

Fig. S1. Amino acid sequence of conserved motifs in SbCys proteins.

Motif 1



SbCys5	73	2.66e-27	QEVGRWAVSE	HVKKANDGLKFSRVVSGQYQVVEGFNYRL	IIDATDSHGK
SbCys15	87	5.90e-26	IELARFAVDE	HNSKTNAMLEFERLVKVRHQVVAGTMHHF	TVQVKEAGGG
SbCys11	65	5.77e-25	QELARFAVEE	HNKKANALLGYEKLVKAKTQVVAGTMYYL	TVEVKDGEVK
SbCys17	29	1.71e-24	IKLVCFTNAE	HNGKTNAILKRVRSVKVRYQVVAGTMHQF	TVKVKEAGST
SbCys2_2	61	1.71e-24	QELGRWAVSE	HGKQASDRLVFGKVVSGEEQIVAGTKYKL	VIQATRAGAG
SbCys10	63	4.41e-24	DGLGRFAVDE	HNKRENALLEFVRVVEAKEQVVAGTLHHL	TLEAIEAGKK
SbCys16	107	1.51e-23	IELARFAVAE	HNSKTNAALEFVRLVKVRTQLVAGRMYF	TVEVREVDGG
SbCys2_1	61	8.02e-23	QEIGRWAVSE	HDAAASDSLVSFVVRGEEQVVAGTNYKL	VIEATKGAGG
SbCys4	141	1.42e-22	QELGGWAVTE	HVRVANDGLRFGEVTSGEQQVSGMNYRL	VLHATDADGD
SbCys9	84	1.07e-20	QKIARWAVTE	HVMLANDGLKFNKLVSGEVYVSLGYLYHL	IIDASDRDGK
SbCys3	68	1.16e-20	LGGWALGQAK	YQKLAANALRFRVVRGEEQVSGMRYRL	YVDAADRAGR
SbCys14	59	3.19e-20	EDAARFAVAH	HNKNQGAALFTRVLKSKRQVVTGTLHDL	I LEAADAGKK
SbCys13	55	3.34e-19	QYIGRWAVAE	HVKQAKDGLKFDKVVGGEMMSIGIDFRL	VIDASSTSDG
SbCys12	85	8.74e-17	RFSVAEYNRQ	LRGDGGGRLEFGRVVAAQRQVVSGLKYYL	RVAAVEEGAQ
SbCys1	49	5.56e-16	QQLGRWAVTE	HDKKANDKVKFNRVVSGEETLDPVLGVIK	YHLVIDASDG

Motif 2



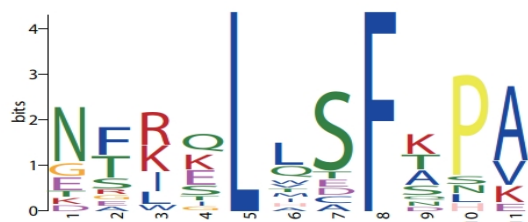
SbCys2_2	44	6.77e-20	PQAVGGWKPI	NVNDPHIQELGRWAV	SEHGKQASDR
SbCys2_1	44	1.99e-18	ENVGRWTPIT	DVNDPEIQEIGRWAV	SEHDAAASDS
SbCys5	56	2.36e-17	LQGGFYQPIV	NINDPHVQEVGRWAV	SEHVKKANDG
SbCys4	124	4.54e-15	PLAGGWSPIR	NVSEPHIQELGGWAV	TEHVRVANDG
SbCys11	48	5.01e-15	LAGGIKDVPA	NENDLHLQELARFAV	EEHNKKANAL
SbCys9	67	1.20e-14	TSTMAETTP	NVNDPVYQKIARWAV	TEHVMLANDG
SbCys8	97	1.17e-13	PPASNWTPVA	NVKDPKIQQVAQFAV	RIHALSSTEL
SbCys3	49	6.34e-13	PLLGGWNPIP	DVGDKHIQELGGWAL	GQAKYQKLAA
SbCys1	32	8.78e-13	ADSQGWFFLP	DIDAPKVQQLGRWAV	TEHDKKANDK
SbCys13	38	1.80e-12	AQTFGVWYPV	DLSEGHVQYIGRWAV	AEHVKQAKDG
SbCys14	70	1.80e-12	VGDVRDAPEG	HENDLEAIELARFAV	DEHNSKTNAM
SbCys15	64	4.95e-12	KVGARTEVRD	VESDGEVQELGRFSV	AEYNRQLRGD
SbCys16	90	4.18e-11	LCGGVVDAPG	HEMHPDAIELARFAV	AEHNSKTNAA
SbCys7	31	6.85e-11	SAQAAWVPVL	DVNELVIKQVAQFAV	LVIYGLAHRD

