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                                                                   ::* : *:   .:
P22219|VPS15_YEAST  LPPLRDYKEFGPIQEIV------------------RSPNMGNLRG-KLIATLMENEPNSITSSAVSPGE-    50
A1DNG9|A1DNG9_NEOFI ENYPTDLFELGPFVKEADPRRPIKKASGHGENKVWK------PG-GSLVALFGEHSG-PVNRV-VVAPD-    60
Q8NJL6|Q8NJL6_ASPFU ENYPTDLFELGPFVKEADPRRPIKKSSGHGENKVWK------PG-GRLVALFGEHSG-PVNRV-VVAPD-    60
A1CU03|A1CU03_ASPCL ENYPTDLFDLGPFVKEEDARRPIKKANGHDANRVWK------PE-GSLVALFGEHSG-PVNRV-VVAPD-    60
Q0CMN6|Q0CMN6_ASPTN ENYPTDLFDLGPFVKDVDLRKPIPKASGNDPTKVWK------PT-GGLVAIFGEHSG-PVNRV-VVAPD-    60
A7KAP0|A7KAP0_PENCH ENYPTDLFDLGPYVKEVDTRQPIRSATDQEPSKIWK------PE-GNLVATFGEHSA-PINRV-VVAPD-    60
Q1EB23|Q1EB23_COCIM ENYPTDLFDFGPVVAPVSSRSPIKKASGQSTNTPWR------PQ-GNLVALFGEHTG-PINRV-AVAPN-    60
A7S9N0|A7S9N0_NEMVE ------------------------------KRDEWS------PK-GLLVAHLHEHKA-AINRL-QVSQD-    30
Q29CG0|Q29CG0_DROPS TPYP----------------------------PNWR------LN-GTLVAHLHEHSE-SVIKLASLRPH-    33
Q9VHH2|Q9VHH2_DROME TPYPP-----G-----------------------WR------MT-GTLVAHLHEHSE-SVIKLASLRPH-    33
Q7PRZ4|Q7PRZ4_ANOGA QRELRESTSAGPALP-----------------AGWR------LS-GTLVAHLAEHKA-AVARMAALKPHA    45
Q17GU5|Q17GU5_AEDAE ----RDLRD--------------PATNAHPLPSGWK------MN-GTIIAHLHEHKA-AVSRMTTLKPY-    43
A9JTK7|A9JTK7_XENTR KREQCNAERIAKHMMES------AEWESKPPPTGWH------PK-GLLVAHLHEHKG-PVNRI-RVSDE-    54
Q99570|PI3R4_HUMAN  KREQCNAERIAKQMMEN------AEWESKPPPPGWR------PK-GLLVAHLHEHKS-AVNRI-RVSDE-    54
A6QLW1|A6QLW1_BOVIN KREQCNAERIAKQMMEN------AEWESKPPPPGWR------PK-GLLVAHLHEHKS-AVNRI-RVSDE-    54
P0C0R5|PI3R4_RAT    KREQCNAERIAKQMMEN------AEWESKPPPPGWR------PK-GLLVAHLHEHKS-AVNRI-RVSDE-    54
Q8VD65|PI3R4_MOUSE  KREQCNAERIAKQMMEN------AEWESKPPPPGWR------PK-GLLVAHLHEHKS-AVNRI-RVSDE-    54
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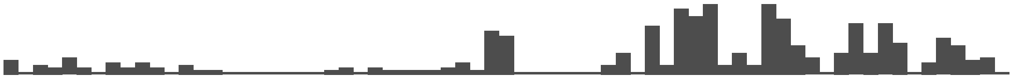

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A1DNG9|A1DNG9_NEOFI HAFFITASDDGTVKIWDTTRLE-KNL-TPRSRQTYRHSSEAKVKTLTFVENTHAFISGATDGSIHVVKVD   128
Q8NJL6|Q8NJL6_ASPFU HAFFVTASDDGTVKIWDTTRLE-KNL-TPRSRQTYRHSSQAKVKTLTFVENTHAFISGATDGSIHVVKVD   128
A1CU03|A1CU03_ASPCL HAFFITASDDGSVKIWDTTRLE-KNL-TPRSRQTYRHSAEAKVKTLAFVENTHTFISGATDGSLHVVKVD   128
