



PHD1 domain

Sc 235 IIRPNIFFYFDELFDRYTLKYYKVYSTDKILNKWNSKSPFLYVLNRRFRYIYTEPKYPLEN  
 Mo 370 RKNEDCFWFEKLYDRYIQKNYEVIPTFQIINVPE---KVKVLDERWKYILVEQGRGKE-  
 Nc 435 KRLRDCFWFEKLYDRYIQKNYEVIPTKQIINVPE---HVKKVLDERWKYILVEQGRGKE-  
 Fg 304 RKTSDSFWDKLYDRYIQKNYDLIPTRSIINVPA---NVKKVLDERWKYILVEQGRGKE-  
 Fo 325 RKDEDSFWYDKLYDRYIQKNYDLIPTRSIINVPA---NVKKVLDERWKYILVEQGRGKE-  
 Fv 273 RKAHDSFWYDKLYDRYIQKNYDLIPTRSIINVPA---NVKKVLDERWKYILVEQGRGKE-  
 consensus 481 .. . . . \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 295 VLKKYVFHELEVNELSPADYQWDKRCQFCKEWCIQKESLSCDECVCAHLYCNDPPLDRK  
 Mo 426 ---L---TSAVKTCRRCSGYCASNDSVDCAVCEHTYHMNCVRPPLLKK  
 Nc 491 ---L---TSAVKTCRRCVGYCASNDSVDCAVCQNTYHMNCVRPPLLKK  
 Fg 360 ---L---TSAVKLCKRCTGYCA-----  
 Fo 381 ---L---TSAVKLCKRCAGYCA-----  
 Fv 329 ---L---TSAVKLCKRCAGYCASNDSVDCAVCQNTYHMNCVNPPLLKK  
 consensus 541 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 355 PNKDVVWTCFSCLOKQOQTKDSH-----VRFLEEQALELDFIR---SV  
 Mo 468 PSRGFAWSCAACSRAQERKLEARNTPNVSLDPNAEAE---EEFFDE-EEEDAGLDTG---  
 Nc 533 PSRGFAWSCAACSRAQERKLEARNTPNVLD-PNGTHFDDDEFLEDEDEDPGVQTMSS  
 Fg 376 --RGFAWSCAACSRAQERKLEARNTPNVND-PTLDADD--DEPMDEEDEEMQVDTG---  
 Fo 397 --RGFAWSCAACSRAQERKLEARNTPNVND-PSFDAED--DDPMDEEDEEMQGLETN---  
 Fv 371 PSRGFAWSCAACSRAQERKLEARNTPNVND-PSFDAED--DDPMDEEDEEMQGLETN---  
 consensus 601 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

