Table S13. The regulated proteins in the different growth stages

CB9615	EDL933	Gene	Product	COG	Category	Description	CB9615	EDL933
G2583_4753	Z5496	metF	5,10-methylenetetrahydrofolate reductase	COG0685	E	Amino acid transport and metabolism	down	down
G2583_0771	Z0751	uspG	hypothetical protein	COG0589	T	Signal transduction mechanisms	down	down
G2583_1094	Z1090	artJ	arginine 3rd transport system periplasmic binding protein	COG0834	ET	Amino acid transport and metabolism/ Signal transduction mechanisms	down	down
G2583_1856	Z2215	gadB	glutamate decarboxylase isozyme	COG0076	E	Amino acid transport and metabolism	down	down
G2583_4253	Z4930	gadA	glutamate decarboxylase isozyme	COG0076	E	Amino acid transport and metabolism	down	down
G2583_4629	Z5351	metE	tetrahydropteroyltriglutamate methyltransferase	COG0620	E	Amino acid transport and metabolism	down	down
G2583_1040	Z1034	dps	global regulator, starvation conditions	COG0783	P	Inorganic ion transport and metabolism	down	down
G2583_1845	Z2228	osmC	osmotically inducible protein	COG1764	O	Posttranslational modification, protein turnover, chaperones	down	down
G2583_2171	Z2754	yniA	orf, hypothetical protein	COG3001	G	Carbohydrate transport and metabolism	down	
G2583_1042	Z1036	ompX	outer membrane protein X	COG3637	M	Cell envelope biogenesis, outer membrane	down	
G2583_1164	Z1276	ompF	outer membrane protein 1a (Ia;b;F)	COG3203	M	Cell envelope biogenesis, outer membrane	down	
G2583_1601	Z2549	trpC	N-(5-phosphoribosyl)anthranilate isomerase and indole-3-glycerolphosphate synthetase	COG0134	E	Amino acid transport and metabolism	down	
G2583_3175	Z3886	clpB	heat shock protein	COG0542	O	Posttranslational modification, protein turnover, chaperones	down	
G2583_3576	Z4259	yggE	putative actin	COG2968	S	Function unknown	down	
G2583_0014	Z0014	dnaK	chaperone Hsp70; DNA biosynthesis; autoregulated heat shock proteins	COG0443	O	Posttranslational modification, protein turnover, chaperones	down	
G2583_0585	Z0590	htpG	chaperone Hsp90, heat shock protein C 62.5	COG0326	O	Posttranslational modification, protein turnover, chaperones	down	
G2583_3311	Z3964	ygaU	orf, hypothetical protein	COG1652	S	Function unknown	down	
G2583_3870	Z4505	yraL	orf, hypothetical protein	COG0313	R	General function prediction only	down	
G2583_4200	Z4871	nikD	ATP-binding protein of nickel transport system	COG0444	EP	Amino acid transport and metabolism/ Inorganic ion transport and metabolism	down	
G2583_4611	Z5331	orf	orf; conserved hypothetical protein	COG1912	S	Function unknown	down	
G2583_4622	Z5343	recQ	ATP-dependent DNA helicase	COG0514	L	DNA replication, recombination, and repair	down	
G2583_4870	Z5644	yjbJ	orf, hypothetical protein	COG3237	S	Function unknown	down	
G2583_5241	Z5983	deoC	2-deoxyribose-5-phosphate aldolase	COG0274	F	Nucleotide transport and metabolism	down	
G2583_2417	Z3059	hchA	hypothetical protein	COG0693	R	General function prediction only	down	
G2583_4715	Z5455	yiiM	orf, hypothetical protein	COG2258	S	Function unknown	down	
G2583_1751	Z2335	uspF	hypothetical protein	COG0589	T	Signal transduction mechanisms	down	
G2583_3560	Z4245	pepP	proline aminopeptidase P II	COG0006	E	Amino acid transport and metabolism	down	

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CB9615	EDL933	Gene	Product	COG	Category	Description	CB9615	EDL933
