



Supplementary Material

Table S1. Putative SUMOylation sites in published proteins involved in *Entamoeba histolytica* phagocytosis.

Function	Protein	Number access	Position	Peptide/sequence	Score	Site	Reference
Retromer	Vacuolar sorting protein 29	EHI_025270	3 - 7	****ML VLVIG DFHVPHR	64.072	SUMO Interaction	[1]
			56 - 60	LRTLARE VHVVK GDFDEMQ	65.27	SUMO Interaction	
			60	AREVHV VK GDFDEMQ	44.952	Sumoylation	
			110 - 114	QRQLDVD ILITG HTHKLET	60.6	SUMO Interaction	
			173	TLVDGS VK CERVDFN	45.097	Sumoylation	
	Vacuolar sorting protein 26	EHI_062490	9-13	AFLFGTP IQIDI LLDNDHE	72.761	SUMO interaction	[1]
			40	TEIPIYM K NEDVNGK	30.527	Sumoylation	
			145 - 149	GLSKEQE IWVIN YQDEPTK	74.151	SUMO interaction	
			238	LMDGAP VK GESMPIR	43.592	Sumoylation	
			342	PQQSEEP K EEIKEPV	21.38	Sumoylation	
			362	QSIQEEP K EEIKEEK	21.38	Sumoylation	
			366	EEPKEEI K EEKKEEP	45.815	Sumoylation	
			374	EEKKEEP K EEVKEEI	21.902	Sumoylation	
			378	EEPKEEV K EEIKEEP	42.644	Sumoylation	

			382	EEVKEEI K EEPKEEV	47.766	Sumoylation	
			386	EEIKEEP K EEVKEKP	21.902	Sumoylation	
			390	EEPKEEV K EKPKAID	39.231	Sumoylation	
			406	SSFIQDD K QDDDNLF	37.443	Sumoylation	
			86	TPLFMFL K DEYEGSL	25.295	Sumoylation	
			309	KVLVNFI K SEETTL	49.647	Sumoylation	
			462 - 466	SNMLEVI IDLIS KVQDQPD	59.445	SUMO interaction	
			476	QDQPDDI K EEEIGVD	48.626	Sumoylation	
			556	AISKMVA K LEHYVLA	17.505	Sumoylation	
ESCRT	Tumor susceptibility gene 101 protein putative	EHI_178530	35	TSVMQYY K FSATVRT	25.383	Sumoylation	[2]
			47 - 51	VRTYADG IILAS LVGTIPI	56.467	SUMO interaction	
			67 - 71	YRGSQFC LPLCI MYPYDYP	56.376	SUMO interaction	
			283	TLTPLNT K *****	38.49	Sumoylation	
	Vacuolar sorting protein VPS4	EHI_118900	78	MISGERV K SDDPDKE	45.994	Sumoylation	[2]
			128 - 132	EALQEAV ILPIK FPQLFTD	59.356	SUMO interaction	
			231	TEASRRV K TEFLVQM	41.814	Sumoylation	
Vesicular trafficking	EhRabB	EHI_181240	82 - 86	YYRGSQG ILIVY DVSNFDS	63.59	SUMO Interaction	[3]
			105	TYWIGEL K KENVVDGI	28.197	Sumoylation	
	EhRab7	EHI_001870	83-87	FRGTDGC VLVCS VTSIESF	60.125	SUMO interaction	[4]
			120	PFVAVAN K SDLDPIE	39.109	Sumoylation	
Actin related proteins	Actin related protein 2/3 complex, subunit 4	EHI_030820	51 - 55	KEVIFKP VVIVR VPSEPSG	61.242	SUMO interaction	[5]

	EhABPH (actin-binding protein)	EHI_122800	422	RRSSVSLKPEHMKSI	26.543	Sumoylation	[6]
			523 - 527	TEEIEGK VGIVI EIDEESE	63.088	SUMO interaction	
			586	KQETKEVKEEKTQR	44.223	Sumoylation	
			674 - 678	QLTSKGN VIHLA CKNEEEL	62.786	SUMO interaction	
			698	ACTPNNLKGEADEE	24.332	Sumoylation	
			753 - 757	NRTDSTP ILKIY LKDIENI	61.532	SUMO interaction	
			787	KGNKHEFKTEECKAW	18.512	Sumoylation	
			795	TEECKAWKEEIMERK	24.947	Sumoylation	
			930	VILLTHGKDDRETDM	37.458	Sumoylation	
			973 - 977	QDKEEPE IIRIY RIVHNEK	61.19	SUMO interaction	
			1236 - 1240	KIFKGKF IVHLG GYSEYYD	63.428	SUMO interaction	
			1297 - 1301	VFKTIKG IEVIE GKDSNEE	67.442	SUMO interaction	
			1426	ERGLKEVKIEQENEE	42.552	Sumoylation	
			1467 - 1471	PVCQKKE IELIT QVIDGTF	60.742	SUMO interaction	
			1486	NEIDPALKNEISVEG	25.939	Sumoylation	
	EhNCABP166	EHI_093850	51 - 55	LKDLQDG IILSR YLQIETG	60.206	SUMO interaction	[7]
			111 - 115	MNGEPPK IITLM FYLMYRF	61.066	SUMO interaction	
			129 - 133	FRLNDTP VRIID FSKWIKC	73.317	SUMO interaction	
			152	NNPLFDLKTEFSDGI	28.859	Sumoylation	
			340	LEAMELVKEESSTPI	45.139	Sumoylation	