Q0CMN6|Q0CMN6_ASPTN HAFFVTASDDGTAKIWDTTRLE-KNL-TPRSRQTYRHSTEAKVKSLTFVENTHTFICGATDGSIHAVKVD   128
A7KAP0|A7KAP0_PENCH HSFFATASDDSTVKIWDTTRLE-RNL-TPRSRQTHRHATGSRVKALTFVENTYTFVSAATDGSVHAVRVD   128
Q1EB23|Q1EB23_COCIM HAFFVTASDDGTVKVWDTTRLE-KNL-TPRSRQTHRHAAGTKVKCVTFVENTYTFISAATDGSVHAVRID   128
A7S9N0|A7S9N0_NEMVE LMYFATASDDGTVKLWDLQKLDGKRV-INKSRQTYS-RQGCKMKALVFCQSSSSIACASDEGLLNIFRIE    98
Q29CG0|Q29CG0_DROPS GSLFASGSIDGTVRLWDCSKLN-GNQGINKSRQVYF--ANTPIYALAACDSGQSLAVGGKDGSLLMMRID   100
Q9VHH2|Q9VHH2_DROME GSLFASGSIDGTVRLWDCSKLN-GNQGVNKSRQVYS--ANTPIYALAACDSGQSLAVGGKDGSMLMMRID   100
Q7PRZ4|Q7PRZ4_ANOGA GSLFASASIDGTVRLWDCNKLD-GQQSVNRSRQSYH--ANTPLHAVAACDAGQSLAVAGKDGTLLLLKID   112
Q17GU5|Q17GU5_AEDAE GSLFATASIDSTVRLWDCNKLD-GQQSINRSRQSYQA--NTPLHAIAACDAGQSLAIAGKDGALLLLKID   110
A9JTK7|A9JTK7_XENTR HSIFATCSNDGTVKIWNSQKME-GKTTTTRSILTY-SRIGGHVKTLTFCQGSHYLAVASDNGNIQLLGIE   122
Q99570|PI3R4_HUMAN  HSLFATCSNDGTVKIWNSQKME-GKTTTTRSILTY-SRIGGRVKTLTFCQGSHYLAIASDNGAVQLLGIE   122
A6QLW1|A6QLW1_BOVIN HSLFATCSNDGTVKIWNSQKME-GKTTTTRSILTY-SRVGGCVKTLTFCQGSHYLAVASDNGAVQLLAIE   122
P0C0R5|PI3R4_RAT    HLLFATCSNDGTVKIWNSQKME-GKTTTTRSILTY-SRIGGRVKTLTFCQGSHYLAIASDNGAVQLLGIE   122
Q8VD65|PI3R4_MOUSE  HLLFATCSNDGTVKIWNSQKME-GKTTTTRSILTY-SRIGGRVKTLTFCQGSHYLAIASDNGAVQLLGIE   122
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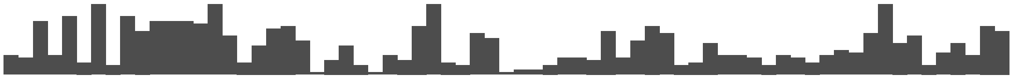

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P22219|VPS15_YEAST  HYQQES-EVKFLNC-ECIRKINL------KNFGKNEYAVRMRAFVNEEKSLLVALTNLSRVIIFDIRTLE   178
A1DNG9|A1DNG9_NEOFI YHNVNE-TVRYGKL-QLVREYQLPA----TDDGSVEYALWIEHFRSDAQSTLLIATNTCRILALDMKTML   192
Q8NJL6|Q8NJL6_ASPFU YHNVND-TVRYGKL-QLVRDYQLPA----TEDGSVEYPLWIEHFRSDAQSTLLIATNTCRILALDMKTML   192
A1CU03|A1CU03_ASPCL YHNVND-TVRYGKL-QRVREYQLPA----ADDGSVEYATWIEHFRSDAQSTLLIATNTCRILALDMKTML   192
Q0CMN6|Q0CMN6_ASPTN YHCAND-TVRYGKL-QLVREYQLPA----ADDGTTEYAVWIEHFRVEAQSILLVATNTCRVLAIDMKTML   192
A7KAP0|A7KAP0_PENCH YQKASQTAVRYGKL-QIVREYQLPI----AEDGSPEYAVWMQHFRDEGQSTLIIATNTCRIIALDMKTML   193
Q1EB23|Q1EB23_COCIM YQNYND-TVRYGKP-HIVRQYQIT-----PSGGENEYAVWMEHYRTDVHSLLLMATNRSKIIGLDLKSMN   191
A7S9N0|A7S9N0_NEMVE QSSQLP-PTR-------LQVYQKK-----INRSEEGHVVDMAHFDTGSQSVLTYATSHGLICGWDLRSGA   155
