

SUPPORTING INFORMATION

Characterization of Lipids and Proteins Associated to the Cell Wall of the Acapsular Mutant *Cryptococcus neoformans* Cap 67 by Larissa V. G. Longo, Ernesto S. Nakayasu, Jhon H. S. Pires, Felipe Gazos-Lopes, Milene C. Vallejo, Tiago J. P. Sobreira, Igor C. Almeida, & Rosana Puccia

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Fig. S1. Tandem-MS spectrum of C16:0/C18:2-PC (Li⁺ adduct) identified in the positive-ion mode. Fragmentation was performed by total-ion mapping (TIM) using PQD and spectra were analyzed manually. ChoP, phosphatidylcholine; Me₃N, trimethylamine. Assigned peaks are indicated. *m/z*, mass to charge ratio.

Fig. S2. Tandem-MS spectrum of C16:0/C18:2-PC (HCOO⁻ adduct) identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. Me, methyl. Assigned peaks are indicated.

Fig. S3. Tandem-MS spectrum of C16:0/C18:1-PE identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. GroP, glycerophosphate. Assigned peaks are indicated.

Fig. S4. Tandem-MS spectrum of C16:0/C18:2-PS identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. GroP, glycerophosphate; Ser, serine. Assigned peaks are indicated.

Fig. S5. Tandem-MS spectrum of C16:0/C18:1-PI identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. GroP, glycerophosphate; Ins, *myo*-inositol. Assigned peaks are indicated.

Fig. S6. Tandem-MS spectrum of C16:0/C18:2-PA identified in the negative-ion mode. Fragmentation was performed by total-ion mapping using PQD and spectra were analyzed manually. GroP, glycerophosphate. Assigned peaks are indicated.

Fig. S7. Tandem-MS spectrum of the glycolipid Hex-C18:1-OH/d19:2-Cer identified at *m/z* 874.7. Fragmentation was performed in the positive-ion mode by total-ion mapping using PQD and spectra were analyzed manually. Assigned peaks are indicated.

Table S1. Cell wall-associated proteins identified in *C. neoformans* cap 67. The proteins are organized according to GO functions. Orthologs previously reported in cell wall (CW) or extracellular vesicles (EV) from *H. capsulatum* (Hc), *P. brasiliensis* (Pb), *S. cerevisiae* (Sc), *C. albicans* (Ca), and *A. fumigatus* (Af) are indicated. Proteins were classified by the Fungal Secretome Database (FSD) into SP (containing signal peptide as identified by SignalP 3.0); SP3 (bearing signal peptide predicted by SigPred, SigCleave or RPSP); SL (subcellular localization predicted by PSort II and/or Target 1.1b); NS (nonclassical secretion, predicted by SecretomeP 1.0f); and not classified as secretory (-).

These files are included in the following pages of this document.

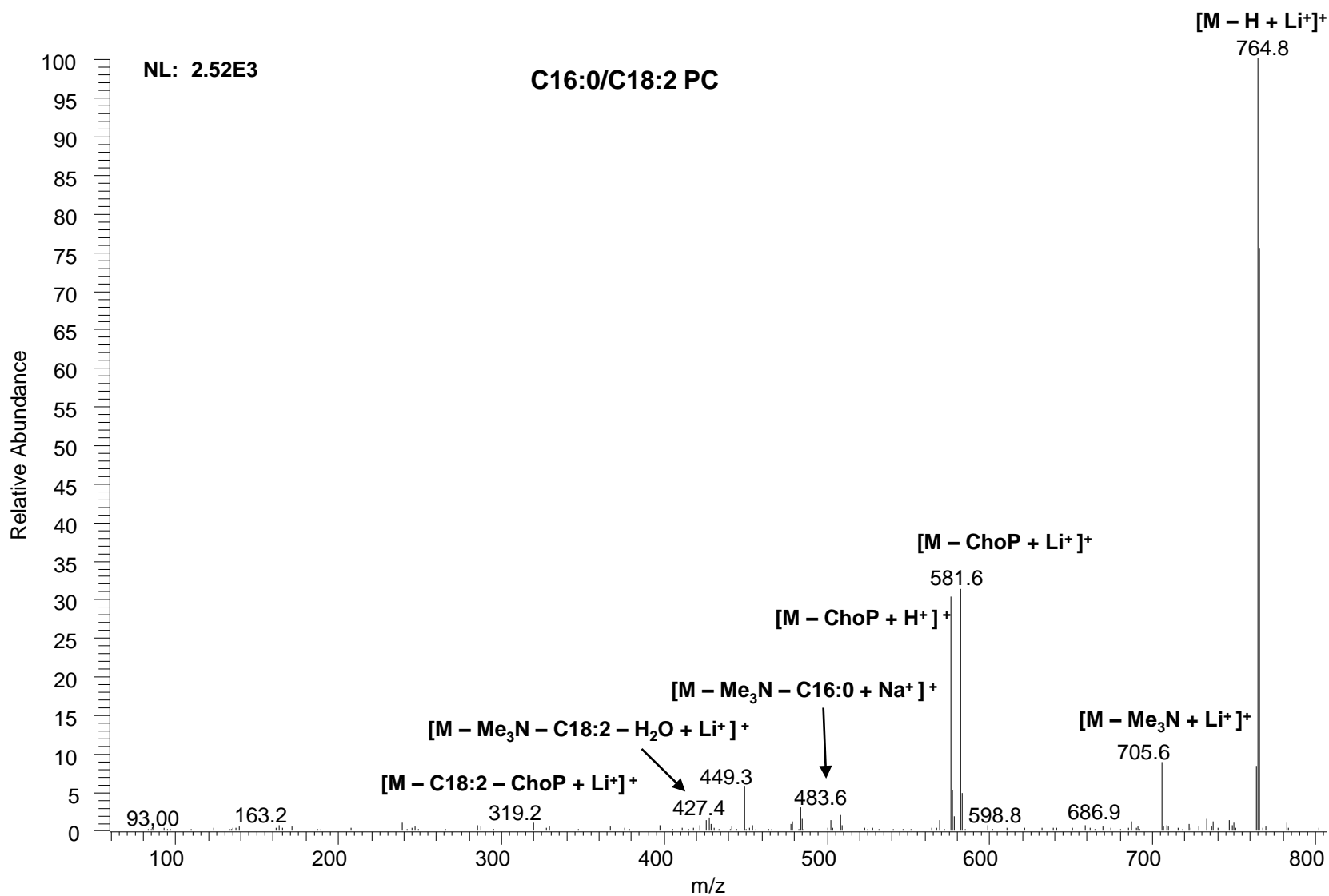


Figure S1 - Tandem-MS spectrum of C16:0/C18:2-PC (Li^+ adduct) identified in the positive-ion mode. Fragmentation was performed by total-ion mapping (TIM) using PQD and spectra were analyzed manually. ChoP, phosphatidylcholine; Me_3N , trimethylamine. Assigned peaks are indicated. m/z , mass to charge ratio.

