRRLGFCVPIEREFRRIPRPSARVAGWFCINR--FRSWLIALFFVUNTFVAVAGGFGHVSYGFMVLDLSEALEAFCPGTFVVISLIRMTIFFGHHFRHCHVINSMFQI : 110
BlatOR22c:  -----
BcucOR22c:  --NRRLGFCVPIEREFRRIPRPSARVAGWFCINR--FRSWLIALFFVUNTFVAVAGGFGHVSYGFMVLDLSEALEAFCPGTFVVISLIRMTIFFGHHFRHCHVINSMFQI : 110
BmirOR22c:  --NRRLGSEVPIEREFRRIPRPSARVAGWFLSHDR--ELSWLIALFFVUNTFVAVAGGFGHVSYGFMVLDLSEALEAFCPGTFVVISLIRMTIFFGHHFRHCHVINSMFQI : 110
CcacOR22c:  MIQPLIGSCVPIEREFRRIPRPSARVAGWFCPAVR--FRSLTLVLPFCUNTFVAVAGGFGHVSYGFMVLDLSEALEAFCPGTFVVISLIRMTIFFGHHFRHCHVINSMFQI : 111
RzcrOR22c:  --NRRLGFCVPIEREFRRIPRPSARVAGWFCINR--FRSWLIALFFVUNTFVAVAGGFGHVSYGFMVLDLSEALEAFCPGTFVVISLIRMTIFFGHHFRHCHVINSMFQI : 111
DmelOR22c:  --NTD--SGGFAIADHFYRIPRISGLIVGWFPCIRIGGGGRFHHHILFVFAFAMVGVAGVGSYGCVLINLVLEAFCPGTFVVISLIRMTIFFGHHFRHCHVINSMFQI : 110
      m      lc      vnie      effrpr      ss      is      fwpc      wlt      lrf      vn      favauq      qe      vcF      vl      dlf      aleefcpq      tkvisllkmt      ff      r      rw      vl      1

120      130      140      150      160      170      180      190      200      210      220
BcorOR22c:  LILDISAEKFRIVEGLASFCSSLEFVILLSGSLINTFFNILELIMCYKWCSS--LEVEILLFFNVIL--EENFNNWYFYATYVILILLSGAMTVETSSAUDGFFICACVWTCAI : 221
BlatOR22c:  -----
BcucOR22c:  LILDISAEKFRIVEGLASFCSSLEFVILLSGSLINTFFNILELIMCYKWCSS--LEVEILLFFNVIL--EENFNNWYFYATYVILILLSGAMTVETSSAUDGFFICACVWTCAI : 221
BmirOR22c:  LILDISAEKFRIVEGLASFCSSLEFVILLSGSVINTFFNILELIMCYKWCSS--LEVEILLFFNVIL--EENFNNWYFYATYVILILLSGAMTVETSSAUDGFFICACVWTCAI : 221
CcacOR22c:  LILDISAEKFRIVEGLASFCSSLEFVILLSGSLINTFFNILELIMCYKWCSS--LEVEILLFFNVIL--EENFNNWYFYATYVILILLSGAMTVETSSAUDGFFICACVWTCAI : 222
RzcrOR22c:  LILDISAEKFRIVEGLASFCSSLEFVILLSGSLINTFFNILELIMCYKWCSS--LEVEILLFFNVIL--EENFNNWYFYATYVILILLSGAMTVETSSAUDGFFICACVWTCAI : 223
DmelOR22c:  LIVESRCEACRMVLGATTANFLSLLLSGGIATNAFLCGLLI--MGLRFRIVLPGGILEFFNILL--EENFNNWYFYATYVILILLSGAMTVETSSAUDGFFICACVWTCAI : 221
      ll      d      s      ekzri      lasf      s      lsfvll      sqs      tntftr      rl      km      yvkw      1      llllfrvll      re      vr      r      vratvl      ltlaGAmvtf      fsaudoffilcav      y      al

230      240      250      260      270      280      290      300      310      320      330      34
BcorOR22c:  FFMICHIRINAEAEIC--ELEFSLIACNMRIHFLAVLVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 332
BlatOR22c:  FFMICHIRINAEAEIC--ELEFSLIACNMRIHFLAVLVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 332
BcucOR22c:  FFMICHIRINAEAEIC--ELEFSLIACNMRIHFLAVLVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 332
BmirOR22c:  FFMICHIRINAEAEIC--ELEFSLIACNMRIHFLAVLVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 332
CcacOR22c:  FFMICHIRINAEAEIC--ELEFSLIACNMRIHFLAVLVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 332
RzcrOR22c:  FFMICHIRINAEAEIC--ELEFSLIACNMRIHFLAVLVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 334
DmelOR22c:  FFLVQCIIIFRFDHIDHGDVDFVFEEMNPVPHLACVVERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE : 334
      ff      lc      dir      faeql      cn      richrlavlvERNNKIIILSDASEEELIILMHLSASIVICFSIIDLMNSSEVGLVITYFYSPALITQIILYICIGGTYVSE

0      350      400      450      500      550      600      650      700      750      800      850      900      950      1000
BcorOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 400
BlatOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 400
BcucOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 400
BmirOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 400
CcacOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 401
RzcrOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 402
DmelOR22c:  SELKVAEVYVDWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK-----TFI----- : 402
      SSl      vAeVYVD      DWYKCDVTRFRLIMICRQAKIIIVPFFIPSPAFRSIVSTAGSVIILIK      tf


```

Supplemental figure 3-5 The alignment of OR22c

```

100      100      100      100      100      100      100      100      100      100
BcorCR24a:  NFLNFLQSPTEHNFLIPFAIRIAGFYFG--DGNSEFRICAWIINFWVLVYGSYAEFMGHIHYISIVVUFALLALCPVASSIMSVMFLAEFLWHPFEIERLIKVFTELIP : 111
BlatCR24a:  NFLNFLQSPTEHNFLIPFAIRIAGFYFG--DGNSEFRICAWIINFWVLVYGSYAEFMGHIHYISIVVUFALLALCPVASSIMSVMFLAEFLWHPFEIERLIKVFTELIP : 111
BcucCR24a:  NFLNFLQSPTEHNFLIPFAIRIAGFYFG--DGNSEFRICAWIINFWVLVYGSYAEFMGHIHYISIVVUFALLALCPVASSIMSVMFLAEFLWHPFEIERLIKVFTELIP : 111
BmirCR24a:  NFLNFLQSPTEHNFLIPFAIRIAGFYFG--DGNSEFRICAWIINFWVLVYGSYAEFMGHIHYISIVVUFALLALCPVASSIMSVMFLAEFLWHPFEIERLIKVFTELIP : 111
CcacCR24a:  NFLNFLQSPTEHNFLIPFAIRIAGFYFG--DGNSEFRICAWIINFWVLVYGSYAEFMGHIHYISIVVUFALLALCPVASSIMSVMFLAEFLWHPFEIERLIKVFTELIP : 111
RzcrCR24a:  NFLNFLQSPTEHNFLIPFAIRIAGFYFG--DGNSEFRICAWIINFWVLVYGSYAEFMGHIHYISIVVUFALLALCPVASSIMSVMFLAEFLWHPFEIERLIKVFTELIP : 112
DmelCR24a:  NFBFLIASYMERDEYFNVDEFAISLIGYVFE--QNRVNVNLMSPF--FELLVGCYAEFMGHIHYIPINATALLALCPVASSILSLVMVAMWYCDREIRSLIERVREITE : 111
      N      4FL      qsYpTe      F66D4falr6      GFYF      3      a5      FN      6L      YGSAEFmG6th      6s11      rALIALCPVASSI66v66      f6W6hr      E6      66      FV      eL      sA

120      130      140      150      160      170      180      190      200      210      220
BcorCR24a:  TQNSRLHLAKRPFYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
BlatCR24a:  TQNSRLHLAKRPFYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
BcucCR24a:  EQNGFLHLAKRPFYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
BmirCR24a:  AQDSPLNSAYKHYPYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
CcacCR24a:  EQDSPLNSAYKHYPYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
RzcrCR24a:  EQNSRLHLAKRPFYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
DmelCR24a:  CQKSRRLVGNKPFYHTIATRIGASVIFGTTISTIVTIRACTVNLHSHIRGEEIYEYTFPFMIFFCPLISMEIFELTHISHHAGYITVAGEAGIDGLFICFCMYIGTILKA : 223
      Q      s      lB      K      4      6t      aTrl3a      6L      6G      IsTlY      Ra      6      Nv      s      x      r5EITPFMf6F      L6s      r65r6T6i      shHAGYITVAGEAGIDGLFICFC      Y      qt6LKa

230      240      250      260      270      280      290      300      310      320      330
BcorCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 333
BlatCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 333
BcucCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 333
BmirCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 333
CcacCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 334
RzcrCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 334
DmelCR24a:  IQYITKELLSDVGCGE--EHSSEVEIIPRSMITLIRHNEIIDLVRKESAVMGGITIGFVISAIIIGTCVVMILIFSIY--GVIVIVHIMAVSTELFLYCLGGTVVIECSSC : 334
      6Q      I      KILL      d      E      i      e      6k      6      RHNE6      dL      rfsaVMs      6tL      hFV      S6      IIGT      V6f6LIFS6y      G6      6Y      ht      aV      66Lyc6G63v66E6sS


```

Supplemental figure 3-6 The alignment of OR24a


```

      10          20          30          40          50          60          70          80          90          100          110
BdorOR35a : MDYFVPLQFDNRPILPIQVAGYKFN-FLWPLKEDAGILSRILVNNICLSVSVLYCYIGTIVGFTFIFGENIA--DIAVAECLCTSFMGVQVYIRIFVLLSRQRALRKLNRNF : 109
BlatOR35a : MDYFVPLQFDNRPILPIQVAGYKFN-FLWPLKEDASILSRILVNNICLSVSVLYCYIGTIVGFTFIFGENIG--NIPVAECLCTSFMGVQVYIRIFVLLSRQRALRQLLRNF : 109
BoleOR35a : MDYFVPLQFDNRPILPIQVAGYKFN-FLWPLKEDASILSRILVNNICLSVSVLYCYIGTILGFTFIFGENIG--DIPVAECLCTSFMGVQVYIRIFVLLSRQRALRKLNRNF : 109
BminOR35a : MDYFVPLQFDNRPVILPIQVGYKFN-FLWPLKEDANILSRILVNNICLSVSVLYCYIGTILGFTFISENIS--NIPVAECLCTSFMGVQVYIRIFVLLSRQRPLRKLNRNF : 109
BcucOR35a : MDYFVPLQFDNRPILPIQITGYKFN-CLWPLKEDASVLMRLFMNVCLSVSVLYCYIGTILGFTFIAENIS--DIPVAECLCTSFMGVQVYIRIFVLLSRQRPLRQLLRNF : 109
CcaphOR35a : MDFVPLQHDNSPILPIQVAGYKFN-FLWPLKEDANVFMRLISSLCGLSVILCYIGTILGVEFVAENFS--DIPVADCLCTSFMGVQVYIRIFVLLSRQRPMRKLNRNF : 109
RzepOR35a : MDYFVPLQFDGGLSLEVMIGYKFN-FLWPLKEDANLSESVVNYIGSVNLLIFGFTILGSEFTENMG--NIPVADCLCTSFMGVQVYIRIFVLLSRQRPMRKLNRNF : 109
DmelOR35a : MVRVYERFADGQKVKLAWPLAVFRLNHIFWELDPSTGKVGWFLDKVLAVAMSVEFQGHNDALRLYLRFEASNRNLDHFLTGMPFTLLIWEAQFGLSLHILHFEKQKQFLEIE : 112
      MdyFVPLQfdNrpi Lpiq gykfn flWPLkeda l Rl ci vs L yigtI gE tti en ipAva cl TsfmgvqyIIRifvll rqr lr lL nF

      120          130          140          150          160          170          180          190          200          210          220
BdorOR35a : YRDIVFTFADDAALYKEINSIMRFMNIPTQFYVPMMLIFVLYVYDVASVGLASPDKPFIVRMSFRWYDAQVPLQFIITAIYSGWLTISCVTIWTAEEDYTLGLVLCHASFXY : 221
BlatOR35a : YRDIVFTFADDAALYKEINSIMRFMNIPTQFYVPMMLILVLYVYDVASVGLASPDKPFIVRMSFRWYDAQVPLQFIITAIYSGWLTISCVTIWTAEEDYTLGLVLCHASFXY : 221
BoleOR35a : YRDIVFTFADDAALCKEINSIIRFMNIPTQFYVPMVLILALYVYDVASVGLASPDKPFIVRMSFRWYDAQVPLQFIITAIYSGWLTISCVTIWTAEEDYTLGLVLCHASFXY : 221
BminOR35a : YRDIVFTFADDAALCKEINTVIRFMKMTQFYVPMMLILLYVYDVASIGLASPHKPFIVRMSFRWYDAQAPQFIITAIYSGWLTISTVTIWTAEEDYTLGLVLCHASFXY : 221
BcucOR35a : YRDIVFTDADDAALCKEINSIIRFINIPTQFYVPMVLILGLVYVEVASVGLASPDKPFIVRMSFRWYDAQAPQFIITAIYSGWLTISCVTIWTAEEDYTLGLVMVLCHASFXY : 221
CcaphOR35a : YRDIVFTSADDGALYKEINTIIRFVNIFTRFYVPMVLILGLYTYDVASVGLAYDPPKPFIVRMSFRWYDAQAPLQFIITAIYSGWLTISTVTIWTAEEDYTLGLVMVLCHASFXY : 221
RzepOR35a : YRDIVFTDADDAALYRQLKATVRYANIPTQFYVAPMLILIAQYAYDVISVGLASPDKPFIVRMSFRWYDAQVPLQFIITAIYSGWLTISTVTIWTAEEDYTLGLVLCHASFXY : 221
DmelOR35a : YANIVIDPKEPEMPFRKVDGKMIINRLVSAMYGAVISYLIAFWFSIING-----SKDLGSMIEF-FSDSPLYIVPPLLNTNVVGVGVVIDTMMFGTNTLGLVILHNGSY : 218
      YrdIftf add al keIn i rf niftqfYy pm Lil lvydyvasvglaspdKpFyRMsFrwyDag pl FiitaiysgWltIs vTIwtaEdytLC vlCHasfry

      230          240          250          260          270          280          290          300          310          320          330
BdorOR35a : KKLRLDQLLEMARADIKCGEPTCTNQNLIHAFRRRLREIFRRQORLNGFVAEAKAHFTHQIFVIMSGFVLLLCVVSFQFQSGEITVASSKYISWLSITAQFLLIGYFGQ : 333
BlatOR35a : KKLRLDQLLEMARADIKCGEPTCTNQNLIHAFRRRLREIFRRQORLNGFVAEAKAHFTHQIFVILSGFVLLLCVVSFQFQSGEITVASSKYISWLSITAQFLLIGYFGQ : 333
BoleOR35a : KKLRLDQLLEMARADIKCGEPTCTNQNLIHAFRRRLCEIFRRQORLNGFVVEAKAHFTHQIFVIMSGFVLLLCVVSFQFQSGEITVASSKYISWLSITAQFLLIGYFGQ : 333
BminOR35a : KKLRLDQLLEMARADIKSGETRCTNRNLHAFRRRLCEIFRQQLNGFVAEAKAHFTYQIFVVMFSGFVLLLCVVSFQFQNAHITVDSSKYISWLSITAQFLLIGYFGQ : 333
BcucOR35a : KKLRLDQLLEMARADIKSGETRCTNLRNLHAFRRRLCEIFRQORLNGFVAEAKAHFTHQIFVVMFSGFVLLLCVVSFQFQSSISVSWSKYISWLSITAQFLLIGYFGQ : 333
CcaphOR35a : KKLRLDQELLEASRADIRCGEARRKNEDLEHAFRRRLCEIFRQORLNGFVAEAKAHFTHQIFVTLFSGFVLLLCVVSFQFQSTQMTGWSKYISWLSITAQFLLIGYFGQ : 333
RzepOR35a : KKLRLDQLLELLEAAR-----EAHFRNEDMHTAFRRRLHYDVERQORLNGFVAEAKAHFTHQIFVIMSGFVLLLCVVSFQFQSTQMTGWSKYISWLSITAQFLLIGYFGQ : 328
DmelOR35a : MLKKRDLQALIKILVAR-----DRPHMAKQLKVLITKTLRKNVAVNGGQQLKQIFVVRVIMFAAGLLGALSEKAYTNGMAN--YIHAIFGAGVELGLSLGQFAS : 321
      kklrldq llE aradi ge n lh afrrrl if rqq lNgFvaeaKhAhThqifY fsgvlllcVvsfGfq p v skti WlIsqT qflllGyfgq

      340          350          360          370          380          390          400          410          420
BdorOR35a : MLMDTEETERNSPYCCORWEDLLVLG-DPHSNKLLIGDVQFAIMNSQEPVFDGMKFPPLTYSTVSAAIRSAVSYFMFLNTMNGEN--- : 417
BlatOR35a : MLMDTEETERNSPYCCORWEDLLVLG-DLHSNKLLIGDVQFAIMNSQEPVFDGMKFPPLTYSTVSAAIRSAVSYFMFLNTMNGEN--- : 417
BoleOR35a : MLMDTEETERNSPYCCORWEDLLVLG-DPHSNKLLIGDVQFAIMNSQEPVFDGMKFPPLTYSTVSAAIRSAVSYFMFLNTMNGEN--- : 417
BminOR35a : MLMDTEETERNSPYCCORWEDLLVHG-DPHSNKLLISDVQFAIMNSQEPVLDGMKFPPLTYSTVSVALRSAVSYFMFLNTMNGEN--- : 417
BcucOR35a : MLMDTEETERNSPYCCORWEDLLALG-DLRSNKLLIGDVQFAIMNSQEPVFDGMKFPPLTYSTVSAAIRSAVSYFMFLNTMNS-EN--- : 416
CcaphOR35a : MLMDTEEDQONSPIYFHWEDLLSLG-DIRSNKLLIRDLFAIMNAQKPIVFDGMKIFPLTYSTVSAAIRSAVSYFMFLNTMNTN--- : 417
RzepOR35a : MLMDTEETERNSPYCCORWEDLLPLG-DQKSNKLLIRDLKFAIMNAQKPIVLEGMKIFPLTYATVTALRSAVSYFMFLNTMNNAN--- : 412
DmelOR35a : DLAFTTDSLSTMYVYLHEDIQIYSTNPSENLRLKLNLAITEMNSKEFYVTGLKYRVSILQAGLKILQASFSYFTLTSQRRQMSN : 409
      mLmdeTteL nsfY crWEdLL l g d sNkLL d fAlmn q Piv dGmK FpLtystvs aLrsavSYFmFLntMn n

```

Supplemental figure 3-8 The alignment of OR35a

```

      10          20          30          40          50          60          70          80          90          100          110
BdorOR43a : -MVAVDNPPLLSINVKIKWFLSVLFAR--DWRRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
BlatOR43a : -MVXAVDNPPLLSINVKIKWFLSVLFAR--DWRRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
BoleOR43a : -MSTAVDNPPLLSINVKIKWFLSVLFAR--DWRRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
BminOR43a : -MSTAVDNPPLLSINVKIKWFLSVLFAR--DWRRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
BcucOR43a : -MSTAVDNPPLLSINVKIKWFLSVLFAR--DWRRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
RzepOR43a : -MPTPIEDNPPLLSINVKIKWFLSVLVLR--DWSRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
CcaphOR43a : MPTTRIEDNPPLLAIVNRKFLSVLFAR--NWLRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFATSIFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 109
DmelOR43a : --MTPIEDNPPLLSINVKIKWFLSVLFAR--DWSRCVAVLAPVCLMNAQGFVYLYQQWGLDSTFIILNTFFAVSVFNALLRTOCLIKNRDKFALMEELVILYDNLQDSGDDY : 108
      m t Dnp ls Nw l fLSVlfr dw RcvA VaPvcLmNAqGFVYlyqgWGLDStFIILntFFavs FNALLRtC IknRdkfEalm eLvTlyd I s ddy

      120          130          140          150          160          170          180          190          200          210          220
BdorOR43a : AKSVLAAATKSARNISIFNLSASFSDILIVAMAYPLFQQQHVHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFATFAMFGKAAQLQILQNNLRNLCNMMKS : 219
BlatOR43a : AKSVLTAATKSARNISIFNLSASFSDILIVAMTFPLFQQQHVHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFATFAMFGKAAQLQILQNNLRNLCNMMKS : 219
BoleOR43a : AKSVLAAATKSARNISIFNLSASFSDILIVAMAYPLFQQQHVHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFATFAMFGKAAQLQILQNNLRNLCNMMKS : 219
BminOR43a : AKSVLAAATKSARNISIFNLSASFSDILIVAMAYPLFQQQHVHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFATFAMFGKATLQILQNNLRNLCNMMKS : 219
BcucOR43a : AKSVLAAATKSARNISIFNLSASFSDILIVAMAYPLFQQQHVHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFASFAMFGKATLQILQNNLRNLCNMMKS : 219
RzepOR43a : AKSVLAETATRSARNISIFNLSASFSDIIVAMGYPLFRDQIHHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFASFAMFGKAAQLQILQNNLRNLCNMMKS : 219
CcaphOR43a : AKRELAAATKAARKISIFNLSASFCDIIAATLFLPQENRIHHPFGVALPGIDVTRSPLEYLIYIGQLSFPFTLSSMYMPYVSLFASFAMFGKAAQLQILQNNLRNLCNMMKS : 220
DmelOR43a : GRGIRRREREARNLAIFNLSASELDIVGALVSLPEREERAHHPFGVALPGVMSSTSSVYEVYLAQLPTPELLSSMYMPYVSLFAGLAIFGKAMLOITVHRLGGTGG--EE : 217
      aksvLaaAtksaRnisIFnLSASfSD iVAm PLF qR HPFGvALPgIdVTrSPlEy iYI QL PftLssMYMPyVSLfA famFgKa LqilQnnL nLcdnm

      230          240          250          260          270          280          290          300          310          320          330
BdorOR43a : KTEBELFGLLRKNIAYHARIARYSDFNELVTYVLIIEFLLFSCVICSLFLFCINIT---TSTAEEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 327
BlatOR43a : KTEBELFGLLRKNIAYHARIARYSDFNELVTYVLIIEFLLFSCVICSLFLFCINIT---TSTAEEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 327
BoleOR43a : KTEBELFGLLRKNIAYHARIARYSDFNELVTYVLIIEFLLFSCVICSLFLFCINIT---TSTAEEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 327
BminOR43a : KTEBELFGLLRKNIAYHARIARYSDFNELVTYVLIIEFLLFSCVICSLFLFCINITVSKTSTAEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 330
BcucOR43a : KTEBELFGLLRKNIAYHARIARYSDFNELVTYVLIIEFLLFSCVICSLFLFCINITVSTTSTAEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 330
RzepOR43a : KSEPLEEDTLIRANIAYHARIARYVNDENELVTYVLIIEFLLFSCVICSLFLFCINIT---NSAAEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 327
CcaphOR43a : KSEMLENLNLRNISYHARISKYVNDENELVTYVLIIEFLLFSCVICSLFLFCINIT---NSTAEKISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 328
DmelOR43a : QSEERERLASCIAHYTQVMRYWQNLKLMANIVAVNAIIGSILCSLLECLNI---TSPQTOISIVMYIGTMLVILVFTYYWQANGVLEMSHVSDAAYEMQWYDCSPR : 325
      k E ElF Lr nIaYHariaRyV dNeLvTy VliEfllFscvICSLLFCINi tS aekISIVMYIGTMLVILVFTYYWqAng l emsllVsdAaYemqWY cs r

      340          350          360          370          380
BdorOR43a : FKRTLLIFITARTQNPLOIRVGQMHFMTMEVFQSLLNNAYSYFTLLHNLYND : 378
BlatOR43a : FKRTLLIFITARTQNPLOIRVGQMHFMTMEVFQSLLNNAYSYFTLLHNLYND : 378
BoleOR43a : FKRTLLIFITARTQNPLOIRVGQMYFMTMEVFQSLNNTSYSYFTLLHNLYND : 378
BminOR43a : FKRTLLIFIGRTQKPLQIRVGQMYFMTMEVFQSLNNTSYSYFTLLHNLYND : 381
BcucOR43a : FKRTLLIFIGRTQKPLQIRVGQMYFMTMEVFQSLNNTSYSYFTLLHNLYND : 381
RzepOR43a : FKRTLLIFITRTQKPLQIRVGQMSFMTMEVFQSLNNTSYSYFTLLHNLYND : 378
CcaphOR43a : FKRTLLIFIGRTQKPLQIRVGQMSFMTMEVFQSLNNTSYSYFTLLHNLYND : 379
DmelOR43a : FKRTLLIFLMOTQHMEIRVGNVYEMTLAMFQSLLNNAYSYFTLLHRGVTK : 376
      FkrTLLIFi rTQ PlqIRVGqM PMTmevFQSLLn sSYFTLLhnlynd

```

Supplemental figure 3-9 The alignment of OR43a

```

      10      20      30      40      50      60      70      80      90      100      110
BdorOR45a2 : -----MENFADVDKIVAAMTINVQLFTTSGKRF : 28
BlatOR45a2 : ----- : -
BcucOR45a2 : -----MRITTLKDIKPIITDAFVRIGLSIELGGSKGIFSHPERYATVMIGVIVWAVALPTYTMEYLADVDKIVAAMTINVQLFTTSGKRF : 84
CcaphOR45a2 : -----MRIIVLKDITPVVDFAFACIGFNIDLNKAKGSGSQPVRYFVLLIGVIAWTAALAAATMQYLTVDVKMVAAMTINVQLFTTSGKRF : 84
BoleOR45a2 : -----MENLTDVDKILAAVTINSQGLFTSSSKHF : 28
RzepOR45a2 : ----- : -
BminOR45a3 : -----MYKYLAIYPVFSFRVIGINLWAAQDQRITSAFCRYVSWTLATAIITILMGFY--IYTSQDQDKAIQVITVFLQGVLCILHSG : 78
CcaphOR45a3 : -----MYEVLQIHFSPFRVIGINLWAAQDQRITSAFCRYVSWTLATAIITILMGFY--IYTSQDQDKAIQVITVFLQGVLSVFKSG : 78
BdorOR45a3 : -----MYEVLRIQFSPFRVIGINLWAAQDQRITSAFCRYVSWTLATAIITILMGFY--IYTSQDQDKAIQVITVFLQGVLSVFKSG : 78
RzepOR45a3-1 : -----MHKYLRIQGISFLLGLDMFATDRHILRAPRYVGCWTLATATITILMGVY--IYNSQDQAVKVITVFLQGVLSVFKSF : 78
RzepOR45a3-2 : ----- : -
CcaphOR45a3 : -----MDGLGIGGDGNS--GIRAGEIGKTDANSDSVDGANVTSSMDNALMQ-----KPDQAITVITVFLQGVLSVFKSG : 69
BdorOR45a1 : -----MTTRSARVVKIYFLLTQIIALATILPIAIVSWQHIGQEVETVNAMAPFMOATISLWKIIV : 60
BlatOR45a1 : -----MVMVFAQSCTSKTRQLPHLDMTTRSARVVKIYFLLTQIIALATILPIAIVSWQHIGQEVETVNAMAPFMOATISLWKIIV : 81
CcaphOR45a1 : -----MTNRSARVVKIYFLLTQIIALATILPIAIVSWQHIGQEVETVNAMAPFMOATISLWKIIV : 60
BminOR45a1 : -----MFKSGLNIKGYFHLQKFTFHLRGIDITTRSARVVKIYFLLTQIIALATILPIAIVSWQHIGQEVETVNAMAPFMOATISLWKIIV : 85
BcucOR45a1 : -----MTTREARVTQICFLIIQIFALASILPIAIVSWQHIGQEVETVNAMAPFMOATISLWKIIV : 60
CcaphOR45a1 : MLVSHYKSHSICSLCVRRTSGSKMFHSDLVINGYFQLQKHTFQRLGIDMTTRNASITHIYFLALQIVALTITMPMVIVSCQHLQETAEVETNAMAPFMOATISLWKIIV : 110
DmelOR45a : -----MDASYFAVQRRALIEIVGDPSTPQLSKHPIWAGILILSLISHNWMVVVALQDLSLTRLTDNFVAFVMSQGSSTFFKFL : 79
                                     q k

