Table S3. Expression changes in *B. fragilis NCTC9343* during growth in neutral porcine mucin *O*-glycans (PMOG) relative to growth in glucose (Glc)

Formatting descriptions and notes:

Color-coding for PUL genes that are upregulated more than 10-fold in PMOG relative to Glc

Color-coding for genes associated with upregulated PULs that are not themselves upregulated more than 10-fold in PMOG relative to Glc

B. fragilis starch utilization PUL genes

B. fragilis inulin utilization PUL genes

B. fragilis PULs containing validated recombinational shufflons that were not probed

Other putative PULs (minimum susC-/susD-like gene pair) that are not regulated in response to PMOG

PUL genes in bold text represent *susC* homologs probed by qPCR during growth in starch and PMOG mixtures

[1] Values shown are RPKM normalized counts

	Total mapped reads :	**5,582,206**	**5,294,358**	**5,109,030**	**4,867,823**	**5,937,185**	**5,830,264**		

Locus tag/gene name	**Description**	**[1]Glc1**	**[1]Glc2**	**[1]Glc3**	**[1]PMOG1**	**[1]PMOG2**	**[1]PMOG3**	**Fold change**	**P value**
BF0001	putative SpoU rRNA methylase family protein	72.5	75.7	67.7	71.3	72.4	61.9	0.95	5.1E-01
BF0002	putative outer membrane protein	169.4	141.2	172.4	194.2	244.6	175.7	1.27	1.6E-01
BF0003	hypothetical protein	38.7	37.7	44.8	103.4	118.3	85.2	2.52	4.2E-03
BF0004	putative sugar transferase	32.1	37.5	37.9	106.1	116.5	93.1	2.93	1.3E-03
BF0005	hypothetical protein	69.1	72.4	70.2	430.3	416.6	379.1	5.78	4.1E-05
BF0006	hypothetical protein	38.4	34.8	32.3	175.1	175.1	200.4	5.22	2.3E-04
BF0007	hypothetical protein	28.8	25.3	31.5	106.1	118.9	94.4	3.73	9.6E-04
BF0008	putative glycosyltransferase	12.6	11.6	15.6	60.1	59.0	54.8	4.40	7.2E-04
BF0009	putative glycosyltransferase	12.7	12.6	8.7	56.2	50.7	55.2	4.83	1.4E-03
BF0010	hypothetical protein	11.1	6.4	12.1	43.8	51.7	36.7	4.59	7.5E-03
BF0011	putative ABC transporter ATP-binding protein	9.5	7.3	7.4	25.3	30.1	27.7	3.45	1.4E-03
BF0012	hypothetical protein	50.0	42.5	47.3	29.3	38.8	29.3	0.69	4.6E-02
BF0013	hypothetical protein	16.2	15.0	15.4	10.2	11.7	11.0	0.71	5.2E-03
BF0014	putative SAM superfamily protein	97.1	97.2	106.9	96.4	99.0	89.5	0.95	3.4E-01
BF0015	hypothetical protein	64.7	60.4	72.4	70.8	65.7	59.4	0.99	9.4E-01
BF0016	putative arylsulfatase precursor	67.2	72.3	75.4	84.4	85.1	74.5	1.13	1.2E-01
BF0017	conserved hypothetical iron transport-related transmembrane protein	899.4	901.2	944.9	609.6	627.1	502.8	0.63	8.6E-03
BF0018	putative iron transport receptor protein	327.9	334.0	326.3	389.9	359.3	315.1	1.07	3.9E-01
BF0019	putative sulfate permease transmembrane protein	66.2	70.6	80.6	40.4	41.0	38.2	0.55	2.9E-03
rbr	putative rubrerythrin	1055.4	1147.2	1183.9	2702.6	3595.0	2832.4	2.68	2.3E-03
nadB	putative exported L-aspartate oxidase	149.4	148.9	151.3	183.4	174.7	186.9	1.21	3.2E-03
BF0022	hypothetical protein	63.2	62.6	53.1	67.1	91.1	75.9	1.30	1.0E-01
pdhD	putative dihydrolipoamide dehydrogenase	73.7	70.2	67.9	110.9	120.7	127.8	1.69	1.9E-03
dacB	putative exported D-alanyl-D-alanine carboxypeptidase penicillin-binding protein	33.4	32.7	32.0	52.1	59.0	50.9	1.65	2.2E-03
BF0025	putative CoA transferase	233.5	234.9	233.9	502.7	479.7	438.5	2.02	5.7E-04
BF0026	hypothetical protein	127.3	128.0	112.5	181.4	211.7	148.2	1.46	5.0E-02
BF0027	putative SAM/TRAM family methylase protein	175.2	170.5	172.9	181.5	167.0	177.9	1.01	6.8E-01
BF0028	putative alpha-L-fucosidase protein	91.9	75.1	73.0	79.6	77.9	88.5	1.03	7.9E-01

BF0029	putative beta-galactosidase	15.4	12.2	16.8	33.5	27.4	28.4	2.02	1.0E-02
BF0030	putative AraC family/two component family regulatory protein	0.8	1.3	1.8	1.4	1.9	0.8	1.04	9.4E-01
BF0031	hypothetical protein	19.8	13.8	13.4	17.6	19.5	12.1	1.04	8.8E-01
BF0032	hypothetical protein	52.0	48.0	61.6	65.5	70.7	64.6	1.25	7.9E-02
BF0033	hypothetical protein	69.7	60.3	79.5	59.4	72.9	58.6	0.91	5.1E-01
BF0034	hypothetical protein	7.2	5.8	12.6	9.3	25.2	5.2	1.33	6.7E-01
BF0035	hypothetical protein	100.6	104.1	112.0	155.4	161.2	125.6	1.39	3.4E-02
BF0036	hypothetical protein	12.1	11.9	23.6	32.7	23.8	26.0	1.81	1.1E-01
BF0037	hypothetical protein	3.6	2.6	3.3	13.1	12.1	10.2	3.74	2.2E-03
BF0038	hypothetical protein	0.0	3.6	4.3	11.6	11.0	9.7	2.72	7.7E-03
BF0039	hypothetical protein	1.4	4.7	0.0	12.9	10.2	12.0	4.60	1.4E-01
BF0040	hypothetical protein	15.7	14.5	13.7	18.2	19.2	18.0	1.26	1.5E-02
BF0041	hypothetical protein	16.6	12.5	18.0	15.8	18.4	25.2	1.25	3.4E-01
BF0042	hypothetical protein	92.6	97.0	124.7	164.4	165.1	132.6	1.48	5.3E-02
BF0043	hypothetical protein	25.0	25.6	21.3	74.1	84.0	73.6	3.23	6.8E-04
BF0044	hypothetical protein	2.5	3.3	5.4	13.3	18.8	12.0	4.06	1.5E-02
BF0045	conserved hypothetical lipoprotein	5.1	7.5	6.8	12.4	12.1	11.7	1.90	1.4E-02
BF0046	hypothetical protein	91.6	99.4	90.0	54.4	47.7	47.6	0.53	1.7E-03
BF0047	hypothetical protein	58.3	66.3	59.6	28.0	34.2	25.0	0.47	5.6E-03
BF0048	hypothetical protein	29.5	22.8	25.4	15.4	16.4	13.4	0.58	1.3E-02
BF0049	hypothetical protein	8.4	8.9	5.6	4.8	5.8	3.2	0.60	1.3E-01
BF0050	hypothetical protein	39.6	30.8	34.3	27.8	34.0	29.2	0.87	2.8E-01
BF0051	hypothetical protein	49.8	37.7	44.8	36.4	34.0	37.6	0.82	1.3E-01
BF0052	hypothetical protein	60.1	60.4	57.1	36.6	34.8	33.2	0.59	7.2E-04
BF0053	hypothetical protein	51.1	51.9	55.1	28.8	29.8	21.2	0.50	9.3E-03
BF0055	hypothetical protein	13.8	12.2	12.6	9.4	11.9	9.2	0.79	8.7E-02
BF0056	hypothetical protein	21.4	14.2	22.1	13.9	13.9	16.7	0.78	2.5E-01
BF0057	hypothetical protein	16.1	19.4	14.7	12.6	6.5	12.1	0.60	1.4E-01
BF0058	hypothetical protein	11.9	11.1	11.5	5.2	7.8	7.2	0.58	2.5E-02
BF0059	putative lipoprotein	8.7	5.6	6.7	3.8	2.3	3.5	0.46	3.4E-02
BF0060	hypothetical protein	9.6	6.2	5.8	5.5	7.3	8.3	0.99	9.6E-01
BF0061	hypothetical protein	11.7	8.3	10.3	6.2	7.0	7.4	0.68	4.9E-02
BF0062	hypothetical protein	7.7	10.4	11.5	7.5	7.1	2.9	0.56	2.0E-01
BF0063	hypothetical protein	5.1	3.1	3.3	1.7	2.7	3.8	0.69	3.3E-01
BF0064	hypothetical protein	102.0	112.6	70.5	100.3	74.1	196.9	1.22	6.4E-01
BF0065	hypothetical protein	382.1	379.6	297.6	338.8	287.5	414.3	0.98	9.0E-01
ftsX	putative cell division protein	174.5	137.9	162.6	102.2	99.6	104.0	0.65	9.9E-03
BF0067	hypothetical protein	260.2	186.1	213.4	215.8	234.8	232.9	1.05	7.4E-01
BF0068	putative undecaprenol kinase	280.2	208.3	257.6	245.7	268.8	273.0	1.06	6.2E-01
BF0069	putative tRNA pseudouridine synthase	163.9	132.9	124.6	160.8	145.2	189.8	1.18	2.9E-01
BF0070	putative S-adenosylmethionine:tRNA ribosyltransferase-isomerase	502.5	433.3	499.1	516.6	558.1	516.1	1.11	1.8E-01
BF0071	putative 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (HPPK)	223.0	225.9	222.1	214.7	213.6	240.4	0.99	9.2E-01
SAM_alpha	RF00521	214.1	230.2	277.2	178.4	209.7	209.9	0.83	1.7E-01
metK	S-adenosylmethionine synthetase	446.2	443.7	476.2	281.7	281.7	319.4	0.65	3.3E-03
BF0073	putative lysine decarboxylase	128.9	100.9	98.3	72.0	66.0	104.9	0.73	1.9E-01
BF0074	hypothetical protein	94.3	89.7	98.0	75.9	76.9	79.6	0.82	8.3E-03
BF0075	possible uroporphyrinogen-III synthase	911.8	915.5	984.7	868.8	887.7	825.5	0.92	9.7E-02

rnpA	ribonuclease P	199.9	203.9	248.9	162.6	182.2	171.4	0.79	6.9E-02
BF0077	hypothetical protein	144.7	126.8	146.2	88.1	81.9	111.3	0.67	3.5E-02
BF0078	putative tatD-related DNAse protein	86.3	91.5	89.2	46.5	50.1	54.3	0.56	1.6E-03
tyrS	putative tyrosyl-tRNA synthetase 1	559.0	527.2	591.2	634.4	700.7	702.6	1.21	3.0E-02
BF0080	putative peptidase/protease family protein	45.0	41.6	42.6	55.3	54.6	50.7	1.24	1.0E-02
BFt01	tRNA-Gln-TTG	77.0	95.2	98.5	49.5	43.2	107.3	0.68	3.3E-01
BF0081	putative choline-sulfatase	34.2	39.4	34.0	73.4	77.6	77.8	2.13	9.1E-04
BF0082	putative 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	22.2	21.2	16.8	19.6	31.5	34.5	1.39	2.2E-01
gno	gluconate 5-dehydrogenase	26.5	26.8	27.2	50.5	45.9	69.0	2.02	1.2E-02
BF0084	hypothetical protein	22.7	25.0	24.8	45.5	41.2	65.1	2.05	1.7E-02
BF0085	putative iron-sulfur cluster-binding protein	34.5	32.5	33.0	32.7	25.3	29.3	0.87	2.0E-01
BF0086	putative polysaccharide deacetylase	321.1	365.3	316.6	286.1	241.8	279.4	0.80	6.1E-02
BF0087	hypothetical protein	362.3	425.1	305.9	301.8	256.4	299.8	0.79	1.4E-01
BF0088	hypothetical protein	17.8	19.4	19.8	5.8	4.1	7.9	0.30	9.7E-03
BF0089	hypothetical protein	3.6	3.7	4.1	1.4	2.0	2.1	0.48	1.6E-02
BF0090	hypothetical protein	1.2	0.5	1.3	1.4	1.1	1.6	1.47	3.7E-01
BF0091	putative metal uptake system ABC transporter ATP-binding protein	96.9	113.5	72.0	88.8	66.1	124.8	0.97	9.3E-01
BF0092	putative metal ABC transporter substrate-binding precursor	46.1	60.8	47.3	50.4	40.1	65.1	1.00	9.9E-01
BF0093	hypothetical protein	97.0	91.1	75.0	79.9	63.6	100.2	0.92	6.6E-01
BF0094	putative transmembrane protein	78.1	94.0	69.7	90.1	69.0	95.5	1.05	7.8E-01
BF0095	putative transmembrane protein	172.5	179.0	161.0	131.7	120.4	144.2	0.77	2.7E-02
purD	putative phosphoribosylamine--glycine ligase	257.0	251.3	213.8	236.8	205.7	293.1	1.01	9.4E-01
BF0097	putative exported dipeptidyl peptidase IV	167.7	174.1	151.8	162.6	145.2	160.3	0.95	4.6E-01
BF0098	putative methylase	202.1	238.2	199.8	229.2	206.9	224.9	1.04	6.8E-01
BF0099	putative serine acetyltransferase	211.5	228.6	209.0	180.2	168.4	179.4	0.81	1.2E-02
BF0100	putative two-component regulator sensor kinase	35.6	32.5	36.5	26.3	29.5	25.7	0.78	2.3E-02
BF0101	putative two-component response regulator	28.7	27.1	30.3	31.0	35.9	29.8	1.12	2.2E-01
BF0102	hypothetical protein	12.1	16.0	13.3	24.3	19.2	14.5	1.38	1.9E-01
BF0103	hypothetical protein	33.4	31.8	32.9	22.4	17.5	15.0	0.55	1.7E-02
polA	putative DNA polymerase I	201.7	207.5	199.7	170.2	175.6	148.7	0.81	3.2E-02
BF0105	putative octaprenyl-diphosphate synthase	272.2	267.6	253.1	264.1	263.0	256.6	0.99	7.2E-01
BF0106	hypothetical protein	88.0	74.2	84.0	31.2	41.3	45.4	0.47	1.1E-02
BF0107	hypothetical protein	94.3	97.1	105.0	57.7	52.8	68.1	0.60	9.3E-03
BF0108	putative deoxyribose-phosphate aldolase	297.0	293.4	323.8	377.9	376.5	375.5	1.24	7.4E-03
BF0109	hypothetical protein	246.2	160.6	221.8	220.0	204.9	214.2	1.03	8.5E-01
dtd	D-tyrosyl-tRNA deacylase	268.8	234.9	241.1	226.7	223.2	208.5	0.89	1.0E-01
uvrC	putative excinuclease UvrC protein	83.8	71.3	77.0	106.2	98.8	89.7	1.27	4.5E-02
apt	adenine phosphoribosyltransferase	184.7	176.5	174.0	240.7	252.6	245.9	1.38	9.6E-04
gidA	glucose-inhibited division protein A	84.8	81.5	81.3	83.8	76.1	74.9	0.95	2.9E-01
BF0114	putative lipoprotein	35.0	30.2	35.3	26.4	31.0	25.8	0.83	1.1E-01

BF0115	hypothetical protein	25.6	15.0	24.9	11.4	8.7	11.1	0.49	4.0E-02
BF0116	hypothetical protein	25.4	24.7	28.7	15.2	20.5	15.9	0.65	3.0E-02
BF0117	hypothetical protein	88.5	79.3	81.6	72.4	90.1	64.0	0.90	4.5E-01
BF0118	hypothetical protein	345.8	331.1	336.8	227.0	245.1	207.2	0.67	4.8E-03
BF0119	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF0120	hypothetical protein	76.6	72.7	78.9	71.1	74.3	66.0	0.93	2.0E-01
BF0121	hypothetical protein	54.4	53.4	58.6	61.4	74.8	63.9	1.20	8.5E-02
BF0122	hypothetical protein	10.5	5.6	4.3	6.2	9.1	22.6	1.72	3.8E-01
BF0123	hypothetical protein	11.1	10.6	8.2	3.4	4.2	4.6	0.40	6.8E-03
BF0124	hypothetical protein	83.3	104.3	75.6	52.6	62.4	48.6	0.62	3.5E-02
BF0125	putative transmembrane spore maturation-like protein	39.5	37.4	38.0	27.4	28.7	29.2	0.74	1.6E-03
BF0126	hypothetical protein	40.1	22.3	23.6	39.2	38.0	49.4	1.52	1.6E-01
BF0127	hypothetical protein	16.4	23.3	9.0	18.2	34.8	30.2	1.77	2.3E-01
ruvB	Holliday junction DNA helicase RuvB	126.7	130.1	108.2	110.0	87.8	130.5	0.89	4.9E-01
BF0129	possible polysaccharide biosynthesis transmembrane protein	146.0	152.7	153.6	120.8	118.9	120.1	0.80	1.1E-03
BF0130	hypothetical protein	102.0	95.8	99.9	84.4	85.7	97.9	0.90	1.5E-01
BF0131	hypothetical protein	165.1	168.3	152.2	133.2	120.7	138.2	0.81	2.8E-02
BF0132	putative transmembrane protein	52.3	58.4	51.5	43.4	37.8	39.2	0.74	1.6E-02
BF0133	hypothetical protein	7.6	13.9	8.3	1.6	1.9	3.2	0.23	1.5E-02
BF0134	putative RNA helicase dead-box protein	245.1	243.3	228.0	130.0	91.3	152.7	0.51	2.6E-02
BF0135	hypothetical protein	316.6	331.1	274.5	301.9	323.3	289.7	0.99	9.5E-01
frk	putative fructokinase	128.2	122.7	132.9	202.5	176.3	175.2	1.44	7.0E-03
BF0137	putative sugar isomerase SIS-domain protein	170.3	162.6	156.5	289.8	245.4	268.7	1.64	3.3E-03
BF0138	putative lysine decarboxylase	168.5	169.7	131.0	220.5	185.4	236.2	1.37	7.8E-02
BF0139	putative peptidase	71.7	78.9	69.4	71.8	71.4	57.5	0.91	3.8E-01
BF0140	hypothetical protein	289.5	292.9	246.5	125.8	113.5	138.2	0.46	2.7E-03
BF0141	possible acetyltransferase protein	482.8	448.5	414.6	373.2	379.7	318.8	0.80	5.6E-02
uxuA	mannonate dehydratase	37.9	42.4	43.2	55.9	55.6	56.7	1.36	5.7E-03
uxuB	D-mannonate oxidoreductase	48.0	58.2	46.4	45.9	44.2	66.8	1.02	9.4E-01
BF0144	hypothetical protein	33.1	26.8	31.6	40.7	32.9	39.1	1.23	1.3E-01
BF0145	putative exported signal peptidase I	132.0	119.5	129.3	131.7	132.7	125.3	1.02	6.1E-01
BF0146	possible signal peptidase	263.9	277.7	254.9	233.1	241.8	219.8	0.87	4.1E-02
BF0147	putative dihydrodipicolinate reductase	296.5	282.2	266.0	260.1	243.0	235.5	0.87	6.2E-02
BF0148	hypothetical protein	40.7	47.8	44.3	49.7	51.4	57.9	1.20	8.3E-02
BF0149	hypothetical protein	121.1	99.7	97.0	228.9	194.8	224.8	2.05	4.4E-03
BF0150	hypothetical protein	62.0	61.4	65.4	92.0	75.1	88.9	1.35	2.2E-02
BF0151	conserved hypothetical outer membrane protein	83.8	80.4	85.9	83.7	79.1	84.3	0.99	7.4E-01
BF0152	hypothetical protein	293.0	308.1	289.9	414.2	382.8	396.6	1.34	2.7E-03
BF0153	UDP-N-acetylglucosamine acyltransferase	181.0	170.6	155.7	253.8	257.8	227.5	1.46	8.9E-03
BF0154	putative outer membrane lipoprotein	141.0	140.0	127.2	174.0	156.3	156.3	1.19	4.3E-02
BF0155	putative AcrB/AcrD family RND transport protein	101.9	104.2	86.4	128.4	125.0	119.1	1.28	3.5E-02
BF0156	putative AcrA/AcrE RND transport or HlyD secretion family protein	65.8	59.2	55.7	100.8	90.9	88.4	1.55	7.0E-03
BF0157	putative exported beta-galactosidase	66.7	61.8	52.3	177.6	167.2	155.5	2.78	1.4E-03

BF0158	hypothetical protein	304.7	313.8	280.1	206.4	203.0	189.7	0.67	3.0E-03
BF0159	hypothetical protein	302.3	312.8	275.0	202.7	175.1	213.7	0.66	1.2E-02
BF0160	putative phenylacetic acid degradation protein	143.3	171.5	141.5	108.2	104.4	128.7	0.75	5.6E-02
cysS	cysteinyl-tRNA synthetase	449.5	463.6	446.7	479.0	437.5	470.3	1.02	6.3E-01
BF0163	putative haloacid dehalogenase-like hydrolase	21.1	28.0	22.5	36.8	28.8	35.0	1.41	6.8E-02
BF0164	putative two-component system, response regulator protein	12.2	9.4	12.9	17.8	18.1	13.5	1.43	9.3E-02
BF0165	putative two-component regulatory system, sensor kinase protein	18.9	18.2	22.0	11.7	12.8	9.9	0.58	1.3E-02
BF0166	hypothetical protein	10.0	6.7	5.0	9.4	7.3	1.7	0.71	6.4E-01
BF0167	hypothetical Kelch-like protein	3.0	3.4	4.4	2.0	1.4	1.6	0.46	1.5E-02
BF0168	putative two-component response regulator transcriptional regulatory protein	82.2	85.0	65.3	69.9	59.5	71.7	0.87	3.0E-01
BF0169	putative two-component regulator sensor kinase	49.9	44.0	52.3	38.4	44.5	37.5	0.82	9.3E-02
mgtA	putative Mg2+ transport ATPase protein	179.7	169.9	168.7	183.0	175.1	183.6	1.05	2.1E-01
BF0171	hypothetical protein	256.7	222.4	239.4	207.7	205.4	228.5	0.89	1.5E-01
BF0172	putative lipoprotein	134.7	111.7	123.4	93.9	122.4	110.5	0.88	3.2E-01
BF0173	putative SNF family helicase	40.1	40.1	40.2	37.7	40.8	38.9	0.97	3.9E-01
BF0174	putative tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	45.0	43.4	38.0	43.1	44.2	57.7	1.14	3.5E-01
BF0175	putative plant auxin-regulated protein	173.5	185.1	173.1	191.6	198.9	176.0	1.06	2.8E-01
pfkA	6-phosphofructokinase	138.9	127.2	124.7	171.7	169.9	164.9	1.30	6.0E-03
BF0177	putative ribonuclease III	95.6	100.0	106.4	140.8	128.0	140.0	1.35	7.1E-03
BF0178	putative 3-oxoacyl-[acyl-carrier-protein] synthase II	2006.1	2016.0	2182.1	5337.8	5302.9	5035.0	2.53	1.6E-04
acpP	putative acyl carrier protein	4214.0	5033.5	4895.3	7274.4	7958.7	7745.3	1.63	4.9E-03
purN	putative phosphoribosylglycinamide formyltransferase	93.0	77.0	91.2	86.3	105.1	87.6	1.07	5.7E-01
pdxB	erythronate-4-phosphate dehydrogenase	79.9	93.2	96.5	86.7	90.9	90.1	1.00	9.6E-01
BF0182	hypothetical protein	264.8	268.1	257.7	301.4	292.9	292.5	1.12	5.6E-03
BF0183	hypothetical protein	119.6	123.0	147.0	188.6	171.7	181.1	1.39	2.0E-02
BF0184	putative lipopolysaccharide 1,2-glucosyltransferase/general stress protein	168.7	190.7	204.5	228.3	231.1	208.3	1.19	9.3E-02
BF0185	putative lipopolysaccharide core biosynthesis protein	246.7	222.0	261.5	205.7	217.5	190.1	0.84	7.9E-02
BF0186	putative glycosyltransferase	330.5	296.7	331.1	291.8	304.4	278.5	0.91	1.6E-01
BF0187	putative glycosyltransferase	257.5	225.5	231.1	200.7	190.6	166.1	0.78	4.3E-02
BF0188	putative transport ATP-binding protein	253.3	219.5	245.0	151.3	163.8	157.7	0.66	4.1E-03
BF0189	hypothetical protein	195.1	183.9	205.6	123.4	131.1	135.1	0.67	2.8E-03
rnh1	putative ribonuclease H1	35.9	38.7	32.4	31.9	35.0	44.1	1.03	8.4E-01
BF0191	hypothetical protein	2028.8	2467.0	2280.7	1028.7	1040.1	1034.5	0.46	1.1E-03
BF0192	putative shikimate kinase	87.2	76.8	68.4	53.0	48.0	54.9	0.67	1.9E-02
BF0193	hypothetical protein	92.6	80.7	77.0	54.2	63.8	73.5	0.76	9.4E-02
BF0194	putative heat-shock protein	64.2	59.5	60.8	60.1	62.8	66.2	1.02	6.1E-01

BF0195	hypothetical protein	52.1	54.6	55.1	65.7	78.7	61.6	1.27	6.1E-02
BF0196	arginine decarboxylase	213.6	194.3	208.6	247.2	251.7	242.5	1.20	1.0E-02
BF0197	putative acetylglutamate kinase	85.1	83.1	81.6	98.7	95.9	98.4	1.17	2.3E-03
BF0198	putative extracytoplasmic function alternative sigma factor	1695.7	1688.1	1629.1	1370.0	1273.0	1404.0	0.81	7.8E-03
BF0199	hypothetical protein	869.5	818.8	891.5	691.6	788.7	761.7	0.87	6.7E-02
BF0200	hypothetical protein	773.9	770.0	809.4	467.4	538.3	525.9	0.65	3.2E-03
BF0201	putative lipoprotein	364.4	349.6	352.0	159.7	199.1	151.0	0.47	3.8E-03
BF0202	putative lipoprotein	508.0	399.4	415.3	173.8	192.9	170.9	0.41	2.1E-03
BF0203	hypothetical protein	103.2	92.6	103.7	100.5	125.1	131.3	1.18	1.9E-01
BF0204	putative transmembrane protein	145.1	116.7	146.1	193.6	210.9	169.3	1.41	4.6E-02
BF0205	putative transmembrane protein	39.6	35.5	46.6	27.9	39.1	36.5	0.85	3.4E-01
BF0206	hypothetical protein	7.7	10.7	12.8	8.1	9.9	13.4	1.00	1.0E+00
BF0207	hypothetical protein	15.9	22.5	21.1	16.3	20.7	15.2	0.88	4.9E-01
BF0208	hypothetical protein	13.0	11.9	15.8	6.7	4.8	5.8	0.42	7.8E-03
BF0209	hypothetical protein	10.4	9.6	10.3	5.1	5.8	4.8	0.52	2.1E-03
fucR	putative GntR-family regulatory protein	315.1	282.2	280.5	801.4	985.0	757.3	2.88	1.6E-03
fucI	putative L-fucose isomerase	43.7	40.5	42.2	936.5	972.4	1052.9	23.41	5.0E-06
fucO	putative lactaldehyde reductase	41.4	43.9	46.1	895.1	963.4	855.2	20.65	9.8E-06
fucA	putative aldolase	144.4	136.0	139.6	1133.0	1269.9	1200.8	8.57	1.6E-05
fucK	putative fuculokinase	72.8	77.4	82.9	709.0	741.7	654.8	9.03	4.6E-05
fucP	putative L-fucose permease	40.3	44.5	42.4	547.8	595.1	506.7	12.95	3.2E-05
BF0217	hypothetical protein	467.5	410.3	368.7	311.2	250.1	408.7	0.77	2.3E-01
BF0218	transcription elongation factor NusA	1001.6	939.3	1030.7	696.6	710.4	673.4	0.70	1.8E-03
infB	translation initiation factor IF-2	855.2	783.2	790.3	650.6	652.1	725.9	0.83	3.3E-02
BF0220	hypothetical protein	195.7	214.9	203.2	128.4	144.7	157.2	0.70	1.3E-02
BF0221	putative ABC transporter membrane protein	264.8	285.8	258.4	168.5	160.6	175.2	0.62	1.6E-03
BF0222	hypothetical protein	138.0	133.2	135.3	75.7	86.1	83.4	0.60	1.4E-03
BF0223	putative ABC transporter, ATP-binding protein	262.0	266.5	257.3	185.7	187.7	185.7	0.71	1.2E-04
BF0224	putative ABC transporter protein	368.4	384.9	380.3	225.1	238.3	201.1	0.58	2.3E-03
BF0225	putative aminotransferase	522.5	537.4	527.4	240.0	251.7	237.3	0.46	5.7E-05
BF0226	hypothetical protein	431.0	445.5	346.2	136.0	122.8	122.3	0.31	1.1E-03
BF0227	putative exported alpha-galactosidase	15.8	16.5	14.3	6.0	7.3	4.9	0.39	5.4E-03
BF0228	hypothetical protein	2.5	3.3	2.7	8.9	7.8	8.3	2.95	1.4E-03
BF0229	putative outer membrane protein	9.6	11.8	10.5	14.0	12.6	14.3	1.28	4.9E-02
BF0230	hypothetical protein	53.5	52.6	57.4	68.4	78.9	57.7	1.24	1.2E-01
BF0231	putative regulatory protein	132.1	114.2	125.6	72.5	77.2	79.7	0.62	3.0E-03
BF0232	putative ECF-type sigma factor	26.3	20.3	23.8	38.8	39.5	36.0	1.63	1.0E-02
BF0233	putative exported alpha-galactosidase	74.5	76.9	72.9	134.6	130.1	127.3	1.75	2.2E-04
BF0234	putative lipoprotein	35.9	40.6	37.5	52.1	45.6	45.8	1.26	3.1E-02
BF0235	putative inorganic pyrophosphatase	16.6	18.7	16.0	53.5	59.1	60.6	3.38	3.9E-04
BF0237	hypothetical protein	2.8	3.3	3.7	7.7	6.5	7.8	2.27	4.4E-03
BF0238	hypothetical protein	0.0	0.9	1.8	3.9	3.8	1.6	2.27	2.4E-01
rnhB	ribonuclease HII	61.4	58.5	49.7	61.8	49.2	73.7	1.08	6.6E-01
BF0240	putative cationic transporter	77.7	72.3	76.5	39.3	34.4	33.6	0.47	1.0E-03
gpmI	phosphoglyceromutase	413.6	394.6	415.2	535.5	486.9	523.9	1.26	6.7E-03
BF0242	putative two-component system sensor kinase	181.1	177.7	166.3	142.5	157.8	159.2	0.87	6.6E-02

BF0243	putative two-component sensor histidine kinase	39.4	28.2	31.4	21.4	21.5	25.9	0.70	6.5E-02
BF0244	hypothetical protein	131.6	115.5	131.2	68.4	75.5	97.7	0.63	3.3E-02
BF0245	hypothetical protein	107.0	108.2	99.5	80.9	81.0	91.5	0.80	2.4E-02
BF0246	DNA gyrase subunit B	508.0	565.4	550.6	568.0	503.2	533.8	0.99	8.5E-01
rpsT	30S ribosomal protein S20	3277.2	2897.0	3655.2	2098.0	1981.2	2252.4	0.65	1.2E-02
BFt02	tRNA-Glu-TTC	138.8	127.6	139.9	285.4	337.8	451.4	2.60	7.0E-03
BF0248	possible DNA repair protein RecO	28.8	26.5	24.5	46.3	50.7	43.9	1.77	3.4E-03
BF0249	hypothetical protein	672.9	545.1	558.3	619.9	584.3	632.7	1.04	6.8E-01
ftsZ	cell division protein FtsZ	227.6	204.9	195.0	203.6	197.0	225.1	1.00	9.8E-01
ftsA	putative cell division protein	245.9	227.0	214.3	209.7	207.9	213.6	0.92	1.6E-01
ftsQ	putative cell division protein	158.1	142.9	150.8	124.8	135.9	129.1	0.86	3.6E-02
murC	UDP-N-acetylmuramate--L-alanine ligase	259.1	277.4	263.0	215.3	214.4	202.9	0.79	4.4E-03
murG	N-acetylglucosaminyl transferase	220.0	225.2	203.3	209.7	190.8	208.4	0.94	2.9E-01
ftsW	putative transmembrane rod-shape determining protein	195.0	236.6	216.9	172.3	181.0	173.8	0.82	4.5E-02
murD	putative UDP-N-acetylmuramoylalanine--D-glutamate ligase	257.6	251.2	241.7	212.3	205.2	191.7	0.81	1.1E-02
mraY	putative UDP-N-acetylmuramoyl-pentapeptide:undecaprenyl-phosphate-ph osphatase	309.5	301.3	313.4	218.2	223.3	204.2	0.70	1.4E-03
murE	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopimelate ligase	216.8	211.6	197.6	194.0	185.4	211.4	0.94	3.5E-01
ftsI	putative cell division specific transpeptidase/penicillin-binding protein	190.3	178.1	179.0	147.1	131.3	144.6	0.77	9.4E-03
BF0260	hypothetical protein	169.7	150.9	166.5	109.0	102.1	109.9	0.66	2.9E-03
mraW	S-adenosyl-methyltransferase MraW	277.3	245.1	245.9	223.5	199.8	245.9	0.87	1.8E-01
mraZ	putative cell division protein	193.8	185.3	159.3	132.9	115.6	170.7	0.77	1.6E-01
BF0263	hypothetical protein	64.1	58.1	56.2	38.7	44.9	46.6	0.73	2.2E-02
BF0264	hypothetical protein	158.8	154.3	151.1	36.2	62.4	66.8	0.34	1.4E-02
sigE	putative extracytoplasmic function alternative sigma factor	4443.3	4152.5	4240.2	2253.9	2659.8	2135.5	0.55	3.8E-03
BF0266	hypothetical protein	1596.3	1657.4	1594.8	506.1	504.2	513.8	0.31	3.9E-06
BF0267	hypothetical protein	239.1	224.5	213.9	46.5	43.8	47.0	0.20	5.0E-05
BF0268	hypothetical protein	183.1	184.7	175.4	20.9	28.4	25.5	0.14	3.2E-04
BF0269	hypothetical protein	487.3	409.8	441.5	307.1	380.4	393.3	0.80	1.2E-01
BF0270	putative hemolysin A	274.9	210.8	245.5	254.3	256.9	272.3	1.08	4.8E-01
dgt	putative deoxyguanosinetriphosphate triphosphohydrolase	74.0	72.3	68.9	91.2	85.0	76.4	1.17	7.7E-02
dut	deoxyuridine 5'-triphosphate nucleotidohydrolase	384.1	399.1	327.0	327.9	327.3	363.1	0.92	3.7E-01
BF0273	hypothetical protein	413.8	398.7	385.0	290.5	289.9	264.4	0.71	3.1E-03
BF0274	putative lipoprotein	359.2	369.0	352.6	266.5	253.6	269.2	0.73	1.0E-03
BF0275	putative exported peptidase	136.2	118.3	110.9	82.3	77.6	97.4	0.70	3.6E-02
BF0276	putative two-component system sensor histidine kinase/response regulator fusion protein	79.8	75.0	77.8	82.1	83.8	84.2	1.08	3.9E-02
BF0277	hypothetical protein	96.5	97.6	99.2	154.0	153.6	153.1	1.57	1.9E-05

BF0278	putative beta-glucosidase	0.4	0.4	0.2	1.1	1.0	0.9	3.55	2.6E-02
BF0279	putative glycosylhydrolase	2.3	2.6	0.8	5.2	3.7	4.9	2.68	9.1E-02
BF0280	putative exported glycosylhydrolase	1.3	1.4	1.4	4.5	3.1	2.7	2.46	1.3E-02
BF0281	hypothetical protein	0.9	0.6	0.6	1.3	1.7	1.7	2.42	1.6E-02
BF0282	hypothetical protein	1.2	1.5	0.9	1.8	1.8	1.3	1.34	2.3E-01
BF0283	putative lipoprotein	26.9	31.2	29.5	35.4	33.0	40.4	1.24	7.1E-02
BF0284	putative exported glycosylhydrolase	4.9	4.3	4.5	15.3	15.3	14.3	3.28	1.5E-04
BF0285	putative exported glutaminase	4.6	5.5	4.7	15.5	15.7	15.8	3.18	4.2E-04
BF0286	hypothetical protein	13.8	13.5	13.9	16.7	18.0	14.3	1.19	9.9E-02
BF0287	putative glycosylhydrolase	1.0	1.2	1.5	1.0	1.0	0.8	0.75	9.6E-02
BF0288	putative TonB dependent receptor outer membrane protein	3.6	2.4	3.6	12.6	13.6	10.9	3.91	3.4E-03
BF0289	putative lipoprotein	7.6	5.7	6.4	13.4	12.7	11.6	1.93	7.0E-03
BF0290	hypothetical protein	13.5	13.3	14.0	22.7	24.8	15.3	1.51	8.3E-02
BF0291	hypothetical protein	7.1	4.5	4.6	3.6	10.7	3.6	0.98	9.7E-01
BF0292	putative exported endo-arabinase	6.1	4.8	3.8	6.8	7.9	6.4	1.46	1.1E-01
BF0295	putative exported glycosylhydrolase	1.6	1.0	2.4	2.7	2.9	2.0	1.59	2.4E-01
BF0296	hypothetical protein	0.5	0.3	0.3	1.2	1.1	1.1	3.55	1.0E-02
BF0297	putative exported glutaminase	7.2	9.3	6.7	9.6	9.0	9.8	1.24	1.5E-01
BF0298	putative exported alpha-1,2-mannosidase	43.4	49.5	39.4	32.9	35.0	38.7	0.81	9.1E-02
BF0299	hypothetical protein	60.1	62.2	57.1	80.0	73.8	68.8	1.24	2.8E-02
BF0300	putative aldose 1-epimerase	80.0	75.6	80.9	111.9	104.7	95.7	1.32	1.4E-02
BF0301	putative transmembrane protein	5.5	7.1	4.6	6.4	5.9	7.5	1.16	4.2E-01
BF0302	putative exported carbohydrate-binding protein	3.9	3.6	3.4	3.5	3.5	4.5	1.05	7.1E-01
BF0303	putative exported glycosylhydrolase	4.4	5.2	4.2	3.1	3.2	3.8	0.73	5.5E-02
BF0305	hypothetical protein	1.8	1.3	0.0	1.7	0.0	0.6	0.65	6.0E-01
BF0306	conserved hypothetical lipoprotein	0.5	1.8	0.5	0.3	0.4	0.2	0.34	1.4E-01
BF0307	hypothetical protein	2.5	1.8	2.3	3.2	1.4	1.2	0.81	6.2E-01
BF0309	hypothetical protein	1.5	0.0	1.6	2.1	0.0	0.0	1.35	
BF0310	hypothetical lipoprotein	26.3	23.8	26.0	36.9	35.8	31.5	1.37	1.4E-02
BF0311	hypothetical protein	22.7	31.3	28.0	21.5	29.4	32.1	1.01	9.7E-01
BF0312	putative transmembrane acyltransferase protein	113.1	111.6	120.3	91.2	106.5	88.5	0.83	6.4E-02
BF0313	putative cAMP-binding DNA-binding protein	75.1	58.6	59.3	59.3	72.8	67.2	1.04	7.8E-01
BF0314	hypothetical protein	461.9	467.8	474.9	287.6	332.2	271.1	0.63	5.6E-03
BF0315	putative transcriptional regulator	62.6	63.1	53.2	71.0	79.8	72.2	1.25	5.2E-02
BF0316	hypothetical protein	20.8	19.6	18.1	44.2	40.8	53.8	2.36	3.0E-03
BF0317	putative exported carbohydrate-binding protein	6.0	5.3	7.1	12.7	10.7	13.0	1.99	8.3E-03
BF0318	putative exported rhamnosidase protein	5.2	5.4	5.0	7.7	7.4	8.1	1.49	1.8E-03
BF0319	putative peptidase/deacetylase	48.8	52.7	36.4	77.6	61.6	69.0	1.52	5.8E-02
BF0320	putative AMP binding long chain acyl-CoA synthetase	269.0	285.4	286.0	265.6	268.2	268.6	0.96	1.3E-01
BF0321	putative peptide chain release factor	617.4	618.4	670.3	782.5	760.1	831.9	1.25	1.2E-02
BF0322	hypothetical membrane protein	909.7	1067.7	1111.1	955.1	1107.7	1364.2	1.10	5.4E-01
BF0323	hypothetical protein	69.8	63.3	69.8	62.5	84.0	79.1	1.10	4.3E-01
BF0324	hypothetical protein	18.4	16.7	18.6	26.3	25.6	34.1	1.59	2.0E-02

BF0325	putative transmembrane protein	115.9	123.8	116.5	75.1	83.4	80.1	0.67	2.1E-03
BF0326	putative TonB-dependent receptor exported protein	87.9	87.5	93.0	214.2	215.4	195.2	2.33	3.1E-04
BF0327	hypothetical protein	4.3	5.7	6.0	29.2	27.1	27.3	5.25	7.2E-04
BF0328	putative beta-galactosidase	10.9	12.0	8.4	75.4	68.8	71.2	6.95	5.8E-04
BF0329	putative exported beta-hexosaminidase	3.4	3.9	6.1	23.6	25.8	27.0	5.86	2.6E-03
BF0330	hypothetical protein	7.5	7.4	8.1	36.3	40.8	34.0	4.81	2.0E-04
BF0331	putative exported hydrolase	7.0	8.7	9.0	35.2	32.5	28.4	3.91	1.1E-03
BF0332	hypothetical protein	13.2	11.2	10.8	24.9	26.6	25.2	2.18	1.6E-03
BF0333	hypothetical protein	4.8	5.1	5.3	10.1	6.9	8.1	1.64	2.8E-02
BF0334	hypothetical protein	2.6	1.9	2.4	10.8	9.6	11.9	4.69	1.0E-03
BF0335	putative two-component system sensor histidine kinase	7.2	8.2	7.5	10.2	12.3	12.4	1.52	1.2E-02
BF0336	putative two-component sensor histidine kinase	34.4	38.8	34.4	44.8	51.6	42.7	1.29	4.1E-02
BF0337	hypothetical protein	19.4	18.7	19.3	5.2	4.9	3.9	0.24	7.4E-04
BF0338	hypothetical protein	41.3	49.4	38.7	15.3	12.5	16.7	0.34	3.0E-03
BF0339	putative exported beta-glucosidase	58.9	76.6	50.8	20.8	16.2	22.4	0.32	6.0E-03
BF0340	hypothetical protein	62.0	65.8	53.8	23.4	16.7	23.1	0.35	4.2E-03
BF0341	putative TonB-dependent outer membrane exported protein	73.2	83.6	77.0	27.7	23.8	24.8	0.33	4.7E-04
BF0342	hypothetical protein	13.0	10.8	8.7	1.1	1.3	1.1	0.11	6.2E-04
BF0343	putative DNA-binding protein	148.8	152.6	154.6	42.1	45.2	53.0	0.31	5.9E-04
BF0344	hypothetical protein	244.6	248.9	229.1	49.3	49.5	39.8	0.19	3.3E-04
BF0345	hypothetical protein	53.2	58.6	62.1	54.3	61.0	55.7	0.98	8.4E-01
BF0346	hypothetical protein	11.8	6.7	9.5	5.2	3.6	9.8	0.63	3.0E-01
BF0347	hypothetical protein	180.0	208.0	202.6	103.4	115.8	136.5	0.60	1.3E-02
BFt03	tRNA-Leu-TAG	76.8	117.0	59.4	72.8	38.5	169.3	0.96	9.5E-01
BF0349	putative TonB dependent outer membrane exported protein	2.1	2.3	1.8	0.4	0.2	0.6	0.17	1.5E-02
BF0350	putative outer membrane protein	4.4	4.7	4.0	2.9	3.4	3.3	0.74	2.0E-02
BF0351	hypothetical protein	58.0	59.1	47.8	62.7	50.3	68.7	1.10	5.3E-01
BF0352	hypothetical protein	116.0	126.6	114.6	113.8	106.8	111.3	0.93	1.7E-01
BF0353	DNA topoisomerase IV subunit A	252.7	230.9	220.1	234.2	226.7	238.7	1.00	9.4E-01
glyS	glycyl-tRNA synthetase	742.3	758.8	765.4	591.4	613.9	566.7	0.78	2.6E-03
BF0355	putative fkbp-type 22 kDa peptidyl-prolyl cis-trans isomerase	702.3	685.5	724.8	544.1	622.1	569.5	0.82	2.2E-02
BF0356	hypothetical protein	29.8	30.0	32.6	19.2	21.1	22.1	0.67	5.2E-03
BF0357	hypothetical protein	7.9	10.8	10.2	4.4	5.9	5.3	0.54	2.1E-02
BF0358	putative transmembrane protein	7.4	6.1	6.8	8.3	10.0	6.4	1.20	3.3E-01
BF0359	putative nitroimidazole resistance-like protein	35.4	33.9	37.0	64.7	66.9	47.7	1.67	2.2E-02
BF0360	putative NapC/NirT cytochrome c-type protein	32.1	28.1	31.1	47.5	44.1	44.6	1.49	3.8E-03
nrfA	putative exported cytochrome c552	25.7	18.1	21.9	31.5	27.7	39.7	1.50	8.1E-02
BF0362	putative transmembrane protein	42.8	35.1	34.6	42.8	34.2	49.2	1.12	5.0E-01
BF0363	putative cytochrome c biogenesis protein	13.6	10.7	14.0	16.3	16.0	15.0	1.24	1.1E-01
BF0364	hypothetical protein	8.8	7.4	10.3	11.2	17.9	12.0	1.53	1.1E-01
BF0365	putative FNR-family transcriptional regulatory protein	129.7	124.6	120.2	100.5	106.2	95.1	0.81	1.3E-02

BF0366	putative beta-lactamase/acylhydrolase	18.2	18.4	18.4	29.6	30.8	28.2	1.61	4.8E-04
BF0367	hypothetical protein	18.1	15.3	17.0	42.9	38.4	38.6	2.38	9.7E-04
BF0368	hypothetical protein	17.3	17.7	20.0	47.4	46.6	39.0	2.42	1.7E-03
BF0369	putative transmembrane protein	15.3	17.9	17.2	36.9	38.4	29.4	2.07	5.6E-03
BF0370	putative FAD-binding oxidoreductase	23.3	25.9	25.0	41.4	41.7	37.7	1.63	2.0E-03
BF0371	hypothetical protein	20.5	26.6	19.5	43.4	35.9	42.6	1.84	1.5E-02
BF0372	putative transmembrane permease	10.3	10.4	9.3	33.2	34.0	30.9	3.27	2.2E-04
BF0373	hypothetical protein	14.7	15.5	12.3	37.0	37.7	35.3	2.60	1.2E-03
BF0376	putative PQQ-binding exported phosphoesterase	3.3	4.0	3.6	20.7	16.9	16.7	4.93	5.5E-04
BF0377	possible exported xanthan lyase/N-acetylmuramoyl-L-alanine amidase	5.5	3.4	4.6	28.8	28.5	28.1	6.45	1.1E-03
BF0378	putative cation symporter	4.4	5.3	4.4	23.4	23.8	19.4	4.75	5.9E-04
BF0379	hypothetical protein	16.7	21.0	18.4	43.6	52.0	42.5	2.46	2.7E-03
BF0380	conserved hypothetical lipoprotein	4.1	3.6	4.3	29.2	30.2	25.9	7.08	1.6E-04
BF0381	hypothetical protein	15.8	15.6	17.4	39.4	45.9	42.7	2.62	5.8E-04
BF0382	hypothetical protein	71.9	65.2	68.2	89.0	99.6	99.3	1.40	6.2E-03
asd	putative aspartate-semialdehyde dehydrogenase	434.2	386.3	444.9	794.3	722.4	729.5	1.78	2.1E-03
BF0385	putative Na+/H+ antiporter	195.4	223.1	219.1	186.8	194.7	202.9	0.92	2.0E-01
BF0386	putative ThiF family protein	111.7	88.7	103.8	95.5	112.9	115.2	1.07	5.9E-01
BF0387	putative ABC transporter ATP-binding protein	87.0	85.6	78.5	82.7	75.9	91.5	0.99	9.5E-01
BF0388	hypothetical protein	38.5	35.8	36.4	24.8	31.4	34.5	0.81	1.6E-01
BF0389	putative sodium-dependent transporter	238.9	260.4	239.6	204.3	208.2	208.1	0.84	1.1E-02
BF0390	putative transmembrane protein	546.4	633.7	571.0	443.8	473.6	516.0	0.82	5.6E-02
murF	putative UDP-N-acetylmuramoyl-tripeptide--D-alanyl-d-alanine ligase	126.7	131.5	123.6	109.7	106.8	118.1	0.88	3.7E-02
BF0392	putative transporter/antibiotic resistance protein	12.4	17.9	12.3	3.2	2.5	3.4	0.22	2.9E-03
gadB	putative glutamate decarboxylase	470.7	524.6	482.5	97.1	86.8	86.0	0.18	1.0E-04
glsA	putative glutaminase	489.2	552.8	513.3	139.0	124.4	161.9	0.27	7.7E-04
BF0395	putative two-component system sensor histidine kinase	48.6	48.5	43.3	15.8	20.4	19.6	0.40	2.1E-03
folP	putative dihydropteroate synthase	162.9	181.1	160.7	189.2	168.5	182.4	1.07	3.2E-01
BF0397	putative transmembrane protein	60.7	66.5	72.1	100.8	96.9	88.5	1.44	1.2E-02
BF0400	hypothetical protein	0.0	2.2	1.5	2.6	1.6	1.3	0.97	9.3E-01
BF0401	putative transmembrane protein	30.3	28.9	37.9	39.8	48.3	33.4	1.24	2.4E-01
BF0402	hypothetical protein	17.8	20.6	18.7	33.0	33.2	39.3	1.84	4.1E-03
BF0403	hypothetical protein	11.5	12.3	15.3	18.5	20.7	18.1	1.47	3.2E-02
BF0404	hypothetical protein	14.5	19.7	15.3	69.5	67.3	45.6	3.66	5.0E-03
BF0405	hypothetical protein	6.9	8.2	9.9	16.5	19.5	12.6	1.93	3.3E-02
BF0406	hypothetical protein	15.8	13.5	15.2	16.3	17.7	13.8	1.07	5.4E-01
BF0409	hypothetical protein	12.0	9.1	11.9	10.3	8.6	11.5	0.92	6.1E-01
BF0411	hypothetical protein	7.1	8.5	8.7	10.7	8.2	10.3	1.20	2.2E-01
BF0412	hypothetical protein	7.7	5.6	8.4	6.2	7.2	6.9	0.94	7.4E-01
BF0413	hypothetical protein	15.6	7.0	8.6	9.7	10.4	8.6	0.97	9.4E-01
BF0414	hypothetical protein	19.7	17.3	20.4	12.4	12.7	11.1	0.63	6.5E-03
BF0415	possible acetyltransferase	728.0	844.2	866.4	389.9	392.0	486.1	0.52	6.3E-03
BF0416	hypothetical protein	677.6	725.2	678.2	292.0	305.8	278.8	0.42	2.3E-04

BF0417	putative LrgB family transmembrane protein	99.4	115.1	104.1	85.1	79.3	79.0	0.76	1.4E-02
BF0418	putative transmembrane holin-like protein LrgA	118.7	121.8	117.5	79.4	71.7	86.4	0.66	5.7E-03
BF0420	hypothetical protein	132.6	116.6	117.0	116.6	100.1	128.7	0.94	5.7E-01
BF0421	hypothetical protein	36.5	29.9	29.0	36.9	30.7	43.7	1.16	3.7E-01
BF0422	hypothetical protein	11.8	11.0	10.9	8.7	8.7	8.7	0.78	2.7E-03
ptaA	putative phosphate acetyltransferase	134.1	139.5	146.7	193.8	181.1	180.2	1.32	4.9E-03
ackA	putative acetate kinase	142.0	168.7	189.4	216.3	236.2	229.5	1.37	4.2E-02
BF0425	putative alkaline phosphatase	137.9	121.4	133.1	189.1	189.7	183.2	1.43	3.4E-03
BF0426	hypothetical protein	744.1	722.3	726.9	600.3	652.4	600.0	0.84	1.2E-02
BF0427	putative UDP-2,3-diacylglucosamine hydrolase	525.7	489.7	521.2	446.2	504.4	500.1	0.94	3.4E-01
radC1	putative DNA repair protein	72.3	75.0	86.9	56.5	67.2	70.1	0.83	1.4E-01
BF0429	putative glycosyltransferase	65.5	59.6	58.3	62.6	62.3	53.8	0.97	7.3E-01
efp	elongation factor P	1202.8	1244.3	1214.1	1580.0	1567.7	1568.3	1.29	2.4E-04
BF0432	50S ribosomal protein L34	1715.5	1890.8	1844.7	2131.8	1828.5	1891.3	1.07	3.4E-01
BF0433	putative transmembrane PASTA-domain protein	254.5	235.0	201.9	203.4	189.3	208.0	0.87	1.9E-01
rluD	ribosomal large subunit pseudouridine synthase	149.0	147.5	149.6	168.3	143.6	184.9	1.11	3.0E-01
ddl	D-alanylalanine synthetase	107.5	100.7	106.0	99.1	90.1	117.0	0.97	7.6E-01
BF0436	hypothetical protein	130.4	104.7	108.2	129.0	145.1	162.6	1.27	1.0E-01
BF0437	hypothetical protein	77.3	78.7	69.8	76.2	88.1	128.9	1.27	2.8E-01
BF0438	conserved hypothetical rhodanese-domain protein	103.8	83.9	96.7	129.7	131.0	145.3	1.43	1.8E-02
BF0439	putative ornithine carbamoyltransferase	295.7	304.2	285.1	309.7	312.1	303.4	1.05	1.4E-01
BF0440	hypothetical protein	116.2	111.0	99.4	97.5	83.8	107.7	0.88	2.9E-01
BF0441	hypothetical protein	42.8	47.2	35.5	36.8	38.5	38.4	0.91	4.1E-01
proA	gamma-glutamyl phosphate reductase	138.4	117.2	120.2	137.2	120.5	136.9	1.05	5.7E-01
proB	gamma-glutamyl kinase	350.0	319.6	308.0	284.1	272.0	285.3	0.86	4.1E-02
BF0445	hypothetical protein	580.0	559.9	504.2	303.4	304.3	323.6	0.57	1.5E-03
murI	putative glutamate racemase	102.4	100.0	107.2	99.8	86.5	82.9	0.87	1.2E-01
BF0447	putative outer membrane protein	3912.7	4212.7	4162.3	3649.4	3557.8	2991.6	0.83	7.7E-02
ompH	putative cationic 19 kDa outer membrane protein precursor	466.1	539.4	456.8	430.7	456.1	365.1	0.85	1.9E-01
BF0449	putative outer membrane protein	736.8	774.2	749.2	488.9	516.7	470.3	0.65	1.1E-03
uppS	putative undecaprenyl pyrophosphate synthetase	605.2	590.4	568.9	398.2	389.1	394.1	0.67	3.6E-04
BF0451	hypothetical protein	1210.0	1180.1	1228.3	670.2	693.7	611.6	0.55	7.7E-04
BF0452	putative riboflavin biosynthesis protein [includes: diaminohydroxyphosphoribosylaminopyrimidine deaminase	45.0	47.3	55.5	52.3	52.1	53.3	1.07	4.1E-01
BF0453	putative protoporphyrinogen oxidase	71.9	59.4	56.4	45.8	34.2	42.1	0.65	3.7E-02
BF0454	putative transcriptional regulatory protein	82.0	63.0	72.3	67.3	67.2	59.3	0.90	3.4E-01
pyrE	orotate phosphoribosyltransferase	1005.1	1087.1	1063.9	1022.8	1034.9	1021.2	0.98	4.4E-01
BF0456	putative conserved hypothetical protein	306.5	295.9	330.9	286.1	290.3	272.2	0.91	1.1E-01
argH	argininosuccinate lyase	363.0	389.8	403.9	323.2	321.9	306.7	0.82	1.4E-02

BFt04	tRNA-Gly-GCC	0.0	0.0	0.0	0.0	0.0	0.0		
BFt05	tRNA-Leu-TAA	0.0	0.0	0.0	0.0	0.0	0.0		
BF0458	putative bacteriophage resolvase/recombinase	27.2	29.2	32.2	23.2	22.2	39.8	0.93	7.7E-01
BF0462	putative regulatory protein	19.4	10.3	14.7	34.5	33.7	27.9	2.23	3.0E-02
BF0463	hypothetical protein	0.6	0.0	1.3	1.1	0.0	0.6	0.91	9.0E-01
BF0465	putative integrase/recombinase	4.2	5.4	4.0	1.4	1.4	1.4	0.32	1.6E-03
BF0466	putative TonB-dependent receptor	85.9	55.6	82.8	64.4	83.2	79.9	1.03	9.0E-01
BF0467	putative phage-derived protein	38.4	41.0	44.1	72.9	98.7	76.2	1.99	7.8E-03
BF0468	hypothetical protein	149.8	153.5	173.5	224.0	285.2	206.5	1.49	3.9E-02
BF0469	putative transmembrane protein	2.8	0.7	0.0	0.0	0.0	0.0		
BF0470	hypothetical protein	46.2	45.0	50.5	72.7	79.2	55.2	1.45	5.6E-02
BF0471	hypothetical protein	14.0	14.0	15.8	18.6	17.5	15.1	1.17	1.5E-01
BF0472	hypothetical protein	13.8	6.8	13.2	24.4	30.9	16.8	2.17	8.8E-02
BF0473	hypothetical protein	36.0	39.7	42.8	40.2	52.4	27.9	0.99	9.6E-01
BF0474	hypothetical protein	7.8	6.9	7.7	16.3	16.8	18.2	2.28	7.3E-04
BF0475	hypothetical protein	517.9	628.4	583.9	374.4	338.4	389.9	0.64	8.9E-03
BF0476	putative Acyl-CoA synthetase	124.1	130.9	111.6	200.9	190.2	182.9	1.57	4.4E-03
BF0477	putative regulatory protein	107.5	105.8	114.5	191.0	177.4	134.2	1.52	3.7E-02
BF0478	putative pyrroline-5-carboxylate reductase	229.8	231.1	239.5	245.2	233.1	208.6	0.98	7.4E-01
argD	putative acetylornithine aminotransferase	385.4	454.6	422.1	405.4	391.1	347.7	0.91	2.8E-01
argC	putative acetylglutamyl phosphate reductase	298.1	299.4	283.3	316.5	309.5	232.3	0.97	7.9E-01
argG	putative argininosuccinate synthase	307.4	284.5	298.9	340.9	315.6	254.5	1.02	9.0E-01
BF0482	putative acetyltransferase	178.0	151.1	165.8	177.6	180.3	149.4	1.02	8.1E-01
argR	putative arginine repressor	173.1	151.7	160.3	203.2	191.8	158.9	1.14	2.6E-01
BFt06	tRNA-Pro-CGG	79.8	105.4	18.6	48.1	11.2	190.1	0.87	9.2E-01
BFt07	tRNA-Phe-GAA	44.7	68.1	37.3	34.4	22.4	144.9	0.99	9.9E-01
BF0486	putative two-component histidine sensor kinase	115.6	115.4	126.9	61.3	64.1	70.0	0.55	1.5E-03
BF0487	putative glutamate:gamma-aminobutyrate antiporter	230.9	288.9	246.8	62.5	55.7	59.6	0.23	4.2E-04
BF0488	putative ion transport protein	44.2	47.0	58.7	11.8	10.8	11.2	0.23	6.4E-04
BF0489	putative malate dehydrogenase	219.9	259.2	243.0	128.2	108.3	107.8	0.48	2.6E-03
BF0491	hypothetical protein	270.6	259.5	253.8	223.8	230.3	236.1	0.88	1.6E-02
BF0492	hypothetical protein	104.4	107.0	99.8	340.4	352.4	316.8	3.24	1.2E-04
BF0493	hypothetical protein	142.4	148.4	144.1	387.7	419.6	317.8	2.57	1.8E-03
BF0494	hypothetical protein	116.4	137.9	129.1	399.3	380.7	398.7	3.08	3.3E-04
BF0495	putative bioynthetic peptidoglycan transglycosylase	12.4	16.3	14.7	20.0	18.8	23.8	1.45	4.7E-02
BF0496	putative mismatch repair-like protein	76.3	77.3	77.0	68.7	76.3	74.7	0.95	2.6E-01
BF0497	hypothetical protein	56.9	55.9	49.2	71.2	87.8	63.1	1.36	7.5E-02
BF0498	putative melibiase	2.8	4.8	3.1	7.8	9.6	7.5	2.36	1.9E-02
BF0499	putative glycosyl hydrolase, alpha-xylosidase	1.0	1.1	0.8	4.4	4.4	3.2	4.13	2.9E-03
BF0500	putative outer membrane protein	1.2	1.8	1.4	6.2	6.0	6.5	4.35	1.1E-03
BF0501	putative outer membrane protein	1.5	2.0	2.2	6.5	4.6	5.7	2.98	6.7E-03
BF0502	putative anti-sigma factor	4.2	4.2	3.8	8.8	6.6	7.1	1.84	8.8E-03

BF0503	putative ECF-type RNA polymerase sigma factor	15.1	13.4	19.7	15.2	16.8	19.3	1.07	6.9E-01
BF0504	hypothetical protein	0.0	2.3	2.4	1.0	1.3	1.0	0.47	5.3E-03
BF0505	hypothetical protein	7.1	0.0	7.8	4.5	2.7	0.0	0.47	1.4E-01
BF0506	putative outer membrane transport/efflux protein	200.3	202.1	170.2	205.7	194.8	182.9	1.02	8.1E-01
BF0507	putative transport/efflux component protein	131.9	147.8	135.2	178.8	176.8	151.4	1.22	6.1E-02
BF0509	putative ATP-binding component of ABC transporter	88.7	86.4	69.6	89.2	75.9	91.2	1.05	7.0E-01
BF0510	putative ABC transporter	187.4	205.1	169.9	142.7	133.4	124.0	0.71	1.8E-02
BF0511	putative ABC transporter ATP-binding protein	275.1	288.2	259.6	151.4	157.8	152.3	0.56	5.7E-04
BF0512	putative ROK family transcriptional repressor	1619.7	1564.5	1600.0	1647.3	1574.8	1823.9	1.05	3.8E-01
BF0513	50S ribosomal protein L19	3955.7	4105.8	3754.9	3237.0	2724.4	3037.4	0.76	1.9E-02
BF0514	putative 5'nucleotidase/UDP-sugar hydrolase	112.0	96.1	89.4	116.2	106.7	122.9	1.17	1.7E-01
BF0515	possible secreted 5'-nucleotidase	116.0	108.6	120.0	125.3	127.5	137.9	1.13	6.6E-02
BF0516	possible beta-N-acetylglucosaminidase/beta-lactamase fusion protein	68.8	70.6	63.0	79.3	72.7	86.3	1.18	8.9E-02
BF0517	putative hydrolase/beta lactamase fusion protein	55.7	60.0	51.2	73.2	75.3	76.6	1.35	9.4E-03
BF0518	putative outer membrane protein	22.8	28.5	26.4	160.1	163.5	142.1	6.01	2.9E-04
BF0519	hypothetical protein	18.6	21.4	17.2	186.2	181.7	170.2	9.44	1.1E-04
BF0520	putative arylsulfatase	15.1	14.4	14.8	84.6	92.1	91.0	6.05	1.4E-05
BF0521	hypothetical protein	1007.2	1110.9	1103.2	286.7	262.9	305.1	0.27	2.3E-04
BF0522	hypothetical protein	1412.7	1560.5	1509.0	311.0	293.0	307.0	0.20	3.3E-05
BF0523	hypothetical protein	31.1	34.7	31.5	89.0	95.9	81.9	2.74	5.6E-04
BF0524	putative MarR family transcriptional regulator	114.6	143.3	109.6	97.2	98.9	99.3	0.81	1.0E-01
BF0525	putative pyridine nucleotide oxidoreductase	113.8	132.2	106.9	97.5	88.8	91.4	0.79	4.8E-02
BF0526	putative aspartate kinase	0.7	1.5	0.3	0.1	0.4	0.2	0.34	2.1E-01
BF0527	putative two-component response regulator-like protein	145.3	138.1	133.0	155.7	141.2	154.2	1.08	1.7E-01
kdpA	potassium-transporting ATPase subunit A	2.3	1.8	2.5	0.5	1.0	0.7	0.32	1.6E-02
kdpB	putative potassium-transporting ATPase B chain	2.0	1.8	1.7	0.7	0.6	1.6	0.46	1.1E-01
kdpC	potassium-transporting ATPase c chain	0.6	0.7	1.3	0.3	0.4	0.6	0.48	1.4E-01
frrB	hypothetical protein	2.8	2.5	1.6	2.0	1.4	1.4	0.70	2.4E-01
kdpD	putative osmosensitive potassium transport sensor protein	0.8	1.7	1.7	0.9	0.9	0.8	0.65	2.3E-01
frrD	putative two-component sensor histidine kinase	32.1	32.2	34.0	37.2	39.2	33.6	1.12	1.3E-01
rpoE	putative RNA polymerase ECF sigma factor	73.8	65.2	85.1	90.4	114.1	98.4	1.35	7.1E-02
frrF	putative anti-sigma factor	59.9	62.6	65.0	79.7	81.0	73.2	1.25	1.3E-02
frrG	putative outer membrane protein	22.7	20.1	23.6	32.1	30.5	34.0	1.46	8.9E-03

frrH	putative outer membrane protein	5.3	5.3	4.6	14.3	14.1	14.3	2.82	3.8E-04
frrI	hypothetical protein	6.6	8.9	10.4	19.3	20.2	21.4	2.38	8.8E-03
BF0539	hypothetical protein	17.7	16.3	15.0	12.2	13.4	12.9	0.79	2.7E-02
BF0540	hypothetical protein	79.4	75.7	86.1	131.4	142.4	122.9	1.64	3.7E-03
BF0541	conserved hypthetical protein	25.5	18.3	29.9	26.2	34.5	22.9	1.14	5.9E-01
BFt08	tRNA-Met-CAT	9.2	2.4	10.1	6.5	8.0	8.8	1.26	7.0E-01
BF0542	hypothetical protein	822.1	775.0	808.3	719.9	775.5	635.6	0.88	1.6E-01
BF0543	putative permease	293.0	297.8	315.9	229.1	253.3	220.7	0.77	1.4E-02
ribA	putative riboflavin biosynthesis protein [includes: GTP cyclohydrolase ii; 3,4-dihydroxy-2-butanone 4-phosphate synthase (dhbp synthase)]	314.7	325.6	328.2	351.3	347.9	344.3	1.08	1.5E-02
aspC1	putative aspartate aminotransferase	737.6	670.7	683.1	951.0	903.0	902.0	1.32	4.6E-03
BF0546	putative exported rhamnosidase A	11.7	9.8	9.9	8.3	8.5	9.7	0.84	1.2E-01
BF0547	hypothetical protein	2828.3	3250.2	3349.5	4063.2	4902.9	4068.9	1.38	3.3E-02
metA	homoserine O-succinyltransferase	142.2	127.8	132.7	155.0	167.8	151.8	1.18	3.8E-02
BF0549	putative protease	138.9	130.1	115.2	130.0	118.7	153.2	1.04	7.2E-01
BF0550	putative transmembrane protein	213.7	212.9	183.1	173.1	157.8	183.9	0.84	1.1E-01
BF0551	putative TonB dependent receptor	3040.6	3117.2	2663.8	2729.9	2227.9	2790.2	0.88	2.6E-01
BF0552	putative LuxR family transcriptional regulator	36.8	40.4	36.3	39.6	28.3	35.5	0.90	4.6E-01
BF0553	hypothetical protein	59.7	66.1	49.6	62.9	47.2	74.3	1.04	8.5E-01
BF0554	hypothetical protein	72.1	74.2	71.0	71.5	65.4	63.7	0.92	1.4E-01
radA	putative DNA repair protein	103.8	115.1	80.4	128.0	91.1	163.8	1.26	3.9E-01
BF0556	putative L-asparaginase I	8.6	9.0	7.6	9.6	10.0	11.5	1.24	7.9E-02
thrA	putative aspartokinase I-homoserine dehydrogenase	514.9	520.5	430.7	519.3	438.4	569.6	1.04	7.6E-01
BF0559	cofactor-independent phosphoglycerate mutase	525.9	539.7	381.4	434.1	294.6	556.0	0.87	6.2E-01
thrC	threonine synthase	1176.1	1211.2	993.3	871.1	689.3	1023.7	0.76	1.5E-01
BF0561	hypothetical protein	947.7	927.0	789.1	638.3	592.7	675.5	0.72	2.0E-02
BF0562	putative transmembrane protein	181.6	194.0	178.0	86.2	85.5	93.1	0.48	4.2E-04
BF0563	hypothetical protein	131.8	134.5	108.0	92.7	89.0	118.8	0.80	1.7E-01
BF0564	putative nicotinamide mononucleotide transporter	37.6	39.0	34.2	15.2	11.1	16.0	0.38	4.7E-03
BF0565	putative TonB-dependent transmembrane receptor protein	15.1	13.7	12.5	5.7	5.0	8.5	0.45	2.1E-02
TPP	RF00059	7.4	5.9	0.0	0.0	2.1	14.1	0.83	9.0E-01
BF0566	putative transmembrane protein	177.4	154.1	162.6	133.3	136.6	161.2	0.87	1.8E-01
BF0567	hypothetical protein	2318.1	2626.1	2079.0	740.7	790.8	675.0	0.31	9.7E-04
BF0568	putative RNA polymerase ECF-type sigma factor	112.8	110.8	115.0	83.1	96.6	93.3	0.80	2.2E-02
BF0569	putative anti-sigma factor	90.3	80.8	87.7	68.1	66.3	78.3	0.82	5.7E-02
BF0570	hypothetical protein	6.6	7.2	7.0	4.4	4.2	5.4	0.67	1.8E-02
BF0571	putative TonB-linked outer membrane receptor protein	3.7	4.1	4.4	5.4	5.7	5.3	1.34	1.7E-02
BF0572	putative outer membrane protein	3.4	4.1	3.7	7.0	7.3	6.2	1.84	4.6E-03
BF0573	putative beta-galactosidase	3.5	3.6	3.6	5.0	6.6	5.8	1.62	9.6E-03
BF0574	putative glycosyl hydrolase	4.9	3.8	4.0	5.9	5.6	7.9	1.53	5.6E-02
BF0575	putative glycosyl hydrolase/xylanase	8.1	7.8	6.5	11.2	10.6	12.6	1.53	1.8E-02
BF0576	hypothetical protein	44.9	37.1	39.5	47.2	42.7	66.9	1.27	2.4E-01

