

Analytical and Bioanalytical Chemistry

Electronic Supplementary Material

**Part II: Defining and Quantifying Individual and Co-cultured Intracellular Proteomes of Two Thermophilic Microorganisms by GeLC-MS<sup>2</sup> and Spectral Counting**

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**Table S1** List of unique *T. maritima* proteins identified having < 1% FDR and  $\geq 4$  spectral counts from the *T. maritima* culture grown at 75°C as compared with *T. maritima* proteins detected in the co-culture.

<b>Tma Proteins Unique to Tma75 with <math>\geq 4</math> SpC, with respect to Co75_Tma</b>	<b>MW, kDa</b>	<b>SpC</b>	<b>Normalized SpC</b>
EFGL Elongation factor G-like protein	75.8	85	0.00773
Q9WZ17 Aspartokinase II	81.4	81	0.00681
PORA Pyruvate synthase subunit porA	44.1	68	0.01077
ATPB ATP synthase subunit beta	51.2	58	0.00770
Q9WZD3 Cysteine synthase	31.1	51	0.01088
Q9X1E6 Putative uncharacterized protein	53.6	50	0.00648
Q9WYB0 Fructose-bisphosphate aldolase	34.9	44	0.00868
Q9X1J8 Putative uncharacterized protein	47.8	44	0.00673
Q9WZZ9 SpoVS-related protein	9.7	43	0.02935
Q9WYM3 Putative uncharacterized protein	47.0	39	0.00597
Q9S5Y0 Response regulator DrrA	28.4	38	0.00955
ILVC Ketol-acid reductoisomerase	38.0	38	0.00702
SYL Leucyl-tRNA synthetase	95.5	37	0.00279
Q9WZ19 Acetolactate synthase, small subunit	19.4	37	0.01344
RS4 30S ribosomal protein S4	24.7	36	0.01070
Q9WXT1 Xylosidase	86.8	35	0.00279
Q9WXN8 Oligopeptide ABC transporter, periplasmic oligopeptide-binding protein	69.9	35	0.00359
Q9WXZ9 Putative uncharacterized protein	24.4	34	0.00982
Q9X0E9 SpoVS-related protein	9.1	34	0.02427
Q9X259 Purine nucleoside phosphorylase	33.3	32	0.00665
Q9X283 Transketolase, putative	69.9	32	0.00313
RL10 50S ribosomal protein L10	20.3	32	0.01110
EFTS Elongation factor Ts	22.8	30	0.00936
SYI Isoleucyl-tRNA synthetase	107.1	29	0.00196
RS10 30S ribosomal protein S10	11.6	29	0.01766
RL5 50S ribosomal protein L5	21.3	28	0.00945
RL1 50S ribosomal protein L1	25.9	27	0.00720
KPRS Ribose-phosphate pyrophosphokinase	34.9	26	0.00513
ATPA ATP synthase subunit alpha	56.0	25	0.00309
GLGA Glycogen synthase	55.4	24	0.00307
LEUD1 3-isopropylmalate dehydratase small subunit 1	18.7	24	0.00898
RECA Protein recA	38.8	24	0.00419
SYM Methionyl-tRNA synthetase	72.9	24	0.00237
PUR9 Bifunctional purine biosynthesis protein purH	49.8	23	0.00316
SYV Valyl-tRNA synthetase	101.7	23	0.00165
G6PI Glucose-6-phosphate isomerase	50.4	23	0.00319
RL25 50S ribosomal protein L25	24.2	23	0.00664
GYRB DNA gyrase subunit B	72.4	22	0.00215
Q9WZT6 Putative uncharacterized protein	16.8	21	0.00869
SYA Alanyl-tRNA synthetase	98.0	20	0.00144
PDXT Glutamine amidotransferase subunit pdxT	21.1	20	0.00661
SYFB Phenylalanyl-tRNA synthetase beta chain	90.0	19	0.00150
Q9WYE9 K <sup>+</sup> channel, beta subunit	36.1	19	0.00370
Q9WZQ9 3-oxoacyl-(Acyl carrier protein) synthase II	43.8	19	0.00286
RL17 50S ribosomal protein L17	14.8	19	0.00901
RL4 50S ribosomal protein L4	26.6	19	0.00502

