

Supplementary Material - Table 2. Protein spots identification by MALDI-TOF/MS of 2-DE gel spots from stressed 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
190	Peroxiredoxin osmC	<i>Escherichia coli</i> (strain K12)	osmC	P0C0L2	15193	5.57	5	46	74	Stress response: Oxidative stress	[1]
191	Protein yhfA	<i>Escherichia coli</i> O157:H7	yhfA	P0ADX3	14678	5.52	3	44	68	Stress response: Oxidative stress	[2]
196	Outer membrane protein X	<i>Escherichia coli</i> O157:H7	ompX	P0A919	18648	5.30	6	43	76	Stress response: Antibiotic resistance	[2]
198	DNA protection during starvation protein	<i>Escherichia coli</i> O139:H28	dps	A7ZJM7	18684	5.70	13	66	164	Stress response: Starvation	[3]
200	DNA protection during starvation protein	<i>Escherichia coli</i> O139:H28	dps	A7ZJM7	18684	5.70	7	42	74	Stress response: Starvation	[3]
202	Protein translocase subunit SecD	<i>Escherichia coli</i> O157:H7	secD	P0AG91	66648	8.62	7	13	78	Transport	[2]
205	Thiol peroxidase	<i>Escherichia coli</i> O157:H7	tpx	P0A864	17995	4.75	8	64	87	Stress response: Oxidative stress	[2]
206	Glucose-specific phosphotransferase enzyme IIA component	<i>Escherichia coli</i> O6	crr	P69784	18240	4.73	6	52	100	Transport	[4]
207	Single-stranded DNA-binding protein (SSB)	<i>Escherichia coli</i> O157:H7	ssb	P0AGE2	18963	5.45	9	43	82	DNA damage	[2]
208	Single-stranded DNA-binding protein (SSB)	<i>Escherichia coli</i> O157:H7	ssb	P0AGE2	18963	5.45	5	27	97	DNA damage	[2]
209	Superoxide dismutase [Fe]	<i>Escherichia coli</i> O157:H7	sodB	P0AGD5	21310	5.58	8	55	99	Stress response: Oxidative stress	[2]

210	ATP-dependent Clp protease proteolytic subunit	<i>Escherichia coli</i> O139:H28	clpP	A7ZIJ5	23286	5.52	8	37	64	Stress response: General / Heat	[3]
211	Inorganic pyrophosphatase	<i>Escherichia coli</i> O157:H7	ppa	P0A7B0	19805	5.03	7	39	85	Phosphate-containing compound metabolic process	[2]
212	Alkyl hydroperoxide reductase subunit C	<i>Escherichia coli</i> O157:H7	ahpC	P0AE10	20862	5.03	10	53	85	Stress response: Oxidative stress	[2]
213	Transcriptional regulator slyA	<i>Escherichia coli</i> O127:H6	slyA	P0A4U5	16427	7.03	4	29	82	Transcription	[5]
214	Uracil phosphoribosyltransferase	<i>Escherichia coli</i> O139:H28	upp	A7ZPU1	22576	5.32	7	34	61	Nucleoside metabolic process	[3]
214	Protein yhbO	<i>Escherichia coli</i> (strain K12)	yhbO	P45470	18904	5.27	6	51	65	Stress response: General	[1]
215	FKBP-type 22 kDa peptidyl-prolyl cis-trans isomerase	<i>Escherichia coli</i> (strain K12)	fkfB	P0A9L3	22203	4.85	4	25	59	Protein folding	[1]
216	Uncharacterized protein ycaC	<i>Escherichia coli</i> (strain K12)	ycaC	P21367	23200	5.20	5	32	74	Unknown function	[1]
217	Purine nucleoside phosphorylase deoD-type	<i>Escherichia coli</i> O139:H28	deoD	A7ZVS7	26161	5.39	13	56	98	Nucleoside metabolic process	[3]
218	Flavoprotein wrbA	<i>Escherichia coli</i> O139:H28	wrbA	A7ZKA9	20832	5.59	8	61	103	Stress response	[3]
