

GxGxFA
 SmSak MDVDPETSFTVSKFHTDFQVFE LLGRGGFAQAYRAKSTITGQEVAIKMI DKKGM LQHLANRVRREVEIHSRLKHPSILELYTCFEDENYVYLVEI CHNGELQTYIRQN-GPVTEDTARHYLKQLISG 129
 hPlk4 -----MATCI GFKIE DFKVG NLLGKGSFAGVYRAES IHSGL E VAIKMI DKKAM YKAGMVQRVQNEVKIHCQLKHPSILELYNYFEDSNVYLVLEMCHNGEMNRYLKNRMKPFSENEARHFMHQIITG 123
 MmSak -----MAACI GERIE DFKVG NLLGKGSFAGVYRAES IHTGLE VAIKMI DKKAM YKAGMVQRVQNEVKIHCQLKHPSILELYNYFEDSNVYLVLEMCHNGEMNRYLKNRMKPFSENEARHFMHQIITG 123
 Plx4 -----MAGSI GERRE DFKVL NLLGKGSFACVYRAQS INTGIDVAIKMI DKKAM QKVG MVQRVQNEVKIHCQLKHPSILELYNYFEDSNVYLVLEMCHNGEVNRYLKNRKRKPFSEDEARHFMHQIVTG 123
 DmSak -----MLSNRAFGETIE DYEVQ HLLGKGGFATVYKARCLHTHQDVAIKMI DKKL LQGTGLTNRVRQEV E IHSRLKHPSVLELYTFEQDANYVYLVELELAHNGELHRYMNH IARPFTE TEAASILKQVVAG 125

HRDLxLxN **DFG** **GTPNYIxPE**
 SmSak LLYLHSHNIIHRDLTIANLLTKDMKVKIADDFGLATKIE-EGEDHKTMCGTPNYISPEVASHNQQGLETDVWSLGCMFYTLIVGHPPFDTRVRSFLNRLVAVDYELFSTLSAEAADLINSLLRREPOER 258
 hPlk4 MLYLHSHGILHRDLTSLNLLTRNMNIK IADDFGLATQLKMPHEKHHTLCGTPNYISPEIATRSAHGLSDVWSLGCMFYTLIIIGRPPFDTRVKNFLNKVVLADYEMPTFLSIEAKDLIHOQLLRNPADR 253
 MmSak MLYLHSHGILHRDLTSLNLLTRNMNIK IADDFGLATQLNMPHEKHHTLCGTPNYISPEIATRSAHGLSDVWSLGCMFYTLIIIGRPPFDTRVKNFLNKVVLADYEMPAFLSREACDLIHOQLLRNPADR 253
 Plx4 MLYLHSHGILHRDLTSLNLLSSDMNIK IADDFGLATQLKMPNEKHHTMCGTPNYIAPETATRSAHGLSDVWSLGCMLYTFIVGRPPFDTRVKNFLNKVVLADYEMPTDFVSREAKDLIFOLLRKNPADR 253
 DmSak LLYLHSHNIMHRDISLSNLLSREMHVKIADDFGLATQLKRPDERHMTMCGTPNYISPEVVSRTSHGLPADVWSVGCMLYTLIVGRPPFDTRAVQSTLNKVVMS EYIMPAHLSYEACDLINKLLKKLPER 255

SmSak LKLIKAIIOHPFM LKKS R PQRHMKTSNDSGIDSIYRTPGLYLSNSLKSHHLRKKVKNESNTHPCNTFISIAISD-----TQCDSIPIYFLASAPQLSHAVTSDWDP SIN V 361
 hPlk4 LLSLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASSSTISGSLFDKRRLLIGQPLPNKMTVFP-KNKSSDFSSSDGNSFYTQWGN--QETSNSGRGRV IQDAEERPHSRYLRRAYSSD 380
 MmSak LLSLSSVLDHPFMSRNPSPKSKDVGTVEDSMDSGHATLSTTITASSGTSLSGSLD-RRLLVGQPLPNKMTVFP-QKNKSSDFSS-GDGSNFTQWGNPEQEANSRGRGRVIEDAEERPHSRYLRRAHSSD 380
 Plx4 LLSLSSVLDHAFMFGFSNVQSKVMGAVEDSMDSGHATISTGFTGSSGVSISGRFQE-KRILSGPSPNKNVNI FQFKDKHPTERSN--GGSFHNTQREN--NDFSENGRKPVACEDRPHSRYLRRAHSSD 377
 DmSak ITTEAVLCHPFMLKCSNG-----GHSAPGALNVS-----QSMESGDSGITTFAS--SDSRNSQQIR SVE 313