      120      130      140      150      160      170      180      190      200      210      220
BdorOR45a2 : IFLARRKRFRLRNEALERLALKGNKYERELWNATNRPVLP-----ITTAISISQCLLVNICLLLEIFKLLFYIYWNEVVLTLPPLGFIIFYDYTLFFYILT : 125
BlatOR45a2 : ----- : -
BcucOR45a2 : IFLARRKRFRLRNEALERLALTGNNIERELWNTSNRRVLP-----ITTAISISQCLLVNICLLLEIFKLLFYIYWNEVVLTLPPLGFIIFYDYTLFFYILT : 181
CcaphOR45a2 : IFLARRKRFRLRNEALERLALNGESERILWNTNRPVLP-----ITTAIRISSELTVSCVLLLEIFKLLFYIYWNEVVLTLPPLGFIIFYDYTLFFYILT : 181
BoleOR45a2 : IFLARRKRLRLRNEALERLALTGNKFERDLWNTNRPVLP-----IVTASISQCLLVNICLLLEIFKLLFYIYWNEVVLTLPPLGFIIFYDYTLFFYILT : 125
RzepOR45a2 : ----- : -
BminOR45a3 : MFVAKGRRFKILIRNLDALADAATVKEWSEMRHENDWQOC-----IVRVVYICCTSTGTLYCTVPAIILLYSCFREDHTVILPFDAAPFLDTGHLEFYPVTS : 175
BoleOR45a3 : MFVAKGRRFKILIRSLDMLADEANVKEGREWRHENDWQOR-----IVRVVYICCMSTGTLYCTVPAIILLYSCFREDHTVILPFDAAPFLDTGHLEFYPVTS : 175
BdorOR45a3 : MFVAKGRRFKILIRSLDMLAAEANVKEGKWKHENDWQOR-----IARVVYSCCMSTGTLYCAVPAIILLYSCFNGHATFILPFDAAPFLDTGHLEFYPVTS : 175
RzepOR45a3-1 : MFVTKGRRFKILIRNLDALADAATVKEWSEMRHENDWQORXAEWTHENDWQORIRVYVYSCCTATGTLYCTVPAIILLYSCFNEHAVILLPFDAAPFLVNOQFFFYIITA : 188
RzepOR45a3-2 : ----- : -
CcaphOR45a3 : MFVLKSGRFKILIRNLDMLAE----KEHSAWRLENWQOR-----IVSVVYICCTSTGTLYCTVPAIILLYTRFREQTVILPFDAAPFLDTGHLEFYPVTS : 162
BdorOR45a1 : RVIYRRKEMAQMAENIYLISTRASAK--ELTHLIQENNRE-----RMNTAYYSVLNTGMLAALAPVLVSFIQYLRLGFEFSYIVVLKATYRIDEARPLNVLFI : 157
BlatOR45a1 : LVYIYRRKEMAQMAENIYLISTRASAK--ELTHLIQENNRE-----RMNTAYYSVLNTGMLAALAPVLVSFIQYLRLGFEFSYIVVLKATYRIDEARPLNVLFI : 178
CcaphOR45a1 : RVIYRRKEMAQMAENIYIMISAKASTK--ELTHLIQENNRE-----RMNTAYYSVLNTGMLAALAPVLVSFIQYLRLGFEFSYIVVLKATYRIDEARPLNVLFI : 157
BminOR45a1 : LVYIYRRKEMAQMAENIYLISTRASAK--ELTHLIQENNRE-----RMNTAYYSVLNTGMLAALAPVLVSFIQYLRLGFEFSYIVVLKATYRIDEARPLNVLFI : 182
BcucOR45a1 : RVIYRRKEMAQMAENIYLISTRASAK--ELTHLIQENNRE-----RMNTAYYSVLNTGMLAALAPVLVSFIQYLRLGFEFSYIVVLKATYRIDEARPLNVLFI : 157
CcaphOR45a1 : RVIYRRKEMAQMAENIYIMISAKASTK--ELTHLIQENNRE-----RMNTAYYSVLNTGMLAALAPVLVSFIQYLRLGFEFSYIVVLKATYRIDEARPLNVLFI : 207
DmelOR45a : VMMAKRRRIGSLIRHLRHLKLNQAASATPNHLEKIERENLQD-----RYVARSFNAAYGVICASAIAPMLLGLWGVETGVTTPTTPEMFNFVLDKREKHEFYMPI : 178
                                     y t p p y

      230      240      250      260      270      280      290      300      310      320      330
BdorOR45a2 : TILTVLLVQLCANTITVVGCGFGFVYINSAHLOIMRLKLEQLQLHVDVDPN---FHRDFVALINRREIISLTLLELDAVWAPILFLEVTSSSPICFLAYQLSYLSDDPA : 232
BlatOR45a2 : -----VGGFCGFVYINSAHLOIMRLKLEQLQLHVDVDPN---FHRDFVALINRREIISLTLLELDAVWAPILFLEVTSSSPICFLAYQLSYLSDDPA : 90
CcaphOR45a2 : TILTVLLVYFCVYITCAVIGFCGFVYINSAHLOIMRLKLEQLQLHVDVDPN---FHRDFVALINRREIISLTLLELDAVWAPILFLEVTSSSPICFLAYQLSYLSDDPA : 288
BcucOR45a2 : TILTVLLVYLCAYITVAIGFCGFVYINSAHLOIMSLRLEQLQLHVDVDPN---FHRDFVALINRREIISLTLLELDAVWAPILFLEVTSSSPICFLAYQLSYLSDDPA : 288
BoleOR45a2 : LILTVLLVQFCNSNIIIVGCGFGFVYINSAHLOIMRLKLEQLQLHVDVDPN---FHRDFVALINRREIISLTLLELDAVWAPILFLEVTSSSPICFLAYQLSYLSDDPA : 232
RzepOR45a2 : VILSVLLVYFCVYITCAVIGFCGFVYINSAHLOIMRLKLEHLVQLQADPQ---QADFAAFISYRREIISLTLLELDAVWAPILFLEVTSSSPICFLAYQLSYLSDDPA : 121
BminOR45a3 : YLWCSIFIIYVAIHAIAMASFCFPIFINSAHFRILQHEIQNVAKTSADVDSACLHSHKITETLHYRRIIELSAEFDLWAPIVFIEIYAVSYIKLCPASYNLNLGSDIS : 285
BoleOR45a3 : YLWCSIFIIYVAIHAIAMASFCFPIFINSAHFRALQRELETVVAASAGADDDSLSHSRITQTLHYRRIIELSAEFDLWAPIVFIEIYAVSYIKLCPASYNLNLGSDIS : 285
BdorOR45a3 : YLWCSIFIIYVAIHAIAMASFCFPIFINSAHFRALQRAVETVGAAMTAEADYASLHGRIITRLHYRRIIELSAEFDLWAPIVFIEIYAVSYIKLCPASYNLNLGSDIS : 285
RzepOR45a3-1 : YLWCSIFIIYVAIHAIAMASFCFPIFINSAHFRILQHKLEAUAAT--LAEDYVSFQONITEALRYRRIIELSAEFDLWAPIVFIEIYAVSYIKLCPASYNLNLGSDIS : 297
RzepOR45a3-2 : YLWCSIFIIYVAIHAIAMASFCFPIFINSAHFRILQHKLEAUAAT--LAEDYVSFQONITEALRYRRIIELSAEFDLWAPIVFIEIYAVSYIKLCPASYNLNLGSDIS : 123
CcaphOR45a3 : YLWCSIFIIYVAIHAIAMASFCFPIFINSAHFRILQKQLTQVSVSPNASTDHATFQDDITQTLFYRRIIELSAEFDLWAPIVFIEIYAVSYIKLCPASYNLNLGSDIS : 272
BdorOR45a1 : WLWTAVAIYGVYIGSVSVSYISYIYHNLVGNFKILQSKVLTAEASE----LSERRELIYYCIAXQRIIATMEQNLNIYQPIVVFQFSLNLAQICFLAYQIGSGVVD : 263
BlatOR45a1 : WLWTAVAIYGVYIGSVSVSYISYIYHNLVGNFKILQSKVLTAEALANE----PSORCELIYYCIAXQRIIATMEQNLNIYQPIVVFQFSLNLAQICFLAYQIGSGVVD : 284
BoleOR45a1 : WLWSAAAIYGVYIGSVSVSYISYIYHNLVGNFKILQSKVLTAEAWTD----LSERRELIYYCIAXQRIIATMEQNLNIYQPIVVFQFSLNLAQICFLAYQIGSGVVD : 263
BminOR45a1 : WLWSAAAIYGVYIGSVSVSYISYIYHNLVGNFKILQSKVLTAEASTAD----LSERRTHIYYCIAXQRIIATMEQNLNIYQPIVVFQFSLNLAQICFLAYQIGSGVVD : 288
BcucOR45a1 : WLWTAVAIYGVYIGSVSVSYISYIYHNLVGNFKILQSKVLTAEASTADLGKRRLEIYYCIAXQRIIATMEQNLNIYQPIVVFQFSLNLAQICFLAYQIGSGVVD : 267
CcaphOR45a1 : WLWSAAAIYGVYIGSVSVSYISYIYHNLVGNFKILQSKVLTAEALAE----YSERRASIIYYCIAXQRIIATMEQNLNIYQPIVVFQFSLNLAQICFLAYQIGSGVVD : 313
DmelOR45a : YVWGVGLVAAAALATATITFSLKLTHTNVVVIQFQLLELVLEEKDLNG-----DSRLTGTFVSRRIALDLAKELSSIFGEIVFVKYMLSVYIQLMLAFRFSRS-GWS : 279
      D L W N i l yH ii y pi f L Cf Ay

      340      350      360      370      380      390      400      410      420      430
BdorOR45a2 : N-VFFICILLSSIVQLMIYCFGGEKQVNECEDLSQNIYLLIP-WHKLPKHCRLILPPIRSQRVLVLTGYFFETANRSLVNIIFRAGSFTAMLPAKKEKVF--- : 333
BlatOR45a2 : N-VFFICILLSSIVQLMIYCFGGEKQVNECEDLSQNIYLLIP-WQNLPKHCRLILPPIRSQRVLVLTGYFFETANRSLVNIIFRAGSFTAMLPAKKEKVF--- : 191
BcucOR45a2 : N-VFFICILLSSIVQLMIYCFGGEKQVNECEDLSQNIYLLIP-WHKLPKHCRLILNPFPIRSQRVLVLTGYFFETANRSLVNIIFRAGSFTAMLPAKKEKVF--- : 389
CcaphOR45a2 : N-VFFICILLSSIVQLMIYCFGGEKQVNECEDLSQNIYLLIP-WQNLPKHCRLILNPLIRSRQRVLVLTGYFFETANRSLVNIIFRAGSFTAMLPAKKEKVF--- : 389
BoleOR45a2 : N-VFFICILLSSIVQLMIYCFGGEKQVNECEDLSQNIYLLIP-WQNLPKHCRLILNPFPIRSQRVLVLTGYFFETANRSLVNIIFRAGSFTAMLPAKKEKVF--- : 334
RzepOR45a2 : N-VFFICILLSSIVQLMIYCFGGEKQVNECEDLSQNIYLLIP-WHKLPKHCRLILPPIRSQRVLVLTGYFFETANRSLVNIIFRAGSFTAMLPAKKEKVF--- : 202
BminOR45a3 : G-LPVIAGVLVITTFQLCIYCFSGEKLKSVSKVSDRIYLAFF-WERVVPPSLRRLILPLMRAQRATNLTCFLFIVDHSILVNIIFKTTGSIIGFLSATKSENTTS : 388
BoleOR45a3 : G-LPVIAGVLVITTFQLCIYCFSGEKLKSVSKVSDRIYLAFF-WERVVPPSLRRLILPLMRAQRATNLTCFLFIVDHSILVNIIFKTTGSIIGFLSATKSENTTS : 388
BdorOR45a3 : A-NTFQSPSPVS---GATDYLKSLNLLNISCVAASECIGAARKNLQQAEPK-----LNANARHLAITGQSAVLACE----- : 354
RzepOR45a3-1 : S-FFVIVVGLVITTFQLCIYCFSGEKLKSVSKVSDRIYLAFF-WARMSSMRRLILPLMRAQRSTNLTCFLFIVDHSILVNIIFKTTGSIIGFLSATKENTVDVN : 401
RzepOR45a3-2 : S-FFVIVVGLVITTFQLCIYCFSGEKLKSVSKVSDRIYLAFF-WARMSSMRRLILPLMRAQRSTNLTCFLFIVDHSILVNIIFKTTGSIIGFLSATKENTVDVN : 227
CcaphOR45a3 : S-LPVIAGVLVITTFQLCIYCFSGEKLKSVSKVSDRIYLAFF-WERVVPPSLRRLILFVPMRAQRPMHLTGFLFIVDHSILVNIIFKTTGSIIGFLSATKENTNII : 375
BdorOR45a1 : VDLPFLFLFMIISVGIQLMIYCYGGQHLQNESVNVVSKSIYQTIN-SSSWBNELRKVLLISMMRAQKPSKLTGIFEDVDLPFLFVWVRTAGSVVTLRSVDQKTM--- : 365
BlatOR45a1 : MDLPFLFLFMIISVGIQLMIYCYGGQHLQNESVNVVSKSIYQTIN-SATWBNELRKVLLISMMRAQKPSKLTGIFEDVDLPFLFVWVRTAGSVVTLRSVDQKTM--- : 386
BoleOR45a1 : VDLPFLFLFMIISVGIQLMIYCYGGQHLQNESVNVVSKSIYQTIN-SSSWBNELRKVLLISMMRAQKPSKLTGIFEDVDLPFLFVWVRTAGSVVTLRSVEQKTM--- : 365
BminOR45a1 : VDLPFLFLFMIISVGIQLMIYCYGGQHLQNESVNVVSKSIYQTIN-SSAWBNELRKVLLISMMRAQKPSKLTGIFEDVDLPFLFVWVRTAGSVVTLRSVDQKTM--- : 390
BcucOR45a1 : VDLPFLFLFMIISVGIQLMIYCYGGQHLQNESVNVVSKSIYQTIN-SSPWNELRKVLLISMMRAQKPSKLTGIFEDVDLPFLFVWVRTAGSVVTLRSVDQKTM--- : 369
CcaphOR45a1 : VDLPFLFLFMIISVGIQLMIYCYGGQHLQNESVNVVSKSIYQTIN-STIWBELRKVLLISMMRAQKPSKLTGIFEDVDLPFLFVWVRTAGSVVTLRSVDQSS--- : 415
DmelOR45a : AQVFRATFVLAIIILSSYCYGGEYIKQSLAIAQAVGQIN-WPEMTPKRRRLWQMVIMRAQPAKIFCFMEVVDLPFLFVWVRTAGSVVTLRSVEQKTM--- : 378
      p Ql iYc g iY yGQIN-WPEMTPKRRRLWQMVIMRAQPAKIFCFMEVVDLPFLFVWVRTAGSVVTLRSVEQKTM--- : 378

```

Supplemental figure 3-10 The alignment of OR45a

```

RzepOR46a : -----10-----20-----30-----40-----50-----60-----70-----80-----90-----100-----110-----
CcaphOR46a : MITPRKASSPIIKYTRITMEEPKEKIVNCEYERQKFFKFLGLFGLPPNYSRCQILFKLYFWHVTVVVMLLFDISMWVK--VIGNITDLDNEIKVVFYCSMAIAVMKRFV : 50
BdorOR46a : -----MGH-----KQLLGLFGLPAHYPSLLQYLYKLYFWHVAIFWMLLDISMWIK--IIGNISNLNEIKVVFYCSMAIAVMKRFV : 76
BlatOR46a : -----MEDAKRIVHSEYNIQLLFKLLGLFGLSAHYSSPSHLYKLYKLYFWHVAIFWMLLDISMWIK--IIGNISNLNEIKVVFYCSMAIAVMKRFV : 90
BoleOR46a : -----MDDAKGIVSEYKQVYLFKLLGLFGLPAHYSSPSHLYKLYKLYFWHVAIFWMLLDISMWIK--IVGINSNLNEIKVVFYCSMAIAVMKRFV : 90
BminOR46a : -----MVSPOQSTTPEIDYLLGLFGLPKHYSSPSHLYKLYKLYFWHVAIFWMLLDISMWIK--IIGNISNLNEIKVVFYCSMAIAVMKRFV : 85
DmelOR46aB : -----MVT--EDFYKYQVWYFQILGLVWQLPWTA--ADHQRRFQSMRFGFLVLLDMLLLFSFEMLNISQVREILKVEFMFATDSCMAKLL : 84
DmelOR46aA : -----MSKGVETIKYKGQKAFNLNLSLWQPIERR--WRILHQVNYVHVIVLFDLLLV--HVMANLNTMSVVKAFILPATAGHTTKLL : 84
          f          lgl l          yfwhv fw llfd smw k          Nis inEi kvfy csmaIavmaKf

RzepOR46a : HTRIKSSSFLALFARMHDDLLFPVNKFEMETTSQLSCKVNCYMYLSLTSLSLIEVTVQVQLVSDPCELPISYIPIPNVEN-IFWFLILVLPQIFGASLCFFINISFDSLS : 160
CcaphOR46a : HTRIKNSRYVAFARMHDDLLPANPSLKKPKIKSVHLSCAVNCYMLSLTSLALIVFPVKLISDPCELPISYIPIPNVEN-TLCPLVAVLPQIFGASLCFFLNISFDSLS : 219
BdorOR46a : RTRIKNSRYVALFARIHDDLLFPNVNSELKFTOSSHLSCRVNSYMYLSLTSLSLIEVTVQISEPCELPISYIPIPNVEN-FWCYLIAMLPQIFGASLCCLLNISFDSLS : 186
BlatOR46a : RTRIKNSRYVALFARIQDDELLFPNVNSELKFTOSSHLSCRVNSYMYLSLTSLSLIEVTVQISEPCELPISYIPIPNVEN-FWCYLIAMLPQIFGASLCCLLNISFDSLS : 200
BoleOR46a : RTRIKNSRYVALFARIHDDLLFPNVNSELKFTOSSHLSCRVNSYMYLSLTSLSLIEVTVQISEPCELPISYIPIPNVEN-FWCYLIAMLPQIFGASLCCLLNISFDSLS : 200
BminOR46a : RTHLKNSRYVEIFARMHDDLLFPNVNSELKIAOSSHLSCRVNSYMYLSLTSLTLIEVTKLISEPCELPISYIPIPNVEN-FWRVLIAMLPQIFGASLCCLLNISFDSLS : 195
DmelOR46aB : HLKIKSRKLAVDAMLSPEFGVKSECEMQMLELDRAVVVMKNSYVIGISGASLILIVPCDFNFGELPIAMLEVCSTIEGWICWQQLFHSICLCLPTVLTNITYDGA : 194
DmelOR46aA : SKANVYQVMELEFRDLNEEFPERGANELIFAAACERSKRLDFYKALGSAALSMILIPQFALDWSHLPIKTYNLEGTGSPAWLLCYQCLALSVSITNIGFDSLC : 195
          i kn lfar dlpp n E s rsc lRn Y lSltslsif s p eLPIsiy p ve y aYqfIGslsc lNI FDSls

RzepOR46a : ASFFIYLRGQLINISNLENIPDKDDTTQD-VINMQLKDCIRYNNKLLDITEIMDLLSPMSVQVSSVFLVANFYAMTFLTDPN-DYATFMKFLVYQLCMLQIFILC : 269
CcaphOR46a : ASFFIYLRGQLIDISNLENIGKFNITQD-VITLQLKECIRYAKRLVYTDIMEDLLICPMSVQVSSVFLVANFYAMTFLTDPS-DYVTFMKFLVYQLCMLQIFILC : 328
BdorOR46a : ASFFIYLRGQLIDIANLENIGKDYVDND-IINQLRDCIQHYVKLRKIAETIMEDLLISPMSVQVSSVFLVANFYAMTFLTDPS-DYVTFMKFLVYQLCMLQIFILC : 295
BlatOR46a : ASFFIYLRGQLIDIANLENIGKDYVDND-IINQLRDCIQHYVKLRKIAETIMEDLLISPMSVQVSSVFLVANFYAMTFLTDPS-DYVTFMKFLVYQLCMLQIFILC : 309
BoleOR46a : ASFFIYLRGQLIDIANLENIGKDYVDND-IINQLRDCIQHYVKLRKIAETIMEDLLISPMSVQVSSVFLVANFYAMTFLTDPS-DYVTFMKFLVYQLCMLQIFILC : 309
BminOR46a : ASFFIYLRGQLIDIANLENIGKDYVDND-IINQLRDCIQHYVKLRKIAETIMEDLLISPMSVQVSSVFLVANFYAMTFLTDPS-DYVTFMKFLVYQLCMLQIFILC : 304
DmelOR46aB : YSLCLFVQLQMLVLRLEKGLPVIEPDQNEKAMELRECAATYNNRIVRGLDVLFPKCGSGVQLMCSVLVLSNLDPMSTMSIANGDAVLMKTCIQVLMVQIFILC : 305
DmelOR46aA : SLLFELKQGLDIHVALEKGLRLTISGGS-TVEQQLKEMIRYHMTLVLESKTVLPLCKESVQIFCSVLVLANFYAMTFLTDPS-DYVTFMKFLVYQLCMLQIFILC : 302
          SffiyLRgQLdIL RLenig i qL ci y k i mE ll PmsVQ iSSVlVlvaNfYamtfltd dy tf KflvYqLcMl QIf lC

RzepOR46a : VFANFVSIRSESPPSYSSEWTHCNRRNRLMLLMAQFDPIRIRKTNRCYSFNLSAFTS-----420-----430-----440----- : 331
CcaphOR46a : VFANFVSIRSAQSYALYSSEWTHCNQNRRLMLLMAQFDVPIRIRKTNRCYSFNLPATSIINSYSYVALLKMKD-----420-----430-----440----- : 407
BdorOR46a : VFANFVSIRSAEISYSLYSSEWTRCSKINRLMLLMAQMDVPIRIRKTNRCYSFNLPATSIINSYSYVALLKMKD-----420-----430-----440----- : 374
BlatOR46a : VFANFVSIRSAEISYSLYSSEWTRCSKINRLMLLMAQLDVPPIRIRKTNRCYSFNLPATSIINSYSYVALLKMKD-----420-----430-----440----- : 388
BoleOR46a : VFANFVSIRSAEISYSLYSSEWTRCSQTNRLMLLMAQFDVPIRIRKTNRCYSFNLPATSIINSYSYVALLKMKD-----420-----430-----440----- : 388
BminOR46a : VFANFVSIRSAEISYSLYSSEWTRCSKMNRLMLLMAQFGVPIRIRKTNRCYSFNLPATSKKKPKESSSKEQDSTEHQSRNVINSTLETRKICSSDITGIEFVK : 412
DmelOR46aB : KASNEVTVQSSRLCHSYSSWGTGNRANRNLIVLMMQRFNSMMLSTNPTAFSLAEGSVINCYSYFALLKRVNS-----420-----430-----440----- : 384
DmelOR46aA : YVAGETORSLDIPHELYKTSVVDWYDRSRRIALLFQRLHSTLRITNPSLGDMLLESIVNCYSYFALLKRVNS-----420-----430-----440----- : 381
          Y anEvS rS L sLYseWt c nrr mLlMmaq piriKt NrcysFnL aFtSi n sysy allk

```

Supplemental figure 3-11 The alignment of OR46a

```

BcucOR47bX1 : -MISLSTQATINNTISHTNSVLEDSNTHLKHHTASKRLTILAPYR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 102
BcucOR46bX2 : -MISLSTQATINNTISHTNSVLEDSNTHLKHHTASKRLTILAPYR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 91
BdorOR47b : -MISLSSKATISNTIASHNSYLTNHSYTHLKHHTASKRLTILAPYR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 102
BlatOR47b : -MISLSSKATISNTIASHNSYLTNHSYTHLKHHTASKRLTILAPYR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 102
BoleOR47b : -MISLSSKATISNTIASHNSYLTNHSYTHLKHHTASKRLTILAPYR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 102
BminOR47b : -MISLSSKATISNTIASHNSYLTNHSYTHLKHHTASKRLTILAPYR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 102
CcaphOR47b : MLHECSDKSTISNTIFNHQSSRRRSR----KYSSSKLETLIAPIR-VLKEMLRSEAVHVEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 109
RzepOR47b : -MIFILRESTISNTEHNN-FNLNNGNIFLQNTIGMAKTILEPVR-VARVILRRGGDGHSEHTCIFYFRAYIRLLGLWFAERAVENPVPYVNLMLLEGFFT----- : 101
DmelOR47b : -----MNDSSQNSLRLRVLEDFRSVLRQESFGLIFDLRFYVVRAPFLSLCQYPNKKLASLPYRWINLFTMCNVMTIFWTMVFALPEKSVINEMGGDLVMTISG----- : 101
          mi          ti nti hnsyl n          l t skl tilapyr vlkemlr g a p htcl yfr y rllglwp r e lyy N l m f ff

BcucOR47bX1 : -----120-----130-----140-----150-----160-----170-----180-----190-----200-----210-----220-----2 : 2
BcucOR46bX2 : -----LCIFFKMILFRLGNADTDIINEFDALHVKHFNFESH-DSEPNRRRTROWRSFFFGEMCFFSGFYILSLFLFAAMSLOPLLSCQILPFRCCKFFGLDD : 199
BdorOR47b : -----LYLIFPMILFRMGNVDTDIINEFDALHVKHARGLS-CGFNRNRILQWRSPFFGEMCFFSGFYILSLFLFAAMSLOPLLSCQILPFRCCKFFGLND : 199
BlatOR47b : -----LYLIFPMILFRMGNVDTDIINEFDALHVKHARGLS-DSEPNRRRILQWRSPFFGEMCFFSGFYILSLFLFAAMSLOPLLSCQILPFRCCKFFGLND : 199
BoleOR47b : -----LYLIFPMILFRMGNVDTDIINEFDALHVKHARGLS-DSEPNRRRILQWRSPFFGEMCFFSGFYILSLFLFAAMSLOPLLSCQILPFRCCKFFGLND : 199
BminOR47b : -----LYLIFPMILFRMGNVDTDIINEFDALHVKHARGLS-DSEPNRRRILQWRSPFFGEMCFFSGFYILSLFLFAAMSLOPLLSCQILPFRCCKFFGLND : 199
CcaphOR47b : SSDFVLLGEDLVVALGYSYILFPMILFRMSTADVVDVDFDHALHVKHARGLS-DSEHRRIRIQLORSFFFGEMCFFSGFYILSLFLFAAMSLOPLLSCQILPFRCCKFFGLND : 222
RzepOR47b : -----LYLILEKMFVYSSIAEISIVNEFDTLHAKYAHALLPKSQSNRRIRQWNRFFEIGHVILTGTGFILSFLFLFAAMSLOPLLSCQILPFRCCKFFGLND : 199
DmelOR47b : -----MALVFETIMFYMHLRCDIEDELSDFEYNNRELR-----PHNIDEVLGWRQCLCYVIESGLYINCFCVUNFFSAIFLOPLLGEGLKPFHSVSEYQWHR : 194
          1 lVfEtm lfr          D ii eFdalh k          p nrr qwrk ff ge f gf lIsL lFAamsLOPLls q LPFrckffFgYl

BcucOR47bX1 : PDEHPMGFVVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----GSTSELVVRKLIKETVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 304
BcucOR46bX2 : PDEHPMGFVVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----GSTSELVVRKLIKETVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 293
BdorOR47b : PDEHPPIAFVVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----ASSSTSEAVAWRELREAVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 310
BlatOR47b : PDEHPPIAFVVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----ASSSTSEAVAWRELREAVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 310
BoleOR47b : PDEHPPIAFVVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----DSSSTSEAVVWRELREAVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 310
BminOR47b : PDEHPPIAFVVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----DSSSTSEAVVWRELREAVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 313
CcaphOR47b : PDKHHTIFVVCVYAFQCFCTLYMLVSIIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----STTTEAVLWRELREAVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 332
RzepOR47b : RDEHPPIAFVVCVYAFQCFCTLYMLVSIIVVMDSLGGNSFNQTTNLNLRILCENIRNLGN-----GATEVWVWRELREAVEFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 303
DmelOR47b : LDIHPTTEWFLXIQSLSQNNHMSILMVDMVGISTELQALNMLLQIIEIKRG-----MEVSDKRPFEEFCRVVRFHQOITIKLMNRINOTFYWNVYVSCMGASTFMIC : 299
          pDeHp F cVY fQcFctlymLv iVvmDslGgnsFnQTTnLnrILCeniR lG          se v wrEl e VeFhQ II l iN tFywnvysQmgAstfmic

BcucOR47bX1 : LTAPEALLAQDK-PMVALKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEVRTWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFTLLRTMSD : 417
BcucOR46bX2 : LTAPEALLAQDK-PMVALKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEVRTWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFTLLRTMSD : 406
BdorOR47b : LTAPEALLAQDK-PMVAMKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEIRAWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFALLRTMSD : 423
BlatOR47b : LTAPEALLAQDK-PMVAMKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEIRAWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFALLRTMSD : 423
BoleOR47b : LTAPEALLAQDK-PMVAMKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEVRTWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFALLRTMSD : 423
BminOR47b : LTAPEALLAQDK-PMVAMKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEVRTWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFALLRTMSD : 426
CcaphOR47b : LTAPEALLAQDK-PMVAMKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEVRTWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFALLRTMSD : 445
RzepOR47b : LTAPEALLAQDK-PMVAMKQTYMFSAFMQLLYWCWGNRTYDSMEVATAAYEVRTWYRHSFLLQRLIIFIKRAQKPLEFRAKFLFGFTFASFTSILSTSISYFALLRTMSD : 416
DmelOR47b : ISTPEPMANAAVDKPMIAKEVLLMLVAIQLSLKVSSTLVITQSYEVAQAQFINDNHTKSEIGDISVILRAQKPLMYVAEFLPTELTGYMLVLRKNCRLRLAMQESM- : 412
          ltaPEallA d PmvA KfQtyMfsAFmQL yWC mGnrtYdSmEvataaY Wy hSP lQR i F lKraQkPlEfrak fPgTfAsftSILstsYsfalLrtmsd

```

Supplemental figure 3-12 The alignment of OR47b

Supplemental figure 3-13 The alignment of OR49a

Supplemental figure 3-14 The alignment of OR49b