219	3'(2'),5'-bisphosphate nucleotidase CysQ	<i>Escherichia coli</i> O157:H7	cysQ	Q8XCG6	27314	5.59	7	48	86	Stress response: Oxidative stress	[2]
221	Stringent starvation protein A	<i>Escherichia coli</i> O157:H7	sspA	P0ACA5	24346	5.22	10	43	90	Unknown function	[2]
222	Lysine-arginine-ornithine-binding periplasmic protein	<i>Escherichia coli</i> (strain K12)	argT	P09551	28088	5.19	14	60	117	Transport	[1]
223	Glutaredoxin-2	<i>Escherichia coli</i> O157:H7	grxB	P0AC61	24449	7.72	4	26	74	Transport	[2]
225	Adenylatekinase	<i>Escherichia coli</i> O139:H28	adk	A7ZIN4	23628	5.55	9	49	91	Nucleotide biosynthesis	[3]

227	Uncharacterized protein ydhL	<i>Escherichia coli</i> (strain K12)	ydhL	P64474	9638	8.75	5	59	59	Unknown function	[1]
228	50S ribosomal protein L1	<i>Escherichia coli</i> O139:H28 (strain E24377A / ETEC)	rplA	A7ZUJ7	24714	9.64	10	47	58	Translation regulation	[3]
230	2,5-diketo-D-gluconic acid reductase A	<i>Escherichia coli</i> (strain K12)	dkgA	Q46857	31147	6.00	6	28	113	Ascorbate biosynthesis	[1]
231	Nitrate/nitrite response regulator protein narL	<i>Escherichia coli</i> O157:H7	narL	P0AF30	23912	5.73	7	48	75	Transcription	[2]
232	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	<i>Escherichia coli</i> O127:H6	gpmA	B7ULM8	28539	5.85	9	46	77	Glycolysis	[5]
234	Maltose-binding periplasmic protein	<i>Escherichia coli</i> O157:H7	malE	P0AEY0	43360	5.22	8	28	58	Transport	[2]
235	Pyridoxine 5'-phosphate synthase	<i>Escherichia coli</i> O157:H7	pdxJ	P0A795	26596	5.61	11	59	95	Pyridoxine biosynthesis	[2]
236	Transcriptional regulatory protein CpxR	<i>Escherichia coli</i> O157:H7	cpxR	P0AE89	26296	5.39	6	37	96	Transcription	[2]
237	Uncharacterized sugar isomerase yihS	<i>Escherichia coli</i> (strain K12)	yihS	P32140	47687	5.71	6	20	88	Mannose metabolic process	[1]
239	Ornithine carbamoyltransferase	<i>Escherichia coli</i> O6:K15:H31	argI	Q0T9E0	36736	6.62	5	19	81	Amino-acid biosynthesis	[6]
240	FKBP-type peptidyl-prolyl cis-trans isomerase slyD	<i>Escherichia coli</i> O157:H7	slyD	P0A9L1	21182	4.86	8	29	106	Protein folding	[2]
241	3-mercaptopyruvate sulfurtransferase	<i>Escherichia coli</i> O157:H7	sseA	P58388	30864	4.56	15	63	214	Sulfurtransferase activity	[2]
242	D-galactose-binding periplasmic protein	<i>Escherichia coli</i> O6	mgIB	P0AEE6	35690	5.25	19	63	180	Transport	[4]
243	Elongation factor Ts	<i>Escherichia coli</i> O139:H28	tsf	A7ZHR0	30518	5.22	19	73	244	Protein biosynthesis	[3]

244	Transaldolase B	<i>Escherichia coli</i> O157:H7	talB	P0A871	35368	5.11	15	60	139	Pentose shunt	[2]
245	Enoyl-[acyl-carrier-protein] reductase [NADH] FabI	<i>Escherichia coli</i> O157:H7	fabI	P0AEK5	28074	5.58	16	58	127	Stress response: Antibiotic resistance	[2]
245	Chaperone protein hchA	<i>Escherichia coli</i> O81	hchA	B7MWF3	31271	5.63	11	38	93	Stress response: General / Heat	[7]