Degron motif

SmSak HADVQRPTQLNTP-----NIRQTCYSDGAFEQRSRVSFSQVSDSEIKKSLLSHRNQLVNSTVTRAHNNLS-----G 428
 hPlk4 RSGTSNRQSQAQTYT-MERCHSAEMLSVSKRSGGGENEERYSPDTNANNI FNFFKEKTS SSSSGSFERPDNNQALSNHLCPGKTPFPFADPTQPTETVQQWFGNLQINAHLRKTEYDYSIS-PNRDFQGHF 508
 MmSak RASPSN-QSRAKTY S-VERCHSVEMLSKPRRS-----LDENQHSSNHCLGKTPFPFADPTQPMEMVQQWFGNLQMNALHGETNEHHTV S-PNRDFQDYP 472
 Plx4 RSGTSQSQTYAKPSSYSERCHSVEMLAKPHTHLG----YRTSSPPNSYGDIPQMFTDERSLERHTSPPVKEKTPSEFMGPAKQATAPRSND--KAE TVQQWF GAMQLNGQFKNTPDTSVSNMGGDFYSQQ 501
 DmSak NSGFPQ-----VLPQITREEFKQVHHKLPYEQTGLFGQAS----- 347

SmSak PSLFSPSHPTATVIKTOHADGVKGN TNIS-----KSELSSNSIS-----KPELTHPLPINTFR LKPMRYTRILAVINILQDESVCLEFLGSSAKTRQNTSVI 522
 hPlk4 DLQKDTSKNAWTDTKVKNSDASDNAHSVKQNTM KYMTALHSKPEIIQQECVFGSDPLSEQSKTRGM EPPWGYQNTLRISITSPVAHRLKPIRQKTKKAVVSIIDSEEVQVELVKEY--ASQ EY---- 632
 MmSak DLQ-DTLRNAWTDTRASKNADTSANVHAVKQLS AMKYSAHHHKPEVMPQE--PGLHPHSEQSKNRSMESTLGYQKPTLRISITSPVAHRLKPIRQKTKKAVVSIIDSEEVQVELLREC--ASEGY---- 593
 Plx4 ATQNGAPQYAWNDVKKRKN TSSLESVLLG-----IKKNPGTGQRK--AEKSQFGEQSKSR--VPQQAFGSSTLRSIISPLNAERLPIRQKTKNAVVSIIESGEVCFLEQ--NSQER----- 611
 DmSak ---TGLAEPNWPG--AAKSSAFCMEAGNVP-----NSKQASLKED-----RISVPP LNTKRLPTRKTKNAIIMSILRNGEVVLEFLKFRPTYNEDR---- 429

SmSak KGSQNLRWVVMGINNTGONLIIYRPNMGKGVPLNVQGLGDSSQTNLANSETMNFSGPPASEGDPLEFYTLNLTLPQKYWRKYCFISKSVOMVRAHTPKVTLYTDKVKCMLMENGPSGDFVTFHNDGIR 652
 hPlk4 -----VKIVLQISSDGNITITTYYPNGRGRFP LAD-----RPP--SPTDNISRY SFDNLEEKYWRKYQYASRFVQLLRSKPKIT YFTRYAKCILMENS PGADFEVWFY-DGVMK 732
 MmSak -----VKIVLQISSDGMITVYYPNDGRGRFP LAD-----RPP--LPTDNISRY SFDNLEEKYWRKYQYASRFIQLVRSKTPKIT YFTRYAKCILMENS PGADFEVWFY-DGAK 693
 Plx4 -----VKIVLRLISCDGNLIYVYHPNEGKGFPLVD-----RPP--SPPENRLSYTFDSLBEKYWRKYQYAAKFIKLVRSKTPKVITYYTRYAKCILMENSPTADVEVCFY-DGAK 711
 DmSak -----INVICRISDDGQRILIIYQDPGRGLEVRE-----QPPDLQIPSGDCVNYNDNLPSKHWKYYIYCARFVGLVKS KTPKVITYFSTL GKQLMETMT--DFEIRFY-SCAK 529

