

Supplemental file 1

>BminOBP8a [gene=OBP8a] [protein=odorant-binding protein 8a] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi011412] [locus=Contig914:542161:543131:+ len:468nt odorant-binding protein 8a]

MKGTALVFIIPFSALFANINADYEEKTEDDFLSAGERCFQRRERLAASYQHRFDNFDYPDEQ
PVHRYVHCIWTELKLWNDRTGFNVEHIAALYRDKANTEVLVPILSDCNRNAQNDPILNWC
YKAFKCVLNSRVGQWFKEDVGRKLQERHVGHNHVA*

>BminOBPlush [gene=OBPlush] [protein=odorant-binding protein lush]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi007112]
[locus=Contig2134:556799:557867:- len:330nt odorant-binding protein lush]

MQQFETSLDMMRNGCAPKFKVSTEILDNLAGEFAENNSDLKLTKKGDFSVQKALAQIPI
ILPPEMQDAAKEALNACKDVQKNYKDSCDRVFYTTKCVRDYPSTFKFP*

>BminOBP19a1 [gene=OBP19a1] [protein=odorant-binding protein 19a1]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi003171]
[locus=Contig1349:2158519:2162429:- len:348nt odorant-binding protein 19a1]

MLNKNPFILTAVFIALVLHSDQVSGGATEDQMISAGKLMRDVCLPKFNKMKKGKFLYESS
LKQVDLLMPDSYKDDYRNLGKCKDVANGIKNNCDASYAVLICLRDNISKFVFP*

>BminOBP19a2 [gene=OBP19a2] [protein=odorant-binding protein 19a2]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi003172]
[locus=Contig1349:2167677:2170122:+ len:444nt odorant-binding protein 19a2]

MNFCKVLFTTSVLAFLFATSISAGVTEEQMWATAKLMRDVCLPRFPKISIELANQLRDGNIP
DNNKDVKCYINCVLEMMQTMKKKGKFLYEASLKQVDLVLDPDNYKDDYRAGLLKCKDAN
GGIKRDNCEAAYRILKCLCGEIKKFIFP*

>BminOBP19b [gene=OBP19b] [protein=odorant-binding protein 19b] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi003173]
[locus=Contig1349:2174610:2175352:- len:465nt odorant-binding protein 19b]

MFKVFTVFTGTILIVTREVLAEEMMTLPMSSLLETIEPYAMECEPNPERVHAEELFLNKED
AHPITKCLRRCLMDQFELFAEDSTDVNTEKLVSWMVLLYSEKMDELKELSNGCNEKTIEM
GIIDKCEVAHSFAMCMLKEMREREYEIPEVEQ*

>BminOBP19c [gene=OBP19c] [protein=odorant-binding protein 19c] [organism=Bactrocera minax]
[moltype=protein] [country=China] [ID=Bmi003174]
[locus=Contig1349:2177516:2178547:- len:555nt odorant-binding protein 19c]

MANSSSVLLFAGFICLMAVQSLSALNEDSHKLFGRKPLMTREDPSTLEDYKRTKRQLSQ
PLQDFQDFIITSKTQCAREMDINPNELQKALLYEDQPTPKCKLMCEILKRMEVMDKDDT
LSTSAIGRIADIIGENNALITSIAMATAENCKKFITAKDSCERAYQINKCIAAEMKMRKIKLI
Y*

>BminOBP19d1 [gene=OBP19d1] [protein=odorant-binding protein 19d1]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi003187]
[locus=Contig1349:2323057:2325125:- len:426nt odorant-binding protein 19d1]

MKFLNIGLIVCVTLISNAMCDYEEAKAAAELCKEEVGATDDDVETILKFEPAGTMEAKCL
HACIIKRFGVMNGDGKIDRDKAMEILTIASGNGEQQALGVEVLEACADIDVNEDHCEAA
EEYRTCMHAKAKENGFMGRV*

>BminOBP19d2 [gene=OBP19d2] [protein=odorant-binding protein 19d2]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi003188]

[locus=Contig1349:2327243:2328975:- len:432nt odorant-binding protein 19d2]
 MKYFVVFLAICSSAICFSEAGELLEKVKNIAEECKNQVGASDDDDVAGLLKYEPAANDKAK
 CLRACTMKKFGIMDENNKLVAAAIDYIKAVAAGDAEFEKLSTEVFNECKNTPASSDECE
 FAETFSSCIENSKSKGIKILPQ*

>BminOBP19d3 [gene=OBP19d3] [protein=odorant-binding protein 19d3]
 [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi003186]
 [locus=Contig1349:2317823:2320040:- len:477nt odorant-binding protein 19d3]
 MEVFKVLPFIALLSLVFAIIAADTGSNPPHYSSLRVMAEAAIEDCYEDAAESVKVQITDES
 DEIVKGSRTNLSRNAKCLRYCIMRKNGLLNEDNSIDRENILQIFQIIHPQIEKDFPLDVIQKC
 SREMDKQADNCECAFVASSCILRELQVDGVTDI*

>BminOBP28a [gene=OBP28a] [protein=odorant-binding protein 28a] [organism=Bactrocera
 minax] [moltype=protein] [country=China] [ID=Bmi003166]
 [locus=Contig1349:2007997:2008688:- len:444nt odorant-binding protein 28a]
 MAKFILIAALCILSAVVSKAAFNKEEVIKTFMTRAEECRGEVGAADSDVQDILSKLPAAGK
 EGKCLRNCLMKKYSAVDNNGKFVKSVAEEHAQIYTDGDADKMKIAHEIIDACAGIPVPD
 DPCEAAEVYGKCFLEQAKAHGIEKFDF*

>BminOBP47a [gene=OBP47a] [protein=odorant-binding protein 47a] [organism=Bactrocera
 minax] [moltype=protein] [country=China] [ID=Bmi004519]
 [locus=Contig1553:5809231:5809976:- len:666nt odorant-binding protein 47a]
 MDSKLIVLTATMLAAIVELTPFLSVSEARSASVKMSLDLSVSEDQHRISADMVSLCALETDL
 SMGELRRFSENDFRNATKAIECFTHCLYEHMGLLNNGVFVERDIISLLGDVTDLKRMLER
 ECLGQYSDNKCERAFLIHQCYRAGQVRMMAPNRQPESIDQLNEERDGEEEKSVANLPKS
 DMAMPSVHRMATDSERQLLIKILAKRLPKKQTINQGLVEE*

>BminOBP50c [gene=OBP50c] [protein=odorant-binding protein 50c] [organism=Bactrocera
 minax] [moltype=protein] [country=China] [ID=Bmi005981]
 [locus=Contig1765:1515036:1516529:+ len:765nt odorant-binding protein 50c]
 MKYFVGSLLLILLGVNAYDFDSDVFNEYLFKELQSHYEEDQVYLHRRARREATDAADAK
 ECSKRNWKKDMQCKGKNVIGDQLELFKSVKKQCIADLKGEPADDAFDPFDCCKMQQV
 KEQMICITECIAKKFKSLDENGELQRDAILEGLRAQIGTVQWKVDAIEGYVDKCLAEVKE
 KLDQKKKAGELKEGGCSRSPLAFHSCMWRQFWNGCPADLRVDSPKCNKLRERVANGDT
 RFFGKHFLNKYYPSPRDEE*

>BminOBP56a [gene=OBP56a] [protein=odorant-binding protein 56a] [organism=Bactrocera
 minax] [moltype=protein] [country=China] [ID=Bmi006859] [locus=Contig2076:264209:264928:-
 len:501nt odorant-binding protein 56a]
 MKSSIICCILATVLLSLCTFGTDAALGRKPKKLTPELESKFVLTAWIAYRLNLKHAKEACV
 GEYGFSDLATNLVKIRVANPSDNEKCYVNCLYNKLVFYKDNAINKQAMKESLYEIVGEQ
 RLMNIVNGCLNAGGTNACDKVYKFHACASPEFDKVRSDIFLPDE*

>BminOBP56b [gene=OBP56b] [protein=odorant-binding protein 56b] [organism=Bactrocera
 minax] [moltype=protein] [country=China] [ID=Bmi006857] [locus=Contig2076:216452:217185:-
 len:417nt odorant-binding protein 56b]
 MKSLGFLYLFVAVFICGPITQLYAADDKAAREICIKETKLT PADANLVRGA AVISKLIQNEPE
 ALKCFRLCYKELGLIDAAGKT NAPKILEYMMQVSGVSDKTRLASALGACESVKGTSNC
 DKWYQFEKCALAKLGA*

>BminOBP56c [gene=OBP56c] [protein=odorant-binding protein 56c] [organism=Bactrocera

minax] [moltype=protein] [country=China] [ID=Bmi006858] [locus=Contig2076:218158:219269:-len:852nt odorant-binding protein 56c]

MYIISLFAILLCAAVQHAKSRTITLSVNMSLTMGVERHKELLEMRHQQRQQEQTRPAFTA
TLLRSCMKQTELSMAELQHFRSLFCRDPCLDCSDEPSTELPNFYEMEEDNLVSGETQIDG
IYEPASDINEQNNNALEYEDPLTIKSDGKTDESLQCFVYCLYEQLGLIAKGVYMESELF
LYALVGRERHLVKECMNLNTNNKCESSYKMHLCYASLKILEEENRIRKILENAKDDQERE
EILEAETAQETHAMEETEPTQSIFAYAEGAKTEEVGVEQ*

>BminOBP56d [gene=OBP56d] [protein=odorant-binding protein 56d] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi006856] [locus=Contig2076:208209:208978:-len:414nt odorant-binding protein 56d]

MKFFTIVAVFAFVAVAAAQEGIKLSEEQKQKVHTLGAELTETGASEAAVRAVGKGDLSQV
DDKVKCFKCLQGKLGYPFENGQVNEAVVQSSLGKVVGEEKIKAIQAKCNGLKGTDDCD
TAFLLHKCYVAENASTLV*

>BminOBP56g [gene=OBP56g] [protein=odorant-binding protein 56g] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi006852] [locus=Contig2076:13872:14887:+len:516nt odorant-binding protein 56g]

MKSFITIALFVVSACAVVLCNANDPEMRKQIEECNKEHNVTPKDYHDFMEGKLTIPENLK
CSSHCVMKQKQIMDDSGKFKAEEVAKAKMNDDKFSATVDECKDLSGSTPCDTAMKITEC
LLSHK*

>BminOBP56h1 [gene=OBP56h1] [protein=odorant-binding protein 56h1] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi006853] [locus=Contig2076:112291:113005:+len:408nt odorant-binding protein 56h1]

MHTLYVLTIIIVLTLAVCQSPADLEKFKHACMDEAKVTNEELKKFFQNGMKYDAAKENI
KCHTKCLMQKHGVWKNAGFAEAKAKELMQIPKLKEHEVQIKQALSNCCKNEKGANEC
DTAFKITMCLKEFKAQID*

>BminOBP56hlike [gene=OBP56hlike] [protein=odorant-binding protein 56h-like] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi008922] [locus=Contig3340:32457:32990:-len:402nt odorant-binding protein 56h-like]

MKVVLLCFVSALLVAAQAEVPLKELIETCSKETGVPSEELQQFLDSEMDPAEATNGIKCH
MKCVLEKIGLYKNNMLDEALTIKFFKDNNKQDPVDVEALKQSVQNCNQQKGVDPCDTA
FQIAKCFMSQHPIFN*

>BminOBP58c [gene=OBP58c] [protein=odorant-binding protein 58c] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi002479] [locus=Contig1300:1346081:1386904:-len:606nt odorant-binding protein 58c]

MKNSTLIIFSFAWLLKFGNSLKIDCDNPEFIREDRIHYCCKHPDGYQEFVDSCAKETGFNYI
QSNEESIVDITADHATMGTCFAKCVFNKLQFMKGDELDMASVRQHFESKYKADPEYAKE
MINAFDHCHGKSVENTAKFLSNPIFHNIGAEFCDPKPGVIMACVIREFFHNCPADRWAKTE
ECNTVLEFSKKCKDALTTI*

>BminOBP73a [gene=OBP73a] [protein=odorant-binding protein 73a] [organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi005271] [locus=Contig1697:132056:133593:+len:795nt odorant-binding protein 73a]

MISNVVYRAYIALILLDRAGILAKDLHGNSFTKVLRSKGSQLSRCLNPPRTARRVESFIQDC
QEDVKNKLFSEAYYILKSEVNKEYTELDITVDNIAEIDSTPASPAAPSLIFHTIEGNSNLASS
HNSYQFQSDRQQVTSLMHRIGRISYDPRSAIYHPTLVPAEEKRLAGCLLHCYAKNNAIDK

LGWPTLDGLVNFYSEGVNEHGFFMATLRSVNLCLHAITIKYNINRRKLPLKGESCDLAFD
VFDCISDQLTGYCLNQYE*

>BminOBP83a [gene=OBP83a] [protein=odorant-binding protein 83a] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi002228]
[locus=Contig1291:2252022:2252987:+ len:447nt odorant-binding protein 83a]

MYSIKSILGTLLWFGFLTTVIWAQKELRRDETYPPPELLKALRPVHDSCVSKTGVTTEEAIKE
FSDGDVHEDELLKCYMYCVFEETDVLHEDGEVHLEKILDSLPQSMHDIALHMGKKCLYP
KGDNCERAFWLHRCWKESDPKHXYFLI*

>BminOBP83b [gene=OBP83b] [protein=pheromone-binding protein-related protein 83b]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi002229]
[locus=Contig1291:2258164:2261909:+ len:531nt pheromone-binding protein-related protein 83b]

MVLTGIWRCQAFNAFLIVALSSSLTLMHVQAQEPRRDDKWPPPAVLKMAKIFHDICVEKT
GVTEEAIKEFSDGQIHEDEALKCYMNCLFHEIDVVDDNGDVHLETLYNTVPGTVRDKLIN
MARGCEHPEGDTLCHKAWWFHQCWKKADPVIAEVRGGRPATRTPLSSPAALVTPAF*

>BminOBP83cd [gene=OBP83cd] [protein=odorant-binding protein 83cd]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi002221]
[locus=Contig1291:2006182:2011265:- len:1599nt odorant-binding protein 83cd]

MKLILIFLFAAAIISPSVAVVQPNAAEEVRIISECLQSYGGLTEDNSQRLVRFKDWSEKYEEIPC
FTKCYIKNMFD MFDES VGFKDEQVIKQFGQPLYIACEHRMKPSTDNCQQAYNGFHCLVN
LEDDPFVIIESMKNVSTEAKTAMKDC LHRFDQYEWERIKDYAKNPVREPIPCFTKCFIDRL
QLYSQQTRQWNIPALTAKLGVPAAGANIQHCLKQRRNRNACVNSAATTKAANQDVE

>BminOBP83g [gene=OBP83g] [protein=odorant-binding protein 83g] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi002220]
[locus=Contig1291:2004665:2005886:+ len:429nt odorant-binding protein 83g]

MQTQLILLMACVALVAGKFHVRTAQDALDAHEACHEEYRVPEDIYQKFLNYEFAPHKRTN
CYVKCFVERMGLFTEEKGFDEKAIQAQFTAKSSKNLAKISHGLEKCLDHNEHDSDTCTWA
NRVFSCWISVNRPIVRRTYIEN*

>BminOBP84a2 [gene=OBP84a2] [protein=odorant-binding protein 84a2]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi011107]
[locus=Contig900:3020516:3021247:- len:513nt odorant-binding protein 84a2]

MSNSNVLVVCPFMIMLLYCSIMISIQDRAKDNGDIFVQHKEQQECVRPIIVQANDSISSEGT
DVVLMCNSSFSIPSDYIAQFNMNGALSDTLDKTGMCFIRCYFEKAGLIKWNQNLKDMIM
QTMRLIKAN SIEFCEPEAKQETNACIRTYAIAKCLMKRGFEDTCIQTV*

>BminOBP99b [gene=OBP99b] [protein=odorant-binding receptor 99b]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi011411]
[locus=Contig914:535616:536235:+ len:465nt odorant-binding receptor 99b]

MKFFLALLSLIFAVVLADEHDHAAHSDYVVKTNADLLRYRDECVSKLSIPADLVEKYKQ
WNFPDDEKTPCYLKCILEKFGLYDEEKGFVDVHKIHHQLDGDKVDHSDATHGAIENCAKE
AAAAGDDACVRAYRGFSCFLKDNIQLVQAGVDKGSK*

>BminOBP99d [gene=OBP99d] [protein=odorant-binding protein 99d] [organism=Bactrocera
minax] [moltype=protein] [country=China] [ID=Bmi011413] [locus=Contig914:542542:560860:-
len:672nt odorant-binding protein 99d]

TEELFNPAVPISEYEEASRRLYKAQGICIQKISSPTTRDNVASTEQAAGAYVRCIASNMGL
WTDATGYNSKRVAKFFIKEHNENEVMTVVDYCNQKHQQADLDLWAFEAYRCATAGRMG

IWLREYVLSAKL*

>BminOBP99c1 [gene=OBP99c1] [protein=odorant-binding protein 99c1]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi011415]
[locus=Contig914:665977:666592:+ len:450nt odorant-binding protein 99c1]

MKFFIVILAVVALACAEDEWVPKNVAEIKVIRQECIKESLSEEHIQKLKNLEYPDDEEPVRK
YLLCTAEKLGVFCEHEGFHANRIAKQFKMDLDEAEVLAIAEGCVDKNEEGSSPDVWAYR
GHKCLIDSKIGESVKAYIKKSADEAKKQ*

>BminOBP99c2 [gene=OBP99c2] [protein=odorant-binding protein 99c2]
[organism=Bactrocera minax] [moltype=protein] [country=China] [ID=Bmi011416]
[locus=Contig914:669005:669795:- len:426nt odorant-binding protein 99c2]

MKYFIVILAIIALVQADDWSPKTTDEIKSIRENCVKQVPSSDEEFKNRKKDEYPDIESVRNY
VLCTSKAWGLYEDGKGFKEHVAQQFKGDLSEDEIKSIVHDCDEKTKEDSDDERAYHVL
MCILSSKLGGDVKELLKRSE*

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP8a : MPQAMKKTAFVF---ILFLAALFAH---INADYEKTEDDFLSAGERQFQERLAASYQRRFDNFYDPEEPVQRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 103
BlatOBP8a : MQQAMKKTAFVF---ILFLAALFAH---INADYEKTEDDFLSAGERQFQERLAASYQRRFDNFYDPEEPVQRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 103
BoleOBP8aX1 : MPQAMKKTAFVFH---ILFLAALFAH---INADYEKTEDDFLSAGERQFQERLAAPYQRRFDTFDYDPEEPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 103
BoleOBP8aX2 : MPQAMKKTAFVFH---ILFLAALFAH---INADYEKTEDDFLSAGERQFQERLAAPYQRRFDTFDYDPEEPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 103
BminOBP8a : ---MKRTALVF---IIPFSALFAN---INADYEKTEDDFLSAGERQFQERLAASYQRRFDNFYDPEEPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 99
BcucOBP8a : MPQAMKKTAFIL---ILFSTLIAL---INADHEETEDDFLSAGERQFQERLAASYQRRFDNFYDPEEPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 103
CcapOBP8a : MTEAMKKTSTIAFTWIIILLFNEINP---IGADFEKTEEDFLTASERQFQERLAASYQRRFDNFYDPEAPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 106
RzepOBP8aX2 : ---MKRTTLAY---IIFLFTTQMP---ISADFEKTEEDFLTASEHVERERLPASYQRRFDNFYDPEEPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 99
RzepOBP8aX1 : ---MKRTTLAY---IIFLFTTQMPYGGISADFEKTEEDFLTASEHVERERLPASYQRRFDNFYDPEEPVHRYVHCITWELKLNWDRDTGFNVHEHIAALYR--DKANTE : 102
DmelOBP8a : ---MMRRSQIGLLSRLLLLLLVVELTPPAIPVPMRSSPQSALLLRARDQGRELTAQRLQLDRMQFEDAHHVRYHLHCFSWSRLQLWLDETFGQAQRIVQSGFGERRLNVE : 108
      Mk t      ii      i ad eekteddfl a erc rerL A yqrrfd f ype pV rYvHCITwELkLNwDrTGFNVehIAaLYr dkaNtE

      120     130     140     150     160     170
BdorOBP8a : VLVPIILSDNNRQAQN---EPTLKWQYRAFKQVLNSRVGQWFKEDVGRKLEERRVGNHVA : 159
BlatOBP8a : VLVPIILSDNNRQAQN---EPTLKWQYRAFKQVLNSRVGQWFKEDVGRKLEERRVGNHVA : 159
BoleOBP8aX1 : VLVPIILSDNNRQAQN---EPSLKWQYRAFKQVLNSQVGQWFKEDVERKLQERRVGNHVA : 159
BoleOBP8aX2 : VLVPIILSDNNRQAQN---EPSLKWQYRAFKQVLNSQVGQWFKEDVERKLQERRVGNHVA : 159
BminOBP8a : VLVPIILSDNNRQAQN---DPIILNWQYKAFKQVLNSRVGQWFKEDVGRKLQERRVGNHVA : 155
BcucOBP8a : VLVPIILSDNNRNTQN---EPTLKWQYKAFKQVLNSRVGQWFKEDVGRKLHERRVGNHVG : 159
CcapOBP8a : VLVPIILSDNNRNTNN---APTILKWQYNAFKQVLNSRVGQWFKEDVERKLHERRTGNHVA : 162
RzepOBP8aX2 : VLVPIILSDNNRQAQN---EPTLKWQYNAFKQVLNSRVGQWFKEDVGRKLQDTKTTNHLG : 155
RzepOBP8aX1 : VLVPIILSDNNRQAQN---EPTLKWQYNAFKQVLNSRVGQWFKEDVGRKLQDTKTTNHLG : 158
DmelOBP8a : QALPAINGNAKTSRSGAQTVVDWQFRAFVQLVATPVGEWYKRHMSDVIN---GNA--- : 163
      vLVpIILsdCnRn qn p l WC AFKCVLns VGqWfKedv rkl nGh