Motif3



SbCys10	99	2.47e-17	HHLTLEAIEA GKKKLYEAKVWVKPW LNFKELQDFS
SbCys15	124	9.24e-16	HFTVQVKEAG GGKKLYEAKVWEKVV ENFKQLQSFQ
SbCys14	95	1.05e-14	HDLILEAADA GKKSlyRAKVVVKPW EDFKSVVEFR
SbCys5	110	1.94e-14	RLIIDATDSH GKVAKYEAVVWEKEW ENFLQLTSFK
SbCys11	101	3.15e-14	YYLTVEVKDG EVKKLYEAKVWEKPV ENFKELQEFK
SbCys16	145	7.93e-14	FTVEVREVDG GASKLYEAKVWLRPW ENFKGLHAFD
SbCys2_1	99	1.23e-12	LVIEATKGAG GKIATYGAVVYEKVD NTRQLLSFAP
SbCys13	93	2.22e-12	LVIDASSTSD GKHANYEARVHERDW MDGISLLSFK
SbCys2_2	100	2.69e-12	VIQATRAGAG GNSATYGAVVYEKVD KTRQLLSFSP
SbCys8	151	1.40e-11	NYRLLITVSG GKNTQYEAfVWGILG TTSWKLLSFT
SbCys7	89	1.53e-11	VVVAARPDDG GSTAQYDCLVWGVPG SRSDTWKLRR
SbCys4	178	2.37e-11	RLVLHATDAD GDVAAYGALVYEQSW TNTRELMSFA
SbCys3	105	9.88e-11	RLYVDAADRA GRSVTYVAVIYEQVW TNTRKLASFT
SbCys12	126	1.01e-9	AAVEEGAQNA GGERAFDAVVVKPW LESRTLLTFA
SbCys6	85	1.46e-9	KMVVTAADAS GATAQYQVLAWGIPG TYQWMLLEFK

Motif4



SbCys15	140	8.21e-12	EAKVWEKWE NFKQLQSFQEV GDAAVA
SbCys5	126	1.23e-11	EAVVWEKEWE NFLQLTSFKPA N
SbCys2_1	114	9.57e-11	YGAVVYEKVD NTRQLLSFAPE N
SbCys2_2	115	1.90e-10	YGAVVYEKVD KTRQLLSFSPA N
SbCys11	117	1.34e-9	EAKVWEKPWE NFKELQEFKPV EEGASA
SbCys4	194	1.62e-9	GALVYEQSWT NRELMSFASA N
SbCys13	109	1.78e-9	EARVHERDWM DGISLLSFKPA K
SbCys8	167	3.71e-9	EAFVWGILGT TSWKLLSFTPK Y
SbCys1	104	4.84e-9	YEAVLGEEWI GRIILISFNPA R
SbCys3	121	5.28e-9	VAVIYEQVWT NTRKLASFTLA SRAH
SbCys9	137	6.27e-9	TAVVRQSTLG GELSLSWFKPA N
SbCys12	142	1.57e-8	DAVVVKPWL ESRTLLTFAPA AAK
SbCys10	115	1.85e-8	EAKVWVKPWL NFKELQDFSHK GEATTFTNAD
SbCys16	161	5.07e-8	EAKVWLRPWE NFKGLHAFDPV ADAA
SbCys17	17	2.30e-7	DTPAGCEKGL EAIKLVCFNTA EHNGKTNAIL

Motif5



SbCys8	82	1.88e-9	PSPPPPAYSS	PPPPPP	ASNWTPVANV
SbCys8	41	1.88e-9	TPSPLPDTPT	PPPPPP	PSSSTAPPP
SbCys8	69	3.98e-9	SQPPPAASSS	PPPSPP	PPAYSSPPPP
SbCys15	31	6.94e-9	FPLAVVPVVS	PPPPLPP	GSRRRTASSA
SbCys5	33	2.72e-7	MASRARGGRA	PPTPSPT	QAEIGRLQGG
SbCys8	55	4.61e-7	PPPESSSTA	PPASQP	PPAASSSPPP