

Sc 1 -----
 Mo 1 MA-----O K G S G G S D A A T P N T T T T S A H K G T A E S K Q S S N A P S S G -
 Nc 1 MAQKTQHVIPSEEQTNSASRTLSAKEKEGAATASVN-----ANSTKQSANPPAATS
 Fg 1 -----
 Fo 1 -----HHLWAC-----LLTRFTTS
 Fv 1 -----
 consensus 1 -----

Sc 1 -----
 Mo 39 PSTTSSSSASVLPKMSDPGPPQALG-----SPASESTTK--SSSTAKDATAGTTASPYG
 Nc 52 SGTSSSTSISNVLPRMLDPSPLPNNSEFSTDAPMGKSTQTSAQAAAAAAKDGSTAANPYG
 Fg 1 -----MAQQNDSKVSDPDA--QSASDEMT--TQSGLD SAAK DASADAASGYG
 Fo 15 RCCASDSL LN VMAQHND SNTSDPGA--QSVSDPMT--TQSSLD SAAKEAGADSAFPYG
 Fv 1 -----MT--NQSSLDSTAKEAGVDSAFPYG
 consensus 61

Sc 1 -----
 Mo 91 TRSRNRGCNSRPNYAEDKDIDMDIFEQLHPQKRDDDSK KTSRQNASSSATNTGDTHNTPP
 Nc 112 TRSRNRGTGNSRINYAEDRDLDMDIFELYPDRREGGEA-KKGSSKQAAASASSATTQAATP
 Fg 44 TRSRNRNSSSRINYAEDRDIDADVYDYHDKKDGDSK KTSRQSSAAVN-----SDAP-
 Fo 69 TRSRNRGTGTSRINYAEDRDIDGADVYDYHDKKDSDSK KTSRQSSAAVN-----GDAP-
 Fv 24 TRSRNRGTGTSRINYAEDRDIDGADVYDYHDKKDSDSK KTSRQSSAAVN-----GDGP-
 consensus 121

Sc 1 -----MP-----KEED
 Mo 151 PP--PRTTNGLSSRK-----PLPMDNKQSQAAA--AKE--
 Nc 171 SASSSSPTNGASQPAPRTAVNGTSAATTVTSTSTSTSRKPLPTIDDSRKGHSNNGTKDQO
 Fg 96 -----PRGGASSRKA--VIDETS-----KPAQSANTPKEQQ
 Fo 121 -----RGGASSRKA--GTDE-P-----KAAQVANTPKEQQ
 Fv 76 -----RGGASSRKA--GTDE-Q-----KAAQVANAPKEQR
 consensus 181*

Sc 7 FOLPRRREAANKVNYNEME-----IDTKLVQOIQIAEKS GAK--TKGSNSQTPRN
 Mo 180 --SSSNANQATGAGSTGSTQ-----TTSKKRKAASQ--TSSNQPPATES---THVPAN
 Nc 231 ARQPSTSPAANGAATT TTTNGPTK--SKKRKADPAAIASSSQTP TSAANSSTSHNKR-
 Fg 125 SGSSNS-----S--STTTQPPASSSQPTRKRKV--ASSSTG-----STNQA-
 Fo 148 SGSSNN-----V--PTTTQOPAA--SQPARKRKV--VGNPAG-----STNPA-
 Fv 103 SGSSNN-----V--PTTTQQSAA--SQPARKRKV--AGNPAG-----STNPA-
 consensus 241

Sc 55 CKRTSNPASRNEKFKYQKFLHDKNTCWNFIPTLPPSFRKNSRFSNILDLD DAMIDLKMS
 Mo 226 AKKPSN--NN-----HNSN-----AASHGADKGYAATNLLTFENC GARPKDGK
 Nc 286 VKTISNDNNGNSKTPTNG-----PVSDLGTAAGYGETNLLTFENTKAMPKDDK
 Fg 162 ---TSTTSNTTKKA-----TTSGTAAGISWPETNMLTFENSKGQPV DGO
 Fo 184 ---TSV--NNSTKKT-----AASGTPSRIPWPETNMLTFDNCKSRPVNGK
 Fv 139 ---ASV--NNSTKKA-----AASGTPSIVWPESNMLTFDNCRSRPVNGK
 consensus 301 . . * *

