

Supplementary material - Table 1. Protein identification by MALDI-TOF/MS of 2-DE gel spots from wild-type strain ESBL-*E. coli* C5478

Spot	Protein Description	Species	Protein Name	Accession Number	Protein MW	Protein PI	Peptide Count	Sequence coverage %	Protein Score	Biological function	References
1	DNA protection during starvation protein	<i>Escherichia coli</i> O139:H28	dps	A7ZJM7	18684	5.70	19	92	177	Stress response: Starvation	[1]
2	Ferric uptake regulation protein	<i>Escherichia coli</i> O157:H7	fur	P0A9B1	17012	5.68	5	41	61	Transcription	[2]
5	Universal stress protein G	<i>Escherichia coli</i> O157:H7	uspG	Q8XBT3	15926	5.89	7	66	125	Stress response: General stress	[2]
7	Peroxiredoxin osmC	<i>Escherichia coli</i>	osmC	P0C0L2	15193	5.57	4	31	65	Stress response: Oxidative stress	[3]
8	30S ribosomal protein S6	<i>Escherichia coli</i> O139:H28	rpsF	A7ZV71	15177	5.26	3	28	59	Translation	[1]
9	10 kDa chaperonin	<i>Escherichia coli</i> O139:H28	groS	A7ZV11	10381	5.15	6	74	69	Protein folding	[1]
12	UPF0313 protein ygiQ	<i>Escherichia coli</i> (strain K12)	ygiQ	Q46861	84223	9.24	7	13	100	Unknown function	[3]
14	Outer membrane protein X	<i>Escherichia coli</i> O157:H7	ompX	P0A919	67648	5.30	8	49	118	Stress response: Antibiotic resistance	[2]
17	L(+)-tartrate dehydratase subunit beta	<i>Escherichia coli</i> O157:H7	ttdB	Q8XBK5	22988	6.08	4	31	73	L(+)-tartrate dehydratase activity: Energy metabolism	[2]
18	Glyceraldehyde-3-phosphate dehydrogenase A	<i>Escherichia coli</i> O157:H7	gapA	P0A9B4	35681	6.58	17	51	154	Glycolysis	[2]
20	Thiol peroxidase	<i>Escherichia coli</i> O157:H7	tpx	P0A864	17995	4.75	7	58	96	Stress response: Oxidative stress	[2]
21	S-ribosylhomocysteine lyase	<i>Escherichia coli</i> (strain 55989 / EAEC)	luxS	B7LEA1	19576	4.98	7	44	63	Autoinducer synthesis	[1]

24	Inorganic pyrophosphatase	<i>Escherichia coli</i> O157:H7	ppa	P0A7B0	19805	5.03	4	22	77	Phosphate-containing compound metabolic process	[2]
25	Alkyl hydroperoxide reductase subunit C	<i>Escherichia coli</i> O157:H7	ahpC	P0AE10	20862	5.03	12	63	105	Stress response: Oxidative stress	[2]
26	Superoxide dismutase [Fe]	<i>Escherichia coli</i> O157:H7	sodB	P0AGD5	21310	5.58	8	55	104	Stress response: Oxidative stress	[2]
28	Modulator of drug activity B	<i>Escherichia coli</i> O157:H7	mdaB	P0AEY7	21877	5.85	5	34	64	Stress response: Oxidative stress	[2]
30	Glutathione S-transferase	<i>Escherichia coli</i> O157:H7	gst	P0A9D3	22968	5.85	8	63	93	Transport	[2]
31	Oxygen-insensitive NAD(P)H nitroreductase	<i>Escherichia coli</i> (strain K12)	nfnB	P38489	23947	5.80	17	65	149	Stress response: Oxidative stress	[3]
32	F1845 adhesin operon regulatory protein	<i>Escherichia coli</i>	daaA	Q47133	9843	7.94	3	61	66	Transcription	[1]
33	Purine nucleoside phosphorylase deoD-type	<i>Escherichia coli</i> O139:H28	deoD	A7ZVS7	26161	5.39	11	68	79	Nucleoside metabolic process	[1]
34	F1845 adhesin operon regulatory protein	<i>Escherichia coli</i>	daaA	Q47133	9843	7.94	3	61	72	Transcription	[4]
35	Uncharacterized protein ycaC	<i>Escherichia coli</i>	ycaC	P21367	23200	5.20	60	30	5	Unknown function	[3, 5]
36	UPF0234 protein yajQ	<i>Escherichia coli</i> O127:H6	yajQ	B7UJP9	18301	5.94	5	37	103	Unknown function	[6]
39	Phosphoribosylamino imidazole-succinocarboxamide synthase	<i>Escherichia coli</i> O139:H28	purC	A7ZPS1	27149	5.05	9	41	90	Purine biosynthesis	[1]
40	Lysine-arginine-ornithine-binding periplasmic protein	<i>Escherichia coli</i> (strain K12)	argT	P09551	28088	5.19	8	41	84	Transport	[1]
41	Cystine-binding periplasmic protein	<i>Escherichia coli</i> O6	fliY	P0AEN0	29021	5.29	9	31	84	Transport	[7]