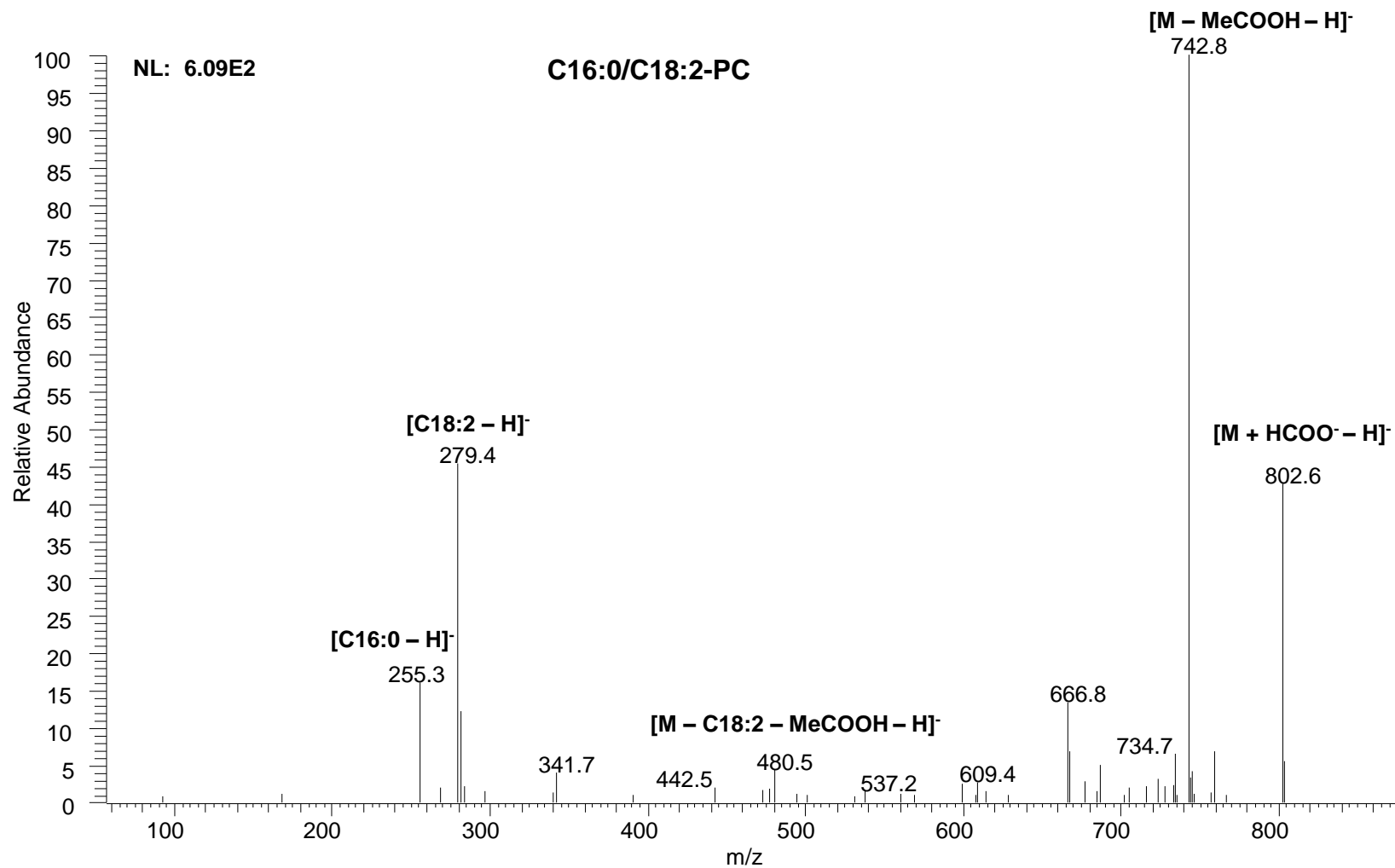


Figure S2 - Tandem-MS spectrum of C16:0/C18:2-PC (HCOO⁻ adduct) identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. Me, methyl. Assigned peaks are indicated.

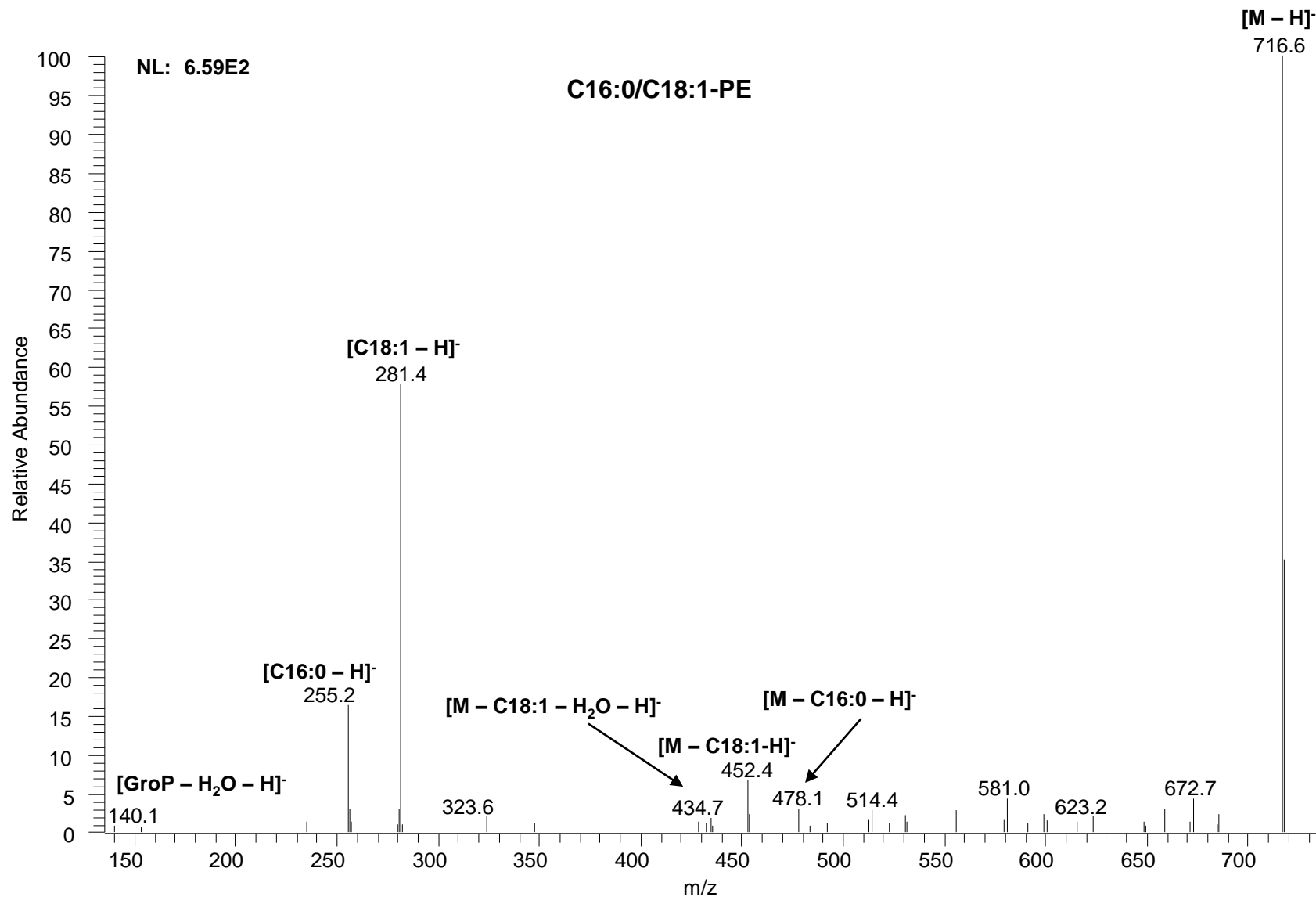


Figure S3 - Tandem-MS spectrum of C16:0/C18:1-PE identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. GroP, glycerophosphate. Assigned peaks are indicated.

