Fig. S6

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>EER22217.1 hypothetical protein REIS_1424 [Rickettsia endosymbiont of Ixodes scapularis]
MEFISSALKPQQASAFSAGEEELTAKQQEELKRQEEERLQEILDEPGVEPVYPEMLVLSLISAPFRLVKS
LYGLFKDQIIDLVSDSYKDKAIKLSREIDNNTIDVSNNITKLQKHIEDITGVKLDNLELEKYGKYLEEYE
IWVQLPEIVKKIPEKLGFPKFSEKGTGLLYGDKVNGMRIMKGRSNVEFSHQKVDYAVIVDKGCRIDKYGN
QLRYNSNTKVTEVIDPVSNKIIKEIPGFKLKKIPEAHINLEEWIKKWITHNKP
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🟩 Ubiquitin associated domain
⬛ VENN motif (manual prediction)
🟥 CRCT (CDI-like/Rhs-like CT toxin)

Rickettsia buchneri REIS_1424

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REIS_1424	EEERLQEILD	E.PGVEPVYP	EMLVLSLISA	PFR.LVKSLY	GLFK	CdiA-like/Rhs-like C-terminal toxin (CRCT)
YBE7_YEAST_1	KSLAVEELSG	M..GFTEE..	.EAHNALEKC	NWD.LEAATN	FLLD	EH domain-containing and endocytosis protein 1
HSU75362-1	DESSVMQLAE	M..GFPLE..	.ACRKAVYFT	GNMGAEVAFN	WIIV	Solution structure of tandem UBA of USP13
UBPC_YEAST_1	NQCSISQLIE	M..GFTQN..	.ASVRALFNT	GNQDAESAMN	WLFQ	Ubiquitin carboxyl-terminal hydrolase 12
UPBA_DICDI	NSQDVDNIIG	M..GFTDS..	.QAKLALKNT	KGN.LERAAD	WLFS	Ubiquitin carboxyl-terminal hydrolase A
RNMARK1_1	DAKRIDIMVT	M..GFARD..	.EINDALVSQ	KYD.EVMATY	ILLG	Serine/threonine-protein kinase MARK1 isoform X1
UBPC-YEAST_2	DEVSLTSMLS	M..GLNPN..	.LCRKALILN	NGD.VNRSVE	WVFN	Ubiquitin carboxyl-terminal hydrolase 12
DMUBCD4_1_1	CDSKIQRLRD	M..GIDEH..	.EARAVLSKE	NWN.LEKATE	GLFS	AT12021p
HSDKG24_1	FEEKVKQLID	I.TGKNQD..	.ECVIALHDC	NGD.VNRAIN	VLLE	Ubiquitin-associated protein 2-like
CET12G3_4_1	TEKTFDRLLE	M..GFSYN..	.VTVAAIRAN	GSN.LEMCLQ	ALLH	SeQueSTosome related
KP78_HUMAN_1	DQKRIDIMVG	M..GYSQE..	.EIQESLSKM	KYD.-EITAT	YLLL	MAP/microtubule affinity-regulating kinase 3
OSU63530-1	EDEAILRLEP	M..GFDRA..	.LVLDVFFAC	NKD.EQLAAN	YLLD	osRAD23
CBL_MOUSE_1	LSSEIERLMS	Q..GYSYQ..	.DIQKALVIA	HNN.IEMAKN	ILRE	E3 ubiquitin-protein ligase CBL
MMU27462+1_3	SQESINQLVY	M..GFDTV..	.VAEAALRVF	GGN.VQLAAQ	TLAH	Solution structure of RSGI RUH-012
UBC1_BOVIN_1	YTKKIENLCA	M..GFDRN..	.AVIVALSSK	SWD.VETATE	LLLS	Ubiquitin-conjugating enzyme E2 K
MMU27462_1_1	DPSKVHNLLQ	L..GFTAQ..	.EARLGLRAC	DGN.VDHAAT	HISN	Nub1 protein
RA23_YEAST_1	RNETIERIME	M..GYQRE..	.EVERALRAA	FNN.PDRAVE	YLLM	UV excision repair protein RAD23
HSNADGLCT_1	PATDIDRILR	A..GFTLQ..	.EALGALHRV	GGN.ADLALL	VLLA	Regulatory solute carrier protein family 1 member 1
HS467511_1	LIESLSQMLS	M..GFSDEG.	GWLTRLLQTK	NYD.IGAALD	TIQY	NMR structure of the UBA domain of p62 (SQSTM1)
HUMHHR23A_1_1	YETMLTEIMS	M..GYERE..	.RVVAALRAS	YNN.PHRAVE	YLLT	Solution structure (Internal UBA Domain of HHR23A)
ATHAKIN10A_1_1	DEEILQEVIN	M..GFDRN..	.HLIESLRNR	TQN.DGTVTY	YLIL	Serine/threonine protein kinases, catalytic domain
HSSTPKEMK_1	DPRRTELMVS	M..GYTRE..	.EIQDSLVGQ	RYN.EVMATY	LLLG	Serine/threonine-protein kinase MARK2 isoform X5