ELM2 domain

Sc 395 RQKIE---EISSKAIKENVGYNTENCWFQYLGITYSISHIGDALNDSMFFPYPFKPSRVG  
 Mo 522 RTSPADGANDMHIP-ATEEOMYHASLWPYRYLGIHCKVEDALDYDDRI---YPRASTRVG  
 Nc 592 RTSPA-T-EDLHOE-ATAEQIYQCSLWPYRYLGMHCKVEDALDYDDRI---FPRASTRLG  
 Fg 428 RTSPEEG-DHAPHE-GTAEQIYQASLWPYRYLGMHCKPEDALDYDDRI---HPRAATRIG  
 Fo 449 RTSPEEG-DHPHHE-GTAEQIYQASLWPYRYLGMHCKPEDALDYDDRI---YPRASTRIG  
 Fv 425 RTSPEEG-DHTHHE-GTAEQIYQASLWPYRYLGMHCKPEDALDYDDRI---YPRASTRIG  
 consensus 661 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 451 VK----YQWNGCNHNVPWRRNSYISANSEE-----ERGSTKTSELAWVLD-  
 Mo 578 PRHOATVLDWPGRPVQYVKAPEIEIKKTGRKDGKLNKEAQAALAEAKVAKARKPKWIQDE  
 Nc 646 PRHOAVVLPWYGRPVQYVKP--LEIKKTGRKDGKLNKEQAALAEARKKRETRPQWIQDE  
 Fg 483 PRHOATVLPWPGPVEYVKP--LEFKKNGKDKTKS-KEALAAIEAEKISRGNRPKWQDM  
 Fo 504 PRNOANVLPWPGKPVYVKP--LEIKKNGKDKTKS-KEALAAIEADKISRGRPKWVQDM  
 Fv 480 PRNOANVSPWPGKPVYVKP--LEIKKNGKDKTKS-KEALAAIEADKISRGRPKWVQDM  
 consensus 721 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 492 -----ASKITTRKLSEYIEQCKSEICP  
 Mo 638 PPGYVPRGEDYPNDDPRNTAQLHWRPPELDLPEESGPEEAHISESEIDKYMEQAKGM-AL  
 Nc 704 PAGYVERGGDDTV-----TVLYKPPPELC-----GKOMPNEAIDEFMDKARGM-AV  
 Fg 540 PPGYTVRGEDCDEDDPNCTAKPMWIPPS-----EDVIKEKDINOYMEKAKAM-AK  
 Fo 561 PPGYTARGEDFDDDDPRCTATRMWIPPP-----EKVIKEKDMNEYMEKAKGM-TK  
 Fv 537 PPGYTARGEDFDNDDPKCTATRMWIPPP-----DKVIKEKDINEYMEKAKGM-TK  
 consensus 781 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 514 ILNVRGETCNFIDVVLKNLLFTNYDTAEAFKKCKRELSRKFLKEPSFTAVEIRKFEEAVE  
 Mo 697 DLDLPEHSTNLLDQALRLLYEHGYDAERALEEL-PKLSKEAFDEPOLTADELKKFEEGVS  
 Nc 748 ELGLPERSTNLQDVAARDLFLKNDFDPKKALQOL-SKVPKAEFKEPELTPAELKKFEEGVS  
 Fg 589 DLGLPERSTNLQDVAADTLFHTGFDTKRALKAL-PEKDKAEFKEPELTPAEQKKFEEAVI  
 Fo 610 DLGLPERSTNLQDVAANKLFRAEFDTEHALKDL-SETKKEAFKEPELTPAEQKKFEEAVI  
 Fv 586 DLGLPERSTNLQDVAANKLFLAEFDTOHALKDL-SETKKEAFKEPELTPAEQKKFEEAVI  
 consensus 841 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 574 KFGSELRPVCEYVGTQPMMSMIVRFYYNWKKTTERGLTVRGKLSKLSKNKRKKEI-----  
 Mo 756 KFGSELYSVKHKHKTVPKPTLVRFYYTWKKTTERGKQVWGNYSGRKSKKEAKEAKKAETAS  
 Nc 807 KYGSELHLVMKHVKTLPATVTRFYYTWKKTTERGKQIWNFAARKGKRDAKKAEE----AA  
 Fg 648 KYGSELYLVRKHVKSMYVGMVTRYYYAWKKSERGMQVLENMAGRKGGKKEAKRAE----AA  
 Fo 669 KYGSELYLVRKHVKTMHYGMVTRYYYAWKKSARGKQVLENQAGRKGKKEAKRAE----AA  
 Fv 645 KYGSELYLVRKHVKTMHYGMVTRYYYAWKKSARGKQVLENQAGRKGKKEAKRAE----AA  
 consensus 901 \* . . . . \* . . . . \* . . . . \* . . . . \* . . . . \*

Sc 627 ANHENDVETKYIDSSFDTEKLSLAESSFQCMFCKTDYSPMWYRVVTGGS DDEKIKIRMQT  
 Mo 816 QNKMQDDVADDHDDSAFDAAKAEKKRSFICKFCNTKSSROWRRAPNASGALV-----  
 Nc 863 ATKQADDVADDHDDSAFDAGKAKARKKAFMCKFCGTKASROWRRAPTISQPIG-----  
 Fg 704 ANKMADDVADNDDSAFDAEKANQKKRGFVCFQFCSTTSSROWRRAPNPTSGVV-----  
 Fo 725 ASKLADDVADNDDSAFDIEKANQKKQGFVCFQFCSTTSSROWRRAPNPVPGVV-----  
 Fv 701 ASKLADDVADNDDSAFDIEKANQKKQGFVCFQFCSTTSSROWRRAPNPVPGIV-----  
 consensus 961 .....\*.....\*\*\*.\*\*..\*.....\*.\*.\*.\*.....\*.\*.\*.....

