Table S2. Expression changes in *B. massiliensis* during growth in neutral porcine mucin *O*-glycans (PMOG) relative to growth in N-acetylglucosamine (GlcNAc)

Formatting descriptions and notes:

Color-coding for PUL genes that are upregulated more than 3-fold in PMOG relative to GlcNAc

Color-coding for genes associated with upregulated PULs that are not themselves upregulated more than 3-fold in PMOG relative to GlcNAc

B. massiliensis starch utilization PUL genes

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

	GlcNac1	**GlcNac2**	**GlcNAc3**	**PMOG1**	**PMOG2**	**PMOG3**
Total mapped reads :	**5,872,261**	**5,050,601**	**4,822,703**	**5,581,153**	**6,482,255**	**6,466,140**

Locus Tag	**Description**	**[1]GlcNac1**	**[1]GlcNac2**	**[1]GlcNAc3**	**[1]PMOG1**	**[1]PMOG2**	**[1]PMOG3**	**Fold (PMOG/GlcNAc)**	***P* value**
B035DRAFT_00001	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	64.2	50.5	60.5	57.1	49.5	23.6	0.70	4.8E-01
B035DRAFT_00002	Signal transduction histidine kinase	73.9	58.8	64.0	70.0	71.4	52.8	0.98	9.4E-01
B035DRAFT_00003	small GTP-binding protein domain	89.8	93.5	88.8	93.2	93.6	108.1	1.08	4.1E-01
B035DRAFT_00004	Acetyltransferases	38.5	51.4	48.5	56.8	59.2	81.8	1.42	2.3E-01
B035DRAFT_00005	hypothetical protein(EC:5.3.3.1)	98.5	117.4	112.0	146.8	154.7	178.7	1.46	6.7E-02
B035DRAFT_00006	Helicase conserved C-terminal domain./SNF2 family N-terminal domain./N-6 DNA Methylase.	8.5	5.2	8.8	10.1	9.0	3.2	0.90	9.0E-01
B035DRAFT_00007	Domain of unknown function (DUF1896).	27.0	20.6	33.1	37.3	30.9	11.0	0.88	8.8E-01
B035DRAFT_00008	Topoisomerase IA(EC:5.99.1.2)	6.0	3.5	6.6	7.0	5.8	1.7	0.78	8.0E-01
B035DRAFT_00009	hypothetical protein	6.6	2.3	3.2	5.0	4.5	0.9	0.74	8.0E-01
B035DRAFT_00010	hypothetical protein	3.6	2.2	2.5	2.2	3.3	0.7	0.64	6.1E-01
B035DRAFT_00011	DNA binding domain, excisionase family	13.9	5.8	10.9	12.9	11.9	2.0	0.71	7.8E-01
B035DRAFT_00012	hypothetical protein	12.8	8.7	13.6	8.1	9.9	4.0	0.60	3.7E-01
B035DRAFT_00013	Site-specific recombinase XerD	17.6	12.3	16.2	15.0	15.4	7.4	0.79	6.2E-01
B035DRAFT_00014	Alpha-L-fucosidase (GH29)	72.2	70.8	62.4	90.1	74.6	46.0	0.99	9.8E-01
B035DRAFT_00015	Alpha-galactosidase	23.5	25.0	25.2	20.1	24.0	18.8	0.85	2.7E-01
B035DRAFT_00016	Arylsulfatase A and related enzymes	42.3	42.0	47.2	39.6	46.2	45.1	1.00	9.7E-01
B035DRAFT_00017	ribonuclease III, bacterial(EC:3.1.26.3)	550.0	624.5	557.4	402.1	541.9	491.4	0.82	3.0E-01
B035DRAFT_00018	beta-ketoacyl-acyl-carrier-protein synthase II(EC:2.3.1.179)	3374.3	3928.0	3738.8	2882.0	3671.2	3990.5	0.95	7.9E-01
B035DRAFT_00019	acyl carrier protein	4101.2	5146.9	4656.6	3951.2	4823.8	5795.6	1.04	8.8E-01
B035DRAFT_00020	phosphoribosylglycinamide formyltransferase, formyltetrahydrofolate-dependent(EC:2.1.2.2)	75.9	90.0	87.9	72.6	83.0	86.8	0.95	7.4E-01
B035DRAFT_00021	Alpha-L-fucosidase (GH95)	119.7	104.1	115.7	125.1	136.6	96.4	1.05	8.4E-01
B035DRAFT_00022	Alpha-N-acetylglucosaminidase (GH89)	58.0	51.0	50.4	99.6	120.1	92.5	1.95	2.7E-02
B035DRAFT_00023	hypothetical protein	53.0	49.3	49.0	102.5	121.3	95.8	2.10	1.4E-02
B035DRAFT_00024	hypothetical protein	57.1	55.5	57.3	113.4	159.5	124.0	2.31	2.2E-02
B035DRAFT_00025	Alpha-galactosidase	40.0	33.6	35.4	73.4	97.4	74.7	2.24	2.6E-02
B035DRAFT_00026	Uncharacterized conserved protein	16.0	19.6	20.6	74.1	109.7	132.2	5.50	1.8E-02
B035DRAFT_00027	SusD family	43.6	42.1	45.1	312.3	428.3	459.8	9.06	1.9E-03
B035DRAFT_00028	**TonB-linked outer membrane protein, SusC/RagA family**	44.9	46.6	42.6	271.2	378.2	456.9	**8.07**	**5.3E-03**
B035DRAFT_00029	Fe2+-dicitrate sensor, membrane component	47.9	45.0	49.5	349.2	448.0	414.6	8.47	4.5E-04
B035DRAFT_00030	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	41.6	46.0	40.5	47.0	42.9	48.2	1.08	4.3E-01
B035DRAFT_00031	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	162.7	213.2	240.4	140.4	135.0	161.1	0.72	2.0E-01
B035DRAFT_00032	hypothetical protein	568.4	630.4	599.1	332.6	374.8	466.2	0.65	8.6E-02
B035DRAFT_00033	Protein of unknown function (DUF1703).	142.6	164.5	146.1	152.1	169.6	177.1	1.10	4.1E-01

B035DRAFT_00034	Phosphoglycerate dehydrogenase and related dehydrogenases(EC:1.1.1.290)	111.6	97.5	114.2	129.9	116.7	71.6	0.96	9.1E-01
B035DRAFT_00035	hypothetical protein	251.4	290.3	241.8	310.5	355.5	421.8	1.38	1.6E-01
B035DRAFT_00036	ADP-heptose:LPS heptosyltransferase (GT9)	342.9	350.7	376.1	382.9	372.1	334.3	1.02	8.6E-01
B035DRAFT_00037	Mn2+-dependent serine/threonine protein kinase	194.4	228.0	210.2	196.1	204.0	244.2	1.02	9.3E-01
B035DRAFT_00038	Lauroyl/myristoyl acyltransferase(EC:2.3.1.)	118.1	129.6	115.4	116.6	114.6	130.5	1.00	9.7E-01
B035DRAFT_00039	UDP-galactopyranose mutase(EC:5.4.99.9)	93.7	99.2	86.9	87.8	80.4	66.5	0.83	3.0E-01
B035DRAFT_00040	hypothetical protein	57.8	92.8	85.8	63.2	77.1	88.5	0.98	9.5E-01
B035DRAFT_00041	Glycosyltransferase (GT4)	46.1	55.3	57.0	37.5	34.9	46.9	0.75	2.0E-01
B035DRAFT_00042	hypothetical protein	103.0	116.5	104.3	100.3	95.2	113.6	0.95	6.9E-01
B035DRAFT_00043	Mannosyltransferase OCH1 and related enzymes (GT32)	96.7	102.8	101.5	86.0	91.8	105.2	0.94	5.7E-01
B035DRAFT_00044	Glycosyltransferases, probably involved in cell wall biogenesis (GT2)	242.0	260.6	254.5	316.1	286.6	358.0	1.26	1.3E-01
B035DRAFT_00045	hypothetical protein	42.2	38.6	32.9	43.9	33.9	50.2	1.12	6.6E-01
B035DRAFT_00046	Nucleoside-diphosphate-sugar epimerases	122.5	125.8	121.5	128.2	139.7	95.5	0.97	9.0E-01
B035DRAFT_00047	Predicted membrane protein	113.4	124.4	120.7	103.0	115.2	115.3	0.93	3.9E-01
B035DRAFT_00048	Glycosyltransferases involved in cell wall biogenesis (GT2)	228.7	229.6	241.8	245.6	227.6	191.5	0.94	6.8E-01
B035DRAFT_00049	4-amino-4-deoxy-L-arabinose transferase and related glycosyltransferases of PMT family (GT83)	233.2	228.9	253.9	263.7	270.8	224.9	1.06	6.4E-01
B035DRAFT_00050	4-alpha-L-fucosyltransferase (Fuc4NAc transferase) (GT56)	148.1	180.1	178.7	125.3	137.3	159.3	0.83	3.1E-01
B035DRAFT_00051	TDP-4-keto-6-deoxy-D-glucose transaminase	273.5	301.8	283.1	237.1	253.4	249.8	0.86	8.6E-02
B035DRAFT_00052	Glycosyltransferases involved in cell wall biogenesis	73.6	82.5	75.5	78.4	75.8	87.3	1.04	6.8E-01
B035DRAFT_00053	Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily (GT2)	130.4	127.8	129.3	121.1	134.5	135.1	1.01	9.2E-01
B035DRAFT_00054	Predicted double-stranded RNA/RNA-DNA hybrid binding protein(EC:3.1.26.4)	231.2	217.0	206.9	225.8	238.1	176.8	0.97	8.8E-01
B035DRAFT_00055	arginyl-tRNA synthetase(EC:6.1.1.19)	304.4	271.4	265.0	266.0	310.5	263.7	1.00	9.9E-01
B035DRAFT_00056	Collagenase and related proteases(EC:3.4.)	121.2	111.3	114.5	123.2	131.0	83.2	0.95	8.7E-01
B035DRAFT_00057	putative TIM-barrel protein, nifR3 family	201.5	197.4	209.5	454.7	457.4	355.6	2.07	2.1E-02
B035DRAFT_00058	Protein of unknown function (DUF2807).	432.5	357.7	395.0	1060.9	1181.6	842.9	2.59	2.1E-02
B035DRAFT_00059	PAP2 superfamily	142.3	141.1	146.3	93.1	88.8	97.0	0.65	3.3E-03
B035DRAFT_00060	Nucleoside-diphosphate-sugar epimerases(EC:5.1.3.2)	222.7	182.8	174.4	103.6	105.4	91.0	0.52	2.7E-02
B035DRAFT_00061	cation diffusion facilitator family transporter	442.0	359.6	377.3	218.2	206.4	153.4	0.49	4.8E-02
B035DRAFT_00062	ribonuclease R(EC:3.1.)	416.1	367.2	367.5	397.4	369.3	356.0	0.98	8.1E-01
B035DRAFT_00063	hypothetical protein	62.9	70.0	62.1	55.1	53.4	50.0	0.81	8.2E-02
B035DRAFT_00064	Serine acetyltransferase(EC:2.3.1.30)	83.6	82.9	83.2	93.6	92.9	99.8	1.15	4.4E-02
B035DRAFT_00065	Signal transduction histidine kinase	93.9	107.3	97.6	93.4	103.3	111.0	1.03	8.2E-01
B035DRAFT_00066	hypothetical protein	8.7	8.4	7.0	9.1	14.4	10.5	1.39	2.6E-01
B035DRAFT_00067	Signal transduction histidine kinase	14.3	18.4	16.3	16.9	17.5	21.1	1.14	4.8E-01
B035DRAFT_00068	Glycoside hydrolase (GH5)	7.1	8.4	8.0	49.8	32.8	32.1	4.78	1.3E-02
B035DRAFT_00069	**TonB-linked outer membrane protein, SusC/RagA family**	**7.2**	**6.3**	**6.4**	**34.1**	**34.0**	**32.9**	**5.10**	**1.2E-04**
B035DRAFT_00070	SusD family	8.0	8.0	8.2	38.5	35.4	34.6	4.47	7.0E-05
B035DRAFT_00071	hypothetical protein	9.2	8.7	9.9	40.7	45.4	46.7	4.78	3.8E-04
B035DRAFT_00072	Arabinogalactan endo-1,4-beta-galactosidase(EC:3.2.1.89) (GH53)	28.2	25.8	26.0	83.6	89.0	78.2	3.14	6.5E-04
B035DRAFT_00073	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	16.7	20.3	9.6	18.2	14.9	12.4	1.01	9.8E-01
B035DRAFT_00074	hypothetical protein	46.1	50.6	50.8	26.6	30.7	36.9	0.63	7.5E-02
B035DRAFT_00075	hypothetical protein	253.4	319.7	270.1	585.9	483.9	462.5	1.82	4.4E-02
B035DRAFT_00076	hypothetical protein	135.9	159.0	168.6	256.1	234.5	333.0	1.76	7.4E-02
B035DRAFT_00077	Predicted N6-adenine-specific DNA methylase(EC:2.1.1.)	227.1	225.4	203.3	230.2	240.5	222.6	1.06	4.6E-01
B035DRAFT_00078	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases(EC:3.4.14.5) (CE1)	173.8	162.9	149.3	161.9	190.4	176.2	1.09	4.7E-01

B035DRAFT_00079	phosphoribosylamine--glycine ligase(EC:6.3.4.13)	330.0	297.9	291.7	313.5	314.9	219.1	0.91	6.8E-01
B035DRAFT_00080	hypothetical protein	124.2	156.5	150.7	137.4	155.9	177.0	1.09	6.4E-01
B035DRAFT_00081	Predicted membrane protein	204.3	188.8	199.8	177.4	191.1	119.7	0.81	4.2E-01
B035DRAFT_00082	Uncharacterized conserved protein	158.0	141.9	137.0	139.3	135.7	126.8	0.92	3.8E-01
B035DRAFT_00083	ABC-type metal ion transport system, periplasmic component/surface adhesin	90.6	87.7	86.7	93.7	93.2	100.9	1.09	1.8E-01
B035DRAFT_00084	ABC-type Mn/Zn transport systems, ATPase component(EC:3.6.3.)	122.8	113.9	101.9	111.8	110.6	95.2	0.94	6.4E-01
B035DRAFT_00085	Beta-glucosidase-related glycosidases(EC:3.2.1.21) (GH3)	34.3	31.5	34.2	28.4	31.2	15.2	0.71	4.2E-01
B035DRAFT_00086	Inorganic pyrophosphatase	214.6	205.1	207.1	235.5	247.7	218.0	1.12	1.8E-01
B035DRAFT_00087	Predicted xylanase/chitin deacetylase (CE4)	99.1	108.4	99.4	107.5	125.9	102.3	1.09	4.9E-01
B035DRAFT_00088	Arylsulfatase A and related enzymes	67.9	64.3	61.3	66.4	82.7	73.7	1.15	3.1E-01
B035DRAFT_00089	Predicted phosphohydrolases	38.9	27.9	32.9	25.6	32.7	31.2	0.90	6.4E-01
B035DRAFT_00090	hypothetical protein	101.5	67.8	68.5	53.2	58.6	66.2	0.76	3.2E-01
B035DRAFT_00091	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)(EC:1.1.1.69)	170.2	129.6	103.2	111.2	116.3	145.3	0.94	8.5E-01
B035DRAFT_00092	5-keto 4-deoxyuronate isomerase(EC:5.3.1.17)	20.2	24.0	26.6	25.5	24.7	17.3	0.95	8.5E-01
B035DRAFT_00093	D-alanyl-D-alanine carboxypeptidase, serine-type, PBP4 family(EC:3.4.16.4,EC:3.4.21.)	38.7	38.2	42.7	59.9	67.7	45.4	1.43	1.7E-01
B035DRAFT_00094	Por secretion system C-terminal sorting domain	4.7	3.7	2.9	5.0	4.6	4.7	1.29	3.5E-01
B035DRAFT_00095	Pregnancy-associated plasma protein-A.	3.7	4.4	3.1	4.6	4.8	6.1	1.38	2.3E-01
B035DRAFT_00096	hypothetical protein	2.9	1.9	6.5	1.7	6.3	8.2	1.36	7.9E-01
B035DRAFT_00097	hypothetical protein	6.8	6.4	6.3	13.2	7.4	6.9	1.35	4.3E-01
B035DRAFT_00098	Predicted P-loop ATPase and inactivated derivatives	3.2	4.3	4.6	5.6	3.4	2.9	0.96	9.3E-01
B035DRAFT_00099	hypothetical protein	28.2	27.0	25.3	59.3	54.4	75.6	2.33	2.2E-02
B035DRAFT_00100	Large extracellular alpha-helical protein	37.6	33.3	40.5	45.7	46.9	37.6	1.17	3.6E-01
B035DRAFT_00101	hypothetical protein	11.0	15.1	16.2	14.0	15.1	19.1	1.14	6.2E-01
B035DRAFT_00102	signal peptidase I, bacterial type(EC:3.4.21.89)	13.0	15.6	18.4	13.3	15.1	17.1	0.97	9.1E-01
B035DRAFT_00103	Transglutaminase-like enzymes, putative cysteine proteases	17.4	13.6	18.1	17.9	15.8	15.9	1.01	9.4E-01
B035DRAFT_00104	dihydrolipoamide dehydrogenase(EC:1.8.1.4)	259.1	222.0	266.6	244.3	256.9	125.4	0.80	6.1E-01
B035DRAFT_00105	Protein of unknown function (DUF1200).	91.8	99.4	91.4	106.7	137.2	145.6	1.37	1.5E-01
B035DRAFT_00106	Protein of unknown function (DUF1200).	107.4	112.3	98.6	128.6	142.3	149.5	1.32	7.0E-02
B035DRAFT_00107	L-aspartate oxidase(EC:1.4.3.16)	196.4	188.9	196.5	209.5	235.2	189.1	1.09	4.8E-01
B035DRAFT_00108	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	129.6	131.5	122.3	131.7	152.6	131.0	1.08	4.3E-01
B035DRAFT_00109	Histidinol phosphatase and related hydrolases of the PHP family	13.2	13.8	9.5	9.7	14.9	10.4	0.95	8.8E-01
B035DRAFT_00110	Predicted phosphohydrolases	7.4	3.9	7.2	6.3	8.1	4.7	1.05	9.3E-01
B035DRAFT_00111	SusD family	5.0	5.7	6.1	4.3	3.8	3.9	0.72	6.4E-02
B035DRAFT_00112	TonB-linked outer membrane protein, SusC/RagA family	13.9	12.3	10.4	6.8	6.1	7.3	0.55	4.4E-02
B035DRAFT_00113	Rubrerythrin	4289.3	3591.8	2762.7	1960.7	1150.7	1732.8	0.45	1.0E-01
B035DRAFT_00114	high affinity sulphate transporter 1	69.5	68.7	66.9	46.0	50.3	52.0	0.72	2.1E-02
B035DRAFT_00115	hypothetical protein	21.9	18.6	13.3	10.6	16.8	21.4	0.89	8.1E-01
B035DRAFT_00116	Outer membrane protein	15.5	15.9	14.4	9.3	11.4	12.0	0.71	9.3E-02
B035DRAFT_00117	ABC-type bacteriocin transporter	13.5	14.0	13.6	10.9	12.5	13.0	0.88	2.4E-01
B035DRAFT_00118	Multidrug resistance efflux pump	11.7	11.3	10.2	8.8	8.5	8.0	0.77	5.5E-02
B035DRAFT_00119	hypothetical protein	31.9	34.3	34.9	22.9	20.2	29.7	0.71	1.7E-01
B035DRAFT_00120	hypothetical protein	29.0	39.7	38.9	25.6	30.9	43.0	0.91	7.9E-01
B035DRAFT_00121	hypothetical protein	34.7	31.5	26.4	27.4	27.5	45.3	1.06	8.8E-01
B035DRAFT_00122	hypothetical protein	41.5	39.7	22.5	23.3	35.1	36.1	0.93	8.8E-01
B035DRAFT_00123	hypothetical protein	25.3	9.4	19.6	12.1	10.4	13.6	0.72	5.5E-01
B035DRAFT_00124	hypothetical protein	15.7	12.2	14.3	16.5	10.7	16.7	1.02	9.5E-01
B035DRAFT_00125	hypothetical protein	11.8	16.5	14.9	11.9	10.2	16.9	0.89	7.3E-01

B035DRAFT_00126	hypothetical protein	5.0	7.3	4.6	9.2	2.3	8.0	1.00	1.0E+00
B035DRAFT_00127	Signal transduction histidine kinase(EC:2.7.13.3)	12.3	12.6	11.6	14.0	17.2	23.7	1.47	2.2E-01
B035DRAFT_00128	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	23.0	25.6	19.4	20.1	19.9	23.1	0.93	6.8E-01
B035DRAFT_00129	Mismatch repair ATPase (MutS family)	71.0	72.4	68.9	56.5	59.1	76.3	0.90	5.2E-01
B035DRAFT_00130	Fe-S oxidoreductases	218.2	192.7	207.8	188.3	192.1	218.7	0.97	7.7E-01
B035DRAFT_00131	hypothetical protein	54.7	45.8	45.5	33.0	36.3	40.2	0.75	1.3E-01
B035DRAFT_00132	hypothetical protein	70.3	103.8	84.3	89.1	88.2	113.6	1.13	6.2E-01
B035DRAFT_00133	rRNA methylases	108.6	112.1	95.8	112.7	110.8	120.4	1.09	4.0E-01
B035DRAFT_00134	quinolinate synthetase complex, A subunit(EC:2.5.1.72)	171.8	193.8	166.8	198.2	208.5	223.6	1.18	1.7E-01
B035DRAFT_00135	hypothetical protein	42.6	40.8	45.1	41.3	43.6	48.3	1.04	7.3E-01
B035DRAFT_00136	hypothetical protein	13.8	43.6	30.5	25.0	27.2	33.0	1.07	9.2E-01
B035DRAFT_00137	non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family(EC:3.6.1.15)	70.8	88.1	59.7	78.5	90.2	72.0	1.11	6.6E-01
B035DRAFT_00138	Predicted transcriptional regulator	21.6	21.0	24.6	34.7	30.7	33.6	1.48	4.0E-02
B035DRAFT_00139	Antirepressor regulating drug resistance, predicted signal transduction N-terminal membrane component	17.8	13.7	15.8	16.8	17.5	24.8	1.24	4.2E-01
B035DRAFT_00140	hypothetical protein	13.7	10.8	9.5	10.2	9.3	14.2	0.99	9.7E-01
B035DRAFT_00141	hypothetical protein	21.4	23.1	17.9	15.8	15.4	23.0	0.86	5.7E-01
B035DRAFT_00142	hypothetical protein	25.6	32.7	15.6	25.6	19.7	30.2	1.05	9.2E-01
B035DRAFT_00143	hypothetical protein	74.1	77.0	75.3	94.0	103.6	88.3	1.26	6.8E-02
B035DRAFT_00144	Uncharacterized conserved protein	182.5	180.6	160.6	162.8	190.7	232.8	1.11	6.1E-01
B035DRAFT_00145	leucyl-tRNA synthetase, eubacterial and mitochondrial family(EC:6.1.1.4)	241.3	218.3	210.0	209.3	251.2	239.7	1.04	7.3E-01
B035DRAFT_00146	hypothetical protein	33.8	29.3	34.4	31.2	32.9	44.6	1.10	6.6E-01
B035DRAFT_00147	Uncharacterized protein related to the periplasmic component of the Tol biopolymer transport system(EC:3.4.21) (PL22)	41.7	39.7	41.9	45.8	54.6	52.4	1.24	1.1E-01
B035DRAFT_00148	Arylsulfatase A and related enzymes	127.8	129.4	121.6	128.6	150.6	155.0	1.14	2.6E-01
B035DRAFT_00149	ATPase components of ABC transporters with duplicated ATPase domains	29.5	25.6	28.1	23.7	35.7	27.9	1.04	8.9E-01
B035DRAFT_00150	hypothetical protein	94.3	99.7	104.0	129.8	128.8	158.7	1.39	7.7E-02
B035DRAFT_00151	Outer membrane receptor for ferrienterochelin and colicins	117.9	129.9	135.7	134.0	145.6	178.9	1.19	3.3E-01
B035DRAFT_00152	hypothetical protein	34.4	47.3	48.0	43.5	32.3	52.3	0.98	9.6E-01
B035DRAFT_00153	hypothetical protein	51.0	65.9	57.8	59.3	61.4	79.6	1.14	5.3E-01
B035DRAFT_00154	succinate CoA transferases	149.3	167.6	161.4	168.2	179.3	218.0	1.18	3.2E-01
B035DRAFT_00155	hypothetical protein	69.8	94.0	69.7	104.4	134.8	177.1	1.76	1.5E-01
B035DRAFT_00156	hypothetical protein	24.6	32.1	32.4	29.1	32.5	42.8	1.17	5.6E-01
B035DRAFT_00157	tRNA-N(6)-(isopentenyl)adenosine-37 thiotransferase enzyme MiaB	336.4	302.1	282.8	258.1	321.7	291.6	0.94	7.0E-01
B035DRAFT_00158	FKBP-type peptidyl-prolyl cis-trans isomerases 1(EC:5.2.1.8)	205.9	203.7	214.8	197.7	218.6	231.0	1.04	7.0E-01
B035DRAFT_00159	Putative stress-responsive transcriptional regulator	285.1	269.3	288.8	330.9	310.1	315.5	1.13	8.2E-02
B035DRAFT_00160	Methyltransferase domain.	410.0	340.6	386.8	357.4	364.6	235.2	0.83	5.0E-01
B035DRAFT_00161	Cell division protein	263.7	265.0	256.1	251.8	279.3	294.0	1.05	5.7E-01
B035DRAFT_00162	Protein of unknown function (DUF3098).	215.8	219.0	186.2	179.3	244.7	269.6	1.10	6.9E-01
B035DRAFT_00163	Uncharacterized bacitracin resistance protein(EC:3.6.1.27)	332.2	316.5	304.2	293.5	357.5	332.3	1.03	8.1E-01
B035DRAFT_00164	tRNA pseudouridine 55 synthase(EC:5.4.99.25)	378.8	341.8	340.5	332.2	379.7	280.3	0.93	6.7E-01
B035DRAFT_00165	S-adenosylmethionine:tRNA ribosyltransferase-isomerase(EC:5.)	446.0	437.0	427.8	454.7	477.7	469.1	1.07	1.2E-01
B035DRAFT_00166	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase(EC:2.7.6.3)	165.2	187.4	181.8	165.0	177.1	211.1	1.03	8.5E-01
B035DRAFT_00167	Uncharacterized protein conserved in bacteria	81.9	90.0	99.6	95.5	95.4	98.3	1.07	5.2E-01
B035DRAFT_00168	Metal-dependent hydrolase	77.6	75.1	82.1	79.7	92.2	96.4	1.14	2.9E-01
B035DRAFT_00169	drug resistance transporter, EmrB/QacA subfamily	161.8	149.8	177.1	141.1	96.0	78.8	0.63	2.0E-01
B035DRAFT_00171	S-adenosylmethionine synthetase(EC:2.5.1.6)	878.7	869.0	870.7	963.4	909.3	725.0	0.98	9.3E-01
B035DRAFT_00172	TIGR00730 family protein	326.9	327.9	310.1	261.9	304.4	215.9	0.80	2.7E-01

B035DRAFT_00173	hypothetical protein	281.5	302.9	299.4	241.0	272.5	271.0	0.89	2.0E-01
B035DRAFT_00174	Uroporphyrinogen-III synthase(EC:4.2.1.75)	1095.3	1255.9	1202.4	903.8	838.5	1034.1	0.78	1.3E-01
B035DRAFT_00175	ribonuclease P protein component, eubacterial(EC:3.1.26.5)	431.4	408.8	394.2	407.2	427.6	295.6	0.90	6.4E-01
B035DRAFT_00176	conserved hypothetical protein YidD	253.4	250.3	287.0	265.9	289.7	291.1	1.07	4.7E-01
B035DRAFT_00177	Mg-dependent DNase(EC:3.1.21.)	225.2	201.7	250.3	224.7	238.7	128.4	0.85	6.6E-01
B035DRAFT_00178	tyrosyl-tRNA synthetase(EC:6.1.1.1)	624.0	656.1	657.5	558.4	640.0	517.3	0.88	3.1E-01
B035DRAFT_00179	Periplasmic protease (PL22)	54.6	53.4	55.3	45.4	54.7	44.4	0.88	3.2E-01
B035DRAFT_00180	(tRNA)	105.0	130.0	100.0	93.7	97.3	62.2	0.75	3.4E-01
B035DRAFT_00181	hypothetical protein	388.1	386.2	380.7	408.4	374.8	303.8	0.93	6.7E-01
B035DRAFT_00182	hypothetical protein	28.5	38.6	32.6	30.0	34.7	37.6	1.03	8.9E-01
B035DRAFT_00183	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	11.7	12.7	15.4	10.6	9.4	9.3	0.74	1.5E-01
B035DRAFT_00184	hypothetical protein	10.6	10.8	12.5	6.9	7.2	7.4	0.64	2.4E-02
B035DRAFT_00185	His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	51.9	54.7	53.2	56.3	54.8	46.8	0.99	9.0E-01
B035DRAFT_00186	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	67.1	61.5	60.2	45.9	58.1	32.0	0.70	3.0E-01
B035DRAFT_00187	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	87.9	89.6	73.7	74.2	78.8	82.3	0.94	6.2E-01
B035DRAFT_00188	DNA mismatch repair protein MutS	140.4	131.4	128.4	119.3	132.2	91.6	0.85	4.2E-01
B035DRAFT_00189	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	96.2	87.3	89.6	80.3	96.3	70.8	0.90	5.3E-01
B035DRAFT_00190	hypothetical protein	62.8	70.0	63.8	50.3	57.8	82.0	0.95	8.5E-01
B035DRAFT_00191	hypothetical protein	206.5	205.9	197.7	321.5	344.6	233.1	1.45	1.6E-01
B035DRAFT_00192	Protein of unknown function (DUF1703)./Predicted AAA-ATPase.	159.6	158.9	164.4	183.6	181.4	190.1	1.15	2.3E-02
B035DRAFT_00193	Chloramphenicol O-acetyltransferase(EC:2.3.1.28)	55.5	52.3	60.1	58.2	64.3	64.7	1.12	2.9E-01
B035DRAFT_00194	prolipoprotein diacylglyceryl transferase	64.1	56.7	59.6	62.5	70.1	68.2	1.11	2.7E-01
B035DRAFT_00195	2-dehydropantoate 2-reductase(EC:1.1.1.169)	78.1	59.1	69.2	64.1	71.7	61.8	0.96	8.3E-01
B035DRAFT_00196	GTP-binding protein YchF	200.0	200.3	173.0	176.7	189.7	132.7	0.86	5.0E-01
B035DRAFT_00197	hypothetical protein	90.4	94.4	106.8	131.9	112.0	141.2	1.32	1.5E-01
B035DRAFT_00198	DNA polymerase I(EC:2.7.7.7)	58.4	58.3	53.4	80.9	98.3	95.0	1.61	3.0E-02
B035DRAFT_00199	Geranylgeranyl pyrophosphate synthase(EC:2.5.1.90)	265.4	300.9	278.3	259.4	246.1	250.0	0.90	1.8E-01
B035DRAFT_00200	deoxyribose-phosphate aldolase(EC:4.1.2.4)	298.6	303.7	292.2	289.4	294.6	345.7	1.04	7.4E-01
B035DRAFT_00201	Predicted pyrophosphatase	86.8	88.1	93.5	98.6	95.4	89.4	1.06	4.2E-01
B035DRAFT_00202	D-tyrosyl-tRNA(Tyr) deacylase(EC:3.1.)	67.5	65.0	62.2	71.1	84.2	81.7	1.21	1.3E-01
B035DRAFT_00203	excinuclease ABC, C subunit	23.5	29.2	27.8	25.4	26.9	28.0	1.00	9.9E-01
B035DRAFT_00204	adenine phosphoribosyltransferase(EC:2.4.2.7)	166.0	158.2	136.3	161.9	175.9	157.9	1.08	5.3E-01
B035DRAFT_00205	glucose-inhibited division protein A	115.1	101.0	101.8	114.0	118.0	97.5	1.04	8.0E-01
B035DRAFT_00206	metalloprotein, YbeY/UPF0054 family	57.9	74.9	64.6	55.9	54.0	49.3	0.81	2.1E-01
B035DRAFT_00207	Uncharacterized membrane protein, required for spore maturation in B.subtilis.	41.1	48.1	54.2	44.9	43.8	49.7	0.97	8.6E-01
B035DRAFT_00208	hypothetical protein	24.7	29.8	21.8	17.1	29.4	28.7	0.96	9.3E-01
B035DRAFT_00209	hypothetical protein	144.5	141.3	133.8	124.9	111.8	125.6	0.86	1.4E-01
B035DRAFT_00210	Uncharacterized protein conserved in bacteria	128.3	106.3	107.9	115.2	110.3	101.0	0.96	7.3E-01
B035DRAFT_00211	Bacterial regulatory proteins, luxR family	21.3	19.5	21.9	25.6	23.5	20.9	1.11	3.9E-01
B035DRAFT_00212	hypothetical protein	7.6	7.4	9.4	9.7	7.6	8.7	1.07	7.3E-01
B035DRAFT_00213	Site-specific recombinase XerD	239.4	177.3	206.7	186.7	156.4	188.6	0.86	4.2E-01
B035DRAFT_00214	Pyruvate kinase	28.1	26.9	26.0	21.4	17.2	26.3	0.79	3.2E-01
B035DRAFT_00215	Predicted ATPase	8.6	8.6	8.1	5.2	4.7	7.2	0.66	1.5E-01
B035DRAFT_00216	hypothetical protein	75.0	74.0	70.5	36.0	46.2	53.6	0.61	8.6E-02
B035DRAFT_00217	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	12.7	14.8	15.4	8.4	7.0	14.6	0.67	3.5E-01

B035DRAFT_00218	Protein of unknown function (DUF1703).	69.2	73.2	53.3	69.0	80.5	66.1	1.11	6.2E-01
B035DRAFT_00219	Predicted AAA-ATPase.	49.7	47.9	46.4	51.3	53.0	61.5	1.15	2.4E-01
B035DRAFT_00220	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	20.0	28.8	29.3	24.8	18.6	19.8	0.82	4.6E-01
B035DRAFT_00221	hypothetical protein	60.2	66.0	61.0	41.6	48.7	54.7	0.77	1.6E-01
B035DRAFT_00222	hypothetical protein	0.0	9.1	0.0	1.6	1.4	1.4	0.16	
B035DRAFT_00223	K+-dependent Na+/Ca+ exchanger related-protein	46.0	47.9	46.7	37.1	50.4	39.4	0.89	5.1E-01
B035DRAFT_00224	hypothetical protein	518.7	556.3	512.2	471.2	495.2	553.6	0.96	6.5E-01
B035DRAFT_00225	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit(EC:5.99.1.)	311.0	305.5	291.5	255.1	311.6	250.6	0.90	4.1E-01
B035DRAFT_00226	pantetheine-phosphate adenylyltransferase, bacterial(EC:2.7.7.3)	373.0	358.7	330.0	291.6	320.5	236.2	0.79	2.3E-01
B035DRAFT_00227	C-terminal peptidase (prc)(EC:3.4.21.102)	231.9	199.9	209.0	162.2	177.7	118.5	0.71	2.0E-01
B035DRAFT_00228	Membrane-associated phospholipid phosphatase	88.4	90.4	82.1	80.0	71.6	66.0	0.83	1.7E-01
B035DRAFT_00229	succinate dehydrogenase (or fumarate reductase) cytochrome b subunit, b558 family	505.8	503.6	508.1	378.2	460.5	467.9	0.86	2.5E-01
B035DRAFT_00230	succinate dehydrogenase or fumarate reductase, flavoprotein subunit, Bacillus subtilis subgroup(EC:1.3.99.1)	1017.0	950.9	1004.7	928.4	1127.9	1037.4	1.04	7.4E-01
B035DRAFT_00231	Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit(EC:1.3.99.1)	1251.5	1363.4	1434.8	1350.2	1550.3	1659.5	1.12	3.9E-01
B035DRAFT_00232	AraC-type DNA-binding domain-containing proteins	23.5	20.5	20.2	21.4	26.8	32.2	1.24	3.7E-01
B035DRAFT_00233	hypothetical protein	9.4	7.4	5.9	5.8	8.2	10.5	1.07	8.8E-01
B035DRAFT_00234	hypothetical protein	2.5	2.8	2.5	2.0	3.5	1.2	0.79	6.7E-01
B035DRAFT_00235	Protein of unknown function (DUF3575).	3.5	3.4	3.9	4.0	4.4	3.9	1.13	2.6E-01
B035DRAFT_00236	TonB-linked outer membrane protein, SusC/RagA family	70.8	75.7	76.4	55.3	61.2	68.3	0.83	1.7E-01
B035DRAFT_00237	SusD family	50.2	55.5	58.3	30.3	33.8	39.2	0.63	5.5E-02
B035DRAFT_00238	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	92.2	92.3	84.2	67.3	90.7	76.4	0.87	4.0E-01
B035DRAFT_00239	DNA protecting protein DprA	101.3	105.4	107.9	95.0	105.9	93.4	0.93	4.0E-01
B035DRAFT_00240	Predicted thioesterase(EC:3.1.2.)	71.9	83.6	83.0	103.8	99.5	92.3	1.24	1.2E-01
B035DRAFT_00241	tRNA-dihydrouridine synthase	60.3	59.2	68.3	81.9	77.5	64.0	1.19	3.1E-01
B035DRAFT_00242	lactaldehyde reductase(EC:1.1.1.77)	111.3	125.1	119.1	137.8	144.4	147.9	1.21	6.8E-02
B035DRAFT_00243	Protein of unknown function (DUF2851).	32.8	40.5	32.1	43.1	43.2	49.7	1.29	1.7E-01
B035DRAFT_00244	dihydrodipicolinate reductase(EC:1.3.1.26)	180.1	156.1	175.9	219.9	238.0	158.6	1.19	4.7E-01
B035DRAFT_00245	hypothetical protein(EC:3.4.21.89)	247.0	228.5	259.4	259.6	272.9	238.8	1.05	6.2E-01
B035DRAFT_00246	signal peptidase I, bacterial type(EC:3.4.21.89)	228.2	239.3	247.4	268.2	245.3	214.6	1.01	9.2E-01
B035DRAFT_00247	WbqC-like protein family	131.6	132.4	143.4	114.5	132.7	140.8	0.95	6.7E-01
B035DRAFT_00248	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	161.4	144.2	143.4	118.3	140.9	93.5	0.78	2.9E-01
B035DRAFT_00249	mannonate dehydratase(EC:4.2.1.8)	148.3	123.1	122.4	108.0	118.4	80.5	0.77	3.1E-01
B035DRAFT_00250	hypothetical protein	92.0	86.2	101.9	117.1	98.4	69.9	1.00	1.0E+00
B035DRAFT_00251	Trehalose and maltose hydrolases (possible phosphorylases) (GH95)	63.0	59.7	56.2	68.8	77.2	61.9	1.16	2.9E-01
B035DRAFT_00252	Predicted Zn-dependent peptidases	19.1	28.6	23.2	28.3	21.9	28.8	1.12	6.7E-01
B035DRAFT_00253	TIGR00730 family protein	151.2	116.2	113.6	122.2	142.2	78.2	0.88	7.3E-01
B035DRAFT_00254	Predicted sugar phosphate isomerase involved in capsule formation(EC:5.3.1.13)	344.0	326.0	348.7	317.3	290.5	273.7	0.86	1.6E-01
B035DRAFT_00255	Chitinase(EC:3.2.1.14) (GH18)	520.6	445.5	560.4	402.9	353.5	265.2	0.66	1.7E-01
B035DRAFT_00256	Aminopeptidase N(EC:3.4.11.2)	120.5	107.5	115.2	89.9	95.8	94.9	0.82	6.0E-02
B035DRAFT_00257	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase(EC:2.8.1.)	52.7	59.7	50.7	61.0	73.4	75.1	1.28	1.6E-01
B035DRAFT_00258	hypothetical protein	81.2	79.2	67.2	108.2	116.3	107.9	1.47	4.4E-02
B035DRAFT_00259	AraC-type DNA-binding domain-containing proteins	50.3	69.1	62.5	21.9	25.2	37.1	0.45	8.3E-02
B035DRAFT_00260	hypothetical protein	1186.7	1203.7	1119.7	128.6	198.1	246.0	0.16	1.6E-02
B035DRAFT_00261	hypothetical protein	17.3	15.5	15.3	16.8	19.8	18.7	1.15	2.5E-01

B035DRAFT_00262	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_00263	hypothetical protein	17.6	19.2	16.4	19.4	18.9	21.9	1.13	3.1E-01
B035DRAFT_00264	hypothetical protein	5.0	7.6	4.1	4.4	5.3	8.3	1.07	8.9E-01
B035DRAFT_00265	Predicted nucleotidyltransferases	14.1	16.4	21.9	38.5	47.0	49.1	2.60	3.9E-02
B035DRAFT_00266	hypothetical protein	2.0	6.5	3.1	3.8	1.4	3.3	0.74	7.3E-01
B035DRAFT_00267	hypothetical protein	5.3	3.0	2.1	3.6	2.4	4.4	1.06	9.3E-01
B035DRAFT_00268	hypothetical protein	11.7	12.3	8.6	18.5	14.9	29.9	1.88	1.9E-01
B035DRAFT_00269	Aspartyl aminopeptidase(EC:3.4.11.21)	16.5	13.4	14.0	10.1	7.1	12.0	0.65	2.1E-01
B035DRAFT_00270	hypothetical protein	49.3	68.2	51.4	49.4	47.9	59.7	0.94	7.7E-01
B035DRAFT_00271	hypothetical protein	94.9	99.0	83.8	192.0	207.5	248.7	2.33	1.7E-02
B035DRAFT_00272	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	509.3	494.5	492.2	435.4	568.1	607.3	1.07	7.4E-01
B035DRAFT_00273	hypothetical protein	50.6	55.5	51.8	53.4	57.1	59.8	1.08	3.4E-01
B035DRAFT_00274	Peroxiredoxin	53.9	50.1	51.0	47.0	47.5	38.1	0.85	2.7E-01
B035DRAFT_00275	Arabinose efflux permease	70.5	58.4	70.6	47.6	44.0	45.3	0.69	5.1E-02
B035DRAFT_00276	Protein of unknown function (DUF2721).	118.7	104.7	113.3	78.9	64.8	84.6	0.67	7.8E-02
B035DRAFT_00277	hypothetical protein	349.1	330.0	367.5	249.4	212.9	263.9	0.69	6.1E-02
B035DRAFT_00278	Lactate dehydrogenase and related dehydrogenases(EC:1.1.1.28)	711.9	636.9	693.0	637.3	510.4	499.8	0.80	2.0E-01
B035DRAFT_00279	MAF protein	131.2	133.9	136.0	101.1	133.4	143.5	0.93	7.2E-01
B035DRAFT_00280	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase, YrbI family(EC:3.1.3.45)	127.9	122.2	110.9	102.4	115.1	111.8	0.91	3.7E-01
B035DRAFT_00281	NADP oxidoreductase coenzyme F420-dependent./Domain of unknown function (DUF2520).	101.7	92.6	99.1	82.0	100.3	87.9	0.92	4.7E-01
B035DRAFT_00282	hypothetical protein	99.1	112.1	92.6	91.7	125.7	131.7	1.14	5.7E-01
B035DRAFT_00283	Nitroreductase	94.1	88.1	74.3	87.4	104.4	67.8	1.00	1.0E+00
B035DRAFT_00284	hypothetical protein	46.1	42.6	41.1	46.9	45.1	58.4	1.15	3.8E-01
B035DRAFT_00285	methylmalonyl-CoA epimerase(EC:4.4.1.5)	293.8	337.7	314.8	263.3	335.1	334.9	0.98	9.2E-01
B035DRAFT_00286	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	603.2	604.8	633.2	522.4	614.3	638.8	0.96	7.4E-01
B035DRAFT_00287	Oxaloacetate decarboxylase, gamma chain.	511.7	497.7	499.7	398.3	534.8	568.9	0.98	9.4E-01
B035DRAFT_00288	Acetyl/propionyl-CoA carboxylase, alpha subunit	537.3	585.0	550.5	455.7	630.9	726.0	1.06	8.2E-01
B035DRAFT_00289	sodium ion-translocating decarboxylase, beta subunit(EC:4.1.1.3)	530.5	549.9	594.0	484.3	588.6	685.8	1.04	8.5E-01
B035DRAFT_00290	Cyclo-malto-dextrinase C-terminal domain.	293.8	304.4	244.4	492.8	482.8	453.2	1.70	2.8E-02
B035DRAFT_00291	Short-chain alcohol dehydrogenase of unknown specificity	127.8	128.8	129.7	115.5	127.9	88.2	0.85	4.2E-01
B035DRAFT_00292	Predicted esterase (CE1)	56.1	53.7	51.8	63.4	60.9	38.3	0.98	9.6E-01
B035DRAFT_00293	Fe2+/Zn2+ uptake regulation proteins	64.1	57.3	66.6	56.4	54.9	68.2	0.95	7.5E-01
B035DRAFT_00294	MazG family protein(EC:3.6.1.19)	151.1	126.4	117.7	89.1	130.5	66.6	0.70	3.6E-01
B035DRAFT_00295	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	58.5	61.6	56.6	47.1	57.3	48.8	0.86	2.5E-01
B035DRAFT_00296	Protein of unknown function (DUF1349).	14.9	13.6	11.7	11.8	14.9	13.9	1.01	9.5E-01
B035DRAFT_00297	valyl-tRNA synthetase(EC:6.1.1.9)	422.5	400.9	374.5	387.2	450.8	346.9	0.98	9.3E-01
B035DRAFT_00298	Predicted Zn-dependent peptidases	70.2	71.0	76.3	75.8	89.5	119.2	1.29	3.2E-01
B035DRAFT_00299	hypothetical protein	57.6	60.1	47.7	118.6	149.7	166.0	2.61	2.4E-02
B035DRAFT_00300	RNA polymerase sigma factor, sigma-70 family	21.5	27.9	25.5	43.4	41.8	42.5	1.72	3.1E-02
B035DRAFT_00301	hypothetical protein	59.0	76.5	65.8	83.0	80.0	104.8	1.33	2.2E-01
B035DRAFT_00302	hypothetical protein	470.4	565.1	546.8	617.6	667.3	769.3	1.30	1.6E-01
B035DRAFT_00303	hypothetical protein	103.0	105.4	104.7	152.2	172.6	151.4	1.52	1.6E-02
B035DRAFT_00304	preprotein translocase, SecA subunit	863.3	817.6	846.6	871.8	868.1	794.2	1.00	9.8E-01
B035DRAFT_00305	Arylsulfatase A and related enzymes	226.4	262.3	261.7	273.3	268.4	291.5	1.11	3.1E-01
B035DRAFT_00306	hypothetical protein	78.3	86.3	79.1	72.5	81.1	56.2	0.85	4.4E-01
B035DRAFT_00307	pantothenate kinase, type III(EC:2.7.1.33)	144.1	171.0	150.0	178.3	151.7	159.8	1.05	6.9E-01
B035DRAFT_00308	hypothetical protein	367.3	402.6	363.1	418.0	398.6	456.1	1.12	2.5E-01

B035DRAFT_00309	Tetratricopeptide repeat.	820.6	933.0	819.3	805.6	897.8	1098.1	1.08	6.7E-01
B035DRAFT_00310	Protein of unknown function (DUF1239).	184.3	199.2	171.8	162.2	191.2	218.9	1.02	9.0E-01
B035DRAFT_00311	Hemolysins and related proteins containing CBS domains	103.8	128.9	108.2	107.4	117.8	142.8	1.08	7.1E-01
B035DRAFT_00312	hypothetical protein(EC:5.2.1.8)	991.9	1079.0	989.0	841.6	909.1	1090.3	0.92	5.9E-01
B035DRAFT_00313	ketol-acid reductoisomerase(EC:1.1.1.86)	564.7	632.3	578.1	458.0	497.8	493.8	0.82	7.3E-02
B035DRAFT_00314	Acyl-ACP thioesterase	199.5	214.6	178.9	173.3	194.3	178.2	0.92	4.7E-01
B035DRAFT_00315	acetolactate synthase, small subunit(EC:2.2.1.6)	252.8	258.3	231.8	221.7	234.6	254.5	0.96	6.4E-01
B035DRAFT_00316	acetolactate synthase, large subunit, biosynthetic type(EC:2.2.1.6)	231.5	237.8	219.6	196.6	202.5	151.4	0.79	2.3E-01
B035DRAFT_00317	dihydroxy-acid dehydratase(EC:4.2.1.9)	234.1	239.9	264.2	147.7	156.8	103.8	0.55	7.6E-02
B035DRAFT_00318	hypothetical protein	1.0	5.5	1.2	1.0	2.6	1.7	0.90	9.3E-01
B035DRAFT_00319	hypothetical protein	2.8	3.3	2.3	2.0	0.9	2.6	0.59	4.1E-01
B035DRAFT_00320	FKBP-type peptidyl-prolyl cis-trans isomerases 2(EC:5.2.1.8)	1589.4	1566.4	1482.2	2267.1	1985.8	1734.3	1.28	1.5E-01
B035DRAFT_00321	hypothetical protein	28.8	19.5	24.8	32.8	31.5	35.9	1.39	1.9E-01
B035DRAFT_00322	hypothetical protein	30.4	47.8	37.0	33.9	51.9	66.6	1.30	5.4E-01
B035DRAFT_00323	hypothetical protein	111.9	133.4	117.6	138.6	137.4	186.7	1.27	2.9E-01
B035DRAFT_00324	hypothetical protein	36.1	37.0	35.7	30.9	42.2	26.1	0.89	6.6E-01
B035DRAFT_00325	hypothetical protein	24.1	24.5	13.5	19.1	21.0	23.8	1.06	8.9E-01
B035DRAFT_00326	hypothetical protein	19.8	28.3	31.5	11.2	11.0	11.1	0.43	4.3E-02
B035DRAFT_00327	TonB-linked outer membrane protein, SusC/RagA family	36.3	31.5	31.1	12.9	18.4	17.1	0.48	4.2E-02
B035DRAFT_00328	SusD family	41.3	37.1	39.2	14.1	20.3	22.5	0.47	6.1E-02
B035DRAFT_00329	Glycoside hydrolase (GH123)	22.4	26.0	28.0	20.8	25.9	20.1	0.87	4.7E-01
B035DRAFT_00330	Galactose mutarotase and related enzymes	116.8	111.7	124.9	128.9	135.4	87.9	0.98	9.4E-01
B035DRAFT_00331	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	15.3	13.5	16.8	15.9	17.5	21.1	1.19	3.8E-01
B035DRAFT_00332	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	10.2	8.6	8.0	8.3	9.4	10.9	1.06	7.6E-01
B035DRAFT_00333	Protein of unknown function (Porph_ging).	4.1	3.1	5.4	3.2	4.2	3.3	0.87	6.7E-01
B035DRAFT_00334	hypothetical protein	22.0	14.9	21.4	12.2	13.2	8.0	0.57	1.8E-01
B035DRAFT_00335	Putative regulator of cell autolysis	39.5	34.7	42.3	27.4	27.3	35.6	0.77	2.2E-01
B035DRAFT_00336	Response regulator of the LytR/AlgR family	33.7	37.1	37.2	28.2	35.4	41.9	0.97	8.8E-01
B035DRAFT_00337	Arylsulfatase A and related enzymes	113.0	112.8	123.6	109.0	126.2	128.4	1.04	7.3E-01
B035DRAFT_00338	hypothetical protein	121.1	119.1	121.5	107.8	122.6	117.0	0.96	5.4E-01
B035DRAFT_00339	protein RecA	1108.4	1106.1	1050.2	1148.4	1218.6	1138.9	1.07	2.1E-01
B035DRAFT_00340	Peroxiredoxin(EC:1.11.1.15)	611.8	579.4	509.1	597.1	694.7	666.6	1.15	3.0E-01
B035DRAFT_00341	Saccharopine dehydrogenase and related proteins(EC:1.5.1.7)	549.1	549.6	542.5	578.3	668.4	645.7	1.15	1.5E-01
B035DRAFT_00342	hypothetical protein	166.8	174.1	164.1	166.3	157.6	137.0	0.91	4.0E-01
B035DRAFT_00343	Heat shock protein	1237.2	1228.7	1224.0	1299.2	1042.8	1138.1	0.94	5.9E-01
B035DRAFT_00344	hypothetical protein	154.1	161.9	147.9	135.7	126.3	142.7	0.87	1.6E-01
B035DRAFT_00345	hypothetical protein	105.1	117.2	111.5	92.9	81.5	120.7	0.87	5.3E-01
B035DRAFT_00346	chaperone protein DnaK	2083.6	1775.8	1928.5	1801.4	1738.7	1896.6	0.94	5.2E-01
B035DRAFT_00347	DNA binding domain, excisionase family	55.4	55.7	34.8	45.3	56.0	60.2	1.12	7.2E-01
B035DRAFT_00348	Site-specific recombinase XerD	44.9	44.0	37.2	37.7	51.8	52.0	1.11	6.2E-01
B035DRAFT_00349	Predicted transcriptional regulator	52.0	53.9	51.2	53.3	60.7	72.6	1.18	3.3E-01
B035DRAFT_00350	hypothetical protein	75.0	74.0	72.0	69.5	95.8	113.5	1.24	4.2E-01
B035DRAFT_00351	hypothetical protein	43.3	38.4	40.0	35.8	66.9	77.0	1.41	4.3E-01
B035DRAFT_00352	hypothetical protein	6.1	3.3	4.0	4.4	6.4	7.3	1.37	4.6E-01
B035DRAFT_00353	hypothetical protein	3.7	4.7	5.2	5.0	5.3	7.0	1.28	3.7E-01
B035DRAFT_00354	hypothetical protein	6.9	4.8	2.6	5.0	4.0	5.2	1.07	9.1E-01
B035DRAFT_00355	Plasmid recombination enzyme.	3.0	3.7	3.0	3.2	3.6	2.2	0.92	7.9E-01
B035DRAFT_00356	Site-specific recombinase XerD	6.0	4.4	7.1	6.5	5.6	6.7	1.10	7.4E-01
B035DRAFT_00357	Restriction endonuclease S subunits	69.8	72.4	64.6	64.7	83.9	99.5	1.18	4.7E-01
B035DRAFT_00358	Restriction endonuclease S subunits	117.7	144.5	129.9	154.4	146.4	173.4	1.21	2.2E-01

B035DRAFT_00359	Restriction endonuclease S subunits(EC:3.1.21.3)	59.9	59.2	54.3	57.0	70.2	83.5	1.20	3.9E-01
B035DRAFT_00360	AIPR protein.	87.2	102.1	91.9	82.1	100.8	132.0	1.10	7.2E-01
B035DRAFT_00361	Prophage maintenance system killer protein	62.7	79.1	66.4	66.4	71.4	91.0	1.09	6.8E-01
B035DRAFT_00362	hypothetical protein	94.5	107.7	93.4	96.5	112.6	144.5	1.18	4.6E-01
B035DRAFT_00363	Type I restriction-modification system methyltransferase subunit(EC:2.1.1.72)	99.6	95.3	90.9	95.2	116.9	137.1	1.21	3.5E-01
B035DRAFT_00364	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases(EC:3.1.21.3)	105.4	111.1	106.2	105.8	107.7	110.0	1.00	9.5E-01
B035DRAFT_00365	Predicted transcriptional regulators	82.4	92.0	79.4	93.6	83.6	82.3	1.02	8.5E-01
B035DRAFT_00366	hypothetical protein	3.3	4.6	5.1	2.5	3.8	4.7	0.83	6.6E-01
B035DRAFT_00367	hypothetical protein	2.3	2.1	2.2	1.1	1.2	2.2	0.66	3.1E-01
B035DRAFT_00368	hypothetical protein	1.0	5.6	4.7	6.1	4.4	4.4	1.66	6.2E-01
B035DRAFT_00369	hypothetical protein	4.0	6.2	6.4	4.9	6.0	4.2	0.92	8.2E-01
B035DRAFT_00370	pyruvate:ferredoxin (flavodoxin) oxidoreductase, homodimeric(EC:1.2.7.)	923.7	904.7	947.5	959.9	1123.3	1065.0	1.13	2.1E-01
B035DRAFT_00371	Predicted ATPase (AAA+ superfamily)	487.6	495.8	462.4	485.7	503.0	527.2	1.05	4.2E-01
B035DRAFT_00372	hypothetical protein	98.1	104.0	109.7	123.5	106.0	77.0	0.97	9.0E-01
B035DRAFT_00373	Predicted membrane protein	55.8	50.8	61.2	51.2	57.0	37.4	0.86	5.3E-01
B035DRAFT_00374	putative DNA modification/repair radical SAM protein	47.2	45.2	52.3	89.1	80.5	59.6	1.57	1.3E-01
B035DRAFT_00375	probable DNA metabolism protein	71.7	72.6	80.0	78.5	88.3	81.4	1.11	2.9E-01
B035DRAFT_00376	pseudouridylate synthase I(EC:5.4.99.12)	125.0	122.0	122.5	125.7	133.9	98.9	0.96	8.3E-01
B035DRAFT_00377	hypothetical protein	136.1	152.7	152.6	135.1	139.7	113.3	0.88	3.5E-01
B035DRAFT_00378	Phosphate starvation-inducible protein PhoH, predicted ATPase	143.9	141.2	124.2	124.8	156.7	125.5	0.99	9.6E-01
B035DRAFT_00379	Phosphoribosylaminoimidazolesuccinocarboxamide (SAICAR) synthase(EC:6.3.2.6)	366.1	348.3	317.6	291.1	357.0	359.2	0.97	8.6E-01
B035DRAFT_00380	ubiquinone/menaquinone biosynthesis methyltransferases(EC:2.1.1.- ,EC:2.1.1.163)	107.1	113.4	117.3	103.9	128.3	133.8	1.08	6.2E-01
B035DRAFT_00381	Shikimate 5-dehydrogenase(EC:1.1.1.25)	96.3	90.0	91.4	92.5	110.9	116.4	1.15	3.2E-01
B035DRAFT_00382	Hydrolases of the alpha/beta superfamily	122.6	110.1	127.7	110.6	112.5	83.5	0.84	3.9E-01
B035DRAFT_00383	chorismate synthase(EC:4.2.3.5)	263.7	261.6	242.0	341.8	390.3	358.2	1.42	2.7E-02
B035DRAFT_00384	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases	108.6	114.8	103.3	100.5	136.2	134.1	1.13	5.2E-01
B035DRAFT_00385	Nitroreductase	86.1	95.7	90.9	89.2	96.9	105.5	1.07	5.2E-01
B035DRAFT_00386	xanthine phosphoribosyltransferase(EC:2.4.2.22)	81.6	79.7	72.9	85.9	82.4	85.8	1.09	2.6E-01
B035DRAFT_00387	xanthine permease	99.3	115.7	112.3	104.1	115.2	123.3	1.05	7.2E-01
B035DRAFT_00388	Uncharacterized protein conserved in bacteria	68.5	71.0	70.2	74.5	81.4	61.2	1.03	8.7E-01
B035DRAFT_00389	hypothetical protein	35.3	46.9	32.2	55.3	66.1	73.1	1.71	1.0E-01
B035DRAFT_00390	N-acetylmuramoyl-L-alanine amidase(EC:3.5.1.28)	177.5	168.5	167.2	176.3	202.5	159.4	1.04	7.5E-01
B035DRAFT_00391	Peroxiredoxin	117.2	125.9	110.8	120.2	147.3	113.5	1.07	6.7E-01
B035DRAFT_00392	hypothetical protein	12.5	18.3	13.6	8.9	9.7	11.4	0.68	1.8E-01
B035DRAFT_00393	Lysyl-tRNA synthetase (class II)(EC:6.1.1.6)	521.3	544.1	539.8	517.6	542.8	589.1	1.03	7.3E-01
B035DRAFT_00394	Glycerol-3-phosphate dehydrogenase(EC:1.1.1.94)	388.7	429.2	423.9	386.0	413.7	490.8	1.03	8.2E-01
B035DRAFT_00395	Glucose-6-phosphate isomerase(EC:5.3.1.9)	543.4	592.2	578.5	500.5	557.7	613.6	0.97	8.2E-01
B035DRAFT_00396	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	182.5	203.6	195.2	173.5	188.3	214.1	0.99	9.3E-01
B035DRAFT_00397	Transcriptional regulator/sugar kinase	243.8	243.3	212.2	226.4	313.2	350.1	1.25	3.8E-01
B035DRAFT_00398	glucosamine-6-phosphate isomerase(EC:3.5.99.6)	1095.7	1076.5	1104.9	1178.1	1109.4	1202.0	1.06	2.2E-01
B035DRAFT_00399	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase(EC:3.5.99.6) (CE14)	1955.1	1891.2	2044.4	2062.7	1734.2	1812.9	0.95	6.2E-01
B035DRAFT_00400	Domain of unknown function (DUF303).(EC:3.1.1.53) (CE6)	28.7	24.7	25.0	23.8	21.3	25.0	0.89	3.7E-01
B035DRAFT_00401	Beta-galactosidase/beta-glucuronidase (GH2)	20.9	20.7	23.9	22.5	21.6	21.0	0.99	9.6E-01
B035DRAFT_00402	TIGR02757 family protein	31.1	36.4	32.5	36.4	34.8	41.4	1.12	3.7E-01