42	Stringent starvation protein A	<i>Escherichia coli</i> O157:H7	sspA	P0ACA5	24346	5.22	12	47	111	Unknown function	[2]
43	Adenylate kinase	<i>Escherichia coli</i> O139:H28	adk	A7ZIN4	23628	5.55	8	40	67	Nucleotide biosynthesis	[1]
44	Triosephosphate isomerase	<i>Escherichia coli</i> O139:H28	tpiA	A7ZUD3	27126	5.64	9	50	75	Glycolysis	[1]
46	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	<i>Escherichia coli</i> O127:H6	gpmA	B7ULM8	28539	5.85	13	48	123	Glycolysis	[6]
48	Succinate dehydrogenase iron-sulfur subunit	<i>Escherichia coli</i> (strain K12)	sdhB	P07014	27379	6.31	7	30	72	Transport	[3]
49	Pyrimidine monooxygenase RutA	<i>Escherichia coli</i>	rutA	C9QZ64	40146	5.14	4	16	72	Pyrimidine biosynthesis	[8]
50	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	<i>Escherichia coli</i> O127:H6	gpmA	B7ULM8	28539	5.85	7	33	116	Glycolysis	[6]
51	30S ribosomal protein S2	<i>Escherichia coli</i> O139:H28	rpsB	A7ZHQ9	26798	6.61	9	44	65	Translation	[1]
52	Aerobic respiration control protein ArcA	<i>Escherichia coli</i> O157:H7	arcA	P0A9Q3	27389	5.20	10	43	110	Transcription	[6]
56	UPF0234 protein yajQ	<i>Escherichia coli</i> O127:H6	yajQ	B7UJP9	18301	5.96	3	29	64	Unknown function	[6]
57	3'(2'),5'-bisphosphate nucleotidase CysQ	<i>Escherichia coli</i> O157:H7	cysQ	Q8XCG6	27314	5.59	4	33	75	Sulfur metabolism	[2]
61	3-mercaptopyruvate sulfurtransferase	<i>Escherichia coli</i> O157:H7	sseA	P58388	30864	4.56	12	53	148	Sulfurtransferase activity	[2]
62	D-alanine--D-alanine ligase B	<i>Escherichia coli</i> (strain K12)	ddlB	P07862	32933	4.75	5	27	88	Cell shape	[3]
65	D-galactose-	<i>Escherichia</i>	mglB	P0AEE6	35690	5.25	4	18	72	Transport	[1]