G2583_0531	Z0522	yajO	putative NAD(P)H-dependent xylose reductase	COG0667	C	Energy production and conversion	down	
G2583_0598	Z0606	ybaS	putative glutaminase	COG2066	E	Amino acid transport and metabolism	down	
G2583_1108	Z1105	poxB	pyruvate oxidase	COG0028	EH	Amino acid transport and metabolism/Coenzyme metabolism	down	
G2583_1134	Z1243	ycaC	orf, hypothetical protein	COG1335	Q	Secondary metabolites biosynthesis, transport and catabolism	down	
G2583_1238	Z1423	wrbA	trp repressor binding protein	-	-	-	down	
G2583_1599	Z2551	trpA	tryptophan synthase, alpha protein	COG0159	E	Amino acid transport and metabolism	down	
G2583_2348	Z2950	otsB	trehalose-6-phosphate phophatase, biosynthetic	COG1877	G	Carbohydrate transport and metabolism	down	
G2583_2807	Z3526	elaB	orf, hypothetical protein	COG4575	S	Function unknown	down	
G2583_2986	Z3720	talA	transaldolase A	COG0176	G	Carbohydrate transport and metabolism	down	
G2583_2987	Z3721	tktB	transketolase 2 isozyme	COG0021	G	Carbohydrate transport and metabolism	down	
G2583_4609	Z5329	yigB	putative phosphatase	COG1011	R	General function prediction only	down	
G2583_5260	Z6004	arcA	negative response regulator of genes in aerobic pathways	COG0745	TK	Signal transduction mechanisms/Transcription	down	
G2583_2831	Z3555	yfbU	orf, hypothetical protein	COG3013	S	Function unknown	up	down
G2583_0849	Z0837	pgm	phosphoglucomutase	COG0033	G	Carbohydrate transport and metabolism	up	up
G2583_3939	Z4577	gltD	glutamate synthase, small subunit	COG0493	ER	Amino acid transport and metabolism/ General function prediction only	up	up
G2583_4803	Z5560	rpoB	RNA polymerase, beta subunit	COG0085	K	Transcription	up	up
G2583_4859	Z5632	malE	periplasmic maltose-binding protein	COG2182	G	Carbohydrate transport and metabolism	up	up
G2583_0102	Z0108	secA	preprotein translocase; secretion protein	COG0653	U	Intracellular trafficking, secretion, and vesicular transport	up	up
G2583_3032	Z3772	guaB	IMP dehydrogenase	COG0516	F	Nucleotide transport and metabolism	up	up
G2583_3345	Z3999	alaS	alanyl-tRNA synthetase	COG0013	J	Translation, ribosomal structure and biogenesis	up	up
G2583_0273	Z0298	pepD	aminoacyl-histidine dipeptidase (peptidase D)	COG2195	E	Amino acid transport and metabolism	up	up
G2583_4754	Z5497	katG	catalase; hydroperoxidase HPI(I)	COG0376	P	Inorganic ion transport and metabolism	up	up
G2583_5250	Z5993	yjjK	putative ATP-binding component of ABC transport system	COG0488	R	General function prediction only	up	up
G2583_0034	Z0038	carB	carbamoyl-phosphate synthase large subunit	COG0458	EF	Amino acid transport and metabolism/ Nucleotide transport and metabolism	up	
G2583_0646	Z0681	cysS	cysteine tRNA synthetase	COG0215	J	Translation, ribosomal structure and biogenesis	up	

CB9615	EDL933	Gene	Product	COG	Category	Description	CB9615	EDL933
G2583_4525	Z5227	glmS	L-glutamine:D-fructose-6-phosphate aminotransferase	COG0449	M	Cell envelope biogenesis, outer membrane	up	
G2583_0118	Z0124	aceE	pyruvate dehydrogenase (decarboxylase component)	COG2609	C	Energy production and conversion	up	
G2583_0258	Z0280	lpcA	phosphoheptose isomerase	COG0279	G	Carbohydrate transport and metabolism	up	
G2583_0278	Z0303	proB	gamma-glutamate kinase	COG0263	E	Amino acid transport and metabolism	up	
G2583_0835	Z0821	asnB	asparagine synthetase B	COG0367	E	Amino acid transport and metabolism	up	
G2583_0841	Z0827	glnS	glutamine tRNA synthetase	COG0008	J	Translation, ribosomal structure and biogenesis	up	