B035DRAFT_00403	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	32.3	49.0	43.1	39.5	38.8	45.6	1.01	9.8E-01
B035DRAFT_00404	Fe2+-dicitrate sensor, membrane component	83.6	88.0	92.1	119.8	110.2	127.0	1.35	4.3E-02
B035DRAFT_00405	TonB-linked outer membrane protein, SusC/RagA family	7.5	6.8	6.6	5.0	4.3	5.0	0.69	3.9E-02
B035DRAFT_00406	SusD family	5.4	6.7	6.4	3.5	4.4	4.4	0.66	8.6E-02
B035DRAFT_00407	NPCBM/NEW2 domain (CBM51)	9.1	7.7	6.7	8.7	8.9	7.3	1.07	7.6E-01
B035DRAFT_00408	Glycoside hydrolase 97 (EC:3.2.1.20)	24.1	23.9	20.4	21.1	23.8	21.6	0.97	8.2E-01
B035DRAFT_00409	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	54.7	49.3	49.0	41.9	55.3	39.8	0.89	5.4E-01
B035DRAFT_00410	DNA-binding protein, histone-like, putative	63.3	57.8	60.2	71.3	73.3	24.0	0.83	7.9E-01
B035DRAFT_00411	Acetyltransferase (isoleucine patch superfamily)	17.1	11.8	18.2	18.6	18.5	17.7	1.18	5.0E-01
B035DRAFT_00412	AraC-type DNA-binding domain-containing proteins	32.5	41.3	31.6	29.0	30.6	30.3	0.86	3.5E-01
B035DRAFT_00413	hypothetical protein	16.5	16.6	14.9	25.3	25.0	34.3	1.74	6.2E-02
B035DRAFT_00414	hypothetical protein	8.5	9.9	8.6	10.5	11.9	16.0	1.40	2.2E-01
B035DRAFT_00415	ABC-type multidrug transport system, ATPase component	20.4	27.6	23.9	22.8	27.9	30.3	1.13	5.9E-01
B035DRAFT_00416	N-acetylglucosamine-6-phosphate deacetylase(EC:3.5.1.25) (CE9)	328.4	323.2	309.6	258.0	313.4	259.4	0.86	2.5E-01
B035DRAFT_00417	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	316.2	280.8	306.1	500.6	534.8	507.0	1.71	5.9E-03
B035DRAFT_00418	alpha-1,2-mannosidase, putative (GH92)	221.0	193.9	198.5	308.6	360.9	370.6	1.69	2.6E-02
B035DRAFT_00419	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	167.4	156.2	162.1	226.7	271.9	248.3	1.53	2.5E-02
B035DRAFT_00420	cyclically-permuted mutatrotase family protein	118.1	112.7	118.1	172.1	201.5	176.1	1.57	2.0E-02
B035DRAFT_00421	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	233.7	218.0	225.2	323.7	414.7	448.9	1.74	5.3E-02
B035DRAFT_00422	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.25) (GH2)	128.9	123.7	124.3	182.0	238.0	191.7	1.61	4.7E-02
B035DRAFT_00423	Lysophospholipase L1 and related esterases(EC:3.1.1.53) (CE3)	38.2	35.8	36.2	102.7	119.9	129.0	3.18	2.7E-03
B035DRAFT_00424	Lysophospholipase L1 and related esterases (CE3)	31.7	35.4	36.7	91.6	126.0	137.2	3.37	1.7E-02
B035DRAFT_00425	N-acetyl-beta-hexosaminidase (GH20)	30.9	33.0	33.4	108.2	118.5	121.3	3.57	3.1E-04
B035DRAFT_00426	BNR/Asp-box repeat.(EC:3.2.1.18) (GH33)	117.8	109.8	122.0	395.5	496.2	465.6	3.87	1.9E-03
B035DRAFT_00427	SusD family	485.1	511.5	477.0	643.2	824.7	854.8	1.56	6.7E-02
B035DRAFT_00428	**TonB-linked outer membrane protein, SusC/RagA family**	**424.7**	**429.1**	**437.8**	**431.0**	**455.8**	**456.8**	**1.04**	**3.2E-01**
B035DRAFT_00429	(tRNA)	27.0	23.6	35.6	23.7	12.3	43.0	0.82	7.8E-01
B035DRAFT_00430	aspartate--ammonia ligase, AsnA-type(EC:6.3.1.1)	334.9	428.8	344.0	381.3	361.7	399.7	1.04	8.2E-01
B035DRAFT_00431	uracil-DNA glycosylase(EC:3.2.2.27)	110.1	125.3	119.4	133.8	121.0	137.1	1.10	3.3E-01
B035DRAFT_00432	hypothetical protein	286.9	309.6	291.4	327.5	313.8	324.0	1.09	1.5E-01
B035DRAFT_00433	Predicted HD superfamily hydrolase involved in NAD metabolism	75.8	84.1	85.4	96.7	88.4	112.4	1.21	2.3E-01
B035DRAFT_00434	Uncharacterized protein conserved in bacteria	37.1	47.0	40.7	55.0	50.9	58.7	1.32	1.3E-01
B035DRAFT_00435	Periplasmic protease	71.8	88.9	72.9	96.3	94.6	113.3	1.30	1.7E-01
B035DRAFT_00436	Uncharacterized lipoprotein NlpE involved in copper resistance.	703.8	720.4	662.2	684.9	481.2	537.6	0.81	3.0E-01
B035DRAFT_00437	hypothetical protein	1710.9	1636.7	1684.0	1733.5	1243.9	1309.6	0.84	3.8E-01
B035DRAFT_00438	hypothetical protein	2388.6	2503.9	2607.3	2579.5	2160.4	2675.3	0.99	9.2E-01
B035DRAFT_00439	Glycosyltransferases involved in cell wall biogenesis(EC:2.4.1.83) (GT2)	320.5	304.2	292.2	356.1	334.4	335.3	1.12	1.4E-01
B035DRAFT_00440	dihydroorotase, multifunctional complex type(EC:3.5.2.3)	292.5	291.5	298.9	333.6	335.8	321.8	1.12	2.6E-02
B035DRAFT_00441	Vitamin B12 dependent methionine synthase, activation domain.	195.8	212.7	215.7	230.3	230.8	246.4	1.13	1.4E-01
B035DRAFT_00442	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_00443	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_00444	SusD family	22.0	30.2	27.5	13.7	13.7	15.2	0.54	4.2E-02
B035DRAFT_00445	TonB-linked outer membrane protein, SusC/RagA family	9.0	10.0	9.7	5.2	5.0	6.0	0.56	1.9E-02
B035DRAFT_00446	Signal transduction histidine kinase	45.2	40.0	39.5	26.3	30.3	31.5	0.71	6.5E-02
B035DRAFT_00447	6-phosphofructokinase(EC:2.7.1.11)	103.9	114.2	114.9	131.4	130.4	119.7	1.15	1.6E-01
B035DRAFT_00448	GH3 auxin-responsive promoter.	228.4	228.2	211.8	207.2	240.7	208.4	0.98	8.5E-01
B035DRAFT_00449	hypothetical protein	370.8	355.5	360.1	507.2	522.8	473.0	1.38	1.4E-02
B035DRAFT_00450	Protein of unknown function (DUF3108).	175.8	172.2	163.3	199.5	219.8	148.2	1.10	6.8E-01
B035DRAFT_00451	hypothetical protein	52.2	49.0	52.6	62.5	72.9	76.3	1.37	6.5E-02
B035DRAFT_00452	hypothetical protein	10.6	4.1	8.6	7.4	11.2	3.2	0.89	9.1E-01
B035DRAFT_00453	N-acetyl-beta-hexosaminidase (GH20)	39.9	36.4	42.2	38.4	45.4	44.2	1.08	5.3E-01

B035DRAFT_00454	cysteinyl-tRNA synthetase(EC:6.1.1.16)	768.0	752.7	724.3	679.6	723.9	636.4	0.91	2.4E-01
B035DRAFT_00455	Uncharacterized conserved protein	254.2	213.1	209.7	297.3	286.4	200.2	1.14	5.9E-01
B035DRAFT_00456	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase(EC:2.8.1.)	37.9	38.8	40.6	40.9	46.7	42.9	1.11	2.3E-01
B035DRAFT_00457	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	135.7	136.2	138.7	117.6	136.9	125.1	0.92	3.4E-01
B035DRAFT_00458	Bacterial nucleoid DNA-binding protein	690.5	894.1	778.5	1006.4	852.0	957.7	1.20	3.0E-01
B035DRAFT_00459	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	215.0	221.9	204.3	215.6	252.1	213.3	1.06	5.9E-01
B035DRAFT_00460	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	314.4	263.6	266.0	286.8	331.9	289.0	1.08	5.8E-01
B035DRAFT_00461	Metal-dependent hydrolase	131.2	134.4	135.1	123.2	155.3	128.2	1.01	9.5E-01
B035DRAFT_00462	Zn-dependent oligopeptidases(EC:3.4.15.5)	184.9	156.4	162.1	160.3	206.8	143.7	1.01	9.8E-01
B035DRAFT_00463	protein-export membrane protein, SecD/SecF family	1183.8	1178.5	1138.5	858.2	1025.3	1048.5	0.83	1.8E-01
B035DRAFT_00464	Sugar kinases, ribokinase family(EC:2.7.1.45)	68.0	75.9	70.6	78.9	96.4	78.5	1.18	2.6E-01
B035DRAFT_00465	Nucleoside-diphosphate-sugar epimerases	686.5	703.5	673.1	761.6	907.7	905.0	1.24	1.1E-01
B035DRAFT_00466	2-amino-3-ketobutyrate coenzyme A ligase(EC:2.3.1.29)	688.0	707.5	729.2	768.0	941.5	923.2	1.23	1.5E-01
B035DRAFT_00467	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	28.2	27.6	24.3	29.1	33.2	22.1	1.04	8.7E-01
B035DRAFT_00468	(tRNA)	11.3	15.7	5.5	2.4	8.2	10.2	0.59	6.0E-01
B035DRAFT_00469	2-oxoacid:acceptor oxidoreductase, alpha subunit(EC:1.2.7.3)	292.4	300.9	319.7	241.5	277.8	265.2	0.86	1.5E-01
B035DRAFT_00470	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit(EC:1.2.7.3)	412.0	427.1	415.6	320.8	365.7	344.3	0.82	6.3E-02
B035DRAFT_00471	Uracil phosphoribosyltransferase(EC:2.4.2.9)	112.9	130.3	112.7	122.3	127.6	115.8	1.03	7.8E-01
B035DRAFT_00472	phosphoenolpyruvate carboxykinase (ATP)(EC:4.1.1.49)	6005.1	6247.1	6247.4	5215.2	5870.2	6969.6	0.97	8.5E-01
B035DRAFT_00473	Nitroreductase	138.6	133.6	124.8	204.9	196.2	207.7	1.53	7.4E-03
B035DRAFT_00474	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	91.5	109.9	94.9	132.8	123.6	173.5	1.44	1.5E-01
B035DRAFT_00475	Fe2+-dicitrate sensor, membrane component	116.4	133.0	120.8	127.5	132.3	161.8	1.13	4.1E-01
B035DRAFT_00476	TonB-linked outer membrane protein, SusC/RagA family	65.8	57.1	65.0	49.9	55.0	59.6	0.87	3.1E-01
B035DRAFT_00477	SusD family	35.2	32.1	37.0	31.9	33.4	37.2	0.98	8.9E-01
B035DRAFT_00478	Arylsulfatase A and related enzymes	106.7	117.6	115.6	125.2	136.1	147.5	1.20	1.4E-01
B035DRAFT_00479	GTP-binding protein TypA/BipA	1014.9	986.7	943.9	986.9	1012.7	948.0	1.00	9.9E-01
B035DRAFT_00480	Response regulator containing a CheY-like receiver domain and a GGDEF domain	20.0	20.7	21.8	12.9	16.9	20.0	0.78	3.2E-01
B035DRAFT_00481	hypothetical protein	16.7	19.4	15.4	26.7	20.8	23.8	1.39	1.4E-01
B035DRAFT_00482	Bacteriophage CI repressor helix-turn-helix domain.	66.3	68.7	62.7	82.8	99.2	99.4	1.42	5.7E-02
B035DRAFT_00483	hypothetical protein	1.6	4.7	4.0	4.3	0.0	0.0	1.37	
B035DRAFT_00484	hypothetical protein	4.2	2.9	0.0	0.9	0.8	2.3	0.33	2.1E-01
B035DRAFT_00485	hypothetical protein	2.6	3.0	2.1	1.8	2.4	3.1	0.94	8.6E-01
B035DRAFT_00486	(tRNA)	2.0	2.3	2.4	0.0	0.0	0.0	0.00	
B035DRAFT_00487	hypothetical protein	2.5	5.9	2.0	5.3	5.3	3.1	1.42	6.0E-01
B035DRAFT_00488	hypothetical protein	3.8	2.7	3.7	2.4	2.1	2.8	0.72	2.4E-01
B035DRAFT_00489	hypothetical protein	4.8	4.8	4.7	4.5	4.9	1.9	0.73	5.7E-01
B035DRAFT_00490	hypothetical protein	6.0	5.9	6.9	6.5	6.9	4.6	0.95	8.4E-01
B035DRAFT_00491	hypothetical protein	6.6	3.3	4.6	7.0	6.4	1.3	0.83	8.7E-01
B035DRAFT_00492	hypothetical protein	3.9	1.8	4.1	2.7	5.0	1.4	0.87	8.8E-01
B035DRAFT_00493	hypothetical protein	4.3	3.3	0.9	3.8	3.2	0.6	0.86	9.2E-01
B035DRAFT_00494	hypothetical protein	6.7	2.1	3.7	1.3	6.0	3.3	0.79	8.3E-01
B035DRAFT_00495	hypothetical protein	10.9	7.3	7.7	7.3	10.9	7.3	0.98	9.6E-01
B035DRAFT_00496	hypothetical protein	11.5	11.1	9.2	11.4	11.3	4.8	0.81	6.9E-01
B035DRAFT_00497	hypothetical protein	7.2	7.5	7.8	7.6	12.4	12.4	1.40	2.9E-01
B035DRAFT_00498	hypothetical protein	8.6	12.4	15.7	7.8	9.5	13.4	0.84	6.9E-01
B035DRAFT_00499	hypothetical protein	19.7	9.5	15.7	14.8	17.5	6.9	0.85	8.1E-01
B035DRAFT_00500	Protein of unknown function (DUF3164).	34.3	29.0	33.8	29.8	27.1	10.1	0.62	4.6E-01
B035DRAFT_00501	hypothetical protein	11.6	5.4	11.3	8.6	11.6	5.3	0.90	8.8E-01
B035DRAFT_00502	hypothetical protein	7.5	8.7	9.5	8.3	9.0	2.9	0.70	6.0E-01

B035DRAFT_00503	hypothetical protein	2.1	2.5	0.6	2.5	1.0	1.7	1.06	9.5E-01
B035DRAFT_00504	hypothetical protein	225.9	276.6	255.3	435.4	314.8	183.4	1.16	7.6E-01
B035DRAFT_00505	Phage Mu protein F like protein.	22.3	30.5	30.7	30.8	28.4	33.7	1.12	5.9E-01
B035DRAFT_00506	Mu-like prophage protein gp29	7.9	5.8	6.5	8.5	7.9	4.8	1.02	9.6E-01
B035DRAFT_00507	Protein of unknown function (DUF1320).	3.6	2.8	5.8	3.8	3.2	1.1	0.61	5.4E-01
B035DRAFT_00508	hypothetical protein	5.4	4.1	5.8	4.1	5.6	2.7	0.79	5.6E-01
B035DRAFT_00509	Transcriptional regulator, contains sigma factor-related N-terminal domain	4.2	4.4	3.2	2.4	3.4	2.7	0.73	2.5E-01
B035DRAFT_00510	Protease subunit of ATP-dependent Clp proteases	15.9	9.6	16.2	8.1	9.4	2.5	0.42	3.2E-01
B035DRAFT_00511	hypothetical protein	44.6	36.1	40.3	26.2	24.8	11.2	0.48	2.0E-01
B035DRAFT_00512	N-acetylmuramoyl-L-alanine amidase.(EC:3.5.1.28)	12.7	12.7	21.7	11.1	12.2	4.0	0.54	4.0E-01
B035DRAFT_00513	hypothetical protein	46.7	35.5	40.4	20.2	25.7	5.6	0.35	2.7E-01
B035DRAFT_00514	hypothetical protein	34.7	25.2	42.1	22.1	16.6	5.8	0.39	2.6E-01
B035DRAFT_00515	hypothetical protein	25.9	23.4	25.3	18.1	11.0	6.6	0.44	1.8E-01
B035DRAFT_00516	hypothetical protein	37.2	34.8	31.8	18.2	23.7	8.0	0.44	2.2E-01
B035DRAFT_00517	hypothetical protein	20.6	20.4	33.4	13.4	16.5	6.6	0.47	2.4E-01
B035DRAFT_00518	tape measure domain	15.4	12.3	15.4	8.3	8.1	2.4	0.38	2.4E-01
B035DRAFT_00519	hypothetical protein	8.0	4.6	6.2	4.2	3.6	1.0	0.40	3.3E-01
B035DRAFT_00520	hypothetical protein	10.4	8.3	9.8	5.0	5.3	2.4	0.42	1.5E-01
B035DRAFT_00521	hypothetical protein	13.2	7.7	16.8	6.4	8.0	4.5	0.51	2.4E-01
B035DRAFT_00522	hypothetical protein	23.7	14.5	22.8	15.1	11.9	4.2	0.46	3.3E-01
B035DRAFT_00523	hypothetical protein	6.0	7.0	7.3	5.0	5.4	1.1	0.46	4.2E-01
B035DRAFT_00524	Retron-type reverse transcriptase	97.0	68.6	104.4	71.9	62.5	16.2	0.47	4.1E-01
B035DRAFT_00525	hypothetical protein	88.6	94.9	89.7	80.9	88.2	46.8	0.76	4.5E-01
B035DRAFT_00526	hypothetical protein	34.1	39.6	49.1	28.5	39.1	23.4	0.73	3.6E-01
B035DRAFT_00527	Thymidylate synthase	66.3	52.1	74.6	57.6	55.6	27.6	0.70	4.5E-01
B035DRAFT_00528	Site-specific DNA methylase	79.2	79.0	80.3	72.4	63.6	66.4	0.85	8.2E-02
B035DRAFT_00529	Two component regulator propeller.	81.9	92.4	77.0	70.5	74.2	85.0	0.91	5.2E-01
B035DRAFT_00530	hypothetical protein	702.2	812.0	708.2	999.2	890.0	992.3	1.30	8.2E-02
B035DRAFT_00531	Protein of unknown function (DUF3575).	4.4	2.7	3.2	2.8	3.7	1.6	0.75	5.8E-01
B035DRAFT_00532	OmpA family	5.2	3.5	6.0	3.5	3.7	3.0	0.71	3.0E-01
B035DRAFT_00533	conserved hypothetical protein (putative transposase or invertase)	389.7	373.5	381.5	465.5	445.2	397.0	1.14	2.0E-01
B035DRAFT_00534	hypothetical protein	42.7	30.0	35.0	21.1	21.4	21.4	0.60	6.3E-02
B035DRAFT_00535	Protein of unknown function (DUF1812).	15.7	14.2	15.1	6.4	7.9	6.9	0.47	1.1E-02
B035DRAFT_00536	hypothetical protein	10.8	6.8	10.9	5.5	5.6	5.2	0.58	1.3E-01
B035DRAFT_00537	hypothetical protein	9.7	10.0	10.5	4.9	5.8	4.8	0.51	1.3E-02
B035DRAFT_00538	hypothetical protein	17.5	11.6	18.3	7.9	5.7	9.1	0.48	1.1E-01
B035DRAFT_00539	hypothetical protein	16.3	19.6	23.7	6.1	9.1	11.0	0.43	9.0E-02
B035DRAFT_00540	hypothetical protein	33.1	31.4	40.9	22.6	20.4	26.2	0.66	1.0E-01
B035DRAFT_00541	AraC-type DNA-binding domain-containing proteins	40.8	43.8	48.5	26.3	24.7	26.7	0.59	1.6E-02
B035DRAFT_00542	Response regulator containing a CheY-like receiver domain and an HD-GYP domain	57.6	70.9	66.2	47.1	41.7	45.8	0.69	6.1E-02
B035DRAFT_00543	ribosomal protein S15, bacterial/organelle	4379.1	5463.3	5067.2	4558.2	4370.0	4147.9	0.88	3.3E-01
B035DRAFT_00544	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	16.7	17.2	21.8	28.5	27.5	26.3	1.49	7.5E-02
B035DRAFT_00545	FOG: WD40-like repeat	9.4	7.1	10.0	10.0	12.2	10.2	1.23	3.5E-01
B035DRAFT_00546	Predicted phosphohydrolases	9.5	9.6	10.3	11.3	11.0	13.0	1.20	1.6E-01
B035DRAFT_00547	SusD family	8.7	6.5	6.3	6.5	8.7	7.9	1.07	7.8E-01
B035DRAFT_00548	TonB-linked outer membrane protein, SusC/RagA family	19.0	17.7	18.5	15.7	23.7	26.1	1.16	6.1E-01
B035DRAFT_00549	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	24.5	30.0	34.0	32.5	35.7	41.5	1.24	3.3E-01
B035DRAFT_00550	LuxS protein involved in autoinducer AI2 synthesis(EC:4.4.1.21)	152.2	139.0	139.6	183.3	167.3	168.4	1.20	7.8E-02

B035DRAFT_00551	5''-methylthioadenosine/S-adenosylhomocysteine nucleosidase(EC:3.2.2.9)	105.3	93.7	92.4	128.3	102.3	76.8	1.03	9.2E-01
B035DRAFT_00552	Bacterial membrane protein YfhO.	125.9	124.5	127.1	108.6	131.9	107.4	0.92	4.8E-01
B035DRAFT_00553	Glycosyltransferases involved in cell wall biogenesis (GT2)	99.2	117.9	114.9	112.9	117.7	149.4	1.14	4.8E-01
B035DRAFT_00554	Glycosyltransferase (GT4)	156.6	146.9	140.6	153.3	169.9	162.9	1.09	2.8E-01
B035DRAFT_00555	hypothetical protein (GT13)	35.0	41.1	33.8	42.5	48.0	46.6	1.25	1.5E-01
B035DRAFT_00556	hypothetical protein	39.8	45.7	40.5	42.5	55.4	61.2	1.25	3.2E-01
B035DRAFT_00557	hypothetical protein (GH99)	65.1	64.6	62.9	69.3	74.8	75.6	1.14	7.7E-02
B035DRAFT_00558	Acetyltransferase (isoleucine patch superfamily)	27.5	28.2	26.1	30.6	30.2	29.4	1.10	1.0E-01
B035DRAFT_00559	Lipopolysaccharide biosynthesis proteins, LPS:glycosyltransferases (GT8)	22.8	30.7	29.4	19.8	23.0	30.9	0.88	6.7E-01
B035DRAFT_00560	Membrane protein involved in the export of O-antigen and teichoic acid	71.6	84.7	75.1	67.7	80.2	87.7	1.02	9.3E-01
B035DRAFT_00561	methionyl-tRNA synthetase/methionyl-tRNA synthetase C-terminal region/beta chain(EC:6.1.1.10)	415.4	391.3	381.6	369.6	388.9	350.6	0.93	3.4E-01
B035DRAFT_00562	hypothetical protein	2.7	2.1	1.6	1.4	0.8	1.2	0.54	1.8E-01
B035DRAFT_00563	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	4.8	4.5	7.6	4.5	3.6	4.5	0.76	4.0E-01
B035DRAFT_00564	hypothetical protein	4.2	9.1	7.3	6.9	8.1	6.5	1.10	8.4E-01
B035DRAFT_00565	hypothetical protein	6.0	4.6	5.7	3.2	8.5	5.1	0.95	9.4E-01
B035DRAFT_00566	hypothetical protein	5.7	7.6	13.9	14.6	14.8	14.1	1.72	2.9E-01
B035DRAFT_00567	hypothetical protein	7.3	8.5	3.6	5.2	4.4	9.3	0.98	9.8E-01
B035DRAFT_00568	hypothetical protein	7.4	7.8	5.7	7.8	9.2	11.8	1.37	2.9E-01
B035DRAFT_00569	radical SAM enzyme, rSAM/lipoprotein system	7.8	4.5	4.4	5.1	9.9	3.4	1.04	9.7E-01
B035DRAFT_00570	putative lipoprotein, rSAM/lipoprotein system	11.4	8.0	7.1	6.9	13.5	5.3	0.91	8.8E-01
B035DRAFT_00571	Mg chelatase-related protein	52.4	58.2	53.4	67.0	61.9	51.6	1.10	5.5E-01
B035DRAFT_00572	AhpC/TSA family	83.5	71.1	75.0	71.3	71.3	58.9	0.88	3.7E-01
B035DRAFT_00573	hypothetical protein	2133.4	2336.8	2081.4	1528.2	1838.3	2329.9	0.86	5.0E-01
B035DRAFT_00574	tyrosine recombinase XerD	14.8	14.4	14.0	11.9	11.9	11.6	0.82	1.1E-02
B035DRAFT_00575	3-dehydroquinate dehydratase, type II(EC:4.2.1.10)	177.7	145.3	129.3	92.9	136.8	103.1	0.73	2.8E-01
B035DRAFT_00576	pyruvate kinase(EC:2.7.1.40)	386.2	363.6	339.6	280.2	348.7	311.0	0.86	2.9E-01
B035DRAFT_00577	Predicted O-methyltransferase	297.1	281.5	259.3	234.6	278.2	253.9	0.91	4.4E-01
B035DRAFT_00578	ribosome-binding factor A	337.8	344.8	313.8	273.1	321.3	339.9	0.93	6.0E-01
B035DRAFT_00579	ABC-type transport system, involved in lipoprotein release, permease component	353.6	320.0	351.1	255.1	295.0	260.0	0.79	8.6E-02
B035DRAFT_00580	Pyridoxal/pyridoxine/pyridoxamine kinase(EC:2.7.1.35)	148.7	142.2	148.6	138.1	134.8	136.5	0.93	8.2E-02
B035DRAFT_00581	glutamate racemase(EC:5.1.1.3)	85.8	85.5	89.5	80.2	74.9	98.1	0.97	8.2E-01
B035DRAFT_00582	Outer membrane protein	1374.8	1477.8	1349.6	1718.3	1429.8	1682.0	1.15	2.8E-01
B035DRAFT_00583	Outer membrane protein	326.7	339.1	302.0	369.8	386.7	414.7	1.21	9.5E-02
B035DRAFT_00584	outer membrane protein assembly complex, YaeT protein	636.0	634.6	606.0	657.3	695.4	729.2	1.11	1.6E-01
B035DRAFT_00585	undecaprenyl diphosphate synthase(EC:2.5.1.31)	438.7	461.9	431.9	492.2	485.5	457.0	1.08	2.3E-01
B035DRAFT_00586	hypothetical protein	513.4	553.6	514.7	527.3	495.9	543.6	0.99	9.0E-01
B035DRAFT_00587	riboflavin biosynthesis protein RibD(EC:1.1.1.193,EC:3.5.4.26)	28.0	28.5	30.8	39.3	42.5	40.8	1.41	1.7E-02
B035DRAFT_00588	protein-(glutamine-N5) methyltransferase, release factor-specific(EC:2.1.1.)	67.4	70.1	72.9	72.9	73.2	64.4	1.00	9.9E-01
B035DRAFT_00589	Uncharacterized protein conserved in bacteria	44.1	40.8	43.1	26.0	48.8	31.6	0.80	5.1E-01
B035DRAFT_00590	Predicted amidophosphoribosyltransferases	60.6	65.5	67.1	49.1	59.5	47.7	0.81	1.8E-01
B035DRAFT_00591	orotate phosphoribosyltransferase(EC:2.4.2.10)	1240.4	1408.3	1372.3	1308.8	1318.0	1419.7	1.01	9.4E-01
B035DRAFT_00592	Polyketide cyclase / dehydrase and lipid transport.	208.2	259.5	233.5	168.6	217.8	202.2	0.84	3.4E-01
B035DRAFT_00593	argininosuccinate lyase(EC:4.3.2.1)	259.9	264.0	267.6	195.2	234.1	197.6	0.79	9.5E-02
B035DRAFT_00594	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	295.7	277.4	303.7	236.6	238.7	180.6	0.74	1.5E-01
B035DRAFT_00595	(tRNA)	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_00596	(tRNA)	324.4	426.2	577.0	375.9	189.7	104.7	0.45	3.1E-01

B035DRAFT_00597	Fic/DOC family	385.2	417.7	442.3	425.7	399.6	450.5	1.02	8.1E-01
B035DRAFT_00598	hypothetical protein	148.2	185.3	165.2	112.0	126.5	150.5	0.78	2.4E-01
B035DRAFT_00599	hypothetical protein	133.1	149.4	145.8	137.4	137.2	172.0	1.04	8.1E-01
B035DRAFT_00600	Predicted P-loop ATPase and inactivated derivatives	103.9	79.2	107.9	76.0	69.5	28.6	0.55	3.4E-01
B035DRAFT_00601	hypothetical protein	19.3	26.2	5.9	5.1	8.8	5.8	0.44	3.7E-01
B035DRAFT_00602	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	30.6	36.7	21.8	15.3	22.7	25.0	0.71	3.8E-01
B035DRAFT_00603	Fe2+-dicitrate sensor, membrane component	31.9	30.0	35.4	11.1	16.2	15.1	0.43	3.5E-02
B035DRAFT_00604	TonB-linked outer membrane protein, SusC/RagA family	66.6	57.6	59.3	28.2	32.4	39.0	0.54	4.4E-02
B035DRAFT_00605	SusD family	63.5	55.5	60.9	29.8	32.5	36.5	0.55	2.1E-02
B035DRAFT_00606	Glycoside hydrolase (GH110)	217.9	221.8	215.1	215.5	217.2	200.8	0.97	4.8E-01
B035DRAFT_00607	Glycoside hydrolase (GH109)	1186.8	1170.3	1124.7	967.4	1179.7	1209.3	0.96	7.6E-01
B035DRAFT_00608	5"-nucleotidase/2",3"-cyclic phosphodiesterase and related esterases	29.1	31.6	25.4	23.7	27.2	29.2	0.93	6.6E-01
B035DRAFT_00609	Outer membrane cobalamin receptor protein	830.6	782.3	624.6	358.0	397.6	300.1	0.47	4.0E-02
B035DRAFT_00610	hypothetical protein	2185.2	1766.0	1499.2	613.8	939.3	490.5	0.37	7.5E-02
B035DRAFT_00611	Uncharacterized iron-regulated membrane protein	1849.4	1544.5	1510.2	490.3	662.3	332.2	0.29	4.5E-02
B035DRAFT_00612	Mg2+ and Co2+ transporters	348.3	339.4	287.6	138.2	190.7	176.8	0.52	4.7E-02
B035DRAFT_00613	peroxiredoxin(EC:1.11.1.15)	7030.7	4328.3	2588.5	3234.7	2097.1	3525.3	0.67	5.1E-01
B035DRAFT_00614	hypothetical protein	1986.1	1526.3	1055.6	1265.0	734.9	1717.3	0.79	6.8E-01
B035DRAFT_00615	N-acetylglucosamine-6-phosphate deacetylase(EC:3.5.1.25) (CE9)	182.6	214.1	214.7	211.1	226.5	208.9	1.06	5.9E-01
B035DRAFT_00616	Sua5/YciO/YrdC/YwlC family protein	134.6	123.8	126.3	139.5	138.8	106.9	0.99	9.8E-01
B035DRAFT_00617	Chloride channel protein EriC	109.6	108.9	113.1	106.7	120.5	120.2	1.05	5.5E-01
B035DRAFT_00618	methionyl-tRNA formyltransferase(EC:2.1.2.9)	153.9	138.6	150.5	146.3	153.3	119.2	0.94	6.9E-01
B035DRAFT_00619	hypothetical protein	14.2	19.2	19.3	47.6	42.6	56.3	2.79	2.3E-02
B035DRAFT_00620	RNA polymerase sigma factor, sigma-70 family	46.4	49.5	37.9	75.3	72.2	60.5	1.56	8.6E-02
B035DRAFT_00621	hypothetical protein	42.2	37.2	40.1	67.0	68.4	68.0	1.70	4.4E-03
B035DRAFT_00622	ribulose-phosphate 3-epimerase(EC:5.1.3.1)	219.8	227.3	193.6	231.7	264.3	236.2	1.14	2.8E-01
B035DRAFT_00623	ComEC/Rec2-related protein	45.6	43.0	43.0	46.8	57.5	48.8	1.16	2.5E-01
B035DRAFT_00624	Exopolyphosphatase-related proteins	260.1	250.7	245.6	207.4	252.1	271.5	0.96	8.0E-01
B035DRAFT_00625	hypothetical protein	810.0	832.6	798.1	930.5	920.4	864.6	1.11	9.1E-02
B035DRAFT_00626	phosphoglucosamine mutase(EC:5.4.2.8)	913.8	947.9	954.4	924.2	1074.6	1029.9	1.07	4.1E-01
B035DRAFT_00627	Beta-glucanase/Beta-glucan synthetase (GH16)	207.5	204.8	201.1	216.9	213.3	190.0	1.01	9.2E-01
B035DRAFT_00628	putative oxygen-independent coproporphyrinogen III oxidase(EC:1.3.99.22)	153.3	164.2	169.8	178.8	175.1	176.5	1.09	1.8E-01
B035DRAFT_00629	small GTP-binding protein domain	90.3	91.5	89.3	93.8	132.8	156.4	1.38	2.7E-01
B035DRAFT_00630	Signal transduction histidine kinase(EC:2.7.13.3)	600.0	642.0	618.2	572.9	527.8	486.7	0.85	1.5E-01
B035DRAFT_00631	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	2529.5	2988.7	2988.6	3062.7	2419.4	3162.5	1.01	9.5E-01
B035DRAFT_00632	Site-specific recombinase XerD	104.2	103.9	103.3	110.8	112.5	129.7	1.13	2.2E-01
B035DRAFT_00633	Transcription antiterminator	106.9	130.2	88.3	65.6	74.1	75.5	0.67	1.4E-01
B035DRAFT_00634	Periplasmic protein involved in polysaccharide export	132.3	150.4	127.6	73.5	111.9	71.6	0.61	1.5E-01
B035DRAFT_00635	capsular exopolysaccharide family	130.9	143.2	136.9	103.3	119.6	105.6	0.80	8.3E-02
B035DRAFT_00636	Capsular polysaccharide biosynthesis protein	112.4	112.0	104.8	69.3	88.5	79.6	0.72	7.9E-02
B035DRAFT_00637	hypothetical protein	105.2	108.5	107.1	68.1	86.9	84.8	0.74	1.1E-01
B035DRAFT_00638	Glycosyltransferase (GT4)	91.3	93.3	94.1	60.4	70.7	74.6	0.74	6.8E-02
B035DRAFT_00639	Glycosyltransferase (GT4)	115.3	117.4	119.3	71.5	86.8	66.3	0.63	5.0E-02
B035DRAFT_00640	Glycosyltransferases involved in cell wall biogenesis (GT2)	82.1	82.7	69.8	41.7	67.9	55.2	0.69	2.3E-01
B035DRAFT_00641	hypothetical protein	75.7	83.6	71.2	46.2	65.2	59.5	0.74	1.9E-01
B035DRAFT_00642	hypothetical protein	76.8	81.9	72.5	41.9	63.9	62.0	0.71	2.3E-01
B035DRAFT_00643	Uncharacterized protein conserved in bacteria	74.3	82.6	68.5	46.0	58.5	63.6	0.74	1.9E-01
B035DRAFT_00644	Glycosyltransferase (GT4)	88.6	101.8	96.4	68.6	74.9	73.0	0.76	4.6E-02
B035DRAFT_00645	hypothetical protein	91.8	106.0	90.3	53.1	74.0	87.9	0.73	3.0E-01

B035DRAFT_00646	Mannosyltransferase OCH1 and related enzymes (GT32)	107.2	117.0	129.6	69.0	84.8	84.0	0.67	7.4E-02
B035DRAFT_00647	Glycosyltransferases, probably involved in cell wall biogenesis (GT2)	85.0	86.0	81.6	52.8	64.4	54.4	0.68	4.2E-02
B035DRAFT_00648	Glycosyltransferase (GT4)	87.3	86.4	78.2	60.0	69.1	56.7	0.74	7.7E-02
B035DRAFT_00649	Phd_YefM.	265.6	268.7	239.4	315.2	332.7	269.1	1.18	2.5E-01
B035DRAFT_00650	toxin-antitoxin system, toxin component, Txe/YoeB family	269.3	259.7	239.8	322.8	334.5	280.3	1.22	1.6E-01
B035DRAFT_00651	hypothetical protein	498.4	490.0	488.0	684.1	639.4	811.2	1.44	6.1E-02
B035DRAFT_00652	hypothetical protein	429.6	475.5	489.1	575.6	545.4	740.6	1.33	1.9E-01
B035DRAFT_00653	hypothetical protein	285.4	293.6	325.5	332.6	344.5	391.6	1.18	2.0E-01
B035DRAFT_00654	Negative regulator of beta-lactamase expression	194.9	161.1	184.8	202.8	177.3	96.3	0.84	6.9E-01
B035DRAFT_00655	hypothetical protein	168.9	157.1	164.4	181.2	156.0	119.9	0.92	7.1E-01
B035DRAFT_00656	DNA-binding protein, histone-like, putative	176.8	163.2	196.9	150.4	143.1	80.0	0.67	3.2E-01
B035DRAFT_00657	hypothetical protein	223.8	200.5	225.3	178.6	163.3	86.4	0.63	3.0E-01
B035DRAFT_00658	DNA primase (bacterial type)	169.6	121.1	189.3	121.9	91.0	24.3	0.41	3.5E-01
B035DRAFT_00659	hypothetical protein	69.2	69.4	72.4	52.9	55.1	41.3	0.70	1.0E-01
B035DRAFT_00660	hypothetical protein	57.4	64.2	64.5	39.5	42.0	37.1	0.64	2.0E-02
B035DRAFT_00661	hypothetical protein	37.0	56.8	43.3	37.4	36.3	35.0	0.81	3.6E-01
B035DRAFT_00662	Nucleoside-diphosphate-sugar epimerases(EC:5.1.3.2)	74.2	82.4	74.2	49.1	62.6	67.5	0.77	2.1E-01
B035DRAFT_00663	Sugar transferases involved in lipopolysaccharide synthesis	53.6	54.3	48.7	41.9	49.6	50.7	0.91	4.3E-01
B035DRAFT_00664	hypothetical protein	76.1	80.7	77.1	56.7	67.1	78.9	0.86	3.9E-01
B035DRAFT_00665	hypothetical protein	91.6	95.9	91.9	73.6	74.8	92.8	0.86	3.0E-01
B035DRAFT_00666	hypothetical protein	70.1	74.3	63.3	47.3	55.6	67.2	0.81	3.2E-01
B035DRAFT_00667	Aldo/keto reductases, related to diketogulonate reductase	72.3	70.5	75.1	55.1	61.6	76.1	0.88	4.5E-01
B035DRAFT_00668	Diaminopimelate decarboxylase(EC:4.1.1.20)	60.8	66.3	67.8	55.0	60.1	59.8	0.90	2.2E-01
B035DRAFT_00669	Carbamoylphosphate synthase large subunit (split gene in MJ)(EC:6.3.5.5)	65.2	70.9	58.9	46.6	62.3	62.9	0.87	5.1E-01
B035DRAFT_00670	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	71.1	56.8	68.2	49.9	52.3	27.6	0.64	2.9E-01
B035DRAFT_00671	Predicted nucleoside-diphosphate sugar epimerases	66.6	53.3	60.3	44.7	56.4	28.4	0.69	3.5E-01
B035DRAFT_00672	Bacterial putative lipoprotein (DUF940).	63.9	46.3	53.0	40.9	47.3	12.1	0.53	4.3E-01
B035DRAFT_00673	Bacterial putative lipoprotein (DUF940).	54.7	46.2	52.7	36.5	51.2	17.9	0.63	4.2E-01
B035DRAFT_00674	hypothetical protein	260.1	232.0	235.6	171.1	189.6	102.7	0.62	2.2E-01
B035DRAFT_00675	Site-specific recombinase XerD	14.3	16.1	14.0	11.7	10.2	11.2	0.75	6.4E-02
B035DRAFT_00676	Protein of unknown function (DUF1812).	33.0	35.8	39.9	27.6	25.4	19.1	0.66	1.3E-01
B035DRAFT_00677	Protein of unknown function (DUF1812).	16.1	12.4	15.2	14.0	13.8	11.8	0.91	5.9E-01
B035DRAFT_00678	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	8.9	8.6	12.4	6.2	5.6	4.1	0.53	1.1E-01
B035DRAFT_00679	Protein of unknown function (DUF3575).	11.2	5.8	11.8	5.3	6.4	4.0	0.56	2.6E-01
B035DRAFT_00680	hypothetical protein	9.0	6.2	9.9	6.6	6.8	5.1	0.74	3.5E-01
B035DRAFT_00681	Protein of unknown function (DUF3575).	12.8	9.0	10.5	8.8	8.4	8.1	0.79	2.5E-01
B035DRAFT_00682	Site-specific recombinase XerD	37.1	39.9	40.2	45.7	32.8	36.6	0.97	8.9E-01
B035DRAFT_00683	hypothetical protein	720.0	1347.7	1203.0	1207.9	1062.7	1623.3	1.21	6.4E-01
B035DRAFT_00684	Transcriptional regulators	187.8	213.5	169.7	162.3	156.2	159.7	0.84	2.1E-01
B035DRAFT_00685	ribosomal protein S6	3304.0	3576.1	2958.2	2875.1	3162.9	3348.6	0.96	7.3E-01
B035DRAFT_00686	ribosomal protein S18	3743.2	3924.4	3582.0	3270.0	3684.7	4159.9	0.98	9.2E-01
B035DRAFT_00687	ribosomal protein L9	3439.0	3746.8	3562.0	3263.3	3507.4	4061.4	1.00	9.8E-01
B035DRAFT_00688	hypothetical protein	143.5	135.0	125.0	179.8	198.0	192.1	1.41	3.1E-02
B035DRAFT_00689	hypothetical protein	3251.3	4898.2	4349.9	2654.8	1935.7	2115.2	0.54	9.4E-02
B035DRAFT_00690	Long-chain acyl-CoA synthetases (AMP-forming)(EC:6.2.1.3)	120.7	138.4	107.4	113.8	130.1	134.6	1.04	8.4E-01
B035DRAFT_00691	MiaB-like tRNA modifying enzyme	163.5	131.8	124.7	137.0	182.7	101.6	0.98	9.6E-01
B035DRAFT_00692	Predicted glycosyltransferases (GT27)	158.6	129.6	119.3	119.6	187.4	124.1	1.04	9.0E-01
B035DRAFT_00693	Methylglyoxal synthase(EC:4.2.3.3)	234.9	216.2	233.4	279.4	317.6	274.3	1.27	7.7E-02

B035DRAFT_00694	dihydroneopterin aldolase(EC:4.1.2.25)	107.6	110.7	97.5	115.7	118.3	111.5	1.10	2.7E-01
B035DRAFT_00695	ribonucleoside-diphosphate reductase, adenosylcobalamin-dependent(EC:1.17.4.1)	827.7	803.2	693.3	638.5	612.2	617.7	0.81	1.0E-01
B035DRAFT_00696	hypothetical protein	12.2	3.5	3.7	11.2	8.3	2.8	1.17	8.9E-01
B035DRAFT_00697	Nitroreductase	261.0	259.7	204.2	250.3	269.7	288.8	1.12	4.9E-01
B035DRAFT_00698	chromosomal replication initiator protein DnaA	495.3	587.7	540.7	635.2	645.2	707.6	1.23	1.3E-01
B035DRAFT_00699	ABC-type transport system involved in resistance to organic solvents, periplasmic component	75.3	83.4	71.8	80.3	84.0	86.3	1.09	3.5E-01
B035DRAFT_00700	N-acetylmuramoyl-L-alanine amidase(EC:3.5.1.28)	39.3	42.5	38.2	48.9	44.4	44.6	1.15	1.6E-01
B035DRAFT_00701	Predicted Na+-dependent transporter	14.2	14.5	15.3	12.3	13.8	12.3	0.87	1.7E-01
B035DRAFT_00702	Acetyltransferases(EC:2.3.1.)	47.4	63.9	58.9	31.2	37.6	41.3	0.65	1.2E-01
B035DRAFT_00703	cytidine deaminase, homotetrameric(EC:3.5.4.5)	92.3	122.2	108.1	172.9	144.3	157.8	1.48	9.3E-02
B035DRAFT_00704	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	16.4	21.0	16.5	15.5	14.1	12.6	0.79	2.3E-01
B035DRAFT_00705	Fe2+-dicitrate sensor, membrane component	16.3	14.9	17.8	14.0	15.0	13.9	0.88	2.4E-01
B035DRAFT_00706	TonB-linked outer membrane protein, SusC/RagA family	12.3	11.4	12.7	9.7	11.2	12.8	0.92	6.0E-01
B035DRAFT_00707	SusD family	11.8	10.6	11.1	11.7	13.9	14.1	1.18	2.3E-01
B035DRAFT_00708	Arylsulfatase A and related enzymes(EC:3.1.6.1)	9.4	9.7	9.2	6.2	8.7	12.3	0.92	8.4E-01
B035DRAFT_00709	Arylsulfatase A and related enzymes	15.3	17.2	17.1	15.8	19.2	15.4	1.01	9.4E-01
B035DRAFT_00710	hypothetical protein	41.9	48.1	44.3	65.6	66.4	72.7	1.53	2.2E-02
B035DRAFT_00711	RNA polymerase sigma factor, sigma-70 family	83.0	79.0	84.2	130.1	136.6	124.9	1.59	4.3E-03
B035DRAFT_00712	hypothetical protein	126.6	115.8	117.8	158.7	173.0	150.1	1.34	4.5E-02
B035DRAFT_00713	hypothetical protein	443.6	405.6	363.6	669.5	646.3	737.8	1.70	2.6E-02
B035DRAFT_00714	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	216.1	235.0	221.0	249.2	268.0	316.4	1.23	1.8E-01
B035DRAFT_00715	hypothetical protein (CBM9)	168.9	156.9	156.6	175.9	203.7	187.0	1.17	1.5E-01
B035DRAFT_00716	Uncharacterized conserved protein	228.0	249.5	240.6	261.6	316.4	306.8	1.23	1.5E-01
B035DRAFT_00717	Zn-dependent protease with chaperone function(EC:3.4.24.)	214.6	224.0	218.5	217.0	251.7	273.4	1.12	3.6E-01
B035DRAFT_00718	Muramidase (flagellum-specific) (GH73)	140.0	150.5	144.6	121.5	145.4	143.4	0.94	5.8E-01
B035DRAFT_00719	Multidrug resistance efflux pump	15.6	12.4	14.2	49.4	81.8	66.9	4.62	1.6E-02
B035DRAFT_00720	ABC-type antimicrobial peptide transport system, permease component	17.5	17.5	16.1	51.2	68.1	82.6	3.89	1.6E-02
B035DRAFT_00721	ABC-type antimicrobial peptide transport system, permease component	16.5	16.3	20.5	62.1	71.1	80.1	4.01	5.8E-03
B035DRAFT_00722	ABC-type antimicrobial peptide transport system, ATPase component	39.2	39.4	41.0	131.0	154.7	143.5	3.58	5.6E-04
B035DRAFT_00723	ABC-type antimicrobial peptide transport system, permease component	39.0	37.3	37.4	134.7	128.5	122.0	3.39	1.3E-04
B035DRAFT_00724	ABC-type antimicrobial peptide transport system, permease component	71.5	62.5	71.2	265.3	256.4	237.4	3.70	7.1E-04
B035DRAFT_00725	Outer membrane protein	18.5	18.5	16.4	71.2	87.3	87.8	4.60	1.5E-03
B035DRAFT_00726	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	130.6	132.6	137.0	226.0	222.9	141.6	1.44	2.3E-01
B035DRAFT_00727	HAMP domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	64.7	66.7	69.9	97.7	119.6	110.5	1.62	2.6E-02
B035DRAFT_00728	Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein (GH23)	29.3	31.9	31.3	49.7	52.9	43.4	1.57	3.1E-02
B035DRAFT_00729	uridine kinase(EC:2.7.1.48)	54.9	51.0	47.4	81.1	85.8	94.1	1.70	2.0E-02
B035DRAFT_00730	Stress responsive A/B Barrel Domain.	180.2	195.1	152.1	217.5	225.6	220.6	1.27	1.5E-01
B035DRAFT_00731	Uncharacterized protein, possibly involved in aromatic compounds catabolism	162.7	172.8	171.7	177.1	183.9	159.5	1.02	7.8E-01
B035DRAFT_00732	ATP phosphoribosyltransferase(EC:2.4.2.17)	92.0	83.9	70.0	51.8	64.9	59.5	0.72	1.5E-01
B035DRAFT_00733	histidinol dehydrogenase(EC:1.1.1.23)	70.8	64.2	65.0	54.6	58.2	38.8	0.75	2.5E-01
B035DRAFT_00734	histidinol-phosphate aminotransferase(EC:2.6.1.9)	65.5	66.2	66.4	48.3	61.9	54.4	0.83	2.0E-01
B035DRAFT_00735	histidinol-phosphatase(EC:3.1.3.15,EC:4.2.1.19)	65.2	76.3	73.1	55.9	62.4	40.9	0.73	2.4E-01
B035DRAFT_00736	NAD+ synthetase(EC:6.3.5.1)	60.0	76.3	70.2	75.4	86.7	81.1	1.18	2.9E-01
B035DRAFT_00737	Fe2+/Zn2+ uptake regulation proteins	934.4	940.2	616.2	915.7	411.2	1103.3	0.92	8.9E-01
B035DRAFT_00738	Rubrerythrin	4047.7	3443.8	2320.3	3043.0	1823.9	3190.6	0.82	6.5E-01
B035DRAFT_00739	thioredoxin	128.0	111.7	69.9	100.6	63.4	132.8	0.95	9.2E-01

B035DRAFT_00740	hypothetical protein	6.1	3.2	3.3	2.9	4.3	3.1	0.84	7.1E-01
B035DRAFT_00741	Predicted transcriptional regulator	42.7	53.5	37.9	48.4	44.5	65.9	1.18	5.6E-01
B035DRAFT_00742	hypothetical protein	10.9	1.1	0.0	4.8	4.9	5.0	1.44	8.8E-01
B035DRAFT_00743	hypothetical protein	6.2	7.2	3.8	2.4	7.0	3.5	0.71	6.1E-01
B035DRAFT_00744	hypothetical protein	4.6	8.2	7.6	7.4	8.6	7.9	1.22	5.7E-01
B035DRAFT_00745	Integrase core domain.	4.6	4.4	4.3	2.7	3.0	2.0	0.57	7.6E-02
B035DRAFT_00746	Uncharacterized ATPase, putative transposase	6.8	5.9	5.0	2.2	3.3	2.1	0.43	6.4E-02
B035DRAFT_00747	hypothetical protein	7.6	5.3	9.7	5.6	6.2	2.4	0.60	4.2E-01
B035DRAFT_00748	hypothetical protein	19.9	12.4	25.7	17.0	8.6	5.8	0.51	3.5E-01
B035DRAFT_00749	hypothetical protein	5.2	6.9	5.4	5.5	3.4	3.4	0.68	2.9E-01
B035DRAFT_00750	Protein of unknown function (DUF2786).	9.3	9.1	12.4	7.3	7.8	6.9	0.72	1.5E-01
B035DRAFT_00751	hypothetical protein	11.7	8.5	8.9	9.2	7.3	8.6	0.87	5.2E-01
B035DRAFT_00752	hypothetical protein	15.6	5.8	9.9	7.9	4.0	5.1	0.56	3.8E-01
B035DRAFT_00753	hypothetical protein	9.2	8.8	9.2	8.4	8.7	2.9	0.66	5.2E-01
B035DRAFT_00754	Protein of unknown function (DUF3164).	23.0	20.8	18.4	16.7	22.4	9.4	0.74	5.2E-01
B035DRAFT_00755	hypothetical protein	21.9	17.9	15.1	12.5	16.7	8.6	0.67	3.3E-01
B035DRAFT_00756	hypothetical protein	22.9	17.8	27.1	17.6	10.7	11.4	0.58	1.9E-01
B035DRAFT_00757	hypothetical protein	26.2	22.6	25.4	31.2	32.6	22.9	1.16	5.0E-01
B035DRAFT_00758	hypothetical protein	14.5	12.7	16.2	16.1	13.1	8.2	0.83	6.4E-01
B035DRAFT_00759	Phage virion morphogenesis family	8.9	4.9	10.8	9.3	8.0	11.9	1.24	6.6E-01
B035DRAFT_00760	phage putative head morphogenesis protein, SPP1 gp7 family	7.7	5.8	6.6	7.6	8.1	5.9	1.07	7.8E-01
B035DRAFT_00761	Mu-like prophage protein gp36	3.2	0.5	1.9	0.8	2.9	1.4	1.07	9.6E-01
B035DRAFT_00762	hypothetical protein	3.1	4.4	3.2	2.5	2.6	3.0	0.76	2.6E-01
B035DRAFT_00763	Transcriptional regulator, contains sigma factor-related N-terminal domain	1.9	1.7	0.5	1.6	3.0	1.4	1.64	6.0E-01
B035DRAFT_00764	Caudovirus prohead protease.	13.4	9.6	10.2	5.9	6.8	2.5	0.43	2.1E-01
B035DRAFT_00765	hypothetical protein	21.5	18.7	20.7	11.9	9.2	5.1	0.41	1.2E-01
B035DRAFT_00766	N-acetylmuramoyl-L-alanine amidase.(EC:3.5.1.28)	30.9	23.2	35.8	21.0	13.2	4.3	0.36	2.8E-01
B035DRAFT_00767	hypothetical protein	13.3	9.0	11.5	10.3	7.3	2.4	0.51	4.1E-01
B035DRAFT_00768	hypothetical protein	16.3	13.8	16.4	8.9	9.5	4.6	0.47	1.5E-01
B035DRAFT_00769	hypothetical protein	9.2	9.4	6.4	6.7	4.5	3.5	0.57	2.2E-01
B035DRAFT_00770	hypothetical protein	8.8	7.1	8.4	6.1	5.9	2.1	0.52	3.3E-01
B035DRAFT_00771	hypothetical protein	4.8	5.2	5.0	3.9	1.3	2.0	0.44	2.0E-01
B035DRAFT_00772	hypothetical protein	9.1	7.1	7.9	5.6	5.6	3.4	0.59	1.7E-01
B035DRAFT_00773	hypothetical protein	10.0	5.5	11.5	6.6	5.2	3.3	0.57	3.3E-01
B035DRAFT_00774	hypothetical protein	13.0	9.8	12.6	10.1	8.0	4.1	0.59	3.3E-01
B035DRAFT_00775	hypothetical protein	30.7	27.1	28.3	29.5	23.8	10.6	0.68	5.0E-01
B035DRAFT_00776	Retron-type reverse transcriptase	65.1	61.2	61.3	50.1	53.4	45.1	0.79	8.0E-02
B035DRAFT_00777	hypothetical protein	130.3	124.7	125.0	122.4	120.0	74.3	0.81	4.8E-01
B035DRAFT_00778	Site-specific DNA methylase(EC:2.1.1.72)	148.1	151.4	157.0	175.7	147.7	149.0	1.03	7.8E-01
B035DRAFT_00779	Outer membrane protein	435.2	519.2	457.3	490.9	495.6	601.9	1.12	4.5E-01
B035DRAFT_00780	hypothetical protein	85.6	90.8	82.2	113.8	117.1	123.5	1.37	2.1E-02
B035DRAFT_00781	Xaa-His dipeptidase(EC:3.4.13.)	195.4	188.9	181.4	231.6	287.3	249.9	1.35	7.6E-02
B035DRAFT_00782	Predicted extracellular nuclease	194.7	196.0	190.8	217.8	255.2	253.6	1.25	8.6E-02
B035DRAFT_00783	Divergent AAA domain.	22.8	23.4	21.0	19.9	24.1	30.5	1.09	7.0E-01
B035DRAFT_00784	Uncharacterized conserved protein	11.1	15.7	11.5	11.0	15.6	11.3	0.99	9.8E-01
B035DRAFT_00785	Arylsulfatase A and related enzymes	3.5	3.7	4.7	2.4	4.3	2.0	0.70	4.2E-01
B035DRAFT_00786	Arylsulfatase A and related enzymes(EC:3.1.6.1)	2.7	3.4	3.1	3.5	3.2	1.9	0.92	8.3E-01
B035DRAFT_00787	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	4.4	3.1	3.5	2.4	3.3	2.4	0.72	2.7E-01
B035DRAFT_00788	SusD family	9.4	8.0	9.4	6.7	6.2	7.5	0.76	1.2E-01
B035DRAFT_00789	TonB-linked outer membrane protein, SusC/RagA family	9.9	6.3	7.8	5.5	6.4	6.2	0.77	3.2E-01
B035DRAFT_00790	Fe2+-dicitrate sensor, membrane component	17.8	17.6	17.6	15.0	14.8	22.3	0.97	8.9E-01

