

**TABLE S1.** *B. pertussis* genes with increased transcript abundance under conditions of iron limitation<sup>a</sup>

Locus tag	Description	Fold change	FC category <sup>b</sup>	MultiFun heading <sup>c</sup>
BP0101	putative exported protein	2.3	4.1.0	Periplasmic/exported/lipoproteins
BP0131	<i>leuA</i> 2-isopropylmalate synthase	2.4	3.1.12	Amino acid biosynthesis
BP0134	putative bacterioferritin-associated ferredoxin	2.1	1.6.3	Adaptation
BP0248	<i>fumC</i> fumarate hydratase class II	2.0	3.5.8	Energy metabolism, carbon
BP0249	putative membrane protein	1.6	4.1.1	Cell envelope
BP0343	<i>bhuV</i> putative ATP-binding component of hemin transport system	1.7	1.6.3	Adaptation
BP0345	<i>bhuT</i> putative hemin binding protein	1.8	1.6.3	Adaptation
BP0346	<i>bhuS</i> putative hemin transport protein	3.7	1.6.3	Adaptation
BP0347	<i>bhuR</i> outer membrane heme receptor	4.8	1.6.3	Adaptation
BP0348	<i>hurR</i> heme uptake transmembrane sensor	4.5	6.1.1	Global regulatory functions
BP0349	<i>hurI</i> heme uptake regulator	8.5	6.1.1	Global regulatory functions
BP0454	putative exported protein	1.9	4.1.0	Periplasmic/exported/lipoproteins
BP0500	<i>bteA</i> ( <i>bopC</i> ) T3SS effector protein	2.7	0.0.0	Unknown proteins, no known homologs
BP0501	two component sensor kinase , C-terminal region of two component sensor kinase (partial)	1.6	6.1.1	Global regulatory functions
BP0663	conserved hypothetical protein	2.1	0.0.2	Conserved in organism other than <i>E. coli</i>
BP0703	outer membrane ferrichrome receptor (pseudogene)	1.4	1.6.3	Adaptation
BP0720	conserved hypothetical protein	1.5	0.0.2	Conserved in organism other than <i>E. coli</i>
BP0809	<i>argH</i> putative argininosuccinate lyase (pseudogene)	5.5	3.1.02	Amino acid biosynthesis
BP1001	phosphoglycerate kinase	1.7	3.5.5	Energy metabolism, carbon
BP1004	phosphate acetyl/butaryl transferase	3.1	7.0.0	Some information, but not classifiable
BP1136	<i>fecI</i> ECF-family sigma factor	2.6	6.1.1	Global regulatory functions
BP1139	putative iron uptake protein	1.8	1.6.3	Adaptation
BP1140	putative iron uptake protein (pseudogene)	1.7	1.6.3	Adaptation
BP1152	putative exported protein	7.6	4.1.0	Periplasmic/exported/lipoproteins
BP1153	putative exported protein	5.7	4.1.0	Periplasmic/exported/lipoproteins
BP1154	putative membrane protein	3.0	4.1.1	Cell envelope
BP1155	putative regulatory protein	2.0	6.1.1	Global regulatory functions
BP1201	<i>tcfA</i> tracheal colonization factor precursor	1.6	4.1.5	Cell envelope
BP1211	putative exported protein	3.0	4.1.0	Periplasmic/exported/lipoproteins
BP1212	putative exported protein	3.8	4.1.0	Periplasmic/exported/lipoproteins
BP1240	conserved hypothetical protein	2.9	0.0.2	Conserved in organism other than <i>E. coli</i>
BP1380	<i>flgI</i> , <i>flaM</i> , <i>fla</i> FIX flagellar P-ring protein precursor	1.8	1.1.1	Chemotaxis, motility