BF0577	conserved hypothetical lipoprotein	2.6	2.9	3.3	5.9	5.8	5.7	1.98	3.2E-03
BF0578	putative TonB-dependent outer membrane receptor protein	3.3	3.3	1.7	2.7	1.3	3.4	0.87	7.8E-01
BF0581	putative AraC family transcriptional regulatory protein	145.0	152.4	151.8	248.3	261.2	230.3	1.65	1.4E-03
BFt09	tRNA-Lys-TTT	14.5	28.3	27.9	22.9	26.6	40.6	1.29	4.8E-01
BF0582	putative transmembrane protein	67.5	64.4	63.4	69.5	70.2	61.3	1.03	6.5E-01
tdk	putative thymidine kinase	113.2	109.5	105.6	91.7	90.6	90.0	0.83	3.6E-03
BF0584	hypothetical protein	377.4	407.0	334.0	260.6	219.5	409.6	0.77	3.2E-01
BF0585	putative tetrapyrrole (corrin/porphyrin) methylase	1035.5	1089.1	900.7	414.0	398.3	412.5	0.41	7.6E-04
BF0586	hypothetical protein	1709.2	1768.6	1769.3	1270.5	1244.1	1074.7	0.68	6.7E-03
BF0587	putative haloacid dehalogenase-like hydrolase protein	138.5	141.4	129.3	41.3	50.1	50.8	0.35	8.9E-04
BF0588	putative amino acid transporter	80.7	82.4	91.6	61.2	76.3	63.2	0.79	6.6E-02
BF0589	hypothetical protein	819.0	849.1	856.6	499.1	495.7	400.8	0.55	4.6E-03
BF0590	putative surface membrane protein	769.6	863.1	828.1	610.6	588.1	497.9	0.69	1.5E-02
BF0591	putative outer membrane receptor protein	122.3	128.0	140.5	92.8	93.4	71.9	0.66	2.5E-02
BF0592	putative surface membrane protein	109.6	119.2	126.6	98.3	100.0	82.7	0.79	5.7E-02
BF0593	putative integrase/transposase	15.8	13.3	16.3	9.3	8.8	8.5	0.59	5.3E-03
BF0594	hypothetical protein	1661.4	1832.4	1848.3	937.4	980.0	799.4	0.51	2.9E-03
BF0595	hypothetical protein	2155.8	2343.2	2355.7	1023.0	1023.9	829.5	0.42	1.7E-03
BF0596	putative surface membrane protein	808.4	864.8	830.9	394.0	396.8	361.1	0.46	3.3E-04
BF0597	hypothetical protein	869.0	891.2	854.9	406.6	404.8	358.8	0.45	4.7E-04
BF0598	putative GTP-binding protein	366.7	344.8	299.2	323.0	283.3	373.4	0.97	8.0E-01
BF0599	hypothetical protein	397.7	383.8	363.5	240.8	244.7	261.6	0.65	1.7E-03
BF0600	putative aminopeptidase	171.4	186.0	163.6	122.0	106.5	141.1	0.71	3.5E-02
fumB	putative fumarate hydratase class I, anaerobic	460.4	492.1	452.0	497.8	452.2	501.3	1.03	5.6E-01
BF0602	putative transmembrane acyl-transferase protein	57.4	58.0	52.1	59.0	60.4	59.1	1.07	2.0E-01
BF0603	putative alpha-N-acetylglucosaminidase	51.9	48.5	44.0	64.2	54.6	69.3	1.30	6.3E-02
BF0604	putative amino acid transporter	79.8	87.5	76.5	83.1	71.6	83.2	0.98	7.6E-01
BF0606	putative outer membrane protein	22.9	20.0	18.3	57.1	50.4	52.6	2.63	1.3E-03
BF0607	putative AcrB/AcrD/AcrF family efflux transporter	16.9	17.5	15.8	54.1	53.0	45.7	3.04	5.2E-04
BF0608	putative HlyD-family efflux transporter component	35.5	35.2	34.6	86.6	91.3	101.4	2.65	3.7E-04
BF0609	putative HlyD-family transporter	21.5	22.6	25.9	136.7	143.8	120.6	5.74	2.9E-04
BF0610	putative ATP-binding transporter component	30.5	28.9	36.3	217.1	231.2	175.6	6.50	5.8E-04
BF0611	putative transmembrane amino-terminal protease	52.2	63.6	62.6	327.3	354.1	264.7	5.28	7.6E-04
BF0612	hypothetical protein	403.4	420.2	410.4	3641.2	3735.7	3045.5	8.41	1.1E-04
BF0614	possible glycosyl transferase	72.3	87.4	101.3	350.6	401.1	296.1	4.02	2.2E-03
BF0615	hypothetical protein	99.8	111.7	110.3	570.9	706.7	521.5	5.55	5.5E-04
BF0616	hypothetical protein	2.4	2.6	0.0	1.5	0.0	1.5	0.62	1.1E-02
BF0618	ribosome-associated GTPase	202.7	198.4	178.3	264.6	259.5	245.5	1.33	9.5E-03
frr	ribosome releasing factor	580.9	540.0	539.6	1202.6	1029.5	1163.8	2.04	1.1E-03

BF0620	hypothetical protein	1.7	2.0	3.1	5.8	5.4	4.8	2.46	2.3E-02
BF0621	putative ErfK/YbiS/YcfS/YnhG family protein	1.6	1.0	1.1	4.8	7.4	1.2	2.95	1.8E-01
BF0622	hypothetical protein	2.5	2.3	1.8	6.2	4.5	5.6	2.45	8.5E-03
dnaK1	putative chaperone protein	2.0	1.8	3.7	15.9	15.7	13.8	6.43	4.6E-03
BF0624	possible Hsp-70 cofactor	2.9	2.0	3.2	10.4	8.9	8.0	3.42	5.8E-03
BF0625	hypothetical protein	74.0	64.7	81.7	51.6	60.9	49.3	0.73	5.3E-02
BF0626	putative uridylate kinase	300.5	279.8	282.3	402.9	376.1	435.7	1.41	6.7E-03
dinF	putative DNA-damage-inducible protein F	63.1	63.4	61.5	43.9	44.0	42.3	0.69	2.9E-04
BF0629	putative endo-beta-galactosidase	30.4	25.0	39.5	25.0	27.9	27.7	0.86	4.1E-01
BF0630	hypothetical protein	218.0	201.8	198.2	117.8	133.5	135.6	0.63	3.7E-03
BF0631	hypothetical protein	163.0	166.4	170.0	115.8	115.3	88.6	0.64	1.7E-02
BF0632	putative biotin/lipoate A/B protein ligase family protein	13.1	15.4	16.4	33.0	27.8	26.6	1.95	6.7E-03
BF0633	hypothetical protein	24.7	15.8	29.9	35.6	32.0	35.1	1.51	1.5E-01
BF0634	hypothetical protein	26.5	20.0	30.8	12.3	10.6	15.3	0.50	2.8E-02
BF0636	hypothetical protein	58.8	59.4	51.5	87.9	59.4	99.8	1.43	1.4E-01
BF0637	possible cytosine deaminase	139.4	120.8	124.2	142.4	120.3	146.9	1.06	5.3E-01
BF0638	hypothetical protein	501.2	473.8	407.5	164.3	176.6	151.6	0.36	1.1E-03
BF0639	putative phosphatidylserine synthase	220.9	230.7	235.0	242.0	235.6	217.6	1.01	8.1E-01
BF0640	phosphatidylserine decarboxylase	370.9	361.2	392.3	381.0	364.9	327.7	0.95	4.8E-01
dnaE	putative DNA polymerase III alpha subunit	234.2	221.4	226.6	183.1	189.3	188.9	0.82	2.7E-03
trxA	putative thioredoxin	732.1	642.3	729.7	1262.0	1310.7	1061.9	1.72	6.9E-03
BF0643	hypothetical protein	1603.3	1507.6	1560.8	2215.9	2185.8	1966.8	1.36	5.9E-03
BF0644	putative transmembrane protein	70.6	66.2	58.1	55.7	55.8	54.3	0.85	8.5E-02
BF0647	putative transmembrane protein	147.7	139.0	124.1	99.0	89.7	110.4	0.73	3.1E-02
BF0648	putative transmembrane protein	244.7	260.1	265.3	316.7	350.6	330.0	1.29	7.6E-03
BF0649	hypothetical protein	155.2	154.9	144.5	222.7	235.4	215.7	1.48	1.8E-03
BF0650	hypothetical protein	93.5	98.2	91.9	123.3	131.0	128.2	1.35	1.9E-03
BF0651	putative methanol denhydrogenase-related protein	176.6	177.9	162.6	220.4	212.9	196.7	1.22	2.4E-02
BF0652	putative transmembrane protein	148.3	154.8	150.3	151.9	164.4	164.1	1.06	1.7E-01
BF0653	putative transmembrane protein	165.3	155.6	173.3	161.2	162.9	161.7	0.98	6.9E-01
BF0654	putative ATP/GTP-binding transmembrane protein	260.1	215.4	219.3	329.3	317.6	339.8	1.42	1.3E-02
BF0655	putative ABC transporter membrane protein	68.2	82.5	63.6	72.9	65.3	78.0	1.01	9.2E-01
BF0656	hypothetical protein	100.1	95.4	88.2	73.5	56.0	82.4	0.74	1.0E-01
BF0657	putative aminopeptidase	122.7	116.5	105.3	170.9	164.3	179.1	1.49	5.2E-03
BF0658	hypothetical protein	165.0	160.8	153.4	187.9	163.9	201.2	1.15	1.4E-01
BF0659	putative alpha-1,2-mannosidase precursor	7.6	6.3	5.0	5.0	4.3	5.4	0.78	2.1E-01
BF0660	putative transmembrane protein	130.7	136.3	115.7	110.4	107.0	128.1	0.90	3.0E-01
BF0661	putative outer membrane protein	4.9	5.5	4.8	8.6	8.5	8.7	1.70	1.5E-03
BF0662	hypothetical protein	3.6	3.1	2.7	6.1	6.1	6.8	2.04	5.6E-03
BF0663	hypothetical protein	1.1	4.9	2.4	7.3	4.4	7.4	2.64	1.5E-01
BF0664	hypothetical protein	5.6	5.0	2.9	14.5	10.7	17.0	3.17	2.0E-02
BF0665	putative beta-galactosidase	10.3	8.5	8.1	15.7	16.6	17.2	1.85	4.8E-03

aroA	putative 3-phosphoshikimate 1-carboxyvinyltransferase	113.6	123.3	104.0	139.0	128.2	141.5	1.20	5.9E-02
BF0667	putative AraC-family regulatory protein	406.5	324.6	368.2	561.1	634.3	604.6	1.64	7.8E-03
BF0668	putative histidine kinase	267.8	205.2	236.2	350.9	391.8	407.0	1.63	1.4E-02
BF0669	putative glycosyl hydrolase, beta-N-acetylhexosaminidase	103.5	111.8	114.6	283.2	281.9	266.3	2.52	2.1E-04
BF0670	putative transmembrane acyltransferase protein	75.3	71.0	64.2	36.9	39.0	35.1	0.53	1.7E-03
BFt10	tRNA-Pro-GGG	13.6	7.2	10.0	2.1	2.6	17.4	0.46	4.0E-01
BF0671	hypothetical protein	58.4	60.7	63.8	105.2	87.7	78.7	1.48	2.5E-02
aroB	putative 3-dehydroquinate synthase	128.4	121.2	125.3	176.1	175.2	168.0	1.38	9.0E-04
BF0673	putative transmembrane protein	201.3	196.5	207.3	265.1	267.3	193.5	1.19	2.5E-01
BF0674	hypothetical protein	58.2	57.6	56.6	62.3	66.6	62.8	1.11	2.0E-02
cls	putative cardiolipin synthetase	119.6	116.5	109.0	107.0	115.9	115.3	0.98	6.8E-01
BF0676	putative methyltransferase	117.0	102.6	134.3	139.4	113.6	126.2	1.07	5.7E-01
BF0677	hypothetical protein	191.3	205.9	227.5	275.6	287.5	297.5	1.38	1.1E-02
BF0678	hypothetical protein	1708.8	1693.6	1826.8	2709.0	2782.4	2302.6	1.49	9.7E-03
BF0679	putative ATP-dependent exodeoxyribonuclease	33.7	29.6	34.1	41.4	44.8	39.0	1.29	2.9E-02
BF0680	conserved hypothetical lipoprotein	8.3	9.4	9.9	43.8	39.9	38.8	4.44	2.5E-04
BF0681	putative outer membrane protein	9.1	10.4	8.2	37.5	34.4	30.6	3.70	9.2E-04
BF0682	putative alpha-1,2-mannosidase precursor	17.1	19.6	18.1	41.4	41.1	36.6	2.18	1.0E-03
BF0683	putative alpha-1,2-mannosidase precursor	13.8	14.6	15.2	28.4	26.9	26.4	1.88	5.9E-04
BF0684	putative anti-sigma factor	129.3	119.9	119.4	135.9	120.7	134.5	1.06	3.4E-01
BF0685	putative RNA polymerase ECF-type sigma factor	103.0	98.4	93.5	164.2	127.0	149.8	1.49	1.8E-02
BF0686	putative alpha-1,2-mannosidase precursor	94.3	96.4	88.0	123.0	116.6	112.8	1.26	9.4E-03
BF0687	putative efflux transporter bicyclomycin resistance protein	0.4	0.6	1.0	0.8	1.7	0.9	1.65	2.6E-01
BF0688	putative AraC-family transcriptional regulator	28.3	25.7	28.9	25.2	25.8	23.8	0.90	1.2E-01
alaS	alanyl-tRNA synthetase	280.0	297.4	272.7	344.1	300.8	324.8	1.14	8.0E-02
BF0690	putative transmembrane peptidase	280.2	283.4	266.1	250.9	236.8	237.2	0.87	1.8E-02
BF0691	putative transcriptional regulator protein	422.3	379.5	329.1	266.4	247.3	274.3	0.70	2.3E-02
BF0692	putative RelA/SpoT GTP pyrophosphokinase	295.6	296.9	287.8	371.0	388.3	378.5	1.29	7.4E-04
BF0693	putative lytic murein transglycosylase	95.7	108.9	103.0	145.4	134.0	142.6	1.37	6.7E-03
BF0694	hypothetical protein	125.8	141.6	122.1	110.3	100.6	111.7	0.83	5.1E-02
parB	putative ParB-like chromosome partitioning protein	201.0	203.3	196.7	200.3	174.9	199.1	0.95	4.3E-01
parA	putative ParA chromosome partitioning protein	512.8	492.9	475.6	317.9	325.1	325.5	0.65	4.9E-04
BF0697	hypothetical protein	0.8	1.7	0.9	0.7	0.9	0.0	0.79	5.0E-01
surE	acid phosphatase	171.2	168.1	168.5	237.4	198.4	218.0	1.28	2.0E-02
BF0699	putative lipid-A-disaccharide synthase	289.1	271.4	284.6	263.7	235.5	245.3	0.88	5.2E-02
BF0700	hypothetical protein	26.1	22.2	24.5	22.0	22.5	23.7	0.94	3.5E-01

BF0701	putative phosphatidate cytidylyltransferase	519.5	552.1	560.0	318.1	342.4	325.7	0.60	7.2E-04
BF0702	putative transmembrane AAA-metalloprotease FtsH	535.6	545.9	513.6	399.7	392.6	408.6	0.75	1.2E-03
BF0703	hypothetical protein	564.2	602.7	605.0	428.3	429.6	368.6	0.69	7.8E-03
BFt11	tRNA-Gln-CTG	9.5	7.6	2.6	0.0	5.5	2.3	0.62	5.5E-01
BF0704	hypothetical protein	831.5	872.9	870.3	1176.5	1324.0	1089.2	1.39	1.3E-02
BF0705	putative transmembrane Mg2+ transporter	138.0	146.3	144.0	146.8	142.1	124.5	0.96	5.9E-01
ksgA	dimethyladenosine transferase	257.2	281.4	268.8	267.1	252.7	263.1	0.97	4.5E-01
BF0707	putative transmembrane protein	97.8	100.1	97.4	71.8	79.8	77.5	0.77	5.1E-03
BF0708	putative aminoacyl-histidine dipeptidase	360.4	352.1	370.9	582.0	612.9	553.3	1.61	9.2E-04
BF0709	hypothetical protein	17.3	15.9	17.7	1.6	3.2	1.5	0.12	3.5E-03
BF0710	hypothetical protein	0.8	1.0	0.8	2.9	2.3	1.0	2.22	1.1E-01
BF0711	putative TonB-dependent outer membrane receptor protein	2.8	3.8	3.2	2.1	2.5	2.1	0.68	3.5E-02
BF0712	hypothetical protein	46.4	49.4	37.5	22.6	25.1	24.2	0.54	7.3E-03
BF0713	hypothetical protein	147.3	160.9	143.6	90.5	96.1	86.2	0.60	2.1E-03
BF0714	hypothetical protein	38.2	48.1	56.5	50.0	58.2	51.6	1.13	4.4E-01
BF0715	hypothetical protein	79.7	75.4	81.3	36.0	43.8	32.7	0.47	4.2E-03
BF0716	possible oxidoreductase	25.6	27.2	23.8	15.1	19.2	12.4	0.60	3.6E-02
BF0717	hypothetical protein	348.2	329.6	330.2	221.2	224.4	211.7	0.65	6.0E-04
BF0718	arginine/ornithine transport system ATPase	299.3	300.1	299.8	296.3	276.1	287.6	0.96	1.4E-01
BF0719	putative transmembrane permease	89.5	78.5	82.1	46.7	53.9	45.1	0.58	4.7E-03
BF0722	putative transmembrane transport protein	100.5	113.2	109.6	76.7	90.2	73.9	0.74	2.8E-02
BF0723	putative AraC-family regulatory protein	102.2	104.6	110.2	139.0	145.6	116.4	1.26	5.6E-02
BF0724	possible HipA-like protein	43.8	50.6	51.2	66.4	76.8	64.1	1.42	2.1E-02
BF0726	putative DNA-binding protein	42.5	43.8	43.2	45.2	46.9	32.6	0.95	7.4E-01
BF0727	hypothetical protein	7.4	4.2	5.6	6.0	4.5	4.8	0.91	6.8E-01
BF0728	hypothetical protein	16.9	16.7	13.3	8.7	4.2	6.7	0.40	3.1E-02
BF0729	hypothetical protein	30.6	27.6	26.9	5.8	8.8	8.1	0.26	2.6E-03
BF0730	hypothetical protein	17.2	16.8	17.4	8.2	3.3	11.0	0.39	9.4E-02
upgY	putative transcriptional regulator	9.2	14.0	10.1	2.5	2.3	3.8	0.25	7.4E-03
upgZ	putative transcriptional regulator	10.8	10.4	13.5	6.5	7.1	6.6	0.59	9.8E-03
BF0733	putative capsular polysaccharide biosynthesis protein	10.2	10.2	11.6	4.6	4.2	4.1	0.40	6.0E-04
BF0734	putative DegT/DnrJ/EryC1/StrS aminotransferase family O-antigen related protein	11.5	12.2	12.7	6.9	7.4	4.2	0.49	3.5E-02
BF0735	putative capsular polysaccharide related hexapeptide transferase family protein	12.7	8.6	14.7	5.8	3.7	5.6	0.42	3.1E-02
BF0736	putative sugar-phosphate nucleotidyl transferase	6.9	10.8	14.2	6.5	6.0	5.1	0.57	1.1E-01
BF0737	putative polysaccharide transporter/flippase	5.8	4.9	6.3	1.8	2.8	1.5	0.35	1.5E-02
BF0738	possible glycosyltransferase protein	15.2	18.5	20.9	5.3	5.3	5.5	0.30	1.3E-03

BF0739	possible O-antigen related transmembrane protein	5.3	7.3	5.8	1.8	2.2	2.3	0.35	3.8E-03
BF0740	possible glycosyltransferase	10.0	12.8	9.9	4.8	4.6	3.8	0.40	4.5E-03
BF0741	hypothetical protein	10.0	10.1	7.8	5.1	5.8	4.5	0.55	1.5E-02
BF0742	possible capsular polysaccharide related protein	8.2	6.2	7.3	2.9	3.3	2.0	0.38	1.3E-02
BF0743	putative UDP-ManNAc dehydrogenase	16.3	12.1	11.9	5.0	6.4	7.7	0.47	2.2E-02
BF0744	putative UDP-GlcNAc 2-epimerase	12.5	10.0	13.7	7.9	5.3	5.2	0.50	2.9E-02
BF0746	putative transposase_11 DDE family protein	11.3	11.4	11.5	5.3	6.3	5.2	0.49	1.6E-03
BF0747	hypothetical protein	8.1	7.9	10.5	3.2	2.8	2.6	0.33	2.3E-03
BF0748	putative glycosyltransferase protein	7.0	4.6	6.2	4.0	4.4	3.1	0.64	8.5E-02
BF0749	putative UDP-galactose phosphate transferase	6.1	6.8	8.3	0.8	2.3	1.9	0.22	2.4E-02
BF0750	putative acetyltransferase	6.6	6.1	3.3	4.3	1.7	4.3	0.62	3.4E-01
BF0751	putative FIC family protein	141.9	139.5	145.7	111.8	113.5	97.1	0.75	1.3E-02
BF0752	putative DegT/DnrJ/EryC1/StrS family aminotransferase protein	9.6	10.6	8.4	3.0	2.5	3.7	0.32	3.9E-03
BF0753	hypothetical protein	0.0	4.4	2.3	2.0	0.0	2.0	0.62	3.6E-01
BF0754	putative non-specific DNA binding protein	5.5	2.7	2.8	4.2	3.0	2.1	0.85	6.8E-01
BF0755	hypothetical protein	0.0	2.0	0.0	1.8	0.0	0.0	0.89	
BF0756	hypothetical protein	179.1	173.4	192.2	144.6	167.2	143.3	0.83	6.3E-02
BF0757	putative aldo/keto-reductase	57.2	56.0	64.6	68.8	77.3	63.9	1.18	1.2E-01
BF0758	putative glycosyl hydrolase	5.8	4.1	4.0	2.0	2.3	2.3	0.48	1.2E-02
BF0759	putative outer membrane protein	8.7	11.5	9.7	6.3	6.1	5.2	0.59	1.6E-02
BF0760	putative outer membrane protein	6.9	7.2	5.2	4.7	4.7	4.8	0.74	6.5E-02
BF0761	putative lipoprotein	16.1	15.8	16.5	9.1	12.7	13.2	0.71	7.8E-02
BF0762	hypothetical protein	4.7	3.7	5.4	3.0	3.5	3.0	0.70	7.8E-02
BF0763	putative secreted glucosidase	6.4	6.9	7.1	3.7	4.1	3.8	0.57	9.5E-04
BF0764	putative mannanase	10.4	8.9	11.8	3.4	3.1	3.3	0.32	1.2E-03
BF0766	putative beta-glucosidase	7.7	6.5	6.8	8.2	7.8	8.0	1.14	1.1E-01
BF0767	possible methyltransferase	14.2	12.0	9.0	11.9	12.9	17.1	1.20	4.3E-01
BF0768	putative B12-binding methyltransferase	7.9	5.2	7.8	10.5	10.0	10.4	1.51	6.6E-02
BF0769	hypothetical protein	5.3	4.5	3.3	4.7	7.2	5.5	1.34	2.5E-01
BF0770	putative methylcobamide:CoM methyltransferase	10.0	9.3	9.7	8.0	8.7	7.4	0.83	4.3E-02
manA	putative mannosidase	16.3	21.9	15.9	8.2	10.9	8.4	0.51	1.8E-02
BF0772	hypothetical protein	44.5	45.1	36.4	28.9	29.1	42.6	0.79	2.4E-01
BF0773	putative cation symporter	22.4	23.9	21.3	17.2	18.7	16.3	0.77	1.8E-02
BF0774	hypothetical protein	14.1	15.0	14.2	12.2	11.4	12.9	0.85	2.9E-02
BF0775	putative transmembrane protein	19.6	21.2	16.4	32.2	30.3	36.3	1.73	1.1E-02
BF0776	hypothetical protein	13.8	14.3	15.3	50.4	48.0	57.6	3.59	3.8E-04
BF0777	possible endoribonuclease	24.0	24.2	21.1	84.4	60.5	131.1	3.79	1.2E-02
BF0778	hypothetical protein	13.7	11.3	16.2	11.5	16.4	16.5	1.08	7.2E-01
BF0779	hypothetical protein	1.1	1.2	0.2	1.2	0.0	1.4	2.10	4.0E-01
BF0780	hypothetical protein	0.0	0.0	0.0	0.3	0.3	0.1		
BF0781	putative TonB-dependent receptor protein	0.1	0.1	0.1	0.2	0.0	0.1	1.24	7.8E-01
BF0782	putative two-component system sensor histidine kinase	34.7	31.3	31.5	24.2	24.5	28.5	0.79	3.7E-02

nuoN	putative NADH dehydrogenase chain N	101.8	139.7	131.1	88.2	92.7	83.0	0.71	5.3E-02
nuoM	putative NADH-ubiquinone oxidoreductase subunit	75.6	113.2	89.8	77.3	71.5	70.1	0.80	1.9E-01
nuoL	putative NADH dehydrogenase chain L	85.1	116.2	96.6	75.5	66.8	67.7	0.71	4.6E-02
nuoK	putative NADH dehydrogenase chain K	56.0	79.4	71.6	45.6	43.2	40.7	0.63	2.8E-02
nuoJ	putative NADH dehydrogenase chain J	79.5	97.3	81.1	70.1	53.8	52.1	0.68	5.0E-02
nuoI	putative NADH dehydrogenase I subunit I	87.9	115.0	91.5	61.3	57.0	54.7	0.59	1.2E-02
nuoH	putative NADH dehydrogenase subunit H	102.6	116.8	108.6	78.7	79.1	81.3	0.73	4.6E-03
nuoC	putative NADH-quinone oxidoreductase chain C/D	115.1	108.5	111.4	95.0	84.0	100.5	0.83	5.4E-02
nuoB	NADH-quinone oxidoreductase chain B	58.8	61.9	64.1	77.8	70.9	79.3	1.23	1.9E-02
nuoA	NADH-quinone oxidoreductase chain A	93.5	105.9	96.9	111.5	105.3	92.1	1.04	6.5E-01
BF0793	hypothetical protein	483.6	476.7	485.2	166.4	199.4	261.5	0.43	8.6E-03
BF0794	putative potassium uptake protein	78.3	76.8	77.9	94.7	81.7	100.3	1.18	8.3E-02
BF0795	putative potassium uptake protein	113.8	113.1	105.2	152.6	141.2	148.6	1.33	4.2E-03
dxs	1-deoxy-D-xylulose-5-phosphate synthase	298.7	331.6	276.1	300.7	260.6	327.6	0.98	8.5E-01
BF0799	hypothetical protein	69.5	74.0	58.8	74.3	78.7	76.3	1.14	1.9E-01
BF0800	putative transmembrane protein	162.2	151.7	143.3	158.8	185.0	145.3	1.07	5.4E-01
BF0801	putative phosphoglycolate phosphatase	189.3	177.3	172.7	182.7	164.3	178.7	0.97	6.4E-01
BF0802	putative secreted sulfatase	8.3	7.5	8.1	10.8	9.8	9.6	1.27	2.0E-02
BF0803	possible alpha-galactosidase	2.6	2.7	2.6	3.0	3.6	3.5	1.27	3.7E-02
BF0804	hypothetical protein	3.2	4.3	3.7	3.1	5.0	3.9	1.07	7.5E-01
BF0805	putative sulfatase	7.8	8.5	6.7	5.9	4.5	7.8	0.77	2.8E-01
BF0806	hypothetical protein	0.6	0.5	0.6	0.3	0.4	0.5	0.68	2.1E-01
BF0807	putative outer membrane protein	1.0	1.0	0.9	0.5	0.8	0.5	0.60	4.6E-02
BF0808	putative two-component system sensor histidine kinase/response regulator fusion protein	32.5	30.6	33.3	29.7	34.9	30.1	0.98	8.0E-01
BF0809	putative hexuronate transporter	12.9	17.6	14.3	14.4	15.8	23.6	1.18	4.7E-01
BF0810	putative alpha-L-fucosidase	174.1	182.0	170.4	273.2	295.8	281.1	1.61	7.2E-04
BF0811	hypothetical protein	271.2	255.5	265.9	305.1	331.0	303.3	1.18	1.7E-02
BF0812	hypothetical protein	41.7	45.6	41.4	57.1	51.7	58.5	1.30	1.4E-02
BF0813	putative transmembrane acyltransferase	77.1	78.6	83.6	43.7	58.3	38.9	0.58	2.5E-02
BF0814	putative Sec-independent protein translocase component	15.5	11.8	12.5	30.1	35.2	30.0	2.40	3.7E-03
BF0815	putative Sec-independent protein translocase component	99.1	92.2	89.5	112.2	113.8	111.4	1.20	1.1E-02
BF0816	putative alanine racemase and UDP-N-acetylmuramoylalanyl-D-glutamyl, 6-diaminopimelate-D-alanyl-D-alanyl ligase fusion protein	184.6	189.1	181.7	201.4	187.4	174.9	1.01	8.1E-01
BF0817	hypothetical protein	26.5	30.8	34.3	36.9	29.6	31.7	1.08	5.8E-01
BF0818	hypothetical protein	43.0	41.4	45.3	16.7	14.7	22.1	0.41	6.3E-03
BF0820	putative regulatory protein	165.4	168.7	146.0	80.0	89.3	86.0	0.53	1.8E-03
BF0821	hypothetical protein	94.8	94.3	91.2	71.5	78.6	71.3	0.79	7.0E-03
BF0822	hypothetical protein	28.4	34.5	33.5	34.6	32.9	34.1	1.06	5.0E-01

BF0823	putative transmembrane protein	70.9	63.0	68.8	47.6	50.4	55.1	0.75	1.7E-02
BF0824	hypothetical protein	17.6	16.4	20.7	32.0	33.2	31.1	1.77	4.6E-03
miaA	tRNA delta(2)-isopentenylpyrophosphate transferase	75.6	75.2	82.4	108.4	98.3	96.0	1.30	1.4E-02
BF0826	hypothetical protein	865.4	828.3	843.7	1004.9	983.1	898.3	1.14	4.6E-02
lpxA	UDP-N-acetylglucosamine acyltransferase	496.7	522.3	518.9	578.4	550.1	518.0	1.07	1.8E-01
lpxC	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	441.9	489.3	474.4	546.4	508.5	494.5	1.10	1.3E-01
lpxD	putative UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase	394.3	407.1	391.2	380.3	366.0	372.7	0.94	3.5E-02
BF0830	hypothetical protein	176.9	198.4	190.4	219.4	208.1	182.1	1.08	3.9E-01
BF0831	putative orotidine 5'-phosphate decarboxylase	450.0	503.9	480.2	488.5	484.6	443.4	0.99	8.4E-01
prfA	peptide chain release factor 1	254.9	229.5	219.1	248.7	225.6	245.2	1.02	7.4E-01
BF0833	possible phosphoribosylformylglycinamidine cyclo-ligase	278.2	276.8	263.1	270.0	254.9	267.6	0.97	3.5E-01
BF0834	hypothetical protein	8.3	10.4	12.5	5.0	1.7	4.3	0.33	5.8E-02
BF0835	putative LemA family protein	203.4	170.3	181.6	144.0	139.4	141.4	0.77	1.7E-02
BF0836	hypothetical protein	139.9	133.7	137.3	88.6	84.1	103.3	0.67	9.0E-03
BF0837	hypothetical protein	216.2	209.4	207.4	122.4	123.5	125.1	0.59	6.5E-05
aroE	putative shikimate 5-dehydrogenase	181.4	170.3	175.8	215.1	209.0	180.0	1.14	1.3E-01
ubiE	ubiquinone/menaquinone biosynthesis methyltransferase	144.4	145.2	162.2	218.7	217.9	203.0	1.42	5.3E-03
hemH	phosphoribosylaminoimidazole-succinocarboxamide synthase	346.4	347.0	394.8	657.6	637.1	591.8	1.74	2.3E-03
BF0841	putative phosphate starvation-inducible PhoH-like protein	177.1	176.8	180.9	219.0	214.2	192.6	1.17	3.5E-02
BF0842	hypothetical protein	135.5	100.0	110.1	126.0	116.4	122.5	1.06	6.1E-01
BF0843	hypothetical protein	219.6	207.5	211.2	302.3	301.3	277.7	1.38	2.6E-03
BF0844	putative transmembrane protein	126.5	134.5	132.7	168.9	196.5	131.9	1.25	1.9E-01
BF0845	conserved hypothetical protein, possible ATP/GTP-binding site	92.6	95.4	98.3	147.4	142.9	150.6	1.54	4.8E-04
BF0846	hypothetical protein	96.2	103.4	101.4	185.2	190.5	171.5	1.82	7.3E-04
truA	putative tRNA pseudouridine synthase A	21.9	23.7	27.4	25.3	24.5	27.2	1.06	5.5E-01
BF0848	putative transmembrane protein	16.1	15.8	14.5	16.7	13.8	16.2	1.01	9.5E-01
BF0849	hypothetical protein	198.3	181.1	180.9	160.6	172.7	142.1	0.85	9.7E-02
BF0850	putative desulfatase	97.7	102.1	88.0	378.7	343.1	325.8	3.64	3.7E-04
BF0851	putative beta-galactosidase	44.5	50.0	42.2	156.6	139.6	139.7	3.19	4.9E-04
BF0852	putative transmembrane protein	46.7	54.1	46.0	162.4	158.4	142.3	3.16	5.7E-04
BF0853	putative GFO/IDH/MOCA family oxidoreductase	286.1	309.7	286.2	1141.0	1051.3	914.6	3.51	5.2E-04
BF0854	hypothetical protein	35.4	32.4	25.8	81.9	74.7	104.7	2.79	5.9E-03
BF0855	hypothetical protein	4.0	6.5	5.4	16.7	14.0	14.9	2.92	7.1E-03
BF0856	putative beta-glucuronidase	10.8	9.3	9.3	12.2	12.8	12.9	1.30	1.7E-02
BF0857	putative TPR-domain protein	2.1	2.4	1.6	5.3	4.6	4.8	2.44	6.8E-03
BF0858	putative sugar-proton symporter	1.4	1.4	1.4	4.5	4.4	3.2	2.87	3.1E-03
BF0859	putative AraC transcriptional regulatory protein	64.3	60.3	50.7	32.3	35.8	40.2	0.62	1.7E-02

BF0860	putative beta-glucosidase	7.5	6.8	6.4	60.0	55.7	50.5	8.03	1.1E-04
BF0861	putative cytochrome c binding protein	2.0	2.1	3.1	32.5	29.9	38.8	14.33	6.7E-04
BF0862	putative transmembrane protein	1.6	1.1	1.5	26.8	24.3	21.6	17.29	3.4E-04
BF0863	putative outer membrane protein	8.3	8.6	8.4	387.1	373.0	331.9	43.06	4.6E-06
BF0864	hypothetical protein	6.1	9.2	8.8	405.0	390.8	300.2	45.88	2.6E-04
BF0865	hypothetical protein	6.0	6.0	5.7	19.9	18.3	16.7	3.10	3.4E-04
BF0866	putative outer membrane protein	2.6	2.5	3.5	17.9	18.3	15.4	6.02	8.7E-04
BF0867	possible outer membrane protein	4.8	3.6	6.2	16.1	18.8	13.3	3.36	8.2E-03
BF0868	putative TonB-linked outer membrane protein	4.2	3.5	4.5	12.0	15.0	10.5	3.08	4.0E-03
BF0869	putative RNA polymerase ECF-type sigma factor	212.5	194.9	204.9	186.1	234.8	206.9	1.02	8.2E-01
BF0870	putative anti-sigma factor	77.4	74.0	84.1	155.9	159.4	160.2	2.02	4.9E-04
BF0871	hypothetical protein	22.2	26.2	29.2	196.7	210.9	163.1	7.35	5.3E-04
BF0872	possible outer membrane protein	35.6	34.2	37.0	174.0	195.7	146.3	4.80	5.3E-04
BF0873	hypothetical protein	3.3	2.0	4.0	4.3	5.0	5.1	1.60	1.3E-01
BF0874	putative GFO/IDH/MOCA family oxidoreductase	34.8	26.0	30.6	39.4	33.9	37.4	1.22	1.6E-01
BFt12	tRNA-Gly-TCC	297.2	261.8	301.7	400.5	360.2	730.6	1.65	1.3E-01
BFt13	tRNA-Tyr-GTA	41.7	72.0	71.7	196.7	176.7	355.2	3.86	2.0E-02
ribH	riboflavin synthase subunit beta	149.0	131.2	155.0	216.2	219.1	194.6	1.45	1.1E-02
BF0876	hypothetical protein	736.3	729.1	775.5	991.7	920.5	879.1	1.24	1.4E-02
BF0877	putative DNA replication and repair protein	105.4	65.9	85.2	67.6	75.3	83.5	0.90	5.7E-01
BF0878	hypothetical protein	57.6	54.2	50.7	54.6	54.1	69.2	1.09	4.6E-01
BF0879	putative histidinol-phosphatase	70.2	72.3	68.5	53.4	56.4	50.2	0.76	5.9E-03
BF0880	putative 5-formyltetrahydrofolate cyclo-ligase	106.4	101.3	84.4	97.6	88.7	95.4	0.97	7.5E-01
BF0881	putative carboxy-terminal protease	241.6	228.7	226.2	179.5	175.0	183.2	0.77	2.2E-03
BF0882	putative deoxycytidylate deaminase	305.8	305.1	296.8	193.6	214.6	195.2	0.66	1.6E-03
BF0883	hypothetical protein	355.7	352.9	362.7	249.2	242.7	229.0	0.67	8.2E-04
dcp	putative peptidyl-dipeptidase	290.3	305.8	286.6	186.2	167.4	170.8	0.59	1.1E-03
gap	putative glyceraldehyde 3-phosphate dehydrogenase	5806.7	6112.6	6690.8	10183.9	10646.9	9790.0	1.65	2.3E-03
mscL	putative large-conductance mechanosensitive channel	119.6	107.7	104.4	108.5	102.4	103.3	0.95	3.7E-01
guaA	bifunctional GMP synthase/glutamine amidotransferase protein	599.4	613.6	577.6	667.0	615.7	644.0	1.08	1.0E-01
BF0888	hypothetical protein	35.3	15.6	29.1	25.1	13.6	18.3	0.73	4.3E-01
BF0889	hypothetical protein	6.6	6.0	6.2	15.7	16.1	13.0	2.37	1.6E-03
BF0890	putative outer membrane receptor protein	4.5	4.2	4.5	16.5	14.2	15.1	3.46	1.9E-04
BF0892	hypothetical protein	2.3	3.4	3.0	1.9	1.7	1.3	0.56	3.7E-02
BF0893	putative outer membrane receptor protein	0.7	1.0	1.7	1.4	1.1	1.1	1.10	7.9E-01
BF0894	putative enoyl-[acyl-carrier-protein] reductase [NADH]	831.3	851.6	890.4	781.0	814.1	785.6	0.93	5.6E-02
BF0895	hypothetical protein	729.1	779.8	798.5	828.9	881.6	782.3	1.08	2.1E-01
BF0896	hypothetical protein	99.6	104.1	110.9	121.0	121.7	129.4	1.18	2.4E-02
BF0897	putative transmembrane protein	233.7	233.8	217.9	107.9	108.3	99.5	0.46	3.3E-04
BF0898	lipoyl synthase	52.9	55.2	52.4	82.0	78.2	76.0	1.47	9.7E-04

BF0899	putative dipeptidyl peptidase	157.1	163.9	149.0	248.1	233.5	213.9	1.48	5.5E-03
BF0901	putative transmembrane protein	15.0	12.1	11.2	17.4	16.8	18.6	1.39	4.4E-02
BF0902	putative transmembrane and transcriptional regulatory protein	29.9	31.2	36.2	37.3	34.7	34.9	1.10	2.6E-01
BF0903	hypothetical protein	208.1	209.1	194.5	179.2	182.9	215.2	0.94	4.6E-01
BF0904	putative flavoprotein	555.8	523.5	562.2	747.3	695.6	667.4	1.28	9.3E-03
nagB	glucosamine-6-phosphate deaminase	1148.4	1163.8	1175.1	2147.5	2252.7	1987.6	1.83	6.7E-04
BF0906	hypothetical protein	1576.9	1462.3	1481.0	569.2	607.6	485.6	0.37	9.6E-04
BF0907	putative Sua5/yciO/yrdC family protein	92.1	103.5	89.1	99.3	91.3	93.6	1.00	1.0E+00
BF0908	putative outer membrane protein	134.6	132.5	125.0	125.3	120.2	109.6	0.90	1.4E-01
BF0909	putative helicase protein	72.0	71.4	65.6	87.6	74.0	76.1	1.13	1.5E-01
BF0910	putative haloacid dehalogenase-like hydrolase	159.4	162.1	152.5	158.7	146.1	137.8	0.93	2.6E-01
BF0911	putative aminotransferase	107.2	88.7	89.7	99.9	98.3	113.4	1.09	3.8E-01
BF0912	putative O-acetylhomoserine synthase	123.1	111.9	115.1	107.2	100.5	101.5	0.88	4.3E-02
BF0913	putative RNA polymerase ECF-type sigma factor	94.6	90.3	87.8	33.0	37.2	48.0	0.43	5.6E-03
BF0914	putative anti-sigma factor	159.6	158.5	162.0	108.2	106.3	115.6	0.69	9.6E-04
BF0915	putative outer membrane protein	100.2	93.6	87.1	103.0	111.8	100.8	1.12	1.3E-01
BF0916	putative FNR-like protein	346.7	327.6	321.6	324.7	328.5	290.3	0.95	3.6E-01
BF0917	putative transmembrane protein	54.4	39.6	52.4	33.6	45.9	34.6	0.78	2.1E-01
BF0918	putative transmembrane protein	21.1	22.4	20.1	17.3	15.4	17.2	0.78	1.9E-02
BF0919	hypothetical protein	477.2	508.6	514.3	809.1	925.9	743.9	1.65	6.0E-03
BF0920	putative glycosyl transferase	184.5	184.3	211.2	425.9	459.1	401.2	2.22	1.1E-03
BF0921	putative glycosyl hydrolase	257.6	268.0	295.6	780.3	855.8	698.1	2.84	9.0E-04
BF0922	hypothetical protein	935.3	1011.6	997.6	721.7	740.8	619.7	0.71	1.2E-02
BF0923	possible glycogen synthase	944.1	965.5	1008.8	786.5	793.6	624.8	0.75	4.4E-02
panC	putative pantoate--beta-alanine ligase	118.5	114.7	121.1	153.6	149.9	145.8	1.27	2.0E-03
panD	aspartate 1-decarboxylase precursor	284.6	302.7	298.6	279.7	284.5	256.8	0.93	1.5E-01
BF0926	putative NADPH-dependent glutamate synthase	199.9	204.7	189.1	242.3	204.6	235.5	1.15	1.2E-01
BF0927	putative sugar transporter	60.0	63.6	65.4	87.6	89.5	76.5	1.34	1.5E-02
serS	seryl-tRNA synthetase	411.2	419.2	416.9	500.7	474.3	430.2	1.12	9.4E-02
rpmA	50S ribosomal protein L27	3233.0	3003.7	3344.9	2947.7	2926.6	3079.0	0.94	1.9E-01
BF0930	putative 50S ribosomal protein L21	3055.7	2925.1	3240.2	3054.4	3052.8	3210.9	1.01	8.0E-01
BF0931	putative haloacid dehalogenase-like hydrolase	41.9	49.1	49.1	119.7	114.8	109.3	2.46	7.8E-04
BF0932	putative lipoprotein	46.5	40.4	44.1	91.7	77.6	89.6	1.98	2.4E-03
BF0933	putative ATP-binding component of ABC transporter protein	74.0	69.7	67.2	140.8	143.4	113.3	1.88	5.2E-03
BF0934	putative transmembrane protein	62.6	72.3	71.5	131.5	142.5	114.5	1.88	4.8E-03
BF0935	putative zinc protease	264.6	271.6	252.5	485.2	471.4	396.3	1.71	4.8E-03
kdsA	2-dehydro-3-deoxyphosphooctonate aldolase	160.4	177.9	168.4	230.7	231.0	225.5	1.36	2.7E-03
BF0937	hypothetical protein	184.8	170.1	188.2	219.4	196.8	199.6	1.13	8.7E-02
BF0938	tRNA delta(2)-isopentenylpyrophosphate transferase	137.4	138.4	133.3	139.5	138.6	154.2	1.06	2.7E-01
BF0939	putative ATP/GTP-binding transmembrane protein	143.4	159.2	154.3	128.5	131.8	121.6	0.84	2.3E-02
BF0940	putative ATP-binding component of ABC transporter	247.0	254.3	249.7	218.6	236.6	213.6	0.89	4.1E-02

BF0941	hypothetical protein	384.6	400.7	420.5	367.5	351.4	298.1	0.84	1.0E-01
BF0942	hypothetical protein	163.9	173.8	173.5	127.2	120.2	147.4	0.77	3.0E-02
BF0943	hypothetical protein	186.0	200.5	182.4	132.3	120.1	142.8	0.69	9.2E-03
BF0944	putative nucleoside/H+ permease	179.1	189.3	169.2	191.3	197.6	184.1	1.07	2.3E-01
BF0946	hypothetical protein	84.3	56.9	70.8	38.7	57.0	45.8	0.67	1.0E-01
BF0947	hypothetical protein	294.8	307.2	305.0	262.7	252.8	239.1	0.83	1.0E-02
BF0948	putative 3'-5' exonuclease	246.1	265.2	251.0	236.3	252.0	218.4	0.93	2.4E-01
BF0949	conserved hypothetical protein, possible C-terminal metal binding site	306.9	299.2	317.7	271.6	255.4	227.3	0.81	3.9E-02
BF0950	putative FtsK/SpoIIIE-like protein	275.0	293.7	286.1	233.4	234.6	214.8	0.80	8.3E-03
BF0951	hypothetical protein	550.8	585.6	543.8	245.3	248.5	279.3	0.46	6.4E-04
trxB	putative thioredoxin reductase	1096.7	1143.7	1173.6	919.3	848.0	952.5	0.80	1.2E-02
BF0953	putative beta-N-acetylhexosaminidase	92.5	93.4	92.6	266.3	252.6	248.5	2.75	3.0E-05
BF0954	putative FNR-family transcriptional regulator protein	382.1	397.0	357.9	388.3	380.4	306.0	0.94	5.7E-01
glnA	glutamine synthetase	220.0	238.4	222.6	145.8	148.0	135.7	0.63	1.4E-03
BF0957	hypothetical protein	138.3	119.8	132.4	64.7	81.1	70.6	0.55	5.6E-03
BF0958	putative reverse transcriptase	45.5	44.2	40.0	38.0	39.1	41.4	0.91	1.8E-01
rpsA	putative 30S ribosomal protein S1	2256.6	2643.2	2539.1	2819.8	2734.4	2701.3	1.11	1.4E-01
BF0960	ribonuclease Z	208.7	226.7	211.9	193.7	205.6	201.5	0.93	1.1E-01
BF0961	putative RNA polymerase ECF-type sigma factor	207.8	186.7	201.3	170.6	174.3	179.4	0.88	4.2E-02
BF0962	hypothetical protein	128.7	119.7	124.8	105.4	125.8	121.0	0.94	4.3E-01
BF0963	hypothetical protein	121.4	114.0	143.1	147.8	146.5	137.1	1.14	1.9E-01
BF0964	hypothetical protein	87.3	70.9	82.1	126.8	130.7	111.3	1.54	1.4E-02
BF0965	putative transmembrane zinc-binding protein	39.7	41.0	39.0	25.5	26.4	20.7	0.60	8.2E-03
valS	putative valyl-tRNA synthetase	310.3	295.1	290.8	273.8	268.6	308.2	0.95	3.9E-01
BF0967	putative two-component sensor histidine kinase	21.6	22.2	21.0	8.5	10.0	13.5	0.49	1.5E-02
BF0969	putative RNA polymerase ECF-type sigma factor	24.6	29.9	26.1	83.8	79.6	95.2	3.21	8.6E-04
BF0970	putative anti-sigma factor	34.9	36.0	27.1	45.2	48.6	62.4	1.59	4.6E-02
BF0971	putative outer membrane protein	11.1	10.2	11.5	19.2	21.8	21.2	1.89	1.5E-03
BF0972	hypothetical protein	12.5	9.9	10.7	25.7	28.5	25.5	2.41	1.8E-03
BF0973	putative endonuclease/exonuclease/phosphatase family protein	6.7	4.6	5.7	13.3	11.7	14.3	2.35	7.5E-03
BF0974	hypothetical protein	64.1	77.8	78.9	117.3	116.0	114.3	1.58	7.5E-03
BF0975	putative RNA polymerase ECF-type sigma factor	103.2	107.9	117.4	103.9	104.3	84.9	0.89	2.7E-01
BF0976	putative anti-sigma factor	13.7	13.2	12.5	691.0	705.3	797.2	55.59	4.8E-06
BF0977	**putative TonB-dependent outer membrane receptor protein**	**5.0**	**5.2**	**5.0**	**1313.9**	**1283.0**	**1235.9**	**253.44**	**4.4E-08**
BF0978	putative outer membrane protein	5.8	6.1	7.9	1376.5	1276.9	1425.0	207.78	2.2E-05
BF0979	putative arylsulfatase precursor	3.6	6.2	6.8	1507.4	1366.2	1672.4	282.14	1.8E-04
BF0980	putative arylsulfatase	77.5	78.5	71.0	304.6	290.4	356.2	4.18	3.7E-04
BF0981	hypothetical protein	1047.7	940.5	962.4	703.0	813.5	695.3	0.75	2.0E-02
BF0982	hypothetical protein	290.9	261.3	275.5	231.8	246.0	219.1	0.84	3.8E-02
secA	translocase	569.7	589.9	511.5	506.1	455.0	486.0	0.87	8.7E-02
BF0984	putative alkaline phosphatase	321.3	344.3	285.0	216.8	181.7	197.2	0.63	9.7E-03

BF0985	putative transmembrane protein	196.9	211.2	174.7	139.0	127.2	134.0	0.69	1.0E-02
BF0989	putative regulatory protein	148.0	150.5	138.8	93.9	90.4	90.4	0.63	6.2E-04
BF0990	putative outer membrane protein	880.9	771.7	818.0	609.8	593.2	650.2	0.75	1.0E-02
BF0991	hypothetical protein	1435.6	1483.4	1521.6	2164.0	2249.2	1992.5	1.44	3.2E-03
BF0992	hypothetical protein	229.2	225.8	229.1	284.2	289.0	270.0	1.23	2.6E-03
BF0993	putative transmembrane CBS domain transporter	151.0	157.5	168.2	220.2	219.4	204.3	1.35	5.6E-03
BF0994	hypothetical protein	1265.2	1342.8	1392.2	1470.6	1464.6	1341.1	1.07	2.4E-01
BF0995	hypothetical protein	409.3	400.8	384.1	317.2	329.0	310.1	0.80	3.8E-03
BF0996	hypothetical protein	299.6	317.7	303.4	358.6	398.8	355.5	1.21	2.2E-02
BF0997	putative 4-hydroxythreonine-4-phosphate dehydrogenase	426.3	446.0	415.5	546.0	486.7	498.1	1.19	2.8E-02
BF0998	putative sigma-54 dependent transcriptional regulator	371.0	370.5	362.6	429.5	411.7	429.5	1.15	3.7E-03
BF0999	hypothetical protein	294.1	305.6	291.8	333.5	355.7	319.7	1.13	4.2E-02
BF1000	hypothetical protein	161.5	161.4	170.4	188.0	185.4	191.4	1.15	7.8E-03
BF1001	possible protein-export transmembrane protein	1102.7	1254.2	1157.7	1270.3	1275.1	1221.8	1.07	2.1E-01
BF1002	putative transmembrane transporter	151.8	145.1	158.2	290.3	294.4	234.0	1.79	5.9E-03
BF1003	hypothetical protein	132.6	123.0	150.9	215.0	221.6	215.2	1.61	5.1E-03
BF1004	hypothetical protein	782.0	773.1	695.9	571.7	562.2	559.1	0.75	5.7E-03
BF1005	putative YjeF-related sugar kinase	91.4	99.7	85.3	98.9	72.2	91.0	0.94	6.6E-01
BF1006	putative transmembrane protein	0.0	0.6	0.1	0.0	0.0	0.1	0.44	
BF1007	putative methyltransferase	51.3	44.3	53.8	77.6	71.6	76.7	1.52	8.3E-03
upcY	putative transcriptional regulator	20.4	20.3	20.6	8.7	5.5	8.2	0.36	6.4E-03
upcZ	putative transcriptional regulator	18.0	16.7	17.8	11.5	14.6	14.2	0.76	4.8E-02
rmlA2	glucose-1-phosphate thymidyl transferase	12.7	15.0	13.8	10.2	14.0	9.0	0.79	2.2E-01
rmlC1	dTDP-6-deoxy-D-glucose-3,5 epimerase	7.4	13.3	8.5	10.4	11.2	6.8	0.98	9.5E-01
wcfA	putative acetyl transferase	9.1	10.8	14.5	2.9	5.9	4.2	0.37	3.1E-02
wzx2	putative O-antigen flippase	9.0	7.5	8.9	3.8	4.5	3.7	0.48	3.8E-03
wcfB	putative fucosyl transferase	9.6	11.7	11.7	5.0	6.1	3.9	0.45	1.4E-02
wcfC	putative glycosyltransferase	11.9	10.3	10.0	8.1	7.7	7.1	0.71	1.4E-02
wcfD	putative acetyltransferase	12.6	10.6	10.4	5.9	5.9	4.9	0.50	4.9E-03
wzy2	putative polysaccharide polymerase	3.5	3.7	4.9	1.7	2.2	1.4	0.43	1.9E-02
wcfE	putative glycosyltransferase	6.6	5.6	4.7	2.7	5.8	4.3	0.73	3.4E-01
wcfF	putative UDP-glucose-6 dehydrogenase	11.6	13.2	12.0	11.5	14.1	11.8	1.01	9.0E-01
wcfG	putative glycosyltransferase	12.8	12.9	11.7	9.7	10.8	7.3	0.74	1.0E-01
wcfH	putative deacetylase	9.0	8.9	10.2	6.9	7.1	6.7	0.73	7.6E-03
wcfI	putative glycosyltransferase	7.5	6.8	5.8	7.3	6.3	5.1	0.92	6.2E-01
wcfJ	putative glycosyltransferase	5.3	4.9	7.1	4.6	6.4	4.0	0.86	5.2E-01
wcfK	putative epimerase/dehydratase	6.4	5.9	6.1	4.1	4.0	3.3	0.62	7.6E-03
wcfL	putative phosphate transferase	10.3	10.4	12.4	4.5	4.5	3.2	0.37	5.4E-03
BF1027	putative iron-regulated transmembrane protein	1133.6	1167.9	1311.2	1208.2	1236.1	1049.4	0.97	7.0E-01
BF1028	conserved hypothetical lipoprotein	1347.1	1369.1	1386.9	1867.6	1780.6	1552.4	1.26	2.9E-02
BF1029	putative TonB-dependent outer membrane receptor protein	234.8	237.2	247.7	304.7	290.0	266.9	1.20	2.8E-02

BF1031	putative hypoxanthine guanine phosphoribosyltransferase	381.2	363.5	398.7	208.3	191.0	214.4	0.54	9.6E-04
adk	adenylate kinase	694.4	622.0	679.4	610.3	625.4	675.6	0.96	4.7E-01
obg	putative Spo0B-related GTP-binding protein	430.2	338.6	372.9	229.0	253.1	298.0	0.68	4.0E-02
BF1034	hypothetical protein	87.0	61.6	65.2	37.6	43.7	55.2	0.64	7.3E-02
BF1035	hypothetical protein	55.9	43.4	49.6	36.9	34.0	56.9	0.84	4.5E-01
BF1036	putative M23/M37-family peptidase	48.9	35.2	36.1	48.0	39.3	56.8	1.20	3.6E-01
BF1037	hypothetical protein	13.4	13.7	15.2	14.8	21.9	20.2	1.33	1.3E-01
BF1038	hypothetical protein	43.2	51.0	50.8	55.9	52.5	45.6	1.06	5.8E-01
tmRNA	RF00023	31100.7	16870.8	17786.5	12045.9	13293.3	27299.9	0.78	5.5E-01
BF1040	hypothetical protein	121.5	112.1	142.6	113.1	136.6	155.3	1.07	6.4E-01
dinB	putative DNA polymerase IV	37.9	36.7	31.7	36.7	28.4	41.5	0.99	9.7E-01
BF1044	hypothetical protein	78.1	72.6	87.0	53.8	63.3	50.9	0.71	2.9E-02
BF1045	possible transglutaminase-family protein	138.3	150.1	137.5	224.1	216.7	210.0	1.53	1.4E-03
BF1046	putative C4-dicarboxylate anaerobic carrier	53.1	56.9	51.6	78.3	83.1	71.6	1.44	6.9E-03
BF1047	hypothetical protein	4932.8	4617.1	5030.3	472.0	559.9	408.8	0.10	2.3E-04
BF1048	hypothetical protein	150.3	140.8	149.3	75.8	87.8	75.8	0.54	1.7E-03
BF1049	hypothetical protein	7.8	5.8	4.1	1.9	2.0	1.3	0.30	1.5E-02
mmdB	putative transmembrane methylmalonyl-CoA/oxaloacetate decarboxylase, beta-subunit	2.9	5.4	6.1	4.0	2.4	3.9	0.73	4.0E-01
BF1051	putative 3,4-dihydroxy-2-butanone 4-phosphate/shikimate 5-dehydrogenase fusion protein	3.8	2.9	3.9	6.1	5.5	4.1	1.47	1.0E-01
BF1052	putative AraC-family transcriptional regulator	22.8	18.2	20.4	19.5	24.5	19.7	1.04	7.8E-01
BF1053	hypothetical protein	16.0	13.7	11.8	10.1	26.0	21.5	1.30	5.0E-01
BF1054	hypothetical protein	49.8	49.3	45.3	44.6	45.9	39.0	0.89	1.9E-01
BF1055	putative acetyltransferase	41.4	36.1	42.7	41.6	42.0	42.7	1.05	4.5E-01
BF1056	putative ribosomal large subunit pseudouridine synthase	69.7	68.9	68.2	71.5	66.6	65.5	0.98	6.5E-01
BF1057	putative restriction enzyme of type III restriction-modification system	99.5	102.4	98.7	115.7	114.2	102.4	1.10	1.1E-01
BF1058	putative modification enzyme of type III restriction-modification system	122.9	127.1	123.2	136.3	135.1	130.1	1.08	3.1E-02
BF1059	putative glycosyl hydrolase	84.0	86.7	84.6	167.3	171.1	154.9	1.93	3.6E-04
BF1060	putative dehydrogenase/oxidoreductase	66.4	61.3	56.9	76.3	87.0	69.8	1.26	7.0E-02
BF1061	hypothetical protein	31.0	48.9	42.4	22.3	28.5	20.5	0.59	5.8E-02
BF1062	hypothetical protein	61.8	70.0	56.0	49.1	62.3	48.8	0.85	2.5E-01
BF1064	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF1066	putative ATP/GTP-binding protein	57.9	44.7	57.9	103.2	105.6	93.1	1.89	7.8E-03
BF1067	hypothetical protein	78.5	59.0	70.7	131.0	136.5	101.5	1.77	2.3E-02
BF1068	possible type I restriction-modification system protein	52.2	41.5	53.4	101.5	106.9	82.7	1.98	1.0E-02
BF1069	hypothetical protein	99.1	73.4	100.0	158.8	165.8	120.8	1.64	4.7E-02
BF1070	hypothetical protein	16.6	19.6	21.3	11.1	8.0	7.5	0.46	1.4E-02
BF1071	hypothetical protein	16.5	15.9	19.2	6.5	7.4	6.6	0.40	1.3E-03

BF1072	hypothetical protein	21.5	26.9	29.1	11.7	13.5	12.8	0.49	6.8E-03
BF1073	putative DNA-binding protein	42.1	33.3	33.3	56.3	47.5	61.1	1.52	3.5E-02
BF1074	hypothetical protein	67.6	59.1	66.5	91.6	97.8	82.0	1.40	1.7E-02
BF1076	putative DNA-binding protein	77.1	95.5	97.2	94.2	101.2	83.9	1.04	7.6E-01
BF1077	putative modification protein of type I restriction-modification system	96.2	88.6	95.8	137.0	144.2	116.1	1.41	1.9E-02
BF1078	putative modification protein of type I restriction-modification system	82.5	77.5	80.0	119.1	123.6	94.4	1.40	3.5E-02
BF1079	putative type I restriction enzyme	96.0	89.3	93.8	133.9	142.7	106.0	1.36	5.3E-02
BF1080	hypothetical protein	54.1	62.0	56.8	87.5	94.2	80.5	1.52	7.3E-03
BF1081	hypothetical protein	43.8	52.0	58.7	69.3	67.8	55.2	1.25	1.7E-01
BF1082	hypothetical protein	51.3	38.4	42.6	47.0	52.5	41.9	1.07	6.1E-01
BF1083	hypothetical protein	44.3	34.8	48.8	38.8	42.2	43.9	0.99	9.2E-01
BF1088	hypothetical protein	0.0	0.0	0.6	0.0	0.6	0.0	1.05	
BF1089	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF1090	hypothetical protein	0.8	1.4	1.2	0.3	0.3	0.8	0.36	8.6E-02
BF1091	hypothetical protein	5.3	1.1	2.3	5.0	4.9	4.0	1.93	2.8E-01
BF1092	hypothetical protein	7.1	11.3	6.5	8.9	4.1	13.5	0.99	9.8E-01
BF1093	hypothetical protein	29.0	30.6	33.6	35.6	37.9	27.9	1.08	5.7E-01
BF1095	hypothetical protein	4.2	1.3	1.3	1.7	0.7	1.2	0.58	3.8E-01
BF1096	hypothetical protein	0.0	0.8	0.0	0.0	0.9	0.0	1.09	
BF1097	putative ATP-binding protein	65.4	64.8	46.8	116.5	79.1	152.1	1.92	7.0E-02
BF1098	hypothetical protein	2.7	1.0	5.0	0.9	4.2	2.6	0.90	9.0E-01
BF1099	hypothetical protein	1.8	0.9	0.0	1.7	0.0	0.0	1.30	
BF1100	putative ATP-binding protein	40.1	47.2	42.8	73.0	77.9	51.2	1.53	6.3E-02
BF1101	hypothetical protein	39.5	31.9	37.4	42.4	50.0	36.7	1.18	2.7E-01
BF1102	conserved hypothetical protein with RecF/RecN/SMC N-terminal domain	28.1	24.0	27.4	33.8	43.2	28.5	1.31	1.6E-01
BF1103	putative ATP-dependent DNA helicase	27.6	21.0	27.6	35.5	41.8	27.6	1.37	1.6E-01
BF1104	hypothetical protein	29.3	25.7	29.0	32.3	36.9	28.6	1.16	2.1E-01
BF1106	hypothetical protein	4.7	6.5	6.0	3.2	3.1	3.2	0.56	1.0E-02
BF1107	hypothetical protein	183.1	179.2	192.8	192.6	193.5	110.3	0.87	5.6E-01
BF1108	putative beta-lactamase protein	72.9	69.9	77.8	89.2	99.4	80.6	1.22	7.5E-02
BF1109	putative ATP/GTP-binding protein	48.2	41.1	50.3	66.7	78.2	59.8	1.46	3.6E-02
BF1110	hypothetical protein	58.8	41.9	57.8	62.2	73.0	69.5	1.30	1.4E-01
BF1111	hypothetical protein	58.8	82.6	77.2	90.1	78.6	102.0	1.24	2.2E-01
BF1112	hypothetical protein	19.8	23.0	24.3	9.4	9.8	12.6	0.47	7.3E-03
BF1113	hypothetical protein	17.9	11.8	15.7	6.5	4.9	5.6	0.38	8.2E-03
BF1114	hypothetical protein	12.4	13.9	18.4	6.0	6.0	5.8	0.40	5.3E-03
BF1116	putative DNA-binding protein	188.9	181.4	163.4	237.2	205.8	195.6	1.19	1.1E-01
BF1117	hypothetical protein	149.0	155.1	151.0	214.0	209.4	183.9	1.33	1.1E-02
BF1118	hypothetical protein	153.4	147.0	144.2	169.6	200.9	154.5	1.17	1.6E-01
BF1119	hypothetical protein	92.6	86.4	85.2	119.3	122.8	118.8	1.37	1.8E-03
BF1120	putative modification enzyme of type III restriction-modification system	120.9	117.1	117.4	163.0	163.1	156.1	1.36	5.9E-04
BF1121	putative DNA-binding protein	149.5	125.5	135.0	176.1	172.3	161.5	1.25	3.6E-02
BF1122	putative restriction enzyme of type III restriction-modification system	145.9	140.4	132.5	200.9	194.5	194.3	1.41	1.8E-03
BF1123	putative ATP/GTP-binding protein	61.6	68.9	65.5	76.6	83.4	68.2	1.16	1.3E-01
BF1124	putative ATP/GTP-binding protein	61.3	59.9	69.9	99.9	99.5	90.1	1.52	6.7E-03
BF1125	hypothetical protein	71.4	55.1	65.1	79.9	90.8	76.8	1.30	7.7E-02

