

1 **Supplemental material for:**

2

3 **A 1 MDa protein complex containing critical components of the Escherichia coli**
4 **divisome.**

5

6 **Erik N. Trip and Dirk-Jan Scheffers**

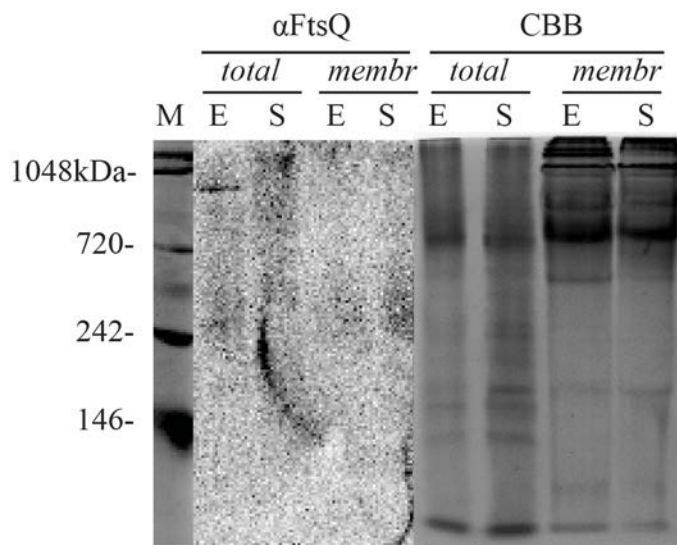
7

8 **contents:**

9 supplemental figures (S1-S5) with legends, supplemental tables (S1, S2), supplemental text,
10 supplemental file S1.

11

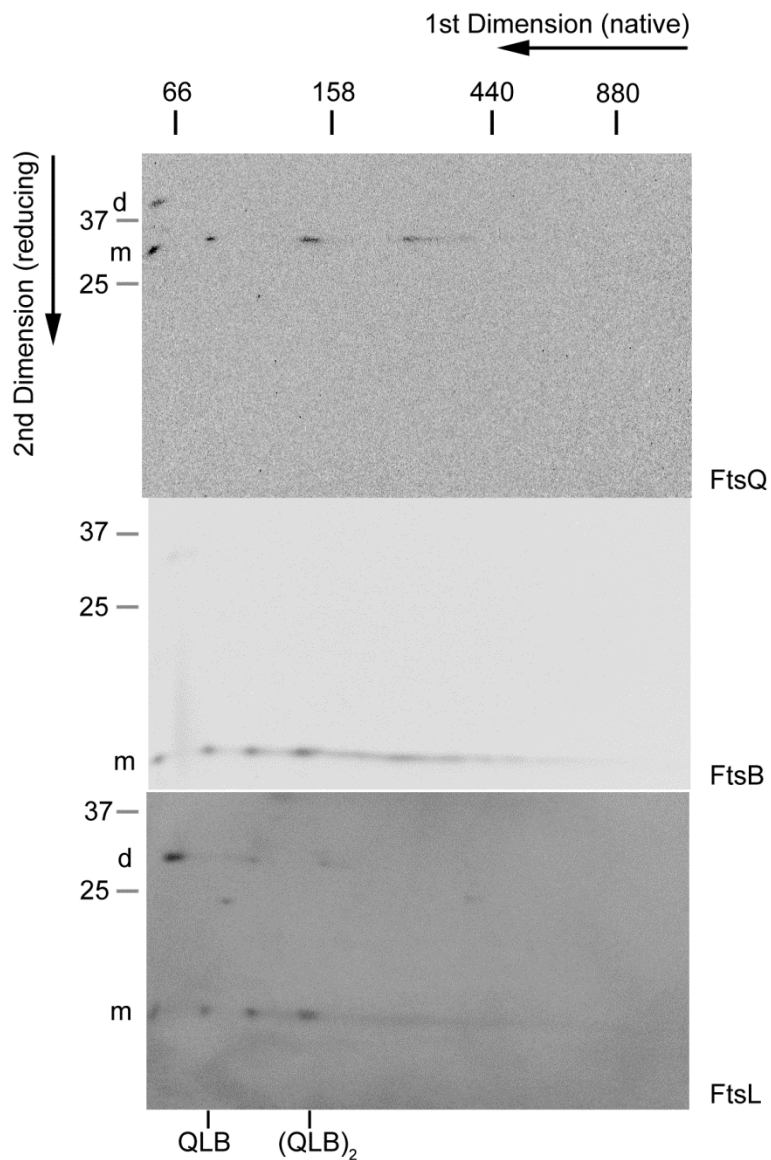
12 **Figure S1**



13

14 **Figure S1.** Native PAGE followed by Western blotting with antibodies against FtsQ of total
15 cell fractions vs membrane fractions. On the far left side, a coomassie stained lane containing
16 Native MarkTM unstained protein standard (novex). On the far right side, four coomassie
17 stained lanes containing total cell fractions and membrane fractions sampled at mid-
18 exponential growth phase (E) and early stationary growth phase (S). In the middle, an
19 immunoblot probed with antibodies against FtsQ. Only in the total cell fraction sample taken
20 during exponential growth the 1 MDa cell division complex is visible. In contrast to the total
21 cell fraction sampled during stationary phase and in contrast to both membrane fractions
22 where no bands were visible.

23



25

26 **Figure S2. Two-dimensional native/SDS-PAGE of *E. coli* inner membrane vesicles**

27 **(IMVs) shows complexes of FtsQ, FtsB and FtsL.** Immunoblots of two-dimensional Blue

28 Native/SDS PAGE gels reveal monomers (m) as well as dimers (d) that have not disintegrated

29 upon equilibration in SDS-buffer. Two distinct sets of spots of FtsQ/B/L running at the same

30 height in the 1st dimension can be resolved that could correspond to a FtsQLB complex (QLB)

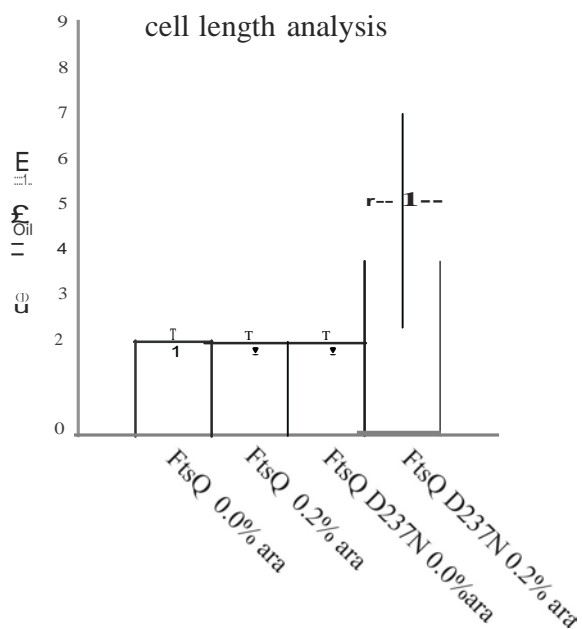
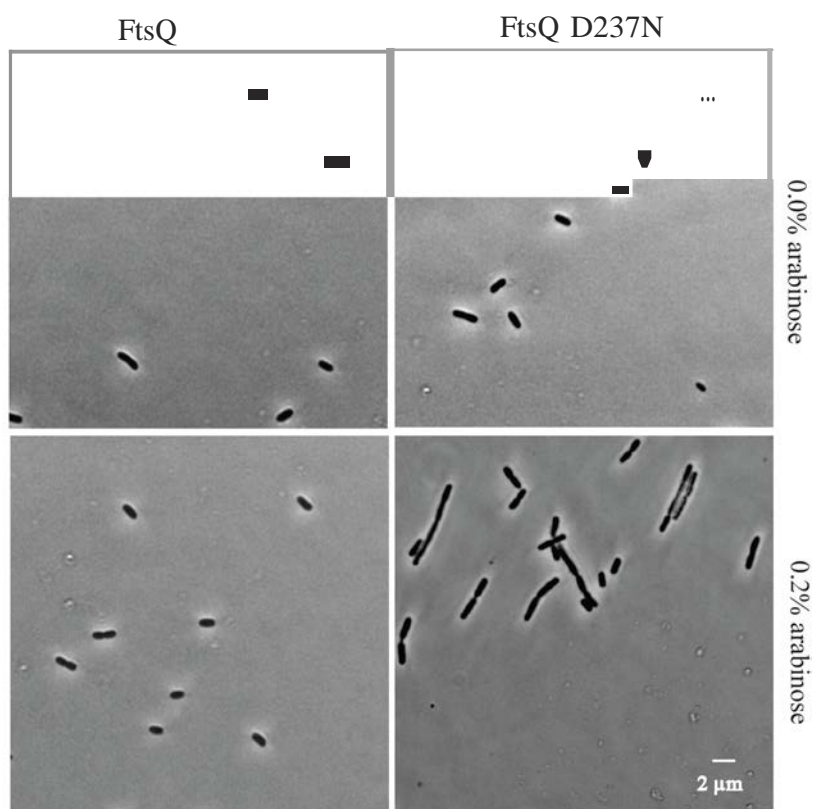
31 and a dimer of this complex (QLB₂). Additional spots corresponding to a potential complex

32 containing FtsB and FtsL are found between the two putative QLB complexes, as well as a

33 smeared signal at higher molecular weight, indicating a disintegrating high Mw complex.

34 Molecular weight markers are indicated on the sides of the blots. Two-dimensional
35 Native/SDS-PAGE was performed as described in ⁶⁴. Briefly, *E. coli* MC4100 cytoplasmic
36 membranes were resuspended in 750 mM Aminocaproic acid; 50 mM Bis-Tris/HCl pH 7.0,
37 and solubilized with 0.5% dodecyl-maltoside. After removal of unsolubilized material, 0.5%
38 Serva-Blue G was added to the samples. Samples (30 µg total protein per lane) were run on a
39 5-14% gradient gel cast on a GelBond PAG backing (Cambrex). Blue Native electrophoresis
40 was performed using a step gradient with constant cooling. Ferritin (440 and 880 kDa),
41 aldolase (158 kDa), and albumin (66 kDa) (GE Healthcare) were used as molecular mass
42 markers. Lanes were cut from the gel, equilibrated for 15 min in 2% SDS, 5 mM
43 tributylphosphine and 15 min in 2% SDS, 260 mM iodoacetamide, and mounted on top of a
44 1.5-mm-thick second dimension gel. Next to the lane, two pieces of filterpaper spotted with
45 IMVs solubilized in SDS-sample buffer or with a prestained molecular weight marker,
46 respectively, were loaded onto the gel. Samples were separated in the second dimension on
47 10% Duracryl (Genomic Solutions) gels using a Tricine-SDS buffer system in an Ettan
48 DALTwelve system (GE Healthcare) with constant cooling. Proteins were transferred from
49 the gels onto PVDF sheets in wet-blot systems (BioRad TransBlot, 15V, O/N, 4°C).
50 Immunodetection was done as described in the text.

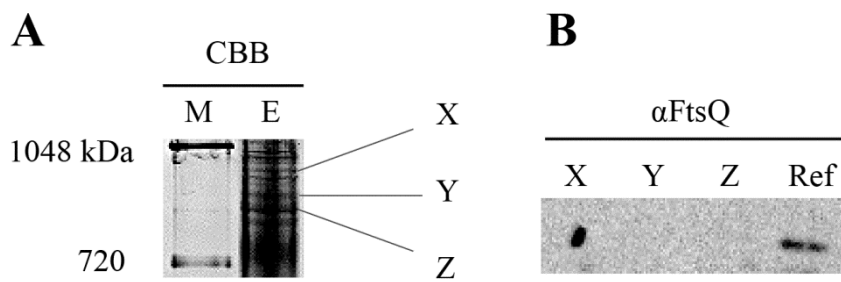
51



54 **Figure S3. Cell-length analysis of cells expressing mutant FtsQ D237N.** (A). Phase
55 contrast microscopy images of the cells expressing additional FtsQ or FtsQ D237N. An
56 aliquot of cells was fixed simultaneous to sample preparation for Native Page. (B). Cell length
57 analysis of the cells depicted in (A). Microscopy images were analyzed with the ObjectJ
58 plugin for Fiji (ImageJ). Average lengths and standard deviations were: MC4100 pBAD-*ftsQ*
59 - 0% arabinose: $2.00 \pm 0.28 \mu\text{m}$ (n=173); 0.2% arabinose: $1.98 \pm 0.23 \mu\text{m}$ (n=176). MC4100
60 pBAD-*ftsQD237N* - 0% arabinose: $1.98 \pm 0.24 \mu\text{m}$ (n=135); 0.2% arabinose: $5.09 \pm 2.75 \mu\text{m}$
61 (n=187).

62

63 **Fig. S4**



64

65 **Figure S4. Pinpointing the 1 MDa band of interest in a coomassie stained native gel.**

66 **A:** Boxed region of the coomassie stained native gel in the region ranging from 1048 to 720

67 kDa. (M) is the lane containing the Native MarkTM unstained protein standard (novex), (E) is

68 the lane containing the exponential phase sample; X, Y and Z are the bands in this lane that

69 potentially could be the 1 MDa band of interest. **B:** these bands were excised from the

70 coomassie stained native gel and subjected to SDS-Page and Western blotting and probed

71 with antibodies against FtsQ as described above. (Ref) is a conventional whole cell SDS-Page

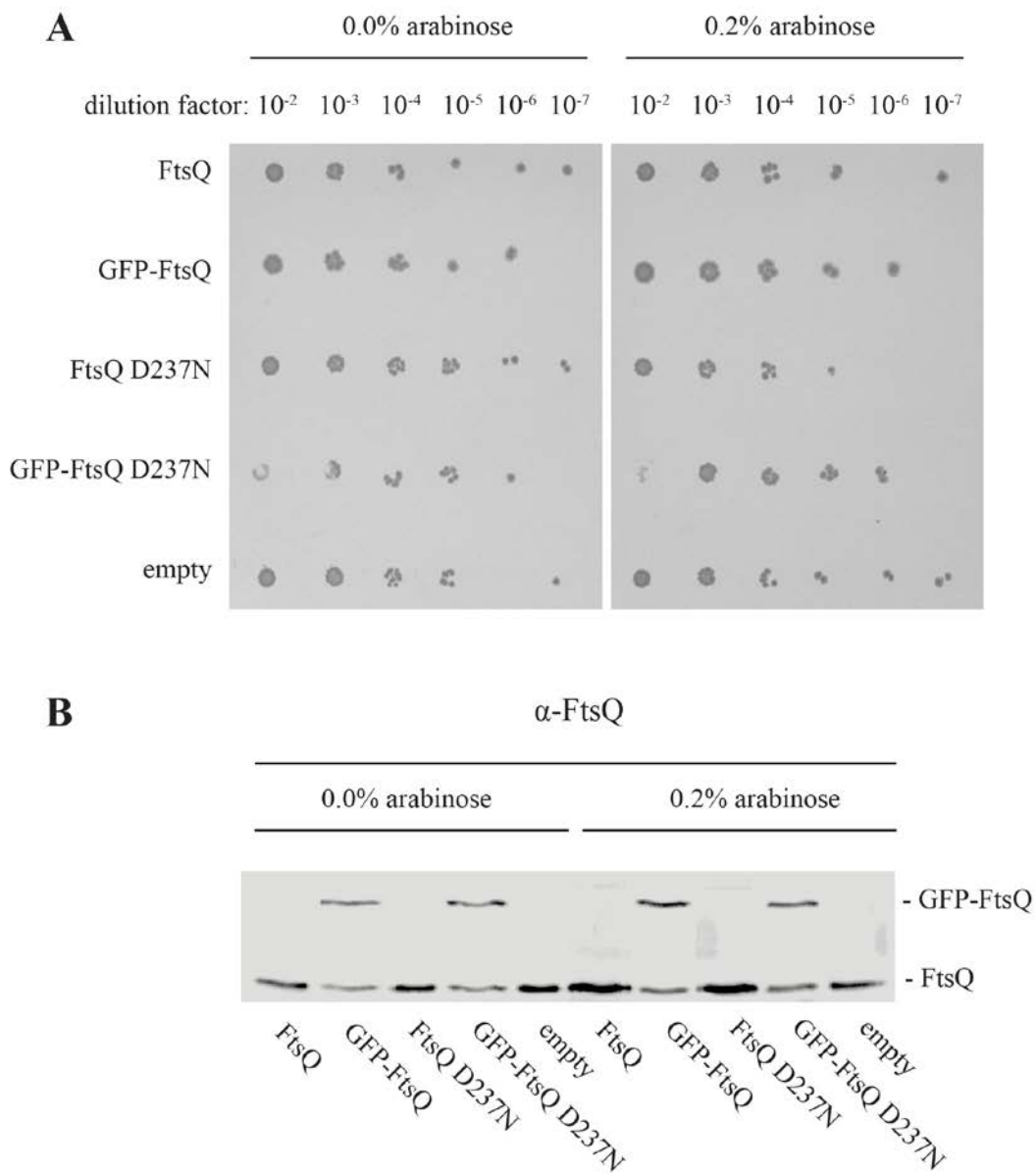
72 sample for reference purposes. Band X was found to be the 1 MDa band of interest in the

73 coomassie stained native gel. Subsequently, this band X from the exponential phase sample

74 lane as well as a corresponding band from the stationary phase sample lane (control) were

75 excised for further analysis.