246	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	<i>Escherichia coli</i> O139:H28	dapD	A7ZHQ6	30044	5.55	18	59	204	Amino-acid biosynthesis	[3]
247	Putative quinone oxidoreductase YhdH	<i>Escherichia coli</i> (strain K12)	yhdH	P26646	34873	5.63	13	45	100	Stress response: Oxidative stress	[1]
248	Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	<i>Escherichia coli</i> O139:H28	accA	A7ZHS5	35333	5.76	11	46	97	Fatty acid biosynthesis	[3]
249	Malate dehydrogenase	<i>Escherichia coli</i> O139:H28	mdh	A7ZSD0	32488	5.61	7	30	82	Tricarboxylic acid cycle	[3]
250	6-phosphofructokinase isozyme 1	<i>Escherichia coli</i> O157:H7	pfkA	P0A797	35162	5.47	11	33	88	Glycolysis	[2]
251	Glyceraldehyde-3-phosphate dehydrogenase A	<i>Escherichia fergusonii</i>	gapA	B7LQ20	35689	6.61	10	34	71	Glycolysis	[7]
252	DNA-directed RNA polymerase subunit beta	<i>Escherichia coli</i> O139:H28	rpoB	A7ZUK1	150937	5.14	12	15	80	Transcription	[3]
253	Cysteine synthase A	<i>Escherichia coli</i> O157:H7	cysK	P0ABK6	34525	5.83	19	80	211	Amino-acid biosynthesis	[2]
253	Transaldolase A	<i>Escherichia coli</i> O157:H7	talA	P0A869	35865	5.89	10	31	65	Pentose shunt	[2]
254	Cysteine synthase A	<i>Escherichia coli</i> O157:H7	cysK	P0ABK6	34525	5.83	16	74	149	Amino-acid biosynthesis	[2]
254	Transaldolase A	<i>Escherichia coli</i> O157:H7	talA	P0A869	35865	5.89	19	73	179	Pentose shunt	[2]

256	ADP-L-glycero-D-manno-heptose-6-epimerase	<i>Escherichia coli</i> O139:H28	hldD	A7ZTH2	34985	4.80	16	61	178	Carbohydrate metabolism	[3]
257	Uncharacterized protein ybbN	<i>Escherichia coli</i> (strain K12)	ybbN	P77395	31885	4.50	10	32	79	Cell redox homeostasis	[1]
260	Multiphosphoryl transfer protein	<i>Escherichia coli</i> O157:H7	fruB	P69812	39624	4.77	7	35	59	Transport	[2]
261	Cell division protein ftsZ	<i>Escherichia coli</i> O157:H7	ftsZ	P0A9A8	40299	4.63	25	85	275	Cell division	[2]
262	Transcriptional regulator slyA	<i>Escherichia coli</i> O127:H6	slyA	P0A4U5	16427	7.03	4	29	82	Transcription	[5]
263	Putative outer membrane porin protein nmpC	<i>Escherichia coli</i> (strain K12)	nmpC	P21420	40277	4.55	10	35	105	Transport	[1]
266	Maltose-binding periplasmic protein	<i>Escherichia coli</i> O157:H7	malE	P0AEY0	43360	5.22	8	28	58	Transport	[2]
267	NH(3)-dependent NAD(+) synthetase	<i>Escherichia coli</i>	nadE	B7L6L4	30791	5.30	12	38	106	NAD biosynthetic process	[7]
268	Phosphoglycerate kinase	<i>Escherichia coli</i> O139:H28	pgk	A7ZR34	41264	5.08	20	68	179	Glycolysis	[3]
269	DNA-directed RNA polymerase subunit alpha	<i>Escherichia coli</i> O139:H28	rpoA	A7ZSI4	36717	4.97	21	58	236	Transcription	[3]
270	Succinyl-CoA ligase [ADP-forming] subunit beta	<i>Escherichia coli</i> O139:H28	sucC	A7ZJA8	41652	5.37	23	57	227	Tricarboxylic acid cycle	[3]
271	Aminomethyltransferase	<i>Escherichia coli</i> O139:H28	gcvT	A7ZR14	40235	5.36	10	40	75	Glycine catabolic process	[3]