```

      10      20      30      40      50      60      70      80      90     100     11
BdorOR63a1-1 : --MMSESVEEIYKRNYSIKVLIGVSFSLGVNLTAPSKIKDALKLFNVIVWVASLLSLAHWSYFIRHIDNIP--LLAETVCTALQTLISAVKMYVYLFQRTFYRLDQ : 106
BoleOR63a1-1 : --MLESVEEYKRNYSIKVLIGVSFSLGVNLTAPSKIKDALKLFNVIVWVASLLSLAHWCYFLRYIDNIP--LLAETVCTALQTLISAVKMYVYLFQRTFYRLDQ : 105
BcucOR63a1 : --MVFEDEEYKRNYSIKVLQVSFSLGVNLTAPSKIKDALKLFNVIVWVASLLSLAHWCYFLRHFNIP--LLAETVCTALQTLISAFKMYVYLFQRTFYRLDQ : 106
CcparOR63a1 : --MILEVEDYKRNYSIKVLIRVSFSLGVNLTAPTRFSDSRIRFNVLVTSLSLHAHCYLIIRHFDNIP--LLAETVCTALQTLISAFKMYVYLFQRTFYRLDQ : 106
RzepOR63a1 : --MILDKLAEYVRNNSIKVLFGVSYGLGVNLTAPN-----FPVKYQLKQEDINIMDTIWRTRRQIIFVSSCCLAIVCNYPFAALFVNLYNQ : 87
BlatOR63a1-2 : --MILENKKEELYKRNYSIKVLFRVSYTLGVNLTAPDKFDSLKII-----P-----LLAETVFTALQIGMAAIKMYIFFTHRTFYRLDQ : 80
BdorOR63a1-2 : --MTSENKEELYKRNYSIKVLFRVSYTLGVNLTAPNKIKDALK-----TVFTALQIGMAAIKMYIFFTHRTFYRLDQ : 73
BoleOR63a1-2 : --MTLENKEELYKRNYSIKVLFRVSYTLGVNLTAPDKFDSLRIVQIILIASLSLSLFAHMYLKRHIDNIP--LIAEAVFTALQIGMAAIKMYIFFTHRTFYRLDQ : 106
BminOR63a1-1 : --MMENAEDEYKRNYSIKVLIRVSFSLGVNLTAPSKIKDALKLISVILSVTSLSLMSGHCCYLMRHLDRMP--LIAEAVFTALQILMAAIKMYIFFTHRTFYRLDQ : 106
BminOR63a1-2 : --MILENKKEELYKRNYSIKVLFRVSFALGVNLTAPSKIKDALKLISVILSVTSLSLMAHCYLMRHLDRMP--LIAEAVFTALQILMAAIKMYIFFTHRTFYRLDQ : 106
DmelOR63a : --MYSPDEAEELKRNYSIKVREMLRSLYTVGNNLQPSRCQVLRITWILSVLSLASLGHWMQLARVYHIDP--RIGETAGALQPLSTAKMYVYLFQRTFYRLDQ : 107
BdorOR63a2-1 : --MYSISEIKELTRNHWIRIRELKRISYIIGINNAQTKCKRWMRIINILPIASCIALPHWLMIKQAEGDIP--LIAETSTTALQTTGLIKMAYMLFTQHRPHRLLRK : 107
BlatOR63a2-1 : -----NINAQTKCKRWMRIINILPIASCIALPHWLMIKQAEGDIP--LIAETSTTALQTTGLIKMAYMLFTQHRPHRLLRK : 77
BoleOR63a2-1 : --MYSITEIKTLRVNHLIRELKRISFIIGINNAQTNLKEWRIINILPITSCIALPHWLMIKQAEGDIP--LIAETSTTALQTTGLIKMAYMLFTQHRPHRLLRK : 107
BminOR63a2 : --MYSIERKELRVNHWIRIRELKRISYIIGINNAQTKLRSRIINVLIIIFSCIALPHWLMIKQAEGDIP--LIAETSTTALQTTGLIKMAYMLFTQHRPHRLLRK : 107
CcparOR63a2 : --MYSORINDLKVNRNHWIRIRELKRSYVLIGVNLSTQTFKLGWLIINVLIIASCIALPHWLMIEHAEGNLIS--LIAETSTTALQTTALVKMAFIFQHRHLLHLYK : 107
RzepOR63a2 : --MYSAGEIQALKRRNHWIRIRELKRISYIIGINNAQTKLRSRIINVLIIIFSCIALPHWLMIQQAEGHIE--LIAETVTTITQTTAIVKLIYIYFMHRFSALHK : 107
BlatOR63a2-2 : --MYNAEFAELKSNRFRKIRELRKVSYILGINYGETSLKCLRVNLFLIITCGISLVPRLMLERADGNVP--LIAETITITMLQTTTMMVKMIFCLFMQSCRALLMK : 107
BdorOR63a2-2 : --MYNAEFAELKNNRFRKIRELRNVSYILGINYGETSLKCLRVNLFLIITCAISLVPRLMLERADGNVP--LIAETITITMLQTTTMMVKMIFCLFMQSCRALLMK : 107
BoleOR63a2-2 : --MYNTEEFVLKYNRFRKIRELRKAVSYILGINYGETSLKCLRVNLFLIITCGISLVPRLMLERADGNVP--LIAETITITMLQTTTMMVKMIFCLFMQSCRALLMK : 107
      n i l s g Nl      k l      y w      p l aet t l q      k F      11

      0      120     130     140     150     160     170     180     190     200     210     2
BdorOR63a1-1 : TLTHEIRKKEIEFQ--DFFINRQLKQEDVDDIMNGVNRSAARQLIFFVCCCVGIVCNVFFGALFVNLYHQLKQTP-DYEHILFPFALPFWEDQGMFTFVYPLQMYLSG : 212
BoleOR63a1-1 : TLTHEIRKKEIEFQ--DFFINRQLKQEDVDDIMNGVNRSAARQLIFFVCCCVGIVCNVFFGALFVNLYHQLKQTP-DYKHILFPYALPFWEEKGMFTFVYPLQMYMTG : 211
BcucOR63a1 : ALKHVIRIETIEFKH--DFFINQQLKREIDEMNGVNRQNAARQLIFFVCCCVGIVCNVFFGALFVNLYHQLKQTP-DYKYILFPFELPFWEDQGMFTFVYPLQMYFSS : 212
CcparOR63a1 : ALTHEVIRKKEIEFKY-----LQQTTPNYKH-----LFPFALPFWENKGMFTFVYHLEMLFSG : 148
RzepOR63a1 : -----LQQTTPNYKH-----LFPFALPFWENKGMFTFVYHLEMLFSG : 125
BlatOR63a1-2 : TLTHEIRKKEIELT--DFFIDRQLKQEDVDDIMNRVNRNTLHLFIFFVCCCVGIVANVFFTAFFVNLYHQLKQTP-DYEFFLPVLPALPFWEEKGMFTFVYHLEMLFSG : 185
BoleOR63a1-2 : ALTHEIRKKEIELT--RFFINRQLKQEDVDDIMNRVNRNTLHLFIFFVCCCVGIVANVFFTAFFVNLYHQLKQTP-DYEFFLPVLPALPFWEEKGMFTFVYHLEMLFSG : 154
BdorOR63a1-2 : TLTHEIRKKEIELT--DFFIDRQLKQEDVDDIMNRVNRNTLHLFIFFVCCCVGIVANVFFTAFFVNLYHQLKQTP-DYEFFLPVLPALPFWEEKGMFTFVYHLEMLFSG : 211
BminOR63a1-1 : TLTHEIRKKEIELTQ--DFFINRQLKREIDEMNAVMNRNIRLFIFFVCCCVGIVANVFFTAFFVNLYHQLKQTP-DYEFFLPVLPALPFWEEKGMFTFVYHLEMLFSG : 212
BminOR63a1-2 : TLTHEIRKKEIELTQ--DFFINRQLKREIDEMNAVMNRNIRLFIFFVCCCVGIVANVFFTAFFVNLYHQLKQTP-DYEFFLPVLPALPFWEEKGMFTFVYHLEMLFSG : 212
DmelOR63a : ANCHELLQKELFERMSDLPVWIKRQCVESVNRVNRNASTRQIILVLYSGICITITNFIINSFVNLYHQLKQTP-DYKHILFPFELPFWEDQGMFTFVYHLEMLFSG : 216
BdorOR63a2-1 : AETHELLQGLEIFQT--DMPKTKSLKKEINAMVMEINWQAARGQLFTLGTGICIMSNVFFYAFKKNLYNHQLQTP-NVYVILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
BlatOR63a2-1 : AETHELLQGLEIFQT--DMPKTKSLKKEINAMVMEINWQAARGQLFTLGTGICIMSNVFFYAFKKNLYNHQLQTP-NVYVILPFTG-YPMFLDKGMASFYVAMDMFFGA : 182
BoleOR63a2-1 : AETHELLQGLEIFQT--GMPKTKSLKKEINAMVMTNWKQTRQLFIITGTGICIMSNVFFYAFKKNLYNHQLQTP-NVYVILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
BminOR63a2 : VETHDQLQGLEIFLT--GMPKTKSLKKEINAMVMTNWKQTRQLFIITGTGICIMSNVFFYAFKKNLYNHQLQTP-NVYVILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
CcparOR63a2 : AETHELLQGLEIFMT--DMPKTKSLKKEINAMVMTNWKQTRQLFIITGTGICIMSNVFFYAFKKNLYNHQLQTP-NVYVILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
RzepOR63a2 : AETHELLQGLEIFKT--DMPKTKSLKKEINAMVMTNWKQTRQLFIITGTGICIMSNVFFYAFKKNLYNHQLQTP-NVYVILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
BlatOR63a2-2 : AENYELLQGLKIFET--DMDKAEKLVKVINAMMATIKWESRQLSCILTSCLSNVFLYAFETNLYHQIKKTP-NVYHILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
BdorOR63a2-2 : AENYELLQGLKIFLT--DMDKAEKLVKVINAMMATIKWESRQLSCILTSCLSNVFLYAFETNLYHQIKKTP-NVYHILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
BoleOR63a2-2 : AENYELLQGLKIFST--DMDKAEKLVKVINAMMATIKWESRQLSCILTSCLSNVFLYAFETNLYHQIKKTP-NVYHILPFTG-YPMFLDKGMASFYVAMDMFFGA : 212
      he i      i l k e im w r l c i nyf f nly tp y lp yp      kgm pYY M

      20      230     240     250     260     270     280     290     300     310     320
BdorOR63a1-1 : SAVYIAGCMVSVFEGVIVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYQIRINIFAQQIQTIFKHVLSQFVLSLIVFGVFLFMSFGLES----SIVI : 317
BoleOR63a1-1 : SAVYISGICVSVFEGVIVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYQIRINIFYVQQIQNSKHHVLSQFVLSLIVFGVFLFMSFGLES----SIVI : 316
BcucOR63a1 : SAVYIAGCMVSVFEGVIVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYQIRIYTVVQQIQTSKHHVLSQFVLSLIVFGVFLFMSFGLESVNCSSII : 321
CcparOR63a1 : SAVYIAGICVSVFEGVIVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYQIRVRYVYVQQIYIYKHVLSQFVLSLIVFGVFLFMSFGLES----SITI : 253
RzepOR63a1 : SAVYIAGCMVSVFEGVIVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYQIRIYVYVQQIQTIFKHVLSQFVLSLIVFGVFLFMSFGLES----SITI : 230
BlatOR63a1-2 : AALVYSGIGVSVFEGVIMVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYRRISKYLQEIKTIFRHISLVQELLSLVMGVFLFMSFGLES----EASIVI : 290
BoleOR63a1-2 : AALVYSGIGVSVFEGVIMVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYRRISKYLQEIKTIFRHISLVQELLSLVMGVFLFMSFGLES----ESSIVI : 259
BdorOR63a1-2 : AALVYSGIGVSVFEGVIMVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYRRISKYLQEIKTIFRHISLVQELLSLVMGVFLFMSFGLES----GNI : 275
BminOR63a1-1 : SALVYSGIGVSVFEGVIMVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYRRISKYLQEIKTIFRHISLVQELLSLVMGVFLFMSFGLES----GNI : 317
BminOR63a1-2 : SALVYSGIGVSVFEGVIMVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYRRISKYLQEIKTIFRHISLVQELLSLVMGVFLFMSFGLES----GNI : 321
DmelOR63a : CSLYICMCMVSVFEGVIVLQCHAVGLVKNHNLVLRSTSLIPERRRVEYLYRTIYRRISKYLQEIKTIFRHISLVQELLSLVMGVFLFMSFGLES----SSIT : 322
BdorOR63a2-1 : CSLIVAGMSAISFGCCVILVCKKSCGLVQVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLES----NKIT : 317
BlatOR63a2-1 : CSLIVAGMSAISFGCCVILVCKKSCGLVQVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLES----NKIT : 287
BoleOR63a2-1 : CSLIVAGMSAISFGCCVILVCKKSCGLVQVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLES----NKIT : 317
BminOR63a2 : CSLIPAAGMSALSFGGSVILVCKKSCGLVQVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLES----NKVT : 317
CcparOR63a2 : CSLHCAAMCAICVQCTVILVCKKSCGLVQVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLES----NKVI : 317
RzepOR63a2 : CSLHVAAGMSAISFNCAVILVCKKSCGLVQVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLES----SKVT : 317
BlatOR63a2-2 : CSLITCGMCSVSFHCIMILCKHACGLVKVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLET----NKTT : 317
BdorOR63a2-2 : CSLITCGMCSVSFHCIMILCKHACGLVKVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLET----DKTT : 317
BoleOR63a2-2 : CSLITCGMCSVSFHCIMILCKHACGLVKVLCMLLRSTSLIPVKKRVEYLYRCVIOHQHTLRFINDVNRFRPHICLSQFLHSLAIVGLVFLFEMNFGLET----NKTT : 317
      g a sf F vlc H glv v l TS P r r eYLy i qr f hi ls f sl g vlife gl

      330     340     350     360     370     380     390     400     410     420
BdorOR63a1-1 : VIRIMIMYFAAGGTQIIILCYNGQQLTSVSEETPLAFYNQCNWYEESEKFKQLLRMMIMRTNRFPNLEVSFTLMNLATLIALFRMGSFYLLLRNLQEK-- : 415
BoleOR63a1-1 : VIRIMIMYFAAGGTQIIILCYNGQQLTSVSEETPLAFYNQCNWYEESEKFKQLLRMMIMRTNRFPNLEVSFTLMNLATLIALFRMGSFYLLLRNLQEK-- : 414
BcucOR63a1 : FIRIMIMYISAGGTQIIILCYNGQQLTSVSEETPLAFYNQCNWYEESEKFKQLLRMMIMRTNRFPNLEVSFTLMNLATLIALFRMGSFYLLLRNLQES-- : 419
CcparOR63a1 : FIRIMIMYISAGGTQIIILCYNGQQLTSVSEETPLAFYNQCNWYEESEKFKQLLRMMIMRTNRFPNLEVSFTLMNLATLIALFRMGSFYLLLRNLQES-- : 351
RzepOR63a1 : FIRIMIMYIAAGGTQIIILCYNGQQLTSVSEETPLAFYNQCNWYEESEKFKQLLRMMIMRTNRFPNLEVSFTLMNLATLIALFRMGSFYLLLRNLQEK-- : 328
BlatOR63a1-2 : LIRIMIMYISAGISQITTIYCYHGAQLTSACEEPLAYNCDWYGEKNTKRLNLIIMIRTKNEEFNMEVSWFTLMNLTLISLRASGSFYLLLRNLQED-- : 388
BminOR63a1-2 : LIRIMIMYISAGISQITTIYCYHGAQLTSACEEPLAYNCDWYGEKNTKRLNLIIMIRTKNEEFNMEVSWFTLMNLTLISLRASGSFYLLLRNLQED-- : 357
BdorOR63a1-2 : ----- : -
BminOR63a1-1 : FRLIMIMYISAGISQITTIYCYHGAQLTSACEEPLAYNCDWYGEKNTKRLNLIIMIRTKNEEFNMEVSWFTLMNLTLISLRASGSFYLLLRNLQED-- : 415
BminOR63a1-2 : FRLIMIMYISAGISQITTIYCYHGAQLTSACEEPLAYNCDWYGEKNTKRLNLIIMIRTKNEEFNMEVSWFTLMNLTLISLRASGSFYLLLRNLQED-- : 419
DmelOR63a : MIRTMIMYLAAGVQIVVYCYNGQFPATASDEANAFYQVRVYGESEKFKQLLRMMIMRTNRFPNLEVSFTLMNLATLIALFRMGSFYLLLRNLQEK-- : 420
BdorOR63a2-1 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 415
BlatOR63a2-1 : FIRITLMY----- : 294
BoleOR63a2-1 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 415
BminOR63a2 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 399
CcparOR63a2 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 415
RzepOR63a2 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 415
BlatOR63a2-2 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 417
BdorOR63a2-2 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 417
BoleOR63a2-2 : FIRIMIMYLCATTAATGCTHYVNGQFLANELKVLACYNDEYHETDAEKKTLRMIIMRSNKKKCFQISWFTVMSLATLMGIFKASGSFYVLLLRDIDET-- : 417
      irm my a      gq l e ip y c w e fk m imr n f swf m l t l s sy l

```

Supplemental figure 3-16 The alignment of OR63a

[illegible]

	20	230	240	250	260	270	280	290	300	310	320		
BdorOr67d1		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALSSLY	HCII	TTNTQCNSTFE	322
BlatOr67d1		RDILILKVEHNEAAQAQ--	NNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALSGSLY	HCII	TTNTQCNSTFE	322
Bmor67d1		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALGGLY	HCII	TTNTQCNSTFE	322
BminOr67d1		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALGGLY	HCII	TTNTQCNSTFE	322
Bmco67d1		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALGGLY	HCII	TTNTQCNSTFE	322
Bcuo67d1		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALGGLY	HCII	TTNTQCNSTFE	322
CcapOr67d1		RDILILKVEHNEAAQAQ--	NNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALSGSLY	HCII	TTNTQCNSTFE	322
RzepOr67d1-1		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALGGLY	HCII	TTNTQCNSTFE	322
RzepOr67d1-2		RDILILKVEHNEAAQAQ--	DNKTESLLISIE	WHQYY	TDYNERCNEIF	IFYIIT	MQILTSGVSTVF	MTILMGM	DWGAVL	ILIALGGLY	HCII	TTNTQCNSTFE	322
RzepOr67d2		LDLILVKVRLNEISNKR--	DKRSERLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
BdorOr67d2		LDLILVKVKSLEAAAE--	SSNAERLLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
BlatOr67d2		LDLILVKVKSLEAAAE--	SSNAERLLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
BoleOr67d2		LDLILVKVKSLEAAAE--	SSNAERLLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
BminOr67d2		LDLILVKVKSLEAAAE--	SSNAERLLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
BcuoOr67d2		LDLILVKVKSLEAAAE--	SSNAERLLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
CcapOr67d2		LDLILVKVKSLEAAAE--	SSNAERLLDIEI	WHQYY	TDYNERCNR	IFYINSM	IVTSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
BminOr67d3		YDIFALVGDGHLHLENNKDKRKS	LINDITE	WHQYY	LEFNDCNR	IFYISV	ITPSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
RzepOr67d3		YDFPKLVGDLHLENNKDKRKS	LINDITE	WHQYY	LEFNDCNR	IFYISV	ITPSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322
DmelOr67d		KDTCFVLLTFENLVMKRNDFPKVRAM	CDLV	WHQYY	LEFNDCNR	IFYISV	ITPSGISIC	LCYLLILG	DWGAVL	ILIAFSGGLY	CIMT	TKTQCNSTFC	322