76



78

79 **Figure S5. Influence of GFP-tags to FtsQ on cell growth.** (A.) Dilution series of cells
 80 expressing additional FtsQ, GFP-FtsQ, FtsQ D237N and GFP-FtsQ D237N spotted on LB
 81 agar plates. (B.) Protein expression control. The presence of FtsQ and GFP-FtsQ was
 82 monitored in the cell samples from panel A.

83

84 **Table S1. Proteins identified by Mass spectroscopy in the Native gel fragment of interest**
 85 **excized from exponential phase lane**

Protein name	Protein accession numbers	Protein molecular weight (Da)	Protein identification probability	Exclusive unique peptide count	Exclusive unique spectrum count	Total spectrum count	Percentage of total spectra	Percentage sequence coverage
Serine transporter.	sp P0AAD6 SDAC_ECOLI	46.909,00	100,00%	3	5	7	0,13%	7,69%
Inosine-5'-monophosphate dehydrogenase (sp P0ADG7 IMDH_ECOLI	52.022,20	100,00%	8	9	9	0,17%	23,60%
Maltose/maltodextrin import ATP-binding	sp P68187 MALK_ECOLI	40.989,90	100,00%	5	5	5	0,09%	13,70%
Chaperone protein dnaK (Heat shock prote	sp P0A6Y8 DNAK_ECOLI	68.984,90	100,00%	23	30	47	0,88%	39,40%
Mannose permease IID component (PTS syst	sp P69805 PTND_ECOLI	31.304,00	100,00%	5	6	7	0,13%	21,00%
Hypothetical protein yqjD.	sp P64581 YQJD_ECOLI	11.051,70	96,10%	1	1	1	0,02%	15,80%
D-ribose-binding periplasmic protein pre	sp P02925 RBSB_ECOLI	30.950,50	100,00%	11	12	14	0,26%	50,30%
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	sp P0A9P0 DLDH_ECOLI	50.557,70	100,00%	9	11	12	0,22%	23,70%
Rod shape-determining protein mreC.	sp P16926 MREC_ECOLI	39.530,60	100,00%	3	3	3	0,06%	13,10%
Iron(III) dicitrate transport protein fe	sp P13036 FECA_ECOLI	85.323,80	100,00%	7	7	8	0,15%	11,80%
Hypothetical protein yggE.	sp P0ADS6 YGGE_ECOLI	26.635,50	100,00%	2	2	2	0,04%	6,91%
PTS system maltose- and glucose-specific	sp P19642 PTOCB_ECOLI	56.628,40	100,00%	2	2	2	0,04%	4,15%
Thiamine biosynthesis protein thil.	sp P77718 THII_ECOLI	54.973,70	100,00%	3	3	3	0,06%	6,43%
NADH-quinone oxidoreductase chain G (EC	sp P33602 NUOG_ECOLI	100.168,30	100,00%	2	2	2	0,04%	2,43%
Glutamate synthase [NADPH] large chain p	sp P09831 GLTB_ECOLI	166.713,70	100,00%	8	8	8	0,15%	6,33%
UPF0234 protein yajQ.	sp P0A8E7 YAJQ_ECOLI	19.047,00	100,00%	4	5	5	0,09%	31,40%
Hypothetical UPF0135 protein ybgl.	sp P0AFP6 YBGI_ECOLI	26.892,70	96,10%	1	1	1	0,02%	6,88%
Protein dcrB precursor.	sp P0AEE1 DCRB_ECOLI	19.787,70	100,00%	3	4	4	0,07%	22,70%
Dihydrolipoyllysine-residue acetyltransf	sp P06959 ODP2_ECOLI	65.964,70	99,80%	1	1	1	0,02%	2,23%
Hypothetical protein yefG (GalF transfer	sp P37749 YFEG_ECOLI	37.759,10	100,00%	2	2	2	0,04%	6,36%
Probable ornithine aminotransferase (EC	sp P42588 OAT_ECOLI	46.401,60	95,20%	1	1	1	0,02%	2,80%
Succinyl-CoA synthetase beta chain (EC 6	sp P0A836 SUCC_ECOLI	41.392,70	100,00%	4	5	5	0,09%	14,70%
DNA-directed RNA polymerase beta' chain	sp P0A8T7 RPOC_ECOLI	155.164,10	100,00%	6	6	7	0,13%	5,83%
50S ribosomal protein L22.	sp P61175 RL22_ECOLI	12.226,60	96,10%	1	1	1	0,02%	11,80%
Hypothetical protein yhaM.	sp P42626 YHAM_ECOLI	45.361,20	96,10%	1	1	1	0,02%	2,52%
Serine hydroxymethyltransferase (EC 2.1.	sp P0A825 GLYA_ECOLI	45.316,70	100,00%	2	2	2	0,04%	4,56%
DNA-directed RNA polymerase beta chain (sp P0A8V2 RPOB_ECOLI	150.635,90	100,00%	27	34	43	0,80%	23,40%

Pyroline-5-carboxylate reductase (EC 1.	sp P0A9L8 PROC_ECOLI	28.145,00	100,00%	7	11	21	0,39%	34,90%
Inner membrane protein yjiY.	sp P39396 YJIY_ECOLI	77.860,40	100,00%	2	2	2	0,04%	3,74%
keratin 1, type II, cytoskeletal - human	KRHU2	65.495,20	100,00%	3	3	3	0,06%	5,29%
Tripeptide permease tppB.	sp P77304 TPPB_ECOLI	53.993,30	97,80%	1	1	1	0,02%	2,60%
Maltoporin precursor (Maltose-inducible	sp P02943 LAMB_ECOLI	49.912,80	100,00%	4	4	4	0,07%	13,00%
Elongation factor Ts (EF-Ts).	sp P0A6P1 EFTS_ECOLI	30.291,60	100,00%	12	15	16	0,30%	40,80%
Phosphate-binding periplasmic protein pr	sp P0AG82 PSTS_ECOLI	37.024,70	100,00%	11	11	16	0,30%	41,00%
Heat shock protein hslJ.	sp P52644 HSLJ_ECOLI	15.166,00	100,00%	2	2	2	0,04%	19,30%
ATP synthase gamma chain (EC 3.6.3.14) (sp P0ABA6 ATPG_ECOLI	31.577,90	100,00%	5	5	5	0,09%	15,70%
Lipoprotein 34 precursor.	sp P0A903 NLPB_ECOLI	36.842,30	100,00%	9	10	13	0,24%	35,20%
Protease VII precursor (EC 3.4.23.-) (Om	sp P09169 OMPT_ECOLI	35.563,90	100,00%	10	12	20	0,37%	34,40%
Cytochrome o ubiquinol oxidase subunit I	sp P0ABJ3 CYOC_ECOLI	22.623,20	96,10%	1	1	1	0,02%	5,39%
2,3,4,5-tetrahydropyridine-2,6-dicarboxy	sp P0A9D8 DAPD_ECOLI	29.891,60	100,00%	3	3	3	0,06%	13,10%
Hypothetical protein yjel precursor.	sp P0AF70 YJEL_ECOLI	11.958,30	99,90%	1	1	1	0,02%	16,20%
UPF0283 membrane protein ycjF.	sp P0A8R7 YCFJ_ECOLI	39.392,90	99,90%	1	1	1	0,02%	3,68%
Cell division proteinftsZ.	sp P0A9A6 FTSZ_ECOLI	40.324,00	100,00%	3	3	3	0,06%	9,14%
Tagatose-1,6-bisphosphate aldolase gatY	sp P37192 GATY_ECOLI	30.811,50	100,00%	3	3	3	0,06%	9,86%
GTP-binding protein lepA.	sp P60785 LEPA_ECOLI	66.571,70	99,60%	1	1	1	0,02%	1,84%
Probable ABC transporter ATP-binding pro	sp P0A9V1 YHBG_ECOLI	26.670,30	100,00%	4	5	7	0,13%	19,60%
Purine nucleoside phosphorylase deoD-tyt	sp P0ABP8 DEOD_ECOLI	25.819,30	100,00%	2	2	2	0,04%	9,66%
Isoaspartyl dipeptidase (EC 3.4.19.-).	sp P39377 IADA_ECOLI	41.084,40	100,00%	4	4	5	0,09%	11,50%
Thymidine phosphorylase (EC 2.4.2.4) (Td	sp P07650 TYPH_ECOLI	47.208,30	98,20%	1	1	1	0,02%	1,59%
DNA-directed RNA polymerase alpha chain	sp P0A7Z4 RPOA_ECOLI	36.512,10	100,00%	5	6	6	0,11%	16,70%
Galactoside transport system permease pr	sp P23200 MGLC_ECOLI	35.551,90	96,10%	1	1	1	0,02%	3,87%
Signal peptidase I (EC 3.4.21.89) (SPase	sp P00803 LEP_ECOLI	35.961,20	100,00%	2	2	2	0,04%	7,41%
Pyruvate kinase II (EC 2.7.1.40) (PK-2).	sp P21599 KPYK2_ECOLI	51.226,60	100,00%	8	9	9	0,17%	19,00%
Putative xanthine dehydrogenase yagR, mo	sp P77489 YAGR_ECOLI	78.089,00	99,40%	1	1	1	0,02%	1,23%
ATP synthase C chain (EC 3.6.3.14) (Lipi	sp P68699 ATPL_ECOLI	8.256,70	99,70%	2	2	6	0,11%	20,30%
Phosphoenolpyruvate carboxylase (EC 4.1.	sp P00864 CAPP_ECOLI	99.066,00	100,00%	18	18	22	0,41%	21,20%
Biotin carboxylase (EC 6.3.4.14) (A subu	sp P24182 ACCC_ECOLI	49.321,90	100,00%	9	9	13	0,24%	20,50%
10 kDa chaperonin (Protein Cpn10) (groES	sp P0A6F9 CH10_ECOLI	10.387,00	100,00%	4	5	5	0,09%	52,60%
Hypothetical adenine-specific methylase	sp P39199 YFCB_ECOLI	35.002,40	100,00%	4	4	4	0,07%	13,20%

30S ribosomal protein S20.	sp P0A7U7 RS20_ECOLI	9.553,70	100,00%	2	2	2	0,04%	23,30%
30S ribosomal protein S3.	sp P0A7V3 RS3_ECOLI	25.852,30	100,00%	3	3	3	0,06%	13,40%
Tryptophanase (EC 4.1.99.1) (L-tryptophan)	sp P0A853 TNAE_ECOLI	52.774,80	100,00%	17	23	43	0,80%	42,70%
Aspartyl-tRNA synthetase (EC 6.1.1.12) (Asp)	sp P21889 SYD_ECOLI	65.915,50	100,00%	6	6	6	0,11%	11,20%
Formate acetyltransferase 1 (EC 2.3.1.54)	sp P09373 PFLB_ECOLI	85.229,10	100,00%	20	34	44	0,82%	30,60%
Hypothetical lipoprotein yedD precursor.	sp P31063 YEDD_ECOLI	14.983,50	100,00%	4	5	6	0,11%	41,60%
CTP synthase (EC 6.3.4.2) (UTP→ammonia)	sp P0A7E5 PYRG_ECOLI	60.243,40	100,00%	5	5	5	0,09%	10,70%
50S ribosomal protein L5.	sp P62399 RL5_ECOLI	20.171,50	100,00%	11	16	25	0,47%	65,70%
50S ribosomal protein L6.	sp P0AG55 RL6_ECOLI	18.772,30	100,00%	2	2	2	0,04%	13,10%
Phenylalanyl-tRNA synthetase alpha chain	sp P08312 SYFA_ECOLI	36.832,50	100,00%	20	38	72	1,34%	53,80%
Protein hflK.	sp P0ABC7 HFLK_ECOLI	45.545,50	100,00%	5	5	6	0,11%	14,80%
ATP-dependent hsl protease ATP-binding subunit	sp P0A6H5 HSLU_ECOLI	49.595,20	100,00%	13	14	16	0,30%	31,40%
NADH-quinone oxidoreductase chain B (EC 1.1.1.13)	sp P0AFC7 NUOB_ECOLI	25.055,60	100,00%	2	2	2	0,04%	9,55%
Ferrienterobactin receptor precursor (Eno)	sp P05825 FEPA_ECOLI	82.108,40	100,00%	4	4	4	0,07%	8,98%
Putative metalloprotease yggG (EC 3.4.24)	sp P25894 YGGG_ECOLI	26.842,40	100,00%	2	2	2	0,04%	10,70%
Glyceraldehyde-3-phosphate dehydrogenase	sp P0A9B2 G3P1_ECOLI	35.401,40	100,00%	15	20	33	0,62%	43,90%
Sulfate/thiosulfate import ATP-binding protein	sp P16676 CYSA_ECOLI	41.058,90	99,90%	1	1	1	0,02%	3,01%
Biopolymer transport exbB protein.	sp P0ABU7 EXBB_ECOLI	26.287,80	100,00%	2	2	3	0,06%	9,84%
Protein-export membrane protein secF.	sp P0AG93 SECF_ECOLI	35.383,50	100,00%	2	2	2	0,04%	9,91%
Lipid A export ATP-binding/permease protein	sp P60752 MSBA_ECOLI	64.462,70	100,00%	12	13	17	0,32%	20,30%
Enoyl-[acyl-carrier-protein] reductase [NADPH-dependent]	sp P0AEK4 FABI_ECOLI	27.733,40	96,10%	1	1	1	0,02%	3,83%
Acyl-CoA thioester hydrolase ybgC precursor	sp P46130 YBHC_ECOLI	46.081,90	100,00%	7	7	10	0,19%	21,80%
Chaperone protein htpG (Heat shock protein 70)	sp P0A6Z3 HTPG_ECOLI	71.425,00	100,00%	16	17	22	0,41%	29,30%
Glycogen phosphorylase (EC 2.4.1.1).	sp P0AC86 PHSG_ECOLI	93.175,30	99,60%	2	2	2	0,04%	2,21%
Alkyl hydroperoxide reductase subunit C	sp P0AE08 AHPC_ECOLI	20.630,70	100,00%	2	2	2	0,04%	15,60%
Colicin I receptor precursor.	sp P17315 CIRA_ECOLI	73.896,60	100,00%	11	11	12	0,22%	23,70%
Alkyl hydroperoxide reductase subunit F	sp P35340 AHPF_ECOLI	56.178,20	100,00%	11	11	12	0,22%	26,10%
ATP synthase beta chain (EC 3.6.3.14).	sp P0ABB4 ATPB_ECOLI	50.194,30	100,00%	19	29	52	0,97%	54,50%
Putative 6-hydroxy-D-nicotine oxidase OS=Arthrobacter nicotinovorans GN=6-HDNO PE=1 SV=1	tr Q8GAG1 Q8GAG1_ARTNI,tr Q8GAGL L138H_ARTNI,tr Q8GAGM H130C_ARTNI	49.922,80	98,80%	1	1	1	0,02%	2,57%
Glycerol-3-phosphate transporter (G-3-P)	sp P08194 GLPT_ECOLI	50.312,50	99,60%	1	1	1	0,02%	2,43%