	bindingperiplasmicpr otein	<i>coli</i> O6									
66	Putative ribosome biogenesis GTPase RsgA	<i>Escherichia coli</i> O139:H28	rsgA	A7ZV32	39440	5.59	4	17	75	GTP binding	[1]
67	Transaldolase B	<i>Escherichia coli</i> O157:H7	talB	P0A871	35368	5.11	10	42	84	Pentose shunt	[2]
72	Putative quinone oxidoreductase YhdH	<i>Escherichia coli</i> (strain K12)	yhdH	P26646	34873	5.63	9	45	118	Unknown function	[3]
73	2,3,4,5- tetrahydropyridine- 2,6-dicarboxylateN- succinyltransferase	<i>Escherichia coli</i> O139:H28	dapD	A7ZHQ6	30044	5.55	12	54	119	Amino-acid biosynthesis	[2]
74	Malate dehydrogenase	<i>Escherichia coli</i> O139:H28	mdh	A7ZSD0	32488	5.61	14	58	133	Tricarboxylic acid cycle	[1]
76	Putative glucose-6- phosphate 1- epimerase	<i>Escherichia coli</i> (strain K12)	yeaD	P39173	32874	5.89	9	25	84	Carbohydrate metabolism	[3]
79	Cysteine synthase A	<i>Escherichia coli</i> O157:H7	cysK	P0ABK6	34525	5.83	18	78	225	Amino-acid biosynthesis, Cysteine biosynthesis	[2]
80	Putative glucose-6- phosphate 1- epimerase	<i>Escherichia coli</i> (strain K12)	yeaD	P39173	32874	5.89	9	25	84	Carbohydrate metabolism	[3]
83	Curved DNA- binding protein	<i>Escherichiacoli</i> O139:H28	cbpA	A7ZKA5	34404	6.33	3	17	57	Transcription	[1]
84	Xaa-Pro dipeptidase	<i>Escherichia coli</i> O8	pepQ	B7M650	50322	5.54	4	14	71	Proteolysis	[9]
88	Multiphosphoryl transfer protein	<i>Escherichia coli</i> O157:H7	fruB	P69812	39624	4.77	7	35	128	Transport	[2]
89	Protein kleA	<i>Escherichia coli</i>	kleA	Q52278	8636	5.08	3	42	71	Unknown function	[10]
92	Putative outer membrane porin protein nmpC	<i>Escherichia coli</i> (strain K12)	nmpC	P21420	40277	4.55	7	31	70	Transport	[3]

93	Alcohol dehydrogenase, propanol-preferring	<i>Escherichia coli</i> (strain K12)	adhP	P39451	35870	5.94	10	47	112	Stress response: Oxidative stress	[3]
94	Ribosomal RNA small subunit methyltransferase G	<i>Shewanella piezotolerans</i>	rsmG	B8CVV5	23626	5.39	5	28	85	rRNA processing	[11]
95	3-oxoacyl-[acyl-carrier-protein] synthase 2	<i>Escherichia coli</i> O157:H7	fabF	P0AAI7	43247	5.71	11	43	81	Fatty acid biosynthesis	[2]
97	Phosphoglycerate kinase	<i>Escherichia coli</i> O139:H28	pgk	A7ZR34	41264	5.08	18	57	137	Glycolysis	[1]
98	Maltose-binding periplasmic protein	<i>Escherichia coli</i> O157:H7	malE	P0AEY0	43360	5.22	13	45	108	Transport	[2]
102	Aminomethyltransferase	<i>Escherichia coli</i> O139:H28	gcvT	A7ZR14	40235	5.36	16	52	172	Glycine catabolic process	[1]
103	Aspartate aminotransferase	<i>Escherichia coli</i>	aspC	P00509	43831	5.54	11	38	112	Aspartate biosynthetic process	[1]
105	ATP synthase subunit alpha	<i>Escherichia coli</i> O139:H28	atpA	A7ZTU6	55416	5.80	12	31	135	Transport	[1]
108	Serine hydroxymethyltransferase	<i>Escherichia coli</i> O139:H28	glyA	A7ZPZ4	45459	6.03	10	26	84	Amino-acid biosynthesis	[2]
109	Der GTPase-activating protein YihI	<i>Escherichia coli</i> O7:K1	yihI	B7NV06	19034	6.37	4	28	62	Ribosome biogenesis	[9]
110	Elongation factor Tu 1	<i>Escherichia coli</i> O139:H28	tuf1	A7ZSL4	43457	5.30	17	54	164	Protein biosynthesis	[1]
111	Isocitrate dehydrogenase [NADP]	<i>Escherichia coli</i> (strain K12)	icd	P08200	46070	5.15	20	47	138	Tricarboxylic acid cycle	[1]
111	30S ribosomal protein S20	<i>Clostridium difficile</i> (strain 630)	rpsT	Q182G1	9777	11.17	6	60	36	Translation	[12]
114	Glutamate decarboxylase alpha	<i>Escherichia coli</i> O6	gadA	P69909	53221	5.22	20	129	129	Stress response: acid resistance	[7]

