•Supplemental Figure 1

			PISA	
SAS6-like SAS6	Drome_DSAS6 (3) Casel_sas-6 (18) Chlre_XP_001697086.1 (18) Physo_143809 (11) Toxgo_SAS6 (268) Trybr_Tb09_211.1930 (41) Chlre_XP_001690222.1 (23) Physo_128318 (16) Toxago_SAS6-like (37)	-MSQVLFHQLVPLOV	TTVDSAS 80 ETLNNEK 73 LEVSEED 85 WSVSEEE 76 AEVGETD 33 LDLLEDD 108 HDLADVT 94 HTCDLES 87 HALNEDL 109) 3 5 5 8 7 9 9
SAS6-like SAS6	Physo 143809 Toxgo_SAS6 Trybr_Tb09.211.1930 Chire_XP_001690222.1 Physo_128318 Toxgo_SAS6-like	FQSLKFQQGLLVDFLAFPQKFIDLLQQCTQEHAK EIP RFLLG FQDLKQDQSLNVSFSGFIDNVVRMLKDCQSGKL ELHL YQILARDHDLTVDFDAFPKVIIQHL-LCKN FQSLKNDQGILVDFASFPGKIISLLEKCILAQPG DSP RFQA FHELKTQQRLLVDFASFPGKIISLLEKCILAQPG DSP RFQA FHELKTQQRLLVDFATFPANLIELLQCCVKDSKKIAQEEEKEGEAEVSAEGDAPVVNKVANETTQGSQKTRSAGPVPLSYLA FARMRSEQRLLIDPQAFPGKFVDLLEECAFSYAS - AQGGDTGPPQRLAAVFNCP - GFCGSRAPAAPAETHAGNAEFSSFLP YGVFKQKLELLVDFSGFPKYLVTMLDNVCSGIV PYVV FKQMQETORLMIEFPDYPTVLMRMLNQCIREPH IYLA FHAMQEQQKLMVDFADYANVLIRMLNNCIKEPH NHLAF FRQMQERQKLMJEFGDYPSVLIKMLNSCIKEPH CFLAF FLRREHQSLVCDFADFLMTFLKMLNRCIKEPP RFLM*	TTR 120 100 VL T 160 VLN 160 SLECCSS 420 SFV 140 VFI 134 VYL 141	20 02 29 52 23 48 34 27
SAS6-like SAS6	Physo_143809 Toxgo_SAS6 Trybr Tb09 211 1930	SPAAILDNS-PAFLNVVETNPFKHLTHLSLKLLPGNDVEIKKFLAG-CLKCSKEEKLSLMQSLDDATKQLI -DQNLSSGREVHDYYLQFVEIRSFKNLVHLSLPCRSAPLNTVLFYINS-MLEASHK	AHAERL 200 128 AQL 199 RSEATL 233 H 509 EALKRE 224 PSLLLQ 200 PSLLLQ 200 PSLLLH 223	00 28 99 37 05 24 08 01

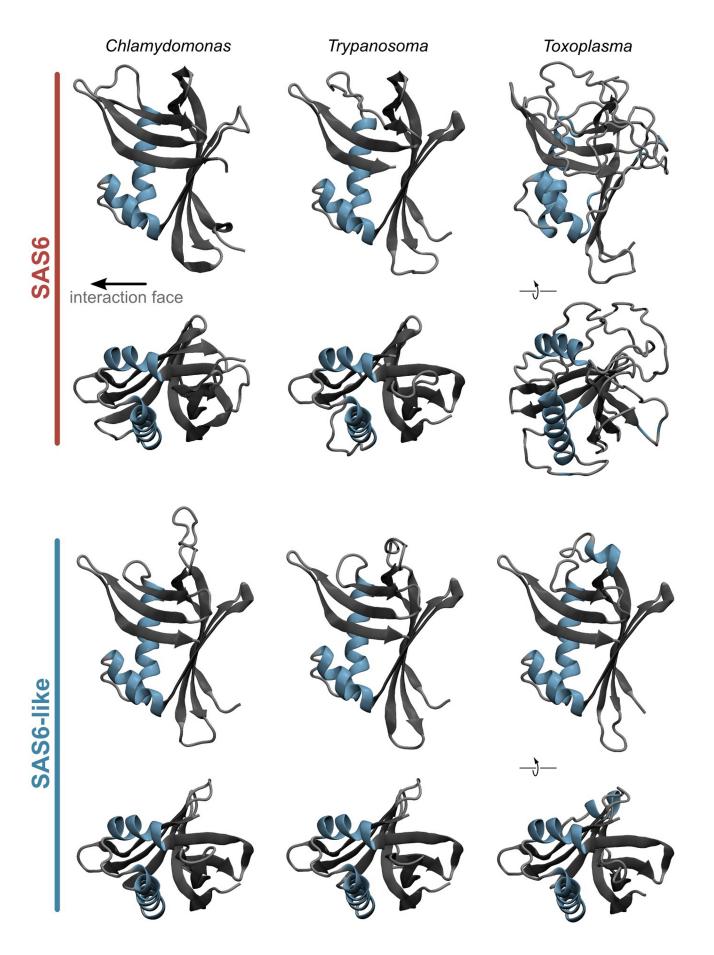


Figure S1: Alignment of the conserved domain of SAS6 and SAS6-like proteins. Domains from 7 representative species are shown: Caeel: Caenorhabdatis elegans; Chlre: Chlamydomonas reinhardtii; Drome: Drosophila melanogaster, Homsa: Homo sapiens; Physo: Phytophthora sojae; Toxgo: Toxoplasma gondii; Trybr: Trypanosoma brucei. Individual residues are shaded according to their degree of conservation. Orange bar highlights the position of the "PISA" motif previously described for SAS-6 proteins (42). Numbers in brackets at N-terminus indicate preceding residues not shown in alignment.

Figure S2: Structures of SAS6L proteins predicted by homology modeling. Conserved head domain structures from the SAS-6 and SAS6L homologues present in *Toxoplasma gondii* and *Trypanosoma brucei* and also the *Chlamydomonas reinhardtii* SAS6L protein were predicted by template-based modeling based on the solved structure of the *Chlamydomonas reinhardtii* SAS-6 head domain (Protein Data Bank entry: 3Q0Y) (50). Modeling was performed using the program I TASSER (91) and models visualised with PyMOL (http://pymol.org/). Two orthogonal views are shown for each protein. The direction of the interaction face through which SAS-6 dimers can multimerize, is also indicated.