```

330      340      350      360      370      380      390
DdorOR67d1 : ELYN-INNWEDLVKHKMLMILVMKSNPSEIKIGGVPLPSVQTALQITTTTYGIFTMMGLFLDEEQ : 388
BlatOR67d1 : ELYN-INNWEDLVKHKMKMLILVMKSNPSEIKIGGVPLPSVQTALQITTTTYGIFTMMGLFLDEEQ : 388
BoleOR67d1 : ELYN-INNWEDLVKHKMKMLILVMKSNPSEIKIGGVPLPSVQTALQITTTTYGIFTMMGLFLDEEQ : 388
BminOR67d1 : ELYN-INNWEDLVKHKMKMLILVMKSNPSEIKIGGVPLPSVQTALQITTTTYGIFTMMGLFLDEEQ : 388
BcucOR67d1 : ELYN-INNWEDLVKHKMKMLILVMKSNPSEIKIAGVLPSVETALQITKSMVGIFTMMGLVMQAEEL : 371
CcapOR67d1 : ELYN-INNWEDLVKHKMKMVFIIKKSSPAEIKIGGVPLPSVQTALQITKTSYGLFTMIIGVIEENN : 388
RzepOR67d1-1 : ELYN-INNWEDLVKHQKMLVFLVKKSNPSEIKIGGVPLPSVQTALSTKSYGIFTMMGLFLDEEQ : 388
RzepOR67d1-2 : ELYN-INNWEDLVKNQKMIIFILMRSNPSEIKIGGVPLPSVQTALSTKSYGIFTMMGLFLDEEQ : 388
RzepOR67d2 : ELYN-INNWEDLVKNQKMIIVILIKKSNPSEIKVAGFLPSVQTALSTKSYGIFTMMGLRLDEESQ : 388
DdorOR67d2 : ELWN-INFWEDLVKNQKMIIPILMKAONPSEIKVGGFLPSVQTALQITTTTYGIFTMMGLFRLEESQ : 388
BlatOR67d2 : ELWN-INFWEDLVKNQKMIIPILMKAONPSEIKVGGFLPSVQTALQITTTTYGIFTMMGLFRLEENQ : 388
BoleOR67d2 : ELWN-INFWEDLVKNQKMIIPILMKAONPSEIKIGGFLPSVQTALQITTTTYGIFTMMGLFRLEENQ : 388
BminOR67d2 : ELCN-INFWEDLVKNQKMIIVPLMKAONPSEIKIGGFLPSVQTALQITTTTYGIFTMMGLFRLEENQ : 388
BcucOR67d2 : ELCN-INFWEDLVKSKQEMIVLILMKAONPVEIKVGGFLPSVQTALKITTTTYGIFTMMGLFRLEEQ : 388
CcapOR67d2 : ELYN-IDWNKLNKSKQMLVFILIKKSKPAEIKVGGFLPSVQTALSTTTTYGIFTMMGLFRLEDEN : 386
BminOR67d3 : GYID-INWEDLVSDQKTVSLMLMESQVERVITITAGIEPLSVNTALKITRTSYSLVMMVVOQNE-- : 386
RzepOR67d3 : GYID-INWSDLVKNQKAILRLMLMQSAERNITITAGIEPLSVSTALKITRTSYSLVMMVVOFRNK-- : 389
DmelOR67d : VYITCNLVKEDLVFKKEKLIIMMLAKAONNEVVLTAAADMAPLSMNLTALITKGTGSFSMMLMNLNYG-- : 391
el n in Y L vk qkm l k Qnp eik g lPLSVgTAL iTk lYgiftMml fl e

```

Supplemental figure 3-18 The alignment of OR67d

10 20 30 40 50 60 70 80 90 100 110
DmelOR69aB : ----MQLEDPMRYFDLVCGQAQLPRYTWSG--RRSLEVRRNLRKRIIFWLGAVNLVYHNIGCVMYGFGDGRGTRKDP--AYLAELASVASMLGFTIVGTLNLNWKMLSKTH : 103
DmelOR69aA : ----MQHDDHMKIIDLCKMACIPRYQWKG--RPTREQVASEQRIVFLGTCIQPQITGVLIIVYQNGRLATETG--TFVAQLSEMCSSFKLTFFUCQNVIAISNNRQ : 103
BdorOR69a1 : -MSYIYSWKHCKLYPVFTLLDLAETPEFTWSG--ARTYSRRRLWLRALFTGAINLVYQNGIMLYLMPHESASQ---STIVQVTEGGMGLTMVGSNNMLVMWYVGR : 105
BlatOR69a1 : -MSYIYSWKHCKLYPVFTLLDLAETPEFTWSG--ARTYSRRRLWLRALFTGAINLVYQNGIMLYLMPHESASQ---STIVQVTEGGMGLTMVGSNNMLVMWYVGR : 105
BminOR69a1 : -MSYIITNCKLCKLYPVFTLLDLAETPEFTWSG--ARTYSRRRLWFRRLFTGAINLVYQNGIMLYLMPHESASQ---STIVQVTEGGMGLTMVGSNNMLVMWYVGR : 105
BcurOR69a1 : -MSEYTTIDKDLKLYPVFTLLDLAETPEFTWSG--APGTHSYRKLWLRALFTGAINLVYQNGIMLYLMPHESASAE---TTIAQITETGGIMGLTMVGSNNMLVMWYVGR : 105
CcaphOR69a1 : -MSGVYSSMMHFLKYPNFTLLDLANSNPPAWSG--ARQYGVHMLWIRRLFTGGAANLVYQNGMIMYLCPHVESNE---STIGQITETGGIMGLTMVGASNMVFMWYHADR : 105
RzepOR69a1 : -MSPRIYTTQHFLLHYPLQLTLNLNSDPPAWSG--SRKYSSSHAIWLRRLFTGAINLVYQNGMIMLYLMPHEISTE---SVIGQITETGGIMGLTMVGACNMVFMWYVGR : 105
BcurOR69a2 : ----- : -
CcaphOR69a2 : ----- : -
BdorOR69a2 : ----- : -
RzepOR69a2 : ----- : -
BoleOR69a2 : MSLRTYNNKTFLEYPQAFKLVCFESFIWCDNEHRHESALWYRKQLIFISTITLLVHVSALVAGVFPVPRATPEALYSSSDSKVFEALATISYSSCGIYKVNLLYRRHD : 112

120 130 140 150 160 170 180 190 200 210 220
DmelOR69aB : FENILNEFEELIQLIKRH-----AYRIHHYQEKYTHIRHTNFTPHSTAVVYVNSLPIILLMIREHFSNSQQLGVRICNSNTWYVQVQ---SIPGEFAA : 193
DmelOR69aA : FETILLBEHLQIYPRYKRN-----HYRCQHYFDMAMTIMRIEFLFYMILYVYNSAPLWLLWEHLHEEYDLSFKTQNTWTFPKVHG---SALGEGMA : 193
BdorOR69a1 : FAMILLEKFPQOLFPTARLQRAKAKFTKQS---LRGVVEFPHRIEHFVLKSNKMLKATLLYMFAPAYVNSLPIVEFLYEWMTTFPGVWVKRYQSNWYVQVONERNAKSFASFTLA : 213
BlatOR69a1 : FAMILLEKFPQOLFPTAGLRQRAKAKFTKRS---LRGVVEFPHRIEHFVLKSNKMLKATLLYMFAPAYVNSLPIVEFLYEWMTTFPGVWVKRYQSNWYVQVONERNAKSFASFTLA : 213
CcaphOR69a1 : FAMILLEKFPQOLFPTERVLQRAKAKFTKRR---LRGVVEFPHRIEHFVLKSNKMLKATLLYMFAPAYVNSLPIVEFLYEWMTTFPGVWVKRYQSNWYVQVONERNAKSFASFTVA : 213
BcurOR69a1 : FAMILLEKFPQOLFPTERVLQRAKAKFTKRR---LRGVVEFPHRIEHFVLKSNKMLKATLLYMFAPAYVNSLPIVEFLYEWMTTFPGVWVKRYQSNWYVQVONERNAKSFASFTVA : 213
CcaphOR69a2 : FAMILLEKFORLEPFTQLQWRKAHANGR---LRGVKFPHSEYFALKSNKMLKATLLYMFAPAYVNSLPIVEFLYVSLTPGVELKHQYQSNWYVQVONERNAKSFASFTLA : 213
RzepOR69a1 : FSALLLEQLNLFPTARARQWRAN-CGR---LRGVRIPIRYVEYFAVKSNRLMKHTTAYIPFYSYVNSLPIIEYLYEWLKPPEELKFRYSQSNWYVQVONERNAKSFASFTLA : 212
BcurOR69a2 : -----MEELKALFFSIKQRRLAEINESKEGI-IGSGGIYRLLEYEKESSRTIMQFIRYFMFAYVANSIEVWQLCFVAVITQOEHTTFAQANAWYVNNHNDHSSGEMLAS : 107
CcaphOR69a2 : ----- : -
BdorOR69a2 : IRLVLELEKDLFFSVAKORRIAEINESKEGQ-IGSGVIYRLLEYEKESSRSMRRLRFRINCIVYVNSVPIQLCYAIVTHQEKIMYRAQANWYVNNHNDHSSGEMMAA : 121
RzepOR69a2 : ICPFLLEKFNELFFSVVIOKRLAEANDYKTELKRGSGGYRYFAYFEKSRAMRMFTMYFVYFYFYNIIPILQLIYELSPNQTVTYKTKSNANWFWNNHNDHSSGEMV : 122
BoleOR69a2 : IARILLKELKDIFPSVAKORRLAEINESKDKQ-LGSGGIYRLLEYEKESSRSMRMTTTHFFKAYCANNAIPILQLCFAIMTHQEKITYKAQANAWYVNNHNDHSSGEMV : 223
i lle lfp q r ks m rr t a yyn pi y q n wypw n sf f

230 240 250 260 270 280 290 300 310 320 330
DmelOR69aB : VACIFSCQTNMCMNMFIQFLINFGIOLIEHFDGLARQLETDARNPHAKDKLKYIVYHTKLNLDADRVRNSFTLELISLSVSMISNCFALFMTDFDGTSLKHLGL : 305
DmelOR69aA : VLSITVGSFVGVGFSIVTQNLICLLTFOLKLYHDGISSQLVSLDCRRPGAHKDELILIAHHSRIQLQGDQVNDMMNFVSGSLVGATIAICMSSVSIMLLDASAFAKYSGL : 305
BdorOR69a1 : VYCVQSSSLGTGVARIMAAEFMLCFFTTQLQIHFDYLANALETIDAGANANEDKYLINYSQSLSYKETNAIFNVSEPMVNLCISAICMLGFSMVMISLAHAFKYSIGL : 325
BlatOR69a1 : VYCVQSSSLGTGVARIMAAEFMLCFFTTQLQIHFDYLANALETIDAGANANEDKYLINYSQSLSYKETNAIFNVSEPMVNLCISAICMLGFSMVMISLAHAFKYSIGL : 325
BminOR69a1 : VYCVQSSSLGTGVARIMAAEFMLCFFTTQLQIHFDYLANALETIDAGANANEDKYLINYSQSLSYKETNAIFNVSEPMVNLCISAICMLGFSMVMISLAHAFKYSIGL : 325
BcurOR69a1 : VYCVQSSSLGTGVARIMAAEFMLCFFTTQLQIHFDYLANALETIDAGANANEDKYLINYSQSLSYKETNAIFNVSEPMVNLCISAICMLGFSMVMISLAHAFKYSIGL : 317
CcaphOR69a1 : VYCVQSSSLGTGVARIMAAEFMLCFFTTQLQIHFDYLANALETIDAGANANEDKYLINYSQSLSYKETNAIFNVSEPMVNLCISAICMLGFSMVMISLAHAFKYSIGL : 317
RzepOR69a1 : VYCVQSSSLGTGVARILSAKFMLYFTTQLQMHFDYLAGALEIADAGELANDKYLINYSQSLSYKETNAIFNVSEPMVNLCISAICMLGFSMVMISLAHAFKYSIGL : 324
BcurOR69a2 : YLTGALVEYTSIAEVMSEGFIFCEFTQMLMHNLYLCSALSDASAPAVDQRLKALISYTHLRLSLKILMSIFNLTPALDLITITPAILSGMLTMMVMWRGQAVMSAF : 219
CcaphOR69a2 : FALILEKFLQIFPTERVQVY-----MFTN-----FSLKILMSIFNLTPALDLITITPAILSGMLTMMVMWRGQAVMSAF : 52
BdorOR69a2 : FLTQIATBYVVICIVFVCSENLFCFTTQMLMHN-----FSLSALS-----ALASAPADALLQKALISYHNLRAVMSAF : 195
RzepOR69a2 : YLVQASAFAGINIRIMCEGYLFGFTNQMLHFDYLAIAETLDATAPDSMKQKHTIITYANLRLPNEINSVENITLALDLINATFPIISGMLAMVIEFGRAVMSAF : 234
BoleOR69a2 : FLTQASAEYYSVAIRISGEFLFCFTTQMLMHN-----YLSAFN-----SLDASAPADALLQKALISYHNLHLR----- : 289
q f ff tq hf l d l l h l s n fn f a l a a g

340 350 360 370 380 390 400 410 420 430 440
DmelOR69aB : LLEITYNFSMCRSGTHLILTSKGVLPAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
DmelOR69aA : VAEVLNVFCIVCMGTETVLASGKVLPAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BdorOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BlatOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BminOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BcurOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
CcaphOR69a1 : LSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
RzepOR69a1 : LSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BcurOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 307
CcaphOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 162
BdorOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 283
RzepOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 322
BoleOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 322
f c g e k a fy nwy g yr mi f imr p ay sm t l sy ft a

450 460 470 480 490 500 510 520 530 540 550
DmelOR69aB : LLEITYNFSMCRSGTHLILTSKGVLPAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
DmelOR69aA : VAEVLNVFCIVCMGTETVLASGKVLPAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BdorOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BlatOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BminOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BcurOR69a1 : TSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
CcaphOR69a1 : LSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
RzepOR69a1 : LSFIVFTFFICVYTGKBLTETSDBKLLNAFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 393
BcurOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 307
CcaphOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 162
BdorOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 283
RzepOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 322
BoleOR69a2 : SFELLGLVFLCQNNGDELIRETMQINSAPFYNWYEGDLVYRRMLLILMKRATFYMWKTYKLAPVSIITYMA-----TLKFSYQMFECVRSILK- : 322
f c g e k a fy nwy g yr mi f imr p ay sm t l sy ft a

Supplemental figure 3-19 The alignment of OR69a

10 20 30 40 50 60 70 80 90 100 110
BoleOR71a : -----MTETITLLWMEITLLSGVDVYVFQWMLRAITETCLVILVNLINHYHAQTANELLQEWDRKSDM : 62
RzepOR71a1-2 : -----MEAYSEVILKIALSETVVVLVILVNLINHPFAPNAAKLLHEQSEFE : 44
BdorOR71a : MAINKLANFRTLEPVITLGLW---EGGDSSWFKRQRYRYQLPMHTITITFACILMIEFTYESLDYAI DVLKYMVEMAIISKVLNANYVEEQQTAEVLNLEANSAL : 106
BlatOR71a : MAIKKLANFRTLEPVITLGLW---QGGDSSWFKRHYRYQLPMHTITITFASLMHVLVEVYESLDYAI DVLKYMVEMAIICVLNANYVAQQTAEVLNLEDSAIL : 106
BminOR71a : MAFDSMANFRTTLRLIILGLW---HGGNGSFWFERHYRYQLFHTLITITFLLMCLVEVYESINAYAI DVLKYMCEMALVFKVLNANYVARKISELMMNQVSEIF : 106
BcurOR71a : MAIDTMNFRFTTIRLITLS---VTGELLILLSLEIITYSGDLDAIDVLKYLIVVMALGILVNLNANYVTRQITVEVMYVWENSEL : 81
CcaphOR71a : MTFDNIAHSFRTALVLLGLWVPVITVHG--SWLQNRVCYQYQLFTITFTESSPLMLLEVICSESLDHATEVVKFLITELMALVFLNATYVARKAAAPLHEWETGEM : 108
RzepOR71a1-1 : M5PTITANSFRTALVLLGLWVPVITVHG--SWLQNRVCYQYQLFTITFTESSPLMLLEVICSESLDHATEVVKFLITELMALVFLNATYVARKAAAPLHEWETGEM : 108
DmelOR71aX1 : MDYDRIRPVNFTLGVNWRWLW---RKESVSTPDWTNNQAYALHPVFTLEVLVLLWLEAKRDIQHTADVLICITTTTALGGWNLINIKYAHVAGQILSEMSTWDL : 106
DmelOR71aX2 : MDYDRIRPVNFTLGVNWRWLW---RKESVSTPDWTNNQAYALHPVFTLEVLVLLWLEAKRDIQHTADVLICITTTTALGGWNLINIKYAHVAGQILSEMSTWDL : 106
m r l tf f l ie i s vl l Kv N W y Ew F

120 130 140 150 160 170 180 190 200 210 220
BoleOR71a : ALKTLLEKQKMQGAQRYEKKVVAVVSLLSICSVFMAFLFSVFPMDTALIPYNNMAS-WRGSNA-PLPLMEDIVVPSLNCNQTIEFFFLCLMFIHTICLRLMIGIMERL : 171
RzepOR71a1-2 : VRTPTQOVQWRRRAQYAKKVLAFVRIWISICVLLAFSLVVFMTPTQLPVYVIEVKKKREGNGPLYLDEFAVITPCCNIEIDSLQCYLHLHTICLRLIGLRLM : 154
BdorOR71a : EIRTSAEQKMQKSKQKFNKLTIXMGTGLNSAFCALLAAALMDAKELLYALALYD-WRDTYFGIYCECIAMPFTCLCNITIDLFQAYLLHLHTICLRFVISMRLERL : 215
BlatOR71a : EIRTSAEQKMQKSKQKFNKLTIXMGTGLNSAFCALLAAALMDAKELLYALALYD-WRDTYFGIYCECIAMPFTCLCNITIDLFQAYLLHLHTICLRFVISMRLERL : 215
BminOR71a : ALRDSAEQKMQKQKQKFNKLTIXMGTGLNSAFCALLGVLMLGATEQYALMMKN-WRDTYFGIYCECIAMPFTCLCNITIDLFQAYLLHLHTICLRFVISMRLERL : 215
BcurOR71a : VLRNDDAEQKMAKQKTKFRKLGMTSFGLGNSAMCAGLVLLMGATEQYALMMKN-WRDTYFGIYCECIAMPFTCLCNITIDLFQAYLLHLHTICLRFVISMRLERL : 190
CcaphOR71a : VLRNDAENKMAKQKTKFRKLMGLIYWSISSAVCALLSCFLINDQALFFYPLTNK-WLEDYVLMYFELLTMTPTCLCNIEIDVFQCYLLHLHTICLRFVISMRLERL : 217
RzepOR71a1-1 : VLQTVGEQEMRACQARAFHKVILFVGCFSNAIACFVAVPMMNTRLEFPFALTNK-WREDYVLMYFELLTMTPTCLCNIEIDVFQCYLLHLHTICLRFVISMRLERL : 219
DmelOR71aX1 : EIRSKQVDMWRFEHRRNRNVFMYCLCSAGVIFPIVQPLFDIPNRLFFWMTEFDWQQPVLFWYAFIQATTITIAACQNVMTDAVNNWILMLSLCLRMLGQLRSLK : 216
DmelOR71aX2 : EIRSKQVDMWRFEHRRNRNVFMYCLCSAGVIFPIVQPLFDIPNRLFFWMTEFDWQQPVLFWYAFIQATTITIAACQNVMTDAVNNWILMLSLCLRMLGQLRSLK : 216
l E MW q f k y a lP W P w W Y pf C cN d Yl lHl LC R Rl rL

230 240 250 260 270 280 290 300 310 320 330
BoleOR71a : GDQVNDVIEITLENITIKHQRIEGMAKSCQRIIMWFLAQITFSSLLICSSISQIQ-----ISFSSNPNFLGFIQVVMAMALEIFLPCYVNLNITVESENISNHL : 274
RzepOR71a1-2 : EDAGTIEITSLKLLKLMQGVKRMVKRCEIIVSLVQVIFSSMLICFTAYASQ-----LSFSSNPNFADVAMQVGVMSQIFLPCYVNLNITVESENISNHL : 257
BdorOR71a : ESAGTIEITSLKLLKLMQGVKRLAKCEQVSIALLSQMLTFLILCPIINNMQNVETANDIAHFSNPAHLAMQVALISMEMEFLPCYVNLNITVESENISNHL : 325
BminOR71a : DNAGTDEAIEKFEFLNNKMQGVKVD-----ENPVHCLAMLQVNLIVSQMLPCYVNLNITVESENISNHL : 281
BcurOR71a : ANAGADAEIARLMDKMHQGVKEMAKISCEHIIISLMLTQITITFLITCPIIYNLAN-----ANFREDPVHCLAMLQVALIVSQMLPCYVNLNITVESENISNHL : 293
CcaphOR71a : ANAGDENAIEKFEFLKTKMHKINEW-----IMLSALITCPIIYRMS-----VHFSNPNTEYLAQVNVAMSMQIFLPCYVNLNITVESENISNHL : 305
RzepOR71a1-1 : GNATEDDAVAFKFKVIMKMHQGVIDMSKRCVQMSVPLVMQIMLSFFIICPIIYRMS-----VHFSNPNTEYLAQVNVAMSMQIFLPCYVNLNITVESENISNHL : 322
DmelOR71aX1 : QHD--DKDLREKFLLELHLHQRLKQALSTIEFISKSTFTQILVSSLIICFTTISMQM-----SPVLQDLPGFAAMQVNLVAMIMQVMLFTTICNAVDASNNMTDSM : 317
DmelOR71aX2 : QHD--DKDLREKFLLELHLHQRLKQALSTIEFISKSTFTQILS-----PVLQDLPGFAAMQVNLVAMIMQVMLFTTICNAVDASNNMTDSM : 302
t e i hqR qi i c y p am QY fLPcy Ne t s L l

340 350 360 370 380 390
BoleOR71a : NCDWTV--MSLYNRQIFLYMEHLKOPITTYAGNYQIFGLPVESKTMNNAYSLALLANVNEE--- : 337
RzepOR71a1-2 : XSCNWD--MSAYNRKIFLYVMDLQKOPALRAGSYFEIQLGVQESKTMNNAYTLALLANVADEDE-- : 321
BdorOR71a : XSCNWD--AMSAVNRKIFLYVMSKKKPVVLCAGRFFEIGIPISKAMNNAYSVLALLLVNNDDEQH- : 390
BlatOR71a : XSCNWD--AMSAVNRKIFLYVMSKKKPVVLCAGRFFEIGIPISKAMNNAYSVLALLLVNNDDEEH- : 390
BminOR71a : XSCNWTGLVDFSPAAPNRSTAPSQRSTFAIQRSAPVQHAVG-QIVHTTYNNHMFQGFDLWSLQY : 348
BcurOR71a : XSSDWTG--MSAYNRKIFLYVMSKKKPVVLHAGSFFEIGIPISKAMNNAYSVLALLLVNNDDEQH- : 357
CcaphOR71a : XNADWTG--MSAYNRKIMLLYMQYKLKPL-----TMNNAYSLALLLVNNDDEKDKK : 354
RzepOR71a1-1 : XCCDWTG--MSAYNRKIFLYVMDLQKOPALRAGSYFEIQLGVQESKTMNNAYSLALLLVNNDNNKN- : 387
DmelOR71aX1 : XNSDWD--MNCMRRLVLMFMVYVNRVTKAGGFHIGLPLFTKTMNQYSLALLLVNNDNQ- : 378
DmelOR71aX2 : XNSDWD--MNCMRRLVLMFMVYVNRVTKAGGFHIGLPLFTKTMNQYSLALLLVNNDNQ- : 363
Y dWT m rr m l p l ag f ig f k mn aYs lall n

Supplemental figure 3-20 The alignment of OR71a

```

      10      20      30      40      50      60      70      80      90      100      110
BdorOR74a1 : -----MLYRRLKNGKLIPLSWPVAAYRLLNHHCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 105
BlatOR74a1 : -----MLYRRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 105
BoleOR74a1 : -----MLYRRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 105
BminOR74a1 : -----MLYRRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 105
BcucOR74a1 : -----MLYRRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 105
CcaphOR74a1 : -----MLYRRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 105
DmelOR74a1 : ---MSFHYRRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASVLLRLYDRFFWAFGFIIFMQHNDABLRVIIVNNNLDDEMLICGPTYLIVVEIHLRAFQLGLKKKPAKR : 108
BdorOR74a2 : MRYLPISYHKPLPNGHHPIDMOLYGFCCAN--GWPAAAHITKTRYIADIMVTIMQMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 109
BlatOR74a2 : -----PAAAHITKTRYIADIMVTIMQMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 75
BoleOR74a2 : MRYLPISYHKPLPNGHHPIDMOLYGFCCAN--GWPAAAHITKTRYIADIMVTIMQMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 109
BcucOR74a2 : -----MVTIACMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 60
BminOR74a2 : MRYLPISYHKPLPNGHHPIDMOLYGFCCAN--GWPAAAHITKTRYIADIMVTIMQMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 109
CcaphOR74a2 : MRYLPSSYHKPLPNGHHPIDMOLYGFCCAN--GWPAAAHITKTRYIADIMVTIMQMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 109
RzepOR74a2 : MRYLPSSYHRELPLNGHHPIDMOLYGYMGAC--GWPAAAHITKTRYIADIMVTIMQMSSEGMVLIGEAVVMHNDLNDISFVCTVLAAPNLILFEMMLRAYNIYRRNSPFT : 109
      p l n g p w n w p l d f e n
      120      130      140      150      160      170      180      190      200      210      220
BdorOR74a1 : FLQKFVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
BlatOR74a1 : FLQKFVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NAIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
BoleOR74a1 : FLQKFVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
BminOR74a1 : FLQKFVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
BcucOR74a1 : FLQKFVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
CcaphOR74a1 : FLKRYVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
RzepOR74a1 : FLKRYVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 215
DmelOR74a1 : LLQKFVAEIVDESSSHKLYANIQKSLRPIWFYSLLYFSTLSSVYVIMFVNNVNNVKAPLYKMYPPDITP-NPIYVAIVLSNINWVGFTVITMVSGEDNIVSEVMLHLNGR : 218
BdorOR74a2 : HIEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
BlatOR74a2 : HIEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
BoleOR74a2 : HIEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
BcucOR74a2 : HIEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
BminOR74a2 : HVEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
CcaphOR74a2 : HVEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
RzepOR74a2 : HLEEFVKKIIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTVVVVYVPSGLKIKERLVPPFPIFGFDYTVVPWPRVLVFLTMSMTGFAVVGVLVAHANILAMQILHLNGR : 220
      f y i y p l i p y t l y p y n n f d t y W G f v E N l L H L N g
      230      240      250      260      270      280      290      300      310      320      330
BdorOR74a1 : FLLIQOKLRHDAERLLHVVDNRNI-----ADGLRRRIIEAEENVRLYKTAEDFEREFSPRIFVNLSPFAGLICVLGFKVYI----- : 292
BlatOR74a1 : FLLIQOKLRHDAERLLHVVDNRNI-----ADGLRRRIIEAEENVRLYKTAEDFEREFSPRIFVNLSPFAGLICVLGFKVYI----- : 292
BoleOR74a1 : FLLIQOKLRHDAERLLHVVDNRNI-----ADGLRRRIIEAEENVRLYKTAEDFEREFSPRIFVNLSPFAGLICVLGFKVYI----- : 292
BminOR74a1 : FLLIQOKLRHDAERLLHVVDNRNI-----ADGLRRRIIEAEENVRLYKTAEDFEREFSPRIFVNLSPFAGLICVLGFKVYI----- : 292
BcucOR74a1 : FLLIQOKLRHDAERLLHVVDNRNI-----ADGLRRRIIEAEENVRLYKTAEDFEREFSPRIFVNLSPFAGLICVLGFKVYI----- : 292
CcaphOR74a1 : FLLIQOKLRHDAERLLHVVDNRNI-----ADGLRRRIIEAEENVRLYKTAEDFEREFSPRIFVNLSPFAGLICVLGFKVYI----- : 292
DmelOR74a1 : YIQIGQDLRRSAQMLLKSSSLNV-----AIAYRLNLTHILRRNAALRDFGQKVEKEFTLRIFFVFAFAGLICVLGFKVYI----- : 320
BdorOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
BlatOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
BoleOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
BcucOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
BminOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
CcaphOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
RzepOR74a2 : YSLILDDLRNISRESIAEHEKCKRK-DNMLVTQRFRRYLYDIIRRNVELNDFAKSMQEQYSFRFVVMALASATLLCVLGLTATLGLTAQNRIRFVSWIIGKVVELLIFGR : 330
      l l L r r i N v l F a s f R F v S A L l C v L g f t
      340      350      360      370      380      390      400      410
BdorOR74a1 : -----VSRLS----- : 297
BlatOR74a1 : -----TNEMSYTFTECNWELVLLKSGDSKANVRLMKTLTLAISTIQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 369
BoleOR74a1 : GSTVIYTNEMSYTFTECNWELVLLKSGDTSKANVRLMKTLTLAISTSQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 402
BminOR74a1 : -----TNEMSYTFTECNWELVLLKSGDTSKANVRLMKTLTLAISTSQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 368
BcucOR74a1 : GSTVIYTNEMSYTFTECNWELVLLKSGDTSKANVRLMKTLTLAISTSQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 402
CcaphOR74a1 : GSTVIYTNEMSYTFTECNWELVLLKSGDTSKANVRLMKTLTLAISTSQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 401
RzepOR74a1 : SSTIATPNTQISAFYESSWELVHQSCKDSKANVRLMKTLTLAISTSQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 402
DmelOR74a1 : GSILLKTDDELGMYYITADWEQVHQSCKDSKANVRLMKTLTLAISTSQKPFVLTGFKYFVSLSLTAVLKTLQAGAGSYFTFLTSMR- : 404
BdorOR74a2 : GTTLSTTMDKLSYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 414
BlatOR74a2 : GTTLSTTMDKLSYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 380
BoleOR74a2 : GTTLSTTMDKLSYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 414
BcucOR74a2 : GTTLSTTMDKLSYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 365
BminOR74a2 : -----TDELSTYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 368
CcaphOR74a2 : GTTLSTTMDKLSYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 414
RzepOR74a2 : GTTLSTTMDKLSYSYCCWEDVILHSTDAENKKMLKLIALAHLSNSPFRLTGLNFSVNNYETVVAIFRGAGSYFTVIYAYR- : 415
      t t s y w e s n l m k l a i p f l t g v v i g a s y f t r

```

Supplemental figure 3-21 The alignment of OR74a

```

      10          20          30          40          50          60          70          80          90          100          110
BdorOR82a : MPEDLFRIQRNCLRMVGHQDIFDNN EASSSDEQKSKSKRQR--RCFRHQALKYVLLLLFMVSAQLPMNNYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 111
Blator82a : MPEDLFRIQRNCLRMVGHQDIFDNN EASSSDEQKSKSKRQRRCFRHQALKYVLLLLFMVSAQLPMNNYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 113
BoleOR82a : MPEDLFRIQRNCLRMVGHQDIFDNN EAPS--DQKSKSKQR--WCLHHQCTVAKYVLLLLFMVSAQLPMMDYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 110
BminOR82a : -----HMDYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 46
BcucOR82a : MPEDLFRIQRNCLRMVGHQDIYDDNETAGDEQKSKSQQR--CFRHSQTLKVAALLLLMMSAQLPMMDYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 110
Ccapor82a : -----MKYVLLLLMMSAQLPMMDYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 62
RzepOR82a : -----MKHALLFMISAQWPMMDYIYHIDDLALATACLSIVFTNVLTVIKTSFTFYKREFKSLM : 62
DmelOR82a : -MGRFLQGLQECYCLRAMGHKDDMDSTDTA-----LSLKHSSMLFVISAQYELISVAIYNRNDEMKVTAACLSIVFTNVLTVIKTSFTFYKREFKSLM : 92
      k llll m saq pmm YIYhidl1 laTaCLsivFTNVLTVIKTSFTFYKREFKslm

      120          130          140          150          160          170          180          190          200          210          220
BdorOR82a : AEFESMYDELQERAGAKR-----CLVTNVNGAKRFVKLYFGACTSGLYFTINPLVSMINAKFOAKPIPLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 219
Blator82a : AEFESMYDELHEAGAKR-----CLVTNVNGAKRFVKLYFGACTSGLYFTINPLVSMINAKFOAKPIPLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 221
BoleOR82a : AEFESMYDELHEAGAKR-----CLVTNVNGAKRFVKLYFGACTSGLYFTINPLVSMINAKFOAKPIPLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 218
BminOR82a : AEFESMYDSE--SGAKR-----CLVTNVNGAKRFVKLYFGACTSGLYFTINPLVSMINAKFOAKPIPLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 151
BcucOR82a : AEFESMYDELHEAGAKR-----CLVTNVNGAKRFVKLYFGACTSGLYFTINPLVSMINAKFOAKPIPLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 218
Ccapor82a : TEFELMYDELRGAGAKP-----LLVTNVNGAKRFVKLYFGACTSGLYFTINPLIGMFWAKFOAKPIPLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 170
RzepOR82a : LFEFMYDELHEADAKR-----LLVAANVGAKRFVKLYFGACTSGLYFTINPLVGMINWDLQKSVLLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 170
DmelOR82a : HRRKMYHSGSASHIPRYREGLDYVAEANKLASFLGRAVCVSCGLTGLYFMELGPIKIGVCRWHGTTCDKLELPMMPMRFPDFDFFESTPGYQIAYIYITITIVVMHATSVDGLFV : 205
      eFe Meysal agak lvt NvgAkrfivklyf s TGLYfti Plv m wakfg kp lELPMMPMRFPdfdestPGY ay Yti itivVMhAtsVDGLFv

      230          240          250          260          270          280          290          300          310          320          330          34
BdorOR82a : SFTTNLRGHFQAQYFIETNTFDKSEALLQRELGIYVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 332
Blator82a : SFTTNLRGHFQAQYFIETNTFNKSEALLQRELGIYVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 334
BoleOR82a : SFTTNLRGHFQAQYFIETNTFDKSEALLQRELRIYVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 331
BminOR82a : LFTTNLRGHFQAQYFIETNTFDKSDALLQRELRFYVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 225
BcucOR82a : SFTTNLRGHFQAQYFIETNTYDKSDALLQRELRIYVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 331
RzepOR82a : SFTTNLRGHFQAQYFIETNTFNKSEALLQRELRFYVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 283
DmelOR82a : SFTTNLRGHFQAQYFIETNTFDKSDALLQRELRAIVQHVRLLELQAGSVQVRFKPIIFGQFLMTSLQVCVYIYQLVMNMGVIMEMVYCTFLSSILLQLLIYCYGAEFLKTE : 283
      SFTTNLRGHFQAQYFIETNTf KS allQ eL yV YHVrLL L svqrifKPIifGQFLMTSLQVCVYIYqlv nmgv memv yctflssillqliiycygaeFlk e

      0          350          360          370          380          390          400
BdorOR82a : SSAVSTAIQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 399
Blator82a : SSAVSTAIQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 401
BoleOR82a : SSAVSTAIQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 398
BminOR82a : CSAVGTAVQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 292
BcucOR82a : SSAVGTAVQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 398
Ccapor82a : SSAVGTAVQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 350
RzepOR82a : SSAVGTAVQMSQWYNLPRRRHVLRMLMLRSQREIISAGFYEASLANFMSILKAAMSYYITFIQSIE : 350
DmelOR82a : SLQVDTAVRLNHLASRTKTSLSIILOSQKVLTRAGFVASLANFVGCRTALSLTLTKSIE : 385
      ssaV TA qmSqWynlpPrhRhvirLmmlrSqREiIsAGFYeASLANFmsIlkaAmSyITFIqSIE

```

Supplemental figure 3-22 The alignment of OR82a

```

      10          20          30          40          50          60          70          80          90          100          110          120
BdorOR83a1 : -MSSNEEQKPDISATVHDGCGSTCRMRDRMRRCIRIWHMLWFSAMYRLPFLERYFPARLRFLAVTLWDTYELFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 120
Blator83a1 : -----MQRDRMRRCIRIWHMLWFSAMYRLPFLERYFPARLRFLAVTVWDTYELFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 96
BminOR83a1 : -MSSNEEQKPDISATVHDGCGSTCRMRDRMRRCIRIWHMLWFSAMYRLPFLERYFPARLRFLAVTLWDTYELFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 119
BoleOR83a1 : -MSSNEEQKPDISATVHDGCGSTCRMRDRMRRCIRIWHMLWFSAMYRLPFLERYFPARLRFLAVTLWDTYELFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 120
BcucOR83a1 : -MADEETQKTQIPTTVNKGYPYV-MERDRMRRCIRIWHMLWFSAMYRLPFLERYFPACQLCLAITLDMAYEVFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 118
Ccapor83a1 : -----MALADRKTPTPTDEHIGCPVYSTQRDRMRRCIRIWHMLWFSAMYRLPFLERYFPARLRFLAVTLWDTYELFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 118
DmelOR83a1 : -----MAITLDYELFLYLLTHDILEICTIYLNQKDGDELEIVNMQIYVYVWAIKARVFFKR : 62
RzepOR83a1 : -----MKSFTKEERIKDDSKRRDLFLVFMTCIAAMYFPFGYVNGSGVLAIVLRCDLTVELENYFVSVAHAGYICTIYINYGQDLOFFVNCQIATITVYVWAIKARVFFKR : 109
BcucOR83a2-1 : -MSPFSKRNIGLTGSCCTPNPGCISNEKRSBLFLVFWMLFFSAIRIPIFDKHPLPRMHGSLVNVNWIIFLYLVVHLVLEIITVYVWAIKARVFFKR : 120
Ccapor83a2-2 : -----MVLHILVLEIITVYVWAIKARVFFKR : 47
BminOR83a2 : -MIPFSKRNIDTTERCANPFGCITNEKRCBLFLVFWMLFFSAIRIPIFDKHPLPRMHGSLVNVNWIIFLYLVVHLVLEIITVYVWAIKARVFFKR : 120
DmelOR83a2 : -----MVLHILVLEIITVYVWAIKARVFFKR : 47
Ccapor83a2 : MILTDAPTAAHAAGLCAASPNGCLSNVKBRLERVFWMLMGAARIPFENPHLPRLCGNYSAINVILIFLLTLTVIHFLVLEIITVYVWAIKARVFFKR : 121
      p r d f r a e f l h i l f t i y n d g l e c i q y w a i k f r

      130          140          150          160          170          180          190          200          210          220          230          240
BdorOR83a1 : IQPKRKVKELMRYLNEECRTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 241
Blator83a1 : IQPKRKVKELMRYLNEECRTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 217
BminOR83a1 : IQPKRKVKELMRYLNEECRTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 240
BoleOR83a1 : IQPKRKVKELMRYLNEECRTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 241
BcucOR83a1 : IQPKRKVKELMRYLNEECRTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 239
Ccapor83a1 : IQPKRKVKELMRYLNEECRTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 239
RzepOR83a1 : VQAKRLNLYLMEYLAESMSSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 183
DmelOR83a1 : FRFGLNLTLSINIDYEYTRSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 240
BcucOR83a2-1 : IYELVNGIVDFVNEEYVQHSALGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 241
Ccapor83a2-2 : IYELVNGIVDFVNEEYVQHSALGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 79
BminOR83a2 : IYELVNGIVDFVNEEYVQHSALGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 143
DmelOR83a2 : ----- : 143
Ccapor83a2 : VRELVRDINDVNEKYIVHSAAGFTYVTFKESVDLSNMWTVFLICCYAGTVFWLVPFIHQDSSLPACWYFDIKKVPYVVEYFIYFLQTVGQLOIAAAGCTSAFYVLIIVFSGQFDI : 242
      p n s a g f t y t p p l c m y p y p q q q f s g q d