Sc 115 LFNTESVLLSANDTIYMISEPAGEPYVGRVVNFVSKPEFSNTIHEAIKTTSVFPAKFFQ
 Mo 268 LIADDGTYLEVNDHVYLVCEPPGEPYLLARIMEFLHAKNDPS-----QPVDA
 Nc 334 MVADDGTVLEVNDHVYLVCEPPGEPYLLGRIMEFLHTKNDPT-----KPVDA
 Fg 203 MIADDGTVLEVNDHVYLVCEPPGEPYLLGRIMEFLHVQNDNS-----RPVEA
 Fo 224 MVADDGTALEVNDHVYLVCEPPGEPYLLGRIMEFLHVQNDSS-----KPVEA
 Fv 179 MVADD-----DHVYLVCEPPGEPYLLGRIMEFLHVQNDSS-----KPVEA
 consensus 361 * *

Sc 175 VRMNWFYRPRDIOEHVNTFNPRLVYASLHODICPISSYRGKCSIFHKDEVFDVLPNEKEC
 Mo 315 LRVNWYYRPKDIARKVN--DTRAVFATMHSDISPLTSLRGKCTIKHKAEIKGKLE---EY
 Nc 381 LRVNWYYRPKDIGRRVQ--DTRMVFATMHSDISPLTALRGKCOIRHKTEIP-DLA---AY
 Fg 250 IRINWYYRPKDIGRKST--DTRMVFATMHSDISPLTALRGKCOIHHKAEIS-NMD---AY
 Fo 271 VRINWYYRPKDIGRKST--DTRMVFATMHSDISPLTALRGKCOIHHKAEIK-NME---LY
 Fv 219 VRINWYYRPKDIGRKST--DTRMVFATMHSDISPLTALRGKCOIHHKAEIE-DME---LY
 consensus 421 . * . * . * . * * . * . * . * . * . .

PHD1 domain

Sc 235 IIRPNIFYFDELFDRYTLKYVKVYSTDKILNKWNSKSPFLYVLNRRFRYIYTEPKYPLEN
 Mo 370 RKNEDCFWFEKLYDRIQKNYEVIPTFOIINVPE---KVKKVLDERWKYILVEQGRGKE-
 Nc 435 KRLRDCFWFEKLYDRIQKNYEVIPTKQIINVPE---HVKKVLDERWKYILVEQGRGKE-
 Fg 304 RKTSDSFWYDKLYDRIQKNYDLIPTRSIINVPA---NVKKVLDERWKYVLVEQGRGKE-
 Fo 325 RKDEDSFWYDKLYDRIQKNYDLIPTRSIINVPA---NVKKVLDERWKYVLVEQGRGKE-
 Fv 273 RKAHDSFWYDKLYDRIQKNYDLIPTRSIINVPA---NVKKVLDERWKYVLVEQGRGKE-
 consensus 481*.....*...*...*...*...*...*...*...*...*...*...*

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

Sc 355 PNKDVVWTCFSCLOKQOQTKDSH-----VRFLEEQALELDFIR---SV
 Mo 468 PSRGFAWSAACSRQERKLEARNTPNVSLDPNAEAE---EEFFDE-EEEDAGLDTG---
 Nc 533 PSRGFAWSCAACSRQERKLEARNTPNVLD-PNGTHFDDDEFLEDDDEDPGQVOTGMSS
 Fg 376 --RGFAWSCAACSRQERKLEARNTPNVND-PTLDADD-DEPMDEEDEEMQGVDTST--
 Fo 397 --RGFAWSCAACSRQERKLEARNTPNVND-PSFDAED-DDPMDEEDEEMQGLETN---
 Fv 371 PSRGFAWSCAACSRQERKLEARNTPNVND-PSFDAED-DDPMDEEDEEMQGLETN---
 consensus 601*...*...*...*...*...*...*...*...*

ELM2 domain

Sc 395 RQKIE---ETSSKAIKENVGYNTENCWFQYLGITYSISHIGDALNDSMFFFPYPFKPSRVG
 Mo 522 RTSPADGANDMHIP-ATEEQMYHASLWPYRYLGIHCKVEDALDYDDRI---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 PRHQATVLDWPGRPVQYVKAPETLEIKKTGRKDGKLNKEAQAALEAEKVAKARKPKWTQDE
 Nc 646 PRHQAVVVPWYGRPVQYVKP--LEIKKTGRKDGKLNKEQAALEAEKKKRETRPQWQODE
 Fg 483 PRHQATVLPWPGQPVEYVKP--LEFKKNGKDDTKS-KEALAAIEAEKISRGNRPKQVQDM
 Fo 504 PRNQANVLPWPGKPVVEYVKP--LEIKKNGKDDTKS-KEALAAIEADKISRGRPKWVQDM
 Fv 480 PRNQANVSPWPGKPVVEYVKP--LEIKKNGKDDTKS-KEALAAIEADKISRGRPKWVQDM
 consensus 721*...*...*...*...*...*...*...*...*