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Supplemental figure 1-1 The alignment of OBP8a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP19a2 : -----MWATAKLMRDVCLPRFPKISIELANQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEASLKQVDLVLDPDSYKDD : 78
BlatOBP19a2 : MMYFQKAIPTTSLAFLFLTP--ISAGITEEQMWATAKLMRDVCLPRFPKINIELANQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEASLKQVDLVLDPDSYKDD : 108
BcucOBP19a2 : -MHFQKVLFTTSLAFLFATP--ISAGVTEEQMWATAKLMRDVCLPRFPKISIELANQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEASLKQVDLVLDPDSYKDD : 107
BminOBP19a2 : -MNFQKVLFTTSLAFLFATS--ISAGVTEEQMWATAKLMRDVCLPRFPKISIELANQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEASLKQVDLVLDPDSYKDD : 107
RzepOBP19a2 : -----MWATAKLMRDVCLPRFPKISIELADQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEDASL----- : 64
CcapOBP19a2X2 : -----MWATAKLMRDVCLPRFPKIATELADQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEASLKQVDLILPDSYKDD : 78
CcapOBP19a2X1 : -MKYFKVLITLQIMLVFIAP--TFAGVTEEQMWATAKLMRDVCLPRFPKIATELADQLRDGNIPDNNKDVKQYINQVLEMMQTMKKGKFLYEASLKQVDLILPDSYKDD : 107
BdorOBP19a1 : MLNKINSFVLATVFIALVLHSDQVSGGATEEQMISAGKLMRDVCLPKPFKISPEVADGIKEGNVPD-TKDVKQYINQIMEMMQTMKKGKFLYESALKQIDLLMPDDYKDD : 109
BlatOBP19a1 : MLNKINSFVLATVFIALVLHSDQVSGGATEEQMISAGKLMRDVCLPKPFKNISPEVADGIKEGNVPD-TKDVKQYINQIMEMMQTMKKGKFLYESALKQIDLLMPDNYKDD : 109
BoleOBP19a1 : MSNKINFLVLAVFIALVLHSDQVFGGATEEQMIAAGKLMRDVCLPKPFKNISPEVADGIKEGKVPD-TKDVKQYINQIMEMMQTMKKGKFLYESALKQVDLLMPDSYKDD : 109
BminOBP19a1 : MLNKINFFILTAVFIALVLHSDQVSGGATEEQMISAGKLMRDVCLPKPFKN-----MKKGKFLYESSLKQVDLLMPDSYKDD : 76
BcucOBP19a1 : MSNKINFLVLAVFIALVLHSDQVFGGATEEQMIAAGKLMRDVCLPKPFKVPT-DVADGIKDGIVPE-TKEVKQYINQIMEMMQTMKKGKFLYESALKQVDLLMPDSYKDD : 109
CcapOBP19a1 : MLPRMNLFLVPAVLIVLTNDRVYGATEEQMIAAGKLMRDVCLPKPFKVPT-DVADGIKDGIVPE-TKEVKQYINQIMEMMQTMKKGKFLYESALKQVDLLMPDDYKDD : 108
RzepOBP19alp : -----DLY--TFIFSFP---EVADGIKLGNIPT-TKDVKQYINQIMEMMQTMKKGKFLLESSLKQIDLLMPDDYKDD : 66
RzepOBP19a1 : -----MFAAGKLMRDVCLPKPFKVSTEVADGIKLGNIPT-TKDVKQYINQIMEMMQTMKKGKFLLESSLKQIDLLMPDDYKDD : 77
DmelOBP19a : -MKFHLLLVCAISLGPQPQS---EAGVTEEQMWSAGKLMRDVCLPKPKYSVEVADNIRNGDIPN-SKDTNQYINQIMEMMQAIKKGFQLESTLKQMDIMLPDSYKDD : 105
      m kLmrdvcIpl f k e a g pd kdvkcyinc emmqtmKKGKfL e lKq dI pd ykd

      120     130     140     150
BdorOBP19a2 : YRAGLLKCKDASAGIKKD-NC EAAAYTILKCLRGEIKKFIFP : 118
BlatOBP19a2 : YRAGLLKCKDASAGIKKD-NC EAAAYTILKCLRGEIKKFIFP : 148
BcucOBP19a2 : YRAGLLKCKDAAGVIGKD-NC EAAAYTILKCLRGEIKKFIFP : 147
BminOBP19a2 : YRAGLLKCKDANGGIKRD-NC EAAAYRIKCLRGEIKKFIFP : 147
RzepOBP19a2 : ----- : 
CcapOBP19a2X2 : YRAGLLKCKDASAHIKKD-NC ESAYTVLKLRLGEIKKFIFP : 118
CcapOBP19a2X1 : YRAGLLKCKDASAHIKKD-NC ESAYTVLKLRLGEIKKFIFP : 147
BdorOBP19a1 : YRNLAKCKDVTSGIKN--NC DASYALLICMRDNISKFLFP : 148
BlatOBP19a1 : YRNLAKCKDVTSGIKN--NC DASYALLICMRDNISKFLFP : 148
BoleOBP19a1 : YRNLTKCKDVTSGIKN--NC DASYALLICMRDNISMFLFP : 148
BminOBP19a1 : YRNLGKCKDVGANGIKN--NC DASYALLICMRDNISKFVFP : 115
BcucOBP19a1 : YRNLGKCKDAAVGIGK--NC DASYALLICMRDNITKFVFP : 148
CcapOBP19a1 : YKSGFAACKDSPNGIKN--NC DASYALLICMRDKITKFVFP : 147
RzepOBP19alp : YRAGLQCKDAVNGIKN--NC DAAYALLICIRGEIKRFIFP : 105
RzepOBP19a1 : YRAGLQCKDAVNGIKN--NC DAAYALLICIRGEIKRFIFP : 116
DmelOBP19a : YRKGINLCKDSTVGNAPNCPAHALLSLKNNIKVFVFP : 146
      yr gl ckd gik nc y l c r i f fp

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Supplemental figure 1-2 The alignment of OBP19a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP19b : -----MNVKLTVFVAVVLMIAIRKVLAEKIMKPMGLALETLEPPFAMNCKLKPEKAHMEELILNKEDADLITKRLRGQLMEQFQLFVEDSTDVNTKELLWSM : 97
BlatOBP19b : -----MNVKLTVFVSVVLMIAATKEVLAEIIMKVPMLGAVETLEPPFAMNCEHKPEKVHMEELILNKEDADVLTCLRSQLMEQFELFVEDSTDVNTKELLWSM : 97
BoleOBP19b : -----MYKVFTVFVAVIILMIATRKVLAEIIMKIPMGLVLAEVVEPYAMNCEPKPEKAHMEELILNKEDADHLITKRLRGQLMEQFQLFVEDRSTDVNSEKLVSWM : 97
BminOBP19b : -----MFKVFTVFTGTILIIIVTREVLAEEEMMTLPMSLLLETIEPYAMNCEPNPERVHAHEELFLNKEDADHPITKRLRRQLMDQFELFAEDSTDVNTKELLWSM : 97
BcucOBP19b : -----MKGFIVFAIILIVMATKEVLAEEMMTLPMLGLLLETIEPYAMNCEPKPERVHAHEELFLNKEDADHPITKRLRRQLMDQFQLFVEDSTDVNTKELLVSWL : 96
RzepOBP19b : MEVFSVFLASSKVKSGKMLKVFIIFTVTTFISITQNVQANDIMKPLMGLLLEGVAVANAKCPKPELHMEELILNKEDAQHATKFRRLMDQFELFVEGGTQVHTKEVLGYM : 114
CcaphOBP19b : MFHIVAAELISMMGVLADEMMTLPICMLIEGVVEFPYQCDPKPELHMEELILNKEDAQHTTKRLRRQLMDQFELFVEGGTQVHTKEVLGYM : 94
DmelOBP19b : -----MMQSRMTTTLKMTNLLLAVALAAVLMGSATADEEGSMTVDVEVLEIFPGDASTPKPSRENIVEMVLNKEDAKHETKFRHMLMEQFELFMPEDQLQYNEKDTVDMI : 108
      k f l t vlaee m pmgl E eP a C pKPe h eEl LnkEDA TkClR Clm QF Lf Ed t v eKl m

      120     130     140     150     160
BdorOBP19b : VLLYSEKIDELRAISNGNNAKNVEMGITDKEVAHSYAMMLKEMKEREYEIPEVEQ : 154
BlatOBP19b : VLLYSEKIDELRAISNGNNAKNVEMGITDKEVAHSFAMMLKEMKEREYEIPEVEQ : 154
BoleOBP19b : VLLYVEKMDELIDISNGNEKNVEMGITDKEVAHSFAMMLKEMKEREYEIPEVE- : 153
BminOBP19b : VLLYSEKMDDELKELSNNGNEKTIEMGITDKEVAHSFAMMLKEMKEREYEIPEVEQ : 154
BcucOBP19b : VLLYTDKMDDELNEISNGNEKNVEMGITDKEVAHSYAMMLKEMQEREYEIPEVEQ : 153
RzepOBP19b : LLLYPDKMDDELSEISDNGNEQNNQMGIEEKEVAHSYAMMLKEMQSRNVEIPEVEQ : 171
CcaphOBP19b : ALLYPEKADELNEIVDGNQNRNKDMGLNEMKEVAHSFGMMLKEMQSRVEIPIVEQ : 151
DmelOBP19b : NMMFPDREDDDRIVTKTNEELKAE--QDKTEAAHGIAAMLREMRSSSGFKIPEIKE : 163
      lly k Del is gCN n mgl dkCvAhS aMCMCLKEM reyeIpeveq
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Supplemental figure 1-3 The alignment of OBP19b

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP19c : MVKSSSALLIAGFIQLMSLQSLTALSEDADKLSEKRRPLMTRREDPSTLLEDYKTRKRLPQLPQEQDFVTTSTKTQAKEMNNINPNELQKSLLYEQDPTSMEKMMELVKLRIE : 113
BlatOBP19c : MVKSSSALI---ICLMSLQSLTALSEDADKLSEKRRPLMTRREDPSTLLEDYKTRKRLPQLPQEQDFVTTSTKTEAKEMNNINPNELQKSLLYEQDPTSIEKMMELVKRIE : 110
BoleOBP19c : MVNSSSALLIAGFIQLMTLQSLNALIEDAYKLSGKRRPLMTRREDPSTLLEDYKTRKRLPQLPQEQDFVTTLSKAQAKDLNINPNELQKSLLYEQDPTSIEKMMELVKLRME : 113
BcucOBP19c : MANSSSALLIAGFICMMVQSLDALNADVYKLSGKRRPLVTRREDPTALEDYKTRKRLPQLPQEQDFVTTSTKTEAKEMNNINPNELQKSLLYEQDPTSIEKMMELVKLRME : 113
BminOBP19c : MANSSSVLLFAGFICLMAVQSLALNEDSHKLFGRKRPMLTRREDPSTLLEDYKTRKRLSQPLQDFQDFIITSKTQAKEMDINPNELQKALLYEQDPTSIEKMMELVKLRME : 113
CcaphOBP19c : -MYSNKTLLFASLILLLAVESINALNANSYKLSGKRRPLATREDATIIEDYKTRKRLSQPMQEQFQAFITTSKQQAASEMGFKANEMKSLLYEELPTPEKKMMELVKLRME : 112
RzepOBP19cX2 : -MTRQNSLELDGKTRKRLQTLQPMQEQDFITTSKTQKANGMGFSADELQKSLLYEQDPTSIEKMMELVKLRME : 74
RzepOBP19cX1 : MISLRNKMFTVILAAAFQSINALDTNPYKLSGKRRPLMTRREDPTALEDYKTRKRLPQLPQEQDFVTTSTKTQAKANGMGFSADELQKSLLYEQDPTSIEKMMELVKLRME : 113
DmelOBP19cX1 : -MKPSTPVAaipLMTIIVAVLLQTHVRGQTQAFLAKLLEPKTG-----TEPIMAVIDRNLNPQVQELVTAARMEITKLQLPRD--QRLPGKVTNPSKKKGLVEVLKKIK : 104
DmelOBP19cX2 : -MKPSTPVAaipLMTIIVAVLLQTHVRGQTQAFLAKLLEPKTG-----TEPIMAVIDRNLNPQVQELVTAARMEITKLQLPRD--QRLPGKVTNPSKKKGLVEVLKKIK : 104
      l l tr dyktrtkrql p q qf f t sk Ca e qk llye Pt EKC EC Lkr e

      120     130     140     150     160     170     180
BdorOBP19c : VMKDDTLSTTTIGHIADIIGNNALITSIAMAASAENCKKFITAEDSCERAFQINKITAAEMMKRRIKLIY : 184
BlatOBP19c : VMKDDTLSTTTAIGYADIIGNNALITSIAVASAENCKKFITAEDSCERAFQINKITATEMMKRRIKLIY : 181
BoleOBP19c : VMKDNDLSTTTAIGHIADIIGNNALITSIAMAASAENCKKFITAEDSCERAFQINKITGAEMMKRRIKLIY : 184
BcucOBP19c : VMNQDDTLSTSAVGRIADIIGNNALITSIAMAASAENCKKFITAEDSCERAFQINKITANEMMKRRIKLIY : 184
BminOBP19c : VMKDNDLSTTSAIGRIADIIGNNALITSIAMAASAENCKKFITAEDSCERAFQINKITAAEMMKRRIKLIY : 184
CcaphOBP19c : VMDRDNLSTPAIGRIADIIGNNALITSIAMAASADNCKKFITAEDPCERAFQINKITATEMMKRRIKLIY : 183
RzepOBP19cX2 : VMKDNDLSTTAAIGRIANIVGNNNPLITSIAMAATDNCKKFINAEDSCERAHQINILITATEMMKRRIKLIY : 145
RzepOBP19cX1 : VMKDNDLSTTAAIGRIANIVGNNNPLITSIAMAATDNCKKFINAEDSCERAHQINILITATEMMKRRIKLIY : 184
DmelOBP19cX1 : LMDADNKLNVGQVEKILSVTDQNKMAIAVSSSMAQAASRGISGSKNPEVAHLFNQISRLQLERNNVKLWY : 175
DmelOBP19cX2 : LMDADNKLNVGQVEKILSVTDQNKMAIAVSSSMAQAASRGISGSKNPEVAHLFNQISRLQLERNNVKLWY : 175
      vM d Lst g ia i g nN l tsia a A Nckkfi a CERa qin CI emkarkiriLly
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Supplemental figure 1-4 The alignment of OBP19c

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      10      20      30      40      50      60      70      80      90     100     110
DmelOBP19dX1 : -----MSHLVHLTVLLLVGIIIGATSAKFHEEINRDHAAELANEKKAETG-----ATDDEVEQLMSHDLPERHE-AKQLRA : 71
DmelOBP19dX2 : -----MSHLVHLTVLLLVGIIIGATSAKFHEEINRDHAAELANEKKAETG-----ATDDEVEQLMSHDLPERHE-AKQLRA : 71
BdorOBP19d2 : -----MKYFVFLVLAISPAISFS-----EAEF-GEKVKKIAEECKQVGV-----ASDDVVARLFKYPEAANDK-AKQLTA : 64
BlatOBP19d2 : -----MKYFVFLVLAISPAISFS-----EAEF-GEKVKKIAEECKQVGV-----ASDDVVARLFKYPEAANDK-AKQLTA : 64
BoleOBP19d2 : -----MKYFVFLVLAISLVISFS-----EAEF-LEKVKKIAEECKQVGV-----ASDDEVAGVFKYPEAANDK-AKQLTA : 64
BminOBP19d2 : -----MKYFVFLVLAISPAISFS-----EAGEL-LEKVKNIAEECKQVGV-----ASDDVAGLLKYPEAANDK-AKQLRA : 64
CcaphOBP19d2 : -----MKYFVFLVLAISLVISHT-----EAGEL-LEKIKQIAEECKQVGV-----ASDDVTRMLKYPEPATNK-AKQLGA : 64
BcucOBP19d2X1 : -----MKYFVFLVLAISLVMSYS-----EAGEL-PWRLKKIIEEKKARLG-----AGDDVVAAMFKYPEPATNK-VKQLHA : 64
BcucOBP19d2X2 : -----MRLKKIIEEKKARLG-----AGDDVVAAMFKYPEPATNKQ-VKQLHA : 40
RzepOBP19d2 : -----MKYFVFLVLAISLATSIA-----QLEEV-VKKAQKIAGDKKEEVG-----ATDADVAEMFKHEPAGNDK-AKQLTA : 64
CcaphOBP19d2 : MEVFKDSSDLXYDYVPYPSDGLYLSMQLIAIPLNVLVITAEILIRNVINHFVIYFQANDLVDKVTKLAQEKKGSTG-----ASGDADYENLNLNQAPITDR-GKGLTE : 104
BminOBP19d1 : -----MKFLNIGLIVLVALISNA-----MDG-YEEAKAAAECKKEVG-----ATDDDVETILKFEPAETME-AKQLHA : 62
BoleOBP19d1 : -----MKFLNIGLIVLVALISNA-----KGG-HEEAKAAAECKKEVG-----ATDDDVETILKFEPAETME-AKQLHA : 62
BdorOBP19d1 : -----MKFLNIGLIVLVALISNA-----KGN-YEEAKAVANECKKEVG-----ATDDELETILKMAEATTT-EKQLGA : 62
BcucOBP19d1-1 : -----MKLLKILIVLVALISNA-----KGG-SEEAKAAAECKKEVG-----ATDDDVVAAMFKFESAGSME-AKQLHA : 62
BcucOBP19d1-2 : -----MKLLKILIVLVALISNA-----KGS-FEEVKAAAECKKEVG-----ATDDDVVAAMFNFESAGSME-AKQLHA : 62
CcaphOBP19d1 : -----MKFLNIGLIVLVAALANT-----KDD-FEGVKLTAQEKKEVG-----ATDDEVETMFKHEPAGSAG-AKQLHA : 63
RzepOBP19d1 : -----MKSYPILVNVAVFTSVY-----EDG-LEKFKAVAEECKKEVG-----ATDDEVETMINHEPAGTP-AKQLHA : 62
BdorOBP19d3 : -----MEILIVLP-----ILAVS-VFTITIA-----AAESEPPHYSSLRVMAEAAIEDYEDSAQSVKQVITDESFDILKGSRTNLSHNAKRLY : 81
BlatOBP19d3 : -----MEILIVLP-----ILAVS-VFTITIA-----AAESEPPHYSSLRVMAEAAIEDYEDSAQSVKQVITDESFDILKGSRTNLSHNAKRLY : 81
BoleOBP19d3 : -----MEILIVLP-----ILAVS-VFTITIA-----AAESEPPHYSSLRVMAEAAIEDYEDSAQSVKQVITDESFDILKGSRTNLSHNAKRLY : 81
BminOBP19d3 : -----MEVFKVLP-----IPALLSLVFAITIA-----DTGSNPHYSSLRVMAEAAIEDYEDAAESVKVQITDESFDILKGSRTNLSHNAKRLY : 82
CcaphOBP19d3X2 : -----MA-----SADAKPHYSLRVVAAEAAIADYEDSAQSVKQVITDESFDILKGSRTNLSHNAKRLY : 62
BcucOBP19d3X1 : -----MHTFKILP-----IPAVLSSIIYITMA-----SADAKPHYSLRVVAAEAAIADYEDSAQSVKQVITDESFDILKGSRTNLSHNAKRLY : 82
CcaphOBP19d3 : -----MEIPKFFF-----IFAIITIGSKMTLV-----VADSKPHYSSLRLMAEDAIGDYEDAAESVKVQITDESFDILKGSRTNLSHNAKRLY : 82
RzepOBP19d3 : -----MMFTVEVRLFLNIVRIICMRLVLSLTIILAILSLVPSMLADPPPHYDSLRTMAEAAVEDYEDADQNVKVEITDEGFDLLKSGRGNLRLNNAKRLY : 99
      C d aKCl
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      120     130     140     150     160     170     180     190
DmelOBP19dX1 : CVMKKLIQIMDESGLNKHEAIELVVKVMSKHDAEKEDAPAEVVAKEAETPEDHDAAFAYEECIYEQMKHEGLEEEH- : 150
DmelOBP19dX2 : CVMKKLIQIMDESGLNKHEAIELVVKVMSKHDAEKEDAPAEVVAKEAETPEDHDAAFAYEECIYEQMKHEGLEEEH- : 150
BdorOBP19d2 : CVMKKLIGTMDENNKVVEAGAIAIYIKQLSGDAEFKLSLETYNCKSTPESSNCEYAEAFQCVLESAKSKGLKILPQV : 144
BlatOBP19d2 : CLMKKIGILDENNKVVEAAAAIAYVKQVSGGDAEFKLSMETYNECKSTPESSNCEYAEAFQCVLESAKSKDKILPFR- : 143
BoleOBP19d2 : CMKRLGILGIDENNKVVEAGAIAIYIKQVAGDAEYKQSMVELVNCKNTPPESSNCEYAEAFRVCIYESSKSGKIKILPQ- : 143
BminOBP19d2 : CVMKKGILGIDENNKVVEAGAMAYIKSLAAGDAELEKLTVEVNECKNTPPASNECEYAEAVRACTIENSKSGKIKILPQ- : 143
BcucOBP19d2 : CVMRLGILGIDENNKVFEAGAMAYIKSVTASNAELEKLLTVEVNECKYFPASKEGEFSEAFRVCIERSRAKGIHMLLH- : 143
BcucOBP19d2X1 : CVMRLGILGIDENNKVFEAGAMAYIKSVTASNAELEKLLTVEVNECKYFPASKEGEFSEAFRVCIERSRAKGIHMLLH- : 119
BcucOBP19d2X2 : CVMRLGILGIDENNKVFEAGAMAYIKSVTASNAELEKLLTVEVNECKYFPASKEGEFSEAFRVCIERSRAKGIHMLLH- : 142
RzepOBP19d2 : CVMKNGFLDADNKLKVDGVDFLKSISGGDADYKLGTEILDADKTPAGGNNCEETSEALRTCLIEKSQEKGFKLFPF-- : 142
CcaphOBP19d2 : CVLKKSGLGIDENNKVINEAVMVEFIKAGAAGDASIEKIGMEGLQACLKVPQHPNACENAAALNACFTKNLRAGFKGLPA- : 183
BminOBP19d1 : CIIKRFVGMNGDGKIDRDKAMEVLTIIASNGEQQALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKENGFMGRV- : 141
BoleOBP19d1 : CIVKIRFGVMNGDGKIDRDKAMEVLTIIASNGEQQALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKENGFMGRV- : 141
BdorOBP19d1 : CVMKRFGMNGDGKIDRDKAMEVLTIIADGNDEQHALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKEIGFVGRV- : 141
BcucOBP19d1-1 : CVMKRFGLINGDGKMDRDKAIEILENIASGDNEQQALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKEIGFVGRV- : 141
BcucOBP19d1-2 : CVMKRFGLINGDGKMDRDKAIEILENIASGDNEQQALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKEIGFVGRV- : 141
CcaphOBP19d1 : CVMKRFGLMNDGKMDRDKAIEILENIASGDNEQQALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKEIGFVGRV- : 142
RzepOBP19d1 : CVMKRFGLMNDGKMDRDKAIEILENIASGDNEQQALGVEVLEACADIDVNDHCEAAEYRTCMHAKAKEIGFVGRV- : 141
BdorOBP19d3 : CVMKRNGLLSVMSIDENILQIFQIHP-QIKKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
BlatOBP19d3 : CVMKRNGLLSVMSIDENILQIFQIHP-QIKKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
BoleOBP19d3 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
BminOBP19d3 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
CcaphOBP19d3 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
BcucOBP19d3X2 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
BcucOBP19d3X1 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
CcaphOBP19d3 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
RzepOBP19d3 : CVMKRNGLLIDNISIDENILQIFQIHP-QVEKDSLLDLVHKARETDKQTDNERAFVATCILRELQADGVTDI--- : 157
      C m g e l C e a C g
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Supplemental figure 1-5 The alignment of OBP19d

