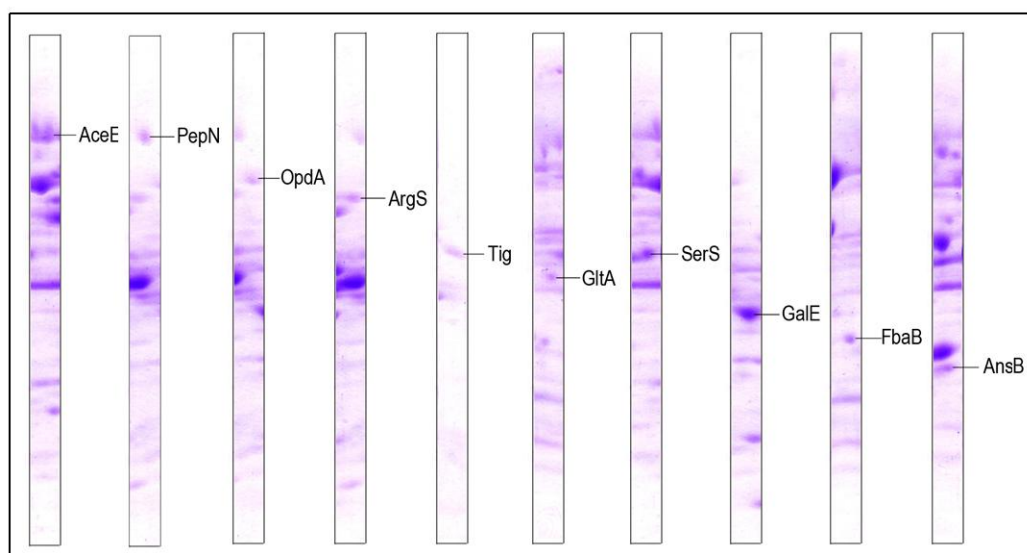


Supplementary Figure 1



Supplementary 1 Enzymes were excluded from homomeric or multimeric protein complexes. They were located in a vertical line alone, but approximately molecular mass of their line locations were not a whole-number multiple of their molecular masses.

Supplemental Table 1 Proteins identified by MALDI-TOF mass spectrometry.

Spot No.	Protein	Gene name	NCBI No.	Protein score	Pred. M.W	Peptides matched	Non-Peptides matched	Sequence coverage (%)
1	Glutamine synthetase	<i>glnA</i>	gi 12518749	73	51883	6	19	20
2	DNA-directed RNA polymerase, beta-subunit	<i>rpoC</i>	gi 409789	110	155047	17	0	19
3	Phenylalanyl-tRNA synthetase beta chain (PheRS)	<i>pheT</i>	gi 16129669	79	87377	10	8	15
4	Alanyl-tRNA synthetase (Alanine-tRNA ligase) (AlaRS)	<i>alaS</i>	gi 2507425	64	95973	14	5	18
5	DNA gyrase subunit A	<i>gyrA</i>	gi 16130166	72	96903	12	0	16
6	Glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex	<i>gcvP</i>	gi 1789269	98	104310	11	18	17
7	Valyl-tRNA synthetase	<i>valS</i>	gi 16132080	97	108124	12	13	17
8	Pyruvate dehydrogenase, decarboxylase component E1, thiamin-binding	<i>aceE</i>	gi 1786304	72	99606	9	17	11
9	leucyl-tRNA synthetase	<i>leuS</i>	gi 1786861	56	97171	8	3	13
10	Phosphoribosylformylglycinamide (FGAM) synthase	<i>purL</i>	gi 49176239	70	141314	10	6	11
11	Aminopeptidase N	<i>pepN</i>	gi 75189987	50	98877	4	16	8
12	Maltodextrin phosphorylase	<i>malP</i>	gi 7246004	114	90322	15	14	27
13	DNA gyrase subunit B	<i>gyrB</i>	gi 49176395	67	89819	10	11	15