Q29CG0|Q29CG0_DROPS RNSAK------MTLQQALEQ----------NEHNDGPVVDMHAYDQATQSVIVYATLYGGIVAWDTRMQH   154
Q9VHH2|Q9VHH2_DROME RNSAK------MTLQQALNQ----------NDHKDGPVVDMHAYDQATQSVIVYATLYGGIVAWDTRMQH   154
Q7PRZ4|Q7PRZ4_ANOGA TNSSKM-ALQQARHFEADTRYTSASSSTGELGPDDGPVVEMHPLDQGAQSVIVYATLYGALVGWDIRMPD   181
Q17GU5|Q17GU5_AEDAE TNSSKMALQQARHLDSSTRVDRIGG-----EPQDDGPVVEMQPLDQGAQSVIVYATLYGALVGWDIRMPG   175
A9JTK7|A9JTK7_XENTR ASKPPK-SPKINPLQS--RTLDL---------QEDGCVVDMHQFNAGSQSVLAYATVNGSLVGWDLRCPS   180
Q99570|PI3R4_HUMAN  ASKLPK-SPKIHPLQSRI-----------LDQKEDGCVVDMHHFNSGAQSVLAYATVNGSLVGWDLRSSS   180
A6QLW1|A6QLW1_BOVIN ASKLPK-SPKIHPLQSRV-----------LDQKEDGCVVDLHHFSSGAQSVLAYATVNGALVGWDLRSSS   180
P0C0R5|PI3R4_RAT    ASKLPK-SPKIHPLQSRI-----------LDQKEDGCVVDMHHFNSGAQSVLAYATVNGSLVGWDLRSSS   180
Q8VD65|PI3R4_MOUSE  ASKLPK-SPKIHPLQSRI-----------LDQKEDGCVVDMHHFNSGAQSVLAYATVNGSLVGWDLRSSS   180
                    .......150.......160.......170.......180.......190.......200.......210
```

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                        :      *  :::  *     *  **  *    **:** : :          : ::
P22219|VPS15_YEAST  RLQIIENSPRHGAVSSICIDEECCVLILGTTRGIIDIWDIRFNVLIRSWSFGDHAPITHVEVCQFY----   244
A1DNG9|A1DNG9_NEOFI PIYSLQNPVHHGTPTTFCCDRKHNWLLVGTTHGVLDLWDLRFRVRLKAWGLPGSGAILRLQVHPTK---G   259
Q8NJL6|Q8NJL6_ASPFU PIYSLQNPVHHGIPTTFCCDRKHNWLLVGTTHGVLDLWDLRFRVRLKAWGLPGSGAILRLQVHPTK---G   259
A1CU03|A1CU03_ASPCL PVYSLQNPVHHGTPTTLCCDRRHNWLLVGTTHGVLDLWDLRFRVRLKAWGLPGSGAIHRLQVHPTK---G   259
Q0CMN6|Q0CMN6_ASPTN PMYTLQNPVHHGTPTTFCCDRKHNWLLIGTTHGLLDLWDLRFRVRLKAWGLPGASNIHRLQVHPTK---G   259
A7KAP0|A7KAP0_PENCH PIYTLENPVHHGTLTTFCCDRRHHWLLVGTTHGILDLWDLRFRVRLKAWGLPGWGAINRIQLHPVK---A   260
Q1EB23|Q1EB23_COCIM EVFILRNPVHYGMPTTFCVDRKRNWLLIGTMHGILNLWDLRFCVLVKSWGLPGGTPINRLLIHPLK---G   258
A7S9N0|A7S9N0_NEMVE MAWKLANNPAHGLITSFVVDPCHCWLAVGTSTGNLVCWDLRFQLPITSLSHPRGARIRRLATHPTE----   221
Q29CG0|Q29CG0_DROPS SAWRLQNELRHGVITTICADPTGSWLATGTSGGKHICWDLRFRLPIAEIKHPADSWIRKVACHPTE----   220
Q9VHH2|Q9VHH2_DROME SAWRLQNELRHGVITTICADPTGSWLATGTSGGKHICWDLRFRLPIAEIKHPADSWIRKVACHPTE----   220
Q7PRZ4|Q7PRZ4_ANOGA YAWRLQSDLRSGVITTFCIDPSSSWLTVGTSSGRHVCWDLRFQLPIAEIKHPHDARIRRVSHHPTE----   247
Q17GU5|Q17GU5_AEDAE YAWRLESDLRKGVITTFCVDPTSSWLTVGTSSGRHICWDLRFRLPIAEIRHPHDSRIRRVSHHPTE----   241