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP28a : ~MAKILFLFAALILSAAVSNAAFNKEEAIKNFMTKAEERGEVGAADSDIQNIIVAKLPAASKEGKGLHSCLMKKYGAMDSNGKFVKVSAQDHAQDFTDGDADKLKTAREII : 110
BlatOBP28a : ~MAKIFLFAALILSAAVSKAAFNKEEAMKNFMTKAEERGEVGAADSDIQDIIAKVPAASKEGKGLRSCLMKKYGAMDSNGKFVKVSAQDHAQDFTDGDADKLKTAREII : 110
BoleOBP28a : ~MAKIFLFAAFILSAAVSKAAFNKEEAIKTFMTRAEEERGEVGAADSDIQDIIVAKVPAAGKEGKGLRSCLMKKYGAMDNNGKFVKVSADEHAQTYTDDGADKLKIAREII : 110
BcucOBP28a : ~MAKIFLILAAALILSAAVTKAAFNKEEAIKTFMTRAEEERGEVGAADSDIQDLIAKVPAAGKEGKGLRSCLMKKYGAMDNNGKFVKVSADEHAQTYTDDGADKLKIAREII : 110
BminOBP28a : ~MAKIFLILAAALILSAAVSKAAFNKEEIVIKTFMTRAEEERGEVGAADSDVDQILSKLPAAGKEGKGLRNLCLMKKYSAVDNNGKFVKVSAEEHAQTYTDDGADKLKIAREII : 110
CcaphOBP28a : ~MAKIFLILAAALILSAAVTKAAFNKEEAIKTFMTRAEEERGEVGAADSDIQDLITKSPAAGKEGKGLRSCIMKKYGVMSDNGKFVKVSAEHEHTKTYTDDGADKLKIAREII : 110
RzepOBP28a : ~MAKILVLGAFILNAAVSKAAFNKEEAIKNFMTNVEERGEVGAADSDIEDLIKKAPAASKEGKGLRSCIMKKYGVMSDNGKFVKVSALEHASTFTDGDAEKMTANEIT : 110
DmelOBP28a : MQSTPIILVAIVLLGAALVR-AFDEKEALAKLMESEASMPPEVGATDADLQEMVKKQPASTYAGKGLRAVMKNIGILDANGKLDTEAGHEKAKQYTGNDPAKLKIALEIG : 110
      mak il aA cilsAav kaAFnkeEaik fMt aBeCrgEvGAdsdIdg K PAa keGKCLrsc MKkyg md nGKfksva eha TdgDadKLK A EII

      120      130      140
BdorOBP28a : DAADIAPVDDHDEATEVYVGKCFMDQAKAHGIQKDFD : 147
BlatOBP28a : DAADIAPVDDHDEATEVYVGKCFMDQAKAHGIQKDFD : 147
BoleOBP28a : DAADIAPVDDHDEASELYGKCFMDQAKAHGIQKDFD : 147
BcucOBP28a : DAADIAPVDDHDEATEVYVGKCFMDQAKAHGIQKDFD : 147
BminOBP28a : DACAGIPVPDDPEAAEVYVGKCFLEQAKAHGIQKDFD : 147
CcaphOBP28a : DAADIAPVDDHDEATELYGKCFMEQTKAHGIDKDFD : 147
RzepOBP28a : DACAGIAPVDDHDEAAEYVGKCFMEQAKAHGLDKDFD : 147
DmelOBP28a : DTAATITVPDDHDEAAEAYGTGFRGEAKKHGLL---- : 143
      DaCa IaVpDdChCEa E YGkCFm qaKahGi kf f

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Supplemental figure 1-6 The alignment of OBP28a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP44a : MKYIVAVLLAALVAMAAAEYKIRNQDDLKARKEEAKKVPTIEHIEKFKKFEFPDDEVTRCYIECFNKFQFLFSPTGFKTQNLIAQLGQNKENKDAVKADIEKADK : 110
BcucOBP44a : MKYIVAVLLAALVAMAAAEYKIRNQDDLKARKEEAKKVPTIEHIEKFKKFEFPDDEVTRCYIECFNKFQFLFSPTGFKTQNLIAQLGQNKENKDAVKADIEKADK : 110
BoleOBP44a : MKYIIAVLLAALVAMAAAEYKIRNQDDLKARKEEAKKVPTIEHIEKFKKFEFPDDEVTRCYIECFNKFQFLFSPTGFKTQNLIAQLGQNKENKDAVKADIEKADK : 110
BlatOBP44a : MKYIVAVLLAALVAMAAAEYKIRNQDDLKARKEEAKKVPTIEHIEKFKKFEFPDDEVTRCYIECFNKFQFLFSPTGFKTQNLIAQLGHNKENKDAVKADIEKADK : 110
CcaphOBP44a : MKYIVAVLLA-LFALAAAEYKIRNQDDLKARKEEAKKVPAEHIEKFKKFEFPDDEVTRCYIECFNKFQFLFSPTGFKTQNLIAQLGHNKENKDAVKADIEKADK : 109
RzepOBP44a : MKYIAVALLA-LFALAAAEYKIRNQDDLKARKEEAKKVVPDHIIEKFKKFEFPDDEVTRCYIECFNKFQFLFSPTGFKTQNLIAQLGQNKENKDAVKADIEKADK : 109
DmelOBP44aX2 : MKNVAIILLALLGLASADYKLRTAEDLQSAARKEAASKVTEALIAKYKTFDYPDDDITRNITQCFIVKFDLFDFAEAGKFKVENLVAQLGGGDEKAAALKADIEKADK : 110
DmelOBP44aX1 : MKNVAIILLALLGLASADYKLRTAEDLQSAARKEAASKVTEALIAKYKTFDYPDDDITRNITQCFIVKFDLFDFAEAGKFKVENLVAQLGGGDEKAAALKADIEKADK : 110
      MKyivAvLLaAl aAaAeeYK RnqdDLlKaRKEc eakKVp hIeK KkFeFPDDevTRcTTeClFnKqLFSpteGFKV NLlAqLgq kEnKdAVKADIEKcADK

      120      130      140
BdorOBP44a : NEQKSDSSTWAYRGFKFISKNLPLVQESLKKN : 143
BcucOBP44a : NEQKSDSSTWAYRGFKFISKNLPLVQESLKKN : 143
BoleOBP44a : NEQKSDSSTWAYRGFKFISKNLPLVQESLKKN : 143
BlatOBP44a : NEQKSDSSTWAYRGFKFISKNLPLVQESLKKN : 143
CcaphOBP44a : NEQKSDSSTWAYRGFKFISKNLPLVQESLKKN : 142
RzepOBP44a : NEQKSDSSTWAYRGFKFISKNLPLVQESLKKN : 142
DmelOBP44aX2 : NEQKSPANEWAFRGFKFISKNLPLVQAAVQKN : 143
DmelOBP44aX1 : NEQKSPANEWAFRGFKFISKNLPLVQAAVQKN : 143
      NEQKSDSstcWayRGFKCFIsKNLPLVQeslKKN

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Supplemental figure 1-7 The alignment of OBP44a

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      10      20      30      40      50      60      70      80      90     100     110
CcaphOBP46aX2 : MFRVTIPIVTWLLLLQYQHAEQ-KTTTCSKLPKSI-----FVECLFNRSGLCHQGGCSYQR--AIDYLDSEFA- : 68
CcaphOBP46aX1 : MFRVTIPIVTWLLLLQYQHAEQ-KTTTCSKLPKSIAPSCCFRPPEP-----FQNPILSECTYLYNDIGQCFVECLFNRSGLCHQGGCSYQR--AIDYLDSEFA- : 97
RzepOBP46a : MIRAIIFPAIWLFLAA--ICRAEQ-KTTTCSKLPKSIAPSCCFRPPEP-----FQNPILDECYNLHNDIGQCFVECLFNRSGLCHQGGCSYQR--AIDYLDREFA- : 95
BdorOBP46a : MIQLFILLSLWTFTE--KCYAEQ-NQQTCSRLPKSIAPHICCFRPPEL-----FEGQLDECHRLHNEFGQCFVECLFGRADICRHKGCSYQR--ANKYLDNKFV- : 95
DmelOBP46a : MSQGLFAPLLLLRLTAFVGRSTFPALDECELSNVDTMHDFCLDLHDESQFSQSCQMEWHEKIPYETDEEEQTYMFTAECSFNSTNPLNGDRRSLSNLNEVKEHLESDLVN : 111
      M i l wll c aeq tDCs lpsksi cc i e CfvECIFnr ic gkcSyqr a yld f
      120      130      140      150      160      170      180      190
CcaphOBP46aX2 : ~LQQSAPKDIYKRAFKKKIAKA~NDVLGNMVKRFSRHGCHPLPEIRIRFVRNEMFTSPNGYWNERNVPGCSKKRDFIRNLIKDN--- : 150
CcaphOBP46aX1 : ~LQQSAPKDIYKRAFKKKIAKA~NDVLGNMVKRFSRHGCHPLPEIRIRFVRNEMFTSPNGYWNERNVPGCSKKRDFIRNLIKDN--- : 179
RzepOBP46a : ~LQQSAPKEIYKRAFKKKIAKA~NDVLGNMVKRFSRHGCHPLPEIRIRFVRNEMFTSPNGYWNERNVAGCSKKRDFIRNLIKENL--- : 178
BdorOBP46a : ~LQQTTFKDIYKSAFKKKIEKG~NGLLTPLVERFRFRNGCHPVEPLIRFVRNEMFISCPNEYWNELMRCTKKQCFIRHCTKEN--- : 177
DmelOBP46a : DADIKLLDYTYVKCHKHALSMPHKGKVKQLSKRLSRLGCHFPYGLVLECVANEMILHPTKRFKRTAQ~CEETRNLHKQCMQYLKYKS : 198
      lqq fkdIYk affkci k n l vkrfsR GCHP Pe i rCF rNEMf sCPn ywn C kkr fir C k n

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Supplemental figure 1-8 The alignment of OBP46a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP47a : ---MDGKVVVLAVGILASIGNLPFFSGVEARSASVKMSLDLSVSEDDQ-HRITADMVRLALETDLSDMLRRFSENDFNATKATCFTHCLFEHMGVLVSNGLFVERDIISFLG : 110
BlatOBP47a : ---MDSKWIVLAGILASIGNLPFFPAVEARSASVKMSLDLSVSEDDQ-HRKTADMVRLALETDLSDMLRRFSENDFSNVTKATCFTHCLFEHMGVLVSNGLFVERDIISFLG : 110
BoleOBP47a : MQSAINKALIVLTVATILATIGLPSFGVKARSASV-----DELRRFSEKDFSNATKATCFTHSLCEHMGVLVSNGLFVERDIISFLG : 83
BminOBP47a : ---MDSKILVLTATMLAAIVELTFFLSVEARSASVKMSLDLSVSEDDQ-HRISADMVRLALETDLSDMLRRFSENDFRNATKAIECFTHCLYEHEMGLLNGVGFVERDIISLLG : 110
CcaphOBP47a : ---MDSKILVFTVLAAVAVELPTFFGVEARSASVKMSFDMSEDDQ-HRINPEMVRLALETDLSDMLRLKFENDFSNATKNTQCFTHCLYEHEMGLVNRNGVGFVERDIISLLG : 110
BcucOBP47a : ---MNN-----PTLTARVASIRMSIDLSISEDDQ-HRINSMDVHLALETDLFMEELRKFSENFNDTVKVTQCFTHCLYEHEMGLVNRDGVGFVERDIISLLG : 91
DmelOBP47aX1 : ---MNR-----VLVLLLVLMKMFALSESFRKAININLGLTVADESPTTTEEMIRLGCQDTDISLRELNLKLRDFSDPSSEVQCFTHCLYEHEMGLMHDGVGFVERDIISLLG : 103
DmelOBP47aX2 : ---MNR-----VLVLLLVLMKMFALSESFRKAININLGLTVADESPTTTEEMIRLGCQDTDISLRELNLKLRDFSDPSSEVQCFTHCLYEHEMGLMHDGVGFVERDIISLLG : 98
      m l f ear as i v i m lc td s eLr f e DF k qCFThcL EhmG1 GvFVerd is Lg
      120      130      140      150      160      170      180      190      200      210      220
BdorOBP47a : DVTDPKRLMEREELGQFSDNKEAFLIHQCYRA--GQRLMKPPNNQPEVPDQILIEERNREETFAVDLPTTDMAMASAHMPPDDERQLLIKNILAKRLPRKQNIKQGLEEE : 221
BlatOBP47a : DVTDPKRLMEREELGHFSDNKEAFLIHQCYQS--GQRLMRPPYQPEVPDQILNEEPNRKEETRAMDLSTTDMAMPSAHRMSPDAEHQLLIKNILAKRLPRKQNIKQGLEEE : 221
BoleOBP47a : DVTDPKRLMEREELGQFSDNKEAFLIHQCYRA--DQRLMK-----DNIYLF-----DELRRFSEKDFSNATKATCFTHSLCEHMGVLVSNGLFVERDIISFLG : 83
BminOBP47a : DVTDPKRLMEREELGQYSDNKEAFLIHQCYRA--GQVMMAPNRQPEPESIDQNEERDGEEEKSVANLPKSDMAMPSVHRMATDSEERQLLIKNILAKRLPRKQNTTNGLVEE : 129
BcucOBP47a : DVTDPKRLMEREELGQYSDNKEAFLIHQCYRA--GQRMMPSPNNHQLPEVPDQILNEEDNABEE--STANLSKSDMAMTFAHRMAPNSERQLMIKNILAKRLPRKQNTTNGLVEE : 220
CcaphOBP47a : DTIDSKHIIIEHEFNQSENKCKRAFLIHQCYHGDGGKGIISSAQGFEEAEDKLNEDKEDEDDSEASDVSLPRTLIESTMPVKAGTERQIILKKLLAKRQPKIH----- : 195
DmelOBP47aX1 : DVSNTDIWPERQCHAIRGNKKEAFLIHQCYQQLKQQQQNLATKEVEVTTTPAGSDETKP-----MNR-----VLVLLLVLMKMFALSESFRKAININLGLTVADESPTTTEEMIRLGCQDTDISLRELNLKLRDFSDPSSEVQCFTHCLYEHEMGLMHDGVGFVERDIISLLG : 165
DmelOBP47aX2 : DVSNTDIWPERQCHAIRGNKKEAFLIHQCYQQLKQQQQNLATKEVEVTTTPAGSDETKP-----MNR-----VLVLLLVLMKMFALSESFRKAININLGLTVADESPTTTEEMIRLGCQDTDISLRELNLKLRDFSDPSSEVQCFTHCLYEHEMGLMHDGVGFVERDIISLLG : 160
      Dv d k Erec s NKCE A lHqCy q e

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Supplemental figure 1-9 The alignment of OBP47a

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      10      20      30      40      50      60      70      80      90     100     110
BlatOBP47b : ----MQKIELFVFCALFVYS---GVKAVEIDRRPPQLVQPSLCKKNEERAAYMETCAQR-LGLSF-EKQKGATALEDVTFAECIVKVELQHLSAPEKINFEAVQYILQTKS : 103
BoleOBP47b : ----MARLR-PLCCFSLLYTVK-YTDAVEIDSRPPQLVQPSLCKKNEERAAYMETCAQR-LGISE-EKQNGATPLEDVTFAECIVKVELQHLSAPEKINFEAVQYILQTKS : 104
BcucOBP47b : ----MKIMLKFKLVPFLALAYS---EARTVEIDRRPPQLVQPNLCKKGGDSVPSLKTCAQR-LGVNL-EDQTGAIPLQTAACFAECIVKVESQYTFPEKVINFEALQTYLQTKS : 106
CcaphOBP47b : MKYRIVLMQKWFVFVFFLLAVFGFGRSKAVEIDRRPPRLVDPACCKKGGDRDQIVAEACQR-MGLAS-QRQNGPPTVEAATFAECILKQLQYMQGPEKINYEAMRKHLLQMKF : 111
DmelOBP47b : ----MSPQLVIFASLALNTRLVFGQATIDRRPPQLVDPALCKKGGDRDQIVAEACQRILGTANGQKAGGPPSLDTAAALAEILTSKSYIDTEPQKLNLANTRSDLSAKF : 108
      M v L veIDC RPPqLV P CCK r e CAQR LG G l CfAECl k q Pek N ea Lq K
      120      130      140      150      160      170      180      190      200
BlatOBP47b : GNDTIVTDMTLTAYRCVSAQQRMQVIKQHS---LGGGVFALRS--SPFSGILLSCVHMEYFMNCPANRWTDNAECALAKQFVTQCAIGTV : 191
BoleOBP47b : GNDTIVTNTMTTAYRCESVAQQRMQSIKQMS---FGGGLSQR--CSLFSGILLSCVHMEYFMNCPSNRWTDNEECALAKQFVTQCAIGSI : 192
BcucOBP47b : GNDTIVTDMTMTTAYRCLEAAQQRMQFQQT---YGGGAIAQRRI--SPFYGILLSCVHMEYFMNCPAQRWTDNEECALAKQFVKQCTVGS : 195
CcaphOBP47b : SNTDITVNTMLQAYRCPEPSVQQRMQILKQTP---LGGGAALRRG--SPFSGMLLCTYMEYFMNCPAHRWNNEEQCALAKQFVTQCSFNA : 199
DmelOBP47b : SNTDITVBTMTWAFSCPEPSQQRLLAMIMQQQQQVQQKQTQQQQPR--SPFSIAVLGCTYMEYFMNCPDHRWTFNAQCTLAKAYVTCGLGA- : 199
      NDT YV TM Ay Kce Qqrmq Q ggg r CSpsgill C MEYF NCP Rwt N CaLAKqFvtQc g

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Supplemental figure 1-10 The alignment of OBP47b

Supplemental figure 1-11 The alignment of OBP50a

Supplemental figure 1-12 The alignment of OBP50c

Supplemental figure 1-13 The alignment of OBP50e


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      10      20      30      40      50      60      70      80      90      100     110
BlatOBP56a1 : MKSSIIICILATVLLSLVFSAEAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
BlatOBP56a2 : MKSSIIICILATVLLSLVFSAEAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
BdorOBP56a : MKSSIIICILATVLLSLVFNADAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
BcucOBP56a : MKSYIICILATVLLSLVFSADAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
BoleOBP56a1 : MKSSIVICILATVLLSLVFSADAGL-RKPKQLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIRVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
BoleOBP56a2 : MKSSIVGILATVLLSLVFSADAGL-RKPKQLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIRVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
BminOBP56a : MKSSIIICILATVLLSLVTFGTDAALGRKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIRVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 110
CcaphOBP56a1 : MKSSIIICILATVLLSLVFLSTEAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
CcaphOBP56a2 : MKSFIVICMLATVLLSLVFLSTEAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
RzepOBP56a2 : MKLTISICILATVLLSLVFNADAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
RzepOBP56a3 : MKLTISICILATVLLSLVFNADAGL-RKPKKLTPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
RzepOBP56a1 : MKSTTSYILAAVFLVSNTEAFGRKAKKLNPELEAKFEVLTAWIAYRNLNKHAKEAIVGEYGFSDLATNLVKIKVANPNDRKKYVYNLYNKLVFYKDDAINKQA : 109
DmelOBP56a : --MNSYFVIALSALFVTLAVGSSNLNSDEQKDLA-----KQHREQAEEVKLTTEEERAKVNAKDFNNFTENIKFANFFKVGTLKDGELQESV : 88
mk i ccilat l lc a l rkpKKL peleakf vltawiaYrnlNKhakEa gEygf d lat lvk vanP d eKcYvNcLy KlVfykd in qa

      120     130     140     150     160
BlatOBP56a1 : MKESLYEIVGEQRLLMIVDGLNAGGANACDKVKFHCACASPEFDKVRSDIFLPDE : 165
BlatOBP56a2 : MKESLYEIVGEQRLLMIVDGLNAGGXNACDKVKFHCACASPEFDKVRSDIFLPDE : 165
BdorOBP56a : MKESLYEIVGEQRLLMIVDGLNAGGTNACDKVKFHCACASPEFDKVRSDIFLPDE : 165
BcucOBP56a : MKESLYEIVGEQRLLMIVDGLNAGGTNACDKVKFHCACASPEFDKVRSDIFLPDE : 165
BoleOBP56a1 : MKESLYEIVGEQRLLDIVDGLSAGGTNACDKVKFHCACASPEFDKVRSDIFLPDE : 165
BoleOBP56a2 : MKESLYEIVGEQRLLDIVDGLSAGGTNACDKVKFHCACASPEFDKVRSDIFLPDE : 165
BminOBP56a : MKESLYEIVGEQRLLMIVDGLNAGGTNACDKVKFHCACASPEFDKVRSDIFLPDE : 166
CcaphOBP56a1 : MKESLYEIVGEERLLMIVNSCMNAGGANDCDKVKFHCACASPEFDKVRSDIFLPDE : 165
CcaphOBP56a2 : MKESLYEIVGEERLLMIVNSCMNAGGANDCDKVKFHCACASPEFDKVRSDIFLPDE : 165
RzepOBP56a2 : MKESLSEIVGEERLLQIVNSCLTAGGANDCDKVKFHCACASPEFDKVRSDIFLPDE : 165
RzepOBP56a3 : MKESLSEIVGEERLLQIVNSCLTAGGANDCDKVKFHCACASPEFDKVRSDIFLPDE : 165
RzepOBP56a1 : MKESLSEIVGEERLLQIVNSCLTAGGANDCDKVKFHCACASPEFDKVRSDIFLPDE : 165
DmelOBP56a : VLEKLGALIGEERTKAALERTIKGENKCDTASKLYDFESFKPAPEAKA----- : 139
mkEsL eivGE r1 iv C1 agG N CdkvYKfhaCaspEfdkvr diFlpde