272	Aspartate aminotransferase	<i>Escherichia coli</i> (strain K12)	aspC	P00509	43831	5.54	15	41	162	Aspartate biosynthetic process	[1]
273	Elongation factor Tu 1	<i>Escherichia coli</i> O139:H28	tuf1	A7ZSL4	43427	5.30	24	68	246	Protein biosynthesis	[3]
274	Fructose-bisphosphate aldolase class 2	<i>Escherichia coli</i> O157:H7	fbaA	P0AB72	39351	5.52	9	32	57	Glycolysis	[2]
276	Fructose-	<i>Escherichia coli</i>	fbaB	P0A992	38313	6.24	15	49	190	Glycolysis	[4]

	bisphosphate aldolase class 1	O6									
277	Flagellar regulator flk	<i>Escherichia coli</i> (strain K12)	flk	P15286	36645	9.48	5	31	96	Regulation of gene expression	[1]
278	Isocitrate dehydrogenase [NADP]	<i>Escherichia coli</i> (strain K12)	icd	P08200	46070	5.15	14	35	94	Tricarboxylic acid cycle	[1]
279	Adenylosuccinate synthetase	<i>Escherichia coli</i> O139:H28	purA	A7ZV47	47543	5.32	22	56	226	Purine biosynthesis	[3]
280	6-phosphogluconate dehydrogenase, decarboxylating	<i>Escherichia coli</i> (strain K12)	gnd	P00350	51563	5.04	18	52	174	Pentose shunt	[1]
281	Thiol peroxidase	<i>Escherichia coli</i> O157:H7	tpx	P0A864	17995	4.75	6	45	71	Stress response: Oxidative stress	[2]
282	Glutamate decarboxylase beta	<i>Escherichia coli</i> O157:H7	gadB	P69911	53204	5.29	19	45	116	Stress response: acid resistance	[2]
283	ATP synthase subunit beta	<i>Escherichia coli</i> O139:H28	atpD	A7ZTU4	50351	4.90	21	66	253	Transport	[3]
284	Trigger factor	<i>Escherichia coli</i> O139:H28	tig	A7ZIJ4	48149	4.82	27	59	287	Cell division	[3]
285	Ribose-phosphate pyrophosphokinase	<i>Escherichia coli</i> O157:H7	prs	P0A719	34425	5.23	14	47	143	Nucleotide biosynthesis	[2]
287	Protein klaB	<i>Escherichia coli</i>	klaB	Q52328	42130	6.05	7	19	114	Stress response: Tellurium resistance	[8]
288	60 kDa chaperonin 1	<i>Escherichia coli</i> O1:K1 / APEC	groL1	A1AJ51	57464	4.85	22	38	152	Protein refolding	[9]
289	Phosphoenolpyruvate -protein phosphotransferase	<i>Escherichia coli</i> (strain K12)	ptsI	P08839	63750	4.78	23	53	132	Transport	[1]
290	Flagellin	<i>Shigella flexneri</i>	fliC	Q08860	56603	4.51	20	46	182	Innate immune response	[10]
291	30S ribosomal protein S1	<i>Escherichia coli</i> O157:H7	rpsA	P0AG69	61235	4.88	31	60	271	Translation	[2]
292	Chaperone protein DnaK	<i>Escherichia coli</i> O139:H28	dnaK	A7ZHA4	69130	4.83	26	52	231	Stress response: General / Heat	[3]

293	Chaperone protein htpG	<i>Escherichia coli</i> O139:H28	htpG	A7ZIN3	71404	5.06	32	61	303	Stress response: General / Heat	[3]
294	Oligopeptidase A	<i>Escherichia coli</i> (strain K12)	prlC	P27298	77461	5.15	25	37	153	Proteolysis	[1]
295	Glutamine synthetase	<i>Escherichia coli</i> O157:H7	glnA	P0A9C7	52099	5.26	13	34	95	ATP-binding	[2]
296	Citrate synthase	<i>Escherichia coli</i> O6	gltA	P0ABH8	48383	6.21	10	26	79	Tricarboxylic acid cycle	[4]
296	Tryptophanase	<i>Escherichia coli</i> O139:H28	tnaA	A7ZTR3	53139	5.88	18	42	170	Tryptophan catabolism	[3]