B035DRAFT_00791	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	14.7	20.5	17.1	15.8	20.9	21.2	1.11	6.8E-01
B035DRAFT_00792	nicotinate-nucleotide pyrophosphorylase(EC:2.4.2.19)	253.2	287.6	244.2	235.0	233.1	199.5	0.85	2.6E-01
B035DRAFT_00793	hypothetical protein	148.9	214.1	219.5	134.6	174.8	179.5	0.85	5.5E-01
B035DRAFT_00794	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II(EC:6.2.1.26)	145.8	151.2	153.7	141.3	157.9	156.0	1.01	9.1E-01
B035DRAFT_00795	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily	125.9	123.3	133.3	124.8	139.5	122.0	1.01	9.3E-01
B035DRAFT_00796	Uncharacterized protein conserved in bacteria	115.7	126.3	113.5	96.8	104.5	123.9	0.91	5.2E-01
B035DRAFT_00797	naphthoate synthase (dihydroxynaphthoic acid synthetase)(EC:4.1.3.36)	132.1	124.5	129.8	128.7	120.7	84.0	0.85	5.0E-01
B035DRAFT_00798	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase(EC:2.2.1.9)	105.1	99.2	110.7	87.9	85.1	87.6	0.83	4.9E-02
B035DRAFT_00799	isochorismate synthases(EC:5.4.4.2)	251.7	220.6	238.3	193.5	155.5	183.2	0.75	1.0E-01
B035DRAFT_00800	uncharacterized domain 1	325.8	373.2	345.5	348.4	239.3	262.4	0.80	3.3E-01
B035DRAFT_00801	putative efflux protein, MATE family	21.3	20.2	21.3	16.5	13.6	17.1	0.75	9.6E-02
B035DRAFT_00802	Thioredoxin.	247.7	202.4	175.1	150.4	168.3	123.2	0.71	2.1E-01
B035DRAFT_00803	Uncharacterized NAD(FAD)-dependent dehydrogenases	121.3	81.2	104.1	63.8	67.0	41.5	0.56	1.6E-01
B035DRAFT_00804	Transcriptional regulators	92.1	92.8	77.2	57.7	71.0	79.6	0.79	2.8E-01
B035DRAFT_00805	Chloride channel protein EriC	134.2	107.6	115.1	64.5	71.3	54.2	0.53	4.2E-02
B035DRAFT_00806	Uncharacterized protein conserved in bacteria	73.2	62.2	62.4	56.9	52.3	29.5	0.68	3.3E-01
B035DRAFT_00807	Periplasmic protease	90.0	87.4	92.6	103.0	109.6	95.7	1.14	1.5E-01
B035DRAFT_00808	hypothetical protein	33.3	35.8	35.5	24.9	25.1	32.2	0.78	1.8E-01
B035DRAFT_00809	Lactoylglutathione lyase and related lyases(EC:4.4.1.5)	169.4	165.4	171.0	215.0	193.9	284.4	1.35	2.0E-01
B035DRAFT_00810	Acyl dehydratase	358.6	380.9	390.8	275.0	263.8	301.1	0.74	3.9E-02
B035DRAFT_00811	O-6-methylguanine DNA methyltransferase	519.8	473.9	544.2	361.9	300.4	325.7	0.64	3.6E-02
B035DRAFT_00812	Protein-tyrosine-phosphatase(EC:1.20.4.1)	1179.6	1034.1	1048.0	956.2	701.4	579.7	0.67	2.0E-01
B035DRAFT_00813	hypothetical protein	43.6	42.5	51.4	38.5	38.3	44.8	0.88	4.0E-01
B035DRAFT_00814	hypothetical protein	90.7	69.1	50.4	38.7	63.8	27.0	0.60	3.6E-01
B035DRAFT_00815	Pseudouridylate synthases, 23S RNA-specific(EC:5.4.99.29,EC:5.4.99.28)	33.0	29.5	32.2	21.8	21.6	16.3	0.63	7.3E-02
B035DRAFT_00816	putative efflux protein, MATE family	124.4	118.0	127.3	44.4	48.1	38.4	0.35	3.9E-03
B035DRAFT_00817	hypothetical protein	5.9	5.7	7.2	6.2	10.7	10.8	1.43	3.3E-01
B035DRAFT_00818	RND family efflux transporter, MFP subunit	493.9	484.2	463.4	110.2	111.3	97.5	0.22	2.3E-04
B035DRAFT_00819	The (Largely Gram-negative Bacterial) Hydrophobe/Amphiphile Efflux-1 (HAE1) Family	365.5	342.2	350.9	111.6	123.3	86.4	0.30	9.9E-03
B035DRAFT_00820	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	406.0	385.2	414.7	147.3	150.5	108.2	0.33	1.4E-02
B035DRAFT_00821	Glycoside hydrolase (GH95)	114.5	93.7	122.5	94.7	86.8	27.1	0.55	4.3E-01
B035DRAFT_00822	Predicted permease	98.2	79.2	89.7	72.0	78.2	33.4	0.65	3.9E-01
B035DRAFT_00823	hypothetical protein	0.0	1.7	1.8	0.0	0.0	0.0	0.00	
B035DRAFT_00824	Undecaprenyl-phosphate glucose phosphotransferase	29.7	30.5	31.2	35.5	34.5	35.6	1.16	2.2E-02
B035DRAFT_00825	Periplasmic protein involved in polysaccharide export	22.8	28.8	16.9	24.5	28.6	27.7	1.21	5.2E-01
B035DRAFT_00826	capsular exopolysaccharide family	53.5	47.2	51.0	65.5	69.8	46.2	1.18	5.0E-01
B035DRAFT_00827	Negative regulator of beta-lactamase expression(EC:3.5.1.28)	7.2	4.0	6.0	8.8	9.6	6.5	1.48	3.3E-01
B035DRAFT_00828	DNA-binding protein, histone-like, putative	4.1	5.2	4.1	5.5	6.5	0.3	0.52	7.1E-01
B035DRAFT_00829	conserved hypothetical protein (putative transposase or invertase)	402.9	351.9	361.9	488.5	441.3	391.6	1.18	2.6E-01
B035DRAFT_00830	hypothetical protein	245.0	232.1	211.8	247.9	231.3	195.4	0.98	8.8E-01
B035DRAFT_00831	VirE N-terminal domain.	12.9	10.6	16.4	11.7	9.5	4.9	0.63	3.8E-01
B035DRAFT_00832	Transcription antiterminator	42.5	26.3	38.2	53.6	48.3	11.6	0.89	9.1E-01
B035DRAFT_00833	Membrane protein involved in the export of O-antigen and teichoic acid	17.9	16.7	19.1	16.4	23.3	22.4	1.14	5.2E-01
B035DRAFT_00834	Acetyltransferase (isoleucine patch superfamily)	16.5	21.9	22.1	21.6	27.5	27.5	1.27	3.2E-01
B035DRAFT_00835	hypothetical protein	12.8	13.4	9.3	9.2	14.9	20.3	1.20	7.0E-01
B035DRAFT_00836	Glycosyltransferases involved in cell wall biogenesis (GT2)	18.3	20.5	17.2	19.7	16.2	22.3	1.03	8.8E-01
B035DRAFT_00837	Coenzyme F420-reducing hydrogenase, beta subunit	26.9	28.2	24.6	25.5	27.9	30.3	1.05	6.7E-01

B035DRAFT_00838	Uncharacterized conserved protein	19.0	30.2	27.2	23.2	24.8	31.1	1.05	8.9E-01
B035DRAFT_00839	Bacterial transferase hexapeptide (three repeats).	15.8	21.1	19.2	18.7	17.8	24.9	1.09	7.3E-01
B035DRAFT_00840	Glycosyl transferases group 1 (GT4)	15.3	15.8	13.2	13.8	15.3	20.0	1.10	6.8E-01
B035DRAFT_00841	Acetyltransferase (isoleucine patch superfamily)(EC:2.3.1.79)	14.4	22.3	18.3	19.5	20.0	21.2	1.12	6.2E-01
B035DRAFT_00842	hypothetical protein	29.5	32.4	33.2	33.5	30.2	38.6	1.07	6.4E-01
B035DRAFT_00843	Glycosyltransferase (GT4)	30.0	26.0	25.5	22.2	25.2	28.1	0.93	6.2E-01
B035DRAFT_00844	bacterial polymer biosynthesis proteins, WecB/TagA/CpsF family (GT26)	21.2	29.6	20.9	21.6	22.7	22.3	0.94	7.8E-01
B035DRAFT_00845	Mannose-1-phosphate guanylyltransferase(EC:2.7.7.22)	26.5	25.0	23.2	21.8	22.7	20.0	0.86	1.8E-01
B035DRAFT_00846	hypothetical protein	19.3	16.8	21.6	15.7	14.6	4.1	0.51	4.1E-01
B035DRAFT_00847	hypothetical protein	34.6	27.0	30.0	21.3	25.0	20.4	0.73	1.4E-01
B035DRAFT_00848	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component, and related enzymes	227.2	142.6	163.7	171.3	154.4	123.2	0.85	5.9E-01
B035DRAFT_00849	Predicted membrane protein	168.1	130.9	130.4	141.4	148.2	176.9	1.09	6.7E-01
B035DRAFT_00850	AraC-type DNA-binding domain-containing proteins	169.7	146.9	144.3	179.7	174.2	222.8	1.25	2.3E-01
B035DRAFT_00851	thioredoxin	358.6	263.9	234.4	358.3	289.0	286.5	1.10	7.2E-01
B035DRAFT_00852	Signal transduction histidine kinase	19.6	23.1	20.0	24.0	24.6	32.9	1.29	2.6E-01
B035DRAFT_00853	Lysine 2,3-aminomutase(EC:5.4.3.2)	66.5	68.0	71.7	94.7	92.5	123.1	1.49	8.5E-02
B035DRAFT_00854	Outer membrane receptor for ferrienterochelin and colicins	48.4	48.8	49.5	54.8	64.8	44.7	1.11	6.0E-01
B035DRAFT_00855	hypothetical protein	204.9	214.6	217.9	239.2	230.4	199.2	1.05	6.7E-01
B035DRAFT_00856	5''-nucleotidase/2'',3''-cyclic phosphodiesterase and related esterases(EC:3.1.4.16)	212.1	213.0	199.3	205.1	231.5	183.4	0.99	9.4E-01
B035DRAFT_00857	Signal transduction histidine kinase	138.6	138.4	136.0	138.0	163.7	146.1	1.08	4.0E-01
B035DRAFT_00858	DnaJ-class molecular chaperone with C-terminal Zn finger domain	389.1	285.0	326.8	343.5	222.7	124.8	0.64	4.3E-01
B035DRAFT_00859	hypothetical protein	292.1	268.6	296.9	281.6	212.1	229.2	0.84	3.1E-01
B035DRAFT_00860	Transcriptional accessory protein	152.9	127.3	137.5	114.7	109.4	91.7	0.75	1.4E-01
B035DRAFT_00861	NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding(EC:3.6.1.22)	87.3	81.1	92.1	93.2	83.0	72.8	0.95	7.4E-01
B035DRAFT_00862	Predicted permease	115.1	125.5	137.2	127.2	122.2	108.9	0.95	6.8E-01
B035DRAFT_00863	Uncharacterized protein conserved in bacteria(EC:3.1.3.11)	127.2	149.8	144.9	125.6	143.7	150.5	0.99	9.8E-01
B035DRAFT_00864	L-aspartate-alpha-decarboxylase(EC:4.1.1.11)	620.3	638.3	616.7	582.1	554.9	500.4	0.87	1.6E-01
B035DRAFT_00865	pantoate--beta-alanine ligase(EC:6.3.2.1)	450.3	500.1	499.9	397.8	400.6	358.8	0.80	7.6E-02
B035DRAFT_00866	Glycogen synthase(EC:2.4.1.21) (GT5)	591.5	689.1	592.5	626.2	541.4	605.5	0.95	6.6E-01
B035DRAFT_00867	hypothetical protein	763.2	792.0	727.3	874.9	843.7	964.7	1.17	1.3E-01
B035DRAFT_00868	Phosphomannomutase(EC:5.4.2.8)	578.4	573.1	533.1	517.4	600.6	642.7	1.04	7.5E-01
B035DRAFT_00869	Dipeptidase	191.8	167.8	168.0	168.7	211.3	175.8	1.05	7.5E-01
B035DRAFT_00870	Membrane proteins related to metalloendopeptidases	106.3	86.9	97.0	136.0	130.2	78.3	1.16	6.7E-01
B035DRAFT_00871	alanine dehydrogenase(EC:1.4.1.1)	25.8	21.8	24.1	42.7	48.8	42.3	1.87	1.7E-02
B035DRAFT_00872	hypothetical protein	51.4	54.9	52.4	60.4	72.5	68.9	1.27	9.1E-02
B035DRAFT_00873	Predicted membrane protein	124.6	123.9	132.2	154.8	148.8	169.2	1.24	6.4E-02
B035DRAFT_00874	Transcriptional regulator	192.7	212.6	202.8	260.1	294.0	326.0	1.44	6.1E-02
B035DRAFT_00875	hypothetical protein	170.1	173.4	149.8	261.5	251.8	178.8	1.39	2.1E-01
B035DRAFT_00876	ATP-dependent chaperone ClpB	641.0	463.4	541.7	528.5	545.7	532.0	0.98	9.3E-01
B035DRAFT_00877	hypothetical protein	718.2	822.9	765.4	845.6	899.7	1015.5	1.20	2.0E-01
B035DRAFT_00878	dephospho-CoA kinase(EC:2.7.1.24)	236.3	228.3	235.5	211.5	238.0	198.5	0.92	4.2E-01
B035DRAFT_00879	YbbR-like protein.	353.8	360.6	345.2	316.0	352.8	402.6	1.01	9.7E-01
B035DRAFT_00880	preprotein translocase, YajC subunit	916.6	1082.5	1026.5	1060.7	990.9	1221.8	1.08	5.9E-01
B035DRAFT_00881	transcription antitermination factor NusB	1067.5	1273.3	1140.2	1094.4	1060.7	1315.3	1.00	9.8E-01
B035DRAFT_00882	Protein of unknown function (DUF3276).	158.9	196.4	143.9	250.9	267.1	299.5	1.65	7.0E-02
B035DRAFT_00883	ribosomal protein L25, Ctc-form	2319.7	2811.9	2511.8	2109.2	2079.9	2431.4	0.87	3.2E-01
B035DRAFT_00884	peptidyl-tRNA hydrolase(EC:3.1.1.29)	275.0	334.6	302.1	283.1	298.1	303.2	0.97	8.1E-01

B035DRAFT_00885	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)	208.3	216.5	200.3	227.2	224.9	195.0	1.03	7.5E-01
B035DRAFT_00886	Kef-type K+ transport systems, membrane components	86.5	96.4	85.8	73.2	94.7	98.5	0.98	9.4E-01
B035DRAFT_00887	glycine cleavage system T protein(EC:2.1.2.10)	718.5	732.5	671.6	691.7	779.7	779.3	1.06	5.0E-01
B035DRAFT_00888	peptidase T(EC:3.4.11.4)	258.4	258.1	234.8	295.5	364.6	394.1	1.39	1.2E-01
B035DRAFT_00889	Glutamine phosphoribosylpyrophosphate amidotransferase(EC:2.4.2.14)	296.8	300.6	306.4	251.3	271.5	236.0	0.84	8.5E-02
B035DRAFT_00890	Abortive infection bacteriophage resistance protein	248.0	276.5	240.9	232.4	244.0	279.5	0.99	9.2E-01
B035DRAFT_00891	hypothetical protein	64.4	47.8	57.6	48.0	53.5	67.4	0.99	9.8E-01
B035DRAFT_00892	protein CrcB	98.8	96.6	89.9	89.9	104.2	90.2	1.00	9.7E-01
B035DRAFT_00893	phosphopyruvate hydratase(EC:4.2.1.11)	1913.0	1684.4	1749.3	2101.9	1425.8	1304.3	0.89	6.6E-01
B035DRAFT_00894	Superfamily II DNA helicase	472.3	498.3	462.6	372.0	468.5	421.4	0.88	3.2E-01
B035DRAFT_00895	(tRNA)	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_00896	hypothetical protein	78.5	93.4	85.5	62.3	74.8	101.2	0.91	7.4E-01
B035DRAFT_00897	Glycosyltransferases involved in cell wall biogenesis (GT2)	87.6	91.4	92.9	92.3	93.7	109.1	1.08	4.4E-01
B035DRAFT_00898	hypothetical protein	89.5	101.2	83.5	97.5	96.8	124.7	1.16	4.2E-01
B035DRAFT_00899	hypothetical protein	74.0	79.7	77.6	73.9	91.0	83.4	1.07	5.6E-01
B035DRAFT_00900	Predicted membrane protein	36.9	40.4	44.5	37.9	34.2	42.9	0.94	7.1E-01
B035DRAFT_00901	Membrane-associated lipoprotein involved in thiamine biosynthesis	62.2	76.7	67.5	69.3	80.7	85.9	1.14	4.1E-01
B035DRAFT_00902	Multiple antibiotic transporter	88.0	86.3	85.6	83.2	89.1	105.1	1.06	6.3E-01
B035DRAFT_00903	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	134.6	136.8	137.3	183.7	151.5	189.6	1.28	1.3E-01
B035DRAFT_00904	Zn-dependent oligopeptidases(EC:3.4.15.5)	328.0	325.6	302.5	449.2	486.8	535.7	1.54	2.6E-02
B035DRAFT_00905	hypothetical protein	258.6	270.5	252.1	331.5	344.4	435.0	1.41	9.7E-02
B035DRAFT_00906	Deoxycytidylate deaminase(EC:3.5.4.12)	217.9	194.1	194.7	267.4	297.5	347.3	1.50	7.0E-02
B035DRAFT_00907	C-terminal peptidase (prc)(EC:3.4.21.102)	232.6	240.0	220.0	307.1	301.6	337.0	1.36	2.8E-02
B035DRAFT_00908	5,10-methenyltetrahydrofolate synthetase(EC:6.3.3.2)	256.9	253.7	240.0	318.8	327.9	370.9	1.35	4.4E-02
B035DRAFT_00909	Protein of unknown function (DUF721).	108.6	118.1	132.1	117.3	111.0	145.1	1.04	8.5E-01
B035DRAFT_00910	recF protein	82.2	78.8	74.6	88.4	95.1	89.0	1.16	9.4E-02
B035DRAFT_00911	Uncharacterized protein conserved in bacteria	834.4	967.6	771.9	820.7	706.9	695.8	0.87	3.6E-01
B035DRAFT_00912	6,7-dimethyl-8-ribityllumazine synthase(EC:2.5.1.78)	282.9	292.6	259.6	250.3	259.2	290.1	0.96	6.7E-01
B035DRAFT_00913	(tRNA)	188.6	427.6	515.6	356.7	202.6	192.1	0.69	5.8E-01
B035DRAFT_00914	(tRNA)	491.7	505.7	639.2	494.5	347.2	291.3	0.68	2.6E-01
B035DRAFT_00915	Pirin-related protein	445.7	438.1	414.0	446.5	355.6	443.6	0.96	7.5E-01
B035DRAFT_00916	hypothetical protein	62.8	69.2	73.4	54.8	52.9	57.3	0.80	8.4E-02
B035DRAFT_00917	hypothetical protein	27.7	21.1	29.1	26.8	32.2	31.0	1.16	4.7E-01
B035DRAFT_00918	hypothetical protein	23.1	27.8	33.0	25.7	27.0	34.6	1.04	8.8E-01
B035DRAFT_00919	hypothetical protein	36.0	41.3	38.6	41.9	46.4	46.9	1.17	1.8E-01
B035DRAFT_00920	exodeoxyribonuclease III(EC:3.1.11.2)	84.8	76.3	76.9	82.2	94.8	81.1	1.08	4.6E-01
B035DRAFT_00921	hypothetical protein	15.9	9.0	14.1	6.1	7.9	7.0	0.55	1.5E-01
B035DRAFT_00922	hypothetical protein	7.4	8.7	10.7	8.2	11.1	5.6	0.90	8.1E-01
B035DRAFT_00923	ABC-type multidrug transport system, ATPase and permease components	8.2	8.1	7.5	5.6	8.6	6.6	0.86	5.2E-01
B035DRAFT_00924	hypothetical protein	21.8	19.3	20.9	17.5	23.7	19.6	0.97	8.9E-01
B035DRAFT_00925	hypothetical protein	17.5	17.9	23.3	19.6	16.4	15.4	0.88	5.3E-01
B035DRAFT_00926	hypothetical protein	38.1	32.1	33.2	29.8	38.0	29.1	0.93	7.1E-01
B035DRAFT_00927	hypothetical protein	23.1	30.2	24.6	18.2	11.8	5.2	0.40	2.3E-01
B035DRAFT_00928	hypothetical protein	38.8	14.7	37.8	24.5	18.5	27.4	0.83	7.7E-01
B035DRAFT_00929	Periplasmic protease	90.3	87.8	84.8	69.9	85.8	79.7	0.89	3.3E-01
B035DRAFT_00930	protein translocase, SecG subunit	920.0	1093.3	1059.5	977.8	895.6	1227.3	1.00	9.9E-01
B035DRAFT_00931	hypothetical protein	167.1	172.1	179.5	199.1	197.5	251.9	1.24	2.0E-01
B035DRAFT_00932	hypothetical protein	188.4	209.4	204.4	215.2	236.9	282.0	1.21	2.5E-01

B035DRAFT_00933	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	289.5	303.9	292.9	316.9	337.1	314.1	1.09	1.4E-01
B035DRAFT_00934	Myo-inositol-1-phosphate synthase(EC:5.5.1.4)	664.2	749.2	743.8	551.6	594.9	674.4	0.84	2.3E-01
B035DRAFT_00935	Sugar kinases, ribokinase family	101.6	112.8	96.4	87.7	89.5	83.8	0.84	1.3E-01
B035DRAFT_00936	Fucose permease	76.5	78.5	77.6	72.1	82.7	71.3	0.97	7.4E-01
B035DRAFT_00937	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED/haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E	123.2	126.5	117.3	106.2	126.8	97.7	0.90	4.5E-01
B035DRAFT_00938	Uncharacterised protein family (UPF0104).	121.0	131.1	133.5	114.3	138.2	127.0	0.98	8.8E-01
B035DRAFT_00939	Phosphatidylglycerophosphate synthase	162.5	153.6	142.7	121.4	139.8	128.0	0.85	1.7E-01
B035DRAFT_00940	hypothetical protein	286.7	255.0	290.4	256.6	242.4	159.1	0.78	3.8E-01
B035DRAFT_00941	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)	240.7	230.2	216.0	202.7	247.0	227.9	0.98	9.0E-01
B035DRAFT_00942	4-hydroxythreonine-4-phosphate dehydrogenase(EC:1.1.1.262)	377.6	363.1	357.9	332.7	394.2	333.3	0.96	7.2E-01
B035DRAFT_00943	hypothetical protein	250.5	255.0	239.9	234.8	288.7	300.3	1.10	5.1E-01
B035DRAFT_00944	23S rRNA m2A2503 methyltransferase(EC:2.1.1.)	240.6	251.1	244.8	248.5	258.3	232.7	1.00	9.6E-01
B035DRAFT_00945	Glycosyltransferases involved in cell wall biogenesis (GT2)	36.2	31.1	32.2	33.6	37.3	35.6	1.07	4.9E-01
B035DRAFT_00946	SpoIID/LytB domain	44.8	43.4	49.2	38.9	45.4	41.6	0.92	4.1E-01
B035DRAFT_00947	Major Facilitator Superfamily	37.0	34.8	40.8	34.6	35.8	32.3	0.91	3.8E-01
B035DRAFT_00948	hypothetical protein	835.5	819.9	804.9	840.1	471.5	479.6	0.70	3.2E-01
B035DRAFT_00949	hypothetical protein	192.8	194.9	208.5	160.1	117.4	131.3	0.68	9.1E-02
B035DRAFT_00950	Predicted P-loop ATPase and inactivated derivatives	120.8	104.3	146.3	105.0	82.4	35.9	0.55	3.5E-01
B035DRAFT_00951	hypothetical protein	463.8	489.9	628.4	531.5	471.9	481.5	0.95	7.7E-01
B035DRAFT_00952	hypothetical protein	16.8	22.4	19.7	17.6	17.3	23.4	0.99	9.6E-01
B035DRAFT_00953	hypothetical protein	11.1	9.7	9.8	8.3	9.3	11.0	0.93	6.7E-01
B035DRAFT_00954	hypothetical protein	3.9	2.1	1.1	2.1	3.8	1.1	0.99	9.9E-01
B035DRAFT_00955	hypothetical protein	10.6	7.4	11.0	6.7	8.9	5.8	0.74	3.6E-01
B035DRAFT_00956	Site-specific recombinase XerD	36.4	36.3	42.9	31.6	33.0	41.5	0.91	6.2E-01
B035DRAFT_00957	Protein of unknown function DUF262./HNH endonuclease.	82.2	84.0	79.7	69.1	90.2	61.1	0.88	5.6E-01
B035DRAFT_00958	hypothetical protein	75.3	81.8	73.3	64.9	69.9	70.8	0.89	2.0E-01
B035DRAFT_00959	hypothetical protein	112.3	129.0	106.2	120.7	136.7	152.4	1.18	3.3E-01
B035DRAFT_00960	Predicted transcriptional regulators	34.8	41.4	35.3	36.6	39.8	47.4	1.11	5.5E-01
B035DRAFT_00961	Predicted N-acetylglucosamine kinase	214.6	215.1	216.6	258.3	263.8	192.6	1.10	6.2E-01
B035DRAFT_00962	N-acetylmuramic acid 6-phosphate etherase(EC:4.2.)	114.1	108.0	113.9	110.5	134.2	63.2	0.87	7.5E-01
B035DRAFT_00963	Uncharacterized protein conserved in bacteria	142.9	129.8	120.3	112.2	131.3	129.2	0.95	6.8E-01
B035DRAFT_00964	Signal transduction histidine kinase	103.5	99.1	101.4	85.2	125.5	99.7	1.01	9.8E-01
B035DRAFT_00965	Ribosomal protein S1	4093.7	4260.2	4044.2	3566.8	4298.5	4801.7	1.01	9.4E-01
B035DRAFT_00966	Cold shock proteins	1293.6	1279.2	1107.8	1787.4	1839.6	2418.2	1.63	7.7E-02
B035DRAFT_00967	ribonuclease Z(EC:3.1.26.11)	238.9	276.8	256.5	237.9	326.3	371.5	1.19	4.8E-01
B035DRAFT_00968	RNA polymerase sigma factor, sigma-70 family	146.9	155.8	152.7	131.8	191.4	212.5	1.15	5.9E-01
B035DRAFT_00969	hypothetical protein	186.5	193.2	191.9	224.3	274.0	280.0	1.36	8.5E-02
B035DRAFT_00970	hypothetical protein	153.7	179.1	174.5	225.4	250.5	283.8	1.49	6.5E-02
B035DRAFT_00971	Predicted acyltransferases	45.0	44.2	44.7	42.6	60.9	59.3	1.20	3.9E-01
B035DRAFT_00972	Plasmid recombination enzyme.	3.9	3.6	3.7	4.6	1.2	2.0	0.59	4.7E-01
B035DRAFT_00973	hypothetical protein	4.0	3.9	1.6	6.3	3.0	1.2	0.97	9.8E-01
B035DRAFT_00974	TonB family C-terminal domain	4.9	6.0	6.8	6.4	5.7	9.0	1.18	5.8E-01
B035DRAFT_00975	TonB family C-terminal domain	4.6	4.7	4.1	4.1	3.0	5.9	0.94	8.7E-01
B035DRAFT_00976	hypothetical protein	8.6	9.7	16.7	17.4	12.6	7.4	1.05	9.4E-01
B035DRAFT_00977	hypothetical protein	35.6	39.5	34.7	49.9	49.0	64.4	1.48	9.3E-02
B035DRAFT_00978	hypothetical protein	41.5	48.7	38.8	45.6	51.4	70.0	1.28	3.6E-01

B035DRAFT_00979	(tRNA)	67.6	131.4	141.2	120.2	66.1	46.7	0.67	5.3E-01
B035DRAFT_00980	Mismatch repair ATPase (MutS family)	36.0	35.6	33.1	32.6	42.4	43.6	1.12	5.1E-01
B035DRAFT_00981	L-serine dehydratase, iron-sulfur-dependent, single chain form(EC:4.3.1.17)	133.6	135.1	143.2	135.0	140.0	139.2	1.01	9.0E-01
B035DRAFT_00982	hypothetical protein	185.7	191.1	207.4	125.0	147.6	193.6	0.79	3.3E-01
B035DRAFT_00983	hypothetical protein	359.3	364.7	341.0	323.2	307.5	381.4	0.95	6.6E-01
B035DRAFT_00984	Protein of unknown function (DUF2874).	427.9	437.7	427.9	400.0	362.2	421.9	0.91	3.0E-01
B035DRAFT_00985	hypothetical protein	49.2	54.4	50.1	68.0	64.5	73.3	1.34	4.3E-02
B035DRAFT_00986	K+ transport systems, NAD-binding component	50.2	56.3	64.3	48.1	36.1	42.2	0.74	1.9E-01
B035DRAFT_00987	Trk-type K+ transport systems, membrane components	108.2	109.8	121.2	104.3	76.1	86.9	0.78	2.2E-01
B035DRAFT_00988	pyridoxal-phosphate dependent TrpB-like enzyme(EC:4.2.1.20)	223.7	263.7	242.3	253.3	280.0	307.3	1.15	3.2E-01
B035DRAFT_00989	Porin subfamily	206.1	151.0	184.7	146.7	175.6	136.7	0.85	4.4E-01
B035DRAFT_00990	(tRNA)	98.4	73.1	76.8	115.3	70.1	59.3	0.95	9.2E-01
B035DRAFT_00991	hypothetical protein	819.1	1058.2	925.0	941.3	787.5	782.2	0.90	5.3E-01
B035DRAFT_00992	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_00993	hypothetical protein	15.3	18.7	18.6	15.0	17.5	15.1	0.91	5.2E-01
B035DRAFT_00994	hypothetical protein	67.3	60.0	66.3	91.5	117.5	109.7	1.64	4.4E-02
B035DRAFT_00995	Beta-glucosidase-related glycosidases(EC:3.2.1.21) (GH3)	27.5	28.3	27.8	32.4	33.2	36.5	1.22	5.6E-02
B035DRAFT_00996	Beta-galactosidase/beta-glucuronidase (GH2)	13.6	13.9	13.0	13.7	16.9	15.5	1.14	2.9E-01
B035DRAFT_00997	Arylsulfatase A and related enzymes	7.5	7.0	7.6	6.2	7.3	7.5	0.95	6.7E-01
B035DRAFT_00998	AraC-type DNA-binding domain-containing proteins	5.2	5.2	7.1	5.1	2.6	5.8	0.74	5.3E-01
B035DRAFT_00999	Beta-galactosidase/beta-glucuronidase (GH2)	8.5	6.9	6.6	5.1	4.6	5.6	0.70	1.2E-01
B035DRAFT_01000	hypothetical protein	5.3	5.2	4.5	2.8	3.0	4.2	0.66	1.7E-01
B035DRAFT_01001	Arabinose efflux permease	1.8	4.4	2.2	1.7	3.0	2.1	0.84	7.6E-01
B035DRAFT_01002	AraC-type DNA-binding domain-containing proteins	42.4	58.8	49.7	63.3	63.3	81.2	1.38	2.1E-01
B035DRAFT_01003	Uncharacterized protein conserved in bacteria	35.6	43.2	44.0	38.7	41.7	50.1	1.06	7.6E-01
B035DRAFT_01004	Carbon starvation protein, predicted membrane protein	61.6	60.9	67.2	59.0	62.4	73.5	1.02	8.7E-01
B035DRAFT_01005	hypothetical protein	62.4	64.6	51.9	39.3	41.4	47.7	0.72	1.1E-01
B035DRAFT_01006	hypothetical protein	165.1	196.0	167.5	120.0	132.3	134.5	0.73	7.0E-02
B035DRAFT_01007	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	95.4	93.2	81.7	81.0	123.2	137.6	1.24	4.9E-01
B035DRAFT_01008	Exonuclease III	57.1	59.5	63.5	70.0	85.8	88.9	1.35	1.1E-01
B035DRAFT_01009	excinuclease ABC, A subunit	76.7	71.4	72.9	92.1	88.0	86.2	1.20	3.8E-02
B035DRAFT_01010	Uncharacterized protein conserved in bacteria	146.2	149.8	142.8	153.0	153.8	133.7	1.00	9.8E-01
B035DRAFT_01011	ResB protein required for cytochrome c biosynthesis	183.4	195.9	180.7	143.1	126.0	154.7	0.75	8.2E-02
B035DRAFT_01012	Cytochrome c biogenesis factor	165.5	148.9	125.5	97.1	89.8	101.4	0.66	7.0E-02
B035DRAFT_01013	Cytochrome c peroxidase(EC:1.11.1.5)	229.0	178.8	146.7	109.7	122.2	104.7	0.62	1.2E-01
B035DRAFT_01014	Chromate transport protein ChrA	98.8	110.7	106.9	73.2	62.0	67.0	0.64	2.5E-02
B035DRAFT_01015	Chromate transport protein ChrA	137.2	180.3	184.2	138.6	116.0	130.3	0.77	2.3E-01
B035DRAFT_01016	Signal transduction histidine kinase	138.3	151.5	139.6	122.1	96.2	121.2	0.79	1.7E-01
B035DRAFT_01017	phosphoribosylformylglycinamidine synthase, single chain form(EC:6.3.5.3)	497.7	491.0	474.7	465.4	500.1	513.8	1.01	8.8E-01
B035DRAFT_01018	Putative threonine efflux protein	149.0	161.3	162.0	161.1	151.5	122.8	0.92	5.8E-01
B035DRAFT_01019	hypothetical protein	152.1	174.3	148.8	150.6	161.3	176.1	1.03	8.4E-01
B035DRAFT_01020	dTDP-4-dehydrorhamnose reductase(EC:1.1.1.133)	228.6	239.4	220.4	208.1	218.3	195.6	0.90	2.1E-01
B035DRAFT_01021	peptide chain release factor 3	250.0	245.0	247.1	235.5	235.8	245.3	0.97	2.3E-01
B035DRAFT_01022	hypothetical protein	68.1	65.5	66.7	79.5	85.8	81.1	1.23	2.2E-02
B035DRAFT_01023	Predicted transcriptional regulator	58.6	68.7	59.5	74.5	101.2	103.2	1.48	1.4E-01
B035DRAFT_01024	TonB family C-terminal domain	86.2	94.2	85.7	132.3	118.4	114.5	1.37	4.5E-02
B035DRAFT_01025	Tetratricopeptide repeat.	66.2	72.4	65.3	91.0	77.6	96.7	1.30	1.2E-01
B035DRAFT_01026	hypothetical protein	95.2	102.2	96.7	103.4	128.8	150.9	1.29	2.5E-01
B035DRAFT_01027	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	145.5	150.5	139.8	144.7	149.8	153.3	1.03	5.8E-01

B035DRAFT_01028	tRNA dimethylallyltransferase(EC:2.5.1.75)	107.9	116.1	96.3	110.7	117.0	124.6	1.10	4.1E-01
B035DRAFT_01029	Plasmid pRiA4b ORF-3-like protein.	714.8	780.6	707.9	834.9	851.9	913.5	1.18	9.4E-02
B035DRAFT_01030	acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase(EC:2.3.1.129)	463.4	522.4	495.1	492.3	489.1	432.4	0.95	6.4E-01
B035DRAFT_01031	UDP-3-0-acyl N-acetylglucosamine deacetylase/beta-hydroxyacyl-[acyl carrier protein] dehydratase FabZ(EC:3.5.1.) (CE11)	411.7	419.2	398.9	401.1	427.6	441.6	1.03	5.8E-01
B035DRAFT_01032	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase(EC:2.3.1.)	343.5	362.9	350.3	345.6	357.7	363.2	1.01	8.3E-01
B035DRAFT_01033	HD superfamily phosphohydrolases	143.5	156.0	148.5	120.7	143.0	153.9	0.93	5.9E-01
B035DRAFT_01034	orotidine 5''-phosphate decarboxylase, subfamily 2(EC:4.1.1.23)	293.8	301.8	282.3	271.6	284.2	320.8	1.00	9.8E-01
B035DRAFT_01035	peptide chain release factor 1	331.5	282.1	299.0	310.3	304.3	187.9	0.86	6.2E-01
B035DRAFT_01036	hypothetical protein	268.9	297.0	286.9	266.0	296.0	306.4	1.02	8.7E-01
B035DRAFT_01037	Phosphoribosylaminoimidazole (AIR) synthetase(EC:6.3.3.1)	379.5	345.7	331.1	340.5	358.2	272.0	0.91	6.0E-01
B035DRAFT_01038	Predicted permease	258.9	281.8	286.6	265.3	182.6	215.3	0.79	2.9E-01
B035DRAFT_01039	Tetratricopeptide repeat./Coatomer epsilon subunit.	140.1	144.5	136.4	123.0	138.5	134.8	0.94	4.0E-01
B035DRAFT_01040	N-acetyl-beta-hexosaminidase(EC:3.2.1.35) (GH84)	124.9	126.0	132.5	118.3	141.3	127.5	1.01	9.5E-01
B035DRAFT_01041	ATP-dependent DNA helicase, RecQ family(EC:3.6.4.12)	155.4	169.5	156.8	152.2	150.5	139.2	0.92	2.6E-01
B035DRAFT_01042	single-stranded-DNA-specific exonuclease RecJ(EC:3.1.)	476.5	494.2	463.9	500.7	509.7	563.4	1.10	2.6E-01
B035DRAFT_01043	Aminopeptidase C	729.5	710.1	609.0	498.5	599.7	677.2	0.86	4.4E-01
B035DRAFT_01044	Xaa-Pro aminopeptidase(EC:3.4.11.9)	314.4	319.9	304.9	323.1	352.6	389.9	1.13	2.6E-01
B035DRAFT_01045	Arylsulfatase A and related enzymes	20.2	20.3	17.8	27.4	30.2	33.4	1.56	4.2E-02
B035DRAFT_01046	Predicted esterase of the alpha-beta hydrolase superfamily	238.9	207.2	230.1	167.2	141.3	112.4	0.62	9.7E-02
B035DRAFT_01047	Subtilisin-like serine proteases	112.2	100.5	113.0	88.1	96.7	66.2	0.76	2.5E-01
B035DRAFT_01048	hypothetical protein	151.5	142.9	157.4	128.5	135.2	84.8	0.76	3.3E-01
B035DRAFT_01049	hypothetical protein	47.6	47.4	47.7	39.2	42.8	46.5	0.90	2.6E-01
B035DRAFT_01050	hypothetical protein	53.4	57.5	50.8	52.9	52.1	63.2	1.04	7.8E-01
B035DRAFT_01051	conserved hypothetical protein YmdA/YtgF	909.1	958.7	907.5	909.6	871.9	824.8	0.94	3.2E-01
B035DRAFT_01052	Cell division protein ZapA.	208.6	307.9	258.7	316.9	339.6	479.4	1.46	2.6E-01
B035DRAFT_01053	hypothetical protein	309.4	372.2	352.3	456.2	420.7	524.7	1.35	1.2E-01
B035DRAFT_01054	6-pyruvoyl-tetrahydropterin synthase(EC:4.2.3.12)	210.5	242.9	209.9	280.9	275.9	247.6	1.21	1.5E-01
B035DRAFT_01055	Organic radical activating enzymes	260.2	296.3	305.3	331.9	307.7	369.7	1.17	2.7E-01
B035DRAFT_01056	(tRNA)	90.0	121.4	116.3	94.8	96.7	83.8	0.85	3.8E-01
B035DRAFT_01057	G:T/U mismatch-specific DNA glycosylase	127.1	142.8	139.5	116.8	135.3	165.7	1.01	9.6E-01
B035DRAFT_01058	hypothetical protein	214.2	244.3	206.9	216.1	219.1	261.3	1.05	7.7E-01
B035DRAFT_01059	amino acid carrier protein	97.8	95.7	91.3	88.2	78.3	74.8	0.85	1.5E-01
B035DRAFT_01060	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen	17.1	21.0	13.3	12.5	17.2	12.3	0.82	5.2E-01
B035DRAFT_01061	Predicted periplasmic ligand-binding sensor domain	18.5	21.3	18.6	16.9	20.4	19.8	0.97	8.6E-01
B035DRAFT_01062	Predicted acetyltransferase	1495.2	1396.6	1357.0	1605.6	968.7	1008.5	0.82	5.1E-01
B035DRAFT_01063	Uncharacterized conserved protein	400.9	400.8	378.6	351.8	298.0	370.8	0.86	2.7E-01
B035DRAFT_01064	Thiol:disulfide interchange protein	239.1	226.7	240.3	286.2	259.7	354.3	1.26	2.2E-01
B035DRAFT_01065	AraC-type DNA-binding domain-containing proteins	19.6	32.2	27.0	28.5	26.3	32.3	1.12	6.9E-01
B035DRAFT_01066	(tRNA)	105.2	138.6	176.5	120.2	66.1	31.8	0.46	3.2E-01
B035DRAFT_01067	hypothetical protein	68.9	60.6	75.0	64.9	63.4	38.1	0.79	4.9E-01
B035DRAFT_01068	hypothetical protein	12.8	10.2	16.0	9.0	9.4	6.0	0.62	2.3E-01
B035DRAFT_01069	hypothetical protein	9.0	6.9	12.3	5.1	3.0	2.0	0.35	1.3E-01
B035DRAFT_01070	hypothetical protein	5.3	5.8	6.9	3.2	2.9	2.1	0.45	5.1E-02
B035DRAFT_01071	hypothetical protein	3.3	3.2	4.1	0.6	3.5	1.0	0.36	3.2E-01
B035DRAFT_01072	hypothetical protein	4.5	5.2	5.5	0.8	1.7	0.3	0.15	9.4E-02
B035DRAFT_01073	hypothetical protein	7.6	3.1	4.8	3.5	1.8	0.6	0.32	3.1E-01
B035DRAFT_01074	hypothetical protein	4.9	3.6	4.2	4.4	3.5	1.9	0.73	5.1E-01
B035DRAFT_01075	hypothetical protein	6.3	3.9	8.7	2.2	3.8	1.9	0.42	1.9E-01

B035DRAFT_01076	hypothetical protein	6.7	6.5	6.0	3.1	3.0	1.6	0.39	8.5E-02
B035DRAFT_01077	Protease subunit of ATP-dependent Clp proteases	6.1	3.2	5.8	2.4	1.9	0.6	0.28	2.0E-01
B035DRAFT_01078	Transcriptional regulator, contains sigma factor-related N-terminal domain	5.3	4.0	4.2	2.8	3.8	1.4	0.55	3.2E-01
B035DRAFT_01079	Terminase-like family	6.3	4.4	5.3	4.1	2.7	1.1	0.44	2.9E-01
B035DRAFT_01080	Protein of unknown function (DUF1320).	3.2	4.1	4.3	2.9	2.5	1.1	0.52	2.9E-01
B035DRAFT_01081	Mu-like prophage protein gp29	8.4	3.9	5.9	6.1	3.0	0.7	0.40	4.6E-01
B035DRAFT_01082	Phage Mu protein F like protein.	10.6	6.1	9.3	8.3	5.8	4.8	0.73	4.5E-01
B035DRAFT_01083	Mu-like prophage protein gpG	12.7	7.2	13.5	8.5	8.1	1.7	0.46	4.4E-01
B035DRAFT_01084	hypothetical protein	17.6	18.7	18.6	16.1	12.2	7.0	0.61	2.9E-01
B035DRAFT_01085	hypothetical protein	25.7	18.2	24.3	24.8	16.2	16.8	0.84	5.8E-01
B035DRAFT_01086	DNA-binding protein, histone-like, putative	27.2	18.5	22.2	19.6	13.7	4.2	0.47	3.9E-01
B035DRAFT_01087	hypothetical protein	14.7	7.0	6.3	6.4	8.6	4.7	0.73	5.9E-01
B035DRAFT_01088	Predicted membrane protein	855.4	850.0	674.4	929.3	887.6	985.6	1.18	3.0E-01
B035DRAFT_01089	hypothetical protein	1052.7	1048.1	679.3	1215.9	1179.6	1063.4	1.27	3.9E-01
B035DRAFT_01090	hypothetical protein	14.4	6.9	8.8	13.8	9.5	8.3	1.08	8.8E-01
B035DRAFT_01091	hypothetical protein	4.4	4.7	5.8	5.7	3.1	5.2	0.91	8.2E-01
B035DRAFT_01092	Protein of unknown function (DUF2786).	1.9	2.0	2.3	3.3	2.8	1.3	1.12	8.5E-01
B035DRAFT_01093	hypothetical protein	3.0	2.8	2.9	4.4	3.2	3.2	1.25	2.7E-01
B035DRAFT_01094	Mu-like prophage host-nuclease inhibitor protein Gam	3.7	2.2	2.7	2.9	2.3	1.1	0.70	5.5E-01
B035DRAFT_01095	hypothetical protein	5.0	1.2	2.4	4.2	1.8	2.7	1.14	8.9E-01
B035DRAFT_01096	hypothetical protein	3.3	1.6	1.4	2.0	1.3	1.3	0.76	6.4E-01
B035DRAFT_01097	hypothetical protein	0.8	1.3	0.9	0.8	1.0	1.7	1.15	7.9E-01
B035DRAFT_01098	hypothetical protein	1.0	0.9	1.8	1.0	1.1	1.1	0.95	9.1E-01
B035DRAFT_01099	AAA domain (dynein-related subfamily).	2.3	1.3	1.2	1.6	2.2	0.2	0.56	7.1E-01
B035DRAFT_01100	Integrase core domain.	1.6	1.0	1.5	1.2	1.0	0.9	0.74	3.3E-01
B035DRAFT_01101	hypothetical protein	1.6	2.7	1.9	4.1	2.1	0.7	0.92	9.3E-01
B035DRAFT_01102	hypothetical protein	4.2	3.9	2.0	3.5	0.0	3.8	1.14	7.7E-01
B035DRAFT_01103	hypothetical protein	2.4	1.8	2.9	0.8	0.7	2.9	0.51	4.3E-01
B035DRAFT_01104	Predicted transcriptional regulator	61.4	73.1	63.4	100.8	106.5	132.2	1.71	5.4E-02
B035DRAFT_01105	hypothetical protein	34.8	48.7	45.3	45.3	46.3	63.2	1.20	5.0E-01
B035DRAFT_01106	(tRNA)	14.1	28.1	14.7	16.9	18.2	12.8	0.88	7.8E-01
B035DRAFT_01107	hypothetical protein	24.1	34.3	27.9	47.4	48.6	54.7	1.76	6.2E-02
B035DRAFT_01108	AraC-type DNA-binding domain-containing proteins	16.8	18.9	17.5	18.3	25.4	25.4	1.29	2.6E-01
B035DRAFT_01109	Hydrolases of the alpha/beta superfamily	11.7	11.5	14.7	11.3	10.3	9.9	0.84	2.9E-01
B035DRAFT_01110	Predicted amidohydrolase	132.6	137.6	139.5	121.4	129.4	80.8	0.79	4.0E-01
B035DRAFT_01111	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits(EC:1.2.7.8)	181.8	190.7	180.4	143.5	183.3	160.4	0.88	3.4E-01
B035DRAFT_01112	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit(EC:1.2.7.8)	144.5	150.8	128.9	96.9	125.5	103.4	0.76	1.7E-01
B035DRAFT_01113	Aspartate/tyrosine/aromatic aminotransferase	130.2	139.6	128.2	100.2	114.0	112.3	0.82	9.1E-02
B035DRAFT_01114	Coenzyme F390 synthetase(EC:6.2.1.30)	182.0	192.1	186.3	128.2	152.0	146.4	0.76	6.1E-02
B035DRAFT_01115	ACT domain-containing protein	181.1	216.1	198.2	151.4	168.2	191.8	0.86	3.4E-01
B035DRAFT_01116	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	1064.8	1243.6	1079.4	771.1	860.2	1037.2	0.78	2.2E-01
B035DRAFT_01117	vacuolar-type H(+)-translocating pyrophosphatase(EC:3.6.1.1)	41.7	40.0	44.7	49.9	52.4	44.6	1.16	2.1E-01
B035DRAFT_01118	uncharacterized radical SAM protein YgiQ	150.6	158.3	152.6	185.7	204.0	188.8	1.25	3.2E-02
B035DRAFT_01119	hypothetical protein	159.8	209.9	180.9	282.5	315.9	364.7	1.75	6.0E-02
B035DRAFT_01120	hypothetical protein	16.1	14.3	12.6	15.5	16.8	11.6	1.01	9.6E-01
B035DRAFT_01121	hypothetical protein	1185.7	1220.6	1166.6	1086.4	1108.8	1168.5	0.94	2.3E-01
B035DRAFT_01122	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	

B035DRAFT_01123	Type III restriction enzyme, res subunit./Type I restriction enzyme R protein N terminus (HSDR_N).	241.2	245.5	232.3	275.0	281.2	261.5	1.14	7.0E-02
B035DRAFT_01124	hypothetical protein	113.4	144.4	122.0	125.0	148.2	153.5	1.13	5.0E-01
B035DRAFT_01125	hypothetical protein	242.5	231.7	190.0	225.8	277.4	287.3	1.19	3.8E-01
B035DRAFT_01126	hypothetical protein	246.3	236.4	217.0	269.2	275.8	326.2	1.24	1.6E-01
B035DRAFT_01127	Restriction endonuclease S subunits	237.7	245.5	205.8	242.4	285.8	325.5	1.23	2.8E-01
B035DRAFT_01128	Restriction endonuclease S subunits	215.3	226.5	216.6	205.8	249.4	291.4	1.12	5.3E-01
B035DRAFT_01129	Type I restriction-modification system methyltransferase subunit(EC:2.1.1.72)	360.0	320.3	328.9	358.4	371.5	293.4	1.01	9.5E-01
B035DRAFT_01130	Predicted transcription factor, homolog of eukaryotic MBF1	135.6	130.0	130.3	146.1	150.3	131.2	1.08	3.5E-01
B035DRAFT_01131	Site-specific recombinase XerD	427.7	460.1	435.4	488.6	460.3	519.7	1.11	2.2E-01
B035DRAFT_01132	hypothetical protein	94.4	95.8	84.9	85.8	85.4	111.1	1.02	9.2E-01
B035DRAFT_01133	tRNA modification GTPase TrmE(EC:3.6.)	213.3	206.9	208.4	181.6	183.9	223.6	0.93	5.7E-01
B035DRAFT_01134	GAF domain-containing protein	169.3	149.1	154.0	130.3	129.8	174.1	0.91	6.3E-01
B035DRAFT_01135	Uridine phosphorylase(EC:2.4.2.3)	210.7	198.6	195.8	182.8	192.9	247.0	1.02	9.2E-01
B035DRAFT_01136	Uncharacterized protein conserved in bacteria	132.4	135.0	145.5	139.9	151.9	175.0	1.13	3.7E-01
B035DRAFT_01137	Membrane-bound serine protease (ClpP class)	56.3	73.8	76.0	80.2	66.4	108.9	1.22	5.2E-01
B035DRAFT_01138	Uncharacterized protein conserved in bacteria	95.3	105.6	90.2	149.1	171.0	187.9	1.74	3.3E-02
B035DRAFT_01139	Predicted ATPase of the PP-loop superfamily implicated in cell cycle control	112.4	120.6	115.7	96.4	103.3	88.4	0.82	1.0E-01
B035DRAFT_01140	Uncharacterized protein conserved in bacteria	36.5	37.8	38.6	17.5	21.6	39.6	0.66	3.6E-01
B035DRAFT_01141	Uncharacterized protein conserved in bacteria	39.5	53.8	50.3	37.8	38.3	42.5	0.83	3.3E-01
B035DRAFT_01142	hypothetical protein	22.1	23.7	21.8	22.2	23.7	29.3	1.11	5.2E-01
B035DRAFT_01143	hypothetical protein	14.9	18.0	20.0	14.2	17.6	19.0	0.96	8.6E-01
B035DRAFT_01144	hypothetical protein	11.0	21.6	19.2	10.5	14.3	17.8	0.84	7.1E-01
B035DRAFT_01145	Site-specific recombinase XerD	6.0	6.3	6.3	2.7	2.6	4.4	0.51	9.7E-02
B035DRAFT_01146	DNA repair proteins	6.8	7.0	4.6	0.4	2.4	2.7	0.23	2.4E-01
B035DRAFT_01147	hypothetical protein	7.9	7.3	9.3	7.8	7.2	6.0	0.86	4.2E-01
B035DRAFT_01148	hypothetical protein	6.2	3.6	3.3	5.0	4.1	3.8	1.02	9.7E-01
B035DRAFT_01149	hypothetical protein	5.8	6.7	6.1	4.3	5.9	6.6	0.89	6.4E-01
B035DRAFT_01150	hypothetical protein	27.5	31.7	30.3	42.8	39.6	54.2	1.52	9.4E-02
B035DRAFT_01151	Site-specific recombinases, DNA invertase Pin homologs	12.9	15.3	12.0	13.3	15.2	16.7	1.12	5.0E-01
B035DRAFT_01152	hypothetical protein	50.5	64.2	46.2	80.4	84.9	93.2	1.62	7.7E-02
B035DRAFT_01153	glutamate synthase (NADPH), homotetrameric(EC:1.4.1.13,EC:1.4.1.14)	205.1	219.5	193.7	204.8	213.9	170.9	0.95	7.3E-01
B035DRAFT_01154	seryl-tRNA synthetase(EC:6.1.1.11)	476.6	494.2	448.7	472.8	478.8	508.7	1.03	6.6E-01
B035DRAFT_01155	nicotinamide mononucleotide transporter PnuC	20.1	21.9	16.8	12.0	20.1	16.1	0.81	4.8E-01
B035DRAFT_01156	thiamine pyrophosphokinase(EC:2.7.6.2)	73.8	74.4	61.1	55.1	70.5	75.6	0.96	8.5E-01
B035DRAFT_01157	hypothetical protein	167.2	197.0	211.9	169.9	170.5	224.7	0.98	9.2E-01
B035DRAFT_01158	ribosomal protein L27	3902.5	4172.7	3717.9	3861.6	3780.0	4075.3	0.99	9.4E-01
B035DRAFT_01159	ribosomal protein L21	3533.6	3800.7	3239.7	3663.9	3339.4	3061.3	0.95	6.9E-01
B035DRAFT_01160	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E	30.6	37.1	37.8	50.0	46.1	56.1	1.44	8.8E-02
B035DRAFT_01161	Cell wall-associated hydrolases (invasion-associated proteins)	61.8	78.5	103.4	128.0	98.3	128.1	1.48	2.5E-01
B035DRAFT_01162	ABC-type multidrug transport system, ATPase component	72.2	88.7	85.3	89.8	84.2	93.9	1.09	4.9E-01
B035DRAFT_01163	hypothetical protein	83.9	96.5	99.9	102.7	94.7	121.6	1.14	4.4E-01
B035DRAFT_01164	Predicted Zn-dependent peptidases(EC:3.4.24.)	253.2	232.2	229.5	249.3	223.0	244.4	1.00	9.8E-01
B035DRAFT_01165	thioredoxin-disulfide reductase(EC:1.8.1.9)	787.4	764.1	671.7	838.7	660.8	595.8	0.93	7.5E-01
B035DRAFT_01166	Outer membrane lipoprotein-sorting protein	225.0	202.4	177.6	193.7	170.2	182.1	0.91	4.8E-01
B035DRAFT_01167	DNA segregation ATPase FtsK/SpoIIIE and related proteins	155.4	148.1	150.4	147.6	141.9	149.9	0.97	4.1E-01
B035DRAFT_01168	hypothetical protein	205.0	213.1	196.3	233.1	244.3	276.9	1.23	1.2E-01
B035DRAFT_01169	Ribonuclease D	292.4	272.2	276.8	334.8	310.0	335.2	1.16	7.6E-02