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Supplemental figure 1-14 The alignment of OBP56a

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      10      20      30      40      50      60      70      80      90      100     110
BdorOBP56b : MKSYGLYQLLFAVFMCSAIT---QLHAADDKAAREAIIEAKELTATDANQVRGAIVSKLIQNDSEALKCFQLVYKQLGLIDAAGKTNAAKTLEYMSQVSGITDTSKLAAL : 110
BlatOBP56b : MKSGHLYQLLFAVFMCSAIT---QLHAADDKAAREAIIEAKELTATDANQVRGAIVSKLIQNDSEALKCFQLVYKQLGLIDAAGKTNAAKTLEYMSQVSGITDTSKLAAL : 110
BdorOBP56b : MKSYGLYQLLFAVFMCSAIT---QLHAADDKAAREAIIEAKELTATDANQVRGAIVSKLIQNDSEALKCFQLVYKQLGLIDAAGKTNAAKTLEYMSQVSGITDTSKLAAL : 110
BcucOBP56b : MKSYGLYQLLFAVFMCSAIT---QLHAADDKAAREAIIEAKELTATDANQVRGAIVSKLIQNDSEALKCFQLVYKQLGLIDAAGKTNAAKTLEYMSQVSGITDTSKLAAL : 110
BminOBP56b : MKSYGLYQLLFAVFMCSAIT---QLHAADDKAAREAIIEAKELTATDANQVRGAIVSKLIQNDSEALKCFQLVYKQLGLIDAAGKTNAAKTLEYMSQVSGITDTSKLAAL : 110
RzepOBP56b : MKSYGSKQALLVVLVSLIS---QLLAADDKTARETICQSKLSADDANVRGTSATSKILLQNSATLECFQLVYQVQGLIDTSGKITTLTKVLAYIVQVGTSGDADTKLAAL : 110
CcaphOBP56b : MKSFGLLQSLFVLIIIGPIS---ELLAADDKTARETICEKVNLSADDANVRGTSATSKILLQNSATLECFQLVYQVQGLIDTSGKITTLTKVLAYIVQVGTSGDADTKLAAL : 110
DmelOBP56b : MKLIYLVLQFLFALSEIVAGQSAELAAYKIQQAQIKELNIAASDANLLT---TDKEVANPSESVKCYHSVYKQLGLIDAGKTNAAKTLEYMSQVSGITDTSKLAAL : 109
Mks gl q v c i ql aAddK are CI e k l Dan vr a isKl qN se lKcFqlCyk lGld GKN k l ym q sgi d kL al

      120     130     140
BdorOBP56b : GTEESVKGSSGDRLYQFEKCALAKLGV : 138
BlatOBP56b : GTEESVKGSSGDRLYQFEKCALAKLGV : 138
BoleOBP56b : GSKSVKGTSQDRLYQFEKCALTKLGV : 138
BcucOBP56b : GSKSVKGSSHDRLYQFEKCALGKLG : 138
BminOBP56b : GATESVKGTSNCDKVIQFEKCALAKLGA : 138
RzepOBP56b : RAGESVQATNCDKVIQFEKCTFNKLG : 138
CcaphOBP56b : SGESVNGASQCDKVIQFEKCALGKLG : 138
DmelOBP56b : TSGGTTKSAATFVFNVEKGVVGKISA : 137
Cesvkg s CD YqfEKal klg

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Supplemental figure 1-15 The alignment of OBP56b

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      10      20      30      40      50      60      70      80      90      100     110     120
BdorOBP56c : MYTSLSLAVLCAATVQAKSRT-----ITISMNMSLTMMVERRKELLETNQRQLQEQARFALTAAVLRSIMKETELSMAEHLRFRLLSLTRDPE-LNTTDDTSTELPNLYDMEEDD : 112
BlatOBP56c : MYTSLSLAVLCAATVQAKSRT-----ITISMNMSLTMMVERRKELLETNQRQLQEQARFALTAAVLRSIMKETELSMAEHLRFRLLSLTRDPE-LSTDDPTSTELPNLYDMEEDD : 112
BcucOBP56c : -----MSLTMMVERRHQLEAHRQQLQEQARFALTAAVLRSIMKETELSMAEHLRFRLLSLTRDPE-LSTDDPTSTELPNLYDMEEDD : 82
BoleOBP56c : -----MSLTMMVERRHQLEAHRQQLQEQARFALTAAVLRSIMKETELSMAEHLRFRLLSLTRDPE-LINATDDSTQOTNLYDMEEDD : 83
BminOBP56c : MYIISLFAILLAAVQHAKSRT-----ITLSVNMSLTMGVERRKELLETNQRQLQEQARFALTAAVLRSIMKETELSMAEHLRFRLLSLTRDPE-LSDPESTELPNLYDMEEDD : 112
CcaphOBP56c : -----MLISAQVQNVKTRT-----ITFSVNMSLTMDEQRQRLLNGG---AAQOTRFSITAAVLRSMKETELSMAEHLRFRLLSLTRDPE-LINATDDSTQOTNLYDMEEDD : 101
RzepOBP56c : MYTASLALLLGAQSVNRVKSRY-----ISLFSVNMSLTMDEQRQRLLNGG---AAQOTRFSITAAVLRSMKETELSMAEHLRFRLLSLTRDPE-LINATDDSTQOTNLYDMEEDD : 113
DmelOBP56cX2 : MYFRASLMALLLTLSEFVSKAW-----TRLSVNMSLTMDEQRQRLLNGG---AAQOTRFSITAAVLRSMKETELSMAEHLRFRLLSLTRDPE-LINATDDSTQOTNLYDMEEDD : 101
DmelOBP56cX1 : MYFRASLMALLLTLSEFVSKAWVFFIFYISFTRLSVNMSLTMDEQRQRLLNGG---AAQOTRFSITAAVLRSMKETELSMAEHLRFRLLSLTRDPE-LINATDDSTQOTNLYDMEEDD : 111
1 S1 m r l q rp l a LRaCM Te1sm eL FR1SL d n d T

      130     140     150     160     170     180     190     200     210     220     230     240
BdorOBP56c : LVSEETLEDGIIYEPQADIN-EVNNNALDYEDPLTIRSDGKTDSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 231
BlatOBP56c : LASEETLGGNIYEPQGIN-EASNNALDYEDPLTIRSDGKTDSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 231
BcucOBP56c : -LSEYSEIDGIIYEPVEIN-ASHNNALDYEDPFTFKSNENTDSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 200
BoleOBP56c : FVSEETLEDGIIYEPHEPIN-EPKNNALDYEDALTFKSGGKADSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 202
BminOBP56c : LVSGETQIDGIIYEPASDIN-EQNNNALDYEDPLTIRSDGKTDSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 231
CcaphOBP56c : -FSEEDIDGIIYETESAIVMEPTSAIVEHEEPVAFKIDGKSDSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 220
RzepOBP56c : SVLDED---ISYEENAKR---NIAVYEDSRSLKVGSDSDLSQFAYLVEQLGLISKGVYMEELFGKLYAIVGREERHLVKEIMNLTNTNNKCESSYKMHLYARLKTLEEERAIR : 224
DmelOBP56cX2 : -----LGLDFNGNSQMP-----YLDLKNNEPLQFVSLYETLDLDRVNVLLLEAFKMQVQTIIQHEKAEIKEISDLQCKTRLEAAYKHLIYNHLKTLAEQRIR : 198
DmelOBP56cX1 : -----LGLDFNGNSQMP-----YLDLKNNEPLQFVSLYETLDLDRVNVLLLEAFKMQVQTIIQHEKAEIKEISDLQCKTRLEAAYKHLIYNHLKTLAEQRIR : 208
ye e k d EQCF yCLYELgL kgYm e lf kl aivgrEhivKeCm Ln n CEs YKMHLCY LkLIE E r r

      250     260     270     280     290     300     310     320     330     340     350
BdorOBP56c : KVLSEAYYGERDEAGGEE-----IPEAETTQETAYAVEEITQTSTYTVEENAKTED--LAVKKLMKQLKKKKLKLVDADVQLREMLQNWIAA : 315
BlatOBP56c : KVLGSAYPGERDEAGGED-----MPEAETTQETAYAVEEITQTSTYTADAENAKTEK--FGVKKLMKQLKKKKLKLIESDEQLREFLQDNWIAA : 315
BcucOBP56c : KLMEDAYNGERDEESEE-----IPQAETTQETAYVMEIGQTESTFVVEEDAITEN--VGIKKKLKKKKSKRVADAKFSEMNNQWAAE : 284
BoleOBP56c : KVLSEAYFGQRDEQSE-----IPATETTQETAYVMEIGQTESTFVVEEDAITEN--FALKKKLKKKKSKRVADAKFSEMNNQWAAE : 286
BminOBP56c : KILENAK-----DDQERE-----ILEAETQETAHMEETPTQSTYAYAEAKTEE--VVGQ----- : 293
CcaphOBP56c : DVLGPEIEGEKRDREEMVTQKITTLESVETTMETEPNPKPNPTVEADTTLESKSMMEPEKTMYPFFFDQYAEDEVTKLNMKKMKMKFKLKLSEDLTNRSYNELLGR--- : 327
RzepOBP56c : DALGYGA---DDRVMEE-----EEAIEDKNEEEDVTT----- : 234
DmelOBP56cX2 : EILERTEAENEGFGPEGS-----DFIDGIQHSGEAMTTAKSE----- : 255
DmelOBP56cX1 : EILERTEAENEGFGPEGS-----DFIDGIQHSGEAMTTAKSE----- : 245
1 d q e t

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Supplemental figure 1-16 The alignment of OBP56c

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP56d2 : MKFFAVAVLLAFVAVAAQEGVGKLTTEEQKQKARALGTCLKETGASEEAIHALIKGDDSQVDGKVKCSKCMLEKLGFIENSKVNEEKVQNFLGKLIGEEAKATAQAKCND : 112
BlatOBP56d2 : MKFFAVAILLAFVAVAAQEGVGKLTTEEQKQKAAHVGTDCLKETGASEEAIHALIKGDDSQVDGKVKCTACCCMLEKLGFIENSKVNEEKVQNFLGKLIGEEAKATAQDKCNG : 112
BdorOBP56d1 : MNFFAVAVLLVFAVAVAAQEG--MLTPEQIQKVHTLSNECLKETGASEDAIRALIKGDDSQVDGKVKCTACCCMLVKLGIVENGKVNNEEKVQNFLGKLIGEEAKATAQAKCNG : 110
BlatOBP56d1 : MKFFAVAVLLAFVAVAAQEGAGMLTQEIQKVHTLSCLKETGASEDAIRALIKGDDSQVDGKVKCTACCCMLDKLGIVENGKVNNEEKVQNFLGKLIGEEAKATAQAKCNG : 112
BdorOBP56d3 : MKFFAVAVLLAFVAVAAQEGVGKLTTEEQKQKAVAAABCFKETGASEDAIRALLKGDDSQVDGKVKCPACKTCMLDKLQNGKVNNEEKVQNFLGKLIGEEAKATAQAKCNG : 112
BminOBP56d : MKFFTTAVVAFVAVAAQEG--IKLSEEQKQKVHTLGAECLTETGASEAAVRAVGKGLSQVDGKVKCPACKTCLQGLGYFENGQVNEAVVQSSLGKVGEEKIKATAQAKCNG : 111
BcucOBP56d : MKFFTAVVAVLAFVAVAAQDGLKLSEEQKQKVHTLGAECLKETGASEAAVRAVGKGLSQVDGKVKCPACKTCLQGLGYFVDGKVNEAAVQSSLGKVGEEKIKATAQAKCNG : 112
CcapiOBP56d : MKFFTVAIVLAFVAVAAQEL--IKLTDEQKQKVHALGAECIKETGAEEAAVRAAGKGYDSQVDGKVKCPACKTCLQGLGYVEDGKLINEAAIQASLGKIVGDEQIKATAQAKCNG : 111
BoleOBP56d : MKFFAVVVVAFVAVAAQEGAGLKLTEEQKQKVHTLGAECLKETGAEEAAVRAVVGKDNSQVDGKVKCPACKTCMLGKLGIVENGKVNNEEVQNSLGKLIGDEKVKATAQAKCNG : 112
RzepOBP56d1 : MKLFAAAIVLAFVAVAAQNA--PRLSLDQMLKVSALTSECAKETGTSMESVLPRLQGDFSQVDDKVKCFSKCQERLGLFVNGVNEEAVQKSLGPLAGEEKVKATAQAKCNG : 111
RzepOBP56d3 : MKLFAAAIVLAFVAVAAQNA--PRLILDQMLKVSALTSECAKETGTSMESVLPRLQGDFSQVDDKVKCFSKCQERLGLFVNGVNEEAVQKSLGPLAGEEKVKATAQAKCNG : 111
RzepOBP56d3 : MKYFATVIVLTFVAVAVGQDG--LKLSAEQKEKVHLLVGECAKETGVSKAAILALRQGDFSQVDDKVKCFSKCQYERLGLVNGVNEEAVQKSLGPLAGEEQIKAVQAKCNG : 111
DmelOBP56dX1 : MKFLIVLSVILAICSAE-----LQLSDEQKAVAHANGALCAQQEGITKDQATALRNGNFDSDPKVKCFANCFLEKIGFLINGEVQPDVVVLAKLGPLAGEDAVKAVQAKCDA : 107
DmelOBP56dX2 : MKFLIVLSVILAICSAE-----LQLSDEQKAVAHANGALCAQQEGITKDQATALRNGNFDSDPKVKCFANCFLEKIGFLINGEVQPDVVVLAKLGPLAGEDAVKAVQAKCDA : 107
Mkff      fva a aq      L eQ k h      eC ketG      a Gd sqvD kVKC C      klG      ng vne vq LG L Gee KA QaKCng

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      120      130
BdorOBP56d2 : LKGTDECDTAFQIRQCYAAAGHEGLDF : 138
BlatOBP56d2 : LKGTDECDTAFQIRQCYSSGYSGFAP : 138
BdorOBP56d1 : LKGTDECDTAYQIRQCYSAGYNGFAP : 136
BlatOBP56d1 : LKGADCDTAYQIRQCYSAGYNGFVF : 138
BdorOBP56d3 : LKGTDECDTAYQIRQCYAAAGESFVF : 138
BminOBP56d : LKGTDDCDTAFLLHKCYVAENASTLV : 137
BcucOBP56d : LKGTDDCDTAFLLHKCYATENASTLV : 138
CcapiOBP56d : VKGADDCDTAFELHKCYLAENANIQI : 137
BoleOBP56d : LKGTDDCDTAFQLRQCYVAEHGAI I : 138
RzepOBP56d1 : VKGADDCDTAFEWYKCYVEEKG--LA : 135
RzepOBP56d3 : VKGADDCDTAFEWYKCYVEEKG--LA : 135
RzepOBP56d2 : VKGANDCDTAFELYKCYVEEKATVLA : 137
DmelOBP56dX1 : TKGADKCDTAYQLFECYKKNRAHI-- : 131
DmelOBP56dX2 : TKGADKCDTAYLFECYKKNRAHI-- : 131
KG d CdtA      CY

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Supplemental figure 1-17 The alignment of OBP56d

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      10      20      30      40      50      60      70      80      90     100     110
BcucOBP56e : MKNNILAIIALSAVVAHKS--HKPSQAHQFYERCLKESGASPALDPLKKGDFNAVGDCAKCFLCLENKKGILENGAPNEADI-RKVRK--VGNPEEPKNILAKCINGLMGAN : 110
BoleOBP56e : MKNLNFVATLISLSAVVAHES--NKPTQAHQFYERCLKESGASAAQLDALKRGDFNAIDDKAKCFLCLENKKELLKNGVPNEAGK-GKLPMPAIGNSAPRNVLACINGLQGAN : 112
BdorOBP56e : MKSYNFASRFNFTQRLSRLYLKPNKSTQVHQFYEDCLKESGASAAQLDALKKGDFNAVDDKAKCFLCKLQNKKGILENGVPNEAAI-HKVMTPAVGNSPPKNTLAKCINGLKGAN : 114
BlatOBP56e : MKNFLLVAALIALSTVA-AHELKSNKSTQVHQFYDDCLKQSGASAAQLDALKKGDFNAVDDKVKCFLCKLQNKKGILANGIPNEAII-HKVLKPAVGNAPKDLAKCINGLNGAN : 113
CcapiOBP56e : MNSNFIILITFVLFAALAAANELKSHKPARNHKIYEDCCMKESGASVAQLEALKKGFNSIDNKAKCFLCKLLEDNKGILTNMGPNEAGIRKKVHAPPAGNVSGLDLAKCINGLKAD : 115
DmelOBP56eX1 : -MKVFFVFALAAALSLASAVGLTDSQKAEAKQRAKCQVKEGITEQAIALRSGNFADSDPKVKCFANCFLEQTGLVANGQIKPDVVLAKLGP-IAGEANVKEVQAKCINGSTKAD : 113
DmelOBP56eX2 : -MKVFFVFALAAALSLASA--GLTDSQKAEAKQRAKCQVKEGITEQAIALRSGNFADSDPKVKCFANCFLEQTGLVANGQIKPDVVLAKLGP-IAGEANVKEVQAKCINGSTKAD : 112
a      q      C K G      q aL G F d K KC C      g NG      K      G      k ARC GA

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      120      130
BcucOBP56e : CDTAFLLYKCYWOEHAALI : 130
BoleOBP56e : CDTAFQLYKCYLOEHVILI : 132
BdorOBP56e : CDTAFQIYKCYRQEHVGLI : 134
BlatOBP56e : CDTAFQIYKCYWOEHVILI : 133
CcapiOBP56e : CDTAYQIYKCFMQEKVPLI : 135
DmelOBP56eX1 : KCDTSYLLYKCYYENHAQF- : 132
DmelOBP56eX2 : KCDTSYLLYKCYYENHAQF- : 131
CDT      YKCy      h

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Supplemental figure 1-18 The alignment of OBP56e

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      10      20      30      40      50      60      70      80      90     100
BdorOBP56g : MKSFTVITALLV--VGSAVVLCLNPH-DPEMRGYIEDCKNKEHNVS PKDFHDFIEG--KLTTVPENMKCSSCIMVKQGIMDESNGFKPDAAKAKMK----EDKLV : 94
BlatOBP56g : MKSFTVITALLV--VGSAVVLCLNPN-DPEMRGYIEDCKNKEHNVS LKDFHDFMEG--KLTTVPDNLKCSSCIMVKQGIMDESNGFKPDVAKAKVK----DDKLV : 94
BcucOBP56g : MKSFTITALLV--VYSVVVLCLNPN-DPEMRKFIEDCKNKEHNVS PKDFHDFMEG--KLTTVPESLKCSSCIMVKQGVMDSENGFNKADVAKAKIT----EEKFA : 94
BminOBP56g : MKSFTITALLV--VSSAVVLCLNAN-DPEMRKQIEECKNKEHNVT PKDYHDFMEG--KLTTIPENLKCSSCIMVKQGVMDSENGFKAEVAKAKMN----DDKFS : 94
RzepOBP56g2 : MKSFTITAFVL--VSSVVVMCLEPP-NPQIRQYIDCKNKEHNVS PKDFHEFNEG--KLSSPSEDLKCAICHFVVKQGSMDAEGTFKPDVAKTGMN----DDKFA : 95
RzepOBP56g1 : MKSFTITAFVL--VSSVVVMCLEPP-NPQIRQYIDCKNKEHNVS PKDFHEFNEG--KLSSPSEDLKCSMCFLIKQGSMDAEGTFKPDVAKTGMN----DDKFA : 95
CcapiOBP56g1 : -----CHPPDPPEMRKYIDCTKDHNVT KEFHEFNEG--KAASPSENLKCSSCCVMLKQGIIDEAGNFKPDVAKSKMP----DDKLA : 77
CcapiOBP56g2 : MKSYFALTILFV--ISAVVMCCHPPDPPEMRKYIDCTKDHNVT KEFHEFNEG--KAASPSENLKCSSCCVMLKQGIIDEAGNFKPDVAKSKMP----DDKLA : 95
DmelOBP56gX1 : MRATFALTLLGLSGILAQ--ANIDSSVSKELVTDCKLKENGVT PQDLADLQSGKVKAEADAKDNVCSSCILVKSGFMDSTGKLLTDKIKSYYANSNFKDVIE : 102
DmelOBP56gX2 : MRATFALTLLGLSGILAQ--ANIDSSVSKELVTDCKLKENGVT PQDLADLQSGKVKAEADAKDNVCSSCILVKSGFMDSTGKLLTDKIKSYYANSNFKDVIE : 103
m      c      p r i C KehaV pkd f eG K      KCss C Kqg mD G fkd aK      dk

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      110      120      130
BdorOBP56g : AAVDCCKDLSGSTPCDTAFKITCMLSKKEFLKRWL : 130
BlatOBP56g : AAVDCCKDLSGSTPCDTAFKITACMLSK----- : 123
BcucOBP56g : AAIDCCKDLTGSTPCDTAMKITECMITHK----- : 123
BminOBP56g : ATVDECCKDLSGSTPCDTAMKITECLLSHK----- : 123
RzepOBP56g2 : AAVDCCKDKTGSSACDTAFRITCCVISHK----- : 124
RzepOBP56g1 : AAVDCCKDKTGSSACDTAFETIACCVISHK----- : 124
CcapiOBP56g1 : AAIDCCKDLSGSSACDTAFKITECCVLSHK----- : 106
CcapiOBP56g2 : AAIDCCKDLSGSSACDTAFKITECCVLSHK----- : 124
DmelOBP56gX1 : KDLDCCSAVKGANACDTAFKILCCFQAAN----- : 131
DmelOBP56gX2 : KDLDCCSAVKGANACDTAFKILCCFQAAN----- : 132
a D Ckd Gs CDTafki C

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Supplemental figure 1-19 The alignment of OBP56g