Chain length determinant protein (Polysa	sp P76372 WZZB_ECOLI	36.455,60	100,00%	8	9	11	0,21%	32,20%
PTS system N-acetylglucosamine-specific	sp P09323 PTW3C_ECOLI	68.348,70	100,00%	2	2	2	0,04%	4,94%
Hypothetical protein yrbK.	sp P0ADV9 YRBK_ECOLI	21.702,70	100,00%	2	2	2	0,04%	13,60%
Probable protease htpX (EC 3.4.24.-) (He	sp P23894 HTPX_ECOLI	31.924,10	96,10%	1	1	1	0,02%	3,75%
50S ribosomal protein L18.	sp P0C018 RL18_ECOLI	12.769,70	100,00%	3	4	5	0,09%	22,20%
Transketolase 1 (EC 2.2.1.1) (TK 1).	sp P27302 TKT1_ECOLI	72.213,00	100,00%	6	6	6	0,11%	9,80%
Penicillin-binding protein 5 precursor (sp P0AEB2 DACA_ECOLI	44.445,50	96,10%	1	1	1	0,02%	2,48%
5-methyltetrahydropteroyltriglutamate-h	sp P25665 METE_ECOLI	84.544,00	100,00%	12	13	16	0,30%	18,60%
Outer membrane lipoprotein slyB precursor	sp P0A905 SLYB_ECOLI	15.600,60	100,00%	4	8	12	0,22%	38,70%
Formate dehydrogenase-O, major subunit (sp P32176 FDOG_ECOLI	112.505,50	99,90%	1	1	1	0,02%	1,67%
50S ribosomal protein L17.	sp P0AG44 RL17_ECOLI	14.365,20	100,00%	3	4	7	0,13%	26,00%
Pyruvate dehydrogenase E1 component (EC	sp P0AFG8 ODP1_ECOLI	99.540,00	100,00%	32	42	62	1,16%	39,20%
Rare lipoprotein A precursor.	sp P10100 RLPA_ECOLI	37.527,60	100,00%	5	5	6	0,11%	16,00%
Cystathionine gamma-synthase (EC 2.5.1.4	sp P00935 METB_ECOLI	41.550,90	100,00%	3	3	4	0,07%	9,59%
Magnesium transporting ATPase, P-type 1	sp P0ABB8 ATMA_ECOLI	99.468,80	100,00%	6	6	6	0,11%	8,02%
Glycyl-tRNA synthetase beta chain (EC 6.	sp P00961 SYGB_ECOLI	76.684,10	100,00%	17	19	25	0,47%	30,80%
Transcription elongation protein nusA (N	sp P0AFF6 NUSA_ECOLI	54.871,40	100,00%	4	4	4	0,07%	9,09%
2-amino-3-ketobutyrate coenzyme A ligase	sp P0AB77 KBL_ECOLI	43.117,70	100,00%	2	2	2	0,04%	5,03%
D-methionine transport ATP-binding prote	sp P30750 METN_ECOLI	37.788,80	100,00%	5	5	6	0,11%	21,00%
Isoleucyl-tRNA synthetase (EC 6.1.1.5) (sp P00956 SYI_ECOLI	104.167,10	100,00%	4	4	4	0,07%	4,27%
Lipoprotein yfgL precursor.	sp P77774 YFGL_ECOLI	41.886,90	100,00%	6	6	7	0,13%	22,70%
PhoH-like protein.	sp P0A9K3 PHOL_ECOLI	40.655,80	100,00%	6	7	10	0,19%	20,10%
Inner membrane protein yjgQ.	sp P0ADC6 YJGQ_ECOLI	39.620,10	100,00%	2	2	3	0,06%	6,39%
Inner membrane protein oxaA.	sp P25714 OXAA_ECOLI	61.528,00	100,00%	7	7	7	0,13%	13,10%
Ellmtl	6H-C384S-W42,6H-W42,EII-F97W,sp P00550 PTM3C_ECOLI	67.857,70	100,00%	6	7	9	0,17%	13,00%
30S ribosomal protein S1.	sp P0AG67 RS1_ECOLI	61.157,40	100,00%	9	11	13	0,24%	23,00%
Na(+)/H(+) antiporter 2 (Sodium/proton a	sp P0AFA7 NHAB_ECOLI	56.730,50	100,00%	2	3	3	0,06%	4,87%
Elongation factor G (EF-G).	sp P0A6M8 EFG_ECOLI	77.450,80	100,00%	18	23	35	0,65%	35,80%
Mannose permease IIC component (PTS syst	sp P69801 PTNC_ECOLI	27.636,40	100,00%	2	2	3	0,06%	11,70%
RNA polymerase sigma factor rpoD (Sigma-	sp P00579 RPOD_ECOLI	70.265,30	100,00%	4	5	5	0,09%	6,69%
30S ribosomal protein S16.	sp P0A7T3 RS16_ECOLI	9.190,60	95,70%	1	1	1	0,02%	13,40%

Protein-export membrane protein secD.	sp P0AG90 SECD_ECOLI	66.634,50	100,00%	14	14	16	0,30%	28,30%
RNA polymerase associated protein rapA (sp P60240 RAPA_ECOLI	109.640,50	100,00%	3	3	3	0,06%	3,21%
Preprotein translocase secY subunit.	sp P0AGA2 SECY_ECOLI	48.514,00	100,00%	3	4	4	0,07%	8,80%
Protein ydgH precursor.	sp P76177 YDGH_ECOLI	33.903,30	96,60%	1	1	1	0,02%	3,82%
GTP cyclohydrolase I (EC 3.5.4.16) (GTP-	sp P0A6T5 GCH1_ECOLI	24.699,80	100,00%	5	6	7	0,13%	28,10%
Oligopeptidase A (EC 3.4.24.70).	sp P27298 OPDA_ECOLI	77.169,50	95,00%	1	1	1	0,02%	1,62%
Organic solvent tolerance protein precur	sp P31554 OSTA_ECOLI	89.672,80	100,00%	13	16	20	0,37%	20,40%
Superoxide dismutase [Mn] (EC 1.15.1.1)	sp P00448 SODM_ECOLI	22.966,60	100,00%	5	6	11	0,21%	20,50%
Lipoprotein bor homolog from lambdaoid pr	sp P77330 BORD_ECOLI	10.447,30	97,30%	1	1	1	0,02%	10,30%
Cell division protein ftsY.	sp P10121 FTSY_ECOLI	54.512,50	97,30%	1	1	1	0,02%	2,01%
DNA gyrase subunit B (EC 5.99.1.3).	sp P0AES6 GYRB_ECOLI	89.820,80	100,00%	5	5	5	0,09%	7,85%
Keratin, type I cytoskeletal 9	K1C9_HUMAN	62.131,00	100,00%	3	3	3	0,06%	8,35%
Methionine synthase (EC 2.1.1.13) (5-met	sp P13009 METH_ECOLI	135.868,30	100,00%	3	3	3	0,06%	3,10%
Alanyl-tRNA synthetase (EC 6.1.1.7) (Ala	sp P00957 SYA_ECOLI	96.033,60	100,00%	35	43	60	1,12%	44,50%
Glutamine transport ATP-binding protein	sp P10346 GLNQ_ECOLI	26.731,30	100,00%	2	2	2	0,04%	12,90%
Spermidine/putrescine transport system p	sp P0AFK4 POTB_ECOLI	31.064,80	99,40%	2	2	2	0,04%	6,91%
Succinyl-CoA synthetase alpha chain (EC	sp P0AGE9 SUCD_ECOLI	29.646,60	100,00%	6	6	7	0,13%	22,20%
Hypothetical protein ycfM.	sp P0AB38 YCFM_ECOLI	22.515,20	100,00%	2	2	3	0,06%	12,70%
Adenylosuccinate lyase (EC 4.3.2.2) (Ade	sp P0AB89 PUR8_ECOLI	51.544,10	100,00%	7	7	9	0,17%	16,40%
Chromosome partition protein mukB (Struc	sp P22523 MUKB_ECOLI	170.232,70	99,90%	2	2	2	0,04%	1,08%
Apolipoprotein N-acyltransferase (EC 2.3	sp P23930 LNT_ECOLI	57.068,90	99,40%	2	2	2	0,04%	4,49%
Glucose-6-phosphate isomerase (EC 5.3.1.	sp P0A6T1 G6PI_ECOLI	61.531,40	100,00%	3	3	3	0,06%	6,56%
Rare lipoprotein B precursor.	sp P0ADC1 RLPB_ECOLI	21.357,30	100,00%	5	5	6	0,11%	31,60%
L-threonine 3-dehydrogenase (EC 1.1.1.10	sp P07913 TDH_ECOLI	37.239,60	96,10%	1	1	1	0,02%	3,23%
Hypothetical oxidoreductase yqhD (EC 1.1	sp Q46856 YQHD_ECOLI	42.097,60	100,00%	2	2	2	0,04%	5,94%
Hypothetical lipoprotein ydCL precursor.	sp P64451 YDCL_ECOLI	24.427,30	100,00%	4	4	4	0,07%	21,60%
ATP-dependent Clp protease ATP-binding s	sp P0ABH9 CLPA_ECOLI	84.208,30	100,00%	6	6	7	0,13%	9,63%
Outer membrane protein C precursor (Pori	sp P06996 OMPC_ECOLI	40.369,00	100,00%	7	7	9	0,17%	22,60%
50S ribosomal protein L15.	sp P02413 RL15_ECOLI	14.981,10	100,00%	5	5	5	0,09%	39,60%
NAD(P) transhydrogenase subunit beta (EC	sp P0AB67 PNTB_ECOLI	48.724,00	100,00%	5	7	7	0,13%	11,50%
Branched-chain amino acid transport syst	sp P0AD99 BRNQ_ECOLI	46.209,90	96,10%	1	1	1	0,02%	3,19%

Tryptophanyl-tRNA synthetase (EC 6.1.1.2	sp P00954 SYW_ECOLI	37.438,40	99,80%	2	2	2	0,04%	6,59%
ADP-L-glycero-D-manno-heptose-6-epimeras	sp P67910 HLDD_ECOLI	34.894,30	100,00%	10	10	15	0,28%	35,50%
Hypothetical protein yiaF.	sp P0ADK0 YIAF_ECOLI	30.158,60	100,00%	5	6	7	0,13%	24,60%
Phosphate acetyltransferase (EC 2.3.1.8)	sp P0A9M8 PTA_ECOLI	77.041,50	100,00%	19	23	33	0,62%	31,60%
50S ribosomal protein L10 (50S ribosomal	sp P0A7J3 RL10_ECOLI	17.580,60	100,00%	9	13	33	0,62%	51,80%
30S ribosomal protein S4.	sp P0A7V8 RS4_ECOLI	23.338,50	100,00%	3	3	3	0,06%	13,20%
Peroxidase/catalase HPI (EC 1.11.1.6) (C	sp P13029 CATA_ECOLI	80.025,80	100,00%	27	39	82	1,53%	39,80%
Ribose transport system permease protein	sp P0AGI1 RBSC_ECOLI	33.452,90	96,10%	1	1	1	0,02%	4,05%
Ubiquinol oxidase polypeptide II precurs	sp P0ABJ1 CYOA_ECOLI	34.912,30	100,00%	7	9	16	0,30%	31,10%
S-adenosylmethionine synthetase (EC 2.5.	sp P0A817 METK_ECOLI	41.820,90	100,00%	3	3	3	0,06%	7,57%
3-oxoacyl-[acyl-carrier-protein] synthas	sp P0A953 FABB_ECOLI	42.613,40	99,80%	1	1	1	0,02%	2,46%
Peptidyl-prolyl cis-trans isomerase D (E	sp P0ADY1 PPID_ECOLI	68.151,40	100,00%	11	12	15	0,28%	23,80%
NADH dehydrogenase (EC 1.6.99.3).	sp P00393 DHNA_ECOLI	47.228,80	100,00%	13	16	22	0,41%	40,40%
30S ribosomal protein S2.	sp P0A7V0 RS2_ECOLI	26.613,10	100,00%	6	6	9	0,17%	28,30%
Hypothetical lipoprotein yifL precursor.	sp P0ADN6 YIFL_ECOLI	7.177,40	94,70%	1	2	4	0,07%	34,30%
Putative lipoprotein yceB precursor.	sp P0AB26 YCEB_ECOLI	20.500,30	100,00%	1	1	1	0,02%	6,45%
30S ribosomal protein S6 [Contains: 30S	sp P02358 RS6_ECOLI	15.703,30	96,10%	1	1	1	0,02%	8,15%
UPF0304 protein yfbU.	sp P0A8W8 YFBU_ECOLI	19.536,50	99,70%	1	1	1	0,02%	9,15%
UPF0169 lipoprotein yfiO precursor.	sp P0AC02 YFIO_ECOLI	27.830,30	100,00%	6	6	8	0,15%	27,80%
Phenylalanyl-tRNA synthetase beta chain	sp P07395 SYFB_ECOLI	87.378,60	100,00%	36	46	116	2,17%	47,20%
Anthranilate synthase component I (EC 4.	sp P00895 TRPE_ECOLI	57.495,80	100,00%	8	8	8	0,15%	17,30%
D-3-phosphoglycerate dehydrogenase (EC 1	sp P0A9T0 SERA_ECOLI	44.045,90	100,00%	9	9	11	0,21%	27,40%
Entericidin B precursor.	sp P0ADB7 ECNB_ECOLI	4.809,50	96,10%	1	1	1	0,02%	39,60%
Uridine phosphorylase (EC 2.4.2.3) (UrdP	sp P12758 UDP_ECOLI	27.027,50	100,00%	4	4	4	0,07%	18,30%
NAD(P) transhydrogenase subunit alpha (E	sp P07001 PNTA_ECOLI	54.623,70	100,00%	4	4	4	0,07%	9,61%
50S ribosomal protein L25.	sp P68919 RL25_ECOLI	10.693,60	100,00%	5	5	8	0,15%	44,70%
Nucleoside permease nupC (Nucleoside-tra	sp P0AFF2 NUPC_ECOLI	43.477,70	100,00%	2	2	3	0,06%	5,00%
Glycerol uptake facilitator protein (Aqu	sp P0AER0 GLPF_ECOLI	29.780,60	96,10%	1	1	1	0,02%	4,27%
Peptidoglycan-associated lipoprotein pre	sp P0A912 PAL_ECOLI	18.824,50	100,00%	7	9	13	0,24%	57,20%
Trypsin precursor	TRYP_PIG	24.409,30	100,00%	7	8	35	0,65%	20,80%
Proline/betaine transporter (Proline por	sp P0COL7 PROP_ECOLI	54.848,50	100,00%	2	2	2	0,04%	5,60%
D-methionine-binding lipoprotein metQ pr	sp P28635 METQ_ECOLI	29.431,90	100,00%	12	15	27	0,50%	53,50%
3-phenylpropionate	sp P0ABR5 HCAE_ECOLI	51.109	97,80%	1	1	1	0,02%	2,21%

dioxygenase alpha sub		,70						
30S ribosomal protein S9.	sp P0A7X3 RS9_ECOLI	14.725,40	100,00%	2	2	2	0,04%	15,50%
Glycerol kinase (EC 2.7.1.30) (ATP:glyce	sp P0A6F3 GLPK_ECOLI	56.100,10	100,00%	6	6	6	0,11%	14,40%
Elongation factor Tu (EF-Tu) (P-43).	sp P0A6N1 EFTU_ECOLI	43.182,60	100,00%	19	23	52	0,97%	56,20%
Aerobic glycerol-3-phosphate dehydrogena	sp P13035 GLPD_ECOLI	56.752,30	100,00%	7	8	10	0,19%	13,00%
Bifunctional aspartokinase/homoserine de	sp P00561 AK1H_ECOLI	89.121,90	99,80%	1	1	1	0,02%	1,59%
Keratin, type I cytoskeletal 10	K1C10_HUMAN	59.520,30	100,00%	3	3	3	0,06%	5,06%
Glycyl-tRNA synthetase alpha chain (EC 6	sp P00960 SYGA_ECOLI	34.774,90	100,00%	4	4	4	0,07%	12,50%
Phosphoglucosamine mutase (EC 5.4.2.10).	sp P31120 GLMM_ECOLI	47.413,30	99,90%	2	2	2	0,04%	6,31%
3-oxoacyl-[acyl-carrier-protein] reducta	sp P0AEK2 FABG_ECOLI	25.561,00	100,00%	10	22	39	0,73%	50,00%
Delta-aminolevulinic acid dehydratase (E	sp P0ACB2 HEM2_ECOLI	35.494,70	100,00%	2	2	2	0,04%	6,81%
Phosphoglycerate kinase (EC 2.7.2.3).	sp P0A799 PGK_ECOLI	40.988,00	96,10%	1	1	1	0,02%	3,63%
Cell division protein zipA.	sp P77173 ZIPIA_ECOLI	36.474,50	99,90%	2	2	2	0,04%	9,76%
NADH-quinone oxidoreductase chain F (EC	sp P31979 NUOF_ECOLI	49.294,50	96,10%	1	1	1	0,02%	2,92%
Putative HTH-type transcriptional regula	sp P27434 YFGA_ECOLI	36.191,50	100,00%	2	2	2	0,04%	9,20%
Fructose-bisphosphate aldolase class II	sp P0AB71 ALF_ECOLI	39.016,10	100,00%	5	5	7	0,13%	16,50%
UTP-glucose-1-phosphate uridylyltransfe	sp P0AAB6 GALF_ECOLI	32.830,10	96,10%	1	1	2	0,04%	4,04%
MltA-interacting protein precursor.	sp P0A908 MIPA_ECOLI	27.831,90	100,00%	3	4	5	0,09%	16,50%
Inner membrane lipoprotein yiaD precurso	sp P37665 YIAD_ECOLI	22.197,60	100,00%	2	3	3	0,06%	16,40%
Protein recA (Recombinase A).	sp P0A7G6 RECA_ECOLI	37.843,50	100,00%	4	4	4	0,07%	14,80%
ATP-dependent protease hslV (EC 3.4.25.-	sp P0A7B8 HSLV_ECOLI	18.962,10	100,00%	5	5	8	0,15%	30,30%
Long-chain fatty acid transport protein	sp P10384 FADL_ECOLI	48.773,40	100,00%	3	3	3	0,06%	8,93%
ATP synthase B chain (EC 3.6.3.14).	sp P0ABA0 ATPF_ECOLI	17.264,50	100,00%	12	15	19	0,36%	56,40%
Hypothetical protein yraM.	sp P45464 YRAM_ECOLI	72.825,80	100,00%	2	2	2	0,04%	3,54%
PTS system mannose-specific EIIAB compon	sp P69797 PTNAB_ECOLI	34.916,20	100,00%	9	12	23	0,43%	26,10%
Hypothetical UPF0070 protein yfgM.	sp P76576 YFGM_ECOLI	22.176,40	100,00%	2	2	2	0,04%	21,40%
Aldehyde-alcohol dehydrogenase [Includes	sp P0A9Q7 ADHE_ECOLI	95.998,90	96,10%	1	1	1	0,02%	1,69%
50S ribosomal protein L1.	sp P0A7L0 RL1_ECOLI	24.598,20	100,00%	5	6	6	0,11%	29,20%
ATP-dependent protease La (EC 3.4.21.53)	sp P0A9M0 LON_ECOLI	87.440,60	100,00%	9	9	11	0,21%	12,60%
Small-conductance mechanosensitive chann	sp P0C0S1 MSCS_ECOLI	30.897,00	100,00%	2	2	2	0,04%	8,04%