BF1126	hypothetical protein	85.0	79.1	86.4	87.2	104.5	90.9	1.13	1.8E-01
BF1127	putative transmembrane protein	32.4	22.8	28.3	23.8	25.1	17.6	0.80	2.7E-01
BF1128	hypothetical protein	1.6	1.1	0.8	0.4	0.0	0.6	0.43	7.3E-02
BF1129	hypothetical protein	0.0	0.4	2.3	0.4	0.0	0.8	0.56	6.5E-01
BF1132	hypothetical protein	4.4	5.1	3.8	2.3	2.5	3.0	0.59	2.0E-02
xis	putative excisionase	2.4	2.0	3.6	2.7	2.7	3.6	1.15	5.9E-01
BF1134	putative transmembrane protein	3.1	2.6	4.1	4.9	4.3	2.4	1.14	6.9E-01
int	putative bacteriophage integrase	5.7	5.0	6.4	2.4	2.2	1.2	0.33	1.8E-02
BF1137	putative transposase	4.4	5.8	5.1	3.0	2.3	3.3	0.56	2.5E-02
BF1138	tRNA modification GTPase	144.8	133.4	144.4	146.8	139.6	137.3	1.00	9.5E-01
BF1139	putative two-component system sensor histidine kinase/response regulator fusion protein	45.5	40.8	37.8	39.0	45.8	40.3	1.01	9.3E-01
BF1140	hypothetical protein	87.5	95.1	91.3	47.8	38.0	43.4	0.47	2.2E-03
BF1141	putative exonuclease	208.9	247.4	238.8	255.6	254.2	237.2	1.08	3.3E-01
BF1142	putative purine nucleoside phosphorylase/uridine phosphorylase family protein	207.2	220.1	242.3	461.6	474.8	411.0	2.01	2.0E-03
BF1143	hypothetical protein	266.1	257.0	270.7	523.2	535.6	486.2	1.95	3.9E-04
BF1144	putative transmembrane protein	179.1	208.4	186.1	190.0	224.7	201.3	1.07	4.2E-01
BF1145	hypothetical protein	307.9	296.6	294.4	292.8	343.3	286.4	1.02	7.7E-01
BF1146	hypothetical protein	40.9	33.0	40.2	27.2	17.2	28.4	0.63	8.9E-02
BF1147	hypothetical protein	43.0	41.2	41.1	58.5	48.2	54.1	1.28	2.8E-02
apbE	putative thiamine biosynthesis lipoprotein	81.4	78.8	88.1	135.7	124.4	120.7	1.53	3.7E-03
BF1149	putative transmembrane protein	89.3	82.8	102.0	112.1	103.7	100.1	1.16	1.5E-01
BF1150	hypothetical protein	146.3	152.3	161.1	167.5	177.2	148.9	1.07	3.7E-01
BF1151	hypothetical protein	107.9	104.9	110.8	124.5	136.6	115.4	1.16	7.3E-02
BF1152	putative transmembrane glycosyltransferase	165.4	164.1	192.9	197.9	156.5	151.7	0.96	7.8E-01
BF1153	putative transmembrane protein	217.7	260.5	303.4	187.1	165.7	174.2	0.68	3.8E-02
BFt14	tRNA-Thr-TGT	106.9	167.4	100.1	178.8	143.3	310.0	1.64	2.1E-01
eno	phosphopyruvate hydratase	6667.7	6842.3	6609.0	5346.9	4991.5	4954.8	0.76	2.3E-03
BF1156	hypothetical protein	46.4	42.6	51.9	59.5	61.0	44.0	1.16	3.5E-01
crcB	putative transmembrane camphor resistance and chromosome condensation CrcB homologue	25.7	37.6	38.5	34.8	41.0	26.9	1.01	9.7E-01
susB	putative alpha-glucosidase	118.9	120.1	131.7	21.9	27.5	21.4	0.19	4.3E-04
BF1159	putative DNA-binding protein	29.9	18.2	26.4	57.1	67.0	43.3	2.26	2.9E-02
BF1160	hypothetical protein	5.1	4.7	6.9	11.1	12.7	9.0	1.98	2.4E-02
BF1161	hypothetical protein	13.9	16.5	11.0	13.2	11.9	16.4	1.01	9.7E-01
hslR	putative ribosome-associated heat shock protein	108.1	95.6	111.7	69.9	65.2	67.6	0.64	4.0E-03
pth	peptidyl-tRNA hydrolase	93.5	98.2	105.8	71.8	77.2	62.7	0.71	1.9E-02
BF1164	putative ribosomal L25p family stress protein	1534.3	1567.6	1845.7	1739.1	1687.9	1637.2	1.03	7.4E-01
BF1165	hypothetical protein	545.3	450.1	568.8	457.2	514.2	440.0	0.90	3.8E-01
BF1166	putative N utilization substance protein	947.5	946.3	1070.5	676.3	714.7	556.4	0.65	1.9E-02
BF1167	conserved hypothetical protein with preprotein translocase motif	1862.2	2298.7	2336.4	1643.2	1828.6	1513.7	0.77	7.5E-02
BF1168	hypothetical protein	367.0	405.2	443.4	344.7	367.7	313.7	0.84	1.2E-01

BF1169	putative dephospho-CoA kinase	260.1	247.5	273.8	255.7	250.9	213.7	0.92	3.3E-01
BF1170	hypothetical protein	1344.8	1385.8	1591.2	1680.4	1894.5	1519.8	1.18	1.7E-01
BF1171	hypothetical protein	171.3	171.3	194.3	92.0	93.6	113.6	0.56	5.9E-03
clpB	putative heat shock ClpB protein	327.6	310.7	298.6	92.2	87.2	83.5	0.28	1.1E-04
BF1173	hypothetical protein	299.5	274.4	284.1	209.2	219.7	210.6	0.75	2.7E-03
BF1174	putative transcriptional regulator	182.0	180.6	193.7	146.0	164.4	142.9	0.81	2.8E-02
BF1175	putative transmembrane protein	130.4	125.5	132.3	71.6	80.5	66.6	0.56	2.6E-03
BF1176	hypothetical protein	591.8	510.9	582.9	46.2	67.8	49.5	0.10	4.9E-04
BF1177	hypothetical protein	199.3	155.2	178.1	12.8	13.0	11.1	0.07	1.3E-04
BF1178	putative RNA polymerase ECF-type sigma factor	323.2	283.4	249.3	16.2	25.3	21.3	0.07	5.7E-04
BF1179	hypothetical protein	57.6	72.5	73.7	54.0	64.5	42.6	0.78	2.2E-01
recA	recombinase A	748.0	685.6	736.6	785.7	776.4	735.8	1.06	2.2E-01
bcp	putative bacterioferritin comigratory protein	316.6	280.9	314.7	463.9	443.3	407.9	1.44	7.6E-03
BF1182	hypothetical protein	462.3	445.2	483.0	647.0	659.7	586.4	1.36	6.7E-03
BF1183	hypothetical protein	3.7	4.7	2.5	2.9	4.1	1.8	0.79	5.6E-01
BF1184	hypothetical protein	622.7	574.2	652.1	438.6	456.3	381.3	0.69	1.3E-02
BF1185	putative iron transport-related family system permease protein	40.7	38.7	34.4	41.3	36.8	45.1	1.08	4.4E-01
BF1186	putative iron-related ABC transport periplasmic binding protein	55.4	48.9	47.3	42.3	41.1	40.1	0.82	3.2E-02
BF1187	putative polysialic acid transport protein	2.4	2.4	2.4	1.6	1.1	2.1	0.65	1.1E-01
BF1188	putative transcriptional regulator	7.1	6.4	7.4	5.1	4.7	2.9	0.59	7.2E-02
dnaK	molecular chaperone DnaK	1230.1	1220.7	942.3	430.8	421.3	347.5	0.35	3.1E-03
BF1190	putative transporter periplasmic binding protein	25.7	22.9	23.9	8.5	5.9	9.2	0.32	4.9E-03
nfo	endonuclease IV	105.8	108.8	101.4	130.5	118.6	123.6	1.18	2.0E-02
trpB	tryptophan synthase subunit beta	201.9	203.9	194.2	375.5	376.4	329.1	1.80	1.4E-03
ktrB	putative transmembrane K+/Na+ uptake protein	175.4	185.4	197.6	84.2	95.0	69.9	0.44	4.1E-03
ktrA	putative K+/Na+ uptake protein	135.4	109.0	110.0	83.0	87.1	91.4	0.74	3.4E-02
katA	catalase	419.8	556.9	553.9	1045.5	1418.6	1099.7	2.33	9.0E-03
BF1196	putative alpha-glucosidase, glycosylhydrolase	25.5	29.5	29.1	42.6	44.0	38.5	1.49	8.6E-03
BF1197	putative ECF-type RNA polymerase sigma factor	33.0	33.0	43.1	48.4	67.0	51.8	1.53	5.8E-02
BF1198	putative xylosidase/arabinosidase	93.2	100.6	110.7	51.1	54.4	50.2	0.51	1.6E-03
cepA	beta-lactamase	102.0	86.5	93.2	60.9	60.4	56.1	0.63	4.2E-03
BF1200	hypothetical protein	9.4	8.3	11.2	5.9	5.4	8.3	0.67	9.7E-02
BF1203	putative anti-sigma factor	9.1	9.3	8.4	5.6	5.1	4.2	0.55	8.0E-03
BF1204	putative outer membrane protein	8.3	8.2	8.9	6.7	7.0	7.3	0.83	1.2E-02
BF1205	hypothetical protein	8.9	7.8	7.7	7.6	11.8	7.9	1.10	6.3E-01
BF1206	putative phosphohydrolase, Icc family	40.8	36.9	28.9	33.7	30.2	38.1	0.96	8.1E-01
BF1207	possible phosphodiesterase/nucleotide pyrophosphatase-like protein	82.3	71.1	81.8	61.7	58.8	73.4	0.82	1.2E-01
BF1208	putative endonuclease/exonuclease/phosphatase family protein	83.8	107.7	102.3	83.0	80.8	75.9	0.82	1.1E-01

ahpF	alkyl hydroperoxide reductase subunit F	139.6	274.0	228.8	109.2	156.7	155.7	0.67	2.2E-01
ahpC	alkyl hydroperoxide reductase C subunit	699.3	1273.8	1206.2	2731.8	3176.8	3275.4	2.98	1.4E-02
BF1211	hypothetical protein	0.0	0.0	1.4	0.0	0.0	1.3	0.87	
BF1212	hypothetical protein	30.5	17.2	16.6	20.0	14.4	34.4	1.04	9.2E-01
BF1213	hypothetical protein	85.8	86.2	80.9	91.9	92.4	96.7	1.11	3.2E-02
BF1214	hypothetical protein	224.9	204.6	170.7	84.7	81.4	98.7	0.44	4.6E-03
BF1215	hypothetical protein	275.4	278.3	269.9	119.5	109.7	120.3	0.42	1.7E-04
tdcG	putative L-serine dehydratase	87.0	86.8	73.3	160.5	134.5	168.9	1.87	6.8E-03
BF1217	putative transmembrane magnesium and cobalt transporter protein	74.9	90.5	92.9	61.1	61.4	55.9	0.69	1.8E-02
BF1218	putative DNA mismatch repair MutS protein	104.0	95.3	96.7	70.7	60.1	66.7	0.67	5.8E-03
BFt15	tRNA-Ser-TGA	21.8	34.2	22.9	23.6	14.4	91.6	1.22	7.9E-01
BF1219	putative transposase	8.1	7.9	6.9	1.5	1.5	1.6	0.20	1.9E-04
BF1220	hypothetical protein	4.2	3.8	5.4	2.5	1.1	0.9	0.31	3.9E-02
radC2	putative DNA repair protein	0.8	0.4	1.7	0.4	0.0	0.4	0.45	2.1E-01
BF1222	putative anti-restriction protein	0.3	0.0	0.4	0.0	0.0	0.3	0.91	
BF1223	hypothetical protein	0.8	0.9	0.0	0.0	0.0	0.0		
BF1224	hypothetical protein	0.0	0.0	0.0	0.8	0.0	0.8		
BF1225	hypothetical protein	0.0	1.6	0.4	0.7	0.4	0.7	0.75	7.5E-01
BF1226	hypothetical protein	119.5	138.2	130.6	72.8	74.7	64.6	0.55	2.7E-03
BF1230	hypothetical protein	135.6	131.1	155.9	164.3	181.2	139.0	1.14	2.9E-01
BF1231	hypothetical protein	21.1	21.2	26.3	28.4	30.2	20.8	1.15	4.4E-01
BF1232	conserved hypothetical protein found in conjugate transposon	21.6	22.1	21.6	13.0	11.3	14.7	0.59	7.0E-03
BF1233	conserved hypothetical protein found in conjugate transposon	0.6	0.6	0.0	0.0	0.0	0.3	0.47	
BF1234	conserved hypothetical protein found in conjugate transposon	0.8	1.0	0.6	0.2	0.2	0.4	0.31	2.2E-02
BF1235	conserved hypothetical protein found in conjugate transposon	0.1	0.8	0.0	0.2	0.0	0.4	0.92	9.5E-01
BF1236	conserved hypothetical protein found in conjugate transposon	0.0	0.0	0.0	0.0	0.0	0.0		
BF1237	conserved hypothetical protein found in conjugate transposon	0.0	0.6	0.0	0.3	0.0	0.0	0.45	
BF1238	conserved hypothetical transmembrane protein found in conjugate transposon	0.9	0.7	1.5	0.3	0.6	0.3	0.41	6.7E-02
BF1239	conserved hypothetical protein found on conjugate transposon	0.0	0.3	0.3	0.0	0.3	0.3	0.97	8.4E-01
BF1240	conserved hypothetical protein found on conjugate transposon	0.0	0.0	0.0	0.0	0.0	0.5		
BF1241	conserved hypothetical protein found on conjugate transposon	0.5	0.2	0.2	0.1	0.1	0.2	0.40	1.9E-01
BF1242	conserved hypothetical transmembrane protein found on conjugate transposon	0.0	0.0	0.6	1.5	0.0	0.0	2.58	

BF1243	conserved hypothetical transmembrane protein found in conjugate transposon	0.6	0.0	1.3	0.0	0.0	0.6	0.65	
BF1244	hypothetical protein	0.2	0.0	0.3	0.2	0.3	0.7	1.40	4.8E-01
BF1245	conserved hypothetical protein found in conjugate transposon	0.4	0.0	0.4	0.0	0.0	0.0		
BF1246	conserved hypothetical protein found in conjugate transposon	0.0	0.2	0.0	0.0	0.0	0.2	0.90	
BF1247	hypothetical protein	0.4	0.0	0.4	0.0	0.0	0.0		
BF1248	hypothetical protein	0.0	0.0	0.4	0.0	0.9	0.0	2.10	
BF1249	putative mobilisation protein	0.4	0.2	0.2	0.3	0.0	0.1	0.89	8.5E-01
BF1250	putative transmembrane mobilisation protein	4.5	5.0	5.2	3.6	3.1	3.0	0.66	1.1E-02
BF1251	hypothetical protein	124.7	126.2	151.1	82.8	91.1	74.7	0.62	1.2E-02
BF1252	hypothetical protein	358.7	391.0	431.2	250.2	290.3	215.1	0.64	2.5E-02
BF1253	hypothetical protein	0.7	0.5	0.3	0.2	0.3	0.1	0.42	1.4E-01
exc	putative transposon excision protein	16.4	14.9	20.5	7.9	10.6	10.7	0.56	2.9E-02
BF1255	hypothetical protein	329.6	304.8	380.8	236.5	259.1	228.7	0.72	2.4E-02
BF1256	hypothetical protein	1539.5	1617.5	1817.9	1334.1	1375.2	1192.1	0.78	4.0E-02
BF1257	hypothetical protein	0.6	2.7	2.8	0.0	0.0	0.0		
BF1258	hypothetical protein	0.4	0.8	0.6	0.2	0.3	0.2	0.45	3.2E-02
BF1259	hypothetical protein	1.0	0.0	0.0	0.0	0.6	0.0	0.58	
BF1260	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
bexA	putative transmembrane MatE family multidrug efflux transporter	0.4	0.4	0.6	0.5	0.8	0.5	1.26	3.5E-01
BF1263	putative transcriptional regulator, AraC family	11.1	17.1	13.4	9.5	13.8	10.0	0.80	3.4E-01
BF1264	hypothetical protein	6.7	6.2	5.7	14.4	13.5	9.6	1.99	1.6E-02
BF1265	hypothetical protein	14.6	12.7	9.6	29.0	29.7	24.6	2.28	1.0E-02
BF1266	possible AraC family transcriptional regulator	13.2	11.4	12.5	32.9	34.8	20.0	2.30	2.2E-02
BF1267	hypothetical protein	31.8	26.9	34.5	76.4	80.7	65.2	2.39	3.6E-03
BF1268	putative haloacid dehalogenase-like hydrolase	16.1	15.4	15.3	27.9	33.7	22.7	1.78	1.7E-02
BF1269	putative sugar O-acetyltransferase	18.2	23.8	14.6	22.3	22.8	24.8	1.26	2.5E-01
BF1270	putative AraC-family transcriptional regulatory protein	28.5	32.3	32.0	30.0	29.1	21.7	0.86	3.2E-01
BF1271	hypothetical protein	87.8	85.0	93.8	54.1	71.1	69.9	0.73	4.9E-02
BF1272	hypothetical protein	73.0	70.7	64.8	32.0	41.6	43.9	0.56	1.3E-02
BF1273	hypothetical protein	86.3	64.7	87.9	27.2	30.5	29.4	0.37	2.9E-03
BF1274	putative transmembrane protein	23.5	28.5	27.2	9.5	10.7	10.7	0.39	1.2E-03
BF1275	putative cNMP and DNA binding protein, possible regulator	109.6	109.3	90.0	28.8	35.5	21.1	0.27	5.0E-03
BF1277	putative zinc-binding alcohol dehydrogenase	86.3	64.5	64.6	77.8	87.3	111.2	1.28	2.2E-01
BF1278	putative SpoU-like rRNA methylase	38.6	30.9	35.8	38.7	45.0	42.7	1.20	1.2E-01
BF1279	putative thioredoxin	159.6	148.3	132.5	45.9	39.1	49.6	0.31	1.1E-03
BF1280	putative sulfatase protein	100.5	98.0	101.9	146.7	148.2	134.4	1.43	2.1E-03
BF1281	putative two-component sensor histidine kinase	28.6	31.2	33.6	20.5	23.2	20.1	0.68	1.1E-02
BF1282	putative transmembrane protein	7.3	6.3	7.9	5.8	6.5	5.7	0.84	1.2E-01

BF1283	putative transmembrane cation transport P type ATPase	28.0	19.8	22.1	16.9	24.2	23.6	0.93	7.0E-01
BF1284	hypothetical protein	116.0	91.2	98.1	73.9	79.0	97.6	0.82	2.0E-01
BF1285	putative outer membrane protein	831.7	741.2	906.1	1345.5	1305.0	1093.7	1.51	2.0E-02
BF1286	hypothetical protein	1.1	1.2	1.2	0.0	0.0	2.1	1.82	
BF1287	hypothetical protein	275.6	247.1	242.5	52.1	59.7	47.1	0.21	4.0E-04
purF	putative amidophosphoribosyltransferase precursor	291.7	246.2	297.3	210.6	203.0	203.4	0.74	1.9E-02
pepT	peptidase T	342.2	314.7	335.7	358.7	403.2	333.2	1.10	2.5E-01
gcvT	aminomethyltransferase	333.2	284.5	332.6	381.6	432.5	387.0	1.27	4.3E-02
BF1291	putative transmembrane protein	3.1	4.4	4.0	4.8	4.1	5.4	1.24	2.3E-01
BF1292	hypothetical protein	2.7	4.1	3.5	5.0	3.9	3.5	1.22	3.7E-01
BF1293	putative Na+/H+ family transporter	108.5	108.3	110.9	79.5	79.6	84.2	0.74	9.0E-04
BF1294	putative transmembrane protein	375.8	376.5	363.9	269.0	273.3	261.7	0.72	4.2E-04
BF1295	hypothetical protein	348.7	337.2	344.8	283.0	291.1	323.7	0.87	5.3E-02
rmlD	putative dTDP-dehydrorhamnose reductase	307.2	300.4	303.4	235.4	231.7	256.1	0.79	6.1E-03
prfC	putative peptide chain release factor 3	256.0	256.1	259.2	218.3	204.5	220.7	0.83	5.6E-03
BF1298	hypothetical protein	5.3	2.8	2.9	0.0	0.0	1.7	0.48	
BF1299	putative haloacid dehalogenase-like hydrolase	402.3	411.0	379.8	321.2	327.1	324.3	0.82	4.2E-03
BF1300	possible isochorismate synthase	206.3	201.8	184.5	191.9	157.4	219.0	0.95	7.1E-01
menD	putative menaquinone biosynthesis protein	210.3	227.4	212.8	183.7	179.1	176.5	0.83	7.1E-03
BF1302	hypothetical protein	117.3	125.9	103.4	110.0	106.6	110.1	0.95	4.7E-01
menB	putative naphthoate synthase	187.8	205.0	160.9	235.3	202.3	273.1	1.28	1.4E-01
BF1304	putative muconate cycloisomerase	91.3	94.6	72.4	72.3	66.5	86.3	0.87	3.7E-01
menE	putative O-succinylbenzoate--CoA ligase	60.3	61.9	51.3	45.2	47.2	56.9	0.86	2.3E-01
BF1306	putative endonuclease/exonuclease/phosphatase family protein	41.1	35.4	38.0	52.4	55.0	53.7	1.41	5.6E-03
BF1307	putative alpha-glucosidase protein	30.8	27.9	32.1	45.9	48.0	51.3	1.60	3.5E-03
BF1308	putative RNA polymerase ECF-type sigma factor	63.2	46.9	62.5	113.7	94.7	97.6	1.78	1.7E-02
BF1309	putative anti-sigma factor	196.8	190.4	180.4	571.4	489.1	703.1	3.07	2.3E-03
BF1310	**putative outer membrane protein**	**11.4**	**9.9**	**10.6**	**201.1**	**161.4**	**202.0**	**17.64**	**9.6E-05**
BF1311	hypothetical protein	6.9	6.8	5.9	127.4	96.5	145.7	18.67	3.0E-04
BF1312	possible endo-beta-N-acetylglucosaminidase	6.0	4.5	3.7	114.7	80.9	135.8	23.33	8.2E-04
BF1313	hypothetical protein	7.4	6.2	7.3	123.6	105.8	134.6	17.34	1.1E-04
BF1314	hypothetical protein	10.8	10.4	11.7	162.5	132.8	189.3	14.62	2.3E-04
BF1315	putative transmembrane protein	59.8	64.3	60.8	126.3	131.8	126.7	2.08	1.6E-04
BF1316	hypothetical protein	128.1	129.4	140.2	408.1	407.6	425.3	3.12	7.9E-05
BF1317	putative DNA-binding protein	532.7	760.7	682.1	2400.6	3679.8	2265.2	4.17	5.4E-03
oxyR	redox-sensitive transcriptional activator	141.4	139.1	131.4	160.2	138.8	177.5	1.15	1.9E-01
BF1319	hypothetical protein	129.6	130.6	141.7	163.7	171.5	132.9	1.16	2.1E-01
BF1320	putative RNA polymerase ECF-type sigma factor	48.5	48.9	47.1	46.6	41.7	54.0	0.98	8.3E-01
BF1321	hypothetical protein	94.9	95.0	94.2	93.6	88.8	110.3	1.03	7.6E-01

pflA	putative pyruvate formate-lyase 1 activating enzyme	456.2	522.2	490.6	256.2	265.4	238.3	0.52	1.2E-03
pflB	putative formate acetyltransferase 1	1750.5	1918.1	1819.6	1079.5	1004.9	948.1	0.55	1.3E-03
BF1324	hypothetical protein	1.1	0.0	1.2	0.0	0.0	0.0		
BFt16	tRNA-Ser-TGA	21.8	34.2	22.9	23.6	14.4	91.6	1.22	7.9E-01
BF1325	hypothetical protein	1.7	0.0	0.0	0.0	0.0	0.0		
BF1326	putative transmembrane protein	35.3	46.0	38.5	39.4	44.5	47.1	1.10	4.5E-01
BF1327	hypothetical protein	5.1	4.4	4.8	11.4	12.7	10.3	2.40	1.4E-03
BF1329	hypothetical protein	30.7	20.4	31.0	18.2	47.4	28.2	1.08	8.5E-01
BF1330	hypothetical protein	36.9	57.7	64.8	30.6	42.7	18.8	0.56	1.7E-01
BF1331	hypothetical protein	0.9	0.0	0.0	0.0	0.0	0.0		
BF1332	putative alpha-glucosidase II	55.0	46.9	50.0	96.0	93.8	84.4	1.81	2.8E-03
BF1333	hypothetical protein	5641.3	5431.5	5702.8	2092.2	1956.3	1836.3	0.35	2.0E-04
BF1334	putative transmembrane CorC/HlyC family transporter	674.5	691.5	588.0	354.4	407.5	392.5	0.59	4.8E-03
BF1335	putative peptidase	83.3	82.5	73.0	167.7	145.9	142.9	1.91	2.7E-03
BF1336	putative TonB dependent outer membrane protein	48.3	49.5	42.8	45.5	45.2	45.5	0.97	6.1E-01
BF1337	hypothetical protein	63.7	61.3	54.6	40.5	55.0	39.8	0.75	1.0E-01
BF1338	putative esterase	68.1	59.8	57.7	79.8	75.1	74.4	1.24	3.5E-02
BF1340	hypothetical protein	102.1	101.6	98.8	78.0	72.3	59.7	0.69	2.2E-02
BF1341	hypothetical protein	0.8	1.8	1.9	0.0	0.0	0.0		
metY	putative O-acetylhomoserine sulfhydrylase	7.0	5.3	3.0	1.6	1.7	2.8	0.41	7.0E-02
trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	22.6	21.2	24.5	8.8	6.2	8.3	0.34	3.3E-03
BF1344	putative transcriptional regulatory protein	180.6	161.4	174.8	124.6	116.0	118.8	0.70	3.3E-03
BF1345	hypothetical protein	2069.7	2234.8	2097.2	603.9	517.8	567.4	0.26	1.9E-04
BF1346	putative transmembrane Na+/H+ antiporter	83.8	87.5	80.2	49.4	43.5	46.6	0.55	1.2E-03
BF1347	putative transmembrane protein	124.8	110.0	112.4	85.9	79.7	83.9	0.72	6.0E-03
BF1348	putative transmembrane protein	45.2	43.3	43.9	37.8	37.6	40.6	0.88	2.1E-02
BF1349	putative transmembrane transporter permease protein	95.4	98.2	99.3	93.0	92.7	95.8	0.96	1.1E-01
BF1350	putative penicillin-binding protein	46.9	51.2	41.9	53.2	51.2	54.5	1.14	1.5E-01
BF1351	putative outer membrane protein	150.3	142.8	131.4	183.0	184.0	162.8	1.25	3.3E-02
BF1352	putative ATP-binding PP-loop protein	58.4	54.5	51.4	95.3	90.4	77.5	1.60	8.5E-03
BF1353	putative transmembrane ferrous transport fusion protein	215.7	160.3	159.8	130.1	143.8	124.2	0.75	9.0E-02
BF1354	hypothetical protein	83.7	49.3	61.1	24.3	24.0	27.8	0.40	1.2E-02
BFt17	tRNA-Cys-GCA	12.3	23.5	29.7	4.6	11.3	14.1	0.44	1.9E-01
BF1355	hypothetical protein	8.2	4.3	3.6	1.5	0.0	1.6	0.31	3.5E-02
BF1356	possible cell division protein	113.8	100.4	130.3	95.5	115.3	81.5	0.84	3.2E-01
BF1357	hypothetical protein	23.7	18.7	21.6	14.7	11.9	20.8	0.72	2.0E-01
BF1358	hypothetical protein	9.0	11.2	6.6	0.0	1.7	1.4	0.18	7.5E-03
BF1359	hypothetical protein	80.6	61.0	60.3	451.9	454.5	315.8	6.03	1.7E-03
BF1360	hypothetical protein	35.5	39.5	34.9	84.8	66.7	82.0	2.12	3.7E-03
BF1361	hypothetical protein	71.2	78.2	62.1	79.1	72.7	73.3	1.07	4.8E-01
BF1362	hypothetical protein	146.9	144.9	130.1	144.6	117.5	151.1	0.97	8.2E-01
BF1363	hypothetical protein	82.2	91.3	75.8	89.2	69.1	100.1	1.03	8.7E-01

BF1364	hypothetical protein	36.0	36.4	21.3	20.8	24.4	30.3	0.82	4.7E-01
upaY	putative LPS biosynthesis related transcriptional regulatory protein	700.0	657.1	683.2	328.4	401.5	380.6	0.54	2.8E-03
upaZ	putative LPS biosynthesis related transcriptional regulatory protein	648.9	641.5	660.4	459.0	480.6	383.9	0.68	1.2E-02
wzx3	putative LPS biosynthesis related flippase	323.9	350.8	368.1	173.0	205.7	157.0	0.51	5.4E-03
wcfM	putative LPS biosynthesis related UDP-galactopyranose mutase	285.7	240.5	314.3	179.5	207.5	165.1	0.66	3.1E-02
wcfN	putative LPS biosynthesis related glycosyltransferase	197.4	137.3	192.1	77.3	116.6	84.4	0.53	3.8E-02
wzy3	putative LPS biosynthesis related integral membrane protein	138.2	108.6	141.3	58.8	80.5	61.0	0.51	1.7E-02
wcfO	hypothetical protein	304.6	271.3	332.2	185.3	218.0	177.9	0.64	1.6E-02
wcfP	putative glycosyltransferase	289.7	256.0	330.0	175.3	232.1	170.8	0.66	4.9E-02
wcfQ	putative glycosyltransferase	341.1	278.4	366.0	195.0	236.7	188.2	0.63	2.8E-02
wcfR	putative DegT/DnrJ/EryC1/StrS family amino sugar synthetase	304.0	259.9	291.1	204.8	229.7	245.8	0.79	5.6E-02
wcfS	undecaprenyl-phosphate galactose phosphotransferase	441.7	382.1	413.1	276.2	327.3	289.6	0.72	1.8E-02
BFt18	tRNA-Thr-TGT	106.9	167.4	100.1	178.8	143.3	310.0	1.64	2.1E-01
pdiA	hypothetical protein	267.8	234.5	227.8	293.6	267.9	343.7	1.24	1.1E-01
BF1379	putative transmembrane sodium/sulfate transporter	292.6	295.2	267.3	280.8	263.3	299.9	0.99	8.4E-01
BF1380	putative methyltransferase protein	301.6	307.3	247.1	287.3	251.2	350.5	1.03	8.3E-01
BF1381	hypothetical protein	220.3	164.8	171.7	140.7	134.0	182.7	0.82	2.7E-01
BF1382	putative lactoylglutathione lyase	431.2	407.4	413.1	530.2	542.6	413.6	1.18	1.9E-01
BF1383	hypothetical protein	261.5	242.9	216.5	277.3	254.4	270.2	1.11	2.0E-01
BF1384	hypothetical protein	154.1	157.2	129.8	106.7	117.9	101.4	0.74	3.2E-02
pdxH	putative pyridoxamine 5'-phosphate oxidase	80.7	98.9	81.2	21.7	21.4	23.4	0.26	4.7E-04
BF1386	hypothetical protein	276.1	290.2	268.4	79.2	68.4	71.1	0.26	1.8E-04
BF1387	putative transmembrane AraC family transcriptional regulator	8.6	6.9	8.2	8.9	7.2	9.1	1.06	6.6E-01
BF1388	hypothetical protein	113.1	136.5	133.1	41.6	42.1	46.5	0.34	7.3E-04
ldhA	D-lactate dehydrogenase	875.8	984.3	920.6	268.0	277.4	251.7	0.29	1.6E-04
BF1390	putative outer membrane protein	434.8	491.7	540.3	459.6	452.0	494.3	0.96	6.6E-01
BF1393	hypothetical protein	75.9	79.9	75.3	23.3	17.7	18.9	0.26	7.1E-04
BF1394	putative RNA polymerase ECF-type sigma factor	174.4	146.4	161.1	513.3	754.3	573.0	3.78	2.2E-03
BF1395	putative transmembrane protein	64.5	59.3	45.7	34.6	29.4	29.3	0.56	1.8E-02
BF1396	putative ExsB family protein	73.8	61.7	56.8	41.0	38.4	42.1	0.64	1.3E-02
BF1397	putative GTP-cyclohydrolase protein	133.1	128.0	116.3	96.1	82.0	92.4	0.72	1.5E-02
BF1398	hypothetical protein	101.3	88.7	89.4	128.1	119.8	156.1	1.44	3.2E-02
BF1399	hypothetical protein	397.4	367.3	313.0	291.9	253.7	392.0	0.86	4.3E-01
nadC	putative nicotinate-nucleotide pyrophosphorylase [carboxylating] (quinolinate phosphoribosyltransferase [decarboxylating])	581.0	532.5	533.6	661.8	642.3	738.4	1.24	2.9E-02
BF1401	putative RNA polymerase ECF-type sigma factor	329.2	312.8	213.1	128.0	90.1	179.3	0.45	5.5E-02

BF1402	hypothetical protein	278.3	262.7	225.8	118.9	100.7	144.6	0.47	9.8E-03
BF1403	hypothetical protein	327.8	347.6	343.9	188.4	190.4	192.7	0.56	1.3E-04
BF1404	hypothetical protein	82.6	78.8	68.1	30.6	27.5	40.1	0.42	7.5E-03
BF1405	putative dioxygenase	428.2	443.9	344.8	242.3	184.6	336.6	0.61	9.8E-02
ald	putative alanine dehydrogenase	36.6	42.8	37.6	26.5	26.1	38.4	0.77	1.7E-01
BF1407	putative peptidase	83.6	88.8	72.1	92.6	69.8	114.4	1.11	6.0E-01
BF1408	putative dipeptidase	170.0	188.6	163.7	172.1	171.5	166.6	0.98	7.0E-01
BF1409	putative phosphoglucomutase	592.8	556.3	560.5	600.7	658.9	649.2	1.12	6.1E-02
BF1411	hypothetical protein	25.5	18.8	19.5	15.4	21.3	23.1	0.93	7.3E-01
BF1412	putative RNA polymerase ECF-type sigma factor	165.5	135.8	165.8	131.1	145.7	122.2	0.86	1.9E-01
BF1413	putative anti-sigma factor	45.6	46.5	46.3	42.0	47.6	41.6	0.95	3.4E-01
BF1415	putative outer membrane protein	6.5	7.6	7.7	12.6	13.9	13.0	1.81	2.6E-03
BF1416	putative outer membrane protein	4.3	3.0	3.0	6.6	9.3	6.0	2.13	2.8E-02
BF1417	hypothetical protein	3.7	5.2	6.7	11.1	9.9	10.9	2.11	2.9E-02
BF1418	putative alpha-galactosidase	1.5	1.7	1.6	3.1	5.3	4.2	2.55	1.1E-02
BF1419	hypothetical protein	2.5	0.9	1.8	0.8	1.9	1.6	0.84	7.5E-01
BF1421	putative histidine decarboxylase	121.0	127.6	112.0	29.8	25.7	33.2	0.25	6.1E-04
BF1422	putative NADH pyrophosphatase	50.3	46.3	41.9	47.6	32.6	39.8	0.86	3.5E-01
BF1423	putative ATP-binding ABC transporter protein	5.0	5.0	7.1	1.4	1.7	1.3	0.26	2.9E-03
BF1424	putative pyridine nucleotide-disulfide oxidoreductase	530.0	651.4	525.6	229.8	197.3	246.0	0.39	2.8E-03
BF1425	putative transmembrane protein	69.6	67.2	66.4	124.0	150.1	127.2	1.97	2.0E-03
BF1426	putative AraC family transcriptional regulatory protein	112.2	109.8	110.9	219.6	234.5	216.3	2.01	1.7E-04
cdd	putative cytidine deaminase	131.0	143.5	111.4	263.2	234.8	235.7	1.91	5.2E-03
BF1428	putative hemagglutinin	156.5	128.3	118.3	79.7	74.0	114.0	0.66	8.9E-02
BF1429	hypothetical protein	19.3	16.1	13.0	11.9	10.7	22.6	0.89	7.4E-01
BF1430	putative ABC transporter component protein	13.4	12.0	9.8	5.8	3.9	6.0	0.44	1.7E-02
BF1431	putative permease component of ABC transporter	1.7	3.3	1.5	0.9	0.8	0.9	0.44	4.9E-02
BF1432	putative ABC transporter permease component	2.1	2.8	2.6	0.5	1.0	1.1	0.33	2.1E-02
BF1433	putative ABC transporter permease component	1.3	1.7	1.0	0.8	0.8	0.8	0.58	3.8E-02
BF1434	putative ABC transporter permease component	2.9	3.1	3.2	1.2	1.3	1.3	0.41	4.1E-04
BF1435	putative ABC transporter permease component	2.8	2.4	1.8	1.3	1.1	1.0	0.49	2.0E-02
BF1436	putative ABC transporter permease component	8.5	8.6	8.2	10.9	9.5	9.4	1.18	5.1E-02
BF1437	putative AraC family transcriptional regulator	52.2	53.6	56.1	98.1	107.4	81.3	1.76	7.9E-03
BF1438	putative ATP-binding component of ABC transporter	1.1	0.8	0.6	0.0	0.3	0.0	0.38	
BF1439	putative ABC transporter permease component	1.0	1.2	1.1	0.0	0.5	0.3	0.33	6.2E-02
BF1443	putative ABC transport system ATP-binding protein	5.6	5.1	4.4	1.5	1.2	1.0	0.25	2.3E-03

BF1444	hypothetical protein	4.1	4.7	3.6	1.6	1.9	2.9	0.50	4.4E-02
BF1445	putative ABC transporter permease component	4.1	2.7	1.9	1.7	2.8	2.0	0.75	4.1E-01
BF1446	putative ABC transporter permease component	1.8	2.6	2.5	1.6	1.8	1.5	0.72	8.1E-02
BF1447	putative two-component system sensor histidine kinase	35.2	36.8	34.9	47.0	44.5	46.4	1.29	2.1E-03
BF1448	hypothetical protein	6.5	10.0	5.2	12.3	12.9	19.7	2.11	6.6E-02
BF1449	putative outer membrane protein	2.8	2.1	2.5	0.4	0.8	0.3	0.18	1.7E-02
BF1451	putative two component sensor histidine kinase protein	44.2	44.7	40.6	24.2	23.5	23.6	0.55	4.8E-04
BF1452	aspartate aminotransferase	90.6	97.9	80.7	38.4	31.3	34.8	0.39	1.7E-03
BF1453	putative transmembrane protein	50.6	59.1	46.1	17.7	12.3	20.9	0.32	8.3E-03
BF1454	putative transmembrane protein	20.0	19.8	20.9	14.0	13.7	20.3	0.78	1.7E-01
BF1457	putative type I restriction enzyme	82.7	81.1	89.6	79.9	85.3	75.1	0.95	4.0E-01
BF1458	putative type I RM modification enzyme	130.7	123.8	135.3	120.7	129.9	106.7	0.91	2.9E-01
BF1459	putative DNA-binding protein	113.6	118.9	129.7	99.2	109.1	87.1	0.81	8.6E-02
BF1460	hypothetical protein	63.6	63.4	66.1	49.8	53.9	55.7	0.82	1.5E-02
BF1461	putative type I restriction enzyme specificity protein	47.8	46.3	49.7	40.7	43.8	37.7	0.85	4.7E-02
BF1464	hypothetical protein	0.0	5.5	0.0	1.6	0.0	0.0	0.30	
BF1465	hypothetical protein	2.0	0.5	2.2	1.0	2.3	1.9	1.22	7.8E-01
BF1466	hypothetical protein	0.0	2.7	0.0	1.2	1.5	0.0	0.49	
BF1467	hypothetical protein	0.4	0.4	0.8	1.0	0.8	0.7	1.75	1.6E-01
BF1468	putative bacteriophage-related replication protein	1.7	3.0	1.4	2.1	0.9	4.7	1.07	9.2E-01
BF1469	putative transmembrane protein	0.9	2.4	0.7	1.8	0.7	0.9	0.92	8.9E-01
BF1470	putative DNA primase	3.1	2.9	2.3	1.8	0.9	2.6	0.59	2.4E-01
BF1471	hypothetical protein	0.7	1.0	2.1	0.7	0.6	1.6	0.73	6.0E-01
BF1473	hypothetical protein	1.4	2.1	1.8	1.1	0.3	2.1	0.52	3.8E-01
BF1474	hypothetical protein	1.0	0.0	0.6	1.0	0.6	1.0	1.09	8.6E-01
BF1475	hypothetical protein	1.2	0.7	0.7	1.2	0.0	2.4	2.03	2.4E-01
BF1476	hypothetical protein	0.6	4.1	0.0	1.2	1.5	2.5	1.01	9.9E-01
BF1477	hypothetical protein	9.8	9.4	11.9	12.1	5.7	8.5	0.81	4.8E-01
BF1478	hypothetical protein	0.3	1.8	0.7	0.3	0.4	1.0	0.65	5.7E-01
BF1479	hypothetical protein	2.4	1.9	1.3	1.7	0.0	1.7	0.94	7.9E-01
BF1480	hypothetical protein	3.6	2.4	4.3	3.1	3.8	2.5	0.92	7.6E-01
BF1481	hypothetical protein	2.1	2.2	1.3	2.2	1.4	2.1	1.02	9.6E-01
BF1482	hypothetical protein	2.0	1.5	1.8	0.4	1.2	1.0	0.43	1.2E-01
BF1483	hypothetical protein	1.6	2.9	2.6	0.9	1.5	1.9	0.58	1.9E-01
BF1484	hypothetical protein	3.0	2.8	1.7	1.0	0.9	1.5	0.46	5.2E-02
BF1485	hypothetical protein	2.2	2.8	2.4	1.7	0.8	3.8	0.69	5.4E-01
BF1486	putative transmembrane protein	2.3	3.6	0.6	0.5	1.3	3.3	0.77	7.8E-01
BF1487	putative transmembrane protein	2.6	2.2	0.6	2.0	1.2	0.5	0.71	6.8E-01
BF1488	putative conserved protein found in conjugate transposon	1.6	2.2	1.0	0.9	0.8	1.4	0.65	2.7E-01
BF1489	putative conserved TraI-like protein found in conjugate transposon	0.3	1.8	0.4	0.0	0.4	0.6	0.83	8.1E-01
BF1490	putative transmembrane protein	2.0	1.6	1.9	0.7	0.3	0.9	0.32	6.1E-02
BF1491	putative transmembrane protein	1.9	2.3	1.8	1.0	0.0	0.8	0.45	3.1E-02

BF1492	conserved hypothetical TraM-like protein found in conjugate transposon	0.2	1.7	1.0	0.3	0.0	1.2	0.95	9.7E-01
BF1493	hypothetical protein	2.5	3.9	6.7	12.8	2.8	9.4	1.74	4.4E-01
BF1494	putative transmembrane protein	28.3	28.0	32.9	34.6	35.0	34.7	1.17	6.7E-02
BF1495	conserved hypothetical TraN-like protein found in conjugate transposon	1.5	1.6	0.5	0.9	0.4	1.0	0.63	4.8E-01
BF1496	putative peptidase	1.9	2.7	0.4	0.9	0.4	2.5	0.77	8.1E-01
BF1497	hypothetical protein	0.5	1.1	0.6	0.0	0.0	1.0	1.44	
BF1498	putative DNA-binding protein	0.6	0.0	0.6	0.5	0.7	0.0	1.00	9.9E-01
BF1499	hypothetical protein	6.5	5.2	6.7	4.2	4.3	3.8	0.67	2.2E-02
BF1500	hypothetical protein	111.8	110.8	83.9	97.8	85.0	118.1	0.98	9.2E-01
BF1501	hypothetical protein	68.3	65.9	48.8	77.9	57.8	88.6	1.22	3.6E-01
BF1502	putative protein involved in partitioning	68.1	51.5	48.5	50.1	32.8	89.1	0.95	9.0E-01
BF1503	hypothetical protein	5.8	8.5	7.2	3.4	7.6	5.6	0.74	3.8E-01
BF1504	hypothetical protein	2.7	2.4	2.1	1.8	1.4	2.8	0.81	4.4E-01
BF1505	hypothetical protein	0.0	1.2	0.0	0.0	1.3	1.0	0.99	
BF1506	hypothetical protein	1.9	2.0	1.0	0.9	1.1	1.8	0.77	4.9E-01
BF1507	hypothetical protein	0.0	1.3	0.0	1.2	0.0	0.0	0.89	
cbh	putative choloylglycine hydrolase	463.5	478.5	429.2	93.7	88.8	100.3	0.21	1.0E-04
BF1509	hypothetical protein	234.8	287.8	256.1	36.0	45.6	39.5	0.16	3.7E-04
BF1510	hypothetical protein	1.9	3.1	4.1	18.0	17.4	16.7	6.00	4.8E-03
BF1511	putative outer membrane protein	2.8	2.5	1.5	56.5	48.4	44.9	22.41	7.2E-04
BF1512	**putative outer membrane protein**	**1.0**	**1.1**	**1.2**	**51.7**	**45.2**	**42.6**	**42.22**	**2.4E-05**
BF1513	putative anti-sigma factor	5.3	4.5	3.2	14.0	8.3	8.1	2.29	4.2E-02
BF1514	putative RNA polymerase ECF-type sigma factor	9.9	7.3	7.9	41.8	42.0	37.4	4.85	6.8E-04
BF1516	hypothetical protein	3.5	3.7	2.9	1.7	1.0	3.8	0.55	2.7E-01
BF1517	hypothetical protein	2.3	3.8	1.9	3.3	2.6	3.9	1.26	4.6E-01
BF1518	hypothetical protein	2.9	2.3	1.7	2.0	1.6	2.8	0.92	7.8E-01
BF1519	hypothetical protein	0.5	0.0	0.0	0.9	0.6	1.4	1.85	
mobC	mobilisation protein C	8.9	6.8	7.0	5.0	4.3	9.6	0.79	4.8E-01
mobB	mobilisation protein B	32.1	25.9	23.5	42.4	38.0	56.2	1.67	4.8E-02
mobA	mobilisation protein A	31.8	25.6	25.0	49.3	42.5	54.9	1.78	1.4E-02
BF1523	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF1524	hypothetical protein	45.6	47.9	41.7	22.8	23.8	27.0	0.54	3.1E-03
BF1525	hypothetical protein	8032.9	11179.6	10507.3	8148.4	9011.1	16349.0	1.08	8.0E-01
BF1526	hypothetical protein	25.2	15.4	26.1	16.7	12.4	10.3	0.59	1.2E-01
BF1527	putative cation efflux protein	15.2	18.0	18.4	6.1	5.2	7.9	0.37	6.0E-03
satG	putative acetyltransferase	6.0	4.9	6.0	2.2	1.0	1.6	0.27	1.4E-02
rteA	putative two component system sensor kinase	3.6	3.0	3.4	2.5	2.1	2.4	0.70	2.5E-02
rteB	putative two-component system response regulator	12.4	14.2	9.7	7.8	4.9	15.0	0.70	4.2E-01
BF1531	hypothetical protein	177.2	173.6	205.1	173.8	184.4	176.1	0.96	6.1E-01
BF1532	hypothetical protein	433.4	402.9	462.4	407.8	453.3	351.6	0.93	5.1E-01
BF1533	putative integrase	269.0	243.8	252.4	106.4	106.2	109.1	0.42	1.5E-04
tnpA	putative transposase for insertion sequence element IS21-like	16.7	15.8	10.3	8.1	6.8	11.7	0.62	1.4E-01
tnpB	insertion sequence IS21-like putative ATP-binding protein	5.3	5.2	5.9	5.7	4.6	4.7	0.91	3.6E-01
BF1536	hypothetical protein	14.9	20.1	22.2	17.5	22.4	10.9	0.86	6.4E-01

BF1537	putative type I restriction-modification specificity protein	12.8	15.4	14.2	5.1	7.0	5.9	0.42	4.4E-03
BF1538	putative phage integrase/recombinase	36.1	38.6	39.2	19.9	22.0	36.5	0.66	1.4E-01
BF1539	hypothetical protein	405.2	418.5	397.2	200.7	246.7	214.4	0.54	2.7E-03
BF1540	hypothetical protein	767.1	713.1	790.0	443.9	523.4	444.2	0.62	5.5E-03
BF1541	hypothetical protein	418.4	340.3	435.3	283.5	350.4	308.2	0.79	1.2E-01
BF1542	hypothetical protein	499.8	422.7	530.1	482.8	547.8	463.0	1.03	7.9E-01
BF1543	hypothetical protein	232.7	213.1	272.2	309.4	409.6	295.2	1.40	8.6E-02
BF1544	hypothetical protein	292.1	345.4	341.5	430.8	493.6	400.6	1.35	4.0E-02
BF1545	hypothetical protein	13.8	12.2	13.3	21.9	23.8	18.0	1.62	1.5E-02
BF1546	hypothetical protein	16.7	13.2	15.5	31.0	38.1	31.8	2.22	4.2E-03
BF1547	hypothetical protein	0.8	1.6	2.5	0.0	0.0	0.7	0.50	
BF1548	hypothetical protein	3.7	2.6	4.0	3.5	1.4	1.2	0.53	2.1E-01
upfY	putative transcriptional regulator	5.6	5.9	5.8	1.4	2.4	3.7	0.40	5.4E-02
upfZ	putative transcriptional regulator	5.5	6.6	5.2	2.4	5.9	3.9	0.66	2.6E-01
rmlA1	putative glucose-1-phosphate thymidyl transferase	5.9	4.8	6.3	2.8	3.7	3.2	0.57	1.7E-02
rmlC2	putative dTDP-4-dehydrorhamnose 3,5 epimerase	5.5	3.9	5.4	2.0	2.5	2.4	0.47	1.1E-02
BF1553	hypothetical protein	7.0	5.1	9.2	1.7	2.0	2.1	0.28	7.0E-03
BF1554	putative nucleotide-sugar dehydrogenase	6.7	7.1	9.6	4.2	5.4	4.5	0.61	4.0E-02
BF1555	putative dNTP-hexose dehydratase-epimerase	10.8	14.5	15.2	6.7	6.7	5.6	0.47	1.0E-02
BF1556	putative polysaccharide transporter/flippase	8.2	7.3	6.9	3.4	3.4	2.1	0.39	1.2E-02
BF1557	putative glucosyltransferase	6.9	5.3	8.6	2.7	2.6	2.9	0.41	9.7E-03
BF1558	putative glyocosyltransferase protein	6.6	5.3	5.5	3.8	6.0	3.1	0.72	2.4E-01
BF1559	hypothetical protein	6.5	3.5	6.9	2.6	2.8	1.8	0.43	5.5E-02
BF1560	putative glycosyltransferase	3.8	4.0	5.6	1.3	2.0	1.5	0.36	1.4E-02
BF1561	putative transmembrane protein	5.0	3.5	6.5	1.8	2.0	0.4	0.24	8.1E-02
BF1562	putative glycosyltransferase O-antigen related protein	4.3	4.6	6.2	2.1	1.8	2.0	0.40	5.7E-03
BF1563	putative lipopolysaccharide biosynthesis glycosyltransferase	10.8	8.5	13.8	4.1	3.2	2.7	0.30	8.8E-03
BF1564	putative DNTP-hexose dehydratase-epimerase	8.3	6.0	5.8	2.9	4.0	4.5	0.57	5.5E-02
BF1565	putative glycosyltransferase	4.3	4.4	4.3	0.5	1.5	1.8	0.26	4.5E-02
rne	putative ribonuclease E	844.5	888.4	888.4	663.1	649.7	618.9	0.74	1.7E-03
BF1567	hypothetical protein	2449.5	2294.6	3294.8	1898.9	1979.2	1483.4	0.67	8.0E-02
hup1	putative histone-like DNA-binding protein HU1	3130.8	2905.8	3720.6	2000.2	2103.6	1755.9	0.60	1.3E-02
BF1569	putative A/G-specific adenine glycosylase	91.9	80.0	76.3	79.9	72.2	86.3	0.96	6.9E-01
BF1570	putative arylsulfatase	99.5	106.5	99.3	194.2	197.0	182.4	1.88	4.4E-04
ssb	putative single-strand binding protein	385.6	363.5	359.0	423.0	433.5	411.9	1.15	1.7E-02
BF1572	putative transmembrane CorC/HlyC family transporter associated protein	202.7	206.7	209.9	238.7	263.6	244.0	1.20	1.2E-02
BF1573	hypothetical protein	170.7	167.4	181.9	174.7	184.0	200.1	1.07	2.7E-01
BF1574	hypothetical protein	68.7	57.1	55.9	49.5	52.0	76.0	0.96	8.5E-01
BF1577	hypothetical protein	17.4	14.6	19.1	3.3	2.8	3.5	0.19	6.8E-04

BF1578	hypothetical protein	12.4	16.9	16.6	2.2	2.5	1.9	0.14	7.8E-04
BF1579	hypothetical protein	12.2	12.4	11.9	2.4	3.0	2.6	0.22	2.1E-04
BF1580	hypothetical protein	19.8	23.7	27.8	10.9	11.1	11.6	0.48	5.9E-03
BF1581	hypothetical protein	261.5	304.9	336.8	355.1	364.7	281.0	1.11	4.8E-01
BF1582	hypothetical protein	104.8	123.2	109.7	168.6	147.3	178.6	1.46	1.7E-02
btuB	putative vitamin B12 receptor	81.6	93.1	90.9	137.8	114.7	156.4	1.53	2.7E-02
BF1584	hypothetical protein	817.7	1141.5	1023.0	1810.8	1464.6	2307.7	1.86	3.8E-02
Cobalamin	RF00174	0.0	0.0	0.0	0.0	0.0	2.8		
BF1587	hypothetical protein	114.6	108.3	104.6	112.7	110.4	108.7	1.01	7.1E-01
BF1588	hypothetical protein	44.4	45.0	42.9	47.2	45.2	55.6	1.11	2.3E-01
BF1589	putative two-component histidine kinase sensor protein	32.5	40.3	36.7	29.7	31.8	33.5	0.87	1.7E-01
BF1590	putative two-component response regulator	69.0	79.4	71.8	69.3	71.1	73.1	0.97	6.1E-01
BF1592	hypothetical protein	91.2	98.7	89.3	49.9	49.4	51.7	0.54	5.0E-04
BF1593	hypothetical protein	426.4	361.1	394.4	266.4	274.4	294.3	0.71	1.0E-02
BF1594	hypothetical protein	266.6	269.7	235.7	250.9	256.8	323.3	1.07	5.7E-01
BF1595	hypothetical protein	187.7	162.2	154.8	225.4	209.0	238.5	1.34	2.9E-02
BF1596	putative ATP-binding component of ABC transporter	190.1	198.9	189.7	235.3	230.6	227.7	1.20	2.6E-03
BF1597	possible histidinol-phosphatase	189.1	190.2	181.5	193.5	199.6	185.9	1.03	3.5E-01
BF1598	putative endo-beta-galactosidase	91.8	98.5	98.0	184.5	172.8	168.9	1.83	5.9E-04
BF1599	putative chondroitinase AC precursor	29.5	31.0	31.3	64.7	59.3	60.6	2.01	3.2E-04
BF1600	hypothetical protein	178.9	190.3	162.2	139.5	137.5	135.4	0.78	1.5E-02
BF1601	aspartate aminotransferase	235.6	265.9	260.4	248.9	248.2	254.9	0.99	8.2E-01
BF1602	putative transmembrane permease	160.3	175.5	167.3	149.4	142.6	149.2	0.88	2.6E-02
BF1603	putative transmembrane glycosyltransferase	120.5	124.3	118.4	103.1	106.4	121.4	0.91	1.9E-01
BF1604	putative transmembrane protein	167.3	198.6	185.2	98.4	109.8	104.4	0.57	2.9E-03
BF1605	putative two-component system sensor histidine kinase protein	7.5	7.7	9.0	24.1	21.7	25.0	2.94	8.5E-04
BF1606	putative two-component response regulator transcriptional regulatory protein	16.5	16.6	13.4	28.0	19.5	30.1	1.65	5.3E-02
BF1607	putative outer membrane protein	0.5	0.6	0.7	0.4	0.8	0.4	0.80	4.9E-01
BF1608	putative HlyD-family transporter component	0.4	1.2	0.0	0.5	0.3	0.9	0.77	7.5E-01
BF1609	putative FtsX-related transporter permease	3.6	2.5	2.2	2.6	3.1	2.7	1.04	8.4E-01
BF1610	putative ABC transport system ATP-binding protein	9.1	9.4	5.7	14.7	10.3	11.3	1.52	1.5E-01
BF1611	putative FtsX-related transmembrane transport protein	22.4	22.5	20.2	16.1	17.0	16.6	0.76	6.5E-03
ndh	putative NADH dehydrogenase, FAD-containing subunit	704.9	769.9	659.9	335.5	267.0	368.9	0.45	5.7E-03
BF1613	hypothetical protein	45.7	59.1	61.2	38.2	27.7	30.3	0.58	3.0E-02
bioD	dithiobiotin synthetase	7.4	9.9	8.8	18.8	14.0	20.0	2.01	1.7E-02
BF1615	putative biotin synthesis-related fusion protein	2.6	2.2	2.0	4.9	5.3	3.7	2.03	1.7E-02
bioF	8-amino-7-oxononanoate synthase	5.2	4.1	3.9	5.9	6.3	6.7	1.44	3.5E-02

bioA	putative adenosylmethionine-8-amino-7-oxononanoate aminotransferase	7.6	6.8	6.6	12.7	10.9	13.9	1.77	7.0E-03
BF1618	putative outer membrane receptor protein	83.7	89.8	75.0	24.2	21.2	24.8	0.28	5.6E-04
BF1619	hypothetical protein	86.7	92.7	87.6	24.3	21.1	24.9	0.26	2.5E-04
lctP	putative L-lactate permease	70.8	82.5	69.2	33.2	41.0	35.1	0.49	4.1E-03
BF1621	hypothetical protein	180.7	210.5	188.0	59.8	50.8	53.5	0.28	4.6E-04
BF1622	hypothetical protein	222.8	251.2	222.4	56.9	48.8	46.5	0.22	3.6E-04
BF1623	putative propionyl-CoA carboxylase	65.3	84.8	63.1	48.9	39.0	61.5	0.69	1.3E-01
accC1	putative biotin carboxylase 1	26.0	29.0	29.7	29.4	26.9	39.2	1.11	4.9E-01
BF1625	putative biotin-requiring enzyme	24.2	16.1	14.1	14.3	16.3	23.9	1.01	9.8E-01
BF1626	hypothetical protein	13.8	17.2	13.5	4.0	3.1	3.1	0.23	1.3E-03
BF1627	hypothetical protein	148.0	152.4	149.4	31.5	35.1	36.4	0.23	1.0E-04
BF1628	putative ATP/GTP-binding protein	963.8	914.7	886.2	165.2	205.3	190.2	0.20	2.7E-04
BF1629	hypothetical protein	578.9	647.7	612.4	177.5	173.3	174.9	0.29	6.5E-05
BF1630	hypothetical protein	215.7	233.9	185.9	73.5	79.0	70.3	0.35	1.0E-03
lpd	putative dihydrolipoamide dehydrogenase	228.6	186.9	187.2	56.0	56.6	86.4	0.32	6.5E-03
lplA	putative lipoate-protein ligase	214.4	199.5	206.8	73.6	62.6	82.2	0.35	1.3E-03
BF1635	putative dihydrolipoamide acetyltransferase	499.3	603.4	447.7	260.9	197.4	363.5	0.52	5.2E-02
BF1636	putative 2-oxoisovalerate dehydrogenase, alpha and beta subunits	218.3	265.7	214.4	86.0	85.4	98.8	0.39	1.8E-03
BF1637	flavodoxin	255.1	298.0	266.7	119.4	110.0	120.9	0.43	7.6E-04
prmA	ribosomal protein L11 methyltransferase	152.2	142.5	142.7	142.2	125.3	149.0	0.95	4.9E-01
BF1639	hypothetical protein	26.2	23.3	26.5	5.6	5.6	5.6	0.22	7.1E-05
BF1640	hypothetical protein	144.1	155.1	186.8	279.1	287.2	234.8	1.65	1.7E-02
BF1641	hypothetical protein	167.2	160.3	174.3	335.7	372.2	282.1	1.96	4.9E-03
BF1642	hypothetical protein	51.7	39.4	59.0	66.5	63.2	74.2	1.37	1.1E-01
BF1643	hypothetical protein	443.2	268.8	305.6	385.8	452.2	644.8	1.46	2.1E-01
BF1644	hypothetical protein	600.0	486.5	591.6	884.3	954.2	792.9	1.57	1.6E-02
BF1645	putative nucleotide deaminase	142.9	146.4	139.5	194.8	186.8	192.1	1.34	7.3E-04
BF1646	hypothetical protein	129.5	130.0	124.8	85.9	86.8	85.8	0.67	1.5E-04
BF1647	hypothetical protein	84.3	79.7	77.3	39.8	28.1	28.6	0.40	4.8E-03
BF1648	hypothetical protein	75.8	78.0	68.0	25.9	24.9	26.2	0.35	2.6E-04
BF1649	putative RNA polymerase ECF-type sigma factor	105.8	108.2	83.0	33.0	27.0	41.8	0.34	6.7E-03
BF1650	putative GFO/IDH/MocA-family oxidoreductase	122.1	127.4	118.5	135.7	118.2	133.6	1.05	4.3E-01
BF1651	putative solute-binding protein precursor	45.6	47.5	47.8	69.7	55.7	77.6	1.43	4.2E-02
BF1652	hypothetical protein	140.5	143.2	132.0	132.5	118.4	122.7	0.90	9.5E-02
BF1652A	putative 2-oxoglutarate synthase subunit	805.6	790.8	820.5	605.8	579.0	576.4	0.73	6.4E-04
BF1653	putative 2-oxoglutarate synthase subunit	448.1	512.3	468.9	424.5	399.5	397.0	0.86	4.6E-02
BF1655	hypothetical protein	629.8	682.8	630.9	468.1	494.3	417.4	0.71	1.0E-02
BF1656	2-oxoglutarate ferredoxin oxidoreductase	448.4	489.9	426.5	478.1	415.2	480.3	1.01	9.5E-01

BF1657	putative ferredoxin	338.2	338.3	305.1	303.7	297.5	323.7	0.94	3.1E-01
BF1658	hypothetical protein	386.8	387.6	340.0	205.4	219.1	238.6	0.59	4.1E-03
rpiB	putative ribose 5-phosphate isomerase	377.2	420.2	363.6	283.0	275.7	330.0	0.76	3.7E-02
tktB	putative transketolase	749.2	781.0	721.1	689.5	620.0	672.1	0.88	5.6E-02
galK	putative galactokinase	519.7	550.7	556.0	1770.2	1888.3	1760.0	3.33	5.8E-05
BF1662	putative transmembrane glucose/galactose transporter	451.6	493.6	501.0	1355.7	1417.5	1195.7	2.74	6.3E-04
BF1663	putative aldose 1-epimerase precursor	322.6	310.3	301.9	822.8	829.7	754.0	2.57	2.0E-04
BF1664	putative mannose-6-phosphate isomerase	896.4	750.2	819.0	2225.3	2392.8	2272.7	2.80	4.9E-04
BF1665	hypothetical protein	286.7	257.4	261.3	210.3	256.1	232.8	0.87	1.4E-01
BF1666	putative transmembrane protein	1647.4	1925.6	2028.0	1326.0	1766.0	1596.1	0.83	2.2E-01
BF1667	hypothetical protein	4209.7	4193.5	4291.3	3562.1	3989.5	3284.0	0.85	7.8E-02
BF1668	putative ATP-dependent RNA helicase	619.9	620.7	642.1	192.1	198.4	229.4	0.33	4.0E-04
BF1669	putative short-chain dehydrogenase	247.2	234.2	245.5	239.7	247.5	249.6	1.01	6.2E-01
BF1670	hypothetical protein	821.3	908.3	927.8	1072.3	1103.1	1135.3	1.25	1.5E-02
BF1671	hypothetical protein	66.1	65.7	69.0	20.4	25.1	34.7	0.39	1.1E-02
BF1672	putative beta-galactosidase	51.4	58.2	54.2	49.4	52.8	48.0	0.92	1.8E-01
BF1673	putative sulfite synthesis pathway protein	224.9	209.5	200.9	220.7	207.5	233.1	1.04	5.1E-01
BF1674	possible Na+/sulfite symporter	113.0	98.1	99.8	113.4	103.0	100.0	1.02	8.1E-01
cysC	putative adenylylsulfate kinase	96.2	83.5	90.3	139.2	139.5	145.9	1.58	2.3E-03
cysD	sulfate adenylyltransferase subunit 2	141.6	135.0	134.4	154.4	157.9	156.5	1.14	6.0E-03
cysN	sulfate adenylyltransferase subunit 1	254.9	237.3	247.1	215.0	230.3	221.0	0.90	4.2E-02
BF1678	possible sulfotransferase	159.7	156.0	151.8	122.2	135.1	115.6	0.80	2.0E-02
BF1679	hypothetical protein	214.2	191.4	213.3	151.8	167.4	154.2	0.77	1.3E-02
BF1680	hypothetical protein	85.8	80.0	76.9	49.0	65.5	72.1	0.76	1.3E-01
BF1681	putative outer membrane protein	4.8	9.7	8.6	3.5	3.3	4.5	0.50	7.4E-02
BF1682	hypothetical protein	2.6	3.0	3.6	1.8	2.3	0.4	0.40	2.2E-01
BF1683	hypothetical protein	3.3	4.1	2.6	2.3	2.8	2.8	0.79	2.5E-01
BF1684	hypothetical protein	0.2	0.6	0.2	0.2	0.6	0.2	0.97	9.6E-01
BF1685	putative bacteriophage integrase	14.7	15.5	16.6	4.4	4.0	3.7	0.26	2.5E-04
BF1686	hypothetical protein	249.7	193.5	221.4	203.5	228.8	204.6	0.96	7.2E-01
BF1687	hypothetical protein	2766.1	3009.1	3078.3	3578.6	3687.3	2933.2	1.15	2.1E-01
BF1688	hypothetical protein	2125.2	2310.3	2357.8	2591.3	2669.9	2225.7	1.10	2.8E-01
BF1689	putative outer membrane protein	2411.0	2638.9	2612.7	2701.0	2858.4	2530.8	1.06	3.7E-01
ruvX	Holliday junction resolvase-like protein	226.0	233.1	214.8	127.9	125.9	154.3	0.60	6.2E-03
def	peptide deformylase	453.4	403.8	456.9	410.7	404.9	373.3	0.91	1.7E-01
BF1692	hypothetical protein	20.3	17.1	23.1	20.5	25.5	20.2	1.09	5.5E-01
BF1693	putative exported Tpr repeat-family protein	208.7	207.9	206.4	138.4	156.4	144.8	0.70	2.8E-03
thrS	putative threonyl-tRNA synthetase	761.8	733.7	750.5	784.6	788.8	725.0	1.02	5.6E-01
infC	translation initiation factor IF-3	1445.1	1331.3	1543.3	946.0	962.7	840.6	0.64	5.7E-03
rpmI	putative 50S ribosomal protein L35	4156.4	4778.5	4752.5	3443.6	3810.3	3647.1	0.80	2.9E-02
rplT	50S ribosomal protein L20	4676.2	5137.1	5632.5	3948.4	4297.1	4350.1	0.82	5.5E-02
BF1698	putative ferredoxin	303.9	257.4	274.3	176.1	208.4	191.3	0.69	1.4E-02
BF1699	xanthine phosphoribosyltransferase	133.7	128.1	140.4	190.4	214.7	194.8	1.49	3.7E-03
paaK2	putative phenylacetate-coenzyme A ligase	52.7	50.9	51.0	94.5	98.7	87.6	1.81	6.8E-04
BF1701	putative indolepyruvate oxidoreductase subunit	174.6	193.5	189.7	330.2	295.4	278.9	1.62	4.5E-03

