

Supplementary Table 1 Identification of the proteins that formforming a complex with Sm proteins in the cytoplasm determined by IP-LC-MS / MS.

No.	locus	protein	score (# of unique peptides)
1	AT5G60160.1	Zn-dependent exopeptidases superfamily protein	2076.0 (4)
2	AT4G02840.1,AT4G02840.2	Small nuclear ribonucleoprotein family protein D1b (SmD1b)	1692.0 (5)
3	AT3G07590.1,AT3G07590.2	Small nuclear ribonucleoprotein family protein D1a (SmD1a)	1551.0 (3)
4	AT1G03330.1	Small nuclear ribonucleoprotein family protein (LSM2)	1153.0 (1)
5	AT4G37930.1	Serine transhydroxymethyltransferase 1 (SHM1, STM, SHMT1)	1104.0 (10)
6	AT5G26780.1,AT5G26780.2,AT5G26780.3	Serine hydroxymethyltransferase 2 (SHM2)	1104.0 (7)
7	AT1G76300.1	snRNP core protein (SmD3)	1011.0 (3)
8	AT1G20580.1	Small nuclear ribonucleoprotein family protein D3b (SmD3b)	1011.0 (2)
9	AT1G29250.1,AT2G34160.1	Alba DNA/RNA-binding protein	650.0 (4)
10	AT3G04620.1	Alba DNA/RNA-binding protein	650.0 (3)
11	AT3G13060.1,AT3G13060.2	Evolutionarily conserved C-terminal region 5 (ECT5)	634.0 (3)
12	AT5G27720.1	Sm-like protein (LSM4)	509.0 (3)
13	AT5G20320.1,AT5G20320.2	Dicer-like protein 4 (DCL4)	496.0 (7)
14	AT2G36250.1,AT2G36250.2	Tubulin/FtsZ family protein (FTSZ2-1)	439.0 (5)
15	AT5G04710.1	Zn-dependent exopeptidases superfamily protein	438.0 (5)
16	AT3G52750.1	Tubulin/FtsZ family protein (FTSZ2-2)	326.0 (3)
17	AT2G45290.1	Transketolase 2 (TKL2)	290.0 (4)
18	AT1G26230.1	Chaperonin 60 subunit beta 4 (CPN-60 beta 4)	273.0 (2)
19	AT1G26230.2	Chaperonin 60 subunit beta 4 (CPN-60 beta 4)	273.0 (3)
20	AT4G00620.1	EMBRYO DEFECTIVE 3127 (EMB3127)	272.0 (2)
21	AT4G00600.1	EMBRYO DEFECTIVE 3127 (EMB3127)	272.0 (2)
22	AT4G20440.1,AT4G20440.2,AT4G20440.3,AT4G20440.4,AT5G44500.1,AT5G44500.2	Small nuclear ribonucleoprotein family protein B (SmB)	259.0 (3)
23	AT3G07920.1	Translation initiation factor IF2/IF5	258.0 (2)
24	AT2G04842.1	EMBRYO DEFECTIVE 2761 (EMB2761)	248.0 (4)
25	AT3G43190.1	SUCROSE SYNTHASE 4 (SUS4)	241.0 (5)
26	AT5G20830.1,AT5G20830.2	SUCROSE SYNTHASE 1 (SUS1)	241.0 (7)
27	AT5G28000.1	Polyketide cyclase/dehydrase and lipid transport superfamily protein	230.0 (1)
28	AT5G49190.1	SUCROSE SYNTHASE 2 (SUS2)	224.0 (2)
29	AT4G02280.1	SUCROSE SYNTHASE 3 (SUS3)	224.0 (5)
30	AT1G79270.1,AT5G61020.1,AT5G61020.2	Evolutionarily conserved C-terminal region 8 (ECT8)	219.0 (3)
31	AT4G19045.1,AT5G45550.1	MOB kinase activator-like 1 (MOB1-LIKE)	201.0 (2)
32	AT1G76860.1	Small nuclear ribonucleoprotein family protein (LSM3B)	200.0 (3)
33	AT1G60110.1	Mannose-binding lectin superfamily protein	193.0 (2)
