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
ADNLNDFCEVIYIAMADVTLNIKFLTLFIVRQQLLELRPILKHLDARARTEEEIGVLQDGID
SAKKCFLIILRLFYSAFVTSQLMVIFSVEARLMYPAWYPFDYQASRTKFWIAYGYQTIGFLV
QCTQACSVDTYPQAYMRVLTAHIRALSLRVERIGRKNFSYASSELMCLTKDEMKRNYDEL
VSSIKDHKTIIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVGFNISIMLNMAVFFVSV
TMETLILCYYGDLFCQECEGLSKAIYNCNWTVQSTEFKNALSFFLLRSQRVNILMAGNWI
PVKLPTFVMLIIIIEVMSLLIDDYNKIE*

>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]

MFELITGRGIGIASSKDAFIYFFKGCTIVGLSPPKNSGLLYYMWSFSVNAICIIISPITGPVGF
VIKYLQNTITTVQFLSGLQAALNLIGLPVKCSTVTHALKRLRGIEPTLTIMDARYTRPEDVA
LIRKAALMGNRLVFFFGTSYFMYMLFTVIPPLINGKAPLSVWIPFFDEHQSRIHICVQIVYD
LFTMFFVLFHQSLYDSYGSVYIYVISTHLQLLVRRVGRLGTDATKSQDDNMKELVDCVVT
HQQILELLATIEPIISTTMFTQFLIISSILCVTMVNMFFFADRSTQLASTLYFLCVLLQTSPCC
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
WLRDRNKLSVMEILTCVQASLNVMAVPLKCIALAMAMNRLRGIEPMVTELDERYTTPED
RAKIKQCAVTGNRLVFGFAVSYFLYETLTVISALVGGHAPLSLWIPNVDWHRSTWEYWLQ
VSFDAAVLFFILYHQVLNDSYPAVYIYIIRTQIQLLTSRVEKLGYDDQKSADENYQELSECIV
IHQKILKIVKIVESVVSITVFTQFLVAAAILGVTMINIFIFADLTTKIASVTYFFCVLLQTSPTC
YHASYLLADCDELRIAIFQCNWIAQNKRFNNLLIYFLHRSQDSIPFFALKLVPINLATNLSTS
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
GCSALRTDLELALDTLCPAGTSAVTLLKMALIYYYRKDLAWVLKRMRGFMYTRDVSINT
VKEHIVRAHAVMAARLNFIPFVMGFITCTSYNLKPLLMTLILYVQGQEPMWKLPFNMTAS
ALFHYSMPSFLLQAPYFPLTYIFTSYTGYITIFMYGGCDAFYFEFCSNIAALLELLQNDLKSI
ISFGEGLIKTFKFPSQSVQLATVAFGCDWLACNPRLRRYVLMIILRSHRAINMAVPFFAPSLV
TFTSILQTSVDHDPLGSKKSERCSNEQVEAKDGEEEVEKEKKRKKVEN*

>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
PLASFASLLSFVLLLSGSVTNTFFNTLPLLKMGYYKWQSLEAELLLPFNVILPEMLPIAILPS
HIPGADALRRHDCFSLLVRSMVSSSALARLSRLAVCFFLVVFCCQWSTQRCAKYADTASL
WRWLVERHNKIIDLCSDFALEFYSYSDAFLFRHRWCCASQHFGLMLNSASVGVLTYIFYSI
AALTQLFLYCIGGTYVSESSLKVAEVIYDIDWYKCDVRTRRMLLMMICRAQKAKTIQVPF
FTPSLPAFRSARKSIIDQISPKRCERNQSTLIRAKHEEEEAVE*

>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]

MLLKFLTQSYPTEKNIFLIPRLALRIIGFYPEESSSRRRQAFLIFNWVILVYGCYAEFMFGIQN
LSIDVVRALDALCPVASSIMSVVKVTFLWYHRAELNRLIKRVTELNAAQDSPLKSAYKHR
YFATATRLSASLLFFGFITATLYGTRAGMINYLSYLRKDEIPFETPFKMIIPKSLLSMPLFPLTF
ILSLWHGYITIAGFAGTDGLFLCFCMYIGTLLKALQYDMKDLLSDVHSGVCKSSAEYEIKE
SLKMIIARHNEIIDLVKRFSAVMSGVILGHFVTSSAIIGTGVLDMLLFSDYGVFVYLLHTMT
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]

MGKKLLVVKSSVNTPVDTVACFDIFWMCWKLMGISINSNKWYVTLYDIVVNIFVTIFYPIH
LTVGLFLVPVLSDVFKNLAIIITDVACSTKHYLFRYKLSKIREIQRLLKELDDRVVAQDERD
YFNKSIRSAVRRMMLIFCVSYAGDTLASALEVLAKKDRELMYPAWFPFDWSANRYTYYA
AVIYQIVGVSLQITQNLAHDTFAPVSLCVMSGQVRLLAMRVSKVGYDESKTLAEHEEELN
ECIEDHKKLLRIFDLLQDVFWYTQLVQFSSVGLNICLTVVFLLQFADNIFAYLYYTAYFISM
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
FLNPTPADLFQNLSITITCFICSIKHYLLRRKLPQIHTVQVLLAELDKRVEGADEHAYFQQQ
LVVGAKNVVKLFSIAYGGANMAAISATLLSKERRLLYPAWLPFRWEASTFNYCAAVIYQIA
GVTIQIVQNLANDIYPPMSLCIIAGHVHLLALRVAKVGEDAKKSMKQHNQALIRCIEDHK
KLVRIFELTQDTLSQAELAQFISSGLNMCIVLFYLIFYVDNVFAYIYYAVYFVSMAIELLPSC
FYGSMLIYEFQQLPSAIFKCSWLGQSREFYQNQRIFVQVSLKKIVPLAGGVIGIQLNSFLGT
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]

MAIGISVVACTAKHLMLRPKLHKIIFVNDILHKLDRRVQTDEDMRYYLKKMRDNCIFMIH
FFTVVYFSVAIMAVLSALWTGNILYPAYVIVDWHGSTWKYLLVMLFQIYGLNMQIVQNLT
NDTYGPMILCLLSGHVHLLSRRILRIGHDSETDLDRNYEELVLCIDDYKVLMRIVERIISCS
YVVQFTAVGVNVVVGLIYLLFFADNLFAYCYYVFHILAIMIEIFPCCYYGSMVQAEFHALS
YAIFRSNWLSQSRTFRRTAVTFTELSLKDVTVWAGGMMKIHLDSFFKTCKMGYSIFTGKH

TKHLRLIYDILMNTYITFGFPAHLVLGIIFSTNQEQFFINLVIGIASVSCVFKHLLLRFRMRE
MQSVNEIFAQLDDRVRTNEDYDYYKRLIERPCNFMVNFFTRCYFAVSITALTMALVTGELL
YPAYIPLQWRTSVFKYAVGILFQFAGVTLQIVQNIANDAYGPVVICMLSGHVHLLANRVSR
VGHNNAESVEDSYRELSMCIEDHKLLMSTTTKVERIVSASYLVQFVGVGINICIGLIYLLFF
ADNYFAYVYYTIHIIAIMIELFPCCYYGSMLECEFHDLSYAIFSSNWPTQPRLFRRNIVNFTE
FTLREVTMYAGGMIRINLDSFFATCKMGYSFFTVIQSMK*

>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
TFISENISNIPAVAECLCTSFMGVQYIIRIFVLLRRQRPLRKLLQNFYRDIYFTYADDAALCK
EINTVIRFMKMFTQFYYVPMMLILILYVYDVASIGLASPHKPFIYRMSFRWYDAQAPQQFII
TAIYSGWLTISTVTLWTAEDYTLCLVLCHASFRYKKLRLDLQQLLEMARADLKSGETRCT
NRNLHTAFRRRLCEIFQRQQLLNGFVAEAKAHFTYQIFYVMFFGVLLLCVVSFQFQNAPIT
VDSSKYISWLISQTAQFLLIGYFGQMLMDETTELRNSFYCCRWEDLLVHGDPHSNKLLLS
DVKFAIMNSQEPIVLDGMKFFPLTYSTVSVALRSAVSYFMFLNTMNGEN*

>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
TFILNTFFAVSVFNALLRTCFIIKNRDKFEALMRELVTLYDIIQDSGDDYAKSVLAAATKSAR
NISIFNLSASFSDLVVAMAYPLFRQQRVHPFGVALPGIDVTHSPLYEIIYIGQLSFPFTLSSMY
MPYVSLFATFAMFGKATLQILQNDLKNLCDNMKSKTEEELFELLRTNIAYHARIARYVSDF
NELVTYLVLIEFLLFSCVICSLLFCINIVSKTTSTAEKISIVMYIGTMLYVLFTYYWQANGVL
EMSLLVSDAAYEMQWYKCSRRFKRTLLIFIGRTQKPLQIRVGQMYPMTMEVFQSLLNTSY
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
AVSIYGVIYGSVSVDSLYSWYIHNLVGNFKILQSKLVSAESTADLSERRTHIYYCIAYHQRII
AMTEQLNLIYQPIVFVQFSLNALQICFLAYQIGSGVVATVDLPFLFLFMISVGIQLMIYSYG
GQHLQNESVNVSKSIYQTINSSAWPIDLRKVLLISMMRAQKPSKLTGIFFDVDLPLFLWVW
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]

MYKYLRIPYFSFRVIGINLWAQQDQRITSAPCRYYSWTLATAIIIILMGFYIYTSDQDKAIQV
LTVFLQGVLCIIKSGMFVAKGRRFIKLIRNLDALADAATVKEWSEWRHENDWQQCIVRVY
YICCTSTGTLYCTVPAVILLYSQCFREHTVFILPFDAAFPLDTGHLFFYTVSYLWCISFIIYAIH
AITAMDSLFCWFIFNISAHFRTLQHELQNVAKTSADVEDSACLHSKITETLHYHRRIIELSA
EFDELYAPIVFIEISVSYLKLCFSAYNLINLGDISGLPVIAVGLVTITFQLCNYCFSGEKLKSVS

KVVSDRIYLAFSWERVPPPLRRLLILPLMRAQRATNLTGFLFVVDHSLLVWIFKTTGSIIGFL
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
NLNEIIKVFYLCSMAIAVMAKFMRIHLKNNSYVEIFARMHDDDLLPVNVSELEKLAQSSH
LSCRVRNYYTYLSLTSLTLIFVTKLISEPDELPLSIYIPISVESFWRYLIAYLFQFIGLSLCCLL
NISFDSLSASFFIYLKGQLDILAYRLENIGTNLDVDDNMINLQLRYCIQHYVKVRKITENME
DLLSIPMFVQMISSVLVLVANFYAMTFLTDTSDYVTFIKFLVYQLSMLSQIFMLCYLANEVS
LRSAELSYSLYSSEWTRCSKMNQRLMLLMMAQFGVPIRIKTVNRCYSFNLPAFTSKKKPK
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]
MISLSSKATIDNSISSHNSYLTNKSYTHLKHTASKLQTILAPYRVLKEMLRYGEAVHPPHTC
LFYFRAYIRLLGLWPTERTAENPLYYFYNVLIMILFSFFMLYLIFFKMALFRMRNGETDIIISE
FDALHVQHANLLRDGPRNQRILQWQRRFFFGEICFFSGFYILSLFLFAAMSLQPLLSQQTLP
FRCKFPFGLDDPDEHPMAFACVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCEN
IRHLGESAAGTAGACSITSELVVWRELREAVEFHQKIIGLMNRINQTFYWNYVSQMGASTF
MICLTAFEALLAQDKPMVAMKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATAAYDV
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
SGDILNSFRLGVYISYAIDSNVKFFVFLLNAQRLRVIYQSLSNEYPMTSIKRKVYQVDKYTF
KRAHLMIVAYLSVTNSILLGPMLQSIFVYIIDLSHYGYTVAAFSYLHPTPMSYNFNYCTPHY
YILIYISEYLNGHFCTTTNLGTDLYVCTFAGQFCMQLEYLGYSLEIYEPSVKNSKTDCEFLI
EWIRKHQLMLNLCSELNEVFGTTLLFKLISNCAVFCIIVVQLKLEGFGFGFLNFLSFFFVAVS
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]
MMMENAEEIYKRNYNYIKVLIRVSFSLGVNLTAPSKIKDALKLISVILSVTSLLSMYGHCC
YLMRHLDRMPLIAEAVFTALQILMAAIKLIYFFFTHRTFYRLLDQTLTHEIIRKMEILQQDFP
INRQLKKEIDDIMNAVWRNIRRILLFYFFCCVGIIANYFFTALFQNLYHHLKQTPNYEFILPV
PSQYPFWEKKGMAFPYYHLQMYVTGSALYVSGLGAVSFEGVFMVLCQHAVGLVKVHNL
LVLRATSAQIPVERRLEYLRYTIFNYQRINKYMHEIQTIFRHISLSQFILSLIVIGFVLFEINYG
LGSNIIIFIRLIMYISASITQITIYCYHGQALTTVNEKIPLAYYNCNWYGENKTFKQLIMMMI
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
MRHFDSIPLIAEAVFTALQILMAAIKLIYFFFTHRTFYRLLDQTLTHEIIRKIEILQQDFPINRQ
LKKEIDDIMNAVWRNIRRIFLFYFFCCVGIIANYFFTALFQNLYHHLKQTPNYEFILPVPALY
PFWEKKGMAFPYYHLQMYMTGSALYVSGLGAVSFEGVFMVLCQHAVGLVKVHNLLVLR
ATSAQIPVERRLEYLRYTIFTYQRINKYMQEIQTIFRHISLSQFLLSLIVLGFVLFEINYGLQIF
KGSNIIIFIRLIMYISASITQITIYCYHGQALTTVNEKIPLAYYNCNWYGENKTFKQLIMMMI
MRTNKEFYLEVSWFTLMNLATLISLIRASVSYYLLLQNFQEN*
>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]
MYSIIERKELRVHNIWRIRELKRISYIIGINLNAQTKLKRSLRIINVLIIIFSCIALYPHWLMIK
QAQGDIPLIAETSTTALQTTTALIKMAYMLFNQHKFHKLLQKVETHDLLQRIEIFLTGMPIK
PNLKREINAIMETNWKQTRRQLLFTIGTCICIMCNYFFYALFKNLYNHLQGTPNYVYILPFT
GYPMFLDKGMASPYYAMDMFFGACSLFAAGMSALSFQGSFMVLCKHSCGLVQVVCLLL
LRSTSAMVPKPQRVEYLRYCIVQHQRTLEFINDVNRLYRHICLSQFLHSLAIYGFVLFEMNF
GLESNKVTFIRMIMYLCAALTCDCLQHVNGQFLANELEKIPLACYNCEWYHETDDFKKT
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]
MLPEARTFSEFIYIPIKVYQTIGEDIYEHRSPGRVRRLLLKSLLYIGFFNFNLHVLGEIVYFVK
ALNSFATILEATGVAPCIGFSFVADFKQIALTIHRGTLRKHLDQMEELFPKTAMQQVEYKLR
EHERAMRRVMYIFTLLCLAYTTTFSLYPALKASVQYWLLGAPVFERNFGFAVWYPYNATE
KTWVYWLTYMGQVHGAYLAGVAFLSADLILVASVTQLCMHFDNISRCLEEFSGASQKTS
AQEDLQYLQALVVKHAKCLELSEHVNSIFSFSLLLNFLTASLTICFIGFQVTASSIEDIVKYII
FLTASLVQVFVVCYYGDELMTASMRIGDAAYNQNWFGCDRQYKWLLTIMIMRSQKPACI
RAPTFPPISFRTYMKVISMSYQFFALLRTTYSGKGN*
>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]
MTVKQIRPSDSFAKLIKMARLVSSLVGADVSTENYRVNIVTIIVIFCIIIYFIFTATTVASVFSE
DWTYLLEASCMVGSVLQGITKLISGIGRTTDVSGMRLELEDLYRRYESKGETYCRVLNER
CDRVWQVIKMVGHIYGASVVGILLLTTILVIKTNEKIYVMHFFIPGVDVETSFGYLLTTAVH
TVVFLAGAFGLFAGDLFFLIYLGQPELFRDILILKIKELNEAAAQKDNKTEHLLINIIQWHQ
YYTDYNERCNEVFYYIITMQIMTSGVSIICTMYIILMGDWPGAYLYILIALCGLYLYCIIGTN
IQTCNAAFFDELYNINWYELDVKRQKMMILILMKSQNPSEIKIGGVLPLSVQTALQITKTIY
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]
MAVKRVRPSESFAKIIKFFHLISSLVGADVSDENYRVNIVTIILIFCIVIYFIFTGTTVASVFSEN
WTYLLEASCMVGSVLQGITKLISAFAFAKEICGTRMELENLYREYEAKGDDYSEVLNKSC
ERVWQVIKMVGQMYLIAGAGIILITVVLIFASTEKVFLMHFLIPGIDVHTQAGYLITLAVHT

VCFLFGAFGLFAGDLFFLLFLGQPMLFLDLLALKVKSLNEAAAQKSKTAKRLLIDIIEWHQ
YYTDYNLRCNHMFYYINSMQIVTSGISIICTLYILLMGDWPGAYLYILIAFSGLYLYCIMGT
KIQTCNTAFCQELCNINFYDLEVKNQKMIVPILMKAQNPSEIKIGGFLPLSVQTALQITKTIY
GIFTMMLGFLEENQ*

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

MQTETRPSDNFHKLLRIIRLSSSLIGVDIIDENYKFNYVVAFVLLAIAWNYMCSIYTICKDLT
TDWTVLLDVFSPISCATQGVVKMCSLILYPKLYRELALDLLEIYKKYQVVGPNYEAKLFE
WNKSMKKILIIGGLVYFVSALLALVTPLFLYIYKGERHLIIMCQMPYVDVATDHGYFITIGY
NVLCVFVAAFGLYGADLYVFLFLTHSIFFYDIFALKVGDLHKILHENNKDKRIKSLINDITE
WHQYYLEFNDKCNVIFFWSITAHVLCTTLGILSTLLIIMLKYWPGAYPYIFVCFVWLYMYC
ILGTRVEICIDQFCDGIYDINWYDLDVSDQKTVSLMLMESQVPRVITIAGIEPLSVNTALKIT
RSIYSLVMMVMQFNE*

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

MAFDSMANFRTLTRLLIILGLWHGGNGSWFERHYRYYQLFLHTTLTFTFTLLMCLEVIYSE
SLNYAIDVLKYMLCEMALVFKVLNAWYYARKISELMNEWQVSEIFALRTSDEKQMWQKT
QKNFHKLTMTYICTGFNSAMCALIGVLLMGASELPYALWMPKNWRETYFWGMYCYEFL
AMPFTCVCNITIDLFQAYLLLHLTLCYRVISMRLERLDNAGTDEAITKEFLNNIKMQQRVK
DENPVHCLAMLQYVLIVSLQMFLPCYYANELTVESEKLGIHLYSCDWTGFLVDFSPAAPN
RSTAPSQRRSTFAIQRSAFEVQHAVGQIVHTTYNHMNFGMQFDLWSLQY*

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

MLYRPRLENGKLISLSWPIAAYRLLNNICWPLQDDATQLERLFDRFLWAFGFLIFMQHNDA
ELRYIILNNNNLDEMLICGPTYLILVEIHLRAFQLGLKKNAFKRFLQKFYAEIYIDEVSHPKL
HGNMRKRLRPIWFYSFLYFGTLSSYVIMPLINYLKNVKAPLYKMYYPIDIMPNPIYVAVVL
SNIWVGFTVITMVSGEDNVLSEVMIHLNGRFLLLQQKLRQDAERLLHAADDRNIADELRR
RIVEAIKENVRLYKFAEDFKLEFSFRLFVNLSFSAGLICVLGFKVYTTNEMSSTFYESNWEL
VILRSRDTKANVRLMKTLLLAISTNQKPFVLTGFNYFSVSLTAVLKQQLASTNNNIPMADL
VMAFSCDSFGNKCYIFSRELGLSTAIFNKVIARVANEVSIAEYNIRMEISNNIVRGINTFLIEE
SPHFADKFRPPYTHTHVHTVHSVQGTCHSFGAMKLSWRFTRSDASSGIAAALAC*

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

MRYLPISYHKPLLPNGRHPPIDWQLYGFFCSNGWPLAAHITKTRYIVDILVTMMQFMSES
MVLIGEAVVMYDNLDNISFVCTVLAPNLILFEMMLRAYNIIYKRNSFRTHVEEFYKKIYIQ
RTWNPELFEKIRRQHLPTKYSTFTYIITLVTYVYVPISGLVKNERLLPFPIKFGFDYTVPWPR
YVVFLAMSIWTGFAVVGPLIGEANMLAMQILHLNGRYSLLLQDLRKISRDSIAEHERCKD
KDNMLVTQRFRCRLFEIIRRNVELNDFAKSLQEQYSFRVFVMMALSATLLCVLGFLTATTD
ELSTSYYCCDWEEVIFHSRDAEENKKIMKLIALAIHLNSKPFRLTGLNFSVVNYETVVSLA
FC*

>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
VTLNVGAKRFVKLYFYSVSCTGLYFTIKPLVSMIWAKFQNKPLLLELPMPMRFPFDFESTP
GYQFAYVYTIFITIMVVMHAASVDGLFVLFTTNLRGHFVALQYFIETNTFDKSDALLQREL
RFYVQYHVRLLDLSQSVQHIFKPIIFGQFLMTSLQVIWALSCSAVGTAVQMSQWYNLPPRH
RHVLRLMMLRSQREIIISAGFYEASLANFMSILKAAMSYITFIQSIE*
>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]
MSSNEEKKKSDYLTTVQQGCPLYGQRPDMFRLMRWNLCFAAMYRLPLERYFPACLRLLA
ITLDWTYELCLYSTMLHIDILFMYTLYLNKDKDDLELIVSCMIQTVIYTWAIVIKVFFKRVK
PKRVEELMRYLNEECQTRSAPGFTYVTMKESADLANKCSAVFLIWCYAGVICWLFVPIFN
QDRSLPLACWYPIDYKVPVVYEIVYFLQTVGQLQVASAFGCSSAFYLQVSVLFSGQFDVL
NCSLKNILATTYLILRKPESELILLREKQNIANYELNQYYNAKEHNSDFDCIAHLVDVKTPK
PKKFYEAFKIAFSPCVTQHLYILNGLKMLEELYSFLWFLKTIQVTMLICLVAFACVKRSPWY
LHSSEIKQDVLFFILNAQRPFRLTGGKMYNLNVEKFRSMDLRQPQ*
>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
INVVLEIFLHFSVIHIFVLFICTIYFNYDNGDLEFLISSGIQVLLYFWAIVIKVAFRHIYPELVD
GILDFVNEEYVLHSAVELRDKERIPDEYTNEFFVAKELPFDLDCLPHLLNTADTMRTRSFRE
AFKYAIEPCVKHHIFILNALRKLESLYNKIWLLKTIEVTFAMCMCAFHLVKSSNDTQFLQV
LCLGQYTVLGLLEIFMICYAGEIIYVNSQRCDEALLRSSWYPHLREVRADFLLFLIHAQRSF
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
VMTLSYVTFIVVAYAKWYYLYTYQTERTAFFQRLETLFPCTKSQQEAIKLSEYIRMNKLSTI
SYTISFLMCISTYTFYTIARQFIYTNLLHVPGTERNLPYQAVYPWDWRDNWTYYVCYVSQ
GFAGWHSTCAQMAFDLMLCTLSTHLIMHYDHISRSLEGYQTKFAEIHGKNGLTQQARAA
MELKAVKDDIKFISSIVAYHTELLRFDWSHADIRFQKMTILVAERAQDPAALKATKLITISR
DTMTVIMQMSYKFFTVLRTMYGD*
>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]
MSNQPIHFESFNYLANIFYTSIGLYAYEQAGERTKDRAAYIRRQLLSIFSIIVIVNMNIALLSQ
LMYIFLAFANNNNFVETTMLSSFVVFVIVSDFKIYNICRQRARISAMMQALHALYPQTLAE
QTKYKVQWQLQRYNRLAYAFAVFYEMLVWGYNLFPLLNYLIYEVWLALRVVEKTLPYN
CWTPFDWHNNDWIYYHMYLMLSASGQACISGQLANDLLLSALAVQLIMHYRELARRIEA
HVAGRETSSDDSEYIRHAVYNHNWFDADMSYRKMLIFIMARAQKPSKLQATTFMTVSMS

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]
MSTQIVEFDRFIKTANFWYSFNGIVAYDDIYRQPGDEPKRRSVQTRLATVLRQIFSFVSLAN
LTWVLIIETLFVVVNFVENADFLEAARNFTFMGFVIVAIIKYLSNLKQRSRLSVLMQKLYEI
YPKQSTDQRPYDLQSHLRHYRRIGFIYAFLYAFTVWAYNSLPMVNYLLLAPLLQQTVYER
VLPYSCWVPFEWRDNWLYYPLYVSQALAGHEALAAYLASDLLLCAAMVQLIMHFRKLA
RDIQAYQAGSSCTKQDVMAQQAKRDLSFLSTAVYYHNRTLALCQLINEIFGLPVLINFISTS
FVMCFLAFQFTVGVSFDDLIMLVFYMICSLVQIYMICSYGQELVTASENIGHVVYNHNWL
VTDIRYKKLLIMIIERAQKPAILRATSFLNVSMGTITDLLQLSYKFYALIRTMYAR*
>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
GVLFLKTSYDMLLSGKLEQITDALTMSIMFWSGVYATCYWFLRSQRLLAFLQRINEHYWH
HSLPGLSFVSWHRTFVLTKRLTTVWVLTCVVSTVSYGLAPLVMGVHALPLKCWYPFDPL
NEQATLPETTDDDELNQYMYCREHLTNLSTLQHLYSQQPAVTFPEALHLAIGERSMVRILN
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]
MALQQERNGAAKVCAIDDLCAILHPAQRYLGLNYLNFRRVNGRFAIPRSKLLNIALFLAV
VDCTGNVIKCGKAINARDVTKAQEIFAVFGMGLVMTMRGLQLALNRDKLSKFYNDIDRIF
PRSENLQQHMEVEKVHNYIKRRFFLLHTTLTVTVSAFLTMPAMKFLLFYDFESNDIVADEF
HVNPSWLPFGVKDKVTTYPYIYIYEVILASAAVNMIVTWDEVFVVLISQLCMYYEYLGKL
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]
MRETSASVLGTRIGIARVLMRLLQILGLWPMWQARQQSSTSTRCRIWLTRYYRYLLHAPL
TFTYNTLMWIEALTRWERADHILYISITEVGMMALTLNFWRLDKRAWHFMHELSYSDRL
ALRNKAERQWWRKQQRFFARVVVCYIGGGAGVLVTAFGATLHMSGYYLPYDYWLPFE
WHNAQNYWYAYGYEVIAMSLTCISNVTMDMILCYYLFHVALLYKLIGMRLMALQQLHEP
LAVQQLMNIIELHKRVKRLTAQCESLVSVPILVQIVLSAFILCLCAYRLQSMQISENPGQFLA
MLQFASVLTLQIFLPCYFANEITINSDALTTCVYNSSWEEFSPSTRKQMNLYMELLKRPAHI
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
AGAGMFYMISFVFQCYYLLFSMVHSNLCDVLFCSWLIFACEQLQHLKGIMKPLMELSASL
DTYRPNSAALFRSLSANSKSELINNEEKEHTDLDISGVYSSKADWGAQFRAPSTLQTFNG
MNGMNGTNPNGLTRKQEMMVRSAIKYWVERHKHVVRLVAAIGDTYGGALLLHMLTSTI
MLTLLAYQATKITGVNVYAFTTVGYLGYALAQVFHFCIFGNRLIEESSSVMEAAYSCHWY
DGSEEAKTFVQIVCQQCQKAMSISGAKFFTVSLDLFASFAIEVCGFALFVAIMSGEGCARR
VAIWLVWSVHSGHSPLSQNLFVFALIYITNTVLL*

>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]

MGKLKVLSSRIFPSDPSKGKIGSIQYNVWLAQLFGVPVVGLKAESPCLKIVLGIYGILITLV
VTFIYTGFEIYDMILCWPNLDSLTQNICLSLTHIAGVLKLMAFYHGEFENKIPLTIYASLVGS
TGVLGIMYLLHSQIFPYRVKLPDWMPLGTQLAYMGISVLVFALQIVAIDYLNVTMINQIRF
QLKILNLAFEELKLDCVNKKEHINLNKRLQTIVEHHCLLRDLRNDVEDLFRLPVLIQFFTS
LVIFAMTGFQAIVKAENSNGAALIYCYCGCIFCELFVYCWFGNEVSEQSKTLTSSGYSSHC
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
WLHRSQLLAVHYYLGKLDARCMRHAVDRQHILTAIRICHLYYAAYMFLYELSSSGFAYIGF
KLRQLVYDGWFPQFYADAAQNLTVTLIYQNFAVMTFFVLQNVNNDMYPQCYLAILIGHL
RALTARISRIGKDGVLNVDENIEELTNCVEDHKNLLGYFNCIRPVISRTIFIQFAITAFVLCLT
AVNYVAFERDAAQKLIAATYIFAVLIEALPCCWYVNSLMEECGELTTALYNCQWYDQNRK
FRKMLIIFMQRSQHTMVLMAGDLVPITLQTFLNLFCLCVQSIYALCSDIYSIIYLILLVA

>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]

MKRVGYFDQHRLASCLLTVPIFICVSSAYRTYIIRNDFDEVTISLFKISGAYVTTARSLIVMY
KAQEFLNFFDGIDRWYQELQCDGNEITLKKVHEFMRIVKKASKTILILTALTLFYITVIQLL
ATADYEHKSISFGTFLIKDLQYKLESTTDMTELEALKCIKKCVKDHVMIIKYHNDLEVLFS
SGSSVSVSIFGITPCVIIVFSTMVSSNRSNLFLCYIFKFKFTIILHLQDHDMSLLIADIQLSLLV
MISTFIFFWVANDFCCEVIWDYFPHIYNICYYNL*

>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
RKVTRIGFYTSIIGALCAYIYPFSFEERKFILDIDYFFFDAKQTPFYEFFFLLQALILVPVFIFV
YLPFANFLLMSLKFGEVILMDLCTKLRNISNQDEATQLRELKECISYHEKIITFRNDLEYLV
SIDGFFHIALFSLMLCMLLFFLSLVHDIRLILTALAFISFHIYIIGITYYYADNFSNESLKVAYA
AYDTPWYEGNSELRKCVQVMIARSHRPLEIKSGGLYPMTLENFQAILRISYSYFSMLQGFN
QQ*

>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
AFQLVPYFKTINASNKYLSMWHLSITSIFALHPMLASIYGYISREDENESFEFTLPFMMGYY
YDTNRPLPYVITYFTQCCGAFYMSLLFLSGDLLLVSLVHLVNMHFGYLIYRIESFQPTGTD
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
LKTMQDVLLNLTISVPVAVCTLKYFNIWRNLAKVRHLEQMFNTLYARIDHPEEWIYYRKVI
IPYALKVLHLFYFICVGTAITSELTLLIMGFAYEWRLMYPAYFPFDPYATKAGYVTAHVFQII
GLMVQLAENLVSDTYGGMCLTLLAGHANLLGQRVASIGYDERKTQEENNRELVDCIIDHN
VLFDCHRTLGDIIGFGLFVQITSASLIMGVVIIYVIFFVGNAFEFVYYALFLFACIMEVFPTC
YYATYFEIEFEKLTYQMFSCNWMDQNREFKRNLIVCVEQSLKTRYFRVGGMFRINLQIFFA
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]
MPATETTISGVSVFHFHDVTLQYLGLMPPTKKLYRYLYYVYSLVLNIIITVGYPTHLMIGLI
KSENKSDVFKNMSINFTCSACSIKIFAFWWRLAEVQKIYAIISKLDKHIVRSTDYELYKIYAL
RRAQHVLYFILVIGLGAAISSEVATIIGGFLGEWRLMYPAYFPFDIERSLWGYPIAHIYQCFG
VTAQIFQNLINDTLPPMALAMLAGHVRLLNVRVARIGHDTSVVSVRKQACNTEFLLCVED
YKALLEFRVAIQRLCSLGTFVQILVTAINMGVVIFYLIFFVNGIFTYIYYVVFLIAMPLEIFPL
CYYGTSVQMEFEELTYGIFSCNWMDQNAAFKKNLRIFAEQSLRTQIVIAGGMFAVNLDTF
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
VMAFLLPKLRTANVFMDRLDARCRAEEEIAELRKIVQQGNRFVVLFAMSYWSYASSTFLG
SVIFGRPPYALYNPFIDWRKSRLEFIAASLMEFALMDVACFQQVVDDSYAVIYVCILRTHM
NILLMRLGRLATNTETKLEENLEELKLCIIDHKNLLGLYDIVAPIISVTIFIQFMITASILSATLI
NIFIFADQLSAQIACCFYILAVVVEIFPLCYYAQCLMDDSERLSQQIFHSNWIAQDVRFRKM
LVFFMQRTQRVMELNAGKIFPITLGSFLNIAKFSFSLYTLIKKMGIRERLGLE*
>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]
MSKILRVSRAKIYKSRDAVSYLFNIFTFLGTNPLEHRSRRYYFLYYFYSFTLNFISLLYCPLSF
HIGYIKLTHVLTNSQLLTAIQNAIQVSGIPIKVVAITWYMKRLQHAVEILDELDVNYTQRED
LAKIRECVRRCRKVILLFCLPYYSFGISTIALGVLQNQAPLTVWVPFLDGKRAAWEYWTIV

LWDTLVMFILLCHQLGNDTYPPIFIKVISTHMQLLVTRVNRLGRPGALTADKHYEELLASKI
VAPVISVTLFTQFATTATTLLNWFGDMEYPENIISLAFFCCQLVQILPCCLSASQLIADCERL
PDAIFHCNWMDQDRRFRRAILFFLQRTQTPIRFSCLKLFDANLETSVAIGKFAFSLYTLIHEA
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]