455	ELIIQQLKDEIIQLT	25.181	Sumoylation
503 - 507	IQKKEQE IIDIK KKNEETI	79.148	SUMO interaction
514 - 518	KKKNEET IQLIQ KEMEKER	64.693	SUMO interaction
585	QQELNKKKEENNEYK	54.425	Sumoylation
645	EIKEKEVKELQKIIE	38.869	Sumoylation
721	MKELERIKGEIEVLK	41.473	Sumoylation
724 - 728	LERIKGE IEVLK IKETGDS	61.956	SUMO interaction
749 - 753	IEELKKQ IEIIK NDNEKER	61.44	SUMO interaction
877 - 881	INELNKS IIELK EEWNKKE	59.355	SUMO interaction
881	NKSIHELKEEWNKKE	26.249	Sumoylation
923	NENLKKVKEEIEKKT	43.876	Sumoylation
1016	ENENEIIKKENKKKE	49.683	Sumoylation
1058 - 1062	ERELGTK IKLIE MIKNEKD	60.142	SUMO interaction
1065	IKLIEMIKNEKDIME	45.305	Sumoylation
1076	DIMEKDFKKEVDNKN	18.489	Sumoylation
1100 - 1104	IEKKKND ITLII QKNDEDK	66.441	SUMO interaction
1129	NQEIEKIKSEKNDVQ	47.32	Sumoylation
1168	ENEKLQIKEEHENNI	43.513	Sumoylation
1228	TKKYEEVKGQIDGAH	40.95	Sumoylation
1242	HQEVENIKKETEQQI	42.417	Sumoylation
1253	EQQINQMKECEDMQ	29.943	Sumoylation
1267	QKTTFEAKEELRVQV	16.67	Sumoylation

			1309	ERTIEKLKNERNEKE	26.905	Sumoylation	[8]
			1354	VMPKEVLKIDNTMLY	37.908	Sumoylation	
			7-11	*MNKEEA ISIIQ SAIKEYC	67.784	SUMO interaction	
			69	QNENAKLKNEQTKE	26.214	Sumoylation	
			183	ELADVKKLDTTQQE	36.796	Sumoylation	
			366 - 370	KQKGDEE IIKLH DDLAEQA	62.69	SUMO interaction	
			463	AMDKELMKEEKLKQE	30.951	Sumoylation	
			468	LMKEEKLKQEIQALK	26.856	Sumoylation	
			711	DKEETIAKLEKDKNT	16.977	Sumoylation	
			787	RLDIVDLKGELESKE	25.353	Sumoylation	
			934 - 938	VADLENQ LEIHK DSIEEKD	62.341	SUMO interaction	
			994	KSKYDQLKSDNLMVL	38.597	Sumoylation	
			998 - 1002	DQLKSDN LMVLS EKEDIEE	61.696	SUMO interaction	
			1015	EEELSSVKEEMTKME	44.303	Sumoylation	
			1134	DDDYVRMKADNDKIR	38.706	Sumoylation	
Cholestero l trafficking	Phagosome- associated TMK96 (PATMK)	EHI_167650	17 - 21	YILLFLS IEIVG EYCDWNK	67.129	SUMO interaction	[9]
			49 - 53	FNYNKTG VFHIR NRETETM	61.818	SUMO interaction	
			100 - 104	KELNTSF IVLIN DTTINGD	62.47	SUMO interaction	
			222	PSVLTKLQEVVNST	27.292	SUMOylation	
			483	NQTRQCVKTDIHQEI	37.543	SUMOylation	
			818 - 822	SQCSQCS IGYIV NYNGTRC	60.948	SUMO interaction	