34	AT1G60130.1	Mannose-binding lectin superfamily protein	193.0 (2)
35	AT3G53510.1	ABC-2 type transporter family protein (ABCG20)	184.0 (4)
36	AT1G78370.1	glutathione S-transferase TAU 20 (GSTU20)	176.0 (2)
37	AT1G21190.1	Small nuclear ribonucleoprotein family protein (LSM3A)	175.0 (3)
38	AT2G18740.1,AT2G18740.2,AT4G30330.1	Small nuclear ribonucleoprotein family protein	172.0 (2)
39	AT4G34200.1	D-3-phosphoglycerate dehydrogenase 1 (PGDH1)	163.0 (6)
40	AT5G22440.1,AT5G22440.2	Ribosomal protein L1p/L10e family (RL10e)	160.0 (4)
41	AT5G26860.1	lon protease 1 (LON1)	153.0 (4)
42	AT1G76950.1	Regulator of chromosome condensation (RCC1) family (PRAF1)	151.0 (4)
43	AT2G39730.1,AT2G39730.2,AT2G39730.3	Rubisco activase (RCA)	145.0 (4)
44	AT2G16440.1	Minichromosome maintenance (MCM2/3/5) family protein (MCM4)	140.0 (4)
45	AT3G54640.1	Tryptophan synthase alpha chain (TSA1, TRP3)	123.0 (3)
46	AT2G35120.1	Single hybrid motif superfamily protein	118.0 (2)
47	AT4G04730.1	Unknown protein	118.0 (4)
48	AT2G17130.1,AT2G17130.2,AT4G35260.1	Isocitrate dehydrogenase subunit (IDH)	111.0 (3)
49	AT5G64140.1	Ribosomal protein S28 (RPS28)	110.0 (1)
50	AT3G45450.1,AT3G48870.1,AT3G48870.2	ClpC-like protein	108.0 (2)
51	AT1G75600.1	Histone superfamily protein (HTR14)	107.0 (3)
52	AT2G23420.1,AT4G36940.1	Nicotinate phosphoribosyltransferase (NAPRT)	107.0 (5)
53	AT5G46560.1	Inner nuclear membrane protein (MAN1)	107.0 (3)
54	AT1G27280.1	Paired amphipathic helix (PAH2) superfamily protein	107.0 (2)
55	AT3G24080.1,AT3G24080.2	KRR1 family protein	104.0 (1)
56	AT4G27070.1	Tryptophan synthase beta-subunit 2 (TSB2)	102.0 (3)
57	AT1G64440.1	UDP-GLUCOSE 4-EPIMERASE (RHD1, REB1, UGE4)	100.0 (3)
58	AT3G22960.1	Pyruvate kinase family protein (PKP1, PKP-ALPHA)	95.0 (7)
59	AT3G60750.1,AT3G60750.2	Transketolase (TKL1)	92.0 (4)
60	AT1G20950.1,AT1G76550.1	Phosphofructokinase family protein	90.0 (3)
61	AT5G49030.1,AT5G49030.2,AT5G49030.3	tRNA synthetase class I (I, L, M and V) family protein (OVA2)	87.0 (10)
62	AT3G03120.1	ADP-ribosylation factor B1C (ARFB1C)	84.0 (2)
63	AT5G17060.1	ADP-ribosylation factor B1B (ARFB1B)	84.0 (3)
64	AT5G60930.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	83.0 (7)
65	AT3G55510.1	Noc2p family (RBL)	81.0 (1)
66	AT3G25820.2	Terpene synthase-like sequence-1,8-cineole (TPS-CIN)	79.0 (1)
67	AT1G12920.1,AT5G47880.1,AT5G47880.2	Eukaryotic release factor 1 (ERF1)	79.0 (4)
68	AT4G08320.1,AT4G08320.2	Tetratricopeptide repeat (TPR)-like superfamily protein (TPR8)	75.0 (1)
69	AT2G10260.1,AT2G10260.2	unknown protein, similar to Ulp1 protease family protein (TAIR:AT5G45570.1)	74.0 (3)