MFQDQVRLPLQRRITSPENTRNMRKLTDLLYGRGAAKFESNESFQLIFQCWSLFGIKPLKQ
YRSGRLLHMCFCWFCLILCPFSFYMGYLQTLQTAPVMVQLSLLQATVNVLGLPLKAIVITI
FQTHLRSAEPIFVRLDERYQSTESREQIKNCVALSTRLFTIVGFMYHLYGGITYFQALVTNN
YPLRTWLPFTDYIPQPTIRYWAHFMFEVFHMAFLLSVQFTMDVFPAIYIRNLRTHLNLLTER
VSQLGGNPDFTDEQNYDELVDCIIMPTCYQASMIEEYSTKLPDAIFHCNWLAMDKRCRKL
TIYFMHRAQENVTFVALKLFKINLTTNLSVSKSCCKEQQ*

>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
HLFFIVSVSYFTYGTISWLSSVFTHTQPLNIWLPFVDWIPQPTIRFWMHFIFEVLYVHFLLII
QFTNDVYSVIYLKALRTHITLLAERVSKLGENPEFNDDDNYEELIDCVRSHQELLHLVGSV
LSLTIFLQFTVAAVILCVCMLNIFIFADASHQAITIVYYVCVMLQTLPACYQASMLKADSTN
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
IVGFIRFQKTATITESLTRLQAVINAIFIVVKSLVVLVNLKRLENVEPVMKSLDERYNTTQER
QQISDCVAACTRLYASMGCLYYSYGTLSILSALISHKQPFGVWYPFLDLISNPTIYFYTCLLL
EACYGYFLLAAQYLHDIYPTLYMRTLRTQIQLLRARISRLGEDPDMSDKENHKELVECIDT
HQKILQVVDMVGSVCSPTIFIQFSVVAIVHCICMVNLFIFADTINKVITILYYATVGMQILPT
CYEASTLEMESSKLPDSIFHCNWLALDKRGRRLITFFIQRAQVEVSFVAIQMFEINLRTYVA
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]

MRNVLNLFYRRGKDDFETNESFVLLFRSWSSVGFIPKKPKRIADIIHQLICWTCVIICPYIYF
SGVIETMSYLPITIVLANLGAAINCIAFPLKAFYIKANIDRLHDVGTIFKDLDGRYQRPQDQ
MQIRDLVTNSRRIFAVSFILCWFYATLSGLVALFAHEYPHGNNLPFIDWLPESNFKFWLHFT
FEVMFLQYLVQVNLTNDSFPAIYIRAIRTHVSLLTDRVSRLGSNPDLNDQENFEELVDCIVS
HQKLLQISDTVGTILSLTTFFQFTIYAAIICVCMLNMFIFGNATTKVVTVVYLIPVFWQTIPT
CYQASMLEGDCAKLPLAIFHSNWLALDKRCHKLIIYFMQRTQKEISFTAIKLFQINLRTNLS
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
AMPITGLSNCAFDMIQSYMLLQLSLCFKLISARLACMGALQEDGASSGFCEVKFHREFVDI
VNLIMTLQIFLPCYCGNEIIQHSGSLNNAIYSTEWFRCSPRMRKYLIIYMEMLQRPVCVRA
GNFFEISLDTVAIYPACVRAGTEVRNVQRVACATNHGQTIKATMTYELPGFPCIFAQPLLTL
DHLMTVLARDRVGPLRLHTGANVLHSRHGIINALRKVIN*

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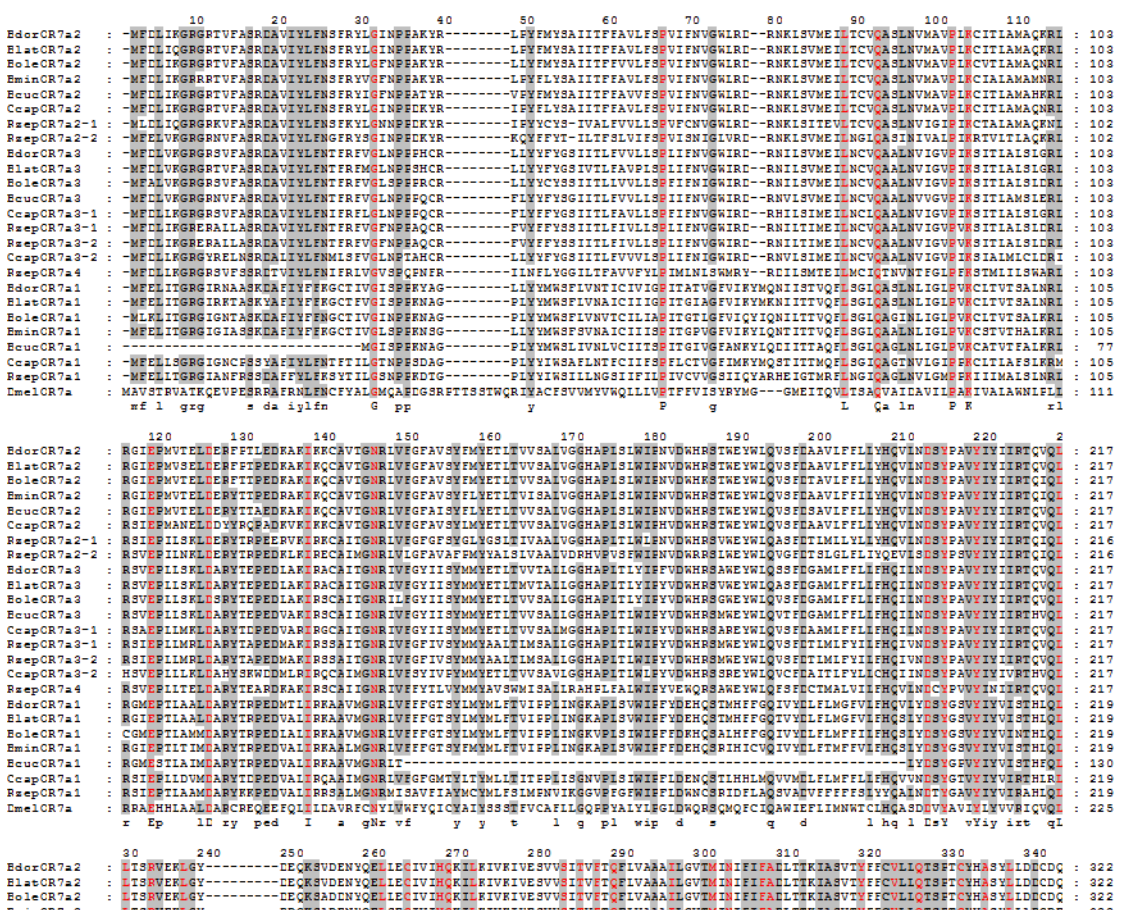
                    10        20        30        40        50        60        70        80        90       100       110
BminOR2a   : --------------MSLKINSWDAFKYHWCVWDLSGFRGPQKQSTWYIPYKLYTIAITLLFPIYYPTCFTVESLLADNLNDFCEVIYIAMADVTLNIKFLTLFIVRQQLLEL :  98
BcucOR2a   : ------------------------------------------------------MIVITLLFPIYYPTCFTVESLLADNLNDFCEVIYIAMADVTLNIKFLTLFIVRQQLLEL :  59
BdorOR2a   : --------------MTLKINSWDAFKYHWRVWDLSGFRGPQRQSVWYIPYKLYTIAITLLFPIYYPICFTVESFLADNLNDFCEVIYIAMADMTLNIKFLTLFIVRRQLLEL :  98
BlatOR2a   : --------------MTLKINSWDAFKYHWRVWDLSGFRGPQRQSVWYIPYKLYTIAITLLFPIYYPICFTVESFLADNLNDFCEVIYIAMADMTLNIKFLTLFCVRRQLLEL :  98
BoleOR2a   : --------------MSLKINSWDAFKYHWRVWDLSGFRGPQKQSAWYIPYKLYTIAITLLFPIYYPTCFTVESLLADNLNDFCEVIYIAMADLTLNIKFLTLFIVRRQLLEL :  98
CcapOR2aX1 : ------------------------------------------------------------------------------------------------------------------ :   -
CcapOR2aX2 : ------------------------------------------------------------------------------------------------------------------ :   -
RzepOR2a   : MTVEIVSRNCTVLVMAARVNSWDAFKYHWRVWDLSGFRGPKTSSPWYIPYKVYTIVITILFPIYYPICFTVKSMLADNLNDFCEVIYIAMSVVTLNVKFLTLFIVRQKLLEL : 112
DmelOR2a   : ----------MEKQEDFKLNTHSAVYYHWRVWELTGLMRPPGVSS--LLYVVYSITVNLVVTVLFPLSLLARLLFTTNMAGLCENLTITITDIVANLKFANVYMVRKQLHEI : 100
                                                             i         p           n    ce   i       n kf     vr  l e

                   120       130       140       150       160       170       180       190       200       210       220
BminOR2a   : RPILKHLDARARTE---EEIGVLQDGIDSAKKCFLIILRLFYSAFVTSQLMVIFSVEARLMYPAWYPFDYQASRTKFWIAYGYQTIGFLVQCTQACSVDTYPQAYMRVLTAH : 207
BcucOR2a   : RPILKRLDARAKTE---EEIGVLQDGIDSAKKCFLIILRLFYSAFVTSQLMVIFSGEARLMYPAWYPFNYKATRTKFWIAYGYQTIGFLVQCTQACSVDTYPQAYMRVLTAH : 168
BdorOR2a   : RPILKRLDARAKTE---EEMNVLQEGIDSAKKCFLIILRLFYSAFVTSQFMVIFSAEARLMYPAWYPFDYQASRTKFWIAYGYQTIGFLVQCTQACSVDTYPQAYMRVLTAH : 207
BlatOR2a   : RPILKRLDARAKTE---EEMNVLQEGIDSAKKCFLIILRLFYSAFVTSQLMVIFSAEARLMYPAWYPFDYQASRRKFWIAYGYQTIGFLVQCTQACSVDTYPQAYMRVLTAH : 207
BoleOR2a   : RPILKRLDARAKSE---KEIIVLQDGINSAKKCFLIILRLFYSAFVTSQLMVIFSSETRLMYPAWYPFDYQASKIKFWIAYGYQTLGFLVQCTQACSVDTYPQAYMRVLTAH : 207
CcapOR2aX1 : ------------------------------------------------------MYPAWYPFDYKASRINFWIAYGYQSVGFLVQCTQACSVDTYPQAYMRILIAH :  52
CcapOR2aX2 : ------------------------------------------------------MYPAWYPFDYKASRINFWIAYGYQSVGFLVQCTQACSVDTYPQAYMRILIAH :  52
RzepOR2a   : GPILKQLDARAKSD---EEINVLQKGIDSANKCFLTVLQLFYSAFVTSQLMVIFSAERRLMYPAWYPFEYKASWTMFWIAYGYQTIGFLVQCTQACSVDTYPQAYIRVLTAH : 221
DmelOR2a   : RSLLRLMDARARLVGDPEEISALRKEVNIAQGTFRTFASIFVFGTTLSCVRVVVRPDRELLYPAWFGVDWMHSTRNYVLINIYQLFGLIVQAIQNCASDSYPPAFLCLLTGH : 212
                l   dara       e   l       a   f       f       s   v       lmYPAWypfdy as   fwiaygYQ  GflVQctQaCsvDtYPqAymr LtaH

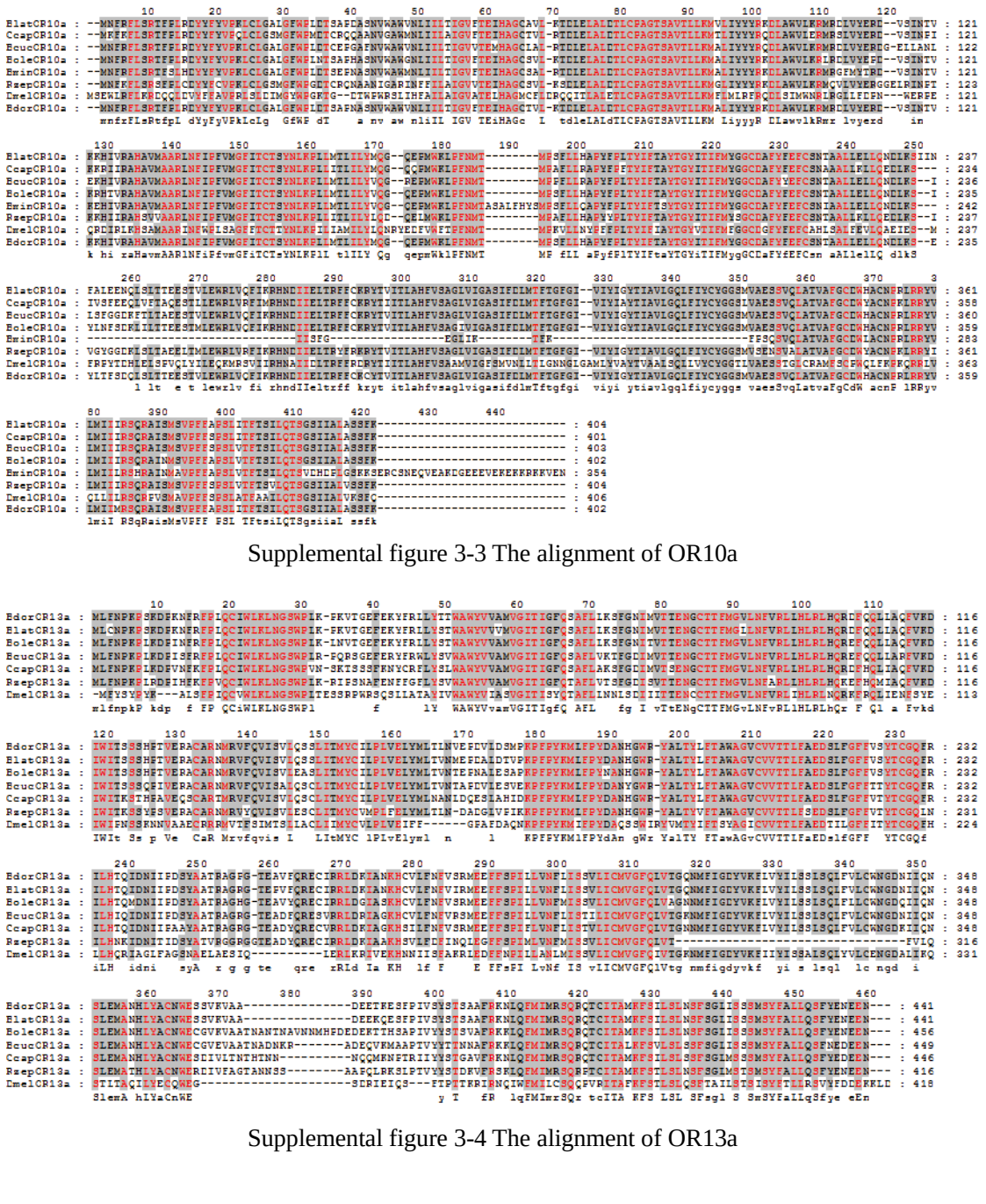
                  230       240       250       260       270       280       290       300       310       320       330
BminOR2a   : IRALSLRVERIGRKNFSYASSELMCLTKDEMKRNYDELVSSIKDHKTIIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVG--FNISIMLNMAVFFVSVTMETLILCY : 317
BcucOR2a   : IRALSLRIEAIGRKSFNCDSSEFIPLTKDEMKRNYDELVSCIKDHKTIIELFSTIQKPISGTAMAQFVCTGVAQCTIGVYMLYVG--FNISIMLNMAVFFVSVTMETLILCY : 278
BdorOR2a   : IRALSLRIERIGRQNFSGVSSELMCSKENEMKRNYESLVSCIKDHKTIIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVG--FNISIMLNMAVFFVSVTMETLILCY : 317
BlatOR2a   : IRALSLRIERIGRQNFSGASSELTCSKEDEMNRNYDELVSCIKDHKTIIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVG--FNISIMLNMAVFFVSVTMETLILCY : 317
BoleOR2a   : IRALSLRIERIGRKNFSSASSEFMCLKKEEMKGNYNELVSCIKDHKTIIELFSTIQKPISGTSIAQFVCTGVAQCTIGVYMLYVG--FNISIMLNMAVFFVSVTMETLILCY : 317
CcapOR2aX1 : MQALSLRIERIGLNANDNTSTSLKYLTKEEMKRNYYELVSCIKDHKTIIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVG--FNLSIMLNMAVFFISVTMETLILCY : 162
CcapOR2aX2 : MQALSLRIERIGLNANDNTSTSLKYLTKEEMKRNYYELVSCIKDHKTIIELFSTIQKPISGTSMAQFVCTGVAQCTIGVYMLYVG--FNLSIMLNMAVFFISVTMETLILCY : 162
RzepOR2a   : MRALSIRIQRIGFQTKSCDSPDTSHLTKAEMKHNYAELVSCIKDHKTIIELFSTIQKTLSGTSLAQFICTGLAQCTIGVYMLYVG--FNLSIMLNMAVFFIAVTIETLILCY : 331
DmelOR2a   : MRALELRVRRIGCRTEKSNKGQTYEAWREEV---VQELIECIRDLARVHRLREIIQRVLSVPCMAQFVCSAAVQCTVAMHFLYVADDHDHTAMIISIVFFSAVTLEVFVICY : 321
              rALslRierIG       s         Emk nY ELvscIkDhktiieLfstIQkpiSgtsmAQFvCtgvaQCTigvymLYVg  fn siMlnmaVFF sVTmEtlilCY

                 340       350       360       370       380       390       400       410
BminOR2a   : YGDLFCQECEGLSKAIYNCNWTVQSTEFKNALSFFLLRSQRVNILMAGNWIPVKLPTFVMLIIIIEVMSLLIDDYNKIE : 396
BcucOR2a   : YGDMFCQECEQLSKAIYNCNWTVQSSEFKKALCFFLLRSQRVNVLMAGNWIPVRLPTFVMVVKSSYSIFTLLSSFK--- : 354
BdorOR2a   : YGDLFCQECEELSKAIYNCNWTVQSSEFKKVLCFFLFRSQRVNVLMAGNWIPVRLPTFVMVVKSSYSIFTLLSSFK--- : 393
BlatOR2a   : YGDLFCQECEELSKAIYNCNWTVQSSEFKKVLCFFLFRSQRVNVLMAGNWIPVRLPTFVMVVKSSYSIFTLLSSFK--- : 393
BoleOR2a   : YGDLFCQECEELSNAIYNCNWTVQSSEFKKALCFFLLRSQRVNVLMAGNWIPVKLPTFVMVMKSSYSIFTLLSSFK--- : 393
CcapOR2aX1 : YGDLFCQECEKLSKAIYNCNWTIQSSEFKRALCIFLLRSQRVNVLMAGNWIPVKLPTFVMVVKSSYSIFTLLSNFK--- : 238
CcapOR2aX2 : YGDLFCQECEKLSKAIYNCNWTIQSSEFKRALCIFLLRSQRVNVLMAGNWIPVKLPTFVMVVKSSYSIFTLLSNFK--- : 238
RzepOR2a   : YGDLFCQECEELSNAIYNCNWTVQSNKFKKALCTFLLRSQRLNVLMAGNWIPVKLPTFVM------------------ : 391
DmelOR2a   : FGDRMRTQSEALCDAFVDCNWIEQLPKFKRELLFTLARTQRPSLIYAGNYLALSLETFEQVMRFTYSVFTLLLRAK--- : 397
             yGDlfcqecE Ls AiYnCNWt Qs eFK  Lc fL RsQRvnvlmAGNwIpv LpTFvmv    ys ftll   k
```

Supplemental figure 3-1 The alignment of OR2a

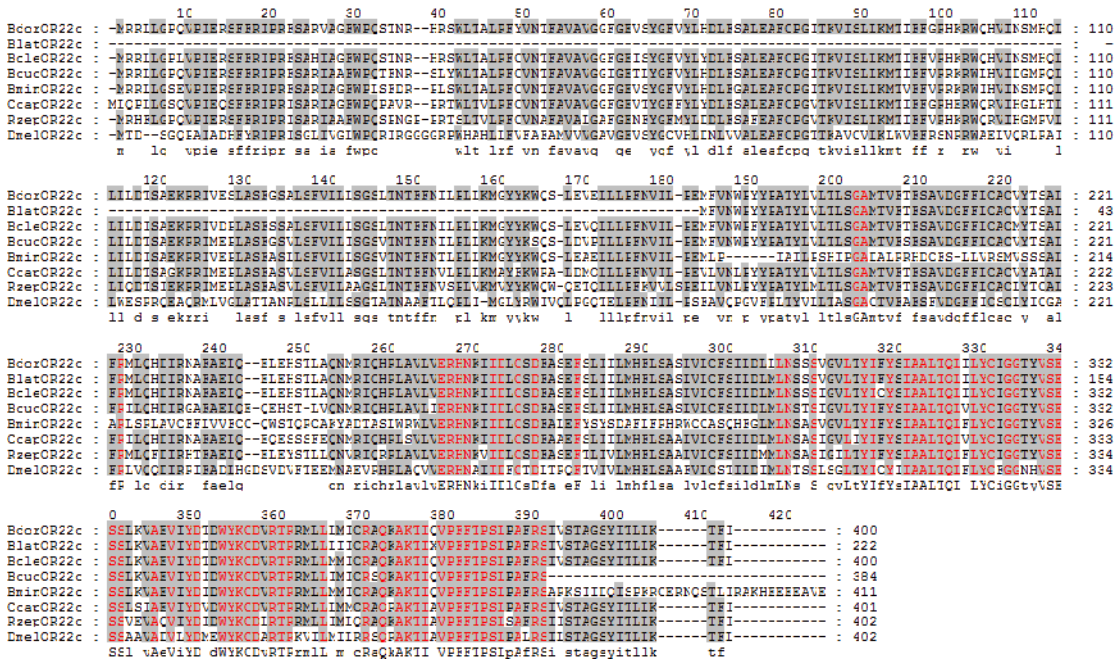


Supplemental figure 3-2 The alignment of OR7a

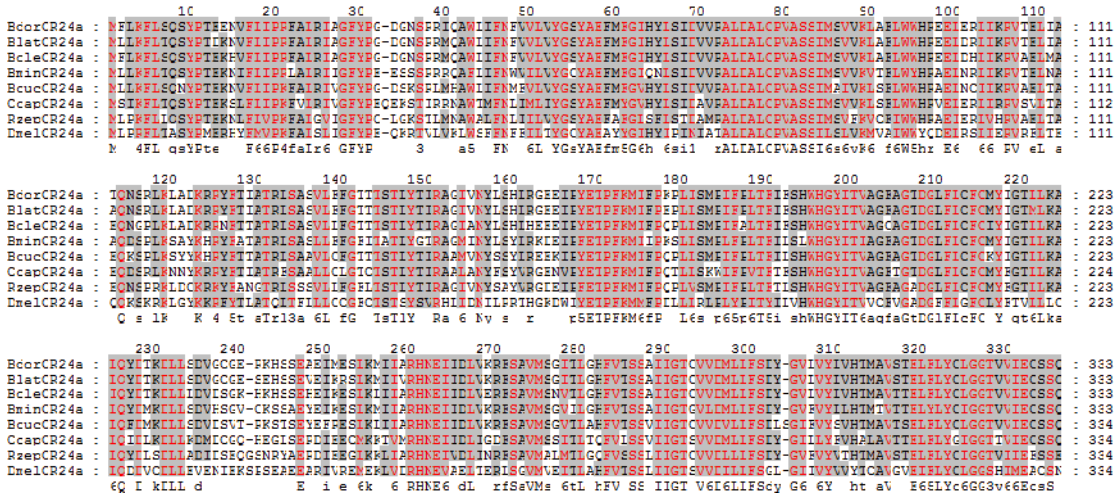


Supplemental figure 3-3 The alignment of OR10a

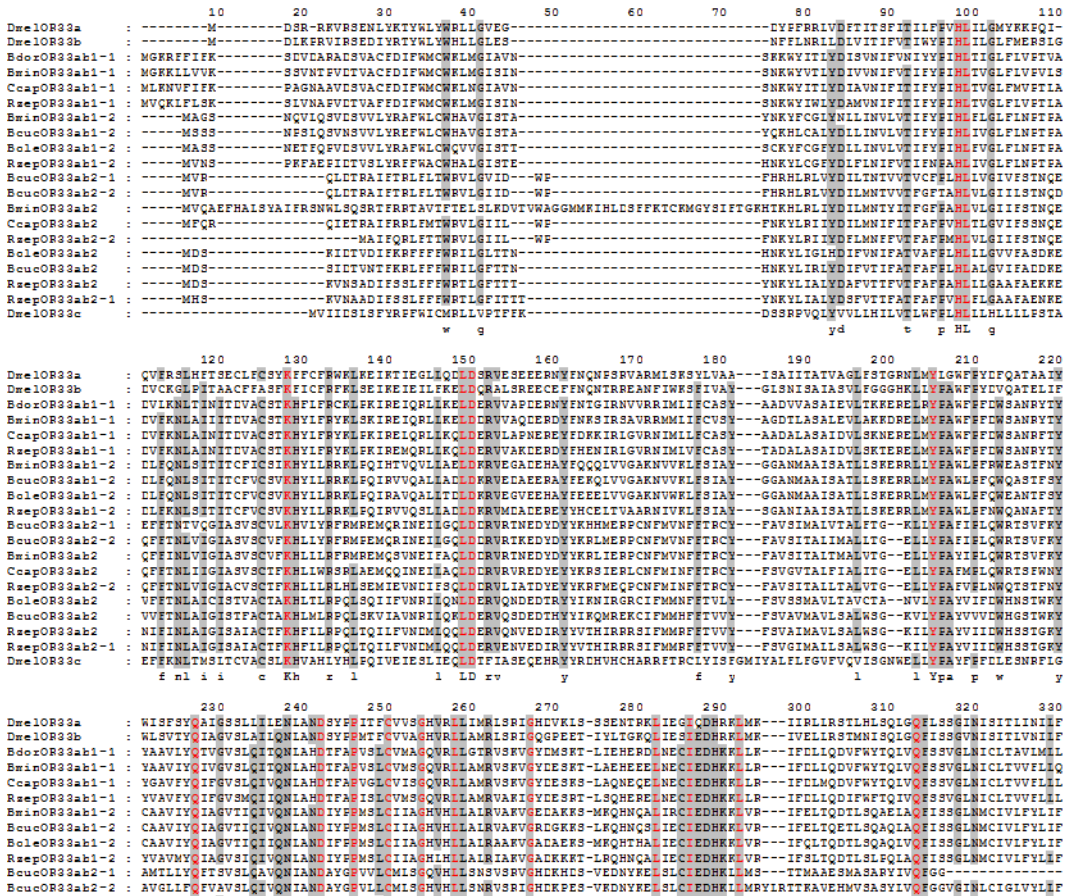
Supplemental figure 3-4 The alignment of OR13a



Supplemental figure 3-5 The alignment of OR22c



Supplemental figure 3-6 The alignment of OR24a



Supplemental figure 3-7 The alignment of OR33abc

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                    10        20        30        40        50        60        70        80        90       100       110
BdorOR35a : MDYFVPLQFDNRPIKLPIQVAGYKFN-FLWPLKEDAGILSRLVNNICLSVSVLCYIGTIVGEFTFIGENIA--DIAAVAECLCTSFMGVQYIIRIFVLLSRQRALRKLLRNF : 109
BlatOR35a : MDYFVPLQFDNRPIKLPIQVAGYKFN-FLWPLKEDASILSRLVNNICLSVSVLFYIGTIVGEFTFIGENIG--NIPAVAECLCTSFMGVQYIIRIFVLLSRQRALRQLLRNF : 109
BoleOR35a : MDYFVPLQFDNRPIILPIQVAGYKFN-FLWPLKEDASILSRLVNNICLGVSVLCYIGTILGEFTFIGENIG--DIPAVAECLCTSFMGVQYIIRIFVLLSRQRALRKLLRNF : 109
BminOR35a : MDYFVPLQFDNRPVKLPIQVTGYKFN-FLWPLKEDANILSRLVHNICLSVSVLCYIGTILGESTFISENIS--NIPAVAECLCTSFMGVQYIIRIFVLLRRQRPLRKLLQNF : 109
BcucOR35a : MDYFVPLQFDNRPIKLPIQITGYKFN-CLWPLKEDASVLWRLFNNVCLSVSVLCYIGTILGEFTFIAENIS--DIPAVAECLCTSFMGVQYIIRIFVLLSRQRPLRQLLRNF : 109
CcapOR35a : MDFFVPLQHDNSPIILPIQVAGYKFN-FLWPLKEDANVFMRLISSLCLGVSILCYIGTILGEVTFVAENFS--DIPAVADCLSTSFMGIQYIIRIFVLLSRQRPMRKLLTNF : 109
RzepOR35a : MDYFVPLQFDGRGISLPVQMIGYKCN-FLWPLKENANLLSRVVNYIGLSVNILFYFGTILGELSFIYENMG--NIPAIADCLSTALMGGQYIIRIFVLTTRNRSMRTLLKKF : 109
DmelOR35a : MVRYVPRFADGQKVKLAWPLAVFRLNHIFWPLDPSTGKWGKYLDKVLAVAMSLVFMQHNDAELRYLRFEASNRNLDAFLTGMPTYLILVEAQFKSLHILLHFEKLQKFLEIF : 112
            MdyfVPlqfDnrpi Lpiq  gykfN flWPLkeda  l Rl    cl vs L yigti gE tfi en     ipAva cl Tsfmgvqyiirifvll rqr lr lL nF

                   120       130       140       150       160       170       180       190       200       210       220
BdorOR35a : YRDIYFTPADDAALYKEINSIMRFMNIFTQFYYVPMMLIFVLYVYDVASVGLASPDKPFIYRMSFRWYDAQVPLQFIITAIYSGWLTISCVTIWTAEDYTLCLVLCHASFRY : 221
BlatOR35a : YRDIYFTYADDAALYKEINSIMRFMNIFTQFYYVPMMLILVLYVCDVASVGLASPDKPFIYRMSFRWYDAQVPLQFIITAIYSGWLTISCVTIWTAEDYTLCLVLCHASFRY : 221
BoleOR35a : YRDIYFTHADDAALCKEINSIIRFMNIFTQFYYTPMVLILALYVYDVASVGLASPDKPFIYRMSFRWYDAQVPLQFIITAIYSGWLTISCVTIWTAEDYTLCLVLCHASFRY : 221
BminOR35a : YRDIYFTYADDAALCKEINTVIRFMKMFTQFYYVPMMLILILYVYDVASIGLASPHKPFIYRMSFRWYDAQAPQQFIITAIYSGWLTISTVTLWTAEDYTLCLVLCHASFRY : 221
BcucOR35a : YRDIYFTDADDAALCKEINSIIRFINIFTQFYYVPMVLILGLYVYEVASVGMASPDKPFIYRMSFRWYDAQAPLQFIITAIYSGWLTISCVTIWTAEDYTLCMVLCHASFRY : 221
CcapOR35a : YRDIYFTSADDGALYKEINTIIRFVNIFTRFYYTPMVLILGLYTYDVASVGLAYPDKPFIYRMSFRWYDAQAPLPFIITAIYSGWLTISTVTIWTAEDYTLCMVLCHASFRY : 221
RzepOR35a : YRNIYFTNADDLALYRQLKAIVRYANIFTQFYYAPMLLLIAQYAYDVISVGLASPDKPFIYRMSFRWYDAQVPLPFIITAIYTGWLTISTVTIWAAEDYTLCLVLCHASFRY : 221
DmelOR35a : YANIYIDPRKEPEMFRKVDGKMIINRLVSAMYGAVISLYLIAPVFSIINQ-----SKDLLYSMIFP-FDSDPLYIFVPLLLTNVWVGIVIDIMMFGETNLLCELIVHLNGSY : 218
            YrdIYft add al kein i rf niftqfYy pm Lil lyvydvasvglaspdKpFiYrMsFrwyDaq pl Fiitaiysg WltIs vTiwtaEdytLC vlcHasfrY

                   230       240       250       260       270       280       290       300       310       320       330
BdorOR35a : KKLRLDLQQLLEMARADLKCGETPCTNQNLHIAFRRRLREIFRRQQRLNGFVAEAKAHFTHQIFYIMSFGVLLLCVVSFQFQSGFITVASSKYISWLISQTAQFLLIGYFGQ : 333
BlatOR35a : KKLRLDLQQLLEMARADLKCGETPCTNQNLHIAFRRRLREIFRRQQRLNGFVAEAKAHFTHQIFYILSFGVLLLCVVSFQFQSGFITVASSKYISWLISQTAQFLLIGYFGQ : 333
BoleOR35a : KKLRLDLQQLLEMARADLKGGETPCTNQNLHTAFRRRLCEIFRRQQRLNGFVVEAKAHFTHQIFYIMSFGVLLLCVVSFQFQSGFITVASSKYISWLISQTAQFLLIGYFGQ : 333
BminOR35a : KKLRLDLQQLLEMARADLKSGETRCTNRNLHTAFRRRLCEIFQRQQLLNGFVAEAKAHFTYQIFYVMFFGVLLLCVVSFQFQNAFITVDSSKYISWLISQTAQFLLIGYFGQ : 333
BcucOR35a : KKLRLDLEQLLETARADLRSGETRCTNLNLHIAFRRRLCDIFQRQQRLNGFVAEAKAHFTHQIFYVMSFGVLLLCVVSFQFQSSFISVEWSKYISWIISQTSQFLLIGYFGQ : 333
CcapOR35a : KKLRLDLQELFEASRADLRCGEARRKNEDLHTAFRRRLCDIFQRQQDLNGFVAEAKAHFTHQIFYTLSFGVLLLCVVSFQFQSTQMTVEWSKYIAWLISQTSQFLLIGYFGQ : 333
RzepOR35a : KELRLELQRLLETARA-----EAHFRNEDMHTAFRRHLYDVFRRQQRLNSFIAEAKAHFTHQIFYIMSFGVLLLCVVSFQFQRTEMGIGWSKYIAWLISQTSQFLLIGYFGQ : 328
DmelOR35a : MLLKRDLQLAIEKILVAR-------DRPHMAKQLKVLITKTLRKNVALNQFGQQLEAQTTVRVFIMFAFAAGLLCALSFKAYTNFMAN--YIYAIWFGAKTVELLSLGQIGS : 321
            kkLrldLq llE aradl  ge    n  lh afrrrl  if rqq LNgFvaeakAhfThqiFy  sFgvlLLCvvSFqfq  p  v  skYi WlisqT qfLliGyfGq

                   340       350       360       370       380       390       400       410       420
BdorOR35a : MLMDETTELRNSFYCCRWEDLLVLG-DPHSNKLLLGDVQFAIMNSQEPIVFDGMKFFPLTYSTVSAALRSAVSYFMFLNTMNGEN--- : 417
BlatOR35a : MLMDETTELRNSFYCCRWEDLLVLG-DLHSNKLLLGDVQFAIMNSQEPIVFDGMKFFPLTYSTVSAALRSAVSYFMFLNTMNGEN--- : 417
BoleOR35a : MLMDETTELRNSFYCCRWEDLLVLG-DPRSNKLLLGDVQFAIMNSQEPIVFDGMKFFPLTYSTVSAALRSAVSYFMFLNTMNGEN--- : 417
BminOR35a : MLMDETTELRNSFYCCRWEDLLVHG-DPHSNKLLLSDVKFAIMNSQEPIVLDGMKFFPLTYSTVSVALRSAVSYFMFLNTMNGEN--- : 417
BcucOR35a : MLMDETTELRNSFYCCRWEDLLALG-DLRSNKLLLGDVQFAIMNSQEPIVFDGMKFFPLTYSTVSSALRSAVSYFMFLNTMS-EN--- : 416
CcapOR35a : MLMDETTDLQNSFYFCHWEDLLSLG-DIRSNKLLLRDLEFAIMNAQKPIVFDGMKIFPLTYSTVSSALRSAVSYFMFLNTMNNTN--- : 417
RzepOR35a : MLMNETTELKNSFYSCRWEDLLPLG-DQKSNKILLRDIKFAIMNAQKPIVLEGMKIFPLTYATVGTALRSAVSYFMFLNTMNNAN--- : 412
DmelOR35a : DLAFTTDSLSTMYYLTHWEQILQYSTNPSENLRLLKLINLAIEMNSKFFYVTGLKYFRVSLQAGLKILQASFSYFTFLTSMQRRQMSN : 409
            mLmdeTteL nsfY crWEdlL lg d  sNklLL d  fAImn q Piv dGmK Fpltystvs aLrsavSYFmFLntMn  n
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Supplemental figure 3-8 The alignment of OR35a

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                    10        20        30        40        50        60        70        80        90       100       110
BdorOR43a : -MVTAVVDNPMLSVNVKLWQFLSVLFAR--DWRRCVALVAPVCLMNAMQFVYLYQQWGDLSTFILNTFFAVSVFNALLRTCLIIKNRDKCEALMEELVTLYDDLQDSDDDY : 108
BlatOR43a : -MVXAVVDNPMLSVNAKLWQFLSVLFAR--DWRRCVALVAPVCLMNAMQFVYLYQQWGDLATFILNTFFAVSVFNALLRTCFIIKNRDKFEXLMEELVTLYDDLQDSGDDY : 108
BoleOR43a : -MSTAVLDNAMLSVNVRLWKFLSVLFAR--DWRRCVAFVAPVCLMNAMQFVYLYQQWGDLATFILNTFFAVSVFNALLRTCLIIKNRDKFEALMEELVTLYDNLQDSDDDY : 108
BminOR43a : -MSTAVEDNPLLSVNVRLWKFLSVLFAR--DWRRCVAFVAPVGLMNAMQFVYLYQQWGDLATFILNTFFAVSVFNALLRTCFIIKNRDKFEALMRELVTLYDILQDSGDDY : 108
BcucOR43a : -MSTAVEDNPLLSINVRLWKSLSVLFAR--DWRRCVAFVAPICLLNAMQCVYLYQQWGDLATFILNTFFAVSVFNALLRTCLIIKNRDKFEALMEELVTLYDNIEESGDDY : 108
RzepOR43a : -MPTPIEDNPLLSINVKLWKFLSVLVR--DWSRCVALVAPVCLMNAMQFVYLYQQWGDLATFILNTFFAVSIFNALLRTCFVIRNRDKFEALMQELVTLYDNIQATGDEH : 108
CcapOR43a : MPITRIEDNPLLAINVRLWKFLSVLFAR--NWLRCAAFVAPVCLMNAMQFVYLYQQWGDLATFILNTFFATSIFNALLRTCLVIKNRDKFEALIQELVTMYDDIEATGNDY : 109
DmelOR43a : ---MTIEDIGLVGINVRMNRHLAVLYPTPGSSWRKFAFVLPVTAMNLMQFVYLLRMWGDLPAFILNMFFFSAIFNALMRTWLVIIKRRQFEEFLGQLAILFHSLLDSTDEW : 108
             m t   Dnp ls Nv lW fLsVLfar  dw RcvA VaPvclmNaMQfVYLyqqWGDLatFILNtFFavs FNALlRTc  IknRdkfEalm eLvTlyd I  s ddy

                   120       130       140       150       160       170       180       190       200       210       220
BdorOR43a : AKSVLAAATKSARNISIFNLSASFSDLIVAMAYPLFQQQRVHPFGVALPGIDVTRSPLYELIYIGQLSFPFTLSSMYMPYVSSFATFSMFGKAALQILQNNLRNLCDNMKS : 219
BlatOR43a : AKSVLTAATKSARNISIFNFSASVSDLVVAMTFPLFQQQRVHPFGVALPGIDVTRSPLYELIYIGQLSFPFTLSSMYMPYVSSFATFSMFGKAALQILQNNLRNLCDNMKS : 219
BoleOR43a : AKSVLAAATKSARNISIFNLSASFSDLVVAMAYPLFQQQRVHPFGVALPVIDVTRSPLYELIYIGQLSFPFTLSSMYMPYVSLFATFAMFGKAALQILQNNLRNLCDKMKS : 219
BminOR43a : AKSVLAAATKSARNISIFNLSASFSDLVVAMAYPLFRQQRVHPFGVALPGIDVTHSPLYEIIYIGQLSFPFTLSSMYMPYVSLFATFAMFGKATLQILQNDLKNLCDNMKS : 219
BcucOR43a : AKSVLAAATKSARNISIFNLSASFSDLIVAMAYPLFQEQRIHPFGVALPGIDVTRSPLYEIIYIGQLSFPFTLSSMYMPYVSLFASFAMFAKATLQILQNNLKNLCDNMKT : 219
RzepOR43a : AKSVLAEATRSTRNISIFNLAASFSDIIVAMGYPLFRDQRIHPFGVALPGIDVTRSPLYEILVVAQLPSPFTLSSMYMPYVSLFASFAMFGKAALQILQNNLRNLCENMQH : 219
CcapOR43a : AKRELAAATKAAKKISIFNLSASFCDIIAATLFPLFQENRIHPFGVALPGIDVTRSPLYEIVISQLPCPFTLTSMYMPYVSLFASFAMFGKVALKVLQDNLRNLCDNMQH : 220
DmelOR43a : GRGILRRAEREARNLAILNLSASFLDIVGALVSPLFREERAHPFGLALPGVSMTSSPVYEVIYLAQLPTPLLLSMMYMPFVSLFAGLAIFGKAMLQILVHRLGQIGG--EE : 217
            aksvLaaAtksaRnisIfNlsASfsD  vAm  PLF  qR HPFGvALPgidvTrSPlYE iYi QL  PftLssMYMPyVSlFA famFgKa LqiLqnnL nlcdnm

                   230       240       250       260       270       280       290       300       310       320       330
BdorOR43a : KTLEELFEILRKNIAYHARIARYVSDFNELVTYMVLIEFLLFSCVICSLLFCINIT---TSTAEKISIVMYIGTMLYVLFTYYWQANGVLEMSHLVSDAAYEMQWYDCSPR : 327
BlatOR43a : KTLEELFGILRKNIAYHARIARYVSDFNELVTYMVLIEFLLFSCVICSLLFCINIT---TSTAEKISIVMYIGTMLYVLFTYYWQANGVLEMSLLVSDAAYEMQWYNCSPH : 327
BoleOR43a : KTLKELFELLRTNIAYHARIARYVSDFNELVTYMVLIEFLLFSCVICSLLFCINIT---TSMAEKISIVMYIGTMLYVLFTYYWQANGVLEMSLLVSDAAYEMQWYNCSPR : 327
BminOR43a : KTLEELFELLRTNIAYHARIARYVSDFNELVTYLVLIEFLLFSCVICSLLFCINIVSKTTSTAEKISIVMYIGTMLYVLFTYYWQANGVLEMSLLVSDAAYEMQWYKCSRR : 330
BcucOR43a : KTLEELFELLRTNIAYHARIARYVSDFNELVTYIVLIEFLLFSCVICSLLFCINIVSTTTSTAEKISIVMYIGTMLYVLFTYYWQANGILEMSLLVSDAAYEMQWYNCSPR : 330
RzepOR43a : KSEPELFDTLRANIAYHARIAKYVNDFNELVTYMVLVEFLLFSCVICSLLFCINIT---NSAAEKMSIVMYIGTMLYVLFTYYWQANGILEMSLLVSDAAYEMQWYNCSQR : 327
CcapOR43a : KSEMELFNLLRSNISYHARISKYVNDSNELVTYMVLIEFMLFSCVICSLLFCINIT---NSTAEKISIVMYIGTMLYVLFTYYWQANGILEQSLLVSDAAYEMQWYKCSQR : 328
DmelOR43a : QSLEERFQRLASCIAYHTQVMRYVWQLNKLVANIVAVEAIIFGSIICSLLFCLNIT---TSPTQVISIVMYILTMLYVLFTYYNRANEICLENNRMAEAVLNVFMWYEAGTR : 325
            k E ElF  Lr nIaYHariaryVV dfNeLVty VliEflIFscvICSLLFCiNI    tS aekiSIVMYIgTMLYVLFTYYwqANg lemsllVsdAaYemqWY cs r

                   340       350       360       370       380
BdorOR43a : FKRTLLIFIARTQNPLQIRVGQMHPMTMEVFQSLLNNAYSYFTLLHNLYND : 378
BlatOR43a : FKXTLLIFIARTQNPLQIRVGQMHPMTMEVFQSLLNNAYSYFTLLHNLYND : 378
BoleOR43a : FKRTLLTFIARTQNPLQIRVGQMYPMTMEVFQSLLNTSYSYFTLLHNLYND : 378
BminOR43a : FKRTLLIFIGRTQKPLQIRVGQMYPMTMEVFQSLLNTSYSYFTLLHNLYND : 381
BcucOR43a : FKRTLLIFIGRTQKPLQIRVGQMYPMTMEVFQSLLNTSYSYFTLLHNLYND : 381
RzepOR43a : FKRTLLIFITRTQRPLQIRVGKMSPMTMEVFQSLLNTSYSYFTLLYNLYND : 378
CcapOR43a : FKRTLLIFIGRTQKPLQIRVGQMSPMTMEVFQSLLNSSYSYFTLLHNLYND : 379
DmelOR43a : FRKTLLIFLMQTQHPMEIRVGNVYPMTLAMFQSLLNASYSYFTMLRGVTGK : 376
            FkrTLLiFi rTQ PlqIRVGqm PMTmevFQSLLN sYSYFTlLhnlynd
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Supplemental figure 3-9 The alignment of OR43a