297	Succinylornithine transaminase	<i>Escherichia coli</i>	astC	B7L6M2	44048	5.82	14	39	85	Arginine metabolism	[7]
298	Dihydrolipoyl dehydrogenase	<i>Escherichia coli</i> O157:H7	lpdA	P0A9P2	50942	5.79	19	39	158	Glycolysis	[2]
299	ATP synthase subunit alpha	<i>Escherichia coli</i> O139:H28	atpA	A7ZTU6	55416	5.80	23	53	215	Transport	[3]
300	Phosphoenolpyruvate carboxykinase [ATP]	<i>Escherichia coli</i> O139:H28 (strain E24377A / ETEC)	pckA	A7ZST1	59863	5.46	19	39	169	Gluconeogenesis	[3]
301	Bifunctional purine biosynthesis protein PurH	<i>Escherichia coli</i> O8	purH	B7M7R5	57721	5.45	18	43	181	Purine biosynthesis	[7]
302	Elongation factor G (EF-G)	<i>Shigella flexneri</i> serotype 5b	fusA	Q0SZX7	77672	5.24	30	53	205	Protein biosynthesis	[11]
303	Polyribonucleotide nucleotidyltransferase	<i>Escherichia coli</i> O139:H28	pnp	A7ZS61	77111	5.08	19	30	116	RNA processing	[3]
304	Phosphoenolpyruvate synthase	<i>Escherichia coli</i> (strain K12)	ppsA	P23538	87836	4.93	28	37	234	ATP-binding	[1]
305	Leucyl-tRNA synthetase	<i>Escherichia coli</i>	leuS	B7L9I6	97800	5.11	16	20	108	Protein biosynthesis	[7]
306	Phenylalanyl-tRNA synthetase beta chain	<i>Escherichia coli</i> O157:H7	pheT	Q8XE32	88119	5.11	12	16	71	Protein biosynthesis	[2]
307	Aminopeptidase N	<i>Escherichia coli</i> (strain K12)	pepN	P04825	99313	5.14	12	16	70	Proteolysis	[1]
309	Pyruvate	<i>Escherichia coli</i>	aceE	P0AFG9	99948	5.46	24	25	190	Glycolysis	[2]

	dehydrogenase E1 component	O157:H7									
310	NADP-dependent malic enzyme	<i>Escherichia coli</i> (strain K12)	maeB	P76558	82878	5.34	23	41	183	Stress response: Oxidative stress	[1]
312	Chaperone protein ClpB	<i>Escherichia coli</i> O157:H7	clpB	P63285	95697	5.37	19	32	119	Stress response: General / Heat	[2]
312	Phosphate acetyltransferase	<i>Escherichia coli</i> (strain K12)	pta	P0A9M8	77466	5.28	26	45	204	Acetate biosynthetic process	[1]
313	Glycyl-tRNA synthetase beta subunit	<i>Escherichia coli</i> O127:H6	glyS	B7ULB9	76936	5.29	26	43	217	Protein biosynthesis	[5]
314	Cell division protein ftsY	<i>Escherichia coli</i> (strain K12)	ftsY	P10121	54480	4.46	16	42	162	Cell division	[2]
315	DNA-directed RNA polymerase subunit beta	<i>Escherichia coli</i> O139:H28	rpoB	A7ZUK1	150937	5.14	28	26	206	Transcription	[3]
316	Polyribonucleotide nucleotidyltransferase	<i>Escherichia coli</i> O139:H28	pnp	A7ZS61	77111	5.08	17	29	200	RNA processing	[3]
317	Carbamoyl-phosphate synthase large chain	<i>Escherichia coli</i> O157:H7	carB	P63737	118580	5.22	11	14	85	Amino-acid biosynthesis	[2]
318	DNA-directed RNA polymerase subunit beta	<i>Escherichia coli</i> O139:H28	rpoC	A7ZUK2	155918	6.67	46	35	265	Transcription	[3]
319	Beta-galactosidase	<i>Escherichia coli</i> O139:H28	lacZ	A7ZI91	117300	5.20	12	16	65	Carbohydrate metabolic process	[3]
320	Isoleucyl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	ileS	A7ZHB5	105013	5.66	35	38	225	Protein biosynthesis	[3]