Sc 687 GVNEKTEISEKSPAHSKKNKELGALCIRCAWMWRRYAIKWVPPLETLRKITGTCONSFYS  
 Mo 869 -----TESGGKGANCKDGVQYVVALCRRCAELWRRYAIQWEDVDQLYSKVAQAGGR-----  
 Nc 916 -----ETSG-RSTKQDKKGEFIPALCRRCAELWRRYAIQWEDVDEVAKKVAQLAGR-----  
 Fg 757 -----NDGGSKSSNKDKGOERVVALCRRCAELWRRYAIRWEDMEEVAKKVAQSGGR-----  
 Fo 778 -----NDGGSKNSNKEKGOERVVALCRRCAELWRRYAIRVEDMDEVNKKITQGR-----  
 Fv 754 -----NDGGPKSSSKEKGOERVVALCRRCAELWRRYAIRVEDVDEVSKKVNOGSGR-----  
 consensus 1021 .....\*.....\*\*\*.\*\*..\*.....\*.\*.\*.\*.....\*.\*.\*.....

Sc 747 AIEGIIENNTNKFTLSPFOAHNKLLLEWELVQDSSELIIRORMKVYKNPNSFVKMKRYSMT  
 Mo 920 -----AWKKKIIDEELLKEIVAA-----EQRSKNTEPSSSG  
 Nc 966 -----NWKPKVDEEDLYKELLAA-----DEMIANTKIRTP  
 Fg 808 -----AWKRKQDEELLKELQAA-----KEMGMMTPERAP  
 Fo 828 -----AWKRKQDEELLKELQAA-----KEMGMMTPERAP  
 Fv 805 -----SWKRKQDEEDLLRELOVA-----KEMGMMTPERAP  
 consensus 1081 .....\*.\*.\*.....\*.\*.\*.....

Sc 807 FHTQLYKMAVRSYRKNEFHPEETMQRDLELFIEDNKEVRKAIPKPERAKNT-----  
 Mo 949 AA-----TPPSNTTPAPAST-----QPAASGOEPARKKQKTTQPPQDK  
 Nc 995 EP-----TPV-----PTLVH-----EPPAAGQEPPrKKLKGSTREKDK  
 Fg 837 TP-----SAA-----P-----AAVANVOEPPRKKLKSVPDKDA  
 Fo 857 TP-----SAT-----P-----A-VATVQEPPrKKLKGASDKDV  
 Fv 834 TP-----SAA-----P-----A-VATVQEPPrKKLKGASDKDV  
 consensus 1141 .. .. ..\*.\*.\*.\*.....

Sc 859 ----KDEFVNIIRQSPGTIKTSDTSRNRKCNDFVIEKASNNNIPKITNASNDLIEISIK  
 Mo 987 DVEMTGTEPVGTTTTAPASKK-----KEK-----  
 Nc 1028 DKAQKEK-----KEN-----  
 Fg 866 DNGHSDT-----ASA-----  
 Fo 885 DNGHSDA-----ASA-----  
 Fv 862 DNVHSDA-----ASA-----  
 consensus 1201 .....

Sc 915 TGGSSSGSVSVDKGFKFVKFDNKTQRLRNSLKLNNKLPKYNEPSTKKIKMINDIALSN  
 Mo 1011 -----ASLEKEKEKEKE-----K-----  
 Nc 1038 -----EKVEKEKEKEKE-----KEKELEP  
 Fg 876 -----AGSTTSKK-----  
 Fo 895 -----AGSTTSKK-----  
 Fv 872 -----TGSTTSKK-----  
 consensus 1261 .....

Sc 975 PLNEPNGASY-NYTVISHSKEETSVALEKYHDGNKPSKMLEKDMILKHTKNPKNPD TAWA  
 Mo 1024 -----EKE-----KEKEKEPVK-EKKEAPAPPVPEI  
 Nc 1057 AVSEPGSVASTPTPVITKKKKE-----KVVEKPVAI-EKPAPPVPEI  
 Fg 884 -----KDKD-----K-----SVESVTVPEM  
 Fo 903 -----K D-----K-----SVENLTVPDI  
 Fv 880 -----K D-----K-----SVENLTAPDI  
 consensus 1321 .. ..\*.....