      250          260          270          280          290          300          310          320          330          340          350          360
BdorOR83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 361
Blator83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 337
BminOR83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 360
BoleOR83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 361
BcucOR83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 330
Ccapor83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 359
RzepOR83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 303
DmelOR83a1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 345
BcucOR83a2-1 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 362
Ccapor83a2-2 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 176
BminOR83a2 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 240
DmelOR83a2 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 303
Ccapor83a2 : LNCSLKNILATTIILIRKPKSELILLREEQSIADYELNQYVIAKEYRTDFDPIHPFE-KETPKPENFYEGKIALRPFIAHVRVLYGLKMLEDLVSLYSLFYLYLEVTLVLCVAFVWVK : 363
      l cslkn a y l lr e n e d d c h t f a f a c h h i l l e l y w k e v t C a F v K

      370          380          390          400          410          420          430          440          450          460          470
BdorOR83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 473
Blator83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 449
BminOR83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 410
BoleOR83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 473
BcucOR83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 442
Ccapor83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 471
RzepOR83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 415
DmelOR83a1 : STAANSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 453
BcucOR83a2-1 : SSDEKSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 470
Ccapor83a2-2 : SSDEKSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 283
BminOR83a2 : SSDEKSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 332
DmelOR83a2 : SSDEKSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 198
Ccapor83a2 : SSDEKSFRLRLSLQVLLALWEMFMICYMGEIIFLCSKRCDALRSPPWHLHSGEIKODTLFIFILNAQRPRFLTGCKMYNINLKMRTILITTSFSLITILQNMMDLRQPPQK : 471
      s t d d k s f r l r l s l q v l l a l w e m f m i c y g e i i f l c s k r c d e a l r s p w h l h s g e i k o d t l f i f i l n a q r p r f l t g c k m y n i n l k m r t i l i t t s f s l i t i l q n m d l r q p p q k

```

Supplemental figure 3-23 The alignment of OR83a


```

10      20      30      40      50      60      70      80      90      100     110
DmelOR85c : -----MKEMKYAVFTYTSVTEIEPTTIDSRSKKASIMHSLFFWANVINLSVIVFGETILVGVAYS DGKFIIDAVTVLSYGFVINGMSKMFIFWKKKTDL : 94
DmelOR85b : -----MEKLMKYASFFVTAVGIRPYTNGEESKMNKLQIFHIVFWSNVINLSFVGLFESIVVYSAPMDNKKFLRAVTALSYIGFIVTGMSKMFYFRKKTKAIT : 95
BdorOR85bc1 : -----MSNIIRFEAFLRIPSPFFYRSVGVLDLWNTNGGP-----LQNAVFIYSIFLNVNVLSELIFAVLMLTKN-PIQATMTLSYAGFVLVGSIKMFMWRKKAEMT : 95
BlatOR85bc1 : -----MSNIIRFEAFLRIPSPFFYRSVGVLDLWNTNGGP-----LQDAVFYFGLNVLNVLSELIFAVLMLTKN-PIQATMTLSYAGFVLVGSIKMFMWRKKAEMT : 95
BolerOR85bc1 : -----MPNVIISFEAFLRIPSPFFYRSVGVLDLWNTNGGP-----LQNAVFIYFGLINVLNVLSELIFSVLMVSKN-PIQATMTLSYAGFVLVGSIKMFMWRKKAEMT : 95
BcucOR85bc1 : MAPLRVCPSSIMSKIIRFEAFLRIPSPFFYRSVGVLDLWNTNGGP-----LQDAVFYFGLNVLNVLSELIFAVLMLVSKN-PIQATMTLSYAGFVLVGSIKMFMWRKKAEMK : 105
CcaphOR85bc1 : -----MCENIESFEAFLRIPSPFFYRSVGVLDLWNTNGGP-----IQRFPIFYFGLNVLNVLSELIFAIITVSEN-PIQATMTLSYAGFVLVGSIKMFMWRKKTENT : 96
RzepOR85bc1 : -----MPDTIRFESFLRLPNELYSVGVLDLWGTGGGL-----LQQALFYLCIINVLNVLSELIVLALMIFGKN-IVQATMTLSYAGFVLVGFIKLYMYWRKKQELT : 95
BlatOR85bc2X1 : -----MSTIIKFPEFLGLSSFFCYNIGIKLRGPDGPF-----WLNFWLYLASINLFLTVFAECIYIIMTIRSD-FIVAIMTLSYVSFVLVAVYKWWYLYNYQTERN : 95
BlatOR85bc2X2 : -----MSTIIKFPEFLGLSSFFCYNIGIKLRGPDGPF-----WLNFWLYLASINLFLTVFAECIYIIMTIRSD-FIVAIMTLSYVSFVLVAVYKWWYLYNYQTERN : 38
BdorOR85bc2 : -----MSTIIKFPEFLGLSSFFCYNIGIKLRGPDGPF-----WLNFWLYLASINLFLTVFAECIYIIMTIRSD-FIVAIMTLSYVSFVLVAVYKWWYLYNYQTERN : 95
BolerOR85bc2 : -----MTLSYVSFVLVAVYKWWYLYNYHTERT : 27
BminOR85bc2 : -----MENLEKFLVRLNFFGNHIMKMPWGRLDGPF-----QRRFLFYFSSINLLITTFIAESSYIIVTITSD-FILAVMTLSYVITVAVAKWWYLYTYQTERT : 92
Ccaph5bc2 : -----MSTIIIRFPEFLRLPSESRNIGILWGGQRGKL-----FDRFMFYFSSINLFLTLAEILWYIISTISTD-ETIAIMGLSYVSFVLVAVYKWWYLYTIYDMKVS : 95
      e f      ff      q      g      n      e      f i a m t L S Y      F v      K y      e

120     130     140     150     160     170     180     190     200     210     220
DmelOR85c : DLVKELEHIYNGKAEEMYRDRVYLSCSRISITVALLYSVLITFNILFNSIMQFLVYEKLKIRVVGQQLFPLMYFPNNWHENITYYV-----LLFCNFIHGTSAAG : 198
DmelOR85b : ELINLEKEIYENGLIREERYNLPMYLGTCRISLIYSLLYSVLITFNILFNSIMQFLVYEKLKIRVVGQQLFPLMYFPNNWHENITYYV-----LLFSQNFAGYTSAG : 199
BdorOR85bc1 : RFLQLMNTIFERTEEQKKMNLRRSHLQCTIVMTVFAMIFMLITWTNLYNYPYMQROQYDCWLHMSRSINKTLPEYSYIPNNHHDHTFYL-----YYTLDSIAGYHSAAG : 199
BlatOR85bc1 : RFLQLMNAIFERTEEQKKMNLRRSHLQCTIVMSAFAMIFMLITWTNLYNYPYMQROQYDCWLHMSRSINKTLPEYSYIPNNHHDHTFYL-----YYTSDSIAGYHSAAG : 199
BolerOR85bc1 : RFLQLMHTIFERTEEQKKMNLRRSHLQCTIVMSGFATIFMLITWTNLYNYPYMQROQYDCWLQVRSVNTKTLPEYSYIPNNHHDHTFYL-----YYTLDSIAGYHSAAG : 206
BcucOR85bc1 : RFLQLMNAIFERTEEQKKMNLRRSHLQCTIVMSGFAMFVLITWTNLYNYPYMQROQYDRLLDVSRSINKTLPEYSYIPNNHHDHTFYL-----YYTLDSIAGYHSAAG : 209
CcaphOR85bc1 : QFLKLMDEIFERTEEQKKMNLRRSHLQCTIVMSGFALIFMLITWTNLYNYPYMQROQYDCWLDRSINKTLPEYSYIPNNHHDHTFYL-----YYTLDSIAGYHSAAG : 200
RzepOR85bc1 : RFLQMDAIFERKASQOQSMDSRHLQSSIVMSIFSLIVMMLICTYNLYPWLHRELYDCWLHMSRSIEKSLPEYSYIPNNHHDHTFYL-----LYVSGSPFAYHAAAG : 199
BlatOR85bc2X1 : AFFQRLDALFHHKKEQENIKLXEYFRLNKLATRGYITTFMVVITWLNLYITISORFIYTKLLHVVH-IERVLEPYQALYPDNRDNTYTV-----IYVTGDFGFHATCA : 198
BlatOR85bc2X2 : AFFQRLDALFHHKKEQENIKLXEYFRLNKLATRGYITTFMVVITWLNLYITISORFIYTKLLHVVH-IERVLEPYQALYPDNRDNTYTV-----IYVTGDFGFHATCA : 141
BdorOR85bc2 : AFFQRLDALFHHKKEQESIKLXEYFRLNKLATRGYITTFMVVITWLNLYITISORFIYTKLLHVVH-IERVLEPYQALYPDNRDNTYTV-----IYVTGDFGFHATCA : 198
BolerOR85bc2 : VEFQRLDALFHHKKEQETIKLKYLRNKLATMSYITTFMVVITWLNLYITISORFIYTKLLHVVH-IERVLEPYQALYPDNRDNTYTV-----IYVTGDFGFHATCA : 130
BminOR85bc2 : AFFQRLDALFHHKKEQENIKLXEYFRLNKLATRGYITTFMVVITWLNLYITISORFIYTKLLHVVH-IERVLEPYQALYPDNRDNTYTV-----IYVTGDFGFHATCA : 196
Ccaph5bc2 : TVLKRLNALFHHKKEQENIQILIKYKMSKFYTLFTYTVFHLVITWTNLYITISORFIYTKLLHVVH-IERVLEPYQALYPDNRDNTYTV-----IYVTGDFGFHATCA : 199
      f      fp t      q      l      r      fm      lw      yn      q r      i y      L      LPY      p W      d      w      y      y      Q      Ag      h

230     240     250     260     270     280     290     300     310     320     330
DmelOR85c : QISTDILLCAVATQVVMHFDYLRAVVE-----KQVLDRDWSSENSRLAKTVOYHORIIR-LMDVLDNDFIGPILLNEMVSTFVICFVGF : 281
DmelOR85b : QISTDILLCAVATQVVMHFDFLNSME-----RHELSGDKKDSRLVDIVRYHERIIR-LSDAVNDIFIGPILLNEMVSSFFVICFVGF : 282
BdorOR85bc1 : QIASDVLVCAMATQIIMHYEYVAQRIT-EYQPOAL-----RAPRHQVKESESYRKDMRELCDIIXYHANVLS-LSDIMNEVLGVPILLNEMTSSFFVICFVGF : 294
BlatOR85bc1 : QIASDVLVCAMATQIIMHYEYVAQRIT-EYQPOAL-----KGAVRDVKESELYRKDMRELCDIIXYHANVLS-LSDIMNEVLGVPILLNEMTSSFFVICFVGF : 294
BolerOR85bc1 : QIASDVLVCAMATQIIMHYEYVAQTIT-EYRPQLVDCCKIS-----RAPRLDXESERSLCKDMRELCDIIXYHANVLS-LSDIMNEVLGVPILLNEMTSSFFVICFVGF : 307
BcucOR85bc1 : QIASDVLVCAMATQIIMHYEYVAQRIT-EYQPOVG-----ADSGSKNEAYCRDMRELCDIIXYHANVLS-LSDIMNEVLGVPILLNEMTSSFFVICFVGF : 301
CcaphOR85bc1 : QIASDVLVCAMATQIIMHYEYVSHKIRSRGERKCVDSKS-----VSLCNALNHWTTEQVATHKDMRELCDIIXYHANVLS-LSDVMDNVLGVPILLNEMTSSFFVICFVGF : 306
RzepOR85bc1 : QIASDVLVCAMATQVIMHYEYVALKIE-QQPKWGTSCCVNRQQQVQLVQASSQWEMKRAAYIEDMRFLGDLIAVYHNSILS-LSNFMNEVFGVPILLNEMTSSFFVICFVGF : 308
BlatOR85bc2X1 : QIAYDILLCILSLQILIMHYDHISRSLE-GQOTKFAEVHGV-----INNGLPQLACAAYELRAVKEDIQFISNIVSYHNELLS-LSKSLNKLFGMPLFVNFFTSATICFLSF : 304
BlatOR85bc2X2 : QIAYDILLCILSLQILIMHYDHISRSLE-GQOTKFAEVHGV-----INNGLPQLACAAYELRAVKEDIQFISNIVSYHNELLS-LSKSLNKLFGMPLFVNFFTSATICFLSF : 247
BdorOR85bc2 : QIAYDILLCILSLQILIMHYDHISRSLE-EKQTKFAEVHGV-----INNGLPQLACAAYELRAVKEDIKFISNIVSYHNELLS-LSKSLNKLFGMPLFVNFFTSATICFLSF : 304
BolerOR85bc2 : QIAYDILLCILSMHILIMHYDHISRSLE-GQOTKFAEVHGV-----TSNSLQQLARVAELKAVKEDIKFISSNIVSYHNELLR-FV-----IYVTGDFGFHATCA : 211
BminOR85bc2 : QMAFDILLITLSHILIMHYDHISRSLE-GQOTKFAEIHG-----KNGLTQQAARAMELKAVKDDIKFISSNIVSYHTELRL-F-----IYVTGDFGFHATCA : 271
Ccaph5bc2 : QILTLLILILISHLIMHYDHARSLL-NYQSKFAELYGKES-----TMKCMPLKARVMMERAVRADMKELADIAVYHTELSS-ETESLDNDFIGPILLNEMTSSATICFLSF : 306
      Qia D1 Lc      q      imHy      y      d      f      i      YH      L      l      n      g      pl      nf      ss      icf      f

340     350     360     370     380     390     400     410     420     430     440
DmelOR85c : QMTVGVPDDIMIKLFLFLFSSLSQVYLICHYGQLIADASSSLSSISAKQNNQONADIRYRRALVFFIARPORTTYLKATIEMNITRATMDLLQVSYKFPALLRTMYIK : 389
DmelOR85b : QMTVGVPDDIVVKLFLFLVSSMSQVYLICHYGQLVADASYGFSVATYNNQKMYKADVRVKRALVIIARSQKVTFLKATIFLDITRSTMTDLLQISYKFPALLRTMYTQ : 390
BdorOR85bc1 : QMTMDAEPDYMVKLFLFLFSSLIQIYLICHYGQQLIDASSNVSRVAVNHDVHSHVHYQRMVLVLTARAQKPAMLKATSEFVRISRGTLIDIMQISYKFPFLVRTMYSN : 402
BlatOR85bc1 : QMTMDAEPDYMVKLFLFLFSSLIQIYLICHYGQQLIDASSNVSRVAVNHDVHSHVHYQRMVLVLTARAQKPAMLKATSEFVRISRGTLIDIMQISYKFPFLVRTMYNN : 402
BolerOR85bc1 : QMTMDAEPDYMVKLFLFLFSSLIQIYLICHYGQQLIDASSNVARAVNHDVHSHVHYQRMVLVLAARAQKPAMLKATSEFVRISRGTLIDIMQISYKFPFLVRTMYSN : 415
BcucOR85bc1 : QMTMDAEPDYMVKLFLFLFSSLVQICLIQYQGLLIDSSNIAHAVNHDVHSHVHYQRMVLVLAARAQKPAMLKATSEFVRISRGTLIDIMQISYKFPFLVRTMYSN : 409
CcaphOR85bc1 : QMTMDAEPDYMVKLFLFLFSSLAQIYLICHYGQQLIDASSNVAAAVNHDVHSHVHYQRMVLVLAARAQKPAMLKATSEFVRISRGTLIDIMQISYKFPFLVRTMYSD : 414
RzepOR85bc1 : QMTMDTEPDYKVKLLFFSLSLTQIYLICHYGQLLIDASSNVAAAVNHDVHSHVHYQRMVLVLAARAQKPAMLKATSEFVRISRGTLIDIMQISYKFPFLVRTMYSN : 416
BlatOR85bc2X1 : QMSVTRVBLMKLAVLFFSVMQVYLICHYGQQLSDASSNVASAAAFQDMSYADIRFQKMTILVAARAQAARALKATNEITISLDMFMVIMQMSYKFPFLVRTMYAD : 412
BlatOR85bc2X2 : QMSVTRVBLMKLAVLFFSVMQVYLICHYGQQLSDASSNVASAAAFQDMSYADIRFQKMTILVAARAQAARALKATNEITISLDMFMVIMQMSYKFPFLVRTMYAD : 355
BdorOR85bc2 : QMSVTRVBLMKLAVLFFSVMQVYLICHYGQQLSDASSNVASAAAFQDMSYADIRFQKMTILVAARAQAARALKATNEITISLDMFMVIMQMSYKFPFLVRTMYAD : 412
BolerOR85bc2 : -----DMSHADIRFQKMTILVAARAQAARALKATNEITISLDMFMVIMQMSYKFPFLVRTMYGD : 330
BminOR85bc2 : -----DMSHADIRFQKMTILVAARAQAARALKATNEITISLDMFMVIMQMSYKFPFLVRTMYGD : 330
Ccaph5bc2 : QMTVNRGFLLLTKLALFIFLSVLQVYLICHYGQQLSDASSNVSTALSDMTNADVRQKMLVLIIRKARSATLKATNEITISLDMFMVIMQMSYKFPFLVRTMYND : 414
      qm      d      kl      f      s      q      ylich      qq      das      a      y      dw      q      m      l      raq      a      lkat      f      is      t      t      imq      sykff      l      rtmY

```

Supplemental figure 3-24 The alignment of OR85bc

10 20 30 40 50 60 70 80 90 100 110 120

BdorOR85d1 : -----MSQIIHFESENTLANIFVTSIGLDAYKAGQRTNN-----IRRQLLS-----IFFIITIANMNIITLSELLYIFMAFANNNNVEATMILLSVGGVVIGDF : 93

Blator85d1 : -----MSNQIHFESENTLANIFVTSIGLDAYKAGQRTNN-----IRRQLLS-----IFFIITIANMNIITLSELLYIFMAFANNNNVEATMILLSVGGVVIGDF : 93

BucurOR85d1 : -----MSNQPIQFERHTLANAYVTSIGLDAYKAGQRTSN-----IRRRLLS-----IFFIITIANMNIITLSELLYIFMAFANNNNVEATMILLSVGGVVIGDF : 93

BminOR85d1 : -----MSNQIHFESENYLANIFVTSIGLYAEQAGERTKDR-----AAYIRQLLS-----IFSIVIVNMNIALSQLMYIFLAFANNNNVEATMILLSVGGVVIGDF : 97

RzepOR85d1 : -----MNEPIHFESENNLANIFVTSIGLDAYEKIGEQTGR-----LAQLRQLQR-----IFFFITMANMNVTLSEIIFIFLAFANNNNVEATMILLSVGGVVIGD : 97

DmelOR85d : MLTKKDTQSAKEQEKKAIPHSLKLYANVFYLSIGMAADHKYSQKWK-----EVLILH-----WTFIAQMVMNLTVISELIYVFLAIGKGSNLEATMILLSVGGVVIGDF : 104

BdorOR85d2 : -----MIEFGAMSTANFWSPNGIVADDIYRQPGDA-PKQKSPFAARFTTLR-----QIYSLIGLVNLWVLIIEASFVVMNLENSDLOARNNFTMGCVVVAII : 99

Blator85d2 : -----MIEFGAMSTANFWSPNGIVADDIYRQPGDA-PKQKSPFAARFTTLR-----QIYCLIGLVNLWVLIIEASFVVMNLENSDLOARNNFTMGCVVVAII : 99

BolOR85d2 : -----MSTKIVEEDARIKKANFWYGNGLIVANDFNHRQAQGE-PQKNIAAARLATVLR-----QIYCFIGLVNLWVLIIEACFVVMNLENSDLOARNNFTMGCVVVAII : 103

BucurOR85d2 : -----MPTKIVEEDARIKKANFWYSGNGVAVDDIYRQAQNE-PNGRSITARLATVLR-----QIYCFISILINLWVLIIEASFVVMNLENSDLOARNNFTMGCVVVAII : 103

BminOR85d2 : -----MSTQIIVEEDRIKTANFWYSPNGIVADDIYRQPGDE-PKRSVSOTRLATVLR-----QIFSFSVLANLWVLIIESTLFVVMNLENSDLOARNNFTMGCVVVAII : 103

RzepOR85d2 : -----MPSNIITESAIRKANFWYNSNGIEPDDVYDAAAEKSAVQESIAANLRTHYLSQFFSLIILIMNFVLTLEAFVVMNLENSDLOARNNFTMGCVVVAII : 108

f F A N Y G a Y 1 N L e a f n F a F g f V K

130 140 150 160 170 180 190 200 210 220 230 240

BdorOR85d1 : FYSIWQRARITAMQALHALYRTLAEIKIEVQRAQVORCFAYAFVLLHELLWWSLMLFLLNFIYEVWLAARVVGKTLFYVWVFFDQHVWWRVYPMFLITQIAAGACISG : 214

Blator85d1 : FYSIWQRARITAMQALHALYRTLAEIKIEVQRAQVORCFAYAFVLLHELLWWSLMLFLLNFIYEXWLAARVVGKTLFYVWVFFDQHVWWRVYPMFLITQIAAGACISG : 214

BucurOR85d1 : FYSIWQRERISAMIQALHALYRTLAEQAKVAVERELQRKRFAYAFVLLHELLWWSLMLFLLNFIYEVWLTWRVVGKTLFYVWVFFDQHNDSRMYTMLITQIAAGACISG : 214

BminOR85d1 : TYNICRQARISAMQALHALYRTLAEQTKYKQVQQLQRNRLAYAFVYFEMLVWYGNLFPLNLIYEVWLTARVVEKTLFYVWVFFDQHNNDWIYHYMLLMSAGQACISG : 218

RzepOR85d1 : FYSIWQRERISAMQALHALYRTLAEIKIEVQRAQVORCFAYAFVLLHELLWWSLMLFLLNFIYELWLEVRTVGKTLFYVWVFFDQHNNDWIYHYMLLMSAGQACISG : 218

DmelOR85d : TWNISQRKRLTQVSRILEELHGGLAQCEPNNIGHHLSGYSRYSKFYFGHMHTVLNLYWAVYLVLCDFWGMQRQFERMLFYCVWFDWSTG-QYSYFPMISQNGGACISG : 224

BdorOR85d2 : TILSNLRQSRISILMKRKYIEIYFKQSTDQPPVELQSHLLRIRLFGFMAHTTAFTVGTYNCLPLMINVLFAPLQHTDVVRELVFFCVWVFVRDNLMLYPLVSVQYASITLGG : 219

Blator85d2 : TILSNLRQSRISILMKRKYIEIYFKQSTDQPPVELQSHLLRIRLFGFMAHTTAFTVGTYNCLPLMINVLFAPLQHTDVVRELVFFCVWVFVRDNLMLYPLVSVQYASITLGG : 219

BolOR85d2 : TILSNLRQSRISILMKRKYIEIYFKQSTDQPPVELQSHLLRIRLFGFMYGTFHTGFTVGTYNCLPLMINVLFAPLQHTDVRELVFFCVWVFVRDNLMLYPLVSVQYASITLGG : 223

BucurOR85d2 : TILSNLRQSRISILMKRKYIEIYFKQSTDQPPVELQSHLLRIRLFGFMYGTFHTGFTVGTYNCLPLMINVLFAPLQHTDVRELVFFCVWVFVRDNLMLYPLVSVQYASITLGG : 223

BminOR85d2 : TILSNLRQSRISILMKRKYIEIYFKQSTDQPPVELQSHLLRIRLFGFMYGTFHTGFTVGTYNCLPLMINVLFAPLQHTDVRELVFFCVWVFVRDNLMLYPLVSVQYASITLGG : 223

RzepOR85d2 : TWHDKRQSRITWLRQVYDIYFKLTVDPQVELQSHLLRIRLFGFMYGTFHTGFTVGTYNCLPLMINVLFAPLQHTDVRELVFFCVWVFVRDNLMLYPLVSVQYASITLGG : 228

i q r m L y F Q Y L Y r v Y N p n Y L 1 p y c W P f W n n Y Y Y q 1 l A

250 260 270 280 290 300 310 320 330 340 350 360

BdorOR85d1 : DLLLSAVVQLIMHVRQLARRIELHVAGGGG-----GSGSKWRTAATNVCQRDLRFIRSVIAHYHQIIL-----LSQALNDVFGISLFISFASTALIIICFVLQITIGAN : 323

Blator85d1 : DLLLSAVSVQLIMHVRQLARRIELHVAGGGGDDGGGSKWRTAATNVCQRDLRFIRSVIAHYHQIILNYFYTPSRLSQALNDVFGNSLFISFASTALIIICFVLQITIGAN : 335

BucurOR85d1 : DLLLSAVAVQLIMHVRQLARRIEAHVAGDSRD-----DSASKRGEANECAHDLHRTIIAHYHQIIL-----ISQVLDNDFGISLFINETSTALIIICFVLQITIGAN : 323

BminOR85d1 : DLLLSAVAVQLIMHVRQLARRIEAHVAG-----RETSS-----

RzepOR85d1 : DLLLSAVAVQLIMHVRQLARRIESHIRKNGD-----GTATREQRISLSEKSEVDFIRFIRGIAHYHQIILK-----LSQAMNDVFGISLFISFASTALIIICFVLQITIGAN : 327

DmelOR85d : DMLMCLLVTLVVMHFRISLASHVAGIGS-----FQHDLEQATVAVYHQSLIH-----LCQDINEIFGVSLLSNFSVSSSIFICVFGQMTIGKIDNLMVIA : 319

BdorOR85d2 : DLLFCATVQLIIMHFRKLARDIEAYAGCSC-----ATADVCTQQAQRDLDFLSAAVYVSHSTIA-----LCQLINEIFGLPVLINIFSTSFVICFLAFQESIVPGLDSMAV : 323

Blator85d2 : DLLFCATVQLIIMHFRKLARDIEAYAGCSC-----ATADVMAQSQRLDFLSAAVYVSHSTIA-----LCQLINEIFGLPVLINIFSTSFVICFLAFQESIVPGLDSMAV : 323

BolOR85d2 : DLLLCATVQLIMHFRKLARDIEAYAGCSC-----ATEEVIAQAQRDLDFLSAAVYVSHSTIA-----LCCLINDIEGLPVLINIFSTSFVICFLAFQESIVPGLDSMAV : 323

BucurOR85d2 : DLLLCATVQLIMHFRKLARDIEAYAGSTN-----ATQPVNAEKARLDLSFISTAVYVHNHTIA-----

BminOR85d2 : DLLLCAMVQLIMHFRKLARDIEAYAGCSC-----TKQDVMAQSQRLDFLSFISTAVYVHNHTIA-----LCQLINEIFGLPVLINIFSTSFVICFLAFQESIVPGLDSMAV : 327

RzepOR85d2 : DLLLCAMVQLIMHFRKLARDIEAYAG-----SVESEMSVSKSLDFLSFISTAVYVHNHTIA-----LCQLINEIFGLPVLINIFSTSFVICFLAFQESIVPGLDSMAV : 327

DLL A vqlimH r Lar le aq d l fl y h l n f g f s c f f q g 1

370 380 390 400 410 420 430 440 450 460

BdorOR85d1 : FFLFSLVQIFPLCYAQQILEASEYISYAVYNNHNFDSLLRYRKMILYIMARAQKPSKIQATALVIVSMPTMDLLQLSKYGFVIRTMYAREPKNFTK : 423

Blator85d1 : FFLFSLVQIFPLCYAQQILEASEYISYAVYNNHNFDSLLRYRKMILYIMARAQKPSKIQATSLVTVSMPTMTNTHGLFDK-----VVQNDP----- : 423

BucurOR85d1 : FFLFSLVQIFPLCYAQQILEASEYISYAVYNNHNFVADLRYRKMILYIMARAQKPSKIQATSLVTVSMPTMDLLQLSKYGFVIRTMYAREPKSVN : 423

BminOR85d1 : -----DDSEYIRHAYVYNNHNFADMSYRKMILYIMARAQKPSKIQATFTMTVSMPTMDVNSKYIVSYNI FHMYSKI----- : 324

RzepOR85d1 : FFLFSLVQIFPLCYAAGLLEASEYIGSAVYNNHMYDADLRYRKMILVIMARAQKAAKLRAATSFVIVSMPTMDVSTK----- : 406

DmelOR85d : LFLFGAMVVFMTATHAGRVADSEYIGSAVYNNHMFADLRYRKMILYIMARAQKPSKIRATMFLNISLTVSDDLQSKYKFALLRTMYVN----- : 412

BdorOR85d2 : FFLFSLVQIFPLCYAQQILEASEYISYAVYNNHNFVADLRYRKMILYIMARAQKPSKIQATSLVTVSMPTMDLLQLSKYGFVIRTMYAREPKSVN : 416

Blator85d2 : SYMIDICQFYMYKSYGQELITTSBENIGHVYNNHNLVADIRYRKMILYIMARAQKPSKIRATMFLNISLTVSDDLQSKYKFALLRTMYAR----- : 416

BolOR85d2 : CYMISCFVQIMKSYGQELITTSBENIGHVYNNHNLVADIRYRKMILYIMARAQKPSKIRATMFLNISLTVSDDLQSKYKFALLRTMYAR----- : 420

BucurOR85d2 : -----

BminOR85d2 : FFLFSLVQIFPLCYAQQILEASEYISYAVYNNHNFVADLRYRKMILYIMARAQKPSKIRATMFLNISLTVSDDLQSKYKFALLRTMYAR----- : 420

RzepOR85d2 : SYMIDICQFYMYKSYGQELITTSBENIGHVYNNHNLVADIRYRKMILYIMARAQKPSKIRATMFLNISLTVSDDLQSKYKFALLRTMYAR----- : 420

c q i se i v y n n h n d r y k m l i i r a q k l a t s m t d

Supplemental figure 3-25 The alignment of OR85d

10 20 30 40 50 60 70 80 90 100 110 120

BucurOR85e1-3 : MKERAERNTR-----ELESNKILVSN-EKKPRIFDPLFVAQVILCKATGQI-----MNLVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 96

BucurOR85e1-2 : -----MDTR-----ALGDTTLVLSH-QKKPRIFDPLFVAQVILCKATGQI-----MNFVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 90

BucurOR85e1-1 : MKDTRAROV-----ELESSTLLVSD-EKKPRITADPLFVAQVILCKATGQI-----FNLVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 96

BdorOR85e : ---KNLSYGYRLRACRDVDKLLDGGTSLVSP-EKKPRITADPLFVAQVILCKATGQI-----FNVVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 105

Blator85e : -----MDVR-----DLTYSH-YDEARITADPLFVAQVILCKATGQI-----FNVVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 85

BminOR85e : -----MDFS-----EQVESTLLVSH-EKKPRITANLPLFVAQVILCKATGQI-----FNVVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 90

BolOR85e : -----MDTR-----ELGDMSLVSH-DKQKPRITADPLFVAQVILCKATGQI-----FDVHG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 90

CcapOR85e : -----MDV-----AGACSLVLSH-KKKPRITADPLFVAQVILCKATGQI-----FNVVG-----LGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 90

RzepOR85e : -----FVVG-----EPQOGASPRVSH-ADPANKPRITADPLFVAQVILCKATGQI-----FNLFPPLHLVNLQGLGVIYCFVIMTQSEHMAVFLFKTAKMLDKEEITDALTMII : 100

DmelOR85e : ---MASLQFVG-----NVDADIRDISLFPANESNLERLMLGLQILVTKESPRNPKWPKRLEMIGKVLPKAYCSMVITTSLELVLETGLVLPTELEQATIDALTMII : 106

Ys D Ri LF aqv katGqi p n y Lgy yC i q l Vlfikt yd Ll G Le ItDALTMii

130 140 150 160 170 180 190 200 210 220 230 240

BucurOR85e1-3 : FWFBSVYACVFLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 218

BucurOR85e1-2 : FFSFSVYACVFLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 212

BucurOR85e1-1 : FWFBSVYACVFLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 218

BdorOR85e : FFSFSVYAAFVWLRLWLRRLAFQIRINQVYVWHSPLGSLFVSAHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 227

Blator85e : FWFBSVYASVWLRLWLRRLAFQIRINQVYVWHSPLGSLFVSAHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 207

BminOR85e : FWFBSVYATCVWLRLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 181

BolOR85e : FWFBSVYACVWLRLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 212

CcapOR85e : FWFBSVYACVWLRLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 212

RzepOR85e : FWFBSVYACVWLRLWLRRLAFQIRINHHVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 222

DmelOR85e : YFTGTGTITLWCLRSRLIMTLEQVNIQVYVWHSPLGSLFVSWHRTFVLAKRIVITVTLGVAAITLYGSTVLVQVRAFLPLKQWYFPDPLQPYVVELVYALQSTQVIMGVTLGNCALFVS : 228

f fsvTa Iw LR Rlafl i n YwhHSLpLsfVs hr f lakt r W C t lYg FLvmgv LFLkcWYFPDPlgpy y q q imq t gn sal vs

250 260 270 280 290 300 310 320 330 340 350 360

BucurOR85e1-3 : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPNTADQ-EVNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 339

BucurOR85e1-2 : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKISDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 333

BucurOR85e1-1 : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKISDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 339

BdorOR85e : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 348

Blator85e : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 328

BminOR85e : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 333

BolOR85e : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 333

CcapOR85e : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 333

RzepOR85e : LVIMLCGGQFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 343

DmelOR85e : LSLILLGCGFDVLYCSLKNLSYYGRIAPFCEVEKLKKEQALPKFSDQ-ELNOVMYCOEHLNLSIQHLHYTQEPAYSLPEALHGVVQCVQLHRFLIDACKKEELFNFPCLVKYSIQVTFL : 347

l lmcgqfdvlycsknl 1 lr eQaaLp dd dLNQMYC EHLnLS lq ly q pa tIpeAlh avvcvqlhrfl c e eelfn clvks qvt ql

370 380 390 400 410 420 430 440 450 460 470 480

BucurOR85e1-3 : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 456

BucurOR85e1-2 : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 450

BucurOR85e1-1 : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 456

BdorOR85e : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 465

Blator85e : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 445

BminOR85e : -----GERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 327

BolOR85e : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 450

CcapOR85e : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 450

RzepOR85e : CLLVFGVGAERSVVRILNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 459

DmelOR85e : CLLVFGVGSREVLVNLQYLTITFELIMFTYFCELLRGHSVSGEAFVRSQWHTAAIRQDILILLANSKRAVRLTAGKFYAMDVERLSVVTQAFSFTLLQLKLAANKP--- : 467

cllvf gv Gers vRIlnl QY LT ELIMFTYFCELLRGHSvR geAFVRSqWCH IR Di lL NSKRAVRLTAGKFYAMDVERLSvvtQafsflltlqlklaank

Supplemental figure 3-26 The alignment of OR85e