BF1702	putative indolepyruvate oxidoreductase/indolepyruvate ferredoxin oxidoreductase	184.2	184.4	190.2	304.1	285.6	252.7	1.50	6.0E-03
BF1703	putative aminodeoxychorismate lyase	51.5	55.0	55.0	52.4	49.0	40.9	0.88	2.2E-01
BF1704	putative endonuclease	13.5	19.0	15.3	17.9	14.6	15.8	1.02	9.0E-01
BF1705	putative surface antigen	249.9	259.7	269.8	117.4	128.1	113.6	0.46	4.9E-04
BFt19	tRNA-Thr-CGT	89.4	138.8	71.9	71.0	47.6	125.2	0.78	5.8E-01
BF1706	putative capsular biosynthesis protein	42.7	41.8	45.6	39.0	54.4	44.0	1.05	7.3E-01
BF1707	putative capsule polysaccharide export protein	273.0	204.1	251.8	180.4	195.8	186.8	0.78	8.0E-02
BF1708	hypothetical protein	402.2	361.4	411.1	393.2	446.6	394.1	1.05	5.2E-01
BF1709	putative LPS-related regulatory protein	455.3	415.3	459.6	508.3	554.4	498.6	1.17	4.6E-02
BF1710	possible O-antigen related protein	373.4	386.7	406.2	408.6	425.7	382.6	1.04	4.2E-01
BF1711	putative ROK family transcriptional repressor protein	232.5	218.6	246.2	286.1	345.7	264.9	1.28	7.6E-02
BF1712	putative N-acetylneuraminate lyase	67.9	61.9	65.8	596.6	714.8	524.8	9.32	2.6E-04
BF1713	hypothetical protein	91.3	93.1	96.2	716.5	841.3	598.3	7.61	3.8E-04
BF1714	putative major facilitator superfamily transporter	50.1	56.4	61.8	579.9	665.6	451.7	10.00	5.3E-04
BF1715	hypothetical protein	33.9	38.6	40.0	526.0	613.3	418.5	13.71	3.3E-04
BF1718	hypothetical protein	0.8	0.7	0.9	3.0	2.5	2.5	3.34	8.9E-04
BF1719	**putative outer membrane protein**	**6.3**	**7.6**	**7.2**	**1087.2**	**1315.2**	**764.8**	**147.11**	**1.4E-04**
BF1720	hypothetical protein	10.4	9.4	9.8	1309.3	1571.9	918.1	125.55	1.3E-04
BF1721	hypothetical protein	2.5	1.6	1.4	133.5	144.0	108.7	73.34	3.3E-04
BF1722	**putative outer membrane protein**	**0.8**	**0.5**	**1.0**	**124.3**	**126.0**	**97.3**	**156.16**	**2.1E-04**
BF1723	hypothetical protein	254.6	269.2	243.1	59.4	64.7	88.8	0.27	2.4E-03
BF1724	hypothetical protein	13.0	15.4	8.4	19.4	21.1	22.0	1.74	6.8E-02
BF1725	hypothetical protein	32.6	29.9	13.4	46.1	20.7	127.0	2.10	3.5E-01
BF1726	hypothetical protein	45.6	42.3	32.9	74.1	65.7	111.2	2.04	3.6E-02
BF1727	putative AraC family transcriptional regulator	20.9	22.0	10.1	21.2	10.6	56.4	1.40	6.4E-01
BF1728	hypothetical protein	5.1	5.4	2.3	5.0	2.9	17.8	1.60	5.5E-01
BF1729	hypothetical protein	1.1	0.8	0.4	0.3	1.2	3.8	1.70	5.9E-01
BF1730	hypothetical protein	0.7	1.1	0.1	0.8	0.1	3.5	1.59	7.8E-01
BF1731	hypothetical protein	1.0	0.5	0.5	0.9	1.1	2.8	2.21	1.7E-01
BF1732	hypothetical protein	9.0	5.7	5.5	1.7	3.3	11.4	0.61	5.1E-01
BF1733	hypothetical protein	1266.2	1577.6	1572.0	463.3	610.8	514.0	0.36	3.0E-03
BF1734	hypothetical protein	744.3	609.5	763.3	421.6	463.4	391.4	0.60	1.2E-02
BF1735	hypothetical protein	1.1	1.6	0.4	0.7	0.0	5.0	2.09	6.1E-01
top1	putative DNA topoisomerase I	1.2	1.1	0.5	1.2	0.6	1.9	1.30	6.5E-01
BF1737	hypothetical protein	0.1	0.4	0.1	0.2	0.0	1.1	2.80	4.0E-01
xerC	putative tyrosine recombinase	49.2	49.8	35.8	96.9	69.9	122.4	2.11	3.6E-02
BF1739	hypothetical protein	63.3	61.8	60.3	102.5	114.4	91.1	1.65	5.8E-03
BF1740	hypothetical protein	91.9	74.3	83.7	121.2	146.1	91.3	1.41	1.2E-01
BF1741	hypothetical protein	85.0	68.1	82.0	117.0	134.6	104.8	1.51	2.9E-02
BF1742	hypothetical protein	55.7	59.8	60.2	82.2	96.8	72.3	1.42	3.3E-02
BF1743	hypothetical protein	61.7	46.9	57.0	94.1	102.7	73.9	1.63	3.6E-02
BF1744	hypothetical protein	55.5	50.1	58.6	90.7	93.2	79.0	1.60	7.4E-03
BF1745	hypothetical protein	62.6	58.2	67.8	108.1	138.8	90.2	1.76	2.7E-02
BF1746	hypothetical protein	37.9	35.1	48.5	63.3	75.1	58.6	1.63	3.2E-02
BF1747	hypothetical protein	35.9	32.4	38.1	58.0	62.4	51.4	1.61	8.5E-03

BF1748	hypothetical protein	56.0	45.1	66.2	75.0	88.4	72.4	1.42	8.2E-02
BF1749	hypothetical protein	50.9	48.2	44.2	92.0	84.9	79.3	1.79	2.8E-03
BF1750	hypothetical protein	43.7	44.8	52.4	81.0	96.5	70.4	1.75	1.6E-02
BF1751	hypothetical protein	32.8	30.5	38.5	58.9	67.2	45.0	1.67	3.9E-02
BF1752	hypothetical protein	54.3	36.6	46.0	81.0	94.1	66.9	1.77	3.7E-02
BF1753	hypothetical protein	26.9	29.8	35.9	66.9	71.8	59.3	2.15	5.6E-03
BF1754	hypothetical protein	25.3	25.0	30.2	53.4	55.7	42.1	1.87	1.1E-02
BF1755	hypothetical protein	15.9	16.9	17.5	32.9	30.6	24.3	1.73	1.2E-02
BF1756	hypothetical protein	6.4	6.8	9.0	12.4	16.4	17.0	2.07	1.7E-02
BF1757	putative transmembrane protein	43.1	42.3	36.0	28.7	35.5	39.3	0.85	2.7E-01
BF1758	putative transmembrane TraG/TraD family mobilization protein	1.5	1.0	1.2	0.6	0.2	1.7	0.48	3.8E-01
BF1759	hypothetical protein	0.0	0.1	0.5	0.3	0.2	0.5	1.09	9.3E-01
BF1760	hypothetical protein	0.4	0.4	0.0	0.0	0.9	0.0	2.25	
BF1761	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
traA	putative conjugative transposon protein	0.2	0.2	0.0	0.2	0.0	0.0	0.92	
traB	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
traD	conserved hypothetical protein found in conjugate transposon	0.0	0.0	0.0	0.0	0.0	0.0		
traE	putative transmembrane conserved protein found in conjugative transposon	0.0	0.0	0.0	0.0	0.0	0.6		
traF	putative transmembrane conserved protein found in conjugate transposon	0.0	0.0	0.0	0.0	0.0	0.0		
traG	putative conserved protein found in conjugate transposon	0.0	0.0	0.2	0.1	0.1	0.3	0.79	
traH	conserved hypothetical protein found in conjugate transposon	0.0	0.0	0.0	0.0	0.0	0.0		
traI	conserved protein found in conjugate transposon	0.0	0.0	0.0	0.3	0.0	0.3		
traJ	conserved transmembrane protein found in conjugative transposon	0.0	0.2	0.2	0.2	0.0	0.2	0.88	3.9E-02
traK	conserved hypothetical protein found in conjugate transposon	0.0	0.0	0.0	0.0	0.3	0.0		
traL	conserved hypothetical protein found in conjugate transposon	0.0	0.7	0.0	0.0	0.0	0.0		
BF1773	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.5		
traM	conserved protein found in conjugate transposon	0.0	0.1	0.0	0.1	0.0	0.1	0.90	
traN	conserved hypothetical protein found in conjugate transposon	0.0	0.0	0.0	0.0	0.2	0.0		
traO	conserved hypothetical protein found in conjugate transposon	0.0	0.0	0.3	0.3	0.0	0.0	0.86	
traQ	conserved protein found in conjugate transposon	0.0	0.0	0.4	0.0	0.0	0.8	1.74	
BF1778	hypothetical protein	0.3	0.0	0.0	0.3	0.0	0.0	0.95	
BF1779	hypothetical protein	0.2	0.7	0.0	0.2	0.0	0.6	0.92	9.5E-01
radC3	putative DNA repair protein	0.0	0.4	0.0	0.0	0.0	0.0		
BF1781	hypothetical protein	0.3	0.3	0.6	0.3	0.0	0.6	1.02	9.8E-01
BF1782	putative ParB-family protein	0.5	0.3	0.5	0.4	0.2	0.3	0.71	2.1E-01
BF1783	hypothetical protein	0.0	0.3	0.3	0.5	1.3	1.6	3.42	6.3E-02
BF1784	hypothetical protein	0.3	0.3	0.0	0.0	0.0	0.8	2.79	

BF1785	putative DNA primase	0.2	0.2	0.6	0.2	0.0	0.2	0.63	3.9E-01
BF1786	hypothetical protein	0.0	0.4	0.5	0.0	0.0	0.0		
BF1787	hypothetical protein	31.6	30.1	28.8	56.1	63.5	44.7	1.80	1.3E-02
BF1788	hypothetical protein	21.9	20.7	19.5	52.1	63.3	42.1	2.50	5.7E-03
BF1789	hypothetical protein	10.7	9.2	10.5	33.7	33.5	40.1	3.52	6.4E-04
BF1790	putative ferredoxin	5.1	4.3	2.7	5.5	5.7	8.3	1.64	1.5E-01
BF1791	putative transcriptional regulator	10.0	8.1	6.8	12.6	11.0	14.1	1.53	5.7E-02
BF1792	hypothetical protein	17.3	17.9	11.8	20.7	15.7	62.7	1.77	3.4E-01
BF1793	hypothetical protein	0.0	4.5	1.3	2.8	1.4	8.1	1.30	8.0E-01
BF1794	hypothetical protein	3.9	3.0	0.0	2.1	1.9	12.8	1.10	9.1E-01
BF1795	putative bacteriophage integrase	20.0	23.0	11.1	28.3	19.4	45.1	1.69	2.5E-01
BF1796	putative alpha-L-fucosidase	36.9	31.5	36.9	59.3	68.6	49.6	1.68	2.0E-02
BF1797	putative outer membrane protein	2.2	2.5	1.2	5.3	4.8	4.2	2.51	3.6E-02
BF1798	putative outer membrane protein	0.9	0.3	0.2	3.9	3.2	2.6	7.67	1.6E-02
BF1799	putative ATP/GTP-binding protein	38.9	40.9	46.1	40.7	44.5	34.9	0.95	6.6E-01
BF1800	hypothetical protein	12.3	20.5	14.5	12.5	14.2	16.0	0.92	7.0E-01
BF1801	hypothetical protein	22.0	19.2	18.8	22.6	25.0	18.3	1.09	5.2E-01
BF1802	possible outer membrane protein	3.3	2.1	4.0	110.6	130.9	98.5	37.46	5.7E-04
BF1803	putative outer membrane protein	0.8	1.3	1.2	121.5	124.3	103.4	109.18	2.0E-04
BF1804	putative TonB-dependent outer membrane receptor protein	11.6	11.7	12.9	90.7	88.3	84.5	7.30	2.5E-05
BF1805	hypothetical protein	12.0	9.3	12.5	78.5	76.8	72.5	6.78	4.0E-04
nanH	neuraminidase precursor	21.3	22.2	20.3	591.8	677.2	513.6	27.81	5.5E-05
nahA	beta-N-acetylhexoosaminidase	14.1	13.6	15.3	264.5	314.3	235.0	18.82	1.1E-04
estA	sialate-O-acetyltransferase	119.8	118.3	105.8	237.6	265.6	208.1	2.06	3.5E-03
estS	sialate O-acetylesterase	174.3	174.1	170.8	355.4	415.0	330.6	2.11	1.9E-03
bmnA	beta-mannosidase	159.6	154.3	161.6	263.1	321.6	300.0	1.85	2.4E-03
nahB	beta-N-acetylhexosaminidase	289.8	287.9	301.2	1193.1	1305.7	1015.5	3.98	4.9E-04
BF1812	putative lipoprotein	75.6	72.1	74.7	142.0	153.3	129.0	1.90	1.4E-03
nahC	beta-N-acetylhexosaminidase	148.9	146.0	144.3	203.9	218.3	201.2	1.42	1.2E-03
BF1814	putative outer membrane protein	143.4	140.6	131.4	183.4	192.4	170.3	1.31	9.8E-03
bgaA	beta-galactosidase	374.8	376.5	349.5	509.5	512.8	491.1	1.38	1.7E-03
BF1816	putative outer membrane protein	59.1	67.3	66.5	52.5	54.6	49.3	0.81	3.0E-02
BF1817	putative outer membrane protein	21.6	24.4	30.7	37.3	37.6	40.9	1.52	3.4E-02
dnaJ	putative chaperone protein	323.9	323.7	234.0	189.0	129.5	168.7	0.55	3.7E-02
grpE	putative GrpE protein (HSP70 cofactor)	753.2	653.1	506.9	165.8	152.9	122.4	0.23	2.6E-03
BF1820	putative ABC transporter component	378.7	392.7	407.3	308.7	290.2	284.5	0.75	3.5E-03
BF1821	putative RNA polymerase ECF-type sigma factor	49.1	54.2	46.9	23.7	17.4	25.5	0.44	8.2E-03
BF1822	putative transmembrane protein	34.6	33.7	44.1	22.1	19.3	22.4	0.57	1.2E-02
BF1823	putative transmembrane protein	67.5	58.5	64.9	46.9	46.4	46.7	0.73	6.2E-03
BF1824	hypothetical protein	399.9	377.3	380.1	325.0	319.0	281.0	0.80	2.3E-02
BF1825	putative transmembrane protease	11.5	13.3	18.4	22.9	18.8	19.8	1.45	1.1E-01
BF1826	hypothetical protein	1.8	2.1	1.5	1.1	1.1	2.0	0.75	3.5E-01
BF1827	hypothetical protein	1.2	2.1	1.1	0.9	0.9	0.7	0.59	1.1E-01
BF1828	hypothetical protein	46.0	38.9	40.6	34.1	37.0	36.7	0.86	9.3E-02
BF1829	putative transmembrane protein	5.9	5.6	6.5	2.5	3.8	6.4	0.66	2.6E-01
BF1830	hypothetical protein	46.8	54.5	55.6	30.7	38.4	39.8	0.69	3.8E-02
BF1831	hypothetical protein	141.6	110.1	133.1	107.4	105.9	88.8	0.79	1.1E-01
BF1832	hypothetical protein	1.4	0.0	1.6	0.7	0.0	1.4	0.64	4.1E-01
BF1833	putative bacteriophage integrase	0.3	0.3	0.0	0.1	0.7	0.1	0.78	7.3E-01

BF1834	hypothetical protein	2.3	0.5	2.6	0.0	0.0	0.9	0.62	
hsdR	putative type I restriction enzyme R protein	167.4	159.0	178.4	164.3	185.5	148.4	0.98	8.7E-01
BF1837	hypothetical protein	106.1	102.9	108.6	95.5	107.0	81.2	0.89	2.8E-01
hsdM	putative type I restriction enzyme methylase	157.2	136.3	157.3	139.8	162.3	122.6	0.94	6.0E-01
BF1839	putative type I restriction enzyme, partial	28.7	27.2	34.0	36.0	31.8	25.0	1.03	8.8E-01
BF1840	putative type I restriction endonuclease specificity subunit, partial	0.6	2.0	2.7	2.6	1.3	0.5	0.83	8.3E-01
BF1841	putative type I restriction-modification system specificity system, partial	90.5	93.0	99.6	74.3	97.3	73.9	0.86	2.5E-01
BF1842	putative type IC restriction-modification system specificity subunit, partial	33.9	25.6	28.8	29.7	26.2	25.4	0.93	5.4E-01
BF1843	putative phage integrase/recombinase	11.1	10.8	11.4	6.6	7.8	6.6	0.63	4.6E-03
BF1844	hypothetical protein	0.0	1.9	1.0	0.0	0.0	0.0		
BF1845	putative integrase/transposase	36.7	36.3	31.2	20.0	17.3	19.6	0.55	3.8E-03
BF1846	hypothetical protein	2.5	0.9	0.0	0.8	0.0	0.0	0.53	
BF1847	hypothetical protein	0.9	1.3	0.3	0.3	0.7	0.9	0.77	7.0E-01
BF1848	hypothetical protein	0.3	0.7	0.5	0.5	0.2	0.2	0.48	2.0E-01
BF1849	hypothetical protein	0.2	0.3	0.7	0.1	0.4	0.1	0.61	4.6E-01
BF1850	hypothetical protein	3.2	3.6	2.2	5.1	3.6	2.9	1.26	4.2E-01
BF1851	hypothetical protein	0.6	0.4	0.4	0.4	0.0	0.4	0.79	1.7E-01
BF1852	possible ATP/GTP-binding chaperonin	0.7	0.8	0.7	0.1	0.5	0.5	0.41	2.4E-01
BF1853	hypothetical protein	0.6	1.5	0.7	0.6	0.7	0.6	0.74	4.1E-01
BF1854	hypothetical protein	0.0	0.2	0.0	0.2	0.2	0.3	1.20	
BF1855	hypothetical protein	0.7	1.0	0.8	0.4	0.6	0.7	0.65	1.9E-01
BF1856	hypothetical protein	0.6	1.0	1.2	0.7	0.2	0.7	0.54	3.3E-01
BF1857	hypothetical protein	1.2	1.3	0.4	0.0	0.0	1.2	1.38	
BF1858	hypothetical protein	0.7	1.0	0.6	0.3	0.6	0.5	0.65	1.8E-01
BF1859	hypothetical protein	1.9	1.1	0.8	0.2	0.4	0.7	0.30	1.1E-01
BF1860	hypothetical protein	0.2	0.7	0.2	0.6	0.4	0.8	2.08	2.9E-01
BF1861	hypothetical protein	1.7	1.0	0.0	0.7	1.1	0.7	0.63	2.9E-01
BF1862	hypothetical protein	2.1	2.1	1.4	0.2	0.8	0.6	0.26	6.1E-02
BF1863	hypothetical protein	2.1	1.1	1.8	0.3	0.2	0.6	0.21	3.7E-02
BF1864	hypothetical protein	0.9	1.4	0.8	0.2	1.3	0.4	0.43	3.0E-01
BF1865	hypothetical protein	1.6	1.2	1.1	1.4	1.2	1.1	0.94	7.2E-01
BF1866	hypothetical protein	1.9	1.8	1.8	0.5	0.9	0.4	0.30	2.0E-02
BF1867	hypothetical protein	1.3	1.7	0.7	0.8	1.0	2.1	1.07	9.0E-01
BF1868	hypothetical protein	0.9	1.6	0.8	0.4	0.5	1.2	0.61	3.5E-01
BF1869	hypothetical protein	0.0	0.0	0.5	0.0	0.0	0.0		
BF1870	hypothetical protein	2.9	3.8	3.0	2.9	2.9	2.1	0.81	2.9E-01
BF1871	putative RNA-binding protein	52.0	64.0	44.4	67.2	62.6	71.8	1.27	1.5E-01
BF1872	putative two-component histidine sensor kinase	105.0	88.3	73.2	51.3	46.3	72.9	0.63	9.2E-02
BF1873	putative 2', 3'-cyclic nucleotide 2'-phosphodiesterase	86.8	68.1	68.4	54.1	61.1	82.6	0.88	5.0E-01
BF1874	putative GAF-domain signal transduction protein	52.9	39.2	49.2	40.6	46.1	58.2	1.02	9.1E-01
BF1875	hypothetical protein	188.9	152.8	193.2	165.3	146.4	177.8	0.92	4.8E-01

BF1876	putative TonB-dependent outer membrane protein	38.3	34.4	32.2	25.5	22.8	30.4	0.75	6.7E-02
BF1877	hypothetical protein	153.1	135.0	145.9	163.7	157.1	177.7	1.15	8.8E-02
BF1878	putative DNA-binding cyclic-nucleotide binding protein	35.8	31.6	37.1	141.7	118.3	126.5	3.70	5.0E-04
BFt20	tRNA-Ser-GCT	1243.3	1652.5	1422.6	797.7	824.2	2115.0	0.78	5.7E-01
BFt21	tRNA-Glu-CTC	56.5	72.6	67.4	84.7	95.3	252.8	1.95	1.9E-01
BF1879	putative transmembrane Na+ driven efflux protein	29.2	30.3	34.8	9.0	7.8	12.3	0.30	4.5E-03
BF1881	hypothetical protein	75.4	65.9	66.1	296.7	306.7	246.9	4.09	5.7E-04
BF1882	putative transmembrane transport efflux protein	81.2	62.0	68.5	11.4	10.0	17.6	0.18	3.4E-03
BF1883	putative antiporter	147.2	144.2	137.1	101.9	93.7	129.2	0.75	7.4E-02
BF1884	hypothetical protein	224.1	223.2	219.1	198.8	200.0	191.1	0.88	5.3E-03
BF1885	hypothetical protein	147.0	131.3	134.6	134.2	131.4	138.4	0.98	6.7E-01
BF1886	hypothetical protein	160.4	174.5	167.8	227.7	204.3	184.9	1.22	6.2E-02
fcl	putative GDP-L-fucose synthetase	49.7	45.4	42.9	49.1	42.8	41.4	0.97	6.9E-01
BF1888	putative GDP mannose 4,6-dehydratase	59.6	60.3	48.8	51.7	43.6	45.1	0.83	1.5E-01
BF1889	hypothetical protein	40.9	38.7	37.1	48.5	44.3	36.5	1.10	4.1E-01
BF1890	hypothetical protein	3.3	2.8	3.4	1.7	2.0	0.8	0.45	7.2E-02
BF1891	hypothetical protein	3.5	1.1	3.4	0.0	0.6	0.0	0.25	
BF1892	hypothetical protein	4.7	8.9	5.2	3.0	6.6	3.0	0.65	3.3E-01
upbY	putative LPS biosynthesis related transcriptional regulatory protein	314.9	294.6	324.9	169.5	165.0	156.7	0.53	5.7E-04
upbZ	putative LPS biosynthesis related transcriptional regulatory protein	265.0	252.2	242.7	153.8	155.1	140.4	0.59	1.3E-03
wcfT	putative LPS biosynthesis related membrane protein	171.6	166.3	163.1	113.3	119.0	105.9	0.67	2.2E-03
wcfU	putative glucose-1-P-cytidylyltransferase	89.9	94.9	85.0	78.0	82.0	84.9	0.91	1.1E-01
aepX	putative LPS biosynthesis related phosphoenolpyruvate phosphomutase	157.9	162.5	147.7	177.9	150.3	197.5	1.12	3.3E-01
aepY	putative LPS biosynthesis related phosphoenolpyruvate decarboxylase	115.2	130.1	104.4	118.4	119.1	138.3	1.08	4.9E-01
aepZ	putative LPS biosynthesis related 2-aminoethylphosphonate pyruvate aminotransferase	141.5	164.2	141.2	111.3	121.9	121.3	0.79	3.3E-02
wzx	putative LPS biosynthesis related flippase	66.7	75.0	81.2	38.5	46.8	31.6	0.52	1.6E-02
wcfV	hypothetical protein	119.0	103.7	116.6	91.6	105.9	69.7	0.78	1.8E-01
wcfW	putative LPS biosynthesis related alpha-1,2-fucosyltransferase	109.3	99.5	104.5	82.1	99.1	72.6	0.80	1.3E-01
wcfX	putative LPS biosynthesis related UDP-glucuronic acid epimerase	105.1	99.8	110.5	91.0	99.3	92.0	0.90	8.4E-02
wcfY	putative LPS biosynthesis related UDP-glucose dehydrogenase	117.6	102.4	117.1	100.2	102.7	96.9	0.89	1.2E-01
wcfZ	putative LPS biosynthesis related glycosyltransferase	69.2	67.0	73.3	48.6	55.1	41.4	0.69	2.7E-02
wcgQ	putative LPS biosynthesis related glycosyltransferase	108.0	109.4	107.5	65.3	80.2	60.3	0.63	1.4E-02

wzy	putative LPS biosynthesis related polymerase	59.6	60.9	63.0	31.1	39.0	25.1	0.51	1.5E-02
wcgR	putative LPS biosynthesis related glycosyltransferase	70.5	86.6	86.5	56.9	69.9	51.1	0.73	8.2E-02
wcgS	putative LPS biosynthesis related dehydratase	153.7	141.6	159.1	147.8	158.3	138.2	0.98	7.4E-01
wcgT	putative LPS biosynthesis related epimerase	160.2	168.4	178.7	144.3	159.0	123.6	0.84	1.4E-01
wcgU	putative LPS biosynthesis related reductase	122.5	118.0	128.0	106.7	122.7	105.0	0.91	2.0E-01
wcgV	putative LPS biosynthesis related glycosyltransferase	87.9	86.7	93.0	63.7	77.9	58.0	0.74	5.1E-02
wcgW	putative LPS biosynthesis related dehydratase	79.1	71.3	92.3	60.9	69.9	54.7	0.76	9.5E-02
wcgX	putative LPS biosynthesis related UndPP-QuiNAc-P-transferase	51.2	46.4	55.8	26.0	28.4	26.2	0.53	2.1E-03
BF1915	hypothetical protein	33.1	24.4	29.3	14.8	22.3	11.5	0.54	7.6E-02
BF1917	hypothetical protein	39.1	33.3	33.6	15.2	14.7	13.6	0.41	9.2E-04
BF1918	putative transmembrane symporter	23.3	28.3	24.1	32.3	36.9	33.6	1.36	2.7E-02
gnd	6-phosphogluconate dehydrogenase	391.5	330.4	315.5	115.0	117.9	171.1	0.38	8.0E-03
zwf	glucose-6-phosphate 1-dehydrogenase	453.6	372.9	398.3	140.4	146.4	164.8	0.37	1.2E-03
pgl	putative 6-phosphogluconolactonase	423.8	370.7	406.8	154.6	153.3	190.5	0.41	2.1E-03
BF1922	hypothetical protein	116.2	103.0	127.2	95.9	115.4	66.1	0.78	3.0E-01
BF1923	hypothetical protein	177.0	178.2	188.8	114.7	126.5	100.0	0.62	8.1E-03
BF1924	hypothetical protein	164.4	141.7	152.1	125.6	140.0	139.1	0.88	1.3E-01
BF1925	putative urea transport protein	29.6	25.1	30.8	52.8	52.0	46.1	1.77	5.7E-03
BF1926	hypothetical protein	29.3	30.2	35.0	45.0	52.7	44.4	1.50	1.6E-02
BF1927	hypothetical protein	48.9	43.6	51.2	25.8	29.8	24.7	0.56	5.0E-03
BF1928	putative RumB/ImpB like DNA repair protein	4.5	2.9	5.4	0.9	1.4	1.5	0.30	1.7E-02
BF1929	putative UmuD/RumA DNA repair protein	1.6	0.9	1.3	0.8	0.5	0.4	0.42	6.1E-02
BF1930	hypothetical protein	1.1	2.5	3.0	2.3	3.2	2.5	1.33	5.1E-01
BF1931	putative two-component system response regulator	18.7	19.9	20.3	33.5	37.7	32.7	1.76	1.9E-03
BF1932	putative transmembrane protein	16.3	15.9	13.3	16.2	17.5	18.3	1.15	1.9E-01
BF1933	putative permease component of ABC transporter	1.3	2.0	1.1	1.0	0.5	0.6	0.45	6.9E-02
BF1934	putative ABC transporter ATP-binding component	2.4	1.8	0.3	0.2	0.3	0.9	0.37	3.6E-01
BF1935	putative HlyD family secretion protein	0.9	0.6	0.5	0.7	0.7	1.1	1.26	4.6E-01
BF1936	putative outer membrane lipoprotein precursor	2.4	2.1	2.4	0.4	1.0	1.2	0.33	7.4E-02
cydA	putative cytochrome d ubiquinol oxidase subunit I	519.4	531.2	515.9	488.7	528.2	571.0	1.01	8.5E-01
cydB	putative cytochrome d ubiquinol oxidase subunit II	415.3	451.0	448.0	503.3	522.9	512.7	1.17	1.4E-02
BF1939	hypothetical protein	89.8	53.8	57.8	48.4	50.6	80.7	0.89	7.0E-01
BF1940	hypothetical protein	41.5	41.2	32.9	36.7	32.3	51.6	1.03	9.0E-01
BF1941	hypothetical protein	37.7	37.9	28.3	40.8	42.4	44.3	1.24	1.4E-01
BF1942	coproporphyrinogen III oxidase	32.0	23.6	26.4	32.7	32.7	47.2	1.36	1.6E-01

BF1943	hypothetical protein	17.6	16.7	14.5	13.5	12.5	19.8	0.92	6.8E-01
BF1944	glycerate dehydrogenase	298.7	326.7	306.0	228.9	232.0	241.6	0.75	3.5E-03
BF1945	putative AAA family ATPase protein	51.2	50.6	48.3	74.9	69.2	70.5	1.43	1.6E-03
BF1946	putative beta-galactosidase	113.9	123.2	105.8	121.3	111.8	131.0	1.06	4.7E-01
BF1947	hypothetical protein	229.8	246.0	233.6	167.4	163.1	162.4	0.70	6.9E-04
BF1948	putative UDP-N-acetylglucosamine 2-epimerase	161.1	147.7	148.9	215.2	193.1	213.6	1.36	7.3E-03
BF1949	putative transmembrane protein	105.0	110.8	131.1	101.1	112.4	96.7	0.90	3.1E-01
BF1950	hypothetical protein	229.6	233.2	225.3	87.8	95.3	96.1	0.41	1.4E-04
BF1951	hypothetical protein	32.3	48.1	45.8	67.3	67.3	67.4	1.63	3.5E-02
htpX	putative transmembrane protease HtpX homolog	118.4	125.7	131.9	242.0	269.9	235.1	1.98	1.2E-03
BF1953	putative LemA antigen-like protein	338.1	297.8	307.2	540.8	561.5	471.9	1.67	5.1E-03
BF1954	putative RNA polymerase ECF-type sigma factor	1297.1	1351.8	1383.2	934.1	1150.3	862.8	0.73	4.1E-02
BF1955	putative pyruvate carboxylase biotin-containing subunit	47.1	46.2	48.1	23.8	22.8	25.9	0.51	6.2E-04
BF1956	putative outer membrane protein	445.3	415.6	417.7	642.7	677.9	600.7	1.50	2.7E-03
BF1957	hypothetical protein	490.8	531.7	511.4	666.1	709.7	608.1	1.29	1.7E-02
mtgA	monofunctional biosynthetic peptidoglycan transglycosylase	68.5	64.8	71.5	38.7	38.6	45.8	0.60	4.7E-03
BF1959	putative outer membrane protein OmpA-family	1367.2	1325.8	1270.0	913.7	825.0	843.4	0.65	1.8E-03
BF1960	putative MatE-family transmembrane protein	79.4	75.3	75.0	58.4	53.2	53.8	0.72	2.9E-03
BF1961	putative transmembrane transporter	38.2	36.5	38.6	33.1	33.6	33.3	0.88	7.1E-03
BF1962	putative outer membrane protein	13.0	11.1	11.3	10.5	10.0	11.0	0.89	1.6E-01
BF1963	possible anti-sigma factor	10.8	11.9	7.8	7.7	6.0	7.8	0.71	1.3E-01
BF1964	putative RNA polymerase ECF-type sigma factor	9.3	7.5	8.8	7.9	11.5	5.5	0.94	8.2E-01
BF1965	hypothetical protein	14.4	13.2	13.8	12.2	17.3	13.9	1.04	7.9E-01
BF1966	hypothetical protein	93.9	96.4	88.0	85.6	94.8	67.3	0.88	3.7E-01
BF1967	putative histone-like DNA-binding protein	12.8	8.8	7.0	6.1	9.6	6.7	0.79	4.2E-01
BF1969	putative ECF-type RNA polymerase sigma factor	17.0	21.9	27.7	5.5	10.5	3.8	0.28	3.5E-02
BF1970	possible anti-sigma factor	18.3	17.3	15.0	8.2	10.5	10.0	0.57	1.1E-02
BF1971	hypothetical protein	7.1	8.3	13.5	5.5	3.7	1.9	0.36	8.7E-02
BF1972	putative AraC family transcriptional regulator	20.6	19.6	27.2	2.0	1.6	2.1	0.08	4.9E-04
BF1973	hypothetical protein	21.3	22.7	28.9	1.7	3.2	2.0	0.09	1.7E-03
BF1974	hypothetical protein	25.3	29.6	36.7	1.8	2.4	1.6	0.06	6.3E-04
BF1975	hypothetical protein	42.0	67.9	84.3	6.1	7.1	5.4	0.10	2.3E-03
BF1976	hypothetical protein	21.2	36.3	38.4	1.6	3.8	1.6	0.07	5.5E-03
BF1977	hypothetical protein	12.9	25.2	28.8	1.5	2.6	1.3	0.08	5.6E-03
BF1978	hypothetical protein	13.7	16.8	24.2	2.7	2.6	2.3	0.14	1.8E-03
BF1979	hypothetical protein	260.4	253.5	274.0	156.5	160.0	160.3	0.61	3.6E-04
BF1980	hypothetical protein	0.7	0.0	2.4	0.0	0.9	0.7	0.58	5.3E-01
BF1981	hypothetical protein	53.7	28.0	35.7	38.0	51.1	37.5	1.10	7.2E-01
BF1982	putative MarR-family regulatory protein	72.5	68.8	77.7	72.9	73.2	67.3	0.98	6.7E-01
BF1983	putative protoporphyrinogen oxidase	315.7	319.6	294.6	256.9	268.9	257.1	0.84	1.2E-02

hemN	coproporphyrinogen III oxidase	536.0	590.7	536.9	462.3	482.5	432.6	0.83	2.9E-02
BF1985	putative transmembrane transporter protein	465.1	597.0	534.1	370.5	368.2	333.9	0.67	1.8E-02
BF1986	putative outer membrane protein	550.8	653.7	606.2	408.7	372.9	370.0	0.64	5.4E-03
BF1987	hypothetical protein	4.3	2.7	4.1	1.3	1.5	1.4	0.38	9.4E-03
BF1988	putative outer membrane protein	9.4	14.5	14.7	2.8	3.9	2.1	0.23	8.7E-03
BF1989	putative AraC-family transcriptional regulator	4.3	2.4	4.3	1.2	1.2	0.4	0.23	4.4E-02
BF1990	hypothetical protein	77.8	72.7	65.7	61.5	55.1	78.8	0.90	4.7E-01
BF1991	putative TonB-dependent outer membrane receptor protein	166.9	159.7	171.5	42.7	47.1	51.1	0.28	3.0E-04
BF1992	putative outer membrane protein	193.7	208.1	225.5	25.2	26.8	31.0	0.13	1.8E-04
BF1993	hypothetical protein	196.5	204.1	237.9	21.4	22.3	24.1	0.11	1.0E-04
BF1994	hypothetical protein	181.2	167.7	191.4	17.8	19.7	25.1	0.11	4.0E-04
BF1995	hypothetical protein	181.1	146.4	180.2	12.2	15.0	17.9	0.09	4.9E-04
BF1996	hypothetical protein	181.1	142.5	170.3	13.1	13.7	14.3	0.08	1.1E-04
BF1997	hypothetical protein	163.7	124.3	139.5	12.1	12.2	15.8	0.09	4.0E-04
BF1998	hypothetical protein	143.0	96.9	119.3	8.3	10.4	12.4	0.09	8.0E-04
BF1999	hypothetical protein	125.7	103.9	112.0	10.5	10.6	13.1	0.10	2.0E-04
BF2000	putative polysialic acid capsule transport protein	116.5	88.2	97.2	10.6	9.4	11.3	0.10	2.8E-04
BF2001	hypothetical protein	160.7	132.2	158.5	160.0	170.5	172.5	1.12	2.3E-01
BF2002	hypothetical protein	156.5	156.2	152.7	186.1	191.4	183.2	1.20	1.4E-03
BF2003	hypothetical protein	178.8	159.8	156.9	210.4	200.6	201.8	1.24	1.8E-02
BF2004	hypothetical protein	154.7	136.1	137.6	162.8	168.7	158.1	1.14	6.9E-02
BF2005	hypothetical protein	142.1	119.9	124.5	169.9	174.3	187.4	1.38	1.4E-02
BF2006	hypothetical protein	151.6	119.2	116.5	178.2	169.3	242.7	1.51	7.0E-02
BF2007	hypothetical protein	300.1	257.8	262.3	369.3	351.0	388.0	1.35	1.4E-02
BF2008	putative transmembrane protein	202.2	234.1	212.2	309.3	296.4	267.6	1.35	1.9E-02
BF2009	putative transmembrane protein	353.3	385.8	418.1	423.5	444.8	326.3	1.03	8.6E-01
BF2010	putative transmembrane protein	415.4	405.3	483.3	463.5	472.5	384.9	1.01	9.2E-01
BF2011	putative transmembrane protein	355.6	331.3	360.7	466.8	519.3	407.9	1.33	3.8E-02
BF2012	hypothetical protein	290.1	264.6	273.6	478.0	474.5	418.3	1.65	2.7E-03
BF2013	hypothetical protein	340.6	297.3	281.2	504.4	455.2	530.1	1.62	7.8E-03
BF2014	hypothetical protein	259.2	245.3	247.6	410.8	382.7	388.8	1.57	6.4E-04
BF2015	putative bacteriophage Gp25 protein	217.3	245.6	211.9	398.9	373.8	388.8	1.72	1.9E-03
BF2016	hypothetical protein	182.2	165.6	153.2	345.0	289.3	347.0	1.96	3.9E-03
BF2017	hypothetical protein	295.8	234.6	255.8	496.5	442.1	506.2	1.84	5.4E-03
BF2018	hypothetical protein	307.5	274.2	298.1	532.9	536.3	536.5	1.83	5.7E-04
BF2019	hypothetical protein	206.8	183.7	213.6	333.4	351.1	293.7	1.62	7.3E-03
BF2020	hypothetical protein	371.2	322.1	376.3	468.7	491.5	377.4	1.25	1.3E-01
BF2021	hypothetical protein	371.5	371.7	378.1	488.2	558.3	436.5	1.32	3.6E-02
BF2022	hypothetical protein	419.1	350.4	393.6	502.1	534.8	415.5	1.25	1.2E-01
BF2023	putative ATP-dependent protease	609.1	588.8	507.0	728.7	658.9	787.5	1.28	5.8E-02
BF2024	hypothetical protein	1237.0	1186.2	1114.7	2929.9	3003.1	2718.4	2.45	3.6E-04
BF2025	hypothetical protein	1607.7	1358.9	1478.9	3296.0	3457.5	2776.9	2.14	3.2E-03
BF2026	hypothetical protein	36030.3	31908.4	39148.8	44437.4	47571.6	41029.2	1.24	6.9E-02
BF2027	hypothetical protein	192.4	165.1	189.6	203.6	233.0	160.8	1.08	6.1E-01
BF2028	putative aminotransferase	249.4	228.7	277.6	314.9	316.4	287.5	1.22	6.3E-02
BF2029	putative ATP-binding protein	32.5	26.3	30.1	46.5	52.7	48.7	1.67	6.5E-03
BF2030	putative tautomerase	19.9	22.2	21.9	39.6	49.4	30.0	1.82	3.1E-02

BF2031	hypothetical protein	0.0	0.0	0.6	0.6	0.0	0.0	0.86	
BF2032	putative TetR-family transcriptional regulator	147.6	124.0	137.8	119.6	111.5	104.4	0.82	6.3E-02
BF2035	hypothetical protein	2.3	4.9	6.6	1.3	1.1	1.8	0.32	5.4E-02
BF2036	hypothetical protein	3.3	4.2	3.4	2.0	1.4	1.2	0.41	1.4E-02
BF2037	putative transmembrane protein	13.0	15.4	13.1	1.4	5.2	3.2	0.21	3.0E-02
BF2038	putative transmembrane protein	7.5	8.0	7.9	5.0	4.4	1.4	0.40	1.3E-01
BF2039	putative transmembrane protein	10.2	9.1	9.9	3.5	5.2	2.4	0.36	2.5E-02
BF2040	putative transmembrane protein	12.0	13.2	15.0	24.3	19.9	18.4	1.55	2.8E-02
BF2041	hypothetical protein	8.7	8.8	8.9	11.2	15.5	15.4	1.58	2.7E-02
BFt22	tRNA-Lys-TTT	14.5	28.3	27.9	22.9	26.6	40.6	1.29	4.8E-01
BF2043	putative ATP-binding component of ABC transporter	220.6	210.4	212.1	231.3	222.7	263.2	1.11	1.6E-01
BF2044	putative TonB-dependent outer membrane receptor protein	238.6	272.1	264.2	355.8	360.0	310.5	1.32	2.3E-02
BF2045	hypothetical protein	298.8	316.9	306.2	350.9	355.6	309.9	1.10	1.6E-01
BF2046	putative transmembrane endonuclease/exonuclease/phosphatase family protein	12.3	11.1	11.5	8.8	5.6	8.4	0.64	6.5E-02
BF2047	putative two-component system sensor kinase/response regulator fusion protein	25.4	21.0	18.6	12.5	8.4	16.2	0.55	8.1E-02
BF2048	putative transmembrane glycosyltransferase	6.4	5.4	5.3	7.5	4.6	9.0	1.18	5.4E-01
BF2049	hypothetical protein	11.6	9.3	10.6	8.0	6.9	8.3	0.74	4.3E-02
BF2050	putative transmembrane acyltransferase	7.3	4.2	7.0	4.7	5.8	3.9	0.80	4.1E-01
BF2051	putative glycosyltransferase	12.8	17.6	16.2	12.4	15.3	14.3	0.90	5.0E-01
BF2052	putative glycosyltransferase protein	13.3	15.3	16.7	12.8	13.3	10.7	0.81	1.3E-01
BF2053	putative glycosyltransferase	9.4	13.6	10.7	10.0	9.3	7.0	0.78	2.4E-01
BF2054	hypothetical protein	37.7	33.4	44.8	33.2	38.2	25.7	0.83	3.4E-01
BF2055	putative transmembrane O-antigen flippase	12.5	13.2	15.0	7.1	8.6	6.6	0.55	8.6E-03
BF2056	putative capsular polysaccharide glycosyltransferase	31.1	28.5	33.6	24.5	24.4	19.0	0.73	5.3E-02
BF2058	putative capsule-related protein	0.6	0.8	0.8	0.0	0.2	0.1	0.22	5.4E-03
BF2059	putative capsule-related glycosyltransferase	4.8	5.3	2.0	0.8	1.1	1.5	0.30	5.6E-02
BF2060	putative transmembrane surface-related protein	3.6	3.1	3.5	0.8	0.8	0.5	0.20	1.7E-03
BF2061	putative transmembrane protein	6.7	6.3	6.3	1.7	1.8	1.7	0.27	9.6E-05
BF2062	putative outer membrane protein	14.4	13.0	14.5	7.1	6.5	6.3	0.48	8.7E-04
BF2063	hypothetical protein	48.0	40.4	37.7	23.5	21.7	30.0	0.59	2.7E-02
BF2064	putative aminopeptidase	147.2	144.9	119.0	274.5	206.8	296.3	1.88	1.9E-02
nqrA	Na(+)-translocating NADH-quinone reductase subunit A	408.1	414.4	358.2	476.5	416.9	547.0	1.22	1.5E-01
nqrB	Na(+)-translocating NADH-quinone reductase subunit B	706.7	757.8	687.9	664.6	627.8	701.7	0.93	2.1E-01
nqrC	Na(+)-translocating NADH-quinone reductase subunit C	453.6	442.4	401.8	413.2	405.3	422.7	0.96	4.0E-01
nqrD	NADH-ubiquinone oxidoreductase	553.3	559.5	526.1	458.4	479.9	487.5	0.87	1.5E-02

nqrE	Na+-translocating NADH-quinone reductase subunit E	533.9	613.4	559.7	498.0	510.2	510.5	0.89	8.2E-02
nqrF	Na(+)-translocating NADH-quinone reductase subunit F	860.9	915.0	749.7	758.9	698.1	853.6	0.91	4.2E-01
dbpA	putative ATP-independent RNA helicase	120.4	112.9	104.7	129.3	118.6	163.2	1.21	2.0E-01
serC	phosphoserine aminotransferase	956.8	931.6	828.0	664.7	646.9	678.7	0.73	8.0E-03
serA	putative D-3-phosphoglycerate dehydrogenase	1180.4	1094.1	1017.9	760.8	712.7	742.5	0.67	4.2E-03
BF2074	hypothetical protein	1859.5	1878.2	1641.8	962.0	864.0	969.8	0.52	1.8E-03
BF2075	putative peptidyl-prolyl cis-trans isomerase	224.4	202.1	202.8	109.3	112.4	115.1	0.54	6.3E-04
BF2076	hypothetical protein	160.2	134.2	118.2	65.2	70.1	86.8	0.54	1.7E-02
BF2077	putative type II restriction enzyme	147.9	110.5	103.5	58.2	51.2	106.9	0.57	1.4E-01
BF2078	hypothetical protein	165.6	121.2	142.8	70.1	91.0	107.5	0.62	6.2E-02
BF2079	glycine dehydrogenase	76.4	73.9	73.6	207.7	197.0	204.2	2.72	2.3E-05
BF2080	putative metallo-beta-lactamase	72.4	61.6	64.8	123.2	123.2	112.9	1.81	2.2E-03
gidB	glucose-inhibited division protein B	78.4	95.8	72.3	133.0	126.3	121.3	1.55	1.7E-02
BF2082	hypothetical protein	149.6	140.1	130.4	155.5	157.5	117.4	1.02	9.1E-01
BF2083	hypothetical protein	111.8	118.5	101.6	63.3	59.3	88.5	0.63	4.4E-02
BF2084	putative TonB-dependent outer membrane receptor protein	4.2	3.1	3.4	5.8	3.7	6.0	1.41	1.8E-01
BF2085	possible exported heavy-metal binding protein	3.4	4.2	4.4	10.2	9.8	13.0	2.75	4.0E-03
BF2086	putative transmembrane cation-transporting ATPase	460.2	503.0	410.3	185.8	169.0	269.9	0.45	1.6E-02
BF2087	putative AraC-type transcriptional regulator	132.3	149.5	140.9	160.1	153.5	141.5	1.08	2.8E-01
BF2088	putative lipoate-protein ligase	53.5	58.6	45.2	70.3	53.4	107.5	1.42	2.4E-01
BF2089	hypothetical protein	41.7	42.4	41.8	41.4	48.3	40.7	1.03	6.6E-01
BF2092	putative transmembrane oligopeptide transporter	61.7	66.9	54.5	118.2	99.4	126.1	1.87	7.5E-03
BF2093	hypothetical protein	1183.0	1156.9	1076.5	599.7	584.0	554.4	0.51	4.9E-04
BF2094	putative two-component sensor histidine kinase protein	2.1	1.4	1.3	11.7	11.0	13.7	7.58	1.4E-03
BF2095	putative two-component response regulator transcriptional regulatory protein	16.8	16.6	10.7	31.6	22.1	35.0	2.01	4.8E-02
BF2096	putative transmembrane protein	3.4	2.6	3.0	19.3	15.9	23.9	6.52	1.1E-03
BF2097	hypothetical protein	0.9	2.2	0.7	6.0	8.5	10.6	7.28	1.6E-02
BF2098	putative transporter permease protein	0.6	0.7	1.0	4.6	5.1	6.5	7.26	2.0E-03
BF2099	putative ATP-binding ABC transporter protein	11.8	11.1	17.3	27.7	30.6	35.4	2.37	1.3E-02
BF2100	hypothetical protein	204.4	223.7	206.9	259.5	218.9	262.7	1.16	1.2E-01
BF2101	putative GTP-binding cell division protein	104.8	84.9	99.1	118.1	105.2	111.2	1.16	1.5E-01
BF2102	putative transmembrane sodium-solute transporter	59.2	60.7	60.7	49.5	44.7	46.6	0.78	4.7E-03
BF2104	putative transmembrane protein	253.7	296.8	328.4	225.3	259.7	223.7	0.81	1.2E-01
BF2105	hypothetical protein	1298.3	1266.8	1370.0	597.3	646.7	507.0	0.44	2.1E-03

recR	putative RecR-family recombination protein	56.8	40.1	41.8	33.8	33.4	49.6	0.84	4.3E-01
BF2107	putative transmembrane protein	48.6	35.5	53.5	56.5	64.0	59.1	1.32	1.4E-01
BF2108	putative acetyltransferase	96.4	92.1	109.0	92.6	113.5	93.7	1.01	9.6E-01
BF2109	putative transcriptional regulator	323.9	354.1	337.6	301.6	352.9	217.7	0.84	3.7E-01
BF2110	putative amino acid transferase	134.0	112.3	130.4	144.3	152.5	123.4	1.11	3.4E-01
BFt23	tRNA-Asp-GTC	0.0	16.6	20.7	19.7	9.1	40.7	1.05	9.4E-01
BF2111	putative bacteriophage integrase	112.1	104.0	128.8	24.1	16.8	28.7	0.20	2.9E-03
BF2112	putative RNA-directed DNA polymerase from retron	50.5	51.5	53.1	32.9	34.2	31.1	0.63	8.6E-04
BF2113	hypothetical protein	2915.8	3471.6	4169.2	2202.5	3412.1	3114.8	0.82	3.8E-01
BF2114	possible DNA-binding protein	2.4	1.3	2.6	0.0	0.7	0.0	0.35	
BF2115	hypothetical protein	1.2	1.2	1.3	0.0	0.0	0.0		
BF2116	hypothetical protein	1.2	0.6	1.3	0.0	0.0	0.0		
BF2117	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF2118	hypothetical protein	0.0	0.0	1.3	0.4	1.8	0.8	0.62	
BF2119	hypothetical protein	2.2	2.3	1.8	0.5	1.3	1.0	0.42	6.5E-02
BF2120	hypothetical protein	0.0	1.1	1.2	0.0	0.6	0.5	0.49	3.4E-02
BF2121	hypothetical protein	0.7	3.9	0.0	0.0	3.4	0.7	0.91	9.6E-01
BF2122	putative aldo/keto reductase	7.0	6.9	7.8	11.2	11.8	10.3	1.53	4.8E-03
BF2123	putative AraC family transcriptional regulator	8.4	11.5	9.2	25.6	26.7	22.3	2.57	3.9E-03
BF2124	hypothetical protein	39.3	37.2	42.6	51.4	57.2	30.7	1.13	6.3E-01
BF2125	putative aldo/keto reductase	2.0	2.1	1.8	2.0	1.7	4.3	1.26	5.5E-01
BF2126	putative flavoredoxin	1.9	2.2	1.4	1.8	1.5	0.9	0.74	3.5E-01
BF2127	putative aldo/keto reductase	2.3	2.4	2.3	1.6	2.6	2.8	0.97	9.1E-01
BF2128	hypothetical protein	0.9	0.0	2.1	0.9	1.1	0.9	0.69	4.9E-01
BF2131	hypothetical protein	4.9	1.9	2.0	1.7	3.1	2.0	0.81	6.5E-01
BF2132	putative cation efflux protein	4.2	4.7	3.1	2.6	2.3	3.9	0.72	2.4E-01
BF2133	putative aminotransferase	2.0	1.3	1.7	1.4	1.4	1.6	0.91	5.9E-01
BF2134	putative aldo/keto reductase	3.0	1.2	3.1	1.6	1.7	3.6	0.97	9.5E-01
BF2135	putative amidohydrolase	2.4	2.6	1.7	2.1	1.4	1.8	0.80	3.4E-01
BF2136	short chain dehydrogenase	2.9	3.1	2.3	2.5	2.2	1.6	0.75	2.2E-01
BF2137	putative AraC family transcriptional regulatory protein	3.5	4.4	3.8	2.9	1.5	3.3	0.63	1.9E-01
BF2138	possible carboxymuconolactone decarboxylase	3.8	4.7	2.8	6.6	4.7	7.7	1.68	1.1E-01
BF2139	flavodoxin	5.5	8.8	6.1	5.0	5.3	7.4	0.87	5.6E-01
BF2140	hypothetical protein	8.6	0.7	4.4	8.8	10.7	8.9	3.16	2.6E-01
BF2141	putative acetyltransferase	7.0	7.4	9.8	5.3	8.6	8.1	0.90	6.6E-01
BF2142	putative outer membrane protein	12.3	11.8	10.2	9.6	9.6	7.6	0.78	9.2E-02
BF2143	hypothetical protein	0.0	0.9	0.5	0.8	0.5	0.0	0.97	9.6E-01
BF2144	putative 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	1.4	0.7	0.5	1.1	0.5	1.1	1.08	8.9E-01
BF2145	putative aldo/keto reductase	0.3	1.1	0.3	0.4	0.5	0.6	1.05	9.4E-01
BF2146	putative RibD-family protein	0.5	0.0	0.9	0.0	0.0	0.0		
BF2147	hypothetical protein	2.5	3.0	2.9	2.0	2.7	2.8	0.90	4.8E-01
BF2148	putative transmembrane protein	2.1	3.2	3.6	1.8	2.1	1.8	0.65	1.0E-01
BF2149	putative aldo/keto reductase	2.6	2.2	2.9	3.3	2.4	3.8	1.22	3.3E-01
BF2150	putative IS element	12.0	12.8	14.1	19.4	13.0	17.4	1.27	1.9E-01

BF2151	hypothetical membrane protein	20.0	23.2	25.6	14.8	13.0	17.1	0.65	3.2E-02
BF2152	hypothetical protein	4.1	0.0	2.2	1.0	0.0	0.0	0.32	
BF2153	putative lipoprotein	2.6	2.3	2.4	0.4	0.2	0.3	0.11	4.2E-03
BF2154	putative cation transport related membrane protein	0.8	1.0	1.0	0.2	0.6	0.7	0.48	1.8E-01
BF2155	hypothetical protein	3.9	4.0	4.6	1.1	1.0	1.7	0.31	6.4E-03
BF2156	hypothetical protein	7.4	6.3	11.5	3.5	4.3	2.1	0.39	4.8E-02
BF2157	putative lipoprotein	71.2	63.3	70.0	41.5	50.9	40.9	0.65	1.4E-02
BF2158	hypothetical protein	64.3	61.3	56.8	45.1	63.4	43.3	0.82	2.5E-01
BF2159	hypothetical protein	8.2	5.0	10.4	11.1	15.0	6.8	1.38	4.3E-01
BF2160	hypothetical protein	24.1	18.1	24.3	23.0	21.6	21.6	1.01	9.7E-01
BF2161	hypothetical protein	756.3	749.4	838.7	905.2	962.9	769.7	1.12	2.7E-01
BF2162	hypothetical protein	4126.7	3799.2	4439.6	2885.2	2938.3	2754.8	0.69	5.8E-03
BF2163	putative lipoprotein	690.3	624.2	666.9	502.5	551.7	468.9	0.77	2.0E-02
BF2164	putative TonB-related exported protein	504.4	444.0	473.6	320.1	358.8	324.9	0.71	7.5E-03
BF2165	conserved hypothetical lipoprotein	354.6	305.7	304.1	224.6	212.8	259.5	0.72	2.9E-02
BF2166	hypothetical protein	366.9	299.8	323.0	194.5	234.9	257.9	0.69	4.2E-02
BF2167	putative exported membrane protein	395.1	314.8	370.3	192.8	220.7	244.8	0.61	1.7E-02
BF2168	hypothetical protein	40.7	31.0	35.7	8.9	7.0	10.0	0.24	2.0E-03
BF2169	putative TetR-family transcriptional regulator	327.5	333.7	330.8	248.9	257.0	269.1	0.78	2.2E-03
BF2170	putative polyketide synthesis O-methyltransferase	8.2	12.1	10.7	7.4	8.5	10.3	0.85	4.1E-01
BF2171	putative transport-related membrane protein	8.9	8.0	9.4	5.4	6.0	6.8	0.69	2.6E-02
BF2172	putative transport-related membrane protein	11.0	9.8	8.6	6.4	8.5	8.8	0.80	2.0E-01
BF2173	putative two-component regulatory system histidine kinase	3.0	4.8	3.0	2.9	2.5	2.1	0.71	1.9E-01
BF2174	putative AraC-family transcriptional regulator	36.8	39.6	42.1	30.3	34.6	28.7	0.79	4.7E-02
BF2175	hypothetical protein	18.1	22.7	20.9	15.7	16.8	17.0	0.80	6.3E-02
BF2176	putative AsnC-family transcriptional regulator	66.7	56.5	69.3	75.4	79.9	75.2	1.20	8.1E-02
BF2177	hypothetical protein	65.4	65.5	78.0	69.2	83.2	82.0	1.12	3.0E-01
BF2178	putative AraC-family transcriptional regulator	137.2	137.3	154.7	123.9	121.8	122.4	0.86	3.8E-02
BF2179	hypothetical protein	238.4	224.2	249.3	328.1	367.8	302.6	1.40	1.6E-02
BF2180	hypothetical protein	101.7	100.4	101.1	143.8	154.2	134.8	1.43	3.4E-03
BF2181	hypothetical protein	122.2	156.8	144.8	190.5	194.2	186.3	1.35	3.1E-02
BF2182	hypothetical protein	3.7	1.7	2.7	0.9	1.4	0.6	0.36	7.0E-02
BF2183	hypothetical protein	0.4	0.9	0.8	0.5	0.4	0.7	0.80	6.0E-01
BF2184	putative lipoprotein	1.9	2.6	1.6	1.5	1.4	1.7	0.77	2.2E-01
BF2185	hypothetical protein	4.3	5.0	7.3	1.7	4.0	2.1	0.45	8.8E-02
BF2186	hypothetical protein	5.0	6.1	5.3	2.1	1.1	1.4	0.27	8.9E-03
BF2187	hypothetical protein	243.2	236.2	234.8	57.3	63.4	56.2	0.25	7.7E-05
BF2188	hypothetical protein	0.0	0.0	0.0	0.5	0.0	0.0		
BF2189	putative NAD dependent epimerase/dehydratase	68.8	62.4	66.0	51.6	65.1	55.2	0.87	1.8E-01

BF2190	putative two component system histidine kinase/response regulator fusion protein	69.1	65.9	75.4	60.8	65.6	47.9	0.82	1.8E-01
BF2191	hypothetical protein	44.6	45.7	44.6	69.1	66.0	54.3	1.40	2.4E-02
BF2192	putative helicase	118.5	119.1	135.5	234.6	240.0	204.0	1.82	3.6E-03
BF2193	putative hydrolase exported protein	67.5	69.9	69.8	222.7	220.9	181.5	3.00	6.8E-04
BF2194	hypothetical protein	253.7	265.8	289.1	118.7	127.2	106.1	0.43	1.3E-03
BF2195	hypothetical protein	287.5	301.2	317.1	75.0	89.5	75.8	0.26	3.6E-04
BF2196	putative lipoprotein	470.8	466.4	474.8	107.0	110.6	100.9	0.23	1.9E-05
BF2197	hypothetical protein	7.0	7.3	8.2	13.7	11.3	12.8	1.68	6.2E-03
BF2198	hypothetical protein	12.2	15.4	13.6	19.2	22.3	17.5	1.43	3.9E-02
BF2199	hypothetical protein	72.6	71.7	79.9	52.3	57.9	54.7	0.74	7.6E-03
BF2200	hypothetical protein	45.0	44.5	37.4	42.7	51.1	48.5	1.12	2.9E-01
BF2201	putative ligase	61.7	59.7	62.6	65.8	54.2	57.8	0.96	6.3E-01
BF2202	cell volume regulation protein CvrA	157.4	163.1	170.8	159.4	172.9	130.9	0.94	5.6E-01
BF2203	putative uracil permease	87.8	80.1	90.3	82.9	91.8	78.4	0.98	7.9E-01
hcp	hydroxylamine reductase	29.8	37.1	34.5	19.2	23.5	24.4	0.66	2.8E-02
BF2205	putative regulatory protein	149.4	150.8	141.8	70.1	72.4	61.3	0.46	9.6E-04
BF2206	putative two-component system, sensor kinase	34.5	33.9	35.8	39.6	39.3	31.0	1.05	6.5E-01
BF2207	putative two-component system, response regulator	83.4	82.4	84.2	88.4	89.9	79.0	1.03	6.1E-01
BF2208	hypothetical protein	24.4	23.7	27.5	46.8	35.3	40.1	1.61	1.7E-02
BF2209	conserved hypothetical lipoprotein	27.2	25.0	23.5	36.8	38.1	24.0	1.28	2.4E-01
BF2210	putative ABC transport system, membrane protein	28.4	28.7	28.8	1.7	4.5	2.3	0.09	4.3E-03
BF2211	putative ABC transport system, ATP-binding protein	13.6	15.8	15.8	3.0	3.9	2.5	0.20	1.8E-03
BF2212	putative ABC transport system, membrane protein	9.7	10.1	9.4	2.0	3.2	2.4	0.26	2.4E-03
BF2213	putative ABC transport system, ATP-binding protein	6.5	8.0	7.7	3.9	3.6	2.5	0.45	1.6E-02
BF2214	putative ABC transport system, membrane protein	6.4	8.9	7.3	2.5	3.3	2.6	0.37	5.3E-03
BF2215	putative ABC transport system, membrane protein	5.8	7.1	8.1	2.5	3.6	3.3	0.44	1.3E-02
BF2216	putative MatE-family transport-related membrane protein	71.4	69.4	68.6	48.1	43.4	44.9	0.65	1.2E-03
BF2217	putative hydrolase	115.0	97.9	107.8	170.0	163.9	143.7	1.49	1.2E-02
pyrD2	dihydroorotate dehydrogenase	35.1	29.4	27.7	28.4	26.7	29.1	0.92	3.8E-01
BF2219	hypothetical protein	13.9	17.6	15.3	9.2	7.1	9.5	0.55	1.5E-02
panB	3-methyl-2-oxobutanoate hydroxymethyltransferase	213.2	199.8	226.2	227.7	203.0	226.1	1.03	6.8E-01
BF2221	putative transport-related membrane protein	217.1	215.2	212.1	199.3	206.6	197.7	0.94	2.6E-02
BF2222	putative diacylglycerol kinase	232.1	244.4	232.5	158.2	174.2	143.9	0.67	7.1E-03
relA	GTP pyrophosphokinase	258.5	243.9	245.5	193.8	198.8	197.7	0.79	1.6E-03
BF2224	hypothetical protein	201.3	219.7	206.1	341.1	357.6	316.1	1.62	2.1E-03
BF2225	putative RNA-binding protein	14612.6	14346.7	15638.1	1271.3	1841.1	2194.4	0.12	1.2E-03
purT	5'-phosphoribosylglycinamide transformylase	170.9	160.7	162.7	252.8	233.9	246.2	1.48	1.2E-03

atpD	ATP synthase subunit B	676.8	630.0	612.9	239.5	238.6	244.3	0.38	1.1E-04
atpC	ATP synthase epsilon chain	493.5	487.5	421.8	208.0	233.4	191.3	0.45	2.3E-03
BF2229	hypothetical protein	283.8	290.1	322.5	98.2	133.3	113.2	0.38	2.6E-03
BF2230	putative ATP synthase A chain	298.4	315.6	283.9	129.5	140.3	131.4	0.45	3.7E-04
atpE	ATP synthase C chain	266.0	307.7	277.1	202.2	202.7	215.2	0.73	8.2E-03
BF2232	putative ATP synthase B chain	575.4	473.4	440.9	393.6	352.8	375.3	0.76	5.6E-02
BF2233	putative ATP synthase delta chain	415.2	378.4	365.4	282.9	290.2	288.5	0.74	5.6E-03
atpA	ATP synthase subunit A	390.0	369.3	346.9	269.2	255.5	283.7	0.73	7.2E-03
atpG	ATP synthase gamma chain	448.1	425.5	404.4	258.4	270.7	251.7	0.61	1.1E-03
BF2236	putative helicase	81.7	76.5	76.9	91.4	84.2	81.9	1.09	1.3E-01
BF2237	putative thioredoxin	221.9	190.8	207.9	233.8	279.8	198.7	1.14	3.7E-01
BF2238	putative cation efflux-related outer membrane exported protein	90.3	80.1	93.5	111.4	113.1	85.9	1.17	2.6E-01
BF2239	putative cation efflux-related lipoprotein	98.7	81.3	88.8	111.0	112.4	102.8	1.22	6.1E-02
BF2240	putative cation efflux-related membrane protein	108.9	97.0	97.2	106.0	120.5	106.9	1.10	2.3E-01
BF2241	putative two component system response regulator	87.3	80.6	74.8	98.4	92.0	107.3	1.23	5.6E-02
BF2242	putative two component system sensor histidine kinase	67.1	66.4	60.1	77.1	78.0	74.1	1.19	2.4E-02
BF2243	putative MarC-family antibiotic resistance related membrane protein	42.3	46.2	50.7	19.3	20.6	20.1	0.43	7.8E-04
BF2244	putative hydrolase lipoprotein	28.7	26.9	24.0	37.7	35.6	45.0	1.48	2.4E-02
BF2245	putative cobalamin synthesis related methyltransferase protein	41.9	44.8	36.2	52.4	53.1	58.8	1.34	3.1E-02
BF2246	putative exported periplasmic protein	156.6	151.3	129.7	106.1	103.8	122.9	0.76	4.6E-02
BF2247	putative iron transport related membrane protein	107.8	108.9	84.8	84.3	84.2	95.7	0.88	3.1E-01
BF2248	putative iron transport related ATP-binding protein	75.5	75.3	66.3	81.7	73.3	91.5	1.13	2.4E-01
BF2249	putative rhamnose biosynthesis-related protein	50.1	51.2	51.7	78.5	72.5	78.7	1.50	9.5E-04
BF2250	hypothetical protein	80.6	62.2	54.6	73.9	71.5	71.3	1.11	4.8E-01
BF2251	hypothetical protein	22.1	21.8	22.3	12.9	12.6	10.0	0.53	5.2E-03
BF2252	putative two component system response regulator	41.8	55.8	44.1	27.6	28.2	28.7	0.60	1.2E-02
BF2253	putative two component system sensor histidine kinase	95.4	109.6	97.9	23.6	25.3	26.2	0.25	1.9E-04
BF2254	hypothetical protein	7.8	6.9	5.6	1.1	1.0	1.6	0.18	2.9E-03
BF2255	putative sensor histidine kinase	9.0	6.8	6.6	1.7	2.1	3.8	0.33	2.5E-02
fhs	formate--tetrahydrofolate ligase	402.7	399.7	414.2	170.6	184.3	168.8	0.43	1.6E-04
BF2257	hypothetical protein	101.5	103.2	118.3	47.7	44.2	41.7	0.41	9.8E-04
glyA	serine hydroxymethyltransferase	1226.1	1146.9	1237.4	1227.8	1272.5	1199.9	1.03	5.2E-01
BF2259	hypothetical protein	56.2	66.7	70.9	94.7	102.8	90.3	1.49	1.7E-02
BF2260	putative flavoredoxin	131.9	116.9	132.9	182.5	195.7	144.6	1.36	6.4E-02
pyrI	aspartate carbamoyltransferase regulatory subunit	184.5	166.2	203.6	302.6	302.9	247.3	1.54	2.0E-02
pyrB	aspartate carbamoyltransferase catalytic subunit	160.8	164.8	173.1	272.2	266.0	233.0	1.54	4.6E-03
BF2263	hypothetical protein	7.7	13.3	16.0	5.4	7.2	4.1	0.46	7.9E-02
BF2264	hypothetical protein	5.1	4.6	4.8	2.0	2.9	2.4	0.49	8.4E-03

