CLUSTAL 2.0.12 MULTIPLE SEQUENCE ALIGNMENT

File: CB2R-3qak.ps
Page 1 of 1

```
                                                .:.  .:   :.:*: * ** * : :  . :*:. ..* *: ***.**
CB2R        MEECWVTEIANGSKDGLDSNPMKDYMILSGPQKTAVAVLCTLLGLLSALENVAVLYLILSSHQLRRKPSYLFIGSLAGAD    80
3QAK.A      ------------------------------IMGSSVYITVELAIAVLAILGNVLVCWAVWLNSNLQNVTNY-FVVSLAAAD    50
            1.......10........20........30........40........50........60........70........80

            : ..*:     :.: . . . .:. :::    :.:*  :*: ***  *****:.:* *  *:.*:*  **   :.* ***
CB2R        FLASVVFACSFVNFHVFHGVDSKAVFLLKIGSVTMTFTASVGSLLLTAIDRYLCLRYPPSYKALLTRGRALVTLGIMWVL   160
3QAK.A      IAVGVLAIPFAITISTGFCAACHGCLFIACFVLVLT-QSSIFSLLAIAIDRYIAIRIPLRYNGLVTGTRAKGIIAICWVL   129
            ........90.......100.......110.......120.......130.......140.......150.......160

            *  :.  *::**. * : *.*       : ::.   :: * * . : .   ::  .: ::   : :* *..     :: :
CB2R        SALVSYLPLMGWTCCPRPCSELFPLIPNDYLLSWLLFIAFLFSGIIYTYGHVLWKAHQHVASLSGHQDRQVPGMARMRLD   240
3QAK.A      SFAIGLTPMLGWNNCGQGCGEGQVACLFEDVVPMNYMVYFNFFACVLVPLLLMLGVYLRIFLAARRQLRST-----LQKE   204
            .......170.......180.......190.......200.......210.......220.......230.......240

            *: **:*.:::.:: :**:*:  : ..::  . ..:.   : : :: *.  **:***.*** *  *:*.: :: :
CB2R        VRLAKTLGLVLAVLLICWFPVLALMAHSLATTLSDQVKKAFAFCSM-LCLINSMVNPVIYALRSGEIRSSAHHCLAHWKK   319
3QAK.A      VHAAKSLAIIVGLFALCWLPLHIINCFTFFCPDCSHAPLWLMYLAIVLSHTNSVVNPFIYAYRIREFRQTFRKIIRSHVL   284
            .......250.......260.......270.......280.......290.......300.......310.......320

CB2R        CVRGLGSEAKEEAPRSSVTETEADGKITPWPDSRDLDLSDC   360
3QAK.A      ------------------------------------------   284
            .......330.......340.......350.......360.
```