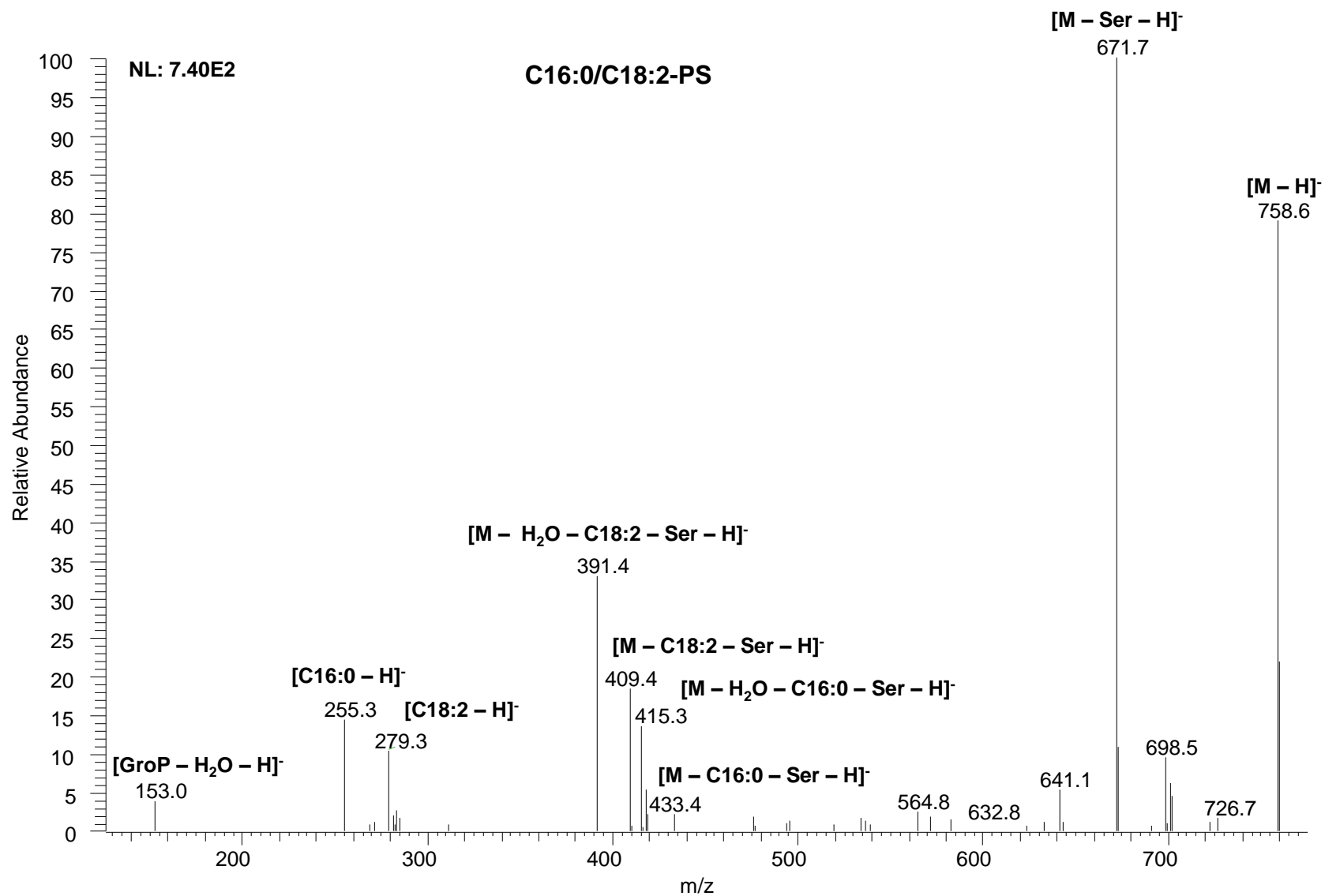


Figure S4 - Tandem-MS spectrum of C16:0/C18:2-PS identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. GroP, glycerophosphate; Ser, serine. Assigned peaks are indicated.

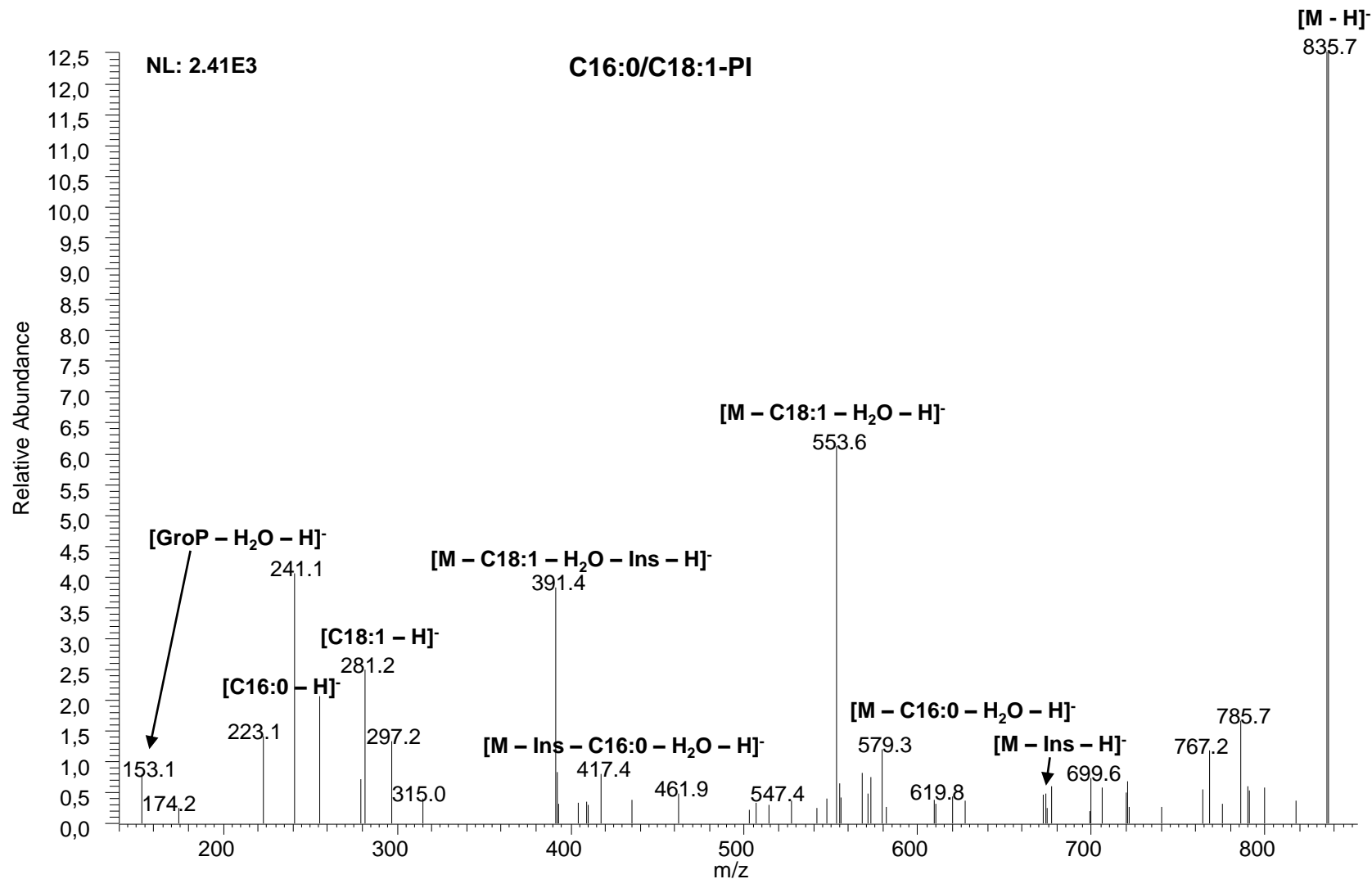


Figure S5 - Tandem-MS spectrum of C16:0/C18:1-PI identified in the negative-ion mode. Fragmentation was performed by TIM using PQD and spectra were analyzed manually. GroP, glycerophosphate; Ins, inositol. Assigned peaks are indicated.