```

10      20      30      40      50      60      70      80      90      100     11
BcucOR88a : -MALRQEKY-GTAK---LDDLCDILHPYQRYLRINYLDFRRVNGRAIFNPSKILNINICILAVFDCIGNCICKVKAINAGEITKQEQIFAVFGMGVMTMRGLMLALNRV : 104
BminOR88a : -MALQQRNN-GAAKVCADLDCALILHPAQRYLGLNLYNFRVNGRAIFNPSKILNINIALFLAVVDCITGNVICKGKAINARDVTKAQEQIFAVFGMGVMTMRGLQLALNRD : 107
BoleOR88a1-2 : -MAQQQWNN-GVWKLCTIDDLCAIQHPYQRYLGLKFLFKRVNGRAIFNPSKILNINVLITLAVVDCAGNIIRKIVKAINRDVTKAQEQIFAVFGMGVMTMRGLMLALNRG : 107
BoleOR88a1-3 : -MALQQRNN-GVSNLCTFDLCAIQHPYQRYLGLKFLFKRVNGRAIFNPSKILNINVLITLALMDAGNIIRKIGKAINRDVTKAQEQIFAVFGMGVMTMRGSMIGLNRG : 107
BoleOR88a1-1 : -MAVQKKRT-FAAKLCALDILCAIQHPYQRYLGLKFLDFKRVNGRAIFNPSKILNINVLITLAVVFLAIIDICNVINIAKAINRDVTKAQEQIFAVFGMGVMTMRGLMLALNRD : 107
BdorOR88a : -MAPQQEVFGAKSKLCAIEDLCAIEHPYQRYLGLKYVEFKRVNGRLVFKPSNINFLFLAVVDCITGNVIKTAIINRDVTKAQEQIFAVFGMGVMTMRGFMGLNLRG : 108
BlatorOR88a : -MAPQQEAFGAKSKLCAIDDLCAIEHPYQRYLGLKYVEFKRVNGRLVFKPSNINFLFLAVVDCITGNVIKTAIINRDITKAQEQIFAVFGMGVMTMRGFMGLNLRG : 108
CcparOR88a : -MALQAGRG-GEPKLRSDLDCALILHPQRYLGLNLYNFRVNGRAIFNPSKILNINVLITLAVVDCMGNITKVCMAINRDITKAQEQIFAVFGMGVMTMRGFMGLNLRG : 107
RzepOR88a : -MGITSGSTTKDKLCTIDDLCAIYHPYQRYLGNFMFDYKRVNGRAIFNPSKILNINVLITLAVVDCIGNATKCVAAIASGNVNLQAQIFAVFGMGVMTMRGFMGLNLRG : 108
DmelOR88a : MKPTEIKKPYRMEEFLRQMFQVAVQMVHFQWRRNPVDSMVMASMPV--FCISAFINVLFFGCGMDLIGHFWLG---HPANQNPPMLSIITIFPSISGLMLALNRK : 102
ma      k      ddical hp qryl l      f rvNgrf ip s      Ln l la      dC gn ik      ain      t Age fav gm      vmtmRG l      R

0      120     130     140     150     160     170     180     190     200     210     2
BcucOR88a : QLSNFYNTICIFPSRAHLQCHMAVEKVVHSYIKRRFFYIMHTLMTVTVAARLTLTGVKEMVFDHDSDDSVADSEYHVNPSKLPFGKDKVSTVPYVVIYBSVLAAAVNM : 213
BminOR88a : KLSKFYNIDIRIFPSRENLCQHMEVEKVVHNYIKRRFFLLHTLTTVTVTSARLTLPAMKELLFVDFESNDIADSEFHVNPSPKLPFGVKDKVSTVPYIYIYBSVLAAAVNM : 216
BoleOR88a1-2 : KLLKMFNAIDISIFPSRQLCQHMEVEKVMHKNIKRRFFLLHTSLTSTVTSARLSALBLAKEMVFYDFKSDNRVTEEFHVNPSPKLPFGIKDKVSTVPYIYVYIMLATAGVHI : 216
BoleOR88a1-3 : NLSKMYNAIDIRIFPSRQLCQHMEVEKVMHKNIKRRFFLLHTSLTSTVTSARLSALBLAKEMVFYDFKSDNRVTEEFHVNPSPKLPFGIKDKVSTVPYIYVYIMLATAGVHI : 216
BoleOR88a1-1 : KVLKMYNAIDIRIFPSRHLQCHMEVEKVMHKNIKRRLLILHRSITALGVIFSVSVSVREVLIVDFESDDLVAEFHVNPSPKLPFGIKDKVSTVPYIYVYIMLATAGVHI : 216
BdorOR88a : KLLKMYNAIDIRIFPSRHLQCHMEVEKVVHNYIKRRFFYLHFLTSTVSCGCFIMFVKEMAFHGKSDAPVEEFHVNPSPKLPFGVKDKVSTVPYIYVYIMLATAGVHI : 217
BlatorOR88a : KLLKMYNAIDIRIFPSRHLQCHMEVEKVMHNYIKRRFFYLHFLTSTVSCGCFIMFVKEMAFHGKSDAPVEEFHVNPSPKLPFGVKDKVSTVPYIYVYIMLATAGVHI : 217
CcparOR88a : RLSELNYSIDIRIFPSSELQTHMEVAKTHDYIKRRFFLLHQGLSFAVLVFCFMEAVLVFFVDFEAQEPVADSEFHVNPSPKLPFGVKDKVSTVPYIYVYIMLATAGVHI : 216
RzepOR88a : KLSKFLVNDLRECFPSAFNLCQRMVEVEKCHRYIKRRFFFFHNFMCAEAVPCVVELIKELLAYDFEEKGVPDEEFHNPSPKLPFGVKENSLVYFYIYAYETILALAVNM : 217
DmelOR88a : EIVSEFVNDLRECFPSDLVSLDMQMDTEYTRNFVQRYRFRIRIYHSLGGPFCVVELIKELLAYDFEEKGVPDEEFHNPSPKLPFGVKENSLVYFYIYAYETILALAVNM : 210
l      yN idrifPrs lQ hMevek h ik Rf h      F      P      kf      f      V      efhn sWlPfg k      Ypyiy ye la m

20     230     240     250     260     270     280     290     300     310     320
BcucOR88a : IITVDELVVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 322
BminOR88a : IITVDELVVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 325
BoleOR88a1-2 : IATNDQVSVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 325
BoleOR88a1-3 : LVTDNHVSVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 325
BoleOR88a1-1 : LKKNQSVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 325
BdorOR88a : LVVNDQSVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 326
BlatorOR88a : LVVNDQSVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 326
CcparOR88a : IITVDELVVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 326
RzepOR88a : IITVDELVVLISQCMYIEYLGRLLSEMNVDLDPKTLDAFYQCHHYYIMHQLNKLAVEFNDLNFNSIIFSDAGIATSIICFNIVLITATDITYQITVYTSPLFVE : 326
DmelOR88a : FVTVDNLNVMQCHLVMLHGLARQFSAIDPQSLTDEKRR--FFVDRLLLVQRCQLNLCCKRYNDIEKVAFVNVFVGGGLLYLPLMLSETSDVITIAQVILATLNL : 317
wD      Fv lis Lcmyy yl      ll e      a      d      k      qh yi      q ln la      NDlFn siL Sd giA SiCfN l      a      Lq      y      P      fve

330     340     350     360     370     380     390     400     410     420
BcucOR88a : VWLIYDAAKGQMTLETVTGRINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQMLTFLKSKS----- : 407
BminOR88a : VWLIYDAAKGQMTLETVTARINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDVCSCKFL----- : 401
BoleOR88a1-2 : VWLIYDAAKGQMTLETVTARINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQLLTFKSKG----- : 410
BoleOR88a1-3 : IWLIYDAAKGQMTLETVSRVNIYELKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQLLX----- : 404
BoleOR88a1-1 : IWLIYDAAKGQMTLETVTARINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAY----- : 400
BdorOR88a : VWLIYDAKSGQMTLETVTARINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQLLTFKAKGYTK----- : 414
BlatorOR88a : VWLIYDAKSGQMTLETVTARINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQLLTFKAKGYTKLWLVGITK----- : 422
CcparOR88a : TWLIYDVSKGQMTLETVTARINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQLLTFKAKGYTKLWLVGITK----- : 328
RzepOR88a : MWLIYDAKSGQMTLETVSRINBIYEQKQYDSSVRFKGYTMMWQSTNEBFRLLTAFNMFYVNMKHFQDMMMLAYQMLTFMKSKS----- : 411
DmelOR88a : VGFTFFICLRCGLKASEGLESSLRSQEWYLGRRYRKFYLLWQYQRTQQLGAGGLIQVNMVHETEMOLAYRLFTFLKSH----- : 401
wliyd kwGt Lltvt rine yeq WY      S      r      kyt m      q      tn      p      rlt      fn      vnmkhfqd m      lay

10      20      30      40      50      60      70      80      90      100     110
DmelOR94a : -----MDKKHDIESMRILIQVMQLFPLPWSKSEBEE---TFTFGVKRRNRFLLPITTFPIGLMWEAFISSNLQAGQVYMSIEMALVVKI : 90
DmelOR94b : -----MES-TNLSASIQTLILVQRWIKLLKWENEGDE---GVLTWLKRIYFPVHLPLTFTYIALMWEAITSSTDFEAGQVYMSIEMALVVKI : 87
BdorOR94ab1 : MWAQHIIKLELKMTPSSAAEQEIGVARVLMHPLQILQAMPILPERHHQNASSTQCTWLARNRYRLHPLTFTYNTLMWEALTR--WERADHILYISITEVGMMLAT : 108
BlatorOR94ab1 : -----MTPSAQRQREIGVARVLMHPLQILQAMPILPERHHQNASSTQCTWLARNRYRLHPLTFTYNTLMWEALTR--WERADHILYISITEVGMMLAT : 96
BoleOR94ab1 : -----MTPPTAQRREIGVARVLMHPLQILQAMPILPERHHQNASSTQCTWLARNRYRLHPLTFTYNTLMWEALTR--WERADHILYISITEVGMMLAT : 96
BminOR94ab1 : -----MRETSASVLGTIGIARVLMHPLQILQAMPILPERHHQNASSTQCTWLARNRYRLHPLTFTYNTLMWEALTR--WERADHILYISITEVGMMLAT : 96
CcparOR94ab1 : -----MATAIEQLREIGIARVLMHPLQILQAMPILPERHHQNASSTQCTWLARNRYRLHPLTFTYNTLMWEALTR--WERADHILYISITEVGMMLAT : 94
BdorOR94ab2 : -----MAVKKSSPNTSSMSRTASANI IIAVLKSLGYWQWTRDRP-----PYIEKVERARIVLHITLPTFTIALMTGVLSRDLDEPTEIHLVLFESLIVKT : 97
BlatorOR94ab2 : -----MAVKKSSPNTSSMSRTASANI IIAVLKSLGYWQWTRDRP-----PYIEKVERARIVLHITLPTFTIALMTGVLSRDLDEPTEIHLVLFESLIVKT : 97
BoleOR94ab2 : -----MAVKKSSPNTSSMSRTAATLFIHVHLLKAIQLWQWTRDSHL-----PYIEKLEHARILHITLPTFTIFITLMTFAVLSQDLDEPTEIHLVLFESLIVKT : 97
R      1      Gw      Yr      LH p tft      lM      l      e      L      TE

120     130     140     150     160     170     180     190     200     210     220
DmelOR94a : LSIHYRTYWRRLMYLQHPADYQLNHQEVDVFRRECRFFKWFYFIYILISLGVVSGCTGVLFLEG--YELFFAYYVFFENQNERRRWFAYGDMAGMTLTCISNITL : 198
DmelOR94b : LNIYVYRREXASILHQLHDPAPNRNSEIKYQQONRKRIFVYIWSGLFVAVMGYSIVFFQED--YELFGYVYVFFENRTRERFYAGNNUVMTCCCLSNITL : 297
BdorOR94ab1 : LNFWRDLQRYHFMHSLCYSDHLARNQAEQWRRAKORSRTIAVCIIGGAGVLTAFGATLLVNG--YSLDYDWLFPFENHNAQNWYAYGVELVAMSLTICIANVTM : 216
BlatorOR94ab1 : LNFWRDLQRYHFMHSLCYSDHLARNQAEQWRRAKORSRTIAVCIIGGAGVLTAFGATLLVNG--YSLDYDWLFPFENHNAQNWYAYGVELVAMSLTICIANVTM : 204
BoleOR94ab1 : LNFWRDLQRYHFMHSLCYSDNLARNQAEQWRRAKORSRTIAVCIIGGAGVLTAFGATLLVNG--YSLDYDWLFPFENHNAQNWYAYGVELVAMSLTICIANVTM : 204
BminOR94ab1 : LNFWRDLKRAWHFMHSLCYSDRLARNKAEQWRRAKORSRTIAVCIIGGAGVLTAFGATLLMSG--YSLDYDWLFPFENHNAQNWYAYGVELVAMSLTICIANVTM : 204
CcparOR94ab1 : LNFWRMERRAQWFMHSHSDGLTCNEVERINRQKQRTFLIVICIGGAGVLTAFGATLLMSG--YSLDYDWLFPFENHNAQNWYAYGVELVAMSLTICIANVTM : 202
BdorOR94ab2 : LNFWRKQGANWFMDHNDPDIYLRQQSSEWTKQQAQSAIVSYNIFVAATTWVVFRCIGAMTADVYVLMNIYVFFEDHHPRRWIAWTNTIASLTATANL : 207
BlatorOR94ab2 : LNFWRKQGANWFMDHNDPDIYLRQQSSEWTKQQAQSAIVSYNIFVAATTWVVFRCIGAMTADVYVLMNIYVFFEDHHPRRWIAWTNTIASLTATANL : 207
BoleOR94ab2 : LNFWRKQGNTRWYNDLNDPDIYLRQQSSEWTKQQAQSAIVSYNIFVAATTWVVFRCIGAMTADVYVLMNIYVFFEDHHPRRWIAWTNTIASLTATANL : 207
L      Wr      A      m      E      L      E      W      QR      F      Yi      v      a      Y      LP      PFewh      Ywya      Y      a      ltc      N

230     240     250     260     270     280     290     300     310     320     330
DmelOR94a : DTLCGYPLFHSLYLPLGLRLRETKN-----MKNDTIFGQDLRAIFMORISLTLCQRIYSPYILSQIILSALITCFSYRLQHVIGIRDNPQIPISMLQFVSM : 301
DmelOR94b : DTLCGYPMFHASIFPLGLRLEALKN-----AAEERAK-PELRRLFOLTKWRRLRECEVLVSYPVLSQVVSFAFICSAVRLVHMCFKQRPGLFVTTVQGVAM : 297
BdorOR94ab1 : DMLCYLPHVALYKILQMRIMALQ-----LSERLAV-QQLINIELKRVKRLTQCEVLVSLPIVQIVLSVFLICLSAYRLQSMOISENPOQFFAMLOFASVL : 318
BlatorOR94ab1 : DMLCYLPHVALYKILQMRIMALQ-----LSERLAV-QQLINIELKRVKRLTQCEVLVSLPIVQIVLSVFLICLSAYRLQSMOISENPOQFFAMLOFASVL : 306
BoleOR94ab1 : DMLCYLPHVALYKILQMRIMALQ-----LSERLAV-QQLINIELKRVKRLTQCEVLVSLPIVQIVLSVFLICLSAYRLQSMOISENPOQFFAMLOFASVL : 306
BminOR94ab1 : DMLCYLPHVALYKILQMRIMALQ-----LSERLAV-QQLINIELKRVKRLTQCEVLVSLPIVQIVLSVFLICLSAYRLQSMOISENPOQFFAMLOFASVL : 306
CcparOR94ab1 : DMMCYLPHVALYKILQMRIMALQY-----LSEFPV-QQLINIELKRVKRLTQCEVLVSLPIVQIVLSVFLICLSAYRLQSMOISENPOQFFAMLOFASVL : 304
BdorOR94ab2 : DLVNCYPMFHSLYLKILQMRISALRR-----SANEPFVIEQMSIEFQMMKVRRLTTECETLVSPVFSQIILSSFILCFGQYRLQOMENMLSMFLSTVEFATVM : 310
BlatorOR94ab2 : DMICYPMFHSLYLKILQMRISALRR-----RADEPFVIEQMSIEFQMMKVRRLTTECETLVSPVFSQIILSSFILCFGQYRLQOMENMLSMFLSTVEFATVM : 310
BoleOR94ab2 : DMICYPMFHSLYLKILQMRISDLRLKNTGVGVKDEPEIDQSEFQMMKVRRLTTECETLVSPVFSQIILSSFILCFGQYRLQOMENMLSMFLSTVEFATVM : 317
D      CY      FH      llyLiLg      RL      al      v      ql      I      H      v      rLT      Ce      lVS      p      l      qi      lS      fliC      YRLq      m      en      g      qFa      V

340     350     360     370     380     390     400     410
DmelOR94a : ILDTLPCYNGEITVYANGLTNEVYHTNMLECRPPIRKLLNNAEMHLEKRFVITRAGNFAVGLPIFVKITNNAYSFLALLNVSN : 387
DmelOR94b : IVDTLPCYNGEITVYANGLTNSVFGTNNLEYSVGTARKLLNNAEMHLEKRFVITRAGNFAVGLPIFVKITNNAYSFFALLNKISK : 383
BdorOR94ab1 : TLDTLPCYFANEITINDALITCVVNSNNEESSPTKRLMNLVEMLLKRFQIKAGNFVLVLGVFTTKMNNAYSLLALLNMSK : 404
BlatorOR94ab1 : TLDTLPCYFANEITINDALITCVVNSNNEESSPTKRLMNLVEMLLKRFQIKAGNFVLVLGVFTTKMNNAYSLLALLNMSK : 392
BoleOR94ab1 : TLDTLPCYFANEITINDALITCVVNSNNEESSPTKRLMNLVEMLLKRFQIKAGNFVLVLGVFTTKMNNAYSLLALLNMSK : 392
BminOR94ab1 : TLDTLPCYFANEITINDALITCVVNSNNEESSPTKRLMNLVEMLLKRFQIKAGNFVLVLGVFTTKMNNAYSLLALLNMSK : 380
CcparOR94ab1 : TLDTLPCYFANEITINDALITCVVNSNNEESSPTKRLMNLVEMLLKRFQIKAGNFVLVLGVFTTKMNNAYSFFALLNMNN : 390
BdorOR94ab2 : AVDTLPCYFNGKVTSSDALITDIPNSDNTTDPVTRRFEMILVEMLLKRNALMSVNYFIIVDIFAKTMKNAYSIFAILNMNN : 396
BlatorOR94ab2 : AVDTLPCYFNGKVTSSDALITDIPNSDNTTDPVTRRFEMILVEMLLKRNALMSVNYFIIVDIFAKTMKNAYSIFAILNMNN : 396
BoleOR94ab2 : TVDTLPCYFGADVTEHNSALINDIPNSDNTTDPVTRRFEMILVEMLLKRNALMSVNYFIIVDIFAKTMKNAYSIFAILNMNN : 403
QIFLPCYf n      T      s      aLT      s      W      f      tRk m lYMELLK      P      gnFF      Glp      F      Kt      nnays      Al      ln

```

Supplemental figure 3-27 The alignment of OR88a

Supplemental figure 3-28 The alignment of OR94ab

