

1	-----RRA-----EEEEESRILRVKVVSG-----	clone 1
1	PGGWLRRALPGRERLQSPVHAVPPQHGTSHSRLVTPGAGRDQDFSSPPLLLLGETDHL	hKIAA0439
1	MAA-----EPIYGLS--EDDEESRILRVKIVSG-----	xNEDD4
20	-IDLA-----KKDIF--GASDPYVKLSLYVADENRELALVQTKTIKKTLNPKWNEEFYF	clone 1
61	HLDLPLSPLPTSDELFLPGICDPYVKLSLYVADENRELALVQTKTIKKTLNPKWNEEFYF	hKIAA0439
30	-TDLA-----KKDIF--GASDPYVKLSLYVADENRELALVQTKTIKKTLNPKWNEEFF	xNEDD4
	C2 domain	
71	RVNPTNHRLLEFVFDENRLTRDDFLGQVDVPLSHLPTEDPSMERPYTFKDFLLRPRSHKS	clone 1
121	RVNPSNHRLLEFVFDENRLTRDDFLGQVDVPLSHLPTEDPTMERPYTFKDFLLRPRSHKS	hKIAA0439
78	RVHPTNHRLLEFVFDENRLTRDDFLGQVDVPLNHLPTEDPTMERPYTFKDFLLRPRSHKS	xNEDD4
131	RVKGFLRLKMAYPKNGGQEEENSQDRDESEHGWDVVDSSDSASQRQEELPPPPLPPGWE	clone 1
181	RVKGFLRLKMAYPKNGGQDEENSQDRDDMEHGWEVVDSSNDSSASQHQEELPPPPLPPGWE	hKIAA0439
138	RVKGFLRLKMAYLPKNGMQEEETNEQRESEQAWDVVDSSSPHQQELPAPMPPPGWE	xNEDD4
191	EKVDNLGRYYVNHNNRRTTQWHRPSLIDVGSDDNNIRQINHEAAHRRFRSRRHISEDLE	clone 1
241	EKVDNLGRYYVNHNNRRTTQWHRPSLMDVSSDNNIRQINQEAHRRFRSRRHISEDLE	hKIAA0439
198	EKVDNLGRYYVNHNNKSTOWQRPSLIDVASEDNNIRYIQEA-HRVFRSRRHISEDLE	xNEDD4
	WW domain	
251	PEPLET-GDIPEPWEAISEEASATGDTLSLSLPPPPASPVSRSSPQELSEELSRRLQITP	clone 1
301	PEPSEG-GDVPEPWETISEEVNIAGDSLGLALPPPPASPGSRTSPQELSEELSRRLQITP	hKIAA0439
257	PEHLEGVGDMPEPWETISEEMTLTADTLNQLSLPPP-ASPDSRATAMELSEELNRRQLISS	xNEDD4
310	DSNGEQLSSLIQRDPSSRLRSCSVTDTVAEQSQLSLPS-----VA	clone 1
360	DSNGEQFSSLIQREPSSRLRSCSVTDAVAEQGHLPPPS-----VA	hKIAA0439
317	DSNGEQFSSIIQREPSTRLRSCSVTDGVPEQAHLSLPSTSTGRARSSTVTGGEDSTPTVA	xNEDD4
350	YVHTTPGLPSGWEERKDAKGRYYVNHNNRRTTTWTRPIMQLAEDGMVGSAAANNHNLSEP	clone 1
400	YVHTTPGLPSGWEERKDAKGRYYVNHNNRRTTTWTRPIMQLAEDGASGSATNSNHLIEP	hKIAA0439
377	YVHTTPGLPSGWEERKDAKGRYYVNHNNRRTTTWTRPIVQHAEDGAVGSTSNSSNHLSEP	xNEDD4
	WW domain	
410	QIRRPRLSSPTVTLSAPLEGMKDSPVRRAVKDTLSNPQSPQSPYNSPKPQHKVAQSFL	clone 1
460	QIRRPRLSSPTVTLSAPLEGAKDSPVRRAVKDTLSNPQSPQSPYNSPKPQHKVTQSFL	hKIAA0439
437	QIRRPRLSSPTVTLSAPLEGTKDFPVRRAVKDTLSNPQSPQSPYNSPKPQHKGAQSFL	xNEDD4
470	PPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFPVHLRRTKASLNPNDLGPLPPGWEERIH	clone 1
520	PPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFPVHMRSKTSLNPNDLGPLPPGWEERIH	hKIAA0439
497	PPGWEMRIAPNGRPFFIDHNTKTTTWEDPRLKFPVHMRTKASLNPNDLGPLPPGWEERIH	xNEDD4
	WW domain	
530	LDGRTFYIDHNNKITQWEDPRLQNPAITGPAVPYSREFKQKR	clone 1
580	LDGRTFYIDHNSKITQWEDPRLQNPAITGPAVPYSREFKQKYDYFRKKLKKPADIPNRF	hKIAA0439
557	MDGRTFYIDHNTKITQWEDPRLQNPAITGPAVPYSREFKQKYDYFRKKLKKPADIPNRF	xNEDD4
	WW domain	
640	MKLRNNIFEESYRRIMSVKRPDVLKARLWIEFESEKGLDYGGVAREWFFLLSKEMFNPY	hKIAA0439
617	MKLRNNIFEESYRRIMSVKRPDVLKARLWIEFESEKGLDYGGVAREWFFLLSKEMFNPY	xNEDD4
700	YGLFEYSATDNYTLQINPNSGLCNEDHLSYFTFIGRVAGLAVFHGKLLDGFFIRPFYKMM	hKIAA0439
677	YGLFEYSATDNYTLQINPNSGLCNEDHLSYFTFIGRIAGLAVFHGKLLDGFFIRPFYKMM	xNEDD4
	Putative E2-binding domain	
760	LGKQITLNDMESVDSEYYNSLKWILENDPTELDLMFCIDEENFGQTYQVDLKPNGSEIMV	hKIAA0439
737	LGKQITLNDMESVDSEYYNSLKWILENDPTELDLMFCIDEENFGQTYQVDLKPNGSEIMV	xNEDD4
820	TNENKREYIDLVIQWRVFNVRVQKQMNAFLEGFTELLPIDLIKIFDENELELLMCGLDVD	hKIAA0439
797	TNDNKREYIDLVIQWRVFNVRVQKQMNAFLEGFTELLIAIDLKIFDENELELLMCGLDVD	xNEDD4
888	VNDWRQHSIYKNGYCPNHPVIQVFWKAVLLMDAEKRIRLLQFVTGTSRVPMNGFAELYGS	hKIAA0439
857	VNDWRQHTLYKNGYCPNHPAVQVFWKAVLLMDAEKRIRLLQFVTGTSRVPMNGFAELYGS	xNEDD4
	HECT domain	
	*	
894	NGPQLFTIEQWGSPEKLPRAHTCFNRLDLPPYETFEDLREKLLMAVENAQGFEGVD	980 hKIAA0439
917	NGPQLFTIEQWGSPEKLPRAHTCFNRLDLPPYDSFEDLREKLLMAVENAQGFEGVD	956 xNEDD4
	*	