A9JTK7|A9JTK7_XENTR NAWTLKHDLRLGLITSFAVDIHQCWLCIGTSSGTMACWDMRFQLPISSHTHPARARIRRLLMHPLSMHTM   250
Q99570|PI3R4_HUMAN  NAWTLKHDLKSGLITSFAVDIHQCWLCIGTSSGTMACWDMRFQLPISSHCHPSRARIRRLSMHPLY----   246
A6QLW1|A6QLW1_BOVIN NAWTLRHDLKAGLITSFAVDIHQCWLCIGTSSGTMACWDMRFQLPISSHCHPSRARVRRLSMHPLY----   246
P0C0R5|PI3R4_RAT    NAWTLKHDLKSGLITSFAVDIHQCWLCIGTSSGAMACWDMRFQLPISSHCHPSRARIRRLSMHPLY----   246
Q8VD65|PI3R4_MOUSE  NAWTLKHDLKSGLITSFAVDIHQCWLCIGTSSGAMACWDMRFQLPISSHCHPSRARIRRLSMHPLY----   246
                    .......220.......230.......240.......250.......260.......270.......280
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                              .   . : :*:: .   :
P22219|VPS15_YEAST  -GKNSVIVVGGSSKTFLTIWNFVKGHCQYAF---------------------------------------   274
A1DNG9|A1DNG9_NEOFI RGRWVCVSSSGSRGNEITVWDIEKVRCREVY------HADSPGSNAVANGGPAVSPVDSAKAKSAFASAR   323
Q8NJL6|Q8NJL6_ASPFU RGRWVCVSSSGSRGNEITVWDIEKIRCREVY------HADSPGSNTVANGGSAASPVDNAKAKSAFVNTR   323
A1CU03|A1CU03_ASPCL RGRWVCASSSGSHGNEITVWDIEKVRCREVY-----QADSPGASAVLPNGGHGGSPADHTPAKKTYPSSR   324
Q0CMN6|Q0CMN6_ASPTN RGRWVCVSSSGSHGNEITVWDIEKVRCREVY-----------QADSPQLGNSDANGDTAKARQPYMSPRD   318
A7KAP0|A7KAP0_PENCH RGRWVCVSSSGSHGNEITVWDIEKFRCREVY-------RATPLGVGTNGPNGTHHPSRTPHAYPTPVVPS   323
Q1EB23|Q1EB23_COCIM RGRWVCVTGGGKSGSEVMVWDIDKMQCREVYRTAVISSASDDNGKPAAAAAQTHRNIHFTPDTTWKAYDP   328
A7S9N0|A7S9N0_NEMVE -QSWVVSAVEG--NNEVSIWDLETGARRQT----------------------------------------   248
Q29CG0|Q29CG0_DROPS ---PSYLISASQSNNEVSVWNIETGQRQTV----------------------------------------   247
Q9VHH2|Q9VHH2_DROME ---PSYLISASQSNNEVSVWNIETGQRQTV----------------------------------------   247
Q7PRZ4|Q7PRZ4_ANOGA ---SSWLVSASQGNSEVYVWNIETGHRQQAY---------------------------------------   275
Q17GU5|Q17GU5_AEDAE ---PSWLVSASQGNNEVYVWNIETGHRQQAF---------------------------------------   269
A9JTK7|A9JTK7_XENTR YQSWVIAAVQG--NNEVSMWDMETGDRR------------------------------------------   276
Q99570|PI3R4_HUMAN  -QSWVIAAVQG--NNEVSMWDMETGDRR------------------------------------------   271
A6QLW1|A6QLW1_BOVIN -QSWVIAAVQG--NNEVSMWDMETGDRR------------------------------------------   271