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      10      20      30      40      50      60      70      80      90     100     110
DmelOBP56hX1 : --MKFTLFLIALAAFLS----MGQNPDFRQ--IMQCMEETNQVTEADLKEFMASGMQS-SAKENLKCYTKLMEKQGHLTNGQFNAQAMLDTLK-NVPQIKDKMDEISS : 100
DmelOBP56hX2 : --MKFTFLIALAAFLS----MGQNPDFRQ--IMQCMEETNQVTEADLKEFMASGMQS-SAKENLKCYTKLMEKQGHLTNGQFNAQAMLDTLK-NVPQIKDKMDEISS : 100
BdorOBP56h1 : --MQKFHILITIAAALVT---LAVQLPADLEK--FHKACMDEAKVTDQMRFQFNGAKASDATENIKCQMKCMQKQGIGWKDGVFDADAKIKELV-QNPFKFGKEADLTk : 103
BlatOBP56h1 : --MQKFYLLITIAAALVT---LAVQLPADLEK--FQKACLDEAKVTDQMRFQFNGAKASDATENIKCLMKCMQKQGIGWKDGVFDADAKIKELV-QHPFKFGKEADLTk : 103
CcaphOBP56h1 : --MQKYLLITIAAALAS---VAVSQLPADVEK--YHRACLDESQVSDDELKQFFQNGMRASDATENIKCHNCKMMQKMGIFKDGVDADAKMKELM-QNPSMGHGEAEITQ : 103
BoleOBP56h1 : --MQFTYLLITIAAALVT---LAVQLPADFEK--FSKACLDEAKVSEDELKQFFQNGMNVNEATENIKCHTKCLMQKLGMMKDGVLDAADAKMKELM-QLPYSGHDAEITQ : 103
BminOBP56h1 : --MHTLVLTITIAAALVT---LAVQSPADLEK--FHKACMDEAKVTNEELKFFQNGMKYDAAKENIKCHTKCLMQKHGVMKNGAFDAEAKAKELM-QIPKLKEHEVQITQ : 103
BcucOBP56h1 : --MHTFLVLTIAAALVT---LAVQSPADMEK--FHKACMDEAKVTNEELKQFFQNGMKADEAKENIKCHTKCLMQKQGIGWKDGVFNADAKVKEIM-QMPKLKDHEAEITQ : 103
RzepOBP56h1 : --MKALVILIGLTALVASVTFVMSQSSDEMdk--WNRIACLESNTTEDEVKFFENGMAKASEATNSIKCHVKCLLEKQGFPNKSVYNADAVATKQLM-KIPAMSGHETEVKQ : 107
RzepOBP56h2 : --MKALVILIGLTALFASVTFVMSQSSSEMdk--WNRIACLESNTTEDEVKFFENGMAKANEATNNIKCHFCKLLEKKGIFPNKSVYNADAAIKQLM-KIPAMSGHETEVKQ : 107
BdorOBP56h2 : --MMKDLFILGILSTLYS---MAVQKEMMADEK--FELPLIEANVTEDALKKPSNGLKANEANANIKCMACKLMEKREVLKKGVDPEKPYVADLI-RMPELKGLEDQIKE : 104
BlatOBP56h2 : --MMKDLFILMLTAAALYS---IVVQKEMIADEK--YELACLIEAHVTEADLKPFSLNGLKANEANANIKCMCKLMEKREILKKGVDPEKAYAEIIM-RMPELKGLEDQIKE : 104
BcucOBP56h2 : --MKALFILVILTVFGS---ITMQQYSRRELINILYELACMDTNTVTESEFRKFTITNGMKANEATSIDIKCMIMCVMEKRGILKKGTFDTERAYKEIM-IVGELKGHEDBIKE : 105
CcaphOBP56h2 : --MKILYILITFAALAT---FALQDLRVEMRK--FFSYQFEANVTETQLNKFIDNGMLASEAKSNIRCLVCKTMERYGLIRNGTYDTERAIDFASKVPKRRKGLEEDVKE : 104
BdorOBP56hlike : -----MTPLQLMDACNKESGITKEELQYFDSQMDPAKATNAIKCHMKQVSEKLGIFYKNMMLDDELTIKYLNENNMNAPKASVNNVVKQ : 82
BlatOBP56hlike : --MLLILLFMAALFGF-----AQADMSPLELMDACNKESGISKAELEQYFDSQMDPAKATNAIKCHMKQVSEKLGIFYKNMMLDETVTIKYLNENNMNAPKASVNTVVKQ : 101
BoleOBP56hlike : --MQFILFLFLFALFLA-----AQAQKTALELMDVCKNESGIVTVFELPKQFDSQMDPAKATNAIKCHMKQVSENLGIFYKNMMLDESLTAHKLKNNLDQNASMEAIKQ : 101
BcucOBP56hlike : --MRTISLFLFALLVA-----AQAQMTAKYVEIKNKEHGVTNTELKQFIDSKMDPAKATNPIKCHMKQVIEKLGIFYKNMMLDEALAAKPFKEHNNKQDQANVTETIKQ : 101
BminOBP56hlike : --MKVVLFLFVALLVA-----AQAEVPLKELIETCSKETGVPSEELQFDSMDPAEATNGIKCHMKQVLEKIGLYKNMMLDEALTIKFFKDNKKNDQPVVDEALKQ : 101
      m      C e v t      f m A i k C k g

      120     130     140     150
DmelOBP56hX1 : GVNAKIDIKGTNDIDTAFKVTMLKEHKAIPGH----- : 134
DmelOBP56hX2 : GVNAKIDIKGTNDIDTAFKVTMLKEHKAIPGH----- : 134
BdorOBP56h1 : AINNCKNEKGANEIDTVFKISMKEFTMQNNL----- : 136
BlatOBP56h1 : ALNDCKNEKGANEIDTVFKINMKKEFTMQNNL----- : 136
CcaphOBP56h1 : ALNDCKNEKGANEIDTSFKITMLKDFSKPQHA----- : 136
BoleOBP56h1 : IVNNCKNEKGANEIDTVFNIAMIKKLSAQIA----- : 136
BminOBP56h1 : ALSNCKNEKGANEIDTAFKITMLKEFKAQID----- : 135
BcucOBP56h1 : AMNNCKNEKGANEIDTAFKITMLKEFKSKNP----- : 135
RzepOBP56h1 : AVNSCKNEKGANYIDTAFKIMCKKEFKAKM----- : 138
RzepOBP56h2 : AVNRCNERGASDIDTAFKIFMKKEFKKE----- : 136
BdorOBP56h2 : AINICKTEKGANDIDTAFKITMLREFKSRNI----- : 136
BlatOBP56h2 : AINVCKTEKGANDIDTAFKIAMLEEFKSRNA----- : 136
BcucOBP56h2 : AVHNCKAEKGHDIDTAFKITMLQEFSSRNK----- : 137
CcaphOBP56h2 : AVNCKAEKGADDIDRAFKITMLKEFKTRFPE----- : 138
BdorOBP56hlike : SIQKNQMKGANTIDAYQIMTFKFS-QPIFT----- : 113
BlatOBP56hlike : SIQKNQMKGANTIDAYQIMTFKFS-QPIFT----- : 132
BoleOBP56hlike : SIQKNQMKGVNPIDAYQIMTFKFS-QPINLFGQGVF : 139
BcucOBP56hlike : TIQKNQMKGADPIDAYQIVTTFVKSELPMFAV----- : 135
BminOBP56hlike : SVQKNQKGVNPIDAYQIAKFMFS-QHPITFN----- : 133
      C k g C d t a f i C

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Supplemental figure 1-20 The alignment of OBP56h

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP57c : MYQFGAHEKRRATTATMSATVLAAGGGKGS-IPGLTWLVLLAVIVVFALPPGAVALTPTAPTSPFVEA QVKNHNTLQELDEFFTPDPSPED-----IDMKFKYADCLL : 104
BlatOBP57c : MYQFGAHEKHATTATMSATVLPAGGGKGMPIPLGLMWLVLLAVIVGFTLPPGAVALTPTAPTSPFVEA QVKNHNTLQELDEFFTPDPSPED-----IDMKFKYADCLL : 104
BoleOBP57c : MYQFGAHGKHATTATV-IISALVVPAGGGKGMSSPLGLTWLALLAVIVVFALPPGAVALTPTAPTSPFVEA QVKNHNTMEELDEFFTPDPSPED-----IDIKFKYADCLL : 103
BcucOBP57cX2 : MYQFGAHEKHATTIT-----ISSGKGMS-LSGLTWSVFLVVFVVLPPAAVTLTPTAPSPSFMEA QVKNHNTLEELDEFFTPDPNPDE-----IDMKFKYADCLL : 96
BcucOBP57cX1 : MYQFGAHEKHATTIT-----ISSGKGMS-LSGLTWSVFLVVFVVLPPAAVTLTPTAPSPSFMEA QVKNHNTLEELDEFFTPDPNPDE-----IDMKFKYADCLL : 96
CcaphOBP57c : MFQFGVGVGKNTTTKS-----EMLASNNGRGMS-LPGLTWLVLLAAILMFFLLPIDKVAASPTASTSPFMEA QVKNHNTMEELDEFFPDSPDADE-----VEMKFKYADCLL : 100
RzepOBP57cX3 : MYQFEVNRKKAIAKE-----ATHSNGLRMA-LPIPAWMLLTAVMLFPSSLGQVNPATPAASTKSFMEA LERNNITHEELDQFPDDPSPED-----VEQKFKYANCLL : 98
RzepOBP57cX4 : MYQFEVNRKKAIAKE-----ATHSNGLRMA-LPIPAWMLLTAVMLFPSSLGQVNPATPAASTKSFMEA LERNNITHEELDQFPDDPSPED-----VEQKFKYANCLL : 98
RzepOBP57cX1 : MYQFEVNRKKAIAKE-----ATHSNGLRMA-LPIPAWMLLTAVMLFPSSLGQVNPATPAASTKSFMEA LERNNITHEELDQFPDDPSPED-----VEQKFKYANCLL : 98
RzepOBP57cX2 : MYQFEVNRKKAIAKE-----ATHSNGLRMA-LPIPAWMLLTAVMLFPSSLGQVNPATPAASTKSFMEA LERNNITHEELDQFPDDPSPED-----VEQKFKYANCLL : 98
DmelOBP57c : -----MLKLWLIILTVSVSVISQLSLLEETNVVSDLASNNISQAEPQLDRNNSSEEDLENTDRRVKFTFHCLA : 72
      myqf k a g m w L v t p a s f e a C Nit Eld fp dp p k f C y a C l l
      120     130     140     150     160     170     180     190
BdorOBP57c : NGMGFMDNSNGKGLDAEGLHEWGILNDESYENMLIEKAANDMEDDDPEYSGFMMLCARMLNSEE-----ENYYSDEVDEAAEERRRK : 184
BcucOBP57c : NGMGFMDNTNGKGLDAEALHEWGILNDESYENMLIEKAANDMEDDDPEYSGFMMLCARMLNSEE-----NDYNSDEVDEAAEERRRK : 184
BoleOBP57c : NGMGFMDNSNGKLNKSLHEWGILNDESYDNMLIEKAANDMEDDDPEYSGFMMLCARMLDSVE-----MDNYSDEMDDAAVEERRK : 184
BcucOBP57cX2 : NGMGFMDKNGKGLDAEAMHEWGILDDSYDNMLIEKAANDLEDDPEYSGFMMLCARMLSSEE-----EES-SGELDVEGDEK--- : 172
BcucOBP57cX1 : NGMGFMDKNGKGLDAEAMHEWGILDDSYDNMLIEKAANDLEDDPEYSGFMMLCARMLSSEE-----EES-SGELDVEGDEK--- : 172
CcaphOBP57c : FGMGLLDENKGLNVEYHMDGILTDPSYESMLIEKAANDMEDDDPEYSGFMMLCARMLGTEEGGSEENIEDIEEVEAEKEEERRK : 186
RzepOBP57cX3 : DGMGILDENKGLMADSMHEWGILDSYENMLIEKAANDMEDDDPEYILELLSVRELI LNIT-----VMRSRSKKSAGSE----- : 174
RzepOBP57cX4 : DGMGILDENKGLMADSMHEWGILDSYENMLIEKAANDMEDDDPEYILELLSVRELI LNIT-----VMRSRSKKSAGSE----- : 174
RzepOBP57cX1 : DGMGILDENKGLMADSMHEWGILDSYENMLIEKAANDMEDDDPEYILELLSVRELI LNIT-----VMRSRSKKSAGSE----- : 174
RzepOBP57cX2 : DGMGILDENKGLMADSMHEWGILDSYENMLIEKAANDMEDDDPEYSGFVIGIARVNIEHH-----SDEIEPIEEERRK----- : 173
DmelOBP57c : EKGMLLDNNGYLDVDDIKQIEPVSDDELRIEYDKKIYDEEDHDEYAFKMTVLTESFEQS-----DEVTEAGKNTNKLNIE-- : 149
      gmg d Ngk a hewgil Desy nm eCKaanD EdDpCEY e

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Supplemental figure 1-21 The alignment of OBP57c

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      10      20      30      40      50      60      70      80      90     100     110
BminOBP58c : MKNSTLIIIPFAWLLKFGNSLKIDCNPEPFIREDRHYCKKHPDGYQEFVDSQAKETGFNVNQSNESIVDITADHATMGTFKAKVFNKIQFMKGDELDMSAVRKHQFES : 110
BcucOBP58c : MKNFLVFIIFAGLLKFGNSLKIDCNPSIESIKEDRIHYCKKHPDGYQEFVDSQAKETGFKFIKHDEEAVDITADHAILGTGFKGVFNKIQFMKGDDLDMSAVRKHQFES : 110
BdorOBP58c : MKNLAILIFSILKLNKNSLKIDCNPSINESIDRIHYCKKHPDGYQEFVDSQAKETGFKYIKHDEEAMVDITVDHAILGTGFKGVFNKIQFMKGADLDMSAVRKHQFES : 110
BlatOBP58c : MKNFVLIIISVSLVLKLSLKIDCNPSIESIKEDRIHYCKKHPDGYQEFVDSQAKETGFKFIKHDEEAMVDITVDHAILGTGFKGVFNKIQFMKGDDLDMSAVRKHQFES : 110
CcaphOBP58c : MGNLAIITIFAFGLAKPTSSSLKIDCNPSIQIEDRIHYCKKHPDGYQEFVDSQAKETGFQYQKPEEAMVDITVDRAITGTGFKGVFNKIEPLKNDLDMSAVRKHQFES : 110
DmelOBP58c : MK--PILIFSFSLIPFAGGKIDCNTEAINEIDRIHYCKKHPDGHNDLIEGQARETNFTLPNQNEEALVDITADRAIRGTGFKGVFNKILNMKNDNLDMSAVRSLFTE : 108
      Mkn Ii l k sLKIDCdNpe I ED IHYCKHPDGyq d CakETgF Eea VDIT D Ai GTCF KcVf KL fmK LDM AVR hfsf
      120     130     140     150     160     170     180     190     200
BminOBP58c : KYKADPEYAKEMINAFDHHGKSVENTAKFLSNPIFHNIGAEFCDPKPGVIMAEVIREFFHNPADRWAKTTEEINTVLEFSKKCKDALTTI : 201
BcucOBP58c : KYKADPEYAKEMINAFDHHGKSIENTAKFLSNPIFHVPGAKYCDPKPVSILAEVIREFFHNPADRWAKTTEEINTVLEFSKKCKDALTTI : 201
BdorOBP58c : KFKTDPYAKEMINAFDHHGKSVENTAKFLSNPIFRQPSAEFCDPKPGVILAEVIREFFHNPADRWAKTTEEINTVLEFSKKCKDALTTI : 201
BlatOBP58c : KSKADPEYAKEMINAFDHHGKSVENTAKFLSNPIFRQANAEEFCDPKPAVILAEVIREFFHNPADRWAKTTEEINTVLEFSKKCKDALTTI : 201
CcaphOBP58c : KFKTDPYAKEMINAFDHHGKSVEHTTKFLSNPLFRATNGEFCDPRSSVILAEVIREFFHNPADRWSKTEEINTVLEFSKKCKDALTTI : 201
DmelOBP58c : RFPDDPEYAKEMINAFDHHGKSEENTSMFLSKPLFKQMSKQFCDPKSSVILAEVIRQFFHNPADRWSKTEEINTLAFSKKCKQDSLATL : 199
      k k DPEYAKEMINAFDHHK S Ent kFLSnP F fCDPk ViLACVIREFFHNCPADRW KTeEC tvLeFSKKCKdabLTti

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Supplemental figure 1-22 The alignment of OBP58c

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP58d : MQLS-----DFLLVLKLFKFSRAFQDTAASDITGLDEKKSNARKGCDNLHITPDEVTAKVLLHEDQ--IPAEDDKSPTKLIGFLSLVEITYKSRNYLTKDADDIMQAVK : 108
BlatOBP58d : MQLPSTTTTDEDTKLSQFIQQLVRAFADTAVSDAGTLDTTKSNARKGCDNLHIFDEVTAKVLLHKDK--IPAEDDKSPTKLIGFLSLVEITYKSRNYLTKDGEDINMQAVK : 114
BcucOBP58d : -----MDEATVNCVMHFHNKGIEPSDDDKNPVKSIIEFLSLAHITYKKNRYLTKGNDINMQGVK : 60
CcaphOBP58d : -----MLLDEPTAKCVLHENN--IPKEDDKDPIKLFGISLVEITYTKRHYIGKNSETLNMKVK : 60
DmelOBP58d : --MVNIVYWFYTLILVAVSKAQDNEETFAVATSSGDLTEDKNSRACGSELYGIEDEELVKCFVIHSPK--LPVGDGADIGKTLRFLSLVEITYKQKYYIGK--SDTINMKVK : 111
      de t k C h iP ddk p K FlSClveCiYk r Y K iNm VK
      120     130     140     150     160     170     180     190     200     210     220
BdorOBP58d : NDVATVYADRPFKEQQYVIEYMDYRKDAAKTYGRLKGNPASKILFKKAKFYPTFVYLQAEVHRKTKPFYFMWEGDEK-TAVKQEKSAKQCYKIDGLTFPFEYEFDS- : 217
BlatOBP58d : NDVATVYADRPFKEQQYVIEYMDYRKDAAKTYGRLKGNPASKILFKKAKFYPTFVYLQAEVHRKTKPFYFMWEGDEK-TPAKQEKSAKQCYKIDGLTAPQYFNHFS- : 223
BcucOBP58d : EHVQSQYAGRPFKEQQYFIELYDVRKDALKMVGLTKNNPAARVFFPKAKFYPTFVYLQAEVHRKTKPFYFMWEGDEK-TPAEQEKAAKQCYKIDGLTFPDVLDVLP : 170
CcaphOBP58d : ADAENLYAARPFKEQQYHVELYEPKAEAFKLYTLIKASPAGLVIFKNSKPYFVFMVLYQIEYHKKKTKPFYFMWQCNEDDETMLSCAKAAKQCYKIDGLTFPPEQK---- : 166
DmelOBP58d : LDAEKTVEVRPFKEQQYHIAFMFPRKDAVGYNLLKASPGAKVLLKGAERYLLMVFVLYISDYHQKHEPFYRWEGTAK-AGTKMRKENAKAEYQIDGTLTPTKSPA---- : 218
      ya RPKE qY ie y CRkDA k Y K P k fk acKPY fvyIcQ eYH K CPYF W g ek Ck AK qCYKIDGLT P

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Supplemental figure 1-23 The alignment of OBP58d

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      10          20          30          40          50          60          70          80          90          100          110          120
BdorOBP59a : MSKRSLASGLSGLPLRTITLVFFYSMT---YALKRTDDGPFSESELKRITRNMKRIKGSVHSIGGSGMSNKNHNPYGPLHQSNFGPQHGGNSRDYDNYDGDADQYQGNANNNNNNNNN : 122
BlatOBP59a : MSKRSLASISFVLWISVLLLYSISIT---YALKRTDDGPFSESELKRITRNMKRIKGSVHSIGGSGMSNKNHNPYGPLHQSNFGPQHGGNSRDYDNYDGDADQYQGNANNNNNNNNN : 122
CcapOBP59a : MLKRSASR-AGHLIGVITLLITFSIT---SLKRTDGFSESELKRITRNMKRIKGSVHSIGGSGMSNKNHNPYGPLHQSNFGPQHGGNSRDYDNYDGDADQYQGNANNNNNNNNN : 119
DmelOBP59a : -----MKQLIFLLITLSITSTIYALKRSQEGLSAEALKRTVNMHRQDDEDEDRGGGQ-----GRQGNG--YEGYGMDDHQDEQDR----- : 78
      m krs a      L      l ycs C yalKCRT dgpSsEsELKRitRnCMrkigE      Ggs      nh ygp hqsfnf q gGnsrYdYnYdydd dgy gn n nn n nnnn

      130          140          150          160          170          180          190          200          210          220          230          240          250
BdorOBP59a : YNNNNNGN-----HD-RDRNVLQQNRDRQNNRSDNNRSASSGSSNN-----NGGRYDNNDGNGNRGGGG-GNGDGGNRNGSGNSGGRNSGGNGSGNSQRGFNQNNNNNNNNNG--NRRN : 230
BlatOBP59a : YNNNNNGN-----HD-GDRNVLQQNRDRQNNRSDNNRSASSGSSNN-----NGGRYDNNDGNGNRGVAG-GNGDGVNRNGSGNSGGRNSGGNGSGNSQRGFNQNNNNNNNNNG--NRRN : 230
CcapOBP59a : GNNNNNGNNYDRDHDGRNRLVQQNRDRQNGNSDNRSSSSSSSSSGNNHNGGGRYDNNNGKSGNGSGGGSGGSGNRNTGSGSSGSGGQRGHTQNHSSNNNNNNNNNNSSNNNNRS : 243
DmelOBP59a : -----NPGNRGGYGM-----RAQRGLRQSDGRNHTSN----- : 105
      nnnngn      hd      rrvlqqrrndrqgn      sdn rs ss ss      nggrydnn g n g g g g g n g g N G r s Gng g Qrg nqnn nNn n nnr

      260          270          280          290          300          310          320          330          340          350
BdorOBP59a : GKNDTADVAVVHHFFDELMLNLSDDYFDRYKVQYGLTRDLRDLRLNFYTDITQDFQYLES--QRRRDKHYSRDLINMTEYAKVNDWQEF-NVVFN : 329
BlatOBP59a : GKNDTADVAVVHHFFDELMLNLSDDYFDRYKVQYGLTRDLRDLRLNFYTDITQDFHYLES--QRRRDKHYSRDLINMTEYAKVNDWQEF-NVVFN : 329
CcapOBP59a : ANNDTADASVHHFFDELMLNLSDDYFDRYKVQYGLTRDLRDLRLNFYTDITQDFHYLES--QRRRDKHYSRDLINMTEYAKVNDWQEF-NVVFN : 342
DmelOBP59a : -----DGGQVACFFFEEMMNSDDYFDRYKVYGLTRDLRDLRLNFYTDITQDFRYLESNGRGRHHRSAARELVKMSSEYAKACEDWEHEHGNMLFN : 202
      ndtat      CVvhCFEElMlnsddyfDRyKVqgLTnDLRDLRLNFYTDITQdCF YLES qfRrdRChysrdLinCmTEYAKvNCdWqEf N vFN