```
                        10        20        30        40        50        60        70        80        90       100       110
BdorOR45a2   : ------------------------------------------------------------------------------------MENFADVDKIVAAMTINVQLFTTSGKNF :  28
BlatOR45a2   : ------------------------------------------------------------------------------------------------------------------ :   -
BcucOR45a2   : --------------------------MRITILKDIKPITDAFVRIGLSIELGGSKGIFSHPERYATVMIGVIVWAVALFTYTMEYLADVDKIVAAMTINVQLCLTTSKNF :  84
CcapOR45a2   : --------------------------MRIIVLKDITPVVDAFACIGFNIDLNKAKGSFSQPVRYFVLLIGVIAWTAALAAYTMQYLTDVDKMVAAMTINVQLFLTTSKNL :  84
BoleOR45a2   : ------------------------------------------------------------------------MENLTDVDKILAAVTINSQLFTSSSKHF :  28
RzepOR45a2   : ------------------------------------------------------------------------------------------------------------------ :   -
BminOR45a3   : ------------------------------MYKYLRIPYFSFRVIGINLWAQQDQRITSAPCRYYSWTLATAIIILMGFY--IYTSDQDKAIQVLTVFLQGVLCIIKSG :  78
BoleOR45a3   : ------------------------------MYEYLQIQHFSFRVIGINLWAQRDQRITSAPCRYLTWTLATAIITLLMGCY--IYTSEQDKAIQVLTVFLQGVLSVIKSG :  78
BdorOR45a3   : ------------------------------MYEYLRIQQFSFRVIGINLWAQRDQRIASAPCRYYSWTLATAIITLFMGFY--IYTSEQDKAIQVLTVFLQGVLSVFKSG :  78
RzepOR45a3-1 : ------------------------------MHKYLRIQQISFLLLGIDMFATRDRHILRAPYRYGCWTLATATITILMGVY--IYNSEQDQAVKVLTVFLQGVLSVLKSF :  78
RzepOR45a3-2 : ------------------------------------------------------------------------------------------------------------------ :   -
CcapOR45a3   : ------------------------------MDGLGIGGDGNS--GIRAGEIGEKTDANSDSDVGANVTSSTMDNALMQ--------KPDQAITVLTVFLQGVLSVFKSG :  69
BdorOR45a1   : ------------------------------------------MTTRSARVIKIYFLTLQIIALATILIPIAVYSWQHIQEIVEVTNAMAPFMQATISLWKIW :  60
BlatOR45a1   : ----------------------------MVMVFAQSCTSKTRQLPHLTDMTTRSARVTKIYFLTLQIIALATILIPIAVYSWQHIQEIVEVTNAMAPFMQATISLWKIW :  81
BoleOR45a1   : ------------------------------------------MTNRSARVTQIYFLTLQIIALSTILIPFAVYSWQHMQEIVEVTNAMAPFMQATISLWKIW :  60
BminOR45a1   : --------------------------MFKSGLNIKGYFHLQKFTFHRLGIDITTRSAHVTRIYLLILQIVALATILISMASYSWQHIQDIGEVTNAMTPFMQATITLWKIW :  85
BcucOR45a1   : ------------------------------------------MTTREARVTQICFLIIQIFALASILIPIAVYSWQHIDDIAEVSNAMAPFMQATISLWKVW :  60
CcapOR45a1   : MLVHSHYKSHSICSLCVRRSTGSQKMFHSDLVINGYFQLQKHTFQRLGIDMTTRNASITHIYFLALQIVALVTITMPMVIYSCQHLQEIAEVTNAMAPFMQATITLWKIW : 110
DmelOR45a    : ------------------------------MDASYFAVQRRALEIVGFDPSTPQLSLKHPIWAGILILSLISHNWPMVVYALQDLSDLTRLTDNFAVFMQGSQSTFKFL :  79
                                                                                                                   q      k

                       120       130       140       150       160       170       180       190       200       210       220
BdorOR45a2   : IFLARRKRFLRLNEALERLALKGNKYERELWNATNRPVLP-------------ITTAYSISCQLTVNICLLLPIFKLLFYYIWYNEVVLTLPLPGIFPYDYTLPFYYILT : 125
BlatOR45a2   : ------------------------------------------------------------------------------------------------------------------ :   -
BcucOR45a2   : IFLARRERFLRLNEALERLALTGNNIERELWNTSNRRVLP-------------ITMAYSISCQMTVSICVLLPILKLLYYYIWHNEVVLTLPLPGIFPYDYTVPFYFILT : 181
CcapOR45a2   : IFLARRKRFLHLNEALERLALNGNESERILWNTTNRFVLP-------------ITRAYRISSELTVSFCVLLPILKLLYYYIFHSEVVLTLPLPGIFPYNYTLPFYFILT : 181
BoleOR45a2   : IFLARRKRLLRLNEALERLALTGNKFERDLWNTTNRTVLP-------------IVTAYSISCQLTVNICVLLPILKLLYYYIWYNEVVLTLPLPGSFPYDYTSPFYFILT : 125
RzepOR45a2   : ------------------------------------------------------------------------------------------FPYDYTIPFYYILT :  14
BminOR45a3   : MFVAKGRRFIKLIRNLDALADAATVKEWSEWRHENDWQQC-------------IVRVYYICCTSTGTLYCTVPAVILLYSQCFREHTVFILPFDAAFPLDTGHLFFYTVS : 175
BoleOR45a3   : MFVAKGRRFIKLIRSLDMLADEANVKEGREWRHENDWQQR-------------IVRVYYICCMSTGTLYCTVPAIILLYSRCFNDHTMFILPFNAAFPYDTGHPFFYTVS : 175
BdorOR45a3   : MFVAKGRRFIKLIRSLDMLAAEANVKEGKEWKHENDWQQR-------------IARVYYSCCMSTGTLYCAVPAIILLYSQCFNGHATFILPFDAAFPFDTAHPFFYPIS : 175
RzepOR45a3-1 : MFVTKGRRFIALIENLESLAEGANVKEHAEWTHENDWQQRXAEWTHENDWQQRIARVYYSCCTATGTLYCTVPVLILLYSVCFNEHAVLILPFDAAFPFNVQQPFFYIIA : 188
RzepOR45a3-2 : ------------------------------------------------------------------------------------------FPFNVQQPFFYIIA :  14
CcapOR45a3   : MFVLKSGRFIELIRNLDMLAE----KEHSAWRLENDWQQR-------------IVSVYYFCCTSTGILYCTVPALVLLYTRYFREQTVFILPFEASFPYDTNQPLFYILS : 162
BdorOR45a1   : RVIYRRKEMAQMAENIYLISTRASAK--ELTHLIQENNRE-----------RLMNTAYYYSVLNTGMLALAAPVLVSFIQYLRLGEFSYIVVLKATYPIEYARPLNYFLI : 157
BlatOR45a1   : LVIYRRKEMAQMVENIYLISYKASAK--ELTHLIQENNRE-----------RLMNTAYYYSVLNTGMLALAAPVLVSFIQYLRLGEFSYIVVLKATYPIDYARPLNYFLI : 178
BoleOR45a1   : RVIYRRKQMAEMVENIYMISAKASTK--ELTHLIQENNRE-----------RLMNTAYYYSVLITGMLALTAPVLVSFIQYLRFGEFSYIVVLKGTYPIDYARPLNYFLI : 157
BminOR45a1   : LVIYRRREMAEIVENIYLISAKASTK--ELTHLIQENNRE-----------RLMNTAYYYSVLNTGMLALTAPVLVSFIQYLRLGEFSYILVLKATYPIDYARPLNYFLI : 182
BcucOR45a1   : RVIYRRKEMAELCENIYLISAKASKL--ELAHLIQENNRE-----------RIMNTAYYYSVLNTGVMALTAPVVVSFIQYLRLGEFSYITALKATYPIDYARPLNYFLI : 157
CcapOR45a1   : RVIYRRKMMAELVEDIYSVSTKATKQ--ELTHLRRENNRE-----------RIMNTFYYYSVFNTGVLALIAPVLVSFIQYLRLGEFSYIVVLKATYPIELARPLNYVLI : 207
DmelOR45a    : VMMAKRRRIGSLIHRLHKLNQAASATPNHLEKIERENQLD-----------RYVARSFRNAAYGVICASAIAPMLLGLWGYVETGVFTPTTPMEFNFWLDERKPHFYWPI : 178
                                                                  y      t       p                          p     p  y

