

Gene	Functional group	Location (kb)	Mean <i>S/EIEC</i>	Mean <i>E. coli</i>	<i>p</i> value
<i>napD</i>	Hypothetical, unclassified, unknown	2300.8	-0.02	-0.42	3.5E-05
<i>b2249</i>	Hypothetical, unclassified, unknown	2360.5	0.23	-0.03	4.6E-04
<i>nucI</i>	Energy metabolism	2393.9	-0.23	0.07	1.6E-04
<i>nucC</i>	Hypothetical, unclassified, unknown	2400.1	-0.19	0.21	9.4E-04
<i>yfdE</i>	Hypothetical, unclassified, unknown	2486.0	-0.01	0.14	1.6E-04
<i>ddg</i>	Hypothetical, unclassified, unknown	2493.6	-0.25	-0.01	9.4E-04
<i>b2392</i>	Hypothetical, unclassified, unknown	2509.5	-0.30	0.04	5.6E-05
<i>yffG</i>	Amino acid biosynthesis and metabolism	2581.6	-0.06	-0.72	3.0E-04
<i>b2529</i>	Hypothetical, unclassified, unknown	2657.9	0.25	0.01	2.3E-04
<i>yfhL</i>	Hypothetical, unclassified, unknown	2697.7	0.23	-0.01	1.8E-04
<i>gabT</i>	Central intermediary metabolism	2790.8	-0.22	-0.77	7.6E-04
<i>ascF</i>	Transport and binding proteins	2837.5	0.31	-0.23	1.2E-04
<i>fucO</i>	Carbon compound catabolism	2929.9	-0.44	-0.22	2.5E-04
<i>ppdC</i>	Other known genes	2960.5	-0.12	-0.50	2.5E-04
<i>ygdB</i>	Hypothetical, unclassified, unknown	2960.8	0.15	-0.17	2.8E-05
<i>galP</i>	Transport and binding proteins	3086.3	-0.03	-0.36	9.0E-04
<b>exbD</b>	Transport and binding proteins	3148.8	0.41	0.17	2.2E-04
<i>rpsU</i>	Translation, post-translational modification	3208.4	-1.11	-0.60	4.3E-04
<i>deaD</i>	Transcription, RNA processing and degradation	3303.6	0.37	-0.50	2.0E-04
<i>nlp</i>	Carbon compound catabolism	3332.6	0.20	-0.33	6.4E-04
<i>yrbB</i>	Hypothetical, unclassified, unknown	3334.6	-0.04	-0.40	1.0E-04
<i>yhcI</i>	Putative enzymes	3367.1	-0.34	-0.78	1.5E-05
<i>yhcJ</i>	Putative enzymes	3368.0	-0.06	-0.46	2.8E-04
<i>smf_1</i>	Hypothetical, unclassified, unknown	3430.4	-0.03	-0.30	1.9E-04
<i>rplR</i>	Translation, post-translational modification	3442.9	0.96	0.57	8.0E-05
<i>rpmC</i>	Translation, post-translational modification	3446.2	0.38	0.09	2.9E-04
<i>rpsS</i>	Translation, post-translational modification	3447.9	0.28	0.03	7.9E-04
<i>bioH</i>	Biosynthesis of cofactors, prosthetic groups and carriers	3541.7	-0.73	-1.03	9.5E-04
<i>gntU_2</i>	Transport and binding proteins	3573.4	0.36	0.06	5.9E-04
<i>livG</i>	Transport and binding proteins	3591.1	0.20	-0.16	3.7E-04
<i>livK</i>	Transport and binding proteins	3594.1	0.65	0.15	3.7E-04
<i>livJ</i>	Transport and binding proteins	3596.2	0.43	0.07	8.3E-04
<i>ftsX</i>	Cell processes (incl. adaptation, protection)	3598.7	-0.41	-0.67	9.4E-04
<i>nikD</i>	Transport and binding proteins	3614.6	0.26	-0.11	1.4E-04
<i>nikE</i>	Transport and binding proteins	3615.4	0.38	0.04	2.9E-04
<i>pitA</i>	Transport and binding proteins	3635.3	0.55	0.07	5.1E-04
<i>yhiP</i>	Transport and binding proteins	3638.5	0.59	0.11	9.9E-04
<i>yhjOP</i>	Hypothetical, unclassified, unknown	3690.2	-1.09	-1.56	1.0E-04
<i>lldD</i>	Energy metabolism	3777.5	-0.62	-1.23	7.4E-04
<i>gmk</i>	Nucleotide biosynthesis and metabolism	3819.1	0.24	0.88	4.9E-04
<i>uhpC</i>	Transport and binding proteins	3844.9	0.50	0.08	1.9E-04
<i>uhpB</i>	Transport and binding proteins	3846.3	-0.47	-0.88	3.4E-05
<i>glvC</i>	Transport and binding proteins	3860.1	0.59	0.14	6.9E-04
<i>wzzE</i>	Cell structure	3966.6	-0.44	-0.82	2.2E-04
<i>yigJ</i>	Hypothetical, unclassified, unknown	4005.6	-0.29	-0.63	7.3E-04
<i>yigK</i>	Hypothetical, unclassified, unknown	4006.0	0.21	0.02	7.4E-04
<i>yihZ</i>	Hypothetical, unclassified, unknown	4074.6	-0.10	-0.41	7.0E-06
<i>yiiT</i>	Putative regulatory proteins	4110.9	-1.17	0.41	5.8E-05
<i>thiC</i>	Biosynthesis of cofactors, prosthetic groups and carriers	4191.8	-1.07	-1.42	3.3E-05
<i>yjeT</i>	Hypothetical, unclassified, unknown	4402.0	0.47	0.09	1.6E-04
<i>sgaH</i>	Hypothetical, unclassified, unknown	4419.8	-0.12	-0.53	3.2E-04
<i>sgaU</i>	Hypothetical, unclassified, unknown	4420.4	-0.04	-0.30	1.3E-04
<i>b4250</i>	Hypothetical, unclassified, unknown	4471.8	0.44	-0.11	9.0E-05
<i>yi4l</i>	Hypothetical, unclassified, unknown	4499.7	-1.26	-0.31	3.9E-04
<i>serB</i>	Amino acid biosynthesis and metabolism	4622.5	0.35	-0.09	1.5E-04

Genes are listed according to their physical position from 0 to 100' on the K12-MG1655 chromosome. Red and green colors indicate