```

      10      20      30      40      50      60      70      80      90      100     110
BminOR1-1 : ----MGKLKLVSSRIFFPSDPSKGIQYNVWLAQLFGVGVVGLKAESPLKIVLGIYGLITLVVTFIYTGFETDMLCWPENLDSLTQNICLSLTHIAGVLK----- : 101
BoleOR1-1 : ----MRKLEVLSSRIFFPSDPSKGIQYNVWLAQLFGVGVVGLKTESPLRLIALGIVGLITLVVTFIYTAETDMLCWPENLDSLTQNICLSLTHIAGVLKVINIYR : 108
BdorOR1-1 : ----MDKLEELSSRIFFPSDASKGIQYNVWLAQLFGVGVVGLKAESPLRLIALGIVGLITLVVTFYTGFEVYDMLCWPENLDSLTQNICLSLTHIAGVFKVINIYR : 108
BlatOR1-1 : ----MDKLEELSSRIFFPSDAYKGIQYNVWLAQLFGVGVVGLKAESPLRLIALGIVGLITLVVTFYTGFEVYDMLCWPENLDSLTQNICLSLTHIAGVFKVINIYR : 108
BcucOR1-1 : ----MDKLAVLSSRIFFPSDPSKGIQYNVWLAQLFGVGVVGLKAESPLRLIALGIVGLITLVVTFIYTGFETDMLCWPENLDSLTQNICLSLTHIAGVLKVINIYR : 108
CcapOR1-1 : ----MDKLEALSSRIFFPSDPSIGKISIEYNVWLAQLFGVGVVGLKKETPRMIALAVIGVATLVVTFIYTGFETDMLCWPENLDSLTQNICLSLTHIAGVGLKVINIYR : 108
BdorOR1-2 : ----- : -
BlatOR1-2 : MAAFQDILKEVYFIVFVPSSEAGKQQLGSIIEFNILSLQISGVLELS----- : 51
BcucOR1-2 : ----- : -
CcapOR1-2 : MHRLLCKFEQVAMRVFSSDVRRGQIGSIEFNILSLQMTGVLELP----- : 55
      r  fps      g  gsi  n  wl  q  gvp      p  l
      120     130     140     150     160     170     180     190     200     210     220
BminOR1-1 : -----LMAPYHGEFENKIPITTIYASLVGSTGVLGIMYLHLS-----QIFPYRVKLPDWMPLGTLAYMGISVLVFAIQIVAIQIVLDYLVNVTMIHQ : 183
BoleOR1-1 : LDEVANVVRRIEYSAKTYVVVSKSQLVAFYRGEFENKIPITTIYAAVLGVTGVLGLIYLLYNPIGVAGQIFPYRVKLPDWMPLGTLAYMGISVLVFAIQIVAIQIVLDYLVNVTMIHQ : 220
BdorOR1-1 : LDEVAFVVRRIEYAAKTYVISKSQLVAFYRGEFENKIPITTIYASLVGSTGVLGLIYLFYNPIGVAGQIFPYRVKLPDWMPLGTLAYMGMMSVLVFAIQIVAIQIVLDYLVNVTMIHQ : 220
BlatOR1-1 : LDEVGVFIRRIEYSAKTYVISKSQLVAFYRGEFENKIPITTIYASLVGSTGVLGLIYLFYNPIGVAGQIFPYRVKLPDWMPLGTLAYMGMMSVLVFAIQIVAIQIVLDYLVNVTMIHQ : 220
BcucOR1-1 : LDEVAHVVRRIEYSAKTYVISKSQLVAFYRGEFENKIPITTIYASLVGSTGVLGLIYLFYNPIGVAGQIFPYRVKLPDWMPLGTLAYMGMMSVLVFAIQIVAIQIVLDYLVNVTMIHQ : 220
CcapOR1-1 : LKEVAGVVRKIEYAAARYVISKNQLKAFYRGEFENKIPITTIYASLVGSTGILGAYLLHNPTGVAGQIFPYRVKLPDWMPLGTLAYMGMFSVLVFAIQIVAIQIVLDYLVNVTMIHQ : 220
BdorOR1-2 : -----MFAVQIVTVDYLVNISMMNL : 19
BlatOR1-2 : -----TRLVNGLLLAY-----EYISSLLFFPDPMAGQIFPYRVTMPANLFFFLQVVIQVTDPMFAVQIVTVDYLVNISMMNL : 124
BcucOR1-2 : -----MAGKIFFFRITLPAWLPFYMQVAYIGVTDPMFAVQIVTVDYLVNISMMNL : 49
CcapOR1-2 : -----IFDRAVEENKLFIVVIYATVIGTGFTAMILVFINP-DMAGKIFPYRVALPAWLPFVRVAYIGVTDPMFAVQIVTVDYLVNISMMNL : 140
      n  l      ag  ifpyrv  lp  w  p      q  ay  g      FA  QIV  DYLVN  MN
      230     240     250     260     270     280     290     300     310     320     330
BminOR1-1 : IRFQIKLLNLAIEELKILDCV---NKK-EHINLNKKLQTIIVEHHCLLRDLNDVEDIFRLPVLIIQFFFTSLVIFAMTGFQAIKVAENNSNGAALICYCGGIFCELFVYCWFGNE : 291
BoleOR1-1 : IRFQIKLLNLAIEELKILDCV---NKG-EQREFNKKLQTIIEHHCLLRDLNDVEDIFRLPVLIIQFFFTSLIIFAMTGFQAIKVAENNSNGAALICYCGGIFCELFVYCWFGNE : 328
BdorOR1-1 : IRFQIKLLNLAIEELKILDCV---NAR-ELEEENKKLQTIIVEHHCLLRDLNDVEDIFRLPVLIIQFFFTSLIIFAMTGFQAIKVAENNSNGAALICYCGGIFCELFVYCWFGNE : 328
BlatOR1-1 : IRFQIKLLNLAIEELKILDCV---NAR-EQEEANKLQTIIVEHHCLLRDLNNVEDIFRLPVLIIQFFFTSLIIFAMTGFQAIKVAENNSDGAALICYCGGIFCELFVYCWFGNE : 328
BcucOR1-1 : IRFQIKLLNLAIEELKILDCG---SKKKAHFNHDKLQTIIVEHHCLLRDLRIDVEIFRMPVLIIQFFFTSLIIFAMTGFQAIKVAENNSNGAALICYCGGIFCELFVYCWFGNE : 329
CcapOR1-1 : IRFQIKLLNLAIEELKIFVSG---QAA-HELSDRLRLTIVDHNHLRNLNNEVEIFRMPVLIIQFFFTSLIIFAMTGFQAIKVAENNSNGASLIICYCGGIFCELFVYCWFGNE : 328
BdorOR1-2 : LRCHINIKKSTFDLILBECHVRDMDKRIKRDPMAMADIVEHHGCIKSVRDDVHEIFRLSILLQFFFTSLVTSVTFQQAIVKNSNSNSCIIIFVCFPIITQLGKWCWFGNE : 131
BlatOR1-2 : LRCHINIKKSTFDLILBECHMRDMDKRIKRDPMAMADIVEHHGCIKSVRDDVHEIFRLSILLQFFFTSLVTSVTFQQAIVKNSNSNSSEMIFVCFPIITQLGKWCWFGNE : 236
BcucOR1-2 : LRCHINIKKSTFDLILBEQNARRDMK--RDPNARMADIVEHHGCIKSVRDDVHEIFRLSILLQFFFTSLVTSVTFQQAIVKNSNSNSMMIMVFCFPIITQLGKWCWFGNE : 159
CcapOR1-2 : LRCHINVMKSSFDLINFNVKCMKSDIKRIRDPNELADLVRRHGVILKSVRDDVHEIFRLPVLIIQFFFTSLVTSVTFQQAIVKNSNSNSSEMIFVCFPIITQLGKWCWFGNE : 252
      R  L  i  F  eL  d      n  R  I  veHhC  L  R  dVE  iFrl  vLLQFFFTSL  i  A  TGFQA  Nsn  iY  YC  CIF  LF  YCWFGNe
      340     350     360     370     380     390     400     410
BminOR1-1 : VSEQSKTLTSSGYSSHCLNRERLSQQA----- : 318
BoleOR1-1 : VSEQSKTLTASGYASHHWYFDDREFKKSLLIFMCNSQTPFVFTAGGEMSLSLPSFTGILSKSYTVIALLRQVYSR : 402
BdorOR1-1 : VSEQSKTLTASGYSSHWWYAFDDREFKKSLLIFMCNSQTPFVFTAGGEMSLSLPSFTGILSKS----- : 389
BlatOR1-1 : VSEQSKTLTASGYSSHWWYAFDDREFKKSLLIFMCNSHIPFVFTAGGEMSLSLPSFTGILSKSYTVIALLRQVYSR : 402
BcucOR1-1 : VSEQSKTLTSSGYSSHWWYFDDREFKKSLLIFMCNSQTPFVFTAGGEMSLSLPSFTGILSKSYTVIALLRQVYSR : 403
CcapOR1-1 : VSEQSKTLTSSGYSSHWWYQFGPRYKKSLLIFMFNSQKPIVFTAGGEMSLSLPSFTGILSKSYTVIALLRQFYGR : 402
BdorOR1-2 : VNEQNKTLAAGGYSSSWYHFDORFRKSLAIFLLNAQOPFNFTGGGFVDLSLPSFTNVLSKAYSFTAVLRQMYSR : 205
BlatOR1-2 : VNEQNKTLATHGYSSSWYHFDORFRKSLAIFLLNAQOPFNFTGGGFVDLSLPSFTNVLSKAYSFTAVLRQMYSR : 310
BcucOR1-2 : VNEQNKTLAARGGYSSSWYHFDORFRKSLAIFLLNAQOPFNFTGGGFIDLSPSTNVMSKAYSFTAVLRHMYGR : 233
CcapOR1-2 : VNEQNKTLAARGYSSSWYFDDREFKKSLLAIFLVNAQOPFEDFTGGGFVALSLPSFTGIMSKAYSFTAVLRQMYSR : 326
      V  EQ  KTL      GY  s  wy  fd  rf  ksl  if  n  q  pf  ft  ggf  lslpsft  sk  y  ia  l  y  r

```

Supplemental figure 3-29 The alignment of OR1

```

      10      20      30      40      50      60      70      80      90     100     110
BdorOR2-1 : -----MSVQPQQQPPQQQQ-----LSAHHFRYLNLNWRLLGMMHPTRRHRLPYIYSACINISLGLFLPATMIAKLFFIENLSQLIGLEYLGVTLTMAT : 88
BlatOR2-1 : -----MSVQLQQSQSQQQ-----LDSAHAFRMLNLNWRLLGMMHPTRRHRLPYIYSAFINISLGVFLPATMIAKLFFIENLSQLIGLEYLGVTLTMAT : 88
BoleOR2-1 : -----MSVQLQEQ-QKQQ-----LDSAHAFRMLNLNWRLLGMMHPTRRHRLPYIYSACINISLGLFLPATMIAKLFFIENLSQLIGLEYLGVTLTMAT : 87
BcucOR2-1 : -----MSAVQPQQQQQQHAAASLHSSHAFRMLNLNWRLLGMMHPTRRHRLPYIYSGGINISLGVFLPATMIAKLFFIENLSQLIGLEYLGVTLTMAT : 93
BminOR2-1 : -----MSALLQVTDGTGAP-----LNSARAFRMLNLNWRLLGMMHPTRRHRCCLYLAYSASINSVFGILLPATMIAKLFFIENLSQLIGLEYLGVTLTMAT : 57
RzepOR2-1 : -----MNKQ-QDAVGRLLDSSDALRNVNLFWRITGTHPTAKYRGIVWLYSLLNLSVSLVFAFYVVTFTISTDLLETITNLSVMVPLIYTS : 85
BcucOR2-2 : -----MANQ-PHSATRLDSSDALRNVNLFWRITGTHPTAKYRGIVWLYSLLNLSVSLVFAFYVVTFTISTDLLETITNLSVMVPLIYTS : 85
CcaphOR2-2 : -----MTKQEQATPTRLDSGDATRVNLFWSITGTHPTAKYRGIVWLYSLLNLSVSLVFAFYVVTFTISTDLLETITNLSVMVPLIYTS : 86
BlatOR2-3 : ---MNMN-----KHKPLHATT-TLDTTEAFKYNFNCWRLFGMMHRLDYERRFNWVLLIVNLNLYCGVIYPMLYVASFETASIESQKLANISVAMPIIYTF : 90
BdorOR2-3 : ---MTN-----KHKPLHATT-TLDTTEAFKYNFNCWRLFGMMHRLDYERRFNWVLLIVNLNLYCGVIYPMLYVASFETASIESQKLANISVAMPIIYTF : 88
BcucOR2-3 : NLQAINNNFTIFQLTILHPGENTSKMSHKPLLTAT-TLDTKEAFSYINWCGFFGMYDLYERRFNWVLLIVNLNLYCGVIYPMLYVASFETASIESQKLANISVAMPIIYTF : 111
RzepOR2-3 : --MSIKQISLD-----DQRLMSSSQTTLSPPSPKLDTHDALRNVNLFWSITGTHPTAKYRGIVWLYSLLNLSVSLVFAFYVVTFTISTDLLETITNLSVMVPLIYTF : 102
      ld a y w wr gmhp r y Ys n p f l l v l

      120      130      140      150      160      170      180      190      200      210      220
BdorOR2-1 : AKQWSLWLHR-PKLLAVNNYAKLQVRCMRHAYDRQHILTAIRICHLIYAGYMFVVELSSSGFAYIGFSLRQLVYDGMFFPOLYADAAQNLTVTLLIYNFAVMTFFVLQNVNN : 199
BlatOR2-1 : AKQWSLWLHR-PKLLAVNNYAKLQVRCMRHAYDRQHILTAIRICHLIYAGYMFVVELSSSGFAYIGFSLRQLVYDGMFFPOLYADAAQNLTVTLLIYNFAVMTFFVLQNVNN : 199
BoleOR2-1 : AKQWSLWLHR-SKLLAVNNYAKLQVRCMRHAYDRQHILTAIRICHLIYAGYMFVVELSSSGFAYIGFSLRQLVYDGMFFPOLYADAAQNLTVTLLIYNFAVMTFFVLQNVNN : 198
BcucOR2-1 : AKQWSLWLHR-SKLLAVNNYAKLQVRCMRHAYDRQHILTAIRICHLIYAGYMFVVELSSSGFAYIGFSLRQLVYDGMFFPOLYADAAQNLTVTLLIYNFAVMTFFVLQNVNN : 204
BminOR2-1 : AKQWSLWLHR-SKLLAVNNYAKLQVRCMRHAYDRQHILTAIRICHLIYAGYMFVVELSSSGFAYIGFSLRQLVYDGMFFPOLYADAAQNLTVTLLIYNFAVMTFFVLQNVNN : 168
RzepOR2-1 : AKQWSLWLHR-SKLLAVNNYAKLQVRCMRHAYDRQHILTAIRICHLIYAGYMFVVELSSSGFAYIGFSLRQLVYDGMFFPOLYADAAQNLTVTLLIYNFAVMTFFVLQNVNN : 199
BcucOR2-2 : TKHLVVPYHIRGKLPQAALHQAALRRVELEPAACEHLRRVQRCRHFILAALAGIGVCLALYALVGIAHRHKLPFEGWLPFDWEHSLNAYILACAYQLFCLSL-VQSIYALCS : 196
BoleOR2-2 : TKHFVVPYHIRGEKPKAALHQAALRRVELEPVACTHLKRLVQRCRHFILAALAGIGVCLALYALVGIAHRHKLPFEGWLPFDWEHSLNAYILACAYQLFCLSL-VQSIYALCS : 196
CcaphOR2-2 : AKQVVPYHIRRTTPQAALHQAALRRBAEQEPAAREQLKRLVQLSRHFIFTALTGTIGICLTLYAMGILRHRRLPFDGWLFPDWEHSLVGAAYVACAYQLFCLSL-VQCIYALCN : 197
BlatOR2-3 : GKHVIVVYVYTRDLPKALAQKALORLAESRPEDCAYMKVMKNCNLFVFFSVFVSFWFALLSYGVLEVLRRHKLPFEGWLPFDWTSSEAAAYGACAVILIGLGL-IETTTAIC : 201
BdorOR2-3 : GKHVIVVYVYTRDLPKALAQKALORLAESRPEDCAYMKVMKNCNLFVFFSVFVSFWFALLSYGVLEVLRRHKLPFEGWLPFDWTSSEAAAYGACAVILIGLGL-IETTTAIC : 199
BcucOR2-3 : GKHVIVVYVYTRDLPKALAQKALORLAESRPEDCAYMKVMKNCNLFVFFSVFVSFWFALLSYGVLEVLRRHKLPFEGWLPFDWTSSEAAAYGACAVILIGLGL-IETTTAIC : 222
RzepOR2-3 : AKQIIFVYIGGLQKAAHLHAMDRAEGHIEDCAYLKRTVRYCHRFIFVNYAGFWLALLVYGLLVMSHKLFPFEGWLPFDWHSRGAYLACTLQMEFCF-SQVTNAVCI : 213
      K L L L D r d cH g L gW P Q f

      230      240      250      260      270      280      290      300      310      320      330
BdorOR2-1 : DMVPCQYLAVMIGHRLATARTSRIGK--DGLVSAEENISELINCIEDHKNLLGYFACIRFVISRTIFPMQGITAFVLCLTAVNNYAFERDAAQMLIAATYIFAVLIGALPC : 309
BlatOR2-1 : DMVPCQYLAVMIGHRLATARTSRIGK--DGLVSAEENISELINCIEDHKNLLGYFACIRFVISRTIFPMQGITAFVLCLTAVNNYAFERDAAQMLIAATYIFAVLIGALPC : 309
BoleOR2-1 : DMVPCQYLAVMIGHRLATARTSRIGK--DGLVSEQNIAELTNCIEDHKNLLGYFACIRFVISRTIFPMQGITAFVLCLTAVNNYAFERDAAQMLIAATYIFAVLIGALPC : 308
BcucOR2-1 : DMVPCQYLAVMIGHRLATARTSRIGK--DGLVSEDNIAELTNCIEDHKNLLGYFACIRFVISRTIFPMQGITAFVLCLTAVNNYAFERDAAQMLIAATYIFAVLIGALPC : 314
BminOR2-1 : DMVPCQYLAILIGHRLATARTSRIGK--DGLVNVDENIEELTNCIVEDHKNLLGYFACIRFVISRTIFPMQGITAFVLCLTAVNNYAFERDAAQMLIAATYIFAVLIGALPC : 278
RzepOR2-1 : DMVPCQYLAVMIGHRLATARTSRIGK--DGLVSEDNIEELTNCIEDHKNLLGYFACIRFVISRTIFPMQGITAFVLCLTAVNNYAFERDAAQMLIAATYIFAVLIGALPC : 309
BcucOR2-2 : DTKSIIYLLLVLAHLRIINARTARIIGGACAAQCGEVANYQQLADQVRDHEWECV---KCISSPAATAITIQIQLSALALCTAAVAFVFNADSSVEQLMKFLPYLLVVLCHIAFC : 305
BoleOR2-2 : DTKSIVYLLLVLAHLRIINARTARIIGGVCAEQHSELANYQQLAACQVRDHEWECV---KCISSPAATAITIQIQLSALALCTAAVAFVFNADSSVEQLMKFLPYLLVVLCHIAFC : 305
CcaphOR2-2 : DTKTVIYLLLVLAHLRIINARTASLG---HGECTEVENYRQLAACQVRDHWACMFNFYNSRPAATAITIQIQLSALALCTAAVAFVFNADSSVEQLMKFLPYLLVVLCHIAFC : 306
BlatOR2-3 : DTKFTVYLLLVLAHLVINGRTERVGS--AGAASDAESYRELVAGVEYHKECMSFYNSRLTSLGIYFIQFLSLGGLGSMFPALAFVGGNFSFSHVIFKLIIFGVILIEVAF : 311
BdorOR2-3 : DTKHVTYLLLVLAHLVINGRTERVGS--AGATSDAESYRELVAGVEYHKECMSFYNSRLTSLGIYFIQFLSLGGLGSMFPALAFVGGNFSFSHVIFKLIIFGVILIEVAF : 309
BcucOR2-3 : DTKHVTYLLLVLAHLVINGRTERVGS--TGDGSDAESYRELVAGVEYHKECMSFYNSRLTSLGTCFIQFLSLGGLGSMFPALAFVGGNFSFSHVIFKLIIFGVILIEVAF : 332
RzepOR2-3 : DTKSVTYLLLVLAHLVINGRTERIGN---CNTRTTETLYGELIAGVQDHRCEMCNYNCRALASGLTFLVQLSLALGLCAPAFVGGDFDLFQLLKFIIFFFATIEVAF : 323
      D Y YL HIR L a r r g g n eL C dH y i rP is t F QF Ta Lc A V q

      340      350      360      370      380      390      400      410      420
BdorOR2-1 : CWYVNSLMECAQLLTALYNCOWYDQNRKFRKMLIIFMQRSQRTVLMAGDLVPITITQFLNLNIIKFSFS-----MYTILKG----- : 385
BlatOR2-1 : CWYVNSLMECGQLLTALYNCOWYDQNRKFRKMLIIFMQRSQRTVLMAGDLVPITITQFLNLNIIKFSFS-----MYTILKG----- : 385
BoleOR2-1 : CWYVNSLMECSQLLTALYNCOWYDQNRKFRKMLIIFMQRSQRTVLMAGDLVPITITQFLNLNIIKFSFS-----MYTILKG----- : 384
BcucOR2-1 : CWYVNSLMECGELLTALYNCOWYDQNRKFRKMLIIFMQRSQRTVLMAGDLVPITITQFLNLNIIKFSFS-----MYTILKG----- : 390
BminOR2-1 : CWYVNSLMECGELLTALYNCOWYDQNRKFRKMLIIFMQRSQRTVLMAGDLVPITITQFLNLNIIKFSFS-----MYTILKG----- : 367
RzepOR2-1 : CWYVNSLMECGQLLTALYSCWFEQSKFRKILIVMQRSQRTATVLMAGNLVPITITQFLNLNIIKFSFS-----MYTILKG----- : 385
BcucOR2-2 : CWMDEAALMLKLTNALFSCCSDGN-----MYTILKG----- : 332
BoleOR2-2 : CWMDEAALMLKLTNALFSCCWYEQNLRFRRSLIIFMQRSQKVEQILAGKIFPVSLVTFIKLKLAFS-----LFTLLNQLKS-- : 384
CcaphOR2-2 : CWMDEAALMQDLTKSLFACRWYEQNKFRRLIIFMQRSQKVEQILAGDLVPVSLVTFVNIKFAFS-----LFTLLNQLKSK- : 386
BlatOR2-3 : CWMDEVLVFMRRLTNMFSCRWYEQNLKFRKALIIIFMQRSQIAQPLLGNLIPVSLDTFTNIIKFAVS-----LFTLLNKLNS-- : 390
BdorOR2-3 : CWMDEVLVFMRRLTNMFSCRWYEQNLKFRKALIIIFMQRSQIAQPLLGNLIPVSLDTFTNIIKFAFS-----LFTLLNQLNS-- : 388
BcucOR2-3 : CWMDEVMAEMHKLNTNMFSCRWYEQNLKFRKALIIIFMQRSQIAHVPVLAGNIIIVSLETFNIIKFAFS-----LFTLLNQLSHN- : 412
RzepOR2-3 : CWMDEVMAEMRQLLTALFSCWYEQNSPRFRDLIIFMQRSQKEDKITAGNITAVSLTFRSVSENLCE----- : 391
      CW E LT a C wy qn fr liifmqrsg ag p l ttf ni k s t

```

Supplemental figure 3-30 The alignment of OR2

10 20 30 40 50 60 70 80 90 100 110

CcapOR4-1-1 : -----MPFAFQQLCFELQLSLKYSVPAMPPLKANNEPAATIQDFVCIPELLTTFMVSVKLFKWTPEEASSKROQLMLGVFCVFATYNFAHILYIMYEFNSSLDTIEII : 104
CcapOR4-1-2 : -----MPFAFQQLCFELQLSLKYSVPAMPPLKANNEPAATIQDFVCIPELLTTFMVSVKLFKWTPEEASSKROQLMLGVFCVFATYNFAHILYIMYEFNSSLDTIEII : 104
BdorOR4-1-2 : -----MTPIFKSSFEVFPVDFVHIFBFLKPLVGLFKWTPEDFITQOITLLGLTFVFSIFNFTSSLHYVYVEDETLLDITIEFV : 82
BlatOR4-1-2 : -----MTPIFKSSFEVFPVDFVHIFBFLKPLVGLFKWTPEDFITQOITLLGLTFVFSIFNFTSSLHYVYVEDETLLDITIEFV : 82
BlatOR4-1 : -----MPSFKSSFEAPVDFVDIPLQIKFMGAFLFKWTPEDFNSKLQIILLGTFCIFATFNFTSSLHYVYVEDETLLDITIEFI : 81
BoleOR4-1 : -----MTPLFKSSFEAPVDFVDIPLQIKFMGAFLFKWTPEDFNSKLQIILLGTFCIFATFNFTSSLHYVYVEDETLLDITIEFI : 82
BdorOR4-1 : -----MMPFSKSSFEAPVDFVDIPLQIKFMGAFLFKWTPEDFNSKLQIILLGTFCIFATFNFTSSLHYVYVEDETLLDITIEFI : 82
BcucOR4-1 : -----MLPPFKSREHAPTVQDFVYVLEQLRFMGVGLFKWTPEERTSKLQITLMGTFCVFATFNFTSSLHYVYVEDETLLDITIEFI : 82
BminOR4-1 : -----MMLFIVYDNLDTLLDITIEFI : 20
BcucOR4-1-1 : MLVLPIARAQRYAHLTAFKFEISMDSPKSHETMKPAKNSFEPTVDFVDIPLVLLTTFIAKLFKWTPEDFNSKSGIILLVIFESGLTVYNFTSMRPFILFENLETLLDITIECI : 115
RzepOR4-1 : -----MSASSEATEPAATVKDFVILFELISLNGEKLFKWTPEDFPSRRQKIFLRATFSTIVTFNFTSSMLFLYIDRLAESALDYTALT : 82
CcapOR4-1 : -----MAPYFHTREPAATIPDFVCIPELLISLNGMOLFKWTPEEASRRKLLLTAFSVIVTYDVCVSLSVFAFVKERLDYTFFA : 81

m e t dfv ip f g klfkwt p e f M l V L Ld Te

120 130 140 150 160 170 180 190 200 210 220 230

CcapOR4-1-1 : LFWGFLNGLMGLAIMILYRNELKSLRGLGARHPQAEERSIYRIVFYVYKILYINXYIAAHLISITTLFSFHLVASTLGWIFRSESSDGYDPTLFMMWYDITTKILYIF : 219
CcapOR4-1-2 : LFWGFLNGLMGLAIMILYRNELKSLRGLGARHPQAEERSIYRIVFYVYKILYINXYIAAHLISITTLFSFHLVASTLGWIFRSESSDGYDPTLFMMWYDITTKILYIF : 219
BdorOR4-1-2 : LFWGFLNALMKGISMVCFRHEIESILKGLIAKHPKTAEEAAYQVVFYRTINISNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 197
BlatOR4-1-2 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTAEEAAYQVVFYRTINISNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 197
BlatOR4-1 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTAEEAAYQVVFYRTINISNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 196
BoleOR4-1 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTEEERVAQVVFYRTINTSNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 197
BdorOR4-1 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTEEERVAQVVFYRTINTSNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 197
BcucOR4-1 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTEEERVAQVVFYRTINTSNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 197
BminOR4-1 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTEEERVAQVVFYRTINTSNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 135
BcucOR4-1-1 : LFWGFLNALMKGISMTMVCFRHEIESILKGLIAKHPKTEEERVAQVVFYRTINTSNKYISLWHLISITISFVHHLIASIHGVSSEDKNKSFDFTFPFMTTFYDINQIAIAI : 230
RzepOR4-1 : IYVQGLNLSLKGSTLWLCRHELEFIIKGLMARHPKTEERHAYRLLEFYKKTAYNKYITLWHLGTTTLNLHLIASAVALWVWEDKEQGNFYRPFMMWFFNEEKIFL : 197
CcapOR4-1 : IYVQGLNLSLKGSTLWLCRHELEFIIKGLMARHPKTEERHAYRLLEFYKKTAYNKYITLWHLGTTTLNLHLIASAVALWVWEDKEQGNFYRPFMMWFFNEEKIFL : 196

l f w g f l n m g l m a i m i l y r n e l k s l r g l g a r h p q a e e r s i y r i v f y v y k i l y i n x y i a a h l i s i t t l f s f h l v a s t l g w i f r s e s s d g y d p t l f m m w y d i t t k i l y i f

240 250 260 270 280 290 300 310 320 330 340

CcapOR4-1-1 : SVVVOFFGAGFMSLLFLSGDLLLISLHVLNMHFDYLRHIESFQFN-GTDEDMKVLGPIVLAYHQBILDYAERIDSTFSLCTLNNYAGSCLVLCLIGLQIVLGSSEFLVYKESIAE : 333
CcapOR4-1-2 : SVVVOFFGAGFMSLLFLSGDLLLISLHVLNMHFDYLRHIESFQFN-GTDEDMKVLGPIVLAYHQBILDYAERIDSTFSLCTLNNYAGSCLVLCLIGLQIVLGSSEFLVYKESIAE : 333
BdorOR4-1-2 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
BlatOR4-1-2 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
BlatOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 310
BoleOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
BdorOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
BcucOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
BminOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
BcucOR4-1-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 249
BcucOR4-1-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 344
RzepOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311
CcapOR4-1 : SVFLQCCGAGHVSLLFLSGDLLLISLHVLNMHFDYLYIKYESFQFT-GTDAIMKVLGPIVYHNMENYAEERIDNTFGATLLNNYVGSCLVLCLIGLQIAMSEAVIVKEIGF : 311

s y Q c g a f S L F l S G D L L I s V L V N M H F Y L I I E s f Q P g t d D k k L G P L Y H E L Y a e r I D T F l t I L N Y g C l v I C l i G L Q i G s e V K F F

350 360 370 380 390 400 410 420 430 440 450

CcapOR4-1-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 427
CcapOR4-1-2 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 427
BdorOR4-1-2 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 405
BlatOR4-1-2 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 405
BlatOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 404
BoleOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 405
BdorOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 405
BcucOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 406
BminOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 355
BcucOR4-1-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 438
RzepOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 404
CcapOR4-1 : LVSTIVQVFFVSYFGNNIMDLISGSDAFYNHNPYDGNRYRSMRLVLPIARAQRYAHLTAFKFFEISMDSPKSLCTTS----YQFYTLRLTSLEEEAG----- : 405

LvsItVqV fSySGNN1 dLS GISDAFYNHNPY nYKY RMLVLPIAR QRYAHLTAFKFFEISMDSPKSLctts yqf t l rts ee

Supplemental figure 3-32 The alignment of OR4

10 20 30 40 50 60 70 80 90 100 110

BdorOR5-1 : -MAFED---VKIEICTHWITINKWMCQVN---HPKTKLYKASILVNVVSLGYPVHLVILQSEKTIQGSLLNLTLSLSVIVLRFYNTWRNFDKVRHLEQMYNNTLYARL : 105
BlatOR5-1 : -MAFED---VKIEICTHWITINKWMCQVT---HPRPKLYNAYSILVNIIFSLGYSILVILQLQEKTIQGSLLNLTLSLSVIVLRFYNTWRNFDKVRHLEQMYNNTLYARL : 105
BminOR5-1 : -MSFEKPGPKVCLFRTHTVWKNLQCVT---HPEPKLHIAITILLNISISGYPVHLVILQLNLTQMQLVLLNLTLSVPVAVCTLYFYNIWRNFAKVRHLEQMYNNTLYARL : 109
BcucOR5-1 : -MAYEAKPGPKVCLFRTHTVWKNLQCVI---HPQPKLHIAITVLLNVGSGYPVHLVILQLNLTQMQLVLLNLTLSVPVAVCTLYFYNIWRNLDKVRHLEQMYNNTLYARL : 109
BoleOR5-1 : -MAFEKPGPKVCLFRTHTVWKNLQCVT---HPEPKLHIAITILLNISISGYPVHLVILQLQKQQTQETLLNLTLSVPVAVCTLYFYNIWRNFAKVRHLEQMYNNTLYARL : 109
RzepOR5-1 : -MALQGPKTVAELFRHWSVWKNLQCVV---HHKPKLYKLAAILLNLICISGYPVHLVILQLNLTQMQLVLLNLTLSVPVAVCTLYFYNIWRNLDKVRHLEQMYNNTLYARL : 109
CcapOR5-1 : -MAFEENPESGSLFRTHTVWKNLQCVT---DPRPKLKVYVAILNVGSLGYPVHLVILQLGLQTLLEEVLLNLTLSVPVAVCTLYFYNIWRNFAKVRHLEQMYNNTLYARL : 109
RzepOR5-2 : MLFVNMKVSIGSALFRHIDTWRVYQTPPSTR-IRIYYLISLILNIITVFGYVPIHMLLIQSESKADIFKHTNLTCLGSLCFIATFWRIADWKRIYALIQRDQOI : 111
BminOR5-2 : -MFATETTISGVSVHFRHIDTWRVYQTPPSTR-IRIYYLISLILNIITVFGYVPIHMLLIQSESKADIFKHTNLTCLGSLCFIATFWRIADWKRIYALIQRDQOI : 111

m y k l Y l N f gYF HL G lNlti p C l k n Wnrl kVr le n L r i

120 130 140 150 160 170 180 190 200 210 220

BdorOR5-1 : DHPEDLAYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 217
BlatOR5-1 : DHAEEDLYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 217
BminOR5-1 : DHPEDLAYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 221
BcucOR5-1 : DHPEDLAYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 221
BoleOR5-1 : DHPEDLAYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 221
RzepOR5-1 : NQRDEWLYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 221
CcapOR5-1 : NQRDEWLYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 221
RzepOR5-2 : IHSDDWLYVRKVTAPNARIRVSAEKVICVCAVTAETQLYGVFVVGNRMLMPYGFFFDPHGSTAGYVTHAIFPIGLLTQISQNLMSDTYGAVCLLALAGHTHLGGLRAR : 223
BminOR5-2 : VRSTDYELKRYALRRAGHYLYFVLVGLGASISSEVATTIGSELGENRMLMPYGFFFDIERSLWGVPIAHYICFGVTAIFONLINDTLPPMALAMAVQVRLNKRVAR : 223

yYr p a V l f i c G a E l l G f WRMLMP YFFDp gYv AH Q i G Q N l s d t Y g m c L lLagH L lG r a r

230 240 250 260 270 280 290 300 310 320 330

BdorOR5-1 : IGYDKDKREQ---HNQDFVDFIVDHNMLNLCORTLVDIGMGLFALISTSLLAIVIMPFFVDNALEYAYVFFMFGALMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 326
BlatOR5-1 : IGYDKDKREQ---HNQDFVDFIVDHNMLNLCORTLVDIGMGLFALISTSLLAIVIMPFFVDNALEYAYVFFMFGALMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 326
BminOR5-1 : IGYDKDKREQ---NNRELVDCTIDHNVLFDCHRTLGDIGLGLFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 330
BcucOR5-1 : IGYDKDKREQ---NNRELVDCTIDHNMLFDCHRTLTDIGLGLFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 330
BoleOR5-1 : IGYDKDKREQ---NNRELVDCTIDHNMLFDCHRTLTDIGLGLFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 249
RzepOR5-1 : IGYDASKTECE---NNRALVDCTIDHNMLFDCHRAIGELIGVGMFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 330
CcapOR5-1 : IGYDNQKTEMD---TGRELANCIDHNMLFDCHSLIGELIGVGMFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 330
RzepOR5-2 : IGYDRKRASVR-ETNDAAELQCEVYKALLDFRAAQRIASIGFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 334
BminOR5-2 : IGYDRKRASVR-ETNDAAELQCEVYKALLDFRAAQRIASIGFVQITISASLIMGVVIIVIFVGNAFEVYVYALFLFACIMEVFPTCYATYHFFYEIEEGLTYKIFSCNW : 335

Igyd t n ci Dh n l i g f i v i y f v y y e f p c y t e e f l t f s c n w

340 350 360 370 380 390

BdorOR5-1 : VDQNRSPKKNLIVCLVEQSLKARYVFGGMFRINMQIFIAICKGAYSVTTLALNYK : 381
BlatOR5-1 : VDQNRSPKKNLIVCLVEQSLKARYVFGGMFRINMQIFIAICKGAYSVTTLALNYK : 381
BminOR5-1 : MDQNRSPKKNLIVCLVEQSLKARYVFGGMFRINLQIEFATCKGAYSVLAVALARL : 385
BcucOR5-1 : MDQNRSPKKNLIVCLVEQSLKARYVFGGMFRINLQIEFATCKGAYSVLAVALARL : 385
BoleOR5-1 : ----- : -
RzepOR5-1 : MDQREKPNKKNLIVCLVEQSLKARYVFGGMFRINLQIEFATCKGAYSVLAVALARL : 385
CcapOR5-1 : MDQNRSPKKNLIVCLVEQSLKARYVFGGMFRINLQIEFATCKGAYSVLAVALARL : 385
RzepOR5-2 : LDQSAAPKKNLIVCLVEQSLKARYVFGGMFRINLQIEFATCKGAYSVLAVALARL : 389
BminOR5-2 : MDQNRSPKKNLIVCLVEQSLKARYVFGGMFRINLQIEFATCKGAYSVLAVALARL : 390

dq f k n l e q s l g g m f n f a k g a y s k

Supplemental figure 3-33 The alignment of OR5

10 20 30 40 50 60 70 80 90 100 110 120
BdorOR6-2 : MTTTCRLMH--IKALGLALVN--KTSEIRCNMRQSPQATAEMPFGIALAIHNEIATQDRIKI---KASSAKALSSENIEEEA-----AEQHVSQDQTTKYLKRSAGFMGLVMSRY : 106
Blator6-2 : ---MQMLHTSIKALGLALAN--YTSEIRCNMRQSPQATAEMPFGIALAIHNEIATQDQTKINKPKASSAKALSSENIEEEA-----AEHHVVSQDQTTKYLKRSAGFMGLVMSRY : 108
BoleOR6-2 : MTHIGRHFFTSDAVLTALRRKRTTEIRCNMRKLPRSTADMAKVGIALAIHNEIATPDNTSKRKLKRSASAKVLSSELSEAEA-----AEHHVVSQDQTTKYLKRSAGFMGLVMSRY : 114
BcucOR6-2 : ---MLCKMSKLPQLTAVMAKO--VKTARQNTNVQKPLSV---LEAKNLVKTLSSETVEED-----VVPQVSTQDQTTKYLKRSAGFMGLVMSRY : 83
Ccapor6-2 : ---MNRFRKQSARAETENNNKALALSLSEKELSGKNGEQRIRAKPAKASAVREKQGEFGNVFFSLTFLVASPASSEKATNVYFKKAAFGMGIMLTPRH : 96
RzepOR6-2-3 : ---CRKAGSFVGLKTALELLLFNKEQTIALRLPEAEKQQLAS---LSTAKFVVSQDTEEAEC-----VDLPVQSQDQTTKYLKRSAGFMGLVMSRY : 87
RzepOR6-2-2 : ---MSKQSGSLDRLPFAEKQQLAS---LSTAKFVVSQDTEEAEC-----VDLPVQSQDQTTKYLKRSAGFMGLVMSRY : 69
RzepOR6-2-1 : ---MMSKSKQSLALRLAARAKQQLAS---LSTAKFVVSQDTEEAEC-----VDLPVQSQDQTTKYLKRSAGFMGLVMSRY : 70
RzepOR6-1-1 : ---MSEAPCNSRQ---LRYDNVGGVRSASASNVQA-----TPSVRTVHALNVLKSGFRVLGIYMPARR : 56
RzepOR6-1-2 : ---MSEAPCNSRQ---LRYDNVGGVRSASASNVQA-----TPSVRTVHALNVLKSGFRVLGIYMPARR : 56
BdorOR6-1 : ---MMANVFSSTVQ---LEASIAALSRAAETTDK-----PAVRTVQATNVLKSGFRVLGIYMPARR : 54
Blator6-1 : ---MANATSSTVH---LEASIAALSRAAETTDK-----PAVRTVQATNVLKSGFRVLGIYMPARR : 54
BoleOR6-1 : ---LRESS---AEATVE-----PAVRTVQATNVLKSGFRVLGIYMPARR : 38
BcucOR6-1 : ---MEDAFSSSHQ---LQADIAAQRR-TETTDK-----PAVRTVQATNVLKSGFRVLGIYMPARR : 53
BminOR6-1 : ---MSEAR : 5
Ccapor6-1 : ---MLPRTQFYKFTFSLFYKYLVVALILNLLSKKKITDLPATMADTAINSRQ---LQDTDLN-NGLKKKGQDQ-----LAVRTEHATNVLKSGFRVLGIYMPARR : 94
RzepOR6-3-1 : ---MANFLPQRLKLVFGQLRPEKVIKVAEQPPAEFVLSNAQLIRIQERATRTVPVSKRESSAQEEHEV---RPYGAVDHSHKDGTLVYLSRFSMALGVLMPEKY : 99
RzepOR6-3-2 : ---MANFLPQRLKLVFGQLRPEKVIKVAEQPPAEFVLSNAQLIRIQERATRTVPVSKRESSAQEEHEV---RPYGAVDHSHKDGTLVYLSRFSMALGVLMPEKY : 99
Ccapor6-3 : ---MSNLLQRLNLQLLPS--RTTQKSIDVVK-QVSPSLSNAELIRIQERATRTPK---ERSAPVG-----RPYGAVDHSHKDGTLVYLSRFSMALGVLMPEKY : 90
y l f g m P r
130 140 150 160 170 180 190 200 210 220 230 240
BdorOR6-2 : RALVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 228
Blator6-2 : RALVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 230
BoleOR6-2 : RPLVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 236
BcucOR6-2 : RALVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 205
Ccapor6-2 : RILVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 219
RzepOR6-2-3 : RFFVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 210
RzepOR6-2-2 : RFFVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 192
RzepOR6-2-1 : RFFVLIIGFLVNFVTFYFPIGTLILFLP-DDNVVSNLLTSLOVTFDYGCSAIIIIKPVLEKLRAHQILQRLDKKCRASDVEELQOMVRFKKVVIFFYTLFLCSASTFLASVSS : 193
RzepOR6-1-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 179
RzepOR6-1-2 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 179
BdorOR6-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 177
Blator6-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 177
BoleOR6-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 161
BcucOR6-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 176
BminOR6-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 128
Ccapor6-1 : KWLIALVALIPHVLTIVLILSLSFVSATMSAADLPSSLLTSIQVAINVICGSVIVVNAFLPKLRATANAFMDRLDARCRDEDEICELRKIVQNNRFVLFAMSYNSKATSTFLGSVVF : 217
RzepOR6-3-1 : KFLDLKALLPGLITFYLPAFVLSYFKLDYSTIKIGNLLTSVQVSIASFVGAICLCVNAFKPKLRAGEAIMSELDAKCKDEDEIEVLRKVVRQNNRLVLVILICNLVISTSTFLGATLK : 222
RzepOR6-3-2 : KFLDLKALLPGLITFYLPAFVLSYFKLDYSTIKIGNLLTSVQVSIASFVGAICLCVNAFKPKLRAGEAIMSELDAKCKDEDEIEVLRKVVRQNNRLVLVILICNLVISTSTFLGATLK : 222
Ccapor6-3 : KFLDLKALLPGLITFYLPAFVLSYFKLDYSTIKIGNLLTSVQVSIASFVGAICLCVNAFKPKLRAGEAIMSELDAKCKDEDEIEVLRKVVRQNNRLVLVILICNLVISTSTFLGATLK : 213
l y l y l T P f t LLTS Qv v g s K Maf L KLR LD RCr E eL k v G Y STf l s G
250 260 270 280 290 300 310 320 330 340 350 360 37
BdorOR6-2 : YPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 351
Blator6-2 : YPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 353
BoleOR6-2 : YPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 359
BcucOR6-2 : YPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 328
Ccapor6-2 : YPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 342
RzepOR6-2-3 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 333
RzepOR6-2-2 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 315
RzepOR6-2-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 316
RzepOR6-1-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 302
RzepOR6-1-2 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 302
BdorOR6-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 300
Blator6-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 300
BoleOR6-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 284
BcucOR6-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 299
BminOR6-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 251
Ccapor6-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 340
RzepOR6-3-1 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 345
RzepOR6-3-2 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 345
Ccapor6-3 : RPPVSLVFFFLKRRSRHTFIASLSLEFIIMDFALQQTVDNGCPVIVIMNMLRCHKIQLQVVEKICNNPMLTQVEHLSLKLCKDHQILIELYDIAPISIVILIQFALSRAVCIGTGLIN : 336
PPY l Y P WR S eF As EF mD aC qq v D y viy l r HM l L R L tn l eLKlCi DH L L yd apIis T F iQf a tLLN
0 380 390 400 410 420 430 440 450 460 470 480
BdorOR6-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 463
Blator6-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 465
BoleOR6-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 471
BcucOR6-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 442
Ccapor6-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 456
RzepOR6-2-3 : TVIPANFSSRIASCFYILAVTVIIFTQYYSCLIDDSNQSDVIFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 447
RzepOR6-2-2 : TVIPANFSSRIASCFYILAVTVIIFTQYYSCLIDDSNQSDVIFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 429
RzepOR6-2-1 : TVIPANFSSRIASCFYILAVTVIIFTQYYSCLIDDSNQSDVIFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 430
RzepOR6-1-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 416
RzepOR6-1-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 416
BdorOR6-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 414
Blator6-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 414
BoleOR6-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 398
BcucOR6-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 413
BminOR6-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 365
Ccapor6-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 454
RzepOR6-3-1 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 452
RzepOR6-3-2 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 459
Ccapor6-3 : TVIPANFSTQVACCFPIILAVLIIYFAIYFSCLINECDKADVPFHSNWEISPEYKRLIIFFLQSRQRMFTTACKLFPVTLSSFI--AKFSFSLYTTEKNNKERIRGLE : 416
i IFA a f iAlav E i P CY QcL d s L IFH nW i Q Rk fF Qr Q m L AGK fp t l sf akfsfalyt i m er

Supplemental figure 3-34 The alignment of OR6

