Table S7. Common features of acidocalcisome proteins identified by the ELM server

Protein	Signal peptide and other characteristics	CK1 phosphorylation site (MOD_CK1_1)	CK2 phosphorylation site (MOD_CK2_1)	GSK3 phosphorylation recognition site (MOD_GSK3_1)	Phosphothreonine motif binding a subset of FHA domains that show a preference for a large aliphatic amino acid at the pT+3 position (LIG_FHA_1)	NEK2 phosphorylation motif with preferred Phe, Leu or Met in the -3 position to compensate for less favorable residues in the +1 and +2 position (MOD_NEK2_1)	Tyrosine-based sort signal responsibl for the interactio with μ sub of adaptor protein complex (TRG_END TIC_2)
VP1 Tb927.4.4380	Yes (1-24) 14 TMD 826 aa	SITSGIK (63-69) SGGSDDD (228-234) SCETGAA (503-509)	LFGSFGE (364-370) IAASSAE (378-384)	YVISKRVS (125-132) AVYTNSRT (213-220) AASSAELS (379-386) AELSADFT (383-390) SCETGAAT (503-510) VAISASNT (742-749)	SITSGIK (63-69) HLTDEVM (115-121) EITDALD (588-594)	LMQTYF (277-282) LGGSSV (301-306) LFGSFG (364-369)	YRPV (4944-4 YGPI (566-569
Vtc4 Tb927.11.12220	No 2 TMD 793 aa	*257-263 *303-309 *367-373 *405-411	NPATPDE (40-46) DYLSEEE (81-87) HALSIDE (167-173) RASTKPE (503-509)	MKASDYLS (77-84) DYLSEEET (81-88) TNMSMVFS (90-97) MVFSMVGS (94-101) QTQTVGAS (539-546) HMNSVAPT (572-579) VAPTMSPT (576-583) GVESLCFT (626-633) DPKTLLTS (664-671) PMLTGSDT (785-792)	AITYELL (118-124) LNTDTIE (132-138) GHTPFIK (483-489) DPTIGIA (514-520) RTTDRVI (526-532) AQTQTVG (538-544) PRTDCLR (552-558)	LYNSLL (47-52) MVFSMV (94-99) FMLSKV (176-181) LCFTST (630-635) FTSTGG (632-637) FGNSMS (695-700)	YPDF (12-15) YNSL (48-51) YELL (121-124 YAVL (147-150 YHAL (166-169 YEHV (182-18 YQRV (560-56 YTAF (614-617 YGPM (783-78
Vtc1 Tb927.7.3900	No 3 TMD 180 aa	*96-102		RNTSGSVS (42-49) YYRTASSS (165-172)	*141-147	*75-80 *84-89 *91-96 *114-119 *149-154	YEDL (33-36)

PMC1 Tb927.8.1180	No 8 TMD 1106 aa	SDGSVAV (31-37) SSVTGEN (244-250) SPLTTVQ (833-839) SDASSLL (1049-1055)	TVVSTAE (266-272)	KDTSNYGT (5-12) AFLSTGLT (22-29) HKVTVDVT (204-211) LSGTVVST (263-270) FSLTVVGT (818-825) EGKSSPLT (829-836) GKSSPLTT (830-837) ALATEQPT (854-861) QRETDGTS (1042-1049) TDGTSDAS (1045-1052) DGTSDASS (1046-1053)	KVTVDVT (205-211) DVTEIVV (209-215) QFTVNLV (810-816) LTTVQLL (835-841) GSTRQLY (1094-1100)	FLSTGL (23-28) LSGTVV (263-268) LMESRL (291-296) LAYSQS (378-383) LQFTVN (809-814) FSLTVV (818-823) LMDTLA (846-851) LYDTLR (1099-1104)	YGTL (10-13) YREL (940-943 YDTL (1100-11
