

PROTEOMICS

**Supporting Information
for Proteomics**

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**Proteome analysis of *Schizosaccharomyces pombe* by two-dimensional gel
electrophoresis and mass spectrometry**

Supplementary material 1. List of identified *S. pombe* proteins by MALDI-TOF-MS and/or nanoLC-MS/MS (only in the 3-10 *pI* range)

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	<i>pI</i>	MW (kDa)	<i>pI</i>
1	214	2ABA_SCHPO	Protein phosphatase PP2A regulatory subunit B	Q12702	nanoLC-MS/MS	29%	11	46	52.8	5.41	54.0	5.49
2	40	6PGD_SCHPO	Fragment of the 6-phosphogluconate dehydrogenase, decarboxylating	P78812	MALDI-TOF-MS	20%	9	25	53.7	6.73	22.1	5.31
3	172	6PGD_SCHPO	6-phosphogluconate dehydrogenase, decarboxylating	P78812	MALDI-TOF-MS nanoLC-MS/MS	46% 29%	23 12	26 53	53.7	6.73	41.3	6.69
4	228	6PGD_SCHPO	6-phosphogluconate dehydrogenase, decarboxylating	P78812	MALDI-TOF-MS nanoLC-MS/MS	41% 11%	22 5	21 34	53.7	6.73	49.5	7.06
5	235	ACH1_SCHPO	Acetyl-CoA hydrolase	Q9UUJ9	MALDI-TOF-MS nanoLC-MS/MS	26% 13%	14 6	12 109	57.9	6.35	59.0	6.93
6	259	ACON_SCHPO	Aconitate hydratase, mitochondrial [Precursor]	O13966	MALDI-TOF-MS	28%	25	21	84.9	8.08	31.2	8.89
7	134	ACT_SCHPO	Actin	P10989	MALDI-TOF-MS nanoLC-MS/MS	44% 50%	19 15	19 56	41.8	5.31	39.3	5.19
8	143	ACT_SCHPO	Actin	P10989	MALDI-TOF-MS	31%	11	14	41.8	5.31	42.2	5.50
9	148	ACT_SCHPO	Actin	P10989	MALDI-TOF-MS nanoLC-MS/MS	50% 32%	23 11	18 86	41.8	5.31	40.3	5.64
10	18	ADH_SCHPO	Alcohol dehydrogenase	P00332	NanoLC-MS/MS	20%	5	77	37.4	6.46	14.2	5.82
11	68	ADH_SCHPO	Alcohol dehydrogenase	P00332	nanoLC-MS/MS	18%	6	92	37.4	6.46	19.9	8.88
12	186	ADH_SCHPO	Alcohol dehydrogenase	P00332	MALDI-TOF-MS	59%	18	9	37.4	6.46	38.0	6.88
13	195	ADH_SCHPO	Alcohol dehydrogenase	P00332	MALDI-TOF-MS nanoLC-MS/MS	40% 28%	14 9	17 41	37.4	6.46	35.3	7.72
14	94	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	35%	9	8	39.6	5.92	32.5	5.77
15	98	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	30%	6	21	39.6	5.92	31.5	6.08
16	163	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	39%	9	10	39.6	5.92	39.3	6.02
17	166	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	41%	10	19	39.6	5.92	38.3	6.20
18	167	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	65%	18	8	39.6	5.92	39.3	6.28
19	178	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	39%	9	11	39.6	5.92	34.8	6.45
20	266	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS nanoLC-MS/MS	55% 6%	15 2	20 8	39.6	5.92	39.3	6.11
21	267	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS nanoLC-MS/MS	33% 18%	8 5	21 27	39.6	5.92	31.5	6.20
22	105	AROF_SCHPO	Putative phospho-2-dehydro-3-deoxyheptonate aldolase	Q09755	nanoLC-MS/MS	12%	3	80	39.8	6.31	26.9	6.59
23	31	ATPA_SCHPO	ATP synthase alpha chain, mitochondrial [Precursor]	P24487	nanoLC-MS/MS	6%	3	81	58.6	9.18	16.3	8.80
24	132	ATPB_SCHPO	ATP synthase beta chain, mitochondrial [Precursor]	P22068	nanoLC-MS/MS	6%	3	49	56.9	5.72	34.9	5.16

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
25	206	ATPB_SCHPO	ATP synthase beta chain, mitochondrial [Precursor]	P22068	MALDI-TOF-MS nanoLC-MS/MS	51% 26%	22 9	16 43	56.9	5.72	48.4	4.99
26	189	BGL2_SCHPO	Glucan 1,3-beta-glucosidase [Precursor]	O13990	MALDI-TOF-MS nanoLC-MS/MS	63% 23%	13 11	14 135	35.4	6.35	39.9	6.95
27	7	BTF3_SCHPO	Transcription fator BTF3 homolog	Q92371	MALDI-TOF-MS	64%	8	23	16.2	5.95	16.3	4.20
28	256	BUT2_SCHPO	Uba3-binding protein but2	P87167	nanoLC-MS/MS	5%	3	21	43.6	9.13	145.9	4.50
29	190	CAP_SCHPO	Adenylyl cyclase-associated protein	P36621	nanoLC-MS/MS	5%	2	39	60.2	6.39	43.1	6.89
30	189	CISY_SCHPO	Probable citrate synthase, mitochondrial [Precursor]	Q10306	MALDI-TOF-MS nanoLC-MS/MS	30% 22%	13 12	15 29	53.0	7.75	39.9	6.95
31	190	CISY_SCHPO	Probable citrate synthase, mitochondrial [Precursor]	Q10306	MALDI-TOF-MS nanoLC-MS/MS	43% 42%	22 20	16 34	53.0	7.75	43.1	6.89
32	213	CPGL_SCHPO	Glutamate carboxypeptidase-like protein	Q9P6I2	MALDI-TOF-MS nanoLC-MS/MS	40% 37%	19 15	28 39	52.6	5.27	53.2	5.36
33	78	CYP5_SCHPO	40 kDa peptidyl-prolyl cis-trans isomerase	Q11004	MALDI-TOF-MS nanoLC-MS/MS	23% 35%	9 10	9 42	40.2	8.05	26.6	5.10
34	29	CYPH_SCHPO	Peptidyl-prolyl cis-trans isomerase	P18253	MALDI-TOF-MS nanoLC-MS/MS	57% 45%	12 9	8 58	17.4	8.81	14.4	8.71
35	30	CYPH_SCHPO	Peptidyl-prolyl cis-trans isomerase	P18253	MALDI-TOF-MS nanoLC-MS/MS	57% 28%	10 5	17 56	17.4	8.81	14.2	8.81
36	171	CYSD_SCHPO	O-acetylhomoserine (Thiol)-lyase	O13326	MALDI-TOF-MS nanoLC-MS/MS	39% 11%	14 5	9 35	46.4	6.05	43.5	6.40
37	221	DAK1_SCHPO	Dihydroxyacetone kinase 1	O13902	MALDI-TOF-MS nanoLC-MS/MS	35% 31%	24 17	10 105	62.3	5.93	52.7	5.98
38	222	DAK1_SCHPO	Dihydroxyacetone kinase 1	O13902	MALDI-TOF-MS nanoLC-MS/MS	27% 7%	16 4	20 24	62.3	5.93	53.3	5.98
39	249	DAK2_SCHPO	Dihydroxyacetone kinase 2	O74215	nanoLC-MS/MS	16%	7	87	62.1	5.50	61.6	5.57
40	71	DHE4_SCHPO	NADP-specific glutamate dehydrogenase	P78804	nanoLC-MS/MS	9%	3	42	48.8	7.14	26.1	4.19
41	221	DYR_SCHPO	Dihydropteridine reductase	P36591	nanoLC-MS/MS	8%	3	96	51.5	6.15	52.7	5.98
42	61	EF1A1_SCHPO	Elongation factor 1-alpha-A	P50522	MALDI-TOF-MS	21%	9	15	49.7	9.12	20.1	7.35
43	126	EF1A1_SCHPO	Elongation factor 1-alpha-A	P50522	MALDI-TOF-MS nanoLC-MS/MS	29% 21%	13 10	12 32	49.7	9.12	32.2	9.34
44	205	EF1A1_SCHPO	Elongation factor 1-alpha-A	P50522	MALDI-TOF-MS	43%	18	15	49.7	9.12	37.9	8.75
45	260	EF1A1_SCHPO	Elongation factor 1-alpha-A	P50522	MALDI-TOF-MS	35%	14	17	49.7	9.12	39.9	8.88
46	28	EF1A2_SCHPO	Elongation factor 1-alpha-B/C	Q10119	nanoLC-MS/MS	18%	6	32	49.7	9.12	14.4	8.55
47	30	EF1A2_SCHPO	Elongation factor 1-alpha-B/C	Q10119	nanoLC-MS/MS	16%	5	46	49.7	9.12	14.2	8.81
48	61	EF1A2_SCHPO	Fragment of the elongation factor 1-alpha-B/C	Q10119	MALDI-TOF-MS	33%	11	23	49.7	9.12	20.1	7.35