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Supplemental figure 1-24 The alignment of OBP59a

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      10          20          30          40          50          60          70          80          90          100          110
BdorOBP69a : MNTKQF-VFLVVIYYQTFYTGVTTLLEVPKHMVSQVKKLTNLIKESGASEDLFKDIRATGELPNNQNLKFMHCVLDKIGLIIDDDNIHVLNDNLIEIMPPDFVPIIEQLH : 108
BlatOBP69a : MNTKQF-VFLVVIYYQTYWTGVDADEVFKHLISGVKKLTNLIKESGATEDLFKFEETGELPNNQNLKFMHCVLDKIGLIIDADNIHVLNDNLIEIMPPDFVPIIEQLN : 108
CcapOBP69a : MMYRRL-VILLIIYQCVLLRNVSQLEVPHKMRSGAKKLTNLIKETGVTEDLFIEAQETGKMPNNQRLKCFIHCVLDKIGLIIDADNIHVLNDNLIEILPEFVPIVEELH : 108
RzepOBP69aX1 : MNTKQF-VFLVVIYQCVFLAIVKPLEVPHKMRSGAKKLTNLIKETGATEEMTEAKRTQQLPGDNRLLCFMCHMDKIGLIIDENIITHLDNLDIMPPEFPMIEQLH : 108
RzepOBP69aX2 : MNTKQF-VFLVLIYQCVFLAIVKPLEVPHKMRSGAKKLTNLIKETGATEEMTEAKRTQQLPGDNRLLCFMCHMDKIGLIIDENIITHLDNLDIMPPEFPMIEQLH : 108
DmelOBP69a : MVARHSEFFLALLILYDLIPSNQGVENIPTTIKQVKRLRMRLNQTGASVDVIDKSVKNRILPTDPEIKFLYCMFDMFGLIDSQNMHLEALLEVLPPEEIHKTINGLV : 109
      Mn      f vFL i yq      v      Evpkh      sg kKltn C ke Ga e f      t lP      lKCF hC ldkIGLID NI HldnL i Pp f p ie L

      0          120          130          140
BdorOBP69a : TTGTGKSGADGCTAFLTIEYIKKEPIISKMLFSTFAD : 147
BlatOBP69a : TTGTGKSGADGCTAFLTIEYIKTEPIISKMLFVKFAK : 147
CcapOBP69a : TTGTGKSGADGCTAFLTTEYIKTNPVILKLLFTTFSE : 147
RzepOBP69aX1 : TTGTGKSGADGCTAFLTVDYIKTNPVILTLL----- : 141
RzepOBP69aX2 : TTGTGKS--KWCR--WL----- : 121
DmelOBP69a : SSTGTQKGKDGDTAYETVKYIAVNGKFIWEEIIVLLG : 148
      ttCGT sg dgC ta lt cyi

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Supplemental figure 1-25 The alignment of OBP69a

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      120          130          140          150          160          170          180          190          200          210          220
DmelOBP73aX1 : -----LDHSFNISQYIEYI-----YDEFEFQRHVARLMRNIRRLDVAS--SGIYHPTLVPLEDKRIAGCLLHCVYAKNNAIDQRGWPTLDGLVHFYSEGVHEHG : 188
DmelOBP73aX2 : -----LDHSFNISQYIEYI-----YDEFEFQRHVARLMRNIRRLDVAS--SGIYHPTLVPLEDKRIAGCLLHCVYAKNNAIDQRGWPTLDGLVHFYSEGVHEHG : 188
BlatOBP73aX1 : I--IFHTIEENSKLASQHDA-----YQFQPERQVQVTSLMNHIRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 196
BlatOBP73aX2 : I--IFHTIEENSKLASQHDA-----YQFQPERQVQVTSLMNHIRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 195
BdorOBP73aX2 : I--IFHTIEENSKLASQHDA-----YQFQPERQVQVTSLMNHIRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 195
BdorOBP73aX1 : I--IFHTIEENSKLASQHDA-----YQFQPERQVQVTSLMNHIRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 196
BdorOBP73aX3 : I--IFHTIEENSKLASQHDA-----YQFQPERQVQVTSLMNHIRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 178
BoleOBP73a : I--IFHTIEENSKLASQHDA-----YQFQPERQVQVTSLMNHIRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 209
BminOBP73a : I--IFHTIEENSKLASSHNS-----YQFQSDRQVQVTSLMHRIGRISYDPR--SALYYPTLVPAEKKRAGCLLHCVYAKNNAIDKLGWPTLDGLVNFYSEGVHEHG : 207
BcucOBP73aX2 : V--I--HTIEDNSLNSRRHDVL-----YQFEPDKRHVTHLAHQFRRTSYDPR--SGIYHPTLVPAEKKRAGCLLHCVYAKNNAIDKFGWPTLDGLVNFYSEGVHEHS : 198
BcucOBP73aX1 : V--I--HTIEDNSLNSRRHDVL-----YQFEPDKRHVTHLAHQFRRTSYDPR--SGIYHPTLVPAEKKRAGCLLHCVYAKNNAIDKFGWPTLDGLVNFYSEGVHEHS : 206
BcucOBP73aX3 : V--I--HTIEDNSLNSRRHDVL-----YQFEPDKRHVTHLAHQFRRTSYDPR--SGIYHPTLVPAEKKRAGCLLHCVYAKNNAIDKFGWPTLDGLVNFYSEGVHEHS : 170
CcapOBP73a : -----VIQEPSVWHMPSAAP-----YPTGSPRPSIRLLHGIQRIAHADPA-NAVYHTITVSIEDKRIAGCLLHCYAKNNAIDKLGWPTLDGLVDFYSEGVHEHE : 197
RzepOBP73a : IGVQSGGS-----TVSAYSSSSNAGFELPSGYDTYEDSSKRRVTRLHHIRIAHDSPTNIIYHPTLVPFEDKRIAGCLLHCVYAKNNAIDGFGWPTLDGLVDFYSEGVHEHG : 211
RzepOBP73ap : IGVQSGSGSAGSTVSAYSSSSNAGFELPSGYDTYEDVSSKRRVTRLHHIRIAHDPATNIIYHPTLVPFEDKRIAG----- : 179
      s      Y      vt L i rRi      s Y PtlVp E KR AGcllhcvyaknnaid gwptldglv fysegvneh

      230          240          250          260          270          280          290
DmelOBP73aX1 : FFMATLRSVNLRLRTMTARYGVNRKELPKKGESDLAFDVFDSHMNTNFKDLPFWAPFISYVNESRAINYI : 259
BdorOBP73aX2 : FFMATLRSVNLRLRTMTARYGVNRKELPKKGESDLAFDVFDSIDQITG--YCLDQYSRY----- : 247
BlatOBP73aX1 : FFMATLRSVNLRLHAITIKYNIDRRKLPKKGESDLAFDVFDSIDQITG--YCLNQYE----- : 253
BlatOBP73aX2 : FFMATLRSVNLRLHAITIKYNIDRRKLPKKGESDLAFDVFDSIDQITG--YCLNQYE----- : 252
BdorOBP73aX2 : FFMATLRSVNLRLHAITIKYNIDRRKLPKKGESDLAFDVFDSIDHITG--YCLNQYE----- : 252
BdorOBP73aX1 : FFMATLRSVNLRLHAITIKYNIDRRKLPKKGESDLAFDVFDSIDHITG--YCLNQYE----- : 253
BdorOBP73aX3 : FFMATLRSVNLRLHAITIKYNIDRRKLPKKGESDLAFDVFDSIDHITG--YCLNQYE----- : 235
BoleOBP73a : FFMATLQSVNLRLHAITIKYNINRRKLPKKGESDLAFDVFDSIDQITG--YCLNQYE----- : 266
BminOBP73a : FFMATLRSVNLRLHAITIKYNINRRKLPKLGESDLAFDVFDSIDQITG--YCLNQYE----- : 264
BcucOBP73aX2 : FFMATLRSANLRLHAISIKYNINRRKLPKKGESDLAFDVFDSIDQITG--YCLNQYE----- : 255
BcucOBP73aX1 : FFMATLRSANLRLHAISIKYNINRRKLPKKGESDLAFDVFDSIDQITG--YCLNQYE----- : 263
BcucOBP73aX3 : FFMATLRSANLRLHAISIKYNINRRKLPKKGESDLAFDVFDSIDQITG--YCLNQYE----- : 227
CcapOBP73a : FFMATLRSVNLRLHAITIKYINRRKLPEHGESDLAFDVFDSIDQITG--YFDQYN----- : 254
RzepOBP73a : FFMATLRSVNLRLRAVTIKYQVNRKLPERGESDLAFDVFDSIDQITG--YCLDQYK----- : 268
RzepOBP73ap : ----- : -
      fpmatlrs ncl a ky rrlkpk gescdlafdvfdcdisd tg ycl qy

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Supplemental figure 1-26 The alignment of OBP73a

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      10          20          30          40          50          60          70          80          90          100          110
BcucOBP83aX2 : -----MHALNSLATLTLWFGFLSN--VWIAQKELRRDETYPPELLKALQPVHDSVAKIGVTAAIKFSDGQVHEDELLKYMVFVEETDV : 87
BcucOBP83aX1 : -----MHALNSLATLTLWFGFLSN--VWIAQKELRRDETYPPELLKALQPVHDSVAKIGVTAAIKFSDGQVHEDELLKYMVFVEETDV : 87
BdorOBP83a : -----MHSRKTLLGTLLWIGFLNL--LWIAQKELRRDETYPPELLKELRPVHDSVAKTGVTAAIKFSDGQVHEDELLKYMVFVEETDV : 87
BlatOBP83a : -----MHSRKTLLGTLLWIGFLNL--LWIAQKELRRDETYPPELLKELRPVHDSVAKTGVTAAIKFSDGQVHEDELLKYMVFVEETDV : 87
BoleOBP83a : -----MHSRKSLLSILLWFGFLSN--LWIAQKELRRDETYPPELLKELRPVHDSVAKTGVTAAIKFSDGQVHEDELLKYMVFVEETDV : 87
BminOBP83a : -----MYSIKSILGTLLWFGFLT--VWIAQKELRRDETYPPELLKALRPVHDSVSKTGVTAAIKFSDGQVHEDELLKYMVFVEETDV : 87
CcapOBP83a : -----MYILRTILGALLMSVLLN--LWIAQKELRRDETYPPELLEALRPVHDSVAKTGVTAAIKFSDGEIHDEPLKYMVFVEETDV : 87
RzepOBP83a : -----MHKMYSLKMLLGTLLFLFYLSS--MAKAQELRRDETYPPEMLKALRPVHDSVKGKTGVTAAIKFSDGQVHEDEALKYMVFVEETDV : 90
DmelOBP83aX2 : -----MALNGFGRVRSASVLLIALSLSGALILPPAAQQRDENYPPGILKMAKPFHDAVEKTVGTAAIKFSDGEIHDEDEKLKYMVFVEIEV : 93
DmelOBP83aX3 : MDQEGFRSSGKERNGKSHIKMALNGFGRVRSASVLLIALSLSGALILPPAAQQRDENYPPGILKMAKPFHDAVEKTVGTAAIKFSDGEIHDEDEKLKYMVFVEIEV : 113
DmelOBP83aX1 : -----MALNGFGRVRSASVLLIALSLSGALILPPAAQQRDENYPPGILKMAKPFHDAVEKTVGTAAIKFSDGEIHDEDEKLKYMVFVEIEV : 93
      L1      L      i      RDE YPFP Lk      P HD CV KtGVTE AIKEFSDG HEDE LKCYM C F E V

      120          130          140          150          160
BcucOBP83aX2 : LHEDGEVHLEKILDSIPESMHVIALHMGKKLYPKGDNKCERAFWLHRWKESDPKHYFLI : 148
BcucOBP83aX1 : LHEDGEVHLEKILDSIPESMHVIALHMGKKLYPKGDNKCERAFWLHRWKESDPKHYFLI : 148
BdorOBP83a : LHEDGEVHLEKILDKIPESMHVIALHMGKKLYPKGDNKCERAFWLHRWKESDPKHYFLI : 148
BlatOBP83a : LHEDGEVHLEKILDKIPESMHVIALHMGKKLYPKGDNKCERAFWLHRWKESDPKHYFLI : 148
BoleOBP83a : LHEDGEVHLEKILDKIPESMHVIALHMGKKLYPKGDNKCERAFWLHRWKESDPKHYFLI : 148
BminOBP83a : LHEDGEVHLEKILDSIPQSMHDIALHMGKKLYPKGDNKCERAFWLHRWKESDPKHYFLI : 148
CcapOBP83a : LHEDGEVHLEKILDSIPNSMHNIALHMGKKLYPKGDTKCERAFWLHRWKESDPKHYFLI : 148
RzepOBP83a : LHDDGEVHLEKILDSIPQSMHNIALHMGKKLYPKGDTKCERAFWLHRWKESDPKHYFLI : 151
DmelOBP83aX2 : VDDNGDVHLEKLFATVPLSMRDKLMEKSGGVHPEGDTLCHKAWWFHQWKKADPKHYFLP : 154
DmelOBP83aX1 : VDDNGDVHLEKLFATVPLSMRDKLMEKSGGVHPEGDTLCHKAWWFHQWKKADPKHYFLP : 174
DmelOBP83aX1 : VDDNGDVHLEKLFATVPLSMRDKLMEKSGGVHPEGDTLCHKAWWFHQWKKADPKHYFLP : 154
      G VHLEK      P SM      M K C P GD C A W H CWK DPKHYFL

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Supplemental figure 1-27 The alignment of OBP83a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP83bX2 : MVLVTGTRRGQAFHAFILVALS--SSLTLMH-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGVTTEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BdorOBP83bX3 : MVLVTGTRRGQAFHAFILVALS--SSLTLMH-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGVTTEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BdorOBP83bX1 : MVLVTGTRRGQAFHAFILVALS--SSLTLMH-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGVTTEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BlatOBP83bX1 : MVLVTGTRRGQAFHAFILVALS--SSLTLMH-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGVTTEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BlatOBP83bX2 : MVLVTGTRRGQAFHAFILVALS--SSLTLMH-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGVTTEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BoleOBP83b : MALIGIWRKQAFHAFILVALS--SSLTLMH-VQAQEPRRDDKVRNLIKHLNISTFX-----SEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 100
BcucOBP83bX2 : MVLNGLIRGHPLSAFLIVALA--SSLTLVH-VRAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGSEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BcucOBP83bX1 : MVLNGLIRGHPLSAFLIVALA--SSLTLVH-VRAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGSEEAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
BminOBP83b : MVLVTGIWRKQAFNAFLIVALS--SSLTLMH-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGTEAAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 110
CcapiOBP83b : MALNGSRRSQAFNAFLIVALALSSTLLMHVVQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGSEEAIKEFSDGQIHDEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 112
RzepOBP83b : -----WPPALLKMAKIFHDIIVVEKTVGTEAAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 71
RzepOBP83b : MILNGLIREQAFSAFLMVVLLSLSLRENY-VQAQEPRRDDKWPPPAVLKMAKIFHDIIVVEKTVGTEAAIKEFSDGQIHEDEALKCYMNCFLPHEIDVDDNGDVHLETLFNTV : 111
DmelOBP83b : -----MVKYP-LILLIGLAAAQEPRRDGEWPPAILKLGRHFHDIIVAPKGTVDAAIKEFSDGQIHEDEALKCYMNCFLPHEFVDDNGDVHMEKVLNAI : 95
      m   g   r   aflival  ssl l h v aqeprddkwppavLkmaKiFhdiIcvektgv eEAIKEFSDGQIHeDEALKCYMNCFLPHeIdVDDNGDVHleIc Ntv

      120     130     140     150     160     170
BdorOBP83bX2 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BdorOBP83bX3 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BdorOBP83bX1 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BlatOBP83bX1 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BlatOBP83bX2 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BoleOBP83b : PG-TVRNQLINMAKDEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 145
BcucOBP83bX2 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BcucOBP83bX1 : PG-TVRNQLINMAKEEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 155
BminOBP83b : PG-TVRDKLINMARGEHPEGDTLCHKAWWFHCWKKADPVIAEVRGGRPATRTPLSSPAALVTPAF : 176
CcapiOBP83b : PG-TVRDKLINMAKDEHPEGDTLCHKAWWFHCWKKADPVHYFLP----- : 157
RzepOBP83b : PG-TVRDKLINMAKDEHVPQGDTLCHKAWWFHCWKKADPVHYFLP----- : 116
RzepOBP83b : PG-TVRDKLINMAKDEHVPQGDTLCHKAWWFHCWKKADPVHYFLP----- : 156
DmelOBP83b : PG-TEKRLNIMMEASGRIHPEGDTLCHKAWWFHCWKKADPVHYFLV----- : 141
      PG tvR linmak CeHPeGDTLCHKAWWFHCWKKADPVhyflp

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Supplemental figure 1-28 The alignment of OBP83b

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      10      20      30      40      50      60      70      80      90     100     110     120
BdorOBP83cd : MELILIFLPAATIIISP-AVAVVQPNAAEIRTLSDQLQSYGGITEENSKRLARFKDSETYEEIPIPTKCIYKNNMFDFESVGFNDEQVIKQFGQPLHKAQKHRMEP----AADSQQAYNGFHL : 121
BlatOBP83cd : MESISIFLFAAIIISP-AVAVIQPNXVIRILSDQLQSYGGITEENSKRLVRFKDSETYEEIPIPTKCIYKNNMFDFESVGFNDEQVIKQFGQPLHKAQKHRMEP----AADSQQAYNGFHL : 121
BoleOBP83cd : MELILIFLFAAIIITP-SVAVVEPNAQEVRIISELQSYGGITENAAQRLVRFKQWSETYEEIPIPTKCIYKNNMFDFESVGFNDEQVIKQFGQPLHKAQKHRMEP----SANSQQAYNGFHL : 121
BminOBP83cd : MKLILIFLPAATIIISP-SVAVVQPNAAEIRIISLQSYGGITENQRLVRFKQWSETYEEIPIPTKCIYKNNMFDFESVGFNDEQVIKQFGQPLHKAQKHRMEP----STONQQAYNGFHL : 121
CcapiOBP83cd : MELPISLLAIVIAIP-ITAVVQPNAAEIRIINELKSFGGLTEENARLVRFKQWSETYEEIPIPTKCIYKNNMFDFIDESSGFKEQVVRVQFGQPLYNAAQHRMVP----LADAQQAYNGFHL : 121
RzepOBP83cd : MEYIIFLLAGALLPLAS-AVAVVQPNVQEGLIADQLKSYGGITEDKAQRLVRFKQWSETYEEIPIPTKCIYKNNMFDFIDESSGFKEQVVIKQFGQPLHKAQKHRMVP----AADTQQAYNGFHL : 122
DmelOBP83cd : MQMKSGILLALLLTS-LNGLLALLEHEGETINRIQNYGGLTAENAERLERFKQWSESYEEIPIPTKCIYSEMDFYNNLTGFNKGQIGVGFGRPVYEAARKKLELFFESGESSKHAYGFGHL : 125
      M   i   L   A       av   pn   E       cl   yGG Te n  RL  RFX  wS  YEIEPCtKcYi nMF  fdes GF  eqv  qGqPl  AC  hrm p       C  qAY GFHC

      130     140     150     160     170     180     190     200     210     220     230     240
BdorOBP83cd : VNLNEDPFVILIESMKNVNSTEAKTAMKDLHRFDQYEWERVKDYSKNPVREPIPIPTKCFIDRLQLYSQQTQWNIPALTAKLGVPAAGANIQHQLKQRRNRNNAVVMYQEFFFLVAHD : 240
BlatOBP83cd : VNLNEDPFVILIESMKNVNSTEAKTAMKDLHRFDQYEWERVKDYSKNPVREPIPIPTKCFIEKLQLYSQQTQWNIPALTAKLGVPAAGANIQHQLKQRRNRNNAVVMYQEFFFLVAHD : 240
BoleOBP83cd : VNLNEDPFVILIESMKNVNIEAKTAMKDLHRFDQYEWERVKDYSKNPVREPIPIPTKCFIDRLQLYGGQSRQWNIPALTAKLGVPAAGANIQHQLKQRRNRNNAVVMYQEFFFLVAHD : 240
BminOBP83cd : VNLNEDPFVILIESMKNVNSTEAKTAMKDLHRFDQYEWERIKDYAKNPVREPIPIPTKCFIDRLQLYSQQTQWNIPALTAKLGVPAAGANIQHQLKQRRNRNNAVNSAATKAAQNDVE : 240
RzepOBP83cd : VNLNEDPFVILIESMQNISTEAKTVMKDLHRFDQYEWELKDYSKNPVREPIPIPTKCFIERLQVYKASTHRWDIQAALRTKLGVPAAGANIQHQLRRRRNRNNAVVMYQDFFFLALAH : 239
CcapiOBP83cd : VSLNEDPFVILIESMKNVNSTEAKTAMKDLHRDYRYEWEMKDYAANFVREPIPIPTKCFVEHLQVFNQTRQWNIPALTAKLGVPAAGADIKHLERRRRNRNVGMWYQDFFGLPVP : 240
DmelOBP83cd : TNMESFPFVILNWNIPISPAKDAHQDLQVHQDEWKSFDAAFYVPNPIPIPTKCFVFDKLHIFEKTRLMKLEAMQNLOIPAKGARIRVRRHRGRDRATYTKQFTYAMAV- : 242
      vnLE dFfV IesM N S eAktAMKdCLhr dqyEWe kdy nVv:EPiPcTKCF Lq tr W i al kLgVPA gA I hcl R rn c y f c

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Supplemental figure 1-29 The alignment of OBP83cd