IP$_3$R Tb927.8.2770	No 5 TMD 3099 aa	SAGTRMA (216-222) SSKSQGS (347-353) SQGSDSH (350-356) SLDSDPC (362-368) SVVSQRS (471-477) SQRSCCN (474-480) SEGSETL (549-555) SMCSVGT (866-872) SVGTHGV (869-875) SDRSRVC (988-994) SELTQAV (1049-1055) SAVTTQL (1251-1257) SGSTKDV (1258-1264) STQTQNE (1373-1379) SSSSAPE (1422-1428) SETSRVP (1469-1475) SYGTSYT (1678-1684) SFGSITL (2012-2018) SVITDIF (2050-2056) SFETDYA (2060-2066) SLYSSLK (2188-2194) STGTGIT (2328-2334) SNSTDNK (2341-2347) SAITHNG (2764-2770) SWNSSTL (2848-2854) SSQSSSL (3063-3069)	ADGTFSE (399-405) AVDTILE (457-463) FLWSQCE (582-588) QTETDGE (611-617) TSPTLME (630-636) CQRTLAE (679-685) VRNSSLE (836-842) VLDSGGE (898-904) YVQSELE (940-946) HQVSATE (1094-1100) YTWTRLE (1129-1135) FVTSPTE (1207-1213) IRGSVEE (1354-1360) STQTQNE (1373-1379) VTGTTNE (1380-1386) SSSSAPE (1422-1428) VHITMLE (1490-1496) LSQSNAE (1520-1526) LMQSRTE (1757-1763) VGATFHE (1808-1814) LLLSCRE (1987-1993) VQCTNAE (2147-2153) DCCTLNE (2351-2357) LNETDSE (2355-2361) CLLSLIE (2389-2395) AYDSILE (2426-2432)	SQGSDSHS (350-357) DSHSAGAT (354-361) AGATSLDS (358-365) SLDSDPCS (362-369) VEGSAVDT (453-460) GDGSPEGS (464-471) YLCTSEGS (5454-552) SEGSETLS (549-556) GSETLSLS (551-558) LSLSWKPS (555-558) FLWSQCET (582-589) QVLTTEGT (598-605) RYPSAEGS (622-629) AEGSTSPT (626-633) PKGSNVGT (660-667) NVGTGYAS (664-671) DSLTRLFS (824-831) SVGTHGVT (869-876) HQVSATET (1094-1101) KGPSDYQS (1239-1246) YQSTVAGS (1244-1251) VAGSAVTT (1248-1255) SAVTTQLS (1251-1258) RICTVRRS (1312-1319) RRRSVGLS (1462-1469) GPSSPAFS (1502-1509)	RQTHSVM (323-329) NLTGDIV (480-486) SETLSLS (552-558) VGTHGVT (870-876) ELTQAVK (1050-1056) EGTLHVI (1057-1063) SNTHFVR (1065-1071) TETACLV (1099-1105) AVTTQLS (1252-1258) GSTKDVA (1259-1265) SETSRVP (1469-1475) DPTPHLT (1562-1568) RFTACIV (1640-1646) PVTHLLE (1668-1674) SYTPLVE (1682-1688) SRTETVL (1760-1766) VQTGNLV (1852-1858) IATADVP (1919-1925 AATKCLD (1945-1951) GATRAIA (2082-2088) EFTRMLL (2173-2179) LLTNALT (2178-2184) ALTQCLL (2385-2391) QHTNKLC (2472-2478) CFTFILW (2825-2831) RSTCFIC (2899-2905)	MALSAV (221-226) LATSVA (285-290) LLKTRQ (319-324) LQCSCT (412-417) LQRTLF (511-516) LSLSWK (555-560) FLWSQC (582-587) LHLTRS (852-857) LTRSGR (854-859) LLCSMC (863-868) LLGSSK (1027-1032) LGSSKL (1028-1033) LSGSTK (1257-1262) LSETSR (1468-1473) FTLSQS (1518-1523) LSQSNA (1520-1525) FNLSSN (1539-1544) LRESAR (1572-1577) FTKTTV (1601-1606) LGRSAL (1662-1667) LEITLS (1673-1678) LWESNS (1695-1700) LLLSRQ (1745-1750) LMQSRT (1757-1762) MCMSVA (1815-1820) LSGTML (1863-1868)	YVAV (450-45 YNHI (645-648 YASL (669-672 YLQL (860-863 YSFV (895-898 YCSL (1191-11 YNDL (1398-14 YPFI (1498-15 YIDI (1531-153 YDAF (1621-1 YTPL (1683-16 YRRL (1776-17 YRDV (1804-1 YRRL (1843-1 YKKI (1882-18 YSAV (2100-21 YSSL (2190-21 YDNL (2249-22 YDSI (2427-24 YRLL (2726-27 YLYF(2933-29