BF2265	putative lipoprotein	2.2	3.5	3.0	1.5	0.7	1.3	0.40	4.3E-02
BF2266	hypothetical protein	82.6	84.0	89.4	25.0	26.3	22.3	0.29	2.8E-04
BF2267	hypothetical protein	77.5	89.7	95.3	34.0	36.8	38.9	0.42	1.6E-03
BF2268	putative peroxidase family protein	438.3	448.0	474.6	305.6	319.6	269.3	0.66	5.8E-03
BF2269	putative lipoprotein	2.1	2.1	2.7	0.2	0.3	0.7	0.14	2.6E-02
BF2270	hypothetical protein	4.7	3.9	5.3	0.9	1.1	1.1	0.22	1.4E-03
BF2271	hypothetical protein	137.9	136.4	150.6	32.2	31.9	36.1	0.24	1.5E-04
BF2272	hypothetical protein	165.8	170.2	192.2	88.6	108.7	89.0	0.54	5.6E-03
BF2273	hypothetical protein	237.7	233.0	252.2	205.6	214.2	178.4	0.83	5.9E-02
BF2274	3-deoxy-manno-octulosonate cytidylyltransferase	367.3	363.9	414.6	348.8	398.7	298.4	0.91	4.3E-01
BF2275	hypothetical protein	16.6	14.8	15.8	14.3	14.4	20.3	1.02	8.8E-01
BF2276	putative penicillin-binding peptidoglycan biosynthesis-related exported protein	265.5	259.7	263.6	197.0	185.7	182.3	0.72	1.1E-03
BF2278	putative peptidase	159.0	133.3	158.7	162.0	164.1	147.6	1.05	5.6E-01
BF2279	hypothetical protein	422.6	237.4	301.9	122.8	144.3	171.6	0.46	3.3E-02
prs	ribose-phosphate pyrophosphokinase	359.6	333.5	366.6	1006.2	956.7	951.1	2.75	1.4E-04
BF2281	putative two component system sensor histidine kinase	75.6	72.6	73.9	44.3	48.1	40.7	0.60	2.3E-03
BF2282	putative two component system response regulator	128.5	111.5	111.4	89.2	103.7	92.0	0.81	5.9E-02
BF2283	putative transport-related membrane protein	121.1	118.7	136.7	78.6	96.7	78.6	0.67	1.9E-02
BFt24	tRNA-Arg-TCT	16.0	7.3	10.1	8.7	13.3	15.4	1.14	7.2E-01
BF2284	putative phage integrase	8.2	11.4	11.7	5.5	5.3	4.4	0.49	1.5E-02
BF2285	hypothetical protein	14.5	13.5	12.6	20.0	13.2	14.3	1.15	4.2E-01
BF2286	hypothetical protein	7.9	9.3	10.6	18.2	17.5	15.9	1.87	8.0E-03
BF2287	hypothetical protein	10.2	12.5	7.7	6.6	6.2	7.7	0.69	1.1E-01
BF2288	hypothetical protein	3.8	3.6	3.2	4.1	4.1	4.4	1.18	7.4E-02
BF2289	hypothetical protein	12.5	12.3	13.8	14.3	13.5	13.6	1.08	2.0E-01
BF2290	hypothetical protein	7.5	7.7	6.8	8.6	9.6	8.5	1.21	5.1E-02
BF2291	hypothetical protein	5.8	9.1	6.0	9.0	11.2	12.1	1.57	9.2E-02
BF2292	hypothetical protein	7.8	4.2	0.9	8.2	6.4	9.8	2.62	2.9E-01
BF2293	hypothetical protein	0.7	1.0	0.9	0.7	1.4	1.5	1.31	4.5E-01
BF2294	hypothetical protein	1.6	1.7	1.3	2.2	2.4	2.2	1.50	2.9E-02
BF2295	hypothetical protein	2.3	2.7	0.9	4.3	2.6	5.7	2.24	1.6E-01
BF2296	hypothetical protein	2.9	2.3	1.6	2.1	5.9	4.5	1.72	2.7E-01
BF2297	hypothetical protein	59.2	76.6	64.8	73.9	89.9	121.7	1.40	1.6E-01
BF2298	hypothetical protein	207.6	216.0	227.5	212.5	236.3	167.8	0.94	6.4E-01
BF2299	hypothetical protein	118.3	107.6	145.3	153.4	187.7	114.3	1.21	3.9E-01
BF2300	hypothetical protein	93.3	99.3	80.7	53.1	72.2	59.8	0.67	4.2E-02
BF2301	putative lipoprotein	615.3	659.9	702.9	1009.6	1029.1	746.1	1.40	6.8E-02
BF2302	hypothetical protein	288.2	273.3	312.4	227.3	233.7	192.9	0.75	3.1E-02
BF2303	hypothetical protein	465.3	539.3	491.1	418.4	385.3	715.7	0.98	9.4E-01
BF2304	hypothetical protein	5.8	5.5	5.0	6.5	10.1	6.8	1.40	1.3E-01
BF2305	hypothetical protein	5.1	5.4	3.9	8.9	7.0	9.4	1.75	2.8E-02
BF2306	hypothetical protein	4.6	5.3	3.4	6.6	6.0	6.7	1.47	7.2E-02
BF2307	hypothetical protein	6.3	6.3	2.9	9.4	7.3	7.6	1.65	1.9E-01
BF2308	hypothetical protein	5.0	6.5	6.4	6.9	9.3	5.9	1.23	3.4E-01
BF2309	hypothetical protein	45.5	51.9	52.5	15.0	18.7	17.5	0.34	1.1E-03

BF2310	hypothetical protein	5.5	8.6	5.5	7.6	6.4	3.9	0.90	7.4E-01
BF2311	putative type I restriction modification system related protein	7.3	7.0	7.0	7.8	7.7	4.1	0.88	6.4E-01
BF2312	hypothetical protein	5.6	3.7	5.6	5.1	5.8	6.8	1.19	4.2E-01
BF2313	hypothetical protein	2.3	2.5	1.9	1.7	3.0	3.1	1.12	7.0E-01
BF2314	hypothetical protein	2.5	2.6	2.0	1.2	3.5	4.1	1.09	8.7E-01
BF2315	hypothetical protein	4.2	4.9	6.4	4.7	4.0	8.5	1.07	8.4E-01
BF2316	hypothetical protein	40.9	38.2	30.5	62.0	58.7	74.8	1.79	1.7E-02
BF2317	hypothetical protein	59.3	78.7	67.7	104.3	103.0	103.7	1.52	1.7E-02
BF2318	hypothetical protein	55.2	64.3	52.1	97.7	88.2	108.2	1.71	9.5E-03
BF2319	hypothetical protein	89.9	96.9	87.2	138.9	135.1	152.8	1.56	3.4E-03
BF2320	hypothetical protein	15.5	18.9	22.6	19.4	29.1	29.0	1.35	2.1E-01
BF2321	hypothetical protein	12.9	20.5	16.3	45.4	45.2	40.3	2.68	6.9E-03
BF2322	hypothetical protein	6.4	5.1	4.1	7.6	10.5	4.1	1.34	4.6E-01
BF2323	hypothetical protein	21.9	17.1	17.7	9.6	13.6	10.3	0.59	3.2E-02
BF2324	putative single-strand binding protein	6.8	4.8	8.0	4.7	4.2	5.2	0.73	1.8E-01
BF2325	putative DNA primase	3.7	4.1	4.5	4.9	5.1	4.8	1.21	5.7E-02
BF2326	hypothetical protein	1.3	2.3	2.9	4.5	1.0	2.9	1.15	8.3E-01
BF2327	putative lipoprotein	1.1	0.6	1.5	1.1	2.3	1.9	1.64	3.1E-01
5S		2411.0	157.8	1128.0	23.7	45.2	127.3	0.07	7.8E-02
BF2328	hypothetical protein	2.2	0.8	4.9	2.1	1.7	2.1	0.97	9.6E-01
BF2329	hypothetical protein	2.0	0.0	2.2	0.0	4.7	2.9	1.74	2.1E-01
BF2329A	hypothetical protein	2.7	1.4	0.0	3.2	3.1	1.9	1.37	5.2E-01
BF2330	putative DNA binding protein	8.6	5.8	7.0	6.9	5.2	7.8	0.93	7.5E-01
BF2331	hypothetical protein	3.5	3.7	4.6	2.0	6.5	3.4	0.90	8.1E-01
BF2332	hypothetical protein	264.2	228.8	298.8	336.9	375.1	240.1	1.19	4.0E-01
BF2334	hypothetical protein	505.9	484.2	498.1	993.7	1088.2	820.2	1.94	5.1E-03
BF2335	para-aminobenzoate synthase component I	28.9	26.9	34.0	35.2	34.0	30.1	1.11	3.5E-01
BF2336	hypothetical protein	38.1	32.1	42.0	55.5	50.0	43.1	1.33	9.4E-02
BF2337	hypothetical protein	225.2	260.4	269.8	210.2	257.7	177.4	0.85	3.1E-01
BF2338	putative hydrolase	225.7	216.5	247.5	266.9	276.4	225.5	1.11	2.9E-01
BF2339	putative amylase	165.6	168.5	166.6	136.7	142.7	108.6	0.77	6.3E-02
BF2340	putative oxidoreductase	158.5	152.8	171.9	131.1	148.2	111.9	0.81	1.1E-01
BF2341	hypothetical protein	205.3	208.2	235.0	172.0	184.5	152.3	0.78	4.8E-02
fsr	putative fosmidomycin resistance protein	18.7	19.3	20.3	16.1	12.6	13.4	0.72	2.7E-02
BF2343	putative glutamine synthetase I	65.5	69.5	75.6	164.6	190.7	143.0	2.35	3.3E-03
BF2344	conserved putative DNA-binding hypothetical protein	18.8	26.4	28.7	46.8	41.8	41.3	1.78	2.8E-02
BF2345	putative oxidoreductase	68.0	56.3	66.4	38.2	39.5	30.3	0.56	1.3E-02
BF2346	hypothetical protein	236.8	236.3	217.3	122.0	122.7	112.9	0.52	6.2E-04
BF2347	hypothetical protein	241.2	255.6	231.3	121.0	140.1	138.6	0.55	2.0E-03
BF2347A	hypothetical protein	109.5	113.0	116.0	4.6	3.8	4.7	0.04	3.7E-05
BF2347B	hypothetical protein	2796.2	2448.4	3063.3	61.8	33.1	51.9	0.02	3.7E-04
BF2348	hypothetical protein	54.4	53.9	54.9	17.6	14.7	21.4	0.33	2.4E-03
BF2349	hypothetical protein	514.9	587.2	529.5	331.5	308.2	303.9	0.58	1.8E-03
sucD	succinyl-CoA synthetase alpha chain	429.6	412.1	410.0	292.2	278.3	307.0	0.70	1.9E-03
sucC	succinyl-CoA synthetase beta chain	470.1	494.9	456.9	319.6	327.5	355.8	0.70	3.8E-03
fabD	malonyl CoA-acyl carrier protein transacylase	439.5	494.6	487.9	776.9	746.5	721.5	1.58	2.2E-03

thiD	phosphomethylpyrimidine kinase	40.6	35.6	39.6	51.1	47.0	47.7	1.26	2.0E-02
BF2354	hypothetical protein	8.9	11.8	9.8	312.5	383.7	298.3	32.59	1.2E-04
BF2355	putative xylulose kinase	6.0	5.1	5.5	215.0	224.2	207.6	38.95	6.4E-06
BF2356	xylose isomerase	14.3	12.4	15.5	606.4	604.0	554.3	42.03	2.2E-05
BF2357	putative sugar-transport membrane protein	6.0	8.2	5.4	290.3	314.5	258.5	44.88	1.7E-04
BF2358	putative phosphodiesterase-nucleotide pyrophosphatase	143.5	155.9	139.3	134.7	116.9	124.8	0.86	7.4E-02
BF2359	putative carbon-nitrogen hydrolase	47.2	47.1	50.1	45.2	40.4	40.0	0.87	5.8E-02
BF2360	putative thioredoxin peroxidase	1258.9	1599.9	1634.8	1401.0	1727.9	1483.6	1.03	8.3E-01
rbp	RNA binding protein	3607.2	4435.8	4696.4	1145.5	1562.1	1297.8	0.31	2.9E-03
ccp	cytochrome-C peroxidase	203.5	288.3	300.7	64.0	69.4	68.8	0.26	2.1E-03
BF2363	putative cytochrome C biogenesis-related protein	189.2	185.3	184.7	73.4	105.0	78.4	0.45	6.5E-03
BF2364	hypothetical protein	336.8	299.5	328.7	277.8	338.6	275.5	0.92	4.1E-01
BF2365	hypothetical protein	24.5	25.6	26.9	24.6	30.7	20.3	0.97	8.4E-01
BF2366	hypothetical protein	47.4	45.4	46.4	14.3	16.0	13.2	0.31	3.6E-04
ileS	isoleucyl-tRNA synthetase	391.4	383.7	411.9	347.8	352.8	302.7	0.84	5.8E-02
BF2368	putative regulatory protein	1206.5	1212.3	1176.5	1314.6	1439.7	1179.6	1.09	2.7E-01
BF2369	putative signal peptidase	403.6	443.9	475.8	394.4	444.1	340.2	0.89	3.3E-01
BF2370	putative lipoprotein	227.5	221.7	253.5	231.4	251.5	199.7	0.97	7.6E-01
BF2371	hypothetical protein	117.1	133.1	141.9	94.3	117.0	97.5	0.79	8.4E-02
BF2372	putative tRNA/rRNA methyltransferase	182.7	170.4	200.2	141.8	147.7	111.7	0.72	5.3E-02
BF2373	hypothetical protein	51.9	50.1	52.3	74.0	80.8	70.3	1.46	3.7E-03
BF2374	putative surface membrane protein	44.9	40.8	46.5	49.2	52.5	41.7	1.08	4.4E-01
BF2375	hypothetical protein	2202.6	1929.0	2416.7	2131.3	2429.8	1772.4	0.96	8.0E-01
BF2376	hypothetical protein	864.5	977.9	937.4	236.7	297.1	202.9	0.26	1.7E-03
BF2377	hypothetical protein	328.5	332.0	324.9	415.9	475.9	331.8	1.23	1.8E-01
BFt25	tRNA-Lys-CTT	43.0	64.2	51.1	28.6	37.6	50.1	0.73	2.4E-01
BF2378	hypothetical protein	15.6	12.8	16.1	12.4	12.3	13.0	0.85	1.4E-01
BF2379	hypothetical protein	77.0	85.3	93.6	21.8	18.7	19.1	0.23	4.1E-04
BFt26	tRNA-Lys-CTT	43.0	64.2	51.1	28.6	37.6	50.1	0.73	2.4E-01
BF2380	putative metallo-beta-lactamase superfamily protein	215.3	215.5	252.1	201.6	202.8	175.0	0.85	1.3E-01
BF2381	putative transport-related membrane protein	49.7	50.8	55.1	118.8	114.7	92.9	2.09	3.7E-03
uxaC	uronate isomerase	51.7	47.9	57.0	55.5	67.1	49.7	1.09	4.9E-01
BF2383	hypothetical protein	258.4	261.1	246.7	308.5	283.1	254.9	1.10	2.3E-01
BF2384	hypothetical protein	411.4	369.2	408.4	293.8	313.0	263.2	0.73	1.7E-02
rfbC2	putative LPS biosynthesis related dTDP-4-dehydrorhamnose 3,5-epimerase	92.6	69.7	78.2	87.1	87.4	79.9	1.06	5.9E-01
rkpK	UDP-glucose 6-dehydrogenase	154.6	144.7	159.4	231.5	234.5	202.9	1.46	7.1E-03
BF2387	putative lipoprotein	82.0	79.5	88.9	78.7	88.2	77.8	0.98	7.4E-01
rhlE	putative ATP-dependent RNA helicase	287.8	284.7	307.8	309.5	321.6	307.7	1.07	1.2E-01
BF2389	putative phosphoserine phosphatase	258.5	219.1	258.4	152.6	165.2	153.1	0.64	6.1E-03
BF2390	hypothetical protein	2539.5	2428.9	2547.3	924.7	902.1	1038.6	0.38	3.6E-04
BF2391	hypothetical protein	182.7	187.0	186.2	124.6	136.4	113.3	0.67	6.0E-03
tgt	queuine tRNA-ribosyltransferase	288.5	286.3	280.4	230.2	229.9	208.6	0.78	6.1E-03
lon	ATP-dependent protease	437.4	431.6	395.1	253.9	249.3	253.1	0.60	7.2E-04
BF2394	hypothetical protein	28.4	38.6	35.6	53.4	53.8	48.8	1.53	2.6E-02

BF2395	hypothetical protein	29.6	28.3	37.0	47.9	47.3	50.1	1.54	1.7E-02
BF2396	hypothetical protein	24.1	30.8	26.5	35.2	52.5	37.9	1.53	6.9E-02
BF2397	hypothetical protein	104.0	109.6	119.0	154.3	165.2	156.2	1.43	4.7E-03
BF2398	hypothetical protein	66.5	64.3	75.5	100.7	107.5	109.3	1.54	5.0E-03
BF2399	hypothetical protein	100.2	90.0	110.0	177.0	196.7	150.8	1.74	1.2E-02
BF2400	hypothetical protein	87.7	74.6	83.0	137.5	157.4	132.8	1.74	5.0E-03
BF2402	hypothetical protein	0.6	2.2	1.3	0.5	0.3	0.8	0.46	2.3E-01
BF2403	hypothetical protein	1.2	0.7	0.0	1.2	0.7	0.0	1.02	9.8E-01
BF2404	putative lipoprotein	1.4	0.8	0.0	1.4	0.0	1.4	1.31	5.6E-01
BF2405	hypothetical protein	0.0	0.4	0.4	1.1	1.8	0.4	2.15	2.6E-01
BF2406	hypothetical protein	0.5	0.5	0.5	0.9	0.0	1.4	2.22	5.7E-02
BF2407	hypothetical protein	0.8	0.0	0.9	0.0	0.0	0.8	0.91	
BF2408	hypothetical protein	0.0	0.6	0.7	1.1	0.0	1.1	1.76	4.1E-03
BF2409	hypothetical protein	0.0	0.4	1.3	0.7	0.5	0.8	0.86	8.5E-01
BF2410	hypothetical protein	2.0	0.0	1.1	0.9	0.0	1.0	0.64	3.5E-01
BF2411	hypothetical protein	1.1	1.1	0.6	1.0	1.2	1.0	1.22	5.0E-01
BF2412	hypothetical protein	0.0	0.5	0.0	1.9	0.0	0.0	3.56	
BF2413	hypothetical protein	1.5	3.1	0.8	0.0	3.4	1.4	1.41	6.6E-01
BF2414	hypothetical protein	1.9	0.7	0.0	0.0	0.0	0.6	0.54	
BF2415	hypothetical protein	1.8	2.1	0.9	1.1	2.0	0.9	0.88	7.8E-01
BF2416	hypothetical protein	2.0	1.3	1.6	1.2	1.4	1.2	0.78	1.9E-01
BF2417	hypothetical protein	2.9	0.8	0.8	0.3	0.8	1.0	0.55	4.1E-01
BF2418	hypothetical protein	1.5	0.0	0.4	1.5	1.3	1.5	1.76	5.2E-01
BF2419	putative proteinase	2.5	4.6	3.4	1.9	2.4	4.7	0.83	6.6E-01
BF2420	hypothetical protein	8.1	7.7	6.1	5.3	5.7	8.0	0.86	4.5E-01
BF2421	hypothetical protein	9.3	6.2	6.4	7.6	4.7	8.3	0.93	8.0E-01
BF2422	hypothetical protein	1.7	2.8	1.0	2.5	0.4	4.5	1.00	1.0E+00
BF2423	hypothetical protein	0.5	0.0	1.1	2.4	0.0	3.0	3.52	1.4E-01
BF2424	hypothetical protein	2.9	3.6	1.4	2.7	1.8	3.5	1.05	9.1E-01
BF2425	hypothetical protein	3.8	4.9	3.4	3.5	2.5	6.2	0.95	9.0E-01
BF2426	hypothetical protein	1.6	1.7	1.1	0.9	1.1	1.3	0.76	2.4E-01
BF2427	putative lipoprotein	1.6	1.7	0.4	2.2	0.4	4.4	1.52	7.2E-01
BF2428	hypothetical protein	0.6	1.3	2.0	1.7	1.4	0.6	0.97	9.6E-01
BF2429	hypothetical protein	1.4	1.1	1.4	0.7	1.4	1.6	0.90	7.4E-01
BF2430	hypothetical protein	102.6	107.4	96.1	70.3	79.6	65.0	0.70	1.5E-02
BF2431	hypothetical protein	258.0	302.1	272.9	148.1	164.4	248.3	0.66	1.0E-01
BF2432	hypothetical protein	0.2	1.6	0.4	1.1	0.4	2.5	2.11	4.8E-01
BF2433	hypothetical protein	1.1	0.9	1.0	1.0	0.8	1.3	1.00	9.9E-01
BF2434	hypothetical protein	0.9	0.9	1.0	0.4	0.0	0.9	0.64	3.7E-01
BF2435	hypothetical protein	0.4	0.4	0.4	1.9	0.9	0.4	2.08	2.5E-01
BF2436	hypothetical protein	1.0	2.5	1.2	1.2	0.9	1.0	0.72	3.9E-01
BF2437	hypothetical protein	0.6	0.8	0.7	0.6	0.2	1.2	0.71	6.2E-01
BF2438	hypothetical protein	1.5	1.3	0.6	1.4	0.3	1.0	0.66	5.6E-01
BF2439	hypothetical protein	0.6	3.1	1.0	1.4	0.9	1.6	1.01	9.9E-01
BF2439A	hypothetical protein	4.0	5.1	5.3	2.1	1.6	2.7	0.45	2.1E-02
BF2439B	hypothetical protein	6.8	7.5	8.7	4.5	4.2	4.6	0.59	7.0E-03
BF2440	hypothetical protein	0.4	2.2	0.0	0.0	0.5	1.2	0.79	8.6E-01
BF2441	hypothetical protein	1166.1	1209.1	1508.0	1796.0	1751.3	1392.2	1.27	1.5E-01
BF2442	hypothetical protein	141.6	121.8	103.7	11.8	10.2	10.0	0.09	2.7E-04
BF2443	hypothetical protein	280.2	329.9	368.6	30.4	31.0	31.8	0.10	1.5E-04
BF2444	putative integrase	80.2	71.5	86.5	30.8	27.9	29.0	0.37	7.0E-04

BFt27	tRNA-Pro-TGG	29.4	45.7	32.4	21.4	5.8	84.6	0.62	6.4E-01
BFt28	tRNA-Pro-TGG	54.3	65.0	27.4	30.0	20.4	86.8	0.82	7.6E-01
BF2445	hypothetical protein	1488.2	1249.5	1188.9	329.9	252.8	260.5	0.21	9.6E-04
BF2447	putative conserved membrane protein	212.1	203.1	206.2	40.1	52.0	44.1	0.22	4.1E-04
BF2448	hypothetical protein	766.7	758.3	648.8	273.9	267.7	310.3	0.39	1.2E-03
BF2449	putative two component system histidine kinase	205.3	201.6	200.2	87.4	79.3	93.1	0.43	5.3E-04
BF2450	putative two component system response regulator	30.4	25.4	23.9	32.8	33.8	37.5	1.31	5.4E-02
BF2451	putative exported outer membrane protein	0.8	1.0	0.7	1.2	0.7	0.8	1.07	8.0E-01
BF2452	hypothetical protein	0.3	0.0	0.5	1.7	2.0	1.4	4.59	2.5E-02
BF2453	putative conserved membrane protein	2.7	2.7	3.4	3.7	4.0	3.8	1.32	4.3E-02
BF2454	putative ABc transport system, membrane protein	4.7	3.4	3.6	3.4	3.2	3.8	0.88	3.7E-01
BF2455	putative ABC transport system, membrane protein	2.9	2.6	2.3	4.2	4.1	2.3	1.32	3.3E-01
BF2456	hypothetical protein	1.5	2.0	2.7	3.1	4.5	3.3	1.79	8.1E-02
BF2457	hypothetical protein	1.5	1.7	1.6	1.6	2.1	1.1	0.98	9.5E-01
BF2458	hypothetical protein	2.3	1.7	2.2	1.6	2.1	1.7	0.87	4.2E-01
BF2459	putative ABC transport system, ATP-binding protein	53.9	51.7	56.7	52.3	59.0	41.1	0.93	6.1E-01
BF2460	hypothetical protein	54.9	52.1	64.8	18.6	28.0	29.5	0.44	1.6E-02
BF2461	putative 8-amino-7-oxononanoate synthase	610.8	384.2	594.1	315.3	375.5	397.8	0.70	1.4E-01
BF2462	hypothetical protein	172.4	167.0	186.9	148.0	148.3	134.6	0.82	2.7E-02
aspS	aspartyl-tRNA synthetase	522.7	538.6	577.8	623.8	634.2	578.5	1.12	8.2E-02
BF2464	hypothetical protein	740.3	754.7	828.8	660.2	721.9	614.1	0.86	9.4E-02
BF2465	putative hydrolase	174.1	163.7	171.0	165.7	178.7	163.0	1.00	9.4E-01
BF2466	putative deiminase	94.9	76.4	93.5	94.4	106.2	78.4	1.05	7.4E-01
BF2467	hypothetical protein	87.9	88.5	88.7	97.2	115.7	116.4	1.24	4.2E-02
BF2468	putative ABC transport system, ATP-binding protein	85.0	77.4	90.1	64.9	79.3	73.6	0.86	1.6E-01
BF2469	putative ABC transport system, membrane protein	36.2	30.0	41.5	30.3	31.1	31.1	0.87	2.7E-01
BF2470	hypothetical protein	20.7	15.8	22.1	20.8	19.5	24.8	1.12	5.0E-01
BF2471	hypothetical protein	119.9	123.7	142.2	193.4	220.8	167.1	1.50	2.8E-02
BF2472	hypothetical protein	161.5	165.9	169.4	183.4	194.9	179.1	1.12	3.3E-02
BF2473	hypothetical protein	180.2	157.5	177.4	161.9	175.2	161.4	0.97	6.3E-01
BF2474	hypothetical protein	781.5	742.3	865.1	1024.3	982.6	917.2	1.23	4.1E-02
BF2475	putative outer membrane exported protein	43.4	52.8	43.8	10.3	10.0	11.3	0.23	3.9E-04
BF2476	putative transport-related protein	43.0	48.2	41.2	11.3	10.2	12.0	0.25	3.7E-04
BF2477	putative drug resistance transport-related membrane protein	60.3	71.6	61.6	16.9	17.3	18.3	0.27	3.1E-04
BF2478	hypothetical protein	54.1	62.6	54.4	56.5	60.8	56.0	1.02	8.4E-01
BF2479	AMP nucleosidase	189.9	171.7	170.8	174.8	184.6	160.1	0.98	7.2E-01
BF2480	hypothetical protein	119.9	124.9	132.8	119.0	119.8	113.5	0.93	1.6E-01
BF2481	putative DNA-binding protein	11.2	10.7	8.5	30.4	34.9	17.1	2.61	3.1E-02
pyrK	putative dihydroorotate dehydrogenase electron transfer subunit	136.5	119.8	153.3	136.7	129.1	124.8	0.96	6.6E-01

pyrD1	putative dihydroorotate dehydrogenase, catalytic subunit	120.9	117.1	133.6	128.7	130.8	118.0	1.02	8.0E-01
trmD	tRNA (guanine-N(1)-)-methyltransferase	105.1	112.4	117.8	111.7	123.2	98.4	0.99	9.3E-01
ligA	putative DNA ligase	132.1	118.4	127.3	111.4	119.7	105.0	0.89	1.2E-01
dapA2	putative dihydrodipicolinate synthase	534.1	543.3	566.8	444.5	412.9	389.9	0.76	8.0E-03
BF2487	putative chloramphenicol acetyltransferase	57.4	59.6	69.7	133.9	138.1	126.6	2.14	1.7E-03
BF2488	hypothetical protein	67.3	64.1	77.7	95.0	104.1	64.6	1.24	3.1E-01
BF2489	hypothetical protein	145.1	149.5	160.4	180.5	223.7	167.6	1.25	1.1E-01
BFt29	tRNA-Arg-ACG	128.0	146.2	221.2	181.9	177.1	462.8	1.53	3.7E-01
BFt30	tRNA-Arg-ACG	136.3	121.8	53.4	68.4	69.7	241.3	1.09	9.0E-01
BFt31	tRNA-Arg-ACG	0.0	0.0	0.0	0.0	0.0	0.0		
BF2490	hypothetical protein	99.2	103.6	108.3	82.5	89.7	72.8	0.78	4.0E-02
htpG	heat shock protein 90	655.1	679.6	529.2	197.8	193.1	129.0	0.28	4.7E-03
clpB	negative regulator of genetic competence	647.1	671.9	560.2	254.2	239.2	238.8	0.39	7.2E-04
gyrA	DNA gyrase A subunit	588.8	647.0	639.3	707.0	692.2	614.3	1.07	3.2E-01
BF2494	hypothetical protein	1932.8	1981.5	2293.4	2136.6	2239.1	1735.4	0.98	8.8E-01
BF2495	hypothetical protein	268.5	275.0	308.1	178.1	190.5	153.1	0.61	9.0E-03
BF2496	putative DNA-binding protein	1026.5	985.2	987.2	1478.7	1645.8	1139.2	1.41	6.3E-02
batE	aerotolerance-related exported protein	349.7	272.0	312.0	210.0	249.4	190.5	0.70	5.0E-02
batD	aerotolerance-related exported protein	438.8	388.6	433.0	293.0	330.2	264.2	0.70	2.1E-02
batC	aerotolerance-related exported protein	454.1	378.0	456.1	306.3	317.1	260.2	0.69	2.6E-02
batB	aerotolerance-related membrane protein	405.4	345.2	390.3	239.0	262.6	235.1	0.65	6.1E-03
batA	aerotolerance-related membrane protein	433.2	422.7	453.0	260.4	284.0	250.5	0.61	1.6E-03
BF2502	putative conserved membrane exported protein	392.7	414.7	434.7	281.7	305.1	250.4	0.67	9.9E-03
BF2503	hypothetical protein	579.9	530.9	611.5	472.3	494.5	407.2	0.80	5.9E-02
BF2504	putative magnesium chelatase	648.4	612.1	640.3	563.2	615.7	472.8	0.86	1.9E-01
BF2505	hypothetical protein	236.9	200.5	227.2	180.3	202.9	180.7	0.85	9.8E-02
hup2	putative histone-like DNA-binding protein HU2	215.3	210.9	229.7	190.2	249.9	162.3	0.90	5.5E-01
BF2507	putative oxidoreductase	250.3	181.2	229.0	165.2	202.1	179.2	0.83	2.4E-01
ftsY	putative recognition particle-docking protein	223.0	160.1	199.8	134.3	156.4	158.9	0.78	1.3E-01
rpmG	50S ribosomal protein L33	2290.1	1901.7	2551.6	2778.4	2605.0	2419.1	1.16	2.5E-01
rpmB	50S ribosomal protein L28	1648.9	1385.7	1756.2	2099.8	2021.8	1967.1	1.28	5.2E-02
BF2511	putative competence-damage inducible	123.1	87.5	108.3	76.0	87.8	89.9	0.80	1.7E-01
BF2512	putative glycoprotease	143.9	106.0	116.4	82.6	89.5	95.9	0.74	6.5E-02
BF2513	hypothetical protein	89.4	91.6	91.8	61.2	65.7	60.1	0.68	1.2E-03
BF2514	putative conserved hypothetical membrane protein	225.5	228.1	240.2	217.3	219.8	199.5	0.92	1.2E-01
proS	prolyl-tRNA synthetase	371.2	318.5	321.9	415.2	372.3	383.4	1.16	1.1E-01
BF2516	hypothetical protein	40.6	40.3	39.9	25.9	27.5	21.2	0.61	9.9E-03
BF2517	putative exported tricorn protease	158.5	168.2	146.6	174.0	166.3	167.1	1.07	2.3E-01
BFt32	tRNA-Gly-CCC	7.0	12.3	5.1	15.4	13.4	33.4	2.51	1.2E-01
cobP	bifunctional cobalamin biosynthesis protein	35.0	35.1	36.7	47.7	40.1	42.4	1.22	4.0E-02

BF2519	putative phosphoribosyltransferase	41.6	41.8	38.9	74.9	68.3	75.2	1.78	8.6E-04
BF2520	putative cobalamin 5'-phosphate synthase	40.1	44.1	38.7	68.8	72.5	70.5	1.73	1.3E-03
BF2521	putative alpha-ribazole-5'-phosphate phosphatase	47.2	35.4	46.3	61.3	59.9	65.4	1.46	3.4E-02
BF2522	putative cobalamin biosynthesis protein	58.8	53.3	54.4	64.7	49.7	79.3	1.14	4.6E-01
BF2523	putative histidinol-phosphate aminotransferase	95.4	100.1	83.0	113.8	100.5	140.2	1.27	1.5E-01
cbiP	cobyric acid synthase	105.3	108.3	90.4	96.4	80.5	139.7	1.02	9.4E-01
BF2525	conserved hypothetical DNA-binding protein	18.7	14.9	13.0	6.1	8.5	12.0	0.56	9.0E-02
BF2526	hypothetical protein	141.0	109.5	127.9	124.9	124.5	96.8	0.91	5.4E-01
BF2527	hypothetical plasmid-stabilisation protein	80.6	74.7	74.4	65.0	95.8	63.2	0.96	8.1E-01
BF2528	putative outer membrane protein	54.0	64.2	47.8	13.8	9.9	16.1	0.24	3.9E-03
BF2529	hypothetical protein	54.2	55.4	52.1	13.9	10.8	14.1	0.24	6.4E-04
BF2530	hypothetical protein	47.1	56.8	54.5	11.0	11.6	12.1	0.22	2.6E-04
BF2531	hypothetical protein	48.7	52.6	40.1	11.8	8.1	12.4	0.23	3.0E-03
BF2532	putative two-component system sensor histidine kinase	29.7	33.7	31.9	18.2	18.6	24.2	0.64	2.3E-02
BF2533	putative cobalamin adenosyltransferase	38.3	38.8	41.5	49.1	44.3	61.7	1.30	9.8E-02
cobB	cobyrinic acid A,C-diamide synthase	114.2	119.9	118.9	136.4	122.4	152.8	1.16	1.3E-01
BF2535	hypothetical protein	45.4	56.7	61.3	98.5	96.7	90.3	1.76	1.1E-02
BF2536	hypothetical protein	38.1	39.8	48.8	82.2	68.5	80.8	1.83	9.2E-03
BF2537	hypothetical protein	59.0	78.4	89.4	105.9	103.5	104.8	1.40	8.2E-02
BF2538	hypothetical protein	36.5	44.7	55.2	64.6	61.1	72.2	1.47	7.0E-02
Cobalamin	RF00174	180.9	210.5	140.2	136.1	101.2	240.7	0.85	6.6E-01
Cobalamin	RF00174	167.9	184.7	178.6	267.0	197.7	431.4	1.60	1.6E-01
BF2539	putative iron transport-related exported protein	67.2	90.1	106.2	277.1	223.2	244.9	2.87	6.5E-03
BF2540	putative cobalt chelatase	88.0	121.5	137.7	330.9	299.6	278.7	2.66	7.3E-03
BF2541	putative transport-related exported protein	98.6	142.4	162.1	286.0	266.9	259.4	2.06	2.0E-02
BF2542	hypothetical protein	50.6	75.8	93.1	142.5	128.4	130.9	1.89	4.6E-02
BF2543	putative cobalamin biosynthesis-related membrane protein	21.5	31.3	35.4	57.1	52.2	53.1	1.88	2.9E-02
BF2544	hypothetical protein	10.7	13.0	20.1	28.9	32.8	27.5	2.10	3.6E-02
BF2545	putative transport-related membrane protein	18.6	26.1	29.2	52.2	55.5	49.0	2.16	1.4E-02
BF2546	putative conserved membrane protein	14.6	22.4	20.2	52.2	50.0	49.2	2.69	5.6E-03
cobJ	precorrin-3B C17-methyltransferase	74.8	79.5	77.2	87.1	87.1	92.7	1.15	1.6E-02
BF2548	putative bifunctional CbiE/CbiT cobalamin biosynthesis protein	125.1	145.5	145.3	184.0	149.3	236.9	1.35	1.5E-01
BF2549	putative bifunctional CbiF/CbiG cobalamin biosynthesis protein	44.5	53.2	48.5	56.5	53.5	58.4	1.15	1.1E-01
BF2550	putative bifunctional CbiD/CbiJ cobalamin biosynthesis protein	52.5	53.9	50.9	53.1	52.8	57.5	1.04	3.8E-01
BF2551	putative lipoprotein	78.3	98.1	96.9	68.2	53.9	55.2	0.65	3.0E-02
BF2552	putative hexokinase	183.2	167.8	168.6	62.5	58.6	53.1	0.33	4.1E-04
BF2553	hypothetical protein	106.9	134.0	104.7	61.9	44.0	43.3	0.43	1.1E-02

BFt33	tRNA-Gly-GCC	0.0	0.0	0.0	0.0	0.0	0.0		
BFt34	tRNA-Leu-CAG	1100.4	1518.4	1161.7	2020.0	1423.1	2442.5	1.54	1.3E-01
BFt35	tRNA-Gly-GCC	1513.7	1535.7	1292.6	2605.2	1997.2	3826.4	1.88	5.7E-02
BFt36	tRNA-Leu-GAG	497.8	681.5	557.5	862.1	775.8	1731.1	1.83	1.3E-01
BFt37	tRNA-Leu-CAG	628.8	404.9	335.6	754.1	672.7	2128.0	2.33	1.6E-01
BFt38	tRNA-Gly-GCC	0.0	0.0	0.0	0.0	0.0	0.0		
BF2554	putative carboxynorspermidine decarboxylase	52.2	55.6	49.3	72.6	73.5	83.3	1.46	7.8E-03
BF2555	putative helicase	79.4	85.9	63.0	97.7	80.0	132.6	1.34	2.2E-01
sodB	superoxide dismutase [Fe]	4746.9	5519.4	4446.6	2335.9	2048.5	2631.1	0.48	5.4E-03
TPP	RF00059	119.5	125.1	108.6	41.4	24.2	51.0	0.32	1.7E-02
BF2557	putative thiamine biosynthesis-related protein	94.5	79.6	63.8	16.9	17.5	29.1	0.26	8.8E-03
thiE	thiamine-phosphate pyrophosphorylase	21.8	20.8	17.7	6.0	4.0	9.1	0.30	1.9E-02
thiG	thiazole synthase	19.3	20.5	17.3	14.9	8.9	17.6	0.70	2.2E-01
thiC	thiamine biosynthesis protein ThiC	15.9	17.8	14.2	13.2	9.2	16.3	0.79	3.2E-01
BF2561	hypothetical protein	12.4	13.5	9.5	9.9	10.7	12.8	0.95	7.7E-01
thiH	thiamine biosynthesis protein ThiH	14.1	14.5	13.6	14.3	12.0	14.4	0.96	6.2E-01
BF2563	putative molybdopterin biosynthesis-related protein	9.0	10.7	8.3	11.7	9.6	16.4	1.32	2.5E-01
BF2564	putative thiamine phosphate pyrophosphorylase	551.7	525.8	593.8	460.2	485.4	437.5	0.83	3.1E-02
BF2565	hypothetical protein	104.2	107.2	120.1	61.3	64.1	57.4	0.55	1.9E-03
BF2566	hypothetical protein	816.0	804.8	777.5	793.9	901.4	823.2	1.05	3.7E-01
ppdK	pyruvate phosphate dikinase	203.4	225.1	217.5	732.6	719.5	839.3	3.54	3.1E-04
BF2568	putative RNA methyltransferase	147.6	141.5	146.0	165.8	168.3	161.4	1.14	5.9E-03
BF2569	putative RNA pseudouridylate synthase	189.9	226.3	200.4	219.7	200.7	210.0	1.02	7.5E-01
BF2570	putative lipoprotein	186.5	190.9	189.0	196.6	224.5	214.4	1.12	7.6E-02
BF2571	putative lipoprotein	232.0	198.9	203.7	219.5	240.0	247.5	1.12	2.0E-01
BF2572	hypothetical protein	2.4	3.8	1.3	4.6	5.6	2.3	1.69	3.4E-01
BF2573	hypothetical protein	1.3	2.1	6.6	7.0	8.5	5.1	2.53	1.9E-01
BF2575	hypothetical protein	3.9	4.5	2.9	6.0	6.1	6.8	1.69	3.5E-02
BF2576	putative aminopeptidase	123.0	121.2	115.0	89.4	79.8	83.6	0.70	3.4E-03
BF2577	putative DNA recombination-related protein	70.9	71.6	68.4	67.2	59.9	63.2	0.90	7.4E-02
BF2578	hypothetical protein	53.4	59.7	46.5	46.8	49.2	45.5	0.89	2.6E-01
BF2579	putative Na+/H+ antiporter	204.8	223.3	211.3	127.9	144.0	141.8	0.65	2.8E-03
BF2580	putative transport-related membrane protein	292.9	275.6	279.5	230.1	236.9	194.7	0.78	3.4E-02
BF2581	GTP-binding protein LepA	265.0	278.7	259.1	274.4	257.3	288.6	1.02	6.8E-01
BF2582	hypothetical protein	2145.5	2487.6	2605.2	1348.7	1567.2	1896.6	0.66	4.2E-02
BF2583	hypothetical protein	94.9	84.8	85.2	96.0	86.1	116.9	1.12	3.7E-01
BF2584	hypothetical protein	150.3	140.2	132.8	127.8	138.7	154.5	0.99	9.3E-01
exoA	exodeoxyribonuclease	249.6	246.1	248.4	174.0	172.7	191.3	0.72	2.7E-03
BF2586	putative manganese transport-related membrane protein	147.3	149.7	158.7	52.1	65.2	59.8	0.39	1.0E-03
BF2587	putative lipoprotein	236.2	269.8	273.9	183.0	181.4	151.6	0.66	1.5E-02
BF2588	hypothetical protein	571.0	587.5	578.2	594.8	563.9	611.7	1.02	5.7E-01
BF2589	hypothetical protein	632.6	564.1	643.7	734.9	730.0	733.3	1.20	2.7E-02

pheT	phenylalanyl-tRNA synthetase beta subunit	348.5	337.7	348.1	358.6	377.7	367.4	1.07	4.3E-02
BF2591	putative LPS biosynthesis related glycosyltransferase	13.7	13.6	14.3	8.4	7.9	7.6	0.58	6.0E-04
BF2592	putative LPS biosynthesis related DNTP-hexose dehydratase-epimerase	13.8	14.5	13.0	6.9	9.8	6.0	0.54	2.9E-02
BF2593	putative LPS biosynthesis related glycosyltransferase	16.4	15.6	16.2	8.4	8.5	7.2	0.50	1.4E-03
BF2594	putative LPS biosynthesis related glycosyltransferase	13.4	13.3	13.1	6.3	6.6	6.4	0.48	4.1E-05
BF2595	putative LPS biosynthesis related glycosyltransferase	12.2	13.3	12.9	5.5	11.0	5.6	0.54	9.1E-02
BF2596	putative LPS biosynthesis related polysaccharide polymerase	8.9	6.6	6.7	1.0	2.2	1.7	0.21	1.0E-02
BF2597	putative LPS biosynthesis related glycosyltransferase	7.7	7.0	10.1	2.8	4.8	2.6	0.39	3.0E-02
BF2598	putative LPS biosynthesis related polysaccharide transporter/flippase	10.1	9.9	16.6	5.1	4.7	4.1	0.39	1.6E-02
BF2599	putative LPS biosynthesis related glycosyltransferase	19.9	24.9	20.1	11.9	13.0	9.2	0.52	1.6E-02
rfbE	DNTP-hexose dehydratase-epimerase	26.8	27.4	27.2	13.0	16.6	14.4	0.54	4.0E-03
BF2601	putative LPS biosynthesis related DNTP-hexose dehydratase-epimerase	29.5	28.0	31.0	11.3	14.2	13.9	0.44	2.4E-03
BF2602	putative LPS biosynthesis related DNTP-hexose dehydratase-epimerase	26.3	21.5	25.7	14.1	14.8	13.6	0.58	4.6E-03
BF2603	putative LPS biosynthesis-related sugar-phosphate nucleotidyltransferase	22.5	15.7	17.5	7.7	7.6	12.2	0.49	3.6E-02
BF2604	putative LPS biosynthesis related DNTP-hexose dehydratase-epimerase	20.6	21.9	25.3	14.1	20.9	14.2	0.72	1.2E-01
upeZ	putative transcriptional regulatory protein	19.0	19.0	19.7	11.8	12.7	13.0	0.65	1.1E-03
upeY	putative transcriptional regulatory protein	43.5	41.6	40.1	17.1	21.3	15.7	0.43	3.5E-03
BF2607	hypothetical protein	95.5	95.2	104.0	179.9	184.4	163.5	1.79	1.4E-03
BF2608	hypothetical protein	105.9	98.4	107.2	153.0	173.3	147.7	1.52	5.6E-03
BF2609	putative DNA helicase	106.6	108.8	105.6	113.0	120.0	119.3	1.10	2.4E-02
BF2610	putative terpenoid biosynthesis-related protein	38.3	37.3	40.0	54.7	56.7	56.6	1.45	7.3E-04
BF2611	putative lipoprotein	26.1	27.6	28.7	62.2	68.9	56.2	2.27	1.4E-03
BF2612	putative lipoprotein	23.9	27.6	25.1	30.0	31.8	27.4	1.16	1.0E-01
galE	UDP-glucose 4-epimerase	1022.6	1095.1	1187.4	1135.4	1246.7	1054.6	1.04	6.5E-01
rnfA	electron transport complex protein RnfA	106.2	113.7	119.4	397.2	422.5	377.8	3.53	1.8E-04
rnfE	NADH-ubiquinone oxidoreductase	54.6	71.2	68.1	237.8	256.1	213.6	3.66	1.1E-03
rnfG	electron transport complex protein RnfG	46.7	60.6	64.5	201.0	230.6	208.2	3.75	1.4E-03
rnfD	electron transport complex protein RnfD	48.9	55.4	62.8	205.3	232.1	196.7	3.81	8.0E-04
rnfC	electron transport complex protein	52.1	54.3	59.7	231.1	242.0	239.5	4.30	9.1E-05
BF2619	ferredoxin	31.9	46.7	46.7	193.1	184.2	214.3	4.78	1.7E-03

BF2620	hypothetical protein	75.2	87.6	96.2	117.1	110.4	134.2	1.40	4.1E-02
BF2621	hypothetical protein	181.2	159.9	165.0	128.0	151.3	120.0	0.79	6.5E-02
BF2622	hypothetical protein	626.3	632.8	674.8	631.6	637.9	564.6	0.95	3.7E-01
BF2623	hypothetical protein	0.7	0.7	0.0	0.0	0.0	0.6	0.93	
pyrG	CTP synthetase	608.0	592.9	627.7	629.8	595.9	559.9	0.98	6.2E-01
BF2625	putative inner membrane protein translocase component YidC	775.8	796.1	807.9	644.4	673.8	594.6	0.80	1.2E-02
BF2626	putative transpor-related membrane protein	29.7	35.8	38.2	27.0	28.4	23.5	0.76	7.6E-02
BF2627	putative exported aminopeptidase	200.5	197.1	182.9	241.5	221.3	237.7	1.21	2.0E-02
BF2628	hypothetical protein	56.2	38.1	41.2	22.2	24.8	32.8	0.59	5.9E-02
BF2629	hypothetical protein	77.3	92.1	79.3	72.5	62.0	70.4	0.82	9.0E-02
BF2630	putative PadR-family transcriptional regulatory protein	27.8	17.9	18.5	20.9	15.2	20.7	0.89	6.2E-01
BF2631	putative acetyltransferase	46.8	44.1	40.6	114.5	109.9	102.7	2.49	5.7E-04
BF2632	putative transport-related membrane protein	308.8	344.0	338.9	674.3	702.0	609.4	2.00	1.3E-03
BF2633	putative regulatory protein	56.6	57.5	58.3	57.1	63.0	58.9	1.04	3.5E-01
uvrA1	UvrABC SOS-repair system protein excinuclease A	178.6	169.0	178.0	170.5	163.5	168.4	0.96	1.6E-01
BF2635	conserved exported hypothetical protein	273.1	275.3	274.9	166.2	176.9	159.6	0.61	6.5E-04
BF2636	putative conserved exported protein	189.9	192.7	227.0	150.0	146.9	133.9	0.71	1.6E-02
BF2637	hypothetical protein	308.6	266.5	329.0	246.0	285.6	259.6	0.88	2.2E-01
BF2638	hypothetical protein	1319.2	1223.9	1433.0	1560.9	1569.3	1396.0	1.14	1.4E-01
BF2639	conserved hypothetical lipoprotein	918.9	917.2	1024.2	645.2	719.1	604.7	0.69	1.1E-02
BF2640	hypothetical protein	129.2	119.0	138.7	362.0	408.6	331.0	2.84	1.0E-03
paaK1	putative phenylacetate-coenzyme A ligase	125.6	120.1	120.3	142.3	144.7	126.7	1.13	8.6E-02
uvrB	excinuclease ABC subunit B	158.1	163.6	153.6	148.2	165.5	141.7	0.96	4.9E-01
BF2643	putative transport-related membrane protein	45.3	46.7	48.3	34.8	43.8	42.1	0.86	1.5E-01
BF2644	hypothetical protein	20.7	17.6	16.0	21.1	20.0	18.1	1.09	4.4E-01
BF2646	putative heat-shock related protein	1044.7	1187.8	803.5	88.5	76.2	71.8	0.08	4.2E-04
BF2647	putative two-component system sensor kinase/response regulator fusion protein	40.1	34.0	38.1	26.1	25.4	25.8	0.69	5.7E-03
BF2648	putative ABC transport system, membrane protein	20.3	19.3	24.1	17.5	17.9	15.7	0.80	8.1E-02
BF2649	putative ABC transport system, membrane protein	22.1	28.3	30.2	19.4	17.4	17.8	0.68	3.7E-02
BF2650	putative BAC transport system, two-fused ATP-binding domains protein	36.4	38.4	32.5	32.2	30.2	35.1	0.91	2.9E-01
BF2651	putative ABC transport system, lipoprotein	37.8	33.5	36.4	35.8	28.9	37.4	0.94	6.1E-01
BF2652	hypothetical protein	28.2	31.5	28.6	39.5	33.3	46.1	1.34	7.3E-02
BF2654	conserved hypothetical lipoprotein	45.7	45.6	48.7	210.3	224.7	197.0	4.51	8.9E-05
BF2655	putative AraC-family transcriptional regulator	15.7	15.0	16.4	21.8	19.8	20.2	1.31	7.3E-03
BF2656	putative thioredoxin	730.2	744.4	618.2	198.2	190.5	196.6	0.28	3.5E-04

carB1	putative carbamoyl-phosphate synthase large chain 1	471.4	544.1	420.5	251.2	216.3	286.2	0.52	1.1E-02
carA	carbamoyl-phosphate synthase small subunit	199.4	188.9	163.3	89.8	79.5	116.6	0.51	1.6E-02
BF2659	putative phosphoribosylpyrophosphate amidotransferase	212.1	178.3	151.2	83.4	76.8	119.4	0.51	3.2E-02
asnB	asparagine synthetase B	39.0	42.0	36.8	8.2	6.7	10.8	0.21	2.1E-03
BF2662	hypothetical protein	121.6	119.0	115.3	154.7	172.4	166.8	1.39	3.3E-03
BF2663	hypothetical protein	9.5	7.7	7.1	4.5	7.6	6.6	0.75	2.6E-01
BF2664	hypothetical protein	9.9	8.4	9.8	21.0	17.7	18.4	2.04	2.9E-03
dapF	diaminopimelate epimerase	331.1	319.0	275.4	76.0	55.1	102.9	0.25	5.8E-03
BF2666	aspartate aminotransferase	230.1	247.4	212.4	126.7	108.2	138.3	0.54	6.0E-03
BF2667	hypothetical protein	504.8	608.1	500.7	531.8	524.6	656.5	1.06	6.4E-01
BF2668	polyphosphate kinase	9.3	11.4	9.9	3.9	3.4	4.4	0.38	2.9E-03
BF2669	putative phosphatase	57.9	54.2	58.2	23.9	28.4	31.8	0.49	4.4E-03
BF2670	putative alcohol dehydrogenase	609.7	618.6	587.5	374.3	324.1	376.8	0.59	2.4E-03
trpB	tryptophan synthase subunit beta	152.1	181.9	179.2	100.9	90.0	103.6	0.57	5.3E-03
trpE	anthranilate synthase component I	130.9	211.3	200.2	57.4	61.3	62.6	0.34	6.9E-03
trpG	glutamine amidotransferase	117.1	191.7	168.3	45.0	51.2	48.3	0.31	5.3E-03
trpD	anthranilate phosphoribosyltransferase	149.3	208.2	190.4	52.4	58.9	61.0	0.32	2.2E-03
trpC	indole-3-glycerol phosphate synthase	168.6	222.5	225.8	57.2	48.0	54.8	0.26	1.4E-03
trpF	N-(5'-phosphoribosyl)anthranilate isomerase	116.2	171.1	160.5	44.4	51.6	36.0	0.30	5.4E-03
trpA	tryptophan synthase alpha chain	164.4	210.2	235.3	58.7	58.0	52.8	0.28	1.8E-03
ansA	putative L-asparaginase I	23.3	30.8	28.4	25.1	21.7	21.8	0.84	1.9E-01
BF2681	hypothetical protein	7.3	6.0	6.6	2.3	2.0	2.9	0.36	4.5E-03
BF2682	putative response regulator	103.7	94.4	101.9	52.1	53.0	48.1	0.51	6.9E-04
BF2683	putative sugar transferase-related membrane protein	15.4	14.7	14.9	9.8	11.4	9.8	0.69	7.0E-03
BF2684	hypothetical protein	7.3	6.3	7.6	4.3	3.2	4.0	0.54	1.2E-02
BF2685	putative acetyltransferase	14.3	14.3	11.4	9.0	9.7	7.3	0.65	3.9E-02
BF2686	putative DNA-binding response regulator	450.8	388.0	422.4	425.1	438.4	428.1	1.03	6.6E-01
BF2687	hypothetical protein	780.6	731.1	781.6	720.4	707.8	729.2	0.94	9.9E-02
BF2688	5-aminoimidazole-4-carboxamide ribonucleotide transformylase	29.4	28.1	23.5	40.0	35.6	40.2	1.43	2.3E-02
fldA	flavodoxin	3314.5	2981.3	3277.6	6226.8	5444.1	6157.7	1.86	1.8E-03
BF2690	hypothetical protein	3595.6	3401.7	3952.4	5615.1	5398.8	4694.1	1.43	1.6E-02
BF2692	hypothetical membrane protein	139.7	176.4	174.5	53.4	54.9	58.8	0.34	1.2E-03
BF2693	hypothetical protein	114.2	124.4	120.9	42.2	35.9	37.3	0.32	3.6E-04
BF2694	putative exported thioredoxin	206.2	212.4	205.9	97.0	93.3	97.5	0.46	3.7E-05
BF2695	putative exported methylamine utilization protein	50.2	62.2	58.8	82.9	72.9	82.4	1.39	2.6E-02
BF2696	hypothetical protein	172.8	216.5	199.3	149.1	144.5	197.8	0.83	2.6E-01
Cobalamin	RF00174	279.9	335.7	192.4	237.2	146.3	430.5	0.94	9.0E-01
BF2697	putative exported TonB-dependent receptor protein	988.3	1015.1	924.3	665.6	586.8	648.2	0.65	3.3E-03
BF2698	hypothetical protein	1641.8	1494.4	1396.7	733.9	792.9	818.9	0.52	1.7E-03
BF2699	hypothetical protein	48.9	50.2	48.7	60.8	54.7	58.4	1.18	1.8E-02
BF2700	hypothetical protein	54.9	67.3	59.4	13.1	13.2	15.6	0.23	5.4E-04
BF2701	hypothetical protein	88.6	95.6	87.6	22.6	19.2	26.1	0.25	8.3E-04

BF2702	hypothetical protein	146.2	152.7	147.0	233.1	202.2	255.7	1.54	9.6E-03
BF2703	putative metal transport-related membrane protein	254.1	274.2	256.5	224.3	223.6	242.6	0.88	4.4E-02
BF2704	hypothetical protein	139.8	163.1	143.5	238.4	230.0	232.6	1.57	3.2E-03
BF2705	hypothetical protein	0.0	0.0	0.0	1.2	1.4	0.0		
BF2706	putative lipoprotein	816.2	721.7	844.3	1855.3	1835.5	1464.9	2.16	4.1E-03
BF2707	putative lipoprotein	372.1	372.6	385.4	758.0	715.9	700.8	1.92	2.2E-04
BF2708	putative exported TonB-dependent receptor protein	209.0	198.7	189.9	417.7	387.1	381.2	1.98	5.8E-04
BF2709	putative cobalamin biosynthesis-related protein	281.8	279.4	240.4	426.3	381.4	467.2	1.59	1.1E-02
BF2710	hypothetical protein	197.6	221.4	207.1	340.1	320.2	359.8	1.63	2.3E-03
BF2711	hypothetical protein	366.7	352.3	354.8	499.5	447.9	433.2	1.28	1.3E-02
BF2712	hypothetical protein	420.9	411.0	404.6	581.5	537.3	501.6	1.31	1.0E-02
Cobalamin	RF00174	86.8	89.4	77.5	132.3	96.2	161.4	1.51	9.4E-02
BF2713	ribonucleotide-diphosphate reductase alpha subunit	91.0	88.3	96.2	120.1	105.2	125.5	1.27	3.1E-02
BF2714	ribonucleotide-diphosphate reductase beta subunit	68.7	79.4	88.1	119.0	103.9	124.1	1.47	2.7E-02
BF2715	hypothetical protein	104.2	95.0	92.1	27.5	27.1	34.0	0.30	9.0E-04
BF2716	hypothetical protein	140.2	161.5	146.9	50.8	49.1	53.6	0.34	3.2E-04
BF2717	hypothetical protein	170.7	195.2	169.1	50.0	50.2	46.8	0.28	2.2E-04
BF2718	keto-hydroxyglutarate-aldolase/keto-deoxy- phosphogluconate aldolase	34.0	35.9	38.0	24.2	27.8	44.5	0.86	5.5E-01
BF2719	putative kinase	37.8	28.2	32.2	12.7	13.7	18.1	0.45	1.2E-02
BF2720	putative LacI-family transcriptional regulator	119.0	122.3	125.3	103.3	104.4	101.6	0.84	2.6E-03
BF2721	putative aceyltransferase	54.5	51.6	39.6	49.0	50.3	47.7	1.02	8.9E-01
BF2722	putative regulatory protein	27.2	21.6	20.1	27.6	22.3	37.9	1.26	3.4E-01
BF2723	putative two-component system histidne kinase/reponse regulator fusion protein	10.9	10.3	10.4	5.2	4.0	5.2	0.45	3.5E-03
BF2724	hypothetical protein	11.7	11.5	12.2	5.1	4.0	6.1	0.42	6.5E-03
BF2725	hypothetical protein	17.5	14.7	13.3	7.0	8.6	6.2	0.48	1.1E-02
BF2726	putative peptide chain release factor	14.8	13.3	13.1	5.7	3.6	4.6	0.33	4.5E-03
BF2727	hypothetical protein	15.0	16.2	16.1	6.3	7.0	6.4	0.42	3.3E-04
BF2728	putative cation antiporter	32.3	33.3	35.7	29.7	23.7	25.2	0.77	4.6E-02
BF2729	hypothetical protein	21.3	24.0	20.4	21.6	22.4	25.3	1.05	5.4E-01
BF2730	hypothetical protein	1.0	1.0	1.1	1.8	1.1	1.4	1.39	1.3E-01
rpsP	30S ribosomal protein S16	2565.0	2976.9	2798.9	2891.7	2809.5	3510.5	1.10	3.8E-01
BF2732	hypothetical protein	18.7	15.2	19.6	22.8	18.1	23.9	1.21	2.4E-01
BF2733	putative lipoprotein	20.1	23.2	23.4	23.0	20.8	23.6	1.01	9.1E-01
BF2734	putative RNA-binding protein	8002.5	8313.2	7183.4	2550.2	2471.4	2930.0	0.34	7.2E-04
BF2735	putative ABC transport system, lipoprotein	55.8	54.3	48.1	47.1	38.8	52.1	0.87	2.9E-01
BF2736	putative ABC transport system, membrane protein	47.6	48.5	52.2	54.3	51.8	50.2	1.05	2.9E-01
BF2737	putative ABC transport system, membrane protein	68.5	59.5	68.2	64.3	56.1	58.3	0.91	2.7E-01
BF2738	putative ABC transport system, ATP-binding protein	110.6	92.2	93.5	78.7	60.6	88.3	0.76	1.4E-01

BF2739	putative lipoprotein/thioderoxin	534.5	521.6	512.3	522.6	486.3	449.0	0.93	2.4E-01
BF2740	hypothetical protein	113.3	124.3	118.2	158.5	158.8	162.5	1.35	2.1E-03
BF2741	putative glycogen phosphorylase	564.1	579.0	548.5	852.3	828.9	834.3	1.49	3.0E-04
BF2742	putative glycogen biosynthesis-related protein	241.3	221.8	230.3	301.6	291.4	304.4	1.29	3.2E-03
BF2743	putative V(vacuolar)-type Na+-ATP synthase subunit K	607.3	686.6	642.2	1130.5	1213.8	1176.5	1.82	9.0E-04
BF2744	putative V(vacuolar)-type Na+ ATP synthase subunit I	348.1	351.0	313.4	497.4	486.2	518.3	1.48	2.9E-03
BF2745	V-type ATP synthase subunit D	392.2	340.7	312.3	487.4	458.8	450.6	1.34	2.9E-02
BF2746	V-type ATP synthase subunit B	350.0	375.8	342.2	527.0	515.2	566.1	1.51	2.4E-03
BF2747	V-type ATP synthase subunit A	246.8	233.4	220.5	383.1	396.5	440.9	1.74	2.3E-03
BF2748	hypothetical protein	177.1	157.3	191.1	349.0	428.0	371.0	2.18	3.0E-03
BF2749	putative V-type ATP synthase subunit E	292.0	267.1	319.2	562.5	684.8	599.5	2.10	2.9E-03
5S		0.4	8.6	41.3	2.2	5.2	27.2	1.31	9.0E-01
23S		3.0	2.1	2.4	6.8	2.2	10.0	2.15	2.3E-01
BFt39	tRNA-Ala-TGC	87.0	97.6	97.6	47.1	45.1	95.3	0.62	1.8E-01
BFt40	tRNA-Ile-GAT	158.9	177.9	180.8	63.0	65.0	113.6	0.45	3.1E-02
16S		672.5	32.3	99.0	90.9	32.3	230.2	0.68	7.8E-01
BF2751	hypothetical protein	2.2	0.4	0.8	0.0	0.0	0.7	0.80	
BF2752	putative N-acetylglucosamine-6-phosphate deacetylase	111.8	111.4	99.5	148.8	141.3	148.4	1.36	6.0E-03
BF2753	putative two component system response regulator	30.2	26.9	19.5	52.3	44.3	55.2	2.01	2.0E-02
BF2754	putative two component system histidine kinase	29.3	26.7	25.3	48.7	48.0	52.3	1.83	1.6E-03
BF2755	hypothetical protein	209.5	216.0	200.1	217.3	221.1	207.2	1.03	4.2E-01
BF2756	putative lipoprotein	362.4	309.7	320.1	352.9	336.3	313.1	1.01	8.9E-01
BF2757	putative peptidase	370.0	427.9	402.4	189.8	181.2	197.7	0.47	8.0E-04
BF2758	conserved exported hypothetical protein	347.6	315.1	330.1	436.0	400.4	367.6	1.21	5.1E-02
sigA	putative sigma factor A	1801.0	1857.3	1757.5	1836.3	1678.7	1654.2	0.95	3.3E-01
BF2760	hypothetical protein	415.3	460.5	378.2	477.7	436.5	554.7	1.17	2.1E-01
BF2761	putative heat shock-related protease	491.6	552.2	373.7	354.5	278.5	419.0	0.74	2.0E-01
BF2762	putative lipoprotein	84.9	83.8	68.7	191.4	162.1	215.1	2.39	4.6E-03
BF2763	putative muconate cycloisomerase	64.7	61.3	53.1	156.1	125.5	183.3	2.57	5.5E-03
BF2764	putative peptidase	130.7	123.3	111.9	278.9	256.4	284.0	2.24	8.8E-04
RNaseP_bact_a	RF00010	38110.9	37301.0	24749.4	50496.3	23941.3	107440.2	1.55	4.6E-01
BF2765	putative tRNA processing ribonuclease	369.9	374.1	351.7	176.7	184.5	201.0	0.51	7.3E-04
BF2766	putative nitroreductase	212.7	208.2	192.1	245.0	186.5	310.3	1.19	3.9E-01
ribE	riboflavin synthase subunit alpha	156.8	149.1	122.1	228.8	186.0	273.7	1.60	4.7E-02
BF2768	putative phosphate transport chemotaxis-related protein	16.4	18.5	16.1	30.8	26.4	28.9	1.69	4.4E-03
pstB	phosphate import ATP-binding protein	1.6	1.5	1.3	1.1	1.3	1.1	0.81	1.4E-01
pstA	phosphate transport system permease protein	1.0	1.3	0.9	0.4	0.0	1.9	0.82	8.6E-01
BF2771	putative phosphate-related ABC transport system, membrane protein	0.6	0.3	0.3	0.0	0.0	0.0		
BF2772	putative phosphate-related ABC transport system, exported protein	0.4	0.4	0.7	0.4	0.2	0.2	0.53	1.1E-01
glnS	glutaminyl-tRNA synthetase	222.3	224.5	191.3	226.2	197.3	248.3	1.05	6.5E-01