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      10      20      30      40      50      60      70      80      90     100     110
BcucOBP83ef : MIFRVASQAVLLIAAAYIQIMVSSAATTKVEERDVESDAELRKQLHEVGSKD-VLVELQKVARYSKWTSEEIPIPTKCLASMKRWFDADESKNWNKQQTADDGLGDMFNYC : 110
RzepOBP83ef : ----- : -
BdorOBP83ef : MNFRASQVULLIAVAYIQIMVSSAATTKAAEQDVSDSTEILRKQLREVGSKD-LVLELQKVARYSKWTSEEVPIPTKCLASMKHWFDADESKNWNKQQTADDGLGDMYNYC : 110
BlatOBP83ef : MNFRHASKVULLIAVAYIQLVSSAVTTKAAEQDVSDSTEILRKQLREVGSKD-LVLELQKVARYSKWTSEEVPIPTKCLASXKHWFDDXDESKWNKQQTADDGLGDMYNYC : 110
BoleOBP83ef : MNFRASQVILLIA--YIQIMVSSAATTKAAERDVSSTEILRKQLREVGSKD-LVLELQKVARYSKWTLEEVPIPTKCLASMKHWFDADESKNWNKQQTADDGLGDMFNYC : 108
DmelOBP83ef : ---MSSPRAVLSLFLISQALAE-----DLSGDAQTLLEKLQLSLSPEISIAGLDLKRLERYSSWTREEVPIPTKCLAREKGFVDEENKRWKQQTADDGLGADVNYC : 98
      l       c   q       d   d   l   kcl   s       g   l   k   rys  wt  ee  pc  rcla  k  wfd  e  kw  q  digad  nyc

      120     130     140     150     160     170     180     190     200     210     220
BcucOBP83ef : RYELDRYNEDSEFFAYTGLRLKQAELYTLETYKNIIVASELNVNMTKELQKYAAPTKEVVPFLFCFLAEKMDFYTPTYEWNFDKNWKAFGFTRQDPTAS---NVCKVS : 217
RzepOBP83ef : -----MEELQKYAAPTKEVVPFLFCFLAEKMNFTYTPTYEWNFDNNWKAFGFPMRQNRKAS---DVCKVS : 61
BdorOBP83ef : RYELDRYNEDSEFFAYTGLRLKQAELYTLETYKNIIVASELNVNMTKELQKYAAPTKEVVPFLFCFLAEKMNFTYTPTYEWNLDNNWKAFGFPMRQDRTAS---NVCKVS : 217
BlatOBP83ef : RYELDRYNEDSEFFAYTGLRLKQAELYTLETYKNIIVASELNVNMTKELQKYAAPTKEVVPFLFCFLAEKMNFTYTPTYEWNFDNWQAAGFPMRQDRTAS---NVCKVS : 217
BoleOBP83ef : RYELDRYNEDSEFFAYTGLRLKQAELYTLETYKNIIVASELNVNMTKELQKYAAPTKEVVPFLFCFLAEKLNFTYTPSYEWNFDNNWKAFGFPMRQDRTAS---NVCKVS : 215
DmelOBP83ef : RFELRMSGDSCSFAYRGLRLKQAEAMHAGTSLSTLLQSRQLNATNVLELYSKLKSKEPIPIPTKCFADAMGFYDPDGNWRLENWKAFGFSGNEDSSGADYSGLRLS : 209
      r  el  r  d  c  fay  glrcIkqae       c   ln  tm  ElqKYaap  KEvvPCLFQCIA  km  FYtP  yeWn  dnWv  AFGP  rq  aS       vCkVs

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      230     240     250     260     270     280
BcucOBP83ef : SEQ-INKRKKENWYEEYNLERLNVNTDGSYPMETTTLSAVITSSKKPDAVEAAVEKAS----- : 275
RzepOBP83ef : AEQ-QMNRKKENWYEEYNLERLNVNTDGSYPLETTTLSAVIASKKTKEVGVQOKTEEADANS : 124
BdorOBP83ef : AEQ-MKTRKKENWYEEYNLERLNVNTDGSYPLETTTLSAVIARKTAASVEDKTAS----- : 274
BlatOBP83ef : XEQ-MKTRKKENWYEEYNLERLNVNTDGSYPLETTTLSAVITRNTAAAVEDLAKTS----- : 274
BoleOBP83ef : AEQ-TKMRKKENWYEEYNLERLNVNTDGSYPLETTTLSAVITSKTTTETVEDKTAS----- : 272
DmelOBP83ef : GTQREVALSKENWYHEYKWERVWNGN-----KLVEDNEEQ----- : 245
      eQ   rKcEWMYeYnCLERLNyNtdgsyp e ttls vi       Ve  k

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Supplemental figure 1-30 The alignment of OBP83ef

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP83g : MNTQ-LILLIAFVA--LVAG---KFQIRTAQDALDAHEAHEEYRVPEDIYQKFLNYEFPFAHKRTNIVYVKCFVERMGLFTEEGGFDEKAIIAQFTAKSSKNLAKVSHGLEKEL : 107
BlatOBP83g : MNTQ-LILLIAFVA--LVAG---KFQIRTAQDALDAHEAHEEYRVPEDIYQKFLNYEFPFAHKRTNIVYVKCFVERMGLFTEEGGFDEKAIIAQFTAKSSKNLAKVSHGLEKEL : 107
BoleOBP83g : MKTQ-LILLIAFVA--LVAG---KFQIRTAQDALDAHEAHEEYRVPEDIYQKFLNYEFPFAHKRTNIVYVKCFVERMGLFTEEGGFDEKAIIAQFTAKSSKNLAKVSHGLEKEL : 107
BminOBP83g : MNTQ-LILLIAFVA--LVAG---KFHVRTAQDALDAHEAHEEYRVPEDIYQKFLNYEFPFAHKRTNIVYVKCFVERMGLFTEEGGFDEKAIIAQFTAKSSKNLAKVSHGLEKEL : 107
BcucOBP83g : MKTQ-LILLIAFVA--LVAG---KFQIRTAQDALDAHEAHEDEFRIIPDDIEKYLYNIEFPFHKRTNIVYVKCFVERMGLFTEEGGFDEKAIIAQFTAKSSKNLAKVSHGLEKEL : 107
CcapiOBP83g : MKIQ-LILLIAFVA--LVAG---KFELRTAQDALDAHEAHEDEFRIIPDDIEKYLYNIEFPFHKRTNIVYVKCFVERMGLFTEEGGFDEKAIIAQFTAKSSKNLAKVSHGLEKEL : 107
DmelOBP83g : MQQSOLLIVAAVATFLVAQTAKFLFLKHADAQKAFEDREDYVVPDDIYKFLNYEFPFAHRTSIFVAKCFLEKLELFSEKKGFDERAMIAQFTAKSSKSLTVQHGLEKEL : 113
      M   Q  LiIl  A  VA   LVag  KF  rtaqDAL aHaEc  e  r  P  DIY  K  LNYEFP  HKRTNcYkCFvErmgLfTEeKGfDeKaIiAQFTaRsSknLak  sHGLEKc

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      120     130     140
BdorOBP83g : DHNEHDSDTCTWANRVFSWISVNRPIVRRTYIEN : 142
BlatOBP83g : DHNEHDSDTCTWANRVFSWISVNRPIVRRTYIEN : 142
BoleOBP83g : DYNEHDSDTCTWANRVFSWISVNRPIVRRTYIEN : 142
BminOBP83g : DHNEHDSDTCTWANRVFSWISVNRPIVRRTYIEN : 142
BcucOBP83g : DHNEHDSDTCTWANRVFSWISVNRPIVRRTYIEN : 142
CcapiOBP83g : DHNEHDSDTCTWANRVFSWISVNRPIVRRTYIAN : 142
DmelOBP83g : DHNEAESDVCTWANRVFSWLPINRHVVRKVFA-- : 146
      DhNehdSDtCTWANRVFSWISvNRpIVR tyi n

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Supplemental figure 1-31 The alignment of OBP83g


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      10      20      30      40      50      60      70      80      90     100     110     120
BdorOBP84a2 : -----MSNGNVFVMLPLTIIILLYGIMVSAQ-DRAKDNGDIFVQHKE-----QRETVAPIMVQANGSVSSEGMVAH : 66
BlatOBP84a2 : -----MSNRNVFVMIFFTIIILLYGIMVSV-DRAKDNGDIFVQHRE-----QRETVAPIMVHANGSNSSEMDVAH : 66
BoleOBP84a2 : -----MSNNVVLVLPFTIIMLLYSIMMSVQ-DRAKDNGDIFVQHKE-----QRETVAPIIVQSGNSFSSEGTVMH : 66
BminOBP84a2 : -----MSNGNVLVGPFIMIMLLYSIMISIQ-DRAKDNGDIFVQHRE-----QRETVAPIIVQANDSISSEGTVDVL : 66
BcucOBP84a2 : -----MSNNVAVFLPYIMIMLLYSVRMSMQ-DRAKDNGDIFVQHKE-----QRETVAPILVQTNDSISNEGADVLD : 66
CcaphOBP84a2 : -----MFRKAVITKLPLLLLVVY-IVASIQ-DHAKDNGDIFVQHQSKEFNMLEERANATIPQLSINSGTNELEDVVR : 73
RzepOBP84a2 : -----MTSINATLQLTLFTLLIYSNMVRTQ-SRPKDNNGDIFVQKTSVMAGITADQDIPKAAQTYGSNI FNVEEVMR : 74
DmelOBP84aX2 : MFHSYLYLIGILSLIWVAQDQIVPDDEVMQMHAMFYTARVAADENLIPYVRAAVIAFLILSPNARALQDHAKDNGDIFIINVDS--FDGVDVDDISSTTSAPRE-ADYVDFDEVNR : 116
DmelOBP84aX1 : -----MYSA-----LVRAAVIAFLILSPNARALQDHAKDNGDIFIINVDS--FDGVDVDDISSTTSAPRE-ADYVDFDEVNR : 70
BdorOBP84a1 : -----MINHRLLSLALSLLVGLAGTTRAHPTDATDNKLDKQQS-----METPTTPTAGAA-ETGDFDFEEVVR : 63
BlatOBP84a1 : -----MINHRLLSLALSLLVGLAGTWAYFEIDATDNKLDKQQP-----METTFPNAGAA-ETGDFDFLEVR : 63
BoleOBP84a1 : -----MINHRLLSLALSLLVGLAGTANQTDATDNKLDKQQS-----METTTSVRAAN-VSGDFDFEEVVR : 63
BcucOBP84a1 : -----MSEILLEMVNVYKVELLALSLLVGLAGTTADAQSDATDNKLDKQQS-----METTTPMAEAA-ASGDFDFQDVVR : 69
CcaphOBP84a1 : -----MGITITKLLKKTMLDHRHINIILLQLFGFMSSGAADAQTNLTNNASDQLQA-----VENTTEVMVEEH-EMGDFDFDAVVR : 74
RzepOBP84aX2 : -----MVNH-QLGMTLSVLLF--LATSLANAQTNMNNRLDVQPS-----METKTTMAENPS-AMGDFDFEAAGR : 60
RzepOBP84aX1 : -----MVNH-QLGMTLSVLLF--LATSLANAQTNMNNRLDVQPS-----METKTTMAENPS-AMGDFDFEAAGR : 60
                                     D                                     e                                     v
      130      140      150      160      170      180      190      200      210      220      230
BdorOBP84a2 : LNNNSFSIPSDYIVQFNNGDLPEIVDKTG-MFIRYFEKAGLIKNNQLNKDLIMQTMWPIKADSIATPEPAKQ-EMNAVRSYAIAKLMKRGFQDTNDTVA----- : 170
BlatOBP84a2 : LNNNSFSIPSDYIVQFNNGDLPEIVDKTG-MFIRYFEKAGLIKNNQLNKDLIMQTMWPIKADSIATPEPEAKQ-EMNAVRSYAIAKLMKRGFQDTNDTVA----- : 170
BoleOBP84a2 : LNNNSFSIPNDYIVQFNTNGALSDTVDKTG-MFIRYFEKASLIKNNQLNKDLIMQTMWPIKADSIATPELESKQ-EMNAVRSYAIAKLMKRGFEDTNDHTVA----- : 170
BminOBP84a2 : MNNSSFSIPSDYIAQFMNGALSDTLDKTG-MFIRYFEKAGLIKNNQLNKDLIMQTMRLIKANSIEFPEPAKQ-ETNAIRTYAIAKLMKRGFEDTITQTV----- : 170
BcucOBP84a2 : MNNSSFSIPMDYIVQFNTNGALSETADKTG-MFLIRYFEKMGLIKAWQLNKDLIMQTMWPIKADSIATPEPAKQ-EVNNAVRTYGIKLMKRGFEDTNDTVAQNSFRAY : 177
CcaphOBP84a2 : LNNNSFSIPTDHIMQFNTDGAADTVDKTG-MFIRYFEKSGLIQNKNLNDQIVQKMNPLAADSDVDFESEAQK-EMNAVRTYAIAKLMQRFEFTGNPSAV----- : 177
RzepOBP84a2 : TNNASFSIPMDYIVQFNTTGEISDTTDKTG-MFIRFLEKSGLIKNNHNLKDLIMQTMWSIIADSVLESESESES-EVNNAVRTYAIAKLMKRLTEAAGNQTLT----- : 178
DmelOBP84aX2 : NNNASFTTSMNVLPQFNNTGDLPPDKDKVTSMYFHFEEKSGMLTDYKLNLTDLVRKYVWPATGDSVEAEAEAGKD-ETNARMGYAIVKVFTRALTDARNKFTV----- : 221
DmelOBP84aX1 : NNNASFTTSMNVLPQFNNTGDLPPDKDKVTSMYFHFEEKSGMLTDYKLNLTDLVRKYVWPATGDSVEAEAEAGKD-ETNARMGYAIVKVFTRALTDARNKFTV----- : 175
BdorOBP84a1 : TNNASYTIPLEYIQQFNETAELPNITDKTG-MFLKYMEKTGLLRNQNLNPTLIQRTMMPATGDSLPVQNEGSR-ETPKRTYAIAKLMLRALVDARNKFLV----- : 167
BlatOBP84a1 : TNNASYTIPLEYIQQFNETAELPNITDKTG-MFLKYMEKTGLLRNQNLNPTLIQRTMMPATGDSLPVQNEGSR-ETPKRTYAIAKLMLRALVDARNKFLV----- : 167
BoleOBP84a1 : TNNASFTIPLEYIQQFNETAELPNITDKTG-MFLKYMENTGLLRNQNLNPTLIQRTMMPATGDSLPVQNEGSR-ETPKRTYAIAKLMLRALVDARNKFTV----- : 167
BcucOBP84a1 : TNNASFTIPLEYIQRFNETAELPNITDKTG-MFLKYMEKTGLLRNQNLNPTLIQRTMMPATGDSLPVQNEGSR-ETPKRTYAIAKLMLRALVDARNKFTV----- : 173
CcaphOBP84a1 : TNNASFAIPLEIYQRFNETAELPNITDKTG-MFLKYMEGTGLLRNQNLNPTLIQRTMMPATGDSLPVQNEGSR-ESPKRTYAIAKLMLRALVDARNKFTV----- : 178
RzepOBP84aX2 : TNNASFTTPIEYIQQFNETAELPNTADKTS-MFMHMYMEKTGLMRNQLNRALIMQTMMPATGDSLPVQNEGSR-ETPKRTYAIAKLMLRSILVDARNKFTV----- : 165
RzepOBP84aX1 : TNNASFTTPIEYIQQFNETAELPNTADKTS-MFMHMYMEKTGLMRNQLNRALIMQTMMPATGDSLPVQNEGSRKLVLSVVRTPSLVN----- : 149
      CN sf p i qFN L DKT MCF Cy EK gL w LN li qtmpw ds C e e c R yalakl r d n

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Supplemental figure 1-32 The alignment of OBP84a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP99a : MKTIIALLLLAVTSAEYVVKNEENLQQVRRREKATELKVPAEHIEQFRKKWQFPNDATQCYLKVFEKFGFLFDAVTFGNVVEHIHQQLQGAEVAPPGDAHDHDDVVDHKIAAC : 111
BlatOBP99a : MKTVIALGLLAVTSAEYVVKNEENLQQVRRREKATELKVPAEHIEQFRKKWQFPNDXSQCYLKVFEKFG-FADETGFNVVEHIHQQLQGAEVAPPGDAHDHDDVVDHKIAAC : 109
BcucOBP99a : MKNFIAPGLLAVTSAEYVVKNEENLQQVRRREKATLKVPEDHQQFRKKWQFPNDSVQCYLKVFEKFGFLFNAETGFNVVEHIHQQLQGAQVAPPGDAHDHDDVVDHKIAAC : 111
BminOBP99a : MKGVVIFLFLVALTSAEYVVKTEENLLQFRRECVNELKVPPEEHQQFGKKWQFPNDSVQCYLKVFEKFGFGFDALTGFNVVEHIHQQLQGAEVAPPGDAHDHDDVVDHKIAAC : 111
RzepOBP99a : MKKFAAFLFLFAAMVSAEYVVKTEENLRQYRQECVAELQVPDEHVQYQFNRRQFPNDSITQCYLKIFNKFQLFDDDETGFNVVEHIHQQLQGAQVAPPGDAHDHDDVVDHKIAAC : 111
DmelOBP99aX1 : MKVFVAIVLIGLASADYVVKNRHMDLAVRDECVKELAVPVDLVEKYQKWEYPNDAKTQCYIKVFTKMGFLFDVQSGFNVENI HQQLVG-----NHADHNEAFHASLAAC : 105
DmelOBP99aX2 : MKVFVAIVLIGLASADYVVKNRHMDLAVRDECVKELAVPVDLVEKYQKWEYPNDAKTQCYIKVFTKMGFLFDVQSGFNVENI HQQLVG-----NHADHNEAFHASLAAC : 105
      MK a c SA YVVK R EC eL VP kw PND TQCY KcVf K g Fd GFNVE IHQQL G ADH H AAC
      120      130      140
BdorOBP99a : VDTNEQGSNACEWAYRGGVCFIKENLQLVKHSVKPQA : 148
BlatOBP99a : VDTNEQGSNACEWAYRGGVCFIKENLQLVKHSVKPQA : 146
BcucOBP99a : VDSNEQGSNACEWAYRGGVCFIKENLQLVKHSVKPQA : 148
BoleOBP99a : VDNNEQGSNACEWAYRGGVCFIKKNLRLVKHSVKPQA : 148
RzepOBP99a : VDSNEQGSNACEWAYRGGVCGMKANLQFIKTN----- : 143
DmelOBP99aX1 : VDKNEQGSNACEWAYRGATOLLKENLAQIKSLAPKA : 142
DmelOBP99aX2 : VDNNEQGSNACEWAYRGATOLLKENLAQIKSLAPKA : 142
      VD NEQGSNACEWAYRG C K NL s a

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Supplemental figure 1-33 The alignment of OBP99a

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP99b : MKFLLALLSLLMVVFAVAD-HASHSDYVVKTNEDLIRYRDECVSKLSIPSDLVVDKYKWSFPDDEKTHCYLKVLEKFELFDAAGKGFVDVHKIHHQLVGA--NADHSDATH : 108
BlatOBP99b : MKFLLALLSLLLAUVFAVAD-HAGHSYDVVKTKEDLIRYRDECVSKLSIPSDLVVDKYKWSFPDDEKTHCYLKVLEKFELFDESKGFVDVHKIHHQLVGA--NADHSDATH : 108
BoleOBP99b : MKFLLALLSLLIAVVLAVADHHAHSDYVVKTNADLLRYRDECVSKLSIPSDLVVDKYKWSFPDDEKTHCYLKVMEKFDVFAEKGFVDVHKIHHQLVGA--NADHSDATH : 109
BminOBP99b : MKFFLALLSLIFAVVLADEHDAHSDYVVKTNADLLRYRDECVSKLSIPADLVEKYKWNFPDDEKTHCYLKVLEKFGLYDEEKGFVDVHKIHHQLDGD--KVDHSDATH : 109
BcucOBP99b1 : MKFFVALLSLIFAVVLASADHSDYVVKTNEDLLRYRDECVSKLSIPADLVEKYKWSFPDDEKTHCYLKVLEKFELFDAAGKGFVDVHKIHHQLVGA--KVDHSDATH : 109
BcucOBP99b2 : MKFFVALLSFIFAVVLADGVDAHSDYVVKTNEDLLRYRDECVSKLSIPADLVEKYKWNFPDDEKTHCYLKVLEKFELYDAEKGFVDVYVHHQLVGA--KADHTNAMH : 109
CcaphOBP99b : MKFFLALLSLFFAVVVDHGG---HSDYVVKTGEDLARYRDCVAKLSIPADLVEKYKWEYFPDDEKTHCYLKVLESFGLFDDAKGFVDVHKVHHQLVGGG--DVDHSDNLH : 106
RzepOBP99b : MKYFIALLSL-LVVVLAHDSHSDYVVKSKEDLAHARDHCYKSLTIADDLVEKYKWEYFPDDEKTHCYLKVIFEELGLYDDEKGFVDVHKVHHQVAGD--KVDHSDNLH : 108
DmelOBP99bX1 : MK---VLIVLLGLFAVLADHHHHHHHDYVVKTHEDLTNYRTQCEVKVHASEELVEKYKWKQYPPDAVTHCYLKVIFQKFGFYDTEHGFDVHKIHLQLAGFGVEVHSDH : 108
DmelOBP99bX2 : MK---VLIVLLGLFAVLADHHHHHHHDYVVKTHEDLTNYRTQCEVKVHASEELVEKYKWKQYPPDAVTHCYLKVIFQKFGFYDTEHGFDVHKIHLQLAGFGVEVHSDH : 108
      MK all l vv a h H dYVVKT DL yR CV l i dLV kYk w PdDekthCYLkC ekf D KGFVDhK HHQl G dhds H
      120      130      140      150
BdorOBP99b : GAIENAKKAA--GDDACVRAVNGFTFLKNNAQVLVQAGVKESSK : 151
BlatOBP99b : GAIENAKKAA--GDDACVRAVNGFTFLKNNAQVLVQAGVKESSK : 151
BoleOBP99b : GAIENAKKAAAAGDDACVRAVNGFTFLKDNIKVLVQAGVKESSK : 154
BminOBP99b : GAIENAKKAAAAGDDACVRAVNGFTFLKDNILQLVQAGVKESSK : 154
BcucOBP99b1 : GAIENAKKAAAAGDDACVRAVNGFTFLKDNILQLVQAGVKESSK : 154
BcucOBP99b2 : VAIDKAKKAAVASDDACVRAVNGFTFLMDYTHLIPAGN--ASK : 152
CcaphOBP99b : KGIENAKEGDAAGEDACVTRAYRGALFFKENLALVQKQNV--ASK : 149
RzepOBP99b : KTIESAKEGAD-SDDSCVTRAYRGGLLINNNLTLVKQSFVSD-- : 150
DmelOBP99bX1 : QKIAHKAETHSK-EGDSCSKAYHAGMFMNSNLQLVQHSVKV--- : 149
DmelOBP99bX2 : QKIAHKAETHSK-EGDSCSKAYHAGMFMNSNLQLVQHSVKV--- : 149
      I CAK D C rAY g Cf n Lv v