		SQSSSLR (3064-3070) SAASVAE (3077-3083) SKGTWLR (3087-3093)	RGLSAKE (2707-2713) QFGSNGE (2798-2804) NEFTGQE (2946-2952) EADSDDE (2990-2996) SAASVAE (3077-3083) LRHSEPE (3092-3098)	YVFTLSQS (1516-1523) LSQSNAES (1520-1527) IVLSILAT (1552-1559) KDPTPHLT (1561-1568) CLPSPGVT (1626-1633) ITLSYGTS (1675-1682) LMQSRTET (1757-1764) LSGTMLTT (1863-1870) LLISGAAT (1940-1947) QLITMEDS (1967-1974) KHVSAENS (2042-2049) AENSSVIT (2046-2053) SVITDIFT (2050-2057) MLLTNALT (2177-2184) NALTTPPS (2181-2188) TPPSLYSS (2185-2192) VVISKLLS (2309-2316) PDVTGTPS (2321-2328) DCCTLNET (2351-2358) DEVSWNSS (2845-2852) NEFTGQES (2946-2953) INRSSQSS (3060-3067) NRSSQSSS (3061-3068) SAASVAET (3077-3084) ETSTSKGT (3083-3090)	ERTRGLA (3048-3054)	MLTTRR (1867-1872) LAETGP (1902-1907) LLISGA (1940-1945) LLLSCR (1987-1992) FVSTTL (200-2005) LLQTTF (2073-2078) LQTTFS (2074-2079) LGATRA (2081-2086) MLLTNA (2177-2182) LYSSLK (2189-2194) FVCTLF (2222-2227) MLQSAF (2279-2284) FLKTVR (2451-2456) LQHTNK (2471-2476) FNETLQ (2698-2703) LLVTRF (2717-2722) LRSTCF (2898-2903) LASSVV (2997-3002)	
AP-3, β3 Tb927.11.10650	No No TMD 918 aa	SLASERA (11-17) SGGSIVS (23-29) SIVSRAR (26-32) SLVSGDA (33-39) SDSSDEA (276-282) SSETTSS (306-312) SETTSSS (307-313) SSSSSSW (311-317) SSSSSWD (312-318) SSSSWDR (313-319) SLNSAVV (352-358) SIISKLA (433-439) SVCTSQV (479-485) SFKTEGS (575-581)	AALSFVE (213-219) ISDSSDE (275-281) DGESSSE (302-308) IVLTHAE (402-408) AEHTHYE (667-673) GNSTSDE (779-785) EQRTPAE (793-799) TVPTETE *48-854)	EFISSGGS (19-26) SIVSRARS (26-33) VRKTAAIS (170-177) DGESSSET (302-309) GESSSETT (303-310) ESSSETTS (304-311) SSETTSSS (306-313) SETTSSSS (307-314) ETTSSSSS (308-315) TTSSSSSS (309-316) ERHSVVLS (390-397) VVLSTIHT (394-401) TIHTIVLT (398-405) SIISKLAT (433-440)	LDTEPLV (164-170) RKTAAIS (171-177) AATAVIC (360-366) ACTLPLL (376-382) IHTIVLT (399-405) VCTSQVM (480-486) RQTARLV (520-526) KTTASVE (893-899)	FISSGG (20-25) FFVTHY (104-109) LSISAF (119-124) MDHSMH (129-134) LLDSVK (342-347) LLMSLN (349-354) LKLSII (430-435) LVKSFK (572-577) LDGSGA (598-603)	YFFV (103-106 YSIL (195-198) YRNL (232-235 YRLL (527-530 YARL (630-633 YHPL (688-691

		SDNSSDS (737-743) SSDSGTC (740-746) SGSSDAS (749-755) SDASTSV (752-758) SVHSSYT (757-763) SSYTGDD (760-766) SDASSKT (806-812) SSKTNIT (809-815) SGGTPGA (870-876) SSTTAGN (877-883)		VRLSSVCT (475-482) RLSSVCTS (476-483) GNSSGRQT (515-522) GADSGDDS (715-722) DDSSMMYS (730-737) MMYSDNSS (734-741) DNSSDSGT (738-745) DSGTCRGS (742-749) GSGSSDAS (748-755) SGSSDAST (749-756) DASTSVHS (753-760) ASTSVHSS (754-761) GYSSTDGS (767-774) IRPSDASS (803-810) SGGTPGAS (870-877) DTPTREGS (907-914)			