P0C0R5|PI3R4_RAT    -QSWVIAAVQG--NNEVSMWDMETGDRR------------------------------------------   271
Q8VD65|PI3R4_MOUSE  -QSWVIAAVQG--NNEVSMWDMETGDRR------------------------------------------   271
                    .......290.......300.......310.......320.......330.......340.......350
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                                                                                     :::
P22219|VPS15_YEAST  ----------------------INSDEQPSMEHFLPIEKGLEELNFCGIRSLNALSTISVSNDKILLTDE   322
A1DNG9|A1DNG9_NEOFI DYEAWHVESDRPEGMLSRFGTEGPLSGAIESSGPSAASTPAGICAFAVGYDSPEDGKDNSTRCGFIVSAG   393
Q8NJL6|Q8NJL6_ASPFU DYEAWHIESDRPEGMLSRFGTEGQLSGAIESSGPSAASTPAGICAFAVGYDSPEDGKDNSTRCGFIVSGG   393
A1CU03|A1CU03_ASPCL DYEAWLVESDRPEGMLSRFGTEGPLSGAIESSGPSPSSAPAGICAFAVGYDSPEDGKDNSTRCGFIVSAG   394
Q0CMN6|Q0CMN6_ASPTN YEAWHVEGDRPEGMLSRFATGAPASGAVEQASGPSSSAMPARICAFTVGFDAPDDGKDNSTRCGFIVSGG   388
A7KAP0|A7KAP0_PENCH DYEAWRVDSDRPEGMLSRFATNGPEPGTPSSN--NPAGDRLGIWAFAVGLNAPGEDKDSNTKCGYIISAG   391
Q1EB23|Q1EB23_COCIM WRVDDEKPESLLSRFAMASSPDSSSKSVTNDRNGIRAIAVGLDVPDPSAPTGNQTDNNFSSKCGFLISGG   398
A7S9N0|A7S9N0_NEMVE ---------------------------LWASNTPPLSQTKVSPHAVHALYSSPGDAT------PFILTAG   285
Q29CG0|Q29CG0_DROPS ---------------------------LWASPAPVLTNTSLNDPATTCGILSGVVDG-----APFILTGS   285
Q9VHH2|Q9VHH2_DROME ---------------------------LWASPVAALSSASPSDPATTCGILSGVVDGS-----PFILTGS   285
Q7PRZ4|Q7PRZ4_ANOGA ----------------------------WASASPPLSNSNASSHSVCALLPGVNDGN------PFLLTGG   311
Q17GU5|Q17GU5_AEDAE ----------------------------WASPNPPLTSPNASSPSVCALLPGVVDGN------GFILTGG   305
A9JTK7|A9JTK7_XENTR -------------------------FTLWASNSPPLSEMQPSPHSVHGIYCSPADGN------PILLTAG   315
Q99570|PI3R4_HUMAN  -------------------------FTLWASSAPPLSELQPSPHSVHGIYCSPADGN------PILLTAG   310
A6QLW1|A6QLW1_BOVIN -------------------------FTLWASSAPPLSELQPSSHSVHGLYCSPADGN------PILLTAG   310
P0C0R5|PI3R4_RAT    -------------------------LTLWASSAPPLSELQPSPHSVHGIYCSPADGN------PILLTAG   310
Q8VD65|PI3R4_MOUSE  -------------------------LTLWASSAPPLSELQPSPHSVHGIYCSPADGN------PILLTAG   310
                    .......360.......370.......380.......390.......400.......410.......420
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                        :  :.    . .