B035DRAFT_01170	Predicted SAM-dependent methyltransferases(EC:2.1.1.)	369.4	393.9	361.3	430.4	446.5	484.7	1.21	8.2E-02
B035DRAFT_01171	hypothetical protein	500.4	491.1	487.5	495.9	565.8	561.2	1.10	2.8E-01
B035DRAFT_01172	Transglutaminase-like enzymes, putative cysteine proteases	348.4	346.3	349.5	359.1	400.0	365.7	1.08	2.6E-01
B035DRAFT_01173	Transglutaminase-like enzymes, putative cysteine proteases	326.0	328.2	334.0	345.5	366.7	368.5	1.09	9.2E-02
B035DRAFT_01174	RNA polymerase sigma factor, sigma-70 family	223.2	210.6	168.4	270.0	365.9	222.6	1.41	2.9E-01
B035DRAFT_01175	hypothetical protein	195.6	194.5	136.6	206.0	335.7	242.0	1.48	2.8E-01
B035DRAFT_01176	hypothetical protein	539.5	534.8	475.6	883.9	1084.1	1033.5	1.93	1.9E-02
B035DRAFT_01177	Nucleoside H+ symporter.	166.0	182.5	179.0	208.6	202.7	237.6	1.23	1.2E-01
B035DRAFT_01178	Uncharacterized conserved protein	129.0	131.6	150.8	118.9	117.7	121.0	0.87	1.8E-01
B035DRAFT_01179	RNA methyltransferase, RsmE family(EC:2.1.1.)	122.5	131.7	125.3	111.7	109.1	113.7	0.88	6.1E-02
B035DRAFT_01180	hypothetical protein	231.6	239.1	239.1	196.1	213.2	219.9	0.89	1.3E-01
B035DRAFT_01181	ABC-type antimicrobial peptide transport system, ATPase component	172.6	173.5	175.9	149.4	149.8	177.3	0.91	3.7E-01
B035DRAFT_01182	hypothetical protein	202.5	198.6	202.8	190.2	194.1	202.8	0.97	4.3E-01
B035DRAFT_01183	NAD-dependent aldehyde dehydrogenases(EC:1.5.99.8,EC:1.5.1.12)	57.2	62.4	60.8	62.7	68.5	69.5	1.11	2.0E-01
B035DRAFT_01184	Predicted transcriptional regulator	46.5	38.9	47.6	42.6	43.0	44.8	0.98	9.0E-01
B035DRAFT_01185	Antirepressor regulating drug resistance, predicted signal transduction N-terminal membrane component	45.9	38.8	36.4	40.9	45.3	37.5	1.02	9.0E-01
B035DRAFT_01186	Response regulator of the LytR/AlgR family	32.7	26.4	25.8	23.0	28.9	25.8	0.92	6.4E-01
B035DRAFT_01187	Putative regulator of cell autolysis	23.7	22.4	19.4	18.8	24.2	23.6	1.02	9.4E-01
B035DRAFT_01188	Outer membrane protein	16.9	13.9	17.8	20.8	20.1	22.6	1.31	1.5E-01
B035DRAFT_01189	hypothetical protein	5.2	9.7	8.9	9.9	6.6	8.5	1.07	8.7E-01
B035DRAFT_01190	Cation/multidrug efflux pump	10.2	9.7	9.3	9.1	10.8	9.1	0.99	9.5E-01
B035DRAFT_01191	RND family efflux transporter, MFP subunit	8.7	10.5	11.4	5.9	5.5	7.6	0.62	1.1E-01
B035DRAFT_01192	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	115.3	123.3	107.0	106.5	124.3	155.9	1.11	6.4E-01
B035DRAFT_01193	GMP synthase (glutamine-hydrolyzing), C-terminal domain or B subunit/GMP synthase (glutamine-hydrolyzing), N-terminal domain or A subunit(EC:6.3.5.2)	682.1	692.2	651.8	564.0	608.4	641.9	0.89	2.0E-01
B035DRAFT_01194	large conductance mechanosensitive channel protein	154.8	176.0	156.5	122.6	108.6	132.1	0.74	8.6E-02
B035DRAFT_01195	glyceraldehyde-3-phosphate dehydrogenase, type I(EC:1.2.1.12)	8386.7	9799.5	9316.0	8914.9	9857.7	12350.7	1.12	5.4E-01
B035DRAFT_01196	TM2 domain.	315.7	362.3	296.1	278.4	303.1	369.6	0.97	8.9E-01
B035DRAFT_01197	Protein of unknown function (DUF2752).	106.5	123.8	113.5	97.7	102.5	112.3	0.91	3.9E-01
B035DRAFT_01198	hypothetical protein	74.9	79.1	69.5	48.2	63.5	72.9	0.82	3.8E-01
B035DRAFT_01199	Peptidase family M48.	94.3	90.0	77.0	48.4	81.4	77.6	0.78	4.3E-01
B035DRAFT_01200	tRNA dimethylallyltransferase(EC:2.5.1.75)	167.1	157.7	148.2	133.0	167.0	143.1	0.93	6.2E-01
B035DRAFT_01201	lipid kinase, YegS/Rv2252/BmrU family	132.6	117.2	111.2	82.0	135.7	111.3	0.89	7.0E-01
B035DRAFT_01202	3-deoxy-8-phosphooctulonate synthase(EC:2.5.1.55)	247.8	220.1	229.7	177.8	238.6	215.8	0.90	5.3E-01
B035DRAFT_01203	Protein distantly related to bacterial ferritins	1670.5	1575.9	1592.3	1777.2	1404.1	1574.1	0.98	8.8E-01
B035DRAFT_01204	Cbb3-type cytochrome oxidase component FixQ.	666.9	649.4	673.1	575.3	335.3	435.5	0.66	2.0E-01
B035DRAFT_01205	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	149.4	201.7	179.2	178.6	181.5	212.8	1.08	6.7E-01
B035DRAFT_01206	Uncharacterized protein related to glutamine synthetase(EC:6.3.1.2)	120.1	137.4	125.4	150.2	169.2	174.1	1.29	8.6E-02
B035DRAFT_01207	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	30.8	35.8	34.1	34.0	39.3	35.5	1.08	4.8E-01
B035DRAFT_01208	hypothetical protein	24.7	29.7	31.0	38.5	42.2	42.1	1.44	6.6E-02
B035DRAFT_01209	Outer membrane protein	218.9	178.9	193.1	133.4	111.6	127.7	0.63	4.7E-02
B035DRAFT_01210	Multidrug resistance efflux pump	197.2	158.9	176.2	104.3	103.6	94.5	0.57	2.3E-02
B035DRAFT_01211	ABC-type multidrug transport system, permease component	167.5	148.4	192.1	110.9	103.4	120.7	0.66	7.0E-02
B035DRAFT_01212	ABC-type multidrug transport system, permease component	99.4	86.2	117.2	70.6	67.9	74.4	0.71	1.1E-01
B035DRAFT_01213	Glycogen debranching enzyme (GH78)	551.2	563.9	564.7	572.7	619.2	771.1	1.16	3.7E-01
B035DRAFT_01214	Glycosyltransferase (GT5)	459.9	457.1	460.2	373.4	409.1	507.1	0.93	6.6E-01
B035DRAFT_01215	Alpha-amylase/alpha-mannosidase(EC:3.2.1.1) (GH57)	479.8	491.4	483.1	421.9	437.9	545.1	0.96	7.9E-01

B035DRAFT_01216	hypothetical protein	173.0	175.2	197.3	140.1	156.0	116.8	0.75	1.6E-01
B035DRAFT_01217	biotin synthase(EC:2.8.1.6)	29.7	23.4	29.9	4.8	4.6	3.7	0.16	3.1E-03
B035DRAFT_01218	adenosylmethionine-8-amino-7-oxononanoate transaminase(EC:2.6.1.62)	32.6	24.2	33.8	5.9	4.2	2.2	0.13	3.5E-02
B035DRAFT_01219	7-keto-8-aminopelargonate synthetase and related enzymes(EC:2.3.1.47)	42.9	31.0	38.1	6.6	6.1	2.6	0.13	3.5E-02
B035DRAFT_01220	Uncharacterized protein conserved in bacteria	16.1	14.2	18.3	4.1	5.9	2.1	0.23	6.9E-02
B035DRAFT_01221	biotin biosynthesis protein BioC(EC:2.1.1.197)	23.0	23.9	23.7	7.1	7.3	3.7	0.24	4.0E-02
B035DRAFT_01222	dethiobiotin synthase(EC:6.3.3.3)	40.6	36.5	30.6	10.2	8.8	7.4	0.24	9.6E-03
B035DRAFT_01223	hypothetical protein	18.1	16.5	13.9	12.5	20.0	15.6	0.98	9.5E-01
B035DRAFT_01224	Uncharacterized conserved protein	124.4	145.5	138.9	102.0	102.3	102.2	0.75	4.2E-02
B035DRAFT_01225	Aspartate ammonia-lyase(EC:4.3.1.1)	564.5	397.9	526.5	738.3	535.1	610.7	1.27	3.7E-01
B035DRAFT_01226	hypothetical protein	164.8	154.8	135.0	167.0	203.8	187.1	1.23	2.2E-01
B035DRAFT_01227	hypothetical protein	83.8	93.5	86.0	86.2	103.8	107.1	1.12	4.0E-01
B035DRAFT_01228	hypothetical protein	49.6	48.4	34.3	33.2	57.2	68.6	1.17	7.4E-01
B035DRAFT_01229	Cyclic nucleotide-binding domain.	87.8	99.0	88.4	77.7	107.4	104.5	1.04	8.5E-01
B035DRAFT_01230	hypothetical protein	74.2	77.1	74.0	79.3	89.3	104.1	1.20	2.4E-01
B035DRAFT_01231	hypothetical protein	128.8	115.7	106.8	127.0	130.1	118.2	1.07	5.3E-01
B035DRAFT_01232	Long-chain acyl-CoA synthetases (AMP-forming)(EC:6.2.1.3)	66.1	67.9	58.9	65.5	79.6	80.7	1.17	3.1E-01
B035DRAFT_01233	Dihydroorotate dehydrogenase(EC:1.3.98.1)	444.9	434.6	425.4	416.0	416.0	467.5	0.99	9.5E-01
B035DRAFT_01234	pyridoxal phosphate enzyme, YggS family	314.9	309.7	282.4	288.7	308.3	326.6	1.02	8.5E-01
B035DRAFT_01235	hypothetical protein	320.0	330.5	300.9	339.5	325.9	280.3	0.99	9.5E-01
B035DRAFT_01236	Protein kinase domain.	37.4	44.6	48.4	86.7	88.1	104.8	2.15	2.4E-02
B035DRAFT_01237	L-fucose isomerase and related proteins	110.3	119.0	118.1	276.1	282.5	349.4	2.60	7.4E-03
B035DRAFT_01238	hypothetical protein	337.1	237.4	193.7	330.4	304.2	246.3	1.17	6.4E-01
B035DRAFT_01239	Uncharacterized conserved protein	61.6	57.2	68.7	45.1	50.4	57.2	0.81	2.3E-01
B035DRAFT_01240	Aspartate/tyrosine/aromatic aminotransferase(EC:2.6.1.1)	320.7	351.4	341.2	318.7	359.1	324.7	0.99	9.0E-01
B035DRAFT_01241	ABC-type transport system, involved in lipoprotein release, permease component	217.2	226.1	227.1	184.5	213.5	196.9	0.89	1.9E-01
B035DRAFT_01242	hypothetical protein	24.0	24.0	19.2	15.1	24.8	21.9	0.90	7.4E-01
B035DRAFT_01243	hypothetical protein	25.8	18.6	25.2	15.2	19.5	23.8	0.84	5.5E-01
B035DRAFT_01244	Predicted ATPase (AAA+ superfamily)	41.0	40.4	42.5	64.6	69.4	88.4	1.78	4.4E-02
B035DRAFT_01245	Uncharacterized conserved protein	260.7	304.5	251.0	311.2	281.3	342.1	1.15	3.7E-01
B035DRAFT_01246	Glycosyltransferases, probably involved in cell wall biogenesis (GT21)	29.8	35.3	35.7	40.7	38.9	43.8	1.23	1.6E-01
B035DRAFT_01247	hypothetical protein	252.2	257.2	201.5	406.2	511.9	564.1	2.08	4.6E-02
B035DRAFT_01248	diaminopimelate decarboxylase(EC:4.1.1.20)	281.2	314.6	305.4	282.9	290.4	305.5	0.98	7.4E-01
B035DRAFT_01249	aspartate kinase(EC:2.7.2.4)	625.8	791.6	692.0	658.4	615.8	657.5	0.92	5.1E-01
B035DRAFT_01250	Predicted ATPase involved in cell division	196.2	237.0	181.2	195.0	194.5	240.8	1.03	9.0E-01
B035DRAFT_01251	phosphoribosyl-ATP pyrophosphohydrolase(EC:3.5.4.19,EC:3.6.1.31)	214.7	255.4	201.5	219.1	219.9	249.9	1.03	8.6E-01
B035DRAFT_01252	imidazoleglycerol phosphate synthase, cyclase subunit(EC:4.1.3.)	168.7	182.9	188.7	156.4	163.9	121.8	0.81	2.8E-01
B035DRAFT_01253	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase(EC:5.3.1.16)	114.0	128.5	111.9	103.5	127.0	135.4	1.03	8.8E-01
B035DRAFT_01254	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit(EC:2.4.2.)	156.3	171.4	164.9	146.8	162.2	216.4	1.05	8.2E-01
B035DRAFT_01255	(tRNA)	41.1	47.8	53.2	31.2	20.7	43.6	0.65	3.2E-01
B035DRAFT_01256	Protein of unknown function (DUF2582).	72.4	93.5	93.0	170.2	155.3	176.2	1.95	2.9E-02
B035DRAFT_01257	hypothetical protein	58.7	70.0	67.6	75.4	78.2	84.1	1.21	1.6E-01
B035DRAFT_01258	Pantothenate kinase, acetyl-CoA regulated(EC:2.7.1.33)	74.1	58.9	76.9	75.7	75.1	69.6	1.06	7.4E-01
B035DRAFT_01259	Domain of unknown function (DUF303).(EC:3.1.1.53) (CE6)	56.2	53.6	59.4	53.5	52.1	47.2	0.90	2.8E-01
B035DRAFT_01260	Membrane-associated phospholipid phosphatase	96.6	89.4	92.2	75.8	68.0	84.1	0.82	1.6E-01
B035DRAFT_01261	methionine-R-sulfoxide reductase/methionine-S-sulfoxide reductase(EC:1.8.4.12,EC:1.8.4.11)	140.4	116.2	112.6	141.3	124.4	140.9	1.10	5.0E-01
B035DRAFT_01262	Penicillin V acylase and related amidases(EC:3.5.1.24)	332.3	299.1	334.9	240.9	161.1	147.5	0.56	1.1E-01

B035DRAFT_01263	(tRNA)	69.4	64.6	84.5	40.2	27.3	31.5	0.45	4.7E-02
B035DRAFT_01264	hypothetical protein	124.3	186.6	164.2	90.6	139.7	196.1	0.87	7.6E-01
B035DRAFT_01265	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.8E-01
B035DRAFT_01266	hypothetical protein	19.7	20.4	15.1	20.8	23.2	31.9	1.36	3.1E-01
B035DRAFT_01267	Archaeal/vacuolar-type H+-ATPase subunit E(EC:3.6.3.14)	354.7	405.4	392.3	542.8	553.2	661.1	1.52	5.0E-02
B035DRAFT_01268	Protein of unknown function (DUF2764).	261.0	289.3	279.2	319.7	359.1	411.0	1.31	1.3E-01
B035DRAFT_01269	Archaeal/vacuolar-type H+-ATPase subunit A(EC:3.6.3.14)	388.0	377.3	384.6	398.6	474.7	457.7	1.15	2.0E-01
B035DRAFT_01270	Archaeal/vacuolar-type H+-ATPase subunit B(EC:3.6.3.14)	367.0	351.2	344.9	339.5	438.2	392.7	1.10	5.1E-01
B035DRAFT_01271	Archaeal/vacuolar-type H+-ATPase subunit D(EC:3.6.3.14)	376.6	360.0	348.0	360.1	458.4	433.7	1.15	3.3E-01
B035DRAFT_01272	Archaeal/vacuolar-type H+-ATPase subunit I(EC:3.6.3.14)	396.4	390.8	398.7	432.5	496.9	488.3	1.19	9.4E-02
B035DRAFT_01273	ATP synthase subunit C.(EC:3.6.3.14)	612.8	671.0	629.5	780.1	837.4	1023.2	1.37	1.1E-01
B035DRAFT_01274	Glycosyltransferase (GT3)	457.0	452.6	436.2	356.5	405.5	425.4	0.88	2.4E-01
B035DRAFT_01275	alpha-glucan phosphorylases(EC:2.4.1.1) (GT35)	918.0	904.0	893.9	762.3	855.2	898.9	0.92	3.9E-01
B035DRAFT_01276	Peroxiredoxin	1285.7	1265.2	1172.9	1234.8	1242.6	1506.5	1.07	6.2E-01
B035DRAFT_01277	Signal transduction histidine kinase	111.3	114.6	105.7	118.0	129.1	138.6	1.16	1.8E-01
B035DRAFT_01278	spermidine/putrescine ABC transporter ATP-binding subunit(EC:3.6.3.31)	236.6	241.7	221.4	228.4	235.6	212.3	0.97	6.4E-01
B035DRAFT_01279	ABC-type spermidine/putrescine transport system, permease component I	225.4	234.5	259.6	220.2	199.2	231.6	0.90	3.8E-01
B035DRAFT_01280	ABC-type spermidine/putrescine transport system, permease component II	133.5	135.1	137.6	112.3	119.5	134.5	0.90	3.0E-01
B035DRAFT_01281	Spermidine/putrescine-binding periplasmic protein	157.7	135.3	153.0	129.4	150.9	86.9	0.80	4.8E-01
B035DRAFT_01282	ribose-phosphate pyrophosphokinase(EC:2.7.6.1)	968.2	1125.7	1036.3	915.6	949.7	1020.5	0.92	4.2E-01
B035DRAFT_01283	Thiamine monophosphate synthase	98.2	104.8	83.4	139.6	134.3	128.6	1.41	6.9E-02
B035DRAFT_01284	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2	17.6	13.9	17.8	18.7	18.6	18.8	1.15	3.6E-01
B035DRAFT_01285	thiazole biosynthesis protein ThiH	17.8	18.9	21.4	20.6	21.4	20.5	1.08	4.7E-01
B035DRAFT_01286	hypothetical protein	16.8	10.2	16.1	16.0	16.1	19.4	1.22	5.2E-01
B035DRAFT_01287	thiamine biosynthesis protein ThiC	37.9	35.0	39.3	47.3	51.6	43.2	1.26	1.1E-01
B035DRAFT_01288	Uncharacterized enzyme of thiazole biosynthesis	35.1	31.7	32.4	38.8	46.5	40.5	1.26	1.1E-01
B035DRAFT_01289	thiamine-phosphate pyrophosphorylase(EC:2.5.1.3)	37.8	37.8	39.6	51.5	59.4	43.5	1.33	1.5E-01
B035DRAFT_01290	thiamine biosynthesis protein ThiS	71.4	94.8	66.5	108.8	95.2	50.4	1.05	9.3E-01
B035DRAFT_01292	Signal transduction histidine kinase	11.0	14.3	10.9	16.5	13.2	14.3	1.22	3.4E-01
B035DRAFT_01293	hypothetical protein	27.7	31.4	24.2	43.5	43.4	59.2	1.75	8.2E-02
B035DRAFT_01294	Uncharacterized protein related to glutamine synthetase(EC:6.3.1.2)	6.0	4.9	5.4	7.7	7.2	3.1	1.02	9.8E-01
B035DRAFT_01295	LL-diaminopimelate aminotransferase(EC:2.6.1.83)	6.6	6.1	8.0	6.5	6.7	3.2	0.76	5.5E-01
B035DRAFT_01296	diaminopimelate epimerase(EC:5.1.1.7)	4.4	6.3	4.9	4.6	4.4	2.2	0.69	4.4E-01
B035DRAFT_01297	Glutamate synthase domain 2(EC:1.4.1.14,EC:1.4.1.13)	5.1	4.4	6.1	6.2	4.7	2.8	0.84	7.1E-01
B035DRAFT_01298	glutamate synthases, NADH/NADPH, small subunit(EC:1.4.1.14,EC:1.4.1.13)	4.8	3.1	4.3	4.7	4.9	1.3	0.78	7.7E-01
B035DRAFT_01299	asparagine synthase (glutamine-hydrolyzing)(EC:6.3.5.4)	15.6	8.7	13.1	8.3	6.3	4.8	0.52	1.9E-01
B035DRAFT_01300	Superoxide dismutase(EC:1.15.1.1)	2760.0	2605.4	2524.6	3820.5	2570.8	2931.7	1.17	4.8E-01
B035DRAFT_01301	Superfamily I DNA and RNA helicases(EC:3.6.4.12)	85.9	79.4	77.0	72.9	92.8	73.9	0.98	9.3E-01
B035DRAFT_01302	carboxynorspermidine decarboxylase(EC:4.1.1.)	83.3	81.6	72.1	79.1	90.2	100.4	1.14	4.0E-01
B035DRAFT_01303	(tRNA)	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01304	(tRNA)	1034.4	1004.8	1479.5	899.0	473.6	146.9	0.34	3.1E-01
B035DRAFT_01305	(tRNA)	745.6	681.6	1129.4	635.7	325.6	120.0	0.35	2.9E-01
B035DRAFT_01306	(tRNA)	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01307	(tRNA)	1034.4	1004.8	1479.5	899.0	473.6	146.9	0.34	3.1E-01
B035DRAFT_01308	(tRNA)	1978.2	2193.6	2742.5	1906.9	1011.4	331.3	0.38	3.2E-01
B035DRAFT_01309	5"-nucleotidase/2",3"-cyclic phosphodiesterase and related esterases	148.5	145.3	129.9	137.9	169.9	120.4	1.00	9.9E-01
B035DRAFT_01310	Glutamine synthetase(EC:6.3.1.2)	110.9	134.3	127.9	151.4	152.4	201.7	1.35	1.9E-01
B035DRAFT_01311	hypothetical protein	28.6	32.8	29.7	41.9	44.3	57.6	1.57	8.6E-02
B035DRAFT_01312	Predicted amidohydrolase	86.4	95.0	77.9	83.2	90.9	91.2	1.03	8.5E-01

B035DRAFT_01313	PAS fold./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	32.1	41.0	39.8	41.0	42.6	53.0	1.21	3.6E-01
B035DRAFT_01314	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	16.7	15.2	13.7	23.0	24.8	25.5	1.61	2.7E-02
B035DRAFT_01315	Outer membrane protein	6.0	5.2	5.5	6.1	8.3	5.7	1.18	4.5E-01
B035DRAFT_01316	RND family efflux transporter, MFP subunit	6.8	4.2	6.4	8.4	6.9	4.9	1.15	7.2E-01
B035DRAFT_01317	ABC-type antimicrobial peptide transport system, permease component	8.2	8.7	7.3	7.7	9.4	7.1	0.99	9.8E-01
B035DRAFT_01318	ABC-type antimicrobial peptide transport system, ATPase component	22.1	14.2	11.5	12.6	14.7	14.3	0.90	7.9E-01
B035DRAFT_01319	ABC-type antimicrobial peptide transport system, permease component	17.8	15.9	17.1	11.4	12.3	12.2	0.71	2.1E-02
B035DRAFT_01320	Formyltetrahydrofolate synthetase(EC:6.3.4.3)	557.9	512.2	491.0	430.6	441.4	433.6	0.84	7.3E-02
B035DRAFT_01321	AraC-type DNA-binding domain-containing proteins	42.5	53.9	42.3	33.3	43.8	51.5	0.92	7.6E-01
B035DRAFT_01322	hypothetical protein	7.9	6.9	6.0	6.2	9.0	7.2	1.07	7.8E-01
B035DRAFT_01323	RND family efflux transporter, MFP subunit	10.3	5.5	5.8	8.6	8.6	9.7	1.31	4.7E-01
B035DRAFT_01324	The (Largely Gram-negative Bacterial) Hydrophobe/Amphiphile Efflux-1 (HAE1) Family	5.1	4.2	4.8	6.5	7.5	5.7	1.38	1.3E-01
B035DRAFT_01325	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	89.7	73.7	90.6	74.7	65.4	55.7	0.77	2.3E-01
B035DRAFT_01326	hypothetical protein	375.4	403.6	387.5	355.7	316.0	322.9	0.85	1.1E-01
B035DRAFT_01327	hypothetical protein	110.9	120.6	115.9	99.6	153.6	160.3	1.16	5.8E-01
B035DRAFT_01328	glycine dehydrogenase (decarboxylating)(EC:1.4.4.2)	287.3	266.3	268.4	290.8	335.0	325.1	1.16	1.7E-01
B035DRAFT_01329	Zn-dependent hydrolases, including glyoxylases	78.0	92.2	84.6	106.9	117.9	121.8	1.36	6.4E-02
B035DRAFT_01330	16S rRNA (guanine(527)-N(7))-methyltransferase GidB(EC:2.1.1.170)	81.6	96.5	78.7	136.4	132.6	143.5	1.61	3.0E-02
B035DRAFT_01331	Protein of unknown function (DUF3298).	35.1	41.0	42.7	83.1	97.5	118.2	2.50	2.5E-02
B035DRAFT_01332	copper-(or silver)-translocating P-type ATPase(EC:3.6.3.4)	284.9	217.5	254.1	198.3	175.5	145.0	0.68	1.5E-01
B035DRAFT_01333	hypothetical protein	123.5	142.9	147.7	188.0	176.2	206.3	1.38	7.7E-02
B035DRAFT_01334	HD domain.	40.0	34.1	38.2	30.9	29.4	38.9	0.88	4.7E-01
B035DRAFT_01335	lipoate-protein ligase B(EC:2.3.1.181)	38.6	38.6	39.0	44.8	43.9	41.2	1.12	8.2E-02
B035DRAFT_01336	Na+/H+ antiporter	128.7	146.0	135.6	157.1	137.4	155.6	1.10	3.8E-01
B035DRAFT_01337	ABC-type sugar transport system, periplasmic component	66.9	67.8	66.2	84.5	73.0	91.0	1.23	1.5E-01
B035DRAFT_01338	Sugar kinases, ribokinase family(EC:2.7.1.45)	98.7	65.3	47.4	46.8	49.5	42.6	0.69	3.5E-01
B035DRAFT_01339	2-keto-3-deoxy-6-phosphogluconate aldolase(EC:4.1.2.14,EC:4.1.3.16)	122.4	86.4	75.8	55.6	63.3	45.3	0.58	1.5E-01
B035DRAFT_01340	Zn-dependent protease with chaperone function(EC:3.4.24.)	82.6	71.1	77.7	57.1	74.8	59.8	0.82	2.9E-01
B035DRAFT_01341	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases (PL22)	199.8	186.7	191.4	210.4	235.2	189.6	1.10	4.4E-01
B035DRAFT_01342	hypothetical protein	35.0	34.1	30.5	41.9	44.3	27.4	1.12	7.0E-01
B035DRAFT_01343	hypothetical protein	1.5	5.2	3.6	3.1	5.4	4.0	1.35	6.8E-01
B035DRAFT_01344	membrane protein insertase, YidC/Oxa1 family, N-terminal domain	573.8	564.4	525.5	638.5	719.6	660.5	1.21	8.2E-02
B035DRAFT_01345	CTP synthase(EC:6.3.4.2)	366.4	356.8	312.8	354.7	379.9	352.2	1.05	6.2E-01
B035DRAFT_01346	Protein of unknown function (DUF3078).	231.9	265.9	226.1	239.7	201.5	228.8	0.93	5.5E-01
B035DRAFT_01347	UDP-N-acetylglucosamine 2-epimerase(EC:5.1.3.14)	88.0	103.9	94.9	145.5	141.2	134.6	1.47	2.8E-02
B035DRAFT_01348	Predicted membrane protein	236.3	268.3	254.2	247.3	246.4	155.3	0.84	5.3E-01
B035DRAFT_01349	RNA polymerase sigma factor, sigma-70 family	560.7	558.3	531.4	790.0	634.4	778.0	1.33	1.0E-01
B035DRAFT_01350	Pyruvate/oxaloacetate carboxyltransferase(EC:6.4.1.1)	136.2	103.0	118.4	91.4	82.0	61.5	0.65	1.6E-01
B035DRAFT_01351	Protein of unknown function (DUF1460).	132.9	119.8	126.6	140.6	138.8	109.9	1.02	9.1E-01
B035DRAFT_01352	monofunctional biosynthetic peptidoglycan transglycosylase(EC:2.4.1.) (GT51)	134.0	127.6	135.3	104.3	91.5	101.7	0.75	3.6E-02
B035DRAFT_01353	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	1109.5	917.7	1052.6	1088.4	903.7	760.6	0.89	5.8E-01
B035DRAFT_01354	putative efflux protein, MATE family	46.4	53.0	53.7	53.9	48.7	43.6	0.95	7.4E-01
B035DRAFT_01355	Glycine/serine hydroxymethyltransferase(EC:2.1.2.1)	285.2	330.5	293.3	333.6	369.0	346.7	1.16	2.0E-01
B035DRAFT_01356	hypothetical protein	38.3	52.8	48.0	48.1	46.4	57.4	1.10	6.6E-01
B035DRAFT_01357	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family	126.0	147.9	136.7	147.8	148.5	161.6	1.12	2.9E-01
B035DRAFT_01358	aspartate carbamoyltransferase, regulatory subunit	110.1	149.5	120.2	147.2	170.6	143.9	1.22	3.2E-01

B035DRAFT_01359	aspartate carbamoyltransferase(EC:2.1.3.2)	121.0	114.2	95.8	134.8	148.9	156.8	1.33	1.3E-01
B035DRAFT_01360	Membrane carboxypeptidase/penicillin-binding protein(EC:3.4.-,EC:2.4.1.) (GT51)	111.1	110.7	101.9	115.1	140.7	96.0	1.07	7.3E-01
B035DRAFT_01361	hypothetical protein	37.5	36.3	36.0	40.6	55.1	60.6	1.40	1.8E-01
B035DRAFT_01362	fructose-6-phosphate aldolase, TalC/MipB family(EC:2.2.1.2)	68.6	65.2	68.8	89.9	99.5	82.7	1.34	6.0E-02
B035DRAFT_01363	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase(EC:2.7.6.3)	24.1	22.7	26.0	22.9	23.9	31.0	1.06	7.6E-01
B035DRAFT_01364	3-deoxy-D-manno-octulosonate cytidylyltransferase(EC:2.7.7.38)	208.9	220.7	208.8	217.6	236.2	214.9	1.05	4.7E-01
B035DRAFT_01365	Predicted Zn-dependent peptidases	123.2	129.2	111.1	119.9	144.6	150.8	1.14	4.0E-01
B035DRAFT_01366	Uncharacterized protein conserved in bacteria	152.9	138.3	106.4	102.8	186.0	90.3	0.92	8.6E-01
B035DRAFT_01367	Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family(EC:3.1.3.25)	101.1	121.7	108.6	128.4	145.4	122.1	1.19	2.3E-01
B035DRAFT_01368	TIGR02453 family protein	235.9	271.5	234.3	270.2	301.9	316.5	1.20	1.9E-01
B035DRAFT_01369	uncharacterized protein, YhcH/YjgK/YiaL family	204.2	228.4	220.9	226.6	232.3	282.7	1.13	3.9E-01
B035DRAFT_01370	1,4-alpha-glucan branching enzyme(EC:2.4.1.18) (CBM48)	303.8	332.5	339.3	317.3	339.1	362.6	1.04	6.4E-01
B035DRAFT_01371	hypothetical protein	177.4	188.0	179.3	169.2	193.5	211.4	1.05	6.9E-01
B035DRAFT_01372	prolyl-tRNA synthetase, family I(EC:6.1.1.15)	383.8	378.6	355.1	340.7	373.9	363.6	0.96	5.9E-01
B035DRAFT_01373	ABC-type antimicrobial peptide transport system, ATPase component(EC:3.6.3.21)	100.4	100.9	96.0	91.3	107.8	71.0	0.90	6.2E-01
B035DRAFT_01374	ABC-type uncharacterized transport system, permease component	93.1	100.6	87.3	79.6	97.9	111.8	1.02	9.3E-01
B035DRAFT_01375	hypothetical protein	64.9	67.6	55.9	49.6	66.0	65.1	0.95	8.3E-01
B035DRAFT_01376	dinuclear metal center protein, YbgI/SA1388 family	203.9	229.8	190.6	151.9	206.4	144.3	0.80	3.3E-01
B035DRAFT_01377	Zn-ribbon protein, possibly nucleic acid-binding	855.9	974.9	856.2	884.0	903.1	898.6	1.00	9.9E-01
B035DRAFT_01378	hypothetical protein	68.3	72.9	79.5	73.1	78.6	82.6	1.06	5.5E-01
B035DRAFT_01379	AMP nucleosidase, putative(EC:3.2.2.4)	137.4	140.8	109.3	146.0	188.2	180.4	1.33	2.1E-01
B035DRAFT_01380	DNA polymerase III, delta subunit(EC:2.7.7.7)	143.3	151.8	119.0	149.5	196.2	221.6	1.36	2.6E-01
B035DRAFT_01381	Predicted transcriptional regulators	62.8	72.1	57.6	121.6	93.9	102.7	1.65	6.3E-02
B035DRAFT_01382	2-polyprenylphenol hydroxylase and related flavodoxin oxidoreductases	149.2	161.9	162.1	148.6	175.9	162.8	1.03	7.9E-01
B035DRAFT_01383	dihydroorotate dehydrogenase (subfamily 1) family protein(EC:1.3.98.1)	198.6	202.4	193.6	211.0	242.5	231.5	1.15	1.4E-01
B035DRAFT_01384	hypothetical protein	26.1	27.1	25.1	37.6	38.6	52.4	1.62	7.9E-02
B035DRAFT_01385	tRNA (guanine-N1)-methyltransferase(EC:2.1.1.31)	122.4	135.3	115.7	108.3	103.9	121.7	0.89	3.6E-01
B035DRAFT_01386	DNA ligase, NAD-dependent(EC:6.5.1.2)	158.2	151.1	143.8	191.0	203.2	210.6	1.33	2.8E-02
B035DRAFT_01387	dihydrodipicolinate synthase(EC:4.2.1.52)	633.9	755.4	708.6	730.5	710.5	872.3	1.10	5.2E-01
B035DRAFT_01388	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01389	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01390	hypothetical protein	231.1	261.0	239.1	246.9	242.4	286.3	1.06	6.2E-01
B035DRAFT_01391	rRNA methylase, putative, group 3(EC:2.1.1.)	157.3	154.6	149.3	146.4	162.1	171.9	1.04	6.7E-01
B035DRAFT_01392	DNA repair protein RecN	143.4	145.5	132.5	139.4	148.1	156.8	1.05	5.1E-01
B035DRAFT_01393	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase, prokaryotic(EC:6.3.2.5,EC:4.1.1.36)	207.3	206.6	184.3	197.4	215.6	159.3	0.95	7.8E-01
B035DRAFT_01394	DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases(EC:2.7.7.7)	352.8	368.6	329.7	347.0	391.8	396.6	1.08	4.3E-01
B035DRAFT_01395	DNA polymerase III, beta subunit(EC:2.7.7.7)	296.6	314.2	265.1	322.1	350.8	386.6	1.21	2.0E-01
B035DRAFT_01396	Protein of unknown function (DUF3127).	1210.2	1390.1	1400.3	1803.2	1383.4	992.2	1.02	9.7E-01
B035DRAFT_01397	transcription termination factor Rho	1047.4	1054.0	959.6	1111.0	1136.1	1266.9	1.15	1.9E-01
B035DRAFT_01398	hypothetical protein	46.0	49.9	41.5	51.8	49.8	41.6	1.04	8.1E-01
B035DRAFT_01399	endoribonuclease L-PSP, putative	419.9	498.7	491.0	602.1	588.0	682.2	1.33	9.6E-02
B035DRAFT_01400	hypothetical protein	273.0	309.4	298.1	337.7	346.1	436.1	1.27	2.0E-01
B035DRAFT_01401	Predicted Zn-dependent hydrolases of the beta-lactamase fold	228.0	218.4	223.1	216.9	192.6	185.5	0.89	2.2E-01
B035DRAFT_01402	Lactoylglutathione lyase and related lyases(EC:4.4.1.5)	255.6	248.3	203.9	220.6	217.5	227.8	0.95	6.7E-01
B035DRAFT_01403	hypothetical protein	305.9	287.3	256.3	239.5	265.7	227.4	0.86	2.7E-01
B035DRAFT_01404	ATPase components of ABC transporters with duplicated ATPase domains	234.4	218.6	223.3	190.1	217.7	182.4	0.87	2.3E-01

B035DRAFT_01405	His Kinase A (phosphoacceptor) domain./Response regulator receiver domain./Y_Y_Y domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase./Two component regulator propeller.	24.5	26.9	27.3	21.9	24.5	26.2	0.92	4.7E-01
B035DRAFT_01406	hypothetical protein	4.0	2.3	1.2	0.0	2.7	1.8	0.99	9.9E-01
B035DRAFT_01407	hypothetical protein	14.5	11.8	18.2	19.0	18.7	19.2	1.30	2.8E-01
B035DRAFT_01408	Site-specific recombinase XerD	36.8	27.1	28.8	38.3	41.9	22.1	1.07	8.7E-01
B035DRAFT_01409	Uncharacterized conserved protein	41.3	39.4	43.3	49.4	51.4	43.8	1.16	1.9E-01
B035DRAFT_01410	hypothetical protein (CE13)	55.6	53.5	42.1	69.7	79.0	72.5	1.47	9.1E-02
B035DRAFT_01411	hypothetical protein	11.4	7.4	11.5	9.3	12.6	5.2	0.86	7.9E-01
B035DRAFT_01412	hypothetical protein	16.3	12.6	13.9	17.5	19.3	9.6	1.04	9.3E-01
B035DRAFT_01413	DNA primase (bacterial type)	11.1	8.6	11.3	11.1	15.3	9.4	1.14	6.7E-01
B035DRAFT_01414	hypothetical protein	12.9	8.5	11.6	9.8	10.4	10.3	0.94	7.8E-01
B035DRAFT_01415	Transposase DDE domain.	208.0	227.9	251.6	140.2	128.0	154.4	0.61	4.0E-02
B035DRAFT_01416	hypothetical protein	71.9	85.2	86.1	79.9	70.9	82.9	0.96	7.8E-01
B035DRAFT_01417	hypothetical protein	81.1	87.3	78.1	60.1	64.1	73.7	0.80	1.5E-01
B035DRAFT_01418	(tRNA)	254.5	357.0	341.3	233.3	121.3	81.7	0.42	2.0E-01
B035DRAFT_01419	Putative transcriptional regulator	142.9	122.5	132.1	169.9	231.7	251.7	1.62	1.1E-01
B035DRAFT_01420	Acetyltransferases, including N-acetylases of ribosomal proteins(EC:2.3.1.57)	128.1	137.6	128.4	135.1	138.3	166.4	1.11	4.1E-01
B035DRAFT_01421	hypothetical protein	100.3	107.3	99.0	105.5	112.0	134.4	1.14	3.5E-01
B035DRAFT_01422	recombination protein RecR	67.5	62.0	58.5	61.3	66.9	65.1	1.03	7.5E-01
B035DRAFT_01423	Na+/proline symporter	98.5	107.6	99.7	99.0	103.7	114.0	1.03	7.1E-01
B035DRAFT_01424	ribosome biogenesis GTP-binding protein YsxC/EngB	76.2	72.0	61.4	45.1	72.9	60.8	0.84	5.3E-01
B035DRAFT_01425	Leucyl aminopeptidase (aminopeptidase T)	121.2	126.6	130.9	137.7	146.9	149.1	1.15	9.0E-02
B035DRAFT_01426	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	39.1	39.1	32.7	30.9	41.3	46.4	1.06	8.3E-01
B035DRAFT_01427	Signal transduction histidine kinase	35.6	32.6	27.6	27.1	37.8	40.0	1.09	7.6E-01
B035DRAFT_01428	Protein of unknown function (DUF2874).	46.3	41.7	42.7	45.9	60.5	56.8	1.24	2.3E-01
B035DRAFT_01429	UDP-glucoronosyl and UDP-glucosyl transferase.	55.1	55.7	50.8	52.5	47.8	49.3	0.93	3.1E-01
B035DRAFT_01430	Predicted aminopeptidases	70.8	70.3	73.4	80.3	84.8	71.1	1.10	3.5E-01
B035DRAFT_01431	ATP synthase, F1 beta subunit(EC:3.6.3.14)	942.7	810.1	891.4	955.7	601.2	350.2	0.67	4.5E-01
B035DRAFT_01432	F0F1-type ATP synthase, epsilon subunit (mitochondrial delta subunit)(EC:3.6.3.14)	626.8	593.0	614.2	604.9	405.3	377.3	0.74	2.9E-01
B035DRAFT_01433	hypothetical protein	386.2	478.9	497.5	428.3	277.9	337.0	0.76	3.2E-01
B035DRAFT_01434	F0F1-type ATP synthase, subunit a(EC:3.6.3.14)	606.8	587.8	711.8	675.7	476.4	453.1	0.83	4.6E-01
B035DRAFT_01435	ATP synthase, F0 subunit c(EC:3.6.3.14)	298.3	277.4	325.5	287.2	198.1	156.6	0.69	2.9E-01
B035DRAFT_01436	ATP synthase, F0 subunit b(EC:3.6.3.14)	494.3	429.6	536.2	557.3	372.9	207.5	0.72	5.4E-01
B035DRAFT_01437	ATP synthase, F1 delta subunit(EC:3.6.3.14)	254.8	265.0	318.5	284.2	207.8	123.4	0.70	4.3E-01
B035DRAFT_01438	proton translocating ATP synthase, F1 alpha subunit(EC:3.6.3.14)	410.9	387.3	467.6	521.6	343.7	191.2	0.77	6.3E-01
B035DRAFT_01439	ATP synthase, F1 gamma subunit(EC:3.6.3.14)	405.3	417.5	502.9	582.7	416.3	333.0	0.98	9.6E-01
B035DRAFT_01440	hypothetical protein	69.2	79.7	77.8	77.3	86.8	78.2	1.07	5.1E-01
B035DRAFT_01441	hypothetical protein	47.3	45.3	56.0	67.7	66.1	42.7	1.17	6.0E-01
B035DRAFT_01442	MoxR-like ATPases(EC:3.6.3.)	112.7	105.3	102.6	108.3	114.1	90.6	0.97	8.5E-01
B035DRAFT_01443	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain	74.3	80.7	76.3	84.0	81.2	71.0	1.02	8.6E-01
B035DRAFT_01444	2-aminoethylphosphonate--pyruvate transaminase(EC:2.6.1.37)	7.7	11.5	9.2	9.6	12.3	10.5	1.15	5.7E-01
B035DRAFT_01445	phosphonoacetaldehyde hydrolase(EC:3.11.1.1)	5.5	6.2	6.4	7.2	5.6	5.0	0.97	9.1E-01
B035DRAFT_01446	hypothetical protein	6.7	6.9	5.3	3.8	5.7	4.4	0.73	2.8E-01
B035DRAFT_01447	hypothetical protein	7.3	7.6	6.3	5.9	7.0	7.3	0.95	7.5E-01
B035DRAFT_01448	Aldo/keto reductases, related to diketogulonate reductase	17.3	17.4	19.9	18.5	18.9	18.9	1.03	7.1E-01
B035DRAFT_01449	Aldo/keto reductases, related to diketogulonate reductase	19.7	11.7	13.5	13.7	14.4	10.1	0.86	6.6E-01

B035DRAFT_01450	AraC-type DNA-binding domain-containing proteins	35.9	46.0	41.7	44.7	39.6	29.3	0.91	7.2E-01
B035DRAFT_01451	Lipoprotein signal peptidase(EC:3.4.23.36)	28.5	38.0	32.2	28.7	28.9	39.4	0.98	9.3E-01
B035DRAFT_01452	hypothetical protein	30.7	40.0	34.1	31.6	26.8	33.9	0.88	5.0E-01
B035DRAFT_01453	Protein of unknown function (DUF3584).	51.9	53.3	50.0	47.8	55.3	55.5	1.02	8.5E-01
B035DRAFT_01454	hypothetical protein	50.5	73.2	51.9	49.2	49.5	65.2	0.94	8.3E-01
B035DRAFT_01455	hypothetical protein	58.8	79.7	65.0	69.4	80.3	82.2	1.15	4.7E-01
B035DRAFT_01456	ABC-type molybdenum transport system, ATPase component/photorepair protein PhrA	47.5	49.1	43.5	44.8	53.6	51.2	1.07	5.8E-01
B035DRAFT_01457	Dioxygenases related to 2-nitropropane dioxygenase(EC:1.3.1.)	447.8	456.5	435.7	289.1	202.1	159.2	0.47	8.2E-02
B035DRAFT_01458	anaerobic c4-dicarboxylate membrane transporter family protein	274.5	264.8	279.8	181.4	147.9	133.8	0.56	3.9E-02
B035DRAFT_01459	L-asparaginases, type II(EC:3.5.1.1)	494.8	458.4	536.5	443.3	382.3	297.0	0.75	2.4E-01
B035DRAFT_01460	hypothetical protein	193.8	183.1	220.3	171.4	151.1	164.3	0.82	1.6E-01
B035DRAFT_01461	Na+/H+-dicarboxylate symporters	228.0	192.5	234.2	201.4	171.8	153.5	0.80	2.6E-01
B035DRAFT_01462	6-phosphogluconate dehydrogenase (decarboxylating)(EC:1.1.1.44)	1081.0	804.7	1034.9	781.7	542.1	235.4	0.48	3.0E-01
B035DRAFT_01463	glucose-6-phosphate 1-dehydrogenase(EC:1.1.1.49)	701.4	583.9	730.9	589.2	392.5	308.8	0.62	2.3E-01
B035DRAFT_01464	6-phosphogluconolactonase(EC:3.1.1.31)	355.4	289.8	392.1	297.1	214.0	176.5	0.65	2.3E-01
B035DRAFT_01465	Putative translation initiation inhibitor, yjgF family	154.3	146.3	146.7	83.8	83.7	83.6	0.56	2.1E-04
B035DRAFT_01466	ABC-type transport system involved in cytochrome c biogenesis, permease component	65.8	63.9	57.7	11.3	16.8	14.7	0.23	7.4E-03
B035DRAFT_01467	Predicted thiol oxidoreductase	401.8	390.0	289.1	40.8	68.5	55.1	0.15	1.3E-02
B035DRAFT_01468	Imelysin.	483.9	418.5	337.0	55.5	99.1	95.1	0.20	2.6E-02
B035DRAFT_01469	hypothetical protein	646.8	569.2	442.6	138.3	182.0	171.7	0.30	2.0E-02
B035DRAFT_01470	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	30.1	37.7	32.6	50.3	47.6	50.9	1.49	4.8E-02
B035DRAFT_01471	heavy metal-(Cd/Co/Hg/Pb/Zn)-translocating P-type ATPase(EC:3.6.3.3,EC:3.6.3.5)	40.7	29.6	36.7	27.4	35.5	16.3	0.71	4.5E-01
B035DRAFT_01472	Predicted permease	79.3	81.4	83.6	105.7	99.7	89.1	1.20	1.2E-01
B035DRAFT_01473	hypothetical protein	4.3	6.7	3.5	3.0	3.9	1.3	0.54	3.8E-01
B035DRAFT_01474	cobyrinic acid a,c-diamide synthase(EC:6.3.5.9,EC:6.3.5.11)	74.0	60.1	79.5	70.0	67.9	35.1	0.78	5.6E-01
B035DRAFT_01475	cobyric acid synthase CobQ(EC:6.3.5.10)	74.0	72.3	81.1	72.1	77.2	41.9	0.81	5.6E-01
B035DRAFT_01476	Histidinol-phosphate/aromatic aminotransferase and cobyric acid decarboxylase(EC:4.1.1.81)	46.2	54.5	45.9	43.6	50.9	46.2	0.96	7.7E-01
B035DRAFT_01477	cobalamin biosynthesis protein CobD(EC:6.3.1.10)	43.7	46.0	50.1	35.8	41.7	35.8	0.81	1.4E-01
B035DRAFT_01478	alpha-ribazole phosphatase	46.1	53.2	52.2	52.5	61.8	45.1	1.05	8.2E-01
B035DRAFT_01479	Cobalamin-5-phosphate synthase(EC:2.7.8.26)	66.7	78.0	80.9	86.3	83.1	77.8	1.10	4.4E-01
B035DRAFT_01480	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase(EC:2.4.2.21)	101.5	95.5	112.1	124.9	110.8	69.4	0.96	9.1E-01
B035DRAFT_01481	Adenosyl cobinamide kinase/adenosyl cobinamide phosphate guanylyltransferase(EC:2.7.1.156,EC:2.7.7.62)	73.1	72.3	70.5	69.0	79.1	61.6	0.97	8.0E-01
B035DRAFT_01482	FHA domain.	193.4	229.7	169.1	196.1	196.9	201.8	1.01	9.5E-01
B035DRAFT_01483	Sporulation related domain.	246.0	276.1	238.5	294.5	299.9	325.7	1.21	1.2E-01
B035DRAFT_01484	nucleotide sugar dehydrogenase(EC:1.1.1.22)	200.5	189.0	174.7	164.8	197.9	142.5	0.89	5.2E-01
B035DRAFT_01485	hypothetical protein	126.5	127.2	108.1	91.5	140.1	120.6	0.96	8.8E-01
B035DRAFT_01486	Superfamily II DNA and RNA helicases	252.1	264.2	243.3	257.0	280.2	301.1	1.10	3.2E-01
B035DRAFT_01487	phosphoserine phosphatase SerB(EC:3.1.3.3)	245.9	288.7	271.7	337.0	314.2	330.2	1.22	1.0E-01
B035DRAFT_01488	Peroxiredoxin	1105.7	1127.8	1181.8	1186.6	1049.0	1188.8	1.00	9.9E-01
B035DRAFT_01489	hypothetical protein	84.5	124.0	115.4	70.2	86.0	103.7	0.80	4.6E-01
B035DRAFT_01490	hypothetical protein	61.4	72.6	65.0	60.9	66.0	71.6	1.00	9.9E-01
B035DRAFT_01491	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	160.3	158.3	153.2	91.2	105.5	93.5	0.61	1.3E-02
B035DRAFT_01492	Predicted permeases	160.1	175.0	164.6	161.6	171.7	181.3	1.03	7.1E-01

B035DRAFT_01493	tRNA-guanine transglycosylase, queuosine-34-forming(EC:2.4.2.29)	270.5	246.2	264.3	277.0	287.3	245.8	1.04	7.3E-01
B035DRAFT_01494	ATP-dependent protease La(EC:3.4.21.53)	240.4	230.0	201.5	221.0	231.3	217.9	1.00	1.0E+00
B035DRAFT_01495	Predicted O-methyltransferase	58.5	69.1	76.4	64.1	54.5	55.1	0.85	3.7E-01
B035DRAFT_01496	lipid kinase, YegS/Rv2252/BmrU family	402.8	428.0	382.5	365.1	260.2	267.9	0.73	1.8E-01
B035DRAFT_01497	7-keto-8-aminopelargonate synthetase and related enzymes(EC:2.3.1.47)	1554.4	1834.5	1765.9	1570.5	1560.4	1716.8	0.94	5.7E-01
B035DRAFT_01498	Predicted permeases	144.2	158.5	148.1	152.6	179.5	146.0	1.06	6.6E-01
B035DRAFT_01499	ABC-type antimicrobial peptide transport system, permease component	39.3	43.2	44.0	54.0	58.8	51.6	1.30	6.3E-02
B035DRAFT_01500	ABC-type antimicrobial peptide transport system, ATPase component	35.9	34.8	33.0	36.5	36.4	31.7	1.01	9.5E-01
B035DRAFT_01501	ABC-type antimicrobial peptide transport system, permease component	12.1	13.2	11.9	13.0	15.0	16.5	1.19	2.5E-01
B035DRAFT_01502	ABC-type transport system, involved in lipoprotein release, permease component	8.9	8.9	9.4	9.9	10.2	9.2	1.08	3.1E-01
B035DRAFT_01503	ABC-type antimicrobial peptide transport system, permease component	6.8	7.5	6.2	7.6	6.8	7.7	1.08	5.3E-01
B035DRAFT_01504	ABC-type antimicrobial peptide transport system, permease component	5.6	6.7	6.4	5.3	8.1	6.7	1.06	8.2E-01
B035DRAFT_01505	Membrane-fusion protein	3.2	1.7	1.8	2.7	2.3	2.6	1.17	6.8E-01
B035DRAFT_01506	Outer membrane protein	4.4	3.1	4.1	2.9	3.6	2.5	0.78	3.5E-01
B035DRAFT_01507	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	22.7	22.5	24.8	23.3	25.4	18.3	0.95	7.8E-01
B035DRAFT_01508	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	19.6	19.3	19.2	17.2	18.8	21.5	0.99	9.2E-01
B035DRAFT_01509	(tRNA)	20.3	28.8	24.7	33.2	28.6	8.2	0.81	8.1E-01
B035DRAFT_01510	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01511	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01512	Restriction endonuclease S subunits	29.5	29.7	27.9	15.9	15.4	21.1	0.60	6.2E-02
B035DRAFT_01513	type I site-specific deoxyribonuclease, HsdR family(EC:3.1.21.3)	36.4	30.9	31.3	25.6	26.5	26.5	0.80	8.8E-02
B035DRAFT_01514	Uncharacterized protein conserved in bacteria	31.7	27.3	24.4	21.4	17.4	22.0	0.73	1.6E-01
B035DRAFT_01515	helicase, putative, RecD/TraA family(EC:3.1.11.5)	28.0	20.2	25.0	22.0	19.5	7.8	0.62	4.4E-01
B035DRAFT_01516	hypothetical protein	17.4	21.0	16.9	12.4	15.8	7.6	0.62	2.8E-01
B035DRAFT_01517	HIRAN domain.	32.2	31.7	31.3	26.2	27.6	27.4	0.85	2.0E-02
B035DRAFT_01518	hypothetical protein	11.0	5.8	8.7	9.4	11.3	3.2	0.85	8.5E-01
B035DRAFT_01519	ATPases involved in chromosome partitioning	6.2	4.6	5.9	7.4	4.8	3.4	0.90	8.2E-01
B035DRAFT_01520	hypothetical protein	1.2	1.7	2.3	1.7	1.1	1.0	0.73	4.8E-01
B035DRAFT_01521	hypothetical protein	0.0	0.0	1.9	0.8	0.7	1.1	0.45	
B035DRAFT_01522	hypothetical protein	3.6	1.7	3.5	1.5	0.6	0.0	0.36	3.2E-01
B035DRAFT_01523	hypothetical protein	5.6	3.2	4.1	2.3	1.0	2.0	0.40	1.6E-01
B035DRAFT_01524	hypothetical protein	20.7	18.6	20.2	23.1	29.0	16.2	1.12	7.3E-01
B035DRAFT_01525	DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases(EC:2.7.7.7)	19.9	29.1	20.9	29.6	31.4	24.0	1.23	4.4E-01
B035DRAFT_01526	Acetyltransferase (isoleucine patch superfamily)(EC:2.3.1.18)	25.9	25.6	20.9	37.4	31.1	19.4	1.18	6.6E-01
B035DRAFT_01527	Histone H1-like protein Hc1.	6.7	5.5	8.1	6.0	9.5	9.5	1.22	5.6E-01
B035DRAFT_01528	hypothetical protein	9.1	10.0	9.8	9.0	8.0	7.8	0.86	1.8E-01
B035DRAFT_01529	hypothetical protein	6.0	5.6	6.2	4.8	7.1	5.2	0.94	8.0E-01
B035DRAFT_01530	hypothetical protein	5.0	4.7	5.3	5.6	5.4	4.8	1.05	6.4E-01
B035DRAFT_01531	hypothetical protein	5.9	3.7	8.0	3.8	4.7	2.7	0.65	4.1E-01
B035DRAFT_01532	hypothetical protein	7.6	7.5	7.5	5.4	6.6	2.9	0.62	3.2E-01
B035DRAFT_01533	Antirestriction protein	9.0	7.3	9.3	6.3	5.4	2.4	0.51	2.7E-01
B035DRAFT_01534	hypothetical protein	5.9	7.7	10.7	4.6	4.6	0.7	0.31	3.5E-01
B035DRAFT_01535	Mismatch repair ATPase (MutS family)	5.7	2.5	3.3	5.7	3.5	3.2	1.10	8.7E-01
B035DRAFT_01536	hypothetical protein	4.1	3.3	4.2	5.0	3.7	2.6	0.94	8.9E-01
B035DRAFT_01537	Muramidase (flagellum-specific) (GH73)	1.6	0.9	2.0	2.0	2.7	1.2	1.30	6.5E-01
B035DRAFT_01538	hypothetical protein	18.0	9.7	16.0	23.5	17.2	6.5	0.98	9.8E-01
B035DRAFT_01539	Protein-tyrosine-phosphatase(EC:1.20.4.1)	13.9	10.1	14.5	14.2	16.5	9.0	1.01	9.8E-01
B035DRAFT_01540	hypothetical protein	15.6	19.0	15.6	22.7	23.2	9.4	1.02	9.7E-01

