

Table S2. The conserved motifs predicted in StSOT protein sequences

Motif	Sites	E-value	Amino acid sequence of motif	Width (aa)	Specific domain/region
Motif 1	18	4.3e-4	NYQGFWTSPRFJQGVACQQQFQAQDSDIILVTTPKSGTTWL	42	Sulfotransfer_1 (5' PSB)
Motif 2	24	2.1e-4	EEMFELFCKGVSLYGPFWBHVLDYWKQSI	29	Sulfotransfer_1
Motif 3	25	2.0e-3	KYEEJKKDPKIZLKRLAEFLECPFSIEEE	29	Sulfotransfer_1
Motif 4	24	2.5e-5	ENKAFFRKGEVGDWKNYFTIEMSEKLBHITEQKFQGSGLKF	41	Sulfotransfer_1
Motif 5	27	1.5e-3	DEILKMCSFENLSNLEVNKNG	21	-
Motif 6	22	6.2e-3	VYJCRNPKDTFISMWHFTNNLR	22	Sulfotransfer_1 (3' PB)
Motif 7	11	2.2e-3	PIFEQNHPLLVKNP HDLVPFLELTLYVDGQVPBFSSFTSPRLLSTHVPFA	50	-
Motif 8	10	3.2e-1	LQZEGLSEECKLLSTLPKEKGWMSGYIY	29	-