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
49	115	EF1A2_SCHPO	Elongation factor 1-alpha-B/C	Q10119	nanoLC-MS/MS	20%	9	39	49.7	9.12	25.9	7.91
50	261	EF1A2_SCHPO	Elongation factor 1-alpha-B/C	Q10119	MALDI-TOF-MS	20%	6	10	49.7	9.12	40.2	8.88
51	50	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	24%	9	5	47.4	6.23	22.5	6.03
52	63	ENO11_SCHPO	N-terminal fragment of the enolase 1-1	P40370	MALDI-TOF-MS nanoLC-MS/MS	30% 20%	14 9	19 69	47.4	6.23	21.6	8.17
53	79	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS nanoLC-MS/MS	15% 31%	7 9	14 24	47.4	6.23	24.4	5.04
54	84	ENO11_SCHPO	C-terminal fragment of the enolase 1-1	P40370	MALDI-TOF-MS	29%	11	15	47.4	6.23	25.5	5.70
55	85	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS nanoLC-MS/MS	39% 36%	15 10	13 44	47.4	6.23	31.2	5.60
56	92	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	51%	23	15	47.4	6.23	27.9	5.84
57	93	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS nanoLC-MS/MS	31% 22%	12 8	21 30	47.4	6.23	25.4	5.84
58	100	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS Nano-LC-MS/MS	23% 18%	10 7	10 21	47.4	6.23	24.1	5.86
59	103	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS nanoLC-MS/MS	37% 29%	14 11	22 79	47.4	6.23	23.8	6.51
60	107	ENO11_SCHPO	N-terminal fragment of the enolase 1-1	P40370	MALDI-TOF-MS	25%	13	13	47.4	6.23	29.1	6.76
61	108	ENO11_SCHPO	N-terminal fragment of the enolase 1-1	P40370	MALDI-TOF-MS	25%	11	19	47.4	6.23	27.8	6.80
62	112	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	17%	8	4	47.4	6.23	25.3	7.27
63	168	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	38%	16	10	47.4	6.23	38.6	6.27
64	192	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	38%	11	11	47.4	6.23	45.8	6.10
65	193	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	50%	18	25	47.4	6.23	38.6	7.59
66	87	ETFA_SCHPO	Probable electron transfer flavoprotein alpha-subunit, mitochondrial [Precursor]	P78790	nanoLC-MS/MS	6%	3	86	36.4	7.03	32.8	5.54
67	25	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	18%	5	14	35.9	6.24	12.5	6.96
68	31	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS nanoLC-MS/MS	31% 21%	12 17	17 89	35.9	6.24	16.3	8.80
69	47	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	32%	9	15	35.9	6.24	18.7	5.78
70	58	G3P1_SCHPO	C-terminal fragment of the glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	34%	13	23	35.9	6.24	20.5	7.03
71	59	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS nanoLC-MS/MS	26% 16%	10 5	16 41	35.9	6.24	21.1	7.15
72	60	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	nanoLC-MS/MS	7%	2	52	35.9	6.24	21.5	7.33

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
73	86	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS nanoLC-MS/MS	59% 40%	20 11	16 33	35.9	6.24	32.9	5.40
74	91	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	54%	15	11	35.9	6.24	30.0	5.76
75	111	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	40%	13	14	35.9	6.24	24.7	7.22
76	115	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)	P78958	nanoLC-MS/MS	39%	11	39	35.9	6.24	25.9	7.91
77	116	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)	P78958	MALDI-TOF-MS	42%	15	14	35.9	6.24	25.2	8.07
78	117	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS nanoLC-MS/MS	35% 38%	13 13	16 98	35.9	6.24	26.3	8.07
79	118	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)	P78958	MALDI-TOF-MS nanoLC-MS/MS	40% 39%	12 12	18 11	35.9	6.24	25.4	8.17
80	119	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)	P78958	MALDI-TOF-MS nanoLC-MS/MS	35% 35%	13 11	18 11	35.9	6.24	26.4	8.32
81	123	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS nanoLC-MS/MS	47% 46%	16 14	12 67	35.9	6.24	27.7	8.75
82	124	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS nanoLC-MS/MS	50% 35%	16 13	10 25	35.9	6.24	28.0	9.26
83	183	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	63%	22	20	35.9	6.24	36.3	6.89
84	27	G3P2_SCHPO	Glyceraldehyde-3-phosphate dehydrogenase 2	O43026	MALDI-TOF-MS nanoLC-MS/MS	26% 21%	10 7	21 10	35.7	7.69	16.1	8.24
85	55	G3P2_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 2	O43026	MALDI-TOF-MS	26%	8	11	35.7	7.69	22.7	6.71
86	120	G3P2_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 2	O43026	Nano-LC-MS/MS	4%	2	44	35.7	7.69	30.9	8.20
87	198	G3P2_SCHPO	Glyceraldehyde-3-phosphate dehydrogenase 2	O43026	MALDI-TOF-MS nanoLC-MS/MS	62% 38%	22 12	10 27	35.7	7.69	35.7	8.20
88	104	G6PI_SCHPO	Glucose-6-phosphate isomerase	P78917	MALDI-TOF-MS nanoLC-MS/MS	33% 23%	21 12	14 71	60.9	5.97	25.2	6.64
89	160	GBLP_SCHPO	Guanine nucleotide-binding protein beta subunit-like protein	Q10281	nanoLC-MS/MS	20%	4	39	34.9	5.43	41.2	5.88
90	199	GCST_SCHPO	Probable aminomethyltransferase, mitochondrial [Precursor]	O14110	MALDI-TOF-MS nanoLC-MS/MS	44% 54%	17 13	19 53	42.4	8.85	43.5	8.27
91	67	GLYD_SCHPO	C-terminal fragment of the probable serine hydroxymethyltransferase, cytosolic	O13972	MALDI-TOF-MS nanoLC-MS/MS	19% 19%	8 10	22 113	51.9	7.66	19.8	8.65
92	234	GLYD_SCHPO	Probable serine hydroxymethyltransferase, cytosolic	O13972	MALDI-TOF-MS nanoLC-MS/MS	40% 45%	20 22	14 67	51.9	7.66	48.1	7.68
93	103	GNTK_SCHPO	Probable gluconokinase	Q10242	nanoLC-MS/MS	18%	3	83	21.6	6.31	23.8	6.51
94	137	GPD1_SCHPO	Glycerol-3-phosphate dehydrogenase [NAD+] 1	P21696	MALDI-TOF-MS	66%	24	20	42.0	5.25	42.7	5.19
95	137	GPD2_SCHPO	Glycerol-3-phosphate dehydrogenase [NAD+] 2	Q09845	Nano-LC-MS/MS	52%	19	37	40.9	7.91	42.7	5.19
96	65	GPX1_SCHPO	Glutathione peroxidase	O59858	MALDI-TOF-MS nanoLC-MS/MS	63% 46%	10 7	5 69	18.1	8.35	18.2	8.28