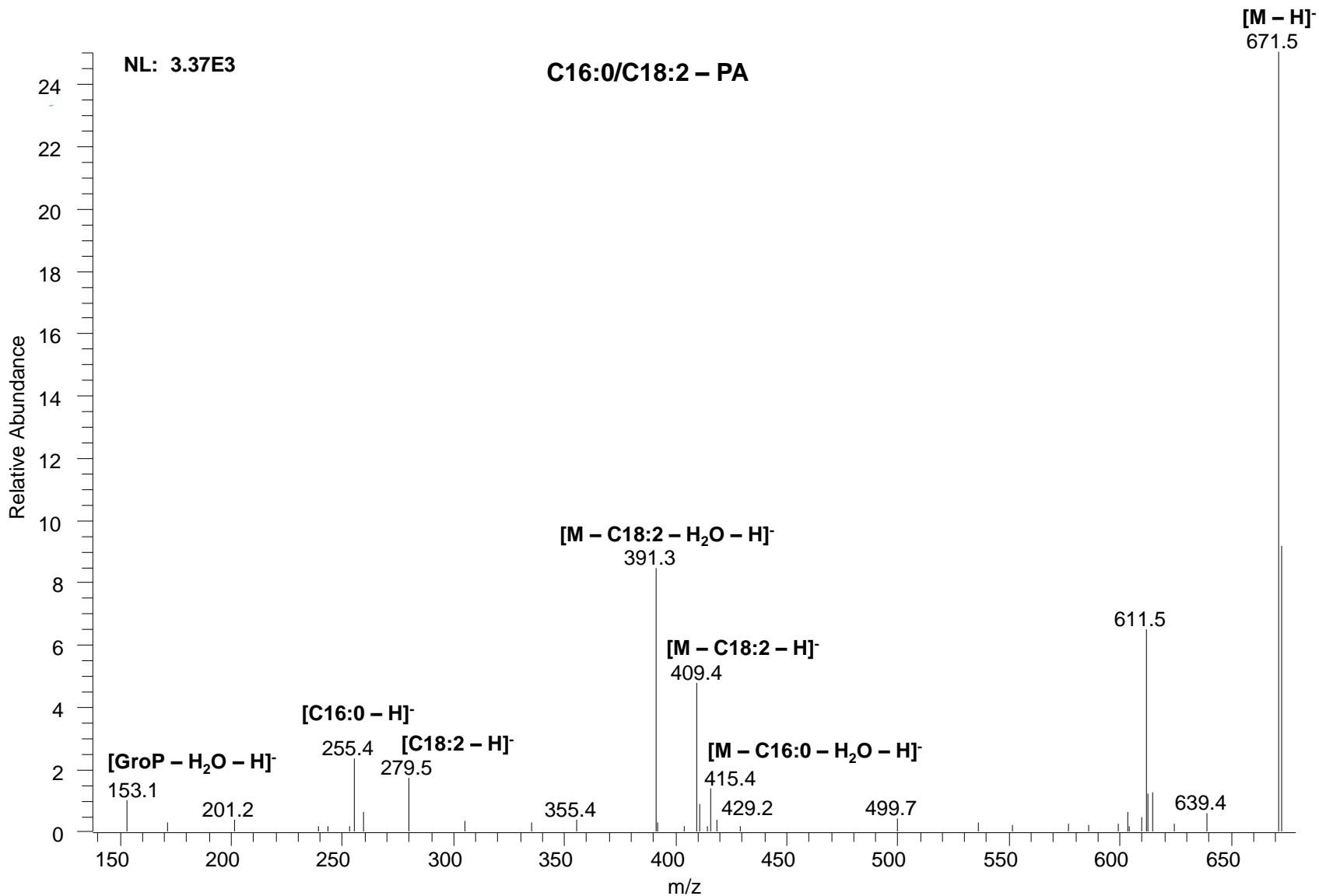


Figure S6 - Tandem-MS spectrum of C16:0/C18:2-PA identified in the negative-ion mode. Fragmentation was performed by total-ion mapping using PQD and spectra were analyzed manually. GroP, glycerophosphate. Assigned peaks are indicated.