                       230       240       250       260       270       280       290       300       310       320       330
BdorOR45a2   : TILTVLLVQLCANTITVVDGLFGWFVYNISAHLQIMRLKLEQLLQLHVDDPN---FHRDFVALINYHREIINLALELDAVYAPIIFLESRLXSLPICFLAYQLSYLSDPA : 232
BlatOR45a2   : ----------------VDGLFGWFVYNISAHLQIMRLKLEQLLQLHVDDPS---FHRDFVALINYHRETIDLALELDAVYAPIIFLEVTSSCLPICFLAYQLSYLSDPA :  90
BcucOR45a2   : TILSVLLVYFCVYTICAVDGLFGWFVYNISAHLQIMRLKLEQLLQLHVDDPN---FQRDLVALVNYHRQIIDLSLELDALYAPIIFLEVTSSSLPICFLAYQLSYLSDPA : 288
CcapOR45a2   : TILTILLVYLCAYTIVAIDGLFGWFIYNISAHLQIMSLRLEQILQLPIEDPR---FHRHFVDLVNYHKEIIRLSLELDAVYAPIIFLEVTSSSLPICFLAYQLSYLSDPA : 288
BoleOR45a2   : LILTVLLVQFCSNSIIIVDGLFGWFVYNISAHLQIMRLKLEQLLQLHVEDPN---FNRDFVAFVNYHREIIDLTLELDAVYAPIIFLEVTSSSLPICFFAYQLSYLSDPA : 232
RzepOR45a2   : VILSVLLVFFCMNAICIVDGLFGWFVYNISAHLQIMRLKLEHLVQLQMADPQ---FQADFAAFISYHREIISLTLELDAVYAPIIFLEVTLSSLPICFLAYQFTYITDPA : 121
BminOR45a3   : YLWCISFIIYAIHAITAMDSLFCWFIFNISAHFRTLQHELQNVAKTSADVEDSACLHSKITETLHYHRRIIELSAEFDELYAPIVFIEISVSYLKLCFSAYNLINLGDIS : 285
BoleOR45a3   : YIWCISFIVYAIHAIAAMDSLFCWFIFNISAHFRALQRELETVVAASAGAEDDSSLHSRITQTLHYHRRIMELSAEFDELYAPIVFIEISVSYLKLCFSAYNLINLSDIS : 285
BdorOR45a3   : YIWCISFIIYAVHAIAAMDSLFCWFIFNISAHFRALQRAVETVGAAMTGAEDYASLHGRITRTLHYHRRIIELSAEFDELYAPIVFIEISVSYLKLCFSAYNLINLAAAA : 285
RzepOR45a3-1 : YIWCISFIVYAIHAVAAMDSLFCWFIFNISAHFRILQHKLEAVAAT-LAEEDYVSFQQNITEALRYHRHIIELAAEFDDLYAPIVFIEIAVSYLKLCFSAYNLINLADIS : 297
RzepOR45a3-2 : YIWCISFIVYAIHAVAAMDSLFCWFIFNISAHFRILQHKLEAVAAT-LAEEDYVSFQQNITEALRYHRHIIELAAEFDDLYAPIVFIEIAVSYLKLCFSAYNLINLADIS : 123
CcapOR45a3   : YIWCISFIIYAIHAIVAMDSLFCWFIFNISAHFRILQQKLTDVSVSPNASTDHAIFQQDITQTLFYHQRIIELSAEFDELYAPIVFVEISVSYLKLCFSAYNLINLDDIS : 272
BdorOR45a1   : WLWTAVAIYGVIYGSVSVDSLYSWYIHNLVGNFKILQSKLVTAESASE----LSERRELIYYCIAYHQRIIAMTEQLNIIYQPIVFVQFSLNALQICFLAYQIGSGVVDT : 263
BlatOR45a1   : WLWTAVAIYGVTYGSVSVDSLYSWYIHNLVGNFKILQSKVLTAELANE----PSQRCELIYYCIAYHQRIIAMTEQLNIIYQPIVFVQFSLNALQICFLAYQIGSGVVDT : 284
BoleOR45a1   : WLWSAAAIYGVIYGSVSVDSLYSWYIHNLVGNFKILQSKLVTAEWATD----LSERREEIYYCIAYHQRIIAMTEQFNIIYQPIVFVQFSLNALQICFLAYQIGSGVVDT : 263
BminOR45a1   : WLWSAVSIYGVIYGSVSVDSLYSWYIHNLVGNFKILQSKLVSAESTAD----LSERRTHIYYCIAYHQRIIAMTEQLNLIYQPIVFVQFSLNALQICFLAYQIGSGVVAT : 288
BcucOR45a1   : WLWTAVAIYGVIYVSVPVDSLYSWYIHNLVGNFKILQSKLVSAESIAESTADLGKRRELIYYCVAYHQRLITMSEQLNIIYQPIVFVQFSLNGLQICFLAYQIGSGVVAM : 267
CcapOR45a1   : WLWSAIAIYGVIYGSVSVDSLYSWYIHNLVGNFKILQTKFVTAELIAE----VSERRASIYYCLGYHQRLITMSEQLNIIYQPIVLVQFSLNALQICFLAYQIGSGDVAV : 313
DmelOR45a    : YVWGVLGVAAAAWLAIATDTLFSWLTHNVVIQFQLLELVLEEKDLNGG--------DSRLTGFVSRHRIALDLAKELSSIFGELIVFVKYMLSYLQLCMLAFRFSRS-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-VPFICLLLSSIVLQLMIYCFGGEKVQNECDELSQNIYLLIP-WHKLPPKHCRLLLIPFIRSQRVLVLTGYFFTANRSLLVWIFRTAGSFTAMLFALKEKEV--- : 333
BlatOR45a2   : N-VPFICLLLSSIVIQLMIYCFGGEKVQSECDELSENIYLLIP-WQNLPPKHCRLLLIPFIRSQRVLVLTGYFFTANRSLLVWIFRTAGSFTAMLFALKEKEL--- : 191
BcucOR45a2   : S-VPFMCLLMSSIVIQLMIYCFGGEKVQNECDQLCENIYLLIP-WHKLPPKHCRLLLNPFIRSQRVLVLTGYFFTANRSLLVWIFRTAGSFTALLFALKEKEV--- : 389
CcapOR45a2   : N-VPFMCLLMSSIVIQLMIYCFGGEKVQSECDQLCENIYLLIP-WQNLPQKHCRLLLNPLIRSQRVLVLTGYFFTANRSLLVWIFRTAGSFTAMLFALKEKDV--- : 389
BoleOR45a2   : N-VPFICLLLASIVLQLMIYCFGGEKVKNECEQLSENIYLLIP-WQNLPPKYCRLLLTPFIHSQRVLVLTGYFFTANRSLLVWIFKTAGSITAMLFAWKEKKVV-- : 334
RzepOR45a2   : N-VPFMCLLLSSIVLQLLIYCFGGEKVQNECEKLCESIYLLIP-WHKLPPKHSRLYLTPLIRSQRALVLTGYFFTANRSLLVW---------------------- : 202
BminOR45a3   : G-LPVIAVGLVTITFQLCNYCFSGEKLKSVSKVVSDRIYLAFS-WERVPPPLRRLLILPLMRAQRATNLTGFLFVVDHSLLVWIFKTTGSIIGFLSATKSENTTS- : 388
BoleOR45a3   : G-LPVLAVGLVTITFQLCIYCFSGEKIKNVSEEVSDRIYLAFP-WERVPPSVRRLLLLPLMRAQRATNLTGFLFIVDHSLLVWIFKTTGSIIGFLSATKSENTTS- : 388
BdorOR45a3   : A-NTFQTSPSVS---QATDYLKSLNLLNISCVAASECIGAAKRNLQQVAEPIK------LNANARHLAITGQSAVLACE---------------------------- : 354
RzepOR45a3-1 : S-FPVIVVGLVTITFQLCIYCFSGEKIKNASLLISDHIYLTFP-WARMPSSMRRLLLLPLMRAQRSTNLTGYLFIVDHSLLVWIFKTTGSIIGFLSATKEKTVDVN : 401
RzepOR45a3-2 : S-FPVIVVGLVTITFQLCIYCFSGEKIKNASLLISDHIYLTFP-WARMPSSMRRLLLLPLMRAQRSTNLTGYLFIVDHSLLVWIFKTTGSIIGFLSATKEKTVDVN : 227
CcapOR45a3   : S-LPVIAVGLVTITFQLCIYCFSGEKIKNASEQFANHIYLSFP-WERVPPSLRRLLFVPIMRAQRPMHLTGFLFIVDHSLLVWIFKTTGSIIGFLSATKKENTNI- : 375
BdorOR45a1   : VDLPFLFLFMISVGIQLMIYCYGGQHLQNESVNVSKSIYQTIN-SSSWPNELRKVLLISMMRAQKPSKLTGIFFDVDLPLFLWVWRTAGSYVTLLRSVDQKTM--- : 365
BlatOR45a1   : MDLPFLFLFMISVGIQLMIYCYGGQHLQNESVNVSKSIYQTIN-SATWPNKLRKVLLISMMRAQKPSKLTGIFFDVDLPLFLWVWRTAGSYVTLLRSMDQKTM--- : 386
BoleOR45a1   : VDLPFLFLFMISVGIQLMIYCYGGQHLQNESVNVSKSIYQTIN-SSAWPIDLRKVLLISMMRAQKPSKLTGIFFDVDLPLFLWVWRTAGSYVTLLRSVEQKTM--- : 365
BminOR45a1   : VDLPFLFLFMISVGIQLMIYSYGGQHLQNESVNVSKSIYQTIN-SSAWPIDLRKVLLISMMRAQKPSKLTGIFFDVDLPLFLWVWRTAGSYVTLLRSVDQKNL--- : 390
BcucOR45a1   : VDLPFLLLFLISVGIQLMIYCYGGQHLQNESVNVSKSIYQTIN-SSPWPNELRKVLLISLMRAQKPCKLTGIFFDVDLPLFLAVWRTAGSYVTLLRSVDQKTM--- : 369
CcapOR45a1   : VDLPFLFLFMTSVGIQLMIYCYGGQYLQNESENVAKFTSQTIN-STIWPIDLRKVLLFSMARAQRPCKLTGIFFDVDLRLFLWVWRTAGSYVTLLRSVDQQSS--- : 415
DmelOR45a    : AQVPFRATFLVAIIIQLSSYCYGGEYIKQQSLAIAQAVYGQIN-WPEMTPKKRRLWQMVIMRAQRPAKIFGFMFVVDLPLLLWVIRTAGSFLAMLRTFER------ : 378
                  p           Ql iYc  g             iy         p      ll    r q    ltG  f     l  w   t gs    l
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Supplemental figure 3-10 The alignment of OR45a

```
                    10        20        30        40        50        60        70        80        90       100       110
RzepOR46a  : ------------------------------------------------------------MYFWYVAIFWIFLFDASMWIK--IISNITDLNEIIKVFYVCSMAIAVMAKFV :  50
CcapOR46a  : MITPRKASSIPIIKYTRITMEEPKKIVNCFYERQFKFFKFLGLFGLPPNYSRFCQILFKLYFWHVTVVWMLLFDISMWVK--VIGNITDLNEIVNVFYICSMAIAVMAKFV : 109
BdorOR46a  : ----------------------------MGFH------QKLLGLFGLPAHYPSLLQYLYKLYFWHVAIFWMLLFDISMWIK--IIGNISNLNEIIKVFYLCSMAIAVMAKFV :  76
BlatOR46a  : -------------------MEDAKRIVHSFYNIQLLFFKLLGLFGLSAHYPSHLEYLYKLYFWHVAIFWMLLFDISMWIK--IIGNISNLNEIIKVFYLCSMAIAVMAKFV :  90
BoleOR46a  : -------------------MDDAKGIVYSFYKVQYLFFKLLGLFDLPAHYSSFWHYMYKLYFWHVAIFWMLLFDISMWIK--IVGNISNLNEIIKVFYLCSMAIAVMAKFV :  90
BminOR46a  : ------------------------MVSPQQSTTPEIDEYLLGLFGLPKHYSSFWHYMYKLYFWHVAIFWMLLFDISMWIK--IIGNISNLNEIIKVFYLCSMAIAVMAKFM :  85
DmelOR46aB : ----------------------MVT--EDFYKYQVWYFQILGVWQLPTWA---ADHQRRFQSMRFGFILVILFIMLLLFSFEMLNNISQVREILKVFFMFATEISCMAKLL :  84
DmelOR46aA : ----------------------MSKGVEIFYKGQKAFLNILSLWPQIERR---WRIIHQVNYVHVIVFWVLLFDLLLVL--HVMANLSYMSEVVKAIFILATSAGHTTKLL :  84
                                     f          lgl  l              yfwhv  fw llFd smw k     Nis lnEi kvfy csmaiavmaKf

                   120       130       140       150       160       170       180       190       200       210       220
RzepOR46a  : HIRIKTSSFLALFARMHDDDLLPVNKFEMETFTQSLQLSCKVRNCYMYLSLTSLSLVFVRQLVSDPGELPLSIYIPMNVEN-IWFFILAYLFQFIGASLCCFINISFDSLS : 160
CcapOR46a  : HIRKKNSRYVAFFARMHNDDLLPANPSELKKFIKSVHLSCAVRNCYMGLSLTSLALVFVPKLISDPGELPLSIYIPLNVEH-TLCFLVAYIFQFVGLSLCCFLNIAFDSLS : 219
BdorOR46a  : RIRLKNSSYVALFARIHDEDLLPVNVSELEKFTQSSHLSCRVRNSYMYLSLTSLSLIFVTQLISEPGELPLSIYVPISVEN-FWCYLIAYLFQFIGLSLCCLLNISFDSLS : 186
BlatOR46a  : RIRLKNRSYVALFARIQDEDLLPVNVSELEKFTQSSHLSCRVRNSYIYLSLTSLSLIFVTQLISEPGELPLSIYIPISVEN-FWCYLIAYMFQFIGLSLCCLLNISFDSLS : 200
BoleOR46a  : RIRLKNSSYVALFARIHDDDLLPVNVSELEKYTQSSHLSCRVRNSYTYLSLTSLSLIFITQIISEPSELPLSIYIPISVEN-FWCYLIAYLFQFIGLSLCCLLNISFDSLS : 200
BminOR46a  : RIHLKNNSYVEIFARMHDDDLLPVNVSELEKLAQSSHLSCRVRNYYTYLSLTSLTLIFVTKLISEPDELPLSIYIPISVES-FWRYLIAYLFQFIGLSLCCLLNISFDSLS : 195
DmelOR46aB : HLKLKSRKLAGLVDAMLSPEFGVKSEQEMQMLELDRVAVVRMFRNSYGIMSLGAASLILIVPCFDNFGELPLAML-EVCSIEGWICYWSQYLFHSICLLPTCVLNITYDSVA : 194
DmelOR46aA : SIKANNVQMEELFRRLDNEEFRPRGANEELIFAAACERSRKLKDFYGALSFAALSMILIPQFALDWSHLPLKTYNPLGENTGSPAYWLLYCYQCLALSVSCITNIGFDSLC : 195
              i  kn     lfar    dllp n  E      s  lsc vRn Y  lSltslslif     s p eLPLsiy p  ve     y  aY fqfiglslcC lNI fDSls

                  230       240       250       260       270       280       290       300       310       320       330
RzepOR46a  : ASFFIYLRGQLNILSNRLENIPTDKDTTQD-VINMQLKDCIRYYNKLLDITEIMEDLLSTPMSVQVISSVFVLVANFYAMTFLTDPN-DYATFMKFLVYQLCMLTQIFILC : 269
CcapOR46a  : ASFFIYLKGQLDILSNRLENIGKFQNITQD-VITLQLKECIRYYAKLRYITDIMEDLLCIPMSVQVISSVLVLVANFYAMTFLTDPS-DYGTFMKFLVYQLCMLSQIFMLC : 328
BdorOR46a  : ASFFIYLKGQLDILANRLENIGKDLYVDDN-IINLQLRDCIQHYVKLRKIAEIMEDLLSIPMSVQMISSVLVLVANFYAMTFLTDPS-DYVTFIKFLVYQLCMLSQIFMLC : 295
BlatOR46a  : ASFFIYLKGQLDILANRLENIGKDLYVDDS-IINLQLRDCIQHYVKLRKIAEIMEDLLSIPMSVQMISSVLVLVANFYAMTFLTDPS-DYVTFTKFLVYQLCMLFQIFMLC : 309
BoleOR46a  : SSFFIYLKGQLDILANRLENIGTNLYVDDN-MINLQLRDCIQQYVKLRNITEIMEELLSIPMSVQMISSVLVLVANFYAMTFLTDPS-DYVTFIKFLVYQLCMLAQIFMLC : 309
BminOR46a  : ASFFIYLKGQLDILAYRLENIGTNLDVDDN-MINLQLRYCIQHYVKVRKITENMEDLLSIPMFVQMISSVLVLVANFYAMTFLTDTS-DYVTFIKFLVYQLSMLSQIFMLC : 304
DmelOR46aB : YSLLCFLKVQLQMLVLRLEKLGFVIEPQDNEKIAMELRECAAYYNRIVRFKDLVELFIKGFGSVQLMCSVLVLVSNLVDMSTMSIANGDAIFMLKTCIVQLVMLWQIFIIC : 305
DmelOR46aA : SSLFIFLKCQLDILAVRLDKIGRLITTSGG-TVEQQLKENIRYHMTIVELSKTVERLLCKFISVQIFCSVLVLTANFYAIAVLSDER---LELFKYVTVQACMLIQIFILC : 302
              SffiyLkgQLdiL  RLenig          i  qL  ci  y k   i   mE ll  PmsVQ isSVlVLvaNfYamtfltd   dy tf KflvYQlcML QIF lC

                  340       350       360       370       380       390       400       410       420       430       440
RzepOR46a  : YFANEVSIRSSELPFSLYSSEWTHCNRINRRLMLLMMAQFDIPIRIKTINRCYSFNLSAFTS------------------------------------------ : 331
CcapOR46a  : YFANEVSLRSAQLSYALYSSEWTHCNQINRRLMMLMMAQFDVPIRIKTINRCYSFNLPAFTSIINSSYSYYALLKNMKD---------------------------- : 407
BdorOR46a  : YFANEVSLRSAELSYSLYSSEWTRCSKINRRLMLLMMAQMDVPIRIKTINRCYSFNLPAFTSIINSSYSYYALLKKMKD---------------------------- : 374
BlatOR46a  : YFANEVSLRSAELSYSLYSSEWTRCSKINQRLMLLMMAQLDVPIRIKTINRCYSFNLPAFTSIINSSYSYYALLKKMKD---------------------------- : 388
BoleOR46a  : YFANEVSLRSAELSYSLYSSEWTRCSQTNRRMMLLMMAQFDVPIRIKTINRCYSFNLPAFTSIVNSSYSYYALLKKMKD---------------------------- : 388
BminOR46a  : YLANEVSLRSAELSYSLYSSEWTRCSKMNQRLMLLMMAQFGVPIRIKTVNRCYSFNLPAFTSKKKPKESSSKEQEDSTEHQSRNVINSTELETRKICSSDLTGIEFVK : 412
DmelOR46aB : YASNEVTVQSSRLCHSIVSSQWTGWNRANRRIVLLMMQRFNSPMLLSTFNPTFAFSLEAFGSIVNCSYSYFALLKRVNS---------------------------- : 384
DmelOR46aA : YYAGEVTQRSLDLPHELYKTSWVDWDYRSRRIALLFMQRLHSTLRIRTLNPSLGFDLMLFSSIVNCSYSYFALLKRVNS---------------------------- : 381
             Y anEVs rS  L  slYsseWt c   nrR mlLmMaq   pirikT NrcysFnL aFtSi n sysy allk
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Supplemental figure 3-11 The alignment of OR46a

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                    10        20        30        40        50        60        70        80        90       100       110
BcucOR47bX1 : -MISLSTQATINNTISTHNSYLSNDSNTHLKHTASKLRTILAPYR-VLKEMLRSGEAVHPPHTCLFYFRAYIRLLGLWPAERAVENPLYYAFNVLIMLLFGFFT---------- : 102
BcucOR46bX2 : -MISLSTQATINNTISTHNSYLSNDSNTHLKHTASKLRTILAPYR-VLKEMLRSGEAVHPPHTCLFYFRAYIRLLGLWPAERAVENPLYYAFN---------------------- :  91
BdorOR47b   : -MISLSSKATISNTIASHNSYLTNHSYTHLKHTASKLQTILAPYR-VLKEMLRCGEAVQPPHTCLFYFRSYIRLLGLWPAKRAAENQLYYFYNLLIMVLFSFFM---------- : 102
BlatOR47b   : -MISLSSKATTSNTIASHNSYLTNHSYTHLKHTVSKLQTILAPYR-VLKEMLRRGEAVQPPHTCLYYFRSYIRLLGLWPAKRDAENQLYYFYNLLIMVLFSFFM---------- : 102
BoleOR47b   : -MISLLSKATISNTISSHNSYLINNSYTHLQHTSSKLQTILAPYR-VLKEMLRFGEAVHPPHTCLFYFRSYMRLLGLWPAARATENQLYYFYNLLLMMLFSFFM---------- : 102
BminOR47b   : -MISLSSKATIDNSISSHNSYLTNKSYTHLKHTASKLQTILAPYR-VLKEMLRYGEAVHPPHTCLFYFRAYIRLLGLWPTERTAENPLYYFYNVLIMILFSFFM---------- : 102
CcapOR47b   : MLHECSDKSTISNTIFNHQSYRRRSR----KYSSSKLETILAPIR-TLKEMLLSGDAAHPSHTCLYYVRAYIRLLGLWPSQRGVEQPMYYAYNVLIMTVFSFFVATIIADLYVA : 109
RzepOR47b   : -MIPILRESTISNTISEHN-FNLNNGNIFLQNTIGMAKTILEPYR-VAREVLRRGDDGHPSHTCLYYFRAYMRLLGLWPLQRRVEQPLYYGYNGLLMTLFGFFV---------- : 101
DmelOR47b   : -----MNDSGYQSNLSLLRVFLDEFRSVLRQESPGLIPRLAFYYVRAFLSLLCQYPNKKLASLPLYRWINLFIMCNVMTIFWTMFVALPESKNVIEMGDDLVWISG-------- : 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

                   120       130       140       150       160       170       180       190       200       210       220       2
BcucOR47bX1 : ----------------LCLIFFKMILFRLGNADTDIIINEFDALHVKHFNESH-DSPRNRRTRQWQRSFFFGEMCFFSGFYILSLFLFAAMSLQPLLSQQILPFRCKFPFGLDD : 199
BcucOR46bX2 : ----------------LCLIFFKMILFRLGNADTDIIINEFDALHVKHFNESH-DSPRNRRTRQWQRSFFFGEMCFFSGFYILSLFLFAAMSLQPLLSQQILPFRCKFPFGLDD : 188
BdorOR47b   : ----------------LYLIFFKMILFRMGNVDTDIIINEFDALHIKHARGLS-GGPRNRRILQWQRSFFFGEMCFFSGFYILSLLLFAAMSLQPLLSQQTLPFRCKFPFGLND : 199
BlatOR47b   : ----------------LYLIFFKMILFRMGNVDTDIIINEFDALHIKHGRGLS-ESPRNRRILQWRRSFFFGEICFFSGFYILSLLLFAAMSLQPLLSQQTLPFRCKFPFGLND : 199
BoleOR47b   : ----------------LYLIFFKMILFRMGNIDTDIIINEFEALHIKHASGLR-DGPRNRRILQWQRSFFIGDMCLFSGFYILSLFLFAAMSLQPLLSQQTLPFRCKFPFGLNN : 199
BminOR47b   : ----------------LYLIFFKMALFRMRNGETDIIISEFDALHVQHANLLR-DGPRNQRILQWQRRFFFGEICFFSGFYILSLFLFAAMSLQPLLSQQTLPFRCKFPFGLDD : 199
CcapOR47b   : SSDFVLLGEDLVVALGLYLILFKMILFRMSTADVDVIVDEFDALHMKFARDTS-DSPHIRRIRQLQRSFFLGEASFFCGFFFLSLFLFAAMSLQPLLTHQALPFRCVFPFGLHD : 222
RzepOR47b   : ----------------LYLILFKMFLYRSSIAEIDSIVNEFDTLHAKYAHALLPKSQSNRRIRQWQRNFFIGEIVLTTGFFILSFLLFAAMSLQPLFSHQTLPFRSKYPFGLDN : 199
DmelOR47b   : ----------------MALVFTKIFYMHLRCDEIDELISDFEYYNRELR-----PHNIDEEVLGWQRLCYVIESGLYINCFCLVNFFSAAIFLQPLLGEGKLPFHSVYPFQWHR : 194
                                l LiffKm lfr       D ii eFdalh k         p nrr   qwqR ff ge   f gf iLsl lfAAmsLQPLls q LPFrckfPFgl

                 30        240       250       260       270       280       290       300       310       320       330       340
BcucOR47bX1 : PDEHPMGFVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCENMRNLGN---------GSTSELVVWRKLKETVEFHQQIIKLMNRINQTFYWNYVSQMGASTFMIC : 304
BcucOR46bX2 : PDEHPMGFVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCENMRNLGN---------GSTSELVVWRKLKETVEFHQQIIKLMNRINQTFYWNYVSQMGASTFMIC : 293
BdorOR47b   : PDEHPIAFVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCENIRHLGIVAAG---ASSSTSEAVAWRELREAVEFHQKIIGLMNRINQTFYWNYVSQMGASTFMIC : 310
BlatOR47b   : PDEHPIAFVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCENIRHLGIVAAG---ASSSTSEAVAWRELREAVLFHQKIIGLMNRINQTFYWNYVSQMGASTFMIC : 310
BoleOR47b   : PDEHPMAFVCVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCENIRHLGNGATG---DCSSTSEVVVWRELRETVEFHQKIIGLMNRINQTFYWNYVSQMGASTFMIC : 310
BminOR47b   : PDEHPMAFACVYFFQCFCTLYMLVAIVVMDSLGGNSFNQTTLNLRILCENIRHLGESAAGTAGACSITSELVVWRELREAVEFHQKIIGLMNRINQTFYWNYVSQMGASTFMIC : 313
CcapOR47b   : PDKHHITFVCVYAFQCFCTLYMLVSIVVMDSLGGNSFNQTTLNLQILCESIRHIGYAGGR----STTITEAVLWRELRENVEFHVKIIELVDGINHTFYWNYVSQMGASTFMIC : 332
RzepOR47b   : RDEHPIAFACIYAFQCFCVLYMLVSIVVMDSLGGNCFNQTTLNLRILCENIRNIRG----------GATEEVIWHELRVTVEFHQQIIGLIDHLNDVFYWNYVSQMGASTFMIC : 303
DmelOR47b   : LDLHPYTFWFLYIWQSLTSQHNLMSILMVDMVGISTILQTALNLKLLCIEIRKLGD---------MEVSDKRFHEEFCRVVRFHQHIIKLVGKANRAFNGAFNAQLMASFSLIS : 299
              pDeHp  F cvY fQcfctlymLv ivvmDslGgnsFnQTtLNLriLCeniR lg             se v wrel e VeFHq II l   iN tFywnyvsQmgAStfmIc

                  350       360       370       380       390       400       410       420       430       440       450
BcucOR47bX1 : LTAFEALLAQDK-PMVALKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATAAYEVRTWYRHSPLLQRQLIFIIKRAQKPLEFRAKFLFGFTFASFTSILSTSYSYFTLLRTMSD : 417
BcucOR46bX2 : LTAFEALLAQDK-PMVALKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATAAYEVRTWYRHSPLLQRQLIFIIKRAQKPLEFRAKFLFGFTFASFTSILSTSYSYFTLLRTMSD : 406
BdorOR47b   : LTAFEALLAQDK-PMVAMKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATAAYEIRAWYEHSPLLQRQLMFIIKRAQKPLEFRAKFLFGFTFASFTSILSTSYSYFALLRTMSD : 423
BlatOR47b   : LTAFEALLAQDK-PMVAMKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATVAYEIRAWYEHSPLLQRQLMFIIKRAQKPLEFRAKFLFGFTFASFTSILSTSYSYFALLRTMSD : 423
BoleOR47b   : LTAFEALLAQDK-PMVAMKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATAAYEVRTWYEHSPLLQRQLMFIIKRAQRPLEFRAKFLFGFTFASFTSILSTSYSYFALLRTMSD : 423
BminOR47b   : LTAFEALLAQDK-PMVAMKFQTYMFSAFMQLLYWCWMGNRTYYDSMEVATAAYDVHAWYEHSPLLQRQIMFIIKRAQKPLEFRAKFLFGFTFASFTSILSTSYSYFALLRTMSD : 426
CcapOR47b   : LTAFEALLAKDQ-PMVAMKFQTYMFSAFMQLFYWCFMGNRTYYDSMEVATAAYEVYAWYEHSPRLQRNLLFMIKRAQKPLEFRSKFFFGFTFASFNSILSTSYSYFALLRTMND : 445
RzepOR47b   : LTAFEALLAKDQ-PMVAMKFQMYMFSAFMQLFYWCSMGNRTYYESMEVATAAFQVHTWYNHSPRLQRNLMFMIKRAQRPLEFRAKFFFGFTFASFTSILSTSYSYFALLRTMSD : 416
DmelOR47b   : ISTFFTMAAAAVDFKMAAKEVLLMLVAFIQLSLWCVSGTLVLTQSVEVAQAAFDINDWHTKSFGIQRDISFVIIRAQKPLMYVAEFLFFTLGTYMLVLKNCNRLLAIMQESM- : 412
              ltaFEallA d  PmvA KFqtyMfsAFmQL yWC mGnrtYydSmEVAtaAy    Wy hSP lQR l F IkRAQkPLefrakF fgFTfasftsiLstsYsyfaLlrtmsd
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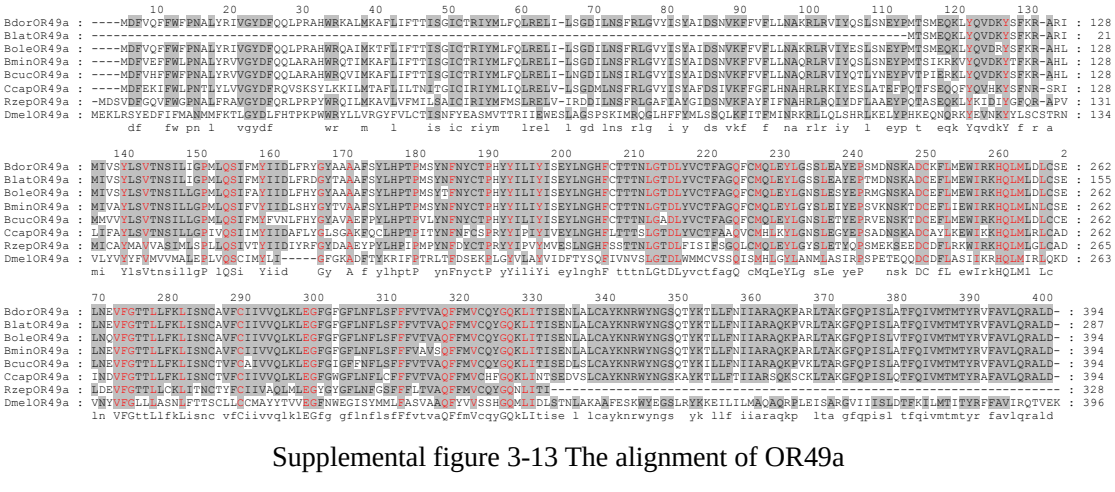
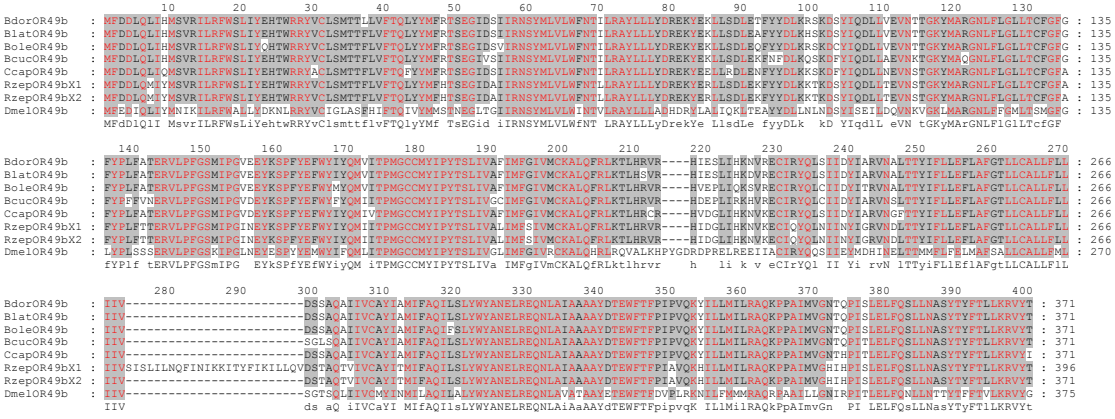
Supplemental figure 3-12 The alignment of OR47b



Supplemental figure 3-13 The alignment of OR49a



Supplemental figure 3-14 The alignment of OR49b

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                    10        20        30        40        50        60        70        80        90       100       110
BminOR59a1  : MS--------------------PSPLPLRQPS---VAAVDTRSFFKLHWTCFKVLG---IKASNSNTYYLGYSVLVQVLVTLCYPLHLVLALFSSPDASTNIQNLAVCVT :  84