Protein rcsF.	sp P69411 RCSF_ECOLI	14.163,50	96,10%	1	1	1	0,02%	10,40%
Hypothetical protein yggT.	sp P64564 YGGT_ECOLI	21.168,60	99,90%	2	2	2	0,04%	11,20%
30S ribosomal protein S10.	sp P0A7R5 RS10_ECOLI	11.735,80	100,00%	2	2	2	0,04%	23,30%
DNA gyrase subunit A (EC 5.99.1.3).	sp P0AES4 GYRA_ECOLI	96.965,00	100,00%	16	16	18	0,34%	21,30%
Transport ATP-binding protein cydD.	sp P29018 CYDD_ECOLI	65.058,60	100,00%	2	2	2	0,04%	4,25%
Transcription antitermination protein nu	sp P0AFG0 NUSG_ECOLI	20.399,80	96,10%	1	1	1	0,02%	7,22%
Inner membrane transport protein ydhC.	sp P37597 YDHC_ECOLI	43.368,60	96,10%	1	1	1	0,02%	3,47%
Alpha-ketoglutarate permease.	sp P0AEX3 KGTP_ECOLI	47.054,00	96,10%	1	1	1	0,02%	2,55%
Acetyl-coenzyme A carboxylase carboxyl t	sp P0A9Q5 ACCD_ECOLI	33.322,50	99,40%	1	1	1	0,02%	3,29%
50S ribosomal protein L9.	sp P0A7R1 RL9_ECOLI	15.768,70	100,00%	2	2	2	0,04%	19,50%
PTS system trehalose-specific EIIBC comp	sp P36672 PTTBC_ECOLI	51.082,60	100,00%	8	9	14	0,26%	14,60%
Antigen 43 precursor (AG43) (Fluffing pr	sp P39180 AG43_ECOLI	106.823,60	100,00%	12	14	14	0,26%	16,90%
Tail-specific protease precursor (EC 3.4	sp P23865 PRC_ECOLI	76.665,70	99,80%	1	1	1	0,02%	1,91%
Glucose-6-phosphate 1-dehydrogenase (EC	sp P0AC53 G6PD_ECOLI	55.705,70	99,90%	1	1	1	0,02%	2,04%
Hypothetical protein yfdI.	sp P76507 YFDI_ECOLI	51.487,90	100,00%	3	4	4	0,07%	7,45%
Aldehyde dehydrogenase A (EC 1.2.1.22) (sp P25553 ALDA_ECOLI	52.142,10	99,80%	2	2	2	0,04%	3,77%
Threonyl-tRNA synthetase (EC 6.1.1.3) (T	sp P0A8M3 SYT_ECOLI	74.015,60	100,00%	9	9	9	0,17%	14,30%
30S ribosomal protein S7.	sp P02359 RS7_ECOLI	19.888,10	99,20%	2	2	2	0,04%	14,60%
Glutamine transport system permease prot	sp P0AEQ6 GLNP_ECOLI	24.365,90	99,80%	1	1	1	0,02%	5,02%
Multidrug resistance protein mdtB (Multi	sp P76398 MDTB_ECOLI	112.081,10	98,00%	1	1	1	0,02%	0,96%
Prolyl-tRNA synthetase (EC 6.1.1.15) (Pr	sp P16659 SYP_ECOLI	63.693,40	100,00%	3	3	3	0,06%	7,17%
30S ribosomal protein S13.	sp P0A7S9 RS13_ECOLI	12.968,90	100,00%	5	5	5	0,09%	52,10%
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysi	sp P0A8N3 SYK1_ECOLI	57.474,30	99,80%	1	1	1	0,02%	2,38%
Outer membrane protein X precursor.	sp P0A917 OMPX_ECOLI	18.603,00	100,00%	5	9	12	0,22%	37,40%
Preprotein translocase secA subunit.	sp P10408 SECA_ECOLI	102.025,30	100,00%	13	13	13	0,24%	16,60%
UDP-galactopyranose mutase (EC 5.4.99.9)	sp P37747 GLF_ECOLI	42.967,60	99,90%	2	2	2	0,04%	5,72%
Bifunctional aspartokinase/homoserine de	sp P00562 AK2H_ECOLI	88.757,50	99,70%	1	1	1	0,02%	0,99%
Enolase (EC 4.2.1.11) (2-phosphoglycerat	sp P0A6P9 ENO_ECOLI	45.525,50	100,00%	8	8	9	0,17%	23,70%
Transcription termination factor rho (EC	sp P0AG30 RHO_ECOLI	47.006,30	100,00%	2	2	2	0,04%	8,11%
3-octaprenyl-4-hydroxybenzoate carboxyl	sp P0AAB4 UBID_ECOLI	55.604,80	99,10%	1	1	1	0,02%	2,41%
Diaminopimelate decarboxylase (EC 4.1.1.	sp P00861 DCDA_ECOLI	46.176,60	96,10%	1	1	1	0,02%	2,62%
Glycine dehydrogenase [decarboxylating]	sp P33195 GCSP_ECOLI	104.246,10	100,00%	3	3	3	0,06%	3,77%

Hypothetical protein yibN.	sp P0AG27 YIBN_ECOLI	15.596,20	100,00%	4	5	5	0,09%	32,90%
Phosphoenolpyruvate-protein phosphotrans	sp P08839 PT1_ECOLI	63.564,30	100,00%	4	4	4	0,07%	8,35%
50S ribosomal protein L24.	sp P60624 RL24_ECOLI	11.185,10	96,10%	1	1	1	0,02%	9,71%
Low-affinity inorganic phosphate transpo	sp P0AFJ7 PITA_ECOLI	53.390,90	99,10%	1	1	1	0,02%	2,00%
Gamma-glutamyl phosphate reductase (GPR)	sp P07004 PROA_ECOLI	44.630,40	100,00%	7	7	9	0,17%	20,40%
ATP-dependent Clp protease ATP-binding s	sp P0A6H1 CLPX_ECOLI	46.226,10	100,00%	8	8	8	0,15%	25,10%
Rod shape-determining protein mreB.	sp P0A9X4 MRB_ECOLI	36.952,40	100,00%	6	6	6	0,11%	22,80%
Cysteine synthase B (EC 2.5.1.47) (O-ace	sp P16703 CYSM_ECOLI	32.664,60	95,80%	1	1	1	0,02%	4,29%
NADP-specific glutamate dehydrogenase (E	sp P00370 DHE4_ECOLI	48.581,20	100,00%	7	7	7	0,13%	21,30%
Small protein A precursor.	sp P0A937 SMPA_ECOLI	12.302,00	100,00%	2	2	2	0,04%	26,50%
Osmotically inducible lipoprotein E prec	sp P0ADB1 OSME_ECOLI	12.020,50	100,00%	4	5	5	0,09%	29,50%
50S ribosomal protein L7/L12 (L8).	sp P0A7K2 RL7_ECOLI	12.163,80	100,00%	5	6	15	0,28%	36,70%
Protein-export membrane protein secG (Pr	sp P0AG99 SECG_ECOLI	11.365,80	100,00%	2	2	3	0,06%	27,30%
Maltose transport system permease protei	sp P02916 MALF_ECOLI	57.016,50	100,00%	2	2	2	0,04%	4,47%
Seryl-tRNA synthetase (EC 6.1.1.11) (Ser	sp P0A8L1 SYS_ECOLI	48.414,80	100,00%	2	2	2	0,04%	4,88%
Polyribonucleotide nucleotidyltransferas	sp P05055 PNP_ECOLI	77.101,00	100,00%	21	28	42	0,78%	38,50%
Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Ty	sp P0AGJ9 SYY_ECOLI	47.397,00	100,00%	2	2	2	0,04%	6,15%
Chaperone surA precursor (Peptidyl-proly	sp P0ABZ6 SURA_ECOLI	47.284,70	100,00%	5	5	6	0,11%	14,00%
Protein ydgA precursor.	sp P77804 YDGA_ECOLI	54.690,10	100,00%	7	7	7	0,13%	13,10%
Putative frv operon regulatory protein [sp P32152 FRVR_ECOLI	66.002,40	97,90%	1	1	1	0,02%	1,20%
Periplasmic oligopeptide-binding protein	sp P23843 OPPA_ECOLI	60.899,80	100,00%	8	10	11	0,21%	17,30%
ATP synthase alpha chain (EC 3.6.3.14).	sp P0ABB0 ATPA_ECOLI	55.223,20	100,00%	21	24	44	0,82%	48,90%
Citrate synthase (EC 2.3.3.1).	sp P0ABH7 CISY_ECOLI	48.016,80	100,00%	10	17	27	0,50%	28,80%
3-hydroxydecanoyl-[acyl-carrier-protein]	sp P0A6Q3 FABA_ECOLI	18.838,40	100,00%	5	5	8	0,15%	31,60%
Cysteine desulfurase (EC 2.8.1.7) (Thil	sp P0A6B7 ISCS_ECOLI	45.090,70	100,00%	2	2	2	0,04%	5,20%
Methionyl-tRNA synthetase (EC 6.1.1.10)	sp P00959 SYM_ECOLI	76.125,50	100,00%	9	9	11	0,21%	15,20%
Uridylate kinase (EC 2.7.4.-) (UK) (Urid	sp P0A7E9 PYRH_ECOLI	25.839,70	96,10%	1	1	1	0,02%	4,58%
Chaperone clpB (Heat-shock protein F84.1	sp P63284 CLPB_ECOLI	95.587,90	100,00%	22	28	35	0,65%	32,70%
Outer membrane protein assembly factor y	sp P0A940 YAET_ECOLI	90.554,40	100,00%	19	23	33	0,62%	30,70%
Soluble pyridine nucleotide transhydroge	sp P27306 STHA_ECOLI	51.429,80	96,80%	1	1	1	0,02%	1,51%
Translation initiation factor IF-2.	sp P0A705 IF2_ECOLI	97.349,00	100,00%	21	23	26	0,49%	26,60%

Pyruvate kinase I (EC 2.7.1.40) (PK-1).	sp P0AD61 KPYK1_ECOLI	50.729,90	100,00%	12	14	18	0,34%	29,40%
Hypothetical ABC transporter ATP-binding	sp P36879 YADG_ECOLI	34.648,40	100,00%	2	2	2	0,04%	6,49%
Nucleoside permease nupG (Nucleoside-tra	sp P0AFF4 NUPG_ECOLI	46.391,50	99,90%	2	2	2	0,04%	4,55%
Multidrug resistance protein A.	sp P27303 EMRA_ECOLI	42.736,10	99,90%	1	1	1	0,02%	3,85%
Major outer membrane lipoprotein precurs	sp P69776 LPP_ECOLI	8.323,70	100,00%	6	13	67	1,25%	48,70%
Hypothetical protein yfgG.	sp P64545 YFGG_ECOLI	7.461,70	96,10%	1	1	1	0,02%	23,80%
Bifunctional glmU protein [Includes: UDP	sp P0ACC7 GLMU_ECOLI	49.190,50	100,00%	3	3	3	0,06%	7,24%
Hypothetical protein yoaF.	sp P64493 YOAF_ECOLI	8.942,30	99,90%	1	1	1	0,02%	21,40%
50S ribosomal protein L28.	sp P0A7M2 RL28_ECOLI	8.875,30	95,90%	1	1	1	0,02%	13,00%
Glucans biosynthesis protein D precursor	sp P40120 OPGD_ECOLI	62.759,70	100,00%	2	2	2	0,04%	3,45%
Putative cytochrome d ubiquinol oxidase	sp P0ADW3 YHCB_ECOLI	15.239,80	99,80%	1	1	2	0,04%	12,70%
Hypothetical protein yrbD precursor.	sp P64604 YRBD_ECOLI	19.577,10	100,00%	3	3	3	0,06%	18,00%
Protein damX.	sp P11557 DAMX_ECOLI	46.161,50	99,90%	3	3	3	0,06%	8,18%
Hypothetical lipoprotein yajG precursor.	sp P0ADA5 YAJG_ECOLI	20.950,40	100,00%	4	5	11	0,21%	25,00%
Nucleoside-specific channel-forming prot	sp P0A927 TSX_ECOLI	33.590,20	100,00%	2	2	6	0,11%	8,16%
Anaerobic C4-dicarboxylate transporter d	sp P0ABN5 DCUA_ECOLI	45.752,20	100,00%	3	3	3	0,06%	6,93%
Protein tolB precursor.	sp P0A855 TOLB_ECOLI	45.955,10	100,00%	7	8	9	0,17%	21,20%
Bifunctional putA protein [Includes: Pro	sp P09546 PUTA_ECOLI	143.818,40	100,00%	7	7	7	0,13%	6,74%
Ribosome recycling factor (Ribosome-rele	sp P0A805 RRF_ECOLI	20.639,30	100,00%	8	10	19	0,36%	44,30%
Protein yicC.	sp P23839 YICC_ECOLI	33.175,20	100,00%	2	2	2	0,04%	8,71%
Ubiquinol oxidase polypeptide I (EC 1.10	sp P0AB18 CYOB_ECOLI	74.370,10	100,00%	5	7	12	0,22%	8,75%
Tyrosine-protein kinase wzc (EC 2.7.1.11	sp P76387 WZC_ECOLI	79.345,10	100,00%	2	3	4	0,07%	3,61%
GTP-binding protein typA/BipA (Tyrosine	sp P32132 TYPA_ECOLI	67.356,00	100,00%	5	6	6	0,11%	9,56%
ProP effector.	sp P45577 PROQ_ECOLI	25.892,40	95,30%	1	1	1	0,02%	4,31%
L-fucose isomerase (EC 5.3.1.25) (6-deox	sp P69922 FUCI_ECOLI	64.977,20	100,00%	4	5	5	0,09%	9,14%
UPF0092 protein yajC.	sp P0ADZ7 YAJC_ECOLI	11.887,60	100,00%	4	6	12	0,22%	27,30%
Inner membrane protein yccF.	sp P0AB12 YCCF_ECOLI	16.275,90	100,00%	2	2	2	0,04%	14,90%
Outer membrane protein A precursor (Oute	sp P0A910 OMPA_ECOLI	37.201,00	100,00%	20	31	116	2,17%	46,50%
30S ribosomal protein S18.	sp P0A7T7 RS18_ECOLI	8.855,80	100,00%	2	2	3	0,06%	29,70%
Probable formate transporter 1 (Formate	sp P0AC23 FOCA_ECOLI	30.991,40	99,90%	1	1	1	0,02%	3,16%
Trigger factor (TF).	sp P0A850 TIG_ECOLI	48.192,90	100,00%	6	7	9	0,17%	17,40%
Outer membrane protein F precursor (Pori	sp P02931 OMPF_ECOLI	39.334,40	100,00%	2	2	2	0,04%	5,80%
Malate dehydrogenase (EC 1.1.1.37).	sp P61889 MDH_ECOLI	32.337,30	100,00%	2	2	2	0,04%	6,09%