G2583_1351	Z1730	fabH	3-oxoacyl-[acyl-carrier-protein] synthase III	COG0332	I	Lipid metabolism	up	
G2583_4670	Z5406	glnA	glutamine synthetase	COG0174	E	Amino acid transport and metabolism	up	
G2583_1130	Z1239	serS	serine tRNA synthetase; also charges selenocystein tRNA with serine	COG0172	J	Translation, ribosomal structure and biogenesis	up	
G2583_1143	Z1254	aroA	5-enolpyruvylshikimate-3-phosphate synthetase	COG0128	E	Amino acid transport and metabolism	up	
G2583_2160	Z2742	pheT	phenylalanine tRNA synthetase, beta-subunit	COG0072	J	Translation, ribosomal structure and biogenesis	up	
G2583_2194	Z2780	astC	acetylornithine delta-aminotransferase	COG4992	E	Amino acid transport and metabolism	up	
G2583_2571	-	cpsG	Phosphomannomutase CpsG	COG1109	G	Carbohydrate transport and metabolism	up	
G2583_3769	Z4400	yqiC	hypothetical protein	COG2960	S	Function unknown	up	
G2583_3906	Z4543	greA	transcription elongation factor: cleaves 3' nucleotide of paused mRNA	COG0782	K	Transcription	up	
G2583_5062	Z5843	mpl	putative ligase	COG0773	M	Cell envelope biogenesis, outer membrane	up	
G2583_0122	Z0128	acnB	aconitate hydrase B	COG1049	C	Energy production and conversion	up	
G2583_0276	Z0301	crl	transcriptional regulator of cryptic csgA gene for curli surface fibers	-	-	-	up	
G2583_0717	Z1931	ompT	outer membrane protein 3b (a), protease VII	COG4571	M	Cell envelope biogenesis, outer membrane	up	
G2583_0883	Z0882	sucC	succinyl-CoA synthetase, beta subunit	COG0045	C	Energy production and conversion	up	
G2583_2650	Z3282	metG	methionine tRNA synthetase	COG0073	R	General function prediction only	up	
G2583_4738	Z5478	hslU	heat shock protein hslVU, ATPase subunit, homologous to chaperones	COG1220	O	Posttranslational modification, protein turnover, chaperones	up	
G2583_2203	Z2789	ynjE	putative thiosulfate sulfur transferase	COG2897	P	Inorganic ion transport and metabolism	up	
G2583_3892	Z4528	rbfA	ribosome-binding factor A	COG0858	J	Translation, ribosomal structure and biogenesis	up	
G2583_3901	Z4538	glmM	similar to phosphoglucomutases and phosphomannomutases	COG1109	G	Carbohydrate transport and metabolism	up	

CB9615	EDL933	Gene	Product	COG	Category	Description	CB9615	EDL933
G2583_4488	Z5190	gyrB	DNA gyrase subunit B, type II topoisomerase, ATPase activity	COG0187	L	DNA replication, recombination, and repair	up	
G2583_5075	Z5856	pyrB	aspartate carbamoyltransferase, catalytic subunit	COG0540	F	Nucleotide transport and metabolism	up	
G2583_0154	Z0161	fhuA	outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and phi80	COG1629	P	Inorganic ion transport and metabolism	up	
G2583_0756	Z0735	entC	isochorismate hydroxymutase 2, enterochelin biosynthesis	COG1169	HQ	Coenzyme metabolism/Secondary metabolites biosynthesis, transport and catabolism	up	
G2583_1033	Z1026	fiu	putative outer membrane receptor for iron transport	COG4774	P	Inorganic ion transport and metabolism	up	
G2583_1360	Z1739	ycfH	orf, hypothetical protein	COG0084	L	DNA replication, recombination, and repair	up	
G2583_2207	Z2793	gdhA	NADP-specific glutamate dehydrogenase	COG0334	E	Amino acid transport and metabolism	up	
G2583_2504	Z3159	yoeE	putative outer membrane receptor for iron compound or colicin	COG1629	P	Inorganic ion transport and metabolism	up	
G2583_2542	Z3183	hisC	histidinol-phosphate aminotransferase	COG0079	E	Amino acid transport and metabolism	up	