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
97	66	GPX1_SCHPO	Glutathione peroxidase	O59858	MALDI-TOF-MS	36%	8	30	18.1	8.35	18.1	8.59
98	24	GRPE_SCHPO	GrpE protein homolog, mitochondrial [Precursor]	O43047	nanoLC-MS/MS	33%	5	28	25.3	7.73	15.8	6.75
99	231	GSHR_SCHPO	Glutathione reductase	P78965	MALDI-TOF-MS nanoLC-MS/MS	22% 32%	9 12	6 46	50.0	6.90	53.6	7.54
100	17	H2B1_SCHPO	Histone H2B-alpha	P04913	nanoLC-MS/MS	9%	2	46	13.7	10.07	13.6	5.76
101	147	HOSM_SCHPO	Homocitrate synthase, mitochondrial [Precursor]	Q9Y823	MALDI-TOF-MS nanoLC-MS/MS	50% 19%	21 7	18 59	46.3	5.69	45.3	5.56
102	1	HSP16_SCHPO	Heat shock protein 16	O14368	nanoLC-MS/MS	20%	2	41	16.0	5.72	15.8	5.37
103	250	HSP71_SCHPO	Probable heat shock protein ssa1	Q10265	nanoLC-MS/MS	34%	21	56	70.0	5.13	66.9	5.33
104	265	HSP71_SCHPO	Probable heat shock protein ssa1	Q10265	MALDI-TOF-MS	21%	11	29	70.0	5.13	42.3	5.55
105	145	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS nanoLC-MS/MS	38% 26%	27 18	14 52	70.1	5.13	44.3	5.45
106	146	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS nanoLC-MS/MS	38% 28%	25 17	25 35	70.1	5.13	43.3	5.54
107	214	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS nanoLC-MS/MS	45% 32%	31 22	17 37	70.1	5.13	54.0	5.49
108	250	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS nanoLC-MS/MS	55% 35%	32 23	17 56	70.1	5.13	66.9	5.33
109	251	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS	25%	14	24	70.1	5.13	72.1	5.13
110	262	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS nanoLC-MS/MS	40% 27%	29 19	10 36	70.1	5.13	48.5	5.66
111	147	HSP75_SCHPO	Heat shock protein sks2	Q10284	nanoLC-MS/MS	23%	13	32	67.2	5.82	45.3	5.56
112	249	HSP75_SCHPO	Heat shock protein sks2	Q10284	MALDI-TOF-MS nanoLC-MS/MS	28% 29%	17 12	17 93	67.2	5.82	61.6	5.57
113	208	HSP90_SCHPO	Heat shock protein 90 homolog	P41887	MALDI-TOF-MS nanoLC-MS/MS	29% 10%	22 7	21 43	80.6	4.89	54.5	5.16
114	209	HSP90_SCHPO	Heat shock protein 90 homolog	P41887	MALDI-TOF-MS nanoLC-MS/MS	34% 9%	25 6	10 41	80.6	4.89	55.9	5.17
115	242	HSP90_SCHPO	Heat shock protein 90 homolog	P41887	nanoLC-MS/MS	6%	4	17	80.6	4.89	69.0	5.63
116	252	HSP90_SCHPO	Heat shock protein 90 homolog	P41887	MALDI-TOF-MS nanoLC-MS/MS	31% 23%	23 17	25 53	80.6	4.89	80.3	4.75
117	162	HXK2_SCHPO	Hexokinase 2	P50521	MALDI-TOF-MS nanoLC-MS/MS	35% 45%	17 18	11 37	50.9	5.89	43.8	5.87
118	124	IDH1_SCHPO	Isocitrate dehydrogenase (NAD) subunit 1, mitochondrial [Precursor]	O13696	nanoLC-MS/MS	9%	3	19	38.8	7.71	28.0	9.26
119	202	IDHP_SCHPO	Probable isocitrate dehydrogenase (NADP), mitochondrial [Precursor]	O14254	MALDI-TOF-MS nanoLC-MS/MS	54% 39%	26 18	16 98	47.3	8.86	43.4	8.65
120	46	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	MALDI-TOF-MS	30%	12	13	45.2	9.47	18.3	5.67

Supplementary material 1. continued

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									MW (kDa)	pI	MW (kDa)	pI
121	118	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	MALDI-TOF-MS nanoLC-MS/MS	41% 41%	15 15	16 14	45.2	9.47	25.4	8.17
122	121	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	MALDI-TOF-MS nanoLC-MS/MS	17% 29%	6 10	18 30	45.2	9.47	26.0	8.61
123	133	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	MALDI-TOF-MS	65%	30	22	45.2	9.47	38.8	5.25
124	193	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	MALDI-TOF-MS nanoLC-MS/MS	64% 53%	28 19	10 91	45.2	9.47	38.6	7.59
125	194	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	nanoLC-MS/MS	13%	4	21	45.2	9.47	38.6	7.72
126	196	ILV5_SCHPO	Probable ketol-acid reductoisomerase, mitochondrial [Precursor]	P78827	MALDI-TOF-MS nanoLC-MS/MS	59% 53%	28 20	16 41	45.2	9.47	38.9	7.97
127	256	INV1_SCHPO	Invertase [Precursor]	O59852	nanoLC-MS/MS	10%	5	24	64.4	4.94	145.9	4.50
128	101	KAD1_SCHPO	Adenylate kinase	P33075	MALDI-TOF-MS	37%	9	14	24.4	6.14	23.6	5.95
129	48	KAPS_SCHPO	Adenylyl-sulfate kinase	Q9P7G9	MALDI-TOF-MS	42%	8	18	22.7	6.23	22.4	5.83
130	95	KPYK_SCHPO	Pyruvate kinase	Q10208	MALDI-TOF-MS	32%	15	19	55.5	8.18	32.4	5.93
131	119	KPYK_SCHPO	Pyruvate kinase	Q10208	MALDI-TOF-MS nanoLC-MS/MS	26% 21%	20 10	13 19	55.5	8.18	26.4	8.32
132	121	KPYK_SCHPO	Pyruvate kinase	Q10208	MALDI-TOF-MS nanoLC-MS/MS	28% 8%	17 4	17 40	55.5	8.18	26.0	8.61
133	122	KPYK_SCHPO	Pyruvate kinase	Q10208	MALDI-TOF-MS	17%	8	9	55.5	8.18	27.6	8.56
134	123	KPYK_SCHPO	Pyruvate kinase	Q10208	MALDI-TOF-MS nanoLC-MS/MS	28% 26%	17 14	15 58	55.5	8.18	27.7	8.75
135	125	KPYK_SCHPO	Pyruvate kinase	Q10208	MALDI-TOF-MS	21%	9	15	55.5	8.18	26.4	9.55
136	146	KPYK_SCHPO	Pyruvate kinase	Q10208	nanoLC-MS/MS	19%	8	82	55.5	8.18	43.3	5.54
137	75	MAOX_SCHPO	NAD-dependent malic enzyme	P40375	MALDI-TOF-MS nanoLC-MS/MS	30% 10%	21 7	19 40	62.5	5.68	32.7	4.64
138	89	MAOX_SCHPO	NAD-dependent malic enzyme	P40375	MALDI-TOF-MS nanoLC-MS/MS	29% 15%	23 8	12 40	62.5	5.68	33.1	5.30
139	117	MAOX_SCHPO	NAD-dependent malic enzyme	P40375	nanoLC-MS/MS	6%	3	96	62.5	5.68	26.3	8.07
140	218	MAOX_SCHPO	NAD-dependent malic enzyme	P40375	MALDI-TOF-MS nanoLC-MS/MS	43% 21%	29 13	14 48	62.5	5.68	56.1	5.74
141	219	MAOX_SCHPO	NAD-dependent malic enzyme	P40375	MALDI-TOF-MS	38%	27	16	62.5	5.68	50.6	5.83
142	229	MET3_SCHPO	Sulfate adenylyltransferase	P78937	MALDI-TOF-MS nanoLC-MS/MS	49% 16%	25 8	22 62	54.8	6.62	53.0	6.75
143	13	METE_SCHPO	Probable 5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase	Q9UT19	MALDI-TOF-MS	11%	8	21	85.3	5.99	16.4	5.33
144	233	METE_SCHPO	Probable 5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase	Q9UT19	MALDI-TOF-MS nanoLC-MS/MS	18% 18%	14 13	23 32	85.3	5.99	61.5	7.60

