```
MDSAGKNRYELLFMDDDVSDPLDNLVAPTAAAAAAAGKKKQPSAAAAAATKTTANKVAN 60
MQLAEKHIVALMFPAIDVSTFTFVSGVKFYIMDNSGNNRYELLFMDDDDSSGLAQPQIAA 60
VIG
Via2
                                 . :..: :: ::*
            * * * * * * **
VIG
            SNNKANAGSNIGGPNAKKPNQAEKENKPNNALNKTDGKKFTPSADNKQQQFNNNASSNYK 120
Vig2
            VVAAPKKPEPAKAPKAPK-SKSEKENKPVVAARKAN----APVAKN------ 101
               VIG
           QQGAPRQGGGANRTREFGSGQGQGQGGQQQGSVNFRQQNGNAETREQRNNRRNVRENV 180
Via2
            --ASPVKGGKGPAGGDVGRPKNP-TANGANNQGRFNNNQRYGNKESNGEFGNELPQRQ-- 156
              VIG
            GAPDGQQSRPYRGPGGGPGAGGDRPQRQNRNYDGQNRKREFDRQSGSDRTGVKSIDKRDG 240
Via2
            ----FNNRDNRGP-----PRVRTGEKFG---KREFDRQSGSDRTGVKSIDKREG 198
                          VIG
           AGSHNWGSVKEAIDDVNKNESETNVTNAEGGAKADESGTEPQNEQATAEEEAKELTLDEW 300
Vig2
           GGAHNWGSPKQDIEDLKTTGETS--PQAEKEDSANEQSADP--AVAAEEDESKQMTLDEW 254
            VIG
            KAOOGORIKPTFNIRKAGEGE-DTTOWKKMVVLTSNKKKENDSEEELEYDPALYPORVGR 359
            KALRDQRAKPNYNLRKAGEGAADNAEWKKMIVLS--KKKESNSEDELEYDPSLYPQRVGR 312
Via2
            VIG
            OORVLDIOFNFNDGRRGGPGGFGGRGGRGGPRPGGFGG-GPRSEGGNRDGGNR-EGGRDN 417
            LQRIVDIQFNFNDGRKVGFR-KGPRPG-AGPREGGFRNDGPRGEGGYRNDGPRGEGGYRN 370
Vig2
             ** * * * * * * * * * * * * *
                              * * * | *** *** | *** | ** * * * * *
           REGGNRGPR-DGQQ-HNNEGGGSSAQNQRPPIDRRGPGNNQNNNQNSGPGPNKRFERQQN 475
VIG
Vig2
           DGPRGEGPRNEGPRGEGYRNDGPRGEGFRGPRFNNGPSNGYENRQDNNRFGEKR--RSAQ 428
               ..*** :* : .. ...*. .:. * * ..**.*. :*.*:.. :** *. :
VIG
            TAPKVNDEROFPTLA 490
Vig2
            KPLKVDDEAQFPTLC 443
             .. **:** *****
```

**Supplementary figure 1**. CLUSTAL 2.0.8 VIG and Vig2 protein sequence alignment. Colors were used as follows: small and hydrophobic residues (AVFPMILW) are red; basic (RK) are in magenta; hydroxyl, amine (STYHCNG) and Q are green; others are grey. An alignment displays the following symbols denoting the degree of conservation observed in each column: "\*" means that the residues or nucleotides in that column are identical; ":" means that conserved substitutions have been observed; "." means that semi-

conserved substitutions are observed.