AP-3, δ Tb927.5.3610	No 1 TMD 1127 aa	SNESEAE (27-33) SEVTSTV (44-50) STVSSPD (135-141) SMLSTIQ (232-238) SNWTLIK (239-245) SDPSRSS (472-478) SRSSQWE (475-481) SNGTAKV (576-582) SAVSAAP (733-739) SATTEGT (815-821) SSSSMRN (879-885) SDRSIFV (943-949) SFYSVLQ (1067-1073) SRKSAAN (1074-1080) SEHTSLA (1105-1111)	FQNTLAE (13-19) KLRSSNE (23-29) SNESEAE (27-33) KLDSSSE (190-196) VLATVIE (395-401) SRSSQWE (475-481) DSLTFEE (556-562) LSPSDSE (671-677) LPPSLTE (971-977) VDTTSVE (1010-1016) EHTSLAE (1106-1112)	KLRSSNES (23-30) DIKSEVTS (41-48) EVTSTVQS (45-52) TVQSVKVT (49-56) YCISTVSS (132-139) YPESLRPT (176-183) PFFSMLST (229-236) SMLSTIQS (232-239) VQTTGAKS (272-279) NGMSKTPS (290-297) MSKTPSLT (292-299) EVLSGLVT (360-367) VAQTDDYS (402-409) NELSQLLS (458-465) LLLSERIS (506-513) LRASILQT (563-570) ILQTEAIT (567-574) VGATGSIS (583-590) AGLSPSDS (669-676) QSATTEGT (814-821) VEISNLAS (872-879) SDRSIFVS (943-950) KGTTTLRT (954-961)	EVTSTVQ (45-51) KVTAVLK (54-60) PKTEVLP (103-109) LLTALLK (110-116) SKTPSLT (293-299) SLTKIVA (297-303) SNTNLLK (465-471) RRTCELL (501-507) LQTEAIT (568-574) NGTAKVV (577-583) GATGSIS (584-590) DVTRSLA (792-798) RVTAFVL (851-857) QITMAVE (867-873) YTTERVR (897-903) KGTTTLR (954-960) LRTKMLL (959-965) SLTEPLL (974-980) KPTESLL (90-996) VDTTSVE (1010-1016) VLTCFVA (1031-1037)	FQNTLA (13-18) LSSTNQ (119-124) MLSTIQ (233-238) FVSTIN (371-376) LDISLV (422-427) LSNTNL (464-469) LRASIL (563-568) FRHSVH (606-611) LQQSAT (812-817) LRVTAF (850-855) FVLSCR (855-860) LASSSS (877-882) MKGTTT (953-958) MLLTFS (963-968) LTFSGS (965-970) FSGSLP (67-972) LLFSLL (979-984) FAKSHV (1005-1010) FMQTIM (1017-1022) LLMTAT (1121-1126)	YKRI (89-92) YRIF (170-173) YPRL (184-187 YECI (282-285) YLGL (319-322 YSYV (408-411 YVKI (417-420) YDAI (693-696) YGRL (809-812 YLRV (849-852 YRYF (1002-10 YSVL (1069-10

				MLLTFSGS (963-970) FSGSLPPS (967-974) LLFSLLYT (979-986) FAKSHVDT (1005-012) LSESPVLT (1026-1033) SFYSVLQS (1067-1074) AVKSEHTS (1102-1109)			
VSP Tb927.11.7060	No No TMD 414 aa	SDRTSPQ (11-17) SLGTNIS (32-38) SMVSADF (153-159)	DLETGRE (189-195) LVRTKPE (211-217)	DSRSDRTS (8-15) SLGTNIST (32-39) NISTGRGS (36-43) KIMSRLFS (79-86) HSRTKCFS (146-153) SMVSADFS (153-160)	NNTHGVD (2-8)	MNNTHG (1-6) FSASLG (29-34) FDVTHL (88-93) LVRTKP (211-216)	YRVL (181-184)
V-H⁺-ATPase, Subunit *a* Tb927.5.1300	No 6 TMDP 783 aa	SDVSAFQ (47-53) SNRTQEH (123-129) SVFSTMN (281-287) SGSTAVA (292-298) SVDTFRS (447-453) SSPSGVT (472-478) SGVTPAR (475-481) SQLSEVF (698-704)	QYQSLLE (115-121) TPFSEGE (183-189) TLNSQLE (239-245) IRASLQE (310-316) QVLTIVE (324-330) EEISTKE (330-336) EAPSLLE (573-579)	LWRSEDMT (9-16) QRETAHDS (23-30) AGLTCVST (80-87) YRITRGNS (167-174) RGNSVLHT (171-178) VLHTDEIT (175-182) DEITTPFS (179-186) TLNSQLET (239-246) QLETMKHT (243-250) MKHTLQQS (247-254) VEKSVFST (278-285) KRPTCFFT (337-344) CFFTNKFT (341-348) CFQSIVDS (350-357) SGVTPARS (475-482) QRTSEAPS (569-576) EAPSLLET (573-580) GCVSNTAS (679-686) WALSLAHS (691-698)	VSTEAIG (85-91) LLTGVIP (149-155) LHTDEIT (176-182) FATPRLW (203-209) ESTERLQ (228-234) RQTVAVE (273-279) PGTVNVP (588-594)	LRLTMQ (18-23) LEESNR (120-125) LWESLK (208-213) MRDTLN (236-241) MKHTLQ (247-252) LQQSLL (251-256) LLTSIS (261-266) LKFSGS (289-294) FSGSTA (291-296) FYNSVK(500-505) LLETMT (577-582) LAHSQL (695-700)	YQSL (116-11 YKEV (363-36 YNSV (501-50 YLRL (687-690