APT Adenine phosphoribosyltransferase	19.7	19	0.00682
Q9WZ98 Nucleotide sugar epimerase, putative	39.1	19	0.00341
LEU1 2-isopropylmalate synthase	56.8	19	0.00230
CHEY Chemotaxis protein cheY	13.2	18	0.00932
LEU22 3-isopropylmalate dehydratase large subunit 2	45.2	18	0.00268
CSP Cold shock-like protein	7.4	18	0.01694
METK S-adenosylmethionine synthetase	43.6	18	0.00283
KAD Adenylate kinase	25.1	18	0.00508
Q9X1S9 Putative uncharacterized protein	26.7	18	0.00453
Q9WXU3 ComE protein, putative	145.1	17	0.00082
Q9X0M4 Putative uncharacterized protein	24.5	17	0.00491
ACKA Acetate kinase	44.8	17	0.00262
RS18 30S ribosomal protein S18	9.0	17	0.01408
Q9X116 Putative uncharacterized protein	12.5	16	0.00857
Q9X2I7 Cold shock protein	7.6	16	0.01506
PNP Polyribonucleotide nucleotidyltransferase	78.6	15	0.00132
Y370 UPF0273 protein TM_0370	26.8	15	0.00385
LEU21 3-isopropylmalate dehydratase large subunit 1	45.4	15	0.00223
REX2 Redox-sensing transcriptional repressor rex 2	23.2	15	0.00457
PURQ Phosphoribosylformylglycinamide synthase 1	23.6	15	0.00437
Q9WYK3 Putative uncharacterized protein	16.2	14	0.00591
HIS6 Imidazole glycerol phosphate synthase subunit hisF	27.7	14	0.00344
PROA Gamma-glutamyl phosphate reductase	46.4	14	0.00210
Q9WY39 Putative uncharacterized protein	17.3	14	0.00557
Q9WYL1 NADH oxidase	47.6	14	0.00196
Q9WXW2 Putative uncharacterized protein	22.4	14	0.00458
Q9WZM7 Phosphomannomutase	52.9	14	0.00185
ILVD Dihydroxy-acid dehydratase	59.7	14	0.00157
RL14 50S ribosomal protein L14	13.7	14	0.00713
LEU3 3-isopropylmalate dehydrogenase	39.1	14	0.00246
Q9S5X2 Maltodextrin glycosyltransferase	73.8	14	0.00136
Q9X0J6 Putative uncharacterized protein	10.7	14	0.00977
GLPK2 Glycerol kinase 2	55.5	14	0.00175
Q9S5W7 Putative uncharacterized protein	29.1	14	0.00344
RL27 50S ribosomal protein L27	9.2	14	0.01048
IF2 Translation initiation factor IF-2	77.7	13	0.00117
RPOA DNA-directed RNA polymerase subunit alpha	38.6	13	0.00240
REX1 Redox-sensing transcriptional repressor rex 1	22.9	13	0.00388
LY41 Uncharacterized AIPM/Hcit synthase family transferase TM_0552	60.2	13	0.00150
Q9X1E8 Putative uncharacterized protein	15.3	13	0.00585
CHEW Chemotaxis protein cheW	16.9	13	0.00535
Q9X292 Putative uncharacterized protein	12.1	13	0.00741
Q9X1V4 DNA-directed DNA polymerase I	102.1	13	0.00090
Q9WZX2 Glutaredoxin-related protein	25.1	13	0.00365
UPP Uracil phosphoribosyltransferase	23.3	13	0.00386
Q9X1E5 Glycerol uptake operon antiterminator	21.6	13	0.00414
RL2 50S ribosomal protein L2	30.6	13	0.00293
Q9WYK8 Putative uncharacterized protein	23.5	13	0.00384
CLPP ATP-dependent Clp protease proteolytic subunit	22.5	13	0.00398
Q9WZD7 Putative uncharacterized protein	22.3	12	0.00365
Q9X0N2 Isocitrate dehydrogenase	45.4	12	0.00187
RS11 30S ribosomal protein S11	14.1	12	0.00573
Y398 Uncharacterized protein TM_0398	42.6	12	0.00198
Q9WXZ4 Putative uncharacterized protein	12.8	12	0.00678