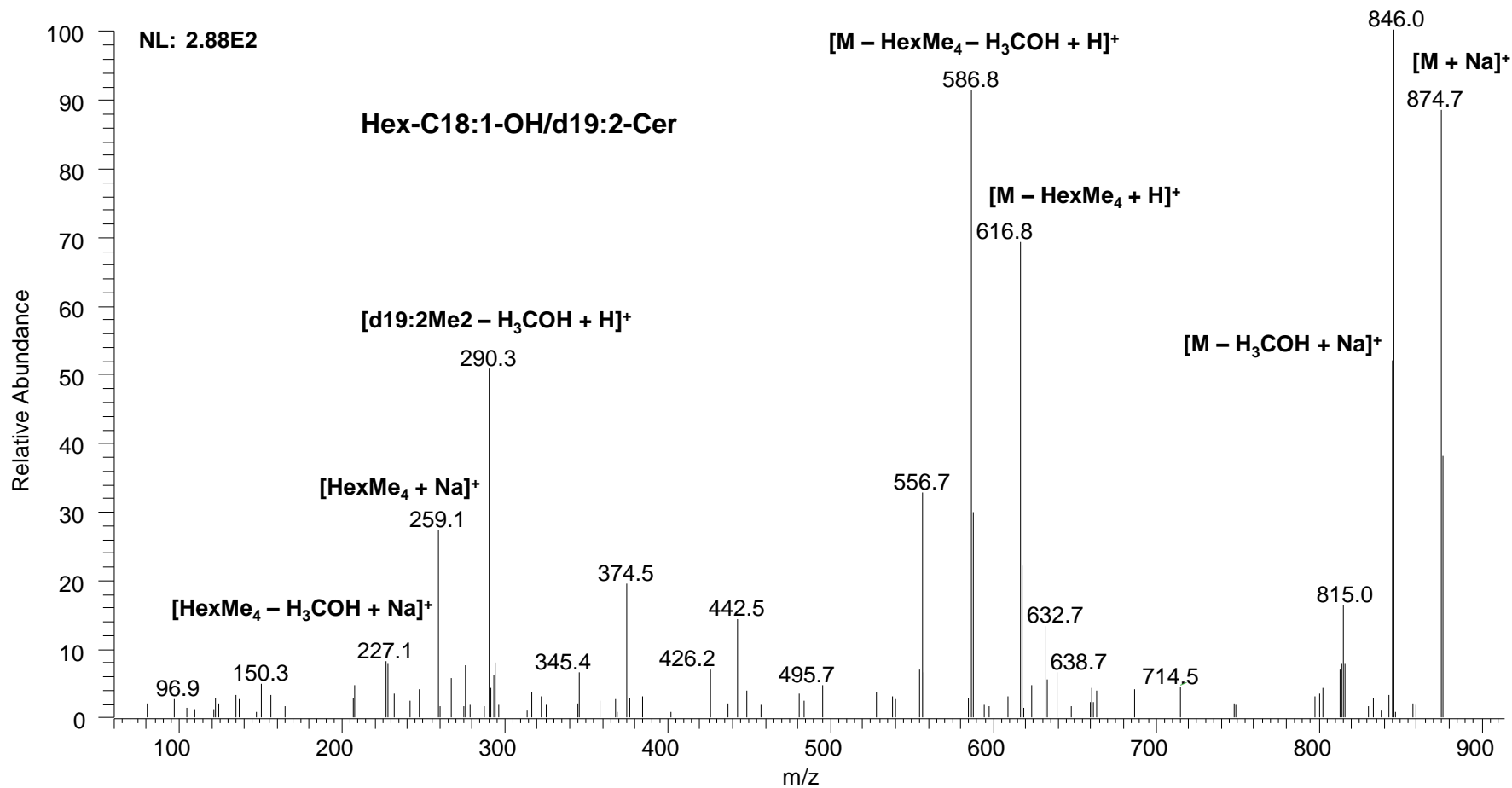


Figure S7 - Tandem-MS spectrum of the glycolipid Hex-C18:1-OH/d19:2-Cer identified at m/z 874.7. Fragmentation was performed in the positive-ion mode by total-ion mapping using PQD and spectra were analyzed manually. Assigned peaks are indicated.

FSD	Access number	Protein name	CW	CW protein code	CW reference	EV	EV reference	EV protein code
Transport								
NS	CNAG_02817	GTP-binding protein vpt2	-	-	-	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_06999, PADG_00282, YFL005W
-	CNAG_02974	voltage-dependent anion channel protein 2	Af	Q4WNT7	7	Cn	14, 15	-
-	CNAG_04851	transitional endoplasmic reticulum ATPase	Ca Pb	CA3333, PABG_05022	3, 9, 10	Hc Sc	11, 13	HCAG_02452, YDL106C
NS	CNAG_04904	clathrin heavy chain	-	-	-	-	-	-
SP3	CNAG_06101	ADP,ATP carrier protein	Ca	Q5A516	10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_06283, PADG_01440, YBL030C
NS	CNAG_06377	solute carrier family 25 , member 3	-	-	-	Cn	15	-
NS	CNAG_00499	solute carrier family 25 , member 20/29	-	-	-	Hc	11	HCAG_06539
NS	CNAG_06096	tricarboxylate carrier	-	-	-	-	-	-
Response to stress								
-	CNAG_00334	hsp75-like protein	Af Ca Sc	Q4WCM2, CA2857, P10591	1, 3, 4, 5, 6, 7, 8, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_05805, PADG_03562, YAL005C
NS	CNAG_01727	hsp71-like protein	Af Ca Sc	Q4WJ30, CA3534, P10592	1, 3, 4, 5, 6, 7, 8, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_05805, PADG_03562, YBL075C
NS	CNAG_01750	hsp72-like protein	Ca Sc	CA1030, P40150	1, 3, 4, 5, 8, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_05805, PADG_03562, YDL229W
-	CNAG_03891	hsp60-like protein	Ca Pb	O74261, PABG_07300	9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_06961, PADG_08369, YLR259C
SP3	CNAG_05199	chaperone DnaK	Af Ca	B0XS36, P83784	7, 10	Hc Pb Sc	11, 12, 13	HCAG_08176, PADG_00430, YJR045C
-	CNAG_06150	hsp90-like protein	Af Ca Pb Sc	P40292, CA4959, PADG_07715, P02829	1, 3, 4, 7, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_04686, PADG_07715, YMR186W
-	CNAG_06208	heat shock 70kDa protein 4	Af Ca Pb Sc	Q6MYM4, Q96VB9, PABG_00374, P32589	1, 4, 7, 9, 10	Hc Pb Sc	11, 12, 13	HCAG_00783, PADG_02785, YPL106C
SP	CNAG_06443	glucose-regulated protein	Ca Sc	Q5A397, P9484	1, 3, 5, 6, 8, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_05805, PADG_03562, YER103W
ATP biosynthetic process								
NS	CNAG_01004	ATP synthase F1, delta subunit	-	-	-	Cn Hc Pb	11, 12, 14	HCAG_03815, PADG_07042
NS	CNAG_04439	V-type proton ATPase subunit B	-	-	-	Cn Sc	13, 15	YBR107C
-	CNAG_05750	ATP synthase subunit alpha, mitochondrial	Ca Pb	Q59RA8, PADG_02561	9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_02813, PADG_02561, YBL099W
NS	CNAG_05918	ATP synthase subunit beta, mitochondrial	Ca Pb	CA4362, PADG_08349	6, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_06944, PADG_08349, YJR101W
-	CNAG_06400	plasma-membrane proton-efflux P-type ATPase	Ca Sc	CA2300, P05030	4, 6	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_06977, PADG_08391, YGL008C
-	CNAG_02326	V-type proton ATPase catalytic subunit A	-	-	-	Hc Sc	11, 13	HCAG_00404, YDL185W
Translation								
-	CNAG_00034	large subunit ribosomal protein L9e	-	-	-	Cn Pb Sc	12, 13, 14, 15	PADG_02329, YGL147C
-	CNAG_00096	small subunit ribosomal protein S3	-	-	-	Hc Pb Sc	11, 12, 13	HCAG_00214, YHR01407, YNL178W
-	CNAG_00640	small subunit ribosomal protein S4-A	Ca	Q5A5Q8	10	Cn Hc Sc	11, 13, 15	HCAG_07237, YHR203C
-	CNAG_00656	large subunit ribosomal protein L7e	Ca Sc	CA3800, P05737	1, 4, 6	Cn Pb Sc	12, 13, 14, 15	PADG_01387, YPL198W
NS	CNAG_00672	small subunit ribosomal protein S9	Sc	P0CX47	1	Cn Hc	11, 14	HCAG_07773
NS	CNAG_01628	small subunit ribosomal protein S20	Ca Sc	Q5A389, P38701	4, 10	Cn Hc	11, 15	HCAG_08821
-	CNAG_01024	large subunit ribosomal protein L18-A	-	-	-	Cn	14	-
-	CNAG_02928	large subunit ribosomal protein L5e	Ca Sc	Q5AGZ7, P26321	1, 4, 10	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_08444, PADG_02142, YPL131W