14	Pyruvate-formate lyase	<i>pflB</i>	gi 16128870	173	85303	12	18	26
15	Molecular chaperone DnaK	<i>dnaK</i>	gi 15799694	63	69072	7	10	19
16	Aspartyl-tRNA synthetase	<i>aspS</i>	gi 16129819	133	65872	16	16	34
17	Protein disaggregation chaperone	<i>clpB</i>	gi 16130513	123	95526	12	29	20
18	Prolyl-tRNA synthetase	<i>proS</i>	gi 16128187	130	63662	11	3	22
19	Protein disaggregation chaperone	<i>clpB</i>	gi 1788943	106	95526	11	13	19
20	Malate synthase	<i>glcB</i>	gi 16130876	61	80438	7	24	15
21	Transketolase 1, thiamin-binding	<i>tktA</i>	gi 48994911	64	72166	9	6	22
22	Uronate isomerase	<i>uxaC</i>	gi 15803633	72	53879	8	1	25
23	Translation elongation factors G(GTPases)	<i>fusA</i>	gi 15803853	72	77532	6	15	14
24	30S ribosomal subunit protein S1	<i>rpsA</i>	gi 1787140	62	61121	7	15	23
25	Bifunctional phosphoribosylaminoimid azolecarboxamide formyltransferase/IMP cyclohydrolase	<i>purH</i>	gi 16131836	63	57293	6	15	19
26	Glycerol kinase	<i>glpK</i>	gi 16131764	82	56195	11	1	31
27	Aminoacyl-histidine dipeptidase (peptidase D)	<i>pepD</i>	gi 1786432	47	52882	4	8	9
28	Bifunctional GMP synthase/glutamine amido transferase protein	<i>guaA</i>	gi 16130432	80	58642	9	4	20
29	Lysine tRNA synthetase,	<i>lysS</i>	gi 16130792	60	57567	6	26	15

	constitutive							
30	Lysyl-tRNA synthetase, heat inducible	<i>lysU</i>	gi 26250946	92	58795	10	10	24
31	S1 ribosomal protein	<i>rpsA</i>	gi 42900	64	60979	7	8	21
32	Oligopeptidase A	<i>opdA</i>	gi 1789913	85	77119	9	0	17
33	Arginyl-tRNA synthetase	<i>argS</i>	gi 16129828	97	64642	12	16	22
34	Phosphoenolpyruvate carboxykinase	<i>pckA</i>	gi 75241506	68	59578	6	30	17
35	Phosphoglyceromutase , cofactor independent	<i>gpml</i>	gi 16131483	134	56158	11	9	30
36	Tagaturonate reductase	<i>uxaB</i>	gi 49176119	102	54774	9	12	27
37	Peptidyl-prolyl cis/trans isomerase (trigger factor)	<i>tig</i>	gi 1786640	120	48163	10	10	27
38	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor)	<i>tig</i>	gi 75189505	111	48149	10	16	28
39	Mixture, components:							
	Phosphoglycerate kinase	<i>pgk</i>	gi 16130827	70	41093	7	9	25
	Alkyl hydroperoxide reductase, C22 subunit	<i>ahpC</i>	gi 1786822	61	20748	5		32
40	Phosphoglycerate kinase	<i>pgk</i>	gi 1789294	63	41093	6	14	22
41	30S ribosomal subunit protein S1	<i>rpsA</i>	gi 24051180	63	61121	6	14	15
42	Chaperonin GroEL	<i>groL</i>	gi 75239112	160	57293	12	0	43
43	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component , Glycine	<i>lpdA</i>	gi 1786307	58	50657	5	31	12