321	Aldehyde-alcohol dehydrogenase	<i>Escherichia coli</i> O157:H7	adhE	P0A9Q8	96580	6.33	23	38	129	Alcohol metabolic process	[2]
322	Aconitate hydratase 1	<i>Escherichia coli</i> (strain K12)	acnA	P25516	98015	5.59	22	29	244	Tricarboxylic acid cycle	[1]
323	Aconitate hydratase 1	<i>Escherichia coli</i> (strain K12)	acnA	P25516	98015	5.59	15	26	95	Tricarboxylic acid cycle	[1]
323	Alanyl-tRNA synthetase	<i>Escherichia coli</i> O157:H7	alaS	Q8X3W8	96315	5.53	20	30	152	Protein biosynthesis	[2]

323	Putative monooxygenase ydhR	<i>Escherichia coli</i> (strain K12)	ydhR	P0ACX3	11281	5.09	3	23	28	Stress response: Oxidative stress	[1]
324	Catalase HPII	<i>Escherichia coli</i> (strain K12)	katE	P21179	84224	5.54	26	31	201	Hydrogen peroxide catabolic process	[1]
325	DNA gyrase subunit B	<i>Escherichia coli</i> O157:H7	gyrB	P0AES7	90179	5.72	18	28	96	Tricarboxylic acid cycle	[2]
325	Malate synthase G	<i>Escherichia coli</i> (strain K12)	glcB	P37330	80780	5.79	23	36	147	Stress response: Antibiotic resistance	[1]
326	Glycine dehydrogenase [decarboxylating]	<i>Shigella boydii</i> serotype 18	gcvP	B2U0S0	105070	5.62	26	30	170	Glycine metabolic process	[3]
327	Formate acetyltransferase 1	<i>Escherichia coli</i> (strain K12)	pflB	P09373	85588	5.69	37	51	291	Carbohydrate metabolism	[1]
328	Formate acetyltransferase 1	<i>Escherichia coli</i> (strain K12)	pflB	P09373	85588	5.69	30	41	249	Carbohydrate metabolism	[1]
329	Acetyl-coenzyme A synthetase	<i>Escherichia coli</i> (strain K12)	acs	P27550	72447	5.50	25	40	204	ATP-binding	[1]
329	Transketolase 1	<i>Escherichia coli</i> (strain K12)	tktA	P27302	72451	5.43	12	19	69	Transketolase activity	[1]
330	Transketolase 1 (TK 1)	<i>Escherichia coli</i> (strain K12)	tktA	P27302	72451	5.43	15	28	144	Transketolase activity	[1]
331	Chaperone protein ClpB	<i>Escherichia coli</i> O157:H7	clpB	P63285	95697	5.37	19	32	138	Stress response: General / Heat	[2]
332	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]	<i>Escherichia coli</i> O157:H7	glmS	Q8XEG2	67095	5.56	23	44	194	Carbohydrate biosynthetic process	[2]
335	Pyruvate kinase I	<i>Escherichia coli</i> O157:H7	pykF	P0AD62	51039	5.77	15	45	140	Glycolysis	[2]
336	CTP synthase	<i>Escherichia coli</i> O139:H28 (strain E24377A / ETEC)	pyrG	A7ZQM3	60792	5.63	11	24	103	Pyrimidine biosynthesis	[3]
337	Elongation factor Ts	<i>Escherichia coli</i> O139:H28	tsf	A7ZHR0	30518	5.22	9	33	77	Protein biosynthesis	[3]
338	Maltose-binding	<i>Escherichia coli</i>	malE	P0AEY0	43360	5.22	6	21	108	Transport	[2]

	periplasmic protein	O157:H7									
339	Phosphoglycerate kinase	<i>Escherichia coli</i> O139:H28	pgk	A7ZR34	41264	5.08	9	34	75	Glycolysis	[3]
340	Glutamate decarboxylase alpha	<i>Escherichia coli</i> O6	gadA	P69909	53221	5.22	6	18	78	Stress response: acid resistance	[4]