BF2774	hypothetical protein	101.8	101.9	86.3	112.5	97.4	119.4	1.14	2.6E-01
BF2775	hypothetical protein	110.5	105.0	103.2	160.7	141.3	143.2	1.40	6.2E-03
BF2776	hypothetical protein	249.5	284.9	249.6	285.0	298.5	314.2	1.15	9.5E-02
tpx	putative thiol peroxidase	2542.9	3010.9	2238.5	1306.9	1085.5	1820.5	0.53	4.2E-02
BF2778	hypothetical protein	296.5	368.3	291.8	83.6	76.5	84.3	0.26	6.2E-04
mpi	multiple promoter invertase	8.9	10.7	6.9	2.5	2.8	1.4	0.25	1.2E-02
BF2780	putative recombinase/integrase	3.6	2.8	2.4	1.2	1.4	1.0	0.42	1.2E-02
BF2782	putative EPS related membrane protein	1.4	0.8	0.4	0.4	0.4	0.8	0.66	4.6E-01
BF2783	putative EPS related membrane protein	0.4	0.0	0.2	0.2	0.5	0.6	1.25	7.2E-01
BF2784	putative EPS related membrane protein	0.4	0.5	0.6	0.7	0.3	0.8	1.18	6.8E-01
BF2785	putative N-acetylmuramoyl-L-alanine amidase	0.0	1.3	2.6	2.2	1.4	0.4	0.58	5.3E-01
BF2786	hypothetical protein	0.8	0.0	0.0	0.0	0.0	0.0		
BF2787	hypothetical protein	0.7	0.8	0.0	1.3	0.0	1.4	1.85	7.8E-03
BF2788	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF2789	hypothetical protein	0.3	0.3	0.2	0.1	0.1	0.3	0.42	1.8E-01
BF2790	putative transcriptional regulator (pseudogene)	1.7	1.1	0.4	0.0	0.4	0.3	0.41	2.0E-01
BF2791	putative transmembrane protein	4.3	2.4	4.7	1.1	0.5	1.2	0.24	2.7E-02
BF2792	putative transmembrane protein	1.5	0.9	1.1	0.5	0.8	0.5	0.49	5.8E-02
BF2793	hypothetical protein	1.8	1.3	0.8	0.8	0.4	0.5	0.46	1.1E-01
BF2794	hypothetical protein	2.4	1.5	1.6	0.3	1.3	0.5	0.31	1.0E-01
BF2795	putative glycosyltransferase protein	1.0	1.2	1.1	0.6	0.6	0.2	0.35	1.2E-01
BF2796	putative glycosyltransferase	0.7	1.5	0.8	0.5	0.2	0.9	0.47	2.5E-01
BF2797	putative glycosyltransferase	1.2	2.1	1.8	1.2	1.2	0.5	0.55	1.9E-01
BF2798	putative acetyltransferase	1.3	1.7	1.4	0.0	0.0	1.2	0.84	
BF2799	possible glycosyltransferase	1.0	1.3	1.7	1.0	0.2	0.8	0.41	2.3E-01
BF2800	putative transmembrane protein	0.6	1.3	0.7	0.7	0.4	0.6	0.65	3.2E-01
BF2801	putative glycosyltransferase protein	0.9	1.1	0.4	0.3	0.4	0.2	0.39	1.3E-01
BF2802	putative acyltransferase transmembrane protein	1.4	1.7	1.0	0.5	0.8	0.3	0.39	6.2E-02
BF2803	putative acetyltransferase	1.9	1.3	2.4	0.3	0.4	0.6	0.22	1.3E-02
BF2804	putative glycosyltransferase	1.2	1.1	1.5	1.3	1.6	1.0	1.01	9.7E-01
BF2805	putative 4Fe-4S binding protein	2.1	1.6	2.7	1.3	0.8	1.9	0.60	2.0E-01
BF2806	hypothetical protein	2.0	1.9	1.3	2.3	1.8	1.6	1.08	7.2E-01
BF2807	putative glycosyltransferase protein	0.9	1.1	0.5	0.8	1.2	0.8	1.22	5.8E-01
BF2808	putative acetyltransferase/glucosyltransferase	3.7	5.0	3.5	0.7	1.4	0.7	0.22	1.2E-02
BF2809	hypothetical protein	2.0	2.4	1.7	0.9	0.3	1.0	0.32	8.3E-02
BF2810	hypothetical protein	1.6	1.4	2.0	0.4	0.2	1.1	0.26	1.1E-01
BF2811	hypothetical protein	1.9	1.0	1.8	1.3	1.4	1.2	0.85	5.6E-01
BF2812	hypothetical protein	3.7	1.6	2.7	1.5	2.1	1.5	0.65	2.5E-01
BF2813	putative transmembrane protein	1.0	1.8	1.1	0.7	1.6	1.3	0.86	7.2E-01
BF2814	hypothetical protein	1.3	1.1	1.2	0.5	0.3	1.0	0.45	1.3E-01
BF2815	hypothetical protein	1.0	0.9	0.7	0.8	0.7	0.0	0.90	4.1E-01
BF2816	hypothetical protein	2.9	3.9	2.3	1.2	1.0	0.4	0.26	4.1E-02
BF2817	putative nucleotidyltransferase	32.1	31.8	34.4	9.9	7.0	9.8	0.27	1.8E-03
BF2818	hypothetical protein	4.5	11.6	7.0	12.0	13.6	16.5	1.95	1.2E-01

BF2819	putative Na+ transport decarboxylase membrane protein	259.0	239.8	234.1	518.8	544.1	504.4	2.14	3.9E-04
BF2820	putative pyruvate carboxylase	138.5	125.2	122.2	318.4	312.7	322.6	2.47	2.8E-04
BF2821	hypothetical protein	123.8	143.3	121.3	238.5	232.8	192.9	1.71	9.4E-03
BF2822	putative nucleotidase	23.5	18.7	21.2	17.9	21.3	21.3	0.96	6.9E-01
BF2823	hypothetical protein	7.3	10.0	9.5	3.6	5.3	2.6	0.41	3.6E-02
BF2824	hypothetical protein	275.1	278.1	315.5	381.2	344.4	324.4	1.21	7.1E-02
BF2825	putative racemase	178.6	181.5	205.6	298.0	281.9	261.6	1.49	7.4E-03
BF2826	dihydroorotate dehydrogenase	306.2	307.6	337.8	601.5	651.0	528.5	1.87	3.4E-03
BF2827	putative phage-related protein	22.4	21.0	22.5	21.2	21.8	22.4	0.99	8.5E-01
BF2828	hypothetical protein	4.2	5.5	5.7	6.4	7.2	8.5	1.44	8.0E-02
BF2829	hypothetical protein	3.5	4.8	3.8	4.0	3.2	3.3	0.87	3.7E-01
BF2830	hypothetical protein	6.7	4.8	10.7	16.9	7.8	14.3	1.77	2.2E-01
BF2831	hypothetical protein	4.9	7.0	5.4	5.4	3.7	7.4	0.93	8.1E-01
BF2832	hypothetical protein	14.8	12.7	15.8	14.4	14.6	10.2	0.90	5.4E-01
BF2833	hypothetical protein	1.6	1.3	4.0	2.7	0.9	3.1	0.98	9.7E-01
BF2835	hypothetical protein	0.5	0.0	0.6	0.0	0.6	0.5	1.00	9.8E-01
BF2836	hypothetical protein	0.6	0.6	0.9	0.4	0.2	0.6	0.53	1.4E-01
BF2837	putative NRPS-secondary metabolite biosyntehsis-related protein	0.9	0.4	0.9	0.4	0.6	0.2	0.54	2.8E-01
BF2838	putative iron-transport related outer membrane protein	1.0	0.8	0.8	0.8	0.6	0.5	0.72	1.9E-01
BF2839	putative two-component system, histidine kinase	0.8	0.7	0.2	0.6	0.2	0.2	0.61	4.6E-01
BF2840	putative two-component system, histidine kinase	0.2	0.1	0.3	0.2	0.4	0.3	1.31	5.0E-01
BF2841	hypothetical protein	0.3	0.7	0.4	0.2	0.4	0.1	0.46	2.1E-01
BF2842	putative anti sigma factor	0.0	0.4	0.0	0.4	0.0	0.4	0.90	
BF2843	putative anti-anti sigma factor	0.0	0.0	0.0	0.0	0.0	0.0		
BF2844	putative regulatory protein	0.0	0.5	0.2	0.0	0.0	0.0		
BF2845	hypothetical protein	0.3	1.2	0.9	1.3	0.3	0.5	0.91	9.1E-01
BF2846	hypothetical protein	2.6	1.7	2.3	0.5	2.4	2.0	0.62	4.8E-01
BF2847	hypothetical protein	1.1	3.4	3.5	2.7	0.0	2.7	1.16	7.8E-01
BF2848	putative capsular polysaccharide biosynthesis protein	82.7	89.4	95.1	150.4	145.8	129.4	1.59	5.5E-03
BF2849	conserved hypothetical PhoH-like protein	229.3	236.9	221.0	290.7	320.9	281.9	1.30	1.1E-02
BF2850	putative folylpolyglutamate synthase	36.8	36.5	31.1	50.2	44.2	50.0	1.39	2.1E-02
BF2851	conserved hypothetical translation inhibitor protein	313.1	380.2	347.5	471.1	452.1	474.5	1.35	1.7E-02
BF2852	hypothetical protein	233.4	232.0	230.6	236.5	242.3	211.0	0.99	8.5E-01
BF2853	putative tRNA:rRNA methyltransferase	223.1	234.5	239.1	216.2	207.0	213.1	0.91	3.9E-02
recN	DNA repair protein	206.1	211.6	208.7	245.8	230.5	223.7	1.12	3.6E-02
dfp	DNA/pantothenate metabolism flavoprotein	315.2	358.1	324.5	382.4	362.7	374.0	1.12	8.1E-02
BF2856	putative DNA polymerase III epsilon chain	426.3	448.6	462.7	515.3	526.3	468.7	1.13	7.9E-02
BF2857	putative DNA polymerase III beta chain	636.5	649.3	676.7	714.9	749.8	656.8	1.08	2.0E-01
BF2858	hypothetical protein	948.6	988.5	841.5	836.2	709.8	895.1	0.88	2.5E-01
BF2859	putative conserved exported protein	151.7	160.5	154.2	210.0	222.5	221.9	1.40	1.1E-03
BF2860	putative hydrolase	181.6	204.5	181.5	124.7	124.4	125.3	0.66	2.3E-03

murB	UDP-N-acetylenolpyruvoylglucosamine reductase	70.5	59.6	53.5	92.1	59.3	140.5	1.51	2.5E-01
BF2862	hypothetical protein	84.2	87.1	84.3	148.9	151.5	166.3	1.82	6.4E-04
BF2863	putative epimerase	223.2	218.4	222.0	352.5	313.1	355.6	1.54	2.3E-03
kbl	2-amino-3-ketobutyrate coenzyme A ligase	378.0	396.4	361.8	778.5	719.5	761.7	1.99	4.2E-04
BF2865	hypothetical protein	246.2	282.7	228.4	102.8	109.5	107.4	0.42	1.2E-03
BF2866	putative lipoprotein	11.4	12.4	10.7	6.9	6.2	7.0	0.58	3.4E-03
BF2867	hypothetical protein	2.4	1.8	0.6	0.6	0.2	0.5	0.30	1.5E-01
BF2868	putative lipoprotein	0.3	0.2	0.5	0.2	0.1	0.4	0.70	5.8E-01
BF2869	putative lipoprotein	1.0	0.5	0.4	0.5	0.0	0.3	0.67	4.1E-01
BF2870	hypothetical protein	0.3	0.7	0.0	0.1	0.1	0.1	0.23	5.6E-02
BF2871	putative lipoprotein	0.3	0.5	0.4	0.0	0.2	0.3	0.62	2.6E-01
BF2872	hypothetical protein	1.2	3.3	1.3	0.0	0.0	1.1	0.66	
BF2873	putative lipoprotein	0.6	0.5	0.3	0.4	0.5	0.3	0.88	6.8E-01
BF2874	hypothetical protein	0.5	0.1	0.4	0.4	0.0	0.6	1.53	5.2E-01
BF2875	hypothetical protein	0.0	0.3	0.0	0.0	0.0	0.0		
BF2876	hypothetical protein	0.0	2.5	0.5	0.0	0.0	0.0		
tsr25	tyrosine site-specific recombinase	4.8	4.9	3.8	1.5	0.9	2.6	0.33	4.8E-02
BF2878	hypothetical protein	36.2	45.5	34.7	32.1	34.3	46.5	0.96	8.4E-01
BF2879	hypothetical protein	117.6	124.0	124.7	135.2	88.3	164.1	1.02	9.2E-01
BF2880	hypothetical protein	272.4	281.8	235.6	241.0	220.1	314.1	0.97	8.7E-01
BF2881	hypothetical protein	18.5	12.7	9.6	2.1	1.3	7.3	0.20	7.6E-02
BF2882	hypothetical protein	116.0	103.5	86.6	54.2	53.5	65.4	0.57	1.5E-02
BF2883	hypothetical protein	426.8	450.0	419.5	354.5	352.7	387.1	0.84	2.2E-02
ftnA	ferritin A	3854.8	4003.2	3870.3	3144.7	3207.8	3175.7	0.81	7.4E-04
BF2885	putative diaminopimelate decarboxylase	960.0	1007.5	957.2	680.6	653.1	624.5	0.67	1.1E-03
BF2886	putative aspartokinase III	1366.0	1456.9	1396.6	1078.6	1012.8	957.4	0.72	4.4E-03
ftsE	Cell division ATP-binding protein	593.7	582.4	531.8	384.7	337.9	439.8	0.68	2.1E-02
hisI	histidine biosynthesis bifunctional protein	1050.1	963.9	820.1	660.2	616.9	700.9	0.70	2.6E-02
hisF	imidazole glycerol phosphate synthase subunit	418.8	336.0	318.4	165.2	158.7	262.3	0.54	4.8E-02
hisA	imidazole-4-carboxamide isomerase	512.7	386.3	391.3	204.6	221.6	250.9	0.53	1.2E-02
hisH	imidazole glycerol phosphate synthase subunit	441.9	455.4	393.9	232.9	217.1	291.0	0.57	1.2E-02
BFt41	tRNA-Asp-GTC	0.0	0.0	0.0	0.0	0.0	0.0		
BFt42	tRNA-Asp-GTC	201.7	232.1	138.2	334.4	237.6	594.7	1.94	1.5E-01
BF2892	hypothetical protein	17.8	21.1	20.3	13.6	15.8	10.5	0.67	6.3E-02
BF2893	hypothetical protein	74.9	82.3	86.7	119.2	139.1	117.7	1.54	9.4E-03
BF2894	hypothetical protein	2.6	0.9	0.9	0.8	2.0	0.0	0.97	9.7E-01
BF2895	hypothetical protein	88.7	90.6	85.2	73.0	75.6	75.1	0.85	4.8E-03
BF2896	putative regulatory protein	91.9	106.9	96.4	97.3	97.9	121.5	1.07	5.5E-01
BF2897	hypothetical protein	9.6	7.7	4.8	6.9	8.4	10.6	1.20	5.7E-01
BF2898	putative regulatory protein	20.8	14.0	14.7	18.7	15.9	32.5	1.31	4.1E-01
BF2899	hypothetical protein	1.7	1.8	1.9	1.4	1.9	1.7	0.93	6.1E-01
BF2900	putative exported hydrolase	1.4	1.5	1.4	1.6	1.7	2.3	1.30	1.2E-01
BF2901	putative uroporphirinogen biosynthesis-related protein	1.2	0.2	1.7	1.2	1.0	0.5	1.14	8.9E-01
BF2902	hypothetical protein	1.2	0.0	0.0	0.3	0.7	1.4	0.55	

BF2903	putative dimethylamine corrinoid protein	1.4	0.3	0.6	0.3	1.0	1.6	1.17	8.6E-01
BF2904	putative methyltransferase	1.1	1.1	0.5	1.5	0.7	1.6	1.41	5.1E-01
BF2905	putative exported hydrolase	0.2	0.6	0.7	0.9	0.9	0.4	1.57	4.6E-01
BF2906	hypothetical protein	1.4	1.2	1.7	3.8	5.8	4.8	3.32	5.9E-03
BF2907	hypothetical protein	1.9	2.3	2.5	5.2	5.8	4.4	2.32	5.8E-03
BF2908	hypothetical protein	17.4	17.7	20.8	27.1	35.8	23.6	1.53	6.1E-02
BF2909	hypothetical protein	14.7	11.4	23.6	22.8	31.0	21.8	1.57	1.8E-01
BF2910	putative ECF sigma factor	102.0	87.7	94.1	157.4	165.6	117.4	1.54	3.9E-02
BF2911	hypothetical protein	0.7	0.0	0.0	0.7	0.8	0.0	1.05	
BF2912	hypothetical protein	62.5	76.0	87.7	153.1	218.1	127.1	2.17	2.9E-02
BF2913	hypothetical protein	173.5	180.7	180.2	617.4	633.5	525.8	3.31	4.0E-04
BF2915	hypothetical protein	67.0	75.7	81.3	232.1	283.5	221.8	3.28	1.3E-03
BF2916	putative CTP pyrophosphohydrolase	55.7	37.3	57.4	23.4	42.1	31.4	0.64	1.6E-01
BF2917	putative restriction enzyme related protein	79.5	81.6	90.6	85.8	93.0	74.0	1.00	9.9E-01
BF2918	hypothetical protein	35.5	40.1	42.5	41.4	45.0	35.8	1.03	7.7E-01
BF2919	hypothetical protein	10.1	16.1	9.8	12.6	13.9	12.1	1.10	6.6E-01
BF2920	hypothetical protein	51.9	48.3	41.1	44.8	43.2	46.7	0.96	6.5E-01
BF2921	putative arsenate reductase	25.7	28.1	23.8	35.6	32.3	40.0	1.39	2.9E-02
BF2922	hypothetical protein	13.4	11.6	11.9	15.7	13.3	17.2	1.25	1.1E-01
BF2923	hypothetical protein	13.2	14.1	14.9	19.4	14.6	18.4	1.23	1.3E-01
BF2924	hypothetical protein	13.1	9.9	15.0	24.9	22.8	25.8	1.96	1.6E-02
BF2925	hypothetical protein	15.5	11.3	12.1	19.3	15.6	17.2	1.34	9.5E-02
BF2926	hypothetical protein	17.2	17.1	17.0	18.6	17.9	25.1	1.19	2.5E-01
BF2927	hypothetical protein	10.7	10.6	5.0	10.1	10.6	8.1	1.15	6.8E-01
BF2928	putative K(+) transport-related membrane protein	6.6	3.4	5.8	1.7	1.4	2.5	0.36	3.4E-02
BF2929	putative AraC-family regulatory protein	42.9	37.5	39.1	38.3	43.5	41.2	1.03	6.8E-01
BF2930	putative antibiotic resistance transport membrane protein	0.3	0.2	0.3	0.4	0.0	0.3	1.40	4.2E-01
BF2931	putative oxidoreductase	38.1	48.8	33.0	64.7	53.9	75.0	1.62	5.6E-02
BF2932	putative AraC-family regulatory protein	25.5	31.4	25.8	32.7	34.2	39.4	1.29	7.5E-02
BF2933	hypothetical protein	173.8	155.7	143.2	125.1	108.2	109.7	0.73	2.5E-02
BF2934	hypothetical protein	399.0	366.1	319.4	141.3	125.4	155.2	0.39	2.2E-03
BF2935	hypothetical protein	281.6	282.9	236.5	111.0	87.7	133.5	0.41	8.2E-03
BF2936	putative hydrolase	84.4	81.4	85.2	65.9	60.0	58.0	0.73	5.4E-03
BF2937	hypothetical protein	217.8	228.0	210.3	221.6	206.4	214.8	0.98	6.2E-01
BF2938	diphosphate--fructose-6-phosphate 1-phosphotransferase	1372.4	1431.7	1511.0	1806.4	1767.6	1670.6	1.22	1.5E-02
BF2939	putative lipoprotein	120.4	136.1	139.7	261.2	252.5	265.0	1.97	9.7E-04
BF2940	hypothetical protein	11.9	11.0	13.6	35.4	31.9	24.0	2.48	7.1E-03
BF2941	hypothetical protein	5.0	6.0	5.1	21.3	26.4	16.8	3.96	2.8E-03
BF2942	hypothetical protein	4.2	4.0	5.4	19.5	25.5	17.4	4.56	2.3E-03
BF2943	hypothetical protein	8.3	6.4	6.3	7.6	10.8	7.2	1.22	3.5E-01
BF2944	putative sigma factor	50.8	57.1	53.4	20.4	32.4	24.4	0.47	1.4E-02
BF2945	putative puter membrane protein	70.1	73.1	62.8	34.2	31.6	34.5	0.49	1.1E-03
acrD	putative aminoglycoside efflux pump	72.7	71.9	65.7	27.5	29.0	30.0	0.41	3.3E-04
BF2947	putative acriflavine resistance protein E precursor	60.3	38.5	43.4	16.0	13.0	23.7	0.37	2.3E-02
BF2948	hypothetical protein	26.7	25.6	21.4	36.3	34.7	32.8	1.42	2.0E-02

BF2949	hypothetical protein	1172.4	1145.6	1240.7	861.0	865.6	699.7	0.68	1.6E-02
BF2950	putative acyltransferase	791.8	842.2	915.1	552.7	645.5	556.1	0.69	1.2E-02
BF2951	putative hydrolase	83.5	89.8	92.2	78.3	80.8	77.1	0.89	4.4E-02
BF2952	putative N-acetylglucosamine-6-phosphate deacetylase	70.0	74.6	66.4	287.3	263.8	291.8	3.99	1.4E-04
BF2953	glucosamine-6-phosphate deaminase	1048.3	1100.5	1071.7	1186.8	1171.0	1084.1	1.07	1.5E-01
BF2954	hypothetical protein	75.7	72.6	69.5	43.4	39.9	34.4	0.54	4.0E-03
BF2955	hypothetical protein	62.2	64.9	60.2	58.0	59.3	60.8	0.95	1.8E-01
BF2956	hypothetical protein	5.1	9.4	8.1	5.6	3.4	4.2	0.59	1.3E-01
BF2957	hypothetical protein	716.0	658.0	632.9	795.0	817.6	691.5	1.15	1.4E-01
BF2958	hypothetical protein	553.5	537.9	562.3	660.6	742.1	601.2	1.21	6.6E-02
BF2959	hypothetical protein	409.3	454.4	441.7	555.1	592.1	495.3	1.26	3.8E-02
BF2960	hypothetical protein	195.9	198.0	212.3	216.7	234.5	243.4	1.15	5.8E-02
BF2961	hypothetical protein	127.6	140.1	141.3	132.9	144.3	160.8	1.07	4.3E-01
BF2962	hypothetical protein	88.9	94.9	84.6	88.1	87.5	96.9	1.01	8.1E-01
BF2963	putative transcription-repair coupling factor	99.7	90.8	84.2	90.9	86.8	96.4	1.00	9.9E-01
BF2964	putative glycosyltransferase	223.6	204.4	196.4	192.3	190.2	208.4	0.95	3.9E-01
BF2965	dihydroorotase	195.4	175.4	185.6	213.8	216.4	205.2	1.14	3.7E-02
BF2966	hypothetical protein	186.5	198.3	212.4	191.8	215.2	165.3	0.95	6.7E-01
BF2967	putative 5-methyltetrahydrofolate--homocysteine methyltransferase	163.3	141.7	147.3	138.0	136.4	130.5	0.90	1.2E-01
BF2968	hypothetical protein	150.6	147.1	128.7	197.9	205.0	187.8	1.39	1.1E-02
BF2969	hypothetical protein	24.6	20.3	23.2	18.6	21.2	19.3	0.87	1.6E-01
BF2970	hypothetical protein	14.4	11.5	12.4	9.5	11.1	9.0	0.77	7.7E-02
BF2971	putative lipoprotein	46.7	36.8	42.7	44.3	41.1	40.2	1.00	9.9E-01
BF2972	hypothetical protein	1.8	0.0	1.0	0.0	0.0	1.7	1.29	
BF2973	hypothetical protein	20.6	29.3	17.2	14.4	21.0	20.5	0.84	5.1E-01
BF2974	hypothetical protein	73.1	73.1	70.8	62.3	66.0	75.7	0.94	4.0E-01
BF2975	putative RNA polymerase sigma factor	59.2	61.1	54.5	96.8	109.1	101.0	1.76	1.7E-03
BF2976	hypothetical protein	45.2	38.8	43.8	96.6	96.7	93.2	2.24	6.2E-04
BF2977	hypothetical protein	75.8	69.0	58.8	50.3	48.1	60.5	0.78	1.1E-01
BF2978	putative ABC transport system, ATP-binding protein	86.9	83.8	71.8	55.5	50.5	70.1	0.72	7.6E-02
BF2979	putative ABC transport system, membrane protein	49.6	50.0	40.4	49.2	43.4	58.0	1.07	6.2E-01
BF2980	hypothetical protein	13.0	10.2	19.6	18.8	16.6	17.1	1.27	3.5E-01
BF2981	putative exonuclease	27.5	23.6	20.2	31.6	24.5	42.6	1.36	2.3E-01
BF2982	putative exonuclease	37.5	41.7	29.6	30.7	27.5	47.9	0.96	8.6E-01
BF2983	putative phospholipids biosynthesis-related protein	140.7	139.7	144.0	106.6	106.1	85.9	0.70	1.8E-02
BF2984	putative ABC transport system, membrane protein	15.4	15.2	15.1	67.7	72.2	66.7	4.51	1.3E-05
BF2985	putative ABC transport system, exported protein	13.9	16.7	14.7	71.1	67.3	61.8	4.42	3.2E-04
BF2986	putative ABC transport system, membrane protein	17.0	19.8	18.9	64.7	70.4	62.8	3.56	3.0E-04
BF2987	putative ABC transport system, lipoprotein	33.8	26.1	23.6	71.2	68.9	69.9	2.54	3.8E-03
BF2988	hypothetical protein	10.7	7.3	9.8	14.6	16.2	16.8	1.73	2.3E-02
BF2989	putative signal peptidase I	14.9	10.5	10.0	7.5	11.9	12.5	0.89	6.8E-01

BF2990	putative lipoprotein	46.3	39.2	42.3	27.8	31.8	32.6	0.72	2.0E-02
BF2991	hypothetical protein	3.7	3.6	2.7	3.8	2.9	4.5	1.10	6.6E-01
BF2992	hypothetical protein	7.3	5.4	7.5	6.6	3.8	4.5	0.73	2.4E-01
BF2993	hypothetical protein	3.3	2.1	2.3	7.4	4.7	8.1	2.56	2.6E-02
BF2994	hypothetical protein	5.6	7.0	4.1	15.9	14.1	31.3	3.53	2.7E-02
BF2995	hypothetical protein	6.9	5.2	5.4	42.7	35.4	58.4	7.67	1.5E-03
BF2996	hypothetical protein	1.5	3.3	3.4	38.1	23.3	38.6	12.55	4.4E-03
BF2997	putative lipoprotein	4.8	6.5	7.1	50.1	44.6	59.2	8.43	9.1E-04
BF2998	hypothetical protein	6.8	6.5	10.5	83.6	64.1	99.1	10.40	1.6E-03
BF2999	hypothetical protein	8.5	7.1	8.7	174.6	140.2	211.1	21.31	2.9E-04
BF3000	hypothetical protein	7.3	8.3	5.6	140.0	116.2	162.8	19.86	4.3E-04
BF3001	hypothetical protein	16.0	14.4	13.1	352.5	335.1	454.8	26.13	1.4E-04
BF3002	hypothetical protein	16.3	12.0	18.6	518.9	478.1	531.8	33.14	2.0E-04
BF3003	putative lipoprotein	37.6	41.7	46.5	1376.0	1214.2	1739.8	34.18	1.5E-04
BF3004	hypothetical protein	49.6	54.5	48.1	1755.2	1460.2	1629.1	31.78	2.1E-05
BF3005	hypothetical protein	35.2	36.5	38.4	14.2	17.7	12.1	0.39	4.6E-03
BF3006	hypothetical protein	55.2	63.5	78.3	103.3	102.9	72.6	1.41	1.3E-01
BF3007	hypothetical protein	43.7	39.6	47.0	26.5	30.1	26.8	0.64	6.9E-03
BF3008	hypothetical protein	304.3	284.8	315.8	128.7	121.1	131.7	0.42	3.2E-04
BF3009	putative regulatory protein	182.9	177.8	175.0	139.2	146.8	143.4	0.80	1.9E-03
BF3010	hypothetical protein	342.5	352.0	354.9	312.8	299.1	265.6	0.83	4.2E-02
BF3011	hypothetical protein	299.9	313.6	307.4	250.9	248.0	217.9	0.78	1.5E-02
BF3012	hypothetical protein	22.2	23.6	17.0	11.9	13.4	20.4	0.71	2.1E-01
BF3013	hypothetical protein	3.6	3.5	4.5	1.3	0.7	1.8	0.31	2.9E-02
BF3014	hypothetical protein	0.9	1.2	0.7	0.2	0.3	0.4	0.31	2.2E-02
BF3015	putative thioredoxin	2461.4	2267.4	2508.3	641.9	726.4	656.0	0.28	2.0E-04
BF3016	putative thioredoxin family protein	2213.6	2143.7	2494.0	668.9	715.5	601.7	0.29	5.1E-04
BF3017	hypothetical protein	288.8	225.8	270.7	215.9	268.5	274.7	0.97	8.1E-01
BF3018	putative rubrerythrin-like protein	2442.2	2022.5	2535.3	1670.9	2193.4	1556.6	0.77	1.5E-01
BF3019	putative iron uptake-related regulatory protein	2761.1	2145.9	2403.3	1960.7	2337.2	1672.6	0.81	2.2E-01
BF3020	hypothetical protein	262.1	316.6	315.5	410.4	483.7	387.7	1.43	3.4E-02
BF3021	putative peptidyl-dipeptidase	151.0	150.9	146.6	222.3	232.1	209.7	1.48	1.3E-03
nadE	NAD(+) synthetase	199.6	200.2	202.9	204.4	203.4	189.6	0.99	7.8E-01
BF3023	hypothetical protein	18.1	22.7	18.5	19.3	26.2	23.0	1.15	3.5E-01
BF3024	hypothetical protein	1.0	1.2	1.3	1.1	0.8	0.5	0.66	2.4E-01
BF3025	hypothetical protein	1.2	1.0	1.2	0.6	0.7	0.7	0.57	8.0E-03
BF3026	hypothetical protein	14.6	12.7	17.0	5.2	6.3	4.7	0.37	4.2E-03
hisB	imidazole glycerol-phosphate dehydratase/histidinol phosphatase	304.8	297.5	306.9	234.7	234.1	227.4	0.77	4.4E-04
BF3028	putative histidine biosynthesis-related aminotransferase	166.1	164.4	178.0	113.1	141.9	127.9	0.75	3.1E-02
hisD	putative histidinol dehydrogenase	169.7	183.2	180.9	113.4	133.2	137.8	0.72	1.6E-02
hisG	ATP phosphoribosyltransferase	234.2	243.2	247.4	160.6	182.7	150.8	0.68	8.2E-03
BF3031	putative thioesterase	82.1	92.7	82.5	125.4	120.0	125.6	1.44	3.8E-03
BF3032	putative Pirin-like protein	832.9	843.0	837.0	217.8	206.9	218.8	0.26	5.8E-06
BF3033	putative exported cytochrome C biogenesis-related protein	377.0	392.2	389.9	301.3	339.1	289.1	0.80	2.3E-02
BF3034	hypothetical protein	171.2	151.4	193.0	175.0	171.6	186.8	1.04	6.9E-01
udk	uridine kinase	134.3	134.9	133.3	170.0	164.8	169.0	1.25	3.1E-04

BF3036	putative exported transglycosylase protein	84.8	86.7	88.9	109.3	114.8	111.8	1.29	1.2E-03
BF3037	putative sodium/proline symporter membrane protein	86.3	84.4	96.4	104.0	110.0	100.4	1.18	5.1E-02
BF3038	putative nitroreductase	115.0	109.0	111.3	102.9	103.8	122.9	0.98	8.0E-01
metH	putative 5-methyltetrahydrofolate--homocysteine methyltransferase	171.4	164.8	175.3	154.4	154.4	161.2	0.92	4.1E-02
BF3040	SsrA-binding protein	306.9	266.8	309.7	273.9	266.1	255.6	0.90	1.7E-01
BF3041	hypothetical protein	199.2	226.1	253.3	208.2	251.7	217.3	1.00	1.0E+00
BF3042	putative lipoprotein	525.2	519.9	587.3	618.6	688.1	538.8	1.13	2.8E-01
BF3043	hypothetical protein	186.0	143.1	182.3	121.5	136.2	150.7	0.80	1.5E-01
BF3044	hypothetical protein	94.1	76.5	81.6	12.8	12.1	15.5	0.16	4.5E-04
BF3045	hypothetical protein	809.9	779.9	765.6	885.7	844.2	790.7	1.07	2.0E-01
BF3046	hypothetical protein	915.1	921.2	911.0	890.6	888.1	832.8	0.95	1.2E-01
BF3047	3-oxoacyl-(acyl carrier protein) synthase	83.2	76.4	84.7	99.3	84.2	82.8	1.09	3.4E-01
BF3048	cytoplasmic alpha-amylase	135.6	124.7	158.0	50.3	55.5	46.5	0.36	1.7E-03
BF3049	putative ribonuclease	64.7	81.4	78.7	19.8	19.4	21.3	0.27	6.1E-04
BF3050	hypothetical protein	161.6	155.5	165.2	46.4	53.5	54.3	0.32	3.3E-04
rho	transcription termination factor Rho	341.1	332.2	322.9	241.8	209.1	228.5	0.68	4.0E-03
BF3053	putative two-component system sensor histidine kinase	21.0	24.2	19.8	16.2	16.2	16.1	0.75	1.9E-02
BF3054	putative two-component system sensor histidine kinase	2.8	3.2	2.9	1.6	1.1	2.0	0.53	3.5E-02
BF3055	putative antiporter membrane protein	32.3	47.5	37.2	29.2	28.9	37.6	0.82	3.1E-01
ffh	signal recognition particle protein	498.9	522.4	482.1	561.8	455.9	571.7	1.05	6.1E-01
BF3057	putative thiol:disulfide oxidoreductase	65.3	69.6	50.1	149.8	144.8	139.0	2.37	4.3E-03
BF3058	putative methenyltetrahydrofolate cyclohydrolase	144.0	137.7	119.4	430.0	355.3	458.9	3.09	1.6E-03
BF3059	hypothetical protein	13.2	15.3	14.2	66.3	59.2	57.6	4.29	2.5E-04
BF3060	hypothetical protein	11.8	14.4	14.9	38.3	35.4	40.5	2.78	1.4E-03
BFt43	tRNA-His-GTG	20.9	17.3	20.5	44.0	37.6	46.8	2.19	3.6E-03
BF3061	hypothetical protein	661.9	679.6	705.6	533.1	570.8	478.4	0.77	2.0E-02
BF3062	hypothetical protein	692.4	707.7	772.0	537.8	597.4	467.8	0.74	3.4E-02
BF3063	putative ABC transport system, ATP-binding protein	659.9	596.0	659.7	433.9	448.8	364.5	0.65	1.1E-02
BF3064	hypothetical protein	607.5	527.2	580.2	368.2	432.7	350.6	0.67	1.5E-02
BF3065	putative lipoprotein	769.8	695.2	738.0	544.6	540.9	504.4	0.72	4.1E-03
BF3066	hypothetical protein	566.3	503.0	500.4	429.4	437.8	423.8	0.82	2.1E-02
BF3067	putative lipoprotein	658.6	619.1	660.3	629.4	685.2	549.3	0.96	6.3E-01
BF3068	hypothetical protein	328.4	295.9	331.8	258.0	232.3	244.2	0.77	1.3E-02
BF3069	hypothetical protein	1.3	6.7	5.5	1.2	1.4	2.4	0.45	3.0E-01
BF3070	hypothetical protein	344.3	306.1	317.1	173.7	176.8	180.8	0.55	6.7E-04
BF3071	putative DNA polymerase III	190.7	195.4	175.6	197.3	206.9	205.2	1.09	1.2E-01
BF3072	putative septum formation initiator-related protein	184.6	171.0	155.2	145.2	124.7	163.1	0.84	2.0E-01
BF3073	hypothetical protein	150.4	134.4	130.7	119.7	111.3	127.6	0.86	1.0E-01
BF3074	hypothetical protein	30.3	29.4	31.9	23.0	26.5	27.0	0.83	5.6E-02
BF3075	hypothetical protein	2.1	2.8	2.9	0.4	1.2	1.7	0.37	1.3E-01
BF3076	hypothetical protein	71.4	63.4	70.4	41.4	43.4	47.8	0.65	5.2E-03
BF3077	hypothetical protein	560.4	540.7	626.2	729.5	740.5	647.1	1.23	5.3E-02

BF3078	hypothetical protein	423.0	372.2	397.7	213.0	216.5	268.4	0.58	8.5E-03
pepD	putative aminoacyl-histidine dipeptidase	493.4	495.6	460.5	439.9	416.7	425.1	0.88	2.7E-02
BF3080	putative conserved exported protein	68.7	78.9	68.0	33.3	37.9	39.1	0.51	2.8E-03
BF3081	hypothetical protein	167.4	173.4	185.5	83.0	92.4	82.6	0.49	8.2E-04
tal	transaldolase	582.8	618.2	565.8	861.9	806.9	916.2	1.46	4.2E-03
BF3083	putative exported fucosidase	75.7	70.8	60.4	481.5	422.6	543.8	6.99	4.2E-04
BF3084	putative exported beta-galactosidase	62.6	65.2	54.1	452.2	415.4	468.3	7.36	1.4E-04
BF3085	putative exported glycosyl hydrolase	8.6	9.6	7.2	380.8	350.7	425.5	45.74	6.2E-05
BF3086	putative exported sulfatase	8.1	6.7	6.0	835.1	809.0	791.0	117.64	2.1E-05
BF3087	putative exported sulfatase	102.5	88.7	93.1	330.3	331.6	343.1	3.54	1.6E-04
BF3088	putative exported hexosaminidase	109.2	109.9	108.0	155.5	165.2	163.5	1.48	3.9E-04
BF3089	putative two-component system histidine kinase/response regulator fusion protein	272.7	335.8	278.6	165.0	119.8	239.5	0.57	9.0E-02
fbaB	fructose-bisphosphate aldolase	1754.8	1992.7	1778.6	594.6	569.8	831.0	0.36	4.5E-03
gpmA	phosphoglyceromutase	1950.9	2157.8	1883.7	574.7	566.7	679.1	0.30	6.2E-04
BF3092	hypothetical protein	17.9	17.4	15.3	49.3	51.1	61.7	3.20	1.1E-03
BF3093	putative ABC transport system, ATP-binding protein	42.4	43.7	35.9	64.9	58.3	71.1	1.59	1.3E-02
BF3094	putative sulfatase	15.1	11.3	12.2	28.7	24.3	28.2	2.11	6.2E-03
BF3095	putative exported hydrolase	9.6	9.3	9.2	18.5	15.9	21.4	1.97	5.3E-03
BF3096	putative lipoprotein	2.3	2.1	2.3	9.4	9.0	8.9	4.09	3.6E-05
BF3097	hypothetical protein	2.8	3.4	2.5	6.3	7.2	6.3	2.27	4.6E-03
BF3098	putative anti-sigma factor	17.7	18.6	20.0	22.9	25.4	26.6	1.33	1.8E-02
BF3099	putative sigma factor	87.4	81.3	84.5	82.0	85.2	86.0	1.00	1.0E+00
BF3100	putative exported amylase	212.5	229.1	207.2	253.2	244.2	243.7	1.14	3.1E-02
ruvC	Holliday junction resolvase	106.4	119.8	125.8	159.9	145.9	181.5	1.38	3.2E-02
BF3102	hypothetical protein	120.6	103.4	96.9	186.1	158.1	182.3	1.64	1.1E-02
BFt44	tRNA-Ala-GGC	21.5	17.8	28.9	18.1	11.0	43.5	0.92	8.9E-01
BF3103	hypothetical protein	19.5	18.3	15.2	21.3	18.7	34.2	1.36	2.6E-01
pheS	phenylalanyl-tRNA synthetase alpha subunit	506.9	525.7	483.5	542.7	464.9	500.9	0.99	9.3E-01
BF3105	putative transport related, membrane protein	53.2	58.8	54.5	70.1	65.9	73.4	1.26	1.5E-02
BF3106	putative endonuclease	34.1	34.9	36.7	89.3	77.7	72.9	2.26	1.3E-03
pgk	phosphoglycerate kinase	1669.3	1714.1	1756.4	2252.1	2216.4	2109.4	1.28	2.6E-03
BF3108	hypothetical protein	296.4	325.9	306.4	212.3	202.6	232.3	0.70	5.9E-03
BF3109	hypothetical protein	23.8	25.0	21.9	25.1	18.1	24.5	0.95	7.2E-01
BF3110	hypothetical protein	24.6	28.8	18.8	17.4	20.4	16.3	0.76	1.8E-01
BF3111	hypothetical protein	268.5	270.1	186.3	63.4	62.2	49.3	0.24	2.9E-03
BF3112	hypothetical protein	120.4	126.6	113.5	53.8	54.5	49.5	0.44	4.6E-04
BF3113	hypothetical protein	86.5	90.8	96.5	61.2	62.8	63.1	0.68	1.7E-03
BF3114	putative endo-beta-galactosidase	184.6	182.5	195.0	235.7	250.7	223.5	1.26	1.1E-02
BF3115	putative non ribosome peptide synthase related, AMP-binding protein	152.5	145.8	149.7	120.2	118.1	118.4	0.80	6.8E-04
BF3116	putative acyl carrier protein	190.2	213.2	207.9	187.2	183.3	163.7	0.87	1.0E-01
BF3117	putative acetyltransferase membrane protein	119.9	135.3	126.9	100.6	108.4	101.7	0.81	1.9E-02
BF3118	hypothetical protein	71.7	76.6	72.6	67.0	63.0	61.0	0.86	2.8E-02
BF3119	putative lipoprotein	810.9	752.2	916.1	600.9	648.7	477.2	0.69	5.1E-02

maf	Maf-like protein	249.8	245.1	267.1	212.9	199.0	218.4	0.83	1.8E-02
BF3121	putative lipopolysaccharide biosynthesis-related protein	61.2	51.1	51.7	96.1	91.6	101.5	1.77	3.8E-03
BF3122	hypothetical protein	111.4	103.8	94.9	151.4	142.9	148.5	1.43	6.2E-03
BF3123	hypothetical protein	98.6	100.9	119.6	141.6	147.8	160.6	1.41	1.9E-02
BF3124	putative nitroreductase family protein	144.6	147.1	131.3	176.6	158.6	191.0	1.24	5.1E-02
BF3125	hypothetical protein	93.2	96.1	82.8	95.7	91.2	101.8	1.06	4.1E-01
BF3126	hypothetical protein	100.1	110.1	88.5	69.5	68.9	74.5	0.72	1.8E-02
BF3127	hypothetical protein	671.8	736.4	673.6	860.5	869.6	791.2	1.21	2.4E-02
mmdA	putative methylmalonyl-CoA decarboxylase, alpha-subunit	544.9	615.2	554.0	980.7	929.6	943.0	1.67	1.4E-03
BF3129	hypothetical protein	591.1	596.3	551.1	1056.1	940.2	886.0	1.65	3.7E-03
bcc	putative biotin carboxyl carrier protein	831.2	832.0	722.8	1117.2	1033.3	930.2	1.29	4.2E-02
mmdB	putative methylmalonyl-CoA decarboxylase, beta subunit	853.8	950.6	847.7	1135.5	1121.9	1017.0	1.23	2.9E-02
BF3132	hypothetical protein	10.1	8.5	9.8	28.8	27.9	24.4	2.87	9.6E-04
BF3133	hypothetical protein	2.6	5.2	4.1	9.4	10.0	8.9	2.48	2.6E-02
BF3134	putative alpha-amylase precursor	51.2	56.7	44.4	12.0	10.9	12.7	0.23	5.8E-04
BF3135	putative MarR-family transcriptional regulator	26.0	20.4	18.1	25.0	14.8	32.6	1.08	8.2E-01
BF3136	putative HlyD-family secretion protein	22.0	22.8	19.1	30.1	20.7	32.0	1.28	2.3E-01
BF3137	putative transport-related membrane protein	12.2	15.1	10.3	9.3	11.4	11.9	0.87	4.3E-01
fba	fructose-bisphosphate aldolase	3667.2	3822.3	4077.1	4460.5	4545.0	4256.8	1.15	3.8E-02
BF3139	hypothetical protein	66.1	48.4	45.9	40.3	33.4	72.0	0.87	6.8E-01
rpmE	50S ribosomal protein L31	3405.8	3669.6	3845.2	2870.2	3016.5	2726.6	0.79	1.6E-02
BF3141	hypothetical protein	32.1	28.9	31.3	5.5	5.6	4.4	0.17	3.7E-04
BF3142	hypothetical protein	70.1	75.2	57.4	444.3	351.6	499.1	6.36	9.7E-04
BF3143	conserved hypothetical lipoprotein	5.2	5.2	5.0	6.3	6.4	6.4	1.24	1.1E-03
BF3144	putative lipoprotein	66.3	72.7	64.3	27.5	23.5	27.8	0.39	9.2E-04
BF3145	hypothetical protein	68.4	85.3	75.3	26.0	26.0	28.4	0.35	8.6E-04
BF3146	hypothetical protein	119.3	143.7	133.2	34.0	35.8	33.5	0.26	2.7E-04
BF3147	putative LacI-family transcriptional regulator	49.7	47.9	36.9	29.8	25.3	35.3	0.67	7.0E-02
BF3148	hypothetical protein	36.2	47.3	32.6	53.8	42.7	80.2	1.49	1.9E-01
BF3149	putative glycosyl hydrolase	49.6	54.1	40.8	79.6	73.2	92.6	1.70	1.9E-02
BF3150	putative conserved lipoprotein	91.2	88.2	80.3	70.1	58.1	74.8	0.78	7.0E-02
BF3151	putative AcrB/AcrD/AcrF family membrane protein	132.9	135.3	102.0	90.2	77.5	97.4	0.72	7.3E-02
BF3152	hypothetical protein	146.1	147.5	118.1	102.2	85.6	95.9	0.69	2.9E-02
BF3153	hypothetical protein	5.3	6.4	5.9	4.5	4.9	6.3	0.89	4.2E-01
BF3154	phosphoribosylformylglycinamidine synthase	412.5	429.6	405.4	425.6	393.4	422.4	0.99	9.0E-01
BF3155	putative two-component system sensor kinase/response regulator fusion protein	135.8	133.0	132.6	120.4	119.0	109.8	0.87	2.2E-02
BF3156	putative chromate transport protein	75.4	78.8	72.6	78.5	71.9	84.8	1.04	6.2E-01
BF3157	putative hromate transport membrane protein	150.4	133.0	140.2	148.0	126.9	132.0	0.96	5.9E-01
BF3158	hypothetical protein	210.5	202.6	190.8	236.2	232.6	244.0	1.18	1.6E-02

uvrA2	UvrABC SOS-repair system protein excinuclease A	124.3	117.5	101.7	121.3	102.7	132.3	1.04	7.8E-01
BF3160	hypothetical protein	233.1	232.8	189.1	322.7	301.6	350.1	1.49	1.9E-02
BF3161	hypothetical protein	59.6	50.4	63.1	104.3	86.7	114.3	1.76	1.5E-02
BF3162	putative carbon starvation-related membrane protein	59.3	65.7	56.7	72.8	69.0	78.4	1.21	5.1E-02
BF3163	hypothetical protein	49.7	54.6	44.7	32.2	26.6	36.0	0.63	2.6E-02
BF3164	putative two-component regulator sensor kinase	48.3	47.5	47.7	25.0	30.4	29.8	0.59	4.1E-03
BF3165	hypothetical protein	18.3	19.0	15.2	33.2	26.3	38.3	1.85	2.0E-02
BF3166	hypothetical protein	260.1	291.5	251.0	229.8	193.4	254.7	0.84	1.9E-01
BF3167	hypothetical protein	190.0	228.2	204.7	214.3	228.3	233.2	1.09	2.9E-01
nifJ	putative pyruvate-flavodoxin oxidoreductase	555.5	674.4	610.5	781.5	757.3	732.4	1.24	4.2E-02
BF3169	hypothetical protein	192.9	240.6	226.7	42.1	47.4	40.6	0.20	3.9E-04
BF3170	putative exported glycine betaine-binding protein	248.3	301.2	264.5	31.9	31.1	42.8	0.13	5.7E-04
opuAB	putative glycine betaine transport system permease protein	338.4	417.5	337.0	31.0	26.0	36.7	0.09	3.9E-04
opuAA	putative glycine betaine transport ATP-binding protein	494.6	566.1	440.5	40.1	36.3	55.3	0.09	6.2E-04
BF3173	conserved DNA methyltransferase protein	6.1	3.8	6.8	17.9	14.2	21.6	3.27	1.4E-02
BF3174	putative two-component system sensor kinase/response regulator fusion protein	32.8	24.4	23.8	52.2	44.1	72.9	2.07	3.2E-02
BF3175	putative fructokinase	53.3	48.7	55.4	219.8	202.0	225.3	4.11	1.7E-04
BF3176	putative sugar transport-related, membrane protein	47.8	51.0	52.4	155.2	181.9	181.2	3.42	3.6E-04
scrL	levanase	39.6	41.6	41.4	131.3	116.6	138.1	3.14	3.2E-04
BF3178	hypothetical protein	12.5	12.1	11.5	24.5	25.5	22.1	2.00	9.7E-04
BF3179	hypothetical DNA-binding protein	56.8	68.3	50.6	24.4	33.2	42.2	0.56	5.7E-02
BF3180	hypothetical protein	1533.4	1727.3	1689.5	873.5	950.9	1056.1	0.58	4.5E-03
BF3181	putative lipoprotein	2087.9	1975.8	2189.7	2057.2	2353.5	2063.0	1.03	6.3E-01
BF3182	putative transport-related, membrane protein	39.9	38.8	44.5	15.7	18.2	16.8	0.41	8.7E-04
BF3183	putative nitroreductase family protein	106.0	120.5	99.2	77.3	74.0	70.1	0.68	1.1E-02
BF3184	hypothetical protein	106.0	103.9	95.3	77.3	75.1	71.2	0.73	5.4E-03
BF3185	conserved hypothetical phospholipase	89.9	89.4	78.2	90.6	85.9	84.6	1.02	8.1E-01
BF3186	putative Na/H exchanger membrane protein	234.5	234.4	227.4	99.8	114.5	119.0	0.48	1.1E-03
BF3187	hypothetical protein	3.4	5.2	3.9	1.6	1.0	2.9	0.40	9.1E-02
BF3188	putative lipoprotein	12.4	12.9	12.0	5.0	6.9	6.9	0.50	8.6E-03
BF3189	hypothetical protein	70.2	79.5	68.8	56.7	54.4	52.6	0.75	1.2E-02
BF3190	putative lipoprotein	130.8	133.8	114.6	111.5	128.1	111.0	0.92	3.8E-01
BF3191	hypothetical protein	214.6	218.4	211.9	172.3	176.5	193.9	0.84	2.1E-02
BF3192	putative transport-related membrane protein	106.1	108.0	90.8	87.9	83.7	90.5	0.86	1.1E-01
BF3193	putative lipoprotein	64.3	44.6	46.4	30.8	31.2	35.3	0.63	4.0E-02
BF3194	putative AraC-family regulatory protein	18.5	15.2	16.6	21.1	26.3	21.4	1.37	4.8E-02
BF3195	hypothetical protein	687.8	656.0	674.6	1062.3	1032.8	997.4	1.53	4.8E-04

BF3196	putative two-component system, response regulator	7.7	8.6	4.7	14.5	13.6	13.5	2.04	3.6E-02
BF3197	putative two component system, sensor protein	0.9	0.8	0.8	0.4	1.0	0.7	0.81	5.5E-01
BF3198	hypothetical protein	9.6	7.4	9.4	7.6	5.1	4.0	0.61	1.2E-01
BF3199	hypothetical protein	13.5	14.5	15.3	37.3	36.7	34.8	2.51	3.1E-04
BF3200	putative lipoprotein	14.3	16.5	14.6	35.3	33.8	34.0	2.28	5.8E-04
BF3201	putative lipoprotein	101.9	107.7	88.6	300.7	276.2	294.4	2.93	6.0E-04
BF3202	putative electron transfer flavoprotein beta-subunit	198.7	208.3	166.9	782.0	637.9	721.1	3.73	8.8E-04
BF3203	putative electron transfer flavoprotein alpha-subunit	143.9	168.0	155.3	780.8	745.5	688.4	4.74	1.8E-04
BF3204	putative acyl-CoA dehydrogenase	209.2	241.2	209.7	1002.8	898.1	967.5	4.35	2.1E-04
BF3205	putative exported beta-galactosidase	86.3	91.6	80.7	209.5	198.0	207.2	2.38	3.3E-04
BF3206	hypothetical protein	155.0	139.0	124.6	53.6	41.3	58.1	0.36	4.2E-03
BF3207	putative chaperone	208.9	182.5	148.9	46.5	41.2	71.5	0.29	8.9E-03
BF3208	putative two-component system, sensor kinase	59.8	67.5	55.1	19.6	20.3	26.5	0.36	3.4E-03
BF3209	putative sulfatase	241.7	283.4	251.4	171.3	163.3	169.2	0.65	3.9E-03
BF3210	hypothetical protein	398.4	417.0	364.3	159.2	151.3	177.2	0.41	9.2E-04
BF3211	hypothetical protein	8.8	8.1	9.0	23.7	31.6	23.3	3.00	2.2E-03
BF3212	putative aldolase	102.1	102.4	90.4	135.9	139.4	143.1	1.42	4.7E-03
BF3213	hypothetical protein	28.0	18.2	24.0	17.5	15.4	20.0	0.76	1.9E-01
BF3214	putative RNA polymerase sigma factor	57.5	50.3	56.3	39.4	39.6	45.7	0.76	2.7E-02
BF3215	hypothetical protein	142.3	147.4	141.8	138.4	148.1	127.5	0.96	4.6E-01
BF3216	hypothetical protein	357.7	320.5	261.7	395.6	375.9	370.2	1.22	1.4E-01
poxB	putative pyruvate dehydrogenase [cytochrome]	38.1	39.7	33.9	12.8	12.9	13.2	0.35	3.2E-04
BF3218	putative flavoprotein	142.4	111.1	102.9	105.7	107.1	149.0	1.01	9.5E-01
BF3219	hypothetical protein	1.9	1.6	0.5	0.5	2.3	0.5	0.67	6.4E-01
BF3220	hypothetical protein	3.5	5.1	3.9	1.8	2.6	0.9	0.40	7.6E-02
BF3221	hypothetical protein	30.4	23.9	24.5	12.8	18.7	11.8	0.54	3.6E-02
groEL	chaperonin GroEL	1787.7	1598.9	1380.2	866.3	928.9	714.4	0.53	1.1E-02
groES	co-chaperonin GroES	2659.1	2477.1	1983.6	618.7	635.3	460.7	0.24	2.2E-03
BF3224	putative lipoprotein	6.3	8.1	6.0	1.8	1.7	1.6	0.25	1.2E-03
BF3225	putative lipoprotein	3.6	4.6	3.1	1.9	3.8	2.1	0.67	2.3E-01
BF3226	putative lipoprotein	0.5	1.7	0.5	1.0	0.9	1.0	1.35	5.8E-01
BF3227	hypothetical protein	1.0	1.0	0.9	0.8	0.6	0.2	0.42	2.1E-01
BF3228	putative lipoprotein	0.6	1.7	2.2	0.6	0.5	0.6	0.41	1.3E-01
BF3229	hypothetical protein	1.1	0.8	1.7	0.4	0.6	0.3	0.35	5.6E-02
BF3230	hypothetical protein	22.7	30.1	25.8	10.5	16.2	12.8	0.50	2.1E-02
BF3231	hypothetical protein	162.4	153.2	165.0	80.0	85.2	84.4	0.52	3.2E-04
BF3232	hypothetical protein	3.4	4.9	3.0	4.0	5.3	3.2	1.12	6.7E-01
BF3233	putative RNA polymerase sigma factor	5.6	2.4	4.5	2.1	4.7	3.6	0.84	7.1E-01
BF3234	hypothetical protein	15.4	18.2	18.3	6.4	8.8	6.3	0.41	6.2E-03
BF3235	putative glycosyl transferase	28.9	30.1	32.0	8.4	11.0	10.1	0.32	1.1E-03
BF3236	hypothetical protein	136.2	142.7	127.4	229.0	207.1	204.7	1.58	3.0E-03
BF3237	conserved exported protein	155.5	160.1	157.8	262.4	270.2	230.8	1.61	2.8E-03
hisS	histidyl-tRNA synthetase	377.9	372.1	409.8	441.2	428.6	426.5	1.12	4.5E-02
BF3239	hypothetical protein	10.3	10.5	7.8	3.5	3.7	2.3	0.33	8.8E-03
BF3240	putative lipoprotein	18.5	20.2	21.2	15.9	17.5	15.1	0.81	4.4E-02

BF3241	hypothetical protein	632.6	684.1	520.7	284.8	293.5	280.9	0.47	3.3E-03
BF3242	putative exported alpha-L-fucosidase protein	159.0	143.8	160.2	271.2	285.7	275.3	1.80	7.7E-04
purA	adenylosuccinate synthetase	490.1	423.3	463.6	494.7	515.2	542.4	1.13	1.1E-01
BF3244	putative iron storage-related regulatory protein	220.5	209.6	215.8	184.3	173.4	194.2	0.85	2.5E-02
BF3245	hypothetical protein	62.9	53.6	52.1	38.7	43.6	41.3	0.73	2.4E-02
BF3246	hypothetical protein	211.6	221.1	218.9	142.8	159.6	150.6	0.69	2.3E-03
BF3247	putative membrane attached peptidase	165.2	156.9	157.7	101.4	112.4	104.9	0.66	1.6E-03
BF3248	putative AraC-family regulatory protein	10592.5	10385.4	11018.4	6969.3	8131.2	6112.2	0.66	1.8E-02
recQ2	putative ATP-dependent DNA helicase	44.7	41.3	42.9	55.6	46.1	58.4	1.24	7.9E-02
BF3250	putative TPR repeat domain exported protein	179.7	171.1	174.2	213.8	201.9	213.1	1.20	5.3E-03
BF3251	putative cysteine synthase	175.5	171.9	128.3	160.2	119.7	198.5	0.99	9.8E-01
BF3252	putative membrane attached sulfatase protein	80.7	82.6	76.6	57.2	59.6	58.5	0.73	1.4E-03
BF3253	hypothetical protein	44.5	43.1	41.4	72.1	73.6	67.9	1.65	7.3E-04
BF3254	hypothetical protein	446.3	456.9	379.1	214.8	212.4	223.6	0.51	1.9E-03
BF3255	hypothetical protein	52.7	55.2	45.1	12.7	8.9	12.9	0.22	1.9E-03
BF3256	hypothetical protein	211.1	186.4	188.6	40.7	44.3	37.9	0.21	2.0E-04
BF3257	hypothetical protein	11.0	16.9	11.2	72.3	72.8	62.2	5.40	1.9E-03
BF3258	hypothetical protein	11.1	10.7	11.2	58.4	59.7	54.9	5.24	1.7E-05
BF3259	putative UDP-glucuronic acid epimerase	237.9	239.9	251.2	152.0	162.7	144.2	0.63	1.6E-03
BF3260	hypothetical protein	98.9	84.9	94.0	100.3	115.3	101.3	1.14	1.6E-01
BF3261	putative transport-related, membrane protein	115.2	98.2	128.6	91.1	98.7	97.7	0.85	1.6E-01
BF3262	putative glycosyl transferase	270.6	227.3	291.3	187.5	200.4	156.4	0.69	4.4E-02
leuB	putative 3-isopropylmalate dehydrogenase	479.7	449.1	514.5	170.5	162.2	153.8	0.34	3.2E-04
BF3264	putative alpha-isopropylmalate synthase 2	314.0	299.6	339.7	70.2	79.1	76.6	0.24	1.6E-04
leuD	putative 3-isopropylmalate dehydratase small subunit	339.5	305.2	356.4	67.1	80.2	62.7	0.21	5.2E-04
leuC	isopropylmalate isomerase large subunit	311.0	251.7	270.9	53.8	64.7	59.8	0.21	4.7E-04
leuA	putative 2-isopropylmalate synthase 1	389.2	293.8	346.9	70.2	90.3	70.7	0.22	1.3E-03
BF3268	putative lipoprotein	3222.0	3659.6	3806.3	2493.2	2686.4	2529.9	0.72	1.1E-02
5S		0.4	8.6	41.3	2.2	5.2	27.2	1.31	9.0E-01
23S		3.0	2.1	2.4	6.8	2.2	10.0	2.15	2.3E-01
BFt45	tRNA-Ala-TGC	87.0	97.6	97.6	47.1	45.1	95.3	0.62	1.8E-01
BFt46	tRNA-Ile-GAT	158.9	177.9	180.8	63.0	65.0	113.6	0.45	3.1E-02
16S		672.5	32.3	99.0	90.9	32.3	230.2	0.68	7.8E-01
BF3269	hypothetical protein	212.1	195.1	172.1	177.9	179.7	260.5	1.05	7.8E-01
BF3270	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0		
BF3271	putative bacterioferritin-related protein	321.9	378.3	374.6	46.0	41.0	52.8	0.13	2.9E-04
sppA	putative protease IV	135.6	132.7	136.1	148.0	158.9	146.3	1.12	2.9E-02
BF3273	putative tetraacyldisaccharide kinase (lipid A biosynthesis) related protein	78.3	75.5	82.0	124.6	123.4	98.1	1.46	2.2E-02
punA	purine nucleoside phosphorylase	175.0	165.6	155.4	274.5	267.1	233.7	1.56	6.0E-03

BF3275	putative thiamine monophosphate kinase	278.4	278.0	283.1	305.2	314.2	285.4	1.08	1.0E-01
BFt47	tRNA-Phe-GAA	44.7	68.1	37.3	34.4	22.4	144.9	0.99	9.9E-01
BF3278	hypothetical protein	49.9	50.7	56.2	61.7	95.2	57.8	1.34	2.0E-01
BF3279	hypothetical protein	90.4	92.5	100.2	130.1	153.4	118.8	1.41	2.7E-02
BF3280	hypothetical protein	0.6	0.0	0.0	1.7	0.7	0.0	1.81	
BF3281	hypothetical protein	0.0	0.0	1.3	0.6	1.4	0.0	0.67	
BF3282	hypothetical protein	0.5	0.3	0.0	0.0	0.0	0.0		
BF3283	putative transposon-related/mobilisation protein	0.2	0.4	0.4	0.0	0.2	0.3	0.89	8.1E-01
bmgB	mobilization protein	0.0	0.5	0.5	0.0	0.0	0.9	1.77	
bmgA	mobilization protein	0.2	0.0	0.2	0.0	0.0	0.4	1.83	
BF3286	hypothetical protein	1.2	0.5	0.3	0.0	0.0	0.2	0.42	
BF3287	hypothetical protein	3.5	5.8	7.7	2.4	1.2	1.4	0.29	3.4E-02
BF3288	hypothetical protein	7.6	8.0	7.9	2.4	3.4	2.8	0.36	2.8E-03
BF3289	hypothetical protein	20.8	15.9	23.1	13.0	14.7	15.5	0.73	9.7E-02
BF3290	putative AraC-family regulatory protein	48.3	50.1	51.7	40.1	48.7	39.6	0.85	1.3E-01
BF3291	hypothetical protein	63.4	59.9	72.6	52.9	59.9	47.2	0.82	1.3E-01
BF3292	hypothetical protein	61.4	68.0	68.5	61.4	59.6	47.7	0.85	1.9E-01
BF3293	hypothetical protein	79.6	79.3	69.8	68.2	75.7	50.1	0.84	3.2E-01
BF3294	hypothetical protein	20.3	20.6	30.7	51.2	55.2	40.6	2.08	2.4E-02
BF3295	hypothetical protein	48.6	40.9	45.8	73.3	74.9	56.7	1.51	3.3E-02
BF3296	hypothetical protein	36.7	40.8	41.8	58.8	59.6	46.1	1.37	4.9E-02
BF3297	hypothetical protein	31.5	39.1	41.4	22.8	23.0	20.9	0.60	1.2E-02
BF3298	putative acetyltransferase	15.3	9.9	11.2	20.4	27.5	22.0	1.93	2.8E-02
BF3299	putative nitroreductase family protein	18.7	20.6	19.0	30.8	32.8	30.2	1.61	1.5E-03
BF3300	putative AraC-family regulatory protein	35.9	32.6	38.9	27.7	32.1	28.2	0.82	7.4E-02
BF3301	putative two-component system sensor kinase/response regulator fusion protein	9.3	10.1	10.7	18.3	20.4	15.1	1.77	1.1E-02
BF3302	hypothetical protein	4.7	3.7	4.7	12.6	15.3	11.4	3.01	3.3E-03
BF3303	hypothetical protein	30.9	22.9	26.0	44.8	40.3	40.6	1.58	1.8E-02
BF3304	hypothetical protein	11.5	11.3	10.1	14.1	17.3	15.3	1.41	2.0E-02
BF3305	putative lipoprotein	29.7	18.8	22.6	30.8	30.2	26.4	1.25	2.5E-01
BF3306	hypothetical protein	1.4	0.7	0.4	2.0	1.6	1.9	2.46	1.0E-01
BF3307	hypothetical protein	1.7	1.8	1.2	2.2	2.8	2.5	1.60	6.6E-02
BF3308	putative membrane attached hydrolase	1.3	0.5	1.1	1.5	1.2	0.8	1.30	5.8E-01
BF3309	putative acetyltransferase	35.1	32.5	30.1	29.3	25.6	21.2	0.77	1.1E-01
BF3310	putative transport-related membrane protein	10.0	8.5	12.1	4.8	4.6	6.7	0.53	3.1E-02
BF3311	hypothetical protein	290.3	318.0	297.1	60.9	45.0	42.4	0.16	7.2E-04
BF3312	uracil-DNA glycosylase	62.3	57.8	70.0	51.7	48.4	38.8	0.73	6.4E-02
BF3313	putative AraC-family regulatory protein	9.7	10.3	11.8	12.7	17.1	14.2	1.38	6.5E-02
BF3314	putative lipoprotein	16.1	15.6	15.7	9.3	10.7	9.0	0.61	3.5E-03
BF3315	hypothetical protein	178.5	186.4	165.5	86.7	93.6	74.8	0.48	2.7E-03
BF3316	hypothetical protein	182.7	194.9	235.3	154.6	178.5	143.7	0.78	1.0E-01
BF3317	hypothetical protein	351.4	357.2	418.3	437.3	502.6	394.3	1.18	1.9E-01
BF3318	hypothetical protein	105.6	110.0	111.4	30.8	31.0	23.9	0.26	7.5E-04
BF3319	hypothetical protein	261.1	279.9	293.6	66.2	68.3	54.3	0.23	4.8E-04
hdhA	putative 7-alpha-hydroxysteroid dehydrogenase (bile acid catabolism)	112.9	118.6	108.4	13.3	11.5	13.2	0.11	5.0E-05

