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Lamprey V1R aligned to V1r pheromone receptor-like AAX10116 [Danio malabaricus]
  Score = 75.5 bits (184),  Expect = 6e-12, Method: Compositional matrix adjust.
  Identities = 70/280 (25%), Positives = 135/280 (48%), Gaps = 24/280 (8%)
Query  17   GTIGNTCVLTVFLHIAVKNGELLPSDRSVINMSIVHLLASVFKNILYVFDFFKMH-LLNN   75
            G + NT VL  + HI + + +L P D + +++    L+  + + +    F M LL++
Sbjct  1    GILTNTLVLLAYTHIRLTDSQLQPVDAILCHLAFADLMLLLTRCVPQTMTVFGMRNLLDD   60

Query  76   IGCRLLLYSINLFRTLSISFTLLLSLFQNKLQNSTYPGINVISLKFEKSICLVSVLLWI   135
            GC++++Y+  + RTLS+ T +LS+FQ  +     P ++ + + +  + +  V LW
Sbjct  61   AGCKVVIYTYRIARTLSVCITCMLSVFQAVTVAPEAGPQLSRLKARLPQLVTPTFVALWF   120

Query  136  ISSAIFTPLLFFDDILTLNNSSGLLQFSSCSISPSGGYHLYFGIGTIILVDGFG------   189
            I+ A+    FF   ++    +G +   + ++  G H+ F     +++G
Sbjct  121  INMAVCIAAPFF----SVAPRNGTVPPFTLNL---GFCHVDFRDNLSYVINGVAVSVRDF   173

Query  190  AF--AIVTMNVLILKILWKHHEMVAARGWVHNANHMATLNAVKIVACLLITYIICWSINI   247
            AF  A++ +  IL +L +H  V RG  +          A + V L++ Y + + I+
Sbjct  174  AFVGAMLGSSGYILVLLHRHGRRV--RGIRRSQGSTMETRAARTVEMLVVLYAVFFGIDN   231

Query  248  IIRILLMRFGASLSAIP--MADIASVFSSLYYSFSPFIII   285
            +I I ++     ++  +P  +AD+    FSS Y S SPF+II
Sbjct  232  VIWIYML----TVPQVPPVVADMRVFFSSCYASVSPFLII   267


                                                            ^    ^
 ^conserved in Mus V1Rs (Pfister and Rodriguez)        AAX10116  G-ILTN- 5
  conserved in fishes                                  3717.V1R311   G-TIGN- 21
  N-linked glycosylation site                          11722.V1R311  G-VVVN- 23
  Not conserved in ORs (Saraiva and Korsching)         18775.V1R342  G-FVGN- 48
  Conserved in ORs (Niimura and Nei)                   2061.V1R320   NLFMTAP 39
  In fish V1R but not mammal V1R (Niimura and Nei)                   .  :


 gi|59891918|gb|AAX10116.1|     ------TLVLLAYTHIRLTDSQLQPVDAILCHLAFADLMLLLTRCVPQTM  49
 3717.V1R311                    ------TCVLTVFLHIAVKNGELLPSDRSVINMSIVHLLASVFKNILYVF  65
 stig_11722.V1R311             ------ALILGVIANTACAYECLPPSDAILVNLAFVNLLISLVRNGPLLF  67
 stig_18775.V1R342             ------SLVI-IITGFKIKKS--TPT-ILIMNLAIADFILILTLPLWIVH  88
 stig_2061.V1R320              SLCLFLSITVTIFTEVKLREN---SRYILFASLLACDTFFLLCSTIMSTF  86
                                       : :             .   . :   . : .:

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 gi|59891918|gb|AAX10116.1|     TVFGMRNLLDDAGCKVVIYTYRIARTLSVCITCMLSVFQAVTVAPEAGPQ  99
 3717.V1R311                    DFFKM-HLLNNIGCRLLLYSINLFRTLSISFTLLLSLFQNKLQNSTYPG  114
 stig_11722.V1R311             WDAGVRMSLSDVGCKLCMGVWVVTSSVSVWTTLTLSMFHYLMVS-RRHTS  116
 stig_18775.V1R342             YALDYHWPYGHLMCKIMPFISYVNVTASIYFVTTLSLDRFLLAV--QHPW  136
 stig_2061.V1R320              IWLQTNLSLTS--CSVNTMVSTILNQSGVLCVTLMSVERYVAIC---HP-  130
                                       * :      :       .:   .  :*: :         .

 gi|59891918|gb|AAX10116.1|     LSRLKARLPQLVTPTFVA-LWFINMAVCIAA--PFFS-VAPRNGTVPPFT  145
 3717.V1R311                    INVISLKFEKSICLVSVL-LWIISSAIFTPL--LFFDDILTLNNSSG--L  159
 stig_11722.V1R311             VKGKTSALRN-AALTLLC-VWAANVLFSLPA--VVFSGNSAGNFTERLML  162
 stig_18775.V1R342             VPKIRT-MNN-TILVCFG-VWLFASLLSIPT--FVFSKALEHNGQVYCYQ  181
 stig_2061.V1R320              FHHPRC-FSHRKTLKFLAIIWSVASVFPLACGILVFTSGVTVNNTRT---  176
                                      : :       .    :*  .      .      *        *

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 gi|59891918|gb|AAX10116.1|     LN------LGFCHVDFRD---NLSYVINGVAVSVRDF-AFVGAMLGSSGY  185
 3717.V1R311                    LQ------FSSCSISPSGG-YHLYFGI-GTIILVDGFGAF--AIVTMNVL  199
 stig_11722.V1R311             VSGTVRPLLG-CVLHFASAREGLAYTT--ASMIINEIVPIV-LMVTVNIK  208
 stig_18775.V1R342             DND----LVDHAAIILAN--FVINFLI---PITIMSF-CYLYIVLKMSRV  221
 stig_2061.V1R320              -----------CSTYLTD-----SLMP--NPMAITVLRESP-NVIIFSVC  207
                                      .       .         . : : .:       :: .

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 gi|59891918|gb|AAX10116.1|     ILVLLHRHGRRV--RGIRRSQGSTMET-RAARTVEMLVVLYAV--FFGID  230
 3717.V1R311                    ILKILWKHHEMVAARGWVHN-ANHMATLNAVKIVACLLITYII--CWSIN  246
 stig_11722.V1R311             TLLILRHRHRRQLHVASLMPS-RVSTEV-KAAKVIMVVTIFVI--CWGIH  254
 stig_18775.V1R342             SYSANRRAINLIIAIVVVFC-LCWLPY-FLVDIVEGSLILHDVNKYWHVS  269
 stig_2061.V1R320              IIALIFTYFNIMMAARKASDDASKAKR-AKQTVILHGLQLFLY--LCSLG  254
                                      . :                        :  : .   :

 gi|59891918|gb|AAX10116.1|     N----VIWIYM-LTV--PQVPPV--VADMRVFFSSCYASVSPFLII----  267
 3717.V1R311                    I----IIRILL-MRFG-ASLSAIP-MADIASVFSSLYYSFSPFIIIFGRS  289
 stig_11722.V1R311             -----VFAINY-YNY--RQDDDLEWLISLARFSTAINISMGPLILVVGHG  296
 stig_18775.V1R342             HETNKAKRILISLAFSHSCLNPIL-YAFLAKGFRTQFKS--AFILQYFEH  316
 stig_2061.V1R320              N---RFFEILFAIIT--TDRNMIT-ILRLCN-YLCLYYS-SRFVVPLIYG  296
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