UPF0141 protein yjP.	sp P32678 YIJP_ECOLI	66.612,50	99,90%	2	2	2	0,04%	5,72%
Hypothetical protein yehM.	sp P33349 YEHM_ECOLI	83.392,30	95,90%	1	1	1	0,02%	1,05%
Transaldolase B (EC 2.2.1.2).	sp P0A870 TALB_ECOLI	35.089,70	100,00%	5	5	5	0,09%	17,70%
Periplasmic beta-glucosidase precursor (sp P33363 BGLX_ECOLI	83.461,40	100,00%	6	6	6	0,11%	10,10%
Macrolide-specific ABC-type efflux carri	sp P75831 MACB_ECOLI	70.702,90	99,60%	2	2	2	0,04%	4,78%
30S ribosomal protein S5.	sp P0A7W1 RS5_ECOLI	17.471,80	100,00%	4	4	4	0,07%	38,00%
Ribonucleoside-diphosphate reductase 1 a	sp P00452 RIR1_ECOLI	85.778,80	100,00%	4	4	4	0,07%	6,44%
Lipoprotein vacJ precursor.	sp P76506 VACJ_ECOLI	28.042,30	100,00%	4	5	9	0,17%	15,50%
Outer membrane protein tolC precursor.	sp P02930 TOLC_ECOLI	54.015,20	100,00%	9	12	12	0,22%	24,00%
Sec-independent protein translocase prot	sp P69428 TATA_ECOLI	9.664,50	100,00%	2	2	2	0,04%	25,80%
ABC transporter periplasmic-binding prot	sp P39325 YTFQ_ECOLI	34.345,60	100,00%	2	2	3	0,06%	8,18%
Putative sensor-like histidine kinase yf	sp P52101 YFHK_ECOLI	55.700,20	95,90%	1	1	1	0,02%	2,42%
Vitamin B12 transporter btuB precursor (sp P06129 BTUB_ECOLI	68.408,20	100,00%	7	7	10	0,19%	15,10%
Cytochrome d ubiquinol oxidase subunit I	sp P0ABK2 CYDB_ECOLI	42.454,10	100,00%	3	7	10	0,19%	7,65%
Septum site-determining protein minD (Ce	sp P0AEZ3 MIND_ECOLI	29.484,10	96,10%	1	1	1	0,02%	5,20%
Magnesium and cobalt transport protein c	sp P0ABI4 CORA_ECOLI	36.591,40	100,00%	5	6	8	0,15%	18,70%
PTS system glucose-specific EIICB compon	sp P69786 PTGCB_ECOLI	50.678,40	100,00%	13	16	39	0,73%	29,80%
NADH-quinone oxidoreductase chain C/D (E	sp P33599 NUOCD_ECOLI	68.696,40	100,00%	5	5	8	0,15%	8,17%
60 kDa chaperonin (Protein Cpn60) (groEL	sp P0A6F5 CH60_ECOLI	57.197,70	100,00%	25	34	78	1,46%	56,70%
Protein hflC (EC 3.4.--).	sp P0ABC3 HFLC_ECOLI	37.650,90	100,00%	5	6	7	0,13%	18,60%
Cytochrome d ubiquinol oxidase subunit I	sp P0ABJ9 CYDA_ECOLI	58.207,40	100,00%	16	20	34	0,64%	27,40%
Inner membrane protein yjgP.	sp P0AF98 YJGP_ECOLI	40.358,90	100,00%	3	3	3	0,06%	8,47%

88 **Table S2. Proteins identified by Mass spectroscopy in the Native gel fragment of interest**
 89 **excized from stationary phase lane (control)**

Protein name	Protein accession numbers	Protein molecular weight (Da)	Protein identification probability	Exclusive unique peptide count	Exclusive unique spectrum count	Total spectrum count	Percentage of total spectra	Percentage sequence coverage
Maltose/maltodextrin import ATP-binding	sp P68187 MALK_ECOLI	40.989,90	100,00%	7	9	16	0,29%	22,10%
Hydroxylamine reductase (EC 1.7.-.-) (Hy	sp P75825 HCP_ECOLI	60.065,50	99,70%	1	1	1	0,02%	1,64%
Phosphate-binding periplasmic protein pr	sp P0AG82 PSTS_ECOLI	37.024,70	100,00%	10	10	12	0,22%	39,30%
Outer-membrane lipoprotein lolB precursor	sp P61320 LOLB_ECOLI	23.551,60	96,30%	1	1	1	0,02%	5,31%
Chaperone protein dnaK (Heat shock prote	sp P0A6Y8 DNAK_ECOLI	68.984,90	100,00%	19	22	26	0,48%	37,20%
Mannose permease IID component (PTS syst	sp P69805 PTND_ECOLI	31.304,00	100,00%	8	10	16	0,29%	32,50%
Hypothetical protein yqjD.	sp P64581 YQJD_ECOLI	11.051,70	100,00%	2	3	5	0,09%	25,70%
Aminoacyl-histidine dipeptidase (EC 3.4.	sp P15288 PEPD_ECOLI	52.785,30	100,00%	7	8	10	0,18%	17,10%
D-ribose-binding periplasmic protein pre	sp P02925 RBSB_ECOLI	30.950,50	100,00%	13	31	86	1,58%	53,40%
Rod shape-determining protein mreC.	sp P16926 MREC_ECOLI	39.530,60	96,30%	1	1	1	0,02%	3,54%
Preprotein translocase secY subunit.	sp P0AGA2 SECY_ECOLI	48.514,00	100,00%	2	3	3	0,06%	5,87%
PTS system maltose- and glucose-specific	sp P19642 PTOCB_ECOLI	56.628,40	96,70%	1	1	1	0,02%	2,26%
Fumarate hydratase class I, aerobic (EC	sp P0AC33 FUMA_ECOLI	60.169,10	100,00%	4	4	4	0,07%	10,60%
Low-specificity L-threonine aldolase (EC	sp P75823 LTAE_ECOLI	36.495,40	100,00%	2	2	2	0,04%	7,51%
Uronate isomerase (EC 5.3.1.12) (Glucuro	sp P0A8G3 UXAC_ECOLI	53.989,00	99,70%	1	1	1	0,02%	2,13%
Hypothetical protein yjeI precursor.	sp P0AF70 YJEI_ECOLI	11.958,30	99,90%	1	1	2	0,04%	16,20%
NADH-quinone oxidoreductase chain G (EC	sp P33602 NUOG_ECOLI	100.168,30	100,00%	8	9	10	0,18%	9,70%
Aconitate hydratase 2 (EC 4.2.1.3) (Citr	sp P36683 ACON2_ECOLI	93.501,00	100,00%	13	13	18	0,33%	18,50%
Protein ycaC.	sp P21367 YCAC_ECOLI	23.100,90	100,00%	4	6	9	0,17%	22,60%
Trypsin precursor	TRYP_PIG	24.409,30	100,00%	6	7	30	0,55%	16,50%
50S ribosomal protein L7/L12 (L8).	sp P0A7K2 RL7_ECOLI	12.163,80	100,00%	5	6	11	0,20%	36,70%
Hypothetical UPF0135 protein ybgl.	sp P0AFP6 YBGI_ECOLI	26.892,70	100,00%	2	4	4	0,07%	14,60%
Hypothetical protein yefG (GalF transfer	sp P37749 YIEG_ECOLI	37.759,10	100,00%	1	1	1	0,02%	3,33%
Succinyl-CoA synthetase beta chain (EC 6	sp P0A836 SUCC_ECOLI	41.392,70	100,00%	17	24	34	0,62%	49,50%
Hypothetical protein yiaF.	sp P0ADK0 YIAF_ECOLI	30.158,60	100,00%	5	6	6	0,11%	24,60%
Protein ygaU.	sp P0ADE6 YGAU_ECOLI	15.932,20	100,00%	3	3	3	0,06%	23,00%
50S ribosomal protein L22.	sp P61175 RL22_ECOLI	12.226,60	100,00%	2	2	2	0,04%	20,90%
Fumarate hydratase class II (EC 4.2.1.2)	sp P05042 FUMC_ECOLI	50.489,50	95,20%	1	1	1	0,02%	3,85%
Serine hydroxymethyltransferase (EC 2.1.	sp P0A825 GLYA_ECOLI	45.316,70	100,00%	4	5	6	0,11%	11,00%

6-phosphogluconate dehydrogenase, decarb	sp P00350 6PGD_ECOLI	51.483,20	100,00%	9	9	9	0,17%	28,20%
Pyrraline-5-carboxylate reductase (EC 1.	sp P0A9L8 PROC_ECOLI	28.145,00	100,00%	5	8	12	0,22%	24,50%
Protein yhdH.	sp P26646 YHDH_ECOLI	34.723,50	100,00%	2	2	2	0,04%	6,48%
Cation/acetate symporter actP (Acetate t	sp P32705 ACTP_ECOLI	59.200,00	99,90%	2	2	2	0,04%	3,83%
Tripeptide permease tppB.	sp P77304 TPPB_ECOLI	53.993,30	96,30%	1	1	1	0,02%	2,60%
Serine transporter.	sp P0AAD6 SDAC_ECOLI	46.909,00	100,00%	4	5	6	0,11%	9,56%
Succinate dehydrogenase flavoprotein sub	sp P0AC41 DHSA_ECOLI	64.421,90	100,00%	3	3	3	0,06%	5,95%
Pyruvate kinase I (EC 2.7.1.40) (PK-1).	sp P0AD61 KPYK1_ECOLI	50.729,90	100,00%	16	18	29	0,53%	37,40%
Adenylate kinase (EC 2.7.4.3) (ATP-AMP t	sp P69441 KAD_ECOLI	23.586,40	100,00%	4	4	6	0,11%	22,00%
Peroxiredoxin osmC (EC 1.11.1.15) (Osmot	sp P0COL2 OSMC_ECOLI	14.957,30	99,80%	1	1	1	0,02%	13,40%
Maltose-binding periplasmic protein prec	sp P0AEX9 MALE_ECOLI	43.389,90	100,00%	13	15	22	0,40%	41,90%
Valyl-tRNA synthetase (EC 6.1.1.9) (Vali	sp P07118 SYV_ECOLI	108.195,30	100,00%	5	5	5	0,09%	7,26%
Succinate-semialdehyde dehydrogenase [NA	sp P25526 GABD_ECOLI	51.721,60	100,00%	4	4	4	0,07%	10,60%
Periplasmic dipeptide transport protein	sp P23847 DPPA_ECOLI	60.294,60	100,00%	6	7	9	0,17%	13,60%
GMP synthase [glutamine-hydrolyzing] (EC	sp P04079 GUAA_ECOLI	58.679,20	100,00%	1	1	1	0,02%	2,67%
Lipoprotein 34 precursor.	sp P0A903 NLPB_ECOLI	36.842,30	96,30%	1	1	1	0,02%	5,52%
Protease VII precursor (EC 3.4.23.-) (Om	sp P09169 OMPT_ECOLI	35.563,90	100,00%	6	6	8	0,15%	22,40%
Cytochrome o ubiquinol oxidase subunit I	sp P0ABJ3 CYOC_ECOLI	22.623,20	96,30%	1	2	3	0,06%	5,39%
ATP synthase C chain (EC 3.6.3.14) (Lipi	sp P68699 ATPL_ECOLI	8.256,70	99,80%	2	2	4	0,07%	20,30%
2,3,4,5-tetrahydropyridine-2,6-dicarboxy	sp P0A9D8 DAPD_ECOLI	29.891,60	100,00%	5	5	7	0,13%	18,60%
Adenylosuccinate synthetase (EC 6.3.4.4)	sp P0A7D4 PURA_ECOLI	47.214,50	100,00%	9	9	10	0,18%	22,30%
GTP pyrophosphokinase (EC 2.7.6.5) (ATP:	sp P0AG20 RELA_ECOLI	83.876,30	99,70%	1	1	1	0,02%	1,88%
2-dehydro-3-deoxyphosphoconate aldolas	sp P0A715 KDSA_ECOLI	30.832,90	98,30%	2	2	2	0,04%	5,99%
Alpha-galactosidase (EC 3.2.1.22) (Melib	sp P06720 AGAL_ECOLI	50.657,80	99,90%	2	3	3	0,06%	4,21%
Cell division protein ftsZ.	sp P0A9A6 FTSZ_ECOLI	40.324,00	100,00%	12	13	14	0,26%	38,90%
Glucosamine-fructose-6-phosphate aminot	sp P17169 GLMS_ECOLI	66.764,50	100,00%	5	5	7	0,13%	8,88%
KHG/KDPG aldolase [Includes: 4-hydroxy-2	sp P0A955 ALKH_ECOLI	22.284,30	100,00%	2	2	2	0,04%	15,00%
Tagatose-1,6-bisphosphate aldolase gatY	sp P37192 GATY_ECOLI	30.811,50	100,00%	6	7	16	0,29%	22,20%
Fructose-bisphosphate aldolase class I (sp P0A991 ALF1_ECOLI	37.978,90	96,30%	1	1	1	0,02%	6,02%
Probable ABC transporter ATP-binding pro	sp P0A9V1 YHBG_ECOLI	26.670,30	100,00%	3	3	4	0,07%	16,20%
Purine nucleoside phosphorylase deoD-ty	sp P0ABP8 DEOD_ECOLI	25.819,30	100,00%	4	4	7	0,13%	18,50%
2-oxoglutarate dehydrogenase E1 componen	sp P0AFG3 ODO1_ECOLI	105.061,90	100,00%	3	3	3	0,06%	3,32%
Galactoside transport system permease pr	sp P23200 MGLC_ECOLI	35.551,90	96,30%	1	1	2	0,04%	3,87%
Putative xanthine dehydrogenase yagR, mo	sp P77489 YAGR_ECOLI	78.089,00	95,30%	1	1	2	0,04%	1,23%
Cystine-binding periplasmic	sp P0AEM9 FLIY_ECOLI	29.039,90	100,00%	3	3	3	0,06%	10,20%