LEUD2 3-isopropylmalate dehydratase small subunit 2	18.4	12	0.00449
Y1081 Putative anti-sigma factor antagonist TM_1081	12.9	12	0.00660
Q9WZP2 Bacteriocin	30.1	12	0.00284
Q9WY44 NADP-reducing hydrogenase, subunit D, putative	67.6	12	0.00123
Q9X0D9 Endoglucanase	37.3	12	0.00220
Q9WYM6 NADH oxidase, putative	47.0	11	0.00161
Q7DFA3 Methyl-accepting chemotaxis protein, putative	31.6	11	0.00246
Q9WZQ7 Putative uncharacterized protein	33.6	11	0.00218
RS8 30S ribosomal protein S8	15.3	11	0.00510
Y1690 UPF0296 protein TM_1690	10.4	11	0.00743
Q9WXV0 Putative uncharacterized protein	18.7	11	0.00432
Q9X102 Putative uncharacterized protein	10.1	11	0.00785
CHEA Chemotaxis protein cheA	75.5	11	0.00102
RL30 50S ribosomal protein L30	7.6	11	0.01020
Q9X0Q6 Putative uncharacterized protein	13.1	11	0.00584
RS13 30S ribosomal protein S13	14.4	11	0.00547
SYT Threonyl-tRNA synthetase	74.5	11	0.00107
K6PF 6-phosphofructokinase	34.4	11	0.00214
DAPA Dihydrodipicolinate synthase	32.4	10	0.00211
Q9WZA6 Polysaccharide export protein, putative	109.5	10	0.00063
DEOC Deoxyribose-phosphate aldolase	27.2	10	0.00250
HIS1 ATP phosphoribosyltransferase	23.5	10	0.00299
TIG Trigger factor	49.8	10	0.00146
Q9WZL4 Putative uncharacterized protein	45.2	10	0.00156
RS3 30S ribosomal protein S3	24.0	10	0.00297
Q9X0P7 2-oxoacid ferredoxin oxidoreductase, alpha subunit	61.4	10	0.00111
Q9WXW6 Alcohol dehydrogenase, iron-containing	42.6	10	0.00160
Q9WZT5 Sugar kinase, pfkB family	35.8	10	0.00195
Q9WZZ4 Putative uncharacterized protein	22.9	10	0.00309
RS17 30S ribosomal protein S17	12.6	10	0.00580
RS6 30S ribosomal protein S6	15.3	10	0.00485
Q9X285 Putative uncharacterized protein	14.0	10	0.00513
Q9X1L1 Aspartate-semialdehyde dehydrogenase	36.6	10	0.00190
RS19 30S ribosomal protein S19	10.9	10	0.00654
Q9WY58 Protein synthesis inhibitor, putative	14.2	9	0.00437
Q9X0P8 2-oxoacid ferredoxin oxidoreductase, beta subunit	31.7	9	0.00198
Q9X0L2 Ferritin	19.3	9	0.00341
Q9X103 Sugar ABC transporter, ATP-binding protein	41.5	9	0.00151
Q9WY50 Putative uncharacterized protein	23.3	9	0.00269
Q9WZX3 Thioredoxin reductase	34.3	9	0.00176
RS20 30S ribosomal protein S20	11.3	9	0.00582
Y1570 Uncharacterized protein TM_1570	21.9	9	0.00291
RL13 50S ribosomal protein L13	17.3	9	0.00375
Q9X0E0 Endoglucanase	36.0	9	0.00169
RL24 50S ribosomal protein L24	12.0	8	0.00473
Q9X1V9 Beta-mannosidase, putative	92.3	8	0.00063
Q9X2I5 Putative uncharacterized protein	14.5	8	0.00376
Q9X0R2 Putative uncharacterized protein	22.5	8	0.00252
FABG 3-oxoacyl-[acyl-carrier-protein] reductase	26.4	8	0.00202
DAPB Dihydrodipicolinate reductase	23.7	8	0.00230
AAT Aspartate aminotransferase	42.4	8	0.00132
Q9X0X1 Putative uncharacterized protein	9.6	8	0.00606
RL28 50S ribosomal protein L28	7.8	8	0.00710
FABZ (3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase	15.3	7	0.00317

