

1 TSDMATASPRTDTSNNHNGRLQMQVTVSSAKLK-RKKNWFGTTFYTELTADGEIKKTAKS clone 2
1 MGSLTMKS-----QLQITVISAALKKENKKNWFGPSPYVEVTVDQSKKTEKC mouse PUL
1 TNHVP TST-----LVQNSC-----CSYV---VNGDNTSPSSPS human WWP1

60 SSSSNPKWDEQLTVNVTPQTTLLEFRVWSHHTLKADALLGRATVDLRQALEIHNRKLDKVK clone 2
49 NNTNSPKWKQPLTVIVTPTSKLCFRVWSHQTLKSDVLLGTAGLDIYETLKSNNMKLEFVV mouse PUL
30 QVAARPKNTPAPKPLASEPA-----DDTVNGES-----SSFAPTDNASVTGTPVV human WWP1

120 EQLKLSLENKSGMVQTGELTVVLDGLVVEQESLTNLSSP-ATKVQONGEAVHENRDASAR clone 2
109 MTLQL-VGDKPETETMGDLSVCLDGLQVEAEVVTNGETSCSESTTONDDGCRTRDDTRVS mouse PUL
75 SEENA-LSPNCTSTTVEDPPV-----QEILTSSE-----NNECIPSTSAELE human WWP1

179 STSRSAACDVSNGNDNQVPSNSVQNAFCIEAVNGNNSPSPTHIAARPKNTPVPKPLGAEL clone 2
168 TNGSEDPEVAASGENKRA-----NGNNSPSSLNNGGFKPSRPPRPSRPPPT mouse PUL
116 SEARSILEPDTNSR-----SSAFEAAKSRQPD----- human WWP1

239 VNSTVNGETSSAPETGNSVSEAMVGSEEPMSDCTNTTAEPPQSTEEAASCSESH TSA clone 2
214 PRRPASVNGSPSTNSDSGSLSTGSL-----PPTNTNVNTSTSEGATSG mouse PUL
145 -----GCM-----DPVRQQSGNANET----- human WWP1

299 LSVASAGLEASTTTDCAQPNTSTAADAAPRESSSASSASGDPVRQQTVNAGTEPLPPGW clone 2
257 LII-----PLTISGGSGRPLNTVLSQA-----PLPPGW mouse PUL
162 -----LPSGW human WWP1

359 EQRKDPHGRTYYYVDHNTRTTTWERPQPLPPGWERRVDDRGRVYYVDHNTRTTTWQRPTME clone 2
285 EQRVDQHGRVYYVDHVEKRTTWDREPLPPGWERRVDNMGRVYYVDHFTRTTTWQRPTLE mouse PUL
167 EQRKDPHGRTYYYVDHNTRTTTWERPQPLPPGWERRVDDRGRVYYVDHNTRTTTWQRPTME human WWP1
WW domain WW domain

419 SVRNFEQWQSQRNQLQGAMQQFNQRYLYSASMLSAEN-----DPLGPLPP-WERRVDSND clone 2
345 SVRNFEQWQLQRSQLOGAMQQFNQRFIYGNQDLFATSQNKEDPLGPLPPGWEKRTDSNG mouse PUL
227 SVRNFEQWQSQRNQLQGAMQQFNQRYLYSASMLAEN-----DPYGPLPPGWEKRVSDTD human WWP1

473 RYFVNHNHTKTQWEDPRTOGLQNE DPLPEGWEIRYTRREGVRYFVDHNTRTTTFNDPRTG clone 1
405 RYFVNHNTRITQWEDPRSQQQLNEKPLPEGWEMRFTVDGIPYFVDHNRRATTYIDPRTG mouse PUL
282 RYFVNHNHTKTQWEDPRTOGLQNEEPLPEGWEIRYTRREGVRYFVDHNTRTTTFKDPRTG human WWP1
WW domain WW domain

533 KSSVNKG-PQIAYERSFRWKLAFRYLCQSNAP clone 2
465 KSALDNG-PQIAYVRDFKAKVQYFRFWCQQLAMPQHIKITVTRKTLFEDSFQQIMSFSPQ mouse PUL
342 KSSVTKGGPQIAYERGFRWKLAFRYLCQSNALP SHVKINVSROTLFEDSFQQIMALKPY human WWP1

525 DLRRRLWVIFPGEGLDYGGVAREWFFLLSHEVLNPMYCLFEYAGKDNVYCLQINPASYIN mouse PUL
402 DLRRRLYVIFRGEGLDYGGLAREWFFLLSHEVLNPMYCLFEYAGKNVYCLQINPASTIN human WWP1
Putative E2-bindng domain

585 PDHLKYFRFIGRFIAMALFHGKFIDTGFSLPFYKRIILNKPVGLKDLESIDPEFYNSLIWV mouse PUL
462 PDHLSYFCFIGRFIAMALFHGKFIDTGFSLPFYKRMLSKKLTIKDLESIDTEFYNSLIWI human WWP1

645 KENNIEECGLEMYFSVDKEILGEIKSHDLKPNNGNILVTEENKEEYIRMVAEWRLSRGVE mouse PUL
522 RDNNIEECGLEMYFSVDEILGKVTSHDLKLGGSNILVTEENKDEYIGLMTIEWRFSRGVQ human WWP1

705 EQTQAFFEGFNEILPQQYLQYFDAKELEVLLCGMQEIDLNDWQRHAIYRHYTRTSKQIMW mouse PUL
582 EQTKAFLDGFNEVPLQWLQYFDEKELEVMLCGMQEVDLADWQRNTVYRHYTRNSKQIWI human WWP1

765 FWQFVKEIDNEKRMRLLOFVTGTCLRPVGGFADLMGSNGPQKFCIEKVGKENWLP RSHTC mouse PUL
642 FWQFVKETDNEVRMRLLOFVTGTCLRPVGGFAELMGSNGPRNS human WWP1
HECT domain

825 FNRLDLPPYKSYEQKELLLFAIEETEGFGQE mouse PUL