protein prec		0						
Phosphoenolpyruvate carboxylase (EC 4.1.	sp P00864 CAPP_ECOLI	99.066,00	100,00%	12	12	14	0,26%	13,70%
Acetate kinase (EC 2.7.2.1) (Acetokinase)	sp P0A6A3 ACKA_ECOLI	43.291,50	96,30%	1	1	1	0,02%	3,75%
Protein csID.	sp P76621 CSID_ECOLI	37.360,80	100,00%	4	4	5	0,09%	16,00%
Hypothetical protein yicH.	sp P31433 YICH_ECOLI	62.274,00	96,30%	1	1	1	0,02%	1,76%
Protein ygfZ.	sp P0ADE8 YGFZ_ECOLI	35.963,60	96,10%	1	1	1	0,02%	3,38%
Biotin carboxylase (EC 6.3.4.14) (A subu	sp P24182 ACCC_ECOLI	49.321,90	100,00%	6	6	10	0,18%	14,90%
10 kDa chaperonin (Protein Cpn10) (groES	sp P0A6F9 CH10_ECOLI	10.387,00	100,00%	2	2	2	0,04%	24,70%
Hypothetical adenine-specific methylase	sp P39199 YFCB_ECOLI	35.002,40	100,00%	2	2	2	0,04%	6,13%
Phosphoheptose isomerase (EC 5.3.1.-) (S	sp P63224 GMHA_ECOLI	20.815,40	100,00%	2	2	2	0,04%	10,40%
2,3-bisphosphoglycerate-independent phos	sp P37689 GPMI_ECOLI	56.194,50	96,30%	1	1	1	0,02%	2,72%
Probable glutamate/gamma-aminobutyrate a	sp P63235 GADC_ECOLI	55.078,90	100,00%	3	3	4	0,07%	7,05%
Tryptophanase (EC 4.1.99.1) (L-tryptopha	sp P0A853 TNAE_ECOLI	52.774,80	100,00%	26	45	141	2,59%	56,50%
Aspartyl-tRNA synthetase (EC 6.1.1.12) (sp P21889 SYD_ECOLI	65.915,50	100,00%	8	8	10	0,18%	15,10%
Formate acetyltransferase 1 (EC 2.3.1.54	sp P09373 PFLB_ECOLI	85.229,10	100,00%	18	24	28	0,51%	32,10%
Hypothetical lipoprotein yedD precursor.	sp P31063 YEDD_ECOLI	14.983,50	100,00%	3	4	5	0,09%	31,40%
CTP synthase (EC 6.3.4.2) (UTP→ammonia	sp P0A7E5 PYRG_ECOLI	60.243,40	100,00%	2	2	2	0,04%	4,41%
6-phosphofructokinase isozyme I (EC 2.7.	sp P0A796 K6PF1_ECOLI	34.843,00	100,00%	2	3	3	0,06%	8,44%
50S ribosomal protein L5.	sp P62399 RL5_ECOLI	20.171,50	100,00%	4	5	5	0,09%	25,30%
50S ribosomal protein L6.	sp P0AG55 RL6_ECOLI	18.772,30	95,30%	1	1	1	0,02%	6,82%
Glucosamine-6-phosphate deaminase (EC 3.	sp P0A759 NAGB_ECOLI	29.774,40	100,00%	2	2	2	0,04%	8,65%
Phenylalanyl-tRNA synthetase alpha chain	sp P08312 SYFA_ECOLI	36.832,50	99,30%	1	1	1	0,02%	3,67%
Protein hflC (EC 3.4.-.-).	sp P0ABC3 HFLC_ECOLI	37.650,90	94,90%	1	1	1	0,02%	5,09%
Putative metalloprotease yggG (EC 3.4.24	sp P25894 YGGG_ECOLI	26.842,40	100,00%	2	2	2	0,04%	10,70%
Glyceraldehyde-3-phosphate dehydrogenase	sp P0A9B2 G3P1_ECOLI	35.401,40	100,00%	17	23	38	0,70%	53,60%
Biopolymer transport exbB protein.	sp P0ABU7 EXBB_ECOLI	26.287,80	99,80%	1	1	1	0,02%	6,15%
Protein-export membrane protein secF.	sp P0AG93 SECF_ECOLI	35.383,50	96,30%	1	1	1	0,02%	4,02%
UDP-glucose 4-epimerase (EC 5.1.3.2) (Ga	sp P09147 GALE_ECOLI	37.265,10	96,30%	1	1	1	0,02%	5,62%
Cysteine synthase B (EC 2.5.1.47) (O-ace	sp P16703 CYSM_ECOLI	32.664,60	99,60%	1	1	1	0,02%	4,29%
Enoyl-[acyl-carrier-protein] reductase [sp P0AEK4 FABI_ECOLI	27.733,40	100,00%	2	2	2	0,04%	8,81%
Acyl-CoA thioester hydrolase ybgC precu	sp P46130 YBHC_ECOLI	46.081,90	100,00%	6	6	8	0,15%	18,00%
Chaperone protein htpG (Heat shock prote	sp P0A6Z3 HTPG_ECOLI	71.425,00	100,00%	3	3	3	0,06%	6,25%
Hypothetical protein yeaG.	sp P0ACY3 YEAG_ECOLI	74.483,00	99,90%	1	1	1	0,02%	2,02%
Glycogen phosphorylase (EC 2.4.1.1).	sp P0AC86 PHSG_ECOLI	93.175,30	100,00%	4	4	4	0,07%	6,01%
Alkyl hydroperoxide reductase subunit C	sp P0AE08 AHPC_ECOLI	20.630,70	100,00%	7	11	16	0,29%	43,00%

Protease degQ precursor (EC 3.4.21.-).	sp P39099 DEGQ_ECOLI	47.207,10	95,30%	1	1	1	0,02%	2,42%
Aminopeptidase N (EC 3.4.11.2) (Alpha-am	sp P04825 AMPN_ECOLI	98.790,60	100,00%	4	4	5	0,09%	5,18%
Colicin I receptor precursor.	sp P17315 CIRA_ECOLI	73.896,60	96,30%	1	1	1	0,02%	1,81%
Alkyl hydroperoxide reductase subunit F	sp P35340 AHPF_ECOLI	56.178,20	100,00%	2	2	3	0,06%	4,41%
Glycerol-3-phosphate transporter (G-3-P	sp P08194 GLPT_ECOLI	50.312,50	100,00%	2	2	2	0,04%	5,09%
Chain length determinant protein (Polysa	sp P76372 WZZB_ECOLI	36.455,60	100,00%	4	4	4	0,07%	15,30%
Isocitrate dehydrogenase [NADP] (EC 1.1.	sp P08200 IDH_ECOLI	45.758,00	100,00%	4	4	6	0,11%	13,50%
Probable protease htpX (EC 3.4.24.-) (He	sp P23894 HTPX_ECOLI	31.924,10	96,30%	1	1	1	0,02%	3,75%
50S ribosomal protein L18.	sp P0C018 RL18_ECOLI	12.769,70	95,50%	1	1	1	0,02%	7,69%
Transketolase 1 (EC 2.2.1.1) (TK 1).	sp P27302 TKT1_ECOLI	72.213,00	100,00%	10	11	14	0,26%	17,60%
Outer membrane lipoprotein slyB precurso	sp P0A905 SLYB_ECOLI	15.600,60	100,00%	4	6	9	0,17%	38,70%
50S ribosomal protein L17.	sp P0AG44 RL17_ECOLI	14.365,20	100,00%	3	3	4	0,07%	26,00%
Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro	sp P21165 PEPQ_ECOLI	50.177,30	99,00%	1	1	1	0,02%	2,26%
Pyruvate dehydrogenase E1 component (EC	sp P0AFG8 ODP1_ECOLI	99.540,00	100,00%	6	6	6	0,11%	7,56%
Phosphoenolpyruvate-protein phosphotrans	sp P37177 PT1P_ECOLI	83.718,50	100,00%	3	3	3	0,06%	5,21%
Ribose transport ATP-binding protein rbs	sp P04983 RBSA_ECOLI	55.043,30	99,90%	1	1	1	0,02%	2,59%
Rare lipoprotein A precursor.	sp P10100 RLPA_ECOLI	37.527,60	100,00%	2	2	2	0,04%	6,91%
Magnesium transporting ATPase, P-type 1	sp P0ABB8 ATMA_ECOLI	99.468,80	100,00%	3	3	3	0,06%	5,23%
Hypothetical protein yibN.	sp P0AG27 YIBN_ECOLI	15.596,20	100,00%	2	2	2	0,04%	17,50%
Transcription elongation protein nusA (N	sp P0AFF6 NUSA_ECOLI	54.871,40	100,00%	2	2	2	0,04%	5,05%
2-amino-3-ketobutyrate coenzyme A ligase	sp P0AB77 KBL_ECOLI	43.117,70	100,00%	7	7	7	0,13%	20,40%
NADH-quinone oxidoreductase chain B (EC	sp P0AFC7 NUOB_ECOLI	25.055,60	100,00%	4	4	6	0,11%	16,80%
Aldehyde dehydrogenase B (EC 1.2.1.-).	sp P37685 ALDB_ECOLI	56.307,40	100,00%	7	9	10	0,18%	18,90%
Isoleucyl-tRNA synthetase (EC 6.1.1.5) (sp P00956 SYI_ECOLI	104.167,10	100,00%	7	7	8	0,15%	7,36%
Lipoprotein yfgL precursor.	sp P77774 YFGL_ECOLI	41.886,90	100,00%	4	4	4	0,07%	13,00%
ADP-L-glycero-D-manno-heptose-6-epimeras	sp P67910 HLDD_ECOLI	34.894,30	100,00%	8	8	9	0,17%	29,00%
Transketolase 2 (EC 2.2.1.1) (TK 2).	sp P33570 TKT2_ECOLI	73.044,10	99,70%	2	2	2	0,04%	2,70%
Inner membrane protein yjgQ.	sp P0ADC6 YJGQ_ECOLI	39.620,10	100,00%	2	2	2	0,04%	6,39%
Inner membrane protein oxaA.	sp P25714 OXAA_ECOLI	61.528,00	100,00%	2	2	2	0,04%	4,56%
EIImtI	6H-C384S-W42,6H-W42,EII-F97W,sp P00550 PTM3C_ECOLI	67.857,70	100,00%	8	8	9	0,17%	15,00%
30S ribosomal protein S1.	sp P0AG67 RS1_ECOLI	61.157,40	100,00%	16	23	30	0,55%	31,40%
Na(+)/H(+) antiporter 2 (Sodium/proton a	sp P0AFA7 NHAB_ECOLI	56.730,50	96,30%	1	1	1	0,02%	2,14%
Elongation factor G (EF-G).	sp P0A6M8 EFG_ECOLI	77.450,80	100,00%	22	30	47	0,86%	43,50%
Mannose permease IIC component (PTS syst	sp P69801 PTNC_ECOLI	27.636,40	100,00%	2	3	6	0,11%	11,70%

Hypothetical zinc-type alcohol dehydroge	sp P27250 YJGB_ECOLI	36.501,80	100,00%	2	2	2	0,04%	7,37%
30S ribosomal protein S16.	sp P0A7T3 RS16_ECOLI	9.190,60	99,70%	1	1	1	0,02%	13,40%
Protein-export membrane protein secD.	sp P0AG90 SECD_ECOLI	66.634,50	100,00%	14	14	19	0,35%	28,00%
Spermidine/putrescine import ATP-binding	sp P69874 POTA_ECOLI	43.028,40	100,00%	3	3	3	0,06%	9,52%
Protein ydgH precursor.	sp P76177 YDGH_ECOLI	33.903,30	100,00%	2	2	2	0,04%	8,60%
GTP cyclohydrolase I (EC 3.5.4.16) (GTP-	sp P0A6T5 GCH1_ECOLI	24.699,80	100,00%	3	3	3	0,06%	15,80%
Oligopeptidase A (EC 3.4.24.70).	sp P27298 OPDA_ECOLI	77.169,50	99,50%	2	2	2	0,04%	3,53%
Organic solvent tolerance protein precur	sp P31554 OSTA_ECOLI	89.672,80	100,00%	12	13	16	0,29%	17,10%
Aspartate aminotransferase (EC 2.6.1.1)	sp P00509 AAT_ECOLI	43.574,10	100,00%	10	11	13	0,24%	28,00%
Superoxide dismutase [Mn] (EC 1.15.1.1)	sp P00448 SODM_ECOLI	22.966,60	100,00%	4	4	6	0,11%	20,00%
Transport ATP-binding protein cydC.	sp P23886 CYDC_ECOLI	62.922,80	99,90%	1	1	1	0,02%	2,62%
Cell division protein ftsY.	sp P10121 FTSY_ECOLI	54.512,50	100,00%	2	2	2	0,04%	4,23%
Alanyl-tRNA synthetase (EC 6.1.1.7) (Ala	sp P00957 SYA_ECOLI	96.033,60	100,00%	31	39	55	1,01%	43,40%
Succinyl-CoA synthetase alpha chain (EC	sp P0AGE9 SUCD_ECOLI	29.646,60	100,00%	11	14	21	0,39%	46,90%
Hypothetical protein ycfM.	sp P0AB38 YCFM_ECOLI	22.515,20	100,00%	4	4	5	0,09%	29,60%
Adenylosuccinate lyase (EC 4.3.2.2) (Ade	sp P0AB89 PUR8_ECOLI	51.544,10	100,00%	8	8	10	0,18%	19,30%
Hypothetical protein ydbA.	sp P33666 YDBA_ECOLI	205.947,30	98,00%	1	1	1	0,02%	0,70%
Ribokinase (EC 2.7.1.15).	sp P0A9J6 RBSK_ECOLI	32.290,60	100,00%	3	3	3	0,06%	12,00%
Xaa-Pro aminopeptidase (EC 3.4.11.9) (X-	sp P15034 AMPP_ECOLI	49.684,60	100,00%	6	6	6	0,11%	14,10%
Glucose-6-phosphate isomerase (EC 5.3.1.	sp P0A6T1 G6PI_ECOLI	61.531,40	100,00%	9	9	11	0,20%	20,20%
Rare lipoprotein B precursor.	sp P0ADC1 RLPB_ECOLI	21.357,30	100,00%	5	6	9	0,17%	31,60%
L-threonine 3-dehydrogenase (EC 1.1.1.10	sp P07913 TDH_ECOLI	37.239,60	100,00%	3	3	3	0,06%	12,30%
Protein-export protein secB.	sp P0AG86 SECB_ECOLI	17.277,20	99,80%	1	1	1	0,02%	9,68%
Hypothetical lipoprotein ydcl precursor.	sp P64451 YDCL_ECOLI	24.427,30	100,00%	9	11	16	0,29%	54,50%
Fumarate reductase flavoprotein subunit	sp P00363 FRDA_ECOLI	65.840,40	100,00%	5	5	5	0,09%	8,82%
Outer membrane protein C precursor (Pori	sp P06996 OMPC_ECOLI	40.369,00	100,00%	4	4	4	0,07%	13,40%
Elongation factor Ts (EF-Ts).	sp P0A6P1 EFTS_ECOLI	30.291,60	100,00%	11	12	14	0,26%	36,90%
NAD(P) transhydrogenase subunit beta (EC	sp P0AB67 PNTB_ECOLI	48.724,00	100,00%	8	13	16	0,29%	22,90%
Superoxide dismutase [Fe] (EC 1.15.1.1).	sp P0AGD3 SODF_ECOLI	21.135,00	100,00%	4	4	7	0,13%	25,50%
Stringent starvation protein A.	sp P0ACA3 SSPA_ECOLI	24.174,60	100,00%	2	2	2	0,04%	11,80%
Spermidine/putrescine-binding periplasmi	sp P0AFK9 POTD_ECOLI	38.868,90	100,00%	2	2	2	0,04%	7,47%
Leucyl-tRNA synthetase (EC 6.1.1.4) (Leu	sp P07813 SYL_ECOLI	97.234,30	100,00%	2	2	2	0,04%	2,79%
2,3-bisphosphoglycerate-dependent phosph	sp P62707 GPMA_ECOLI	28.426,10	100,00%	4	5	7	0,13%	18,10%
Putative HTH-type transcriptional regula	sp P77634 YBCM_ECOLI	30.842,00	99,10%	1	1	1	0,02%	4,15%
50S ribosomal protein L10 (50S ribosomal	sp P0A7J3 RL10_ECOLI	17.580,60	100,00%	8	9	12	0,22%	53,70%