B035DRAFT_01541	hypothetical protein	15.5	18.9	14.9	20.9	20.3	15.1	1.13	5.8E-01
B035DRAFT_01542	O-6-methylguanine DNA methyltransferase(EC:2.1.1.63)	10.5	10.7	14.0	12.5	18.5	15.6	1.31	3.3E-01
B035DRAFT_01543	TraX protein.	8.8	7.4	8.3	5.7	7.7	5.2	0.75	2.6E-01
B035DRAFT_01544	Type IV secretory pathway, VirD4 components	3.4	3.4	2.7	2.1	4.0	2.6	0.89	7.5E-01
B035DRAFT_01545	hypothetical protein	2.5	1.7	0.9	2.6	3.9	0.6	1.23	8.7E-01
B035DRAFT_01546	Bacteroides conjugative transposon TraN protein	3.5	3.8	3.8	3.5	3.2	2.6	0.83	2.7E-01
B035DRAFT_01547	Bacteroides conjugative transposon TraM protein	2.0	1.4	2.8	2.0	1.0	1.5	0.71	5.1E-01
B035DRAFT_01548	hypothetical protein	1.0	0.8	2.1	0.7	1.9	2.5	1.25	8.0E-01
B035DRAFT_01549	Bacteroides conjugative transposon TraK protein	1.1	0.7	0.0	2.4	0.8	0.5	1.14	9.1E-01
B035DRAFT_01550	hypothetical protein	1.5	1.4	1.3	1.9	3.3	0.0	1.83	3.2E-01
B035DRAFT_01551	hypothetical protein	1.7	1.7	0.9	1.6	1.1	0.9	0.84	7.2E-01
B035DRAFT_01552	hypothetical protein	1.9	1.1	2.4	1.8	1.1	1.3	0.80	6.3E-01
B035DRAFT_01553	hypothetical protein	1.8	2.4	2.2	1.4	2.1	0.6	0.58	4.1E-01
B035DRAFT_01554	Bacteroides conjugation system ATPase, TraG family	5.9	5.0	6.2	5.5	4.5	3.6	0.79	3.5E-01
B035DRAFT_01555	hypothetical protein	2.3	5.4	2.1	2.4	4.2	2.1	0.94	9.3E-01
B035DRAFT_01556	hypothetical protein	6.8	7.9	5.7	6.7	1.9	3.5	0.53	3.6E-01
B035DRAFT_01557	hypothetical protein	3.7	2.9	1.2	1.8	2.7	2.2	0.95	9.5E-01
B035DRAFT_01558	hypothetical protein	2.0	3.0	4.1	2.1	1.3	0.8	0.44	2.5E-01
B035DRAFT_01559	hypothetical protein	3.5	0.9	3.8	2.4	1.7	0.7	0.63	6.7E-01
B035DRAFT_01560	ATPases involved in chromosome partitioning	4.0	3.9	3.8	2.1	2.7	1.3	0.49	1.5E-01
B035DRAFT_01561	Relaxase/Mobilisation nuclease domain.	1.0	0.9	1.9	1.4	1.4	1.0	1.08	8.9E-01
B035DRAFT_01562	hypothetical protein	6.5	4.5	9.0	5.9	3.5	2.0	0.54	3.7E-01
B035DRAFT_01563	hypothetical protein	14.7	10.4	18.9	17.2	17.0	11.1	1.04	9.3E-01
B035DRAFT_01564	hypothetical protein	8.0	15.0	3.9	10.2	4.4	7.3	0.88	8.9E-01
B035DRAFT_01565	hypothetical protein	12.5	11.9	11.1	10.5	12.4	12.1	0.98	8.7E-01
B035DRAFT_01566	pyruvate, phosphate dikinase(EC:2.7.9.1)	349.6	354.9	356.6	338.0	387.7	394.3	1.05	5.6E-01
B035DRAFT_01567	23S rRNA (uracil-5-)-methyltransferase RumA	307.5	318.1	304.6	338.0	371.9	404.7	1.20	1.4E-01
B035DRAFT_01568	pseudouridine synthase, RluA family(EC:5.4.99.23)	317.6	327.9	300.0	338.4	382.6	402.8	1.19	1.7E-01
B035DRAFT_01569	HAD-superfamily hydrolase, subfamily IIB	50.9	68.3	56.2	68.9	68.9	97.5	1.33	3.0E-01
B035DRAFT_01570	Uncharacterized protein conserved in bacteria	34.0	34.4	30.2	40.5	55.4	51.1	1.48	1.0E-01
B035DRAFT_01571	Uncharacterized membrane protein	39.7	48.9	42.2	51.2	62.1	52.6	1.27	1.9E-01
B035DRAFT_01572	Signal transduction histidine kinase(EC:2.7.13.3)	25.4	30.4	22.6	24.0	25.4	35.9	1.08	8.0E-01
B035DRAFT_01573	Osmosensitive K+ channel His kinase sensor domain.(EC:2.7.13.3)	27.3	20.8	24.5	16.1	17.0	25.4	0.79	4.4E-01
B035DRAFT_01574	Bacteriophage protein gp37	17.7	22.6	14.7	19.7	20.4	26.0	1.21	4.9E-01
B035DRAFT_01575	NTP pyrophosphohydrolases including oxidative damage repair enzymes(EC:3.6.1.13)	68.8	81.0	75.9	83.0	77.0	105.4	1.17	4.2E-01
B035DRAFT_01576	Methylase involved in ubiquinone/menaquinone biosynthesis	191.4	206.9	202.7	213.0	212.6	234.5	1.10	2.4E-01
B035DRAFT_01577	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain	10.0	10.4	12.2	12.9	10.1	8.6	0.96	8.8E-01
B035DRAFT_01578	Lactoylglutathione lyase and related lyases	6.8	2.6	9.6	10.7	3.1	7.2	1.11	9.2E-01
B035DRAFT_01579	hypothetical protein	6.3	7.8	5.9	0.7	2.1	5.5	0.31	3.0E-01
B035DRAFT_01580	Sugar kinases, ribokinase family(EC:2.7.1.4)	4.1	4.3	3.1	2.2	3.7	4.4	0.88	7.7E-01
B035DRAFT_01581	Threonine dehydrogenase and related Zn-dependent dehydrogenases(EC:1.1.1.14)	7.6	5.5	7.5	5.3	6.0	5.1	0.81	3.4E-01
B035DRAFT_01582	sugar (Glycoside-Pentoside-Hexuronide) transporter	4.5	5.0	5.1	4.6	5.1	5.2	1.02	8.9E-01
B035DRAFT_01583	Transcriptional regulators	35.1	46.1	41.9	42.6	42.4	48.4	1.09	6.1E-01
B035DRAFT_01584	Predicted P-loop ATPase fused to an acetyltransferase	37.0	45.6	40.1	48.4	45.3	53.9	1.20	2.4E-01
B035DRAFT_01585	Beta-lactamase class A(EC:3.5.2.6)	25.9	30.9	28.5	36.1	46.6	53.4	1.58	1.2E-01
B035DRAFT_01586	Glucoamylase and related glycosyl hydrolases (GH15)	6.1	4.2	2.8	2.1	2.9	3.4	0.67	4.2E-01
B035DRAFT_01587	trehalose-phosphatase(EC:2.4.1.15) (GT20)	8.2	7.0	7.1	4.0	3.5	4.9	0.56	5.4E-02
B035DRAFT_01588	Aspartokinases(EC:2.7.2.4)	6.0	3.6	4.9	2.0	1.9	3.2	0.48	1.4E-01

B035DRAFT_01589	Chloramphenicol O-acetyltransferase(EC:2.3.1.28)	34.5	39.8	36.2	52.0	47.9	65.2	1.48	1.0E-01
B035DRAFT_01590	Predicted hydrolase (HAD superfamily)	18.9	24.2	20.6	21.1	20.0	33.6	1.15	6.7E-01
B035DRAFT_01591	Bacterial protein of unknown function (Gcw_chp).	11.8	10.4	12.0	6.6	7.2	10.1	0.69	1.9E-01
B035DRAFT_01592	hypothetical protein	1.5	1.7	9.0	0.0	4.0	6.7	1.83	6.1E-01
B035DRAFT_01593	K+-transporting ATPase, C subunit(EC:3.6.3.12)	6.5	10.3	5.8	4.4	4.0	4.6	0.59	1.7E-01
B035DRAFT_01594	K+-transporting ATPase, B subunit(EC:3.6.3.12)	11.5	8.9	11.0	7.4	7.7	6.3	0.68	1.1E-01
B035DRAFT_01595	K+-transporting ATPase, KdpA(EC:3.6.3.12)	8.3	8.9	7.3	4.6	5.9	6.5	0.69	1.5E-01
B035DRAFT_01596	hypothetical protein	0.0	0.0	0.0	2.5	1.1	0.0	0.00	
B035DRAFT_01597	Arylsulfatase A and related enzymes	64.3	73.3	65.3	46.4	56.9	62.8	0.81	2.8E-01
B035DRAFT_01598	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	77.8	83.4	77.2	71.2	79.5	95.8	1.03	8.8E-01
B035DRAFT_01599	glycine betaine/L-proline transport ATP binding subunit(EC:3.6.3.32)	539.5	512.6	475.4	332.3	193.3	203.1	0.46	8.2E-02
B035DRAFT_01600	ABC-type proline/glycine betaine transport system, permease component	497.4	464.1	471.9	334.5	204.7	216.2	0.51	8.5E-02
B035DRAFT_01601	ABC-type proline/glycine betaine transport systems, periplasmic components	320.2	311.6	337.0	210.2	115.2	104.5	0.42	9.9E-02
B035DRAFT_01602	Permeases of the drug/metabolite transporter (DMT) superfamily	278.6	312.6	306.0	165.3	93.8	123.0	0.42	5.8E-02
B035DRAFT_01603	Acetyltransferase (isoleucine patch superfamily)(EC:2.3.1.79)	256.3	330.1	325.4	198.2	122.7	182.3	0.54	1.2E-01
B035DRAFT_01604	Protein of unknown function (DUF2582).	268.4	304.0	236.5	212.7	229.3	206.8	0.81	1.9E-01
B035DRAFT_01605	Tryptophan-rich sensory protein (mitochondrial benzodiazepine receptor homolog)	182.4	212.4	193.2	30.6	28.3	41.3	0.17	4.2E-03
B035DRAFT_01606	hypothetical protein	1574.4	1852.6	1515.5	186.5	157.1	202.7	0.11	8.3E-04
B035DRAFT_01607	Glucuronate isomerase(EC:5.3.1.12)	185.9	144.6	109.1	154.8	157.8	200.0	1.19	5.9E-01
B035DRAFT_01608	hypothetical protein	17.3	28.7	20.5	19.5	23.5	31.8	1.13	7.6E-01
B035DRAFT_01609	Arylsulfatase A and related enzymes	37.8	43.8	39.5	36.2	39.7	48.2	1.02	9.2E-01
B035DRAFT_01610	hypothetical protein	44.8	47.9	47.5	49.1	54.2	66.3	1.20	3.0E-01
B035DRAFT_01611	ATP-dependent exoDNAse (exonuclease V) beta subunit (contains helicase and exonuclease domains)	80.1	79.0	74.2	75.7	86.9	90.6	1.08	4.6E-01
B035DRAFT_01612	Long-chain acyl-CoA synthetases (AMP-forming)(EC:6.2.1.3)	159.7	156.5	151.3	139.9	138.1	138.9	0.89	3.0E-02
B035DRAFT_01613	Protein of unknown function (DUF2874).	178.3	171.3	164.1	129.9	115.0	142.2	0.75	8.2E-02
B035DRAFT_01614	hypothetical protein	53.1	76.7	52.9	56.7	55.4	56.3	0.94	7.8E-01
B035DRAFT_01615	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	277.4	276.8	251.0	257.7	359.9	407.5	1.25	3.9E-01
B035DRAFT_01616	(tRNA)	63.6	66.3	69.4	97.0	59.7	53.8	1.02	9.6E-01
B035DRAFT_01617	hypothetical protein	151.8	161.7	150.5	187.1	211.7	222.8	1.34	6.1E-02
B035DRAFT_01618	crossover junction endodeoxyribonuclease RuvC(EC:3.1.22.4)	100.8	97.1	76.1	103.6	119.0	131.7	1.30	2.4E-01
B035DRAFT_01619	pullulanase, type I(EC:3.2.1.41) (CBM48)	98.0	105.0	80.1	77.4	104.3	104.0	1.01	9.8E-01
B035DRAFT_01620	mannonate dehydratase(EC:4.2.1.8)	78.9	104.1	87.5	82.1	89.1	91.5	0.98	8.9E-01
B035DRAFT_01621	Predicted esterase of the alpha-beta hydrolase superfamily	40.3	41.0	40.0	33.0	29.0	32.6	0.78	4.5E-02
B035DRAFT_01622	isoleucyl-tRNA synthetase(EC:6.1.1.5)	477.7	492.2	444.7	424.3	501.6	537.8	1.03	8.4E-01
B035DRAFT_01623	DnaK suppressor protein	559.5	641.7	541.7	704.3	747.6	891.7	1.34	1.4E-01
B035DRAFT_01624	Lipoprotein signal peptidase(EC:3.4.23.36)	434.3	513.0	502.1	514.3	557.4	739.4	1.24	3.5E-01
B035DRAFT_01625	hypothetical protein	220.4	262.9	258.7	245.5	276.4	326.5	1.14	4.7E-01
B035DRAFT_01626	hypothetical protein	136.9	190.4	201.8	163.7	157.3	207.0	1.00	9.9E-01
B035DRAFT_01627	rRNA methylases	85.9	102.5	87.4	80.8	86.2	88.9	0.93	5.2E-01
B035DRAFT_01628	Outer membrane protein/protective antigen OMA87	134.0	147.0	139.4	174.5	173.8	191.3	1.28	4.3E-02
B035DRAFT_01629	hypothetical protein	88.2	112.0	97.4	114.3	102.1	125.8	1.15	4.0E-01
B035DRAFT_01630	hypothetical protein	249.7	280.0	242.7	334.9	255.8	316.9	1.17	3.7E-01
B035DRAFT_01631	hypothetical protein	260.0	324.5	253.7	359.4	275.8	350.6	1.18	4.4E-01
B035DRAFT_01632	Metal-dependent hydrolases of the beta-lactamase superfamily I	198.3	235.0	200.2	180.5	169.3	223.8	0.90	5.7E-01
B035DRAFT_01633	(tRNA)	346.7	449.6	503.1	285.5	187.4	147.5	0.47	1.3E-01
B035DRAFT_01634	hypothetical protein	392.0	513.6	529.6	418.5	396.9	483.4	0.91	6.4E-01
B035DRAFT_01635	(tRNA)	35.6	56.8	78.4	44.5	36.3	99.0	1.00	1.0E+00

B035DRAFT_01636	(tRNA)	42.8	31.4	43.9	56.9	36.8	40.9	1.13	6.9E-01
B035DRAFT_01637	ferrous iron transporter FeoB	320.0	274.6	240.1	263.1	197.9	289.0	0.89	6.6E-01
B035DRAFT_01638	tRNA(Ile)-lysidine synthetase, N-terminal domain/tRNA(Ile)-lysidine synthetase, C-terminal domain(EC:6.3.4.)	67.3	69.3	70.9	74.2	62.8	80.8	1.04	7.6E-01
B035DRAFT_01639	hypothetical protein	118.0	111.8	125.0	99.3	93.7	97.7	0.82	5.5E-02
B035DRAFT_01640	hypothetical protein	36.7	35.0	27.1	46.9	28.5	32.1	1.07	8.4E-01
B035DRAFT_01641	(tRNA)	484.2	942.5	1377.2	879.3	706.1	1298.1	1.09	9.1E-01
B035DRAFT_01642	hypothetical protein	200.7	241.8	269.2	180.1	178.3	207.5	0.80	2.5E-01
B035DRAFT_01643	formate acetyltransferase 1(EC:2.3.1.54)	1680.0	1629.0	1473.9	1168.0	1142.7	1212.5	0.74	3.0E-02
B035DRAFT_01644	pyruvate formate-lyase 1-activating enzyme(EC:1.97.1.4)	470.2	461.1	385.7	260.8	318.4	307.0	0.67	7.7E-02
B035DRAFT_01645	hypothetical protein	634.1	651.2	563.9	399.7	461.0	394.4	0.68	4.6E-02
B035DRAFT_01646	Uncharacterized conserved protein	233.0	202.4	188.4	117.6	151.0	100.3	0.59	9.5E-02
B035DRAFT_01647	Uncharacterized conserved protein containing a ferredoxin-like domain	386.1	373.8	363.7	272.6	227.2	167.4	0.58	1.1E-01
B035DRAFT_01648	Fe-S oxidoreductase	566.5	501.9	536.2	451.9	318.2	265.2	0.63	1.7E-01
B035DRAFT_01649	Predicted phosphohydrolases	216.9	212.4	221.5	167.6	214.2	242.8	0.95	8.0E-01
B035DRAFT_01650	Calcineurin-like phosphoesterase.	271.4	250.3	239.3	214.4	246.9	220.8	0.90	3.1E-01
B035DRAFT_01651	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	1265.1	1412.2	1328.2	976.7	997.4	1011.5	0.75	2.0E-02
B035DRAFT_01652	hypothetical protein	1516.7	1662.6	1494.4	1141.3	1131.3	1128.7	0.73	1.6E-02
B035DRAFT_01653	Formate-dependent phosphoribosylglycinamide formyltransferase (GAR transformylase)(EC:2.1.2.2)	191.4	200.2	202.0	200.3	229.6	193.4	1.05	6.4E-01
B035DRAFT_01654	Putative stress-responsive transcriptional regulator	88.1	76.0	89.5	116.2	141.9	126.1	1.51	5.7E-02
B035DRAFT_01655	Predicted transcriptional regulators	104.4	84.1	75.4	174.6	171.9	130.5	1.81	8.0E-02
B035DRAFT_01656	Acetyltransferases	47.1	62.3	46.2	40.4	54.7	63.2	1.01	9.8E-01
B035DRAFT_01657	Predicted DNA alkylation repair enzyme	103.0	105.9	91.8	85.8	92.8	81.8	0.87	2.2E-01
B035DRAFT_01658	O-6-methylguanine DNA methyltransferase(EC:2.1.1.63)	147.7	139.4	115.2	102.4	132.2	119.6	0.88	5.1E-01
B035DRAFT_01659	Peptide-N-glycosidase F, N terminal./Peptide-N-glycosidase F, C terminal.	121.6	128.4	115.3	94.3	111.9	122.3	0.89	4.6E-01
B035DRAFT_01660	hypothetical protein	343.4	332.6	321.7	332.7	403.0	389.7	1.12	3.2E-01
B035DRAFT_01661	(p)ppGpp synthetase, RelA/SpoT family(EC:2.7.6.5)	92.2	112.4	99.8	145.3	146.4	158.1	1.48	4.2E-02
B035DRAFT_01662	Diacylglycerol kinase(EC:2.7.1.107)	55.8	62.7	55.7	62.3	74.4	73.3	1.20	2.0E-01
B035DRAFT_01663	Protein of unknown function (DUF1573).	421.7	464.5	397.4	647.6	582.6	703.2	1.50	4.7E-02
B035DRAFT_01664	Predicted phosphohydrolases	93.2	99.2	90.5	121.6	115.9	134.2	1.31	5.6E-02
B035DRAFT_01665	hypothetical protein	67.1	82.1	78.6	100.7	95.9	117.6	1.38	1.1E-01
B035DRAFT_01666	putative oligopeptide transporter, OPT family	142.0	152.5	136.6	95.9	116.8	106.1	0.74	7.3E-02
B035DRAFT_01667	Esterase/lipase (CE10)	91.7	110.1	116.7	114.2	123.5	107.4	1.09	5.8E-01
B035DRAFT_01668	Ferritin-like protein(EC:1.16.3.1)	178.7	186.2	169.4	180.4	234.0	215.8	1.17	3.1E-01
B035DRAFT_01669	ribosomal protein S16	8440.6	9637.3	8907.7	9192.9	8020.1	8525.0	0.95	6.4E-01
B035DRAFT_01670	Predicted extracellular nuclease	47.6	47.7	40.5	24.8	38.9	41.7	0.76	3.9E-01
B035DRAFT_01671	hypothetical protein	387.1	424.1	363.5	206.9	303.2	386.4	0.74	3.9E-01
B035DRAFT_01672	Outer membrane receptor proteins, mostly Fe transport	275.0	291.7	251.9	127.2	183.3	207.8	0.62	1.5E-01
B035DRAFT_01673	ATP-binding cassette protein, ChvD family	372.5	383.9	379.3	351.4	339.5	282.6	0.85	2.4E-01
B035DRAFT_01674	Arabinose efflux permease	294.7	322.6	322.9	241.4	240.8	240.1	0.77	2.0E-02
B035DRAFT_01675	3-methyl-2-oxobutanoate hydroxymethyltransferase(EC:2.1.2.11)	1034.3	1050.4	1052.5	918.3	765.4	667.1	0.74	1.5E-01
B035DRAFT_01676	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	848.3	895.2	784.6	879.8	761.9	739.8	0.94	6.1E-01
B035DRAFT_01677	NhaP-type Na+/H+ and K+/H+ antiporters with a unique C-terminal domain	149.3	160.5	150.2	129.1	113.1	133.1	0.81	1.1E-01
B035DRAFT_01678	Mn2+ and Fe2+ transporters of the NRAMP family	418.1	426.5	396.2	283.8	255.6	257.0	0.64	1.1E-02
B035DRAFT_01679	hypothetical protein	136.7	148.6	130.0	130.8	135.7	175.9	1.06	7.7E-01
B035DRAFT_01680	hypothetical protein	353.3	392.2	325.8	403.1	434.4	479.9	1.23	1.8E-01
B035DRAFT_01681	RNA polymerase sigma factor, sigma-70 family	6314.3	6183.0	6570.3	7713.2	6770.7	6743.4	1.11	2.6E-01

B035DRAFT_01682	Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain	214.3	190.3	179.1	329.7	414.1	322.8	1.82	4.0E-02
B035DRAFT_01683	(miscRNA)	70807.8	50756.1	114687.4	188739.8	87287.0	20623.3	0.94	9.7E-01
B035DRAFT_01684	Predicted membrane protein	154.0	178.5	176.0	184.0	175.4	203.9	1.11	3.9E-01
B035DRAFT_01685	riboflavin synthase, alpha subunit(EC:2.5.1.9)	287.7	309.5	309.3	338.9	328.7	304.3	1.07	3.6E-01
B035DRAFT_01686	Predicted transcriptional regulators	85.9	104.7	80.7	100.0	103.7	88.0	1.08	6.5E-01
B035DRAFT_01687	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II(EC:6.2.1.)	86.6	86.5	91.2	72.4	84.5	100.1	0.96	8.5E-01
B035DRAFT_01688	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	80.9	68.7	72.4	77.7	87.4	71.1	1.06	6.6E-01
B035DRAFT_01689	cytochrome d oxidase, subunit II (cydB)(EC:1.10.3.)	277.7	208.4	152.3	151.3	148.3	202.8	0.80	5.4E-01
B035DRAFT_01690	Cytochrome bd-type quinol oxidase, subunit 1(EC:1.10.3.)	257.4	193.2	171.7	151.7	139.2	117.8	0.66	1.7E-01
B035DRAFT_01691	hypothetical protein	81.0	75.3	51.6	74.7	62.9	99.5	1.14	7.1E-01
B035DRAFT_01692	Outer membrane protein	1.3	2.3	1.2	1.1	1.6	2.3	1.02	9.7E-01
B035DRAFT_01693	RND family efflux transporter, MFP subunit	2.5	1.9	2.0	2.3	2.8	2.4	1.17	3.8E-01
B035DRAFT_01694	ABC-type antimicrobial peptide transport system, ATPase component	3.4	2.9	1.9	3.3	3.3	2.9	1.19	5.9E-01
B035DRAFT_01695	ABC-type antimicrobial peptide transport system, permease component	4.8	4.5	4.0	3.9	4.0	3.4	0.85	2.6E-01
B035DRAFT_01696	Putative regulator of cell autolysis	6.4	10.6	11.7	16.8	15.7	17.0	1.78	1.6E-01
B035DRAFT_01697	Response regulator of the LytR/AlgR family	14.9	20.6	19.8	20.3	20.2	26.9	1.22	4.3E-01
B035DRAFT_01698	uncharacterized protein TIGR03905	472.0	455.8	482.2	486.6	484.0	376.5	0.95	7.5E-01
B035DRAFT_01699	DNA-binding regulatory protein, YebC/PmpR family	454.4	455.0	406.6	384.2	481.9	474.1	1.01	9.3E-01
B035DRAFT_01700	phenylalanyl-tRNA synthetase, beta subunit, non-spirochete bacterial(EC:6.1.1.20)	446.5	466.1	454.8	401.7	456.0	475.3	0.97	7.8E-01
B035DRAFT_01701	replicative DNA helicase(EC:3.6.4.12)	130.5	126.0	117.6	130.6	136.4	92.1	0.95	8.2E-01
B035DRAFT_01702	4-diphosphocytidyl-2C-methyl-D-erythritol kinase(EC:2.7.1.148)	295.4	319.0	299.6	263.9	200.1	245.7	0.77	1.6E-01
B035DRAFT_01703	(miscRNA)	5132.1	7908.3	8085.1	9719.0	7503.2	7235.7	1.17	6.2E-01
B035DRAFT_01704	UDP-glucose-4-epimerase(EC:5.1.3.2)	989.9	1061.1	1066.5	908.7	991.8	1070.1	0.95	6.0E-01
B035DRAFT_01705	hypothetical protein	500.4	490.8	418.7	406.0	514.7	445.5	0.97	8.5E-01
B035DRAFT_01706	electron transport complex, RnfABCDGE type, A subunit	232.0	260.8	264.9	209.7	236.2	273.2	0.95	7.3E-01
B035DRAFT_01707	electron transport complex, RnfABCDGE type, E subunit	146.1	161.8	166.6	138.6	149.2	153.0	0.93	4.2E-01
B035DRAFT_01708	electron transport complex, RnfABCDGE type, G subunit	209.7	169.3	192.8	156.4	188.0	140.7	0.85	3.9E-01
B035DRAFT_01709	electron transport complex, RnfABCDGE type, D subunit	203.6	193.2	198.5	160.9	201.8	172.6	0.90	3.8E-01
B035DRAFT_01710	electron transport complex, RnfABCDGE type, C subunit	260.6	226.6	241.5	193.0	231.4	152.0	0.78	3.1E-01
B035DRAFT_01711	Predicted NADH:ubiquinone oxidoreductase, subunit RnfB	275.0	242.3	252.8	199.2	223.5	111.3	0.67	3.3E-01
B035DRAFT_01712	Positive regulator of sigma E activity	238.4	292.0	263.4	273.3	226.0	221.0	0.91	5.4E-01
B035DRAFT_01713	Permeases of the drug/metabolite transporter (DMT) superfamily	245.9	213.2	233.0	117.8	90.3	115.7	0.47	2.3E-02
B035DRAFT_01714	Cyanate permease	248.6	245.3	264.9	192.6	145.5	180.5	0.68	8.0E-02
B035DRAFT_01715	glutamate decarboxylase(EC:4.1.1.15)	2703.5	1786.4	2164.2	2316.5	2475.4	2537.5	1.12	6.2E-01
B035DRAFT_01716	glutaminase A(EC:3.5.1.2)	1323.1	971.2	1140.7	1292.1	1362.2	1693.4	1.27	3.1E-01
B035DRAFT_01717	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	145.4	141.3	135.3	125.7	148.5	149.3	1.00	1.0E+00
B035DRAFT_01718	Uncharacterized protein involved in copper resistance	193.1	218.8	187.5	168.6	195.0	199.2	0.94	6.2E-01
B035DRAFT_01719	Transglutaminase-like enzymes, putative cysteine proteases	210.0	188.4	198.7	191.0	203.6	161.8	0.93	5.9E-01
B035DRAFT_01720	Ion channel.	106.6	109.4	111.2	101.6	80.0	90.6	0.83	1.9E-01
B035DRAFT_01721	putative glutamate/gamma-aminobutyrate antiporter	609.8	457.1	536.2	465.2	481.4	483.8	0.90	4.8E-01
B035DRAFT_01722	His Kinase A (phosphoacceptor) domain./PAS fold./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	53.4	59.8	52.1	65.8	64.2	73.1	1.23	1.2E-01
B035DRAFT_01723	Na+/H+ antiporter NhaA	181.9	159.8	157.8	120.5	159.1	141.9	0.84	3.2E-01
B035DRAFT_01724	hypothetical protein	324.4	317.4	315.7	308.0	341.7	350.3	1.04	5.7E-01
B035DRAFT_01725	GTP-binding protein LepA	439.6	443.3	420.0	438.5	474.9	362.6	0.97	8.7E-01
B035DRAFT_01726	Protein of unknown function (DUF2582).	1314.1	1311.0	1145.7	1147.2	1000.6	803.7	0.78	2.6E-01
B035DRAFT_01727	C_GCAxxG_C_C family probable redox protein	76.1	49.7	62.7	57.4	59.7	20.6	0.67	5.4E-01
B035DRAFT_01728	Lactate dehydrogenase and related dehydrogenases(EC:1.1.1.29)	70.1	67.3	65.5	69.9	78.2	45.6	0.93	8.2E-01
B035DRAFT_01729	ATPase related to the helicase subunit of the Holliday junction resolvase	47.3	39.0	32.7	27.6	43.7	21.1	0.75	5.1E-01

B035DRAFT_01730	hypothetical protein	121.3	121.7	132.4	167.8	168.6	160.0	1.32	2.1E-02
B035DRAFT_01731	phosphate transport system regulatory protein PhoU	21.2	19.8	25.5	17.4	12.4	10.4	0.59	1.6E-01
B035DRAFT_01732	phosphate ABC transporter, ATP-binding protein(EC:3.6.3.27)	11.4	9.4	17.5	9.0	8.3	6.3	0.63	2.7E-01
B035DRAFT_01733	phosphate ABC transporter, permease protein PstA	14.3	11.3	13.7	8.2	7.9	5.5	0.55	8.9E-02
B035DRAFT_01734	phosphate ABC transporter, permease protein PstC	20.6	16.8	18.2	15.0	12.6	8.7	0.64	2.0E-01
B035DRAFT_01735	phosphate binding protein	6.8	5.5	6.3	6.3	3.6	3.6	0.70	3.4E-01
B035DRAFT_01736	glutaminyl-tRNA synthetase(EC:6.1.1.18)	257.6	237.9	212.8	259.4	279.2	234.5	1.09	5.1E-01
B035DRAFT_01737	hypothetical protein	147.4	160.8	149.7	165.6	189.3	189.0	1.19	1.4E-01
B035DRAFT_01738	Uncharacterized membrane-associated protein	154.9	166.0	169.2	177.5	196.8	229.9	1.23	2.1E-01
B035DRAFT_01739	Peroxiredoxin(EC:1.11.1.15)	2512.7	2253.9	1883.8	2695.6	1166.1	1618.1	0.78	6.0E-01
B035DRAFT_01740	hypothetical protein	71.1	72.8	74.8	95.5	70.4	89.2	1.16	4.0E-01
B035DRAFT_01741	Predicted P-loop ATPase and inactivated derivatives	28.7	22.9	28.0	12.3	10.4	13.0	0.45	2.2E-02
B035DRAFT_01742	hypothetical protein	777.2	870.1	927.6	896.8	643.8	779.4	0.90	5.8E-01
B035DRAFT_01743	hypothetical protein	21.9	25.3	22.6	14.6	15.0	22.1	0.73	2.6E-01
B035DRAFT_01744	hypothetical protein	676.9	703.9	745.7	715.8	694.6	733.7	1.01	8.9E-01
B035DRAFT_01745	Beta-glucosidase-related glycosidases(EC:3.2.1.21) (GH3)	52.5	50.8	51.4	31.2	46.4	32.6	0.70	1.8E-01
B035DRAFT_01746	Predicted membrane protein	50.4	48.8	46.4	33.2	47.2	54.8	0.91	7.3E-01
B035DRAFT_01747	Alcohol dehydrogenase, class IV(EC:1.1.1.1)	104.3	93.4	105.1	153.3	153.1	141.6	1.48	2.1E-02
B035DRAFT_01748	**TonB-linked outer membrane protein, SusC/RagA family**	**24.5**	**16.1**	**19.3**	**30.7**	**45.1**	**50.8**	**2.10**	**1.1E-01**
B035DRAFT_01749	SusD family	6.5	6.6	7.6	22.3	32.0	35.3	4.25	1.5E-02
B035DRAFT_01750	hypothetical protein (CE1)	7.5	6.8	5.9	10.1	16.1	17.4	2.11	9.2E-02
B035DRAFT_01751	N-acyl-D-glucosamine 2-epimerase(EC:5.1.3.8) (GH76)	112.2	113.5	128.0	400.3	454.2	463.4	3.73	1.1E-03
B035DRAFT_01752	Dihydrodipicolinate synthase/N-acetylneuraminate lyase(EC:4.1.3.3)	91.8	92.8	93.1	332.6	378.0	362.6	3.86	1.6E-04
B035DRAFT_01753	uncharacterized protein, YhcH/YjgK/YiaL family	45.0	50.1	59.3	129.7	168.9	167.6	3.02	1.7E-02
B035DRAFT_01754	Sugar phosphate permease	133.6	108.2	139.9	273.3	299.6	229.2	2.10	3.5E-02
B035DRAFT_01755	Predicted thioesterase(EC:3.1.2.)	161.3	177.8	152.3	146.6	163.1	134.5	0.90	4.3E-01
B035DRAFT_01756	OAH/OAS sulfhydrylase(EC:2.5.1.49)	110.1	128.8	114.4	118.3	118.5	100.1	0.95	7.2E-01
B035DRAFT_01757	Short-chain dehydrogenases of various substrate specificities	75.2	72.4	92.7	78.0	61.3	42.6	0.74	3.9E-01
B035DRAFT_01758	hypothetical protein	17.5	18.5	17.5	13.1	12.8	12.8	0.72	2.7E-03
B035DRAFT_01759	hypothetical protein	113.7	130.1	100.8	1021.3	1195.8	1085.4	9.62	5.2E-04
B035DRAFT_01760	RNA polymerase sigma factor, sigma-70 family	114.3	118.3	103.8	954.3	1025.3	771.8	8.14	8.8E-04
B035DRAFT_01761	hypothetical protein	78.3	71.3	60.5	635.8	667.3	589.8	9.05	5.0E-04
B035DRAFT_01762	hypothetical protein	146.5	146.7	135.7	1292.0	1311.8	1433.5	9.41	3.2E-05
B035DRAFT_01763	hypothetical protein	164.9	183.7	172.9	140.6	198.9	176.9	0.98	9.3E-01
B035DRAFT_01764	hypothetical protein	104.3	88.9	107.5	131.9	103.6	52.9	0.90	8.5E-01
B035DRAFT_01765	Mismatch repair ATPase (MutS family)	96.4	105.8	105.9	167.0	153.2	154.2	1.54	1.3E-02
B035DRAFT_01766	hypothetical protein	575.3	604.0	625.8	745.2	743.0	866.8	1.30	7.2E-02
B035DRAFT_01767	hypothetical protein	631.6	694.8	667.0	768.1	780.3	687.5	1.12	2.4E-01
B035DRAFT_01768	ribosomal protein L17	3981.7	4374.0	4301.2	3591.7	3593.4	4604.4	0.93	6.3E-01
B035DRAFT_01769	DNA-directed RNA polymerase, alpha subunit, bacterial and chloroplast-type(EC:2.7.7.6)	4789.7	5193.6	5041.4	4097.5	4145.8	5465.3	0.90	5.7E-01
B035DRAFT_01770	ribosomal protein S4, bacterial/organelle type	5009.2	5018.0	5045.9	4235.2	4206.7	4966.7	0.89	2.6E-01
B035DRAFT_01771	30S ribosomal protein S11	4289.4	4145.3	3907.6	3307.6	3439.9	4050.2	0.87	2.9E-01
B035DRAFT_01772	30S ribosomal protein S13	3918.0	3532.5	3210.1	3148.1	3242.6	3473.4	0.93	5.2E-01
B035DRAFT_01773	ribosomal protein L36, bacterial type	1895.7	1866.3	1691.9	1547.2	1681.8	2023.3	0.96	8.0E-01
B035DRAFT_01774	translation initiation factor IF-1	2512.3	2435.3	2133.4	2094.1	2195.5	2658.3	0.98	9.0E-01
B035DRAFT_01775	methionine aminopeptidase, type I(EC:3.4.11.18)	3731.1	3621.4	3422.0	3167.9	3379.4	4034.5	0.98	8.8E-01
B035DRAFT_01776	preprotein translocase, SecY subunit	4226.0	4609.6	4452.6	3907.2	4171.2	5700.4	1.02	9.3E-01
B035DRAFT_01777	ribosomal protein L15, bacterial/organelle	5553.7	5530.2	5097.5	4931.8	5408.1	6436.3	1.03	8.5E-01
B035DRAFT_01778	ribosomal protein L30, bacterial/organelle	2943.3	2731.3	2622.3	2568.9	2884.3	3198.8	1.04	7.7E-01
B035DRAFT_01779	ribosomal protein S5, bacterial/organelle type	3865.6	3524.6	3433.9	3162.6	3624.6	3444.1	0.94	5.6E-01

B035DRAFT_01780	ribosomal protein L18, bacterial type	4286.3	3873.3	3624.2	3594.5	4060.1	4356.5	1.02	9.0E-01
B035DRAFT_01781	ribosomal protein L6, bacterial type	3465.6	3491.1	3136.3	2839.6	3383.6	4008.6	1.00	9.8E-01
B035DRAFT_01782	Ribosomal protein S8	4473.5	4479.2	3883.7	3699.8	4400.5	5165.1	1.03	9.0E-01
B035DRAFT_01783	Ribosomal protein S14	4567.1	4678.7	4069.3	4292.7	4716.8	6017.6	1.12	5.7E-01
B035DRAFT_01784	Ribosomal protein L5	2275.6	2456.6	2411.8	1933.1	2192.1	2801.6	0.96	8.5E-01
B035DRAFT_01785	ribosomal protein L24, bacterial/organelle	3840.4	3597.0	3141.0	2882.5	3463.3	3684.1	0.95	7.6E-01
B035DRAFT_01786	ribosomal protein L14, bacterial/organelle	3633.2	3606.4	3352.3	3001.2	3451.6	3944.6	0.98	8.8E-01
B035DRAFT_01787	30S ribosomal protein S17	3836.8	3661.6	3141.5	3231.2	3627.6	4068.9	1.03	8.8E-01
B035DRAFT_01788	ribosomal protein L29	3090.0	3061.2	2783.9	2543.4	2902.3	3542.8	1.00	9.9E-01
B035DRAFT_01789	ribosomal protein L16, bacterial/organelle	3648.4	3282.6	3155.6	3047.6	3479.0	3452.7	0.99	9.3E-01
B035DRAFT_01790	ribosomal protein S3, bacterial type	5009.1	4484.7	4200.1	3974.8	4792.1	4905.0	1.00	9.9E-01
B035DRAFT_01791	ribosomal protein L22, bacterial type	3724.1	3385.0	3150.8	2920.5	3572.2	3763.0	1.00	9.8E-01
B035DRAFT_01792	ribosomal protein S19, bacterial/organelle	3369.7	3226.2	3067.3	2747.7	3197.0	3652.1	0.99	9.4E-01
B035DRAFT_01793	ribosomal protein L2, bacterial/organellar	3542.7	3452.4	3386.9	3078.2	3325.2	3288.2	0.93	2.1E-01
B035DRAFT_01794	Ribosomal protein L23	4609.1	4820.0	4254.5	3899.3	4502.8	5410.7	1.00	9.9E-01
B035DRAFT_01795	50S ribosomal protein L4, bacterial/organelle	2531.7	2603.5	2456.2	2238.3	2513.5	2928.7	1.01	9.8E-01
B035DRAFT_01796	50S ribosomal protein L3, bacterial	3812.8	3669.3	3449.2	3472.2	3867.8	4259.4	1.06	6.4E-01
B035DRAFT_01797	ribosomal protein S10, bacterial/organelle	2482.0	2766.4	2437.8	2253.6	2508.6	3259.6	1.03	8.9E-01
B035DRAFT_01798	translation elongation factor EF-G	4656.1	4517.9	4418.2	3996.0	4488.1	4980.7	0.99	9.2E-01
B035DRAFT_01799	ribosomal protein S7, bacterial/organelle	3872.5	4020.7	3703.0	3172.9	3479.9	3681.6	0.89	2.4E-01
B035DRAFT_01800	ribosomal protein S12, bacterial/organelle	3532.3	3597.1	3257.6	2709.5	2765.5	2474.5	0.77	4.6E-02
B035DRAFT_01801	Protein of unknown function (DUF3467).	908.3	1133.4	920.2	1038.9	1068.8	1259.6	1.14	4.4E-01
B035DRAFT_01802	Signal transduction histidine kinase	146.2	163.8	138.5	143.6	171.3	164.7	1.07	6.1E-01
B035DRAFT_01803	hypothetical protein	88.7	83.5	80.5	63.7	71.5	79.3	0.85	2.3E-01
B035DRAFT_01804	DNA-directed RNA polymerase, beta'' subunit, predominant form(EC:2.7.7.6)	1883.9	1831.5	1924.2	1904.8	1865.1	2027.7	1.03	6.0E-01
B035DRAFT_01805	DNA-directed RNA polymerase, beta subunit(EC:2.7.7.6)	1582.5	1555.4	1590.3	1495.0	1624.8	1790.8	1.04	7.2E-01
B035DRAFT_01806	ribosomal protein L7/L12	6291.7	6493.5	6622.9	5968.9	6110.9	6727.0	0.97	6.5E-01
B035DRAFT_01807	Ribosomal protein L10	6171.1	6700.9	6761.9	5428.7	5874.0	7756.0	0.96	8.5E-01
B035DRAFT_01808	ribosomal protein L1, bacterial/chloroplast	9610.0	9533.0	9417.5	8095.0	9100.9	10592.8	0.97	8.2E-01
B035DRAFT_01809	50S ribosomal protein L11	8588.1	8104.4	7880.0	6834.7	7775.0	8728.6	0.95	6.8E-01
B035DRAFT_01810	transcription termination/antitermination factor NusG	10745.5	10687.9	11614.4	9861.3	9936.1	10435.3	0.92	1.9E-01
B035DRAFT_01811	preprotein translocase, SecE subunit, bacterial	9276.1	9545.3	9471.3	8232.9	8206.0	9531.8	0.92	3.5E-01
B035DRAFT_01812	(tRNA)	90.0	121.4	116.3	94.8	96.7	83.8	0.85	3.8E-01
B035DRAFT_01813	translation elongation factor TU	11959.9	12924.8	12065.2	8681.9	10196.6	11471.6	0.82	2.3E-01
B035DRAFT_01814	(tRNA)	523.2	616.4	562.4	419.9	340.3	411.5	0.69	7.5E-02
B035DRAFT_01815	(tRNA)	491.7	505.7	639.2	494.5	347.2	291.3	0.68	2.6E-01
B035DRAFT_01816	(tRNA)	535.2	673.6	951.7	652.4	402.6	355.9	0.65	3.5E-01
B035DRAFT_01817	(tRNA)	1759.4	2103.9	3417.0	2090.0	1354.3	773.6	0.56	3.7E-01
B035DRAFT_01818	ribosomal subunit interface protein	1852.5	2255.6	1782.2	1266.7	1812.0	1947.7	0.84	5.3E-01
B035DRAFT_01819	Site-specific recombinase XerD	5436.2	5992.9	5773.5	4628.5	5059.8	5422.0	0.88	2.3E-01
B035DRAFT_01820	ribosomal protein S21	2406.3	3036.5	2882.0	2100.6	2200.4	2422.8	0.81	2.1E-01
B035DRAFT_01821	Xaa-Pro aminopeptidase(EC:3.4.11.9)	117.4	125.4	115.5	110.7	114.6	125.6	0.98	8.0E-01
B035DRAFT_01822	Carbonic anhydrases/acetyltransferases, isoleucine patch superfamily	127.0	150.9	124.9	120.9	115.1	121.1	0.89	3.2E-01
B035DRAFT_01823	outer membrane autotransporter barrel domain	280.2	358.0	295.0	242.9	285.4	369.5	0.95	8.6E-01
B035DRAFT_01824	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	94.2	81.9	69.1	59.0	82.1	49.2	0.76	4.0E-01
B035DRAFT_01825	His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.(EC:2.7.13.3)	54.8	59.3	47.7	47.0	58.7	57.2	1.01	9.8E-01
B035DRAFT_01826	hypothetical protein	6.3	7.7	7.2	6.0	8.6	7.3	1.02	9.3E-01
B035DRAFT_01827	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	25.1	19.1	23.7	17.1	20.7	12.1	0.72	3.3E-01

B035DRAFT_01828	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins (GH105)	25.1	16.6	27.6	21.3	19.0	8.9	0.68	5.0E-01
B035DRAFT_01829	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	33.7	22.5	31.1	21.1	24.0	11.4	0.63	3.4E-01
B035DRAFT_01830	SusD family	18.2	17.5	17.1	11.8	13.5	14.5	0.75	8.0E-02
B035DRAFT_01831	TonB-linked outer membrane protein, SusC/RagA family	27.8	26.8	29.4	16.0	17.4	19.6	0.63	3.0E-02
B035DRAFT_01832	Fe2+-dicitrate sensor, membrane component	34.8	42.4	36.3	29.3	31.0	37.2	0.86	3.8E-01
B035DRAFT_01833	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	65.3	71.9	63.2	67.4	70.7	87.4	1.12	4.8E-01
B035DRAFT_01834	3-deoxy-D-manno-octulosonic-acid transferase(EC:2.) (GT30)	318.8	348.8	337.2	336.0	368.0	390.7	1.09	3.7E-01
B035DRAFT_01835	glutamyl-tRNA synthetase, bacterial family(EC:6.1.1.17)	312.8	324.6	309.8	284.9	318.1	305.3	0.96	5.0E-01
B035DRAFT_01836	uncharacterized domain HDIG	60.2	66.0	66.5	84.2	91.9	109.0	1.47	7.2E-02
B035DRAFT_01837	Protein-tyrosine-phosphatase(EC:3.1.3.48)	76.1	67.9	71.1	88.2	91.4	95.7	1.28	4.3E-02
B035DRAFT_01838	Histidinol phosphatase and related hydrolases of the PHP family	52.3	47.2	50.3	53.8	59.4	57.9	1.14	1.5E-01
B035DRAFT_01839	primosomal protein N"(EC:3.6.4.)	48.0	49.2	47.3	51.6	55.0	48.6	1.07	3.3E-01
B035DRAFT_01840	hypothetical protein	384.6	426.1	391.7	409.4	364.9	395.7	0.97	7.5E-01
B035DRAFT_01841	hypothetical protein	17.6	19.8	18.6	13.6	8.0	19.2	0.69	4.2E-01
B035DRAFT_01842	Predicted transcriptional regulators	30.1	30.4	31.8	40.1	33.8	42.5	1.25	1.5E-01
B035DRAFT_01843	hypothetical protein	41.1	55.5	45.0	41.3	37.0	59.2	0.96	9.0E-01
B035DRAFT_01844	DNA modification methylase(EC:2.1.1.72)	96.9	115.8	103.9	104.2	104.3	126.7	1.06	7.2E-01
B035DRAFT_01845	DpnII restriction endonuclease.(EC:3.1.21.4)	167.5	199.3	174.6	181.6	195.2	240.1	1.13	4.8E-01
B035DRAFT_01846	DNA adenine methylase (dam)(EC:2.1.1.72)	164.7	184.5	171.4	190.8	199.7	281.0	1.27	3.2E-01
B035DRAFT_01847	Protein of unknown function (DUF2795).	274.7	308.7	243.5	326.8	310.4	250.3	1.07	7.3E-01
B035DRAFT_01848	ATP:cob(I)alamin adenosyltransferase	190.2	164.3	167.3	132.4	141.7	125.2	0.77	7.5E-02
B035DRAFT_01849	hypothetical protein	93.9	94.7	99.5	98.6	129.8	106.8	1.16	3.5E-01
B035DRAFT_01850	PS-10 peptidase S37.	13.5	16.1	16.7	16.7	18.6	24.7	1.28	3.3E-01
B035DRAFT_01851	Site-specific recombinase XerD	10.9	7.2	9.1	10.1	8.9	5.3	0.87	7.6E-01
B035DRAFT_01852	hypothetical protein	15.2	14.7	13.8	15.7	12.4	7.1	0.76	5.3E-01
B035DRAFT_01853	KilA-N domain.	27.7	26.9	21.5	33.2	26.0	10.5	0.83	7.8E-01
B035DRAFT_01854	hypothetical protein	16.3	11.6	9.9	9.5	13.4	6.3	0.76	5.5E-01
B035DRAFT_01855	hypothetical protein	9.5	8.5	8.9	2.3	5.8	2.0	0.33	1.5E-01
B035DRAFT_01856	hypothetical protein	15.8	6.2	14.7	22.9	10.2	2.7	0.76	8.4E-01
B035DRAFT_01857	hypothetical protein	4.3	7.2	5.3	3.3	4.5	4.5	0.74	3.7E-01
B035DRAFT_01858	TonB-linked outer membrane protein, SusC/RagA family	363.9	365.3	339.7	201.0	279.7	263.7	0.69	1.2E-01
B035DRAFT_01859	SusD family	472.6	432.8	378.2	196.7	353.5	324.6	0.66	2.8E-01
B035DRAFT_01860	hypothetical protein	502.2	491.1	384.0	234.5	360.8	430.3	0.73	3.9E-01
B035DRAFT_01861	Glycoside hydrolase (GH109)	429.1	423.8	360.5	161.4	266.8	262.9	0.56	1.4E-01
B035DRAFT_01862	hypothetical protein	60.3	59.0	61.0	43.4	34.9	24.1	0.55	1.3E-01
B035DRAFT_01863	hypothetical protein	22.7	19.5	24.4	16.5	16.2	6.4	0.54	3.2E-01
B035DRAFT_01864	Protein of unknown function (DUF3408).	12.4	5.8	14.7	8.8	5.8	2.4	0.49	4.1E-01
B035DRAFT_01865	hypothetical protein	8.2	6.9	13.3	4.3	4.9	2.5	0.41	1.6E-01
B035DRAFT_01866	Relaxase/Mobilisation nuclease domain.	13.2	5.5	14.3	8.5	8.6	5.8	0.74	6.2E-01
B035DRAFT_01867	hypothetical protein	29.7	15.7	31.0	24.3	18.5	12.3	0.72	5.4E-01
B035DRAFT_01868	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01869	AraC-type DNA-binding domain-containing proteins	19.7	17.6	22.2	17.8	20.9	20.3	0.99	9.8E-01
B035DRAFT_01870	3-carboxymuconate cyclase	14.9	12.1	16.3	11.1	11.0	10.5	0.76	1.6E-01
B035DRAFT_01871	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_01872	Predicted membrane protein involved in D-alanine export	25.9	28.9	22.6	15.7	25.3	25.8	0.85	6.0E-01
B035DRAFT_01873	Lysophospholipase L1 and related esterases (CE3)	65.9	73.8	70.9	58.2	74.7	63.4	0.93	6.1E-01
B035DRAFT_01874	hypothetical protein (CE3)	121.0	117.3	123.5	124.4	122.8	88.9	0.92	6.7E-01
B035DRAFT_01875	hypothetical protein	155.7	162.3	151.0	189.3	177.1	190.6	1.19	5.4E-02
B035DRAFT_01876	Cation/multidrug efflux pump	192.7	167.3	171.5	179.5	232.1	202.0	1.15	3.8E-01

B035DRAFT_01877	RND family efflux transporter, MFP subunit	148.5	128.4	126.3	131.3	192.3	152.6	1.17	4.8E-01
B035DRAFT_01878	Outer membrane protein	131.5	141.2	122.1	134.8	178.7	155.0	1.18	3.3E-01
B035DRAFT_01879	Transcriptional regulator	475.4	524.2	524.1	765.2	682.0	650.1	1.37	5.4E-02
B035DRAFT_01880	Acyl-[acyl carrier protein]--UDP-N-acetylglucosamine O-acyltransferase(EC:2.3.1.129)	203.0	201.7	191.1	258.6	312.0	335.0	1.51	6.0E-02
B035DRAFT_01881	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	209.0	183.3	174.4	228.2	289.5	264.1	1.38	1.2E-01
B035DRAFT_01882	The (Largely Gram-negative Bacterial) Hydrophobe/Amphiphile Efflux-1 (HAE1) Family	199.0	185.3	188.6	220.7	264.4	263.4	1.30	8.8E-02
B035DRAFT_01883	RND family efflux transporter, MFP subunit	92.0	95.6	88.1	94.2	95.5	86.6	1.00	9.8E-01
B035DRAFT_01884	Malic enzyme(EC:1.1.1.40)	130.2	163.5	132.2	109.9	123.3	139.9	0.88	4.7E-01
B035DRAFT_01885	Glutamate dehydrogenase/leucine dehydrogenase(EC:1.4.1.4)	485.1	660.7	560.0	477.7	481.3	457.3	0.84	3.1E-01
B035DRAFT_01886	hypothetical protein	184.2	188.2	177.5	194.1	205.3	234.9	1.15	2.4E-01
B035DRAFT_01887	hypothetical protein	198.1	184.5	194.4	190.4	232.7	246.0	1.15	3.5E-01
B035DRAFT_01888	hypothetical protein	699.4	771.7	796.5	668.3	585.5	742.8	0.88	3.8E-01
B035DRAFT_01889	hypothetical protein	641.2	632.7	653.7	502.6	426.4	483.6	0.73	4.1E-02
B035DRAFT_01890	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	123.4	124.9	122.3	103.0	108.6	117.0	0.89	1.4E-01
B035DRAFT_01891	hypothetical protein	2.9	0.0	0.0	0.0	1.3	2.6	0.64	
B035DRAFT_01892	Glutamate dehydrogenase/leucine dehydrogenase(EC:1.4.1.4)	486.2	449.5	519.3	609.7	574.2	523.2	1.17	2.0E-01
B035DRAFT_01893	hypothetical protein	95.6	139.8	119.9	108.2	132.6	159.0	1.13	6.8E-01
B035DRAFT_01894	Predicted phosphoadenosine phosphosulfate sulfotransferase	96.9	105.0	105.8	109.5	116.0	125.7	1.14	1.9E-01
B035DRAFT_01895	Predicted transcriptional regulators	70.7	81.4	73.3	76.9	77.8	71.7	1.00	9.6E-01
B035DRAFT_01896	hypothetical protein	49.8	59.3	57.6	48.4	49.0	58.5	0.93	6.5E-01
B035DRAFT_01897	malate dehydrogenase, NAD-dependent(EC:1.1.1.37)	1221.4	1559.4	1376.9	959.0	1144.9	1170.6	0.79	2.2E-01
B035DRAFT_01898	hypothetical protein	65.4	68.2	67.3	67.2	64.4	59.3	0.95	4.6E-01
B035DRAFT_01899	Outer membrane protein	34.3	34.0	33.3	38.7	37.6	27.7	1.01	9.6E-01
B035DRAFT_01900	Multidrug resistance efflux pump	45.9	41.0	39.2	53.9	48.6	26.8	0.98	9.7E-01
B035DRAFT_01901	hypothetical protein	22.5	22.5	24.6	29.0	27.9	32.4	1.28	7.4E-02
B035DRAFT_01902	ABC-type multidrug transport system, permease component	17.7	17.1	23.5	20.3	21.8	17.4	1.03	9.1E-01
B035DRAFT_01903	Uncharacterized lipoprotein NlpE involved in copper resistance	74.9	73.6	61.9	67.9	58.4	71.6	0.94	7.0E-01
B035DRAFT_01904	ABC-type multidrug transport system, ATPase and permease components	88.9	104.1	97.2	107.9	98.9	110.4	1.09	3.9E-01
B035DRAFT_01905	Predicted transcriptional regulator	25.8	30.6	32.6	34.0	28.0	44.0	1.18	5.4E-01
B035DRAFT_01906	TonB family C-terminal domain	44.9	41.8	46.4	43.1	45.8	52.2	1.06	6.3E-01
B035DRAFT_01907	anion transporter	113.2	117.0	114.5	89.7	109.4	122.2	0.92	6.4E-01
B035DRAFT_01908	ATPases involved in chromosome partitioning	185.5	182.5	187.8	168.0	192.6	170.3	0.95	5.5E-01
B035DRAFT_01909	Predicted S-adenosylmethionine-dependent methyltransferase(EC:2.1.1.33)	119.1	131.4	125.9	116.9	120.0	102.1	0.90	3.3E-01
B035DRAFT_01910	branched-chain amino acid aminotransferase, group II(EC:2.6.1.42)	369.0	402.0	379.5	369.8	357.4	381.5	0.96	5.2E-01
B035DRAFT_01911	Exonuclease VII small subunit(EC:3.1.11.6)	79.0	67.4	40.9	68.1	66.3	59.6	1.07	8.6E-01
B035DRAFT_01912	Exonuclease VII, large subunit(EC:3.1.11.6)	110.8	95.3	110.5	89.9	91.0	51.1	0.71	3.5E-01
B035DRAFT_01913	Subtilisin-like serine proteases	118.6	86.2	114.1	99.3	89.8	36.8	0.65	4.8E-01
B035DRAFT_01914	putative efflux protein, MATE family	42.5	45.5	41.2	44.8	44.8	46.9	1.06	3.6E-01
B035DRAFT_01915	hypothetical protein	80.7	81.2	89.2	108.5	118.7	114.4	1.36	2.7E-02
B035DRAFT_01916	polyphosphate kinase 1(EC:2.7.4.1)	40.0	39.7	41.5	36.0	43.9	37.4	0.96	7.6E-01
B035DRAFT_01917	Predicted phosphoesterase	35.0	31.1	30.9	40.5	31.1	24.3	0.97	9.2E-01
B035DRAFT_01918	dTDP-glucose 4,6-dehydratase(EC:4.2.1.46)	124.5	124.9	115.2	126.8	127.6	120.0	1.03	6.5E-01
B035DRAFT_01919	ATPase components of ABC transporters with duplicated ATPase domains	218.1	233.0	218.9	170.8	197.3	142.1	0.75	1.7E-01
B035DRAFT_01920	Predicted permease	432.7	436.4	450.0	343.4	361.1	327.5	0.78	2.3E-02
B035DRAFT_01921	methylmalonyl-CoA mutase, heterodimeric type, beta chain(EC:5.4.99.2)	234.3	237.2	240.1	293.5	305.8	312.4	1.28	6.7E-03
B035DRAFT_01922	methylmalonyl-CoA mutase C-terminal domain/methylmalonyl-CoA mutase N-terminal domain(EC:5.4.99.2)	379.3	338.3	349.1	388.1	426.0	394.6	1.13	1.8E-01
B035DRAFT_01923	hypothetical protein	24.2	33.9	30.8	35.7	35.9	42.4	1.29	2.6E-01