BF3321	putative lipoprotein	0.9	0.9	1.2	0.7	0.5	0.8	0.64	1.2E-01
BF3322	hypothetical protein	0.9	0.7	0.3	0.6	0.4	0.9	0.97	9.5E-01
BF3323	hypothetical protein	1.5	1.0	1.1	0.0	0.0	0.5	0.40	
BF3324	hypothetical protein	0.3	0.3	0.6	0.5	0.0	0.3	1.02	9.8E-01
BF3325	putative lipoprotein	0.6	0.6	0.7	0.3	0.3	0.5	0.57	4.2E-02
BF3326	putative lipoprotein	0.8	0.9	0.7	0.3	0.2	0.3	0.35	2.5E-03
BF3327	putative lipoprotein	0.6	0.6	0.3	0.5	0.1	0.3	0.50	2.7E-01
BF3328	putative lipoprotein	1.0	1.7	0.6	0.4	0.5	0.2	0.31	6.5E-02
BF3330	hypothetical protein	1.5	0.9	1.7	0.4	0.5	0.9	0.43	9.5E-02
BF3331	putative AraC-family regulatory protein	0.4	0.6	1.1	0.6	0.9	0.2	0.71	6.3E-01
BF3332	putative integrase	10.2	8.4	9.1	4.7	5.1	6.7	0.59	2.7E-02
BF3333	putative AraC-family regulatory protein	49.0	48.9	52.2	35.9	52.8	39.6	0.84	2.8E-01
pncB	nicotinate phosphoribosyltransferase	342.3	351.6	349.0	156.2	159.5	152.5	0.45	2.2E-05
BF3335	hypothetical protein	15.9	20.1	22.0	26.4	29.2	19.6	1.29	2.4E-01
BF3336	putative K+ transport related membrane protein	24.9	27.8	25.6	8.6	8.4	11.2	0.36	2.3E-03
Cobalamin	RF00174	581.5	621.1	446.9	254.7	130.0	323.9	0.41	6.2E-02
accC2	putative biotin carboxylase 2	225.8	255.3	207.1	110.2	73.1	130.6	0.44	2.5E-02
BF3338	putative bioin-requiring protein	179.6	189.9	152.8	97.5	63.2	103.1	0.50	2.9E-02
BF3339	putative carboxyl transferase	292.5	383.0	289.2	158.7	120.0	183.6	0.48	2.0E-02
BF3340	hypothetical protein	5.3	8.1	4.0	3.5	4.0	7.6	0.85	6.8E-01
BF3342	putative exported beta-lactamase protein	62.2	61.3	55.1	36.6	28.4	39.0	0.58	1.6E-02
impDH	inositol-5-monophosphate dehydrogenase	212.6	207.8	181.2	221.6	190.6	242.0	1.09	4.7E-01
BF3345	hypothetical protein	36.1	30.6	26.3	15.1	10.6	19.4	0.47	3.7E-02
BF3346	hypothetical protein	177.2	227.0	148.6	20.7	18.3	17.4	0.10	6.0E-04
BF3347	putative AraC-family regulatory protein	22.9	20.0	20.4	13.0	12.1	12.8	0.60	2.3E-03
BF3348	putative transport-related, exported protein	0.8	1.7	0.5	0.2	0.0	0.6	0.34	3.3E-01
BF3349	putative multidrug resistance/siderophore transport related, membrane protein	2.3	2.6	1.5	1.6	1.5	2.2	0.84	5.0E-01
BF3350	putative transport related, lipoprotein	5.4	6.4	4.9	5.3	3.9	7.7	0.97	9.2E-01
BF3351	putative cysteine biosynthesis related protein	305.7	314.3	276.5	383.3	319.3	387.4	1.21	9.4E-02
BF3352	putative cell wall biosynthesis related protein	26.3	21.5	16.4	24.9	20.8	32.7	1.22	4.2E-01
BF3353	hypothetical protein	93.7	106.1	74.7	102.6	96.1	105.8	1.12	4.2E-01
BF3354	hypothetical protein	123.9	136.7	105.6	91.1	77.8	106.0	0.75	1.1E-01
BF3355	hypothetical protein	27.4	37.0	23.6	2.5	4.6	5.1	0.14	5.3E-03
BF3356	hypothetical protein	67.1	74.1	60.5	12.7	22.9	15.3	0.25	5.4E-03
BF3357	hypothetical protein	28.8	30.6	22.8	18.1	22.5	16.3	0.69	7.9E-02
BF3358	putative permease/membrane protein	11.3	9.6	10.2	2.0	1.1	1.1	0.13	2.5E-03
BF3360	putative chaperone/membrane protein	57.7	63.1	45.9	62.8	51.4	64.6	1.08	6.4E-01
BF3361	putative hydrolase	46.2	43.4	41.9	43.1	35.1	58.9	1.02	9.3E-01
BF3362	putative lipoprotein	18.2	19.1	11.8	3.3	3.3	4.7	0.23	5.5E-03
BF3363	hypothetical protein	46.3	56.8	45.7	8.3	7.6	14.5	0.20	5.6E-03
BF3364	putative two-component system, sensor kinase	307.7	312.8	296.7	56.6	55.9	67.6	0.20	2.0E-04

BF3365	putative metal transport-related, exported protein	7.9	8.7	7.4	2.9	2.4	3.6	0.37	5.3E-03
BF3366	hypothetical protein	13.1	13.7	13.0	5.2	4.6	7.1	0.42	7.5E-03
BF3368	putative copper/silver resistance-related transport membrane protein	25.5	29.2	25.5	5.7	5.3	7.0	0.22	7.3E-04
BF3369	hypothetical protein	249.6	267.4	249.7	131.1	143.5	158.1	0.56	2.7E-03
BF3370	putative peptidoglycan biosynthesis-related protein	54.7	61.0	59.8	92.6	98.9	80.1	1.54	1.0E-02
BF3371	putative ion transport related, membrane protein	90.5	104.6	94.0	41.7	49.5	46.9	0.48	1.9E-03
BF3372	hypothetical protein	27.7	23.6	25.2	27.2	28.6	28.3	1.10	1.7E-01
BF3373	hypothetical protein	13.3	16.1	18.3	22.0	24.2	14.6	1.26	3.5E-01
BF3374	hypothetical protein	40.6	44.6	41.5	35.2	34.2	33.1	0.81	9.2E-03
BF3375	hypothetical protein	23.5	21.6	31.1	27.9	29.8	30.6	1.17	3.0E-01
BF3376	hypothetical protein	50.5	42.0	53.6	50.3	59.9	52.7	1.12	3.5E-01
BF3377	hypothetical protein	107.2	108.7	103.2	111.3	129.6	108.3	1.09	2.7E-01
BF3378	bifunctional methionine sulfoxide reductase A/B protein	474.6	513.3	499.0	189.6	199.4	177.5	0.38	2.6E-04
BF3380	hypothetical protein	69.8	63.7	67.5	20.3	19.1	31.4	0.34	7.6E-03
BF3381	putative amino acid transport related, membrane protein	66.5	65.0	67.7	28.1	26.4	25.9	0.40	1.1E-04
BF3382	hypothetical protein	360.4	332.5	353.0	364.6	353.3	327.7	1.00	9.9E-01
BF3383	hypothetical protein	208.1	227.5	188.7	109.8	120.9	103.7	0.54	3.6E-03
BF3384	putative xanthine/uracyl permease, membrane protein	97.1	92.1	91.1	83.1	89.4	78.4	0.89	9.2E-02
BF3385	hypothetical protein	33.6	28.9	34.6	33.5	31.5	26.3	0.94	5.9E-01
BF3386	hypothetical protein	60.9	60.3	43.4	100.7	88.1	92.2	1.73	2.2E-02
BF3387	putative ArsC family related protein	146.5	158.0	160.3	283.5	304.1	248.7	1.79	3.5E-03
BFt48	tRNA-Trp-CCA	0.0	0.0	0.0	0.0	0.0	0.0		
BF3388	hypothetical protein	40.3	34.3	30.2	37.0	32.5	41.5	1.06	6.8E-01
BF3389	putative RNA polymerase sigma fator	24.2	21.5	20.9	35.1	37.2	35.0	1.61	2.8E-03
BF3390	hypothetical protein	30.6	24.9	28.7	55.0	47.0	46.1	1.76	7.5E-03
BF3391	putative cytidylyltransferase	26.6	28.4	31.5	42.5	47.4	42.3	1.53	7.3E-03
BF3392	hypothetical protein	43.5	51.1	39.9	54.7	58.8	50.8	1.22	1.1E-01
BF3393	conserved exported hypothetical protein	10.5	10.3	10.4	6.0	6.6	4.2	0.53	2.0E-02
BF3394	hypothetical protein	84.6	62.6	48.7	18.1	23.3	17.2	0.30	8.8E-03
BF3395	pyridoxine kinase	203.7	209.0	201.4	142.1	143.7	146.2	0.70	2.0E-04
BF3396	hypothetical protein	180.1	188.3	164.8	117.0	109.0	109.3	0.63	2.5E-03
BF3397	hypothetical protein	244.4	231.8	222.2	138.5	133.0	139.8	0.59	6.3E-04
BF3398	hypothetical protein	376.0	401.2	386.2	166.3	170.9	152.8	0.42	3.0E-04
BF3399	hypothetical protein	124.7	117.9	116.4	78.1	77.1	78.4	0.65	4.2E-04
BF3400	putative 6-pyruvoyl tetrahydropterin synthase	126.1	116.1	112.0	108.0	100.6	98.1	0.87	5.9E-02
BF3401	hypothetical protein	64.4	64.2	73.3	81.4	63.1	62.7	1.02	8.8E-01
BF3402	hypothetical protein	11.0	13.6	14.4	9.6	5.4	8.2	0.58	7.7E-02
BF3403	hypothetical protein	248.4	261.5	240.6	153.4	138.3	168.2	0.61	4.8E-03
BF3404	putative copper homeostasis protein	52.7	48.4	47.3	76.1	58.4	69.6	1.37	4.0E-02
BF3405	hypothetical protein	720.7	767.1	719.0	539.2	532.7	611.4	0.76	1.3E-02
BF3406	hypothetical protein	703.4	640.3	628.5	718.4	708.8	605.1	1.03	7.4E-01
BF3407	hypothetical protein	1029.3	911.6	878.3	931.7	881.1	870.6	0.95	4.9E-01

maeB	putative NADP-dependent malic enzyme	528.6	521.2	451.3	508.0	497.6	496.7	1.00	9.6E-01
gdhB2	glutamate dehydrogenase	4803.3	3806.3	4197.6	964.7	981.8	1133.1	0.24	6.2E-04
BF3410	putative RNA polymerase sigma factor	4.2	3.1	4.7	55.7	57.1	39.5	12.65	8.5E-04
BF3411	putative regulatory protein	8.0	11.0	10.2	138.7	132.1	144.0	14.31	1.8E-04
BF3412 (omp117)	**putative outer membrane protein Omp117**	**1.3**	**1.4**	**1.0**	**162.2**	**146.9**	**149.3**	**123.73**	**3.8E-05**
BF3413	hypothetical protein	0.9	1.2	1.7	140.2	106.1	119.5	102.17	3.0E-04
BF3414	hypothetical protein	0.5	0.7	0.0	127.4	99.9	112.4	186.03	7.7E-04
BF3415	putative lipoprotein	0.9	1.0	0.3	171.2	129.5	137.8	221.61	8.0E-04
BF3416	hypothetical protein	0.9	0.9	0.6	229.1	197.6	195.4	272.07	8.1E-05
BF3417	hypothetical protein	2.3	1.5	3.0	9.1	18.5	17.5	6.65	1.0E-02
BF3418	putative DNA methylase	165.0	127.7	157.3	136.7	159.7	109.5	0.90	5.4E-01
BF3419	hypothetical protein	118.6	110.4	121.9	114.9	128.0	106.7	0.99	9.4E-01
BF3420	hypothetical protein	54.6	54.5	65.7	51.8	71.0	42.7	0.93	7.3E-01
BF3421	hypothetical protein	12.3	13.1	14.1	8.2	12.1	10.5	0.77	1.5E-01
BF3422	putative DNA-binding protein	419.8	359.3	393.7	445.6	418.4	449.9	1.12	1.3E-01
BF3423	hypothetical protein	358.0	347.8	411.9	709.3	799.0	626.3	1.91	6.0E-03
BF3424	putative lipoprotein	1445.7	1447.4	1566.9	2329.6	2393.1	2058.3	1.52	5.2E-03
BF3425	hypothetical protein	157.0	152.9	166.3	132.9	149.9	129.2	0.86	7.9E-02
BF3426	hypothetical protein	228.5	237.8	252.1	218.5	247.5	201.0	0.93	3.8E-01
BF3427	hypothetical protein	546.2	479.1	471.0	388.6	371.6	351.5	0.74	1.5E-02
BF3428	hypothetical protein	412.0	426.9	412.4	357.7	366.4	431.9	0.92	3.1E-01
BF3429	hypothetical protein	356.8	275.9	280.1	194.5	202.0	243.7	0.70	5.6E-02
BF3430	putative lipoprotein	568.6	526.7	477.7	449.6	407.6	477.0	0.85	1.1E-01
BF3431	hypothetical protein	764.6	706.3	690.2	577.7	568.4	597.4	0.81	9.5E-03
BF3432	hypothetical protein	694.8	615.7	628.7	625.1	660.2	589.8	0.97	6.1E-01
BF3433	hypothetical protein	393.9	346.3	351.8	557.6	528.3	543.5	1.49	3.2E-03
BF3434	hypothetical protein	363.1	308.4	319.5	535.4	514.8	458.1	1.52	9.9E-03
BF3435	hypothetical protein	82.4	83.7	79.9	99.4	97.5	86.1	1.15	7.1E-02
gdhB	glutamate dehydrogenase	44.2	49.1	43.9	58.1	59.1	52.9	1.24	2.7E-02
BF3438	putative peptidase	270.7	241.7	260.9	334.3	342.4	306.4	1.27	1.7E-02
BF3439	hypothetical protein	11.6	10.6	11.2	11.5	13.5	13.8	1.16	1.2E-01
BF3440	hypothetical protein	11.0	9.0	10.9	10.4	9.0	8.3	0.90	3.8E-01
BF3441	hypothetical protein	1.8	0.0	0.0	0.0	0.0	0.8	0.48	
BF3442	putative polyA polymerase	53.8	49.3	42.1	38.5	38.1	50.6	0.87	3.8E-01
BF3443	putative lipoprotein	106.2	100.4	92.9	134.9	137.4	123.8	1.32	1.3E-02
BF3444	hypothetical protein	88.3	92.2	86.0	142.3	124.3	132.1	1.49	3.3E-03
BF3445	hypothetical protein	91.5	100.9	86.5	100.3	99.5	92.8	1.05	4.6E-01
BF3446	putative lipoprotein	205.2	206.7	218.4	224.4	226.5	180.0	1.00	9.7E-01
BF3447	putative peptidase	207.5	228.4	204.5	136.4	141.5	129.3	0.64	2.3E-03
BF3448	hypothetical protein	415.1	465.3	430.1	202.5	198.4	212.3	0.47	4.3E-04
BF3449	cold shock-like protein	851.2	850.9	867.9	197.5	209.2	282.1	0.26	1.6E-03
BF3450	hypothetical protein	2.5	0.0	0.0	1.2	1.4	2.4	0.64	
BF3451	putative LPS biosynthesis related conserved hypothetical protein	12.1	4.2	10.6	6.3	4.8	7.6	0.76	5.5E-01
rfbC1	putative LPS biosynthesis related dTDP-4-dehydrorhamnose 3,5-epimerase	17.9	18.0	14.7	10.2	7.9	11.8	0.59	3.4E-02

rffH1	putative LPS biosynthesis related glucose-1-phosphate thymidylyltransferase	20.1	18.4	23.2	11.1	15.9	13.2	0.65	4.5E-02
BF3454	putative LPS biosynthesis related glycosyltransferase	17.8	15.5	17.4	8.2	10.3	8.1	0.52	6.1E-03
BF3455	putative LPS biosynthesis related glycosyltransferase	7.9	7.6	9.0	2.9	5.4	4.8	0.52	5.6E-02
BF3456	putative LPS biosynthesis related polysaccharide polymerase	3.8	5.4	5.8	2.5	2.3	2.0	0.46	1.5E-02
BF3457	putative LPS biosynthesis related glycosyltransferase	4.6	7.4	9.7	6.8	7.8	6.9	1.03	9.2E-01
BF3458	putative LPS biosynthesis related glycosyltransferase	7.7	10.3	11.4	6.6	7.5	6.0	0.69	8.2E-02
BF3459	putative LPS biosynthesis related glycosyltransferase	9.5	9.5	8.8	6.5	10.1	8.4	0.89	4.8E-01
BF3460	putative LPS biosynthesis related glycosyltransferase	12.9	13.9	14.6	7.7	13.7	7.0	0.65	1.7E-01
BF3461	hypothetical protein	15.2	14.4	16.6	8.8	8.5	7.6	0.54	2.2E-03
BF3462	hypothetical protein	10.9	9.9	11.0	10.0	7.5	6.3	0.74	1.3E-01
BF3463	putative LPS biosynthesis related polysaccharide transporter	9.3	8.9	9.5	4.1	5.0	3.9	0.47	2.8E-03
BF3464	putative LPS biosynthesis related glycosyltransferase	7.1	10.0	8.7	8.6	6.9	6.2	0.84	3.5E-01
uphZ	putative LPS biosynthesis related transcriptional regulatory protein	8.4	7.3	5.2	5.5	5.9	3.8	0.73	2.4E-01
uphY	putative LPS biosynthesis related transcriptional regulatory protein	11.1	12.9	12.2	7.7	12.1	11.9	0.86	4.5E-01
BF3468	hypothetical protein	5.8	3.8	2.5	2.1	1.6	2.2	0.51	1.0E-01
BF3469	hypothetical protein	2.5	2.3	1.8	2.1	2.2	3.7	1.16	5.8E-01
BF3470	hypothetical protein	149.4	144.5	179.8	261.5	283.4	211.7	1.59	2.8E-02
BF3471	hypothetical protein	221.0	152.6	190.8	249.7	292.2	230.7	1.38	1.0E-01
BF3472	hypothetical protein	32.3	39.7	41.1	63.2	44.0	50.2	1.39	1.0E-01
BF3473	hypothetical protein	23.6	25.5	26.0	9.2	7.8	9.7	0.35	9.3E-04
BF3474	putative ribose 5-phosphate isomerase	193.3	165.8	184.3	90.1	98.4	116.0	0.56	7.8E-03
BF3475	hypothetical protein	90.6	93.2	89.3	84.0	90.5	90.6	0.97	4.1E-01
BF3476	putative acetyltransferase	11.9	8.3	9.4	11.3	11.8	13.7	1.25	1.9E-01
BF3477	putative DNa-binding protein	27.9	20.9	23.9	68.4	66.2	50.0	2.53	6.6E-03
BF3478	hypothetical protein	28.2	21.4	30.8	59.8	69.2	49.8	2.23	1.4E-02
BF3479	hypothetical protein	34.6	27.5	27.4	43.0	40.1	37.1	1.35	5.0E-02
ruvA	Holliday junction DNA helicase motor protein	121.1	101.3	101.0	113.1	103.2	130.2	1.07	5.6E-01
BF3481	putative oxidoreductase	1262.8	1195.6	1060.2	781.2	621.0	837.2	0.63	2.5E-02
BF3482	putative hemolysin	83.5	100.9	77.0	49.6	40.2	58.5	0.56	2.8E-02
BF3483	hypothetical protein	29.2	25.5	9.2	12.9	7.3	12.0	0.55	2.8E-01
Cobalamin	RF00174	102.4	104.0	89.3	58.5	46.2	122.7	0.70	3.7E-01
BF3484	anaerobic ribonucleoside triphosphate reductase	117.2	140.1	146.2	152.7	122.9	150.1	1.05	6.7E-01
BF3485	putative anaerobic ribonucleoside-triphosphate reductase activating protein	83.0	106.7	106.3	103.8	92.6	123.5	1.08	6.2E-01

BF3486	putative transport-related, membrane protein	21.6	26.0	16.8	8.2	6.5	8.7	0.37	8.2E-03
BF3487	putative aminotransferase	3.6	4.0	3.9	4.0	5.3	5.6	1.28	1.3E-01
BF3488	putative hydrolase	2.2	1.2	1.5	1.9	1.0	2.8	1.12	8.0E-01
BF3490	hypothetical protein	39.6	42.1	34.8	74.3	69.2	71.9	1.85	2.3E-03
BF3491	putative protease	487.6	477.5	493.6	376.3	387.8	375.6	0.78	5.7E-04
BF3492	1-deoxy-D-xylulose 5-phosphate reductoisomerase	247.7	260.1	255.1	266.4	249.6	260.4	1.02	5.7E-01
BF3493	putative peptidase	231.8	233.9	242.4	195.0	204.3	190.7	0.83	5.7E-03
rimM	16S rRNA-processing protein	203.7	200.1	214.0	219.9	203.5	221.3	1.04	3.5E-01
BF3495	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	451.3	447.1	446.2	435.2	414.2	405.1	0.93	5.6E-02
BF3496	hypothetical protein	356.0	394.8	382.6	379.4	402.0	343.8	0.99	9.1E-01
BF3497	putative glycoprotease family exported protein	246.1	272.0	267.5	275.7	263.6	252.1	1.01	8.9E-01
BF3499	hypothetical protein	451.1	392.7	412.7	446.3	402.5	387.5	0.98	8.3E-01
gmk	guanylate kinase	373.0	403.1	414.8	328.8	319.9	331.9	0.82	1.2E-02
nadD	nicotinic acid mononucleotide adenyltransferase	165.7	188.3	183.4	138.3	153.0	153.4	0.83	4.1E-02
BF3502	putative phosphoesterase	66.2	71.8	65.5	37.1	39.6	46.6	0.60	7.3E-03
BF3503	putative prenyltransferase	78.9	62.6	63.3	63.9	60.4	64.9	0.93	4.8E-01
rffG	putative dTDP-glucose 4,6-dehydratase	160.8	152.5	180.8	279.9	275.4	252.4	1.64	4.4E-03
rffH2	putative glucose-1-phosphate thymidylyltransferase	117.0	126.4	124.1	129.9	129.1	132.8	1.07	9.7E-02
BF3506	putative phosphoesterase	53.4	62.9	50.2	71.0	63.5	76.7	1.27	8.3E-02
ppk	polyphosphate kinase	14.5	17.5	15.0	44.2	44.5	40.7	2.76	7.6E-04
BF3508	hypothetical protein	41.3	41.6	44.0	39.1	49.8	47.4	1.07	5.0E-01
BF3509	putative response regulator	722.6	688.2	768.4	637.9	742.9	598.6	0.91	3.0E-01
BF3510	putative ABC transport system, ATP-binding protein	91.7	87.1	91.5	131.0	117.3	121.7	1.37	4.0E-03
BF3511	putative metal resistance related exported protein	15.4	17.1	18.4	84.9	72.8	95.3	4.95	5.9E-04
BF3512	putative metal resistance related trasport membrane protein	30.5	32.0	31.3	67.7	63.8	69.4	2.14	1.8E-04
BF3513	putative puter membrane protein	59.7	71.3	64.4	97.9	95.5	88.2	1.44	1.0E-02
BF3514	hypothetical protein	40.7	38.8	34.7	35.2	31.6	39.2	0.93	4.6E-01
BF3515	hypothetical protein	43.2	38.6	36.3	54.3	51.1	60.5	1.40	2.0E-02
BF3516	hypothetical protein	26.8	38.6	27.6	41.8	50.1	51.4	1.56	5.4E-02
BF3517	hypothetical protein	52.7	57.4	53.0	109.3	94.6	103.7	1.88	1.4E-03
BF3518	hypothetical protein	131.0	145.5	144.3	159.5	135.1	150.0	1.06	4.8E-01
BF3519	hypothetical protein	309.3	338.9	332.8	172.8	174.6	156.3	0.51	8.6E-04
BF3520	putative RNA polymerase sigma factor	193.2	183.2	163.2	120.0	113.9	150.2	0.71	4.6E-02
BF3521	hypothetical protein	241.7	211.0	175.5	167.7	129.4	200.1	0.79	2.6E-01
BF3522	putative phospholipid biosynthesis related protein	108.4	86.6	99.5	59.3	59.9	81.8	0.68	6.1E-02
thyB	thymidylate synthase	136.1	130.6	117.1	122.9	112.6	145.6	0.99	9.3E-01
dfrA	putative dihydrofolate reductase	111.3	122.9	114.0	116.2	114.2	131.4	1.04	5.9E-01
BF3525	putative AsnC family regulatory protein	456.9	477.3	491.3	602.0	565.3	546.2	1.20	1.6E-02
BF3526	putative lipoprotein	56.6	56.7	47.0	63.2	61.1	56.3	1.13	2.2E-01
BF3527	hypothetical protein	6323.5	6931.5	7184.2	7500.8	8341.2	7450.7	1.14	1.1E-01

BF3528	hypothetical protein	6721.0	6805.0	7652.7	7897.2	8635.1	6909.4	1.10	3.4E-01
BF3529	hypothetical protein	3689.8	4203.7	4551.0	5669.4	6530.7	5475.1	1.42	2.7E-02
BF3530	hypothetical protein	4345.2	4655.9	4983.5	6965.1	7493.6	6239.6	1.48	1.1E-02
BFt49	tRNA-Ser-GGA	118.3	168.5	88.3	138.7	132.3	265.5	1.40	3.8E-01
BF3531	putative DNAse related protein	115.1	115.9	126.3	115.8	114.4	110.5	0.95	2.9E-01
BF3532	hypothetical protein	175.2	194.8	192.9	183.2	169.5	184.3	0.95	4.1E-01
BF3533	putative isoprenoid biosynthesis related protein	351.1	335.1	357.1	322.8	328.1	297.1	0.91	9.0E-02
BF3534	conserved hypothetical outer membrane protein	2991.2	2822.2	2637.0	3158.2	2892.0	2938.1	1.06	3.1E-01
cmk	putative cytidylate kinase	375.4	347.4	328.6	307.8	254.6	331.4	0.85	1.8E-01
BF3536	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	122.9	126.2	124.6	121.1	114.0	113.2	0.93	6.1E-02
pfkA	6-phosphofructokinase	422.9	400.8	389.8	604.0	503.5	582.7	1.39	1.4E-02
BF3538	conserved hypothetical dehydrogenase protein	43.2	50.1	42.7	70.7	70.2	84.1	1.65	8.7E-03
BF3539	putative oxidoreductase	51.4	44.0	42.1	72.8	64.0	98.3	1.69	3.9E-02
BF3540	putative membrane dehydrogenase protein	72.5	70.9	69.4	60.6	66.2	66.0	0.91	6.1E-02
BF3541	citrate synthase	387.4	413.6	398.0	267.4	265.5	241.6	0.65	1.7E-03
icd	putative isocitrate dehydrogenase [NADP]	276.2	293.1	244.7	167.8	149.9	178.2	0.61	7.6E-03
acn	putative aconitase	364.4	376.6	347.7	194.6	186.8	230.2	0.56	4.0E-03
BF3544	putative DNA-binding protein	33.3	25.9	26.9	20.2	20.2	25.9	0.77	1.2E-01
BF3545	putative lipoprotein	7.7	7.2	8.2	3.2	3.6	2.4	0.39	6.4E-03
BF3546	putative reductoisomerase	2636.4	2895.1	2641.9	1335.7	1308.7	1415.0	0.50	5.2E-04
BF3547	hypothetical protein	375.2	368.3	359.4	158.9	155.1	175.4	0.44	3.7E-04
BF3548	putative acyl-ACP thioesterase	409.6	415.0	419.2	191.3	211.7	181.8	0.47	6.2E-04
BF3549	putative acetohydroxyacid synthase small subunit	449.8	453.7	461.3	203.6	235.2	187.1	0.46	1.7E-03
ilvB	putative acetolactate synthase large subunit	387.9	387.4	333.1	189.4	171.3	210.7	0.52	4.1E-03
ilvD	dihydroxy-acid dehydratase	454.9	426.4	377.6	178.0	176.1	234.8	0.46	6.8E-03
BF3552	hypothetical protein	8.1	6.4	6.6	6.7	8.7	7.8	1.10	5.0E-01
BF3553	hypothetical protein	5.7	4.5	4.8	4.0	3.4	4.6	0.80	1.6E-01
BF3554	putative lipoprotein	2.8	2.6	1.4	1.7	1.3	2.0	0.75	3.7E-01
BF3555	putative lipoprotein	3.7	1.5	2.1	1.2	1.1	2.3	0.64	3.5E-01
BF3556	hypothetical protein	2.6	2.1	1.7	1.3	2.3	0.6	0.57	2.9E-01
BF3557	putative AraC-family regulatory protein	5.4	9.2	7.3	2.1	2.8	1.4	0.28	1.9E-02
BF3558	putative isomerase	1361.2	1207.1	1151.7	584.3	574.5	690.6	0.50	3.4E-03
BF3559	putative lipoprotein	80.9	60.0	67.4	40.3	47.2	61.3	0.71	1.3E-01
BF3560	hypothetical protein	33.2	22.5	29.0	42.4	40.6	52.6	1.61	4.9E-02
BF3561	hypothetical protein	34.9	35.8	38.1	56.6	56.1	49.4	1.49	5.3E-03
BF3562	hypothetical protein	415.4	397.8	413.0	317.3	311.8	265.5	0.73	1.4E-02
BF3563	hypothetical protein	488.9	455.6	484.8	353.0	345.4	316.4	0.71	4.0E-03
BF3567	hypothetical protein	5124.2	4793.8	5629.9	2892.3	3266.6	2853.6	0.58	4.0E-03
BF3568	putative exported phosphatase	25.7	29.0	32.9	36.2	38.5	36.2	1.27	5.6E-02
BF3569	hypothetical protein	29.4	39.0	45.4	41.3	51.3	46.0	1.23	2.8E-01
BF3570	putative exported phosphoesterase protein	28.6	28.2	31.4	38.0	35.0	33.7	1.21	3.5E-02
BF3571	hypothetical protein	5.7	4.0	5.2	23.6	26.2	22.3	4.89	1.1E-03

BF3572	hypothetical protein	3.9	5.1	4.8	16.7	19.0	19.3	4.01	8.6E-04
BF3573	putative anti sigma factor	23.2	19.2	24.2	50.9	56.9	48.5	2.35	2.6E-03
BF3574	putative RNA polymerase sigma factor	55.4	51.8	63.8	83.2	89.1	71.5	1.43	3.3E-02
BF3575	putative lipoprotein	4.2	4.3	3.8	8.3	9.4	7.4	2.03	3.8E-03
BF3576	hypothetical protein	2.6	2.5	2.7	6.8	7.4	6.7	2.66	1.9E-04
BF3579	hypothetical protein	2.9	2.7	2.2	155.4	168.3	130.9	58.13	7.7E-05
BF3580	hypothetical protein	2.6	1.9	2.1	142.9	148.9	125.7	64.01	6.5E-05
BF3581	**hypothetical protein**	**2.0**	**2.5**	**2.2**	**162.8**	**163.6**	**137.4**	**69.33**	**2.3E-05**
BF3582	putative regulatory protein (possible anti-sigma factor)	2.9	5.1	5.6	39.4	45.3	44.6	9.93	2.0E-03
BF3583	putative RNA polymerase sigma factor	37.5	45.1	49.3	73.7	76.9	64.6	1.64	1.7E-02
aroC	chorismate synthase	480.7	471.7	472.5	327.0	328.0	312.5	0.68	2.8E-04
BF3585	putative peptidase	366.1	334.8	366.4	261.1	278.7	262.4	0.75	5.2E-03
BF3586	putative exported hydrolase	162.2	187.0	195.0	44.5	48.8	41.8	0.25	4.2E-04
BF3589	hypothetical protein	64.7	60.5	74.2	19.7	20.1	21.3	0.31	5.0E-04
BF3590	putative DNA topoisomerase	89.1	80.4	81.1	82.4	74.4	80.3	0.95	3.6E-01
BF3591	putative exporte hydrolase	25.7	22.4	27.7	38.4	40.0	38.3	1.55	7.6E-03
mutB	methylmalonyl-CoA mutase	673.1	701.6	578.9	721.7	666.7	684.0	1.06	4.5E-01
mutA	putative methylmalonyl-CoA mutase small subunit	457.3	486.8	441.3	592.7	623.5	558.6	1.28	1.2E-02
BF3594	putative cation transport related, membrane protein	192.6	196.6	209.1	272.9	249.2	243.4	1.28	1.2E-02
BF3595	hypothetical protein	103.9	102.7	92.0	178.4	160.9	201.5	1.81	5.2E-03
BF3596	putative cation transport related membrane protein	3.8	3.2	2.4	6.1	3.9	5.1	1.61	9.2E-02
BF3597	hypothetical protein	49.2	49.7	49.1	44.6	35.1	44.5	0.83	1.3E-01
BF3598	hypothetical protein	29.8	32.4	28.0	35.4	28.2	30.6	1.04	6.9E-01
BF3599	hypothetical protein	67.4	65.1	55.0	24.7	20.8	26.2	0.38	2.3E-03
BF3601	putative cation transport related membrane protein	36.7	38.6	32.5	27.1	21.6	33.6	0.75	1.6E-01
lysS	lysyl-tRNA synthetase	504.0	506.4	488.1	519.3	506.2	485.8	1.01	7.8E-01
BF3603	putative phospholipids biosynthesis	276.5	314.5	303.5	242.6	242.9	250.9	0.82	1.9E-02
pgiA	glucose-6-phosphate isomerase	1040.9	1029.2	1064.4	923.2	869.4	891.9	0.86	5.3E-03
BF3605	putative lipoprotein	448.3	360.6	357.6	386.6	366.7	341.9	0.94	5.8E-01
BF3606	putative hydrolase	105.9	108.4	109.9	85.8	62.6	66.6	0.66	2.6E-02
BFt50	tRNA-Arg-CCG	77.6	55.1	69.9	58.0	43.6	47.4	0.74	1.3E-01
asnA	asparagine synthetase AsnA	647.5	644.1	624.1	424.7	404.2	387.6	0.63	7.2E-04
ung	uracil-DNA glycosylase	705.0	753.9	709.2	441.7	429.5	409.0	0.59	6.0E-04
BF3609	hypothetical protein	380.9	368.8	363.5	248.8	248.9	254.3	0.68	2.2E-04
BF3610	hypothetical protein	101.9	110.1	105.7	80.3	95.1	95.2	0.85	8.9E-02
BF3611	putative glycosyl hydrolase lipoprotein	30.4	33.9	33.9	103.5	105.6	100.6	3.16	1.5E-04
BF3612	hypothetical protein	151.2	151.4	165.8	162.2	200.9	187.3	1.17	1.3E-01
BF3613	putative acetyltransferase	49.9	47.3	43.5	49.5	42.1	41.9	0.95	5.5E-01
BF3614	hypothetical protein	56.5	57.0	53.3	33.3	32.9	30.8	0.58	6.3E-04
BF3615	putative exported N-acetylmuramoyl-L-alanine amidase	205.8	191.0	204.6	93.2	94.7	81.0	0.45	8.8E-04
BF3616	hypothetical protein	204.5	200.7	203.2	196.4	186.2	152.0	0.87	2.2E-01
dnaA	chromosomal replication initiation protein	811.6	773.6	874.8	963.1	960.2	903.4	1.15	5.1E-02
BF3618	putative oxidase	96.8	107.2	112.6	113.7	117.0	98.3	1.04	6.8E-01
BF3619	putative ribonucleoside reductase	342.5	411.4	406.0	497.6	463.6	470.0	1.24	5.0E-02

BF3620	putative alpha-glucanotransferase	66.8	73.4	71.1	61.4	55.4	59.4	0.83	2.5E-02
BF3621	putative acetyltransferase membrane protein	14.2	13.7	12.1	9.1	11.3	11.2	0.78	7.8E-02
BF3622	putative dihydroneopterin aldolase	37.3	24.9	27.9	30.8	36.5	40.4	1.21	3.3E-01
BF3623	hypothetical protein	22.2	25.6	25.1	45.6	48.3	45.0	1.91	1.2E-03
mgsA	putative methylglyoxal synthase	380.4	341.0	355.7	362.8	342.8	358.4	0.99	8.1E-01
BF3625	putative glycosyl transferase	98.0	95.8	81.7	88.3	63.0	125.6	0.97	9.1E-01
BF3626	putative lipd A biosynthesis related exported protein	146.6	126.4	131.5	86.5	93.6	122.7	0.74	9.5E-02
BF3627	hypothetical protein	155.7	132.1	133.5	107.3	93.5	144.3	0.81	2.6E-01
BF3628	putative long-chain-fatty-acid--CoA ligase	109.5	112.9	112.0	147.9	139.7	142.5	1.29	1.2E-03
BF3629	hypothetical protein	1990.9	2635.3	2451.4	1152.3	1151.1	1595.4	0.55	2.6E-02
rplI	putative 50S ribosomal protein L9	2289.5	2546.5	2774.5	3037.4	3113.6	2919.6	1.20	6.6E-02
rpsR	putative 30S ribosomal protein S18	1959.7	1974.5	2425.6	2734.0	2571.2	2105.7	1.16	2.9E-01
rpsF	30S ribosomal protein S6	1579.9	1532.5	1892.3	2281.2	2117.5	1936.6	1.27	7.2E-02
BF3633	putative MarR-family regulatory protein	334.4	278.8	272.5	196.4	207.9	198.8	0.68	1.2E-02
rprY	two-component system, transcriptional regulatory protein	3208.4	3310.0	3395.2	2036.9	2140.6	1908.5	0.61	1.2E-03
rprX	two-component regulatory system, sensor kinase protein	1667.3	1780.9	1601.1	579.4	614.3	525.5	0.34	4.2E-04
BF3636	putative elongation factor G	87.9	95.5	82.6	539.1	531.8	578.1	6.21	6.9E-05
BF3637	hypothetical protein	1.2	0.7	2.0	0.6	0.0	0.0	0.49	
BF3637A	hypothetical protein	0.0	0.0	0.7	0.0	0.0	1.2	1.74	
BF3638	putative oxygen-independent coproporphyrinogen III oxidase	135.5	144.0	125.1	121.1	102.3	138.7	0.89	3.6E-01
BF3639	putative RNA polymerase sigma factor	33.5	29.9	32.0	46.5	39.2	39.7	1.31	2.8E-02
BF3640	hypothetical protein	305.8	294.8	269.3	330.3	322.3	312.3	1.11	1.0E-01
BF3641	putative transmembrane sensor/regulatory protein	427.8	444.3	440.8	305.7	313.1	311.0	0.71	2.1E-04
BF3642	hypothetical protein	140.1	173.5	141.0	111.9	101.9	138.7	0.77	1.3E-01
BF3643	putative lipoprotein	89.2	88.3	96.1	92.7	78.6	86.2	0.94	3.9E-01
BF3646	hypothetical protein	12784.8	11827.5	12303.0	353.8	412.0	401.7	0.03	9.2E-06
BF3647	hypothetical protein	72.4	71.2	78.2	52.8	55.1	45.4	0.69	1.3E-02
BF3648	putative glycosyl transferase	0.4	0.6	1.2	0.0	0.3	0.4	0.48	1.9E-01
BF3649	hypothetical protein	1.0	2.2	0.0	0.0	0.0	0.0		
BF3649A	hypothetical protein	1.0	1.0	2.1	0.0	0.0	0.9	0.70	
BF3650	hypothetical protein	0.0	0.0	1.5	0.0	0.0	0.7	0.44	
BF3651	hypothetical protein	61.0	51.6	61.0	82.7	101.8	62.1	1.40	1.4E-01
BF3653	hypothetical protein	160.0	153.9	159.3	169.5	171.0	198.3	1.14	1.1E-01
BF3654	putative S-adenosylmethionine:tRNA ribosyltransferase-isomerase	78.4	85.0	81.9	90.2	83.6	85.6	1.06	2.1E-01
BF3655	putative NUDIX domain conserved hypothetical protein	125.9	152.7	148.2	133.5	124.7	134.8	0.92	3.6E-01
BF3656	putative glutathione peroxidase	365.0	400.8	374.5	221.0	237.3	234.9	0.61	1.0E-03
BF3657	hypothetical protein	90.2	90.9	83.5	61.5	57.1	70.8	0.71	1.8E-02
BF3658	putative transport-related, membrane protein	0.7	1.0	0.9	0.8	0.7	0.7	0.84	2.2E-01
BF3659	putative lipoprotein	1.0	0.4	0.7	1.1	1.2	0.8	1.53	2.7E-01
BF3660	hypothetical protein	14.1	13.8	14.1	13.9	13.4	14.2	0.98	4.9E-01
BF3661	putative response regulator	11.5	15.6	12.5	17.2	15.7	19.3	1.32	9.8E-02

BF3662	putative iron hydrogenase	80.9	76.5	80.0	123.8	118.0	120.2	1.53	4.5E-04
BF3663	biotin synthase	62.2	61.7	71.3	97.3	86.6	97.7	1.44	1.1E-02
BF3664	thiamine biosynthesis protein ThiH	28.6	32.3	32.3	50.0	43.2	50.3	1.54	7.8E-03
BF3665	hypothetical protein	50.3	52.8	46.4	58.2	57.2	63.5	1.20	4.2E-02
BF3666	putative lipoprotein	259.4	282.6	296.0	162.8	210.4	162.5	0.64	2.0E-02
BF3667	putative glycosyl hydrolase	15.2	13.7	15.3	30.6	30.1	29.5	2.04	4.3E-04
BF3668	putative phosphoglucomutase/phosphomannomutase family protein	382.6	355.9	371.0	528.0	522.6	532.7	1.43	6.5E-04
BF3669	hypothetical protein	931.2	905.0	991.7	672.6	705.0	622.3	0.71	5.4E-03
BF3670	hypothetical protein	217.3	202.8	224.4	128.8	144.9	124.8	0.62	3.6E-03
BF3671	putative competence related membrane protein	22.6	26.5	21.0	9.6	12.2	13.3	0.50	1.2E-02
BF3672	putative ribulose-phosphate 3-epimerase	325.8	309.9	320.9	268.7	259.5	267.8	0.83	2.6E-03
fmt	methionyl-tRNA formyltransferase	181.9	186.7	188.5	170.0	178.1	182.3	0.95	1.5E-01
BF3674	putative transport related, membrane protein	216.5	224.3	220.5	179.9	184.5	196.8	0.85	1.2E-02
BF3675	hypothetical protein	194.9	177.7	174.0	168.4	141.6	232.3	0.97	8.9E-01
BF3676	hypothetical protein	149.3	145.4	150.5	164.9	149.3	147.5	1.04	4.6E-01
BF3677	hypothetical protein	44.1	38.0	41.7	22.9	25.1	28.7	0.62	9.9E-03
BF3679	putative non-specific DNA-binding protein	1.6	2.9	3.9	3.7	0.9	6.4	1.07	9.4E-01
BF3682	putative phosphotransferase	7.4	7.1	9.7	4.4	5.3	6.4	0.67	8.0E-02
BF3683	DNTP-hexose dehydratase-epimerase	11.4	10.3	8.9	7.8	7.1	4.7	0.63	8.8E-02
BF3684	putative glycosyltransferase protein	8.7	8.0	10.6	5.3	7.6	5.8	0.69	8.1E-02
BF3685	putative glycosyltransferase protein	11.2	9.9	15.1	7.6	5.6	4.9	0.50	3.7E-02
BF3686	putative polysaccharide polymerase	7.6	6.2	8.4	4.6	5.8	2.8	0.57	1.2E-01
BF3687	putative glycosyltransferase protein	15.0	13.9	17.1	8.1	7.2	8.1	0.51	3.1E-03
BF3688	putative alpha-1,2-fucosyltransferase	20.9	15.3	16.5	9.2	11.7	9.1	0.57	2.4E-02
BF3689	putative transferase	13.5	17.8	15.3	11.4	10.8	8.6	0.66	4.6E-02
BF3690	putative O-acetyl transferase (capsular polysaccharide synthesis enzyme o-acetyl transferase)	12.3	9.5	11.1	7.1	7.4	4.3	0.56	6.7E-02
BF3691	hypothetical protein	7.9	5.5	8.4	3.3	4.3	3.2	0.50	2.8E-02
BF3692	possible flippase	11.2	10.2	12.2	5.3	7.1	5.9	0.54	9.4E-03
BF3693	hypothetical protein	15.2	19.7	21.6	16.0	14.5	15.2	0.82	1.9E-01
BF3694	putative nucleotidyltransferase	18.1	18.2	17.3	18.7	17.3	13.4	0.91	5.0E-01
BF3695	putative nucleotidyltransferase	11.3	11.3	12.2	9.6	11.4	8.5	0.84	1.8E-01
BF3696	putative haloacid dehalogenase-like hydrolase	11.2	17.2	11.7	11.6	14.8	13.1	1.00	9.9E-01
BF3697	hypothetical protein	12.5	10.0	15.3	11.0	8.6	11.4	0.83	3.6E-01
updZ	putative transcriptional regulator	13.1	12.7	14.0	6.5	9.2	8.4	0.60	2.0E-02
updY	putative transcriptional regulator	15.4	14.9	14.8	5.9	9.5	8.5	0.52	2.3E-02
BF3700	hypothetical protein	17.5	20.5	19.2	2.6	3.2	3.5	0.16	5.1E-04
BF3701	hypothetical protein	13.0	8.4	13.7	7.9	2.3	7.2	0.44	1.8E-01
BF3702	hypothetical protein	13.0	7.8	9.5	5.9	6.8	7.1	0.67	9.8E-02
tag	putative DNA-3-methyladenine glycosylase I	134.6	132.3	142.1	122.0	117.3	133.2	0.91	1.4E-01
BF3705	putative single-stranded-DNA-specific exonuclease	348.8	378.8	347.5	292.0	267.8	293.9	0.79	1.3E-02

BF3706	putative DEAD box helicase	83.8	85.0	83.7	65.3	61.2	68.5	0.77	5.0E-03
BF3707	hypothetical protein	92.2	85.6	90.4	207.7	193.3	200.4	2.24	1.9E-04
BF3708	putative transport related, membrane protein	4.1	3.8	4.4	6.6	8.1	8.9	1.90	8.0E-03
BF3709	putative sialidase	2.0	1.9	3.1	4.4	3.7	3.1	1.64	8.8E-02
BF3710	hypothetical protein	3.4	2.0	1.7	4.0	4.0	5.2	1.92	7.7E-02
BF3711	putative lipoprotein	3.1	3.7	3.0	3.1	2.5	3.3	0.90	4.5E-01
BF3712	hypothetical protein	7.1	8.6	10.1	5.8	7.1	5.8	0.72	9.2E-02
BF3713	putative N-acetylneuraminate lyase (sialic acid lyase)	37.9	38.2	32.5	16.7	23.4	23.3	0.58	2.4E-02
BF3714	putative GntR-family regulatory protein	196.7	207.7	172.0	21.7	23.7	27.2	0.13	2.4E-04
BF3715	putative prefrenate dehydratase	97.0	94.7	96.7	168.8	203.8	172.9	1.88	2.2E-03
BF3716	putative aminotransferase	128.8	139.5	121.2	102.7	100.0	125.9	0.84	1.5E-01
BF3717	putative chorismate mutase	183.3	195.5	193.4	129.4	112.9	146.6	0.68	1.8E-02
BF3718	putative prephenate dehydrogenase family protein	226.4	258.0	292.2	153.2	155.5	147.4	0.59	6.9E-03
BF3719	hypothetical protein	24.9	25.5	32.1	13.2	14.9	13.1	0.50	5.6E-03
BF3720	putative DNA primase	123.0	120.0	93.3	137.6	104.3	149.8	1.16	4.2E-01
BF3721	putative exported sulfatase	3.5	4.6	2.7	6.9	5.3	7.9	1.87	5.7E-02
BF3722	putative exported uslfatase	1.5	1.6	1.4	4.3	3.0	4.8	2.57	8.2E-03
BF3723	hypothetical protein	3.4	3.7	2.8	10.9	10.3	13.1	3.46	2.0E-03
BF3724	hypothetical protein	4.7	4.1	4.5	6.1	6.2	8.2	1.53	2.9E-02
BF3725	hypothetical protein	51.4	40.4	38.5	19.4	16.9	22.0	0.45	7.3E-03
BF3726	putative RNA polymerase sigma factor	121.6	119.0	120.1	111.2	122.4	111.4	0.96	3.0E-01
folE	GTP cyclohydrolase I	189.4	158.8	181.7	125.2	141.8	157.1	0.80	9.1E-02
BF3728	hypothetical protein	188.2	195.2	187.4	164.3	169.8	183.2	0.91	7.6E-02
tpiA	triosephosphate isomerase	1861.6	1906.9	1905.0	2176.7	2252.9	2142.4	1.16	3.8E-03
BF3730	hypothetical protein	280.0	270.0	280.9	149.6	152.0	153.5	0.55	5.0E-05
BF3731	hypothetical protein	420.8	416.2	416.2	205.4	210.7	222.6	0.51	1.6E-04
BF3732	putative exported peptidase	1492.2	1479.8	1523.6	1745.0	1693.8	1566.3	1.11	5.8E-02
BF3733	putative nucleoside diphosphate kinase	1817.7	1770.7	1754.6	1295.8	1231.4	1389.9	0.73	4.1E-03
BF3734	putative ATP-dependent DNA helicase	119.7	100.0	104.3	142.8	142.5	134.5	1.30	2.3E-02
ispD	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	221.9	218.4	203.1	280.5	287.2	320.1	1.38	8.2E-03
BF3736	putative thiamine biosynthesis related protein	411.1	380.8	352.0	485.0	473.0	544.0	1.31	2.5E-02
BF3737	putative TonB exported protein	216.4	168.8	173.8	194.0	179.8	262.9	1.13	5.0E-01
BF3738	putative tansport related protein	255.0	231.8	261.3	236.0	274.7	252.8	1.02	7.9E-01
BF3739	putative transport related membrane protein	328.3	302.7	321.7	372.2	359.1	361.5	1.15	1.6E-02
BF3740	pyridoxal phosphate biosynthetic protein	210.6	216.6	201.6	227.2	228.9	225.0	1.08	3.8E-02
ppnK	inorganic polyphosphate/ATP-NAD kinase	131.0	138.2	149.1	143.3	143.9	115.6	0.96	6.9E-01
5S		4.7	6.9	36.7	1.9	4.5	25.4	0.57	6.6E-01
23S		13.7	7.5	12.2	16.3	9.1	22.1	1.38	4.5E-01
BFt51	tRNA-Ala-TGC	87.0	97.6	97.6	47.1	45.1	95.3	0.62	1.8E-01
BFt52	tRNA-Ile-GAT	158.9	177.9	180.8	63.0	65.0	113.6	0.45	3.1E-02
16S		672.5	32.3	99.0	90.9	32.3	230.2	0.68	7.8E-01
BF3741A	hypothetical protein	0.0	457.3	0.0	96.4	92.4	155.5	0.24	
BF3742	hypothetical protein	43.0	55.7	61.6	33.3	41.5	31.0	0.66	6.9E-02

BF3743	hypothetical protein	222.5	244.0	263.5	188.4	238.5	142.3	0.76	2.2E-01
BF3744	putative RNA polymerase sigma factor	22.4	28.1	30.8	67.8	76.0	67.2	2.61	3.1E-03
BF3745	hypothetical protein	12.7	10.7	8.8	24.7	29.1	21.1	2.33	1.1E-02
BF3746	hypothetical protein	2.5	3.1	2.0	12.2	13.7	13.0	5.27	1.3E-03
BF3747	putative liporotein	1.7	2.0	1.7	9.7	11.3	9.5	5.66	2.7E-04
BF3748	putative lipoprotein	3.3	1.0	2.1	12.0	15.8	7.2	5.86	2.8E-02
BF3749	hypothetical protein	7.9	8.5	6.4	16.9	15.8	17.2	2.21	3.5E-03
BF3750	hypothetical protein	51.2	47.9	51.0	44.2	53.3	47.3	0.96	6.1E-01
BF3751	putative antibiotic resistance-related regulatory protein	74.8	71.1	76.7	87.4	87.7	65.0	1.07	6.2E-01
BF3752	putative exported peptidase	89.1	81.1	86.4	132.2	132.6	139.4	1.58	1.0E-03
mdh	putative malate dehydrogenase	1497.2	1676.2	1709.9	1980.4	1900.0	1907.5	1.19	3.4E-02
BF3754	hypothetical protein	124.1	125.1	127.3	97.7	91.7	95.8	0.76	1.0E-03
BF3755	hypothetical protein	28.8	23.3	26.0	15.1	17.3	14.0	0.59	1.1E-02
BF3756	putative RNA polymerase sigma factor	23.8	15.2	19.6	14.2	14.4	14.9	0.75	1.4E-01
BF3757	hypothetical protein	19.9	14.5	18.5	3.4	3.6	2.9	0.19	9.1E-04
BF3759	putative outer membrane protein	44.1	44.2	31.2	30.8	27.1	25.8	0.71	8.5E-02
BF3760	hypothetical protein	25.6	33.8	26.0	45.5	30.0	41.4	1.36	1.7E-01
BF3761	putative conserved transport-related membrane protein	31.5	28.9	26.6	35.1	32.1	29.2	1.11	2.9E-01
BF3762	putative transport-related membrane protein	25.1	26.4	25.6	25.1	25.1	21.4	0.93	3.1E-01
BF3763	hypothetical protein	44.2	44.7	41.9	40.5	39.3	37.2	0.89	4.7E-02
BF3764	putative acylhydrolase	11.2	14.3	9.9	8.0	9.2	7.2	0.69	8.2E-02
BF3765	hypothetical protein	11.3	11.0	10.9	14.9	12.3	7.7	1.01	9.6E-01
BF3766	hypothetical protein	296.5	250.3	284.0	494.4	490.1	405.6	1.67	9.5E-03
BF3767	hypothetical protein	152.2	159.9	156.8	308.5	309.6	291.7	1.94	1.7E-04
BF3768	putative exported thioredoxin	19.9	25.0	21.4	103.1	93.9	97.8	4.47	3.6E-04
BF3769	hypothetical protein	227.0	175.3	188.5	131.1	131.4	179.1	0.74	1.3E-01
trmB	tRNA (guanine-N(7)-)-methyltransferase	114.5	70.8	95.3	50.0	67.8	74.8	0.69	1.7E-01
BF3771	putative hydrolase	167.7	153.7	149.0	153.6	147.1	207.7	1.07	6.6E-01
BF3772	branched-chain amino acid aminotransferase	460.2	490.0	463.3	541.7	525.3	590.8	1.17	3.4E-02
BF3773	putative exodeoxyribonuclease VII small subunit	99.4	85.5	90.3	113.1	96.9	110.5	1.16	1.2E-01
BF3774	exodeoxyribonuclease VII large subunit	123.4	133.3	98.3	136.3	110.7	195.8	1.22	4.2E-01
BF3775	putative exported serine protease, subtilase family	96.2	97.7	79.7	101.3	81.2	124.8	1.11	5.7E-01
BF3776	putative tRNA methyltransferase	61.1	59.5	37.1	53.1	32.1	82.7	1.01	9.7E-01
BF3777	hypothetical protein	3.1	2.5	5.8	0.7	1.6	0.7	0.26	4.4E-02
BF3778	hypothetical protein	54.8	46.8	42.2	33.4	36.1	42.4	0.78	1.1E-01
BF3779	hypothetical protein	131.6	139.2	126.8	148.7	125.9	129.4	1.01	8.6E-01
ispF	putative 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	178.3	188.1	167.6	188.5	162.2	171.0	0.98	7.4E-01
BF3781	putative hydrolase	325.9	331.1	341.5	273.8	259.4	291.5	0.83	1.5E-02
BF3782	redox-sensing transcriptional repressor Rex	535.5	581.2	555.9	330.2	310.0	331.7	0.58	6.2E-04
BF3783	putative translation initation factor	221.2	201.1	156.1	254.4	206.6	274.4	1.28	2.0E-01
tsf	elongation factor Ts	1530.9	1643.8	1661.3	2096.4	2151.7	2208.1	1.34	2.8E-03
rpsB	30S ribosomal protein S2	2183.4	2258.5	2549.1	2880.2	2905.4	2657.5	1.21	4.7E-02

rpsI	30S ribosomal protein S9	1939.2	2057.8	2185.5	2666.7	2680.0	2566.7	1.28	7.8E-03
rplM	50S ribosomal protein L13	1844.4	1795.6	1917.4	2611.0	2484.2	2449.4	1.36	1.8E-03
BF3788	hypothetical protein	411.7	396.6	433.9	549.3	504.4	573.6	1.31	1.1E-02
BF3789	hypothetical protein	1199.4	1226.7	1358.9	1052.7	1276.3	955.4	0.86	2.5E-01
asnS	asparaginyl-tRNA synthetase	965.5	1016.5	986.3	601.4	611.3	592.2	0.61	1.6E-04
BF3791	putative ribosomal large subunit pseudouridine synthase	1139.3	1240.4	1139.3	923.6	903.2	933.7	0.79	4.7E-03
purB	adenylosuccinate lyase	571.4	552.9	555.9	526.7	521.4	503.2	0.92	2.2E-02
BF3793	putative exported beta-galactosidase	125.6	123.5	122.4	258.1	258.6	249.8	2.06	2.0E-05
BFt53	tRNA-Val-TAC	0.0	0.0	0.0	0.0	0.0	0.0		
BFt54	tRNA-Val-TAC	0.0	0.0	0.0	0.0	0.0	0.0		
BFt55	tRNA-Val-TAC	244.3	271.9	214.2	132.9	104.8	570.8	0.82	7.8E-01
maa	putative maltose O-acetyltransferase	47.3	38.4	41.9	58.8	61.4	61.0	1.43	1.2E-02
BF3795	hypothetical protein	60.2	52.9	50.6	88.1	87.7	83.3	1.59	4.2E-03
BF3796	putative exported hyaluronidase	125.5	122.7	114.2	289.1	291.0	263.2	2.33	4.2E-04
aapH	hypothetical protein	272.0	280.1	319.3	167.2	172.9	199.7	0.62	8.4E-03
aapG	hypothetical protein	290.7	304.1	294.4	207.3	171.3	213.2	0.66	1.1E-02
aapF	hypothetical protein	150.4	146.2	142.6	76.1	73.5	77.3	0.52	1.2E-04
aapE	putative outer membrane protein	149.1	143.6	124.5	73.7	72.2	90.5	0.57	9.3E-03
aapD	hypothetical protein	150.9	163.2	147.6	93.5	86.5	104.5	0.62	5.3E-03
aapC	hypothetical protein	158.4	170.7	168.6	104.5	91.4	111.2	0.62	5.2E-03
aapB	hypothetical protein	275.3	273.1	267.0	173.3	168.4	154.2	0.61	1.1E-03
aapA	putative lipoprotein	579.9	626.2	599.6	431.4	395.1	408.3	0.68	1.9E-03
tsr15	tyrosine site-specific recombinase	61.4	56.2	67.2	46.9	49.3	58.0	0.83	1.4E-01
BF3807	hypothetical protein	139.2	96.4	136.0	125.3	151.4	140.5	1.14	4.6E-01
carB2	putative carbamoyl-phosphate synthase large chain 2	259.9	246.1	227.2	331.5	325.6	341.0	1.36	5.7E-03
trpS	tryptophanyl-tRNA synthetase	176.8	122.2	147.9	94.2	110.2	128.7	0.75	1.5E-01
ompA	putative major outer membrane protein	4554.3	5007.9	4791.8	1611.7	1561.2	1657.4	0.34	9.7E-05
BF3811	putative hemolysin secretion transport system membrane protein	5.5	3.7	4.0	11.5	8.8	18.3	2.85	2.7E-02
BF3812	putative hemolysin secretion transport system ATP-binding protein	13.7	13.3	10.6	19.1	18.4	23.4	1.61	2.6E-02
BF3813	hypothetical protein	2.1	2.2	2.6	2.5	0.7	2.0	0.66	4.4E-01
BF3814	hypothetical protein	5.3	3.1	2.9	3.0	4.3	2.3	0.85	6.4E-01
BF3815	putative LPS biosynthesis-related glycosyltransferase	7.4	4.0	4.7	2.2	2.3	5.9	0.60	3.1E-01
BF3816	putative fucosyltransferase	9.9	9.1	10.7	3.9	5.5	5.5	0.50	1.2E-02
BF3817	hypothetical protein	8.0	7.0	5.7	4.6	5.0	6.9	0.79	2.9E-01
BF3819	hypothetical protein	6.4	8.0	10.0	8.2	7.0	5.9	0.87	4.9E-01
BF3820	putative dehydrogenase	8.9	6.6	6.2	8.4	9.7	8.3	1.22	2.3E-01
BF3821	putative regulatory protein	12.6	10.1	13.0	13.4	14.5	9.1	1.03	9.1E-01
BF3822	hypothetical protein	12.2	12.1	14.5	13.9	15.7	8.7	0.96	8.8E-01
BF3823	hypothetical protein	42.0	37.2	48.1	48.9	61.6	48.7	1.25	1.6E-01
BF3824	hypothetical protein	17.4	13.8	18.5	23.8	23.1	20.5	1.36	6.3E-02
BF3825	hypothetical protein	81.4	67.8	90.3	221.1	236.9	182.7	2.68	4.0E-03
BF3826	putative glycosyltransferase	3.6	1.8	2.8	3.9	4.8	5.5	1.78	9.4E-02
BF3827	hypothetical protein	1.4	0.9	3.3	3.9	3.1	2.6	2.01	2.2E-01
BF3828	hypothetical protein	4.1	3.7	5.1	2.8	4.8	4.0	0.89	6.2E-01
BF3829	hypothetical protein	5.8	6.5	5.8	6.1	9.8	7.3	1.25	2.5E-01
BF3830	hypothetical protein	17.0	15.0	18.3	25.9	33.0	35.8	1.87	1.4E-02

BF3831	hypothetical protein	45.3	40.0	43.9	28.6	32.3	28.1	0.69	8.6E-03
BF3832	hypothetical protein	0.0	2.5	0.0	3.3	2.7	0.0	1.21	
BF3833	hypothetical protein	6.7	15.7	9.0	10.3	9.0	9.3	0.97	9.2E-01
BF3834	putative lipoprotein	21.7	20.4	17.2	20.0	22.6	22.9	1.11	3.5E-01
BF3835	hypothetical protein	2.9	1.0	1.1	0.9	1.1	2.8	0.97	9.6E-01
BF3836	hypothetical protein	1.8	1.7	1.8	0.6	0.8	1.0	0.44	2.0E-02
BF3837	hypothetical protein	1.3	0.5	1.5	0.3	0.2	0.5	0.31	7.7E-02
BF3838	hypothetical protein	0.0	0.0	0.5	0.0	0.0	0.4	0.87	
BF3839	putative phage integrase	1.3	0.6	1.3	0.3	0.2	0.3	0.23	1.8E-02
BF3840	hypothetical protein	1.7	3.1	1.3	4.4	4.7	8.4	2.93	5.5E-02
BF3841	hypothetical protein	2.1	2.3	1.2	1.0	2.5	6.2	1.39	6.5E-01
BF3842	hypothetical protein	1.8	0.0	3.0	0.9	1.1	2.6	0.57	3.5E-01
BF3843	hypothetical protein	1.6	0.7	1.7	1.1	0.3	0.9	0.50	3.2E-01
BF3844	hypothetical protein	1.1	0.0	0.6	1.0	1.9	1.6	1.80	2.5E-01
BF3845	hypothetical protein	2.0	1.5	0.3	1.4	0.7	1.4	1.09	9.2E-01
BF3846	hypothetical protein	0.0	1.0	1.0	0.0	0.0	0.0		
BF3847	hypothetical protein	1.4	1.9	1.5	0.6	1.4	1.3	0.64	2.8E-01
BF3848	hypothetical protein	3.9	1.5	1.5	0.3	0.6	0.5	0.22	4.1E-02
BF3850	putative regulatory protein	1.9	1.6	2.1	0.7	0.8	0.4	0.32	1.6E-02
BF3851	hypothetical protein	0.6	1.5	0.7	0.5	0.7	0.8	0.72	4.4E-01
BF3852	putative transport related membrane protein	0.5	0.5	1.1	0.4	0.3	0.3	0.50	1.0E-01
BF3853	putative outer membrane protein	1.1	0.8	1.0	0.4	0.7	0.2	0.36	8.9E-02
BF3854	hypothetical protein	2.0	4.7	3.9	0.8	1.4	1.1	0.32	4.2E-02
BF3855	putative regulatory protein	83.2	90.5	90.3	61.7	88.0	73.5	0.84	2.3E-01
BF3856	putative iron transport, fusion membrane protein	23.3	22.9	23.8	21.7	29.3	22.4	1.04	7.6E-01
BF3857	putative exported esterase	15.0	11.0	13.1	16.1	18.5	13.8	1.24	2.2E-01
BF3858	putative acetylornithine aminotransferase	10.2	8.8	10.3	7.9	9.4	8.6	0.88	2.1E-01
aspC2	putative aspartate aminotransferase	8.3	6.6	6.5	9.2	13.0	9.1	1.45	9.1E-02
BF3860	putative hydrolase	8.0	10.2	6.5	7.3	9.0	7.7	0.98	9.4E-01
BF3861	pyridoxine kinase	4.9	5.2	5.8	8.2	10.3	6.0	1.52	1.0E-01
dapA1	putative dihydrodipicolinate synthase	11.6	11.7	7.4	12.5	12.1	8.3	1.08	7.8E-01
BF3863	putative copper transport-related membrane protein	5.8	6.4	5.1	5.3	6.4	4.1	0.91	6.1E-01
BF3864	hypothetical protein	0.7	0.4	1.5	0.0	0.0	1.0	1.37	
BF3865	conserved hypothetical fusion protein	0.0	0.2	0.2	0.0	0.0	0.2	0.89	
BF3866	hypothetical protein	0.3	0.2	0.4	0.2	0.0	0.1	0.44	1.9E-01
BF3867	hypothetical protein	0.0	0.0	0.0	0.0	0.9	0.0		
BF3871	hypothetical protein	21.5	29.2	27.5	33.7	42.8	35.1	1.43	6.8E-02
BF3872	hypothetical protein	84.6	67.6	96.9	123.3	150.0	91.3	1.45	1.5E-01
BF3873	hypothetical protein	95.9	87.3	105.3	141.0	182.8	117.4	1.51	7.1E-02
BF3876	putative lipoprotein	13.6	9.8	14.3	10.9	13.1	11.4	0.95	7.6E-01
BF3877	hypothetical protein	1.5	1.9	2.3	3.6	7.3	4.4	2.56	3.5E-02
BF3878	hypothetical protein	5.6	4.8	6.4	7.2	9.0	7.9	1.45	4.6E-02
BF3879	putative transposase	10.7	10.7	5.9	13.1	13.9	17.8	1.69	1.2E-01
BF3880	hypothetical protein	1.0	2.2	4.5	4.9	6.0	1.0	1.41	7.1E-01
BF3881	hypothetical protein	2.7	2.2	3.7	1.3	3.1	0.6	0.49	2.8E-01
BF3882	hypothetical protein	3.1	2.0	1.4	2.4	0.7	1.2	0.62	3.9E-01
ubb	putative ubiquitin	4888.0	4375.3	5488.4	4241.0	4798.6	3256.6	0.83	2.9E-01