CEUT27A3_6	VRFVAGELML	M..GFCEN..	.ACYRAAYYS	NGN.VEIASN	WLME	Ubiquitin specific protease 5 (Zn finger protein)
STSNF1PKN_1	DEEILQQVSR	M..GLDRD..	.QLLDSLQKR	IQD.DATVAY	YLLY	SNF1-related protein kinase
CEU22183_1	RIEKLIQIFQ	L..GFNKA..	.AILESVEKE	KFE.DIHATY	LLLG	H39E23, serine/threonine Kinase
ATTS1169_1_1	LEEKVKRLVE	M..GFGDA..	.QVRSAIESS	GGD.ENLALE	KLCS	Ubiquitin-conjugating enzyme 27
HSU75362_1	PEEIVAIITS	M..GFQRN..	.QAIQALRAT	NNN.LERALD	WIFS	Solution structure of tandem UBA of USP13
T24B8.7	YQDNQDMLIT	M..GFKSE..	.EIDTALRLS	NND.VEKAIQ	YLTR	UBA domain-containing protein
YAUG_SCHPO	YAEQLSQLNE	M..GFVDF..	ERNVQALRRS	GGN.VQGAIE	SLLS	Deubiquitination-protection protein dph1
YSCL9931_9_1	TRMIVERLTE	I..GVSSD..	.EALLALQQN	DMN.ENEAAG	FLTR	UBA (putative ATP-dependent RNA helicase YLR419W)
CEF15C11_2	YASQLEQLQS	M..GFSDR..	ARNVAALTAT	FGD.LNAAVE	RLLN	Ubiquilin
CEZK20_5	QEENVLAITG	M..GYDRE..	.QTIAALRAA	FWN.PDRAVE	FLLN	UV excision repair protein RAD23
HS2671010_1	VDAKIAKLMG	E..GYAFE..	.EVKRALEIA	QNN.VEVARS	ILRE	E3 ubiquitin-protein ligase CBL-B
SC130KBXV_53_1	DNQAVKSLLE	M..GIPHE..	.VAVDALQRT	GGN.LEAAVN	FIFS	Solution structure of UBA of RUP1p
YEX3_YEAST_1	PEQTIKQLMD	L..GFPRD..	.AVVKALKQT	NGN.AEFAAS	LLFQ	DNA damage-inducible protein 1
GTS1_YEAST	YSRQLAELKD	M..GFGDT..	NKNLDALSSA	HGN.INRAID	YLEK	GTS1 transcription factor (heat resistance and flocculation)
CELC06E2_2_1	QKKKVDSLIE	M..GFSRL..	.ESILALGGS	DWN.LADAAE	QLLE	Ubiquitin Conjugating enzyme
HUMORF_1_1	ELTALESLIE	M..GFPRG..	.RAEKALALT	GNQGIEAAMD	WLME	UBA (UBX domain-containing protein 1 and similar proteins)
OSU63530_1	LEATIQSILE	MGGGIWDR..	DIVLHALSAA	FNN.PERAVE	YLYS	osRAD23
MMU27462-1_2	RLENVNTLRG	M..GYSTQ..	.AAKQALHQA	RGN.LDDALK	VLLS	Nub1 protein
CEF49C12_8	YEQQAATLRE	F..GFEND..	ELIQLALEQA	NGD.VQAAME	FLID	UBA domain-containing protein
SPAC3F10_13_1	LDTKIKTLKN	M..GVSES..	.DAKDSLERC	GYD.VESAAE	FIFS	UBA domain protein Ucp6
UPBA-DICDI	NQEVLDTLLS	M..DFPLV..	.RCKKALLAT	GGKDAELAMN	WIFE	Deubiquitinating enzyme, peptidase C19 family
RF2P_DROME	INKSIHAMMA	M..GFSNEG.	AWLTQLLESV	QGN.ISAALD	VMNV	Ref(2) Pp protein
YD28_SCHPO	LNSKIAQLVS	M..GFDPL..	.EAAQALDAA	NGD.LDVAAS	FLL-	UBA domain protein Mud1
HUMHHR23A-1_2	EKEAIERLKA	L..GFPES..	.LVIQAYFAC	EKN.ENLAAN	FLLS	UV excision repair protein RAD23 homolog A
Consensus/60%	.ppplppLbs	M..GFspp..	.psbpALp.s	sss.hpbAhp	bLbp	
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🟩 *Saccharomyces cerevisiae*
🟥 *Homo sapiens*
🟪 *Dictyostelium discoideum*
🟦 *Rattus rattus*
🟧 *Drosophila melanogaster*
🟫 *Pseudonaja textilis*
🟥 *Caenorhabditis elegans*
🟦 *Oryza sativa Japonica Group*
⬛ *Mus musculus*
🟪 *Bos taurus*
🟩 *Arabidopsis thaliana*
🟫 *Piliocolobus tephrosceles*
🟦 *Solanum tuberosum*
⬜ *Schizosaccharomyces pombe*