342	30S ribosomal protein S3	<i>Buchnera aphidicola</i> subsp. <i>Acyrtosiphon kondoi</i>	rpsC	P46172	22718	10.14	6	33	79	Translation	[12]
343	Phenylalanyl-tRNA synthetase alpha chain	<i>Acidovorax ebreus</i>	pheS	B9MHY2	39110	5.67	6	20	75	Protein biosynthesis	[13]
344	Phosphoglycerate kinase	<i>Escherichia coli</i> O139:H28	pgk	A7ZR34	41264	5.08	5	16	74	Glycolysis	[3]
345	6-phosphogluconate dehydrogenase, decarboxylating	<i>Escherichia coli</i> (strain K12)	gnd	P00350	51563	5.04	10	23	77	Pentose shunt	[1]
346	Arginyl-tRNA synthetase	<i>Escherichia coli</i> O157:H7	argS	Q8XCH2	64851	5.31	11	20	88	Protein biosynthesis	[2]
347	Malate synthase A	<i>Escherichia coli</i> (strain K12)	aceB	P08997	60521	5.39	12	30	97	Tricarboxylic acid cycle	[1]
348	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	<i>Escherichia coli</i> O157:H7	sucB	P0AFG7	43984	5.58	16	44	170	Tricarboxylic acid cycle	[2]
349	Phosphoglucomutase	<i>Escherichia coli</i> (strain K12)	pgm	P36938	58610	5.43	12	30	78	Carbohydrate metabolism	[1]
349	Seryl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	serS	A7ZJW2	48669	5.34	19	47	145	Protein biosynthesis	[3]
350	Alkyl hydroperoxide reductase subunit F	<i>Escherichia coli</i> (strain K12)	ahpF	P35340	56484	5.47	13	32	131	Stress response: Oxidative stress	[1]
351	Glucose-6-phosphate 1-dehydrogenase	<i>Escherichia coli</i> O157:H7	zwf	Q8XCJ6	56040	5.55	12	28	90	Carbohydrate metabolism	[2]

352	N-succinylglutamate 5-semialdehyde dehydrogenase	<i>Escherichia coli</i>	astD	B7L6M0	53353	5.52	11	31	98	Arginine metabolism	[7]
353	Xaa-Pro dipeptidase	<i>Escherichia coli</i> O157:H7	pepQ	Q8X8I1	50335	5.60	7	24	54	Protein biosynthesis	[2]
353	Glutamyl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	gltX	A7ZPK7	54181	5.59	13	33	110	Proteolysis	[3]
354	Histidyl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	hisS	A7ZPV7	47285	5.65	14	40	153	Protein biosynthesis	[3]
355	Aspartyl-tRNA synthetase	<i>Escherichia coli</i> O157:H7	aspS	Q8XCI7	66115	5.47	7	16	81	Protein biosynthesis	[2]
356	Methionyl-tRNA synthetase	<i>Escherichia coli</i> O139:H28	metG	A7ZNT3	76648	5.56	9	21	76	Protein biosynthesis	[3]
357	Succinyl-CoA ligase [ADP-forming] subunit alpha	<i>Escherichia coli</i> O157:H7	sucD	P0AGF1	30044	6.31	8	48	104	Tricarboxylic acid cycle	[2]
358	Uncharacterized protein ygiC	<i>Escherichia coli</i> O157:H7	ygiC	P0ADT7	45282	4.67	11	36	119	Catalytic activity	[2]
359	Thioredoxin reductase	<i>Escherichia coli</i> O157:H7	trxB	P0A9P5	34829	5.30	10	47	72	Removal of superoxide radicals	[2]
360	Ribose-phosphate pyrophosphokinase	<i>Escherichia coli</i> O157:H7	prs	P0A719	34425	5.23	15	53	152	Nucleotide biosynthesis	[2]

References

- [1] F.R. Blattner, G. Plunkett, 3rd, C.A. Bloch, N.T. Perna, V. Burland, M. Riley, J. Collado-Vides, J.D. Glasner, C.K. Rode, G.F. Mayhew, J. Gregor, N.W. Davis, H.A. Kirkpatrick, M.A. Goeden, D.J. Rose, B. Mau, Y. Shao, *Science*, 277 (1997) 1453-1462.