Sc 492 -----ASKITTRKLSEYLEQCKSEICP
 Mo 638 PPGYVPRGEDYPNDDEPRNTAQOLHWRPPELDLPEESGPEEAHISESEIDKYMEQAKGM-AL
 Nc 704 PAGYVERGGDDTV-----TVLYKPPELC-----GKOMPNEAIDEFMDKARGM-AV
 Fg 540 PPGYTVRGEDCDEDDPNCTAKPMWIPPS-----EDVIKEKDINOYMEKAKAM-AK
 Fo 561 PPGYTARGEDFDDDDPRCTATRMWIPPP-----EKVIKEKDMNEYMEKAKGM-TK
 Fv 537 PPGYTARGEDFDNDDEPKCTATRMWIPPP-----DKVIKEKDINEYMEKAKGM-TK
 consensus 781*...*...*...*...*...*...*...*...*

Sc 514 ILNVRGETCNFIDVVLKNLLFTNYDTAEAFKKCKRELSRKFLKEPSFTAVEIRKFEEAVE
 Mo 697 DLDLPEHSTNLLDQALRLLYEHGYDAERALEEL-PKLSKEAFDEPOLTADELKKFEEGGS
 Nc 748 ELGLPERSTNLQDVARDLLFKNDFDPKKALQOL-SKVPKAEFKEPELTPAELKKFEEGVC
 Fg 589 DLGLPERSTNLQDVAADTLFHTGFDTKRAALKAL-PEKDKAEFKEPELTPAEQKKFEEAVI
 Fo 610 DLGLPERSTNLQDVAANKLFRAEFDTEHALKDL-SETKKEAFKEPELTPAEQKKFEEAVI
 Fv 586 DLGLPERSTNLQDVAANKLFLAEFDTOHALKDL-SETKKEAFKEPELTPAEQKKFEEAVI
 consensus 841*...*...*...*...*...*...*...*...*

Sc 574 KFGSELRPVCEYVGTQPMMSMIVRFYYNWKKTTERGLTVRGKLSKLSKNKRKKEI-----
 Mo 756 KFGSELYSVKKHKIKTVKPGTLVRFYYTWKKTERGKQVWGNYSGRKSKKEAKEAKKAETAS
 Nc 807 KYGSELHLVMMKHVKTLKPATVTRFYTWKKTERGKQIWGNFAARKGKRDAKKAEE----AA
 Fg 648 KYGSELYLVRKHVKSMYGMVTRYYYAWKKSERGMQVLENMAGRKKGKKEAKRAE----AA
 Fo 669 KYGSELYLVRKHVKTMHYGMVTRYYYAWKKSSARGKQVLENQAGRKKGKKEAKRAE----AA
 Fv 645 KYGSELYLVRKHVKTMHYGMVTRYYYAWKKSSARGKQVLENQAGRKKGKKEAKRAE----AA
 consensus 901*...*...*...*...*...*...*...*...*

Sc 627 ANHENDVETKYIDDSSEFDTEKLSLAESSFQCMFCKTDYSPMWYRVTTGSSDDEKIKIRMQT
 Mo 816 QNKMODDVADHDHDSAFDAAKAAEKKRSFICKFCNTKSSRQWRRAPNASGALV-----
 Nc 863 ATKQADDVADHDHDSAFDAGKAKARKKAFMCKFCGTKASRQWRRAPTISQPIG-----
 Fg 704 ANKMADDVADNDHDSAFDAEKANQKKRGFVCQFCSTTSSRQWRRAPNPTSGVV-----
 Fo 725 ASKLADDVADNDHDSAFDTEKANQKKQGFVCQFCSTTSSRQWRRAPNPVPGVV-----
 Fv 701 ASKLADDVADNDHDSAFDIEKANQKKQGFVCQFCSATFSRQWRRAPNPVPGIV-----
 consensus 961*.....***.**..*.....*.*.*.....*.*.*.....

Sc 687 GVNEKTEISEKSPAHSKKNEKLGALCIRCAWMWRRYAIAKWPPLLETLRKITGTCONSFYS
 Mo 869 -----TESGGKGANKDKGVQYVVALCRRCAELWRRYAIAQWEDVDQLYSKVAQAGGR-----
 Nc 916 -----ETSG-RSTKQDKKGEFIPALCRRCAELWRRYAIAQWEDVDEVAKKVAQLAGR-----
 Fg 757 -----NDGGSKSSNKDKGOERVVALCRRCAELWRRYAIAIRWEDMEEVAKKVAQSGGR-----
 Fo 778 -----NDGGSKNSNKEKGQERVVALCRRCAELWRRYAIAIRYEDMDEVNKKITQGR-----
 Fv 754 -----NDGGPKSSSKEKGQDRVVALCRRCAELWRRYAIAIRYEDVDEVSKKVNOGSGR-----
 consensus 1021*.....***.**..*.....*.*.*.....*.*.*.....