G2583_2702	Z3416	nfo	endonuclease IV	COG0648	L	DNA replication, recombination, and repair	up	
G2583_2726	Z3442	rsuA	16S pseudouridylate 516 synthase	COG1187	J	Translation, ribosomal structure and biogenesis	up	
G2583_3954	Z4593	degQ	serine endoprotease	COG0265	O	Posttranslational modification, protein turnover, chaperones	up	
G2583_4234	Z4910	chuS	putative heme/hemoglobin transport protein	COG3720	P	Inorganic ion transport and metabolism	up	
G2583_4300	Z4983	glyS	glycine tRNA synthetase, beta subunit	COG0751	J	Translation, ribosomal structure and biogenesis	up	
G2583_4662	Z5398	polA	DNA polymerase I	COG0258	L	DNA replication, recombination, and repair	up	
G2583_4781	Z5527	btuB	outer membrane receptor for transport of vitamin B12, E colicins, and bacteriophage BF23	COG4206	H	Coenzyme metabolism	up	
G2583_4878	Z5652	tyrB	tyrosine aminotransferase, tyrosine repressible	COG1448	E	Amino acid transport and metabolism	up	
G2583_4998	Z5778	miaA	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase	COG0324	J	Translation, ribosomal structure and biogenesis	up	
G2583_5001	Z5781	hflK	protease specific for phage lambda cII repressor	COG0330	O	Posttranslational modification, protein turnover, chaperones	up	
G2583_5027	Z5809	rpsF	30S ribosomal subunit protein S6	COG0360	J	Translation, ribosomal structure and biogenesis	up	
G2583_2866	Z3592	aroC	chorismate synthase	COG0082	E	Amino acid transport and metabolism		down
G2583_5172	Z5972	rsmC	putative enzyme	COG2813	J	Translation, ribosomal structure and biogenesis		down

CB9615	EDL933	Gene	Product	COG	Category	Description	CB9615	EDL933
G2583_0921	Z0925	gpmA	phosphoglyceromutase 1	COG0588	G	Carbohydrate transport and metabolism		down
G2583_3735	Z4364	yqhD	putative oxidoreductase	COG1979	C	Energy production and conversion		down
G2583_1010	Z1001	moaB	molybdopterin biosynthesis, protein B	COG0521	H	Coenzyme metabolism		down
G2583_2062	Z2694	ydhR	orf, hypothetical protein	-	-	-		down
G2583_3748	Z4379	mdaB	modulator of drug activity B	COG2249	R	General function prediction only		down
G2583_4356	Z5044	kbl	2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)	COG0156	H	Coenzyme metabolism		down
G2583_1107	Z1104	ltaE	putative arylsulfatase	COG2008	E	Amino acid transport and metabolism		down
G2583_2008	Z2617	ydgA	orf, hypothetical protein	COG5339	S	Function unknown		down
G2583_2846	Z3571	hisJ	histidine-binding periplasmic protein of high-affinity histidine transport system	COG0834	ET	Amino acid transport and metabolism/ Signal transduction mechanisms		down
G2583_3749	Z4380	ygiN	orf, hypothetical protein	COG1359	S	Function unknown		down
G2583_4771	Z5517	argB	acetylglutamate kinase	COG0548	E	Amino acid transport and metabolism		down
G2583_1153	Z1264	kdsB	CTP:CMP-3-deoxy-D-manno-octulosonate transferase	COG1212	M	Cell envelope biogenesis, outer membrane		up
G2583_2541	Z3182	hisD	L-histidinal:NAD+ oxidoreductase; L-histidinol:NAD+ oxidoreductase	COG0141	E	Amino acid transport and metabolism		up
G2583_3043	Z3781	ndk	nucleoside diphosphate kinase	COG0105	F	Nucleotide transport and metabolism		up
G2583_4134	Z4797	asd	aspartate-semialdehyde dehydrogenase	COG0136	E	Amino acid transport and metabolism		up
G2583_0882	Z0881	sucB	2-oxoglutarate dehydrogenase	COG0508	C	Energy production and conversion		up