B035DRAFT_01924	Protein of unknown function (DUF2874).	52.6	70.9	56.2	72.2	57.6	63.4	1.08	7.1E-01
B035DRAFT_01925	DNA topoisomerase III, bacteria and conjugative plasmid(EC:5.99.1.2)	155.1	140.1	150.8	212.9	201.9	180.8	1.33	6.2E-02
B035DRAFT_01926	tRNA and rRNA cytosine-C5-methylases	90.4	86.7	83.3	95.7	91.6	59.8	0.93	8.0E-01
B035DRAFT_01927	Predicted phosphohydrolases	6.6	6.1	5.5	5.1	7.7	5.5	1.00	9.9E-01
B035DRAFT_01928	TonB-dependent receptor	7.5	6.2	5.5	4.4	5.3	4.4	0.74	1.9E-01
B035DRAFT_01929	hypothetical protein	52.3	50.8	48.6	63.5	57.6	50.2	1.12	3.8E-01
B035DRAFT_01930	RNA polymerase sigma factor, sigma-70 family	34.0	37.4	40.3	40.1	38.1	29.8	0.96	8.5E-01
B035DRAFT_01931	hypothetical protein	40.8	56.4	42.7	41.3	40.3	51.6	0.96	8.6E-01
B035DRAFT_01932	thymidylate synthase(EC:2.1.1.45)	107.5	99.3	99.0	106.7	88.2	88.1	0.92	5.1E-01
B035DRAFT_01933	Dihydrofolate reductase(EC:1.5.1.3)	119.4	133.3	132.1	103.1	95.6	112.0	0.81	1.1E-01
B035DRAFT_01934	Transcriptional regulators	538.3	648.0	637.8	476.1	382.0	457.7	0.72	1.2E-01
B035DRAFT_01935	IgA Peptidase M64.	49.1	57.2	51.7	39.0	43.9	45.8	0.81	1.5E-01
B035DRAFT_01936	Acetyltransferases	150.4	174.8	158.9	145.4	124.3	126.1	0.82	1.6E-01
B035DRAFT_01937	Biopolymer transport protein	4772.4	5554.8	5199.9	4463.6	5075.9	6690.3	1.03	9.0E-01
B035DRAFT_01938	Biopolymer transport protein	4212.8	4582.5	4395.2	3752.1	4191.4	5385.8	1.00	1.0E+00
B035DRAFT_01939	hypothetical protein	3320.7	3724.9	3700.4	2897.9	3401.2	4388.9	0.98	9.4E-01
B035DRAFT_01940	Biopolymer transport proteins	3726.5	3960.6	3704.8	2891.0	3487.5	3840.1	0.89	4.6E-01
B035DRAFT_01941	(tRNA)	99.8	111.6	102.8	169.7	146.2	146.5	1.47	3.8E-02
B035DRAFT_01942	hydrolase, TatD family(EC:3.1.21.)	166.1	156.3	159.3	174.4	193.1	149.6	1.07	6.4E-01
B035DRAFT_01943	Geranylgeranyl pyrophosphate synthase(EC:2.5.1.29,EC:2.5.1.1,EC:2.5.1.10)	226.8	205.6	225.9	209.1	251.8	181.2	0.97	8.7E-01
B035DRAFT_01944	TonB family C-terminal domain	1791.5	1909.7	1585.8	1891.3	1906.5	1757.4	1.05	6.4E-01
B035DRAFT_01945	cytidylate kinase(EC:2.7.4.14)	167.5	143.4	174.0	285.8	222.1	95.9	1.13	8.5E-01
B035DRAFT_01946	(E)-4-hydroxy-3-methyl-but-2-enyl pyrophosphate reductase (IPP and DMAPP forming)(EC:1.17.1.2)	117.0	107.3	107.7	153.6	156.3	114.7	1.27	2.5E-01
B035DRAFT_01947	6-phosphofructokinase(EC:2.7.1.11)	316.2	328.3	313.5	389.5	352.9	271.4	1.05	8.3E-01
B035DRAFT_01948	hypothetical protein	46.2	48.9	41.1	61.1	53.7	53.3	1.24	1.5E-01
B035DRAFT_01949	Alpha-N-acetylglucosaminidase (NAGLU).(EC:3.2.1.50) (GH89)	41.0	45.7	42.9	53.5	62.6	75.4	1.47	1.1E-01
B035DRAFT_01950	LAO/AO transport system ATPase(EC:2.7.)	496.2	446.7	535.4	652.8	542.4	258.4	0.92	8.8E-01
B035DRAFT_01951	Protein of unknown function (DUF1573).	363.1	316.2	337.9	459.0	421.9	357.0	1.21	2.5E-01
B035DRAFT_01952	hypothetical protein	158.4	171.9	159.4	203.1	167.1	153.2	1.06	7.1E-01
B035DRAFT_01953	Large extracellular alpha-helical protein	126.7	105.1	116.7	102.5	109.9	69.6	0.80	4.1E-01
B035DRAFT_01954	HipA-like C-terminal domain./HipA-like N-terminal domain.	58.3	60.2	63.7	61.5	68.2	57.2	1.02	8.3E-01
B035DRAFT_01955	HipA N-terminal domain	72.5	83.6	78.7	64.8	92.6	82.0	1.01	9.7E-01
B035DRAFT_01956	transcriptional regulator, y4mF family	71.9	69.1	49.5	70.0	61.7	46.9	0.94	8.5E-01
B035DRAFT_01957	Xaa-His dipeptidase(EC:3.4.13.)	854.3	849.3	807.3	943.9	1035.7	926.4	1.16	1.1E-01
B035DRAFT_01958	conserved hypothetical protein	45.7	40.8	38.2	45.5	45.6	43.2	1.08	4.5E-01
B035DRAFT_01959	dimethyladenosine transferase(EC:2.1.1.182)	154.5	161.8	161.8	187.9	191.7	175.8	1.16	6.5E-02
B035DRAFT_01960	Mg2+ transporter (mgtE)	130.9	126.7	123.7	146.4	146.3	129.5	1.11	2.5E-01
B035DRAFT_01961	Domain of Unknown Function (DUF349).	479.9	540.7	481.9	570.8	639.0	773.6	1.31	1.8E-01
B035DRAFT_01962	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	62.2	71.1	58.1	39.0	47.1	56.6	0.74	2.2E-01
B035DRAFT_01963	hypothetical protein	51.0	50.6	48.4	52.4	64.0	53.5	1.13	3.2E-01
B035DRAFT_01964	5,10-methylene-tetrahydrofolate dehydrogenase/Methenyl tetrahydrofolate cyclohydrolase(EC:1.5.1.5,EC:3.5.4.9)	247.3	239.3	262.0	332.9	335.9	229.8	1.18	4.7E-01
B035DRAFT_01965	signal recognition particle protein	612.0	608.4	598.5	603.1	631.1	478.7	0.94	6.7E-01
B035DRAFT_01966	putative efflux protein, MATE family	70.7	72.9	74.6	86.6	87.5	94.2	1.23	3.5E-02
B035DRAFT_01967	Long-chain fatty acid transport protein	770.9	904.6	786.1	516.9	650.9	680.5	0.75	1.7E-01
B035DRAFT_01968	Protein of unknown function (DUF1812).	188.4	202.0	246.8	205.7	231.4	229.4	1.05	7.7E-01
B035DRAFT_01969	hypothetical protein	339.8	387.1	440.8	449.2	483.4	554.7	1.28	2.2E-01
B035DRAFT_01970	3-phosphoglycerate kinase(EC:2.7.2.3)	1317.4	1437.7	1267.3	1262.7	1484.6	1757.6	1.11	5.7E-01

B035DRAFT_01971	hypothetical protein	852.4	1022.8	926.1	1040.9	1035.6	1111.8	1.14	2.5E-01
B035DRAFT_01972	hypothetical protein	177.5	174.7	178.8	163.5	151.0	175.6	0.92	3.3E-01
B035DRAFT_01973	hypothetical protein	117.1	132.0	116.8	100.6	111.9	119.9	0.91	4.2E-01
B035DRAFT_01974	Glycoside hydrolase (GH123)	404.0	397.0	387.4	447.4	525.0	647.4	1.35	1.8E-01
B035DRAFT_01975	hypothetical protein	45.9	54.4	49.6	65.4	77.1	100.0	1.60	1.2E-01
B035DRAFT_01976	Periplasmic component of the Tol biopolymer transport system	59.8	57.9	58.4	71.8	82.8	88.0	1.37	6.0E-02
B035DRAFT_01977	Beta-galactosidase(EC:3.2.1.23) (GH35)	17.8	15.6	17.1	11.9	15.3	14.9	0.83	2.8E-01
B035DRAFT_01978	Beta-galactosidase/beta-glucuronidase (GH2)	15.7	14.1	17.3	13.4	15.2	11.9	0.86	3.8E-01
B035DRAFT_01979	Beta-galactosidase/beta-glucuronidase (GH2)	15.6	13.2	15.0	13.8	14.8	14.9	1.00	9.7E-01
B035DRAFT_01980	transporter, SSS family	16.8	13.3	17.5	10.4	14.9	11.6	0.77	3.2E-01
B035DRAFT_01981	Gluconolactonase	17.1	19.5	17.8	19.2	17.2	13.7	0.91	6.4E-01
B035DRAFT_01982	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	18.3	7.9	16.6	11.7	13.5	7.6	0.79	6.8E-01
B035DRAFT_01983	L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily(EC:4.2.1.6)	21.1	17.5	15.8	14.7	18.3	11.3	0.81	4.7E-01
B035DRAFT_01984	Demethylmenaquinone methyltransferase	25.8	25.2	25.8	19.5	21.9	22.4	0.83	8.2E-02
B035DRAFT_01985	AraC-type DNA-binding domain-containing proteins	54.2	55.1	57.0	48.3	47.0	48.4	0.86	2.1E-02
B035DRAFT_01986	Glycoside hydrolase (GH95)	44.1	41.3	45.3	39.9	44.2	33.6	0.90	4.7E-01
B035DRAFT_01987	TonB-linked outer membrane protein, SusC/RagA family	5.4	4.9	5.1	3.3	4.4	5.0	0.81	3.7E-01
B035DRAFT_01988	SusD family	15.7	16.5	16.1	15.9	16.7	17.2	1.03	5.1E-01
B035DRAFT_01989	Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities(EC:4.4.1.8)	163.9	140.9	152.4	151.8	176.6	153.0	1.05	6.7E-01
B035DRAFT_01990	Transcriptional regulator containing an amidase domain and an AraC-type DNA-binding HTH domain(EC:3.2.)	84.8	69.2	87.2	80.8	86.4	79.4	1.03	8.6E-01
B035DRAFT_01991	Predicted transcriptional regulators	60.0	62.3	51.8	68.0	81.8	87.0	1.36	1.4E-01
B035DRAFT_01992	hypothetical protein	65.5	46.1	76.2	102.8	82.3	58.0	1.29	5.3E-01
B035DRAFT_01993	hypothetical protein	36.0	60.1	45.4	51.7	30.9	41.1	0.87	7.3E-01
B035DRAFT_01994	Prephenate dehydratase(EC:4.2.1.51)	150.3	146.7	130.7	136.5	140.8	126.9	0.95	5.6E-01
B035DRAFT_01995	Aspartate/tyrosine/aromatic aminotransferase	179.5	175.5	168.8	177.8	182.3	149.2	0.97	8.0E-01
B035DRAFT_01996	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase(EC:5.4.99.5)	256.7	239.2	215.4	246.1	242.3	220.5	1.00	9.9E-01
B035DRAFT_01997	Prephenate dehydrogenase(EC:5.4.99.5)	314.7	339.2	318.7	307.9	321.7	398.3	1.05	7.5E-01
B035DRAFT_01998	hypothetical protein	84.6	86.1	89.0	94.2	112.4	85.2	1.12	4.6E-01
B035DRAFT_01999	Protein of unknown function(DUF2089).	56.3	50.1	51.0	63.1	65.7	33.8	0.99	9.8E-01
B035DRAFT_02000	Lysophospholipase	55.1	46.5	59.0	80.9	78.6	37.4	1.16	7.6E-01
B035DRAFT_02001	Fucose 4-O-acetylase and related acetyltransferases	21.9	27.9	27.2	36.8	35.9	36.4	1.43	7.6E-02
B035DRAFT_02003	MAC/Perforin domain.	1267.3	1444.1	1252.0	1248.8	1283.4	1783.4	1.08	7.5E-01
B035DRAFT_02004	Outer membrane receptor for ferrienterochelin and colicins	336.7	425.4	389.1	406.4	436.5	570.8	1.22	3.8E-01
B035DRAFT_02005	hypothetical protein	814.2	887.7	828.2	922.7	924.5	1235.4	1.21	3.2E-01
B035DRAFT_02006	hypothetical protein	411.8	423.2	382.7	442.2	441.1	517.8	1.15	2.5E-01
B035DRAFT_02007	ABC-type Fe3+-hydroxamate transport system, periplasmic component	294.7	295.4	310.0	322.1	338.2	275.2	1.04	7.7E-01
B035DRAFT_02008	ABC-type cobalamin transport system, permease component	226.7	238.2	269.5	291.2	247.3	228.4	1.04	8.1E-01
B035DRAFT_02009	ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components(EC:3.6.3.34)	116.3	119.2	126.2	126.0	135.8	99.3	0.99	9.6E-01
B035DRAFT_02010	threonine synthase(EC:4.2.3.1)	324.7	363.0	319.9	220.8	270.3	227.5	0.71	7.5E-02
B035DRAFT_02011	proposed homoserine kinase(EC:5.4.2.1)	550.3	491.7	592.4	406.1	352.6	164.4	0.53	2.6E-01
B035DRAFT_02012	aspartate kinase(EC:2.7.2.4,EC:1.1.1.3)	511.1	506.4	468.5	326.3	385.9	295.1	0.67	7.0E-02
B035DRAFT_02013	hypothetical protein	58.1	55.2	54.5	68.0	72.6	79.6	1.31	5.4E-02
B035DRAFT_02014	Alpha-N-acetylglucosaminidase (NAGLU).(EC:3.2.1.50) (GH89)	39.8	38.8	36.5	43.4	47.2	35.2	1.09	6.1E-01
B035DRAFT_02015	DNA repair protein RadA	84.8	78.5	95.9	89.5	83.1	43.4	0.80	6.0E-01
B035DRAFT_02016	Uncharacterized metal-binding protein conserved in archaea	52.1	53.6	52.0	43.1	63.8	51.9	0.99	9.8E-01

B035DRAFT_02017	Uncharacterized FAD-dependent dehydrogenases	88.7	82.7	85.6	92.1	93.1	63.2	0.95	8.5E-01
B035DRAFT_02018	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	29.5	36.9	30.2	24.4	27.3	27.3	0.82	2.2E-01
B035DRAFT_02019	Outer membrane receptor proteins, mostly Fe transport	680.0	902.9	730.8	817.9	892.6	885.5	1.13	4.5E-01
B035DRAFT_02020	hypothetical protein	140.0	154.2	140.9	137.8	160.9	184.7	1.10	5.4E-01
B035DRAFT_02021	Collagenase and related proteases(EC:3.4.)	190.9	178.5	180.1	189.6	201.1	133.2	0.94	8.0E-01
B035DRAFT_02022	homoserine O-succinyltransferase(EC:2.3.1.46)	152.5	157.0	151.6	165.2	176.1	161.0	1.09	1.7E-01
B035DRAFT_02023	His Kinase A (phosphoacceptor) domain./PAS fold./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	34.4	35.3	36.4	44.3	58.2	59.2	1.51	8.2E-02
B035DRAFT_02024	DNA-binding protein, histone-like, putative	175.2	160.5	166.7	277.0	239.8	155.0	1.30	4.2E-01
B035DRAFT_02025	Nitroreductase	129.8	122.6	130.8	173.7	186.7	166.4	1.37	2.3E-02
B035DRAFT_02026	Outer membrane protein	108.0	87.3	100.3	144.5	168.3	123.9	1.47	1.2E-01
B035DRAFT_02027	heavy metal efflux pump (cobalt-zinc-cadmium)	82.7	75.5	87.2	122.3	141.2	127.2	1.59	2.5E-02
B035DRAFT_02028	RND family efflux transporter, MFP subunit	99.9	84.6	82.2	129.6	147.9	99.4	1.40	2.1E-01
B035DRAFT_02029	hypothetical protein	127.5	161.8	145.8	152.0	140.7	142.9	1.01	9.7E-01
B035DRAFT_02030	Predicted metalloendopeptidase(EC:3.4.24.)	177.7	164.7	173.4	134.9	156.6	119.0	0.79	1.8E-01
B035DRAFT_02031	ATPase components of ABC transporters with duplicated ATPase domains	138.3	132.9	131.5	103.0	115.5	114.9	0.83	7.0E-02
B035DRAFT_02032	adenylosuccinate synthase(EC:6.3.4.4)	538.2	556.7	542.6	512.4	530.3	524.3	0.96	1.6E-01
B035DRAFT_02033	Fe2+/Zn2+ uptake regulation proteins	255.7	325.4	304.3	294.3	278.1	289.2	0.98	8.8E-01
B035DRAFT_02034	Predicted DNA alkylation repair enzyme	145.4	155.0	156.1	145.9	140.1	149.2	0.95	3.8E-01
B035DRAFT_02035	Peptidase family M49.(EC:3.4.14.4)	170.7	155.3	150.3	135.3	145.7	140.4	0.89	1.8E-01
B035DRAFT_02036	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	1653.3	2241.1	1965.4	2276.2	2043.7	2724.8	1.20	4.1E-01
B035DRAFT_02037	ATP-dependent DNA helicase RecQ(EC:3.6.4.12)	44.6	55.2	46.1	55.0	52.8	65.6	1.19	3.3E-01
B035DRAFT_02038	Tetratricopeptide repeat.	88.0	99.1	93.5	121.6	135.1	142.5	1.42	4.3E-02
B035DRAFT_02039	3-isopropylmalate dehydrogenase(EC:1.1.1.85)	157.5	172.3	145.9	128.9	157.7	158.6	0.93	6.5E-01
B035DRAFT_02040	Isopropylmalate/homocitrate/citramalate synthases(EC:2.3.1.182)	98.2	105.1	89.4	84.6	96.7	100.5	0.96	7.7E-01
B035DRAFT_02041	3-isopropylmalate dehydratase, small subunit(EC:4.2.1.33,EC:4.2.1.35)	112.9	133.2	90.2	99.8	112.9	121.4	1.00	9.9E-01
B035DRAFT_02042	hypothetical protein	49.5	56.4	35.4	39.9	39.6	65.3	1.01	9.8E-01
B035DRAFT_02043	3-isopropylmalate dehydratase, large subunit(EC:4.2.1.33,EC:4.2.1.35)	103.9	106.5	100.9	80.2	102.3	97.7	0.90	4.3E-01
B035DRAFT_02044	2-isopropylmalate synthase, bacterial type(EC:2.3.3.13)	139.8	166.2	170.1	84.2	90.4	106.9	0.59	5.0E-02
B035DRAFT_02045	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.8E-01
B035DRAFT_02046	Transcriptional regulators	43.7	42.7	43.9	43.3	45.4	42.6	1.01	8.7E-01
B035DRAFT_02047	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	1.4	2.5	3.1	1.5	3.1	3.8	1.17	8.2E-01
B035DRAFT_02048	Glycoside hydrolase (GH32)	8.4	6.4	7.3	9.1	7.3	8.7	1.13	5.1E-01
B035DRAFT_02049	hypothetical protein	8.7	6.0	7.0	7.2	6.6	6.1	0.92	7.2E-01
B035DRAFT_02050	hypothetical protein	5.7	5.1	5.8	4.3	5.4	3.7	0.80	3.2E-01
B035DRAFT_02051	FOG: FHA domain	4.1	3.1	4.0	2.6	3.7	3.4	0.85	5.3E-01
B035DRAFT_02052	FOG: FHA domain	1.4	1.7	1.7	2.4	1.6	1.3	1.06	8.9E-01
B035DRAFT_02053	Serine/threonine protein phosphatase	0.9	1.1	0.6	0.8	0.6	0.4	0.69	4.1E-01
B035DRAFT_02054	Protein kinase domain.(EC:2.7.11.1)	2.1	2.4	1.7	3.7	1.6	3.0	1.26	6.4E-01
B035DRAFT_02055	Serine/threonine protein kinase	1.3	1.7	1.4	1.0	1.4	0.8	0.72	3.5E-01
B035DRAFT_02056	FOG: FHA domain	1.7	2.0	1.8	0.3	2.0	2.2	0.57	6.6E-01
B035DRAFT_02057	Uncharacterized conserved protein	43.7	54.1	51.0	56.3	48.1	59.2	1.10	5.5E-01
B035DRAFT_02058	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	226.9	212.1	196.1	176.6	171.2	199.9	0.86	2.4E-01
B035DRAFT_02059	Small-conductance mechanosensitive channel	94.9	92.9	97.6	82.5	80.2	86.0	0.87	5.2E-02
B035DRAFT_02060	The (Largely Gram-negative Bacterial) Hydrophobe/Amphiphile Efflux-1 (HAE1) Family	412.9	267.6	425.6	268.1	235.7	128.4	0.56	2.7E-01
B035DRAFT_02061	RND family efflux transporter, MFP subunit	197.7	135.1	176.8	112.1	116.8	79.9	0.61	1.6E-01
B035DRAFT_02062	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	177.9	111.4	166.9	86.1	94.7	63.1	0.54	1.5E-01
B035DRAFT_02063	hypothetical protein	140.3	131.3	144.2	122.5	135.4	149.3	0.98	8.5E-01

B035DRAFT_02064	hypothetical protein	25.1	23.9	30.0	45.4	59.2	74.0	2.23	6.1E-02
B035DRAFT_02065	Electron transfer flavoprotein, beta subunit	120.9	131.3	111.7	104.8	156.0	110.2	1.01	9.9E-01
B035DRAFT_02066	Electron transfer flavoprotein, alpha subunit	283.7	249.1	257.1	232.2	292.6	238.7	0.96	8.1E-01
B035DRAFT_02067	S23 ribosomal protein.	550.7	523.6	568.6	451.8	508.0	672.9	0.98	9.3E-01
B035DRAFT_02068	Acyl-CoA dehydrogenases	431.9	394.1	426.5	351.1	459.6	469.3	1.01	9.4E-01
B035DRAFT_02069	Histidine carboxylase PI chain.	823.8	643.6	638.6	791.6	791.8	648.9	1.06	7.6E-01
B035DRAFT_02070	uncharacterized domain 1	89.2	93.6	93.0	77.0	96.5	75.1	0.90	4.5E-01
B035DRAFT_02071	Domain of unknown function (DUF2027)./Smr domain.	62.4	66.9	59.8	58.1	75.4	64.1	1.04	8.0E-01
B035DRAFT_02072	hypothetical protein	11.5	11.0	8.4	7.9	10.2	9.1	0.88	5.8E-01
B035DRAFT_02073	Predicted bile acid beta-glucosidase (GH116)	14.1	14.4	12.6	9.0	12.0	8.1	0.70	1.7E-01
B035DRAFT_02074	SusD family	8.2	6.4	7.6	4.8	5.9	5.8	0.75	1.7E-01
B035DRAFT_02075	TonB-linked outer membrane protein, SusC/RagA family	9.3	9.4	9.0	6.1	7.3	8.2	0.78	1.8E-01
B035DRAFT_02076	Fe2+-dicitrate sensor, membrane component	16.5	19.0	14.8	17.0	21.0	21.2	1.18	3.8E-01
B035DRAFT_02077	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	69.4	61.8	81.0	73.0	71.4	75.2	1.04	7.9E-01
B035DRAFT_02078	S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (queuine synthetase)(EC:5.)	116.7	123.2	104.6	156.7	166.6	132.4	1.32	1.4E-01
B035DRAFT_02079	urocanate hydratase(EC:4.2.1.49)	15.8	11.1	16.6	21.9	22.4	18.7	1.47	1.9E-01
B035DRAFT_02080	glutamate formiminotransferase(EC:2.1.2.5)	14.2	8.7	14.8	10.4	12.9	11.6	0.95	8.8E-01
B035DRAFT_02081	imidazolonepropionase(EC:3.5.2.7)	26.2	21.9	27.7	24.1	21.5	13.3	0.76	4.3E-01
B035DRAFT_02082	Methenyl tetrahydrofolate cyclohydrolase	16.2	11.6	10.5	6.8	12.3	16.0	0.88	8.1E-01
B035DRAFT_02083	histidine ammonia-lyase(EC:4.3.1.3)	14.0	11.8	18.3	8.6	13.4	11.6	0.76	4.2E-01
B035DRAFT_02084	Isopentenyldiphosphate isomerase	58.3	50.2	50.1	55.4	66.6	61.0	1.15	3.1E-01
B035DRAFT_02085	TonB-linked outer membrane protein, SusC/RagA family	26.4	23.9	24.5	13.3	15.6	16.1	0.60	2.6E-02
B035DRAFT_02086	SusD family	28.4	27.1	27.0	13.3	12.4	15.6	0.50	1.4E-02
B035DRAFT_02087	Glycoside hydrolase (GH109)	266.7	288.1	240.8	268.4	334.3	326.5	1.17	3.5E-01
B035DRAFT_02088	Carbonic anhydrase(EC:4.2.1.1)	118.8	103.0	100.7	128.3	126.9	112.4	1.14	3.0E-01
B035DRAFT_02089	hypothetical protein	49.3	41.7	47.5	45.1	40.0	49.4	0.97	8.5E-01
B035DRAFT_02090	Predicted transcriptional regulator	42.6	50.8	45.7	44.8	48.0	54.2	1.06	6.9E-01
B035DRAFT_02091	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	80.7	95.2	83.9	80.7	82.8	64.2	0.87	4.3E-01
B035DRAFT_02092	Na+-driven multidrug efflux pump	6.9	6.5	8.5	6.3	8.7	4.8	0.88	7.3E-01
B035DRAFT_02093	(tRNA)	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02094	hypothetical protein	243.6	287.9	271.1	263.3	300.3	314.8	1.09	4.9E-01
B035DRAFT_02095	chaperonin GroL	1776.6	1568.6	1635.3	1518.8	1527.0	1453.7	0.90	2.1E-01
B035DRAFT_02096	Co-chaperonin GroES (HSP10)	1467.7	1347.2	1117.4	1349.0	1162.8	1118.5	0.93	6.7E-01
B035DRAFT_02097	[FeFe] hydrogenase, group B1/B3	114.7	116.4	114.9	88.4	103.2	95.6	0.83	8.7E-02
B035DRAFT_02098	[FeFe] hydrogenase H-cluster radical SAM maturase HydE(EC:2.8.1.6)	108.8	113.7	127.2	91.6	92.6	89.8	0.79	6.1E-02
B035DRAFT_02099	[FeFe] hydrogenase H-cluster radical SAM maturase HydG	35.6	37.5	35.1	32.5	41.2	29.8	0.95	7.7E-01
B035DRAFT_02100	[FeFe] hydrogenase H-cluster maturation GTPase HydF	38.8	42.3	40.1	37.1	42.1	33.0	0.92	5.5E-01
B035DRAFT_02101	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases (CE10)	58.8	58.9	56.6	48.3	63.0	67.8	1.02	9.3E-01
B035DRAFT_02102	histidyl-tRNA synthetase(EC:6.1.1.21)	200.2	201.8	187.3	180.4	222.8	182.8	0.99	9.5E-01
B035DRAFT_02103	Site-specific recombinase XerD	15.6	13.2	15.0	13.0	12.3	9.6	0.79	2.6E-01
B035DRAFT_02104	hypothetical protein	33.4	31.9	32.3	27.5	25.3	38.3	0.92	7.1E-01
B035DRAFT_02105	hypothetical protein	86.5	96.2	84.6	77.6	73.4	102.9	0.94	7.7E-01
B035DRAFT_02106	hypothetical protein	8.8	8.2	7.0	12.2	10.2	7.7	1.24	4.4E-01
B035DRAFT_02107	hypothetical protein	6.1	7.1	5.5	7.7	6.9	5.1	1.04	8.8E-01
B035DRAFT_02108	Plasmid recombination enzyme.	4.9	5.3	4.9	6.7	6.6	2.6	0.96	9.6E-01
B035DRAFT_02109	hypothetical protein	84.8	99.4	83.0	106.4	93.8	117.1	1.19	3.0E-01
B035DRAFT_02110	hypothetical protein	56.8	69.9	55.7	62.5	66.8	80.5	1.15	4.6E-01
B035DRAFT_02111	Superfamily I DNA and RNA helicases(EC:3.6.4.12)	23.5	30.1	27.9	26.0	26.7	27.2	0.98	9.2E-01
B035DRAFT_02112	Predicted Zn-dependent protease	400.9	424.2	394.2	678.4	627.6	584.8	1.55	1.8E-02

B035DRAFT_02113	AraC-type DNA-binding domain-containing proteins	35.1	36.7	33.3	62.4	53.9	64.3	1.72	1.9E-02
B035DRAFT_02114	Uncharacterized protein conserved in bacteria	68.0	68.2	71.8	76.7	73.5	73.3	1.07	1.5E-01
B035DRAFT_02115	Outer membrane protein/protective antigen OMA87	71.5	65.0	78.4	84.4	89.4	84.3	1.20	1.5E-01
B035DRAFT_02116	hypothetical protein	774.0	770.8	687.4	603.7	762.8	933.9	1.02	9.5E-01
B035DRAFT_02117	hypothetical protein	10.5	13.1	12.8	11.1	18.4	25.2	1.43	4.3E-01
B035DRAFT_02118	Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family(EC:5.2.1.8)	207.6	222.5	176.2	233.7	243.3	227.2	1.17	2.7E-01
B035DRAFT_02119	Predicted Zn-dependent peptidases	126.8	135.9	117.5	125.5	138.7	143.0	1.07	5.1E-01
B035DRAFT_02120	putative efflux protein, MATE family	175.4	162.8	157.1	116.4	119.3	119.5	0.72	1.5E-02
B035DRAFT_02121	Signal transduction histidine kinase	100.7	93.2	89.1	77.1	71.7	75.8	0.79	5.3E-02
B035DRAFT_02122	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	72.7	77.3	74.2	62.4	59.3	67.8	0.84	9.7E-02
B035DRAFT_02123	Protein of unknown function (DUF2874).	2686.8	3112.3	2396.8	457.9	405.8	490.2	0.17	1.6E-03
B035DRAFT_02124	Pseudouridylate synthases, 23S RNA-specific(EC:5.4.99.23)	931.6	1003.7	806.6	686.2	1003.5	1094.8	1.00	1.0E+00
B035DRAFT_02125	3-oxoacyl-(acyl-carrier-protein) reductase(EC:1.1.1.100)	986.0	1046.0	861.6	772.0	1066.4	1212.8	1.04	8.9E-01
B035DRAFT_02126	Transcriptional regulator	90.4	93.9	85.0	94.2	100.0	85.5	1.04	7.1E-01
B035DRAFT_02127	(tRNA)	120.0	93.0	62.2	91.3	50.4	48.5	0.68	4.6E-01
B035DRAFT_02128	SusD family	39.5	41.8	39.8	17.8	19.0	21.6	0.48	7.1E-03
B035DRAFT_02129	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02130	**TonB-linked outer membrane protein, SusC/RagA family**	**170.4**	**166.9**	**156.4**	**426.7**	**614.4**	**711.6**	**3.47**	**2.3E-02**
B035DRAFT_02131	SusD family	228.4	213.6	202.2	577.9	825.5	974.4	3.61	2.2E-02
B035DRAFT_02132	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	140.6	142.9	145.7	115.2	121.0	107.4	0.80	4.1E-02
B035DRAFT_02133	hypothetical protein	148.0	128.4	155.0	93.5	99.1	58.4	0.57	1.5E-01
B035DRAFT_02134	Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases(EC:6.2.1.1)	308.5	280.9	317.7	245.5	249.6	183.8	0.74	1.8E-01
B035DRAFT_02135	Cupin domain.	215.5	208.7	219.3	201.9	186.2	147.7	0.83	2.9E-01
B035DRAFT_02136	hypothetical protein	2.2	1.7	4.4	2.3	2.7	0.0	0.97	9.6E-01
B035DRAFT_02137	His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	31.0	34.3	31.1	57.9	54.5	58.8	1.78	4.5E-03
B035DRAFT_02138	pyrroline-5-carboxylate reductase(EC:1.5.1.2)	80.4	84.4	87.6	150.1	147.2	104.7	1.57	1.1E-01
B035DRAFT_02139	Lysophospholipase L1 and related esterases (CE3)	49.6	62.9	51.4	74.1	72.1	96.7	1.48	1.4E-01
B035DRAFT_02140	Uncharacterized proteins of the AP superfamily	6.0	7.8	7.5	7.7	8.5	7.1	1.10	6.0E-01
B035DRAFT_02141	Phosphate-selective porin	23.4	20.6	17.9	22.4	20.2	20.3	1.02	9.1E-01
B035DRAFT_02142	Ornithine/acetylornithine aminotransferase(EC:2.6.1.11)	292.7	265.8	254.2	288.5	318.6	253.0	1.06	7.1E-01
B035DRAFT_02143	N-acetyl-gamma-glutamyl-phosphate reductase, common form(EC:1.2.1.- ,EC:1.2.1.38)	175.5	171.8	146.8	164.4	210.8	207.5	1.18	3.8E-01
B035DRAFT_02144	Argininosuccinate synthase(EC:6.3.4.5)	177.3	145.5	134.5	160.0	197.3	164.7	1.14	4.8E-01
B035DRAFT_02145	hypothetical protein	166.5	136.9	136.7	136.4	147.4	104.3	0.88	5.5E-01
B035DRAFT_02146	arginine repressor	48.2	53.1	54.7	50.3	49.1	37.7	0.87	4.6E-01
B035DRAFT_02147	His Kinase A (phosphoacceptor) domain.	32.9	39.0	38.2	33.7	34.4	36.7	0.95	6.6E-01
B035DRAFT_02148	His Kinase A (phosphoacceptor) domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	35.6	34.9	32.8	36.4	43.7	42.1	1.18	1.9E-01
B035DRAFT_02149	Sugar (pentulose and hexulose) kinases(EC:2.7.1.5)	42.4	39.0	37.7	40.6	50.8	47.8	1.16	3.0E-01
B035DRAFT_02150	Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases(EC:4.1.2.19)	200.8	201.7	188.0	205.7	211.0	241.7	1.11	3.1E-01
B035DRAFT_02151	hypothetical protein	104.8	106.4	90.2	103.7	111.7	132.5	1.15	3.9E-01
B035DRAFT_02152	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains) (GH23)	48.0	49.6	56.6	65.6	58.6	57.5	1.18	2.1E-01
B035DRAFT_02153	Kef-type K+ transport systems, predicted NAD-binding component	45.8	45.2	51.7	43.3	41.4	40.4	0.88	1.8E-01
B035DRAFT_02154	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	258.9	233.0	234.0	236.2	295.1	260.9	1.09	5.2E-01
B035DRAFT_02155	hypothetical protein	43.3	63.5	66.4	48.8	61.6	63.7	1.02	9.6E-01
B035DRAFT_02156	Glycoside hydrolase (GH109)	153.6	153.2	166.1	177.7	159.8	71.2	0.80	6.8E-01

B035DRAFT_02157	Predicted glycosylase (GH130)	180.1	184.4	176.6	180.2	181.4	107.2	0.84	5.9E-01
B035DRAFT_02158	hypothetical protein	49.4	49.4	61.9	56.7	50.1	32.8	0.85	6.3E-01
B035DRAFT_02159	Metal-dependent hydrolase	76.1	79.1	81.4	73.4	70.0	60.2	0.86	2.2E-01
B035DRAFT_02160	hypothetical protein	72.4	81.6	81.9	43.4	48.8	59.9	0.64	8.2E-02
B035DRAFT_02161	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	28.0	27.1	27.8	10.9	17.1	14.9	0.51	6.3E-02
B035DRAFT_02162	Ion channel.	30.9	33.4	31.7	25.1	30.6	36.5	0.95	8.1E-01
B035DRAFT_02163	hypothetical protein	409.4	520.3	567.2	558.8	491.4	479.0	1.03	9.0E-01
B035DRAFT_02164	hypothetical protein	57.6	57.1	48.8	43.8	51.0	46.9	0.87	2.9E-01
B035DRAFT_02165	Small-conductance mechanosensitive channel	32.1	35.5	34.5	27.3	32.6	37.0	0.94	7.3E-01
B035DRAFT_02166	hypothetical protein	45.7	47.9	45.0	42.7	45.5	55.6	1.03	8.5E-01
B035DRAFT_02167	alpha-1,2-mannosidase, putative (GH92)	69.9	65.0	65.8	58.1	68.3	51.5	0.88	4.1E-01
B035DRAFT_02168	alpha-1,2-mannosidase, putative (GH92)	73.8	63.5	82.2	69.6	69.2	55.9	0.89	5.2E-01
B035DRAFT_02169	alpha-1,2-mannosidase, putative (GH92)	53.7	50.8	53.9	65.4	70.0	63.9	1.26	3.3E-02
B035DRAFT_02170	hypothetical protein	37.9	56.3	45.5	48.7	51.3	55.4	1.13	5.9E-01
B035DRAFT_02171	Predicted membrane protein	213.0	205.5	216.1	151.8	164.7	194.8	0.80	1.7E-01
B035DRAFT_02172	Membrane protein of unknown function (DUF340).	135.6	128.8	123.8	117.9	112.0	137.6	0.94	6.4E-01
B035DRAFT_02173	AraC-type DNA-binding domain-containing proteins	37.9	42.8	36.7	39.3	58.4	59.6	1.32	3.1E-01
B035DRAFT_02174	Periplasmic component of the Tol biopolymer transport system	21.5	19.8	26.4	20.5	19.2	17.8	0.86	3.8E-01
B035DRAFT_02175	hypothetical protein	3.1	2.0	2.9	2.3	2.5	2.2	0.90	6.7E-01
B035DRAFT_02176	hypothetical protein	3.7	0.0	1.5	1.3	4.4	2.2	1.00	1.0E+00
B035DRAFT_02177	TonB-linked outer membrane protein, SusC/RagA family	6.7	5.3	5.4	4.2	4.7	3.9	0.74	1.4E-01
B035DRAFT_02178	SusD family	7.3	5.2	5.7	5.3	5.8	5.0	0.89	5.6E-01
B035DRAFT_02179	Arylsulfotransferase (ASST).(EC:2.8.2.22)	7.6	9.5	7.3	7.2	6.5	6.5	0.83	2.8E-01
B035DRAFT_02180	hypothetical protein	12.9	15.1	16.5	11.0	17.7	11.0	0.88	6.7E-01
B035DRAFT_02181	Alpha-glucosidases (GH31)	35.5	35.9	33.9	29.9	33.5	36.5	0.95	6.1E-01
B035DRAFT_02182	hypothetical protein	14.5	25.8	14.5	18.0	20.9	14.7	1.01	9.9E-01
B035DRAFT_02183	hypothetical protein	5.3	8.2	3.2	9.3	5.6	1.6	0.84	8.8E-01
B035DRAFT_02184	hypothetical protein	3.6	6.6	3.1	2.7	6.1	6.1	1.10	8.9E-01
B035DRAFT_02185	Transposase DDE domain.	11.9	13.2	8.8	10.9	9.4	14.6	1.02	9.5E-01
B035DRAFT_02186	hypothetical protein	7.8	5.6	8.3	8.2	11.4	11.5	1.44	2.6E-01
B035DRAFT_02187	Glycoside hydrolase (GH42)	31.1	38.5	34.5	25.5	30.0	31.4	0.83	2.9E-01
B035DRAFT_02188	hypothetical protein	6.5	7.4	7.1	4.0	3.7	5.9	0.64	1.6E-01
B035DRAFT_02189	hypothetical protein	4.5	5.0	6.1	4.3	4.2	6.6	0.96	9.2E-01
B035DRAFT_02190	hypothetical protein	6.3	7.3	4.6	2.6	6.8	4.5	0.73	5.8E-01
B035DRAFT_02191	hypothetical protein	19.7	10.1	27.3	12.5	10.8	12.1	0.67	4.6E-01
B035DRAFT_02192	hypothetical protein	79.2	55.8	60.9	51.2	47.9	58.1	0.81	3.5E-01
B035DRAFT_02193	hypothetical protein	52.6	59.0	66.3	41.8	29.3	46.1	0.65	1.8E-01
B035DRAFT_02194	AraC-type DNA-binding domain-containing proteins	688.2	878.7	742.4	626.9	600.2	679.2	0.83	2.4E-01
B035DRAFT_02195	hypothetical protein	11695.4	12409.2	11563.8	8235.5	9844.0	12904.4	0.85	5.1E-01
B035DRAFT_02196	hypothetical protein	19.0	15.0	25.6	22.1	22.8	25.3	1.20	5.2E-01
B035DRAFT_02197	hypothetical protein	11.5	16.0	7.7	13.9	10.4	14.6	1.14	7.6E-01
B035DRAFT_02198	hypothetical protein	9.3	5.8	5.2	5.3	8.4	9.7	1.15	7.7E-01
B035DRAFT_02199	hypothetical protein	12.3	8.5	13.0	10.6	10.6	5.5	0.77	5.8E-01
B035DRAFT_02200	TonB-linked outer membrane protein, SusC/RagA family	134.2	148.5	136.1	104.9	142.9	133.9	0.90	5.8E-01
B035DRAFT_02201	SusD family	364.5	358.9	326.8	272.3	450.6	445.8	1.09	8.0E-01
B035DRAFT_02202	Alpha-L-fucosidase (GH29)	117.2	119.9	101.9	70.9	115.9	96.5	0.82	4.7E-01
B035DRAFT_02203	Alpha-L-fucosidase (CBM32)	102.9	90.1	85.9	63.1	107.6	91.4	0.92	7.9E-01
B035DRAFT_02204	(tRNA)	44.5	78.8	55.4	50.3	40.3	41.4	0.76	4.0E-01
B035DRAFT_02205	(tRNA)	85.6	59.2	115.4	104.7	48.2	35.8	0.68	5.6E-01
B035DRAFT_02206	hypothetical protein	369.6	390.5	395.9	406.8	374.3	454.9	1.07	5.6E-01

B035DRAFT_02207	Predicted P-loop ATPase and inactivated derivatives	39.1	22.6	26.6	32.8	27.3	11.4	0.76	6.8E-01
B035DRAFT_02208	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02209	hypothetical protein	25.9	33.0	34.6	23.0	25.3	17.5	0.70	2.2E-01
B035DRAFT_02210	hypothetical protein	39.1	30.3	35.1	17.3	26.1	16.2	0.56	1.3E-01
B035DRAFT_02211	hypothetical protein	36.6	26.7	24.0	19.8	25.1	16.6	0.71	3.0E-01
B035DRAFT_02212	N-acetylmuramoyl-L-alanine amidase(EC:3.5.1.28)	41.3	33.4	27.1	24.4	22.0	22.3	0.68	1.6E-01
B035DRAFT_02213	hypothetical protein	32.0	26.8	29.6	24.0	20.6	25.2	0.79	1.6E-01
B035DRAFT_02214	hypothetical protein	26.7	28.4	28.3	19.4	19.4	22.5	0.73	4.8E-02
B035DRAFT_02215	hypothetical protein	37.2	29.5	30.9	32.9	29.0	25.7	0.90	5.6E-01
B035DRAFT_02216	hypothetical protein	51.2	54.4	50.3	48.9	46.4	45.1	0.90	1.5E-01
B035DRAFT_02217	hypothetical protein	20.2	17.4	19.1	13.6	15.2	21.1	0.87	5.7E-01
B035DRAFT_02218	hypothetical protein	15.1	12.2	13.4	12.5	8.3	15.4	0.87	6.8E-01
B035DRAFT_02219	hypothetical protein	11.5	12.4	13.0	8.3	11.5	15.9	0.93	8.6E-01
B035DRAFT_02220	hypothetical protein	13.5	9.9	5.2	3.8	7.1	13.0	0.79	7.8E-01
B035DRAFT_02221	hypothetical protein	6.6	6.7	6.0	4.4	6.0	7.5	0.90	7.3E-01
B035DRAFT_02222	hypothetical protein	7.3	3.6	3.8	4.4	7.6	7.6	1.36	5.6E-01
B035DRAFT_02223	hypothetical protein	8.5	7.4	8.0	7.7	7.3	5.8	0.86	4.1E-01
B035DRAFT_02224	hypothetical protein	13.0	7.9	5.9	7.2	8.0	7.4	0.88	7.8E-01
B035DRAFT_02225	hypothetical protein	2.7	6.2	4.0	4.2	7.2	7.8	1.53	4.5E-01
B035DRAFT_02226	hypothetical protein	9.9	7.4	7.8	9.8	8.4	11.6	1.19	4.6E-01
B035DRAFT_02227	hypothetical protein	5.8	9.6	7.1	4.4	5.3	11.3	0.87	8.2E-01
B035DRAFT_02228	hypothetical protein	5.9	7.7	5.1	5.9	4.1	5.1	0.81	4.6E-01
B035DRAFT_02229	hypothetical protein	5.2	5.4	2.8	1.2	3.7	2.1	0.49	3.3E-01
B035DRAFT_02230	hypothetical protein	6.6	7.7	4.7	1.7	2.5	3.5	0.40	1.1E-01
B035DRAFT_02231	hypothetical protein	5.8	4.3	0.6	3.4	3.9	2.4	1.24	8.8E-01
B035DRAFT_02232	hypothetical protein	3.9	4.6	3.1	2.3	5.2	2.6	0.82	7.1E-01
B035DRAFT_02233	hypothetical protein	3.1	0.7	5.3	2.0	6.2	2.8	1.42	7.8E-01
B035DRAFT_02234	3''-phosphoadenosine 5''-phosphosulfate sulfotransferase (PAPS reductase)/FAD synthetase and related enzymes	4.5	5.2	2.8	3.1	2.6	3.0	0.72	3.5E-01
B035DRAFT_02235	hypothetical protein	3.5	3.1	6.1	3.2	2.4	5.3	0.86	7.9E-01
B035DRAFT_02236	DNA-methyltransferase (dcm)(EC:2.1.1.37)	7.0	4.3	5.8	5.0	4.7	4.0	0.81	4.6E-01
B035DRAFT_02237	hypothetical protein	4.7	2.2	0.0	0.0	3.4	5.1	1.30	7.6E-01
B035DRAFT_02238	hypothetical protein	5.1	6.1	3.4	4.7	4.8	5.3	1.05	8.9E-01
B035DRAFT_02239	hypothetical protein	3.4	5.0	6.4	3.9	4.8	5.0	0.95	8.9E-01
B035DRAFT_02240	VRR-NUC domain.	6.9	5.7	7.0	4.7	9.6	4.1	0.88	8.0E-01
B035DRAFT_02241	hypothetical protein	4.4	2.2	3.7	6.1	5.7	4.0	1.57	3.3E-01
B035DRAFT_02242	Bacterial nucleoid DNA-binding protein	3.7	1.4	6.7	3.9	5.0	5.6	1.45	6.6E-01
B035DRAFT_02243	hypothetical protein	3.8	1.1	1.1	1.0	1.7	2.6	0.97	9.8E-01
B035DRAFT_02244	Metal-dependent hydrolases of the beta-lactamase superfamily I	2.9	4.5	5.5	4.7	4.9	4.3	1.12	7.5E-01
B035DRAFT_02245	hypothetical protein	11.2	8.4	9.0	11.6	13.9	10.3	1.25	3.3E-01
B035DRAFT_02246	hypothetical protein	4.9	3.4	3.3	5.4	6.4	5.2	1.49	1.8E-01
B035DRAFT_02247	(tRNA)	0.0	0.0	0.0	0.0	1.7	0.0	0.00	
B035DRAFT_02248	hypothetical protein	1.3	1.5	0.8	1.3	1.7	0.0	1.34	5.1E-01
B035DRAFT_02249	hypothetical protein	0.0	0.0	0.0	1.7	2.9	3.6	0.00	
B035DRAFT_02250	hypothetical protein	1.7	0.0	1.0	2.7	0.8	3.1	1.40	7.3E-01
B035DRAFT_02251	hypothetical protein	0.9	1.0	1.1	0.0	0.0	2.4	2.43	
B035DRAFT_02252	hypothetical protein	146.4	168.1	156.2	148.0	162.1	173.2	1.03	8.3E-01
B035DRAFT_02253	hypothetical protein	128.5	146.1	118.6	119.6	121.5	168.4	1.03	9.0E-01
B035DRAFT_02254	hypothetical protein	140.2	160.4	166.5	141.7	148.5	190.9	1.02	9.1E-01
B035DRAFT_02255	Multimeric flavodoxin WrbA	46.8	48.3	35.2	46.0	53.8	47.5	1.14	5.1E-01
B035DRAFT_02256	hypothetical protein	17.4	21.5	12.7	16.2	21.7	20.7	1.15	6.6E-01

B035DRAFT_02257	ABC-type antimicrobial peptide transport system, permease component	17.3	16.6	17.6	13.4	11.0	12.1	0.71	4.5E-02
B035DRAFT_02258	ABC-type antimicrobial peptide transport system, ATPase component	25.3	26.2	18.6	15.5	17.0	19.6	0.75	2.5E-01
B035DRAFT_02259	ABC-type antimicrobial peptide transport system, permease component	20.2	19.6	20.2	18.5	24.8	25.7	1.14	5.0E-01
B035DRAFT_02260	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	26.3	27.9	27.7	29.0	33.6	30.1	1.13	2.1E-01
B035DRAFT_02261	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	27.5	29.3	33.6	32.8	34.7	35.1	1.14	2.9E-01
B035DRAFT_02262	Dipeptide/tripeptide permease	402.7	480.5	458.4	362.7	448.5	632.1	1.05	8.8E-01
B035DRAFT_02263	ybaK/ebsC protein	219.7	223.8	235.6	293.8	265.9	263.8	1.21	7.0E-02
B035DRAFT_02264	excinuclease ABC, A subunit	131.7	133.0	134.3	148.9	153.6	133.9	1.09	2.8E-01
B035DRAFT_02265	Predicted glycosyl hydrolase (CBM50)	177.6	189.2	170.5	208.2	210.5	229.9	1.21	8.2E-02
B035DRAFT_02266	hypothetical protein	198.5	206.4	202.0	227.5	243.7	250.4	1.19	5.0E-02
B035DRAFT_02267	hypothetical protein	110.5	112.4	106.5	169.1	202.2	195.3	1.72	1.6E-02
B035DRAFT_02268	hypothetical protein	184.6	251.8	238.2	213.2	216.0	255.5	1.02	9.3E-01
B035DRAFT_02269	RNA polymerase Rpb6.	1084.4	1296.8	1078.5	1308.8	1131.1	1271.1	1.07	6.0E-01
B035DRAFT_02270	hypothetical protein	492.4	577.4	517.7	498.0	449.3	502.6	0.91	4.1E-01
B035DRAFT_02271	excinuclease ABC, B subunit	198.8	182.9	193.5	243.1	227.7	245.1	1.24	3.7E-02
B035DRAFT_02272	Phosphate-selective porin O and P.	66.6	72.0	67.3	70.5	74.1	84.9	1.11	3.5E-01
B035DRAFT_02273	Uncharacterized conserved protein	70.0	85.2	81.1	91.3	90.5	96.5	1.18	2.0E-01
B035DRAFT_02274	DNA polymerase III, epsilon subunit and related 3''-5'' exonucleases(EC:2.7.7.7)	72.2	79.1	83.2	114.2	115.2	114.3	1.47	1.7E-02
B035DRAFT_02275	hypothetical protein	93.2	102.7	86.2	163.5	149.6	108.5	1.48	1.7E-01
B035DRAFT_02276	RNA polymerase sigma factor, sigma-70 family	67.8	54.5	39.4	41.2	38.5	54.5	0.84	6.2E-01
B035DRAFT_02277	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	109.5	110.7	108.3	112.2	131.4	119.5	1.10	2.8E-01
B035DRAFT_02278	Predicted permease, DMT superfamily	73.3	97.1	84.7	69.2	68.8	87.0	0.88	5.3E-01
B035DRAFT_02279	hypothetical protein	64.1	81.8	68.5	57.6	48.2	68.2	0.81	3.6E-01
B035DRAFT_02280	Uncharacterized conserved protein	264.3	289.0	276.9	213.4	239.0	278.0	0.88	3.7E-01
B035DRAFT_02281	Lactate dehydrogenase and related dehydrogenases(EC:1.1.1.95)	234.0	269.5	268.9	207.4	225.8	262.0	0.90	4.7E-01
B035DRAFT_02282	phosphoserine aminotransferase(EC:2.6.1.52)	415.8	489.2	471.0	403.3	466.7	505.7	1.00	9.9E-01
B035DRAFT_02283	Superfamily II DNA and RNA helicases	98.5	90.3	96.5	99.7	113.7	117.2	1.16	2.0E-01
B035DRAFT_02284	hypothetical protein	37.9	41.1	42.5	53.5	59.9	62.0	1.44	3.6E-02
B035DRAFT_02285	hypothetical protein	135.9	126.4	150.0	172.7	151.4	196.8	1.26	2.1E-01
B035DRAFT_02286	NADH:ubiquinone oxidoreductase, Na(+)-translocating, F subunit(EC:1.6.5.)	1867.2	1876.6	1887.9	1901.6	2040.5	2027.8	1.06	2.1E-01
B035DRAFT_02287	NADH:ubiquinone oxidoreductase, Na(+)-translocating, E subunit(EC:1.6.5.)	1250.4	1285.4	1218.9	1209.3	1438.2	1637.6	1.13	4.4E-01
B035DRAFT_02288	NADH:ubiquinone oxidoreductase, Na(+)-translocating, D subunit(EC:1.6.5.)	776.4	876.4	841.2	795.6	934.1	1051.1	1.11	5.1E-01
B035DRAFT_02289	NADH:ubiquinone oxidoreductase, Na(+)-translocating, C subunit(EC:1.6.5.)	860.1	873.3	819.2	722.9	943.7	913.6	1.00	9.8E-01
B035DRAFT_02290	NADH:ubiquinone oxidoreductase, Na(+)-translocating, B subunit(EC:1.6.5.)	880.1	887.0	886.0	740.4	898.9	743.9	0.89	3.5E-01
B035DRAFT_02291	NADH:ubiquinone oxidoreductase, Na(+)-translocating, A subunit(EC:1.6.5.)	823.1	854.0	830.7	645.6	724.8	583.4	0.78	9.5E-02
B035DRAFT_02292	Aminopeptidase C(EC:3.4.22.40)	128.6	124.1	109.3	116.9	147.9	108.3	1.02	9.1E-01
B035DRAFT_02293	Na+/H+ antiporter NhaC	106.0	115.4	107.1	151.3	138.2	92.5	1.14	6.4E-01
B035DRAFT_02294	Uncharacterized conserved protein	1556.9	1341.1	1499.4	1290.2	1070.8	1173.5	0.80	1.5E-01
B035DRAFT_02295	Family of unknown function (DUF490).	140.3	128.6	130.0	121.2	109.7	111.2	0.86	1.1E-01
B035DRAFT_02296	hypothetical protein	82.5	97.4	85.6	93.5	102.3	93.2	1.09	4.2E-01
B035DRAFT_02297	hypothetical protein	20.0	24.9	27.5	38.5	32.8	40.0	1.55	1.0E-01
B035DRAFT_02298	Zn-ribbon protein, possibly nucleic acid-binding	1.7	2.9	2.7	2.5	4.0	1.1	0.96	9.6E-01
B035DRAFT_02299	hypothetical protein	5.1	4.9	3.2	7.1	4.9	1.6	0.88	9.0E-01