114	Glutamate decarboxylase beta	<i>Escherichia coli</i> O157:H7	gadB	P69911	53204	5.29	20	41	127	Stress response: acid resistance	[2]
115	Glutamate-1-semialdehyde 2,1-aminomutase	<i>Escherichia coli</i> O139:H28	hemL	A7ZHP6	45897	4.75	6	24	60	Porphyrin biosynthesis	[1]
117	Malate dehydrogenase	<i>Escherichia coli</i> O139:H28	mdh	A7ZSD0	32488	5.61	11	52	122	Tricarboxylic acid cycle	[1]
119	ATP synthase subunit beta	<i>Escherichia coli</i> O139:H28	atpD	A7ZTU4	50351	4.90	24	76	242	Transport	[1]
120	Uncharacterized protein ycfD	<i>Escherichia coli</i> (strain K12)	ycfD	P27431	42609	4.69	5	19	89	Unknown function	[3]
124	Uncharacterized zinc-type alcohol dehydrogenase-like protein YahK	<i>Escherichia coli</i> (strain K12)	yahK	P75691	38524	5.80	4	12	73	Unknown function	[3]
126	Glutamate decarboxylase alpha	<i>Escherichia coli</i> O6	gadA	P69909	53221	5.22	12	34	91	Stress response: acid resistance	[7]
126	Glutamate decarboxylase beta	<i>Escherichia coli</i> O157:H7	gadB	P69911	53204	5.29	13	34	91	Stress response: acid resistance	[2]
127	Elongation factor Tu1	<i>Escherichia coli</i> O139:H28	tuf1	A7ZSL4	43457	5.30	9	33	100	Protein biosynthesis	[1]
128	Elongation factor Tu1	<i>Escherichia coli</i> O139:H28	tuf1	A7ZSL4	43457	5.30	9	33	100	Protein biosynthesis	[1]
131	Glyceraldehyde-3-phosphate dehydrogenase	<i>Salmonella typhi</i>	gapA	P0A1P1	35681	6.32	8	19	85	Glycolysis	[13]
132	Biotin carboxylase	<i>Escherichia coli</i> (strain K12)	accC	P24182	49745	6.65	10	29	87	Fatty acid biosynthesis	[3]
134	Dihydrolipoyl dehydrogenase	<i>Escherichia coli</i> O157:H7	lpdA	P0A9P2	50942	5.79	9	31	151	Glycolysis	[2]
135	Periplasmic dipeptide transport protein	<i>Escherichia coli</i> (strain K12)	dppA	P23847	60483	6.21	8	28	75	Transport	[3]
137	Periplasmic	<i>Escherichia</i>	oppA	P23843	60975	5.85	15	35	92	Transport	[3]