```

      10      20      30      40      50      60      70      80      90     100     110
BdorOR7-1 : MSKILVRSATVYKSRDALTYLFNVFTFMGTNLENRSQRYYRLYHFYSFTVNFICCLECPLSFHIGYIKLRRHVLINSQLLAAIONAVQVSSGIPIKILVITWYMKRLRHA : 110
BlatOR7-1 : MSKILRFRSAIVYKSRDALTYLFNIFTFVGTNPLENRSQRYYRLYFYFSTVNFICCLECPLSFHIGYIKLRRHVLINSQLLAAIONAVQVSSGIPIKILVITWYMKRLRHA : 110
BminOR7-1 : MSKILRVRSRAKIYKSRDAVSYLFNIFTFLGNTNLEHRSRRYYVLYFYFSTLNFISLLYCPLSFHIGYIKLTHVLINSQLLTAAIONAVQVSSGIPKVVAITWYMKRLRQA : 110
BcucOR7-1 : MPNLIRVGGACIYKSRDLSYLFKIFTFVGINSEQQSRKYYWLYYSYSLTVNFICCLESPLSFHIGYIKLWHVLNNQLLAIONAVQVSSGIPIKILVITWYMKRLRQA : 110
CcapOR7-1-1 : MLDLIRGRGRVYKSRHALTYLFNVFTFVGTNEGKTRTHKYVTLYYYSYSLTVNFICCLECPLSFHIGYIKSWHLINTTELLAAIONAVQVSGIPIKIFFITWNNMRLQSV : 110
RzepOR7-1 : MLDLIRGRGLEAYKSRDALTYLFNIFTLVGTNPGQGSNKYYVLYLSYSLTVNFICCFESPLSFHIGYIKYLNVLSTTELLAIONAVQVSGIPVKIIVITWNNMRLSA : 110
CcapOR7-1-2 : MSDLIFGRGQIVYKSRHALTYLFNIFTFVGTNPLGGQSYAYYSLYLSYSLTVNFVCCIECHISFHIGYIKLLNVLTNTNELLSAIONAVQVSSGIPKIIVITWNNMRLQSV : 110
      M 1      YKSR altYLFn Ftf GtNP      s YY LYy YS tvNFicc f PlSFHIGYIK      vL      LL AIQNA QV GIPIKi Itw MkrL

      120     130     140     150     160     170     180     190     200     210     220
BdorOR7-1 : FEILDELDVNYTRREDLAKIRECVRRRKRIIVLIFCFPPYYSFELTITIALGVANRAPLAANVPFLDGQR-AAEYWTIVLWDAFVMPFLCHOLGSDYTPPIFINIRTHV : 219
BlatOR7-1 : FDILDELDVNYTRREDLAKIRECVRRRKRIIVLIFCFPPYYSFELTITIALGVVQNRAPLAANVPFLDGQR-AAEYWTIVLWDAFVMPFLCHOLGSDYTPPIFINIRTHI : 219
BminOR7-1 : VEILDELDVNYTQREDLAKIRECVRRRKRIIVLIFCFPPYYSFGISITIALGVLQCAPUTWVPFLDGQR-AAEYWTIVLWDTLVMPFLCHOLGNDDYTPPIFINIRTHM : 219
BcucOR7-1 : FKILDELDVNYTQHEDLAKIRECVRRRKRIIVLIFCFPPYYSFELTITIALGLLQKRAPLAANVPFLDGQR-AAEYWTIVLWDTLVMPFLCHOLGNDDYTPPIFINIRTHV : 219
CcapOR7-1-1 : IPILDELDVNYKSADDLKIRKCVRGSCMIGFFLLPYYSFITITIALGVQNRAPLAANVPFLDGQR-AAEYWTIVVWDIFVMPFLCHOLGSDYTPPIFINIRTHV : 219
RzepOR7-1 : REILDELDANRRADDLIRIQCVRRCHITIVFVPPYYSFITITIALGVLQHNVPLAAWVFLDAQGAEQWVLIWVWDTFVMPFLCHOLASDYTPPEVVISIRTHI : 220
CcapOR7-1-2 : CEILDKLDENYKRAEDLNSIRCVRSCHIIAAEVPPYCFELSTIAFCMYQNRAPITINLYFBATR-TTWEYWHGNDVELILFLAHOLGSDYTPPEVVISIRLHM : 219
      ILD LD NY      DL      IR CVR C K      FC PYYsfe      TIA Gv Q raPL WvP ld r a WeYWTiV WD fvMf LL hQLg DTYpP i Irth

      230     240     250     260     270     280     290     300     310     320     330
BdorOR7-1 : QLLIIARVNRLGRGALTADEHYELLGCIRTHVQIVSIAKIVAPVISVTLTFQFATTATTLNWLNVVEYPENIISLAFFSCQLLOILPCCSSASOLIADCERLP----- : 324
BlatOR7-1 : QLLIITRVNRLGRGALTADEHYELLGCIRTHVQIVSIAKIVAPVISVTLTFQFATTATTLNWLNVVEYPENIISLAFFSCQLLOILPCCSSASOLIADCERLP----- : 324
BminOR7-1 : QLLIVTRVNRLGRPGALTADKHYELL-----ASKIVAPVISVTLTFQFATTATTLNWLNVVEYPENIISLAFFSCQLLOILPCCSSASOLIADCERLP----- : 313
BcucOR7-1 : QLLIVTRVSRLGRDGALSADEHYAELLACIRTHVQIVSIANIVAPVISVTLTFQFATTATTLNWLNVVEYPENIISLAFFSCQLLOILPCCSSASOLIADCERLP----- : 324
CcapOR7-1-1 : QLLIVERVELLGSDKTKSAEEHYAELLGCIRTHGQIKRIVNLIAPVISVTLTFQFATSATTLNWLNVVEYPENIISPAYFTGLTLIQILPCCSSAYLISDCELLP----- : 324
RzepOR7-1 : QLLIVERAKRLGGDRMINADENYAELLACIRTHQILRLARIAPVISITLFTFQFATTATVLNWFGNVEPENIISPAFFSCQLMOILPCCYCASLLIDCDQLP----- : 325
CcapOR7-1-2 : QLLIVERVKRLGTNKALCREKRYAELLVCINTYGILSIANIVAPVISITLFTFQFATTATVLNWFGNMKFPDNIIPMAFFSCQIMQILPCCYYASOLIAWCFMTHSHSL : 329
      QLL Rv rLG      l a Y ELL ci t qi      ivAPVIS TLTFQFATTat LnW G e PeNIIs Aff Cq QILPCC AS LI Dc Lp

      340     350     360     370     380     390     400     410     420     430
BdorOR7-1 : -----DAIFHCNWDQDRFRRAILPFLQRTQPIRESCKLFNVKLETS-----VAIGKFAPSLYT--LEETRKVTDTTEN----- : 394
BlatOR7-1 : -----DAIFHCNWDLDDRFRRAILPFLQRTQPIRESCKLFDVKLETS-----VAIGKFAPSLYT--LEETTVGTNTDN----- : 394
BminOR7-1 : -----DAIFHCNWDQDRFRRAILPFLQRTQPIRESCKLFDANLETS-----VAIGKFAPSLYT--LHEAEDGGKTDN----- : 383
BcucOR7-1 : -----DAIFHCNWDQDRFRRAILPFLQRTQPIRESCKLFEVVKLETS-----VAIGKFAPSLYT--FIQESDVGRKSNN----- : 394
CcapOR7-1-1 : -----NAIFHCNMIERDRFRKRTLLPFLQRTQPIRESCKLFEVVKLETS-----VAIGKFAPSLYT--LQGTEVGGKTEN----- : 394
RzepOR7-1 : -----NAIFHCNMDQNRFRKRTLLPFLQRTQPIRESCKLFEGVNLAG-----NAIGKFAPSLYT--FIKESKVGDKLDR----- : 395
CcapOR7-1-2 : RPIFEQHYRPVAGSVIRATIDQLYTVLTLLDNAPPSAVIATVEQNIKENPNEYIHYREAQLEPCSSTFCKILLKNLGLRTYATQVQVSSKNDQLERCTSAK : 432
      aifh nw      rR      lff qr q p rf ciklf      Let      aigkfafslYt      i e g

```

Supplemental figure 3-35 The alignment of OR7


```

      10      20      30      40      50      60      70      80      90     100     110
BdorOR9 : MELHEHDNLSCGRVRVKKILKLLGLHWHGCVGMRTFYLLVSGLLHSVFTIPYTHMCMQVQVQVSOLEKFTNTMYMTLTELAKLVNVVWSYSKLLVDFEFTAFTHBKLYQLQDAEERQS : 117
BlatorOR9 : MELHEHDNLSCGRVRVKKILKLLGLHWHGCVGMRTFYLLVSGLLHSVFTIPYTHMCMQVQVQVSOLEKFTNTMYMTLTELGMVVKVIVNVVWFVSRLLVDFFAAFTHBKLYQLQDAEERQS : 117
BcucOR9 : MKLEQFDNLISGGRVRVKKILKLLGLHWHGCVGMRTFYLLVSGLLHSSTFTIPYTHMCMQVQVQVSNLEKFTNTMYMTLTELGLVAKLVNVVWSYSRLLVDFEFAAFTHBKLYQLQDAEERQS : 117
BoleOR9 : MELLEVDNLISGGRVRVKKILKLLGLHWHGCVGMRTFYLLVSGLLHSVFTIPYTHMCMQVQVQVSNLEKFTNTMYMTLTELGLVAKLLN----- : 86
CcaphOR9 : MVLQEVDDNNSGGRRIQVVMKLLGLWVYEGSAKMPYLLVSGLLHSFTSTIPYTHMAMDVVHHTOLEKFTNTMYMTLTELGMVAKLVNVVWFVAKLLVDFEFTLSGQKYFELREKDERLN : 117
BminOR9 : MYVREHHDNLISGGRVITVILKLLGLHWHGCVGMRTFYLLVSGLLHSSTFTIPYTHMCMQVQVQVSNLEKFTNTMYMTLTELCLVVKVIVNVVWFVSRLLVDFFAAFTHBKLYQLQDAEERLN : 117
RzepOR9 : -----MCMQVQVQVSNLEKFTNTMYMTLTELAKLVNVVWSYSKLLVDFEFAAFTHBKLYQLQDAEERLN : 65
      m      dn      gr      kilglw      y      py      l      s      llh      ip      t      mM      DV      A      LeKftntMymtLTEL      v      KL      Nvw      y      llvdf      d      e

      120     130     140     150     160     170     180     190     200     210     220     230
BdorOR9 : WQRTQKNYSRVAFELFTMSLSTLATAFVGVIYSEDYELFPFYAPPEDWRTPRGYWYAYCYELLAMPITCLSNCAFDMIQCYMLLQSLSCFKVITSLERLMTLQEQ-CSSTRGFSFVM : 233
BlatorOR9 : WQRTQKNYSRVAFELFTMSLSTLATAFVGVIYSEDYELFPFYAPPEDWRTPRGYWYAYCYELLAMPITCLSNCAFDMIQCYMLLQSLSCFKVITSLERLMTLQEQ-GSTTHGFSFVR : 233
BcucOR9 : WRTTQGNVARIATFLFAMSLGALASAFVGVIYSEDYELFPFYAPPEDWRTPRGYWYAYCYELLAMPITCLSNCAFDMIQCYMLLQSLSCFKVITSLERLMTLQEQ-DSASRGFSFVR : 233
BoleOR9 : ----- : -
CcaphOR9 : WQHAQRTYARIVLFVFIQGLGAMFTGFVGVLPSAKYELFPFYAPPEDWRTPRGYWYAYCYELLAMPITCLSNCAFDMIQCYMLLQSLSCFKVITSLERLMTLQEQ-TAVSRGFSFV : 234
BminOR9 : WRRPQRNFARVVFITVTSFSAMVSATIGVLYREDYELFPFYAPPEDWRTPRGYWYAYCYELLAMPITCLSNCAFDMIQCYMLLQSLSCFKVITSLERLMTLQEQ-DGASSGFSFV : 233
RzepOR9 : WARRGHWGIALLFAMSLATLSTAFVGVIYSEDYELFPFYAPPEDWRTPRGYWYAYCYELLAMPITCLSNCAFDMIQCYMLLQSLSCFKVITSLERLMTLQEQ-VVRESSASNGSSEK : 182
      w      q      y      f      gvl      yelp      pyappf      w      t      gwy      ay      yellam      n      fdmiq      yml      qisicfk      i      rl      mg      gf      e

      240     250     260     270     280     290     300     310     320     330     340     350
BdorOR9 : FHRDFVDIVRLHARTKLLSQCCQTYISFFPLLIQISSSFVLCFSAYRLQKVPILNPSQFTLTVQANLIMLVQITFIPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 350
BlatorOR9 : FHRDFVDIVRLHARTKLLSQCCQTYISFFPLLIQISSSFVLCFSAYRLQKVPILNPSQFTLTVQANLIMLVQITFIPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 335
BcucOR9 : LHREDFVDIVRLHARTKLLSQCCQTYISFFPLLIQISSSFVLCFSAYRLQKVPILNPSQFTLTVQANLIMLVQITFIPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 350
BoleOR9 : -----VPILESQFTLTVQANLIMLVQITFIPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 153
CcaphOR9 : LYRFDFVDIVKLHARIKMLSRCLQTYISFFPLLIQISSSFVLCFSAYRLQKLSLSDPMQFTFVQVNLIMLIEIFLPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 351
BminOR9 : FHRDFVDI-----VNLIMLIEIFLPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 293
RzepOR9 : FYADEFGAVTLHVRTRELSQCC-----ENAYRLQKITFIPCYCGNIIIEYSSGNNATYNNAEWFRCSFMRKRYLVIYME : 256
      fv      Nlim      l      IF      PCy      GN      II      S      LnNa      Y      eWfrCSP      mRkRYLviYMeM

      360     370     380     390     400     410     420     430     440     450     460
BdorOR9 : LQRFVRVRAGDFEDISIT-----IFTKTMNNTYSLLIALLNNMK----- : 389
BlatorOR9 : LQRFVRVRAGDFEDISIT-----IFTKV----- : 358
BcucOR9 : LQRFVRVRAGDFEDISIT-----IFTKTMNNTYSLLIALLNNMK----- : 389
BoleOR9 : LQRFVRVRAGDFEDISIT-----IFTKTMNNTYSLLIALLNNMK----- : 192
CcaphOR9 : LQRFVRVRAGDFEDISIT-----IFTKTMNNTYSLLIALLNNMK----- : 390
BminOR9 : LQRFVRVRAGDFEDISITDVAIYACVACRAGTEVRNVQVACATNHGQTIKATMTYELPGFPCIEAQPLLTDLHMTVLARDRVGRLRHTGANVLHSHRGILINARLVIN : 403
RzepOR9 : LQRFVIVYHFRNCWLIV-----VIAQ----- : 277
      LQRPv      V      a      ff      isL      if

```

Supplemental figure 3-37 The alignment of OR9

```

      10      20      30      40      50      60      70      80      90     100     110     120
BdorORCO : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
BlatorORCO : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
BcucORCO : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
BoleORCO : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
BminORCO : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
RzepORCOX2 : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
RzepORCOX1 : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
CcaphORCOX1 : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
CcaphORCOX2 : ---MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 118
DmelORCOX1 : MTTSMQPSKVTLGLVADLMPNIRLMKYSGLFMNFTGGSAFMKYYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 122
DmelORCOX2 : MTTSMQPSKVTLGLVADLMPNIRLMKYSGLFMNFTGGSAFMKYYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA : 122
      MQPSKVGLVADLMPNIRLMKYSGLFMNFTGGSGLFKKIYSSVHLVLVQVQFLLILVNALNAEVEVNLSGNTITVLFPTHSTKFIYLAVSQKHFYRTLNINWQVNSHPLFAESSA

      130     140     150     160     170     180     190     200     210     220     230     240
BdorORCO : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
BlatorORCO : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
BcucORCO : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
BoleORCO : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
BminORCO : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
RzepORCOX2 : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
RzepORCOX1 : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
CcaphORCOX1 : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 240
CcaphORCOX2 : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 244
DmelORCOX2 : RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL : 244
      RYHIALAKMRKRLFTLVMLTTVASAVAWTTITFFGGSVKFAFKEKNTSTVEIPLRLPIKSFYFNWAGSGMFYISFAFQCYVLLFSMVHNSLCDVLFCSWLIFACEQLQHLKGIMKFMPEL

      250     260     270     280     290     300     310     320     330     340     350     360
BdorORCO : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
BlatorORCO : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
BcucORCO : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
BoleORCO : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
BminORCO : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 356
RzepORCOX2 : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
RzepORCOX1 : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
CcaphORCOX1 : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 353
CcaphORCOX2 : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 366
DmelORCOX2 : SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNM-----GTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL : 366
      SASLDTYRPNASALFRSLNSANSKSELINNEEKETDLDISGVYSSKADWGAQFRAPSTLOTFNQNMGTNPNGLTRKQEMMVRSAIKYWVERHKKHVRLVAAGDGTGGALLHL

      370     380     390     400     410     420     430     440     450     460     470     480
BdorORCO : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
BlatorORCO : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
BcucORCO : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
BoleORCO : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
BminORCO : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
RzepORCOX2 : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
RzepORCOX1 : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
CcaphORCOX1 : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 473
CcaphORCOX2 : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 486
DmelORCOX2 : MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK : 486
      MLTSTIMLTLLAYQATKITGVNVYAFITGYGLYALAQVHFICFQNRLEIESSSVMEAAAYSCHWVDGSEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASVLGAVVTFYFMVLVQLK

```

Supplemental figure 3-38 The alignment of ORCO