

Proteins induced at pH 9

No	gene ID ¹	gene	function	TMH ²	Transcriptome ³		Proteome ⁴								
					pH 6	pH 9	cytoplasm			envelop			membrane		
							6	7.5	9	6	7.5	9	6	7.5	9
1	cg0422	<i>murA</i>	UDP-N-acetylglucosamine enolpyruvyl transferase	0	-0.46	-0.4	2.9	2.6	3.8	2.6	2.3	0.8	-	1.9	-
2	cg0673	<i>rplM</i>	50S ribosomal protein L13	0	-0.84	-0.32	-	-0.8	1.3	2.6	2.3	3.8	-0.9	1.0	2.9
3	cg0766	<i>icd</i>	Isocitrate dehydrogenase	0	-0.06	0.09	5.4	5.1	6.5	3.2	3.8	3.3	1.5	2.2	1.0
4	cg0873	<i>aroA</i>	3-phosphoshikimate 1-carboxyvinyltransferase	0	0.25	0.96	2.2	2.1	3.9	-	-	-	-	-	-
5	cg1408		Putative membrane protein	2	-0.14	0.64	-0.3	-0.5	-	5.0	3.5	5.5	0.1	-	-
6	cg1604		Hypothetical protein	1	-	-0.15	1.2	2.1	2.3	2.8	3.1	5.4	3.9	-0.6	2.0
7	cg1730		Membrane protease subunits	1	0.06	-0.43	1.0	-	-0.8	2.7	2.5	4.2	1.8	0.4	1.9
8	cg1769	<i>ctaA</i>	Cytochrome oxidase assembly protein	8	-	-	-	-	-	0.7	0.7	3.7	3.6	3.0	4.1
9	cg1787	<i>ppc</i>	Phosphoenolpyruvate carboxylase	0	0.36	-	2.4	2.4	4.1	5.7	5.5	5.8	2.3	3.6	4.0
10	cg2299	<i>hisA</i>	Imidazole-4-carboxamideisomerase	0	0.33	-0.28	3.9	2.6	3.8	-	-	-	-	-	-
11	cg2405	<i>qcrC</i>	Menaquinol-cytochrome c reductase subunit	2	-	0.23	-	-	-	4.4	4.8	5.4	3.8	2.4	3.6
12	cg2523	<i>malQ</i>	4-alpha-glucanotransferase	0	0.27	-0.01	3.7	2.8	3.9	5.2	5.6	3.6	2.3	2.2	1.5
13	cg2613	<i>mdh</i>	Malate dehydrogenase	0	0.31	0.21	4.7	3.4	4.6	-	-	-	-0.9	-	-0.6
14	cg2750		Hypothetical membrane protein	2	0.62	0.96	-	-	-	3.2	2.1	4.0	1.4	2.0	3.2
15	cg2780	<i>ctaD</i>	Cytochrome c oxidase polypeptide I	12	0.31	0.52	-	-	-	3.7	2.1	3.9	5.1	5.3	6.3
16	cg2888	<i>cgtR</i>	Two-component system, response regulator	0	-0.21	0.82	3.9	2.1	4.2	-	-	0.7	-	-	-
17	cg3138		Membrane protease subunits	2	-	0.65	-	0.2	-	3.8	2.1	5.0	5.3	3.8	6.0
18	cg3179	<i>fadD</i>	Putative Acyl-CoA synthetase	0	0.18	0.6	1.1	3.2	4.1	1.8	0.8	3.7	-	-	-
19	cg3219	<i>ldh</i>	L-lactate dehydrogenase	0	1.83	0.12	5.1	3.1	4.8	4.3	1.3	2.3	-	-	-0.4
20	cg3315		Transcriptional regulator	0	0.03	0.71	3.6	3.2	4.5	-0.4	-	-	-	-	-0.6
21	cg3327	<i>dps</i>	Starvation-inducible DNA-binding protein	0	0.32	0.75	1.6	-0.8	3.6	-	-	-	-	-	-

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							6	7.5	9	6	7.5	9	6	7.5	9
1	cg0007	<i>gyrB</i>	DNA Gyrase subunit B	0	-0.7	-0.56	1.2	1.9	-0.8	4.2	4.5	3.3	0.2	2.0	-0.4
2	cg0441	<i>lpd</i>	Dihydrolipoamide dehydrogenase	0	-0.2	-0.04	4.1	4.3	0.3	0.6	-	-	0.8	-	-
3	cg0468		Cobalamin/Fe3+-siderophores transport system	8	-0.79	#NV	-	-	-	-	0.8	-	2.8	4.3	1.1
4	cg0628	<i>rpsH</i>	30S ribosomal protein S8	0	-0.48	-0.19	4.5	4.9	3.8	2.2	2.1	4.1	3.7	4.4	4.5
5	cg0674	<i>rpsL</i>	30S ribosomal protein S9	0	-0.92	-0.28	2.8	4.4	3.1	-0.4	-	0.0	-0.7	-0.6	-
6	cg0752		Uncharacterized BCR	1	-1.55	-0.47	0.6	2.7	1.6	3.4	2.3	1.8	4.4	4.7	3.4
7	cg0989	<i>rpsN</i>	30S ribosomal protein S14	0	-0.71	-0.25	2.5	3.9	1.7	0.0	0.7	2.7	1.2	1.0	1.2
8	cg1111	<i>eno</i>	Enolase	0	0.24	0.09	8.4	7.8	6.7	2.5	-0.2	1.4	1.4	-	-0.6
9	cg1314	<i>putP</i>	Na+/proline symporter	13	-0.55	-0.04	-	-	-	3.3	3.8	3.0	4.4	4.5	3.1
10	cg1322		Uncharacterized BCR	0	1.24	-0.62	6.3	5.1	2.7	-	-	-	2.6	-0.6	-
11	cg1333	<i>argS</i>	Arginyl-tRNA synthetase	0	-0.51	-0.17	1.9	2.9	2.2	6.3	6.8	5.9	0.1	3.1	-0.6
12	cg1364	<i>atpF</i>	F0F1-type ATP synthase b subunit	1	-1.52	-0.96	-0.6	0.5	-0.8	4.5	4.8	4.9	4.9	5.4	4.3
13	cg2132		Hypothetical protein	0	#NV	-0.35	4.9	5.1	3.1	-	-	-	-0.9	-	-
14	cg2833	<i>cysK</i>	O-Acetylserine (Thiol)-Lyase	0	0.42	-0.14	6.9	6.7	6.5	4.5	6.0	4.3	4.8	4.1	2.5
15	cg3018		Hypothetical protein	0	0.14	0.2	0.7	2.4	1.1	4.5	4.9	3.6	1.2	1.7	-0.6