P22219|VPS15_YEAST  ATSSIVMFSLNELSSSKAVISPSR-------------------------------------------FSD   349
A1DNG9|A1DNG9_NEOFI CDRKIRFWDLARPELSTIVSGQDI----------VSEGGMSGKPRYELSQPLPNLLVTTEHIPGPPAASS   453
Q8NJL6|Q8NJL6_ASPFU CDRKIRFWDLARPELSTIVSGQDI----------VSEGGVSGKPRYELSQPLPNLLVTTEHIPGPPAASS   453
A1CU03|A1CU03_ASPCL CDRKIRFWDLARPELSAIVSGMEA---------VSEGGVAGKPRYELSQPGPNLMVTTEHIPSPPAASST   455
Q0CMN6|Q0CMN6_ASPTN TDRKIRFWDLARPELSSIVSGLDA----------VSDGVATGKPRYELSQPGPSLLVTTEHLPHPPA-SG   447
A7KAP0|A7KAP0_PENCH CDRKIRFWDLARPDLSSIVSGLDV----------VSDGSASGKPYYEQSQPGPSLLVTTEHLP---SSSS   448
Q1EB23|Q1EB23_COCIM SDRKIRFWDVSHPDASTIICSPDMISDGASLSAKPRYEITNPTPSLTITTEWLPSSGASTSAAGRAGPGS   468
A7S9N0|A7S9N0_NEMVE SDRRIRMWDLSYPEHSQMVAGAAT---------------------------DNLNSVVLQYKSRLIDGTE   328
Q29CG0|Q29CG0_DROPS SDQRIRYWDIASPKNSSL-----------------------KVPAANDNLTDVAFNYSARLIDGSQVIEE   332
Q9VHH2|Q9VHH2_DROME SDQRIRYWDITNPKNSSL----------------------KVPAANDNLADVAFNYGARLIDGSQVIEEQ   333
Q7PRZ4|Q7PRZ4_ANOGA TDQRLRYWDPVNIENCALVVPSAR-----------------DYAPLNVTGTAGNNANTPGGGSAGATPGG   364
Q17GU5|Q17GU5_AEDAE TDQRIRYWDSVNANNCSLVV-----------------------PAPRDYLSTSNISYNAQLIDGTRVFQE   352
A9JTK7|A9JTK7_XENTR SDMKIRFWNLACPKRSYIIAGST---------------------------------NNLPPVSYFSKIIE   352
Q99570|PI3R4_HUMAN  SDMKIRFWDLAYPERSYVVAGSTS----------------------------------SPSVSYYRKIIE   346
A6QLW1|A6QLW1_BOVIN SDMKIRFWDLAYPERSYIVAG----------------------------------SAGSPSVSYYRKVIE   346
P0C0R5|PI3R4_RAT    SDMKIRFWDLVSPERSYVVAGST----------------------------------GSPSVSYYKKIIE   346
Q8VD65|PI3R4_MOUSE  SDMKIRFWDLVSPERSYVVAGST----------------------------------GSPSVSYYKKIIE   346
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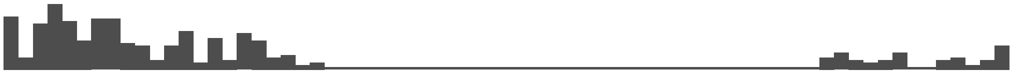

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P22219|VPS15_YEAST  VFIPTQVTANLTMLLRKMKRTSTHSVDDSLYHHDIINSISTCEVDE-TPLLVACDNSGLIGIFQ-----   412