BF3884	hypothetical protein	9.8	8.8	6.6	7.9	6.1	6.5	0.82	2.8E-01
mutL	putative DNA mismatch repair protein	200.4	219.1	199.7	248.9	235.9	257.3	1.20	2.2E-02
BF3886	hypothetical protein	322.6	346.3	320.6	347.4	334.3	357.4	1.05	2.5E-01
BF3887	hypothetical protein	294.9	299.2	290.5	233.4	229.1	219.6	0.77	1.2E-03
BF3888	putative exported peptidyl-prolyl cis-trans isomerase	673.8	663.3	611.5	522.2	511.1	500.3	0.79	6.0E-03
BF3889	hypothetical protein	384.1	351.1	344.1	288.8	296.6	310.6	0.83	2.2E-02
BF3890	putative exported isomerase	96.5	102.5	92.7	91.5	91.1	98.4	0.96	4.6E-01
guaB	putative inosine-5'-monophosphate dehydrogenase	355.5	351.2	309.8	375.6	320.6	418.6	1.09	4.5E-01
recQ1	putative ATP-dependent DNA helicase	1005.8	1042.1	1006.4	982.7	993.5	1038.2	0.99	6.2E-01
clpX	ATP-dependent protease ATP-binding subunit	435.3	462.0	435.3	474.4	458.8	490.5	1.07	1.2E-01
clpP	putative ATP-dependent CLP protease proteolytic subunit	476.2	479.7	442.8	529.9	477.7	470.4	1.06	3.7E-01
BF3895	putative cell division trigger factor	969.2	911.2	1029.7	1231.5	1088.2	1098.8	1.17	6.6E-02
BF3896	hypothetical protein	9.5	17.0	12.9	7.1	6.6	7.1	0.54	4.2E-02
BF3897	putative RNA-binding protein	6129.9	5911.4	6528.9	3494.3	3562.6	3314.7	0.56	6.9E-04
BF3898	putative ABC transport system, ATP-binding protein	179.2	192.9	173.4	195.3	158.2	191.9	1.00	9.7E-01
BF3899	hypothetical protein	201.1	186.2	180.1	151.5	146.1	160.9	0.81	1.8E-02
BF3900	putative ABC amino acid transport system, ATP-binding protein	149.9	140.0	161.0	137.5	144.1	141.8	0.94	2.9E-01
BF3901	putative LuxR-family regulatory protein	258.4	263.0	236.0	205.2	194.2	236.4	0.84	9.3E-02
BF3902	GTP-binding protein EngA	370.1	320.7	394.1	259.4	313.9	297.5	0.80	9.3E-02
BF3903	putative GTP-binding protein (cell growth-related)	370.0	334.7	429.2	248.3	299.8	259.3	0.71	4.1E-02
fabH	3-oxoacyl-(acyl carrier protein) synthase	1431.6	1262.1	1522.3	1827.6	1969.9	1782.2	1.33	2.4E-02
BF3905	hypothetical protein	720.6	681.5	797.5	494.9	495.3	478.5	0.67	4.1E-03
5S		4.7	6.9	36.7	1.9	4.5	25.4	0.57	6.6E-01
23S		13.7	7.5	12.2	16.3	9.1	22.1	1.38	4.5E-01
BFt56	tRNA-Ala-TGC	87.0	97.6	97.6	47.1	45.1	95.3	0.62	1.8E-01
BFt57	tRNA-Ile-GAT	158.9	177.9	180.8	63.0	65.0	113.6	0.45	3.1E-02
16S		672.5	32.3	99.0	90.9	32.3	230.2	0.68	7.8E-01
BF3906	hypothetical protein	212.1	195.1	172.1	177.9	179.7	260.5	1.05	7.8E-01
BF3907	hypothetical protein	0.9	0.0	2.1	0.0	0.0	0.0		
BF3908	putative 5,10-methylenetetrahydrofolate reductase	331.6	336.6	339.7	341.8	357.6	334.7	1.03	3.6E-01
BF3909	putative DNA polymerase III delta prime subunit	217.0	227.9	222.1	218.5	211.1	191.1	0.93	2.2E-01
BF3910	hypothetical protein	246.1	242.9	232.9	226.4	196.0	201.0	0.86	6.1E-02
gldH	putative gliding motility protein	167.1	187.3	191.8	95.9	120.6	140.9	0.65	4.2E-02
mrdB	putative transmembrane rod shape-determining protein	150.9	146.2	143.6	90.6	99.6	95.7	0.65	1.0E-03
mrdA	putative penicillin-binding protein 2	157.5	136.2	134.7	91.1	91.5	102.6	0.67	8.9E-03
BF3914	putative transmembrane protein	155.2	126.6	135.4	87.3	88.2	89.1	0.64	5.7E-03
BF3915	putative rod shape-determining protein MreC	206.7	201.2	200.3	153.8	173.1	162.7	0.80	1.0E-02
mreB	putative rod-shape determining protein	522.8	475.0	472.9	439.9	477.1	515.8	0.97	7.1E-01

purH	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	589.6	609.1	583.9	575.8	553.1	571.8	0.95	9.2E-02
pepO	putative endopeptidase	309.1	291.0	281.5	299.8	305.3	314.3	1.04	3.0E-01
BF3919	putative ATP-binding component of ABC transporter	135.9	108.9	121.5	121.5	117.6	144.9	1.05	6.9E-01
BF3920	hypothetical protein	1.1	1.3	1.8	0.8	0.8	0.9	0.62	5.4E-02
BF3921	hypothetical protein	7.4	2.2	2.3	1.0	2.4	0.0	0.46	3.5E-01
BF3922	hypothetical protein	608.1	671.1	572.8	976.2	955.2	1003.3	1.59	2.9E-03
BF3923	hypothetical protein	164.1	164.5	144.5	95.4	93.5	102.3	0.62	2.9E-03
BF3924	hypothetical protein	169.0	175.9	153.4	103.7	95.9	109.9	0.62	4.2E-03
BF3925	putative two-component system sensor histidine kinase/response regulator fusion protein	162.2	171.7	158.8	112.1	109.1	118.1	0.69	1.8E-03
BF3926	putative transmembrane transport efflux protein	261.9	275.3	283.1	156.5	181.6	155.4	0.60	3.3E-03
BF3927	putative protease	386.7	388.3	368.8	239.7	256.5	254.3	0.66	7.4E-04
BF3928	putative peptidyl-prolyl cis-trans isomerase	455.6	442.6	470.0	314.8	330.3	280.9	0.68	5.4E-03
BF3929	putative two-component response regulator transcriptional regulatory protein	120.9	115.2	116.1	97.1	98.3	96.0	0.83	1.8E-03
BF3930	hypothetical protein	2058.0	2040.9	2151.0	78.0	106.1	91.5	0.04	8.7E-05
BF3931	putative ribosomal large subunit pseudouridine synthase	417.0	488.9	534.5	681.8	763.5	784.6	1.55	1.6E-02
fabG	putative 3-oxoacyl-[acyl-carrier protein] reductase	882.3	889.4	997.3	1740.2	1709.8	1540.3	1.80	2.1E-03
BF3933	putative TetR-family transcriptional regulator	340.2	303.4	308.9	189.6	158.4	174.9	0.55	2.9E-03
BFt58	tRNA-Met-CAT	7.0	2.5	17.9	8.8	5.4	20.0	1.46	6.8E-01
BF3934	hypothetical protein	38.1	24.3	31.6	16.4	26.1	29.2	0.75	3.4E-01
BF3935	putative transmembrane protein	3.2	2.2	2.3	0.2	2.1	0.9	0.29	2.0E-01
BF3936	putative ABC transporter transmembrane component	3.5	3.1	4.3	1.9	4.1	2.6	0.75	3.8E-01
BF3937	hypothetical protein	3.5	2.4	2.9	1.9	2.5	1.9	0.72	1.1E-01
BF3938	hypothetical protein	7.7	5.9	5.6	8.4	6.7	8.5	1.23	2.4E-01
BF3939	putative GntR family transcriptional regulator	6.7	16.3	10.5	6.8	10.0	3.7	0.60	3.3E-01
BF3940	putative transmembrane protein	8.2	7.1	8.1	7.8	8.5	7.1	1.00	9.6E-01
BF3941	putative ATP-binding component of ABC transporter	6.6	5.9	8.6	5.8	8.8	6.9	1.02	9.3E-01
BF3942	putative TPR-repeat family protein	41.8	49.5	45.7	19.0	19.1	17.9	0.41	6.0E-04
BF3943	hypothetical protein	53.4	61.6	61.5	30.5	28.7	27.7	0.49	1.3E-03
BF3944	putative TonB-family outer membrane receptor protein	54.7	58.2	55.5	28.7	28.8	26.3	0.50	3.9E-04
BF3945	hypothetical protein	39.0	42.7	46.9	20.6	24.5	22.1	0.52	3.6E-03
BF3946	hypothetical protein	28.8	34.1	28.2	22.9	21.9	19.8	0.71	2.1E-02
BF3947	putative transmembrane MotA/TolQ/ExbB proton channel family protein	44.5	50.6	53.5	29.4	29.4	26.7	0.58	3.9E-03

BF3948	hypothetical protein	994.7	1170.5	1117.2	276.5	306.9	277.9	0.26	3.0E-04
5S		530.5	7.9	40.9	1.9	5.2	26.8	0.12	2.7E-01
23S		281.3	180.6	242.6	645.1	239.0	1088.6	2.39	1.9E-01
BFt59	tRNA-Ala-TGC	87.0	97.6	97.6	47.1	45.1	95.3	0.62	1.8E-01
BFt60	tRNA-Ile-GAT	158.9	177.9	180.8	63.0	65.0	113.6	0.45	3.1E-02
16S		672.5	32.3	99.0	90.9	32.3	230.2	0.68	7.8E-01
BF3949	putative transmembrane protein	460.4	131.9	402.1	51.6	49.5	83.2	0.21	4.0E-02
BF3950	hypothetical protein	63.1	67.6	71.2	61.3	55.8	49.8	0.82	8.2E-02
BF3951	hypothetical protein	74.1	69.0	69.3	50.5	50.1	53.2	0.72	2.0E-03
BF3954	hypothetical protein	68.5	49.1	65.6	52.0	64.1	54.4	0.94	6.8E-01
BF3955	hypothetical protein	43.3	28.3	38.2	13.5	15.1	16.6	0.42	9.4E-03
BF3956	hypothetical protein	19.9	22.9	25.5	14.9	18.2	15.1	0.71	4.3E-02
BF3957	hypothetical protein	30.6	30.0	29.1	23.3	34.0	34.0	1.00	9.9E-01
BF3958	putative transmembrane polysaccharide modification protein	87.2	74.8	86.7	52.9	60.1	57.9	0.69	1.1E-02
BF3959	hypothetical protein	67.5	52.5	61.4	32.9	36.7	54.3	0.67	1.2E-01
BF3960	putative transmembrane protein	160.2	141.4	141.5	100.8	91.5	111.4	0.68	1.5E-02
BF3961	hypothetical protein	136.2	153.9	112.4	105.8	86.2	161.2	0.85	5.6E-01
BF3962	putative transmembrane Acr-type transport protein	147.8	162.1	130.9	122.1	115.2	123.5	0.82	6.8E-02
BF3963	putative membrane fusion protein transporter	119.2	107.4	94.2	105.7	98.8	96.2	0.94	5.3E-01
BF3964	putative outer membrane efflux protein	118.8	107.1	98.0	97.6	93.0	93.5	0.88	1.3E-01
BF3965	putative TetR transcriptional regulator	80.4	78.3	71.4	70.8	57.0	50.1	0.77	1.1E-01
hutH	putative histidine ammonia-lyase	7.1	8.3	6.6	37.1	33.4	35.3	4.83	3.3E-04
BF3967	putative formiminotransferase-cyclodeaminase	5.9	10.7	5.9	35.3	29.2	39.8	4.80	6.6E-03
hutI	putative imidazolonepropionase	8.4	7.8	7.4	23.9	21.5	28.9	3.12	1.5E-03
ftcD	putative formimidoyltransferase-cyclodeaminase	7.6	10.6	11.2	23.5	26.0	25.5	2.58	5.4E-03
hutU	urocanate hydratase	37.5	35.2	28.4	41.4	40.9	55.8	1.36	1.2E-01
BF3971	hypothetical protein	296.9	301.5	259.4	169.9	167.8	232.1	0.66	4.3E-02
BF3972	putative transmembrane DNA mismatch repair-like protein	94.2	89.7	93.2	64.5	64.6	69.8	0.72	1.9E-03
BF3973	putative transmembrane protein	278.7	270.1	291.1	691.2	653.3	494.4	2.17	6.1E-03
BF3974	hypothetical protein	589.0	558.9	494.3	633.3	626.9	606.6	1.14	1.1E-01
rplQ	putative 50S ribosomal protein L17	5126.2	5644.2	5941.0	4573.2	4710.0	3827.2	0.78	6.0E-02
rpoA	DNA-directed RNA polymerase alpha subunit	3931.9	4466.9	4645.2	3602.6	3894.3	3322.6	0.83	8.4E-02
rpsD	30S ribosomal protein S4	3457.1	3777.6	3953.4	3788.2	4001.8	3558.4	1.01	8.3E-01
rpsK	30S ribosomal protein S11	3011.0	3185.4	3341.5	3163.8	3145.5	2675.9	0.94	4.5E-01
rpsM	30S ribosomal protein S13	2686.6	2648.8	2867.1	2754.8	2699.7	2608.0	0.98	6.6E-01
rpmJ	putative 50S ribosomal protein L36	1416.1	1652.3	1622.5	1475.1	1510.3	1296.3	0.91	3.2E-01
infA	translation initiation factor IF-1	1445.5	1525.5	1510.9	983.6	1083.9	1014.9	0.69	1.8E-03
map	putative methionine aminopeptidase	3128.6	3104.6	3223.3	2353.3	2475.5	2112.6	0.73	8.6E-03
secY	preprotein translocase SecY	3904.0	4570.0	4449.2	2662.0	3031.1	2513.9	0.63	9.9E-03
rplO	putative 50S ribosomal protein L15	3908.8	4651.5	4434.6	2819.1	3345.9	2958.0	0.70	1.9E-02
rpmD	putative 50S ribosomal protein L30	3211.0	3064.5	3104.4	2077.7	2048.7	1714.8	0.62	5.6E-03
rpsE	putative 30S ribosomal protein S5	2932.4	3007.0	3033.2	2215.6	2289.7	2141.6	0.74	1.1E-03
rplR	putative 50S ribosomal protein L18	3488.1	3531.3	3583.6	2560.9	2649.8	2177.0	0.69	1.1E-02
rplF	50S ribosomal protein L6	3487.6	3705.7	3642.0	2615.1	2831.0	2348.2	0.72	1.2E-02

rpsH	putative 30S ribosomal protein S8	3742.9	3951.4	3822.7	2708.7	2935.4	2319.0	0.69	1.5E-02
rpsN	putative 30S ribosomal protein S14	3854.3	3951.5	3972.8	3020.9	3189.0	2989.4	0.78	1.9E-03
rplE	50S ribosomal protein L5	3152.4	3365.3	3442.4	2651.2	2806.2	2522.2	0.80	1.4E-02
rplX	50S ribosomal protein L24	3938.0	3704.6	3889.7	3322.3	3410.5	3073.4	0.85	2.4E-02
rplN	50S ribosomal protein L14	2907.6	2898.9	2958.6	2721.5	2813.2	2615.0	0.93	5.3E-02
rpsQ	putative 30S ribosomal protein S17	3365.0	2993.3	3162.1	2908.7	2923.6	2490.3	0.87	1.4E-01
rpmC	50S ribosomal protein L29	2452.5	2271.2	2404.2	2049.1	2148.1	1781.7	0.84	7.1E-02
rplP	50S ribosomal protein L16	2389.2	2168.1	2415.6	1991.8	2129.3	1951.2	0.87	5.8E-02
rpsC	putative 30S ribosomal protein S3	3327.6	2718.3	3025.6	2402.7	2431.5	2272.9	0.79	3.5E-02
rplV	putative 50S ribosomal protein L22	3477.2	3025.1	3173.1	2590.1	2637.4	2380.3	0.79	2.2E-02
rpsS	30S ribosomal protein S19	2265.8	2282.8	2373.4	1852.6	1861.3	1826.3	0.80	9.3E-04
rplB	50S ribosomal protein L2	2314.0	2264.5	2276.5	2138.0	2124.1	2199.8	0.94	2.1E-02
rplW	putative 50S ribosomal protein L23	2894.2	2855.3	2980.6	2044.2	2349.7	1951.6	0.72	1.3E-02
rplD	50S ribosomal protein L4	2152.9	2089.1	2087.4	1575.5	1721.3	1643.4	0.78	3.4E-03
rplC	50S ribosomal protein L3	2783.8	2507.4	2676.2	2004.7	2137.4	2069.9	0.78	7.0E-03
rpsJ	30S ribosomal protein S10	2724.6	2602.5	2596.4	1852.2	2040.2	1942.8	0.74	2.9E-03
fusA	elongation factor EF-2	2763.8	2896.8	2860.3	2381.7	2566.5	2409.4	0.86	1.4E-02
rpsG	30S ribosomal protein S7	1952.4	2124.8	2168.3	2058.4	2083.2	1839.0	0.96	5.1E-01
rpsL	30S ribosomal protein S12	1393.6	1506.6	1428.3	1754.7	1454.9	1660.8	1.12	1.8E-01
BF4008	hypothetical protein	140.3	119.7	115.2	104.5	89.0	81.4	0.73	5.4E-02
BF4009	hypothetical protein	44.7	48.7	57.6	15.5	17.7	14.6	0.32	1.4E-03
BF4010	hypothetical protein	1406.9	1423.8	1375.7	581.8	481.4	540.9	0.38	5.9E-04
BF4011	putative transmembrane protein, transglycosylase associated	459.1	534.8	443.9	55.7	63.9	97.7	0.15	2.1E-03
BF4012	hypothetical protein	15.2	19.5	14.5	26.9	37.3	24.9	1.80	3.7E-02
BF4013	putative transmembrane protein	15.7	18.0	17.8	55.5	63.1	47.3	3.21	1.4E-03
rpoC	DNA-directed RNA polymerase beta' subunit	1784.8	1908.1	1775.2	1269.0	1308.9	1263.8	0.70	1.1E-03
rpoB	DNA-directed RNA polymerase beta subunit	2142.6	2407.2	2296.2	1567.4	1656.1	1494.9	0.69	4.4E-03
rplL	putative 50S ribosomal protein L7/L12	6830.4	7486.0	7739.4	7415.1	7846.9	7993.9	1.06	3.5E-01
rplJ	putative 50S ribosomal protein L10	5521.6	6442.9	6606.3	5723.9	6238.6	5014.3	0.91	4.2E-01
rplA	50S ribosomal protein L1	6326.0	7181.6	7366.2	7518.5	7800.7	6326.7	1.04	7.4E-01
rplK	50S ribosomal protein L11	5972.4	6303.2	6681.5	7074.8	7205.3	6145.4	1.08	3.6E-01
nusG	putative transcription antitermination protein	6539.5	6680.0	7367.4	7588.5	7943.6	7294.5	1.11	1.2E-01
secE	putative preprotein translocase SecE subunit	4331.4	4597.4	5200.6	5337.6	5403.0	4542.3	1.08	4.4E-01
BFt61	tRNA-Trp-CCA	153.2	185.2	245.4	525.9	564.5	487.8	2.75	6.7E-03
tuf	elongation factor Tu	12627.2	12769.8	14333.3	17495.8	17558.2	16485.0	1.30	1.2E-02
BFt62	tRNA-Thr-GGT	276.9	292.0	242.9	348.4	238.3	322.1	1.11	5.4E-01
BFt63	tRNA-Gly-TCC	0.0	0.0	0.0	0.0	0.0	0.0		
BFt64	tRNA-Tyr-GTA	83.4	85.1	136.2	363.3	338.7	461.7	3.89	6.1E-03
BFt65	tRNA-Thr-TGT	106.9	167.4	100.1	178.8	143.3	310.0	1.64	2.1E-01
BF4023	putative sigma(54) modulation protein	2464.5	2106.5	2393.2	1796.1	2108.3	1925.2	0.84	9.1E-02
BF4024	putative site-specific recombinase	4165.4	3817.8	4150.6	3302.6	3749.0	3570.0	0.87	7.6E-02
BF4025	putative ribosomal protein S21	1052.3	1127.1	1365.2	1104.5	1328.9	1535.0	1.12	4.9E-01
BF4027	putative peptidase	145.1	145.9	147.8	146.2	147.4	145.3	1.00	9.7E-01
BF4028	putative hexapeptide repeat protein	209.8	206.3	224.2	183.9	180.8	173.9	0.84	1.2E-02
kdtA	3-deoxy-D-manno-octulosonic-acid transferase	299.3	280.5	285.2	252.6	273.9	264.2	0.91	7.0E-02

gltX	glutamyl-tRNA synthetase	356.4	330.5	332.5	330.8	323.4	372.2	1.01	9.4E-01
BF4031	putative transmembrane HD family protein	137.9	150.2	136.2	166.5	162.2	158.3	1.15	3.1E-02
BF4032	putative low molecular weight protein-tyrosine-phosphatase	68.5	68.5	61.9	97.0	111.6	113.2	1.62	4.8E-03
BF4033	hypothetical protein	116.8	141.3	121.8	301.9	299.6	294.1	2.37	8.7E-04
BF4034	putative primosomal protein N'	114.4	120.4	92.3	102.2	86.9	116.0	0.93	6.5E-01
BF4035	putative transmembrane protein	1331.2	1214.0	1348.0	1003.4	1131.9	933.2	0.79	4.0E-02
BFt66	tRNA-Pseudo-CGA	48.5	37.1	23.5	31.2	24.7	35.3	0.86	6.4E-01
BF4036	hypothetical protein	65.0	61.0	56.5	60.2	63.3	73.6	1.08	4.3E-01
aspA	putative aspartate ammonia-lyase	28.1	33.9	31.0	14.6	15.5	16.1	0.50	1.8E-03
BF4038	anaerobic C4-dicarboxylate transporter	55.9	63.3	55.7	46.9	42.7	63.3	0.86	3.8E-01
ansB	putative L-asparaginase II precursor	108.8	119.8	94.3	80.1	78.7	82.2	0.75	3.1E-02
BF4040	hypothetical protein	103.2	117.1	107.9	53.6	56.4	60.4	0.52	1.2E-03
BF4041	putative transposase	50.9	52.0	44.3	15.1	18.2	15.8	0.33	9.1E-04
BF4042	hypothetical protein	0.7	0.4	0.4	0.3	0.8	0.3	0.97	9.4E-01
BF4048	putative two-component system sensor histidine kinase/response regulator fusion protein	156.6	143.5	144.0	252.8	265.4	209.7	1.63	9.1E-03
tnpB	putative IstB/TnpB insertion sequence IS21-like protein	4.0	4.7	4.7	8.2	4.1	6.2	1.33	3.0E-01
nanH2	putative neuraminidase precursor	4.1	5.7	4.2	129.6	137.6	117.4	27.75	1.7E-04
BF4052	putative transposase	0.9	0.6	1.1	16.2	13.8	15.8	18.75	7.6E-04
BF4053	hypothetical protein	0.7	1.5	1.8	9.4	9.7	10.0	7.92	6.5E-03
BF4054	putative transmembrane sugar transporter	0.6	0.5	0.8	2.6	2.1	4.0	4.75	8.6E-03
BF4055	hypothetical protein	0.5	0.3	0.7	2.1	1.8	1.9	4.08	8.2E-03
BF4056	**putative outer membrane protein**	**7.0**	**5.2**	**5.1**	**383.8**	**399.2**	**407.7**	**69.46**	**4.5E-05**
BF4057	putative outer membrane protein	4.0	2.6	2.6	126.8	143.1	154.7	46.88	2.4E-04
BF4058	putative endo-beta-galactosidase	8.3	7.4	7.5	302.2	318.7	320.3	40.72	2.3E-06
BF4059	putative beta-hexosaminidase precursor	6.7	5.2	5.5	220.0	223.2	242.6	39.46	3.7E-05
BF4060	putative beta-glucanase	9.4	6.8	9.0	226.1	258.9	289.6	30.89	1.8E-04
BF4061	putative beta-galactosidase	24.1	18.8	20.6	866.8	823.9	879.8	40.66	2.6E-05
BF4062	**putative TonB-linked outer membrane protein**	**14.0**	**11.4**	**10.9**	**914.7**	**801.8**	**975.6**	**74.47**	**3.7E-05**
BF4063	putative outer membrane protein	15.3	12.0	10.3	1041.8	836.7	1281.3	83.72	1.9E-04
BF4064	hypothetical protein	9.7	9.2	9.5	360.6	335.7	446.2	39.97	4.4E-05
BF4065	hypothetical protein	12.9	12.3	7.2	331.9	300.2	454.8	34.21	7.3E-04
BF4069	hypothetical protein	7.6	6.1	6.8	3.1	1.6	3.6	0.39	4.0E-02
BF4070	hypothetical protein	23.7	19.1	19.8	21.7	12.3	12.5	0.72	2.3E-01
BF4071	putative IstB IS21 family transposase protein	19.1	15.6	19.3	16.6	17.3	16.3	0.93	4.5E-01
BF4073	hypothetical protein	70.3	65.4	70.0	87.8	98.6	72.0	1.25	1.2E-01
BF4074	hypothetical protein	66.0	54.6	64.8	98.1	110.3	90.5	1.61	1.2E-02
BF4075	possible recombination enzyme	1.4	1.9	1.8	1.0	0.3	0.3	0.27	5.8E-02
BF4076	hypothetical protein	0.7	1.8	0.2	0.5	0.6	0.3	0.74	7.3E-01
BF4077	hypothetical protein	1.7	2.3	1.8	0.7	1.0	0.9	0.44	1.2E-02
BF4078	hypothetical protein	15.9	10.1	8.2	5.0	3.7	1.0	0.24	8.8E-02
BF4079	putative transmembrane protein	76.0	75.7	79.9	108.7	117.3	89.8	1.36	3.8E-02
BF4080	putative bacteriophage integrase	321.1	278.0	323.1	389.4	402.9	401.1	1.30	1.6E-02

BF4081	hypothetical protein	543.7	529.2	513.8	1188.7	1164.1	1117.8	2.19	1.1E-04
BF4082	putative vitamin B12 related Cobalamin adenosyltransferase	102.9	108.2	102.7	115.0	103.6	102.6	1.02	6.7E-01
BF4083	hypothetical protein	56.7	53.5	51.9	91.6	86.6	77.9	1.58	4.2E-03
BF4084	hypothetical protein	38.3	35.3	35.0	7.6	6.6	8.1	0.20	2.3E-04
BF4085	hypothetical protein	2.1	3.3	1.7	0.0	0.0	0.9	0.39	
BF4086	hypothetical protein	1.8	1.2	1.8	1.0	0.6	1.0	0.56	9.8E-02
BF4087	hypothetical protein	1.0	0.9	1.0	0.3	0.7	0.4	0.47	4.0E-02
tsr26	tyrosine site-specific recombinase	9.3	7.0	5.8	8.2	8.3	6.7	1.07	7.5E-01
BF4089	hypothetical protein	2.4	2.7	3.3	7.7	9.1	8.9	3.08	2.2E-03
BF4090	hypothetical protein	4.2	1.7	1.7	4.2	4.3	4.8	1.92	1.4E-01
BF4091	putative O-antigen related protein	16.4	22.2	20.0	42.3	39.6	53.2	2.31	8.1E-03
BF4092	hypothetical protein	3.9	2.7	3.0	2.7	2.6	2.9	0.86	3.3E-01
BF4093	hypothetical protein	1.6	2.2	2.7	1.5	1.2	1.0	0.57	7.8E-02
BF4094	possible bacterial surface protein	1.6	1.8	1.8	1.2	1.6	1.7	0.83	2.5E-01
BF4095	hypothetical protein	1.3	1.6	1.1	0.7	1.2	1.0	0.70	1.9E-01
BF4096	hypothetical protein	1.8	2.1	2.2	1.0	1.9	0.5	0.49	1.9E-01
BF4097	hypothetical protein	1.6	1.9	1.9	2.1	1.4	1.3	0.90	6.2E-01
BF4098	hypothetical protein	8.9	9.9	13.0	4.2	3.9	5.0	0.41	8.7E-03
BF4099	putative NUDIX/MutT-family protein	71.8	51.8	51.2	103.4	92.6	93.4	1.68	2.5E-02
BF4100	hypothetical protein	83.0	86.6	93.2	91.6	139.9	71.1	1.11	6.9E-01
BF4101	hypothetical protein	18.3	27.1	19.3	30.1	23.9	16.8	1.08	7.7E-01
BF4102	putative two-component sensor histidine kinase transcriptional regulator	8.2	7.7	9.7	4.8	2.9	4.8	0.48	3.1E-02
BF4103	putative two-component response regulator autolysis regulator LytR	4.6	5.2	5.6	5.0	6.9	5.1	1.10	5.3E-01
BF4104	putative transmembrane ferredoxin-like protein	4.5	4.2	3.4	6.8	8.0	6.5	1.77	1.5E-02
BF4105	putative aldo/keto reductase	8.0	6.2	4.9	13.9	10.3	10.8	1.84	4.2E-02
BF4106	putative TonB-dependent outer membrane receptor protein	3.3	2.9	3.4	6.5	5.9	6.0	1.93	1.6E-03
BF4107	putative transmembrane protein	8.9	7.3	6.8	11.7	12.7	10.6	1.52	2.7E-02
BF4108	hypothetical protein	29.3	23.6	26.0	21.8	27.9	25.0	0.95	6.5E-01
lacA	putative thiogalactoside transacetylase	13.2	12.4	13.9	6.8	9.7	7.8	0.61	2.3E-02
BF4110	putative transcriptional regulator GerE, LuxR family	56.1	48.7	49.0	40.8	41.7	41.3	0.81	2.2E-02
BF4111	putative methylated-DNA--protein-cysteine methyltransferase	69.0	56.4	66.6	65.1	72.8	67.8	1.07	4.4E-01
BF4112	hypothetical protein	22.4	20.1	23.6	23.6	22.5	26.3	1.09	3.1E-01
BF4113	putative AraC-family transcriptional regulator	9.8	11.7	11.7	8.8	11.8	11.5	0.96	7.8E-01
BF4114	1-deoxy-D-xylulose-5-phosphate synthase	6.1	4.7	7.5	3.8	4.6	4.5	0.72	1.4E-01
BF4115	flavodoxin	2.9	1.9	3.2	2.8	2.1	1.0	0.70	4.0E-01
BF4116	putative transmembrane protein	1.7	0.6	1.2	0.0	0.0	0.0		
BF4117	hypothetical protein	58.8	72.0	67.7	51.5	64.0	53.9	0.85	2.0E-01
BF4118	hypothetical protein	76.1	76.4	77.7	77.5	77.6	74.7	1.00	9.3E-01
BF4119	hypothetical protein	54.9	54.8	62.6	67.3	74.9	68.6	1.22	4.1E-02
BF4120	putative acetyltransferase	68.1	59.0	75.7	72.8	84.3	62.2	1.08	6.2E-01
BF4124	hypothetical protein	25.1	23.2	24.0	23.8	24.5	17.8	0.91	4.7E-01

BFt67	tRNA-Leu-CAA	16.8	13.4	13.9	6.0	12.2	24.2	0.83	7.2E-01
BF4125	putative mannose-1-phosphate guanylyltransferase	734.2	696.5	734.9	818.7	856.6	707.7	1.10	2.6E-01
BF4126	putative Hit-family protein	392.1	380.0	427.9	376.6	367.2	290.9	0.86	2.2E-01
greA	putative transcription elongation factor	831.4	774.2	822.8	721.5	740.3	775.0	0.92	8.8E-02
BF4128	hypothetical protein	218.3	216.4	231.4	358.9	363.4	304.8	1.54	6.6E-03
pnpA	putative polyribonucleotide nucleotidyltransferase	1695.1	1767.5	1799.4	1402.2	1343.9	1292.3	0.77	3.5E-03
BF4130	putative RNA polymerase ECF-type sigma factor	23.5	18.6	15.3	27.6	33.3	32.3	1.64	4.2E-02
BF4131	putative anti-sigma factor	25.7	27.6	27.7	48.0	51.2	46.3	1.80	7.8E-04
BF4132	putative outer membrane protein	3.2	5.1	3.7	22.1	22.7	19.2	5.41	1.8E-03
BF4133	hypothetical protein	3.5	3.3	2.3	23.0	23.4	23.1	7.83	7.4E-04
BF4134	hypothetical protein	2.0	1.6	2.3	1.2	0.9	1.3	0.57	4.1E-02
BF4135	hypothetical protein	23.4	20.0	16.2	7.8	8.4	12.0	0.47	2.5E-02
BF4136	hypothetical protein	15.8	13.6	11.2	33.0	26.9	32.7	2.29	7.1E-03
BF4137	butyrate kinase	42.8	44.2	42.7	125.9	115.5	126.4	2.83	1.0E-04
BF4138	putative phosphate acetyl/butyryltransferase	41.0	50.2	40.0	96.0	93.3	104.6	2.25	2.5E-03
BF4139	putative endo-beta-galactosidase	66.8	68.7	64.0	179.0	169.9	144.8	2.47	1.1E-03
BF4140	putative muramoyltetrapeptide carboxypeptidase	51.3	57.6	57.5	132.7	127.0	134.5	2.37	3.8E-04
BF4141	hypothetical protein	264.1	247.4	231.0	230.6	211.6	227.6	0.90	1.4E-01
sufE	putative SufE Fe/S-cluster-related protein	593.1	547.3	536.3	519.3	510.5	512.2	0.92	9.1E-02
BF4143	putative DNA-binding protein	105.3	98.8	95.4	199.5	191.7	208.6	2.00	4.9E-04
BF4144	putative transmembrane protein	45.6	47.3	48.0	98.1	105.8	91.7	2.10	6.3E-04
BF4145	putative transmembrane CAAX amino terminal protease family	43.2	44.7	40.6	84.8	95.0	88.2	2.08	6.2E-04
BF4146	hypothetical protein (pseudogene)	2.1	5.6	5.8	1.0	1.2	3.0	0.38	1.6E-01
BF4146A	hypothetical protein	21.5	16.9	23.6	7.1	13.0	14.3	0.54	9.7E-02
ribF	putative riboflavin biosynthesis protein RibF	407.4	414.2	413.8	259.4	294.9	335.7	0.72	2.4E-02
BF4148	putative haloacid dehalogenase-type hydrolase	337.9	331.8	354.0	239.9	232.4	248.5	0.70	1.3E-03
BF4149	putative transmembrane calcium-transporting ATPase	329.2	320.5	303.3	188.4	180.1	221.2	0.62	6.3E-03
BF4150	putative two-component system sensor kinase/response regulator fusion protein	40.5	30.6	34.2	31.9	34.3	33.6	0.95	6.6E-01
BF4151	putative transmembrane Na+/Pi-cotransporter	256.4	254.2	262.8	339.5	355.2	318.5	1.31	4.6E-03
BF4152	putative phosphoribulose/uridine kinase	313.8	339.0	321.3	241.1	274.8	228.2	0.76	2.3E-02
BF4153	putative two-component regulator sensor histidine kinase transcriptional regulator	251.7	255.3	239.3	341.0	341.8	299.7	1.31	1.2E-02
BF4154	hypothetical protein	22.5	26.3	20.2	60.8	57.7	57.5	2.56	1.6E-03
BF4155	conserved hypothetical exported protein, possible ATP/GTP-binding	29.2	37.1	24.4	59.0	46.3	75.9	1.99	4.1E-02
BF4156	hypothetical protein	56.9	61.8	43.8	79.0	69.0	88.7	1.46	6.7E-02

BF4157	hypothetical protein	37.4	34.5	21.9	23.5	26.1	13.2	0.66	2.6E-01
BF4158	putative aminopeptidase	382.3	423.5	302.8	476.8	323.7	718.5	1.31	4.1E-01
BF4160	putative RNA polymerase sigma-54 factor	251.5	251.8	193.3	274.2	210.6	311.3	1.14	5.0E-01
BF4161	putative transmembrane protein	364.3	407.9	384.6	286.3	308.1	307.0	0.78	9.9E-03
BF4162	glycine cleavage system protein H	364.0	409.4	396.3	946.4	973.7	962.8	2.47	2.2E-04
purE	putative transmembrane phosphoribosylaminoimidazole carboxylase	437.5	465.3	409.7	1048.0	1032.3	1088.8	2.42	3.2E-04
BF4164	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	211.4	212.9	199.0	346.0	301.1	358.0	1.61	4.3E-03
BF4165	hypothetical protein	82.5	90.4	75.8	71.7	68.4	85.1	0.90	3.6E-01
BF4166	possible xylosidase/arabinosidase	31.2	30.1	27.6	16.2	11.4	15.2	0.48	8.6E-03
BF4167	hypothetical protein	5.2	3.8	3.9	1.4	0.6	2.2	0.30	5.9E-02
BF4168	putative outer membrane protein	0.3	0.2	0.1	0.9	0.1	1.0	2.21	4.0E-01
BF4169	putative TonB-linked outer membrane protein	0.5	0.5	0.4	0.6	0.5	0.5	1.14	3.2E-01
bglX	periplasmic beta-glucosidase precursor	6.4	6.7	5.7	9.1	5.3	14.2	1.42	3.6E-01
BF4171	hypothetical protein	112.2	114.6	99.1	104.1	88.4	117.5	0.95	6.6E-01
BF4172	putative carboxy-terminal processing protease precursor	407.8	398.1	376.1	291.1	277.1	292.8	0.73	2.2E-03
BF4173	putative PfkB family carbohydrate kinase	106.2	107.5	97.3	108.6	96.6	93.7	0.96	5.7E-01
BFt68	tRNA-Asn-GTT	0.0	0.0	0.0	0.0	0.0	0.0		
BFt69	tRNA-Asn-GTT	850.2	1138.3	767.1	760.2	849.0	2288.5	1.26	6.4E-01
BF4174	hypothetical protein	14.8	10.7	11.6	12.8	12.5	15.0	1.09	5.3E-01
BF4175	hypothetical protein	9.0	8.6	6.7	7.9	11.9	8.1	1.13	5.6E-01
BF4176	hypothetical protein	5.5	6.6	6.1	7.9	9.2	8.4	1.40	1.7E-02
BF4177	putative outer membrane protein	2.4	2.7	2.7	5.5	6.2	4.6	2.08	5.2E-03
BF4178	putative outer membrane protein	2.4	2.0	2.9	5.8	6.0	4.6	2.25	1.3E-02
BF4179	putative two-component system sensor kinase/response regulator fusion protein	3.2	3.4	3.0	3.6	3.3	3.7	1.11	1.3E-01
BF4180	putative pyruvate formate-lyase activating enzyme	1.3	1.2	1.0	2.1	2.3	3.0	2.11	1.4E-02
pflD	putative formate acetyltransferase (pyruvate formate-lyase)	0.7	0.7	0.7	1.9	1.8	1.6	2.51	8.2E-04
BF4182	putative transmembrane sugar transporter	0.8	0.3	0.6	1.5	1.7	1.9	3.33	3.6E-02
BF4183	putative aldose 1-epimerase precursor	2.0	2.5	2.4	2.4	3.4	2.7	1.22	2.6E-01
BF4184	hypothetical protein	1.1	1.0	1.3	3.1	3.4	3.1	2.83	1.7E-03
BF4185	hypothetical protein	286.0	292.8	283.9	291.8	305.0	328.3	1.07	1.8E-01
BF4186	possible amidophosphoribosyl-transferase	58.6	55.0	56.6	69.5	62.2	73.0	1.20	4.3E-02
suhB	putative inositol-1-monophosphatase	46.6	36.3	45.3	58.6	62.5	72.4	1.51	3.0E-02
BF4188	hypothetical protein	53.4	62.8	52.7	15.3	18.4	20.2	0.32	1.8E-03
BF4189	putative alpha-galactosidase/melibiase	38.0	31.8	31.5	37.7	35.1	41.2	1.13	2.6E-01
BF4190	hypothetical protein	44.8	38.6	44.0	22.0	32.6	20.9	0.58	4.1E-02
BF4191	hypothetical protein	115.2	94.4	104.5	41.1	59.9	63.5	0.52	2.4E-02
BF4192	hypothetical protein	1.2	2.7	1.5	1.1	0.5	2.4	0.67	5.4E-01
BF4193	hypothetical protein	2.6	0.3	0.3	0.6	1.7	1.1	1.59	6.5E-01

BF4194	putative lipopolysaccharide biosynthesis protein	8.2	1.5	3.4	2.7	1.6	4.1	0.75	6.9E-01
BF4195	hypothetical protein	6.0	4.4	4.4	5.0	5.4	5.5	1.09	5.2E-01
BF4196	hypothetical protein	7.8	8.3	8.5	9.8	10.6	8.5	1.17	1.3E-01
BF4197	possible regulatory protein	7.5	6.1	6.3	7.9	6.2	7.3	1.08	5.6E-01
BF4198	hypothetical protein	7.1	7.4	8.6	5.8	8.1	6.6	0.88	3.8E-01
BF4199	hypothetical protein	14.1	6.3	11.5	18.3	21.5	15.0	1.79	1.3E-01
BF4200	putative glycosyl transferase	30.8	35.3	36.0	13.8	20.0	13.7	0.46	1.2E-02
BF4202	putative glycosyl transferase	3.4	4.6	4.0	5.7	5.9	4.4	1.33	1.3E-01
BF4203	hypothetical protein	3.5	2.7	1.9	2.1	3.7	2.6	1.03	9.2E-01
BF4204	hypothetical protein	6.8	5.2	7.3	5.7	7.4	8.2	1.10	6.3E-01
BF4205	hypothetical protein	12.8	10.1	15.1	13.9	11.0	10.0	0.92	6.8E-01
BF4206	hypothetical protein	11.2	6.8	8.1	7.8	11.5	9.2	1.10	6.9E-01
BF4207	hypothetical protein	2.5	3.2	2.0	4.4	4.8	4.1	1.77	3.6E-02
BF4208	hypothetical protein	2.5	3.0	3.8	3.0	3.3	3.8	1.10	6.0E-01
BF4209	hypothetical protein	3.5	5.9	6.1	5.6	7.9	8.1	1.42	2.5E-01
BF4210	putative DNA-binding protein	8.8	6.3	4.3	7.9	4.5	8.0	1.06	8.7E-01
BF4211	hypothetical protein	4.0	3.2	2.9	2.3	3.3	1.9	0.71	2.1E-01
BF4212	hypothetical protein	4.5	5.1	5.3	7.8	12.3	6.3	1.71	9.1E-02
BF4213	hypothetical protein	3.8	5.5	4.8	6.3	6.4	7.7	1.44	7.2E-02
BF4214	putative MutT/NUDIX family protein	66.2	64.7	53.7	65.9	61.1	61.9	1.03	7.7E-01
BF4215	putative TPR-repeat protein	174.6	176.1	163.0	181.2	166.5	160.8	0.99	8.5E-01
BF4216	hypothetical protein	231.3	207.7	211.2	185.4	188.6	193.6	0.87	3.8E-02
topA	putative DNA topoisomerase I	395.7	374.7	343.3	296.1	262.1	269.4	0.74	1.5E-02
BF4218	hypothetical protein	151.0	138.3	144.1	55.6	55.4	62.3	0.40	4.0E-04
argS	arginyl-tRNA synthetase	193.7	180.8	180.7	211.7	189.8	236.7	1.15	1.7E-01
hup3	putative histone-like DNA-binding protein HU3	896.5	1091.1	1190.0	3032.3	4161.4	3763.8	3.44	2.7E-03
BF4221	putative transmembrane rhomboid family protein	453.0	473.3	424.0	277.7	289.9	284.9	0.63	1.1E-03
BF4222	putative transmembrane rhomboid family protein	310.2	293.2	285.6	235.1	218.1	258.6	0.80	3.1E-02
BF4223	hypothetical protein	65.9	63.4	64.2	59.6	48.2	63.8	0.88	2.7E-01
BF4224	hypothetical protein	1.6	3.5	3.6	3.1	3.8	2.1	1.06	8.9E-01
BF4225	putative protein-export transmembrane SecDF protein	1341.5	1571.0	1422.9	1400.4	1354.6	1334.0	0.94	3.8E-01
hup4	putative histone-like DNA-binding protein HU4	212.2	223.8	207.0	287.3	194.5	233.8	1.10	5.3E-01
BF4227	hypothetical protein	88.0	125.4	124.4	60.6	59.3	70.3	0.57	2.5E-02
BF4228	hypothetical protein	127.7	174.6	179.9	61.8	68.2	71.6	0.42	6.1E-03
BF4229	hypothetical protein	242.4	348.9	351.3	202.6	200.6	231.7	0.68	7.2E-02
BF4230	hypothetical protein	731.8	888.3	976.9	817.2	792.6	696.8	0.89	3.8E-01
BF4231	hypothetical protein	102.0	102.4	106.0	83.4	91.9	88.5	0.85	1.5E-02
BF4232	hypothetical protein	156.0	135.2	160.7	89.7	111.8	109.8	0.69	2.8E-02
BF4233	hypothetical protein	3.6	1.9	3.0	0.9	0.0	0.9	0.31	1.9E-02
BF4234	putative AraC-family transcriptional regulatory protein	4.4	2.1	3.5	3.6	3.2	2.3	0.93	8.4E-01
BF4235	putative bacteriophage integrase	45.2	41.7	47.2	34.5	36.8	34.9	0.79	1.3E-02
BF4236	hypothetical protein	7.5	4.8	9.1	0.0	3.5	2.2	0.40	9.0E-02
BFt70	tRNA-Arg-CCT	16.5	12.5	10.4	11.1	10.9	9.0	0.80	2.8E-01

porA	putative 2-oxoglutarate ferredoxin oxidoreductase subunit	369.5	384.0	341.9	381.1	327.6	337.8	0.95	5.3E-01
porB	ferrodoxin oxidoreductase beta subunit	299.0	295.2	269.1	362.9	331.4	300.2	1.15	1.4E-01
BF4241	putative transmembrane protein	24.1	22.0	25.6	11.5	13.6	8.8	0.47	1.3E-02
ugpQ	putative glycerophosphoryl diester phosphodiesterase	258.9	247.0	232.3	156.5	142.4	189.5	0.66	2.1E-02
BF4243	uracil phosphoribosyltransferase	229.1	257.1	255.2	325.8	301.4	272.0	1.21	6.9E-02
pckA	phosphoenolpyruvate carboxykinase	10609.8	11246.7	11885.5	8757.9	8903.4	8356.5	0.77	7.3E-03
BF4245	hypothetical protein	55.1	43.7	59.6	28.3	37.8	31.3	0.62	3.6E-02
BF4246	putative outer membrane protein	13.0	14.0	15.0	64.7	69.2	56.6	4.53	3.6E-04
BF4247	hypothetical protein	14.6	13.4	13.8	58.3	66.6	54.2	4.27	3.1E-04
BF4248	putative outer membrane protein	18.8	18.9	19.4	78.8	71.9	70.3	3.87	6.7E-05
BF4249	putative outer membrane protein	9.6	8.8	10.6	55.1	49.7	51.2	5.40	1.7E-04
BF4250	hypothetical protein	13.6	16.8	23.1	85.0	74.1	74.4	4.46	3.1E-03
BF4251	hypothetical protein	8.2	9.4	5.8	23.2	21.1	25.5	3.05	6.4E-03
BF4252	putative transmembrane protein	9.2	9.3	9.0	25.5	27.2	28.4	2.94	1.1E-04
BF4253	hypothetical protein	2.9	6.7	7.0	16.9	12.7	12.7	2.72	5.4E-02
BF4254	hypothetical protein	4.7	6.0	4.7	21.6	15.3	23.4	3.87	3.7E-03
BF4255	hypothetical protein	59.5	60.2	51.3	180.1	157.8	172.5	2.99	6.0E-04
BF4256	putative outer membrane protein	65.4	57.6	61.2	282.2	290.1	285.3	4.66	5.0E-05
BF4257	hypothetical protein	106.2	106.8	104.9	437.0	429.6	392.1	3.96	5.2E-05
typA	putative GTP-binding elongation factor family protein TypA/BipA	1025.5	1102.7	1075.6	666.1	641.8	620.5	0.60	5.9E-04
rpsO	putative 30S ribosomal protein S15	2757.9	3212.2	3407.5	2812.7	3176.3	3596.8	1.02	8.7E-01
BF4260	putative transcriptional regulator	147.0	142.4	145.7	464.5	501.5	402.0	3.13	5.7E-04
BF4261	acyl-CoA synthase	96.0	94.6	95.1	370.5	367.8	339.6	3.77	3.2E-05
BF4262	putative two-component sensor histidine kinase with PAS domain	22.9	19.0	20.6	28.7	26.0	24.9	1.28	4.4E-02
sahH	S-adenosyl-L-homocysteine hydrolase	485.6	536.9	470.4	355.1	304.2	410.5	0.71	4.4E-02
BF4264	hypothetical protein	170.9	184.1	177.0	141.1	142.0	130.2	0.78	6.4E-03
BF4265	hypothetical protein	39.2	36.5	37.8	21.9	25.9	32.9	0.70	7.1E-02
BF4266	putative arylsulfatase	2.2	2.9	2.8	1.2	2.3	2.2	0.69	2.4E-01
BF4267	hypothetical protein	3.3	2.1	2.3	0.9	2.2	2.1	0.62	3.0E-01
BF4270	putative anti-sigma factor	12.8	11.0	12.9	6.9	5.1	6.8	0.51	1.0E-02
BF4271	putative ECF-type RNA polymerase	149.3	154.4	143.6	95.7	103.3	79.7	0.62	1.1E-02
BF4273	putative lipoprotein releasing system transmembrane protein	808.3	759.8	818.0	493.7	561.4	513.4	0.66	3.0E-03
BF4274	putative ribosome-binding factor A	694.7	664.0	765.5	425.4	539.3	463.1	0.67	1.8E-02
BF4275	putative transmembrane protein	72.3	84.1	79.7	32.7	35.2	43.5	0.47	5.0E-03
BF4276	putative O-methyltransferase	329.2	326.6	319.6	181.9	178.1	180.9	0.55	2.0E-05
pyk	pyruvate kinase	711.6	648.5	702.4	437.4	474.3	428.8	0.65	2.4E-03
aroQ	3-dehydroquinate dehydratase	428.1	404.0	422.4	227.4	247.6	194.7	0.53	3.8E-03
xerD	putative tyrosine recombinase	54.9	55.3	53.6	52.6	52.7	52.7	0.96	3.9E-02
BF4280	hypothetical protein	5360.8	5887.0	5899.4	6700.8	6857.9	6266.6	1.16	4.6E-02
BF4281	possible thiol-disulfide oxidoreductase	132.1	128.5	129.7	140.8	161.6	131.8	1.11	2.2E-01
BF4282	hypothetical protein	65.2	66.3	62.9	85.3	88.5	85.8	1.34	8.7E-04
BF4283	hypothetical protein	17.0	18.1	18.9	27.5	28.4	25.3	1.51	3.7E-03
BF4284	hypothetical protein	35.8	36.0	37.8	15.2	18.1	15.8	0.45	8.8E-04
BF4285	hypothetical protein	15.1	13.4	14.2	14.8	16.8	14.4	1.08	3.5E-01

BF4286	putative two-component system sensor kinase/response regulator fusion protein	14.0	13.0	15.4	14.7	16.0	15.0	1.08	3.1E-01
BF4287	putative radical SAM-family protein	44.0	38.4	42.8	50.0	56.8	58.0	1.32	2.5E-02
BF4288	hypothetical protein	74.3	60.3	54.0	89.9	95.3	121.5	1.63	4.0E-02
BF4289	putative CoA-binding protein	99.9	99.0	91.7	156.0	165.2	166.0	1.68	7.8E-04
BF4290	hypothetical protein	21.5	23.9	22.0	20.5	21.4	15.8	0.85	2.4E-01
BF4294	putative transmembrane anchored hypothetical protein	8.7	8.2	10.0	24.5	29.5	23.0	2.86	1.9E-03
BF4295	hypothetical protein	2.0	5.8	3.8	16.5	15.0	11.5	3.99	2.9E-02
BF4296	hypothetical protein	2.6	2.8	1.4	11.7	12.2	7.9	4.80	9.5E-03
metG	methionyl-tRNA synthetase	308.3	332.2	308.1	353.2	315.8	300.5	1.02	7.8E-01
BF4298	putative O-antigen repeat unit transporter	76.5	88.9	82.4	87.2	90.3	81.9	1.05	4.9E-01
BF4299	putative glycosyltransferase	41.1	40.8	34.5	49.0	48.0	43.9	1.21	7.3E-02
BF4300	putative exopolysaccharide biosynthesis protein	44.9	45.1	42.3	50.0	47.3	44.4	1.07	2.3E-01
BF4301	putative glycosyltransferase	50.1	46.0	48.3	53.8	51.9	49.8	1.08	1.4E-01
BF4302	putative transmembrane protein	85.2	92.1	83.1	90.3	92.7	86.7	1.04	4.5E-01
BF4303	putative UDP-N-acetylglucosamine 2-epimerase	120.3	116.2	111.8	112.7	106.6	123.9	0.98	8.0E-01
BF4304	putative UDP-N-acetyl-D-mannosamine dehydrogenase	198.2	188.6	177.2	171.0	164.7	172.9	0.90	7.5E-02
BF4305	putative glycosyltransferase	140.5	139.2	142.0	137.9	137.8	147.9	1.00	9.0E-01
BF4306	putative glycosyltransferase	121.0	109.3	107.6	119.8	125.0	125.1	1.10	1.2E-01
cobB	NAD-dependent deacetylase	98.8	94.9	79.1	92.8	77.2	111.6	1.03	8.9E-01
fklB	putative FkbP-type 22 kDa peptidyl-prolyl cis-trans isomerase	811.4	754.3	819.1	723.5	645.3	716.5	0.87	6.8E-02
BF4309	putative isomerase	1970.0	1876.4	2046.7	1586.8	1483.0	1433.4	0.76	7.2E-03
BF4310	putative AsnC-family transcriptional regulatory protein	1513.3	1470.8	1541.5	1664.8	1667.3	1429.9	1.05	4.8E-01
BF4311	putative transmembrane protein	1421.2	1387.8	1508.3	1670.2	1783.6	1565.3	1.16	5.3E-02
BFt71	tRNA-Met-CAT	271.8	309.4	333.5	336.7	416.9	521.6	1.38	1.3E-01
BF4312	putative two-component response regulator	27.1	27.9	27.4	28.5	33.3	32.4	1.14	8.5E-02
BF4313	putative two-component system sensor, no kinase domain	29.6	29.1	34.3	29.8	27.5	23.4	0.87	2.4E-01
BF4314	putative outer membrane component of efflux transporter	4.6	3.6	3.5	2.6	3.0	2.7	0.72	5.3E-02
BF4315	putative transmembrane AcrB/D/F-family transporter	1.8	1.9	2.2	1.0	0.9	1.2	0.53	6.5E-03
BF4316	putative efflux transporter component	4.6	2.5	2.2	0.6	1.6	0.8	0.32	5.3E-02
5S		0.4	8.3	41.3	1.9	5.2	27.2	1.27	9.1E-01
23S		13.7	7.5	12.2	16.3	9.1	22.1	1.38	4.5E-01
BFt72	tRNA-Ala-TGC	87.0	97.6	97.6	47.1	45.1	95.3	0.62	1.8E-01
BFt73	tRNA-Ile-GAT	158.9	177.9	180.8	63.0	65.0	113.6	0.45	3.1E-02
16S		672.5	32.3	99.0	90.9	32.3	230.2	0.68	7.8E-01
BF4317	hypothetical protein	0.0	0.0	0.0	96.4	92.4	155.5		
BF4318	hypothetical protein	0.0	1.5	0.8	0.0	0.0	0.0		
BF4319	putative D-Ala-D-Ala dipeptidase protein	16.9	18.8	21.0	21.2	21.5	19.0	1.09	3.8E-01

BF4320	hypothetical protein	20.9	18.5	18.3	42.5	43.1	39.2	2.17	8.4E-04
BF4321	hypothetical protein	14.7	14.3	17.6	153.7	157.2	150.6	9.95	9.2E-05
BF4322	putative outer membrane protein	12.2	14.0	12.8	142.1	137.9	113.1	10.05	1.6E-04
BF4323	putative TonB-dependent outer membrane receptor protein	16.5	15.2	15.3	123.6	129.7	113.6	7.80	3.8E-05
BF4324	hypothetical protein	19.5	19.3	18.7	63.8	62.0	67.9	3.37	5.2E-05
BF4325	putative transmembrane sugar transporter	34.5	42.3	35.8	166.4	143.3	198.2	4.49	1.2E-03
BF4326	putative two-component system sensor kinase/response regulator fusion protein	14.7	18.9	16.4	27.3	25.7	25.7	1.58	1.0E-02
BF4327	putative glycosylhydrolase	80.6	83.0	77.4	125.7	124.8	136.9	1.61	1.2E-03
BF4328	putative TonB-dependent outer membrane receptor protein	1.2	1.1	0.8	0.6	0.3	0.6	0.46	7.2E-02
BF4329	putative acid phosphatase	7.8	7.6	5.2	3.9	5.0	6.2	0.73	2.3E-01
BF4330	putative transmembrane ion channel	56.1	55.6	59.8	49.0	39.8	47.3	0.79	4.8E-02
BF4331	putative transmembrane K+ dependent Na+/Ca+ exchanger-related protein	39.1	38.0	42.0	56.6	49.1	52.4	1.33	1.3E-02
BF4332	hypothetical protein	142.3	126.4	130.0	162.8	152.5	147.7	1.16	5.5E-02
parE	DNA topoisomerase IV subunit B	212.4	208.8	185.8	226.3	210.5	221.3	1.09	2.1E-01
coaD	phosphopantetheine adenylyltransferase	218.5	233.3	207.6	172.0	193.9	176.4	0.82	3.4E-02
BF4335	putative carboxy-terminal processing protease precursor	184.4	180.4	176.6	175.3	160.4	163.4	0.92	8.4E-02
BF4336	putative transmembrane PAP2-family protein	107.7	92.6	104.9	96.2	95.3	89.8	0.92	2.5E-01
BF4337	putative AraC-family transcriptional regulator	251.2	230.8	210.9	343.3	351.0	298.7	1.43	1.7E-02
BF4339	fumarate reductase transmembrane cytochrome b subunit	954.3	954.1	909.5	808.2	778.2	736.5	0.82	9.8E-03
BF4340	succinate dehydrogenase	1089.5	1224.1	1096.2	1061.7	997.7	1034.9	0.91	1.3E-01
BF4341	succinate dehydrogenase	1440.6	1657.2	1476.5	1109.4	1135.2	1156.3	0.74	8.2E-03
BF4342	putative iron-regulated transmembrane protein	492.7	493.9	480.0	310.4	304.5	311.5	0.63	5.4E-05
BF4343	hypothetical protein	571.8	556.5	533.7	420.2	386.3	397.6	0.72	2.5E-03
BF4344	putative TonB-dependent outer membrane receptor protein	381.9	351.5	347.2	272.3	247.0	276.7	0.74	8.1E-03
BF4345	putative AraC-family transcriptional regulator	123.1	103.6	102.0	81.6	87.4	84.8	0.78	3.2E-02
BF4346	hypothetical protein	4.5	4.3	9.0	5.0	6.1	7.4	1.08	8.2E-01
BF4347	hypothetical protein	2.0	1.9	0.2	0.2	0.8	0.7	0.51	5.7E-01
BF4348	putative transmembrane protein	8.8	8.8	7.8	5.4	5.0	9.6	0.75	3.2E-01
BF4349	putative DNA processing Smf-like protein	219.1	234.4	207.8	173.3	162.0	190.7	0.79	3.4E-02
BF4350	putative thioesterase protein	274.5	298.0	271.5	237.8	229.0	275.0	0.88	1.5E-01
BF4351	putative peptidase	220.7	209.4	190.8	160.0	159.9	186.1	0.81	6.2E-02
BF4352	hypothetical protein	202.6	196.3	206.6	140.6	133.5	129.8	0.67	9.0E-04
BF4353	putative TIM-barrel protein, possible dihydrouridine synthase	64.2	50.6	47.6	58.8	44.4	64.1	1.03	9.0E-01
BF4354	putative transmembrane protein	126.0	131.3	119.1	130.5	124.1	152.1	1.08	4.0E-01
BF4355	putative UDP-glucose 4-epimerase	90.3	91.2	91.0	108.7	106.6	116.2	1.22	5.9E-03

BF4356	putative transmembrane cation efflux protein	161.2	151.2	143.8	85.8	85.8	128.5	0.65	6.0E-02
BF4357	putative exoribonuclease	259.3	273.3	230.2	231.3	222.0	230.0	0.90	1.6E-01
BF4358	hypothetical protein	39.2	43.1	29.3	22.2	20.5	28.5	0.64	7.3E-02
BF4359	putative RNA polymerase ECF-type sigma factor	11.3	13.5	8.4	6.2	9.2	9.4	0.75	2.8E-01
BF4360	putative transmembrane protein	18.0	18.5	16.9	12.4	10.1	10.8	0.62	6.2E-03
BF4361	putative 5-nitroimadazole antibiotic resistance protein	126.9	128.3	136.1	132.7	136.6	150.3	1.07	2.5E-01
cysK	putative cysteine synthase	109.4	120.0	93.5	104.6	75.0	141.1	0.97	9.0E-01
BF4363	putative lipase/esterase	43.8	48.9	47.1	68.1	65.1	73.1	1.47	4.3E-03
BF4364	putative metalloprotease	21.3	23.2	20.0	61.3	68.1	60.0	2.94	4.7E-04
BF4365	putative ATP/GTP-binding protein	224.2	204.7	216.8	268.3	218.2	235.2	1.11	2.4E-01
BF4366	putative 2-dehydropantoate 2-reductase	172.3	156.0	144.2	144.8	134.0	149.4	0.91	2.5E-01
BF4367	prolipoprotein diacylglyceryl transferase	164.4	171.0	176.4	168.0	184.2	163.6	1.01	9.0E-01
BF4368	possible chloramphenicol acetyltransferase	264.1	240.9	250.9	235.0	233.2	225.4	0.92	7.4E-02
mutS	DNA mismatch repair protein	241.6	230.8	257.9	228.8	235.3	217.8	0.93	2.2E-01
BF4370	hypothetical protein	47.6	50.1	48.0	31.9	39.0	38.8	0.75	2.8E-02
BF4371	putative ATP/GTP-binding protein	53.4	55.8	55.9	40.7	48.0	47.9	0.83	5.0E-02
leuS	leucyl-tRNA synthetase	168.1	177.4	168.2	227.6	216.3	203.0	1.26	1.0E-02
BF4373	putative transmembrane protein	322.3	317.8	334.4	315.1	335.9	267.6	0.94	4.8E-01
BF4374	putative Ham1-like protein	198.8	211.4	191.3	231.8	231.2	232.6	1.16	1.8E-02
nadA	quinolinate synthetase	177.5	158.6	171.8	201.9	189.1	219.7	1.20	5.2E-02
finB	putative resolvase/DNA invertase	56.7	45.2	58.2	50.7	60.5	39.9	0.94	7.3E-01
pBF9343.02	hypothetical protein	31.8	28.6	32.5	14.1	16.2	13.7	0.47	1.7E-03
pBF9343.03	putative DNA-binding protein	260.5	276.3	276.8	149.3	192.1	133.7	0.58	1.7E-02
pBF9343.04	hypothetical protein	216.7	204.0	245.8	193.2	201.5	157.7	0.83	1.6E-01
pBF9343.05	hypothetical protein	268.1	235.3	274.0	260.0	306.7	218.2	1.00	9.9E-01
pBF9343.06	hypothetical protein	180.5	202.3	213.8	187.1	209.0	150.0	0.91	5.0E-01
pBF9343.07	hypothetical protein	190.7	165.2	229.5	208.9	212.2	149.6	0.97	8.9E-01
pBF9343.08	hypothetical protein	124.8	124.3	168.0	127.3	169.3	111.3	0.97	9.0E-01
pBF9343.09	hypothetical protein	121.2	112.5	126.8	117.6	126.2	98.1	0.94	6.0E-01
pBF9343.10	hypothetical protein	111.8	104.0	140.5	112.3	135.2	76.3	0.89	6.5E-01
pBF9343.11	putative integral membrane protein	145.4	127.5	130.8	132.5	114.4	90.5	0.83	2.4E-01
pBF9343.12	putative replication protein	187.3	164.0	201.2	148.9	175.5	132.9	0.83	1.8E-01
pBF9343.13	putative mobilization protein	101.3	86.7	100.1	111.0	146.5	106.2	1.25	1.7E-01
pBF9343.14	putative mobilization protein	107.8	97.9	116.1	148.9	164.7	119.9	1.34	8.3E-02
pBF9343.15	putative ParA-related protein	155.0	131.7	179.4	230.8	233.8	193.7	1.42	5.6E-02
pBF9343.16	hypothetical protein	731.4	708.5	805.8	799.7	865.5	669.7	1.04	7.5E-01
pBF9343.17c	putative regulatory protein	151.8	161.0	191.8	204.0	227.0	181.1	1.21	1.6E-01
pBF9343.18c	putative plasmid transfer protein	93.7	96.2	105.4	118.2	122.6	93.8	1.13	3.3E-01
pBF9343.20c	hypothetical protein	495.5	516.0	539.0	585.6	570.4	444.1	1.02	8.4E-01
pBF9343.21c	hypothetical protein	44.0	28.2	44.8	68.0	74.1	65.7	1.81	3.6E-02
pBF9343.22c	putative HU-like DNA binding protein	22.6	26.8	32.0	64.9	78.6	52.1	2.39	1.3E-02
pBF9343.23c	hypothetical protein	28.9	20.7	28.0	41.1	57.1	36.3	1.72	6.0E-02
pBF9343.24c	putative topoisomerase-related protein	22.1	24.9	28.8	47.6	45.9	31.6	1.63	5.6E-02
pBF9343.25c	hypothetical protein	17.5	12.8	20.4	28.5	28.1	18.2	1.47	1.8E-01
pBF9343.26c	putative integral membrane protein	14.7	19.0	19.7	27.2	24.3	19.5	1.33	1.5E-01

pBF9343.27c	hypothetical protein	19.9	16.4	20.1	36.8	37.2	27.8	1.79	1.7E-02
pBF9343.28c	putative integral membrane protein	18.6	17.2	18.8	54.1	56.3	47.7	2.89	4.8E-04
pBF9343.29c	hypothetical protein	14.2	10.4	16.2	38.8	42.0	29.2	2.70	1.2E-02
pBF9343.30	putative secreted peptidase	19.3	14.9	19.8	28.4	35.0	18.8	1.48	1.8E-01
pBF9343.31c	hypothetical protein	81.0	80.5	84.0	122.5	115.7	117.7	1.45	5.9E-04
pBF9343.32c	hypothetical protein	156.2	146.7	162.3	286.4	270.8	235.4	1.70	4.6E-03
pBF9343.33c	hypothetical protein	170.2	145.5	172.4	233.1	257.5	207.4	1.43	2.7E-02
pBF9343.34c	hypothetical protein	221.5	204.8	232.7	249.7	288.7	202.4	1.11	4.5E-01
pBF9343.35c	putative outer membrane protein	55.8	45.0	61.1	47.9	51.9	41.4	0.88	3.7E-01
pBF9343.36c	hypothetical protein	33.2	36.7	38.9	36.7	37.5	30.5	0.96	7.1E-01
pBF9343.37c	hypothetical protein	32.6	34.6	40.9	33.5	38.9	24.9	0.89	5.4E-01
pBF9343.38c	putative plasmid transfer protein	42.4	45.1	50.0	39.2	42.1	29.6	0.80	1.8E-01
pBF9343.39c	putative plasmid transfer protein	35.1	35.2	33.4	38.9	34.0	27.6	0.96	7.6E-01
pBF9343.40c	putative integral membrane protein	18.4	18.7	19.8	23.2	24.6	18.4	1.16	2.5E-01
pBF9343.41c	putative plasmid transfer protein	21.8	20.1	21.5	22.8	32.6	18.4	1.13	5.7E-01
pBF9343.42c	putative plasmid transfer protein	22.6	23.1	25.6	25.8	30.4	23.7	1.11	3.3E-01
pBF9343.43c	hypothetical protein	14.8	16.6	18.9	24.2	19.9	17.5	1.22	2.2E-01
pBF9343.44c	putative plasmid transfer protein	24.0	16.8	20.4	22.8	25.8	18.0	1.09	6.6E-01
bctA	plasmid transfer protein	23.0	24.9	25.0	33.8	31.2	25.9	1.24	1.0E-01
pBF9343.46c	putative plasmid transfer protein	27.1	20.6	21.4	39.6	53.1	32.7	1.79	4.4E-02
pBF9343.47c	putative plasmid transfer protein	169.7	150.2	159.8	236.3	228.9	209.0	1.41	7.8E-03
pBF9343.48c	putative integral membrane protein	33.5	33.5	31.2	53.8	43.0	39.1	1.37	5.6E-02