BcucOR59a1  : MS--------------------PSPLSLPPPPP-PLAAVDTRSFFKLHWTCFRVLG---INAPSSNTY---YSVLLQVLVTLCYPFHLALALFSSPDASINIQNLTVCVT :  83
BdorOR59a1  : MS--------------------PSPLSLPQQA---LAAVDTRSFFKLHWTCFKVLG---INASTSSAYYLGYSLLLQVLVTLCYPLHLALVLFDSADASKNIQNLAICVI :  84
BdorOR59a1p : MS---------------------TSPLSVPQQA---LAAVDTRSFFKLHWTCFK-------------------------------------------------------- :  30
BlatOR59a1  : MS--------------------PSALSVPQPA---LDAVDTRSFLKLHWACFKVLG---INASNSSVYYRGYSVLLHVLVTFCYPLHLALALFSSADGSTNIQNLAACVV :  84
CcapOR59a1  : MSSPLISSSSSSPSPSPSPSPSPSPLPFPLPQRLAATAVDTRSFFKLHWACFKVLG---VVAPTADVFYLVYSVLLHLLVNLCYPLHLALMLFRSPNSSANIQNLAVCVT : 107
RzepOR59a1  : MS---------------VHSPLPSPLVLPLP-----AALDTRSFFKLHWTCFKVLG---IIAPTSNAYYFGYSVLLHLLVTFCYPLHLAMALFSNTNASANIQNLAVCVT :  87
BdorOR59a2  : MS---------------------------------QPVNSNAFFKIHWLGFRICGGD-LTVCKYRLVYLPYALMVTALVTFCYPLHLALALFRNGSLAGNIKNLAVCVT :  75
BlatOR59a2  : MS---------------------------------QPVNSNAFFKILWLGFRICXGD-LTVCKYRLVYLAYALMVTALVTLCYPLHLALALFRTGSLAGNIKNLAVCVT :  75
BoleOR59a2  : MS---------------------------------QPVNSNAFFKIHWLGFRICGGD-LSVNKYRLVYLAYALMVTALVTFCYPLHLALALFRNGSVAGNIKNLAVCVT :  75
BminOR59a2  : MN---------------------------------QSVNSNAFFKIHWLGFRICGGD-LSVNKYRLIYLAYALTVTALVTLCYPLHLALALFRNGSLAGNIKNLAVCVT :  75
BcucOR59a2  : MN---------------------------------QPINSNVFFKIHWLGFRICGGD-STVNKYRLVYLAYALMVTVLVTVCYPLHLALALFRNGSLGGNIKNLAVCVT :  75
DmelOR59a   : MA--------------------------------EVRVDSLEFFKSHWTAWRYLGVAHFRVENWKNLYVFYSIVSNLLVTLCYPVHLGISLFRNRTITEDILNLTTFAT :  77
BoleOR5-3   : MD-------------------------------KPSVVDSRQFFHTHWRLWLLLG-CVREPVRYQLLYSLYRPIVNALIILFYPGTILLALYNSGNLNDFLQTLPICAA :  77
BcucOR5-3   : MN--------------------------------NSPPVDSRQFFRTHWRLWLLLG-CVREPVHYQLLYRLYSTVVNALIMLFYPGTILIALYNSANLTDFLQTLPICAA :  77
              M                                   v    Ffk hW  f   g            y  y      lv  cyp hl   lf        i nl  c

                   120       130       140       150       160       170       180       190       200       210       220
BminOR59a1  : CVVCSVKFIIYASRMSRISELESIIATMDARAQSLYERRYFMELRKEMRRITFCFLGIYGVVCVTAELMFIFRNEH-TLLYPARLPFDWRATKFKFYLAHAYQIVGISYQ : 193
BcucOR59a1  : CVACSMKFVFYATRLSRIRELESIIAALDARARSLCERRYFVQLRKELRRITICFLCIYTVVGVTAELMFIFHNER-NLLYPAWFPFDWRASNLKFYAAHSYQIVGISYQ : 192
BdorOR59a1  : CVVCSVKFAIYAARMSRIRVLESIIATLDARAQSPCERRYFVEIRKEIRRITLGFLSIYAAVAVTAELMFLLRNEH-NLIYPGWFPFDWRATDLKFYAANFYQIVGVTYQ : 193
BdorOR59a1p : ---------------------------LDARAQSPCERRYFVELRKEMRRITFGFLSIYAVVAVTAELMFFRNEH-NLLYPAWFPFDWRASDLKFYAAHSYQIVGISYQ : 112
BlatOR59a1  : CSICSAKFVIYVTRMSRIRELESIIATLDARAQSPCERRYFVQLRKEIRRITFGFLSIYSAVGVTAELMVFSSNEH-KLFYPAWFPFDWRASDLKFYVAHSYQFVGVSYQ : 193
CcapOR59a1  : CMACSVKFVIYTMKMWRIRELESIVAALDARACSPRERGYFLKLRKDMRRITIGFLSIYAFVGVTAELMFIFCNEH-NLLYPAWFPFDWRASKLKFYAAHFYQIVGISYL : 216
RzepOR59a1  : CVACSMKFIIYATKMERLRELEAIMAALDERVNSSRERRYLAQLRKEIRHIIVGFLSIYTLVGVTAELRFIFRNEH-NLLYPAWFPFDWRASDLKFYAAHLYQIVGISFQ : 196
BdorOR59a2  : CIACSLKFLIYTRKLRIMREIEQTFAELDARVSSEEELKYFALMRTSVRNVVAVFVCAYAAVGVTAELAFLLSKER-SLLYPAWFPFDWRASTRNFYVANVYQIVGICYQ : 184
BlatOR59a2  : CIACSLKFLIYTRKLRIIREIEHTFAELDARVSSEEERKYFALMHTSVRNVVSVFVCAYAAVGVTAELAFLLSNER-SLLYPAWFPFDWRASTRNFYVANVYQIVGISYQ : 184
BoleOR59a2  : CIACSLKFLIYTRKLGIMREIEQTFSELLDSRVSSEVERKYFAWMRISVRNVVSVFLCAYAAVGVTAELAFLLSKER-SLLYPAWFPLDWRASTRNFYVANVYQFVGISYQ : 184
BminOR59a2  : CIACSLKFLIYTRKLRIMREIEQTFSELLDARVSSEVERKYFAWMRTSVRNVVSVFVCAYAAVAVTAELAFLISKER-SLLYPAWFPFDWRASPRNFYVANVYQFVGISYQ : 184
BcucOR59a2  : CIACSSKFLIYTRKLRIMHEIEQTFAELLDARVSSEVERKYFARLRISVRNVVSVFVCAYAAVGMTAELAFLLSKER-SLLYPAWFPFDWRASTRNFYVANVYQFVGISYQ : 184
DmelOR59a   : CTACSVKCLLYAYNIKDVLEMERLLRLLDERVVGPEQRSIYGQVRVQLRNVLYVFIGIYMPCALFAELSFLFKEER-GLMYPAWFPFDWLHSTRNYYIANAYQIVGISFQ : 186
BoleOR5-3   : ALACSAKYISYYRKLKLVRQAEQVFNALDGEVLLEEDRVFFAGIHRATNLILNTLCGLCAFFFVITVMA---SIENRDLAIAIELPFDWHASTASYVGAVALDLFLLACD : 184
BcucOR5-3   : ALACSAKYISYYRRLGLVRQAEQIFNALDEQVLLPEDREFYAGIHRGTNLILNTLRGLCIFFMAITVMAFASSIEERGLAFAIELPFDWRKSSVAYVGAVGLELLLLSCD : 187
              c  cs k   y          e     lD r  s  er yf   r   r     f   y  v vtael f    E   L ypawfPfDWras   fy A  yq vg s q

                   230       240       250       260       270       280       290       300       310       320       330
BminOR59a1  : LLQNFVNDCFPTVALALLSAHIKLLGIRVSQIGYAAALLETNEEELLCCIKDQEQLYNIFIPSVLHIIQNIISLPMFLQFTVTAVNICLALNALLFFVDAPFDRLYYLAY : 303
BcucOR59a1  : LLQNFVNDCFPTMALALLSAHIKLLGIRVSQIGHETASLGANEAELLHCIKDQEQLYN-----VLNIIQNIISLPMFLQFTVTAINLCLGMAALLYFVDAPFDRLYYLAY : 297
BdorOR59a1  : LLQNFINNCLPTIALALLSAHIKLLGIRVSQIGYAGESPEANEEELLCCIKDQEQLYN-----MLSVIQNIISLPIFLQFTVTAVNICLPLAALLCYVDAPFDRLFFVVY : 298
BdorOR59a1p : LLQNFVNDCLPTMALALLSAHIKLLGMRVSKIGYATESSAANEEELLYCIKDQEQLYN-----MLNVIQNIISLPMFLQFTVTAINICLPVAALLFYVDAPFDRLYFLVY : 217
BlatOR59a1  : LLQNFVNDFLPTMGLALLSAHIKLLGIRVSQIGYATESLAANEEELLCCIKDQKQLYN-----MLNVIQNIMSLPMFLQFAVTAVNICLSLAALLFYVDAPFDRLYFVSY : 298
CcapOR59a1  : LLQNFVNDCFPTMALALLSAHIKLLGIRVSQIGHEAKSLDANELELLRCIKDQEHLFN-----MLNTIQNIISLPMFLQFTVTAINICLAMAALFFFVDAPFDRLYYLAY : 321
RzepOR59a1  : LLQNFVNDCFPTMTLVLLSAHIKLLGIRVSQIGYANRSLDENEEELFRCIKDQEQLYN-----MLNVIQNIISLPMFLQFTVTAFNICLAMAALFFFVDAPFDRLYYFTY : 301
BdorOR59a2  : IFQNFIDDTFPPITCCLLSGHIKLLGIRVSRIGYDGVHLADNERELVRCIKDQKNLYK-----LFDLLQEVMSWPMFIQFTVTAFNICVAMVVMLFYVDTPFERLYYLVY : 289
BlatOR59a2  : IFQNFIDDTFPPITCCLLSGHIKLLGIRVSRIGYDRVHLPDNERELVRCIKDQKNLYK-----LFDLLQEVMSWPMFIQFTVTAFNICVAMVVMLFYVDTPFERLYYLVY : 289
BoleOR59a2  : IFQNFINDTFPPITCCLLSGHIKLLGIRVSRIGYDCVRLQDNERELVRCIKDQKNLYK-----LFDLLQEVMSWPMFIQFTVTAFNICVAMVVMLFYVDTPFERLYYLIY : 289
BminOR59a2  : IYQNFIDDTFPPITCCLLSGHIKLLGLRVSRIGNDCVHMQDNELELVRCIKDQKNLYK-----LFDLLQEVMSWPMFIQFTVTAFNICVAMIVMLFYVDTPFERLYYLVY : 289
BcucOR59a2  : IFQNFIDDTFPPITCCLLSGHIKLLGIRVSRIGYDCVNRQDNERELVRCIKDQKNLYK-----LFVLLQEVMSWPMFIQLTVTAFNICVAMFVMLFFVDTPFERLYYLVY : 289
DmelOR59a   : LLQNYVSDCFPAVVLCLISSHIKMLYNRFEEVGLDPAR--DAEKDLEACITDHKHILE-----LFRRIEAFISLPMLIQFTVTAINVCIGLAALVFFVSEPMARMYFIFY : 289
BoleOR5-3   : LLQSLVNDSFPAVALCILSNHTRLLGARLSRIGHTSKDVQANIRELQHCIIDHQRLYR-----LLAIIEEIISMPVFVQYAVTAFQDQFTLITFIFYTNTISDKLLYLTY : 289
BcucOR5-3   : LLQSLANDSFPAIALCVLSNHTRLLGARLARIGHTSKDVQANIREMQRCIIDHQRLYR-----LQAIIEEIISMPVFIQYAVTAFQDQFTLITFIFYTNTVSDKVLYLTY : 292
                Qnf  d fP     llS HiklLg Rvs iG        ne el  CIkDq  ly           q   S Pmf QftVTA n C       f vd pf rly   Y

                   340       350       360       370       380       390       400       410       420
BminOR59a1  : LLSMPLEIFTI-------------------------------------------------------------------------- : 314
BcucOR59a1  : LLALPLQIFPICYYGTTFQLLFDKLHVEMFASNWVEQTHKFRKHMILFCERSLMSQTAMAGGIVRIHLDTFISTCKAAYSLLAVIMKMNE- : 387
BdorOR59a1  : LFAVPLEIFPICYYGTTFQLLFDKLHVEMFFSNWVEQTHKYRKHMILICERSLKNQTATAGVIIRIHLDTFVSTCKTAYSLLAVIMKMNE- : 388
BdorOR59a1p : LLSLPLEIFPICYYGTTFQLLFDKLHVEMFCSNW------------------------------------------------------ : 251
BlatOR59a1  : LIAVPLEIFPICYYGTTFQLLFDKLHVEMFCSNWVEQTQKFRKNMVIFCERSLKSHTAMAGGIVRINLDTFVSICKTAYSLLAVIMKMNE- : 388
CcapOR59a1  : FLSMPLEIFPTCYYGTDFQLLFETLHIEMYASNWVEQTQKFRKHMILFNERSLKKEVAMAGGMIRIHLDTFVSTCKGAYSLLAVIMKMNE- : 411
RzepOR59a1  : FLSMPLQIFPTCYYGTDFQLLFEKLHIEMYSSNWVEQTQKFRKHMILFCERSLKQHTAMAGGIVRIHLDTFVSTCKGAYSLLAVIMKMNE- : 391
BdorOR59a2  : FISMPLQIFPICYYGSSLQFLFGQLQYEVFRCNWPDQTRHFKKQMILFTERALKTTTALAGGMVKIHLDTFFATVKGAYSLFAVIMKVK-- : 378
BlatOR59a2  : FISMPLQIFPICYYGSSLQLLFGQLQYEVFRCNWPDQTRHFKKQMILFTERALKTTTALAGGMVKIHLDTFFATVKGAYSLFAVIMKVK-- : 378
BoleOR59a2  : FISMPLQIFPICYYGSSLQLLFGQLQYEVFRCNWTDQTRRFKKQMMLFTERALKTTTGLAGGMIKIHLDTFFATVKGAYSLFAVIMKVK-- : 378
BminOR59a2  : FVSMPLQIFPICYYGSSLQLLFGQLQYEVFRCNWIDQTRRFKKQMMLFTERALKTTTALAGGMIKIHLDTFFATVKGAYSLFAVIMKVK-- : 378
BcucOR59a2  : FVSMPLQIFPICYYGSSLQHLFSQLQYDVFRCNWTDQTPRFKKQMMLFTERALKTTTALAGGMIKIHLDTFFATVKGAYSLFAVIMKVK-- : 378
DmelOR59a   : SLAMPLQIFPSCFFGTDNEYWFGRLHYAAFSCNWHTQNRSFKRKMMLFVEQSLKKSTAVAGGMMRIHLDTFFSTLKGAYSLFTIIIRMRK- : 379
BoleOR5-3   : LLALQLQIFPICYYGTACAQSMEDLQQKIFASNWVEQDQVYRRLVTIISQCSLKRTTAYAAGLIPIHLGTFVKTLKGAYSFYTFVNGVRKV : 380
BcucOR5-3   : LLALQLQIFPTCYYGTACAQSMDDLQQEIYASNWVEQNQVYRRLVTIFSQRTLKSTTTYAAGLIPIHLSAFVKTLQGAYSFYTFVDGVRKV : 383
                  pL IFp cyyg       f  l        nw  q                lk  t  a g   ihl tf  t k ays
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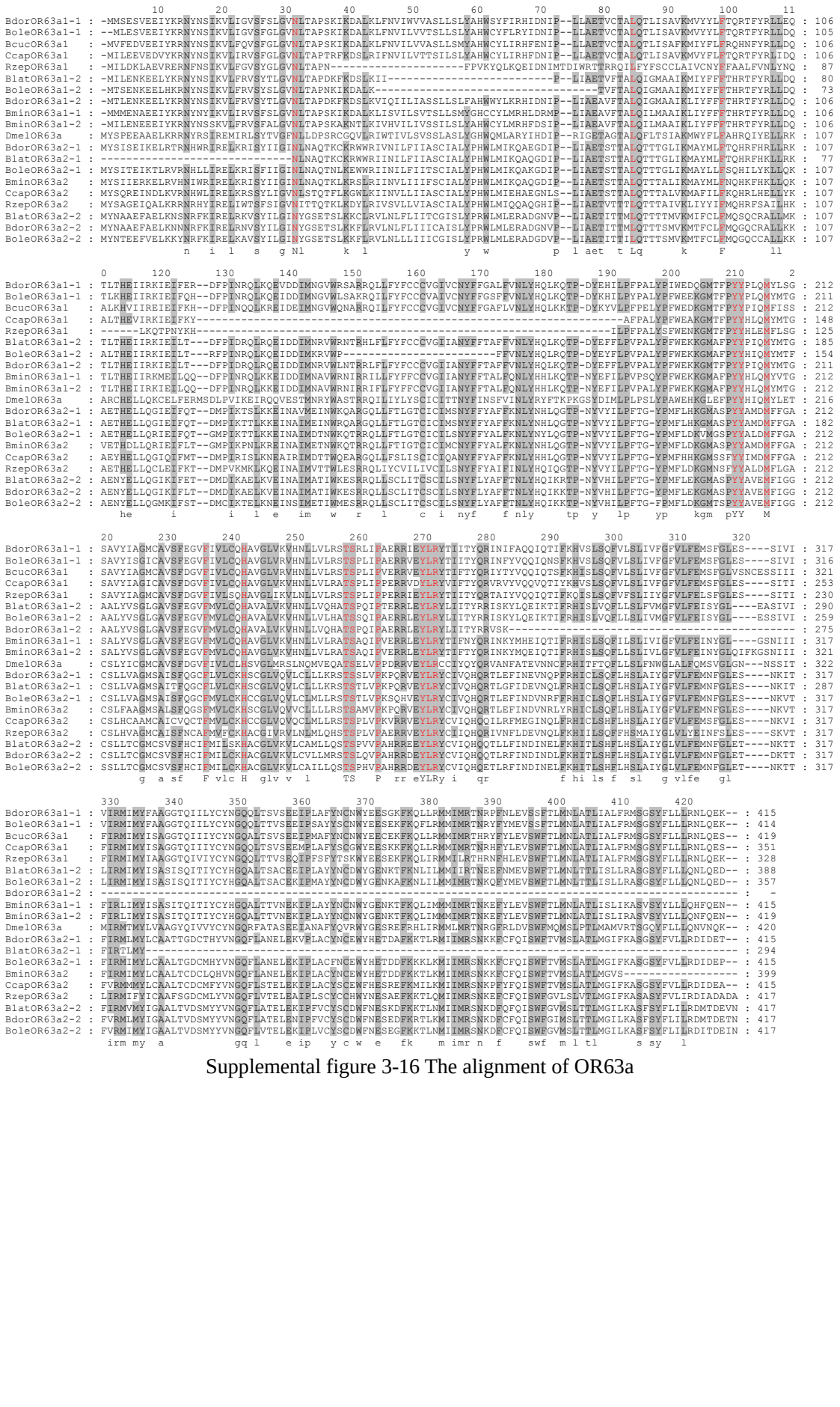
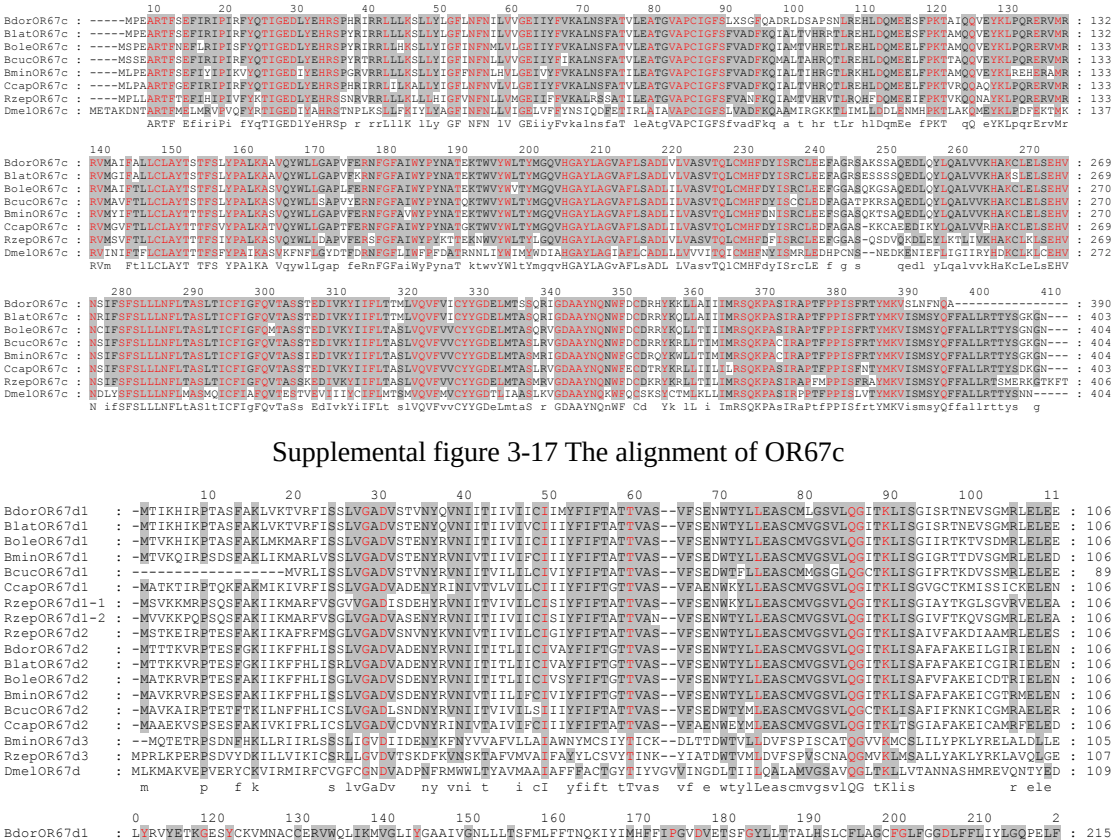
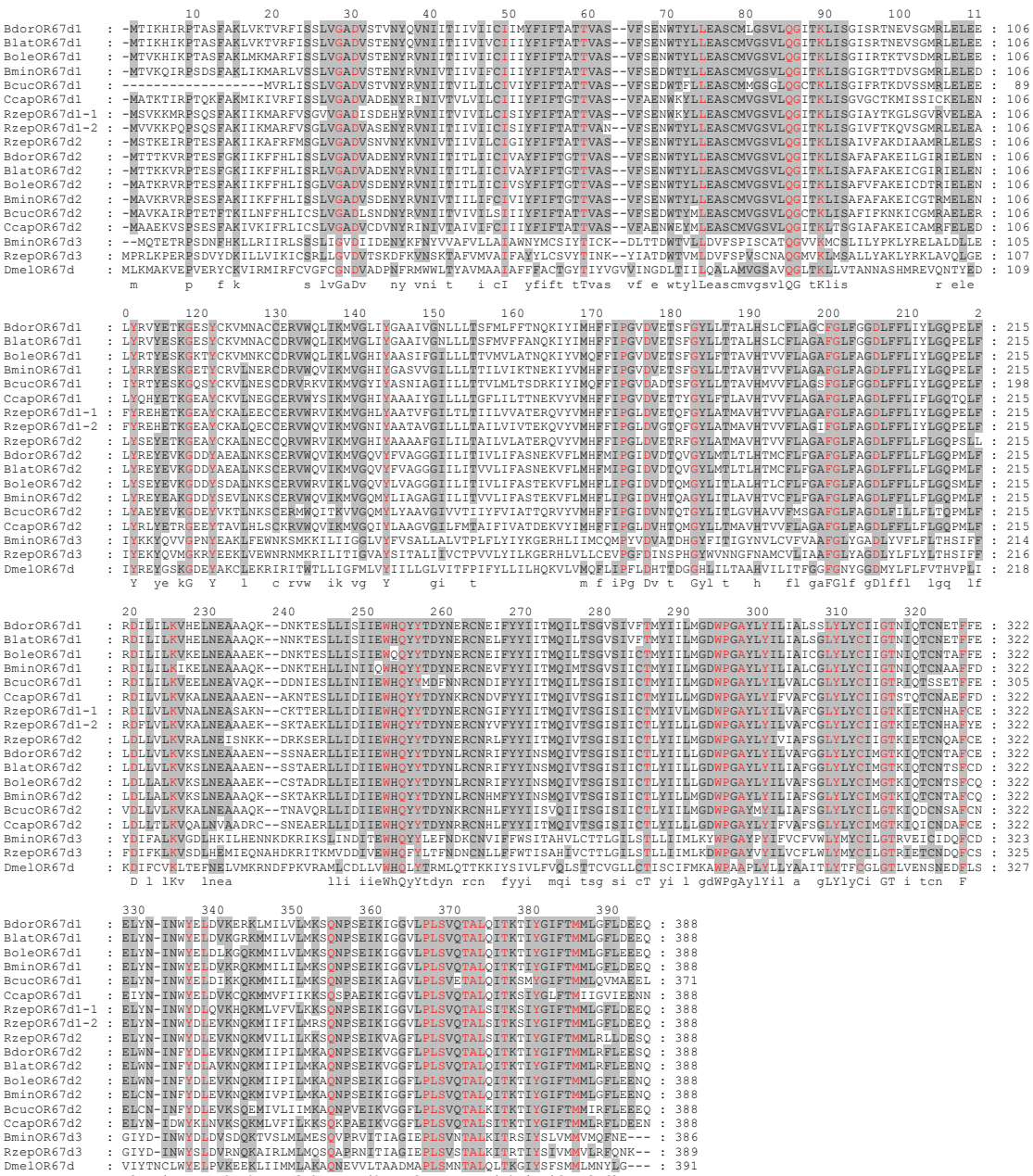
Supplemental figure 3-15 The alignment of OR59a



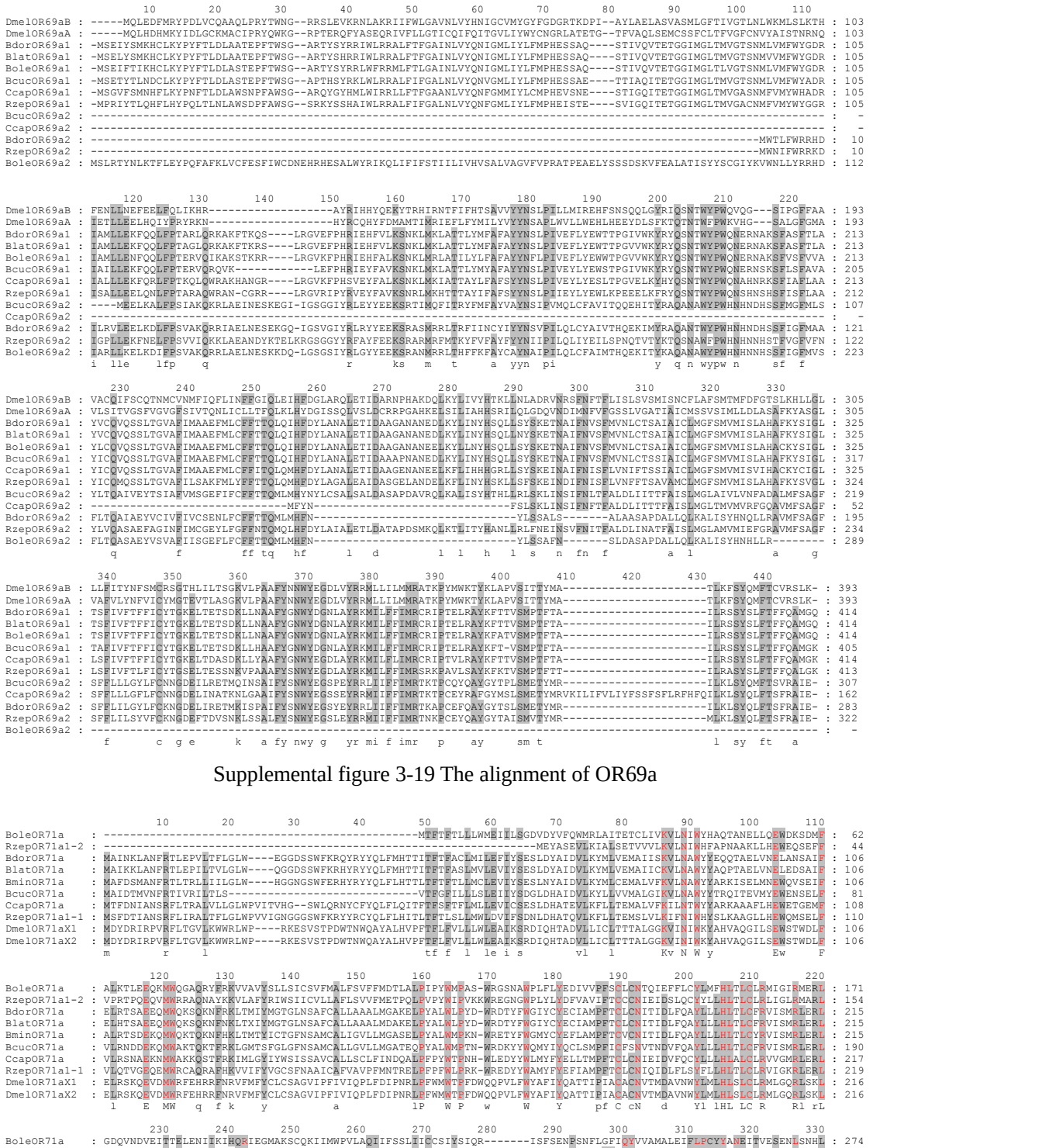
Supplemental figure 3-16 The alignment of OR63a



Supplemental figure 3-17 The alignment of OR67c



Supplemental figure 3-18 The alignment of OR67d



Supplemental figure 3-19 The alignment of OR69a

Supplemental figure 3-20 The alignment of OR71a

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                    10        20        30        40        50        60        70        80        90       100       110
BdorOR74a1 : ------MLYRPRLKNGKLIPLSWPVAAYRLLNHICWPLRDDASYLLRLYDRFFWAFGFFIFMQHNDAELRYIIVNNNNLDEMLICGPTYLVLVEIHLRAFQLGLKKEPFKR : 105
BlatOR74a1 : ------MLYRPRLKNGKLIPLSWPVAAYRLLNHVCWPLRDDASYLLRLYDRFFWAFGFCIFMQHNDAELRYIIVNNNNLDEMLICGPTYLILVEIHLRAFQLGLKKDAFKR : 105
BoleOR74a1 : ------MLYRPRLENGKLIPLSWPVAAYRLLNHVCWPLQDDASWLQRLFDRFFWAFGFFIFMQHNDAELRYIIRNNNNLDEMLICGPTYLILVEIHLRAFQLGLKKEAFKR : 105
BminOR74a1 : ------MLYRPRLENGKLISLSWPIAAYRLLNNICWPLQDDATQLERLFDRFLWAFGFLIFMQHNDAELRYIILNNNNLDEMLICGPTYLILVEIHLRAFQLGLKKNAFKR : 105
BcucOR74a1 : ------MLYRPRLNNGKLIPLSWPIVAYRLLNNICWPLRDHASLLERLFDRFFWSLGFFIFVQHNDAELRYILVNNNNLDEMLICGPTYLILVEIHLRAFQLGLNKEAFKR : 105
CcapOR74a1 : ------MLYRPRLPNGKLIPLSWPLAAYRLLNNICWPLRDNANRLERLFDRFCWALGFFIFIQHNDAELRYILSNNNNLDQMLICGPTYLILVEAHLRAFQLGLKKNNFKN : 105
RzepOR74a1 : ------MLYRPNVSNKELIPLSWPLAAYRLLNNICWPLRDGANLPERLFDRFCWWLCFIIFIQHNDAELRYIVVNRDDLDQMLTCVPEYLILIFIHIRAFQLGLKKDDFKT : 105
DmelOR74a  : ---MSFHRYRPRLPGGELAPMPWPVSLYRVLNHVAWPLEAESGRWTVFLDRLMIFLGFLVFCEHNEVDFHYLIANRQDMDNMLTGLPTYLILVEMQIRCFQLAWHKDRFRA : 108
BdorOR74a2 : MRYLPISYHKPLLPNGLHPFIDWQLYGFFCAN--GWPLAAHITKTRYIADIMVTIMQFMSEGMVLIGEAVVMHDNLDNISFVCTVLAPNLILFFMMLRAYNIIYRRNSFRT : 109
BlatOR74a2 : ------------------------------------PLAAHITRTRYIADIMVTIMQFMSESMVLIGEAVVMQNNLDNISFVCTVLAPNLILFFMMLRAYNIIYRRNSFRT :  75
BoleOR74a2 : MRYLPISYHKPLLPNGRHPFIDWQIYGFLCAN--CWPLAALITKTRYIVDIMVIIMQFMSESMVLIGEAVVMHDNLDNISFVCTVLAPNLILFFMMLRVYNIIYSRNSFRT : 109
BcucOR74a2 : ------------------------------------------------------MVTIAQFMSESMVLIGEGIVMHDNLDNISFVCTVLAPNLILIFMMLRAYNIIYRRSSFRK :  60
BminOR74a2 : MRYLPISYHKPLLPNGRHPFIDWQLYGFFCSN--GWPLAAHITKTRYIVDILVTMMQFMSESMVLIGEAVVMYDNLDNISFVCTVLAPNLILFFMMLRAYNIIYKRNSFRT : 109
CcapOR74a2 : MRYLPSSYHKPLLPNGRHPFIDWQLYGFVCSN--CWPLARDITKTRRIIDMVITAMQFMSESMVLSGETIAMRNNLDDISFVCMVLAPYLILIFLMLRAYNIIYKRNSFRT : 109
RzepOR74a2 : MRYLPSSYHRPLLPNGQYPFIDWQLYGYMGAC--CWPPAINISKWRYIVDAVMIMCQFISECSVLFGEMQLMCASLDDISFVCAILAPFLILFFMMLRAYNIIYKRASFRV : 109
                  p l ng   p  w       n   wpl          d       F         e     n              LiL E  lRa         F

                   120       130       140       150       160       170       180       190       200       210       220
BdorOR74a1 : FLQKFYAEIYIDESSHPKLYANIQKSLRPIWFYSLLYFSTLSSYVIMPVVNYLNNVKAPLYKMYYPFDITP-NPIYVAIVLSNIWVGFTVITMVSGEDNVLSEVMLHLNGR : 215
BlatOR74a1 : FLQKFYATIYIDESSHPKLYANIQKSLRPIWFYSLLYFSTLSSYIIIPIINYLNNVKVPLYKMYYPFDITS-NAIYVAIVLSNIWVGFTVITMVTGEDNVLSEVMLHLNGR : 215
BoleOR74a1 : FLQNFYAEIYIDQSSHSKLYANIQKRLRPIWFNSLLYFSTLSSYVIMPLINYLNNVKVPLYKMYYPFDITP-NPIYVAIVLSNIWVGFTVITMVSGEDNILSEVLLHLNGR : 215
BminOR74a1 : FLQKFYAEIYIDEVSHPKLHGNMRKRLRPIWFYSFLYFGTLSSYVIMPLINYLKNVKAPLYKMYYPIDIMP-NPIYVAVVLSNIWVGFTVITMVSGEDNVLSEVMIHLNGR : 215
BcucOR74a1 : FLQKFYAEIYIDEPAHPKLYASIQKRLRPIWFYSLLYFSTLSSYVIMPFVNYLNNVKAPLYKMYYPFDITP-NPIYVAVVLSNIWVGFTVITMVSGEDNILSEVMLHLNGR : 215
CcapOR74a1 : FLKRYYAEIYIDKPTHPKLYANIQKRLRPIWFYSFLYYSTLFSYVITPLTNYLKNVKAPLFKMYYPFDITP-NPIYVAVVLSNIWVGFTVISLVAGEDNILSEVMLHLNGR : 215
RzepOR74a1 : FLKKFYAEVYVDKSSHPKLYANIQQRLRPIWFFSALYYMTLSSFFLTLNNNLNNAKEPLYKMYYPFDITP-HAIYVAIVFSNIWVGLIAITTISGEDNLLSEVMLHLNGR : 215
DmelOR74a  : LLQRFYAEIYVSEEMEPHLFASIQRQMLATRVNSTVYLLALLNFFLVPVTNVIYHRREMLYKQVYPFDNTQ-LHFFIPLLVLNFWVGFIITSMLFGELNVMGELMMHLNAR : 218
BdorOR74a2 : HIEEFYKKIYIQRTWNPELFEKIRRQQLPTKYSTFTYIITLVTYVYVPVSGLIKNERLVPFPINFGFDYTVPWPRYLVFLTMSMWTGFAVVGPLVAEANILAMQILHLNGR : 220
BlatOR74a2 : HIEEFYKKIYIQRTWTPELFEKIRRQQLPTKYSTFTYIITLVTYVYVPVSGLIKKERLVPFPINFGFDYTVPWPRYLVFLTMSMWTGFAVVGPLVAEANILAMQILHLNGR : 186
BoleOR74a2 : HIEEFYNKIYIQRSWKPEVFEKIRRQQLPTKYSTFTFIITLVTYVYVPVSGLFKNERLLPFPINFGFDYTVPWPRYLVFLAMSMWTGFAVVGPLIAEANILAMQILHLNGR : 220
BcucOR74a2 : HIEEFYKKIYVQRTWNPDLFEQIRRQQLPTKYSTCTYIITLVTYVYVPISGLIKNERLVPFPIRFSFDYTVPWPRYLVFLAMSIWTGFAVVGPLVAEPNLLAMQILHLNGR : 171
BminOR74a2 : HVEEFYKKIYIQRTWNPELFEKIRRQHLPTKYSTFTYIITLVTYVYVPISGLVKNERLLPFPIKFGFDYTVPWPRYVVFLAMSIWTGFAVVGPLIGEANMLAMQILHLNGR : 220
CcapOR74a2 : HIEEFYKKIYVQRTWNPELFEQIRRQHLPTKYSTFTYIITLVTYVYVPISGLVKNERLVPFPIQFSFDFTVPWPRYVVFLIMSIWTGFAVVGPLVSEANMLAMQILHLNGR : 220
RzepOR74a2 : HLEEFYKKIYIERSWNPELFEQIRRQQLPTKYSTSTYIITLVTYFYVPIMGLIHQQRLLPFPVIYKYDYKATFAGYLLFLAMALWTGFAVVGPLIAEANMLAMQILHLNAR : 220
                 fY  iY      p l   i     p       y  tL  y   p      n           fD t     y        W Gf v      E N l    lHLNgR

                   230       240       250       260       270       280       290       300       310       320       330
BdorOR74a1 : FLLLQQKLRHDAERLLHVVDDRNI-------ADGLRRRIIEAIEENVRLYKFAEDFEREFSFRIFVNLSFSAGLLCVLGFKVYT---------------------------- : 292
BlatOR74a1 : FLLLQQKLRHDAERLLHVVDDRNI-------ADGLRRRVIEAIEENVRLYKFAEDFEREFSFRIFVNLSFSAGLLCILGFKVYT---------------------------- : 292
BoleOR74a1 : FLLLQQKLRQDADRLLHIVDERNI-------ADELRRQIIEAVEENVRLYKFAEDFEREFSFRLFVSLSFSAGLLCVLGFKVYTNPMA--SFGFIFWICAKIMEMILVGQL : 317
BminOR74a1 : FLLLQQKLRQDAERLLHAADDRNI-------ADELRRRIVEAIKENVRLYKFAEDFKLEFSFRLFVNLSFSAGLICVLGFKVYT---------------------------- : 292
BcucOR74a1 : FLLLQQKLGQDAERLLHAGDDRNI-------ADDLRQRIVEAIEENVRLYKFAEDFEREFSFRLFVSLSFSAGLICVLGFKVYTNPMA--SFGFMFWICAKVMEMLLIGQL : 317
CcapOR74a1 : FLLLQQKLRQNADRLLHNTDGRYI-------ADALQDQIIEAIEENVRLYEFAKGFEREFSFRIFVNLSFSAGLLCVLCFKVYTNPMA--SYGFMFWICAKIMEMILVGQL : 317
RzepOR74a1 : FLLLQQKLRDDTKRLLDEANGKNVD------ADDLSRQIVEAIRENERLYKFAKEFEREFSFRIFTNLSFSAMLLCALGFKVYTNPMS--SFGFMFWICAKVMEMLLIGQL : 318
DmelOR74a  : YIQLGQDLRRSAQMLLKKSSSLNV-------AIAYRLNLTHILRRNAALRDFGQRVEKEFTLRIFVMFAFSAGLLCALFFKAFTNPWG--NVAYIVWFLAKFMELLALGML : 320
BdorOR74a2 : YSLLLEDLRNISRESIAEHEKCKRK-DNMLVTQRFRYRLYDIIRRNVELNDFAKSMQEQYSFRVFVMLALSATLLCVLGFLTATLGITAQNIRFVSWIIGKVVELLIFGRL : 330
BlatOR74a2 : YSLLLEDLRNIAKESIAEHEKCKWK-DNMLITQRFRYRLYDIIRRNVDMNDFAKSMQEQYSFRVFVMLALSATLLCVLGFLTATLGITAQNIRFVSWIIGKVVELLIFGRL : 296
BoleOR74a2 : YSLLLDDLRNISRESIVEHKNCKGK-DNMLITQRFRFRLYEIIRRNVELNDFAKSMQKQYSFRVFVMLALSATLLCVLGFLTATLGLTLKNIRFVSWIIGKVVELLIFGRL : 330
BcucOR74a2 : YSLLLQDLRKISKESIVEHERLKGK-DTLLVTQRFRYRLFEIIRRNVELNEFAKSLQEQYSFRVFVMMAMSATLLCVLGFLTATLGLTAQNIRFVSWIIGKVVELLIFGRL : 281
BminOR74a2 : YSLLLQDLRKISRDSIAEHERCKDK-DNMLVTQRFRCRLFEIIRRNVELNDFAKSLQEQYSFRVFVMMALSATLLCVLGFLTA---------------------------- : 302
CcapOR74a2 : YSLLLRDLRKIAREAIEEHEKCKGR-DKISVTQRFRYSLFDIIRRNVELNEFAKSLQDQYSFRVFVMMALSATLLCVLGFLTATLGLTAENIRFVSWIIGKVVELLIFGRL : 330
RzepOR74a2 : YTLLLRDLRKIAQNAIEWHAMHKGEGDNVSVTSRFRYGLIDVVRRNVELNKFAESLQEQYSFRVFVMMALSATLLCVLGFLTATIGLSTDNIRFVTWIIGKVIELLIFGRL : 331
                  lL   Lr                          r      i  Nv l  Fa       sfR Fv    SA LlCvLgF   t

                   340       350       360       370       380       390       400       410
BdorOR74a1 : -------VSRLS-------------------------------------------------------------------------- : 297
BlatOR74a1 : -------TNEMSYTFYECNWELVLLKSGDSKANVRLMKTLLLAISTIQKPFVLTGFKYFSVSLTAVLKILQGAGSYFTFLTSMR- : 369
BoleOR74a1 : GSTVIYTTNEMSSTFYECNWELVLLKSGDTKSNVRLMKTLLLAISTSQKPFVLTGFKYFSISLAAVLKILQGAGSYFTFLTSMRK : 402
BminOR74a1 : -------TNEMSSTFYESNWELVILRSRDTKANVRLMKTLLLAISTNQKPFVLTGFNYFSVSLTAVLKQQLASTNNNIPMADL-- : 368
BcucOR74a1 : GSSLIYTTNEISSTFYKSHWELVIQKSSDTNANVRLMKTLLLAITTSQKPFVLTGFNYFSVSLTAVLKILQGAGSYFTFLTSMRK : 402
CcapOR74a1 : GSTMIYTTNEVSSTFYECNWELVLMKSTDTKANVRLLKTLALAISTSGKPFVLTGFNYFSVSLTAVLKILQGAGSYFTFLTSMR- : 401
RzepOR74a1 : SSTLIATTNQISSAFYESSWELVIHQSKDSNANVRLMKLLVLAIGTSQKPFTLSGLNYFSVSLTAVLKILQGAGSYFTFLTSLR- : 402
DmelOR74a  : GSILLKTTDELGMMYYTADWEQVIHQSDNVGENVKLMKLVTLAIQLNSRPFFITGLNYFRVSLTAVLKIIQGAFSYFTFLNSMR- : 404
BdorOR74a2 : GTTLSTTTDKLSTSYYCCDWEDIILHSTNAEENKKLMKLIALAIHLNSNPFRLTGLNFSVVNYETVVAIFRGAGSYFTVIYAYR- : 414
BlatOR74a2 : GTTLSTTTDKLSTSYYCCDWEDVINHSTNAEENKKLMKLIALAIHLNSNPFRLTGLNFSVVNYETVVTILRGAGSYFTVIYAYR- : 380
BoleOR74a2 : GTTLSTTTDELSTSYYCCDWEDIILYSTNTEENKKLMKLIALAIHLNSKPFRLTGLNFSVVNYETVVAILRGAGSYFTVIYAYR- : 414
BcucOR74a2 : GTTLSTTTDELSTSYYCCDWEDVILHSTDAEENKKLMKLIALAVHLNSNPFRLTGLNFSVVNYETVVSILRGAGSYFTVIYAYR- : 365
BminOR74a2 : ------TTDELSTSYYCCDWEEVIFHSRDAEENKKIMKLIALAIHLNSKPFRLTGLNFSVVNYETVVSLAFC------------ : 368
CcapOR74a2 : GTTLSTTTNDLSTSYYCCDWEEIIFHSADAEENRKTMKLIALAIHLNSNPFQLTGLNFFVVNYETVVSILRGAGSYFTVIYAYR- : 414
RzepOR74a2 : GTTLSTTTNELSTSYYSCGWEDVILHSTDAVENAKLMKLMALAIHLNSNPFRLSGLAFFYVNYEVVVSILRGAGSYFTVIYAYR- : 415
                  tt   s   y   we     s     n  lmk   lai     pf ltg     v    v  i  ga syft     r
```
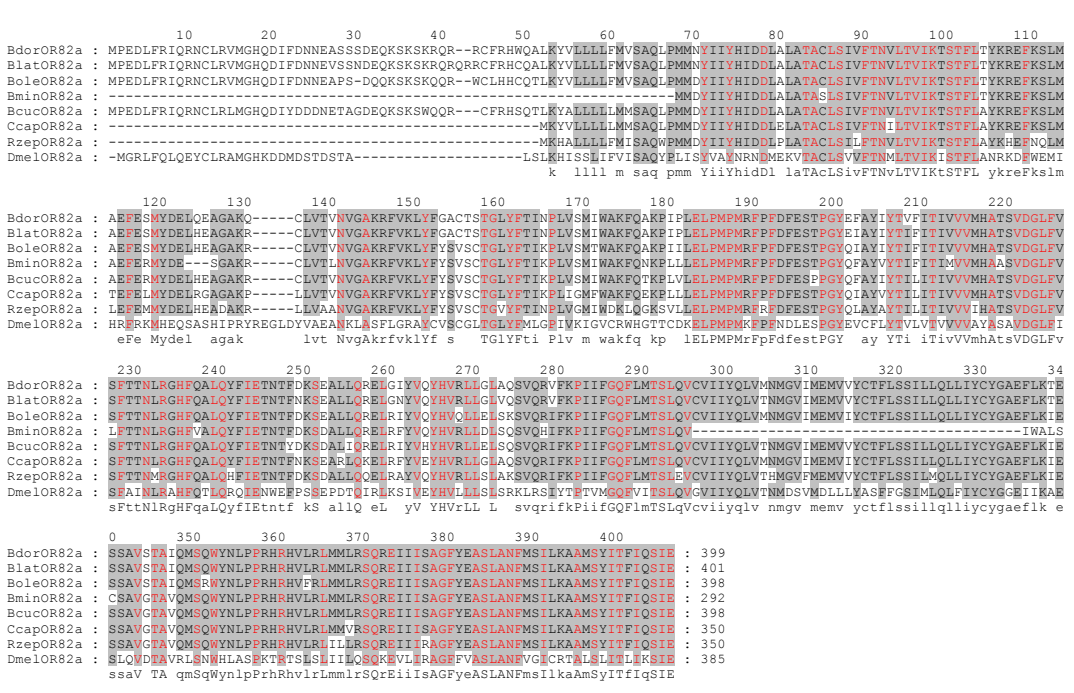
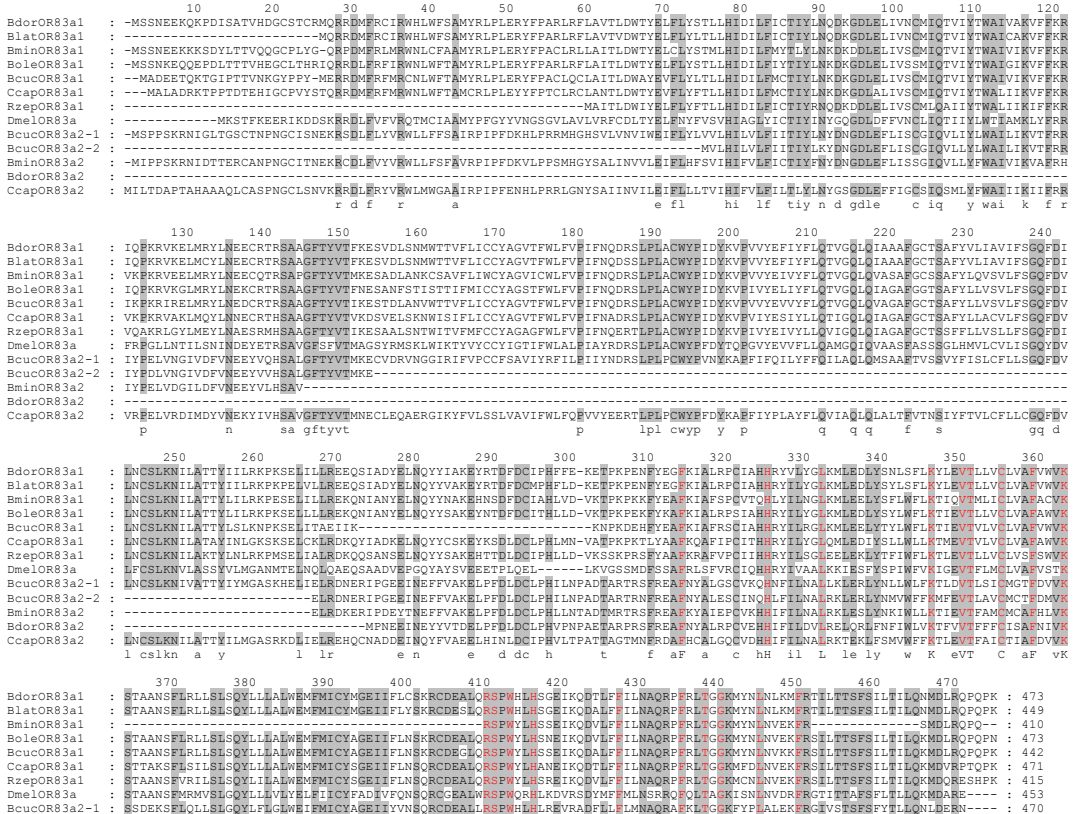