Q9X2B2 Putative uncharacterized protein	32.7	7	0.00151
Q9WYM5 Putative uncharacterized protein	27.3	7	0.00177
Q9WXN4 Oligopeptide ABC transporter, ATP-binding protein	30.6	7	0.00162
KHSE Homoserine kinase	31.3	7	0.00155
RRF Ribosome recycling factor	21.5	7	0.00235
DNLJ DNA ligase	78.8	7	0.00063
Q9X1U8 ATP synthase F1, subunit delta	21.5	7	0.00238
HFQ Protein hfq	10.5	7	0.00473
Y1468 UPF0230 protein TM_1468	32.5	7	0.00151
SYS Seryl-tRNA synthetase	48.8	7	0.00102
RS12 30S ribosomal protein S12	14.0	7	0.00342
PORD Pyruvate synthase subunit porD	11.2	7	0.00439
Q9X082 Putative uncharacterized protein	115.7	6	0.00037
Q9WXM6 NADP-reducing hydrogenase, subunit B	14.0	6	0.00291
Q9WXM4 Putative uncharacterized protein	16.6	6	0.00262
Q9X117 Iron-sulfur cluster-binding protein	31.3	6	0.00129
TRPA Tryptophan synthase alpha chain	26.7	6	0.00156
Q9X2C1 Putative uncharacterized protein	34.4	6	0.00125
Q9WZF4 Putative uncharacterized protein	17.3	6	0.00250
Q9WZ16 Threonine synthase	37.7	6	0.00107
Q9X168 Inosine-5'-monophosphate dehydrogenase	52.0	6	0.00077
SAHH Adenosylhomocysteinase	44.8	6	0.00092
Y508 UPF0189 protein TM_0508	67.4	6	0.00062
Q9X176 Putative uncharacterized protein	12.8	6	0.00321
Q9X2B4 Putative uncharacterized protein	93.4	6	0.00046
Y1442 Putative anti-sigma factor antagonist TM_1442	12.3	6	0.00339
Q9WZU7 Formiminotransferase-cyclodeaminase/formiminotetrahydrofolate cyclodeaminase, putative	34.4	6	0.00123
Q9X252 Outer membrane protein	43.7	6	0.00092
Q9WZZ8 Galactose-1-phosphate uridylyltransferase	39.4	6	0.00111
Q9S5X7 Fe-hydrogenase, subunit gamma	18.3	6	0.00227
ATPE ATP synthase epsilon chain	12.3	6	0.00345
Q9WXP0 Putative uncharacterized protein	44.7	6	0.00094
RL29 50S ribosomal protein L29	7.9	6	0.00565
Q9X1K6 Aspartokinase	43.8	6	0.00093
RS14Z 30S ribosomal protein S14 type Z	7.3	6	0.00611
THYX Thymidylate synthase thyX	26.0	6	0.00169
RL31 50S ribosomal protein L31	8.0	6	0.00525
Q9WZH7 Purine-binding chemotaxis protein	17.0	6	0.00245
Q9X083 Putative uncharacterized protein	129.3	5	0.00028
RL23 50S ribosomal protein L23	11.7	5	0.00311
PANB 3-methyl-2-oxobutanoate hydroxymethyltransferase	29.7	5	0.00115
Q9WZH5 Propionyl-CoA carboxylase, beta subunit	56.4	5	0.00060
Q9WZY7 Putative uncharacterized protein	20.1	5	0.00168
Q9WYT2 Oligopeptide ABC transporter, periplasmic oligo-peptide binding protein, putative	70.7	5	0.00051
Q9WYF6 Heavy metal binding protein	7.8	5	0.00463
ILVE Probable branched-chain-amino-acid aminotransferase	31.1	5	0.00114
RL19 50S ribosomal protein L19	13.4	5	0.00270
Y763 UPF0145 protein TM_0763	11.4	5	0.00293
PYRE Orotate phosphoribosyltransferase	20.4	5	0.00166
Q9WZT1 AstB/chuR-related protein	55.8	5	0.00064
RL22 50S ribosomal protein L22	18.3	5	0.00195
Q9X0R3 Putative uncharacterized protein	20.3	5	0.00173
OMPA Outer membrane protein alpha precursor	45.3	5	0.00078