	oligopeptide-binding protein	<i>coli</i> (strain K12)									
138	PyruvatekinaseI	<i>Escherichia coli</i> O157:H7	pykF	P0AD62	51039	5.77	18	48	160	Glycolysis	[1]
139	Succinate dehydrogenase flavoprotein subunit	<i>Escherichia coli</i> O157:H7	sdhA	P0AC43	65008	5.85	12	28	118	Transport	[2]
141	Fructose-bisphosphate aldolase class 2	<i>Escherichia coli</i> O157:H7	fbaA	P0AB72	39351	5.52	7	27	86	Glycolysis	[6]
142	Seryl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	serS	A7ZJW2	48669	5.34	23	51	142	Protein biosynthesis	[1]
144	Phosphoenolpyruvate carboxykinase [ATP]	<i>Escherichia coli</i> O139:H28	pckA	A7ZST1	59863	5.46	9		108	Gluconeogenesis	[1]
145	Alkyl hydroperoxide reductase subunit F	<i>Escherichia coli</i> (strain K12)	ahpF	P35340	56484	5.47	12	32	96	Cell redox homeostasis	[3]
147	Oligopeptidase A	<i>Escherichia coli</i>	prlC	P27298	77461	5.15	8	14	110	Proteolysis	[3]
149	Phosphoenolpyruvate -protein phosphotransferase	<i>Escherichia coli</i> (strain K12)	ptsI	P08839	63750	4.78	22	43	166	Transport	[3]
150	60kDachaperonin1	<i>Escherichia coli</i> O1:K1/APEC	groL1	A1AJ51	57464	4.85	13	40	125	Protein Refolding	[1]
151	Flagellin	<i>Escherichia coli</i> (strain K12)	fliC	P04949	51265	4.50	9	23	61	Innate immune response	[3]
152	Chromosome partition protein mukF	<i>Escherichia coli</i> O127:H6	mukF	B7UN08	50645	4.75	5	11	86	DNA replication and Cell division	[6]
153	Chaperone protein DnaK	<i>Escherichia coli</i> O139:H28	dnaK	A7ZHA4	69130	4.83	28	54	279	Stress response: General / Heat	[1]
154	30S ribosomal protein S1	<i>Escherichia coli</i> O157:H7	rpsA	P0AG69	61235	4.88	24	52	239	Translation	[2]
155	Glutaredoxin-2	<i>Escherichia</i>	grxB	P0AC61	24449	7.72	4	41	85	Transport	[2]

<i>coli</i> O157:H7											
157	Glycyl-tRNA synthetase beta subunit (GlyRS)	<i>Escherichia coli</i> O127:H6	glyS	B7ULB9	76936	5.29	26	42	223	Protein biosynthesis	[1]
159	Polyribonucleotide nucleotidyltransferase	<i>Escherichia coli</i> O139:H28	pnp	A7ZS61	77111	5.09	17	29	166	RNA processing	[1]
160	Elongation factor G	<i>Escherichia coli</i> O139:H28	fusA	A7ZSL5	77704	5.24	21	40	175	Protein biosynthesis	[1]
161	Elongation factor G	<i>Shigella flexneri</i> serotype 5b	fusA	Q0SZX7	77672	5.24	27	51	180	Protein biosynthesis	[3]
162	Chaperone protein ClpB	<i>Escherichia coli</i> O157:H7	clpB	P63285	95697	5.37	30	42	194	Stress response: General / Heat	[2]
166	DNA-directed RNA polymerase subunit beta	<i>Escherichia coli</i> O139:H28	rpoB	A7ZUK1	150937	5.14	10	12	76	Transcription	[1]
167	Leucyl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	leuS	A7ZJ31	97768	5.16	16	17	82	Protein biosynthesis	[1]
169	Formate acetyltransferase 1	<i>Escherichia coli</i> (strain K12)	pflB	P09373	85588	5.69	33	47	204	Carbohydrate metabolism	[3]
171	Threonyl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	thrS	A7ZMI6	74680	5.80	17	28	100	Protein biosynthesis	[1]
172	Formate acetyltransferase 1	<i>Escherichia coli</i> (strain K12)	pflB	P09373	85588	5.69	23	34	181	Carbohydrate metabolism	[3]
173	Malate synthase G	<i>Escherichia coli</i> (strain K12)	glcB	P37330	80780	5.79	11	21	73	Tricarboxylic acid cycle	[3]
174	Catalase HP II	<i>Escherichia coli</i> (strain K12)	katE	P21179	84224	5.54	22	24	217	Hydrogen peroxide catabolic process	[3]
177	Aspartyl-tRNA synthetase	<i>Escherichia coli</i> O157:H7	aspS	Q8XCI7	66115	5.47	12	22	91	Protein biosynthesis	[2]
178	Transketolase 1	<i>Escherichia coli</i> (strain	tktA	P27302	72451	5.43	9	14	81	Transketolase activity	[3]

K12)											
183	Superoxide dismutase [Mn]	<i>Escherichia coli</i> O157:H7	sodA	P66828	23065	6.45	7	47	74	Superoxide metabolic process	[2]
185	Xaa-Pro dipeptidase	<i>Escherichia coli</i> O157:H7	pepQ	Q8X8I1	50335	5.60	12	33	75	Proteolysis	[2]

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