70	AT5G30510.1	Ribosomal protein S1 (RPS1)	70.0 (3)
71	AT1G50770.1	Aminotransferase-like, plant mobile domain family protein	68.0 (4)
72	AT1G01950.1,AT1G01950.2,AT1G01950.3	Armadillo repeat kinesin 2 (ARK2)	63.0 (2)
73	AT1G59990.1	EMBRYO DEFECTIVE 3108, DEAD-box ATP-dependent RNA helicase 22	61.0 (3)
74	AT4G40020.1	Myosin heavy chain-related protein	61.0 (3)
75	AT3G50240.1	Kinesin-related protein (KICP-02)	61.0 (5)
76	AT3G44716.1,AT3G44716.2	unknown protein	61.0 (1)
77	AT2G17930.1	Phosphatidylinositol 3- and 4-kinase family protein with FAT domain	60.0 (8)
78	AT1G30440.1	Phototropic-responsive NPH3 family protein	60.0 (3)
79	AT5G22450.1	unknown protein	57.0 (6)
80	AT4G32820.1,AT4G32820.2	CALCINEURIN BINDING PROTEIN 1 (CABIN1)	57.0 (5)
81	AT4G36760.1	Aminopeptidase P1 (APP1)	54.0 (3)
82	AT1G15690.1,AT1G15690.2	Inorganic H pyrophosphatase family protein (AVP1, AVP-3)	54.0 (1)
83	AT5G61950.1	Ubiquitin carboxyl-terminal hydrolase-related protein	53.0 (7)
84	AT1G06590.1	unknown protein	51.0 (3)
85	ATMG00090.1	ribosomal protein S3 (RS3)	47.0 (2)
86	AT5G58530.1	Glutaredoxin family protein	47.0 (1)
87	AT1G11990.1	O-fucosyltransferase family protein	47.0 (4)
88	AT3G06720.1,AT3G06720.2,AT4G16143.1,AT4G16143.2	importin alpha isoform (IMPA)	46.0 (1)
89	AT2G36720.1	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain	46.0 (3)
90	AT3G48190.1	PCD IN MALE GAMETOGENESIS 1 (PIG1)	46.0 (15)
91	AT3G44050.1	P-loop containing nucleoside triphosphate hydrolases superfamily protein	45.0 (7)
92	AT1G12470.1	zinc ion binding protein	45.0 (2)
93	AT5G08390.1	Transducin/WD40 repeat-like superfamily protein	45.0 (5)
94	AT1G48300.1	Diacylglycerol acyltransferase 3 (DGAT3)	45.0 (2)
95	AT5G23340.1	RNI-like superfamily protein	43.0 (1)
96	AT3G01310.1,AT3G01310.2	Arabidopsis homolog protein of yeast VIP1 1	43.0 (4)
97	AT5G15070.1,AT5G15070.2	Arabidopsis homolog protein of yeast VIP1 2	43.0 (3)
98	AT3G53940.1	Mitochondrial substrate carrier family protein	42.0 (2)
99	AT4G35350.1	Xylem cysteine peptidase 1 (XCP1)	41.0 (2)
100	AT5G35604.1	similar to: myosin heavy chain-related (TAIR:AT5G32590.1)	39.0 (4)
101	AT1G67120.1	Midasin	38.0 (18)
102	AT3G10220.1	EMBRYO DEFECTIVE 2804, tubulin folding cofactor B	35.0 (2)
103	AT3G04960.1,AT3G04960.2,AT3G04960.3,AT3G04960.4	Domain of unknown function (DUF3444)	35.0 (2)
104	AT4G15360.1	cytochrome P450, family 705, subfamily A, polypeptide 3 (CYP705A3)	34.0 (8)
105	AT3G54050.1,AT3G54050.2	High cyclic electron flow 1 (HCEF1)	34.0 (1)
106	AT1G54460.1	TPX2 (targeting protein for Xkdp2) protein family	33.0 (1)