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
145	240	METE_SCHPO	Probable 5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	Q9UT19	nanoLC-MS/MS	15%	11	93	85.3	5.99	62.3	5.93
146	242	METE_SCHPO	Probable 5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	Q9UT19	nanoLC-MS/MS	7%	5	21	85.3	5.99	69.0	5.63
147	263	METE_SCHPO	Probable 5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	Q9UT19	MALDI-TOF-MS nanoLC-MS/MS	32% 17%	26 13	18 39	85.3	5.99	80.3	5.76
148	148	METK_SCHPO	S-adenosylmethionine synthetase	O60198	MALDI-TOF-MS	18%	8	26	41.8	5.70	40.3	5.64
149	160	METK_SCHPO	S-adenosylmethionine synthetase	O60198	nanoLC-MS/MS	14%	4	42	41.8	5.70	41.2	5.88
150	33	MLO3_SCHPO	Protein mlo3	Q09330	MALDI-TOF-MS nanoLC-MS/MS	74% 29%	18 5	15 96	21.8	10.21	20.5	4.00
151	15	MMF1_SCHPO	Protein mmf1, mitochondrial [Precursor]	O43003	MALDI-TOF-MS	67%	11	18	17.5	9.41	12.4	5.62
152	24	MPG1_SCHPO	Probable mannose-1-phosphate guanylyltransferase	O74484	nanoLC-MS/MS	7%	2	21	39.7	6.02	15.8	6.75
153	130	O42873_SCHPO	SPAC3G9.11c protein	O42873	MALDI-TOF-MS nanoLC-MS/MS	27% 26%	15 12	16 54	62.7	5.45	36.6	4.83
154	215	O42873_SCHPO	SPAC3G9.11c protein	O42873	nanoLC-MS/MS	15%	7	69	62.7	5.45	47.6	5.72
155	217	O42873_SCHPO	SPAC3G9.11c protein	O42873	MALDI-TOF-MS nanoLC-MS/MS	49% 22%	25 11	21 71	62.7	5.45	53.2	5.69
156	188	O42888_SCHPO	SPBC8E4.04 protein	O42888	MALDI-TOF-MS	48%	16	18	36.6	6.61	34.9	7.00
157	3	O74887_SCHPO	SPCC576.03c protein	O74887	nanoLC-MS/MS	23%	4	25	21.2	5.37	13.1	5.47
158	82	O74914_SCHPO	SPCC757.03c protein	O74914	MALDI-TOF-MS	39%	10	10	26.7	5.42	24.2	5.42
159	138	O74960_SCHPO	SPCC736.15 protein	O74960	MALDI-TOF-MS nanoLC-MS/MS	40% 32%	17 10	7 45	39.8	5.24	44.5	5.28
160	36	O94273_SCHPO	Peptidyl-prolyl cis-trans isomerase	O94273	MALDI-TOF-MS	52%	12	27	22.2	5.58	17.8	5.47
161	45	O94273_SCHPO	Peptidyl-prolyl cis-trans isomerase	O94273	MALDI-TOF-MS	61%	10	16	22.2	5.58	17.7	5.60
162	247	ODO2_SCHPO	Probable dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial [Precursor]	O94681	MALDI-TOF-MS	36%	16	20	49.0	7.55	58.9	5.54
163	191	ODPA_SCHPO	Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial [Precursor]	Q10489	nanoLC-MS/MS	43%	11	10	45.1	8.34	43.8	6.90
164	77	NACA_SCHPO	Putative nascent polypeptide-associated complex alpha subunit-like protein	P87147	MALDI-TOF-MS nanoLC-MS/MS	64% 72%	12 13	20 90	18.8	5.00	27.1	4.86
165	149	PDC2_SCHPO	Probable pyruvate decarboxylase C1F8.07c	Q92345	nanoLC-MS/MS	14%	7	23	64.8	5.71	42.7	5.65
166	157	PDX1_SCHPO	Probable pyridoxin biosynthesis PDX1-like protein	O14027	MALDI-TOF-MS	58%	30	17	31.4	5.92	33.7	5.82

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
167	37	PGK_SCHPO	C-terminal fragment of the phosphoglycerate kinase	O60101	MALDI-TOF-MS	21%	7	28	44.0	8.33	20.1	5.40
168	38	PGK_SCHPO	Phosphoglycerate kinase	P60101	MALDI-TOF-MS	41%	17	30	44.0	8.33	20.7	5.40
169	42	PGK_SCHPO	C-terminal fragment of the phosphoglycerate kinase	O60101	MALDI-TOF-MS	44%	19	21	44.0	8.33	22.5	5.61
170	43	PGK_SCHPO	C-terminal fragment of the phosphoglycerate kinase	O60101	MALDI-TOF-MS	43%	16	13	44.0	8.33	23.1	5.67
171	68	PGK_SCHPO	Phosphoglycerate kinase	O60101	nanoLC-MS/MS	25%	9	85	44.0	8.33	19.9	8.88
172	133	PGK_SCHPO	Phosphoglycerate kinase	O60101	MALDI-TOF-MS	36%	16	26	44.0	8.33	38.8	5.25
173	194	PGK_SCHPO	Phosphoglycerate kinase	O60101	MALDI-TOF-MS nanoLC-MS/MS	63% 56%	24 21	16 27	44.0	8.33	38.6	7.72
174	200	PGK_SCHPO	Phosphoglycerate kinase	O60101	MALDI-TOF-MS nanoLC-MS/MS	61% 60%	23 23	13 84	44.0	8.33	43.4	8.42
175	201	PGK_SCHPO	Phosphoglycerate kinase	O60101	MALDI-TOF-MS nanoLC-MS/MS	75% 63%	27 24	13 72	44.0	8.33	43.5	8.52
176	203	PGK_SCHPO	Phosphoglycerate kinase	O60101	MALDI-TOF-MS	76%	30	15	44.0	8.33	43.5	8.75
177	204	PGK_SCHPO	Phosphoglycerate kinase	O60101	MALDI-TOF-MS	41%	14	23	44.0	8.33	39.3	8.87
178	63	PIN1_SCHPO	Peptidyl-prolyl cis-trans isomerase pin1	O74448	nanoLC-MS/MS	16%	2	68	19.8	7.92	19.6	8.13
179	255	PLB1_SCHPO	Lysophospholipase 1 [Precursor]	P78854	MALDI-TOF-MS	14%	8	18	67.1	4.74	137.8	4.60
180	23	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS	47%	8	10	23.8	6.92	14.1	6.71
181	32	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS nanoLC-MS/MS	61% 55%	17 14	27 84	23.8	6.92	17.2	8.66
182	55	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS	51%	9	18	23.8	6.92	22.7	6.71
183	64	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS nanoLC-MS/MS	52% 55%	10 11	26 63	23.8	6.92	19.6	8.13
184	68	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS nanoLC-MS/MS	66% 56%	18 14	11 108	23.8	6.92	19.9	8.88
185	101	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS	56%	10	19	23.8	6.92	23.6	5.95
186	113	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS nanoLC-MS/MS	81% 45%	22 11	22 40	23.8	6.92	23.9	7.26
187	83	PMM_SCHPO	Phosphomannomutase	Q9UTJ2	nanoLC-MS/MS	12%	2	35	29.2	5.25	23.5	5.46
188	90	PNPP_SCHPO	4-nitrophenylphosphatase	Q00472	MALDI-TOF-MS	38%	10	8	32.8	5.58	33.0	5.55
189	220	Q9C0U6_SCHPO	SPCPJ732.02c protein	Q9C0U6	MALDI-TOF-MS nanoLC-MS/MS	23% 28%	12 15	9 77	61.7	5.77	57.3	5.87
190	202	Q9C1X5_SCHPO	SPAP32A8.02 protein	Q9C1X5	nanoLC-MS/MS	7%	2	49	31.8	5.79	43.4	8.65