PHD2

Sc 1034 NNSARTFCSSVCKEKFNDNDNYEVVCGNCGGLTVHYFCYAIKLPKDMKNTNLKTFKWLCDP  
 Mo 1050 PKPRTMPCDICROL-EP LGDQHITCKECRM TVHRNCYGVVDN-----RNP GKWVCDM  
 Nc 1101 PKPRTLPCAI CROM-EP MGDQHLSCKECRM TVHRNCYGVLEH-----RAP GKWTCDM  
 Fg 899 PKPRVLP CAVCGEL-EP QGDQHLSCRECR LTVHRNCYGIMDN-----RNP GKWTCDM  
 Fo 916 PKPVVLP CAVCGQL-EP QGDQHLSCRECR LTVHRNCYGIMDN-----RNP GKWTCDM  
 Fv 893 PKPLVLP CAVCGQL-EP RGEQHLSCRECR LTVHRNCYGIMDN-----RNS GKWTCDM  
 consensus 1381 .....\*.\*.\*.....\*.\*.\*.\*.....\*.\*.\*.\*.....



Sc -----  
 Mo 1553 PPPMQAPPLQPPPIAPPMA--RMSG-----RGQTGVQPPGPVPPSQAYQPLPEPPPT  
 Nc 1566 PPLAHPAPTRPP-VSHPPVPSGVPVAPVAPPPTLPPSLAPRGPSMPQSLFGSA--PP--  
 Fg 1353 PPAM-----QAPSLVADHALG-ARPP-----APH-AYAAPPHR--  
 Fo 1355 PPPM-----QAPALVADHALG-ARPP-----PPA-PYAPLEPPQR--  
 Fv -----  
 consensus 1921 . . . . .

Sc -----  
 Mo 1605 HSAPSGPYGDWHRRTTHGPP-----MNGRPPSRA-----SRISPIIPPLA----  
 Nc 1621 -----RPYDDWHRQPSGHPPPLHPARQLNGTGPS-----PPPLNSMSSLAPPNHLRPS  
 Fg 1385 -----PAYSDWGRPASQQS---SPSRHINGGPPPPPIHNAPPMTNLSSLRPPPVVGPV  
 Fo 1387 -----PSYSDWGRPASQQG---SPPRHINGGPPPI-----HNPPPMSTLSSLRPPPVVGGP  
 Fv -----  
 consensus 1981 . . . . .

Sc -----  
 Mo 1645 -----PPALRPPSLHHSPPHAP-HAHLTNGHMVNGAGAPGRRISGPPPPPSRDGQ  
 Nc 1669 PLSLIANLTHAQPPPPPPQNGHNGHNGHIAHPSPYARMDGLPLSPRRVSGOPTTSGG--  
 Fg 1437 -----PTAPPPANHHGGHPS-----SPYTNGLPLSPRQLNGPAPPSR--  
 Fo 1434 PPV-----GSSPPAAPPANHHGGPPS-----QPYTNGLPPSPRRLNGPAPPPR--  
 Fv -----  
 consensus 2041 . . . . .

Sc -----  
 Mo 1693 GPYMGSYHSPA--P--Y-----HSPAPHQSNGTMVPPERIDHAFASVL  
 Nc 1727 -SYLSGGSLHSHGGPPDLRPPPTDLRTDLRPHSMLNHALPPHHVTGLPPQPAAAEQHQP-L  
 Fg 1474 --YAHPYQHHRPVP-----PA-----HLPPPNMANGAPPPPPPPRGEY  
 Fo 1477 --YTHPYQTHGHNAPPPPPAS-----HLPPPTLTNGAPP--PPPRHDG-F  
 Fv -----  
 consensus 2101 . . . . .

Sc -----  
 Mo 1731 NPPRAYG--NSGSVQPPAHMSPAVARDAPISRDGPLLSQPPPP--ARAPESRPATGAS  
 Nc 1785 SFLRHWNSHTAQONQPPPLHHTSSY-----Q---QVSGLPPPPRDNKP--KDMKTGAS  
 Fg 1513 PHE--I---NPO-----RPPY-----T---PQTSPPGSRNGHPPQNRPASGAS  
 Fo 1518 SHE--L---HPQ-----RPTY-----P---APHGSPPGFRNGPQPPSSRPASGAS  
 Fv -----  
 consensus 2161 . . . . .

Sc -----  
 Mo 1785 ASPSLRNLLS  
 Nc 1833 SSPSLRNLLH  
 Fg 1549 ASPSLRNLLS  
 Fo 1555 ASPSLRNLLS  
 Fv -----  
 consensus 2221 . . . . .