107	AT2G36460.1,AT2G36460.2	Aldolase superfamily protein	33.0 (1)
108	AT4G29640.1	Cytidine/deoxycytidylate deaminase family protein	32.0 (4)
109	AT1G48240.1,AT3G17440.1,AT3G17440.2	novel plant snare 12 (NPSN12)	31.0 (2)
110	AT5G05320.1	FAD/NAD(P)-binding oxidoreductase family protein	30.0 (1)
111	AT4G28630.1	ABC transporter of the mitochondrion 1 (ATM1)	29.0 (1)
112	AT1G16400.1	cytochrome P450, family 79, subfamily F, polypeptide 2 (CYP79F2)	29.0 (2)
113	AT5G61150.1,AT5G61150.2	VERNALIZATION INDEPENDENCE 4 (VIP4)	28.0 (4)
114	AT2G38720.1	Microtubule-associated protein 65-5 (MAP65-5)	28.0 (1)
115	AT1G67950.2	RNA-binding (RRM/RBD/RNP motifs) family protein	25.0 (2)
116	AT1G16760.1	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain	23.0 (7)
117	AT1G79190.1	ARM repeat superfamily protein	23.0 (7)
118	AT5G37010.1	unknown protein	16.0 (3)

The results in the list of protein families were obtained on the basis of a comparison of the masses of obtained peptides and their fragments with those of the TAIR10 database, using the MASCOT program in combination with the MScan software (<http://proteom.ibb.waw.pl/mscan/index.html>). 118 proteins were identified in the interactome studied, of which 5 represented canonical Sm proteins (SmD1a, SmD1b, SmD3, SmD3b, SmB). Interestingly, there was a trend similar to the results obtained for mRNA identified by RIP-seq. A significant part of the cytoplasmic Sm interaction was the ribosome-related / translational proteins (eIF2 / IF5 translation initiators, RL10e ribosome structural proteins, RS1, RS3, OVA2 tNA RNase synthase), mitochondria (SHM1 and SHM2 methyltransferases, IDH isocitrate dehydrogenase, ABC ATM1 transporters) and plastids / photosynthesis (RuBisCO RCA asset, TKL1 transketolase). In addition, 2 families of mRNA binding proteins: Alba and ECT were identified.

**Supplementary Table 2 The cytoplasmic Sm proteins interactome.
The results in the list of protein families.**

locus	protein	score (# of unique peptides)
AT1G29250.1,AT2G34160.1	Alba DNA/RNA-binding protein	650.0 (4)
AT3G04620.1	Alba DNA/RNA-binding protein	650.0 (3)
AT4G19045.1,AT5G45550.1	MOB kinase activator-like 1 (MOB1-LIKE)	201.0 (2)
AT3G53510.1	ABC-2 type transporter family protein (ABCG20)	184.0 (4)
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AT1G76950.1	Regulator of chromosome condensation (RCC1) family (PRAF1)	151.0 (4)
AT3G55510.1	Noc2p family (RBL)	81.0 (1)
AT1G15690.1,AT1G15690.2	Inorganic H pyrophosphatase family protein (AVP1, AVP-3)	54.0 (1)
AT1G06590.1	unknown protein	51.0 (3)