Supplemental figure 3-21 The alignment of OR74a



Supplemental figure 3-22 The alignment of OR82a



Supplemental figure 3-23 The alignment of OR83a

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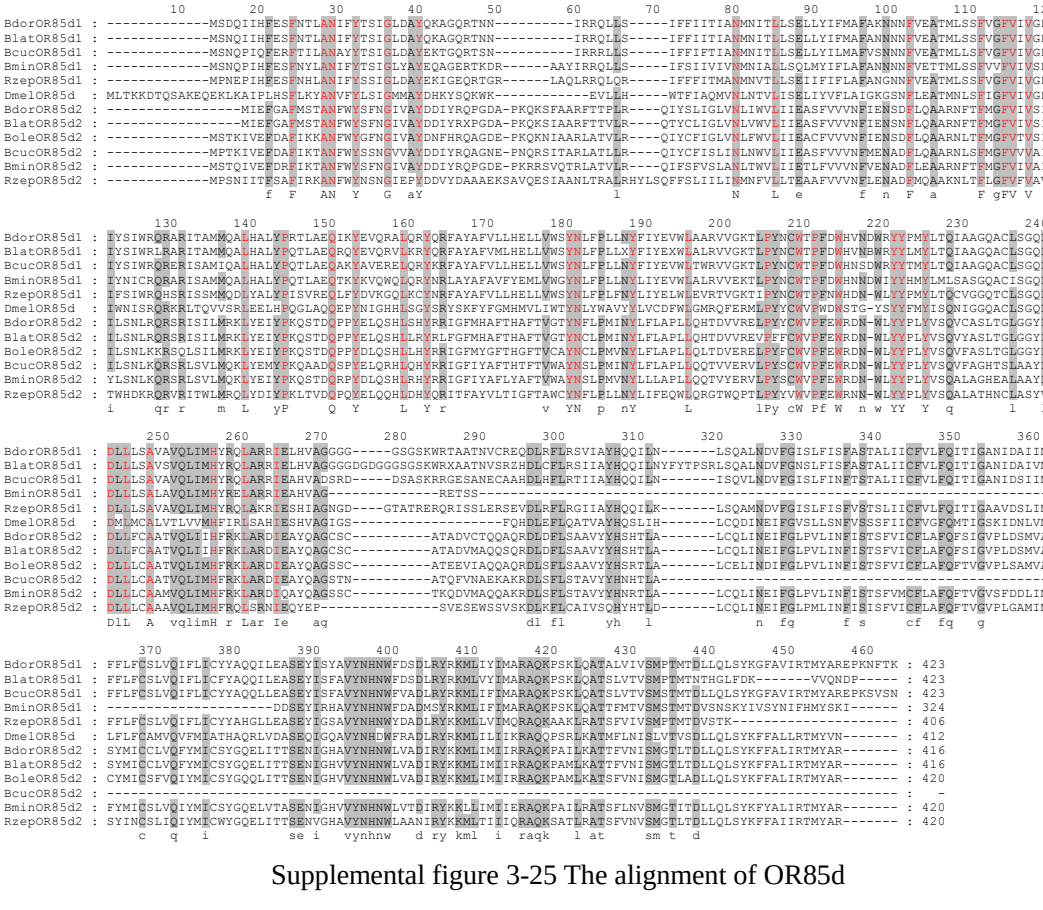
                        10        20        30        40        50        60        70        80        90       100       110
DmelOR85c     : -----------------MKFMKYAVFFYTSVGIEPYTIDSRSKKASLWSHLLFWANVINLSVIVFGEILYLGVAYSDGKFIDAVTVLSYIGFVIVGMSKMFFIWWKKTDLS :  94
DmelOR85b     : ----------------MEKLMKYASFFYTAVGIRPYTNGEESKMNKLIFHIVFWSNVINLSFVGLFESIYVYSAFMDNKFLEAVTALSYIGFVTVGMSKMFFIRWKKTAIT :  95
BdorOR85bc1   : ----------MSNIIRFEAFLRIPSFFYRSVGVDLWNTNGGP-----LQNAVFYISLFNVNVWLLSELIFAVLMLTKN-FIQATMTLSYAGFVLVGSIKMYFMWRKKAEMT :  95
BlatOR85bc1   : ----------MSNIIRFEAFLRIPSFFYRSVGIDLWNTNGGS-----LQSAVFYISLFNVNVWLLSELIFAVLMFTKN-FIQATMTLSYAGFVLVGSIKMYFMWRKKAEMT :  95
BoleOR85bc1   : ----------MPNVISFEAFLRIPSFFYRSVGVDLWNTNGGP-----LQNAVFYFGLINLNIWLLSELIFSVLMVSKN-FIQATMTLSYAGFVLVGTIKMFYMRRKKAEMT :  95
BcucOR85bc1   : MAPLRVCPSIMSKIIRFEAFLRIPNFFYRSVGVDLWNTDGGP-----LQDAVFYFGLLNVNVWLLSELVFAVLMVSKN-FIQATMTLSYAGFVLVGSIKMYFMWRKKAEMK : 105
CcapOR85bc1   : ---------MCENIESFEAFLRIPSFFYRSVGVDLWNTNGGS-----IQRFIFYFGFLNVNLWLLSELIFAIITVSEN-FIQATMTLSYAGFVLVGSIKMYFMWRKKTEMT :  96
RzepOR85bc1   : ----------MPDTIRFESFLRLPNFLYRSVGIDLWGTHGGL-----LQQALFYLCIINVNIWLISEVILALMIFGKN-IVQATMTLSYAGFVLVGFIKLYYMWRKKQELT :  95
BlatOR85bc2X1 : ----------MSTIIKFEQFLGLSSFFCYNIGIKLRGPNDGF-----WLNFWLYLASINLFLTVFAECIYIIMTIRSD-FIVAIMTLSYVSFIVVAYVKWYYLYNYQTERN :  95
BlatOR85bc2X2 : ------------------------------------------------------------------------MTIRSD-FIVAIMTLSYVSFIVVAYVKWYYLYNYQTERN :  38
BdorOR85bc2   : ----------MSTIIKFEKFLELASFFCYNIGIKLWGPNDGF-----WLNFWLYLTSINLFLTVFAECIYIIMTIRSD-FIVAIMTLSYVSFIVVAYVKWYYLYNYQTERN :  95
BoleOR85bc2   : ------------------------------------------------------------------------------------------MTLSYVSFIVVAFVKWYYLINYHTERT :  27
BminOR85bc2   : -------------MENLEKFVRLANFFGNHIGMKPWGRLDGF-----QRRFLFYFSSINLLITFIAESSYIIVTITSD-FILAVMTLSYVTFIVVAYAKWYYLYTYQTERT :  92
Ccap85bc2     : ----------MSIIIRFEEFLRLPSFFSRNIGIILWGQRGKL-----FDRFMFYFSSINLFLTLLAELWYIISTISTD-FITAIMGLSYVSFVVLAEVKFYYLIKYDMKVS :  95
                                e f     ff    q                           n       e            fi a mtLSY  F  v   K y       e

                       120       130       140       150       160       170       180       190       200       210       220
DmelOR85c     : DLVKELEHIYPNGKAEEEMYRLDRYLRSCSRISITYALLYSVLIWTFNLFSIMQFLVVEKLLKIRVVGQTLPYLMYFPWNWHENWTYYV-------LLFCQNFAGHTSASG : 198
DmelOR85b     : ELINELKEIYPNGLIREERYNLPMYLGTCSRISLIYSLLYSVLIWTFNLFCVMEYWVVDKWLNIRVVGKQLPYLMYIPWKWQDNWSYYP-------LLFSQNFAGYTSAAG : 199
BdorOR85bc1   : RFLQLMNTIFFRTETQQKKMNLRSHLRQCTIVMTVFAMIFMILIWTYNLYPYMQRQIYDCWLHMRSINKTLPYESYIPWNWHDHWTFYL-------YYTLQSIAGYHSASG : 199
BlatOR85bc1   : RFLQLMNAIFFRTEPQQKMMNLRSHLRQCTIVMSAFAMIFMILIWTYNLYPYMQRQIYDCWLHMRSVNKTLPYESYIPWNWHDHWTFYL-------YYTSQSIAGYHSASG : 199
BoleOR85bc1   : RFLQLMHTIFFHTEPQQKMMNLRRHLCQCTIVMSGFATIFMLLIWTYNLYPYMQRQIYDCWLQVRSVNKTLPYESYIPWNWHDHWSFYLTILYKLSYYTLQSIAGYHSASG : 206
BcucOR85bc1   : RFLQLMNAIFFRTEQQQKIMHLRRHLRQSTIVMSCFAMMFMVLIWTYNLYPYMQRQIYDRLLDVRSINKTLPYESYIPWNWHEHWTFYL-------YYTLQSIAGYHAASA : 209
CcapOR85bc1   : QFLKLMDEIFFRTAEQQKMMNLRRHLRQSTIVMSGFALIFMILIWTYNLYPFMQRQIYDCWLDTRSINKTLPYESYIPWNWHNHWSFYL-------YYVLQSIAGYHSAAG : 200
RzepOR85bc1   : RFLIQMDAIFFRKASQQQSMDVSRHLRQSSIVMSIFSLIVMMLICTYNLYPWLHRELVDCWLHMRSIEKSLPYESYIPWNWHDHWSYYL-------LYVSQSFAAYHAAAG : 199
BlatOR85bc2X1 : AFFQRLEALFFHTKSEQENIKLXEYFRLNKLATRGYTITFMVVIWLYNLYTISQRFIYTKLLHVH-IERVLPYQALYPWDWRDNWTYYV-------IYVTQDFAGFHATCA : 198
BlatOR85bc2X2 : AFFQRLEALFFHTKSEQENIKLXEYFRLNKLATRGYTITFMVVIWLYNLYTISQRFIYTKLLHVH-IERVLPYQALYPWDWRDNWTYYV-------IYVTQDFAGFHATCA : 141
BdorOR85bc2   : AFFQRLDALFFHTKSEQESIKLSEYFRLNKLATRGYTITFMVVIWIYNLYTISQRFIYTQLLHVH-IERVLPYQAMYPWDWRDNWTYYV-------IYVTQGFAGFHATCA : 198
BoleOR85bc2   : VFFQRLEALFFHTKSEQETIKLSKYLRLNKLATMSYTITFMVVIWIYNLYTISQRFIYTNLLHVH-IERVLPYQAMYPWDWRDNWTYYV-------IYVTQSFAAWHSTCA : 130
BminOR85bc2   : AFFQRLETLFFCTKSQQEAIKLSEYIRMNKLSTISYTISFLMCISTYTFYTIARQFIYTNLLHVPGTERNLPYQAVYPWDWRDNWTYYV-------CYVSQGFAGWHSTCA : 196
Ccap85bc2     : TVLKRLNALFFHTKEEQENIQLIKYLKMSKFYTLFYTVTFMLVIWTYNLYTVSQRFIYTKILQVREIERELPYPAIYFWNWQDNWSYFM-------LYISQSLAGWHATCA : 199
                 f       fP t   q    l    r            fm  Iw ynly   qr iY   L        LPY    pW W d W  y         y  Q  Ag h

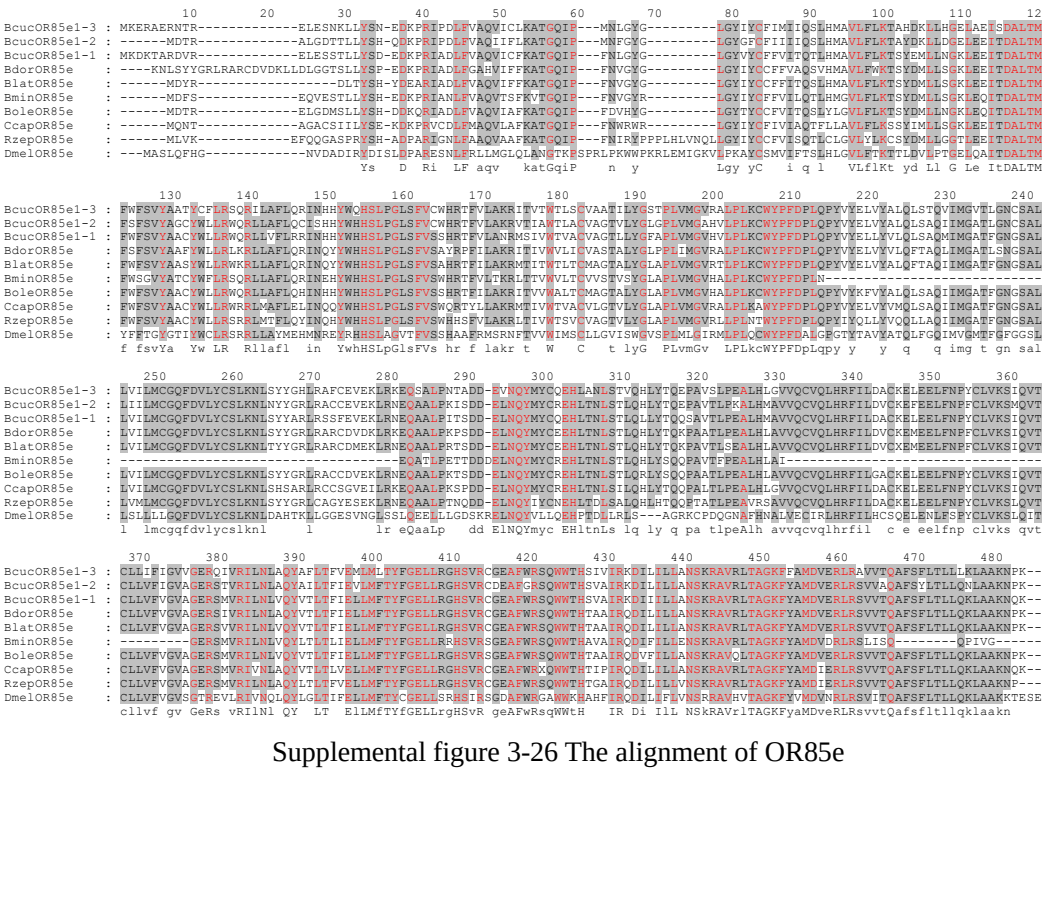
                       230       240       250       260       270       280       290       300       310       320       330
DmelOR85c     : QISTDLLLCAVATQVVMHFDYLARVVE--------------------------KQVLDRDWSENSRFLAKTVQYHQRILR-LMDVLNDIFGIPLLLNFMVSTFVICFVGF : 281
DmelOR85b     : QISTDVLLCAVATQLVMHFDFLSNSME--------------------------RHELSGDWKKDSRFLVDIVRYHERILR-LSDAVNDIFGIPLLLNFMVSSFVICFVGF : 282
BdorOR85bc1   : QIASDLVLCAMATQIIMHYEYVAQRIT-EYQPQAL--------------RAPRHQVKESESYRKDMEFLCDIIAYHANILS-LSDIMNEVLGVPLLVNFMTSSFVICFVGF : 294
BlatOR85bc1   : QIASDLVLCAMATQIIMHYEYVAQRIT-EYQPQAL--------------KGAVRDVKESELYRKDMRFLCDIXEYHANVLS-LSDIMNEVLGVPLLVNFMTSSFVICFVGF : 294
BoleOR85bc1   : QIASDLVLCAMATQIIMHYEYVAQTIT-EYRPQLVDCKIS---------RAPRLDXESERSLCKDMKFLCDIIAYHANILRXLSDIMNEVLGVPLLVNFMTSSFVICFVGF : 307
BcucOR85bc1   : QIASDLVLCAMATQMIMHYEYVAQKIT-EYQPQVG-----------------ADSGSKNEAYCRDMKFLCDIIAYHANVLS-LSDIMNEVLGVPLLVNFMTSSFVLCFVGF : 301
CcapOR85bc1   : QIASDLVLCAMATQMIMHYEYVSHKIRSRYRGERKCVDSKS----VSCLNALNHWTEEQVATHKDMRWLCETIAYHSNLLS-LSDVMNDVLGVPLLVNFMTSSFVICFVGF : 306
RzepOR85bc1   : QIASDLVLCAMATQMVMHYEYVALKIE-QYQPKWGTSCCVNRQQQVKLVQASSQWEMKRAAYIEDMRFLGDLIAYHSNILS-LSNFMNEVFGVPLLVNFMASSFVICFIGF : 308
BlatOR85bc2X1 : QIAYDLLLCILSIQLIMHYDHISRSLE-GYQTKFAEVHGVD---INNGLPQLACAAVELRAVKEDIQFISNIVSYHNELLS-LSKSLNKLFGMPLFVNFFTSSAIICFLSF : 304
BlatOR85bc2X2 : QIAYDLLLCILSIQLIMHYDHISRSLE-GYQTKFAEVHGVD---INNGLPQLACAAVELRAVKEDIQFISNIVSYHNELLS-LSKSLNKLFGMPLFVNFFTSSAIICFLSF : 247
BdorOR85bc2   : QIAYDLLLCILSIQLIMHYDHISRSLE-EYQTKFAEVHGID---INNGLPPLMCAAVELRAVKEDIKFISNIVSYHNELLS-LSMSLNKLFGMPLFVNFFTSSAIICFLSF : 304
BoleOR85bc2   : QIAYDLLLCILSMHLIMHYDHISRSLE-GYQTKFAEVHGVE---TSNSLQQLARVAVELKAVKEDIKFISNIVAYHNELLR-FVVL------------------------- : 211
BminOR85bc2   : QMAFDLMLCTLSTHLIMHYDHISRSLE-GYQTKFAEIHG------KNGLTQQARAAMELKAVKDDIKFISSIVAYHTELLR-F---------------------------- : 271
Ccap85bc2     : QILTDLLICILISHLIMHYDHIARSLL-NYQSKFAELYGKES--TMKCMPKLARVMMEERAVRADMKFLADIIAYHTELLS-LTESLNDVFGVPLFMKFMSSSAIICFLGF : 306
                Qia Dl 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     : QMTVGVPPDIMIKLFLFLFSSLSQVYLICHYGQLIADASSSLSISAYKQNWQNADIRYRRALVFFIARPQRTTYLKATIFMNITRATMTDLLQVSYKFFALLRTMYIK : 389
DmelOR85b     : QMTVGVPPDIVVKLFLFLVSSMSQVYLICHYGQLVADASYGFSVATYNQKWYKADVRYKRALVIIIARSQKVTFLKATIFLDITRSTMTDLLQISYKFFALLRTMYTQ : 390
BdorOR85bc1   : QMTMDAEPDYMVKLFFFLFSSLIQIYLICHYGQQLIDASSNVSRAVYNHDWIHSHVHYQRMLVLVTARAQKPAMLKATSFVRISRGTLTDIMQISYKFFTLVRTMYSN : 402
BlatOR85bc1   : QMTMDAEPDYMVKLFLFLFSSLFQIYLICHYGQQLIDASNNVSRAVYNHDWVHSHVHYQRMLVLVTARAQKPAMLKATSFVRISRGTLTDIMQISYKFFTLVRTMYNN : 402
BoleOR85bc1   : QMTMDAEPDYMVXLFLFLFSSLFQIYLICHYGQQLIDASSNVARAIYNHDWIHSHVHYQRMLVLVAARAQKPAMLKATSFVHISRGTLTDIMQISYKFFTLIRTMYSN : 415
BcucOR85bc1   : QMTMDAEPDYMVKLFLFLFSSLVQICLICQYGQLLIDSSSNIAHAVYNHDWVHSHVHYQRMLVLVAVRAQKPAMLQATSFVRISRGTITDIMQISYKFFTLIRTMYSN : 409
CcapOR85bc1   : QMTMDAEPDYMVKLFLFLFSSLAQIYLICHYGQLLIDASINVAAAVYDQDWFDLNVRYQHMLVLVVARAQKPAMLKATNFVRISRGTLTDIMQISYKFFTLIRTMYSD : 414
RzepOR85bc1   : QMTMDTEPDYKVKLLLFFFSSLTQIYLICHYGQLLLDASINVAQAVFNNDWTNAHTHYQQMLVLVAARAQKPAILKATSFVHVSRGTMNDIMQISYKFFTLIRTMYSN : 416
BlatOR85bc2X1 : QMSVTREVDLLMKLAVFLFFSVMQVYLICHFGQLLSDASTNVASAAYFQDWSYADIRFQKMTILVAERAQEAAALKATNFITISLDTMTVIMQMSYKFFTLLRTMYAD : 412
BlatOR85bc2X2 : QMSVTREVDLLMKLAVFLFFSVMQVYLICHFGQLLSDASTNVASAAYFQDWSYADIRFQKMTILVAERAQEAAALKATNFITISLDTMTVIMQMSYKFFTLLRTMYAD : 355
BdorOR85bc2   : QMSVTREVDLLMKLAVFLFFSVMQVYLICHFGQLLSDASTNVASAAYFQDWSYADVRFQKMTILVAQRAQEAAALKATNFITISLDTMTVIMQISYKFFTVLRTMYAD : 412
BoleOR85bc2   : ------------------------------------------------------------------------------------------------------------- :   -
BminOR85bc2   : ---------------------------------------------DWSHADIRFQKMTILVAERAQDPAALKATKLITISRDTMTVIMQMSYKFFTVLRTMYGD : 330
Ccap85bc2     : QMTVNRGFDLLTKLALFFILSVLQVYLICHFGQLLIDASTNVSTALYSQDWTNADVRYQKMLVLIIKRAQRSATLKATNFIIISRATMTEIMQMSYKFFALIRTMYND : 414
                qm      d   kl  f   s  q ylich gq   das     a y  dw       q m  l   raq  a lkat f  is  t t imq sykff l rtmy
```

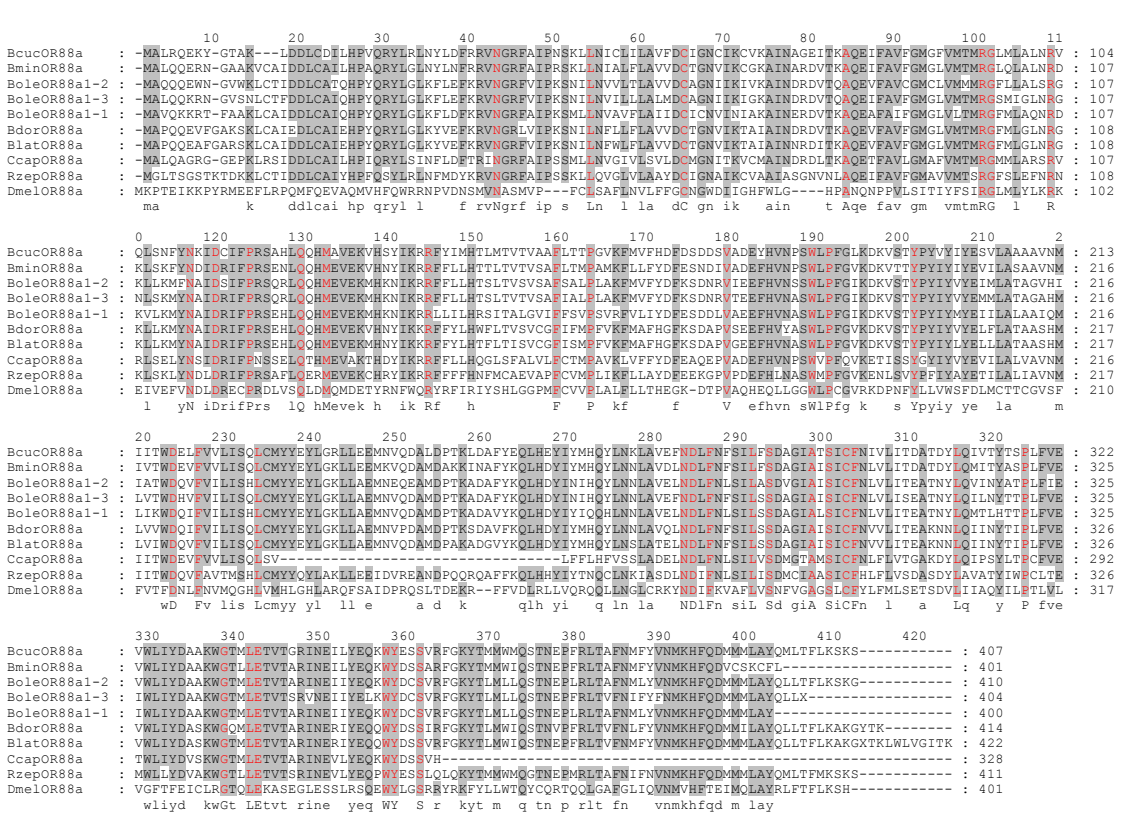
Supplemental figure 3-24 The alignment of OR85bc



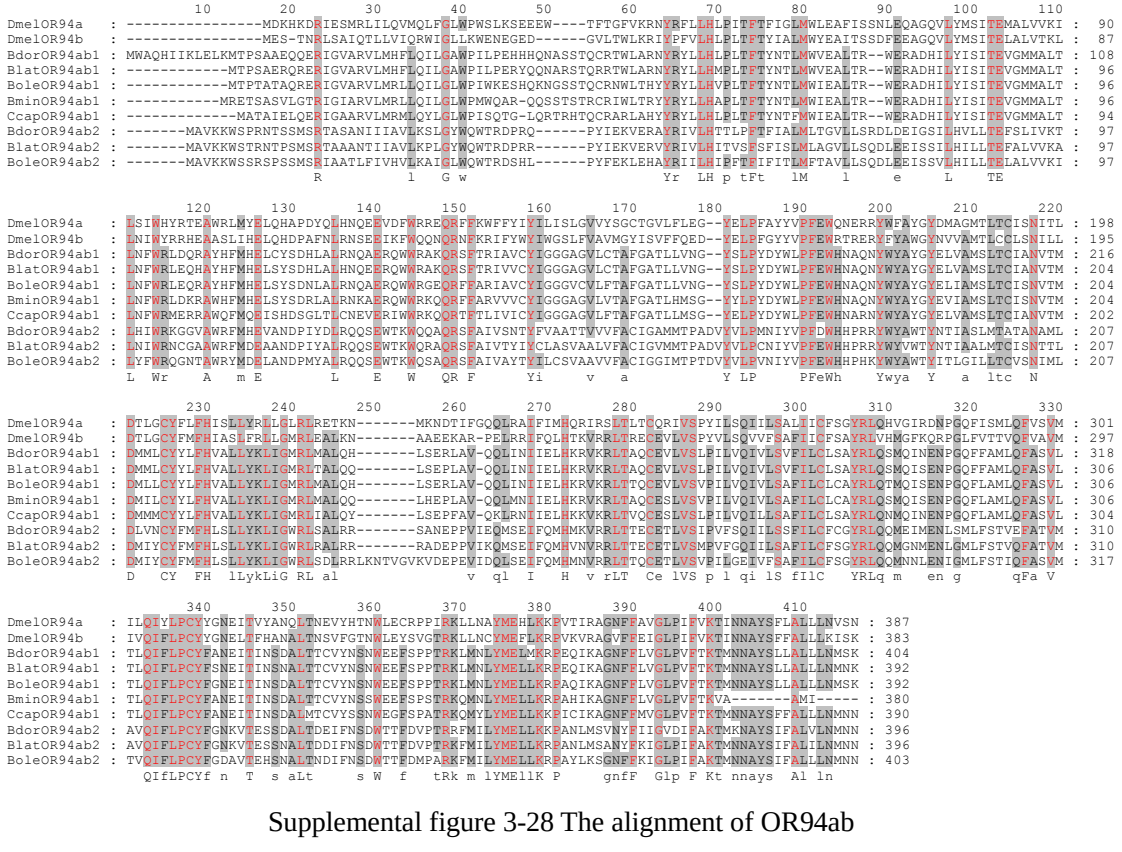
Supplemental figure 3-25 The alignment of OR85d



Supplemental figure 3-26 The alignment of OR85e



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 : ----MGKLKVLSSRIFPSDPSKGKIGSIQYNVWLAQLFGVPVVGLKAESPCLKIVLGIYGILITLVVTFIYTGFEIYDMILCWPNLDSLTQNICLSLTHIAGVLK------- : 101
BoleOR1-1 : ----MRKLEVLSSRIFPSDPSKGKIGSIQYNVWLAQLFGVPVVGLKTESPRLRIALGVYGVLITLVVTFIYTAFEIYDMILCXPNLDSLTQNICLSLTHVAGVLKVINIIYR : 108
BdorOR1-1 : ----MDKLEELSSRIFPSDASKGKIGSIQYNVWLAQLFGVPVVGLKAESTRLRIALGIYGLLMTLVVTFFYTGFEVYDMILCWPNLDSLTQNICLSLTHVAGVFKVINIIYR : 108
BlatOR1-1 : ----MDKLEELSSRIFPSDAYKGKIGSIQYNVWLAQLFGVPVVGLKAESPRLKIALGIYGVLMTLVVTFFYTGFEIYDMILCWPNLDSLTQNICLSLTHIAGVFKVINIIYR : 108
BcucOR1-1 : ----MDKLAVLSSRIFPSDPSKGKIGSIEYNVWLAQLFGVPVVGLKAESPLMRIALGIYGVLLTLLVTFIYTGFEIYDMILCWPNLDDLSQNICLSLTHIAGVLKVINILYR : 108
CcapOR1-1 : ----MDKLEALSSRIFPSDPSIGKIGSIEYNVWLAQLFGVPVLGLKKETPRMRIALAVYGVVATLVVTFLYTGFEIYDMIFCWPNLDKLTQNICLSLTHVAGALKVINIIYR : 108
BdorOR1-2 : ---------------------------------------------------------------------------------------------------------------- :   -
BlatOR1-2 : MAAFQDILKEVYFRVFPSEAGKGQLGSIEFNIWLSQISGVPLS--------------------------------------PWFVPLHR--------------------- :  51
BcucOR1-2 : ---------------------------------------------------------------------------------------------------------------- :   -
CcapOR1-2 : MHRLLCKFEQVAMRVFPSDVRRGQIGSIEFNIWLSQMTGVPLP--------------------------------------PSFVPLRRRFRQ----------------- :  55
                        r fps    g  gsi  n wl q  gvp                                          p    l

                 120       130       140       150       160       170       180       190       200       210       220
BminOR1-1 : ------------------------LMAFYHGEFENKIPLTIYASLVGSTGVLGIMYLLHS------QIFPYRVKLPDWMPLGTQLAYMGISVLVFALQIVAIDYLNVTMINQ : 183
BoleOR1-1 : LDEVANVVRRIEYSAKTYVVSKSQLVAFYRGEFENKIPLTIYAALVGFTGVLGLIYLLYNPIGVAGQIFPYRVKLPDWMPFGTQLAYMGISVLVFALQIVAIDYLNVTMINQ : 220
BdorOR1-1 : LDEVAFVVRRIEYAAKTYVISKSQLVAFYRGEFENKIPLTIYASLVGFTGVLGLIYLFYNPIGVAGQIFPYRVKLPEWMPFGIQLAYMGMSVLVFALQIVAIDYLNVTMINQ : 220
BlatOR1-1 : LDEVGFVIRRIEYSAKTYVISKSQLVAFYRGEFENKIPLTIYASLVGFTGVLGLIYLFYNPIGVAGQIFPYRVKLPEWMPFGTQLAYMGMSVLVFALQIVAIDYLNVTMINQ : 220
BcucOR1-1 : LDEVAHVVRRIEYSAKTYVISKRQLVAFYRGEFENKIPLTIYASLVGFTGVLGIIYLFYNPVGVAGQIFPYRVKLPDWMPFGLQLAYMGISVLVFALQIVSIDYLNVTMINQ : 220
CcapOR1-1 : LKEVAGVVRKIEYAARYYVISKNQLKAFYRGEFENKIPLTIYASLVGFTGILGIAYLLHNPTGVAGEIFPYRVKLPHWMPFGLQLAYMGFSVLVFALQIVAIDYLNVTMINQ : 220
BdorOR1-2 : ---------------------------------------------------------------------------------------------MFAVQIVTVDYLNISMMNL :  19
BlatOR1-2 : ------------------------------TRLVNGLLLAY--------EYISSLLFFPDP-DMAGQIFPYRVTMPAWLPFFLQVVYIGVTDFMFAVQIVTVDYLNISMMNL : 124
BcucOR1-2 : ------------------------------------------------------------MAGKIFPFRITLPAWLPFYMQVAYIGVTDFMFAVQIVTVDYLNISMINL :  49
CcapOR1-2 : --------------------------IFDRAEVENKLFLVIYATVIGFTGFTAMILVFINP-DMAGKIFPYRVALPAWLPLPVRVAYIGTTDFMFAVQIVTVDYLNIGMMNL : 140
                                          n   l                          ag ifpyrv lp w p   q ay g     FA QIV  DYLN  M N

                230       240       250       260       270       280       290       300       310       320       330
BminOR1-1 : IRFQLKILNLAFEELKLDCV---NKK-EHINLNKRLQTIVEHHCLLRDLRNDVEDLFRLPVLIQFFTSLVIFAMTGFQAIVKAENSNGAALIYCYCGCIFCELFVYCWFGNE : 291
BoleOR1-1 : IRFQLKILNLAFEELKLDCV---NKG-EQREFNKRLQTIIEHHCLLRDLRNDVEDIFRLPVLLQFFTSLIIFAMTGFQAIVKAENSNGAALIYCYCGCIFCELFVYCWFGNE : 328
BdorOR1-1 : IRFQLKILNLAFEELKLDCV---NAR-ELEEVNKRLHTIVEHHCLLHDLRNDVEDIFRLPVLLQFFTSLIIFAMTGFQAIVKVENSNGAALIYCYCGCIFCELFVYCWFGNE : 328
BlatOR1-1 : IRFQLKILNLAFEELKMDCV---NAR-EQEEANKRLQTIVEHHCLLRDLRNNVEDIFRLPVLLQFFTSLIIFAMTGFQAIVKVENSDGAALIYCYCGCIFCELFVYCWFGNE : 328
BcucOR1-1 : IRFQLKILNLAFEELKLDCG---SKKKAHFNHDKRLQTIVEHHCLLRDLRIDVEEIFRMPVLLQFFTSLIIFAMTGFQAIVKTENSNGAALIYCYCGCIFCELFVYCWFGHE : 329
CcapOR1-1 : IRFQLKILNLAFEELKFVSG---QAA-HELSLDRRLRTIVDHHNLLRNLRNEVEEIFRLPVLVQFFTSLIIFAMTGFQAIVKSENSNGASLIYCYCGCIFCELFVYCWFGNE : 328
BdorOR1-2 : LRCHLNIIKSTFDDLILDECHVRRDMKRIRDPNARMADIVEHHGILKSVRDDVEHIFRLSILLQFFTSLVISAVTGFQATMNSSNSNSEIIIYFYCFCIFTQLFGYCWFGNE : 131
BlatOR1-2 : LRCHLNIIKSTFDDLILDECHMRRDMRRIRDPNARMTDIVEHHGILKSVRDDVEHIFRLSILLQFFTSLVISAVTGFQATMNSSNSNSEMIIYFYCFCIFTQLFGYCWFGNE : 236
BcucOR1-2 : LRCHLNIIKSTFDELILDEQNARRDMK--RDPNARMADIVEHHGILKSVRDDVEYIFNLAVLLQFFTSLIVSAVTGFQATMHSSNSNSMMIMYFYCFCIFTELFGYCWFGQE : 159
CcapOR1-2 : LRCHLNVMKSSFDELNFNVKCMKSDIKRIRDPNERLADIVRHHGVLKSVRDDVEQIFRLPVLLQFFTSLVISAVTGFQATIYSSNFKSELIIYFYCFCIFTQLFGYCWFGNE : 252
             R  L i    F eL  d              n R   IveHHc L   R dVE iFrl vLlQFFTSL i A TGFQA     Nsn    iY YC CIF  LF YCWFGnE

             340       350       360       370       380       390       400       410
BminOR1-1 : VSEQSKTLTSSGYSSHCLNRERLSQQA------------------------------------------ : 318
BoleOR1-1 : VSEQSKTLTASGYASHWYEFDQRFKKSLIIFMCNSQTPFVFTAGGFMSLSLPSFTGILSKSYTVIALLRQVYSR : 402
BdorOR1-1 : VSEQSKTLSASGYGSHWYAFDQRFKKSLLIFMCNSQTPFVFTAGGFMSLSLPSFTGILSKS------------ : 389
BlatOR1-1 : VSEQSKTLAASGYGSHWYAFDQRFKKSLLIFMCNSHIPFVFTAGGFMSLSLPSFTGILSKSYTVIALLRQVYSR : 402
BcucOR1-1 : VSEQSKTLTTSGYSSHWFEFDQRFKKSLLIFMCNSQTPFVFTAGGFMSLSLPSFTGILSKSYTVIALLRQVYSR : 403
CcapOR1-1 : VSEQSKTLTTSGYNCHWYQFGPRYKKSLLIFMFNSQKPIVFTAGGFMALSLPSFTGILSKSYTVIALLRQFYGR : 402
BdorOR1-2 : VNEQNKTLAAHGYGSSWYHFDQRFRKSLAIFLLNAQQPFNFTGGGFVDLSLPSFTNVLSKAYSFIAVLRQMYER : 205
BlatOR1-2 : VNEQNKTLATHGYGSSWYHFDQRFRKSLAIFQLNAQQPFNFTGGGFVDLSLPSFTNVLSKAYSFIAVLRQMYER : 310
BcucOR1-2 : VNEQNNTLAARGYGSSWYHFDQRFRKSLAIFLLNAQQPFNFTGGGFIDLSLPSFTNVMSKAYSFIAVLHRMYGR : 233
CcapOR1-2 : VNEQNKTLAARGYSSSWYYFDNRFRKSLAIFLVNAQQPFDFTGGGFVALSLPSFTGIMSKAYSFIAVLRQMYDR : 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 : --------------------MSVQPQQQPQQQQ----LDSAHAFRYLWLNWRLIGMHPTRRHRLPYYIYSACINISLGLFLPATMIAKLFFIENLSQLIGLLYLGVTLTMAT :  88
BlatOR2-1 : --------------------MSVQLQQQSQQQQ----LDSAHAFRYLWLNWRLIGMHPTRRHRLPYYIYSAFINISLGVFLPATMIAKLFFIENLSQLIGLLYLGVTLTMAT :  88
BoleOR2-1 : --------------------MSVQLQEQ-QKQQ----IDSAHAFRYLWLNWRLIGMHPTRRHRLPYYIYSACINISLGIFLPATMIAKLFFIENLSQLIGLLYLGVTLTMAT :  87
BcucOR2-1 : -------------------MSAVQPQQQQQQQHAAASLHSSHAFRYLWLNWRLIGMHPTRRHRLPYYIYSGCINISLGVFLPATMIAKLFFIENLSQLIGLLYLGVTLTMAT :  93
BminOR2-1 : ------------------------------------------------------MHPTRRHRWPYYIYSACINISLGIFLPATMIAKLFFIENLSQLIGLLYLGVTLTMAT :  57
RzepOR2-1 : --------------------MSALLQVTDTGAP----LNSARAFRYLWLNWRLIGMHPTRRHRCLYLAYSASINSVFGILLPATMIAKLCFIENLPQLIGLLYLGVTLTMAT :  88
BcucOR2-2 : --------------------------MNNK-QDAVGRLDSSDALRYVWLFWRITGIHPTAKYRGIYWLYSLLLNISSSVLFIAFYVVTFFISTDLLETLTNLSVMVPLIYTS :  85
BoleOR2-2 : -------------------------MANQ-PHSATRLDSSDALRYIWLFWRITGIHPVKKHRYIYYIYSLLLNFTSTVLFISFYVVTLFISNGLLEILTNLSVMVPLIYSS :  85
CcapOR2-2 : --------------------------MTKQEQATPTRLDSGDATRYVWLFWSIIGIHPFKKHRTLYWLYSVLLNFCCSAFFIAFYAVTFFVVSDLLEILANLSVMVPLIYNT :  86
BlatOR2-3 : --MNMIN-------------------KHKPLHATT-TLDTTEAFKYIWFCWRLFGMHRDLYERRFNWVYLIVLNLYCGVIYPMLYVASFFASIELSQKLANISVAVPIIYTF :  90
BdorOR2-3 : ----MTN-------------------KHKPLHATT-TLDTTEAFKYIWSCWRLFGMHRDLYERRLNWIYLILLNLYCGVIYPMLYICSFFTPMDLSQKLANISVAVPIIYTF :  88
BcucOR2-3 : NLQAIVNNFTIFQLTILHPGENTSKMSHKPLLTAT-TLDTKEAFSYIWYCWGFFGMYPDLYERRLNWIYLILLNLYCGVIYPLLYIGSLLTPMDLNQKLANISVAVPILYTL : 111
RzepOR2-3 : --MSIKQISLD--------DQRLMSSSQTTLSSPSPKLDTHDALRYIWLCWRYLGMLPFMQSSYIYYAYSVLIIFYGAILFPLFYVISLFVHIDFADRLANLSVALPLLYTT : 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-PKLLAVNYYLAKLDVRCMRHAVDRQHIRTAIRICHLYYAGYMFVYELSSSGFAYIGFSLRQLVYDGWFPQLYADAAQNLTVTLIYQNFAVMTFFVLQNVNN : 199
BlatOR2-1 : AKQWSLWLHR-PKLLAVNYYLAKLDVRCMRHAVDRQHILTAIRICHLYYAGYMFVYELSSSGFAYIGFSLRQLVYDGWFPQLYADAAQNLTLTLIYQNFAVMTFFVLQNVNN : 199
BoleOR2-1 : AKQWSLWLHR-SKLLAVNYYLSKLDVRCMTHAVDRQHILTAIRICHLYYAGYMFVYELSSSGFAYIGFSLRQLVYDGWFPQLYADAAQNLTVTLIYQNFAVMTFFVLQNVNN : 198
BcucOR2-1 : AKQWSLWLHR-SKLLAVNQYLDKLDARCMPHAVDRQHIRTAIRICHLYYAGYMFVYELCSSGFAYIGFTLRQLVYDGWFPQFYADEATNLTVTLIYQNFAVMSFFVLQNVNN : 204
BminOR2-1 : TKQWSLWLHR-SQLLAVHYYLGKLDARCMRHAVDRQHILTAIRICHLYYAAYMFLYELSSSGFAYIGFKLRQLVYDGWFPQFYADAAQNLTVTLIYQNFAVMTFFVLQNVNN : 168
RzepOR2-1 : AKQFSLWLHR-SKLLDVNLYLAKLDARCNHHAVDRQHLLWAIRICHFYYVAYMFVYELSSSGFAYIGFSLRQLVYDAWFPKLYEDADKNLTITLIYQNFAVMTFFVLQNVNN : 199
BcucOR2-2 : TKHLVVFYHIRGKLPQAAFHLQALDRRVELEPAACEHLRRLVQRCHRIFLAALAGIGVCLALYALVGIARHKLPFEGWLPFDWEHSLNAYILACAYQLFCLS-VQSIYALCS : 196
BoleOR2-2 : TKHFVVFYHIRGELPKAALHLQALDRRVELEPVACTHLKRLVQRCHKIYLAALAGIVVCLALYALVGILRHKLPFEGWLPFDWEHSLNAYILACAFQLFCLS-VQSIYALCN : 196
CcapOR2-2 : AKQLVIFYHIRRTLPQAALHLHALDRRAEQEPAAREQLKRLVQLSHRIFLTALTGIGICLTLYAMGGILRHRLPFDGWLPLDWEHSVGAYVAACAYQLFCLI-VQCIAALCN : 197
BlatOR2-3 : GKHVVIVYYTREDLPKALAQLKALDRLAESRPEDCAYMQKMVKNCHLVFFVSFVSFWFALLSYGVLEVLRHKLPFEGWVPFDWTSSEAAYVGACVIQLIGLI-IETTNAICC : 201
BdorOR2-3 : GKHVVIVYYIREDLPKALAQLKALDRLAESRPEDRAYMQKMVKNCHLVFFVSFVSFWFALLSYGVLEIFRHKLPFEGWVPFDWTRSEAAYVGACAIQLIGLG-IETTTAICC : 199
BcucOR2-3 : GKHVIIVYYLRKDLPKALRQLQALDRLAERRPKDREYMKRMVKNCHWIFLASSVSFWFALLSYGVLEMFRHKLPFEGWVPFDWQRTEFAYVCACALQLFGLG-IETTNAICC : 222
RzepOR2-3 : AKQAIIFYYIQGDLQKAAHHLHAMDRRAEGHIEDCAYLKRTVRYCHRIFIVNYAGFWLALLVYGLLGVMSHKLPFEGWLPFDWQHSRGAYTLACTLQMFCFC-SQVTNAVCI : 213
             K           L      L  lD r      d          cH                    g     L   gW P                Q f

                  230       240       250       260       270       280       290       300       310       320       330
BdorOR2-1 : DMYPQCYLAVMIGHLRALTARISRICK--DGVLSAEENISELINCIEDHKNLLGYFACIRPVISRTIFMQFGITAFVLCLTAVNYVAFERDAAQMLIAATYIFAVLIEALPC : 309
BlatOR2-1 : DMYPQCYLAVMIGHLRALTARISRICK--DGVLSAEENISELVNCIEDHKNLLSYFACIRPVISRTIFMQFGITAFVLCLTAVNYVAFERDAAQMLIAATYIFAVLIEALPC : 309
BoleOR2-1 : DMYPQCYLAVMIGHLRALTARISRICK--DGVLSVEQNIAELTNCIEDHKNLLGYFACIRPVISRTIFMQFGITAFVLCLTAVNYVAFERDAAQMLIAATYIFAILIEALPC : 308
BcucOR2-1 : DMYPQCYLAMMIGHLRALTARISRICK--DGVLSEDENIAELTNCIEDHKNLLGYFACIRPVISRTIFMQFGITAFVLCLTAVNYVAFERDAAQMLIAATYIFAVLIEALPC : 314
BminOR2-1 : DMYPQCYLAILIGHLRALTARISRICK--DGVLNVDENIEELTNCVEDHKNLLGYFNCIRPVISRTIFIQFAITAFVLCLTAVNYVAFERDAAQKLIAATYIFAVLIEALPC : 278
RzepOR2-1 : DMYPQCYLAVMIGHMRALSARISRVCK--DGALSVEDNIEELKNCIEDHKNLLSYFACIRPVISRTIFMQFGITAFVLCLTAVKYVAFGVDTAQMLIAITYIFAVLIEALPC : 309
BcucOR2-2 : DTYSIIYLLLLVAHLRILNARIARIQGACAAQCGEVANYQQLADCVRDHWECM---KCISPTIAATIFVQFLSTAFALCTAAVAFVNADSSVEQLMKFLPYLLVVLCEIAPC : 305
BoleOR2-2 : DIYSIVYLLLLVAHLRILNARIARIQGVCAEQHSELANYQQLAACVRDHWECV---KCISPAIAATIFIQFISTALALCTAAVAFVNADSIGEQLIKFLPYILVVLCEIAPC : 305
CcapOR2-2 : DTYTVIYLLLLATHLRILNARIASLC---HGECTEVENYRQLAACVRDHWACMNFYNSIRPAIAATLFIQFFSTAITLCTSAVAFVNAEDSVAQLFKFLPHLLVVVCEILPC : 306
BlatOR2-3 : DTYPVTYLILLVAHLRVLNGRIERVCS--AGAASDAESYRELVACVEYHKECMSYYNSLRPTLSGIYFIQFLSTGLGLSMPAIAFVGGNFSFSHVIKFLIIFGVILIEVAPC : 311
BdorOR2-3 : DTYAVTYLILLVAHLRVLNGRIERVCS--AGATSDAESYRELVACVEYHKECMSYYNSLRPTLSGIYFIQFLSTGLGLSMPAIAFVGGNFSFSHVIKFLIIFGAIIIEVAPC : 309
BcucOR2-3 : DTYAVTYLVLLVAHLRILNRRIARACN--TGDGSDAENYRELVACVEYHKECISYYNSIRPTLSGTCFIQFLSTGLGLSMPAIAFVGGSFSFSHVIKFLIIFGAIIIEVAPC : 332
RzepOR2-3 : DTYSVTYLALLVAHLRVLNARIERICN--CNTRTETDLYGELIACVQDHRECMCYYNCIRPAISGTLFVQFLSTALGLCAPAIAFVGGDFDLFQLLKFIIFFFAIIIEVAPC : 323
            D Y   YL     HlR L aRI r G    g      n  eL  C  dH     y   irP is t F QF  Ta  Lc  A   V       q            iE  PC

             340       350       360       370       380       390       400       410       420
BdorOR2-1 : CWYVNSLMEECAQLTTALYNCQWYDQNRRFRKMLIIFMQRSQRTMVLMAGDLVPITLQTFLNIIKFSFS--------MYTILKG----- : 385
BlatOR2-1 : CWYVNSLMEECGQLTTALYNCQWYDQNRKFRKMLIIFMQRSQRTVLLMAGDLVPITLQTFLNIIKFSFS--------MYTIMKG----- : 385
BoleOR2-1 : CWYVNSLMEECSQLTTALYNCQWYDQDRKFRKMLIIFMQRSQRTMVLMAGDLVPITLQTFLNIIKFSFS--------MYTILKG----- : 384
BcucOR2-1 : CWYVNSLMEECGELTTALYNCQWYDQNRKFRKMLIIFMQRSQRTMLLMAGDLVPITLQTFLNIIKFSFS--------MYTILKG----- : 390
BminOR2-1 : CWYVNSLMEECGELTTALYNCQWYDQNRKFRKMLIIFMQRSQHTMVLMAGDLVPITLQTFLNLFCLCVQSIYALCSDIYSIIYLILLVA : 367
RzepOR2-1 : CWYVNALLEECGQLTLAIYSCQWFEQSKEFRKILIVFMQRSQRATVLMAGNLVPITLQTFLNIIKFSFS--------MYTILKG----- : 385
BcucOR2-2 : CWLMDEAALEMLKLTNALFSCCCSDGN------------------------------------------------------------ : 332
BoleOR2-2 : CWLMDEAALEMFKLTNALFSCCWYEQNLRFRRSLIIFMQRSQKVEQILAGKIFPVSLVTFIKILKLAFS--------LFTLLNQLKS-- : 384
CcapOR2-2 : CWLMDKAALEMQDLTKSLFACRWYEQNQKFRRSLLIFMQRSQKVEKILAGDLVPVSLETFVNIIKFAFS--------LFTLLNQIKSK- : 386
BlatOR2-3 : CWFMDEVLFEMRRLTNSMFSCRWYEQNLKFRKALIIFMQRSQIAQPLLAGNLIPVSLDTFTNIIKFAVS--------LFTLLNKLNS-- : 390
BdorOR2-3 : CWFMDEVLVEMRRLTNAMFSCRWYDQNLKFRKALIIFMQRSQIAQPILAGNLIPVSLETFTNIIKFAFS--------LFTLLNQLNS-- : 388
BcucOR2-3 : CWFMDEVMAEMHKLTNSMFSCRWYDQNLKYRKALIIFMQRSQIAHPVLAGNIIPVSLETFTNIIKFAFS--------LFTLLNQLSHN- : 412
RzepOR2-3 : CWFMDEVMAEMRQLTTALFSCSWYEQSPRFRRDLIIFMQRSQKEDKIIAGNITAVSLETFRSVSENLC-------------------- : 391
            CW       E   LT a   C wy qn  fr  liifmqrsq      ag   p  l tf ni k   s          t
```