			951 - 955	YELTVSP ITHL KKNEGCI	75.893	SUMO interaction	[10]
			1082 - 1086	AVINKNN VSIIT EYAPYGS	61.53	SUMO interaction	
			1143 - 1147	RDIKLAN VLIIS LEDEMEI	67.864	SUMO interaction	
			1254 - 1258	ISLKIKS LLDLM WCQNPEN	61.691	SUMO interaction	
			325 - 329	IGFIIMG IIVVG FPMEGVI	64.822	SUMO interaction	
			391 - 395	DIIDSAK VSILG QEESCEE	66.998	SUMO interaction	
			431 - 435	FLWKFKW IILTV VILCCIV	63.514	SUMO interaction	
			504 - 508	NQVLTQP LIVQL QQMIDEI	60.057	SUMO interaction	
			758 - 762	LAIGVDN IFILT NTIDEQP	66.525	SUMO interaction	
			1133	MNSIFDV K TFPYAYH	40.095	Sumoylation	
			1150 - 1154	YFQQYFN IVDLC VMDVCLA	60.804	SUMO interaction	
			1191 - 1195	LCVLMCV IDLIG IMYLWGV	60.091	SUMO interaction	
	EhNPC1	EHI_080220					
	EhNPC2a	EHI_068260	104	LPGPISIK F EMEIPN	42.327	Sumoylation	[10]
	EhNPC2b	EHI_188770	143 - 146	SCSEFGP VLVK * *****	59.366	SUMO interaction	[10]
			146	EFGPVLV K *****	37.397	Sumoylation	
	Phosphatidylinositol phosphate kinase	EHI_153770	49	GKTLPEL K NEKYIFK	25.986	Sumoylation	[11]
Kinases	p21-activated kinase 8 protein kinase	EHI_103610	151	FVIKVIP K REEKILC	21.671	Sumoylation	
			103 - 107	TLCEQPS ILLLM QNESDFN	62.875	SUMO interaction	[12]

			180 - 184	AVNGEIP L TILP FSDNVEI	65.13	SUMO interaction	
			312	QAHIEKP K KEPPPEE	21.484	Sumoylation	
			67	KPKMRVA K LENTEQA	16.205	Sumoylation	
			262 - 266	PGLKTGE VLVPQ EFTVTAK	59.917	SUMO interaction	
Calcium related proteins	EhC2PK	EH1_094060	33	VSKKRAI K NEQLLQL	46.539	Sumoylation	[13]
	Cation/calcium exchanger	EH1_001770	46 - 50	VSFLINY LELLY CYNYSWI	59.298	SUMO interaction	[15]
			57 - 61	YCYNYSW IVLVC MVIGIII	62.999	SUMO interaction	
			196 - 200	HSIIFIL IYILY VCFIGYI	60.578	SUMO interaction	
			336 - 340	PFILSIG IILII HFTETQI	66.662	SUMO interaction	
Stress protein	Heat shock protein 70	EH1_002560	27	VAYFDV V KGEPVILQ	45.554	Sumoylation	[16]
			230	IINDNYI K VESSGGD	48.879	Sumoylation	
			287	NKKLIRL K KEAERIK	26.186	Sumoylation	
			294	KKEAERI K IELSGKP	42.012	Sumoylation	
			300	IKIELSG K PDAELDL	36.684	Sumoylation	
			366 - 370	KKGNVQL VLLIG GTCEMPR	61.124	SUMO interaction	
			423 - 427	NSICSKF IYDIV PTPIGIE	64.333	SUMO interaction	
Adhesin	Gal/GalNAc lectin heavy subunit	EH1_012270	206 - 210	TNNTSKC IIDVH KNNVNTH	60.701	SUMO interaction	[17]
			218 - 222	KNNVNTH L AAIL GITDSTV	60.45	SUMO interaction	
			255	GVTIYYL K GDSYATD	37.476	Sumoylation	
			270	NIKLDL K YETLVKY	26.485	Sumoylation	

	437	PKAKPKAKKECPATC	16.996	Sumoylation
	552	VQEKVCVKTSPYIEM	41.585	Sumoylation
	970 - 974	IECKIQE IVITE KDGIKTT	60.791	SUMO interaction

The access number and sequence of proteins (already identified) that participate in *Entamoeba histolytica* phagocytosis were obtained from KEGG (<https://www.genome.jp/kegg>, 29/04/2021), AmoebaDB (<https://amoebadb.org/amoeba/app>, 29/04/2021) and NCBI (<https://www.ncbi.nlm.nih.gov>, 29/04/2021) databases. Then, these proteins were analysed using the GPS-SUMO 1.0 (<http://sumosp.biocuckoo.org>, 29/04/2021) program to predict SUMOylation sites.

The results displayed several hypothetical sites in the studied proteins, suggesting that this posttranslational modification could regulate their function during this virulence event.



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