

```

fly      1                               MQELKQRFERRQLADDLKQKQVIQDHL--LQKILY 33
                                F +   DDL K I L L IL
human    1  MTEPFDEEVVFENSPLYQYLQDLGHTDFEICSSLSPKTEKCTTEGQQKPPTRVLPKQGILLKVAETIKSWIFFSQCNKKDDLHKLDIGFRLDSLHTILQ 100

fly      34  SKRLLVDHVEALEH-----CMQELQTASSASSGRQLLTRNA--CLILGGTLLLEHLITPRGIRYTMVPSILISGTFAALF----AVKSVFVCRNKIVE 120
            + LL + VE +E          Q Q +          L T N  +L + ++ P  +V S L+ G  ++  +++++ R  ++
human    101 QEVLLQEDVELIELLDPSILSAGSQSQQENGHLPTLCSLATPNIWDLISMLFAFISLLVMLPTWW--IVSSWLWGVILFVYL--VIRALRLWRTAKILQ 194
            L A I L+      W  + SS L G L + +  +IR+L WR  +LQ
vez dom                                LIALIIFLLKQAFYW---LSSSSLFKGFKLLLLLstkLIRVlfyWRRQLQ

fly      121 RK-----LEQLVKTIDFEGNCIRRNMTYFQEIIIMKQAEILIES---RQIER-AWDCITAKEVTEILYD-----ATRKLETDYPLPTKYSAY 198
            LE +      F N +R+ +  QE ++ +  + S      +      + + +Y      AT +  +YPL ++
human    195 VTLKKYSVHLEDMATNSRAFTNLVRKALRLIQETEVISRGFTLVSAACPFNKA-GQHPSQHLIGLRKAVYRTLRFQAAARLATLYMLKNYPLNSEDNV 293
            + K      LE+  NS+AF  LVRKAL LIQE E++SRG+ L  PF++  Q S+  IGLRKA+Y TL  F R A  K PL++ DN+
vez dom    IIRHKALNQLLEEFVANSQAFDKLVRKALILIQEVELVSRGyrlslppfsrledQSQSRRCIGLRKALYSTLSFLFLNLRQAIS---KLLPLSN-GDNL

fly      199 -----YAPMEEL-----RECEYFKNNVTD-YSPKHIKDFHNI FAYVQSQYLLRLALTITT--RPSISQLSEDLV--KIDSLVRQ-LVQEEEQHFNSIA 280
            P +EL      + E  +N TD +S  +K + ++  S++ RLAL ++T  P  L+ L+ +I S V Q L      L
human    294 TNYICVVPFKELGLLSEEQISEEEAHNFTDGFSLPALKVWFQLWVAQSSEFFRRLALLSTANSPPGPLLPALLPHRILSDVTQGLPHAHSACLEELK 393
            Y +      EL  GLSEE +S+EEA  TD  SLPALK  FQ +  EF  +L++LLS  + P      A
vez dom    EKYCDIYNINEL--GLSEESlsdeeAEELTDESELPAKFLFQRFNGLRKEFLCQLLALLSdGSKpNFFRWKVAdqfltpdr-----

fly      281 LALQ---NKKQLELAELNATRAEQQSGPIAVLQHSSSLKLSACMVAVAECQALDVTLQKLTVTTEAAKNNSKELVAVANNMHGIENALAVCCDDFQRL 376
            + +      + Q +      ++ QQ+S  + +  L  + A+ E  L+ L+KL T+ ++ S+  + + I+ +  + ++
human    394 RSYEFYRYFETQHQSVPQCLSKT-QQKSRELNNVHTAVRTLQHLKALLNEVIILEDELEKLVCTKETQELVSEAYPILEQKCLKLIQPHVQASNNCWEAA 492
            + + +SR+LN++ T +R
vez dom    -----eraraqsrKLNLSLTLIR

fly      377 MLVYNKFLHSQLDLEGE LPKPKQDL-----DDEFPSILRVEFSQNV---DAPQQRDDFYAYMYDENEEQHFEAEQNAPFPSPPEKELLN 457
            +  +K L  D +G+  ++          D PE  +E +  D+  ++DDFY  ++ E Q  E E++  K +L
human    493 ISQVDKLLRRNTDKKGKPEIACENPHCTVVPLKQPTLHIADKDIPEE-QELEAYVDDIDIDSDFRKDDFYLLSQEDKERQKREHEESKRVLQELKSVLG 591

fly      456 F-EKRITKGRFK-----PVLKQL--KDRIDPIRQVMLEKEREVLASKGINVDELFGKMERVEQQQEDNRLADAAPLPVYESSNSDSADAEAFRRR 547
            F      + ++K      VLK L  D ++PI      E  + +  G  V +  + E  +  DN ++      S  + D++  E F +
human    592 FKASEAERQKWKQLLFSDAHVLKSLFPVDPVEPISNS----EPSMNSDMG-KVSKNDTEESNKSATTDNEIS-RTEYLCENSLEGKNKDNSSNEVFPQG 685

fly      548 SKQH--KERDNFAEMRQFLAQKQAINLFKLPPPPVAAGGEELLESEC 592
            +++      + ++ E +
human    686 AEERMCYQCESEDEPQADGSGLTAPPTPRDSLQPSIKQRLARLQLSPDFTFTAGLAAEVAARSLSFTTMQEQTFGGEEEEEQIIEENKNEIEEK 779

```

Figure S1. Detailed sequence alignment of fly *Vezi*, human *Vezt*, and the "Vezatin domain" consensus sequence. The alignment between fly *Vezi* (NCBI reference sequence NP_650741.1 (isoform A); "fly") and human *Vezt* (NCBI reference sequence NP_060069.3 (isoform b); "human") was generated by PSI-BLAST. The alignment between human *Vezt* and the pfam12632 Vezatin domain consensus sequence ("vez dom") was generated from the consensus sequence alignment at <https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=372233>. Amino acid identities and similarities are indicated between each pair of aligned proteins.