NS	CNAG_00779	large subunit ribosomal protein L27e	Sc	P0C2H6	4	Cn Hc	11, 14	HCAG_00055
-	CNAG_00952	small subunit ribosomal protein S6e	Ca	CA2708	6, 10	Hc Sc	11, 13	HCAG_01666, YPL090C
NS	CNAG_00953	small subunit ribosomal protein S13e	Ca	P33192	10	Cn Pb Sc	12, 13, 14	PADG_07685, YDR064W
-	CNAG_01884	large subunit ribosomal protein L3	Ca Sc	CA0615, P14106	4, 6, 10	Cn Hc Pb	11, 12, 15	HCAG_03923, PADG_07173
-	CNAG_01486	large subunit ribosomal protein L15-A	Ca Pb Sc	Q5A6R1, PABG_01078, P05748	1, 4, 9, 10	Cn Sc	13, 15	YLR029C
NS	CNAG_01951	small subunit ribosomal protein S22-A	-	-	-	Cn Hc Sc	11, 13, 15	HCAG_02272, YJL190C
NS	CNAG_02144	large subunit ribosomal protein L1-A	-	-	-	Cn Hc Pb	11, 12, 14, 15	HCAG_01850, PADG_02828
-	CNAG_02234	large subunit ribosomal protein L6e	Ca Pb	Q9P834, PABG_00475	6, 9, 10	Cn	15	-
-	CNAG_02331	small subunit ribosomal protein S9	Ca	H8WXD5	10	Cn	15	-
-	CNAG_03000	small subunit ribosomal protein S19e	Ca	H8X2Y6	10	Cn	15	-
NS	CNAG_03053	large subunit ribosomal protein L23	-	-	-	Cn Sc	13, 15	YOL107W
-	CNAG_03198	small subunit ribosomal protein S8e	Ca	CA4562	6, 10	Cn Sc	13, 15	YBL072C
NS	CNAG_03510	large subunit ribosomal protein L36e	-	-	-	Hc Pb	11, 12	HCAG_04185, PADG_04065
-	CNAG_03577	large subunit ribosomal protein Lp0	Af Pb Sc	Q4WJR3, PABG_01430, P05317	4, 7, 9	Hc Sc	11, 13	HCAG_04856, YLR340W
NS	CNAG_03739	large subunit ribosomal protein L10-like	Ca Sc	CA2047, P41805	1, 6, 10	Cn Hc Sc	11, 13, 15	HCAG_03695, YLR075W
NS	CNAG_03780	small subunit ribosomal protein S16	Ca	O94017	10	Cn Sc	13, 14, 15	YDL083C
NS	CNAG_04004	small subunit ribosomal protein S1	Ca Sc	CA289, P23248	1, 6, 10	Cn Hc Pb	11, 12, 15	HCAG_06914, PADG_06525
NS	CNAG_04009	large subunit ribosomal protein L37a	-	-	-	Cn	14	-
-	CNAG_04021	large subunit ribosomal protein L24	-	-	-	Cn	15	-
-	CNAG_00494	small subunit ribosomal protein S0	Af Ca Sc	Q4WYK1, O42817, P46654	1, 7, 10	Cn Sc	13, 14	YLR048W
NS	CNAG_04445	small subunit ribosomal protein S7e	Ca Sc	CA1502, P26786	4, 6, 10	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_06613, PADG_00942, YOR096W
NS	CNAG_04726	large subunit ribosomal protein L18Ae	Ca	CA0736	6	Cn	14, 15	-
NS	CNAG_04762	large subunit ribosomal protein L4e	Ca	CA5343	6, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_00468, PADG_05721, YBR031W
NS	CNAG_04799	large subunit ribosomal protein L14e	-	-	-	Cn Pb Sc	12, 13, 14, 15	PADG_04731, YKL006W
NS	CNAG_04883	small subunit ribosomal protein S18	-	-	-	Cn Hc Pb	11, 12, 15	HCAG_08667, PADG_06313
-	CNAG_00417	elongation factor 1-gamma	Pb	PABG_06894	9	Cn Pb Sc	12, 13, 14, 15	PADG_06265, YKL081W
-	CNAG_00785	ATP-dependent RNA helicase eIF4A	Af Ca Sc	Q4WX43, P87206, P10081	1, 4, 7, 10	Cn Hc Pb Sc	11, 12, 13, 14	HCAG_04273, PADG_04144, YKR059W
-	CNAG_04609	argonate	-	-	-	Cn Hc	11, 15	HCAG_06198
NS	CNAG_05555	large subunit ribosomal protein L7Ae	Pb Sc	PABG_04452, P29453	4, 9	Cn Sc	13, 15	YHL033C
-	CNAG_06105	elongation factor 1-alpha	Ca Pb Sc	CA0362, PADG_00692, P02994	1, 3, 6, 8, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14	HCAG_08798, PADG_00692, YPR080W
-	CNAG_06605	small subunit ribosomal protein S2	Af Sc	Q4WA18, P25443	4, 7	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_07961, PADG_08602, YGL103W
NS	CNAG_00689	large subunit ribosomal protein L22e	Pb	PABG_04220	9	Pb	12	PADG_04588
NS	CNAG_05232	large subunit ribosomal protein L8	Ca Pb Sc	Q6FPN7, PABG_06705, P0CX45	4, 9, 10	Cn Hc Sc	11, 13, 15	HCAG_08515, YIL018W
-	CNAG_06231	large subunit ribosomal protein L13	-	-	-	-	-	-
NS	CNAG_06447	large subunit ribosomal protein L22	Ca Sc	CA1440, P05740	4, 6, 10	Cn Sc	13, 14, 15	YKL180W
Protein metabolism								
-	CNAG_04009	aminopeptidase 2	-	-	-	Hc Pb Sc	11, 12, 13	HCAG_06935, PADG_06546, YKL157W
SP	CNAG_00150	peptidase	-	-	-	Cn	15	-
SP	CNAG_00919	carboxypeptidase D	Pb	PABG_06849	9	Cn Sc	13, 15	YGL203C
-	CNAG_01890	5-methyltetrahydropteroyltrylglutamate-homocysteine S-methyltransferase	Ca Pb Sc	CA0653, PABG_07587, P05694	1, 5, 6, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_05565, PADG_08328, YER091C

