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Genomic sequence
AE 003593

244.5 244.2 243.8 243.5 243.2 242.8 242.5 242.2 Kb

Ubiquitin like domain (UBD)

D. melanogaster MLELLQFGGKTLTHTLSIYVKTNTGKTLTVNLEPQWDIKNVKELVAPQLGLQDDDLKIIFAGKELSDATTIEQC DLGQQSVLHAIRLRP-----PV 92
A. gambiae MLAIFSFGKKLSNSLSVYVKTNTGNTLAVDLEPHMDIKDVKEMVAPRLGLEPQELKIIFAGRELSDTTITISECDLGQQSIIHVVKSRPT----AITTPQ 97
R. norvegicus -----MIVFVRFNSSYGFVPEVDSDTISIFQLKEVVAKRQGV PADQLRVIFAGKELQNHLTVQNC DLEQQSIVHIVQ-RPQRKSHE TNASG 85
M. musculus -----MIVFVRFNSSYGFVPEVDSDTISILQLKEVVAKRQGV PADQLRVIFAGKELPNHLTVQNC DLEQQSIVHIVQ-RPRRRSHE TNASG 85
H. sapiens -----MIVFVRFNSSHGFPVEVDSDTISIFQLKEVVAKRQGV PADQLRVIFAGKELRNDWTVQNC DLDQQSIVHIVQ-RPWRKQEMNATG 85

		Unique parkin domain (UPD)																												
<i>D. melanogaster</i>	QRQK--IQSATLEE-EPSSLDEASKPLNETLLDLQLESEE-RLNITDEERV---- <td>183</td>	183																												
<i>A. gambiae</i>	KRQAKPALNATISEEPSPEEQQQHNKPLSETMSELTVLDE--RNGDQSIPIGR----TKAHFFVYCS-QCEKVCTGKLVRVCGICSGGAFTVHRDPTCWD	190																												
<i>R. norvegicus</i>	GDKPQSTPEGSIWEPRSLTRVDLSSHILPADSVGLAVILDTSKSDSEAARGPAAPPTYHSFFVYCKGPCHKVQPGKLRVQCQTCRQATTLTLAGGPS CWD	185																												
<i>M. musculus</i>	GDEPQSTSEGSIWESRSLTRVDLSHTLPVDSVGLAVILDTSKR DSEAARGP-VKPTYNSFFIYCKGPCHKVQPGKLRVQCQTCKQATTLTLAGGPS CWD	184																												
<i>H. sapiens</i>	GDDPRNAAGGCEREPPQSLTRVDLSSVLPGD SVGLAVILHTDSRKDSPPAGSPAGR SIYNSFYVYCKGPCQRVQPGKLRVQCSTCRQATTLTLTLAGGPS CWD	185																												
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	Unique parkin domain (UPD)	RING1	
<i>D. melanogaster</i>	DVLKSRRI [*] IPGH [*] CSLE [*] VAC [*] VDNAAGDP [*] PPFA [*] EFF [*] FKCA [*] EHV [*] SGGE [*] KDFA [*] APLN [*] L [*] IKNN [*]	FKNVP [*] CLACTD [*] VSD [*] TVL [*] VFP [*] CASQ [*] HVT [*] CIDCF [*] RHY [*] CRS [*] RLGER [*]	283
<i>A. gambiae</i>	DVLKRRK [*] RI [*] TGH [*] CEN [*] YV [*] PCVENDEGE [*] PPFT [*] EFY [*] FKC [*] SEH [*] SSGGE [*] KDFA [*] APLS [*] L [*] IKTN [*]	HKNI [*] P [*] CIAC [*] TD [*] TSET [*] ILV [*] FP [*] CVAGH [*] VSCL [*] DCF [*] RQ [*] YCV [*] TRL [*] LER [*]	290
<i>R. norvegicus</i>	DVLIPN [*] RM [*] SGE [*] CQ [*] SPDC [*] PGTR [*] -----AEFF [*] FKCA [*] HPT [*] S-DKDT [*] SVAL [*] NL [*] ITNN [*]	SRSI [*] P [*] CIAC [*] TD [*] VRNP [*] V [*] LVF [*] QC [*] NHR [*] HVIC [*] LD [*] CF [*] HY [*] CV [*] TRL [*] ND [*] R	275
<i>M. musculus</i>	DVLIPN [*] RM [*] SGE [*] CQ [*] SPDC [*] PGTR [*] -----AEFF [*] FKCA [*] HPT [*] S-DKDT [*] SVAL [*] NL [*] ITSN [*]	RRSI [*] P [*] CIAC [*] TD [*] VRSP [*] V [*] LVF [*] QC [*] NHR [*] HVIC [*] LD [*] CF [*] HY [*] CV [*] TRL [*] ND [*] R	274
<i>H. sapiens</i>	DVLIPN [*] RM [*] SGE [*] CQ [*] SPHC [*] PGTS [*] -----AEFF [*] FKCA [*] HPT [*] S-DKET [*] PVAL [*] HL [*] IATN [*]	SRNI [*] T [*] CITC [*] TD [*] VRSP [*] V [*] LVF [*] QC [*] NSNR [*] HVIC [*] LD [*] CF [*] HY [*] CV [*] TRL [*] ND [*] R	275
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Inbetween RING domain (IBR)