B035DRAFT_02300	hypothetical protein	21.1	22.1	24.0	27.3	28.0	34.4	1.33	1.3E-01
B035DRAFT_02301	hypothetical protein	5.1	14.5	11.6	6.9	13.9	14.6	1.18	8.3E-01
B035DRAFT_02302	hypothetical protein	11.3	7.1	8.2	0.7	3.9	2.8	0.23	1.8E-01
B035DRAFT_02303	Peptidylarginine deiminase and related enzymes	107.0	105.5	98.7	127.6	133.0	133.2	1.27	2.2E-02
B035DRAFT_02304	Predicted amidohydrolase(EC:3.5.1.53)	146.7	141.1	143.2	148.5	153.9	157.3	1.07	1.5E-01
B035DRAFT_02305	hypothetical protein	1380.0	1409.8	1481.3	1487.9	856.6	873.3	0.73	3.5E-01
B035DRAFT_02306	aspartyl-tRNA synthetase, bacterial type(EC:6.1.1.12)	712.0	680.7	667.2	585.9	657.5	620.3	0.90	2.0E-01
B035DRAFT_02307	Thioredoxin.	552.3	451.6	418.0	532.3	503.2	460.6	1.06	7.5E-01
B035DRAFT_02308	hypothetical protein	390.3	268.6	251.6	409.8	361.7	169.4	0.98	9.8E-01
B035DRAFT_02309	hypothetical protein	1.6	4.7	6.9	2.5	5.8	4.4	1.08	9.4E-01
B035DRAFT_02310	Predicted DNA-binding proteins	67.5	63.0	49.8	70.3	58.6	66.2	1.09	6.6E-01
B035DRAFT_02311	hypothetical protein	133.6	128.7	123.1	101.5	106.8	124.5	0.86	2.5E-01
B035DRAFT_02312	Resolvase, N terminal domain.	42.2	47.3	49.5	39.5	29.8	48.3	0.83	4.9E-01
B035DRAFT_02313	hypothetical protein	3.8	2.5	3.1	5.8	3.9	5.4	1.60	2.0E-01
B035DRAFT_02314	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.9E-01
B035DRAFT_02315	ABC-type multidrug transport system, ATPase component	258.9	287.4	268.2	416.2	416.9	548.3	1.68	5.5E-02
B035DRAFT_02316	hypothetical protein	196.8	194.2	208.5	242.8	274.2	359.4	1.44	1.5E-01
B035DRAFT_02317	Predicted transcriptional regulators	174.5	149.7	167.4	196.3	188.3	255.5	1.29	2.3E-01
B035DRAFT_02318	putative efflux protein, MATE family	94.3	90.6	88.2	47.6	62.0	50.8	0.58	3.6E-02
B035DRAFT_02319	adenylosuccinate lyase(EC:4.3.2.2)	1085.5	1076.7	1041.0	985.5	1027.7	1068.6	0.96	4.2E-01
B035DRAFT_02320	pseudouridine synthase(EC:5.4.99.22)	1135.9	1001.1	1007.8	947.7	977.1	873.3	0.89	2.6E-01
B035DRAFT_02321	asparaginyl-tRNA synthetase(EC:6.1.1.22)	1087.5	1110.9	1069.9	896.1	936.0	962.6	0.85	3.5E-02
B035DRAFT_02322	hypothetical protein	154.9	141.2	151.2	148.0	192.4	272.9	1.33	3.9E-01
B035DRAFT_02323	Uncharacterized protein conserved in bacteria	250.5	224.0	234.1	255.9	262.4	255.9	1.09	2.0E-01
B035DRAFT_02324	hypothetical protein	108.9	121.4	123.5	108.4	110.1	99.7	0.90	2.8E-01
B035DRAFT_02325	ribosomal protein L13, bacterial type	3791.6	3991.4	3641.7	3175.8	3251.5	3226.3	0.85	4.2E-02
B035DRAFT_02326	Ribosomal protein S9	2624.6	2835.3	2846.9	2313.6	2350.7	2657.9	0.88	2.2E-01
B035DRAFT_02327	ribosomal protein S2, bacterial type	3643.4	3755.8	3794.8	3010.8	3291.4	3403.2	0.87	1.1E-01
B035DRAFT_02328	translation elongation factor Ts	3552.3	3569.0	3429.0	3029.0	3347.8	3187.7	0.91	1.5E-01
B035DRAFT_02329	Translation initiation factor 1 (eIF-1/SUI1) and related proteins	82.6	89.6	73.6	75.8	68.6	65.9	0.86	2.6E-01
B035DRAFT_02330	AT-rich DNA-binding protein	257.1	303.7	276.3	311.1	352.1	357.0	1.22	1.6E-01
B035DRAFT_02331	2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway)	228.0	258.3	234.2	252.4	286.9	245.9	1.09	4.4E-01
B035DRAFT_02332	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase(EC:4.6.1.12)	254.6	275.8	303.8	289.3	292.5	184.4	0.90	7.3E-01
B035DRAFT_02333	1,4-dihydroxy-2-naphthoate octaprenyltransferase(EC:2.5.1.-,EC:2.5.1.74)	69.8	75.6	76.1	67.3	77.7	66.9	0.95	6.5E-01
B035DRAFT_02334	Predicted phosphohydrolases	30.0	29.9	26.4	30.1	34.3	24.7	1.03	9.1E-01
B035DRAFT_02335	hypothetical protein	20.7	29.3	34.3	49.9	28.2	41.7	1.41	4.0E-01
B035DRAFT_02336	hypothetical protein	75.0	64.3	75.3	70.6	71.1	67.0	0.97	8.1E-01
B035DRAFT_02337	Predicted nucleotidyltransferases	115.7	115.2	104.0	210.2	185.3	171.5	1.69	2.5E-02
B035DRAFT_02338	HEPN domain.	123.9	132.0	99.4	184.7	176.1	227.7	1.66	8.2E-02
B035DRAFT_02339	nicotinate (nicotinamide) nucleotide adenylyltransferase(EC:2.7.7.18)	195.0	263.2	244.8	248.8	232.6	237.5	1.03	8.7E-01
B035DRAFT_02340	hypothetical protein	303.0	307.5	253.4	239.9	250.4	276.2	0.89	3.9E-01
B035DRAFT_02341	guanylate kinase(EC:2.7.4.8)	270.6	272.8	244.1	222.4	249.3	204.2	0.86	2.5E-01
B035DRAFT_02342	TIGR00255 family protein	202.6	196.6	178.7	158.9	173.3	168.5	0.87	1.5E-01
B035DRAFT_02343	universal bacterial protein YeaZ	231.1	241.4	246.4	287.0	259.5	186.8	1.00	9.9E-01
B035DRAFT_02344	hypothetical protein	342.7	370.7	324.1	358.5	382.6	396.4	1.10	3.2E-01
B035DRAFT_02345	UDP-N-acetylglucosamine 1-carboxyvinyltransferase(EC:2.5.1.7)	501.8	455.8	451.0	494.8	504.4	410.7	1.00	9.9E-01
B035DRAFT_02346	16S rRNA processing protein RimM	222.4	214.7	191.3	184.1	229.0	208.8	0.99	9.4E-01
B035DRAFT_02347	Membrane proteins related to metalloendopeptidases	184.1	181.0	184.5	161.0	179.0	170.9	0.93	2.3E-01
B035DRAFT_02348	1-deoxy-D-xylulose 5-phosphate reductoisomerase(EC:1.1.1.267)	218.4	218.3	211.1	216.5	220.3	187.9	0.96	6.8E-01

B035DRAFT_02349	RIP metalloprotease RseP(EC:3.4.24.)	270.1	266.5	266.5	251.3	279.8	260.1	0.98	7.9E-01
B035DRAFT_02350	anaerobic ribonucleoside-triphosphate reductase activating protein(EC:1.97.1.4)	195.8	195.9	161.7	136.0	186.2	182.3	0.91	6.5E-01
B035DRAFT_02351	Oxygen-sensitive ribonucleoside-triphosphate reductase(EC:1.17.4.2)	306.6	313.0	250.6	308.6	343.0	326.5	1.13	4.0E-01
B035DRAFT_02353	Predicted membrane protein, hemolysin III homolog	74.8	78.7	63.7	59.8	65.4	59.8	0.85	2.6E-01
B035DRAFT_02354	tRNA nucleotidyltransferase/poly(A) polymerase(EC:2.7.7.19)	170.2	173.1	165.7	171.3	159.6	132.4	0.91	4.8E-01
B035DRAFT_02355	hypothetical protein	235.1	278.3	265.4	295.2	355.8	527.1	1.47	2.7E-01
B035DRAFT_02356	hypothetical protein	64.8	60.7	68.8	87.3	91.6	81.5	1.34	4.4E-02
B035DRAFT_02357	Holliday junction DNA helicase, RuvA subunit(EC:3.6.4.12)	182.3	168.3	170.6	162.3	160.9	173.4	0.95	4.4E-01
B035DRAFT_02358	diaminopimelate dehydrogenase(EC:1.4.1.16)	846.5	893.5	813.3	755.2	623.1	534.8	0.74	1.7E-01
B035DRAFT_02359	prolipoprotein diacylglyceryl transferase	123.5	129.0	120.7	117.9	133.6	118.9	0.99	9.2E-01
B035DRAFT_02360	hypothetical protein	58.3	64.6	61.9	57.0	63.2	60.1	0.98	7.6E-01
B035DRAFT_02361	hypothetical protein	27.3	33.0	29.5	26.5	32.6	30.4	1.00	9.8E-01
B035DRAFT_02362	DNA-binding protein, histone-like, putative	241.5	228.4	244.5	281.6	270.7	190.6	1.03	9.2E-01
B035DRAFT_02363	hypothetical protein	59.4	60.0	55.6	58.7	54.3	56.7	0.97	6.1E-01
B035DRAFT_02364	Beta-fructosidases (levanase/invertase)(EC:3.2.1.65) (GH32)	127.9	115.6	114.8	93.3	106.4	88.2	0.80	1.4E-01
B035DRAFT_02365	Fucose permease	166.9	146.0	173.7	133.3	120.7	141.2	0.81	1.7E-01
B035DRAFT_02366	Sugar kinases, ribokinase family(EC:2.7.1.4)	233.6	192.4	240.0	211.3	182.3	97.0	0.70	4.3E-01
B035DRAFT_02367	ABC-type sugar transport system, periplasmic component	38.2	37.4	39.5	32.6	36.6	32.6	0.88	1.7E-01
B035DRAFT_02368	ACT domain-containing protein	135.5	163.9	158.6	134.7	128.9	178.2	0.96	8.5E-01
B035DRAFT_02369	Coenzyme F390 synthetase(EC:6.2.1.30)	99.7	102.2	102.4	99.7	112.2	108.1	1.05	4.5E-01
B035DRAFT_02370	Protein of unknown function (DUF3256).	153.1	170.9	137.7	160.3	159.1	158.1	1.04	7.5E-01
B035DRAFT_02371	ribosomal protein L31	4279.4	5093.9	4202.2	3483.3	3195.9	4509.3	0.82	3.7E-01
B035DRAFT_02372	fructose-1,6-bisphosphate aldolase, class II, various bacterial and amitochondriate protist(EC:4.1.2.13)	2697.4	3086.3	3072.7	3249.3	3546.9	4410.3	1.26	2.5E-01
B035DRAFT_02373	AraC-type DNA-binding domain-containing proteins	87.4	91.3	93.6	93.3	102.3	121.8	1.16	3.3E-01
B035DRAFT_02374	RND family efflux transporter, MFP subunit	282.6	239.8	257.3	336.7	315.2	224.6	1.11	6.7E-01
B035DRAFT_02375	The (Largely Gram-negative Bacterial) Hydrophobe/Amphiphile Efflux-1 (HAE1) Family	309.0	273.8	302.5	365.1	361.2	347.2	1.21	6.8E-02
B035DRAFT_02376	efflux transporter, outer membrane factor (OMF) lipoprotein, NodT family	319.7	319.3	314.2	394.1	381.0	432.0	1.26	4.1E-02
B035DRAFT_02377	hypothetical protein	88.6	100.8	102.0	89.8	96.9	131.6	1.08	7.4E-01
B035DRAFT_02378	Domain of unknown function (DUF3332).	447.4	509.1	468.5	480.0	528.5	553.7	1.10	3.8E-01
B035DRAFT_02379	Arabinose efflux permease	127.4	134.5	123.1	96.9	116.6	149.7	0.93	7.6E-01
B035DRAFT_02380	hypothetical protein	108.1	173.4	161.1	544.7	365.6	553.2	3.32	4.4E-02
B035DRAFT_02381	hypothetical protein	79.1	89.2	80.9	104.1	120.7	113.8	1.36	5.5E-02
B035DRAFT_02382	yjeF C-terminal region, hydroxyethylthiazole kinase-related/yjeF N-terminal region	75.2	66.9	69.6	59.9	61.0	66.1	0.88	1.9E-01
B035DRAFT_02383	TonB-linked outer membrane protein, SusC/RagA family	404.8	416.5	380.0	132.2	200.5	217.2	0.45	6.1E-02
B035DRAFT_02384	SusD family	495.5	465.2	421.8	152.8	233.0	275.0	0.47	8.6E-02
B035DRAFT_02385	F5/8 type C domain (CBM32)	517.6	509.6	533.2	192.9	256.7	335.6	0.49	7.9E-02
B035DRAFT_02386	hypoxanthine phosphoribosyltransferase(EC:2.4.2.8)	124.6	136.4	124.8	105.3	104.9	96.1	0.79	5.4E-02
B035DRAFT_02387	Adenylate kinase and related kinases(EC:2.7.4.3)	618.8	766.3	691.3	567.3	562.5	508.0	0.79	1.4E-01
B035DRAFT_02388	Obg family GTPase CgtA	309.8	321.3	285.9	338.8	363.1	319.8	1.11	2.7E-01
B035DRAFT_02389	uncharacterized protein, YfiH family	180.8	160.1	165.2	159.7	194.5	147.9	0.99	9.4E-01
B035DRAFT_02390	Uncharacterized conserved protein	172.0	156.8	152.6	161.7	198.6	142.6	1.04	8.6E-01
B035DRAFT_02391	Membrane proteins related to metalloendopeptidases	142.7	130.9	110.7	115.7	153.4	132.1	1.04	8.5E-01
B035DRAFT_02392	hypothetical protein	110.9	114.5	98.5	138.0	154.7	131.9	1.31	9.1E-02
B035DRAFT_02393	Opacity protein and related surface antigens	439.7	512.2	477.1	396.4	414.3	426.5	0.87	1.7E-01
B035DRAFT_02394	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)(EC:2.1.2.3)	105.3	118.4	107.0	108.9	123.6	123.6	1.08	4.7E-01
B035DRAFT_02395	hypothetical protein	19.9	23.6	21.7	25.4	23.1	27.6	1.17	2.6E-01

B035DRAFT_02396	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02397	Predicted transcriptional regulators	110.4	133.0	122.5	158.7	126.2	118.9	1.10	6.2E-01
B035DRAFT_02398	hypothetical protein	18.3	19.6	15.1	18.5	13.9	16.6	0.92	7.1E-01
B035DRAFT_02399	hypothetical protein	16.7	17.0	18.3	14.5	18.9	21.6	1.05	8.5E-01
B035DRAFT_02400	Uncharacterized conserved protein	20.1	20.6	17.8	10.5	14.2	14.0	0.65	9.9E-02
B035DRAFT_02401	Protein-tyrosine-phosphatase(EC:1.20.4.1)	12.8	12.7	16.0	7.5	8.8	10.6	0.65	1.3E-01
B035DRAFT_02402	Predicted permeases	19.2	25.3	22.9	8.6	10.0	13.9	0.48	7.6E-02
B035DRAFT_02403	RteC protein.	46.1	47.2	47.5	20.2	22.4	26.7	0.49	2.0E-02
B035DRAFT_02404	Site-specific recombinase XerD	418.0	434.0	403.4	388.4	376.4	402.5	0.93	2.1E-01
B035DRAFT_02405	(tRNA)	69.4	64.6	84.5	40.2	27.3	31.5	0.45	4.8E-02
B035DRAFT_02406	Predicted permease	21.4	25.1	24.6	20.8	25.2	30.9	1.07	7.7E-01
B035DRAFT_02407	Thymidine kinase(EC:2.7.1.21)	32.7	36.4	34.4	40.1	37.5	41.0	1.15	1.4E-01
B035DRAFT_02408	probable S-adenosylmethionine-dependent methyltransferase, YraL family(EC:2.1.1.198)	828.1	871.0	848.4	1022.2	890.8	745.8	1.04	8.5E-01
B035DRAFT_02409	hypothetical protein	539.8	606.2	581.3	556.5	512.9	649.0	0.99	9.6E-01
B035DRAFT_02410	HAD superfamily (subfamily IA) hydrolase, TIGR02254	126.8	145.1	123.3	125.3	115.0	145.3	0.97	8.7E-01
B035DRAFT_02411	SusD family	66.0	72.9	62.4	29.4	39.5	42.8	0.55	6.7E-02
B035DRAFT_02412	TonB-linked outer membrane protein, SusC/RagA family	42.6	42.6	38.0	14.9	17.5	20.6	0.43	2.1E-02
B035DRAFT_02413	SusD family	257.6	284.2	237.1	76.9	120.3	157.8	0.44	1.1E-01
B035DRAFT_02414	TonB-linked outer membrane protein, SusC/RagA family	188.0	204.5	179.5	54.8	74.0	95.6	0.38	4.6E-02
B035DRAFT_02415	SusD family	393.8	452.8	373.1	118.9	164.4	227.6	0.41	7.4E-02
B035DRAFT_02416	TonB-linked outer membrane protein, SusC/RagA family	275.8	325.7	265.5	79.7	101.9	130.4	0.35	3.5E-02
B035DRAFT_02417	Predicted ATPase (AAA+ superfamily)	178.9	198.8	191.6	210.2	183.0	236.6	1.10	5.1E-01
B035DRAFT_02418	SusD family	57.7	63.4	51.5	28.1	31.5	43.0	0.59	1.1E-01
B035DRAFT_02419	TonB-linked outer membrane protein, SusC/RagA family	36.8	43.9	40.7	18.2	19.7	23.8	0.51	2.9E-02
B035DRAFT_02420	hypothetical protein	30.4	33.8	46.9	16.0	21.3	18.9	0.51	8.2E-02
B035DRAFT_02421	hypothetical protein	42.1	38.4	53.6	25.2	29.3	28.2	0.62	8.2E-02
B035DRAFT_02422	Site-specific recombinase XerD	95.8	89.0	90.2	70.6	56.6	71.3	0.72	8.6E-02
B035DRAFT_02423	TonB-linked outer membrane protein, SusC/RagA family	64.9	73.3	65.0	23.1	28.6	35.3	0.42	3.5E-02
B035DRAFT_02424	SusD family	46.3	58.7	49.0	15.7	31.4	34.5	0.50	2.0E-01
B035DRAFT_02425	hypothetical protein	51.3	56.7	47.7	20.7	28.3	39.1	0.55	1.5E-01
B035DRAFT_02426	Predicted Zn-dependent peptidases	39.9	34.0	36.9	18.1	22.1	21.2	0.55	2.5E-02
B035DRAFT_02427	GTP-binding protein HflX	167.5	159.1	155.7	146.2	162.2	139.7	0.93	4.1E-01
B035DRAFT_02428	Putative GTPases (G3E family)	183.0	182.5	184.7	163.0	184.2	167.4	0.93	3.3E-01
B035DRAFT_02429	putative hydrolase, CocE/NonD family (CE7)	72.1	80.5	76.5	65.9	72.4	78.2	0.94	5.9E-01
B035DRAFT_02430	hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha region/hydro-lyases, Fe-S type, tartrate/fumarate subfamily, beta region(EC:4.2.1.2)	458.0	482.4	454.4	501.4	532.8	535.6	1.13	8.8E-02
B035DRAFT_02431	Amino acid transporters	89.3	97.8	100.2	110.0	99.2	81.9	1.01	9.8E-01
B035DRAFT_02432	hypothetical protein	128.4	141.3	165.4	187.2	146.9	132.9	1.07	7.8E-01
B035DRAFT_02433	Outer membrane protein	63.2	58.0	55.6	76.1	84.0	68.7	1.29	1.1E-01
B035DRAFT_02434	Cation/multidrug efflux pump	75.3	81.8	82.9	117.8	119.4	134.8	1.55	2.1E-02
B035DRAFT_02435	RND family efflux transporter, MFP subunit	86.3	83.1	87.9	169.2	174.8	174.7	2.02	1.6E-04
B035DRAFT_02436	Predicted aminopeptidases	179.4	179.6	181.0	196.0	199.2	170.5	1.05	6.2E-01
B035DRAFT_02437	ribosome small subunit-dependent GTPase A(EC:3.6.1.)	266.7	326.6	280.9	335.6	346.0	423.2	1.26	2.2E-01
B035DRAFT_02438	ribosome recycling factor	348.7	332.9	230.8	417.1	440.5	394.1	1.39	2.2E-01
B035DRAFT_02439	Fructose-2,6-bisphosphatase(EC:5.4.2.1)	10.8	17.1	14.3	22.1	16.9	29.5	1.61	2.5E-01
B035DRAFT_02440	uridylate kinase(EC:2.7.4.22)	295.3	285.3	261.1	324.1	327.8	244.2	1.06	7.8E-01
B035DRAFT_02441	DNA-3-methyladenine glycosylase I(EC:3.2.2.20)	31.8	31.5	34.9	34.3	34.1	34.9	1.05	4.0E-01
B035DRAFT_02442	putative efflux protein, MATE family	58.2	67.7	64.2	81.0	74.0	82.6	1.25	9.4E-02
B035DRAFT_02443	birA, biotin-[acetyl-CoA-carboxylase] ligase region(EC:6.3.4.15)	40.3	50.3	43.2	56.7	58.1	61.9	1.33	9.4E-02
B035DRAFT_02444	Uncharacterized protein conserved in bacteria	49.1	58.6	50.2	69.6	74.2	80.9	1.42	6.3E-02

B035DRAFT_02445	Predicted endonuclease distantly related to archaeal Holliday junction resolvase	62.8	74.6	68.0	100.1	78.2	61.7	1.15	6.0E-01
B035DRAFT_02446	hypothetical protein	74.7	80.4	81.2	69.6	61.6	41.2	0.71	2.8E-01
B035DRAFT_02447	Cytosine/adenosine deaminases	137.1	162.5	147.0	137.4	135.5	112.9	0.86	3.3E-01
B035DRAFT_02448	hypothetical protein	230.5	259.8	256.2	229.7	198.9	272.4	0.93	7.0E-01
B035DRAFT_02449	Phosphatidylserine synthase(EC:2.7.8.8)	252.7	325.3	289.8	248.9	248.9	281.9	0.90	5.0E-01
B035DRAFT_02450	phosphatidylserine decarboxylase precursor-related protein(EC:4.1.1.65)	497.9	550.8	514.3	523.6	468.3	474.0	0.94	4.4E-01
B035DRAFT_02451	DNA-directed DNA polymerase III (polc)(EC:2.7.7.7)	214.7	195.1	212.3	240.6	241.3	194.3	1.08	5.7E-01
B035DRAFT_02452	thioredoxin	541.6	614.0	596.4	558.9	552.7	592.2	0.97	7.4E-01
B035DRAFT_02453	hypothetical protein	774.7	847.4	797.7	736.2	789.3	854.0	0.98	8.6E-01
B035DRAFT_02454	hypothetical protein	144.8	142.7	153.8	134.2	135.8	192.8	1.03	8.9E-01
B035DRAFT_02455	hypothetical protein	59.3	61.3	56.9	51.1	51.9	64.0	0.94	6.3E-01
B035DRAFT_02456	Response regulator of the LytR/AlgR family	35.5	37.5	37.1	23.8	19.2	25.3	0.62	4.8E-02
B035DRAFT_02457	hypothetical protein	55.5	59.1	53.3	34.6	34.7	43.4	0.67	6.3E-02
B035DRAFT_02458	ATPase, YjeE family	163.4	166.4	142.8	110.2	140.2	113.9	0.77	1.7E-01
B035DRAFT_02459	ABC-type Mn2+/Zn2+ transport systems, permease components	95.8	91.9	107.1	84.3	64.2	67.2	0.73	1.4E-01
B035DRAFT_02460	hypothetical protein	167.3	119.7	138.5	155.4	118.1	68.4	0.77	5.8E-01
B035DRAFT_02461	5-enolpyruvylshikimate-3-phosphate synthase(EC:2.5.1.19)	167.5	149.5	139.9	156.2	134.0	118.4	0.89	5.1E-01
B035DRAFT_02462	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes(EC:4.1.2.13)	797.5	657.2	744.7	762.9	486.6	450.7	0.75	3.8E-01
B035DRAFT_02463	phosphoglycerate mutase, BPG-dependent, family 1(EC:5.4.2.1)	591.8	480.5	492.6	563.0	378.8	305.4	0.77	4.6E-01
B035DRAFT_02464	Nucleotidyltransferase/DNA polymerase involved in DNA repair(EC:2.7.7.7)	60.6	54.7	62.3	48.6	45.3	38.9	0.75	1.1E-01
B035DRAFT_02465	Alpha-L-fucosidase (GH29)	48.1	47.1	43.9	40.6	47.0	34.9	0.87	4.2E-01
B035DRAFT_02466	hypothetical protein	49.8	46.4	42.4	34.6	40.5	42.9	0.85	2.9E-01
B035DRAFT_02467	hypothetical protein	40.2	37.4	23.8	27.8	28.1	20.9	0.77	4.5E-01
B035DRAFT_02468	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02469	Site-specific recombinase XerD	29.8	24.0	28.7	35.4	35.0	23.2	1.12	6.9E-01
B035DRAFT_02470	hypothetical protein	20.1	24.9	22.8	12.7	13.4	19.5	0.66	1.8E-01
B035DRAFT_02471	hypothetical protein	55.0	64.9	56.1	61.6	55.5	43.9	0.91	6.4E-01
B035DRAFT_02472	DNA binding domain, excisionase family	8.1	7.9	6.0	5.7	4.9	2.9	0.59	2.5E-01
B035DRAFT_02473	hypothetical protein	6.8	5.0	6.2	6.8	5.7	3.5	0.87	7.2E-01
B035DRAFT_02474	hypothetical protein	4.8	2.9	6.0	3.4	4.3	5.0	0.96	9.4E-01
B035DRAFT_02475	hypothetical protein	7.8	5.1	9.1	6.3	2.0	1.7	0.39	2.8E-01
B035DRAFT_02476	hypothetical protein	2.4	4.6	4.8	3.6	4.4	1.8	0.81	7.5E-01
B035DRAFT_02477	hypothetical protein	5.4	8.3	6.5	5.2	8.9	5.3	0.94	8.9E-01
B035DRAFT_02478	hypothetical protein	11.4	6.0	11.8	6.6	6.2	4.7	0.62	3.1E-01
B035DRAFT_02479	hypothetical protein	2.6	2.2	3.0	2.0	1.4	0.6	0.46	2.6E-01
B035DRAFT_02480	hypothetical protein	3.5	2.3	3.6	1.4	2.0	0.7	0.41	2.0E-01
B035DRAFT_02481	hypothetical protein	3.3	1.9	1.4	1.0	2.5	0.6	0.56	5.1E-01
B035DRAFT_02482	hypothetical protein	2.0	0.8	2.1	0.9	1.6	0.8	0.71	6.4E-01
B035DRAFT_02483	hypothetical protein	3.4	2.6	1.5	2.2	2.6	0.3	0.49	6.1E-01
B035DRAFT_02484	hypothetical protein	3.0	2.0	3.1	2.2	1.9	0.4	0.45	4.5E-01
B035DRAFT_02485	Bacteroides conjugative transposon TraK protein	4.4	1.6	3.3	3.2	3.0	2.5	1.00	1.0E+00
B035DRAFT_02486	hypothetical protein	1.3	2.6	2.7	2.3	2.0	0.0	1.03	9.5E-01
B035DRAFT_02487	DNA N-6-adenine-methyltransferase (Dam).	1.7	1.6	3.4	1.8	1.9	0.3	0.49	5.3E-01
B035DRAFT_02488	Bacteroides conjugative transposon TraM protein	2.5	2.7	2.9	1.9	2.5	0.8	0.58	3.9E-01
B035DRAFT_02489	DNA modification methylase	2.5	2.7	4.6	5.1	2.1	1.0	0.69	6.9E-01
B035DRAFT_02490	Bacteroides conjugative transposon TraN protein	1.8	3.7	2.9	1.7	2.0	2.0	0.70	3.8E-01
B035DRAFT_02491	hypothetical protein	1.0	1.5	2.7	1.7	1.2	0.6	0.66	6.0E-01
B035DRAFT_02492	hypothetical protein	4.9	2.4	5.0	4.1	1.6	1.4	0.54	4.2E-01

B035DRAFT_02493	Bacterial RNA polymerase, alpha chain C terminal domain.	33.3	26.4	34.1	29.8	23.5	22.8	0.81	3.4E-01
B035DRAFT_02494	Type IV secretory pathway, VirD4 components	25.6	15.9	21.2	13.7	15.3	10.5	0.63	2.1E-01
B035DRAFT_02495	Uncharacterized conserved protein	226.1	223.5	203.2	245.6	224.8	199.1	1.02	8.7E-01
B035DRAFT_02496	hypothetical protein	2.9	2.0	3.6	3.7	3.2	0.5	0.67	7.3E-01
B035DRAFT_02497	hypothetical protein	3.6	1.0	4.4	1.4	3.7	0.8	0.64	6.9E-01
B035DRAFT_02498	hypothetical protein	0.0	4.3	1.5	0.7	0.6	2.2	0.37	4.5E-01
B035DRAFT_02499	hypothetical protein	1.8	3.6	1.5	1.9	3.3	0.6	0.72	7.6E-01
B035DRAFT_02500	ParB-like partition proteins	12.0	10.7	13.6	11.3	12.3	9.2	0.90	6.1E-01
B035DRAFT_02501	hypothetical protein	39.7	33.9	36.3	46.7	48.6	39.1	1.22	2.2E-01
B035DRAFT_02502	ATPases involved in chromosome partitioning	50.3	51.2	38.3	59.3	55.7	37.6	1.08	8.2E-01
B035DRAFT_02503	Helicase conserved C-terminal domain./Type III restriction enzyme, res subunit.	2.7	2.1	2.5	2.0	2.2	1.3	0.75	3.6E-01
B035DRAFT_02504	hypothetical protein	7.7	5.3	4.9	3.4	2.7	3.6	0.55	1.2E-01
B035DRAFT_02505	hypothetical protein	4.5	4.4	3.7	2.4	2.0	2.7	0.57	5.7E-02
B035DRAFT_02506	hypothetical protein	377.1	361.2	331.8	401.6	414.3	475.0	1.20	1.7E-01
B035DRAFT_02507	Domain of unknown function (DUF1814).	326.2	315.2	350.6	384.5	369.8	388.0	1.15	9.1E-02
B035DRAFT_02508	Predicted ATPases of PP-loop superfamily	250.5	234.0	248.3	280.9	251.9	192.8	0.98	9.3E-01
B035DRAFT_02509	cob(I)alamin adenosyltransferase(EC:2.5.1.17)	246.7	218.7	225.0	315.6	222.5	155.0	0.96	9.3E-01
B035DRAFT_02510	Membrane proteins related to metalloendopeptidases	52.2	48.3	50.9	56.0	48.9	34.0	0.90	7.0E-01
B035DRAFT_02511	hypothetical protein	17.4	11.4	20.0	11.7	10.9	2.2	0.42	4.0E-01
B035DRAFT_02512	hypothetical protein	15.8	13.1	11.9	7.1	13.6	5.5	0.60	3.4E-01
B035DRAFT_02513	hypothetical protein	22.4	15.7	20.6	12.8	13.6	3.2	0.43	3.5E-01
B035DRAFT_02514	hypothetical protein	18.7	14.3	19.8	11.4	13.1	5.1	0.52	2.9E-01
B035DRAFT_02515	Predicted membrane protein	18.3	16.2	16.1	17.9	14.1	8.3	0.76	5.1E-01
B035DRAFT_02516	hypothetical protein	10.0	10.2	12.8	8.8	10.7	5.6	0.73	4.1E-01
B035DRAFT_02517	hypothetical protein	14.8	9.5	10.5	6.5	6.7	2.2	0.40	2.4E-01
B035DRAFT_02518	hypothetical protein	7.6	3.5	8.3	5.6	3.7	0.7	0.40	4.6E-01
B035DRAFT_02519	Membrane proteins related to metalloendopeptidases	12.4	12.1	13.9	11.3	12.0	2.6	0.55	5.1E-01
B035DRAFT_02520	hypothetical protein	16.3	9.3	13.5	9.3	9.3	2.0	0.44	4.0E-01
B035DRAFT_02521	Mismatch repair ATPase (MutS family)	15.8	7.7	11.6	9.2	9.1	2.6	0.54	4.6E-01
B035DRAFT_02522	Muramidase (flagellum-specific) (GH73)	17.4	11.9	14.7	13.6	12.2	3.1	0.55	5.1E-01
B035DRAFT_02523	hypothetical protein	24.8	4.4	17.4	9.0	7.8	0.9	0.32	4.9E-01
B035DRAFT_02524	hypothetical protein	18.3	10.6	21.6	13.1	11.8	3.0	0.48	4.4E-01
B035DRAFT_02525	Antirestriction protein	19.0	16.9	21.8	15.5	16.9	5.5	0.59	4.3E-01
B035DRAFT_02526	hypothetical protein	8.6	7.3	5.5	7.6	8.6	9.4	1.21	4.6E-01
B035DRAFT_02527	hypothetical protein	5.3	12.3	8.9	4.9	9.0	5.4	0.74	6.0E-01
B035DRAFT_02528	hypothetical protein	9.4	7.1	9.7	4.9	5.6	7.2	0.67	2.0E-01
B035DRAFT_02529	hypothetical protein	4.6	6.0	6.3	3.4	4.9	5.9	0.83	5.9E-01
B035DRAFT_02531	hypothetical protein	1085.0	1204.3	1096.3	1138.0	1442.8	1478.5	1.19	3.1E-01
B035DRAFT_02532	PKD domain (CBM44)	346.6	361.0	312.5	318.4	394.5	407.3	1.09	5.8E-01
B035DRAFT_02533	hypothetical protein	256.1	260.3	230.7	263.8	330.4	393.1	1.31	2.6E-01
B035DRAFT_02534	Glutamine cyclotransferase.	228.8	212.5	217.0	268.7	296.5	198.6	1.14	5.4E-01
B035DRAFT_02535	Transposase and inactivated derivatives	236.6	267.1	219.0	268.3	289.7	323.6	1.22	2.2E-01
B035DRAFT_02536	Outer membrane cobalamin receptor protein	212.1	187.6	202.8	225.7	232.1	122.1	0.93	8.5E-01
B035DRAFT_02537	ABC-type Fe3+-hydroxamate transport system, periplasmic component	232.8	204.6	243.4	268.9	228.8	85.2	0.77	6.9E-01
B035DRAFT_02538	ABC-type Fe3+-siderophore transport system, permease component	222.8	207.4	307.2	294.7	195.0	64.6	0.64	6.0E-01
B035DRAFT_02539	ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase components(EC:3.6.3.34)	153.6	129.1	183.6	169.9	116.2	44.3	0.62	5.2E-01
B035DRAFT_02540	Predicted metal-binding protein	63.7	81.2	70.2	84.9	64.4	66.6	1.00	1.0E+00
B035DRAFT_02541	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	10.4	11.8	11.7	12.6	13.3	11.1	1.09	4.9E-01

B035DRAFT_02542	Plasmid recombination enzyme.	5.5	4.3	5.2	5.7	4.4	4.2	0.95	8.4E-01
B035DRAFT_02543	hypothetical protein	5.0	3.3	5.3	3.8	4.9	3.6	0.92	8.0E-01
B035DRAFT_02544	hypothetical protein	4.0	4.7	2.4	3.0	3.9	1.6	0.74	6.2E-01
B035DRAFT_02545	hypothetical protein	3.8	5.4	2.0	4.0	6.9	3.1	1.26	7.4E-01
B035DRAFT_02546	hypothetical protein	5.3	4.0	6.4	2.0	4.8	3.8	0.64	4.2E-01
B035DRAFT_02547	hypothetical protein	12.1	8.2	10.0	6.3	5.3	4.4	0.53	8.5E-02
B035DRAFT_02548	Resolvase, N terminal domain.	49.4	50.1	41.3	53.8	53.0	32.9	0.97	9.3E-01
B035DRAFT_02549	hypothetical protein	70.8	59.8	47.0	39.0	61.3	30.7	0.72	4.4E-01
B035DRAFT_02550	Bacterial nucleoid DNA-binding protein	84.5	110.7	87.5	123.6	126.0	102.9	1.25	2.8E-01
B035DRAFT_02551	Single-stranded DNA-binding protein	118.8	78.9	110.6	96.1	94.4	54.8	0.78	5.4E-01
B035DRAFT_02552	hypothetical protein	41.9	29.7	31.1	41.4	33.2	32.1	1.05	8.7E-01
B035DRAFT_02553	hypothetical protein	23.5	20.7	21.1	34.6	17.4	24.3	1.13	7.5E-01
B035DRAFT_02554	hypothetical protein	23.9	15.5	26.7	11.1	15.6	21.7	0.72	4.8E-01
B035DRAFT_02555	hypothetical protein	27.0	22.0	28.7	18.1	22.4	23.0	0.82	3.3E-01
B035DRAFT_02556	hypothetical protein	1.1	2.6	2.0	1.7	1.2	3.7	1.13	8.8E-01
B035DRAFT_02557	Antirestriction protein	4.4	5.6	6.5	6.1	7.5	7.3	1.28	3.2E-01
B035DRAFT_02558	hypothetical protein	32.4	33.2	33.2	31.4	46.5	74.9	1.45	4.2E-01
B035DRAFT_02559	hypothetical protein	29.7	34.5	22.8	18.1	26.9	54.0	1.04	9.6E-01
B035DRAFT_02560	hypothetical protein	39.5	38.7	31.7	33.6	42.2	51.7	1.15	6.0E-01
B035DRAFT_02561	Superfamily II DNA helicase	40.8	39.6	39.8	39.1	46.9	62.2	1.21	4.4E-01
B035DRAFT_02562	Domain of unknown function (DUF1848).	32.7	33.8	28.1	32.1	33.3	47.4	1.18	5.1E-01
B035DRAFT_02563	hypothetical protein	42.5	39.6	35.5	52.5	53.3	59.3	1.41	5.8E-02
B035DRAFT_02564	Predicted ATPase (AAA+ superfamily)	37.6	42.2	41.4	57.9	63.5	63.3	1.52	1.8E-02
B035DRAFT_02565	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02566	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	2.7	2.8	2.8	3.2	3.1	2.2	1.00	9.9E-01
B035DRAFT_02567	Plasmid recombination enzyme.	1.9	1.9	2.0	2.8	2.9	1.3	1.15	7.9E-01
B035DRAFT_02568	hypothetical protein	3.1	4.0	3.1	4.3	4.3	4.6	1.30	1.7E-01
B035DRAFT_02569	DNA binding domain, excisionase family	2.7	3.6	3.3	0.5	2.8	3.2	0.51	5.6E-01
B035DRAFT_02570	hypothetical protein	1.7	2.5	2.4	1.4	2.4	2.2	0.88	7.3E-01
B035DRAFT_02571	Site-specific recombinase XerD	5.3	3.5	3.0	5.6	5.0	4.4	1.30	4.4E-01
B035DRAFT_02572	DNA binding domain, excisionase family	3.8	4.7	1.6	3.0	2.4	3.8	0.99	9.9E-01
B035DRAFT_02573	Domain of unknown function (DUF1814).	58.8	66.7	55.1	57.5	61.5	66.0	1.03	8.5E-01
B035DRAFT_02574	hypothetical protein	54.2	65.7	60.7	57.1	56.0	61.2	0.97	7.8E-01
B035DRAFT_02575	single stranded DNA-binding protein (ssb)	8.9	4.7	8.2	4.2	2.4	1.6	0.37	1.7E-01
B035DRAFT_02576	hypothetical protein	2.9	1.1	0.0	0.0	1.3	0.9	0.60	6.2E-01
B035DRAFT_02577	hypothetical protein	3.2	2.0	3.8	1.8	1.6	1.6	0.57	1.8E-01
B035DRAFT_02578	ATPases involved in chromosome partitioning	4.0	3.4	3.8	2.1	3.3	2.7	0.70	2.0E-01
B035DRAFT_02579	hypothetical protein	6.8	1.1	4.7	4.1	4.4	0.9	0.76	8.5E-01
B035DRAFT_02580	hypothetical protein	8.2	7.7	15.2	8.0	8.1	8.1	0.81	6.0E-01
B035DRAFT_02581	hypothetical protein	1.1	2.5	1.3	2.0	1.0	1.2	0.88	8.4E-01
B035DRAFT_02582	hypothetical protein	4.1	4.0	4.2	1.1	5.0	2.5	0.58	5.0E-01
B035DRAFT_02583	hypothetical protein	0.9	0.7	3.2	2.1	1.8	2.4	1.71	5.4E-01
B035DRAFT_02584	Uncharacterized protein conserved in bacteria	0.7	2.0	0.4	1.1	2.2	0.6	1.37	7.8E-01
B035DRAFT_02585	hypothetical protein	1.5	1.7	0.0	1.6	0.0	1.3	0.91	6.5E-01
B035DRAFT_02586	hypothetical protein	6.6	5.6	5.3	6.5	4.9	4.3	0.89	6.4E-01
B035DRAFT_02587	Nucleotidyltransferase/DNA polymerase involved in DNA repair	16.0	14.6	16.5	17.3	17.5	14.6	1.05	7.3E-01
B035DRAFT_02588	Protein of unknown function (DUF2958).	3.5	4.1	3.2	4.1	3.6	2.0	0.86	7.4E-01
B035DRAFT_02589	hypothetical protein	3.7	3.3	4.9	4.3	2.8	2.8	0.83	5.7E-01
B035DRAFT_02590	Protein of unknown function (DUF1653)./Uncharacterised protein family (UPF0227).	20.5	18.9	17.7	22.0	28.1	23.2	1.28	1.7E-01

B035DRAFT_02591	Resolvase, N terminal domain.	14.4	8.4	11.6	11.6	14.5	13.1	1.16	6.2E-01
B035DRAFT_02592	hypothetical protein	0.0	0.0	2.2	0.0	0.0	0.0	0.00	
B035DRAFT_02593	hypothetical protein	2.2	2.3	1.8	2.0	1.9	2.2	0.97	8.5E-01
B035DRAFT_02594	hypothetical protein	1.5	1.7	2.3	2.3	1.7	2.4	1.17	6.0E-01
B035DRAFT_02595	hypothetical protein	0.9	2.7	1.1	0.5	2.1	4.2	1.15	9.2E-01
B035DRAFT_02596	hypothetical protein	5.5	5.0	5.3	1.2	1.4	4.3	0.37	2.2E-01
B035DRAFT_02597	hypothetical protein	7.8	7.5	9.5	6.1	4.6	5.5	0.65	1.0E-01
B035DRAFT_02598	hypothetical protein	6.6	5.8	5.8	3.5	3.7	3.2	0.57	1.7E-02
B035DRAFT_02599	Site-specific recombinase XerD	19.8	25.4	22.7	24.2	25.3	22.8	1.07	6.4E-01
B035DRAFT_02600	Site-specific recombinase XerD	18.4	20.3	20.1	16.7	17.9	19.2	0.91	3.5E-01
B035DRAFT_02601	hypothetical protein	21.8	23.2	22.0	17.6	20.9	17.1	0.83	1.8E-01
B035DRAFT_02602	hypothetical protein	18.1	15.1	16.9	14.2	17.9	15.3	0.94	7.1E-01
B035DRAFT_02603	DNA binding domain, excisionase family	0.7	5.8	3.5	1.5	1.3	3.2	0.76	8.4E-01
B035DRAFT_02604	hypothetical protein	4.5	5.5	4.3	2.7	1.9	1.5	0.42	7.5E-02
B035DRAFT_02605	hypothetical protein	4.3	4.6	3.7	3.5	1.9	5.3	0.79	6.6E-01
B035DRAFT_02606	hypothetical protein	2.5	2.3	4.2	2.6	4.9	3.6	1.24	6.5E-01
B035DRAFT_02607	Bacterial mobilisation protein (MobC).	6.5	3.4	3.5	3.0	4.6	3.9	0.89	8.1E-01
B035DRAFT_02608	Relaxase/Mobilisation nuclease domain.	9.6	8.6	9.6	9.3	7.4	7.3	0.86	3.4E-01
B035DRAFT_02609	hypothetical protein	32.5	36.2	33.7	30.8	31.7	40.4	1.00	1.0E+00
B035DRAFT_02610	hypothetical protein(EC:3.6.4.12)	55.9	60.3	56.8	45.4	51.0	72.1	0.96	8.7E-01
B035DRAFT_02611	hypothetical protein	60.6	69.6	62.0	53.8	68.9	82.2	1.05	8.5E-01
B035DRAFT_02612	Restriction endonuclease(EC:3.1.21.5)	82.2	74.2	76.0	63.5	82.7	99.6	1.04	8.8E-01
B035DRAFT_02613	Adenine specific DNA methylase Mod(EC:2.1.1.72)	96.6	93.6	92.5	88.6	104.1	122.2	1.10	5.6E-01
B035DRAFT_02614	hypothetical protein	57.8	60.6	50.7	48.0	53.7	70.3	1.01	9.8E-01
B035DRAFT_02615	hypothetical protein	56.9	61.6	48.3	42.7	58.8	77.6	1.05	9.0E-01
B035DRAFT_02616	Superfamily II DNA/RNA helicases, SNF2 family	84.3	83.2	83.3	82.7	90.7	110.9	1.13	4.6E-01
B035DRAFT_02617	Helix-turn-helix.	95.8	107.1	93.4	98.5	111.4	134.2	1.15	4.3E-01
B035DRAFT_02618	Virulence protein	131.4	115.6	119.2	83.4	96.7	93.8	0.75	6.6E-02
B035DRAFT_02619	DNA mismatch endonuclease Vsr(EC:3.1.)	159.3	146.7	131.8	117.2	128.2	141.5	0.88	3.9E-01
B035DRAFT_02620	hypothetical protein	180.4	215.7	169.0	142.8	158.3	187.3	0.86	4.5E-01
B035DRAFT_02621	hypothetical protein	165.2	192.1	174.5	143.0	154.4	202.9	0.93	7.4E-01
B035DRAFT_02622	hypothetical protein	115.0	130.9	115.1	93.0	111.7	132.3	0.93	7.0E-01
B035DRAFT_02623	hypothetical protein	125.0	140.2	134.1	119.3	129.1	167.1	1.03	8.9E-01
B035DRAFT_02624	AIPR protein.	111.7	122.8	105.7	98.8	122.0	150.0	1.08	7.6E-01
B035DRAFT_02625	hypothetical protein	163.7	175.0	165.9	161.8	201.8	244.3	1.19	4.3E-01
B035DRAFT_02626	Type III restriction enzyme, res subunit./Z1 domain.	115.7	128.9	104.0	103.7	129.6	162.4	1.12	6.6E-01
B035DRAFT_02627	hypothetical protein	109.2	125.3	106.3	95.6	121.3	147.4	1.05	8.4E-01
B035DRAFT_02628	DNA-methyltransferase (dcm)(EC:2.1.1.37)	143.4	157.9	138.0	135.6	179.1	197.2	1.15	5.1E-01
B035DRAFT_02629	Predicted transcriptional regulators	109.7	109.7	100.6	96.2	137.2	143.6	1.16	5.2E-01
B035DRAFT_02630	hypothetical protein	56.3	49.8	44.3	50.5	68.5	60.8	1.19	4.0E-01
B035DRAFT_02631	HipA-like C-terminal domain./HipA-like N-terminal domain.	80.2	76.4	71.6	79.0	100.2	86.4	1.16	3.1E-01
B035DRAFT_02632	Helix-turn-helix.	53.7	59.9	51.2	57.6	59.2	74.6	1.16	4.0E-01
B035DRAFT_02633	Uncharacterized stress protein (general stress protein 26)	144.4	146.8	143.4	175.2	194.7	239.4	1.39	1.2E-01
B035DRAFT_02634	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02635	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02636	hypothetical protein	110.6	152.3	166.9	284.5	219.0	197.3	1.64	1.7E-01
B035DRAFT_02637	hypothetical protein	34.7	39.8	44.2	41.0	51.0	48.8	1.19	3.4E-01
B035DRAFT_02638	hypothetical protein	43.4	41.7	53.3	57.9	57.8	49.2	1.19	3.2E-01
B035DRAFT_02639	hypothetical protein	58.8	55.1	65.9	74.1	80.2	52.1	1.13	6.4E-01
B035DRAFT_02640	hypothetical protein	75.7	76.1	81.5	95.2	93.5	84.0	1.17	1.3E-01
B035DRAFT_02641	hypothetical protein	154.5	141.6	145.0	170.1	153.1	109.3	0.96	8.9E-01

B035DRAFT_02642	conserved hypothetical protein, YceG family	102.8	108.7	116.4	122.3	112.1	99.2	1.02	9.2E-01
B035DRAFT_02643	4Fe-4S binding domain.	284.2	317.7	300.5	382.5	398.9	394.7	1.30	2.5E-02
B035DRAFT_02644	(miscRNA)	32616.5	45027.0	67728.3	93949.3	50708.4	20323.9	0.99	9.9E-01
B035DRAFT_02645	ribosomal protein L20	2789.4	3380.1	3274.8	3292.6	3135.8	3837.6	1.09	5.9E-01
B035DRAFT_02646	ribosomal protein L35	2742.9	3637.7	3605.5	3117.3	2976.7	3821.0	1.00	9.9E-01
B035DRAFT_02647	translation initiation factor IF-3	1418.9	1622.6	1560.0	1256.6	1181.0	1336.7	0.82	1.1E-01
B035DRAFT_02648	threonyl-tRNA synthetase(EC:6.1.1.3)	733.1	717.8	695.3	726.3	807.5	771.3	1.07	2.9E-01
B035DRAFT_02649	Tetratricopeptide repeat.	478.2	485.6	493.4	560.6	574.5	571.1	1.17	5.3E-03
B035DRAFT_02650	peptide deformylase(EC:3.5.1.88)	328.4	370.4	375.6	465.2	448.3	394.7	1.22	1.6E-01
B035DRAFT_02651	RNAse H-fold protein YqgF(EC:3.1.)	218.2	262.7	209.4	329.3	324.7	316.3	1.41	6.7E-02
B035DRAFT_02652	hypothetical protein (CBM60)	115.4	113.3	98.1	124.5	147.7	138.8	1.26	1.5E-01
B035DRAFT_02653	Cell division protein	1058.0	1133.1	1187.0	1264.3	1141.9	976.6	1.00	9.9E-01
B035DRAFT_02654	hypothetical protein	2150.8	2348.4	2157.3	2796.7	2409.0	2227.6	1.11	4.2E-01
B035DRAFT_02655	Protein of unknown function (DUF1469).	475.5	506.0	492.3	437.8	406.6	596.5	0.96	8.8E-01
B035DRAFT_02656	hypothetical protein	425.2	463.3	421.1	399.6	359.0	479.5	0.94	7.1E-01
B035DRAFT_02657	Periplasmic protease (PL22)	427.7	419.4	408.5	299.6	302.8	309.0	0.73	1.4E-03
B035DRAFT_02658	Transcriptional regulators	50.5	45.1	48.1	50.0	42.1	54.2	1.01	9.3E-01
B035DRAFT_02659	OAH/OAS sulfhydrylase(EC:2.5.1.49)	59.5	66.4	67.2	50.6	43.1	47.2	0.73	6.0E-02
B035DRAFT_02660	Predicted membrane-associated, metal-dependent hydrolase	195.4	186.8	200.2	167.7	119.7	136.0	0.72	1.4E-01
B035DRAFT_02661	Outer membrane protein/protective antigen OMA87	241.2	255.3	257.6	225.2	175.4	203.4	0.80	1.6E-01
B035DRAFT_02662	Outer membrane protein	430.9	401.5	445.0	546.1	351.4	379.2	0.98	9.5E-01
B035DRAFT_02663	Cation/multidrug efflux pump	81.7	64.0	67.2	121.1	132.7	128.4	1.80	2.7E-02
B035DRAFT_02664	RND family efflux transporter, MFP subunit	32.3	26.3	30.0	52.6	53.2	45.1	1.70	3.5E-02
B035DRAFT_02665	AraC-type DNA-binding domain-containing proteins	50.9	55.2	55.5	50.2	54.9	57.1	1.00	9.8E-01
B035DRAFT_02666	hypothetical protein	222.2	189.4	199.3	154.5	162.4	152.4	0.77	6.1E-02
B035DRAFT_02667	Uncharacterized conserved protein	269.6	248.3	247.6	211.7	223.9	256.4	0.90	3.8E-01
B035DRAFT_02668	hypothetical protein	302.7	321.8	249.8	209.9	120.2	99.2	0.47	1.5E-01
B035DRAFT_02669	Gas vesicle protein	853.7	699.7	702.5	1190.3	1034.3	706.4	1.28	4.3E-01
B035DRAFT_02670	(miscRNA)	366.8	413.8	395.0	343.0	310.6	310.3	0.82	9.0E-02
B035DRAFT_02671	tryptophan synthase, beta subunit(EC:4.2.1.20)	583.0	548.1	540.2	254.5	274.7	263.2	0.47	7.7E-04
B035DRAFT_02672	Anthranilate/para-aminobenzoate synthases component I(EC:4.1.3.27)	209.0	189.1	200.1	101.0	134.4	155.6	0.64	1.3E-01
B035DRAFT_02673	glutamine amidotransferase of anthranilate synthase or aminodeoxychorismate synthase(EC:4.1.3.27)	92.8	80.4	82.0	60.9	74.9	81.7	0.85	3.6E-01
B035DRAFT_02674	anthranilate phosphoribosyltransferase(EC:2.4.2.18)	89.0	84.4	87.1	69.6	86.1	97.1	0.96	8.4E-01
B035DRAFT_02675	Indole-3-glycerol phosphate synthase(EC:4.1.1.48)	79.3	74.5	63.8	63.4	68.1	66.9	0.92	4.7E-01
B035DRAFT_02676	Phosphoribosylanthranilate isomerase(EC:5.3.1.24)	67.2	70.2	60.5	46.0	52.5	57.4	0.79	1.5E-01
B035DRAFT_02677	tryptophan synthase, alpha subunit(EC:4.2.1.20)	106.6	116.1	93.6	70.2	81.3	92.1	0.77	2.0E-01
B035DRAFT_02678	L-asparaginases, type I(EC:3.5.1.1)	115.5	118.9	124.1	134.3	127.0	170.0	1.19	3.1E-01
B035DRAFT_02679	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	77.9	70.9	75.1	87.4	80.6	93.9	1.17	1.6E-01
B035DRAFT_02680	Signal transduction histidine kinase(EC:2.7.13.3)	67.0	76.1	74.3	72.3	75.4	87.9	1.08	5.4E-01
B035DRAFT_02681	hypothetical protein	170.1	161.1	156.5	196.7	210.7	184.7	1.21	8.4E-02
B035DRAFT_02683	hypothetical protein	236.0	241.0	223.2	188.4	260.2	204.0	0.92	6.6E-01
B035DRAFT_02684	gliding motility-associated protein GldE	238.4	271.9	251.1	225.1	268.1	308.1	1.05	8.1E-01
B035DRAFT_02685	single stranded DNA-binding protein (ssb)	307.4	303.1	297.1	348.3	354.2	347.4	1.16	6.8E-03
B035DRAFT_02686	A/G-specific adenine glycosylase(EC:3.2.2.)	23.3	23.4	20.8	18.3	24.7	18.0	0.90	5.8E-01
B035DRAFT_02687	Bacterial nucleoid DNA-binding protein	1284.7	1582.3	1088.1	1322.1	1256.1	1420.1	1.02	9.3E-01
B035DRAFT_02688	ribonuclease, Rne/Rng family(EC:3.1.26.)	804.9	846.2	776.3	798.9	854.8	974.3	1.08	5.0E-01
B035DRAFT_02689	Predicted P-loop-containing kinase	74.7	76.3	72.5	77.5	88.6	99.7	1.18	2.5E-01