Supplemental figure 3-30 The alignment of OR2

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                    10        20        30        40        50        60        70        80        90       100       110
BdorOR3-2-5 : -----MTSYENLPLYAVNVKVFVKVGLINSTDWTKGLLFFLILIVAYVGQIINLCKSWNEDIGETTMNFHCFLFVTHCLIRLWIVVKKNKFERFFQCVEQWHR------ :  99
BdorOR3-2-6 : -----MTNYENLPLYAENVKVFVKAGFIDSNGLAKGILFCLMLIITYVGAIINLCKTWNEDIGETTMNFHCFLLVTHCLIRFCIVVKKNKFERFFQCVEQWHR------ :  99
BdorOR3-2-2 : -----MTNYENLPLYAVNVKVFVKVGLIDSTGWTKGLLFCLILIITYVGAIINMCKTWYEDIGETTMNFHRLLLITHCLIRFCIIVKKNKFERFFQCIEQWHR------ :  99
BdorOR3-2-4 : -----MTSYENLPLYAVNVKVFVKVGLIDSIGWTKRFLFCLIPIITYVGQIIHIFKSWNEDMGETSMNLHILLLKTHCLIRLWLMVKKPKDFERFFQCVEQWYR------ :  99
BlatOR3-2-4 : -----MTNYENLPLYGVNVKIFVKLGLIDSIGWTKRFLVCLIPIITYVGQIIHIFKSWDDDIGEMSMNLHILLFTTHSIVRLWLMVTKPKDFERFFLCVEQWYT------ :  99
BdorOR3-2-3 : -----MTSYENLPLYLMNVKVFVKMGLIDSSGWIKRFLYGLILITSFVGQMINVSKTWSEDIGDTSMNFYCLLLVTHCLIRFSIVVKAEKFERFFQCIKQWYT------ :  99
BlatOR3-2-3 : -----MTSYENLPLYLMNVKVFVKMGLIDSSGWIKRFLYGLILIISFVGQMINFCKTWSEDIGDTSMNFYCLLLVTHCLIRFFIVVKAHKFEWFFLCIKQWYT------ :  99
BoleOR3-2-2 : -----MTNYENLPLYAMNVKVFVKLGLIDSSDWTKRFLFSLILVITLVGLVVNMFKTWDEDIGETSMNIHKLLALTHCSIRCCIMVKKAKKFERLFQSIEQWYR------ :  99
BcucOR3-2X1 : -----MASYQNLPLYSVNIKAFVKLGLIESNNSTRRFLLGIIIIVTYIGQLTNMFRTWDVDIGETGMNFHVLALVTHYLLRFIIIVRKEKKFERLFQGIEPWYT------ :  99
BcucOR3-2X2 : -----MASYQNLPLYSVNIKAFVKLGLIESNNSTRRFLLGIIIIVTYIGQLTNMFRTWDVDIGETGMNFHVLALVTHYLLRFIIIVRKEKKFERLFQGIEPWYT------ :  99
BdorOR3-2-1 : -----MQNYKNLPLYSVNVKIFLQLGLIGRSTQTKQILLAFVPVATYLGQIINLYKTWGGVIGETGMNFYMLAHITHCLVRLLMVVRNNERFMCFLQSTDRWYE------ :  99
BoleOR3-2-1 : -----MQNYKNLPLYSINVKIFLQLGLIGPSTRAKQILLAFVPVTTYLGQIINLYKTWSDDIGETGLNFYMLALVTHCLL----------------------------- :  75
BminOR3-2   : -----MTSYQNMPLYSVNIKIFLKLGLIGSGARTMRVLLGLVLILTYSGQLINFCKTWNEDIGESGMNFHVVALIMHSVVRFFVVLKKAKKFERFFQRTEQWFT------ :  99
RzepOR3-2   : -----MLDYQNLELFSVNAKIFLKLRIIGTRSKKRQLLVALEPVLSIFGQILHLFMTRNESISETGLNFFFMAVVLNLVVRLFIVIHNGDKFVRLLRLVANWYH------ :  99
BdorOR3-1-1 : ---------------------MRRIGYFDQHR--LAWLYLISPIFLCLTAYYRTYVIRN-DFDEVIVNLFKISGATTTTVRAFIVMYKAKKFLSFFESIDEWYQGLQVRF :  86
BlatOR3-1   : ------------------------------------------------------------------------------------MYKAKKFLSFFESIDEWYQ------ :  19
BdorOR3-1-2 : ------------------------------------------------------------------------------MTIGRAFIVMCKSKKFLNFFESVDEWYQELHVRF :  34
BoleOR3-1   : -------MHYCGELFNWSLAFMRRVGYFDQHR--LAGLFLISPIFLCLTAYYRTYVIRN-DFDEVIVNLFKISGATVTTARTFIVMYKAQKFLNFFESIDKWYQELQVLF : 100
BcucOR3-1   : ------------------------------------------------------------------------------------MYKSQAFLDFFVFVEKWYE------ :  19
BminOR3-1   : ---------------------MKRVGYFDQHR--LASCLLTVPIFICVSSAYRTYIIRN-DFDEVTISLFKISGAYVTTARSLIVMYKAQEFLNFFDGIDRWYQ------ :  80
RzepOR3-1   : -------MYFCEQLYNINLVYMKRVGSLGDPK--RALFMLAMPTFCCFATIYRIYQIWH-NFDEVVANFFKVSGMITITIRTFMVLSKQKKFLDFFNDIDNWYH------ :  94
CcapOR3-1-1 : -------MLYSEEIYNWNLVFMRSIGYLGNRR--RAYFLLSLPVLICFGAIYGTYKMWS-DFDKVIINLFKTSGLLTVTLRSFVIIQKEKKLYDFEDYISQLYR------ :  94
CcapOR3-1-2 : MATERKSMPNVERLFNWNLEAWTRLGYLDKRKRLLACTIISAPIVVSMFVMPTFFMGVN-TFEQHIYNFYMIIVTSSSVARAILIIIKQRKILDLLNDMENWFV------ : 103
CcapOR3-1-3 : ---------------------------------------MIPPIFCN--LYLGHD-DLGEAIYDFFTAMIDITGLIRSIVILRKQRKFLNLFGVVESWYE------ :  58
                                      g                                       n           r      k   f   f     w

                   120       130       140       150       160       170       180       190       200       210       220
BdorOR3-2-5 : --------------------EIERNDDPQMVGILQEITKRTQLLSKMTIYVAAGGTLAAIFYPLSFD----GRKHMITMQFPHFDVLQTPFYEIFFLIGVTWLTPAFLVI : 185
BdorOR3-2-6 : --------------------EIERNDDPQMVGILKEITKRTQLWSKMTIYVAAGGTFAAIFYPLSFD----GRRHMITMQFPHFDVLQTPFYEIFFLLQVTWLTPATLAL : 185
BdorOR3-2-2 : --------------------EIERNDDPQMVGILQEITKRTQLLSKMTIYVAAGGTLAAIVYPLSFD----ERRHMITMQFPHFDVLQTPFYEIFFLMQVTWFTPAVLVL : 185
BdorOR3-2-4 : --------------------DIERNGDPQMVGTLKEITKRTQLLSKMTIYVAAGGTIAAFFYPLSFD----RRKHMITVQYPFVDALQTPFFEFLFLLQVLCLAPIILVL : 185
BlatOR3-2-4 : --------------------NIKRNDDPQMVGTLQKIIKRTQLVIKIAICVAAGGTIAAFFYPLSFD----GHKHMVSVQYPFFDALQTPFYEFLFLLIQVLCLAPINVIL : 185
BdorOR3-2-3 : --------------------DIEREGDPQMVGTIQEITRKTQKLSKVTIYVAALATLAAFCYPLSFD----ERKHMIEVQYLFFDILQTPYYELFYLMEVVLVTPTILVL : 185
BlatOR3-2-3 : --------------------NIELKGDPQMVGTLQEITIKTQKLSKITIYVAALATISAFLYPVSFD----ECKHMIEVQYLFFDTLQTPFYELFYLMQVVLVTPTILVL : 185
BoleOR3-2-2 : --------------------DIERNGDPEILSTLQEINRKTDKLSKMTIYLAAMAALAGLLYPLSYN----TRTHMVTVQYPFIDALQTPFFEFFFLIQVLWLTPTVLVI : 185
BcucOR3-2X1 : --------------------DIERHGDPHIVSILQKITQKTQRLTRLSFYASVVATLATFIYSLSFD----ERRLLVTVQYPFFDVLQTPFFEFFFLIQMVWLVPTSLLV : 185
BcucOR3-2X2 : --------------------DIERHGDPHIVSILQKITQKTQRLTRLSFYASVVATLATFIYSLSFD----ERRLLVTVQYPFFDVLQTPFFEFFFLIQMVWLVPTSLLV : 185
BdorOR3-2-1 : --------------------DIELNSDAEVVLMLQDVTTHTHKLTRIGFYTITIGALFSYIYPFSFE----ERKFILHIHYIFFDAKQTPFYEFFFLLQALVLVPTFVFV : 185
BoleOR3-2-1 : ------------------------NSDPEVVRMLQDVTTHTQKLTRIGFYTILTGGLCSYIFPFLFE----ERKFILDIHYIFFDAKQTPFYEFFLVLQIVVLVPVFIVI : 157
BminOR3-2   : --------------------DIEQNSDPGVVRMLQDVITHARKVTRIGFYTSIIGALCAYIYPFSFE----ERKFILDIDYFFFDAKQTPFYEFFFLLQALILVPVFIFV : 185
RzepOR3-2   : --------------------EIERDANPEVLRKLQDVNKHARKLTRISIFAACTGMLFAYTFPFSFD----DRKLIVEVSYSFFDTKQSPFYEFFFLLQALVLVPIFCCV : 185
BdorOR3-1-1 : AGVSSLFLFICYSLTFL---HFQREDDDVTLKKAHEFTKKIKKTSKTVLILAGITLFYVIFIQLLATAGVGYKKLLVDVAFPGVDLYESPLWEMMSILQSLWIAPIVLFS : 193
BlatOR3-1   : --------------------ELQREDDDVTLKKAHEYTQKIKKTSKTVLILAGITLFYIAFIQLLATVGVGYKKLLVDVAFPGVDLYESPLWEMMSILQSLWIAPIVLFS : 109
BdorOR3-1-2 : AGGSSLFLFIYYLLTFL---HFQREGDDVTLKKAHEYTKKIKKTSKTVLILTGITIFYIMFVQLLSTAGVGYKKLILDVAFPGVDFYESPLWEMMSILQGLWTAPIVIVS : 141
BoleOR3-1   : ANRKSNFMFIYYLLTFLFNLYFQCEGNEITLNKAHEYTRKIKKATKTVLILTSITLFYVIFIQLLATVGVGYKKLLVDVAFPGIDLYKSPFWEIMSIMQSLCIAPITLFS : 210
BcucOR3-1   : --------------------EQQRDGEEVTLRKTHEFTQKIRKAAKTLLIVTMIILSYMVLIQLLATVGIGYRKLIVDVAFPGIDFYISPNWEMMSFLQCLYVAPFTFVS : 109
BminOR3-1   : --------------------ELQCDGNEITLKKVHEFMRIVKKASKTILILTALTLFYITVIQLLATADYEHK---------------------------------- : 133
RzepOR3-1   : --------------------RLRSENDEVTMKNLEEYTRKTRRASKTIFGIMIVCIFYISAIQLLTSISSTNKKYIIEVRLPFVDLYTSPYYEIISVLQALWLAPIVLLS : 184
CcapOR3-1-1 : --------------------ELQAEGDETTLKRMHEFARKTKRYTKGLFILMIACTFYISLIQVMSTFGIGLKKFLIEMELPFISVNENPYWDIFSTLQAVWLAPSILLS : 184
CcapOR3-1-2 : --------------------EVQEQNDNNALETLNKLTQKVRRYSKYTLWWVIIFGAFLSFQPICT----GYGKFVYDTQIPGIDLHQSPLYEIMYGFQSLWVIPMACVS : 189
CcapOR3-1-3 : --------------------DLKQPNEHKALETLNQIVAKVQLYSKCCLYSLLMVDVTYAFEPIIT----HYGKLVVELQLPSIDLHQSPVYEMVYLIQALWLVPLTSVN : 144
                                      d                                                   d   p  e    q    p