	cleavage system L protein							
44	Trigger factor	<i>tig</i>	gi 91209509	68	47836	6	14	22
45	ATP synthase subunit B	<i>atpD</i>	gi 15804332	105	50294	8	11	28
46	Pyruvate kinase	<i>pykF</i>	gi 75214842	76	48722	8	12	29
47	Glutamine Phosphoribosylpyrophosp hate (PRPP) amidotransferase, Chain B	<i>purF</i>	gi 16130247	145	56453	14	1	40
48	Aldehyde dehydrogenase A, NAD-linked	<i>aldA</i>	gi 16129376	91	52240	8	17	23
49	Citrate synthase	<i>gltA</i>	gi 146196	88	48032	8	14	22
50	Citrate synthase	<i>gltA</i>	gi 1786939	100	47984	9	10	29
51	Tryptophanase (L-tryptophan indole- lyase) (TNase)	<i>tnaA</i>	gi 41018359	125	52768	12	3	27
52	Succinyl-CoA Synthetase, beta subunit	<i>sucC</i>	gi 6980728	131	41052	11	1	40
53	Seryl-tRNA synthetase	<i>serS</i>	gi 15830232	61	20406	7	23	22
54	D-tagatose 1,6-bisphosphate aldolase 2, subunit	<i>gatZ</i>	gi 16130033	72	47109	7	19	28
55	Elongation Factor Complex Ef-TuEF-Ts, Chain C (EF-Tu)	<i>tufA</i>	gi 1942723	68	42150	6	17	22
56	Maltodextrin-Binding Protein (Maltose-Binding Protein) Mutant	<i>malE</i>	gi 809263	82	39897	7	22	29

57	Glycine/Serine hydroxymethyltransferase , Chain D	<i>glyA</i>	gi 7767020	75	45272	7	6	27
58	6-phosphogluconate dehydrogenase	<i>gnd</i>	gi 642410	82	48794	7	1	20
59	Fructose-1,6-bisphosphat e aldolase, Class II	<i>fbaA</i>	gi 2392634	63	38992	6	11	25
60	UDP-galactose-4-epimera se	<i>galE</i>	gi 49176045	95	37242	8	29	33
61	Glutamyl-tRNA synthetase	<i>gltX</i>	gi 16130330	78	53782	8	21	22
62	Enolase	<i>eno</i>	gi 16975437	90	45495	9	23	37
63	Fructose-bisphosphate aldolase, Class I	<i>fbaB</i>	gi 90111385	72	38085	5	15	19
64	Phenylalanyl-tRNA synthetase alpha subunit	<i>pheS</i>	gi 16129670	82	36809	7	12	32
65	Succinyl-CoA Synthetase, alpha subunit	<i>sucD</i>	gi 6980727	63	29646	6	10	36
66	Glyceraldehyde 3-phosphate dehydrogenase	<i>gapA</i>	gi 468157	130	33507	12	14	53
67	Periplasmic L-asparaginase II	<i>ansB</i>	gi 1789327	64	36828	6	7	29
68	D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit	<i>gatY</i>	gi 90111384	65	30793	6	33	31
69	Malate dehydrogenase	<i>mdh</i>	gi 10185998	90	30075	8	7	46
70	Elongation Factor Complex	<i>tsf</i>	gi 1942724	73	30273	6	16	25

	Ef-TuEF-Ts, Chain D (EF-Ts)							
71	Transaldolase B	<i>talB</i>	gi 14277926	70	35022	7	12	33
72	Cysteine synthase A, O-acetylserine sulfhydrylase A subunit	<i>cysK</i>	gi 15802947	230	34468	11	0	74
73	Serine acetyltransferase	<i>cysE</i>	gi 1790035	66	29317	6	16	38
74	Cysteine synthase A, O-acetylserine sulfhydrylase A subunit	<i>cysK</i>	gi 1788754	174	34358	12	7	60
75	Phosphoglyceromutase 1	<i>pgmA</i>	gi 1786970	64	28539	6	9	24
76	Iron-containing superoxide dismutase	<i>sodB</i>	gi 56159892	48	21121	4	16	30
77	Alkyl hydroperoxide reductase, C22 subunit	<i>ahpC</i>	gi 15800320	56	20748	5	15	39