Sc 747 AIEGIIENNTNKFTLSPFQAHNKLLEWELVQDSELIIRORMKVYKNPNSFVKMKRYSMT
 Mo 920 -----AWKKKIIDEELLKEIVAA-----EQRSKNTESSSG
 Nc 966 -----NWKPKVDEDLKELLA-----DEMIANTKIRTP
 Fg 808 -----AWKRKQDEELLKELQAA-----KEMGMMTPERAP
 Fo 828 -----AWKRKQDEELLKELQAA-----KEMGMMTPERAP
 Fv 805 -----SWKRKQDEDLLRELOVA-----KEMGMMTPERAP
 consensus 1081*.....*.....*.....*.....*.....

Sc 807 FHTQLYKMAVRSYRKNEFHPEETMQRDLELFIEDNKEVRKAIPKPERAKNT-----
 Mo 949 AA-----TPPSNTTPAPAST-----QPAASGOEPARKKQKTTPPPQDK
 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 ---KDEFVNIIRQSPGTIKTSDTSRNRKCNDFIEKASNNNIPKITNASNDLIEISIK
 Mo 987 DVEMTGTEPVGTTTTAPASKK-----KEK-----
 Nc 1028 DKAQKEKE-----KDKD-----KEN-----
 Fg 866 DNGHSDT-----K-----ASA-----
 Fo 885 DNGHSDA-----K-----ASA-----
 Fv 862 DNVHSDA-----K-----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-NYTVISHSKETSVALEKYHDGNKPSKMLEKDMILKHTKNKPNPD TAWA
 Mo 1024 -----EKE-----KEKEKEPVK-EKKEAPAPPPVPEI
 Nc 1057 AVSEPGSVASTPTPVITKKKE-----KVVEKPVAI-EKPAPPPPPVPEI
 Fg 884 -----KDKD-----K-----SVESVTVPEM
 Fo 903 -----K-D-----K-----SVENLTVPDI
 Fv 880 -----K-D-----K-----SVENLTAPDI
 consensus 1321 *

Sc 1034 NNSARTFCSVCKEKFNDNDNYEVVCGNCGLTVHYFCYAIKLPKDMKKNNTNLKTFKWLCDP
 Mo 1050 PKPRTMPCDICROL-EPLGDQHITCKECRMVHRNCYGVVDN-----RNPgKWVCDM
 Nc 1101 PKPRTLPCATCROM-EPMGDQHLSCKECRMVHRNCYGVLEH-----RAPGKWTCDM
 Fg 899 PKPRVLPCAVCGEL-EPQGDQHLSCRECRILT VHRNCYGIMDN-----RNPgKWTCDM
 Fo 916 PKPVVLPCAVCGQL-EPQGDQHLSCRECRILT VHRNCYGIMDN-----RNPgKWTCDM
 Fv 893 PKPLVLPCAVCGQL-EPRGQHLSCRECRILT VHRNCYGIMDN-----RNSGKWTCDM
 consensus 1381*.....*.....*.....*.....*.....*.....*.....*.....


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

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

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Sc
Mo      1645  -----PPALRPPSLHHSPHAP-HAHLTNGHVMVNGAGAPGRRISGPPPPPSRDGO
Nc      1669  PLSLIANLTHAQPPPPPPQNGHNGHNGHIAHPSPYARMDGLPLSPRRVSGOPTTSGG--
Fg      1437  -----PTAPPPANHHGGHPS-----SPYTNGLPPLSPRQLNGPAPPSR---
Fo      1434  PPV-----GSSPPAPPPANHHGGPPS-----QPYTNGLPPLSPRRLNGPAPPPR---
Fv
consensus 2041  . . . . . . . . . . . . . . . . . . . .

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Sc
Mo      1693  GPYMGSYHSPA--P--Y-----HSPAPHQSNGTMVPPERIDHAFASVL
Nc      1727  -SYLSGGSLHSHGGPPDLRPPTDLRTDLRPHSMLNHALPPHHVTGLPPQPAAAEQHQP-L
Fg      1474  --YAHPTYQHGGRPVP-----PA-----HLPPPNMANGAPPPPPPPPRGEG-Y
Fo      1477  --YTHPTYQTHGHNAPPPPPPAS-----HLPPPTLTNGAPP--PPPRHDG-F
Fv
consensus 2101  . . . . . . . . . . . . . . . . . . . .

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

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

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