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Supplemental figure 1-34 The alignment of OBP99b

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP99c2 : -MKYFMFIVILAVVALVQAD-DWSPKTVDDIKKIREEMKQVPSSDEEFQKRKENYDPDVESVRKYALNSKSGWGLYKEGKGFYPDRVAEQFKDDMP-EDEIKAIVND : 107
BlatOBP99c2 : -MKYFLLIVILAVIKLVQAD-DWSPKTVDDIKNIREEMKQVPSSDEEFQKRKENYDPDVESVRKYVLCNSKAWGLYKEGKGFNADRIAQFKDEMP-EDEIKAIQD : 107
BoleOBP99c2 : -----MSK-EFHTVSTDDIKSIREEMKQVPSPASDEEFQKRKENYDPDVESVRKYVLCNSKAWGLYEDGKGFNADRIAQFKGDLT-EDEIKTIVHD : 91
BminOBP99c2 : -MKYF--IVILAIILVQAD-DWSPKTTDEIKSIRENCKQVPSSDEEFQKRKKDEYPDIESVRNYVLCNSKAWGLYEDGKGFGEHVAQFKGDLSEDEIKSIVHD : 105
BcucOBP99c2 : -MKYF--IVILAIILVQAD-DWSPKTTDEVKSIRENCAKDIPASDEEFQKRKENYDPDVASVRNYVLCNSKAWGLYEDGKGFYNADRIAQFKGDLSEDEIKAIVHD : 105
BdorOBP99c1 : -MKFF--IVILAVVALAYAEDDWVPKNAAEIKVIRQECCKDFFPLSEEEYIQMKMSFEYDDEEPVRKYLLCTAKKLGVPCEHGQYHADRVAKQFKMDLD-EAEVLAIEGG : 106
BcucOBP99c1 : -MKFF--IVILAVVALAYADDEWVPKNAAEIKVIRQECCKDFFPLSEEEYIQMKMNFEYDDEEPVRKYLLCTAKKLGVPCEHGQYHADRVAKQFKMDLD-EAEVVAIEGG : 106
BdorOBP99c1 : -MKFF--IVILAVVALAYADEWVPKNVAQIKVIRQECCKDFFPLSEEEYIQMKMNFEYDDEEPVRKYLLCTAKKLGVPCEHEGYHADRVAKQFKMDLD-EAEVIAIEGG : 106
BlatOBP99c1 : -MKFF--IVILAVVALAYADEWVPKNVAQIKVIRQECCKDFFPLSEXYIQMKMNFEYDDEEPVRKYLLCTAKKLGVPCEHEGYHADRVAKQFKMDLD-EAEVIAIEGG : 106
BdorOBP99c3 : -MKFF--LVILAVVTQTAYAEDEWVPKNMAELNAIRQECCKEYPLSEEQLOKQKNFEYDDEEPARKILLCTVKKLGVPCEREGYNADRVAKQFKMDLD-EAEALAIIEGG : 106
BlatOBP99c3 : -MKFF--LLILAVISRTYAEDEWVPKNAAEVNVIRQECCKDFFPLSEEEQKQVKNFEYDDEEPARKVLLCTVKKLGVPCEREGYNVDRVTKQFKMDLD-EAEALSIIEGG : 106
BoleOBP99c3 : -MKLF--IVLAVVALVYAD-EWMPKNFAEINVIRQECCKDFFPLSEEEYIQMKMNFEYDDEEPVRKYLLCTVKKVGIFCEREGYLADRVAKQFKMDLD-EAEALIAIEGG : 105
BlatOBP99c4X1 : -MKFF--IVILAVVALAYADEWVPKNVAQIKVIRQECCKDFFPLSDEYIQMKMNFEYDDEEPVRKYLLCTVKKFGIFREDEGYNVNRVAKQFKMDLD-EAEALAIIEGG : 106
BlatOBP99c4X2 : -MKXF--LAFLAHFALAYAEDEWVPKNVAELNAIRQECCKDFFPLSDEYIQMKMNFEYDDEEPVRKYLLCTVKKFGIFREDEGYNVNRVAKQFKMDLD-EAEALAIIEGG : 106
BdorOBP99c4 : -MKFF--IVILAHVALAYAEDEWMPKNMAELNVIRQECCKDFFPLNDEYIEKMNFEYDDEEPVRKYLLCTVKKRFGIFREGQGYNDRAVAKQFKMDLD-EAEVLAIEGG : 106
BdorOBP99c6 : -MKFF--IVILAVIALVYAKDEWVPKTEAELKVIIVKECKDFFPLNNEQLOQYTYTFQDDEEPPIRKYMLCTAKRVGFFSEHEGCHVDRVAKQFKLDLD-EAEVAAIEGG : 106
BdorOBP99c5 : -MKFF--IVILAVVALAYAKDEWPKTEAELKVIANECCKDFFPLSNEQLOQYTYAYQHPDKEISIRNRLCAIKKXOFFSEHEGYHADRIAKQFQIDFH-EAEVAAIEGG : 106
BdorOBP99c7 : -MKFF--IVILVVALITYAEDEWIPKNDTELEVIAQECCKDFFPLSSEEQKFSSFEYDDEEPPIRKYMLCTAKRVGFFTEQEGYHADRVAKQLKMDLD-EAEVIAIEGG : 106
BdorOBP99c8 : -MKFF--IVMLAVVTTLAYAEDEWMPKNDAEVSVIRQECCKDFFPLSEEQLOKQFRIFEYPEEEALRKYLLCTKAVGIFTEHEGYHADRVAKQFNINLD-EAEVTIIIEGG : 106
BminOBP99c1 : -MKFF--IVILAVVALAYAEDEWVPKNVAEIKVIRQECCKEFLSSEEHQKQLKNLEYPDDEEPVRKYLLCTAEKLGVPCEHEGFHANRIAKQFKMDLD-EAEVLAIEGG : 106
CcapOBP99c1 : -MKFL--IVLAVVALAYADDEWTVKQAAEIKERQECCKLENPLDGEYIQMKMSFEYDDEEPVRKYLLCTAKKLGVPCEHGYHVDRIAKQFKMDLD-EAEVVAIEGG : 106
RzepOBP99c1 : -MKYF--IAILAVVALAQAEENWVKTAADIKVIRQECCKEFLPLQBEYIQMKMNFEYDDEEPVRKYLLCTAKKLGVPCEHGQYHADRVAKQFKMDLD-EAEVLAIEGG : 106
DmeLOBP99c : MLKYL--IVLAIAVVAHAD-DWTFPTGEEIRKIRVDCCKENPLSNQISQLKNLIFNPEPVRQYLLCTSAIKLGIFCEHGQYHADRVAKQFKMDLS-EEBALQIAQS : 106
CcapOBP99c4 : -MKYF--IVLAAVVAQAADDDWPKTPEEFNAIRECHKEFFPFSKELQKQDELDLFDSDDETVRKYEVCVFRKWGIIADDDTFHGERLVKQFEAVLDVGEIEQKYNV : 108
CcapOBP99c2X1 : -MKYF--IVLAAVVAQAADDDWPKTPEEFNAIRECHKEFFPFSKELQKQDENLDFSDDETVRKYEVCVFRKWGIIADDENFHGERLVKQFEAVLDDEVENIEQKYNV : 108
CcapOBP99c3 : -MKYF--IVLAAVVAQAADDDYKLTPEEFNAMARECHREFFPFSKELQKQDENLDFSDDETVRKYEVCVFRKLGILDADNNFNGDLRVKQFEAVLD-VEGTEQKYNV : 107
CcapOBP99c2X2 : -MKYF--IVLAAVVAQAADDDYKLTPEEFNAMARECHREFFPFSKELQKQDENLDFSDDETVRKYEVCVFRKLGILDADNNFNGDLRVKQFEAVLD-VEGTEQKYNV : 107
CcapOBP99c5X1 : -MKYF--LTLLAAVLAQAQDD-WKIKSANEVNDIRRECHKEHFPFNEELQKHEEVLRFDPDEDVVRNVECVFTKWGVDPETGFKKDLRVQFPEVLK-REEDIEIGRA : 106
CcapOBP99c5X2 : -MKYF--FLTLAAFLFAQAQDD-WKIKSANEVNDIRRECHKEHFPFNEELQKHEEVLRFDPDEDVVRNVECVFTKWGVDPETGFKKDLRVQFPEVLK-REEDIEIGRA : 106
CcapOBP99c6 : -MKYF--ILLAAVLLAQAGE-KWKTVDDEFNDMRDRCHKEIPFSEELQKKEEVLRFDPDEDVVRKYLLCTAKTWEVDFDEENGFMMDRLIVEFELLN-RDEVLPIAKR : 106
      mk f      a      a      w      k      ir e c k p s e      p d e v R y C      g      g      r      q f      l      e      i      C

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      120      130      140      150
BdorOBP99c2 : EKTKE-ETDDEEYHLLKVMSTKLGDHIDLVKRLE----- : 143
BlatOBP99c2 : EKTKE-ETDDEEYHILKCASTKLGDHIDLIKRS----- : 143
BoleOBP99c2 : AKTKE-DTDDERAYHIMKCTSTKLGEDIKEILKRS----- : 127
BminOBP99c2 : EKTKE-DSDDERAYHVLMOILSSKLGGDVKELLKRS----- : 141
BcucOBP99c2 : EKTKE-DADDEKAFHILKCLTSKIGEAUVKFLHKE----- : 141
BcucOBP99c1 : DKNVEGSSADVWAYRGHKLMAASKIGDRVKAYIKKTVEAAKQ-- : 149
BoleOBP99c1 : DKNVEGSSADVWAYRGHKLMAASKIGDRVKAYIQSVVEAAKQ-- : 149
BdorOBP99c1 : DKNVEGSSADVWAYRGHKLMAASKIGDRVKAYIQSVVEAAKQ-- : 149
BlatOBP99c1 : DKNVEGSSADVWAYRGHKLMAASKIGERVKAYIQSVVEAAKQ-- : 149
BdorOBP99c3 : DKNLEGGSSADVWAYRGHECVVASKIGDRVKAYFLKS---KK--- : 144
BlatOBP99c3 : DKNLEGGSSADVWAYRGHECVVASKIGERVKAYFLKNGEKPKK--- : 148
BoleOBP99c3 : DKNVEGSSADVWAYRGHECVLASKIGDRVKAYFKKSSENTKK--- : 147
BlatOBP99c4X1 : DKNIEGSSDDVWAYRCKCVLASKIGDRVKAKSKEESYKQ----- : 146
BlatOBP99c4X2 : DKNIEGSSDDVWAYRCKCVLASKIGDRVKAKSKEESYKQ----- : 146
BdorOBP99c4 : DKNTEGSSDDVWAYRCKCVMAASKIGDRVKAKSRE----- : 141
BdorOBP99c6 : DKNAEGSSDVWAYRGHKLMAASKIGERLRYIQNLKKEAKKH-- : 149
BdorOBP99c5 : DKIVKGSSDVWAYRSRCKVMTSKIGERLKARNQKI----- : 142
BdorOBP99c7 : DKNVEGSSADVWAYRVHKLMAASKIGEHGKAYFQK----- : 141
BdorOBP99c8 : DKNVEGSSADVWAYRIHKVMAASKIGERVKAYIQNLKKEAKKH-- : 149
BminOBP99c1 : DKNEGSSPDVWAYRGHKLIDSKIGESVKAYIKKSADAQKQ-- : 149
CcapOBP99c1 : DKNEGSSADVWAYRGHKLMAASKIGDRVKSIVKKNVEAAKQ-- : 149
RzepOBP99c1 : DNNEQSSPDVWAYRGHKLMAASKVGEKVKAYIKKRAEDAQKQ-- : 149
DmeLOBP99c : DDNAKNMPTDVWAFRGHQLMAASKIGDKVRAFVAKAEAAKKAA : 151
CcapOBP99c4 : DKNEGSSPDVWAYRSRIQCKIDKTDIAPNLLKVIKGL----- : 144
CcapOBP99c2X1 : DKNEGSSPDVWAYRSRIQCKIDKTDIAPNLLKVIKGL----- : 144
CcapOBP99c3 : DKNEGGRPVDYVRSRIQCKIDKTDIAPNLLKVIKGL----- : 143
CcapOBP99c2X2 : DKNEGGRPVDYVRSRIQCKIDKTDIAPNLLKVIKGL----- : 143
CcapOBP99c5X1 : DKNEGSSPDVWAYRVFQQCVSRSEIIPNFKLIIGKL----- : 142
CcapOBP99c5X2 : DKNEGSSPDVWAYRVFQQCVSRSEIIPNFKLIIGKL----- : 142
CcapOBP99c6 : DKNEGSSPDVWAYRVQQCVGKTKLGPLFEALGKLSK----- : 144
      dkn      g      D      yr      C      g

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Supplemental figure 1-35 The alignment of OBP99c

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      10      20      30      40      50      60      70      80      90     100     110
BdorOBP99d : MLIPRFLIIP-I-TIMFSLVISFPTPSKAVPIS-EHEEASRRLYKAHGCQVNSSAPTSIDKEYRSTKQEPAAVVRVASNMGLWTDASGYQAKRVAKFFVKHEHNEVMTVVD : 111
BlatOBP99d : MFTSRVLIISL-AVGFVAIISLKPAKAVPIS-EHEKASRRLYKAHGCQVNSSTPTSMNKYEYRNTQKTGAYLRVASNMGLWTDASGYHARRVAKFFIKHEHNEVMTVIX : 111
BoleOBP99d : MFIPRFLIIRL-AVVLGVVISFPMASATVPIS-EHEDASRRLYKAHGCQVNSISTPKSTD-SHISTEQIVGAYVRVASNMGLWTDATGYQAKRVAKFFFKHEHSEVMTVVD : 110
BminOBP99d : -----TEELFNPAIAPVIS-EYEEASRRLYKAHGCQVNSISTPKSTD-NVASTEQKAGAYVRVASNMGLWTDATGYNSKRVAKFFIKHEHNEVMTVVD : 93
BcucOBP99d : --MLKTIITIKL-AVVLIVLINLTKTTTAIPIS-EQEEASRRLYKAHGCQVNSISTPKSTD-DTSTRQLAGAYVRVATNVGLWNDATGYNAKRVAKFFIKHEHNEVMTVLD : 108
RzepOBP99d : MFRIRAAVIFPVGVILNFAVISSTASAIAPALTAYEEFVRRILKANKPKAKELSLPLAED---MDNEHIAAGAYIRMATNMGLWNDGGGYNAKRVAKFFIKQRNEHNEVMTVVE : 110
CcapOBP99d : MFTTFRVLLIFSLVLIATSSSPTAVANPTNIS-DYEQPSRRLYKAHELCPVITVTDVSAAE--SEQQMRAATYIRVMVSNMGLWTDVSGYKRVAKFFPMQKSHSEHVALVE : 110
DmeLOBP99d : MNHLRIETIWSGLLIAMAVSTEAASVWKLPT-----ACQMVYDLEKLCQ-----ESQEEDAATLRGLVKKLGLWTDDESGYNARRIAKIFAGHNQMEELMLVVE : 94
      m      r      i      pis      e      sr rlyka      C      q      p      q      ay RC a nmGLWtD      GY      akrvAKff k      e      EvmTtvV

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      120      130      140      150
BdorOBP99d : YCNQKHQQA-DLDLWAYEAYRCATAGRMGIWLRE----- : 144
BlatOBP99d : YCNQKHQQA-DLDLWAYEAYRCATAGXMGVWLKEYVVSAKL-- : 151
BoleOBP99d : YCNQKHQQM-NLDLWAYEAYRCATAGRMGIWLREYMLSAKL-- : 150
BminOBP99d : YCNQKHQQA-DLDLWAFAYRCATAGRMGIWLREYVLSAKL-- : 133
BcucOBP99d : YCNQKHRQT-DLNLWAYEAYRCATAGRMGAWLNAYVRSAKL-- : 148
RzepOBP99d : YCNQQYQQT-DVDLWAFAYRCATAGRMGTWLGVEYMLSAKL-- : 150
CcapOBP99d : YCNQKNQOE-NLDLWAFAYRCATAGRMGTWLGVEYVLSAKL-- : 150
DmeLOBP99d : HNRMQEQTSHLDDWAFLAYRCATSGQGFHWVVKDFMSQKEVER : 137
      yCNqk qq      ldlWA eAYRCAtaGrmG Wl ey sakl

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Supplemental figure 1-36 The alignment of OBP99d


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      10      20      30      40      50      60      70      80      90     100     110
RzepOBPlushX1 : -----MLFGLNIIRNFLPLLAIIIGVSAVTMQQFETSLDMMRNGAPKFKIPVELLDRLRDGDF-VENNSELKQYTRQVAQLAGTTLTKKGFDSVQKALAQIPIILPPEMQDT : 106
RzepOBPlushX3 : -----MLFGLNIIRNFLPLLAIIIGVSAVTMQQFETSLDMMRNGAPKFKIPVELLDRLRDGDF-VENNSELKQYTRQVAQLAGTTLTKKGFDSVQKALAQIPIILPPEMQDT : 106
RzepOBPlushX2 : -----MLFGLNIIRNFLPLLAIIIGVSAVTMQQFETSLDMMRNGAPKFKIPVELLDRLRDGDF-VENNSELKQYTRQVAQLAGTTLTKKGFDSVQKALAQIPIILPPEMQDT : 81
BcucOBPlushX1 : -----MLVKINAFKYFLLTLLATG-VNAITMQQFESSLDMMRNGAPKFKVATEILDNLRAGEF-IENNGELKQYTRQVAQLAGTVTKKGFDSVQKALAQIPIILPPEMQEA : 105
BcucOBPlushX2 : -----MLVKINAFKYFLLTLLATG-VNAITMQQFESSLDMMRNGAPKFKVATEILDNLRAGEF-IENNGELKQYTRQVAQLAGTVTKKGFDSVQKALAQIPIILPPEMQEA : 105
BoleOBPlush : -----MLKINALKYFLLTLLATG-VSAITMQQFETSLDMMRNGAPKFKVPIEILDNLRAGEF-IENNGELKQYTRQVAQLAGTVTKKGFDSVQKALAQIPIILPPEMQNA : 105
BlatOBPlushX1 : -----MQQFETSLDMMRNGAPKFKIATEILDNLRAGEF-VENNGDLKQYTRQVAQLAGTVTKKGFDSVQKALAQIPIILPPEMQGP : 81
BlatOBPlushX2 : -----MLKINAFKYFLLTLLATG-VNAVTMQQFETSLDMMRNGAPKFKIATEILDNLRAGEF-VENNGDLKQYTRQVAQLAGTVTKKGFDSVQKALAQIPIILPPEMQGP : 105
BdorOBPlush : -----MYLKINALKYFLLTLLATG-VSAVTMQQFETSLDMMRNGAPKFKIATEILDNLRAGEF-IENNGDLKQYTRQVAQLAGTVTKKGFDSVQKALAQIPIILPPEMQDP : 105
BminOBPlush : -----MQQFETSLDMMRNGAPKFKVSTEILDNLRAGEF-AENNSDLK-----LTKKGFDSVQKALAQIPIILPPEMQDA : 69
CcapOBPlush : MQEKYKAMILNTNGIKYFFTLTLLAS-VGAVTMQQFEASLDMMRNGAPKFKVSVSDILDKLRAGEF-TENNNDLKQYTRQVAQLAGTTLTKKGFDSVQKALAQIPIILPPEMQDA : 112
Dme1OBPlushX1 : -MKHWKRSSAVFAIVLQVLVLLPDPFAVAMTMEQFLTSLDMIRSGAPKFKLKTEDLDRLRVGDFNFPPSQDLMQYTKQVSLMAGTVNKKGFENAPKALAQLPHLVPEMMEM : 113
Dme1OBPlushX2 : -MKHWKRSSAVFAIVLQVLVLLPDPFAVAMTMEQFLTSLDMIRSGAPKFKLKTEDLDRLRVGDFNFPPSQDLMQYTKQVSLMAGTVNKKGFENAPKALAQLPHLVPEMMEM : 113
      1      a tMqQFetSLDMMRnGCaPKFK e LD LR G F enn Lkcytrc aqlagt tKKG FsvqKALAQIPIILPPEMQ

      120     130     140     150     160     170
RzepOBPlushX1 : AREAMNAKEVQKNY----KESER-VFY-----TTKQVRDYAPDTFKFP---- : 146
RzepOBPlushX3 : AREAMNAKEVRKKK----LQGIVR-AIF-----LHNEMRA----- : 137
RzepOBPlushX2 : AREAMNAKEVQKTRNRASVFSQORNAQVTMLPILSSFHNFVQLFYLLQYMHYTVT : 140
BcucOBPlushX1 : AKAALNAKDVKQSYK----DSERVFYTT-----KQVRDYDPATFKFP---- : 145
BcucOBPlushX2 : AKAALNAKDVRK-----KKL----- : 121
BoleOBPlush : AKEALIAKDVKQAYK----DSQDKVFYTT-----KQVRDYDPSTFKFP---- : 145
BlatOBPlushX1 : AKEALNAKDVKQKNYK----ESQDKVFYTT-----KQVRDFDPATFKFP---- : 121
BlatOBPlushX2 : AKEALNAKDVKQKNYK----ESQDKVFYTT-----KQVRDFDPATFKFP---- : 145
BdorOBPlush : AKEALNAKDVKQKNYK----ESQDKVFYTT-----KQVRDFDPATFKFP---- : 145
BminOBPlush : AKEALNAKDVKQKNYK----DSQDRVFYTT-----KQVRDYDPSTFKFP---- : 109
CcapOBPlush : AKEALNAKDVKQKNYK----ESQDRVFYTT-----KQVRDYDPSTFKFP---- : 152
Dme1OBPlushX1 : SRKSVEARDTHKQFK----ESQERVYQTA-----KQFSENADGQFMMP---- : 153
Dme1OBPlushX2 : SRKSVEARDTHKQFK----ESQERVYQTA-----KQFSENADGQFMMP---- : 153
      a a nAcKdv K sc kc f p

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Supplemental figure 1-37 The alignment of OBPlush