30S ribosomal protein S4.	sp P0A7V8 RS4_ECOLI	23.338,50	100,00%	3	3	4	0,07%	20,00%
Peroxidase/catalase HPI (EC 1.11.1.6) (C	sp P13029 CATA_ECOLI	80.025,80	100,00%	22	29	45	0,83%	32,90%
Ribose transport system permease protein	sp P0AGI1 RBSC_ECOLI	33.452,90	100,00%	2	2	3	0,06%	6,54%
Asparaginyl-tRNA synthetase (EC 6.1.1.22	sp P0A8M0 SYN_ECOLI	52.439,10	100,00%	8	8	8	0,15%	20,90%
Glucokinase (EC 2.7.1.2) (Glucose kinase	sp P0A6V8 GLK_ECOLI	34.723,90	100,00%	3	3	3	0,06%	10,90%
Ubiquinol oxidase polypeptide II precurs	sp P0ABJ1 CYOA_ECOLI	34.912,30	100,00%	6	9	21	0,39%	26,30%
Cold shock-like protein cspC (CSP-C).	sp P0A9Y6 CSPC_ECOLI	7.271,10	100,00%	2	2	3	0,06%	42,60%
S-adenosylmethionine synthetase (EC 2.5.	sp P0A817 METK_ECOLI	41.820,90	100,00%	2	2	2	0,04%	7,83%
Maltoporin precursor (Maltose-inducible	sp P02943 LAMB_ECOLI	49.912,80	100,00%	5	7	10	0,18%	14,80%
3-oxoacyl-[acyl-carrier-protein] synthas	sp P0A953 FABB_ECOLI	42.613,40	100,00%	4	5	6	0,11%	10,30%
Peptidyl-prolyl cis-trans isomerase D (E	sp P0ADY1 PPID_ECOLI	68.151,40	100,00%	13	13	15	0,28%	27,60%
NADH dehydrogenase (EC 1.6.99.3).	sp P00393 DHNA_ECOLI	47.228,80	99,30%	1	1	1	0,02%	2,54%
Hypothetical protein yneA precursor.	sp P76142 YNEA_ECOLI	36.685,00	100,00%	3	3	3	0,06%	9,71%
30S ribosomal protein S2.	sp P0A7V0 RS2_ECOLI	26.613,10	100,00%	5	5	5	0,09%	24,20%
Hypothetical lipoprotein yifL precursor.	sp P0ADN6 YIFL_ECOLI	7.177,40	96,30%	1	1	2	0,04%	34,30%
Phospho-N-acetylmuramoyl-pentapeptide-tr	sp P0A6W3 MRAY_ECOLI	39.875,60	99,70%	1	1	1	0,02%	2,22%
UPF0304 protein yfbU.	sp P0A8W8 YFBU_ECOLI	19.536,50	100,00%	2	2	2	0,04%	17,10%
UPF0169 lipoprotein yfiO precursor.	sp P0AC02 YFIO_ECOLI	27.830,30	100,00%	4	4	4	0,07%	20,40%
Phosphocarrier protein HPr (Histidine-co	sp P0AA04 PTHP_ECOLI	9.119,20	99,90%	1	1	1	0,02%	15,30%
Phenylalanyl-tRNA synthetase beta chain	sp P07395 SYFB_ECOLI	87.378,60	100,00%	3	3	3	0,06%	4,91%
Anthranilate synthase component I (EC 4.	sp P00895 TRPE_ECOLI	57.495,80	100,00%	3	3	3	0,06%	6,54%
Pyruvate dehydrogenase [cytochrome] (EC	sp P07003 POXB_ECOLI	62.012,00	100,00%	3	3	3	0,06%	6,64%
Low affinity tryptophan permease.	sp P23173 TNAB_ECOLI	45.213,70	100,00%	2	2	3	0,06%	5,54%
D-3-phosphoglycerate dehydrogenase (EC 1	sp P0A9T0 SERA_ECOLI	44.045,90	100,00%	2	2	2	0,04%	6,36%
Succinate dehydrogenase iron-sulfur prot	sp P07014 DHSB_ECOLI	26.771,00	100,00%	2	2	2	0,04%	10,10%
Sec-independent protein translocase prot	sp P69428 TATA_ECOLI	9.664,50	99,90%	1	1	1	0,02%	14,60%
Entericidin B precursor.	sp P0ADB7 ECNB_ECOLI	4.809,50	96,30%	1	2	4	0,07%	39,60%
Uridine phosphorylase (EC 2.4.2.3) (UrdP	sp P12758 UDP_ECOLI	27.027,50	100,00%	6	8	10	0,18%	27,80%
NAD(P) transhydrogenase subunit alpha (E	sp P07001 PNTA_ECOLI	54.623,70	100,00%	9	14	22	0,40%	23,70%
Probable formate transporter 1 (Formate	sp P0AC23 FOCA_ECOLI	30.991,40	100,00%	3	4	4	0,07%	9,12%
Nucleoside permease nupC (Nucleoside-tra	sp P0AFF2 NUPC_ECOLI	43.477,70	100,00%	2	2	3	0,06%	5,00%
Peptidoglycan-associated lipoprotein pre	sp P0A912 PAL_ECOLI	18.824,50	100,00%	4	4	7	0,13%	29,50%
Putative betaine aldehyde dehydrogenase	sp P77674 YDCW_ECOLI	50.829,80	100,00%	7	9	11	0,20%	21,30%
Protein dcrB precursor.	sp P0AEE1 DCRB_ECOLI	19.787,70	100,00%	2	2	2	0,04%	16,20%
Lysyl-tRNA synthetase, heat inducible (E	sp P0A8N5 SYK2_ECOLI	57.697,30	100,00%	2	2	2	0,04%	9,13%

D-methionine-binding lipoprotein metQ pr	sp P28635 METQ_ECOLI	29.431,90	100,00%	6	6	6	0,11%	30,60%
Transaldolase A (EC 2.2.1.2).	sp P0A867 TALA_ECOLI	35.659,50	99,50%	1	1	1	0,02%	5,06%
Glutathione reductase (EC 1.8.1.7) (GR)	sp P06715 GSHR_ECOLI	48.772,60	100,00%	2	2	2	0,04%	4,89%
Putative transport protein yidE.	sp P60872 YIDE_ECOLI	58.941,10	99,90%	1	1	1	0,02%	1,99%
Glycerol kinase (EC 2.7.1.30) (ATP:glyce	sp P0A6F3 GLPK_ECOLI	56.100,10	100,00%	5	5	6	0,11%	13,00%
Elongation factor Tu (EF-Tu) (P-43).	sp P0A6N1 EFTU_ECOLI	43.182,60	100,00%	21	29	56	1,03%	61,10%
Aspartate ammonia-lyase (EC 4.3.1.1) (As	sp P0AC38 ASPA_ECOLI	52.356,30	100,00%	16	20	31	0,57%	39,30%
Hypothetical UPF0070 protein yfgM.	sp P76576 YFGM_ECOLI	22.176,40	100,00%	2	2	2	0,04%	21,40%
Inner membrane protein yccF.	sp P0AB12 YCCF_ECOLI	16.275,90	100,00%	2	2	2	0,04%	14,90%
High affinity ribose transport protein r	sp P04982 RBSD_ECOLI	15.292,20	100,00%	3	3	4	0,07%	24,50%
Glycyl-tRNA synthetase alpha chain (EC 6	sp P00960 SYGA_ECOLI	34.774,90	100,00%	4	5	7	0,13%	21,50%
3-oxoacyl-[acyl-carrier-protein] reducta	sp P0AEK2 FABG_ECOLI	25.561,00	100,00%	7	12	17	0,31%	43,00%
Delta-aminolevulinic acid dehydratase (E	sp P0ACB2 HEM2_ECOLI	35.494,70	100,00%	6	6	8	0,15%	21,70%
Phosphoglycerate kinase (EC 2.7.2.3).	sp P0A799 PGK_ECOLI	40.988,00	100,00%	8	9	11	0,20%	23,30%
NADH-quinone oxidoreductase chain F (EC	sp P31979 NUOF_ECOLI	49.294,50	100,00%	7	7	7	0,13%	20,90%
Fructose-bisphosphate aldolase class II	sp P0AB71 ALF_ECOLI	39.016,10	100,00%	8	11	15	0,28%	29,90%
UTP-glucose-1-phosphate uridylyltransfe	sp P0AAB6 GALF_ECOLI	32.830,10	96,30%	1	1	2	0,04%	4,04%
MltA-interacting protein precursor.	sp P0A908 MIPA_ECOLI	27.831,90	96,30%	1	1	2	0,04%	5,24%
Aconitate hydratase 1 (EC 4.2.1.3) (Citr	sp P25516 ACON1_ECOLI	97.517,60	100,00%	3	3	3	0,06%	3,03%
Protein recA (Recombinase A).	sp P0A7G6 RECA_ECOLI	37.843,50	100,00%	5	5	5	0,09%	19,60%
ATP-dependent protease hslV (EC 3.4.25.-	sp P0A7B8 HSLV_ECOLI	18.962,10	100,00%	2	2	2	0,04%	10,30%
Hypothetical UPF0325 protein yaeH.	sp P62768 YAEH_ECOLI	15.097,00	99,90%	2	2	2	0,04%	18,80%
Long-chain fatty acid transport protein	sp P10384 FADL_ECOLI	48.773,40	96,30%	1	1	1	0,02%	2,68%
ATP synthase B chain (EC 3.6.3.14).	sp P0ABA0 ATPF_ECOLI	17.264,50	100,00%	9	11	19	0,35%	46,80%
Outer membrane protein X precursor.	sp P0A917 OMPX_ECOLI	18.603,00	98,80%	2	2	2	0,04%	13,50%
ATP-dependent Clp protease proteolytic s	sp P0A6G7 CLPP_ECOLI	23.187,30	100,00%	2	3	4	0,07%	14,50%
Hypothetical protein yram.	sp P45464 YRAM_ECOLI	72.825,80	100,00%	5	5	5	0,09%	7,67%
PTS system mannose-specific EIIB compon	sp P69797 PTNAB_ECOLI	34.916,20	100,00%	14	23	38	0,70%	42,50%
ATP-dependent hsl protease ATP-binding s	sp P0A6H5 HSLU_ECOLI	49.595,20	99,60%	2	2	2	0,04%	5,42%
Cysteine synthase A (EC 2.5.1.47) (O-ace	sp P0ABK5 CYSK_ECOLI	34.359,70	100,00%	10	11	16	0,29%	38,80%
Catalase HPII (EC 1.11.1.6) (Hydroxypero	sp P21179 CATE_ECOLI	84.165,10	100,00%	22	27	38	0,70%	30,40%
50S ribosomal protein L1.	sp P0A7L0 RL1_ECOLI	24.598,20	100,00%	6	7	9	0,17%	33,90%
Thiosulfate-binding protein precursor.	sp P16700 CYSP_ECOLI	37.615,40	100,00%	3	3	3	0,06%	9,47%
Protein rcsF.	sp P69411 RCSF_ECOLI	14.163,50	95,90%	1	1	1	0,02%	10,40%
30S ribosomal protein S10.	sp P0A7R5 RS10_ECOLI	11.735,80	100,00%	2	2	2	0,04%	23,30%

		0						
Triosephosphate isomerase (EC 5.3.1.1) (sp P0A858 TPIS_ECOLI	26.971,80	100,00%	4	4	4	0,07%	18,00%
ATP synthase beta chain (EC 3.6.3.14).	sp P0ABB4 ATPB_ECOLI	50.194,30	100,00%	5	5	5	0,09%	16,30%
DNA gyrase subunit A (EC 5.99.1.3).	sp P0AES4 GYRA_ECOLI	96.965,00	100,00%	13	13	14	0,26%	18,70%
Phosphoserine aminotransferase (EC 2.6.1	sp P23721 SERC_ECOLI	39.652,90	100,00%	2	2	2	0,04%	7,76%
Alpha-ketoglutarate permease.	sp P0AEX3 KGTP_ECOLI	47.054,00	100,00%	2	2	2	0,04%	5,09%
ATP synthase alpha chain (EC 3.6.3.14).	sp P0ABB0 ATPA_ECOLI	55.223,20	100,00%	10	11	11	0,20%	22,40%
50S ribosomal protein L9.	sp P0A7R1 RL9_ECOLI	15.768,70	100,00%	3	3	3	0,06%	23,50%
PTS system trehalose-specific EIIBC comp	sp P36672 PTTBC_ECOLI	51.082,60	100,00%	5	6	9	0,17%	10,40%
Antigen 43 precursor (AG43) (Fluffing pr	sp P39180 AG43_ECOLI	106.823,60	100,00%	25	39	64	1,17%	34,40%
Tail-specific protease precursor (EC 3.4	sp P23865 PRC_ECOLI	76.665,70	100,00%	9	10	12	0,22%	13,60%
ABC transporter ATP-binding protein yjJK	sp P0A9W3 YJK_ECOLI	62.314,20	100,00%	2	2	2	0,04%	3,97%
Branched-chain-amino-acid aminotransfera	sp P0AB80 ILVE_ECOLI	33.962,60	96,30%	1	1	1	0,02%	5,19%
Glucose-6-phosphate 1-dehydrogenase (EC	sp P0AC53 G6PD_ECOLI	55.705,70	99,70%	2	2	2	0,04%	4,28%
Hypothetical protein yfdI.	sp P76507 YFDI_ECOLI	51.487,90	100,00%	1	2	3	0,06%	2,71%
Aldehyde dehydrogenase A (EC 1.2.1.22) (sp P25553 ALDA_ECOLI	52.142,10	100,00%	15	20	39	0,72%	37,00%
Lysine-arginine-ornithine-binding peripl	sp P09551 ARGT_ECOLI	27.993,10	95,60%	1	1	1	0,02%	2,69%
Glutamine transport system permease prot	sp P0AEQ6 GLNP_ECOLI	24.365,90	95,00%	1	1	1	0,02%	4,11%
Prolyl-tRNA synthetase (EC 6.1.1.15) (Pr	sp P16659 SYP_ECOLI	63.693,40	100,00%	10	11	14	0,26%	20,80%
30S ribosomal protein S13.	sp P0A7S9 RS13_ECOLI	12.968,90	100,00%	2	2	2	0,04%	26,50%
Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysi	sp P0A8N3 SYK1_ECOLI	57.474,30	100,00%	5	5	5	0,09%	10,90%
Lipid A export ATP-binding/permease prot	sp P60752 MSBA_ECOLI	64.462,70	100,00%	10	10	12	0,22%	20,30%
Inner membrane protein yqjE.	sp P64585 YQJE_ECOLI	15.147,60	100,00%	2	2	2	0,04%	13,40%
Maltose transport system permease protei	sp P02916 MALF_ECOLI	57.016,50	100,00%	6	6	8	0,15%	16,90%
Glucose-1-phosphate adenylyltransferase	sp P0A6V1 GLGC_ECOLI	48.566,90	96,30%	1	1	1	0,02%	2,33%
D-lactate dehydrogenase (EC 1.1.1.28) (R	sp P06149 DLD_ECOLI	64.482,90	100,00%	5	5	5	0,09%	8,95%
Tryptophan synthase beta chain (EC 4.2.1	sp P0A879 TRPB_ECOLI	42.852,80	100,00%	2	2	2	0,04%	9,60%
Enolase (EC 4.2.1.11) (2-phosphoglycerat	sp P0A6P9 ENO_ECOLI	45.525,50	100,00%	11	14	25	0,46%	34,60%
Malate synthase G (EC 2.3.3.9) (MSG).	sp P37330 MASZ_ECOLI	80.358,90	100,00%	11	11	13	0,24%	19,30%
Glutamate decarboxylase beta (EC 4.1.1.1	sp P69910 DCEB_ECOLI	52.669,60	100,00%	18	26	51	0,94%	44,00%
Phosphoenolpyruvate carboxykinase [ATP]	sp P22259 PPCK_ECOLI	59.645,30	100,00%	5	5	7	0,13%	13,00%
UPF0076 protein yjgF.	sp P0AF93 YJGF_ECOLI	13.480,20	99,90%	2	2	2	0,04%	17,30%
Diaminopimelate decarboxylase (EC 4.1.1.	sp P00861 DCDA_ECOLI	46.176,60	100,00%	7	9	11	0,20%	27,90%
2-hydroxy-3-oxopropionate reductase (EC	sp P0ABQ2 GARR_ECOLI	30.428,30	100,00%	3	3	4	0,07%	15,30%
Single-strand binding protein (SSB) (Hel	sp P0AGE0 SSB_ECOLI	18.843,20	96,30%	1	1	1	0,02%	7,91%