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
191	67	Q9P7B4_SCHPO	SPAC521.03 protein	Q9P7B4	nanoLC-MS/MS	16%	4	122	28.1	6.01	19.8	8.65
192	101	Q9P7G7_SCHPO	Ssp1 protein [Fragment]	Q9P7G7	MALDI-TOF-MS	28%	6	24	25.1	5.81	23.6	5.95
193	33	RPA8_SCHPO	DNA-directed RNA polymerase I 17 kDa polypeptide	Q9P7P1	nanoLC-MS/MS	8%	2	56	17.0	6.23	20.5	4.00
194	108	Q9UT36_SCHPO	SPAC824.07 protein	Q9UT36	MALDI-TOF-MS	33%	7	20	28.5	6.41	27.8	6.80
195	122	SOU1_SCHPO	Sorbitol utilization protein sou1	Q9Y6Z9	nanoLC-MS/MS	20%	4	55	27.4	8.61	27.6	8.65
196	20	Q9Y7R8_SCHPO	SPCC306.08c protein	Q9Y7R8	MALDI-TOF-MS	27%	7	18	35.8	8.90	16.5	6.36
197	179	Q9Y7R8_SCHPO	SPCC306.08c protein	Q9Y7R8	nanoLC-MS/MS	14%	4	131	35.8	8.90	34.1	6.57
198	74	RAD24_SCHPO	DNA damage checkpoint protein rad24	P42656	MALDI-TOF-MS nanoLC-MS/MS	53% 56%	15 14	11 68	30.1	4.66	29.4	4.49
199	87	RAD24_SCHPO	DNA damage checkpoint protein rad24	P42656	nanoLC-MS/MS	23%	7	128	30.1	4.66	32.8	5.54
200	144	RAD24_SCHPO	DNA damage checkpoint protein rad24	P42656	nanoLC-MS/MS	30%	8	127	30.1	4.66	32.9	5.46
201	129	RAD25_SCHPO	DNA damage checkpoint protein rad25	P42657	nanoLC-MS/MS	45%	13	40	30.4	4.78	34.1	4.80
202	257	RAD25_SCHPO	DNA damage checkpoint protein rad25	P42657	nanoLC-MS/MS	16%	4	129	30.4	4.78	33.9	4.44
203	34	RL17A_SCHPO	60S ribosomal protein L17-A	O14339	MALDI-TOF-MS	51%	13	19	20.8	10.36	20.2	4.38
204	35	RL17B_SCHPO	60S ribosomal protein L17-B	O59794	MALDI-TOF-MS nanoLC-MS/MS	48% 26%	10 5	14 85	20.8	10.33	21.9	4.53
205	72	RL2_SCHPO	60S ribosomal protein L2	P08093	MALDI-TOF-MS	49%	12	20	27.1	10.86	29.4	4.23
206	9	RL31_SCHPO	60S ribosomal protein L31	Q9URX6	MALDI-TOF-MS	55%	9	13	13.3	10.24	14.1	3.80
207	11	RL36A_SCHPO	60S ribosomal protein L36-A	Q92365	MALDI-TOF-MS	61%	12	20	11.3	11.85	12.4	4.20
208	69	RL4A_SCHPO	60S ribosomal protein L4-A	P35679	nanoLC-MS/MS	28%	7	110	39.8	10.78	24.3	4.32
209	12	RL5A_SCHPO	60S ribosomal protein L5-A	P52822	MALDI-TOF-MS	30%	7	18	33.5	9.08	14.2	5.15
210	7	RL8_SCHPO	60S ribosomal protein L8	O13672	MALDI-TOF-MS	42%	13	30	28.5	10.35	16.3	4.20
211	3	RPE_SCHPO	Ribulose-phosphate 3-epimerase	O14105	nanoLC-MS/MS	11%	2	20	25.2	5.53	10.1	5.39
212	41	RPE_SCHPO	Ribulose-phosphate 3-epimerase	O14105	nanoLC-MS/MS	11%	2	35	25.2	5.53	23.4	5.55
213	127	RS0B_SCHPO	40S ribosomal protein S0-B	Q9P546	nanoLC-MS/MS	11%	3	115	31.4	4.95	35.2	4.18
214	131	RS0B_SCHPO	40S ribosomal protein S0-B	Q9P546	MALDI-TOF-MS nanoLC-MS/MS	32% 32%	11 9	6 53	31.4	4.95	36.3	4.99