AT3G48190.1	PCD IN MALE GAMETOGENESIS 1 (PIG1)	46.0 (15)
AT5G15070.1,AT5G15070.2	Arabidopsis homolog protein of yeast VIP1 2	43.0 (3)
AT5G61150.1,AT5G61150.2	VERNALIZATION INDEPENDENCE 4 (VIP4)	28.0 (4)
AT3G07920.1	Translation initiation factor IF2/IF5	258.0 (2)
AT5G22440.1,AT5G22440.2	Ribosomal protein L1p/L10e family (RL10e)	160.0 (4)
AT5G64140.1	Ribosomal protein S28 (RPS28)	110.0 (1)
AT5G49030.1,AT5G49030.2,AT5G49030.3	tRNA synthetase class I (I, L, M and V) family protein (OVA2)	87.0 (10)
AT1G12920.1,AT5G47880.1,AT5G47880.2	Eukaryotic release factor 1 (ERF1)	79.0 (4)
AT5G30510.1	Ribosomal protein S1 (RPS1)	70.0 (3)
AT1G50770.1	Aminotransferase-like, plant mobile domain family protein	68.0 (4)
ATMG00090.1	ribosomal protein S3 (RS3)	47.0 (2)
AT1G67120.1	Midasin	38.0 (18)
AT5G26780.1,AT5G26780.2,AT5G26780.3	Serine hydroxymethyltransferase 2 (SHM2)	1104.0 (7)
AT5G26860.1	Ion protease 1 (LON1)	153.0 (4)
AT2G35120.1	Single hybrid motif superfamily protein	118.0 (2)
AT2G17130.1,AT2G17130.2,AT4G35260.1	Isocitrate dehydrogenase subunit (IDH)	111.0 (3)
AT3G53940.1	Mitochondrial substrate carrier family protein	42.0 (2)
AT4G28630.1	ABC transporter of the mitochondrion 1 (ATM1)	29.0 (1)
AT2G36250.1,AT2G36250.2	Tubulin/FtsZ family protein (FTSZ2-1)	439.0 (5)
AT3G52750.1	Tubulin/FtsZ family protein (FTSZ2-2)	326.0 (3)
AT2G45290.1	Transketolase 2 (TKL2)	290.0 (4)
AT1G26230.1	Chaperonin 60 subunit beta 4 (CPN-60 beta 4)	273.0 (2)
AT1G26230.2	Chaperonin 60 subunit beta 4 (CPN-60 beta 4)	273.0 (3)
AT4G00620.1	EMBRYO DEFECTIVE 3127 (EMB3127)	272.0 (2)
AT4G00600.1	EMBRYO DEFECTIVE 3127 (EMB3127)	272.0 (2)
AT2G04842.1	EMBRYO DEFECTIVE 2761 (EMB2761)	248.0 (4)
AT3G43190.1	SUCROSE SYNTHASE 4 (SUS4)	241.0 (5)
AT5G20830.1,AT5G20830.2	SUCROSE SYNTHASE 1 (SUS1)	241.0 (7)
AT5G49190.1	SUCROSE SYNTHASE 2 (SUS2)	224.0 (2)
AT4G02280.1	SUCROSE SYNTHASE 3 (SUS3)	224.0 (5)
AT2G39730.1,AT2G39730.2,AT2G39730.3	Rubisco activase (RCA)	145.0 (4)
AT3G54640.1	Tryptophan synthase alpha chain (TSA1, TRP3)	123.0 (3)
AT4G04730.1	Unknown protein	118.0 (4)
AT4G27070.1	Tryptophan synthase beta-subunit 2 (TSB2)	102.0 (3)
AT3G22960.1	Pyruvate kinase family protein (PKP1, PKP-ALPHA)	95.0 (7)
AT3G60750.1,AT3G60750.2	Transketolase (TKL1)	92.0 (4)
AT3G25820.2	Terpene synthase-like sequence-1,8-cineole (TPS-CIN)	79.0 (1)
AT1G59990.1	EMBRYO DEFECTIVE 3108, DEAD-box ATP-dependent RNA h	61.0 (3)
AT5G22450.1	unknown protein	57.0 (6)
AT3G54050.1,AT3G54050.2	High cyclic electron flow 1 (HCEF1)	34.0 (1)
AT1G67950.2	RNA-binding (RRM/RBD/RNP motifs) family protein	25.0 (2)