G2583_2693	Z3405	mglB	galactose-binding transport protein; receptor for galactose taxis	COG1879	G	Carbohydrate transport and metabolism		up
G2583_0492	Z0480	psiF	induced by phosphate starvation	-	-	-		up
G2583_0642	Z0677	purK	phosphoribosylaminoimidazole carboxylase	COG0026	F	Nucleotide transport and metabolism		up
G2583_3334	Z3988	luxS	orf, hypothetical protein	COG1854	T	Signal transduction mechanisms		up
G2583_3031	Z3771	guaA	GMP synthetase (glutamine-hydrolyzing)	COG0518	F	Nucleotide transport and metabolism		up
G2583_4599	Z5317	hemX	uroporphyrinogen III methylase	COG2959	H	Coenzyme metabolism		up
G2583_4966	Z5744	aspA	aspartate ammonia-lyase (aspartase)	COG1027	E	Amino acid transport and metabolism		up
G2583_1911	Z2083	-	unknown protein encoded within CP-933O	-		-		up
G2583_0188	Z0197	accA	acetylCoA carboxylase, carboxytransferase component, alpha subunit	COG0825	I	Lipid metabolism		up
G2583_0279	Z0304	proA	gamma-glutamylphosphate reductase	COG0014	E	Amino acid transport and metabolism		up
G2583_1321	Z1699	pyrC	dihydro-orotase	COG0418	F	Nucleotide transport and metabolism		up
G2583_1628	Z2514	rnb	RNase II, mRNA degradation	COG4776	K	Transcription		up

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G2583_1777	Z2306	aldA	aldehyde dehydrogenase, NAD-linked	COG1012	C	Energy production and conversion		up
G2583_2049	Z2676	grxD	orf, hypothetical protein	COG0278	O	Posttranslational modification, protein turnover, chaperones		up
G2583_2328	Z2929	argS	arginine tRNA synthetase	COG0018	J	Translation, ribosomal structure and biogenesis		up
G2583_3447	Z4111	queF	orf, hypothetical protein	COG0780	R	General function prediction only		up
G2583_3557	Z4242	gcvT	aminomethyltransferase of glycine cleavage system	COG0404	E	Amino acid transport and metabolism		up
G2583_3950	Z4588	rpsI	30S ribosomal subunit protein S9	COG0103	J	Translation, ribosomal structure and biogenesis		up
G2583_4262	Z4940	kdgK	ketodeoxygluconokinase	COG0524	G	Carbohydrate transport and metabolism		up
G2583_5056	Z5837	ppa	inorganic pyrophosphatase	COG0221	C	Energy production and conversion		up
G2583_5235	Z5976	prfC	peptide chain release factor RF-3	COG4108	J	Translation, ribosomal structure and biogenesis		up
-	Z2386	-	unknown protein encoded within prophage CP-933R	-	-	-		up
G2583_0058	Z0063	imp	organic solvent tolerance	COG1452	M	Cell envelope biogenesis, outer membrane		up
G2583_0138	Z0145	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	COG0413	H	Coenzyme metabolism		up
G2583_1162	Z1274	ycbL	orf, hypothetical protein	COG0491	R	General function prediction only		up
G2583_1842	Z2231	maeA	NAD-linked malate dehydrogenase (malic enzyme)	COG0281	C	Energy production and conversion		up
G2583_2536	Z3178	yeeZ	putative enzyme of sugar metabolism	COG0451	MG	Cell envelope biogenesis, outer membrane/ Carbohydrate transport and metabolism		up
G2583_2546	Z3187	hisF	imidazole glycerol phosphate synthase subunit in heterodimer with HisH	COG0107	E	Amino acid transport and metabolism		up
G2583_3331	Z3985	mprA	regulator of plasmid mcrB operon	COG1846	K	Transcription		up
G2583_3336	Z3989	gshA	gamma-glutamate-cysteine ligase	COG2918	H	Coenzyme metabolism		up
G2583_4884	Z5658	ssb	ssDNA-binding protein	COG0629	L	DNA replication, recombination, and repair		up
G2583_5030	Z5812	rplI	50S ribosomal subunit protein L9	COG0359	J	Translation, ribosomal structure and biogenesis		up