SmSak VLCTSDGSLRISQTEQNNSLKVKENITPTITLDSNRSLSTLSPEIRKLIIDYVYACRDRCKIEOLLARM DSEENDT SVLSCSSFFVILGHRPKIGFNLVTS-----SQNHPKPTSVTNMITNELG 774
 hPlk4 IHKT-EDFIQVIEKTGK-----SYTLKSESEVNSLKEIKMYMDHANE GHRICLALESIIS----EEERKTRSAFFPIIIGRKPSTSSPKALSPPPSVDSNYPTRDRASFRNMVMHSDA 843
 MmSak IHKT-ENLIHIIEKTGI-----SYNLKNEVEVSLKBEVKVYMDHANE GHRICLSLESVIS----EEEKRSRGSFFPIIIGRKPSTSSPKALSAPP-VDPSCCKGEQASARLSVNSAA 803
 Plx4 IHKT-SDVIRVIEKSGR-----SYTLKSESEVNSLKEIKMYMDHANE GHRICLSLESAIN----TEEKGENISLFPITFGRRPALAESPKTQPTPSVDSARERKEQSYVNRVHLGSA 821
 DmSak LLKTPSEGLKVYDRNG-----MLLSDYSCS----ESRSLIEHGNECFTHCVNISALE-----VAQTKDN--SCFFVTIIGRRPITDVQF-----AQRLDGLRDTNIAFSTPK 621

SmSak DQVSI.SSQIYNI.TSDCI.KEKYKNP LSEN-----QAKHORI.PTNAV FVFNVGWASQFSDDRLOVQFNDGAKI.IIVYNRITLVYAIFHSAPPEFTDQELPKRYVYNTSDPI.PEHTYRRIEVMPTVIKQIR.T 896
 hPlk4 SPTQAPIILNPSMYVNEGLGLTTASGTDISSNSLKDLPKSAQLLKS VFKVNGWATQLTSGAVVQFNDGSQLVVOAG-VSS--ISYTSFNG-----QTRRYGENEKLPEYIKQKLOCLSSILLMFSN 964
 MmSak FPTQSPGLSPSTVTVVEGLGHTATATGTGVSS-----LPKSAQLLKS VFKVNGWATQLTSGAVVQFNDGSQLVVOAG-VSS--ISYTSFNG-----QTRRYGENEKLPEYIKQKLOCLSSILLMFSN 919
 Plx4 SPPQMPNLNPSLISYDGSVFSALTIVQPSPTSIHNH-TPDHAQVLSK VFNVGWASQNSGAVVQFNDGSQLVVOAG-VSS--IITYAENG-----QTRHGENDKLPEYIKSKLOCLSSILLMFSN 940
 DmSak SNQGSINFSLSTISST---RNTSDFGTNCSRS--NMLAAHQNIPIKRIINVEPEIGATELSHG VVOVQFNDGSSVVSIP S-MOGGGLIYQFNG-----TSIFHGKGDLEFPVRDRVQIPNIQLKLT 739

SmSak VAN-----KIIS---- 903
 hPlk4 P-----TPNFH---- 970
 MmSak P-----TPNFQ---- 925
 Plx4 S-----SSR----- 944
 DmSak APLLGSRKTDYNNAMPKTTIPYYNRMLL 769

* * * * *
 * * * * *
 * * * * *
 * * * * *
 * * * * *