SP	CNAG_02500	calnexin	Pb	PABG_03040	-	9	Cn	14, 15	-
NS	CNAG_02966	carboxypeptidase	-	-	-	-	Sc	13	YGL203C
-	CNAG_03507	mitochondrial-processing peptidase subunit beta	-	-	-	-	Cn Hc	11, 15	HCAG_02342
-	CNAG_04604	tryptophan-tRNA ligase	-	-	-	-	-	-	-
SP	CNAG_04625	cerevisin	Ca Pb	Q5A099, PADG_07422	-	9, 10	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_00635, PADG_07422, YEL060C
NS	CNAG_05725	ketol-acid reductoisomerase, mitochondrial	Ca	Q59XR8	-	10	Cn Hc Sc	11, 13, 14	HCAG_08890, YLR355C
-	CNAG_05932	peptidyl-prolyl cis-trans isomerase D	Pb	PADG_06488	-	9	Hc Pb	11, 12	HCAG_08833, PADG_06488
NS	CNAG_06026	aspartate aminotransferase	Pb	PADG_01404	-	9	Hc Pb Sc	11, 12, 13	HCAG_06102, PADG_01404, YLR027C
NS	CNAG_06088	aspartate aminotransferase, mitochondrial	-	-	-	-	-	-	-
NS	CNAG_00136	ubiquitin-activating enzyme E1	-	-	-	-	Sc	13	YKL210W
-	CNAG_05722	alanine-tRNA ligase	Sc	P40825	-	1	Sc	13	YOR335C
NS	CNAG_04906	26S protease regulatory subunit 10B	-	-	-	-	-	-	-
NS	CNAG_05886	ubiquitin-conjugating enzyme E2	Pb	PADG_01802	-	9	-	-	-
-	CNAG_06755	threonine-tRNA ligase	-	-	-	-	Sc	13	YIL078W
Carbohydrate metabolism									
NS	CNAG_00061	citrate synthase, mitochondrial	Ca	Q59ZZ5	-	10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_06981, PADG_04710, YNR001C
-	CNAG_00937	aconitate hydratase, mitochondrial	Ca Pb	P8269, PADG_04898	-	9, 10	Hc Pb Sc	11, 12, 13	HCAG_05266, PADG_04898, YLR304C
-	CNAG_00964	glutamine-fructose-6-phosphate transaminase	-	-	-	-	-	-	-
-	CNAG_01820	pyruvate kinase	Ca Sc	CA3483, P00549	-	1, 2, 3, 4, 8, 10	Cn Hc Sc	11, 13, 15	HCAG_07781, YAL038W
-	CNAG_01896	alcohol dehydrogenase	Ca Pb	CA1592, PADG_03268	-	5, 9	Cn Pb Sc	12, 13, 15	PADG_07606, YOR100W
NS	CNAG_01984	transaldolase	Ca Sc	CA2582, P15019	-	1, 5, 6, 10	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_00638, PADG_07420, YLR354C
NS	CNAG_02035	triose-phosphate isomerase	Ca Sc	CA5950, P00942	-	1, 2, 3, 5, 10	Hc Pb Sc	11, 12, 13	HCAG_0259, PADG_06906, YDR050C
SP3	CNAG_02818	glycine cleavage system T protein	-	-	-	-	Cn Hc	11, 14	HCAG_02105
NS	CNAG_03072	enolase	Af Ca Pb Sc	Q96X30, CA3874, PADG_08054, P00924	-	1, 2, 3, 4, 5, 6, 7, 9, 10	Cn Pb Sc	12, 13, 14, 15	PADG_04059, YGR254W
NS	CNAG_03225	malate dehydrogenase, NAD-dependent	Ca	Q5AMP4	-	10	Cn Hc Pb Sc	11, 12, 13, 14	HCAG_03969, PADG_08054, YKL085W
-	CNAG_03358	phosphoglycerate kinase	Af Ca Sc	Q4WT69, CA1691, P00560	-	1, 2, 3, 4, 5, 6, 7, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_03385, PADG_01896, YCR010W
SP	CNAG_03525	alpha,alpha-trehalase	-	-	-	-	-	-	-
-	CNAG_03674	oxoglutarate dehydrogenase, E1 component	-	-	-	-	Hc	11	HCAG_01535
SP	CNAG_03725	dTDP-4-dehydrothiamine reductase	Pb	PADG_02719	-	9	Cn	15	-
-	CNAG_04640	ATP-citrate synthase subunit I	-	-	-	-	Cn Hc Sc	11, 13, 14, 15	HCAG_04934, YOR142W
NS	CNAG_04659	pyruvate decarboxylase	Ca Pb Sc	CA2474, PABG_02300, P06169	-	1, 2, 3, 4, 5, 6, 9, 10	Cn Sc	13, 15	YGR087C
NS	CNAG_04969	UDP-glucose 6-dehydrogenase	-	-	-	-	Cn	14, 15	-
NS	CNAG_05653	malate synthase A	-	-	-	-	Cn Hc Sc	11, 13, 14, 15	HCAG_05084, YNL97W
-	CNAG_05907	pyruvate carboxylase	-	-	-	-	Cn Hc Sc	11, 13, 15	HCAG_04227, YBR218C
NS	CNAG_06313	phosphoglucomutase	Ca Pb	CA0692, PABG_02271	-	5, 9	Hc Pb Sc	11, 12, 13	HCAG_08808, PADG_00681, YMR105C
NS	CNAG_06666	starch phosphorylase	-	-	-	-	Cn	15	-
-	CNAG_06699	glyceraldehyde-3-phosphate dehydrogenase	Af Ca Pb Sc	B3LEA5, CA5892, PADG_0249, P00359	-	1, 2, 3, 4, 6, 7, 8, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_04910, PADG_0249, YGR192
-	CNAG_06770	fructose-bisphosphate aldolase 1	Ca Pb Sc	CA5180, PADG_00668, P14540	-	1, 3, 5, 9, 10	Hc Pb Sc	11, 12, 13	HCAG_00010, PADG_00668, YKL060C
NS	CNAG_05351	phosphomannomutase	Sc	P07283	-	1	Hc Sc	11, 13	HCAG_04139, YFL045C
-	CNAG_02748	UTP-glucose-1-phosphate uridylyltransferase	Ca	Q59K10	-	10	Cn Sc	13, 15	YKL035W
-	CNAG_04217	phosphoenolpyruvate carboxykinase	Pb	PABG_07421	-	9	Hc Sc	11, 13	HCAG_05681, YKR097W
SP	CNAG_06501	1,3-beta-D-glucanase	Ca Pb Sc	Q5AJY5, PABG_04523, P22146	-	1, 2, 9, 10	Cn Hc Sc	11, 13, 15	HCAG_05285, YMR307W
Lipid metabolism									
SP3	CNAG_02099	fatty acid synthase subunit beta, fungi type	-	-	-	-	Hc Sc	11, 13	HCAG_07637, YKL182W
-	CNAG_02100	fatty acid synthase subunit alpha, fungi type	Sc	P19097	-	4	Cn Sc	13, 14	YPL231W
NS	CNAG_02562	acyl-CoA dehydrogenase	-	-	-	-	-	-	-
NS	CNAG_04308	3-hydroxyacyl-CoA dehydrogenase	-	-	-	-	Hc	11	HCAG_07725
SP	CNAG_04869	carboxylesterase	-	-	-	-	Cn	15	-
SP	CNAG_07004	dihydrolipoyl dehydrogenase	-	-	-	-	Cn Pb Sc	12, 13, 15	PADG_06494, YFL018C
Nucleic acid metabolism									
NS	CNAG_01395	ribose-5-phosphate isomerase	Ca	CA1503	-	5	Pb	12	PADG_04989
NS	CNAG_00165	methylthioadenosine phosphorylase	Pb	PABG_01873	-	9	Hc	11	HCAG_05768
-	CNAG_02285	nucleoside diphosphate kinase	-	-	-	-	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_00544, PADG_07524, YKL067W
NS	CNAG_04577	nucleoside-diphosphate kinase	-	-	-	-	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_00544, PADG_07524, YKL067W
Oxidation/Reduction									
-	CNAG_00452	isovaleryl-CoA dehydrogenase	-	-	-	-	Hc	11	HCAG_00677
NS	CNAG_00938	cytochrome c peroxidase, mitochondrial	Af	Q4WPF8	-	7	Hc	11	HCAG_07098
-	CNAG_01492	hypothetical protein	-	-	-	-	-	-	-
-	CNAG_01594	glycine dehydrogenase	-	-	-	-	Hc	11	HCAG_07571
SP	CNAG_01981	sulfide:quinone oxidoreductase	-	-	-	-	-	-	-
-	CNAG_02399	glutathione-disulfide reductase	Pb Sc	PABG_06068, P41921	-	2, 9	Cn	15	-
-	CNAG_02801	thioredoxin	Ca Pb	CA1755, PABG_00718	-	3, 9	Cn Sc	13, 14, 15	YGR209C
NS	CNAG_03482	peroxiredoxin	Ca Sc	CA5714, P34760	-	1, 5, 6, 10	Cn Sc	13, 14, 15	YML028W
NS	CNAG_03618	NADPH2:quinone reductase	Ca Sc	CA4765, P00330	-	1, 3, 4, 5, 6, 8	Hc Sc	11, 13	HCAG_08561, YBR145W
NS	CNAG_04981	catalase	Pb	PABG_0369	-	9	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_08064, PADG_00225, YGR088W
-	CNAG_06628	aldehyde dehydrogenase	Pb Sc	PABG_07609, P5495	-	1, 9	Cn Hc Sc	11, 13, 15	HCAG_08367, YPL061W
NS	CNAG_06917	thiol-specific antioxidant protein 3	Ca Pb	CA4416, PADG_03095	-	5, 9, 10	Cn Hc Pb	11, 12, 14, 15	HCAG_06210, PADG_03095
NS	CNAG_00162	alternative oxidase, mitochondrial	-	-	-	-	-	-	-
NS	CNAG_03936	NADH:quinone oxidoreductase, type IV	-	-	-	-	Pb Sc	12, 13	PADG_07749, YDR032C
-	CNAG_05753	N-acetyl-gamma-glutamyl-phosphate reductase	-	-	-	-	-	-	-
SP3	CNAG_05721	multifunctional beta-oxidation protein	-	-	-	-	Hc	11	HCAG_08039
-	CNAG_05069	ubiquinol-cytochrome c reductase subunit 10	-	-	-	-	-	-	-
NS	CNAG_06431	acyl-CoA oxidase	-	-	-	-	-	-	-
Signaling									
NS	CNAG_01523	CMGC/MAPK/P38 protein kinase	-	-	-	-	Sc	13	YNL307C