- [2] N.T. Perna, G. Plunkett, 3rd, V. Burland, B. Mau, J.D. Glasner, D.J. Rose, G.F. Mayhew, P.S. Evans, J. Gregor, H.A. Kirkpatrick, G. Posfai, J. Hackett, S. Klink, A. Boutin, Y. Shao, L. Miller, E.J. Grotbeck, N.W. Davis, A. Lim, E.T. Dimalanta, K.D. Potamouisis, J. Apodaca, T.S. Anantharaman, J. Lin, G. Yen, D.C. Schwartz, R.A. Welch, F.R. Blattner, *Nature*, 409 (2001) 529-533. doi: 10.1038/35054089
- [3] D.A. Rasko, M.J. Rosovitz, G.S. Myers, E.F. Mongodin, W.F. Fricke, P. Gajer, J. Crabtree, M. Sebaihia, N.R. Thomson, R. Chaudhuri, I.R. Henderson, V. Sperandio, J. Ravel, *J Bacteriol*, 190 (2008) 6881-6893. doi: 10.1128/JB.00619-08
- [4] R.A. Welch, V. Burland, G. Plunkett, 3rd, P. Redford, P. Roesch, D. Rasko, E.L. Buckles, S.R. Liou, A. Boutin, J. Hackett, D. Stroud, G.F. Mayhew, D.J. Rose, S. Zhou, D.C. Schwartz, N.T. Perna, H.L. Mobley, M.S. Sonnenberg, F.R. Blattner, *Proc Natl Acad Sci U S A*, 99 (2002) 17020-17024. doi: 10.1073/pnas.252529799
- [5] A. Iguchi, N.R. Thomson, Y. Ogura, D. Saunders, T. Ooka, I.R. Henderson, D. Harris, M. Asadulghani, K. Kurokawa, P. Dean, B. Kenny, M.A. Quail, S. Thurston, G. Dougan, T. Hayashi, J. Parkhill, G. Frankel, *J Bacteriol*, 191 (2009) 347-354. doi: 10.1128/JB.01238-08
- [6] B. Hochhut, C. Wilde, G. Balling, B. Middendorf, U. Dobrindt, E. Brzuszkiewicz, G. Gottschalk, E. Carniel, J. Hacker, *Mol Microbiol*, 61 (2006) 584-595. doi: 10.1111/j.1365-2958.2006.05255.x
- [7] M. Touchon, C. Hoede, O. Tenaillon, V. Barbe, S. Baeriswyl, P. Bidet, E. Bingen, S. Bonacorsi, C. Bouchier, O. Bouvet, A. Calteau, H. Chiapello, O. Clermont, S. Cruveiller, A. Danchin, M. Diard, C. Dossat, M.E. Karoui, E. Frapy, L. Garry, J.M. Ghigo, A.M. Gilles, J. Johnson, C. Le Bouguenec, M. Lescat, S. Mangenot, V. Martinez-Jehanne, I. Matic, X. Nassif, S. Oztas, M.A. Petit, C. Pichon, Z. Rouy, C.S. Ruf, D. Schneider, J. Tourret, B. Vacherie, D. Vallenet, C. Medigue, E.P. Rocha, E. Denamur, *PLoS Genet*, 5 (2009) e1000344. doi: 10.1371/journal.pgen.1000344
- [8] E.G. Walter, C.M. Thomas, J.P. Ibbotson, D.E. Taylor, *J Bacteriol*, 173 (1991) 1111-1119.
- [9] T.J. Johnson, S. Kariyawasam, Y. Wannemuehler, P. Mangiamale, S.J. Johnson, C. Doetkott, J.A. Skyberg, A.M. Lynne, J.R. Johnson, L.K. Nolan, *J Bacteriol*, 189 (2007) 3228-3236. doi: 10.1128/JB.01726-06
- [10] J. Wei, M.B. Goldberg, V. Burland, M.M. Venkatesan, W. Deng, G. Fournier, G.F. Mayhew, G. Plunkett, 3rd, D.J. Rose, A. Darling, B. Mau, N.T. Perna, S.M. Payne, L.J. Runyen-Janecky, S. Zhou, D.C. Schwartz, F.R. Blattner, *Infect Immun*, 71 (2003) 2775-2786.
- [11] H. Nie, F. Yang, X. Zhang, J. Yang, L. Chen, J. Wang, Z. Xiong, J. Peng, L. Sun, J. Dong, Y. Xue, X. Xu, S. Chen, Z. Yao, Y. Shen, Q. Jin, *BMC Genomics*, 7 (2006) 173. doi: 10.1186/1471-2164-7-173
- [12] R. Abe, A. Yamashita, K. Isono, *DNA Res*, 1 (1994) 103-114.
- [13] S. Lucas, A. Copeland, A. Lapidus, T. Glavina del Rio, H. Tice, D. Bruce, L. Goodwin, S. Pitluck, O. Chertkov, T. Brettin, J.C. Detter, C. Han, F. Larimer, M. Land, L. Hauser, N. Kyrpides, N. Mikhailova, J.D. Coates, US DOE Joint Genome Institute, (2009).