A1DNG9|A1DNG9_NEOFI AGSKGSSKKGGGARLPRSTVISLQQQQLLKSHLDFIQDVAVLR-VPY-GMIISVDRAGMVFLSDSDESC   520
Q8NJL6|Q8NJL6_ASPFU AGSKGSSKKGGGARLPRSTVISLQQQQLLKSHLDFIQDVAVLR-VPY-GMIISVDRAGMVYVFQ-----   515
A1CU03|A1CU03_ASPCL GGKGSSSKKGGGGRLPRSTVISLQQQQLLKNHLDFIQDVAVLR-VPY-GMIVSVDRAGMVYVFR-----   517
Q0CMN6|Q0CMN6_ASPTN SGGKGGSKKGGSGRLPRSTVISLQQQQLLKSHLDFIQDVAVLR-VPY-GMVVSVDRAGMVYVFQ-----   509
A7KAP0|A7KAP0_PENCH TGSSRDTRKGASPRPPRSTVISLQQQMLLKSHLDIIQDVTVLR-VPY-GMVVSGDRAGMVYIFS-----   510
Q1EB23|Q1EB23_COCIM KKSGAGATGGGAGRPPRSTVISLQQQQLLKSHLDIILDIAVLE-VPY-GMTVSVDRGGMIYVFQ-----   530
A7S9N0|A7S9N0_NEMVE VFQEVYCKPRQSVLHEDMPRRGPAQPPV--GHHECINDIAFSK-SP-QNFILTAARDGVVKIWK-----   388
Q29CG0|Q29CG0_DROPS QVISMGTGDSQQLRTSTEENPRSGPDMPTASHRDAITDLLMCKDKG-QIYIASASRDGVIKLWK-----   395
Q9VHH2|Q9VHH2_DROME IISMASTGDSQQLRSSTEENPRSGPDMPTASHHDAITDLLMCKDKG-QIYIASASRNGVIKLWK-----   396
Q7PRZ4|Q7PRZ4_ANOGA PGSGAGGSGERGGRQPDDDH-RVGPEMPAHGHNDVISDLLMCRSA-KQTFIASSSRDGVIKLWK-----   426
Q17GU5|Q17GU5_AEDAE IHCNSGGPPDRNSRGGSEDVARSGPEMPPPGHHDAISDMLMCRTS-KQTFVVSSSRDGVVKLWK-----   415
A9JTK7|A9JTK7_XENTR GTEVVQEIQNKHTMGPSDDTPRKGPESLPAGHHDIITDIVTFQ-TT-QGFIVTASRDGIVKVWK-----   414
Q99570|PI3R4_HUMAN  GTEVVQEIQNKQKVGPSDDTPRRGPESLPVGHHDIITDVATFQ-TT-QGFIVTASRDGIVKVWK-----   408
A6QLW1|A6QLW1_BOVIN GTEVVQEIQNKQKVGPSDDGPRRGPESLPVGHHDIITDVATFQ-TT-QGFIVTASRDGIVKVWK-----   408
P0C0R5|PI3R4_RAT    GTEVVQEIQNKQKVGPSDDTPRRGPESLPVGHHDIITDIATFQ-TT-QGFIVTASRDGIVKVWK-----   408
Q8VD65|PI3R4_MOUSE  GTEVVQEIQNKQKVGPSDDTPRRGPESLPVGHHDIITDIATFQ-TT-QGFIVTASRDGIVKVWK-----   408
                    .......500.......510.......520.......530.......540.......550.........
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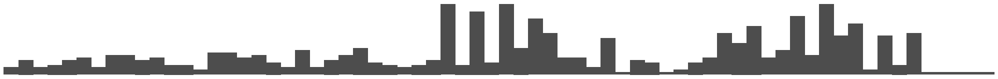
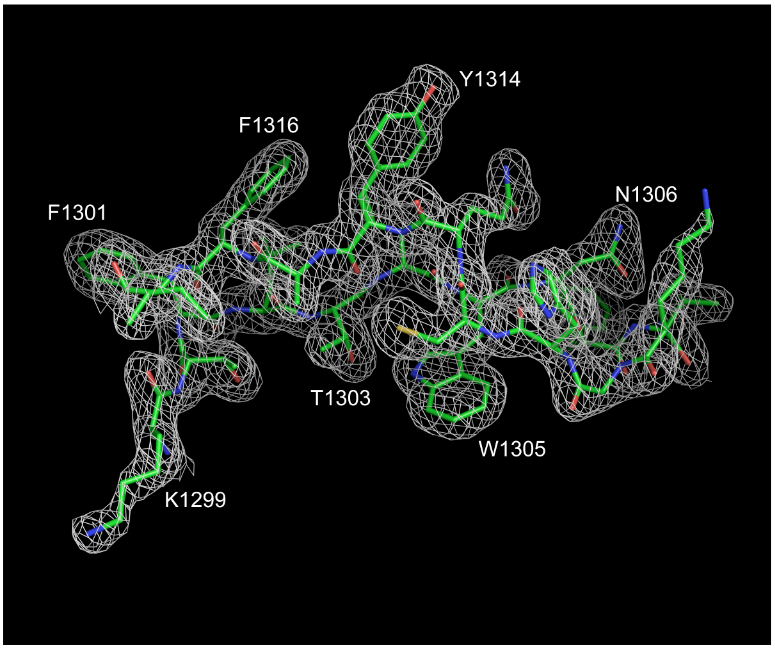


Supporting Figure 1



SUPPORTING FIGURE AND TABLE LEGENDS

Table 1. Phasing and refinement statistics.

Figure 1. Representative electron density of Vps15 WD-like domain.