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
215	7	RS11_SCHPO	40S ribosomal protein S11	P79013	MALDI-TOF-MS	67%	12	30	17.5	10.37	15.1	4.16
216	10	RS19A_SCHPO	40S ribosomal protein S19-A	P58234	MALDI-TOF-MS	53%	13	25	16.2	9.71	9.4	4.15
217	8	RS23_SCHPO	40S ribosomal protein S23	P79057	MALDI-TOF-MS	62%	9	25	15.7	10.32	11.9	4.14
218	8	RS24A_SCHPO	40S ribosomal protein S24-A	O13784	MALDI-TOF-MS	60%	11	14	15.3	10.93	11.9	4.14
219	8	RS24B_SCHPO	40S ribosomal protein S24-B	O59865	MALDI-TOF-MS	62%	13	27	15.4	10.92	11.9	4.14
220	37	RS5A_SCHPO	40S ribosomal protein S5-A	O14277	MALDI-TOF-MS	31%	6	14	22.2	9.91	20.1	5.34
221	69	RS6B_SCHPO	40S ribosomal protein S6-B	Q9C0Z7	nanoLC-MS/MS	41%	7	109	27.5	10.77	26.9	4.20
222	109	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS	76%	20	20	23.8	6.92	23.8	6.92
223	49	SAHH_SCHPO	Adenosylhomocysteinase	O13639	MALDI-TOF-MS	13%	6	24	47.4	5.61	22.7	5.89
224	150	SAHH_SCHPO	Adenosylhomocysteinase	O13639	MALDI-TOF-MS nanoLC-MS/MS	43% 7%	19 3	9 45	47.4	5.61	43.5	5.65
225	19	SODC_SCHPO	Superoxide dismutase [Cu-Zn]	P28758	MALDI-TOF-MS	68%	6	27	15.9	5.80	14.9	6.03
226	60	SODM_SCHPO	Superoxide dismutase [Mn], mitochondrial [Precursor]	Q9UQX0	MALDI-TOF-MS nanoLC-MS/MS	59% 24%	9 4	9 39	24.3	9.12	21.5	7.33
227	62	SODM_SCHPO	Superoxide dismutase [Mn], mitochondrial [Precursor]	Q9UQX0	MALDI-TOF-MS nanoLC-MS/MS	77% 40%	12 9	22 37	24.3	9.12	21.6	7.66
228	209	TBA1_SCHPO	Tubulin alpha-1 chain	P04688	MALDI-TOF-MS	27%	12	15	51.2	4.97	55.9	5.17
229	190	TKT_SCHPO	Probable transketolase	Q9URM2	nanoLC-MS/MS	14%	2	39	75.2	6.33	43.1	6.89
230	191	TKT_SCHPO	C-terminal fragment of the probable transketolase	Q9URM2	MALDI-TOF-MS nanoLC-MS/MS	40% 31%	19 16	9 12	75.2	6.33	43.8	6.90
231	237	TKT_SCHPO	Probable transketolase	Q9URM2	MALDI-TOF-MS	46%	30	21	75.2	6.33	72.0	6.62
232	238	TKT_SCHPO	Probable transketolase	Q9URM2	MALDI-TOF-MS nanoLC-MS/MS	47% 30%	35 17	15 26	75.2	6.33	71.7	6.51
233	155	TOM40_SCHPO	Probable mitochondrial import Receptor subunit tom40	O13656	MALDI-TOF-MS	37%	13	17	37.6	5.90	36.2	5.78
234	81	TPIS_SCHPO	Triosephosphate isomerase	P07669	MALDI-TOF-MS	68%	13	20	27.1	6.61	25.7	5.34
235	104	TPIS_SCHPO	Triosephosphate isomerase	P07669	nanoLC-MS/MS	17%	3	61	27.1	6.61	25.2	6.64
236	110	TPIS_SCHPO	Triosephosphate isomerase	P07669	MALDI-TOF-MS	93%	22	17	27.1	6.61	25.5	7.08
237	111	TPIS_SCHPO	Triosephosphate isomerase	P07669	MALDI-TOF-MS	77%	19	18	27.1	6.61	24.7	7.22
238	179	TPIS_SCHPO	Triosephosphate isomerase	P07669	MALDI-TOF-MS nanoLC-MS/MS	80% 47%	17 12	19 145	27.1	6.61	34.1	6.57

Supplementary material 1. continued

Protein No.	SSP	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
239	35	TPM_SCHPO	Tropomyosin	Q02088	MALDI-TOF-MS nanoLC-MS/MS	86% 45%	18 8	30 102	19.0	4.63	21.9	4.53
240	21	UBC4_SCHPO	Ubiquitin-conjugating enzyme E2 4	P46595	MALDI-TOF-MS nanoLC-MS/MS	47% 38%	6 3	20 35	16.5	6.40	13.9	6.50
241	22	UBC13_SCHPO	Ubiquitin-conjugating enzyme E2 13	O13685	nanoLC-MS/MS	22%	3	64	16.9	6.74	14.2	6.57
242	232	UGPA1_SCHPO	Probable UTP--glucose-1-phosphate uridylyltransferase	P78811	MALDI-TOF-MS nanoLC-MS/MS	25% 12%	13 6	22 36	56.4	7.04	56.6	7.49
243	264	UREA_SCHPO	Urease	O00084	MALDI-TOF-MS nanoLC-MS/MS	17% 17%	13 11	15 45	91.2	5.56	102.1	5.62
244	207	VATB_SCHPO	Vacuolar ATP synthase subunit B	P31411	MALDI-TOF-MS nanoLC-MS/MS	64% 25%	29 13	14 49	55.8	5.19	52.5	5.19
245	114	VDAC_SCHPO	Probable outer mitochondrial membrane protein porin	Q9P544	MALDI-TOF-MS nanoLC-MS/MS	78% 13%	13 4	28 32	29.6	7.10	28.7	7.82
246	257	VIP1_SCHPO	Protein vip1	P87216	MALDI-TOF-MS	69%	16	25	27.5	5.54	33.9	4.44
247	99	YA03_SCHPO	Hypothetical protein C5H10.03 in chromosome I	Q09676	MALDI-TOF-MS	74%	15	12	24.7	5.77	25.7	5.89
248	76	YA14_SCHPO	Hypothetical protein C13C5.04 in chromosome I	Q09686	MALDI-TOF-MS	64%	17	12	28.0	5.05	28.6	5.01
249	142	YD25_SCHPO	Hypothetical protein C56F8.05c in chromosome I	Q10253	MALDI-TOF-MS	57%	19	18	32.7	5.55	34.1	5.51
250	197	YDG7_SCHPO	Probable oxidoreductase C26F1.07 in chromosome I	Q10494	MALDI-TOF-MS nanoLC-MS/MS	73% 55%	21 16	13 74	36.2	7.78	37.8	8.00
251	139	YEAH_SCHPO	Hypothetical protein UNK4.17 in chromosome I	O14082	MALDI-TOF-MS	59%	23	17	45.6	5.31	44.1	5.35
252	153	YEPE_SCHPO	Hypothetical protein C23H3.15C in chromosome I	P78890	MALDI-TOF-MS	64%	16	18	34.7	5.86	38.9	5.75
253	57	YEPF_SCHPO	Hypothetical protein C23H3.15C in chromosome I	P78890	MALDI-TOF-MS	31%	8	19	34.7	5.86	22.0	6.91
254	88	YEPF_SCHPO	Hypothetical protein C23H3.15C in chromosome I	P78890	MALDI-TOF-MS nanoLC-MS/MS	40% 23%	9 5	15 70	34.7	5.86	33.1	5.14
255	158	YEPF_SCHPO	Hypothetical protein C23H3.15C in chromosome I	P78890	MALDI-TOF-MS	74%	22	19	34.7	5.86	39.5	5.88
256	102	YGK3_SCHPO	Hypothetical protein C725.03 in chromosome II	O94322	MALDI-TOF-MS nanoLC-MS/MS	82% 30%	19 7	18 94	29.3	6.11	26.8	6.20
257	44	YHZ8_SCHPO	Hypothetical protein SPBC21B10.08c in chromosome II	P78833	MALDI-TOF-MS	64%	9	15	21.8	5.65	21.4	5.67
258	83	YHZ8_SCHPO	Hypothetical protein SPBC21B10.08c in chromosome II	P78833	nanoLC-MS/MS	67%	7	30	21.8	5.65	23.5	5.46
259	26	YJO6_SCHPO	Very hypothetical protein PB16A4.06c in chromosome III	Q96WU9	MALDI-TOF-MS	50%	6	11	14.4	7.87	17.3	6.83
260	149		Hypothetical protein SPBC16E9.16c		MALDI-TOF-MS	17%	12	24	74.1	6.41	42.7	5.65
261	265		Hypothetical protein SPBC16E9.16c		MALDI-TOF-MS	27%	19	26	74.1	6.41	42.3	5.55