V-H⁺-ATPase, Subunit *d* Tb927.5.550	No No TMD 383 aa	SFGSLVD (245-251) STSSSSA (286-292) SSSSAKG (288-294) SGQTGAS (309-315)	AGASSLE (317-323)	ADLTVLRS (217-224) VLRSTVNT (221-228) LDDSRYNS (279-286) RYNSTSSS (283-290) YNSTSSSS (384-291)	GATAEVM (203-209) VNTMGVP (226-232) EVTVALY (328-334)	LRSTVN (222-227) LDDSRY (279-284) LEVSNL (356-361)	YASL (32-35) YGNF (53-56) YEHM (102-10 YEQF (191-19 YGVF (344-34

				NAVSGAAS (302-309)			YVSI (379-382)
Pho91 Tb927.11.11160	No 9 TMD 728 aa	SPLTGVE (32-38) SHPSAHN (274-280) SVLSFHD (452-458)	SPLTGVE (32-38) KLNSPRE (99-105) AFESSTE (110-116) LGRTHLE (356-362) IRPTLWE (408-414)	FIHSSPLT (28-35) FESSTENS (111-118) KNITINQT (241-248) VASTTVAS (324-331) GMLSPIAS (437-444) IADSLHDT (591-598) PPYTTLVS (603-610)	PLTGVEF (33-39) FMTDVDA (221-227) GRTHLEV (357-363) RPTLWEF (409-415)	FIHSSP (28-33) LGRTHL (356-361) LHDTLV (595-600)	YKRL (22-25) YTTL (605-608 YVVF (721-724
Vacuolar iron transporter Tb927.3.800	No 3 TMD 281 aa	SNSSVAS (78-84) SVASVLI (81-87) SGVSMLR (242-248)	IEMSRME (30-36)	GSNSSVAS (77-84) SGVSMLRS (242-249)	FETGDIE (25-31) DATTIVN (150-156) MMTEELG (169-175)	FGFSNV (88-93) MLRSAA (246-251)	YKSI (15-18) YKEV (42-45)
Zinc transporter Tb927.8.7460	No 5 TMD 471 aa	SLNSTEV (48-54) SIMSLRA (106-112) SRTSCGK (114-120) SIASDYA (410-416)	TEATHME (202-208) EEDSLCE (261-267) HGHSGSE (282-288) HSGSEGE (284-290)	PCSSGPHS (13-20) DQQSLNST (45-52) GNISQRPT (187-194) EMCTSIDS (208-215) FGGSHHHS (247-254) HDHSHSHS (292-299) INYSELLS (385-392) ELLSALRS (389-396) LCHSLCAS (459-466)	HTTIQVD (445-451)	MLATTA (167-172) LATTAQ (168-173) FGGSHH (247-252) LMESTP (377-382) FGITHT (441-446) LCHSLC (459-464) LCASAQ (463-468)	YYGF YSEL YAAL
Acid phosphatase Tb927.10.7020	Yes 0 TMD 435 aa		NDYSDTE (304-310) YSDTEQE (306-312) PEKSVGE (357-363) QLCTLKE (395-401) CNFTITE (420-426)	PVSDMDT (161-168)		LVLTKL (48-53) FNRSRH (116-121) LNTSLS (190-195) FLKTVA (227-232) LNRSTS (292-297) FGFTFN (330-335)	YWSM (68-71) YRDF (108-11) YAFL (225-228) YTSV (279-282) YRIL (286-289) YVRL (371-374)
Polyamine Transporter 1 Tb927.9.10340	Yes 11 TMD 492	SNVTDER (4-40) SAFSKSL (151-157)	WNFSGFE (227-233) FEGSIVE (472-47*)	VDNSLYPT (131-138) TITTVPQS (208-215) WNFSGFES (227-234) QLTTTSRS (321-328)		MHMSNV (1-6) LGISAF (148-153) FSKSLV (153-158) LTTTSR (322-327) MCASLK (439-444) FEGSIV (472-477)	YPTI (136-139) YESL (488-491)

* excluded ELMs falling inside SMART/PFAM domains and/or scoring poorly with the structural filter.