                   230       240       250       260       270       280       290       300       310       320       330
BdorOR3-2-5 : SLPFTNIFLISLMFGELVLKDLCVKLRNIRSE-NEETMLQEFKECIAYHQKIIDLCDDLQDLLSIDGFFHLALFGMMLCMLLFFLSMI---------------------- : 272
BdorOR3-2-6 : SLPFTNIFLISLMF------------------------------------------------------------------------------------------------ : 199
BdorOR3-2-2 : SLPFTNIFLISLMFGELVLKDLCVKLRNIRSE-NEETMLQEFKKCIAYHRKIVDWCAD-------------------------------------------------- : 242
BdorOR3-2-4 : TLPFTNIYLISLMFGELVLKDLCVKLRNIRSE-NEETMLQEFKKCIAYHQKIIALCDDLQDLLSMDGFFHVALFGMMLCMLLFFLSMI---------------------- : 272
BlatOR3-2-4 : TLPLTNIYLISLMFGELVLKDLCVKLRNIRSE-NEEIMLQEFKQCIAYHRKIIDWCDDLQDLLSMDGFFHVALFGMMLCMLLFFLSMI---------------------- : 272
BdorOR3-2-3 : YLPFTNILLISLMFGELALKDLCVKLRNIRSE-NEETMLQEFKECIEYHGKVVDMCDDLEDLISIDGFFHLALFGMILCMLLFVLSVV----------------------- : 272
BlatOR3-2-3 : YLPFTNILLISLMFGELVLKDLCVKLRNIGSE-NEETMLQDFKECLGYHGKVVDLCDDLEDLISVDGFFHVALFGMILCMLLFVLSVV----------------------- : 272
BoleOR3-2-2 : SLPFMNIFLITFTFGVLALKDLCGKLRNIRSE-NEETMLQEFKECIVYHRKVIKLCDDLEDLISIDGFFNLALFGMMLCILLFFLSMI---------------------- : 272
BcucOR3-2X1 : YLSFTNIFLTSLMFGELILKDLCLKLRNIRSE-NEMTMLKEFKDCIAYHNKIIDLCGDIEDLISMDAFFHVTSFGMMLCMLLFFLSMI---------------------- : 272
BcucOR3-2X2 : YLSFTNIFLTSLMFGELILKDLCLKLRNIRSE-NEMTMLKEFKDCIAYHNKIIDLCGDIEDLISMDAFFHVTSFGMMLCMLLFFLSMI---------------------- : 272
BdorOR3-2-1 : YLPFTNILLTSLKFG-------------------EVHDLR--------------------------------LILSALAFIS------------------------- : 216
BoleOR3-2-1 : YLPFTNILLTSLKFGELILMDMCTKLKNINNQ-DETTQLREFKECISYHEKIITFRDDLEYLVSIDGFFHVTLFGLMLCMLLFFL------------------------ : 241
BminOR3-2   : YLPFANFLLMSLKFGEVILMDLCTKLRNISNQ-DEATQLRELKECISYHEKIITFRNDLEYLVSIDGFFHIALFSLMLCMLLFFLSLV---------------------- : 272
RzepOR3-2   : YLAFTNLFLAFLMFGEVVLLDLRVRLDSISSSGNKAAMLHELKECIAYHRKIISYRNDLDNLVKVANFFDVALFGLMFCMMLFFMSLV---------------------- : 273
BdorOR3-1-1 : YVSYLCLTLIAIAFGIFLMKNLQSKLEGMNEM-TDEEALKCIKKCVKDHVMIIKYHRDLEVLFSVGSFADVCIFAIIPCVIIVISTM---------------------- : 279
BlatOR3-1   : YVSYLCLTLIAIAFGIFLMKNLQTKLEGINEK-TDEEALKFIKKCVKDHVMIIKYHQDLEVLFSVGSFADVCIFAIIPCVIIVISTM---------------------- : 195
BdorOR3-1-2 : YVSYLCLTLIAIAFGIFLMKNLQSKLEGMNEM-TDEEALKCIKKCVKDHVMIIKYHRDLEVLFSVNSFADVCIFAVIPCVIIIISTM---------------------- : 227
BoleOR3-1   : YVSYFCLFLIAIAFGIFLMKDLQSKLESMNDM-TDVEALECINKCVKDHIMIIKYHNDLEVLFSVGSSADVCIFGIIPCVIIVFSTM---------------------- : 296
BcucOR3-1   : YVSYLCLTLIAISFGIFLMKDLQFKLENMNDM-TDLEALNCIKKCVKAHVMIIKYHNHLEALFSVGSFADVCIFGIIPCVIIVLSTM---------------------- : 195
BminOR3-1   : ---------SISFGTFLIKDLQYKLESTTDM-TELEALKCIKKCVKDHVMIIKYHNDLEVLFSSGSSVSVSIFGITPCVIIVFSTMVSSNRSNLFLCYIFKFKFTIILH : 232
RzepOR3-1   : YVSYLCVIISISFGIFLMKDLQQKLGNMHEL-NELEGLECIKKCIQQHVLIIKFHRDLEVLFSAGNFVDVSIFCIIPCVIIVYANM---------------------- : 270
CcapOR3-1-1 : YISYLCIIFTTISFGILLMKDLQFKLGNMNEK-NDLEAYEYIKNCVKQHVMIIKYHRQMEVLFSLGSCAEVCNFCIIPCVIIVYSTM---------------------- : 270
CcapOR3-1-2 : SISYADTLLIFISFGIFATKQLQRKLKDISQM-DEQQGLENIKKCVQYHWKIIKFGEDLENAYSLMCLLDFSLYCVTLCMLLFYSVM---------------------- : 275
CcapOR3-1-3 : YVSYSNSLLIFTIFGVFATRHLQQKLMEISQM-EDDEALANLKQCVVYHSKIIKFGENLEELYSLMSLLDISLYCISVCLMLVYLTM---------------------- : 230
                   l    Fg      l  kl            l   k c   h  ii    d   l s         f    c

                   340       350       360       370       380       390       400       410       420       430
BdorOR3-2-5 : --HDLRLILAALSFVSFTTYMLFITYYYANKLVTE-SLEVANAAYDTPWYRGNLEMRKCVITMIARCQKPLQMTAGGIYPMTMETFQAILRVSYSYFSLLQGLNQQ--- : 375
BdorOR3-2-6 : ------------------------------------VANAAYDTPWYRGNLEMRRCVITMIARCQKPLQMTAGGIYPMTMETFQAILRVSYSYFSLLQGLNQQ--- : 266
BdorOR3-2-2 : ------------------------------------LQDLLSMDGFFHLALFGMMLCILLFFLSLIHDLRLFLAALSFVSFTTYIISITYYYANKLATEVLHAT--- : 310
BdorOR3-2-4 : --HDLRLILTILTFVSYTTYMLFTTYYYANNLATE-SLEVANAAYDTPWYRGNLEMRKCVITMIARCQKPLQMKAGGLYPMTMETFQAILRVSYSYFSLLQGLSQQ--- : 375
BlatOR3-2-4 : --HDLRLIVTILTFVSYTTYMLFSTYYYANKLATA-SLEVANAAYDTPWYRGNLEMRKCVITMIARCQKPLQMNAGGLYPMTMETFQAVLRVSYSYFSLLQGLSQQ--- : 375
BdorOR3-2-3 : --HNLRLILMVFVFVSFNIYMIGITYYYANNLATE-SLEVANAIYDTPWYRGNLEMRKSVITMIARCQKPLQMKAGGLYPMNMETFQAILRVSYSYFSLLQGLNQ---- : 374
BlatOR3-2-3 : --HNLRLILMVFVFVSFNIYMIGITYYYANNLATE-SLEVANAIYNTPWYRGNLEMRKCVITMIARCQKPLQMKAGGLYPMNMETFQAILRVSYSYFSLLQGLNQ---- : 374
BoleOR3-2-2 : --DDLRLILVGLVFVSLNTYMIGITYYYANNLATE-SVEVANAAYDTPWYMGNLEMRKCVTIMIARCQKPIQITAGGLYPMNMENFQAILRISYSYFSLLQGLSQQ--- : 375
BcucOR3-2X1 : --DDLELIPAVLVMMGFDMYLIGFSYYYANNLATE-SLEVANAAYDTPWYRGNLEMRKCVLIMIARSQNPLQITAGGLYPLTMENFQAILRISYSYFSLLQGVSQQ--- : 375
BcucOR3-2X2 : --DDLELIPAVLVMMGFDMYLIGFSYYYANNLATE-SLEVANAAYDTPWYRGNLEMRKCVLIMIARSQNPLQITAGGLYPLTMENFQAILRISYSYFSLLQGVSQQ--- : 375
BdorOR3-2-1 : ----------------FNFYVIGITHYYANNFSNETTLKRAYAAYDTPWYEGNMELRKCVQIMIARSHKPLEIKSSGLYPMTLENFQAILRISYSYFSMLXGFNQQ--- : 306
BoleOR3-2-1 : ----------------SLMFFIFVSAYTLYILLLMQSLKVAYAAYDTPWYEGNPELRKCVQIMIARSHKPLEIKAGGLLPMTLENFQAILRISYSYFSMLQGFSQK--- : 331
BminOR3-2   : --HDIRLILTALAFISFHIYIIGITYYYADNFSNE-SLKVAYAAYDTPWYEGNSELRKCVQVMIARSHRPLEIKSGGLYPMTLENFQAILRISYSYFSMLQGFNQQ--- : 375
RzepOR3-2   : --KDIQLVLSAVVFISFPVYVIAISYYYANKFTNE-SIQICNAAYNTPWYEGNLEMRKCVLIMIARSQRPLYITVMGMYPMTLETFQAIIRISYSYFSLLQGLSQQ--- : 376
BdorOR3-1-1 : --DHDMSLLIADIQLSLMVMISTFIIFWVANNFCYESANIAKAAYNCNWENRNKEFRKYIPLIIITSQRPLQLTAGGLKPINMEFFLTMVRCTYSLFTVLFTMKTEGDS : 386
BlatOR3-1   : --DHDMSLLIADIQLSLIVMISTFIIFWVXNNFCYESENIAKAAYNCNWESRNKEFRKYIPLIIMASQRQLQLTAGGLKPLNMEFFLTMVRCTYSLFTVLFTMKTEGDS : 302
BdorOR3-1-2 : --DHDMSMLIGDIQLSIMVMISTFLVFWVGNNFCYENENIAKAAYNCNWENRNKEFRKYIPLIIITSQRPLQLTAGGLKPINMEFFLTIVRCTYSFFTVLFTMTTEGDS : 334
BoleOR3-1   : --DHDMSLLIADIQLSLLVMISTFIFFWVANNFCCESEKIANAAYNCNWEDRNKEFRKYIPLIIITSQRPLQLTAGGLKPINMEFFLTMVRCTYSLFTVLITMKTEGDS : 403
BcucOR3-1   : --DHDISMLIADIQMAAMVMTSTFIFFWVANNFVIESENIANAAYNCNWVDRDKEFRKYIPLIIGNSQKPLQLTAGGIKPINMEFFLTIVRCTYSLFTVLFTMKTGGDS : 302
BminOR3-1   : LQDHDMSLLIADIQLSLLVMISTFIFFWVANDFCCEV-----------------IWDYFPHIYN----------------------ICYYNL-------------- : 285
RzepOR3-1   : --EYNLAFMITDVQLVFVVIFSTYIIFWLANSFYIEGLNIAHAAYNCNWVDRGKDFRKYIVVIMTVGQKPLELTAGGLKPVNMQFFLAIVRVSYSIFTVLQGTKKDY-- : 375
CcapOR3-1-1 : --DYDLAFLMTDIQLAVIAVSSTFFNFWLANNFCVESLNIAYAAYNSNWIDRNKEFRKYIVLIMTMSQKPLQLTAAGLKPINMEFFLAILRAAYSLFTVLQ-------- : 369
CcapOR3-1-2 : --DFTWALMFQAVVVELILTLLIFLTTFLADIFTQESLNVAQTAYDMNWLQRDKAFRVAVLLIILRSQRPLILTAGGIQPLNLETFLAIMRSSYSFFSVLRGVM----- : 377
CcapOR3-1-3 : --DFTWPLLFKGVIVILFLTTLIFLTYHVADVLTHESMNIAELAYNTNWMDRDKEFRSCIQVIIVRSQRPLMLTAGGFQPMNMKTFLAIMRASYSFFSVLRSTV----- : 332
                                                  a aay   w     e rk     i   q pl   agg  p   e f    r  Ys f  l
```
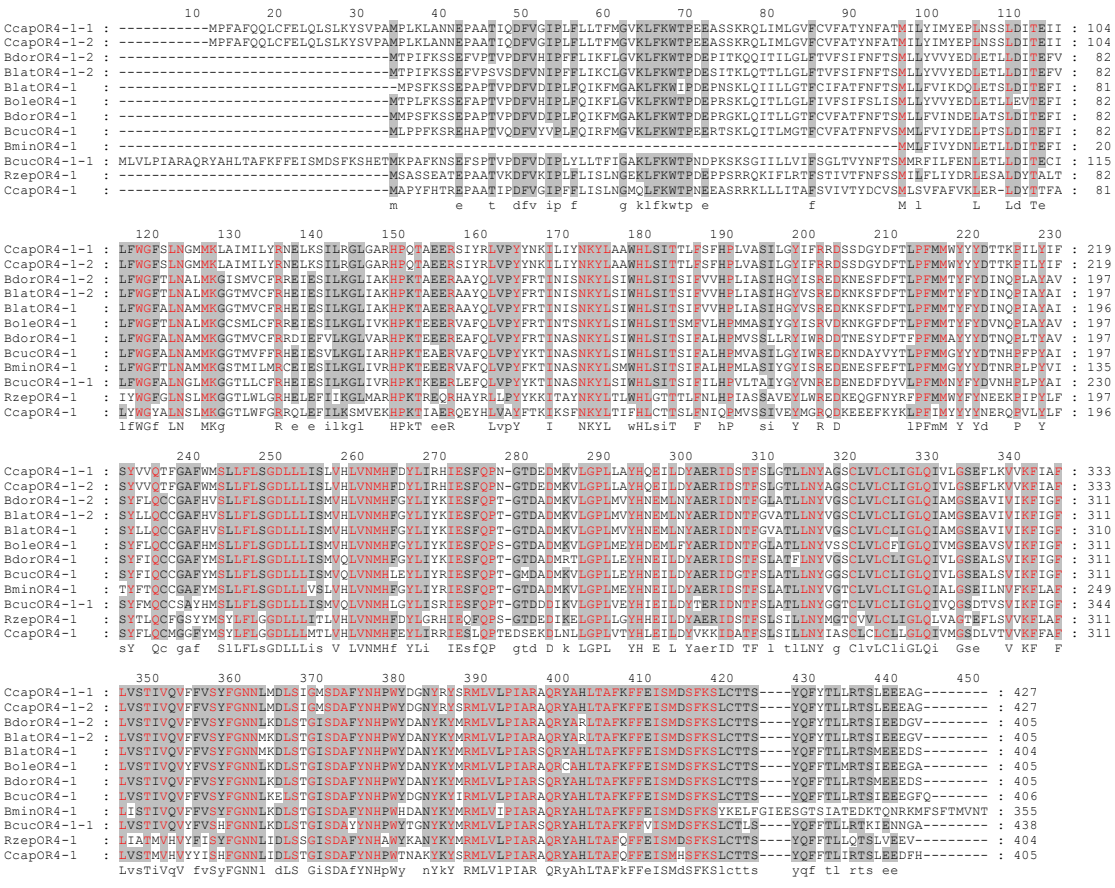
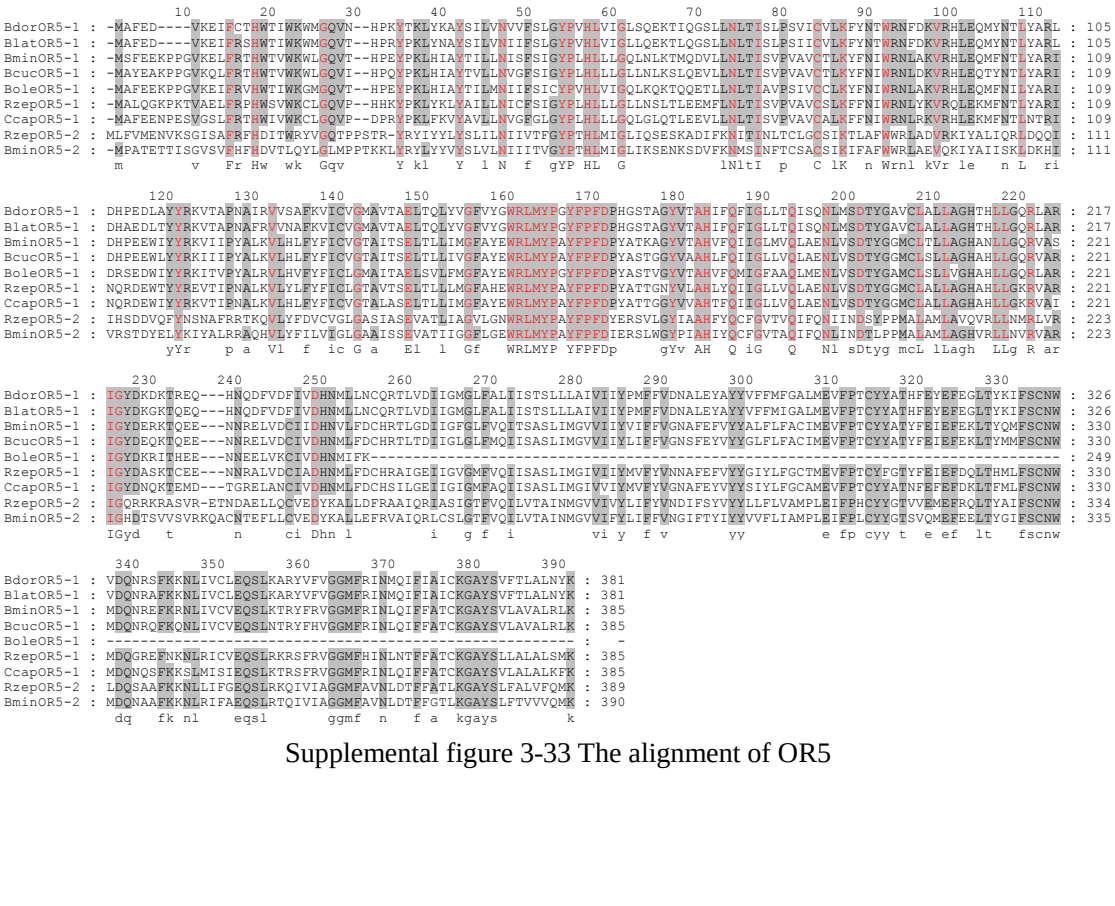
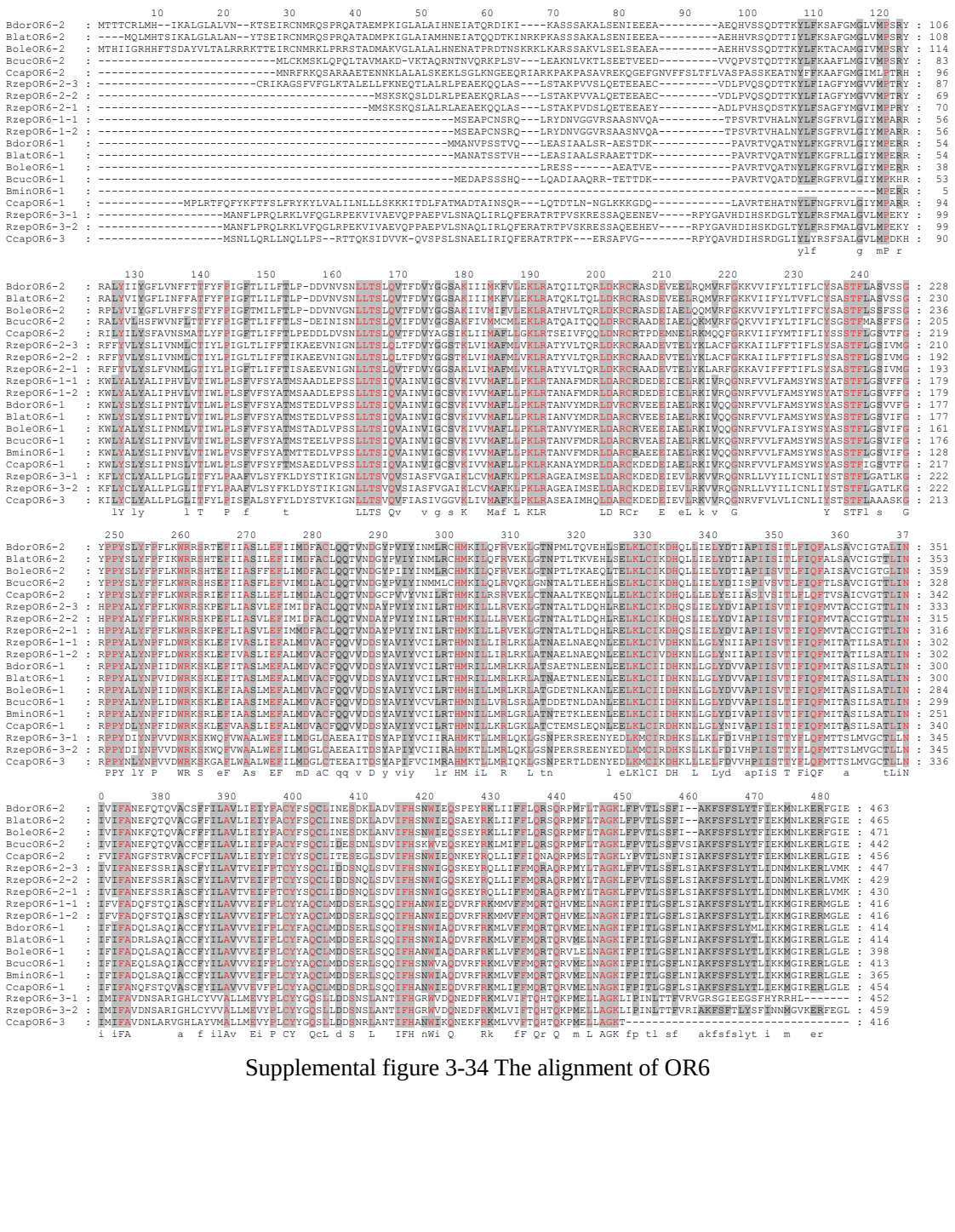

Supplemental figure 3-31 The alignment of OR3



Supplemental figure 3-32 The alignment of OR4



Supplemental figure 3-33 The alignment of OR5

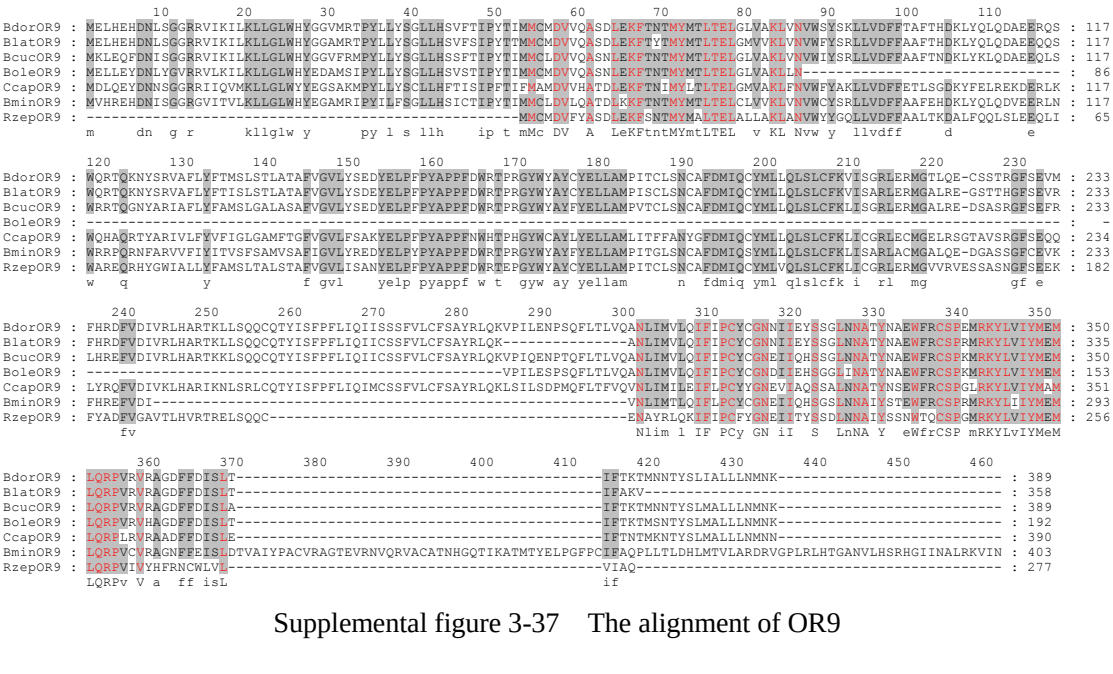


Supplemental figure 3-34 The alignment of OR6

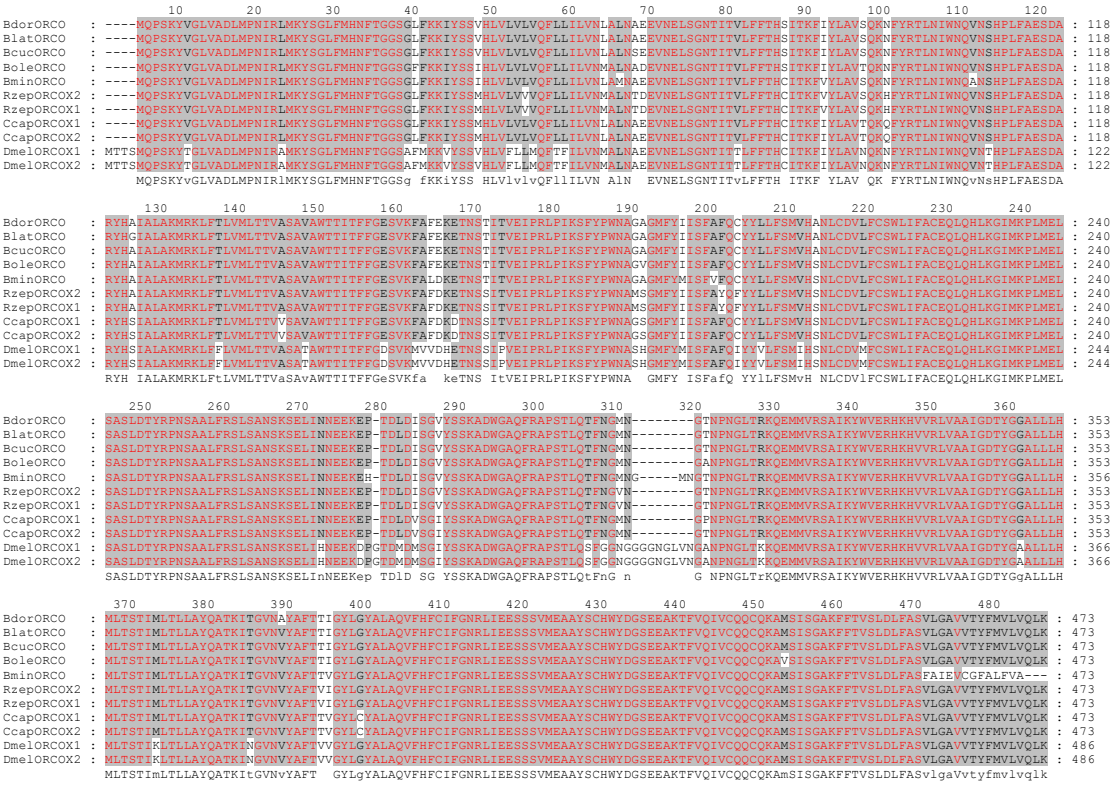
```
                        10        20        30        40        50        60        70        80        90       100       110
BdorOR7-1   : MSKILLVRSATVYKSRDALTYLFNVFTFMGTNPLENRSQRYYRLYHFYSFTVNFICCLFCPLSFHIGYIKLRHVLTNSQLLAAIQNAVQVSGIPIKILVITWYMKRLRHA : 110
BlatOR7-1   : MSKILRFRSAIVYKSRDALTYLFNIFTFVGTNPLENRSQRYYRLYYFYSFTVNFICCLFCPLSFHIGYIKLRHVLTNSQLLAAIQNAVQVSGIPIKILVITWYMKRLRHA : 110
BminOR7-1   : MSKILRVSRAKIYKSRDAVSYLFNIFTFLGTNPLEHRSRRYYFLYYFYSFTLNFISLLYCPLSFHIGYIKLTHVLTNSQLLTAIQNAIQVSGIPIKVVAITWYMKRLQHA : 110
BcucOR7-1   : MPNLIRVGGACIYKSRDSLTYLFKIFTFVGINPSEQQSRKYYWLYYSYSLTVNFICCLFSPLSFHIGYIKLWHVLNNNQLLAAIQNAVQVTGIPIKILVITWYMKRLRQA : 110
CcapOR7-1-1 : MLDLLRGRGRRVYKSRHALTYLFNVFTFVGTNPGKTRTHKYYTLYYTYSLTVNFICCLFCPLSFHIGYIKSWHLLNTTELLAAIQNAVQVTGIPIKIFFITWNMRRLQSV : 110
RzepOR7-1   : MLDLLRGRGLEAYKSRDALTYLFNIFTLVGTNPQGQQSNKYYYLYYLYSVTVNFICCFFSPLSFHIGYIKYLNVLSTTELLAAIQNAVQVTGIPVKIIVITWHMKSLLSA : 110
CcapOR7-1-2 : MSDLLFGRGQIVYKSRHALTYLFNIFTFVGTNPLGGQSYAYYSLYYLYSLLVNFVCCIFCPISFHIGYIKLLNVLNTNELLSAIQNAIQVSGIPIKIIVIAWYMKRLQSV : 110
              M   l       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   : FEILDELDVNYTRREDLAKIRECVRRCRKIVLIFCFPYYSFELTTIALGVAQNRAPLAAWVFFLDGQR-AAWEYWTIVLWDAFVMFFLLCHQLGSDTYPPIFINIIRTHV : 219
BlatOR7-1   : FDILDELDVNYTRREDLAKIRECVRRCRKIVLIFCFPYYSFELSTIALGVVQNRAPLAAWVFFLNGQR-AAWEYWTIVLWDAFVMFFLLCHQLGSDTYPPIFINIIRTHI : 219
BminOR7-1   : VEILDELDVNYTQREDLAKIRECVRRCRKVILLFCLPYYSFGISTIALGVLQNQAPLTVWVFFLDGKR-AAWEYWTIVLWDTLVMFILLCHQLGNDTYPPIFIKVISTHM : 219
BcucOR7-1   : FKILDQLDVNYTQHEDLAKIRECVRRCRKIVLIFCLPYYSFELSTIALGLLQKRAPLAAWVFFLDGQR-AAWEYWTIVLWDTFVMFILLSYQLGGDTYPLIFLNIIRTHV : 219
CcapOR7-1-1 : IPILDELDENYKSAKDLLKIRKCVRGCCKMIGFFCLPYYSYEITTIALGVWQNRAPLAAWVFYLDGQR-AAWEYWTIVVWDIFVMFFLLSHQLGSDTYPPIYINIIRTHV : 219
RzepOR7-1   : REILDELDANYRRADDLLRIRQCVRRCCKIIVIFCVPYYSFEITTIAFGVLQHRVPLAAWVFYLDAQGGAEWQYWTIVVWDTFVMFILLTHQLASDTYPPVYISIIRTHI : 220
CcapOR7-1-2 : CEILDKLDENYKRAEDLNSIRRCVRSCCKIIAAFCVPYYGFELSTIAFGVYQNRAPLTIWLFYFDATR-TTWEYWTHVGWDVFIMLFLLAHQLGSDTYPPVFISVIRLHM : 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   : QLLIARVNRLGRTGALTADEHYELLGCIRTHVQIVSIAKIVAPVISVTLFTQFATTATTLLNWLGNVEYPENIISLAFFSCQLLQILPCCSSASQLIADCERLP----- : 324
BlatOR7-1   : QLLITRVNRLGRAGALTADEHYELLGCIRTHVQIVSIAKIVAPVISVTLFTQFATTATTLLNWLGNVEYPENIISLAFFSCQLLQILPCCSSASQLIADCERLP----- : 324
BminOR7-1   : QLLVTRVNRLGRPGALTADKHYELLL----------ASKIVAPVISVTLFTQFATTATTLLNWFGDMEYPENIISLAFFCCQLVQILPCCLSASQLIADCERLP----- : 313
BcucOR7-1   : QLLVTRVSRLGRDGALSADEHYALLLACIRTHVQIVSIANIVAPVISVTLFTQFATTATTLLTWFGNVEYPENIISFAFFSCQLLQIFPCCSSASQLIADCERLP----- : 324
CcapOR7-1-1 : QLLVERVELLGSDKTKSAEEHYALLGCIRTHGQIKRIVNLIAPVISVTLFTQFATSATTLLNWFGDVEFPENIISFAYFTCLTLQILPCCSSASYLISDCELLP----- : 324
RzepOR7-1   : QLLVERAKRLGGDRMLNADENYALLLACIRTHCQILRLARIVAPVISITLFTQFATTAITVLNWFGNVEFPENIISFAFFSCQLMQILPCCYCASLLIDDCDQLP----- : 325
CcapOR7-1-2 : QLLVERVKRLGTNKALCREKRYALLVCINTYGQILSIANIVAPVISITLFTQFATTATTVLNWFGNMKFPDNIIPMAFFSCQIMQILPCCYYASQLIADWCFLMTHHSL : 329
              QLL  Rv rLG    l a   Y ELL ci t  qi     ivAPVIS TLFTQFATtAtT LnW G  e PeNIIs AfF Cq  QIlPCC  AS LI Dc  Lp

                       340       350       360       370       380       390       400       410       420       430
BdorOR7-1   : --------------------DAIFHCNWVDQDRFFRRAMLFFLQRAQNPIRFSCLKLFNVKLETS------VAIGKFAFSLYT--LIEETKVGTDTEN----- : 394
BlatOR7-1   : --------------------DAIFHCNWVDLDRFFRRAILFFLQRTQNPIRFSCLKLFDVKLETS------VAIGKFAFSLYT--LIEETTVGTNTDN----- : 394
BminOR7-1   : --------------------DAIFHCNWMDQDRFFRRAILFFLQRTQTPIRFSCLKLFDANLETS------VAIGKFAFSLYT--LIHEAEDGGKTDN----- : 383
BcucOR7-1   : --------------------DAIFHCNWVDQDRFFRRAILFFLQRTQKPMRFWCLKLFVVKLETS------VAIGKFAFSLYT--FIQESDVGRKSNN----- : 394
CcapOR7-1-1 : --------------------NAIFHCNWIERDRFFRKTLLFFLQRTQTPLRFSCLKLFVVKLETS------VAIGKFAFSLYT--LIQGTEVGGKTEN----- : 394
RzepOR7-1   : --------------------NAIFHSNWMDQNRFYRKTILFFIQRTQNPIRFSCLKLFGVNLATG------MAIGKFAFSLYT--FIKESKVGDKLDK----- : 395
CcapOR7-1-2 : RPIFEQHYRPAVGSVIRATIDQLYTVLTLLDNAFPPSAVIATVEQNIKENPNEYIHYREAQLEPCSSTFCKILLKNLGLRTYKTQLVQESKQNDQLERCTSAK : 432
                                  aifh nw    rR r   lff qr q p rf clklf   Let        aigkfafslYt   i e   g
```

Supplemental figure 3-35 The alignment of OR7

Supplemental figure 3-36 The alignment of OR8



Supplemental figure 3-37 The alignment of OR9



Supplemental figure 3-38 The alignment of ORCO