- a) Entry name and accession number according to Swiss-Prot (<http://kr.expasy.org/sprot/>)
b) Amino acid sequence coverage for the identified proteins
c) Number of matching peptides according to the MASCOT™ search engine
d) Error in ppm according to the MASCOT™ search engine
e) Theoretical *Mr* and *pI* according to protein sequence and Swiss 2-D PAGE database
f) Gel-estimated *Mr* and *pI* calculated by analysis of the gel images with PDQuest 7.2.0 software

Supplementary material 2. List of identified *S. pombe* proteins by MALDI-TOF-MS and/or nanoLC-MS/MS (in both 3-10 *pI* and 4-7 *pI* ranges)

Protein No.	SSP		Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
	(<i>pI</i> 3-10 & 4-7)	Entry Name ^{a)}							MW (kDa)	<i>pI</i>	MW (kDa)	<i>pI</i>
262	136 364	ACT_SCHPO	Actin	P10989	nanoLC-MS/MS MALDI-TOF-MS	45%	13	45	41.8	5.31	41.7	5.31
						57%	21	12				
263	187 341	ADH_SCHPO	Alcohol dehydrogenase	P00332	MALDI-TOF-MS	59%	17	13	37.4	6.46	37.9	6.76
264	94 334	ADH_SCHPO	Alcohol dehydrogenase	P00332	MALDI-TOF-MS	44%	17	20	37.4	6.46	32.5	5.77
265	49 321	ADH_SCHPO	Alcohol dehydrogenase	P00332	MALDI-TOF-MS	27%	6	6	37.4	6.46	22.4	5.87
266	133 366	ADK_SCHPO	Adenosine kinase	P78825	MALDI-TOF-MS	46%	13	15	36.7	5.26	38.8	5.25
267	156 359	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	39%	12	23	39.6	5.92	35.2	5.79
268	81 331	ALF_SCHPO	N-terminal fragment of the fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	60%	17	8	39.6	5.92	25.7	5.34
269	165 352	ALF_SCHPO	Fructose-bisphosphate aldolase	P36580	MALDI-TOF-MS	76%	18	17	39.6	5.92	39.4	6.19
270	48 322	ATPF_SCHPO	ATP synthase subunit 4. mitochondrial [Precursor]	O94373	MALDI-TOF-MS	51%	14	21	26.7	8.65	22.4	5.83
271	230 388	CATA_SCHPO	Catalase	P55306	MALDI-TOF-MS	64%	33	28	58.3	6.39	55.5	6.79
272	257 370	CLC1_SCHPO	Clathrin light chain	Q9USP6	MALDI-TOF-MS nanoLC-MS/MS	30%	7	6	25.9	4.61	33.9	4.44
						44%	9	126				
273	3 303	COFI_SCHPO	Cofilin	P78929	MALDI-TOF-MS nanoLC-MS/MS	67%	10	26	15.6	5.60	13.1	5.47
						60%	8	13				
274	17 307	COFI_SCHPO	Cofilin	P78929	Nano-LC-MS/MS	42%	4	106	15.6	5.60	13.6	5.79
275	240 391	DAK1_SCHPO	Dihydroxyacetone kinase 1	O13902	MALDI-TOF-MS nanoLC-MS/MS	29%	16	12	62.3	5.93	62.3	5.93
						51%	30	81				
276	173 349	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	42%	16	13	47.4	6.23	37.5	6.41
277	227 386	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS nanoLC-MS/MS	68%	33	13	47.4	6.23	47.3	6.67
						50%	31	96				
278	226 385	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	58%	23	17	47.4	6.23	47.8	6.36
279	224 383	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	51%	22	13	47.4	6.23	49.0	6.04
280	135 365	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	45%	19	10	47.4	6.23	38.1	5.37
281	54 317	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	33%	11	7	47.4	6.23	22.9	6.61
282	176 346	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	38%	16	9	47.4	6.23	36.9	6.54
283	225 384	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	48%	19	7	47.4	6.23	47.8	6.12
284	174 348	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	42%	17	18	47.4	6.23	36.8	6.44
285	223 382	ENO11_SCHPO	Enolase 1-1	P40370	MALDI-TOF-MS	57%	21	12	47.4	6.23	48.0	5.99

Supplementary material 2. continued

Protein No.	SSP		Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
	(pI 3-10 & 4-7)	Entry Name ^{a)}							MW (kDa)	pI	MW (kDa)	pI
286	258 387	ENO11_SCHPO	Enolase 1-1	P40370	nanoLC-MS/MS MALDI-TOF-MS	19% 38%	7 14	98 15	47.4	6.23	58.6	6.83
287	216 381	ENO12_SCHPO	Enolase 1-2	Q8NKC2	MALDI-TOF-MS	60%	25	13	47.9	5.73	46.8	5.81
288	215 380	ENO12_SCHPO	Enolase 1-2	Q8NKC2	MALDI-TOF-MS nanoLC-MS/MS	64% 52%	28 21	27 60	47.9	5.73	47.6	5.72
289	182 343	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	72%	24	15	35.9	6.24	36.4	6.80
290	56 315	G3P1_SCHPO	C-terminal fragment of the glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	40%	16	18	35.9	6.24	20.5	6.75
291	141 368	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	59%	19	17	35.9	6.24	34.0	5.45
292	175 347	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	62%	18	13	35.9	6.24	36.9	6.49
293	55 316	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	40%	14	16	35.9	6.24	22.7	6.71
294	96 335	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	59%	20	20	35.9	6.24	31.0	5.88
295	185 342	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	37%	7	19	35.9	6.24	37.1	6.77
296	155 358	G3P1_SCHPO	Glyceraldehyde 3-phosphate dehydrogenase 1	P78958	MALDI-TOF-MS	30%	8	13	35.9	6.24	36.2	5.78
297	140 362	GBLP_SCHPO	Guanine nucleotide-binding protein beta subunit-like protein	Q10281	nanoLC-MS/MS MALDI-TOF-MS	69% 95%	20 23	31 23	34.9	5.43	35.6	5.53
298	83 325	GRPE_SCHPO	GrpE protein homolog. mitochondrial [Precursor]	O43047	MALDI-TOF-MS	26%	5	13	25.3	7.73	23.5	5.46
299	4 304	HSP16_SCHPO	Heat shock protein 16	O14368	nanoLC-MS/MS MALDI-TOF-MS	75% 89%	24 14	39 19	16.0	5.72	14.9	5.59
300	2 302	HSP16_SCHPO	Heat shock protein 16	O14368	MALDI-TOF-MS	87%	14	24	16.0	5.72	14.7	5.36
301	248 374	HSP60_SCHPO	Heat shock protein 60. mitochondrial [Precursor]	Q09864	MALDI-TOF-MS nanoLC-MS/MS	64% 34%	36 17	12 77	62.2	5.76	59.3	5.35
302	246 377	HSP72_SCHPO	Probable heat shock protein ssa2	O59855	MALDI-TOF-MS	26%	13	23	70.1	5.13	58.2	5.56
303	242 393	HSP75_SCHPO	Heat shock protein sks2	Q10284	MALDI-TOF-MS	22%	12	29	67.2	5.82	69.0	5.63
304	37 327	HSP75_SCHPO	N-terminal fragment of the heat Shock protein sks2	Q10284	MALDI-TOF-MS	12%	7	17	67.2	5.82	20.1	5.40
305	82 332	HSP75_SCHPO	Heat shock protein sks2	Q10284	MALDI-TOF-MS	18%	9	14	67.2	5.82	24.2	5.42
306	15 306	ILV5_SCHPO	C terminal fragment of the probable ketol-acid reductoisomerase. mitochondrial [Precursor]	P78827	MALDI-TOF-MS	32%	13	26	45.2	9.47	12.4	5.62
307	132 367	IPYR_SCHPO	Inorganic pyrophosphatase	P19117	MALDI-TOF-MS nanoLC-MS/MS	60% 42%	20 15	14 59	32.3	5.20	34.9	5.16
308	51 320	KAPS_SCHPO	Adenylyl-sulfate kinase	Q9P7G9	MALDI-TOF-MS	51%	9	18	22.7	6.23	22.6	6.11