BP1561	putative exported protein	4.1	4.1.0	Periplasmic/exported/lipoproteins
BP1604	putative inner membrane component of binding-protein-dependent transport system	1.6	1.5.0	Transport/binding proteins
BP1605	putative iron binding protein	4.8	1.5.2	Transport/binding proteins
BP1879	<i>fhaB</i> filamentous hemagglutinin/adhesin	2.0	4.1.5	Cell envelope
BP1961	putative flavocytochrome	2.1	3.5.3	Energy metabolism, carbon
BP2016	<i>brfB</i> putative ferric siderophore receptor	2.7	1.6.3	Adaptation
BP2043	putative lipoprotein	1.7	4.1.0	Periplasmic/exported/lipoproteins
BP2072	putative lipoprotein	1.5	4.1.0	Periplasmic/exported/lipoproteins
BP2073	conserved hypothetical protein	2.0	0.0.2	Conserved in organism other than <i>E. coli</i>
BP2077	putative efflux system outer membrane component	1.9	1.5.5	Transport/binding proteins
BP2233	hypothetical protein	2.3	0.0.0	Unknown proteins, no known homologs
BP2251	<i>bcrH2</i> putative regulatory protein	1.8	1.3.1	Folding and ushering proteins
BP2252	<i>bopB</i> putative outer protein B	1.9	1.5.5	Transport/binding proteins
BP2256	<i>bsp22</i> putative secreted protein	2.6	1.5.5	Transport/binding proteins
BP2257	<i>bopN</i> putative outer protein N	2.0	1.5.5	Transport/binding proteins
BP2396	putative binding-protein-dependent transport periplasmic protein	1.7	1.5.0	Transport/binding proteins
BP2413	putative lipoprotein	1.6	4.1.0	Periplasmic/exported/lipoproteins
BP2414	conserved hypothetical protein	8.8	0.0.2	Conserved in organism other than <i>E. coli</i>
BP2456	<i>alcA</i> alcaligin biosynthesis enzyme	5.9	1.6.3	Adaptation
BP2457	<i>alcB</i> alcaligin biosynthesis protein	8.0	1.6.3	Adaptation
BP2458	<i>alcC</i> alcaligin biosynthesis protein	6.6	1.6.3	Adaptation
BP2459	<i>alcD</i> hypothetical protein	2.8	1.6.3	Adaptation
BP2463	<i>fauA</i> ferric alcaligin siderophore receptor	1.4	1.6.3	Adaptation
BP2714	putative lipoprotein	1.5	4.1.0	Periplasmic/exported/lipoproteins
BP2900	<i>bfeR</i> transcriptional regulator	1.7	6.1.1	Global regulatory functions
BP2985	<i>bphI</i> histone protein	2.5	6.1.1	Global regulatory functions
BP2985	<i>bphI</i> histone protein	2.8	6.1.1	Global regulatory functions
BP3014	<i>secA, prlD, azi, pea</i> preprotein translocase <i>secA</i> subunit	1.6	1.5.5	Transport/binding proteins
BP3018	<i>ftsZ, sfiB, sulB</i> cell division protein FtsZ	2.6	1.7.1	Cell division
BP3027	<i>murE</i> possible murein precursor biosynthesis bifunctional protein	1.6	4.1.2	Cell envelope
BP3110	probable MerR-family transcriptional regulator	1.5	6.1.1	Global regulatory functions
BP3157	omega-amino acid--pyruvate aminotransferase	1.8	3.3.00	Central intermediary metabolism
BP3159	putative extracellular solute-binding protein	1.9	1.5.0	Transport/binding proteins
BP3344	proline-rich inner membrane	1.4	4.1.1	Cell envelope

BP3530	protein <i>hupB</i> , DNA-binding protein Hu-beta	2.0	1.6.1	Adaptation
BP3531	<i>tonB</i> siderophore-mediated iron transport protein	1.8	1.6.3	Adaptation
BP3532	<i>exbB</i> MotA/TolQ/ExbB proton channel family protein	1.8	1.6.3	Adaptation
BP3533	<i>exbD</i> biopolymer transport protein ExbD/TolR	3.4	1.6.3	Adaptation
BP3663	<i>bfrC</i> ferric siderophore receptor	5.5	1.6.3	Adaptation
BP3664	conserved hypothetical protein	2.4	0.0.2	Conserved in organism other than <i>E. coli</i>
BP3665	putative aldolase (pseudogene)	1.8	7.0.0	Some information, but not classifiable
BP3790	<i>ptlC</i> putative bacterial secretion system protein	3.1	1.5.0	Transport/binding proteins
BP3792	<i>ptlI</i> putative bacterial secretion system protein	1.9	1.5.0	Transport/binding proteins
BP3831	putative ABC transporter periplasmic amino acid-binding protein	2.2	1.5.1	Transport/binding proteins
BP3838	<i>ubiE/COQ5</i> methyltransferase family protein	3.2	7.0.0	Some information, but not classifiable
BP3842	hypothetical protein	1.7	0.0.0	Unknown proteins, no known homologs

<sup>a</sup> Genes with significant differences in transcript abundance between the two nutritional growth conditions, based on SAM analysis (false discovery rate = 0.56%). Genes are listed in chromosomal order.

<sup>b</sup> Functional classification as assigned by Parkhill and coworkers (66).

<sup>c</sup> Descriptive multifunctional classification (78).