<i>D. melanogaster</i>	QFMHPD F G Y T L P C PAGCEHSFIEEIHFFKLLTREEDRYQRFA T E E YVLQAGGVLC P QPGCGMGLLVEPDCRKVTC Q NG---CGYVFCRNCLQGYHIG	379
<i>A. gambiae</i>	QFVEHPTGGYT L QC P AGCDNSFIEDVHHFKLLNKEQYERYQRFA T E E FVLKNGGVLC P QPGCGMGLLVDPCCRITC Q NG---CGYVFCRSCLQGYHIG	386
<i>R. norvegicus</i>	QFVHD A QLGYS L PCVAGCPNSLIKELHHFRILGEEQYNRYQQYGAE C VLMGGVLCPRPGCGAGLLPEQGQ R KVTC E GGNGLGCGFVFCDCKEAYHEG	375
<i>M. musculus</i>	QFVHD A QLGYS L PCVAGCPNSLIKELHHFRILGEEQYTRYQQYGAE C VLMGGVLCPRPGCGAGLLPEQGQ R KVTC E GGNGLGCGFVFCDCKEAYHEG	374
<i>H. sapiens</i>	QFVHD P QLGYS L PCVAGCPNSLIKELHHFRILGEEQYNRYQQYGAE C VLMGGVLCPRPGCGAGLLPEPDQ R KVTC E GGNGLGCGFA F CR E CKEAYHEG	375

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RING2

<i>D. melanogaster</i>	ECLPEGTGASATNSCEYTVDPNRAAEARWDEASNVTIKVSTKECPKCRTPTERDGGCMHMVCTRAGCGFEWCVCQTEWTRDCMAHWFVG- 468
<i>A. gambiae</i>	ECFETPTSPSTPGNEQGAYIDPLRASEEARWDEATKIAlKVTTKECPQCRTATERDGGCMHMVCTRS GCGFEWCVCQTPWTRDCMAAHWFVG- 475
<i>R. norvegicus</i>	ECDSMFE-ASGATSQA YRV DQRAAEQARWE EASKETIKKT TKECPRCNVP IEKN GGCMHMKCPQP QCKLEWCWNCGEWN RACMGDHWFDV 464
<i>M. musculus</i>	DCDSLLE -PSGATSQA YRV DKRAA EQARWE EASKETIKKT TKECPRCNVP IEKN GGCMHMKCPQP QCKLEWCWNCGEWN RACMGDHWFDV 463
<i>H. sapiens</i>	ESAVFE -ASGTTTQA YRV DERAAEQARWE EASKETIKKT TKECPRCHVPVEKN GGCMHMKCPQP QCRLEWCWNCGEWN RVCMGDHWFDV 464
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