Supplementary material 2. continued

Protein No.	SSP (pI 3-10 & 4-7)	Entry Name ^{a)}	Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
									MW (kDa)	pI	MW (kDa)	pI
309	169 353	O13702_SCHPO	SPAC13F5.03c protein	O13702	MALDI-TOF-MS	57%	25	17	49.4	7.23	41.3	6.28
310	143 363	O13702_SCHPO	SPAC13F5.03c protein	O13702	MALDI-TOF-MS	34%	12	13	49.4	7.23	42.2	5.50
311	170 354	O13702_SCHPO	SPAC13F5.03c protein	O13702	MALDI-TOF-MS	53%	22	16	49.4	7.23	42.0	6.23
312	128 371	O42932_SCHPO	Qcr6 protein	O42932	MALDI-TOF-MS	55%	20	16	24.3	4.41	35.8	4.21
313	151 379	O59711_SCHPO	SPBC3B8.03 protein	O59711	MALDI-TOF-MS	39%	17	13	49.9	5.41	46.7	5.56
314	39 326	O74887_SCHPO	SPCC576.03c protein	O74887	nanoLC-MS/MS MALDI-TOF-MS	50% 72%	13 11	31 9	21.2	5.37	21.3	5.36
315	16 308	O74887_SCHPO	SPCC576.03c protein	O74887	MALDI-TOF-MS	27%	5	11	21.2	5.37	12.8	5.76
316	52 319	P25_SCHPO	P25 protein	P30821	MALDI-TOF-MS	58%	10	27	21.9	6.29	20.4	6.30
317	69 329	NACA_SCHPO	Putative nascent polypeptide-associated complex alpha subunit-like protein	P87147	nanoLC-MS/MS	25%	6	96	18.8	5.00	24.3	4.32
318	24 312	PDC2_SCHPO	Probable pyruvate decarboxylase C1F8.07c	Q92345	nanoLC-MS/MS	15%	12	31	64.8	5.71	15.8	6.75
319	97 336	PDX1_SCHPO	Probable pyridoxin biosynthesis PDX1-like protein	O14027	MALDI-TOF-MS	40%	17	7	31.4	5.92	30.8	5.96
320	256 396	PLB1_SCHPO	Lysophospholipase 1 [Precursor]	P78854	nanoLC-MS/MS	25%	13	32	67.1	4.74	145.9	4.50
321	109 314	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS	83%	23	10	23.8	6.92	23.8	6.92
322	53 318	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS	80%	19	18	23.8	6.92	22.5	6.49
323	22 311	PMGY_SCHPO	Phosphoglycerate mutase	P36623	MALDI-TOF-MS nanoLC-MS/MS	50% 51%	11 10	11 61	23.8	6.92	14.2	6.57
324	1 301	PMP20_SCHPO	Putative peroxiredoxin pmp20	O14313	MALDI-TOF-MS nanoLC-MS/MS	87% 62%	10 10	20 29	16.7	5.18	15.8	5.37
325	254 395	Q9USU5_SCHPO	SPBC29A10.08 protein	Q9USU5	MALDI-TOF-MS	19%	9	21	50.6	5.32	145.0	5.35
326	102 337	Q9UT63_SCHPO	SPAC513.02 protein	Q9UT63	MALDI-TOF-MS	44%	9	17	25.2	5.94	26.8	6.20
327	57 313	SERC_SCHPO	Putative phosphoserine aminotransferase	Q10349	MALDI-TOF-MS	17%	5	19	42.8	6.02	22.6	6.91
328	5 309	SODC_SCHPO	Superoxide dismutase [Cu-Zn]	P28758	nanoLC-MS/MS MALDI-TOF-MS	62% 90%	11 8	22 16	15.9	5.80	14.5	5.93
329	87 333	SPEE_SCHPO	Spermidine synthase	Q09741	nanoLC-MS/MS	8%	4	88	33.1	5.49	32.8	5.54
330	243 394	STI1_SCHPO	Heat shock protein sti1 homolog	Q9USI5	MALDI-TOF-MS nanoLC-MS/MS	17% 15%	8 9	9 138	65.5	5.42	67.8	5.57
331	106 338	TPIS_SCHPO	Triosephosphate isomerase	P07669	MALDI-TOF-MS	82%	23	17	27.1	6.61	24.8	6.77
332	70 330	TPIS_SCHPO	Triosephosphate isomerase	P07669	MALDI-TOF-MS	50%	8	12	27.1	6.61	24.7	4.55

Supplementary material 2. continued

Protein No.	SSP		Protein Name	Swiss-Prot Accession Number ^{a)}	identified by	Sequence coverage ^{b)}	Number of peptides ^{c)}	Error in ppm ^{d)}	Theoretical ^{e)}		Gel-estimated ^{f)}	
	(p/ 3-10 & 4-7)	Entry Name ^{a)}							MW (kDa)	pI	MW (kDa)	pI
333	41 324	UCRI_SCHPO	Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial [Precursor]	Q09154	MALDI-TOF-MS nanoLC-MS/MS	25% 15%	6 2	17 30	24.7	8.32	23.1	5.52
334	144 369	VIP1_SCHPO	Protein vip1	P87216	MALDI-TOF-MS nanoLC-MS/MS	69% 38%	15 9	11 131	27.5	5.54	32.9	5.46
335	87 333	VIP1_SCHPO	Protein vip1	P87216	MALDI-TOF-MS nanoLC-MS/MS	74% 37%	15 8	18 135	27.5	5.54	32.8	5.54
336	71 328	YAAB_SCHPO	Hypothetical protein C22G7.11c in chromosome I	Q09802	MALDI-TOF-MS nanoLC-MS/MS	56% 27%	9 6	22 92	15.4	4.24	26.1	4.19
337	127 372	YBI8_SCHPO	Protein C16A3.08c in chromosome II	O42914	MALDI-TOF-MS nanoLC-MS/MS	48% 30%	19 10	10 120	30.9	10.14	35.2	4.18
338	14 305	YBL5_SCHPO	Hypothetical protein C106.05c in chromosome II	Q9URV6	MALDI-TOF-MS	65%	7	11	11.2	5.77	12.1	5.56
339	236 389	YDGE_SCHPO	Putative flavoprotein C26F1.14C.	Q10499	MALDI-TOF-MS nanoLC-MS/MS	62% 40%	31 15	15 96	62.1	6.20	61.4	6.50
340	160 360	YEPF_SCHPO	Hypothetical protein C23H3.15c in chromosome I	P78890	MALDI-TOF-MS nanoLC-MS/MS	91% 36%	28 11	20 33	34.7	5.86	41.2	5.88
341	42 323	YHZ8_SCHPO	Hypothetical protein SPBC21B10.08c in chromosome II	P78833	MALDI-TOF-MS	78%	13	18	21.8	5.65	22.5	5.61

- a) Entry name and accession number according to Swiss-Prot (<http://kr.expasy.org/sprot/>)
b) Amino acid sequence coverage for the identified proteins
c) Number of matching peptides according to the MASCOT™ search engine
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f) Gel-estimated *Mr* and *pI* calculated by analysis of the gel images with PDQuest 7.2.0 software