RL18 50S ribosomal protein L18	14.0	5	0.00255
Y964 UPF0272 protein TM_0964	45.0	5	0.00077
Q9X211 Putative uncharacterized protein	14.3	5	0.00250
Q9X208 Putative uncharacterized protein	7.9	5	0.00463
SYD Aspartyl-tRNA synthetase	66.4	5	0.00054
Q9WZP3 Putative uncharacterized protein	13.3	5	0.00272
AROE Shikimate dehydrogenase	28.9	5	0.00123
RL15 50S ribosomal protein L15	16.2	5	0.00211
Q9X076 Putative uncharacterized protein	13.1	5	0.00263
Q9WYU2 Putative uncharacterized protein	27.2	5	0.00134
FER Ferredoxin	6.2	5	0.00518
CH10 10 kDa chaperonin	10.3	4	0.00270
Q9X118 Iron-sulfur cluster-binding protein, putative	30.7	4	0.00088
Q9X2G7 Putative uncharacterized protein	34.2	4	0.00084
FTSZ Cell division protein ftsZ	38.3	4	0.00071
Y466 UPF0082 protein TM_0466	28.4	4	0.00098
Q9X2F2 Transposase	15.1	4	0.00193
PYRF Orotidine 5'-phosphate decarboxylase	22.8	4	0.00124
PUR6 Phosphoribosylaminoimidazole carboxylase catalytic subunit	18.6	4	0.00145
Q9WZF2 DNA polymerase III, gamma and tau subunit	54.8	4	0.00052
Q9WZ52 Lipopolysaccharide biosynthesis protein	48.6	4	0.00057
CHEX CheY-P phosphatase cheX	16.4	4	0.00160
Q9X091 Putative uncharacterized protein	8.5	4	0.00311
Q9WXN1 Laminarinase	72.5	4	0.00039
Q9WXS1 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase	22.2	4	0.00121
AROA 3-phosphoshikimate 1-carboxyvinyltransferase	45.3	4	0.00061
RIMM Probable 16S rRNA-processing protein rimM	20.4	4	0.00141
Q9WXM7 NADP-reducing hydrogenase, subunit A	19.9	4	0.00141
SYE1 Glutamyl-tRNA synthetase 1	54.6	4	0.00053
MINC Probable septum site-determining protein minC	22.7	4	0.00118
Q9X2B1 Putative uncharacterized protein	27.9	4	0.00102
Q9X2F4 Cyclomaltodextrinase, putative	55.1	4	0.00053
Q9WZU0 Cell division protein FtsA, putative	47.0	4	0.00059