-	CNAG_05235	protein BMH2	Ca Pb Sc	CA5050, PADG_04056, P2939	1, 2, 3, 4, 8, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_04527, PADG_04440, YDR099W	
NS	CNAG_05465	guanine nucleotide-binding protein subunit beta-like protein	Af Ca Pb Sc	Q4WQK8, CA3852, PABG_01053, P3809	1, 5, 7, 9, 10	Hc Sc	11, 13	HCAG_07031, YMR96C	
Nucleosome assembly									
NS	CNAG_06745	histone H3	-	-	-	-	-	-	
NS	CNAG_06746	histone H2B	Ca Pb	P48989, PABG_05589	9, 10	Cn Hc Pb Sc	11, 12, 13, 15	HCAG_03525, PADG_05907, YBL002W	
Cytoskeleton									
SP3	CNAG_00483	actin	Ca Pb Sc	CA5255, PABG_06867, P60010	1, 4, 6, 9, 10	Cn Hc Pb Sc	11, 12, 13, 14, 15	HCAG_08210, PADG_06295, YFL039C	
-	CNAG_01840	tubulin beta chain	-	-	-	Cn Pb Sc	12, 13, 14	PABG_00486, YFL037W	
NS	CNAG_03787	tubulin alpha-1A chain	Ca	P87066	10	Cn	14, 15	-	
-	CNAG_04948	tubulin beta	-	-	-	-	-	-	
Others									
NS	CNAG_00356	survival factor 1	-	-	-	-	-	-	
NS	CNAG_00490	acetyl-CoA acyltransferase	Pb	PADG_01687	9	Hc	11	HCAG_01596	
-	CNAG_00700	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	Ca	Q5A6R2	10	Sc	13	YLR028C	
-	CNAG_00747	succinyl-CoA synthetase beta subunit	-	-	-	Hc	11	HCAG_07697	
-	CNAG_00797	acetyl-CoA synthetase	-	-	-	Hc	11	HCAG_01606	
SP3	CNAG_00866	transketolase	-	-	-	-	-	-	
-	CNAG_00930	argininosuccinate synthase	-	-	-	Cn Sc	13, 14	YOL058W	
-	CNAG_00935	DNA-binding protein	-	-	-	Cn Hc	11, 15	HCAG_06523	
-	CNAG_01016	6-phosphogluconolactonase	Ca Pb	CA1704, PADG_07771	5, 9	-	-	-	
-	CNAG_01400	3-deoxy-7-phosphoheptulonate synthase	-	-	-	Sc	13	YBR249C	
NS	CNAG_01744	phosphatase	Af Ca Pb Sc	Q4WT47, CA5788, PABG_03355, P41077	1, 5, 7, 9	Sc	13	YER062C	
-	CNAG_01893	glutathione S-transferase Gst3	Pb	PABG_00949	9	-	-	-	
-	CNAG_02545	inorganic pyrophosphatase	Ca Sc	CA0870, P00817	1, 2, 5	Hc Pb Sc	11, 12, 13	HCAG_04307, PADG_04175, YBR09C	
-	CNAG_02673	NAD dependent epimerase/dehydratase family protein	Pb	PABG_00254	9	-	-	-	
-	CNAG_02858	adenylosuccinate synthetase	-	-	-	Sc	13	YNL220W	
-	CNAG_02918	acetyl-CoA C-acetyltransferase	Pb	PABG_0794	9	Hc Pb Sc	11, 12, 13	HCAG_08621, PADG_02751, YPL028W	
-	CNAG_02943	cytoplasmic protein	-	-	-	Cn	14	-	
-	CNAG_03322	UDP-glucuronate decarboxylase	-	-	-	Cn	14	-	
NS	CNAG_03621	peptidyl-prolyl cis-trans isomerase	Ca Sc	CA3978, P23285	1, 5	Cn Hc Sc	11, 13, 15	HCAG_04485, YDR155C	
-	CNAG_03629	NADH dehydrogenase, G subunit	-	-	-	Hc	11	HCAG_06929	
NS	CNAG_03765	trehalose-phosphatase	-	-	-	-	-	-	
-	CNAG_03769	hexokinase	Pb Sc	PABG_06490, P04807	1, 4, 9	Hc Pb Sc	11, 12, 13	HCAG_03191, PADG_07950, YFR053C	
NS	CNAG_04189	succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Sc	P32614	1	Hc	11	HCAG_06317	
-	CNAG_04259	H/ACA ribonucleoprotein complex subunit 1	-	-	-	-	-	-	
NS	CNAG_04351	methylmalonate-semialdehyde dehydrogenase	-	-	-	-	-	-	
SP3	CNAG_04485	long-chain acyl-CoA synthetase	-	-	-	Pb Sc	12, 13	PADG_00434, YOR317W	
-	CNAG_04531	enoyl-CoA hydratase	-	-	-	Hc Pb	11, 12	HCAG_08058, PADG_01009	
NS	CNAG_04584	poly-binding protein 2/3/4	Pb	PABG_01674	9	Cn Hc	11, 14	HCAG_06295	
SP	CNAG_04601	glycine hydroxymethyltransferase	-	-	-	Cn Hc Pb Sc	11, 12, 13, 14	HCAG_07418, PADG_05277, YLR058C	
NS	CNAG_04985	nascent polypeptide-associated complex subunit alpha	Ca Sc	CA2956, P38879	1, 6, 10	Pb	12	PADG_04730	
NS	CNAG_05229	stomatin family protein	-	-	-	Pb	12	PADG_01002	
NS	CNAG_06079	proliferating cell nuclear antigen	Pb	PADG_03905	9	Hc Pb	11, 12	HCAG_04835, PADG_03905	
-	CNAG_06453	benzodiazepine receptor	-	-	-	-	-	-	
NS	CNAG_06672	formate dehydrogenase	Af Pb	Q4WDJ0, PABG_06935	7, 9	Sc	13	YNL274C	
NS	CNAG_06764	short-chain dehydrogenase	Pb	PABG_04304	9	Hc	11	HCAG_05071	
NS	CNAG_06908	pyridoxal biosynthesis lyase pdxS	Ca Pb	CA4184, PABG_05508	5, 9	Cn Hc	11, 14	HCAG_02994	
-	CNAG_06923	phosphoketolase	-	-	-	Cn	15	-	
Unknown									
NS	CNAG_03544	hypothetical protein	-	-	-	-	-	-	
NS	CNAG_00275	hypothetical protein	Ca	CA5239	5	-	-	-	
SL	CNAG_00995	hypothetical protein	-	-	-	-	-	-	
SP	CNAG_01052	hypothetical protein	-	-	-	-	-	-	
-	CNAG_02109	hypothetical protein	-	-	-	Cn	14	-	
NS	CNAG_02585	hypothetical protein	Pb	PABG_03438	9	Hc	11	HCAG_01318	
NS	CNAG_06075	hypothetical protein	Pb	PADG_04806	9	Cn	15	-	
-	CNAG_00659	hypothetical protein	-	-	-	-	-	-	

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