Glycine dehydrogenase [decarboxylating]	sp P33195 GCSP_ECOLI	104.246,10	100,00%	10	10	12	0,22%	13,20%
Outer membrane protein slp precursor.	sp P37194 SLP_ECOLI	20.964,10	100,00%	3	3	3	0,06%	20,20%
Phosphoenolpyruvate-protein phosphotrans	sp P08839 PT1_ECOLI	63.564,30	100,00%	7	8	9	0,17%	13,90%
Glutamate decarboxylase alpha (EC 4.1.1.)	sp P69908 DCEA_ECOLI	52.686,80	96,30%	1	1	1	0,02%	44,00%
ATP-dependent Clp protease ATP-binding s	sp P0A6H1 CLPX_ECOLI	46.226,10	100,00%	2	2	2	0,04%	6,38%
Rod shape-determining protein mreB.	sp P0A9X4 MREB_ECOLI	36.952,40	99,80%	1	1	1	0,02%	4,03%
Hypothetical GST-like protein yghU.	sp Q46845 YGHU_ECOLI	32.392,20	100,00%	2	2	2	0,04%	8,68%
NADP-specific glutamate dehydrogenase (E	sp P00370 DHE4_ECOLI	48.581,20	100,00%	12	15	18	0,33%	36,00%
Small protein A precursor.	sp P0A937 SMPA_ECOLI	12.302,00	100,00%	2	2	2	0,04%	32,70%
Protein grpE (HSP-70 cofactor) (Heat sho	sp P09372 GRPE_ECOLI	21.797,80	96,30%	1	1	1	0,02%	7,11%
Osmotically inducible lipoprotein E prec	sp P0ADB1 OSME_ECOLI	12.020,50	100,00%	5	9	12	0,22%	37,50%
Protein-export membrane protein secG (Pr	sp P0AG99 SECG_ECOLI	11.365,80	100,00%	2	2	3	0,06%	27,30%
Seryl-tRNA synthetase (EC 6.1.1.11) (Ser	sp P0A8L1 SYS_ECOLI	48.414,80	100,00%	6	6	8	0,15%	16,50%
Glucose-1-phosphatase precursor (EC 3.1.	sp P19926 AGP_ECOLI	45.682,90	100,00%	6	6	7	0,13%	17,40%
Glutamate-1-semialdehyde 2,1-aminomutase	sp P23893 GSA_ECOLI	45.366,30	100,00%	3	3	3	0,06%	9,86%
30S ribosomal protein S6 [Contains: 30S	sp P02358 RS6_ECOLI	15.703,30	96,30%	1	1	1	0,02%	8,15%
Bifunctional protein hldE [Includes: D-b	sp P76658 HLDE_ECOLI	51.050,60	99,50%	1	1	1	0,02%	2,52%
Polyribonucleotide nucleotidyltransferas	sp P05055 PNP_ECOLI	77.101,00	100,00%	20	26	34	0,62%	36,40%
Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Ty	sp P0AGJ9 SYT_ECOLI	47.397,00	100,00%	2	2	2	0,04%	6,15%
D-galactose-binding periplasmic protein	sp P0AEE5 DGAL_ECOLI	35.713,30	100,00%	9	11	16	0,29%	34,90%
Isocitrate lyase (EC 4.1.3.1) (Isocitras	sp P0A9G6 ACEA_ECOLI	47.522,00	100,00%	13	16	19	0,35%	47,70%
Chaperone surA precursor (Peptidyl-proly	sp P0ABZ6 SURA_ECOLI	47.284,70	100,00%	4	4	5	0,09%	12,10%
Protein ydgA precursor.	sp P77804 YDGA_ECOLI	54.690,10	100,00%	7	7	7	0,13%	18,30%
Hypothetical lipoprotein ygdI precursor.	sp P65292 YGDI_ECOLI	8.174,30	96,30%	1	2	2	0,04%	26,70%
Periplasmic oligopeptide-binding protein	sp P23843 OPPA_ECOLI	60.899,80	100,00%	23	34	61	1,12%	47,10%
Citrate synthase (EC 2.3.3.1).	sp P0ABH7 CISY_ECOLI	48.016,80	100,00%	24	33	74	1,36%	61,80%
3-hydroxydecanoyl-[acyl-carrier-protein]	sp P0A6Q3 FABA_ECOLI	18.838,40	99,70%	2	2	3	0,06%	11,70%
4-aminobutyrate aminotransferase (EC 2.6	sp P22256 GABT_ECOLI	45.775,60	100,00%	5	5	6	0,11%	15,50%
Methionyl-tRNA synthetase (EC 6.1.1.10)	sp P00959 SYM_ECOLI	76.125,50	100,00%	4	4	4	0,07%	7,84%
Outer membrane protein assembly factor y	sp P0A940 YAET_ECOLI	90.554,40	100,00%	18	21	25	0,46%	31,50%
Translation initiation factor IF-2.	sp P0A705 IF2_ECOLI	97.349,00	100,00%	3	3	3	0,06%	3,26%
Putative Na(+)/H(+) exchanger yjcE.	sp P32703 YJCE_ECOLI	60.525,40	97,90%	1	1	1	0,02%	2,55%
NAD-dependent malic enzyme (EC 1.1.1.38)	sp P26616 MAO1_ECOLI	63.198,80	100,00%	10	10	10	0,18%	19,50%
Hypothetical ABC transporter ATP-binding	sp P36879 YADG_ECOLI	34.648,40	100,00%	2	2	2	0,04%	7,47%
D-amino acid dehydrogenase	sp P0A6J5 DADA_ECOLI	47.607,60	100,00%	4	4	4	0,07%	10,40%

small subunit		0						
Transaldolase B (EC 2.2.1.2).	sp P0A870 TALB_ECOLI	35.089,70	100,00%	14	15	20	0,37%	58,90%
Biosynthetic arginine decarboxylase (EC	sp P21170 SPEA_ECOLI	73.899,00	100,00%	9	9	10	0,18%	16,40%
Thiol peroxidase (EC 1.11.1.-) (Scavenga	sp P0A862 TPX_ECOLI	17.704,00	96,30%	1	1	2	0,04%	7,78%
Major outer membrane lipoprotein precurs	sp P69776 LPP_ECOLI	8.323,70	100,00%	5	12	49	0,90%	48,70%
Phosphopentomutase (EC 5.4.2.7) (Phospho	sp P0A6K6 DEOB_ECOLI	44.371,10	96,30%	1	1	1	0,02%	2,95%
Trigger factor (TF).	sp P0A850 TIG_ECOLI	48.192,90	100,00%	10	12	15	0,28%	26,60%
50S ribosomal protein L28.	sp P0A7M2 RL28_ECOLI	8.875,30	99,90%	2	2	3	0,06%	13,00%
Putative cytochrome d ubiquinol oxidase	sp P0ADW3 YHCB_ECOLI	15.239,80	100,00%	6	11	16	0,29%	63,40%
Hypothetical lipoprotein yajG precursor.	sp P0ADA5 YAJG_ECOLI	20.950,40	100,00%	4	4	9	0,17%	25,00%
Putative aldolase yneB (EC 4.2.1.-).	sp P76143 YNEB_ECOLI	31.893,00	100,00%	16	23	42	0,77%	59,10%
Ribulose-phosphate 3-epimerase (EC 5.1.3	sp P0AG07 RPE_ECOLI	24.554,90	96,30%	1	1	1	0,02%	6,67%
Nucleoside-specific channel-forming prot	sp P0A927 TSX_ECOLI	33.590,20	100,00%	2	2	6	0,11%	8,16%
Anaerobic C4-dicarboxylate transporter d	sp P0ABN5 DCUA_ECOLI	45.752,20	100,00%	3	3	4	0,07%	7,16%
Phosphoglucosyltransferase (EC 5.4.2.2) (Glucose	sp P36938 PGM_ECOLI	58.361,60	100,00%	3	3	3	0,06%	6,59%
Protein tolB precursor.	sp P0A855 TOLB_ECOLI	45.955,10	100,00%	4	4	4	0,07%	11,40%
Bifunctional putA protein [Includes: Pro	sp P09546 PUTA_ECOLI	143.818,40	100,00%	21	23	29	0,53%	19,50%
Ribosome recycling factor (Ribosome-rele	sp P0A805 RRF_ECOLI	20.639,30	100,00%	7	8	11	0,20%	40,00%
UTP-glucose-1-phosphate uridylyltransfe	sp P0AEP3 GALU_ECOLI	32.810,80	96,30%	1	1	1	0,02%	4,32%
Protein yicC.	sp P23839 YICC_ECOLI	33.175,20	100,00%	3	4	4	0,07%	13,60%
Ubiquinol oxidase polypeptide I (EC 1.10	sp P0AB18 CYOB_ECOLI	74.370,10	100,00%	7	11	16	0,29%	11,50%
NADP-dependent L-serine/L-allo-threonine	sp P39831 YDFG_ECOLI	27.248,70	96,30%	1	1	1	0,02%	7,26%
D-serine/D-alanine/glycine transporter.	sp P0AAE0 CYCA_ECOLI	51.660,80	96,30%	1	1	1	0,02%	2,98%
Tyrosine-protein kinase wzc (EC 2.7.1.11	sp P76387 WZC_ECOLI	79.345,10	100,00%	2	3	5	0,09%	3,61%
GTP-binding protein typA/BipA (Tyrosine	sp P32132 TYPA_ECOLI	67.356,00	100,00%	2	2	2	0,04%	3,46%
ProP effector.	sp P45577 PROQ_ECOLI	25.892,40	96,30%	1	1	1	0,02%	4,31%
Galactoside transport ATP-binding protei	sp P0AAG8 MGLA_ECOLI	56.417,70	96,30%	1	1	1	0,02%	2,57%
L-fucose isomerase (EC 5.3.1.25) (6-deox	sp P69922 FUCI_ECOLI	64.977,20	100,00%	2	2	2	0,04%	3,21%
UPF0092 protein yajC.	sp P0ADZ7 YAJC_ECOLI	11.887,60	100,00%	4	4	10	0,18%	27,30%
Flavoprotein wrbA (Trp repressor binding	sp P0A8G6 WRBA_ECOLI	20.714,20	98,00%	1	1	1	0,02%	8,63%
Outer membrane protein A precursor (Oute	sp P0A910 OMPA_ECOLI	37.201,00	100,00%	15	20	42	0,77%	42,80%
Hypothetical lipoprotein yddW precursor.	sp P64426 YDDW_ECOLI	49.575,10	99,80%	1	1	2	0,04%	2,51%
30S ribosomal protein S18.	sp P0A7T7 RS18_ECOLI	8.855,80	100,00%	2	2	3	0,06%	24,30%
Inner membrane protein ybaL.	sp P39830 YBAL_ECOLI	59.425,90	96,30%	1	1	1	0,02%	3,05%
Outer membrane protein F precursor (Pori	sp P02931 OMPF_ECOLI	39.334,40	100,00%	7	8	11	0,20%	20,70%

Malate dehydrogenase (EC 1.1.1.37).	sp P61889 MDH_ECOLI	32.337,30	100,00%	11	15	28	0,51%	38,10%
Trehalose-6-phosphate hydrolase (EC 3.2).	sp P28904 TREC_ECOLI	63.838,50	100,00%	2	2	2	0,04%	3,81%
50S ribosomal protein L3.	sp P60438 RL3_ECOLI	22.242,80	95,60%	1	1	1	0,02%	4,78%
Aspartate-semialdehyde dehydrogenase (EC	sp P0A9Q9 DHAS_ECOLI	40.018,60	100,00%	2	2	3	0,06%	8,99%
Periplasmic beta-glucosidase precursor (sp P33363 BGLX_ECOLI	83.461,40	100,00%	3	3	3	0,06%	4,71%
Inorganic pyrophosphatase (EC 3.6.1.1) (sp P0A7A9 IPYR_ECOLI	19.572,80	100,00%	3	3	3	0,06%	16,00%
Glycyl-tRNA synthetase beta chain (EC 6.	sp P00961 SYGB_ECOLI	76.684,10	100,00%	23	30	44	0,81%	39,70%
Starvation-sensing protein rspA.	sp P38104 RSPA_ECOLI	45.969,40	99,00%	2	2	2	0,04%	9,16%
30S ribosomal protein S5.	sp P0A7W1 RS5_ECOLI	17.471,80	100,00%	5	6	6	0,11%	48,20%
Hypothetical protein yhil precursor.	sp P37626 YHII_ECOLI	38.828,50	100,00%	2	2	2	0,04%	7,89%
Sensor protein kdpD (EC 2.7.3.-).	sp P21865 KDPD_ECOLI	98.719,90	98,60%	2	2	2	0,04%	3,24%
Ribonucleoside-diphosphate reductase 1 a	sp P00452 RIR1_ECOLI	85.778,80	100,00%	3	3	3	0,06%	5,65%
Lysophospholipase L2 (EC 3.1.1.5) (Lecit	sp P07000 PLDB_ECOLI	38.978,50	95,00%	1	1	1	0,02%	5,59%
Hypothetical UPF0142 protein ycaO.	sp P75838 YCAO_ECOLI	65.653,60	100,00%	2	2	2	0,04%	3,92%
Phosphoenolpyruvate synthase (EC 2.7.9.2	sp P23538 PPSA_ECOLI	87.304,40	99,80%	2	2	2	0,04%	3,41%
Outer membrane protein tolC precursor.	sp P02930 TOLC_ECOLI	54.015,20	96,30%	1	1	1	0,02%	3,23%
HTH-type transcriptional regulator maltT	sp P06993 MALT_ECOLI	103.121,50	100,00%	3	3	3	0,06%	3,88%
ABC transporter periplasmic-binding prot	sp P39325 YTFQ_ECOLI	34.345,60	100,00%	7	10	19	0,35%	29,20%
Vitamin B12 transporter btuB precursor (sp P06129 BTUB_ECOLI	68.408,20	100,00%	7	7	7	0,13%	14,80%
Cytochrome d ubiquinol oxidase subunit I	sp P0ABK2 CYDB_ECOLI	42.454,10	100,00%	3	7	11	0,20%	7,65%
Septum site-determining protein minD (Ce	sp P0AEZ3 MIND_ECOLI	29.484,10	100,00%	3	3	3	0,06%	14,90%
PTS system glucose-specific EIICB compon	sp P69786 PTGCB_ECOLI	50.678,40	100,00%	8	11	20	0,37%	20,80%
D-lactate dehydrogenase (EC 1.1.1.28) (D	sp P52643 LDHD_ECOLI	36.535,70	100,00%	2	2	2	0,04%	7,60%
NADH-quinone oxidoreductase chain C/D (E	sp P33599 NUOCD_ECOLI	68.696,40	100,00%	14	16	20	0,37%	26,80%
Cytochrome d ubiquinol oxidase subunit I	sp P0ABJ9 CYDA_ECOLI	58.207,40	100,00%	19	26	57	1,05%	30,10%
Inner membrane protein yjgP.	sp P0AF98 YJGP_ECOLI	40.358,90	100,00%	3	3	3	0,06%	10,40%
Carbon starvation protein A.	sp P15078 CSTA_ECOLI	75.107,10	100,00%	6	8	11	0,20%	8,27%
Pyruvate kinase II (EC 2.7.1.40) (PK-2).	sp P21599 KPYK2_ECOLI	51.226,60	100,00%	13	15	22	0,40%	30,90%
Peptidase B (EC 3.4.11.23) (Aminopeptida	sp P37095 PEPB_ECOLI	46.181,80	100,00%	8	9	11	0,20%	23,20%

92

93

94 **Supplemental text.**

95 To further investigate the role of tags fused to cell division proteins we compared the effects
96 of mild overexpression of GFP-fusions to FtsQ and FtsQ D237N to that of untagged FtsQ and
97 FtsQ D237N. FtsQ, GFP-FtsQ, FtsQ D237N and GFP-FtsQ D237N were expressed at
98 endogenous levels in *E. coli* MC4100 in addition to the chromosomal *ftsQ* and subsequently
99 dilutions of these cultures were spotted on a plate and incubated to form colonies. GFP-FtsQ
100 and GFP-FtsQ D237N are both expressed at endogenous levels from a leaky *Trc99_{down}*
101 promotor, FtsQ and FtsQ D237N are both expressed at endogenous levels from a pBAD
102 promotor after induction with 0.2% arabinose (Fig. S5B). A clear difference was observed
103 between strains expressing FtsQ D237N and GFP-FtsQ D237N. As previously shown, mild
104 overexpression of FtsQ D237N disrupts the 1 MDa cell division complex. Here, mild
105 expression of FtsQ D237N and of GFP-FtsQ D237N results in less growth on the plate as
106 compared to empty vector. GFP-FtsQ D237N is always expressed and thus this strain is
107 inhibited in growth by one order of magnitude as compared to empty vector. FtsQ-D237N is
108 expressed after induction with 0.2% arabinose. When not induced, this strain grows similar to
109 empty vector; when FtsQ D237N is induced, growth is inhibited by two orders of magnitude
110 as compared to empty vector and by one order of magnitude as compared to GFP-FtsQ
111 D237N (Fig. S5A). Thus, addition of a GFP-tag to the mutant FtsQ D237N makes it less
112 inhibitory on growth. Also, a difference in growth can be observed between strains expressing
113 additional FtsQ and GFP-FtsQ. Here, mild expression of GFP-FtsQ results in less growth.
114 GFP-FtsQ is always expressed and thus this strain is inhibited in growth by one order of
115 magnitude as compared to empty vector. FtsQ is expressed after induction with 0.2%
116 arabinose. Whether induced or not, this strain grows similar as compared to empty vector
117 (Fig. 5A). Thus, addition of a GFP-tag to the mutant FtsQ D237N makes the mutant less
118 growth-inhibiting, whereas addition of a GFP-tag to wild type FtsQ makes it more growth-

119 inhibiting. This observation is in agreement with the finding that GFP-FtsQ protein
120 complexes at a different size than 1 MDa (Fig. 5).

121

122 **Supplementary reference**

123 1. Wagner, S. *et al.* Consequences of membrane protein overexpression in *Escherichia coli*.
124 *Mol. Cell. Proteomics* **6**, 1527-1550 (2007).

125

126

127 **Supplementary file S1** Raw data of the Mass Spectrometry experiment. The data can be
128 viewed with the freely available demo version of the Scaffold proteome software package
129 (<http://www.proteomesoftware.com/products/scaffold/>)

130