B035DRAFT_02690	Nucleoside-diphosphate-sugar pyrophosphorylase involved in lipopolysaccharide biosynthesis/translation initiation factor 2B, gamma/epsilon subunits (eIF-2Bgamma/eIF-2Bepsilon)(EC:2.7.7.13)	85.4	89.3	81.9	79.2	96.4	107.3	1.09	5.9E-01
B035DRAFT_02691	5-methyltetrahydrofolate--homocysteine methyltransferase(EC:2.1.1.13)	325.1	301.4	323.7	283.2	312.3	196.1	0.82	4.4E-01
B035DRAFT_02692	SsrA-binding protein	234.2	211.5	200.6	218.3	230.5	276.5	1.12	4.6E-01
B035DRAFT_02693	Protein of unknown function (DUF1282).	195.3	211.9	212.8	220.6	227.5	253.2	1.13	2.3E-01
B035DRAFT_02694	hypothetical protein	567.8	704.0	677.0	717.2	705.8	798.7	1.14	3.5E-01
B035DRAFT_02695	hypothetical protein	87.9	97.6	83.7	83.2	117.9	110.4	1.15	5.1E-01
B035DRAFT_02696	hypothetical protein	2613.3	2568.7	2419.2	3112.5	3439.3	2982.5	1.25	7.2E-02
B035DRAFT_02697	hypothetical protein	2357.1	2510.6	2483.3	3077.6	3466.3	3497.5	1.36	3.3E-02
B035DRAFT_02698	Site-specific recombinase XerD	22.9	26.6	27.5	22.5	24.9	31.3	1.01	9.5E-01
B035DRAFT_02699	hypothetical protein	2.1	3.6	2.5	2.2	3.8	3.8	1.18	7.2E-01
B035DRAFT_02700	hypothetical protein	1.5	1.8	3.7	4.8	0.0	1.4	1.20	9.0E-01
B035DRAFT_02701	hypothetical protein	7.4	6.5	7.4	6.1	6.9	5.7	0.87	3.1E-01
B035DRAFT_02702	Protein of unknown function (DUF1071).	1.1	1.1	1.1	2.6	1.4	1.0	1.43	4.7E-01
B035DRAFT_02703	hypothetical protein	4.3	3.6	5.1	5.3	7.2	8.2	1.59	1.8E-01
B035DRAFT_02704	hypothetical protein	0.0	1.0	0.0	0.0	0.8	0.0	0.78	
B035DRAFT_02705	hypothetical protein	1.7	0.4	2.4	1.4	1.5	0.9	1.07	9.6E-01
B035DRAFT_02706	hypothetical protein	0.8	0.0	1.0	0.0	0.8	0.0	0.82	
B035DRAFT_02707	hypothetical protein	0.0	0.0	0.0	0.0	0.9	0.0	0.00	
B035DRAFT_02708	hypothetical protein	1.0	2.3	0.6	1.0	0.9	1.3	0.97	9.8E-01
B035DRAFT_02709	hypothetical protein	1.0	0.6	1.2	1.5	0.9	0.9	1.23	7.0E-01
B035DRAFT_02710	Site-specific recombinases, DNA invertase Pin homologs	0.0	0.6	0.9	0.5	0.5	1.1	0.89	8.7E-01
B035DRAFT_02711	hypothetical protein	0.7	0.0	1.8	1.5	0.7	0.0	0.89	9.3E-01
B035DRAFT_02712	hypothetical protein	2.6	2.0	2.8	0.9	2.4	2.4	0.70	5.5E-01
B035DRAFT_02713	hypothetical protein	18.4	21.8	21.1	25.6	23.3	26.4	1.23	1.5E-01
B035DRAFT_02714	ATPases with chaperone activity, ATP-binding subunit	96.4	100.2	107.8	150.2	146.1	99.3	1.28	3.4E-01
B035DRAFT_02715	hypothetical protein	21.2	25.5	14.1	24.4	22.1	17.1	1.06	8.8E-01
B035DRAFT_02716	hypothetical protein	27.1	18.2	23.0	19.5	28.3	13.8	0.88	7.7E-01
B035DRAFT_02717	hypothetical protein	13.9	13.8	11.0	8.1	13.7	11.1	0.83	5.7E-01
B035DRAFT_02718	hypothetical protein	6.5	8.3	4.8	4.1	8.3	7.7	1.00	9.9E-01
B035DRAFT_02719	hypothetical protein	17.8	18.7	20.3	19.4	18.8	10.4	0.82	6.0E-01
B035DRAFT_02720	hypothetical protein	27.9	18.7	24.7	27.6	22.6	16.9	0.94	8.6E-01
B035DRAFT_02721	hypothetical protein	26.2	18.2	25.2	24.1	24.9	15.4	0.91	8.1E-01
B035DRAFT_02722	Phage baseplate assembly protein W	24.0	22.0	23.4	29.4	29.0	24.4	1.19	2.0E-01
B035DRAFT_02723	hypothetical protein	17.9	16.2	16.9	21.9	17.8	15.0	1.06	7.9E-01
B035DRAFT_02724	hypothetical protein	6.3	6.5	9.4	9.5	7.8	8.7	1.19	4.8E-01
B035DRAFT_02725	hypothetical protein	11.1	10.7	11.0	14.6	14.8	9.9	1.18	4.8E-01
B035DRAFT_02726	Uncharacterized protein conserved in bacteria	13.0	13.9	12.8	13.7	14.8	8.8	0.92	7.8E-01
B035DRAFT_02727	hypothetical protein	9.7	5.8	12.6	12.0	12.8	7.0	1.14	8.1E-01
B035DRAFT_02728	hypothetical protein	9.5	14.5	9.2	11.0	9.2	8.3	0.88	6.7E-01
B035DRAFT_02729	FOG: PKD repeat	11.2	8.9	10.4	11.6	12.2	5.4	0.90	8.5E-01
B035DRAFT_02730	hypothetical protein	13.9	11.6	11.6	14.4	15.6	8.2	0.99	9.9E-01
B035DRAFT_02731	hypothetical protein	7.6	10.1	7.5	11.5	10.1	11.9	1.34	1.9E-01
B035DRAFT_02732	Domain of unknown function (DUF1911)./Domain of unknown function (DUF1910).	19.8	17.2	14.2	20.8	20.8	26.5	1.33	2.5E-01
B035DRAFT_02733	hypothetical protein	26.5	21.4	37.0	30.0	28.5	41.5	1.19	6.3E-01
B035DRAFT_02734	hypothetical protein	23.7	21.2	21.2	24.7	26.8	22.9	1.13	2.9E-01
B035DRAFT_02735	hypothetical protein	13.4	9.7	10.1	17.5	15.5	10.5	1.30	4.4E-01
B035DRAFT_02736	hypothetical protein	29.0	28.8	26.8	24.9	29.4	40.7	1.10	7.3E-01
B035DRAFT_02737	hypothetical protein	42.3	38.1	40.6	30.1	34.3	57.4	0.97	9.3E-01

B035DRAFT_02738	Type IV secretory pathway, VirD4 components	23.2	16.5	20.9	15.8	15.8	14.5	0.77	2.2E-01
B035DRAFT_02739	Relaxase/Mobilisation nuclease domain.	6.5	5.5	8.1	8.4	7.8	6.0	1.11	7.0E-01
B035DRAFT_02740	hypothetical protein	5.2	4.2	3.9	3.8	8.7	4.7	1.23	6.7E-01
B035DRAFT_02741	ATPases involved in chromosome partitioning	4.5	2.2	7.0	5.6	4.0	2.5	0.94	9.4E-01
B035DRAFT_02742	Protein of unknown function (DUF3408).	6.4	2.2	5.5	7.9	10.2	5.5	1.79	4.0E-01
B035DRAFT_02743	hypothetical protein	5.5	4.2	4.6	5.7	4.3	2.1	0.79	6.7E-01
B035DRAFT_02744	hypothetical protein	41.4	45.9	44.5	45.2	41.2	58.6	1.09	6.7E-01
B035DRAFT_02745	hypothetical protein	38.6	41.0	30.7	35.9	34.7	47.1	1.06	8.0E-01
B035DRAFT_02746	hypothetical protein	16.3	33.8	29.8	37.3	32.1	46.2	1.50	3.8E-01
B035DRAFT_02747	hypothetical protein	3.6	2.8	3.0	1.3	3.3	1.5	0.59	3.5E-01
B035DRAFT_02748	hypothetical protein	1.0	1.2	2.5	2.2	2.3	0.0	1.54	4.2E-01
B035DRAFT_02749	Bacteroides conjugation system ATPase, TraG family	2.1	1.2	3.3	1.5	1.9	0.7	0.62	5.1E-01
B035DRAFT_02750	hypothetical protein	1.4	1.7	2.9	2.5	0.9	0.0	0.77	8.2E-01
B035DRAFT_02751	hypothetical protein	2.9	0.9	2.3	2.0	2.4	0.2	0.57	7.1E-01
B035DRAFT_02752	Bacteroides conjugative transposon TraJ protein	2.5	1.2	1.4	2.5	1.8	0.5	0.79	8.3E-01
B035DRAFT_02753	Bacteroides conjugative transposon TraK protein	3.0	1.3	2.0	1.4	1.7	1.0	0.69	4.9E-01
B035DRAFT_02754	hypothetical protein	0.6	1.3	1.4	1.8	1.5	0.5	1.11	9.1E-01
B035DRAFT_02755	Bacteroides conjugative transposon TraM protein	2.1	1.8	3.0	2.4	2.7	1.4	0.94	9.0E-01
B035DRAFT_02756	Bacteroides conjugative transposon TraN protein	2.2	2.8	3.4	4.3	3.0	2.5	1.16	6.8E-01
B035DRAFT_02757	Conjugative transposon protein TraO.	3.2	2.7	4.2	5.4	4.7	2.9	1.27	5.7E-01
B035DRAFT_02758	hypothetical protein	2.9	4.7	4.0	5.0	1.7	2.3	0.71	5.9E-01
B035DRAFT_02759	Phage-related lysozyme (muraminidase) (GH24)	8.1	3.7	5.6	7.0	5.7	2.9	0.89	8.7E-01
B035DRAFT_02760	hypothetical protein	6.1	6.0	8.0	8.9	10.3	2.9	0.97	9.8E-01
B035DRAFT_02761	hypothetical protein	4.2	3.3	4.5	4.7	4.7	1.3	0.76	7.5E-01
B035DRAFT_02762	hypothetical protein	4.6	3.5	4.8	4.9	5.3	3.5	1.05	8.8E-01
B035DRAFT_02763	Type I restriction-modification system methyltransferase subunit(EC:2.1.1.72)	4.1	3.4	1.9	6.2	7.4	2.5	1.61	5.1E-01
B035DRAFT_02764	hypothetical protein	5.1	4.1	4.3	7.6	6.1	2.8	1.14	8.3E-01
B035DRAFT_02765	hypothetical protein	5.4	2.1	3.7	7.6	4.9	6.1	1.75	3.3E-01
B035DRAFT_02766	hypothetical protein	11.6	17.5	17.0	18.9	15.8	14.8	1.09	7.7E-01
B035DRAFT_02767	hypothetical protein	43.1	38.1	52.4	61.3	44.8	32.9	1.02	9.7E-01
B035DRAFT_02768	hypothetical protein	30.2	27.9	33.5	39.5	34.9	22.9	1.04	9.2E-01
B035DRAFT_02769	hypothetical protein	13.2	9.5	13.5	16.7	15.1	7.0	1.01	9.8E-01
B035DRAFT_02770	DnaJ-class molecular chaperone with C-terminal Zn finger domain	13.4	13.1	13.1	18.1	17.1	8.6	1.05	9.2E-01
B035DRAFT_02771	hypothetical protein	12.1	8.4	5.9	14.4	13.1	3.7	1.05	9.6E-01
B035DRAFT_02772	hypothetical protein	8.4	11.1	8.9	8.3	10.2	4.1	0.75	5.8E-01
B035DRAFT_02773	hypothetical protein	13.8	10.5	10.3	11.3	14.5	5.4	0.84	7.7E-01
B035DRAFT_02774	hypothetical protein	13.2	14.8	11.5	12.1	20.5	16.8	1.23	5.0E-01
B035DRAFT_02775	hypothetical protein	20.1	7.8	9.8	9.9	10.3	4.3	0.66	5.7E-01
B035DRAFT_02776	hypothetical protein	12.7	14.6	13.9	16.6	19.7	10.7	1.11	7.7E-01
B035DRAFT_02777	hypothetical protein	18.6	12.2	16.5	18.4	20.8	5.4	0.82	8.1E-01
B035DRAFT_02778	hypothetical protein	14.8	13.9	13.2	13.8	18.0	6.2	0.83	7.6E-01
B035DRAFT_02779	Site-specific recombinase XerD	155.1	133.2	136.2	165.2	168.5	102.7	1.01	9.9E-01
B035DRAFT_02780	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02781	(tRNA)	44.5	78.8	55.4	50.3	40.3	41.4	0.76	4.0E-01
B035DRAFT_02782	thiamine-monophosphate kinase(EC:2.7.4.16)	432.0	437.2	424.5	352.1	324.3	336.5	0.78	1.5E-02
B035DRAFT_02783	purine nucleoside phosphorylase I, inosine and guanosine-specific(EC:2.4.2.1)	400.0	409.2	373.1	325.9	311.7	338.4	0.83	5.8E-02
B035DRAFT_02784	tetraacyldisaccharide 4''-kinase(EC:2.7.1.130)	177.2	173.2	164.9	145.2	140.2	152.4	0.85	6.2E-02
B035DRAFT_02785	signal peptide peptidase SppA, 67K type(EC:3.4.21.)	321.5	304.4	296.0	274.6	234.8	253.5	0.83	1.1E-01
B035DRAFT_02786	Predicted oxidoreductase related to nitroreductase	578.7	542.1	575.3	531.1	430.3	528.7	0.87	3.3E-01

B035DRAFT_02787	Predicted kinase related to galactokinase and mevalonate kinase	317.6	277.6	310.9	221.4	192.9	164.2	0.63	7.0E-02
B035DRAFT_02788	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02789	Uncharacterized protein involved in exopolysaccharide biosynthesis	145.1	157.7	141.8	144.0	161.2	185.7	1.10	5.1E-01
B035DRAFT_02790	Glycosyltransferases involved in cell wall biogenesis (GT2)	72.2	79.7	72.8	88.2	73.0	99.0	1.15	4.2E-01
B035DRAFT_02791	Glycosyltransferase(EC:2.4.1.) (GT4)	75.3	85.6	89.6	83.6	71.7	98.4	1.01	9.8E-01
B035DRAFT_02792	hypothetical protein	47.6	48.4	53.6	56.0	45.5	67.6	1.12	6.1E-01
B035DRAFT_02793	hypothetical protein	103.5	123.9	120.6	127.3	111.9	143.5	1.10	5.7E-01
B035DRAFT_02794	Glycosyltransferases involved in cell wall biogenesis (GT2)	147.3	173.8	154.1	178.7	157.4	209.0	1.14	4.4E-01
B035DRAFT_02795	Predicted glycosyltransferases (GT2)	134.0	146.7	141.0	137.0	119.3	153.5	0.97	8.3E-01
B035DRAFT_02796	Membrane protein involved in the export of O-antigen and teichoic acid	131.7	156.6	145.5	125.4	117.3	159.8	0.92	6.8E-01
B035DRAFT_02797	Glycosyl transferase (GT11)	122.5	150.3	139.0	136.5	132.5	182.7	1.09	6.9E-01
B035DRAFT_02798	Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis	189.5	209.0	200.5	192.3	196.6	245.1	1.05	7.4E-01
B035DRAFT_02799	Acetyltransferase (isoleucine patch superfamily)	169.2	179.4	160.7	130.3	157.5	190.8	0.93	7.3E-01
B035DRAFT_02800	WxcM-like, C-terminal.	168.5	172.8	149.9	101.1	138.1	150.6	0.78	3.2E-01
B035DRAFT_02801	WxcM-like, C-terminal.	203.6	231.8	204.0	145.3	169.6	180.1	0.77	1.4E-01
B035DRAFT_02802	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	242.7	255.5	263.6	202.1	184.2	224.8	0.80	1.2E-01
B035DRAFT_02803	Transcription antiterminator	505.6	513.2	564.8	473.3	418.9	456.5	0.85	1.5E-01
B035DRAFT_02804	hypothetical protein	95.2	102.9	93.0	60.7	42.5	48.7	0.52	4.2E-02
B035DRAFT_02805	Nucleoside-diphosphate-sugar epimerases(EC:1.1.1.271)	251.4	252.1	225.1	199.1	241.8	225.2	0.91	4.6E-01
B035DRAFT_02806	GDP-mannose 4,6-dehydratase(EC:4.2.1.47)	290.4	280.9	262.3	233.5	274.2	232.5	0.89	3.1E-01
B035DRAFT_02807	Mannose-1-phosphate guanylyltransferase(EC:2.7.7.22)	152.4	165.8	144.4	184.7	197.8	202.2	1.27	6.8E-02
B035DRAFT_02808	glucose-1-phosphate thymidylyltransferase, short form(EC:2.7.7.24)	180.2	185.3	170.5	179.0	177.9	200.9	1.04	6.4E-01
B035DRAFT_02809	dTDP-4-dehydrorhamnose 3,5-epimerase(EC:5.1.3.13)	224.0	269.2	239.4	233.0	245.1	272.9	1.03	8.6E-01
B035DRAFT_02810	Periplasmic protein involved in polysaccharide export	220.1	201.4	206.8	192.2	186.4	140.8	0.82	3.1E-01
B035DRAFT_02811	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	337.4	370.2	301.0	403.8	420.5	388.0	1.21	1.7E-01
B035DRAFT_02812	Sugar transferases involved in lipopolysaccharide synthesis	183.1	208.0	189.0	241.7	219.8	264.8	1.25	1.3E-01
B035DRAFT_02813	Outer membrane protein	77.6	97.6	73.3	87.3	88.9	99.9	1.12	5.2E-01
B035DRAFT_02814	hypothetical protein	44.0	57.0	52.9	51.7	50.1	58.1	1.04	8.1E-01
B035DRAFT_02815	O-Antigen ligase.	31.8	40.4	51.0	49.7	30.1	42.2	0.99	9.8E-01
B035DRAFT_02816	Predicted glycosyltransferases (GT2)	25.4	37.7	40.2	50.1	34.5	38.1	1.20	5.9E-01
B035DRAFT_02817	Glycosyltransferases, probably involved in cell wall biogenesis (GT2)	17.9	14.0	20.5	19.9	15.6	16.2	0.99	9.8E-01
B035DRAFT_02818	hypothetical protein	12.1	16.7	19.8	12.8	11.8	13.0	0.79	3.8E-01
B035DRAFT_02819	Glycosyltransferases, probably involved in cell wall biogenesis (GT2)	6.4	5.5	5.8	6.8	4.6	5.5	0.95	8.1E-01
B035DRAFT_02820	Acetyltransferase (isoleucine patch superfamily)(EC:2.3.1.18)	6.9	4.2	4.0	5.2	6.2	8.0	1.31	4.8E-01
B035DRAFT_02821	hypothetical protein	9.4	7.6	10.2	6.5	9.1	11.4	0.97	9.3E-01
B035DRAFT_02822	Glycosyltransferases involved in cell wall biogenesis (GT2)	21.1	22.6	21.3	17.0	16.4	19.1	0.81	8.8E-02
B035DRAFT_02823	Glycosyltransferases involved in cell wall biogenesis (GT2)	30.3	32.0	40.4	23.7	25.5	21.8	0.70	1.2E-01
B035DRAFT_02824	hypothetical protein	33.2	34.8	32.0	27.7	26.4	23.9	0.78	6.3E-02
B035DRAFT_02825	ABC-type polysaccharide/polyol phosphate transport system, ATPase component	26.8	23.2	20.7	16.0	18.6	13.1	0.67	1.5E-01
B035DRAFT_02826	ABC-type polysaccharide/polyol phosphate export systems, permease component	37.0	30.3	34.7	28.4	35.8	30.4	0.93	6.4E-01
B035DRAFT_02827	Glycosyltransferase (GT4)	45.8	47.8	46.7	50.5	55.8	49.3	1.11	2.1E-01
B035DRAFT_02828	hypothetical protein	76.1	68.1	73.6	86.7	106.9	107.7	1.38	9.0E-02
B035DRAFT_02829	Predicted acyltransferases	6.8	5.7	6.8	8.3	7.8	9.4	1.32	1.3E-01
B035DRAFT_02830	hypothetical protein	1.5	4.4	1.8	2.4	1.4	5.5	1.14	9.0E-01
B035DRAFT_02831	Glycosyltransferase (GT4)	62.2	70.5	64.1	88.2	81.6	75.5	1.25	1.1E-01
B035DRAFT_02832	Glycosyltransferase (GT4)	55.9	54.7	53.1	57.4	63.7	56.0	1.08	3.3E-01

B035DRAFT_02833	Glycosyltransferase (GT4)	47.8	46.7	48.5	57.4	53.2	44.2	1.08	6.0E-01
B035DRAFT_02834	Glycosyltransferase (GT4)	38.7	36.0	45.3	45.5	40.0	42.2	1.07	6.4E-01
B035DRAFT_02835	Glycosyltransferase (GT4)	34.0	41.1	36.2	41.4	29.6	30.8	0.91	6.6E-01
B035DRAFT_02836	Glycosyltransferase (GT4)	26.5	28.8	34.8	26.6	24.3	29.2	0.89	5.1E-01
B035DRAFT_02837	Glycosyltransferase (GT2)	22.3	24.5	24.7	25.1	19.8	24.1	0.96	8.0E-01
B035DRAFT_02838	Glycosyltransferase (GT4)	22.9	27.1	26.2	24.7	16.8	21.1	0.81	3.7E-01
B035DRAFT_02839	Glycosyltransferase (GT2)	39.3	55.8	52.7	54.9	50.0	63.7	1.15	5.6E-01
B035DRAFT_02840	FOG: CheY-like receiver	97.8	137.6	108.6	135.1	133.7	176.1	1.30	3.2E-01
B035DRAFT_02841	His Kinase A (phosphoacceptor) domain./Response regulator receiver domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	121.2	134.0	129.5	147.6	146.7	180.0	1.23	1.8E-01
B035DRAFT_02842	Metal-dependent hydrolase	56.1	63.4	62.1	51.4	52.8	56.5	0.88	2.0E-01
B035DRAFT_02843	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02844	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02845	(miscRNA)	82741.8	73753.8	81225.4	102951.3	112466.6	93360.2	1.30	9.4E-02
B035DRAFT_02846	Beta-glucosidase-related glycosidases(EC:3.2.1.21) (GH3)	10.3	7.5	7.3	9.6	10.0	7.2	1.06	8.3E-01
B035DRAFT_02847	3-carboxymuconate cyclase	64.6	67.3	69.9	83.0	86.0	80.1	1.23	3.3E-02
B035DRAFT_02848	Predicted glycosylase (GH130)	61.8	69.5	69.4	58.5	68.3	57.7	0.92	4.8E-01
B035DRAFT_02849	Exonuclease III	45.1	46.9	45.7	34.3	46.1	50.0	0.93	7.5E-01
B035DRAFT_02850	hypothetical protein	108.6	106.2	109.6	109.0	119.3	110.8	1.04	4.2E-01
B035DRAFT_02851	Alpha-glucosidases, family 31 of glycosyl hydrolases (GH31)	133.2	125.7	122.3	115.1	134.5	112.4	0.95	6.3E-01
B035DRAFT_02852	Na+/proline symporter	102.0	111.3	108.2	81.6	95.5	100.9	0.86	2.7E-01
B035DRAFT_02853	Cytosine/adenosine deaminases	220.0	227.8	211.0	184.9	186.5	200.6	0.87	8.8E-02
B035DRAFT_02854	Phosphomannose isomerase(EC:5.3.1.8)	247.7	251.5	237.1	205.6	251.7	265.0	0.98	8.8E-01
B035DRAFT_02855	hypothetical protein	21.8	20.1	24.3	17.4	17.5	13.9	0.74	1.4E-01
B035DRAFT_02856	Outer membrane receptor proteins, mostly Fe transport	14.4	13.2	14.3	8.7	11.5	9.9	0.72	9.6E-02
B035DRAFT_02857	Threonine aldolase(EC:4.1.2.5)	69.4	78.0	72.0	89.2	86.9	74.0	1.14	3.2E-01
B035DRAFT_02858	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	50.0	60.8	61.6	44.2	43.2	45.4	0.77	1.1E-01
B035DRAFT_02859	hypothetical protein	262.2	283.1	273.6	199.6	226.3	284.3	0.86	4.3E-01
B035DRAFT_02860	proton-translocating NADH-quinone oxidoreductase, chain N(EC:1.6.5.3)	37.9	38.7	37.9	39.9	42.1	44.8	1.11	1.7E-01
B035DRAFT_02861	proton-translocating NADH-quinone oxidoreductase, chain M(EC:1.6.5.3)	37.2	31.5	40.1	37.7	38.2	34.4	1.02	9.1E-01
B035DRAFT_02862	proton-translocating NADH-quinone oxidoreductase, chain L(EC:1.6.5.3)	26.5	25.2	28.8	33.8	30.4	31.2	1.19	1.3E-01
B035DRAFT_02863	NADH:ubiquinone oxidoreductase subunit 11 or 4L (chain K)(EC:1.6.5.3)	18.0	20.3	14.6	15.0	17.3	24.3	1.06	8.8E-01
B035DRAFT_02864	NADH:ubiquinone oxidoreductase subunit 6 (chain J)(EC:1.6.5.3)	24.5	31.9	31.4	33.9	32.8	28.3	1.09	6.6E-01
B035DRAFT_02865	NADH-quinone oxidoreductase, chain I(EC:1.6.5.3)	29.1	28.6	30.4	25.1	27.0	26.1	0.89	8.5E-02
B035DRAFT_02866	NADH:ubiquinone oxidoreductase subunit 1 (chain H)(EC:1.6.5.3)	54.6	50.7	53.6	48.9	46.9	50.3	0.92	1.8E-01
B035DRAFT_02867	NADH:ubiquinone oxidoreductase 49 kD subunit 7(EC:1.6.5.3)	65.1	59.5	59.5	55.7	53.7	36.6	0.78	3.4E-01
B035DRAFT_02868	NADH-quinone oxidoreductase, B subunit(EC:1.6.5.3)	60.3	53.1	59.8	52.0	42.4	39.2	0.77	1.8E-01
B035DRAFT_02869	NADH:ubiquinone oxidoreductase subunit 3 (chain A)(EC:1.6.5.3)	56.8	65.5	71.4	59.3	44.5	48.6	0.78	2.5E-01
B035DRAFT_02870	hypothetical protein	55.0	81.6	75.9	75.2	56.1	90.5	1.04	9.2E-01
B035DRAFT_02871	Trk-type K+ transport systems, membrane components	65.6	76.0	76.9	57.9	65.7	69.7	0.88	3.8E-01
B035DRAFT_02872	K+ transport systems, NAD-binding component	121.2	124.6	120.9	116.6	116.2	114.5	0.95	6.7E-02
B035DRAFT_02873	1-deoxy-D-xylulose-5-phosphate synthase(EC:2.2.1.7)	172.2	163.6	172.5	178.4	162.5	146.8	0.96	6.8E-01
B035DRAFT_02874	GSCFA family	64.2	58.5	62.7	73.9	86.9	78.9	1.29	7.2E-02
B035DRAFT_02875	alanine racemase(EC:5.1.1.1)	171.1	148.2	147.9	231.1	240.0	257.4	1.56	2.5E-02
B035DRAFT_02876	hypothetical protein	63.5	60.2	58.3	166.8	145.5	138.3	2.47	3.9E-03
B035DRAFT_02877	Superfamily I DNA and RNA helicases and helicase subunits	71.2	61.3	62.4	61.0	70.1	55.0	0.95	7.6E-01
B035DRAFT_02878	Zn-dependent protease with chaperone function	46.4	43.0	39.8	38.0	57.7	45.8	1.08	7.4E-01
B035DRAFT_02879	Nitrate/nitrite transporter	34.3	29.1	24.4	28.0	33.2	31.6	1.06	7.7E-01
B035DRAFT_02880	5-keto 4-deoxyuronate isomerase(EC:5.3.1.17)	117.7	76.3	65.3	53.3	68.6	65.0	0.74	4.0E-01
B035DRAFT_02881	Phosphotransferase system, galactitol-specific IIC component	78.9	62.2	47.1	40.2	48.0	58.6	0.79	4.8E-01

B035DRAFT_02882	hypothetical protein	80.4	86.0	74.4	94.8	84.6	87.7	1.11	3.1E-01
B035DRAFT_02883	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_02884	TonB-linked outer membrane protein, SusC/RagA family	72.9	55.7	48.5	37.8	45.2	59.9	0.80	5.0E-01
B035DRAFT_02885	SusD family	63.5	61.5	59.7	35.7	32.5	50.0	0.63	1.2E-01
B035DRAFT_02886	Predicted metal-sulfur cluster biosynthetic enzyme	198.4	204.3	153.0	211.1	236.1	217.6	1.20	3.2E-01
B035DRAFT_02887	Uncharacterized protein conserved in bacteria(EC:3.6.1.)	178.2	190.7	178.0	167.6	208.2	211.3	1.07	6.4E-01
B035DRAFT_02888	Alpha-galactosidase(EC:3.2.1.22) (GH36)	244.9	232.1	241.3	225.3	272.6	254.7	1.04	6.8E-01
B035DRAFT_02889	acetate kinase(EC:2.7.2.1)	475.2	446.7	430.3	341.7	449.4	463.8	0.92	6.5E-01
B035DRAFT_02890	phosphate acetyltransferase(EC:2.3.1.8)	441.5	406.9	358.8	340.7	392.3	384.9	0.93	5.8E-01
B035DRAFT_02891	Putative effector of murein hydrolase LrgA	68.2	86.0	70.8	111.0	106.4	103.2	1.43	6.8E-02
B035DRAFT_02892	Putative effector of murein hydrolase	92.5	82.9	74.4	103.0	115.5	94.2	1.25	2.0E-01
B035DRAFT_02893	Uncharacterized conserved protein	750.9	604.1	592.8	558.9	440.4	277.6	0.63	2.8E-01
B035DRAFT_02894	hypothetical protein	460.4	401.9	434.8	351.2	267.2	209.9	0.63	1.6E-01
B035DRAFT_02895	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase(EC:6.3.2.10)	52.0	62.0	48.1	54.7	47.6	41.7	0.89	5.5E-01
B035DRAFT_02896	dihydropteroate synthase(EC:2.5.1.15)	87.9	92.8	92.2	95.8	94.8	76.1	0.97	8.5E-01
B035DRAFT_02897	TIGR00159 family protein	57.2	59.6	51.1	56.5	65.1	53.4	1.04	7.8E-01
B035DRAFT_02898	hypothetical protein	30.8	26.9	25.8	25.4	31.3	18.9	0.89	6.8E-01
B035DRAFT_02899	Beta-xylosidase (GH43)	57.4	47.1	50.3	57.7	59.8	38.3	0.99	9.8E-01
B035DRAFT_02900	Beta-galactosidase(EC:3.2.1.23) (GH35)	98.2	82.1	87.2	72.4	96.0	67.6	0.87	5.3E-01
B035DRAFT_02901	exonuclease SbcD	91.2	79.9	69.2	60.3	78.0	51.8	0.78	3.6E-01
B035DRAFT_02902	ATPase involved in DNA repair	123.3	106.6	113.4	94.2	105.1	64.0	0.75	3.3E-01
B035DRAFT_02903	DNA-binding protein, histone-like, putative	164.3	182.6	155.0	159.1	162.5	138.3	0.92	4.9E-01
B035DRAFT_02904	Predicted sugar kinase(EC:2.7.1.23)	99.8	107.5	109.8	139.5	117.0	120.5	1.19	1.8E-01
B035DRAFT_02905	pyridoxine 5''-phosphate synthase(EC:2.6.99.2)	191.4	177.9	193.8	257.3	241.9	197.6	1.23	2.2E-01
B035DRAFT_02906	Biopolymer transport proteins	361.9	359.3	400.2	487.3	444.9	328.9	1.11	6.4E-01
B035DRAFT_02907	Biopolymer transport protein	339.9	387.1	488.4	503.0	421.5	377.2	1.08	7.7E-01
B035DRAFT_02908	TonB family C-terminal domain	169.3	115.0	136.8	165.1	146.3	51.5	0.78	7.2E-01
B035DRAFT_02909	DJ-1 family protein	263.8	233.4	239.8	253.9	289.1	160.5	0.93	8.3E-01
B035DRAFT_02910	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase(EC:2.7.7.60)	258.2	232.7	250.1	268.4	277.5	164.5	0.93	8.4E-01
B035DRAFT_02911	ATP-dependent DNA helicase RecG(EC:3.6.4.12)	123.6	119.7	114.7	124.4	135.3	121.7	1.06	3.8E-01
B035DRAFT_02912	Nucleoside diphosphate kinase(EC:2.7.4.6)	952.1	1117.4	1041.5	1017.6	968.5	966.7	0.95	5.7E-01
B035DRAFT_02913	Membrane proteins related to metalloendopeptidases (CBM50)	690.7	752.0	763.6	735.3	677.8	626.7	0.92	4.3E-01
B035DRAFT_02914	Domain of Unknown Function (DUF1599).	338.8	335.2	312.3	319.0	323.2	284.7	0.94	4.6E-01
B035DRAFT_02915	Predicted membrane protein	213.6	242.6	219.1	202.2	221.6	255.0	1.00	9.9E-01
B035DRAFT_02916	triosephosphate isomerase(EC:5.3.1.1)	1815.5	2165.7	1890.2	1646.1	1805.5	2139.2	0.95	7.7E-01
B035DRAFT_02917	Sporulation related domain.	473.6	463.7	455.0	447.1	485.4	488.3	1.02	7.3E-01
B035DRAFT_02918	GTP cyclohydrolase I(EC:3.5.4.16)	454.2	445.0	437.8	438.3	444.7	455.7	1.00	9.7E-01
B035DRAFT_02919	DNA primase, catalytic core(EC:2.7.7.)	114.4	124.5	122.9	151.9	148.8	155.5	1.26	2.3E-02
B035DRAFT_02920	Glycoside hydrolase (GH4)	164.2	168.5	161.9	181.4	141.7	146.8	0.94	6.9E-01
B035DRAFT_02921	hypothetical protein	84.5	93.5	67.8	99.2	109.4	100.3	1.27	2.3E-01
B035DRAFT_02922	hypothetical protein	58.0	47.1	53.1	48.1	51.0	60.1	1.01	9.8E-01
B035DRAFT_02923	hypothetical protein	95.7	90.7	73.5	100.7	81.2	91.3	1.05	7.8E-01
B035DRAFT_02924	hypothetical protein	801.3	828.7	1005.7	1090.3	788.8	762.9	0.99	9.8E-01
B035DRAFT_02925	hypothetical protein	44.5	46.3	66.5	54.8	53.4	59.1	1.08	7.5E-01
B035DRAFT_02926	Predicted phosphohydrolases	48.0	52.3	45.5	46.9	36.4	45.6	0.88	4.3E-01
B035DRAFT_02927	1-acyl-sn-glycerol-3-phosphate acyltransferases(EC:2.3.1.51)	142.0	153.9	152.3	150.2	157.4	173.3	1.07	4.4E-01
B035DRAFT_02928	hypothetical protein	374.2	417.0	400.0	499.9	459.2	486.2	1.21	6.8E-02
B035DRAFT_02929	Peptidase S46.	131.3	123.4	104.3	92.5	110.8	114.3	0.88	4.8E-01
B035DRAFT_02930	Peptidase S46.	195.5	162.3	153.9	144.9	170.7	155.6	0.92	6.2E-01
B035DRAFT_02931	hypothetical protein	233.7	254.4	244.3	312.6	289.9	284.8	1.21	6.1E-02

B035DRAFT_02932	Septum formation initiator	176.3	177.2	148.8	207.2	188.2	145.8	1.07	7.7E-01
B035DRAFT_02933	DNA polymerase III, subunit gamma and tau(EC:2.7.7.7)	155.5	158.2	155.4	152.0	171.2	162.6	1.03	5.9E-01
B035DRAFT_02934	7-cyano-7-deazaguanine reductase(EC:1.7.1.13)	177.1	169.7	157.3	156.8	167.9	181.1	1.00	9.8E-01
B035DRAFT_02935	queuosine biosynthesis protein QueC	144.5	120.4	147.4	113.9	125.4	103.8	0.83	2.7E-01
B035DRAFT_02936	conserved hypothetical integral membrane protein	148.3	161.5	159.2	125.8	134.4	126.3	0.82	4.9E-02
B035DRAFT_02937	endonuclease III(EC:4.2.99.18)	92.2	98.6	80.9	79.4	81.7	85.9	0.91	4.2E-01
B035DRAFT_02938	Metal-dependent hydrolases of the beta-lactamase superfamily I	165.9	191.6	190.3	139.1	175.3	163.0	0.87	3.6E-01
B035DRAFT_02939	UDP-N-acetylenolpyruvoylglucosamine reductase(EC:1.1.1.158)	161.9	164.4	154.9	112.9	140.3	100.7	0.73	1.5E-01
B035DRAFT_02940	hypothetical protein	142.4	153.0	145.9	120.0	131.8	118.6	0.84	7.9E-02
B035DRAFT_02941	phenylalanyl-tRNA synthetase, alpha subunit(EC:6.1.1.20)	674.4	717.2	652.6	585.9	546.8	579.7	0.84	6.2E-02
B035DRAFT_02942	Arabinose efflux permease	246.3	236.7	250.8	202.0	200.2	210.9	0.84	2.5E-02
B035DRAFT_02943	hypothetical protein	259.2	254.1	253.0	202.7	216.2	218.9	0.83	2.7E-02
B035DRAFT_02944	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase(EC:4.1.3.38)	143.3	162.6	135.7	104.5	144.1	138.3	0.87	5.0E-01
B035DRAFT_02945	Anthranilate/para-aminobenzoate synthases component I(EC:2.6.1.85)	213.6	226.7	204.1	164.1	225.3	203.9	0.91	6.1E-01
B035DRAFT_02946	Polysaccharide lyase family 8, super-sandwich domain./Polysaccharide lyase family 8, N terminal alpha-helical domain (PL8)	217.0	200.8	180.9	111.7	184.4	144.6	0.72	2.8E-01
B035DRAFT_02947	hypothetical protein	259.9	268.1	233.7	156.7	193.7	161.9	0.67	6.1E-02
B035DRAFT_02948	(tRNA)	68.0	89.3	74.7	80.8	61.6	55.8	0.85	5.1E-01
B035DRAFT_02949	Bacterial capsule synthesis protein PGA_cap.	99.9	98.0	97.0	98.5	135.0	118.4	1.18	3.3E-01
B035DRAFT_02950	transcription-repair coupling factor (mfd)(EC:3.6.4.)	156.1	147.4	148.1	147.4	186.0	144.4	1.05	7.5E-01
B035DRAFT_02951	Predicted membrane protein	52.9	54.7	57.6	54.6	64.4	77.4	1.18	3.9E-01
B035DRAFT_02952	Tetratricopeptide repeat.	168.8	171.6	166.1	170.1	163.7	203.5	1.06	6.6E-01
B035DRAFT_02953	hypothetical protein	126.2	144.3	128.8	154.9	180.0	207.7	1.35	1.5E-01
B035DRAFT_02954	aspartate-alanine antiporter	1056.7	916.0	975.4	949.9	686.2	664.3	0.77	2.7E-01
B035DRAFT_02955	aspartate 4-decarboxylase(EC:4.1.1.12)	967.2	883.2	994.9	1026.5	769.2	723.2	0.88	5.2E-01
B035DRAFT_02956	hypothetical protein	60.5	68.6	71.1	47.0	43.2	53.3	0.72	8.5E-02
B035DRAFT_02957	hypothetical protein	40.1	46.7	58.3	40.5	34.9	36.5	0.78	2.7E-01
B035DRAFT_02958	hypothetical protein	20.2	18.5	15.5	16.8	12.5	24.1	0.96	9.2E-01
B035DRAFT_02959	hypothetical protein	15.6	16.0	23.3	15.1	18.5	29.4	1.12	8.0E-01
B035DRAFT_02960	ATPase components of ABC transporters with duplicated ATPase domains	408.7	403.9	369.7	305.9	329.6	296.0	0.79	5.7E-02
B035DRAFT_02961	Molecular chaperone GrpE (heat shock protein)	473.7	432.1	398.6	425.2	400.7	409.4	0.95	5.9E-01
B035DRAFT_02962	chaperone protein DnaJ	474.6	414.9	398.9	385.7	358.6	314.2	0.82	2.2E-01
B035DRAFT_02963	folylpolyglutamate synthase/dihydrofolate synthase(EC:6.3.2.12,EC:6.3.2.17)	92.0	82.2	90.6	71.4	71.4	83.1	0.85	2.0E-01
B035DRAFT_02964	Galactose mutarotase and related enzymes(EC:5.1.3.3)	279.2	316.0	279.1	354.8	399.7	477.8	1.40	1.2E-01
B035DRAFT_02965	Fucose permease	582.3	632.8	647.7	660.1	734.2	910.6	1.23	2.9E-01
B035DRAFT_02966	galactokinase(EC:2.7.1.6)	975.1	1019.6	1011.6	1036.8	1113.5	1367.3	1.16	3.4E-01
B035DRAFT_02967	hypothetical protein	78.6	65.5	84.9	91.1	109.3	159.0	1.54	2.4E-01
B035DRAFT_02968	hypothetical protein	16.4	20.1	20.0	16.1	18.8	16.2	0.91	5.2E-01
B035DRAFT_02969	DNA gyrase, B subunit(EC:5.99.1.3)	780.5	739.3	726.5	712.4	755.0	620.0	0.93	5.0E-01
B035DRAFT_02970	4-alpha-glucanotransferase(EC:2.4.1.25) (CBM20)	36.8	36.3	38.1	35.8	39.3	38.8	1.02	6.9E-01
B035DRAFT_02971	Major Facilitator Superfamily	46.4	57.4	52.9	61.2	59.3	56.7	1.13	3.2E-01
B035DRAFT_02972	hypothetical protein	50.1	51.8	45.3	50.7	58.3	54.6	1.11	3.2E-01
B035DRAFT_02973	Glycosidases (GH13)	4.5	3.6	4.9	8.2	5.3	5.7	1.46	2.4E-01
B035DRAFT_02974	Glycoside hydrolase 97.(EC:3.2.1.20) (GH97)	40.5	42.3	38.6	52.5	34.6	35.4	0.99	9.8E-01
B035DRAFT_02975	**TonB-linked outer membrane protein, SusC**	**39.9**	**36.2**	**38.0**	**54.3**	**36.7**	**43.9**	**1.17**	**4.6E-01**
B035DRAFT_02976	SusD family	22.7	20.0	20.5	35.3	22.9	32.4	1.41	2.2E-01
B035DRAFT_02977	hypothetical protein	22.6	23.6	25.8	50.6	39.3	37.7	1.76	4.9E-02
B035DRAFT_02978	hypothetical protein	18.0	13.3	17.9	40.0	30.5	25.7	1.95	9.0E-02
B035DRAFT_02979	1,4-alpha-glucan branching enzyme (GH13)	7.0	7.0	7.1	9.9	9.2	5.7	1.14	6.8E-01

B035DRAFT_02980	RNA-binding proteins (RRM domain)	4063.3	4055.1	3913.0	4344.1	3659.2	2517.8	0.85	5.9E-01
B035DRAFT_02981	hypothetical protein	38.4	43.6	28.0	29.6	24.7	27.9	0.76	3.1E-01
B035DRAFT_02982	hypothetical protein	111.5	119.2	111.6	106.1	110.7	120.3	0.98	8.5E-01
B035DRAFT_02983	Protein of unknown function (DUF3109).	198.2	209.2	209.4	180.0	211.3	199.2	0.96	6.2E-01
B035DRAFT_02984	2,3-bisphosphoglycerate-independent phosphoglycerate mutase(EC:5.4.2.1)	788.8	821.2	749.6	664.2	756.6	807.0	0.94	6.0E-01
B035DRAFT_02985	hypothetical protein	20.1	19.4	16.3	25.2	26.8	19.3	1.27	3.0E-01
B035DRAFT_02986	Transcriptional regulators	33.1	42.0	39.6	216.8	270.5	350.4	7.20	6.7E-03
B035DRAFT_02987	L-fucose isomerase(EC:5.3.1.25)	165.4	155.8	162.6	493.6	656.4	562.2	3.52	3.8E-03
B035DRAFT_02988	L-fucose:H+ symporter permease	33.0	39.3	48.5	107.3	143.2	178.1	3.52	3.3E-02
B035DRAFT_02989	hypothetical protein	30.1	29.1	30.1	21.3	30.4	47.3	1.05	9.2E-01
B035DRAFT_02990	hypothetical protein	37.0	48.0	38.5	38.7	46.9	49.9	1.10	6.4E-01
B035DRAFT_02991	hypothetical protein	64.6	77.9	78.0	79.2	95.0	86.5	1.18	2.9E-01
B035DRAFT_02992	Ribonuclease HII(EC:3.1.26.4)	46.8	53.8	47.8	43.7	45.2	44.3	0.90	2.3E-01
B035DRAFT_02993	Membrane protein of unknown function (DUF340).	28.2	31.3	29.2	27.1	24.4	19.6	0.80	2.5E-01
B035DRAFT_02994	Predicted membrane protein	56.6	55.4	62.4	45.5	50.8	56.5	0.87	3.2E-01
B035DRAFT_02995	cysteine desulfurases, SufSfamily(EC:2.8.1.7,EC:4.4.1.16)	568.4	508.6	557.3	500.3	487.6	405.1	0.85	2.6E-01
B035DRAFT_02996	FeS assembly protein SufD	538.4	492.8	509.9	408.8	456.1	423.2	0.84	8.2E-02
B035DRAFT_02997	FeS assembly ATPase SufC	547.2	475.4	488.9	406.9	438.8	371.1	0.80	1.4E-01
B035DRAFT_02998	FeS assembly protein SufB	392.5	345.4	345.8	282.5	311.3	264.0	0.79	1.1E-01
B035DRAFT_02999	Uncharacterized membrane protein, required for colicin V production	173.3	184.3	155.4	116.8	174.4	158.1	0.87	5.4E-01
B035DRAFT_03000	translation initiation factor IF-2	912.6	856.3	845.1	797.3	945.0	706.2	0.93	6.5E-01
B035DRAFT_03001	transcription termination factor NusA	754.2	746.7	687.6	627.0	760.2	723.2	0.96	7.5E-01
B035DRAFT_03002	Uncharacterized protein conserved in bacteria	536.7	519.9	449.3	389.1	454.8	261.4	0.72	3.2E-01
B035DRAFT_03003	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03004	hypothetical protein	60.4	58.3	50.4	43.6	42.6	41.9	0.76	6.8E-02
B035DRAFT_03005	Site-specific recombinase XerD	61.6	51.2	58.0	39.6	47.4	34.7	0.71	1.4E-01
B035DRAFT_03006	Site-specific recombinase XerD	67.4	69.9	81.0	45.7	49.9	34.1	0.59	8.9E-02
B035DRAFT_03007	Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain	86.8	90.3	74.7	47.1	43.7	41.5	0.53	1.7E-02
B035DRAFT_03008	Uncharacterized protein conserved in bacteria	32.1	30.5	31.1	30.8	29.2	27.2	0.93	3.2E-01
B035DRAFT_03009	Uncharacterized proteins of the AP superfamily	14.6	11.1	12.8	12.3	14.0	9.6	0.92	7.5E-01
B035DRAFT_03010	Glycosyl Hydrolase (GH88)	8.6	8.1	9.5	6.5	9.6	9.5	0.96	8.8E-01
B035DRAFT_03011	Heparinase II/III-like protein (PL12)	6.7	4.4	6.3	4.8	4.9	5.4	0.88	5.9E-01
B035DRAFT_03012	SusD family	7.2	8.4	6.8	5.2	6.2	6.9	0.81	2.9E-01
B035DRAFT_03013	TonB-linked outer membrane protein, SusC/RagA family	12.7	12.3	12.4	7.9	8.8	8.3	0.67	7.4E-03
B035DRAFT_03014	Site-specific recombinases, DNA invertase Pin homologs	30.2	31.9	27.8	24.3	24.2	31.9	0.89	5.1E-01
B035DRAFT_03015	TonB-linked outer membrane protein, SusC/RagA family	17.1	15.0	15.0	10.7	9.2	10.4	0.64	3.3E-02
B035DRAFT_03016	SusD family	10.4	9.4	9.4	6.0	6.5	7.0	0.67	3.2E-02
B035DRAFT_03017	Signal transduction histidine kinase	74.2	93.7	83.5	83.0	91.9	118.4	1.16	5.1E-01
B035DRAFT_03018	hypothetical protein	238.4	323.6	280.5	339.0	362.5	501.2	1.42	2.4E-01
B035DRAFT_03019	Transcriptional regulators	299.3	380.1	328.4	452.0	451.1	591.0	1.48	1.3E-01
B035DRAFT_03020	hypothetical protein	76.7	97.5	93.9	97.9	102.5	119.0	1.19	3.2E-01
B035DRAFT_03021	Hemolysins and related proteins containing CBS domains	41.9	51.1	50.3	70.7	66.2	82.3	1.53	7.2E-02
B035DRAFT_03022	NTP pyrophosphohydrolases containing a Zn-finger, probably nucleic-acid-binding	52.4	47.9	45.8	69.4	116.4	67.8	1.68	1.7E-01
B035DRAFT_03023	Uncharacterized protein conserved in bacteria	117.5	107.6	105.3	167.8	200.1	194.8	1.70	2.2E-02
B035DRAFT_03024	Outer membrane receptor proteins, mostly Fe transport	133.6	123.2	128.3	185.2	220.9	226.2	1.64	2.8E-02
B035DRAFT_03025	DNA topoisomerase I, bacterial(EC:5.99.1.2)	431.6	424.4	419.6	464.3	516.6	417.1	1.09	4.4E-01
B035DRAFT_03026	Shikimate kinase(EC:2.7.1.71)	316.4	335.8	321.2	293.0	350.6	282.6	0.95	6.7E-01
B035DRAFT_03027	arginine decarboxylase, biosynthetic(EC:4.1.1.19)	315.3	333.3	314.0	294.0	332.8	323.9	0.99	8.7E-01

B035DRAFT_03028	acetylglutamate kinase(EC:2.7.2.8,EC:2.7.2.)	199.7	191.3	193.9	187.0	209.9	119.4	0.86	6.3E-01
B035DRAFT_03029	RNA polymerase sigma factor, sigma-70 family	750.6	683.6	671.1	1152.8	1146.1	634.0	1.34	4.2E-01
B035DRAFT_03030	hypothetical protein	564.5	539.5	542.9	815.9	863.5	585.4	1.36	2.2E-01
B035DRAFT_03031	Protein of unknown function (DUF2807).	144.7	150.1	153.1	195.4	174.7	233.2	1.34	1.3E-01
B035DRAFT_03032	Predicted metal-dependent hydrolase	62.3	65.5	72.9	74.7	69.7	40.9	0.90	7.6E-01
B035DRAFT_03033	hypothetical protein	18.5	20.0	16.6	19.8	23.0	26.6	1.26	2.6E-01
B035DRAFT_03034	hypothetical protein	30.7	37.7	41.5	32.3	32.5	55.8	1.07	8.7E-01
B035DRAFT_03035	Lanthionine synthetase C-like protein.	42.5	43.9	34.3	44.6	46.6	55.4	1.22	3.2E-01
B035DRAFT_03036	natural product precursor, GG-Bacteroidales family	52.8	63.8	57.5	54.2	53.6	49.9	0.91	3.8E-01
B035DRAFT_03037	hypothetical protein	22.5	26.3	23.4	16.1	23.4	23.0	0.85	5.1E-01
B035DRAFT_03038	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03039	riboflavin kinase/FMN adenylyltransferase(EC:2.7.7.2,EC:2.7.1.26)	190.6	225.1	231.7	239.2	223.1	265.0	1.12	4.1E-01
B035DRAFT_03040	haloacid dehalogenase superfamily, subfamily IA, variant 3 with third motif having DD or ED	171.9	201.5	176.1	178.7	201.9	235.2	1.12	5.1E-01
B035DRAFT_03041	plasma-membrane calcium-translocating P-type ATPase(EC:3.6.3.8)	184.5	165.9	168.5	218.7	223.8	183.1	1.20	2.1E-01
B035DRAFT_03042	(tRNA)	125.0	229.5	304.3	258.7	192.9	175.5	1.00	1.0E+00
B035DRAFT_03043	hypothetical protein	26.9	28.6	23.2	19.3	22.4	22.7	0.82	2.3E-01
B035DRAFT_03044	hypothetical protein	13.3	14.3	13.2	13.1	12.8	18.2	1.07	7.6E-01
B035DRAFT_03045	hypothetical protein	2.8	0.0	0.0	0.0	1.3	2.6	0.64	
B035DRAFT_03046	hypothetical protein	6.6	7.0	3.5	4.2	6.5	7.0	1.06	9.1E-01
B035DRAFT_03047	hypothetical protein	1.6	2.3	1.0	0.8	1.1	1.4	0.72	5.3E-01
B035DRAFT_03048	hypothetical protein	1.2	0.9	1.3	1.4	1.8	0.7	1.09	8.8E-01
B035DRAFT_03049	hypothetical protein	88.2	67.8	82.5	29.4	21.8	35.6	0.36	4.0E-02
B035DRAFT_03050	hypothetical protein	9.3	3.6	12.8	4.6	6.2	5.6	0.72	6.4E-01
B035DRAFT_03051	hypothetical protein	4.0	3.1	1.6	1.4	2.4	4.9	0.94	9.4E-01
B035DRAFT_03052	Site-specific recombinase XerC	4.3	5.0	4.8	2.1	4.1	3.1	0.64	2.6E-01
B035DRAFT_03053	hypothetical protein	1.8	2.1	4.4	1.9	1.6	3.3	0.85	8.1E-01
B035DRAFT_03054	hypothetical protein	9.4	6.3	8.2	1.8	3.4	5.8	0.42	2.3E-01
B035DRAFT_03055	hypothetical protein	14.6	19.1	16.2	15.3	10.9	20.7	0.92	8.2E-01
B035DRAFT_03056	hypothetical protein	24.7	20.4	19.2	19.3	16.3	21.8	0.89	5.7E-01
B035DRAFT_03057	hypothetical protein	9.1	7.6	7.5	12.3	11.5	9.2	1.36	1.8E-01
B035DRAFT_03058	hypothetical protein	6.8	7.4	6.2	6.2	8.4	8.9	1.14	5.7E-01
B035DRAFT_03059	hypothetical protein	6.7	3.4	2.7	7.8	6.0	7.4	1.78	2.9E-01
B035DRAFT_03060	Cell division protein FtsI/penicillin-binding protein 2	11.7	7.7	7.9	10.3	6.9	11.0	1.03	9.4E-01
B035DRAFT_03061	hypothetical protein	6.1	8.1	6.3	5.7	3.7	8.0	0.81	6.4E-01
B035DRAFT_03062	hypothetical protein	54.0	57.2	57.5	95.2	101.2	127.1	1.90	3.0E-02
B035DRAFT_03063	Uncharacterized conserved protein	31.7	40.0	32.4	48.2	50.3	57.6	1.50	7.9E-02
B035DRAFT_03064	ORF6N domain.	48.6	52.4	36.6	54.3	45.4	51.4	1.11	6.4E-01
B035DRAFT_03065	hypothetical protein	23.0	8.9	17.1	18.9	10.4	15.1	0.95	9.3E-01
B035DRAFT_03066	TonB-linked outer membrane protein, SusC/RagA family	63.8	65.0	62.5	34.6	52.1	63.6	0.76	4.1E-01
B035DRAFT_03067	SusD family	50.1	44.5	45.7	26.6	43.8	55.7	0.86	7.1E-01
B035DRAFT_03068	F5/8 type C domain (CBM32)	97.0	84.3	84.9	46.5	87.7	92.2	0.82	6.2E-01
B035DRAFT_03069	Uncharacterized protein conserved in bacteria	67.8	65.5	61.4	49.9	67.0	69.0	0.95	7.8E-01
B035DRAFT_03070	thioredoxin	404.8	331.8	362.0	370.6	383.0	400.1	1.05	6.4E-01
B035DRAFT_03071	hypothetical protein	960.0	837.8	1041.1	1274.8	1002.3	767.4	1.05	8.7E-01
B035DRAFT_03072	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	140.4	150.6	143.9	167.5	153.1	148.4	1.08	3.4E-01
B035DRAFT_03073	Signal transduction histidine kinase	50.6	56.9	53.3	68.1	65.9	74.7	1.30	6.1E-02
B035DRAFT_03074	hypothetical protein	42.0	40.0	29.2	56.0	43.5	20.8	1.01	9.9E-01
B035DRAFT_03075	hypothetical protein	92.6	108.2	117.0	169.5	106.4	91.6	1.12	7.6E-01
B035DRAFT_03076	SufE protein probably involved in Fe-S center assembly	163.0	161.1	153.3	197.3	153.8	188.6	1.12	4.2E-01

B035DRAFT_03077	Predicted aminopeptidases	130.9	118.6	112.9	111.5	115.5	91.0	0.87	4.0E-01
B035DRAFT_03078	Zn-dependent dipeptidase, microsomal dipeptidase homolog	55.8	50.2	49.2	52.9	55.0	41.1	0.95	8.0E-01
B035DRAFT_03079	Phosphotransacetylase(EC:2.3.1.19)	76.2	67.6	80.3	137.1	114.4	96.8	1.54	1.0E-01
B035DRAFT_03080	butyrate kinase(EC:2.7.2.7)	129.1	99.2	134.1	139.3	131.4	94.0	1.00	1.0E+00
B035DRAFT_03081	hypothetical protein	1385.7	1343.0	1265.2	1148.4	1211.9	1191.6	0.89	1.1E-01
B035DRAFT_03082	hypothetical protein	763.9	960.0	907.1	1116.9	1103.2	1499.1	1.41	1.8E-01
B035DRAFT_03083	hypothetical protein	16.1	15.6	22.8	9.9	8.5	21.9	0.69	5.1E-01
B035DRAFT_03084	hypothetical protein	101.5	114.0	102.8	111.5	111.3	114.9	1.06	3.9E-01
B035DRAFT_03085	Transposase and inactivated derivatives	93.4	112.9	96.4	84.4	93.2	91.1	0.89	3.5E-01
B035DRAFT_03086	(tRNA)	335.7	425.5	397.9	275.9	108.0	51.2	0.30	2.2E-01
B035DRAFT_03087	tryptophanyl-tRNA synthetase(EC:6.1.1.2)	289.1	302.9	284.4	285.0	298.3	293.9	1.00	9.8E-01
B035DRAFT_03088	hypothetical protein	131.5	171.2	158.1	291.8	278.8	352.1	2.00	3.6E-02
B035DRAFT_03089	hypothetical protein	64.2	95.9	106.8	113.0	109.2	155.9	1.43	3.2E-01
B035DRAFT_03090	carbamoyl-phosphate synthase, large subunit(EC:6.3.5.5)	250.3	263.2	253.8	228.5	240.1	253.8	0.94	3.4E-01
B035DRAFT_03091	hypothetical protein	24.4	27.2	25.2	33.0	19.3	36.2	1.11	7.8E-01
B035DRAFT_03092	hypothetical protein	22.7	20.0	20.1	21.0	21.8	34.3	1.20	5.3E-01
B035DRAFT_03093	ABC-type uncharacterized transport system, ATPase component	47.7	59.7	47.5	43.3	47.9	42.5	0.87	3.6E-01
B035DRAFT_03094	ABC-type Na+ efflux pump, permease component	85.5	81.0	91.6	73.6	95.1	82.4	0.97	8.5E-01
B035DRAFT_03095	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	131.5	136.4	126.8	199.1	199.8	237.2	1.61	2.5E-02
B035DRAFT_03096	Peroxiredoxin	173.6	179.1	167.8	370.6	344.2	438.5	2.20	1.2E-02
B035DRAFT_03097	Uncharacterized protein conserved in bacteria	71.0	74.9	79.5	65.8	55.0	67.0	0.83	2.0E-01
B035DRAFT_03098	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	2870.4	2509.4	2779.9	2552.8	2287.6	2642.8	0.92	4.2E-01
B035DRAFT_03099	DNA mismatch repair protein MutL	311.3	308.2	301.3	317.7	370.2	354.0	1.13	2.0E-01
B035DRAFT_03100	hypothetical protein	296.3	279.0	269.9	301.2	370.2	356.2	1.21	1.8E-01
B035DRAFT_03101	hypothetical protein	230.8	245.0	228.8	245.3	277.2	313.4	1.18	2.5E-01
B035DRAFT_03102	Parvulin-like peptidyl-prolyl isomerase(EC:5.2.1.8)	501.1	508.6	467.9	539.9	595.9	532.5	1.13	1.9E-01
B035DRAFT_03103	hypothetical protein	267.2	275.8	262.5	305.1	318.2	309.2	1.16	2.5E-02
B035DRAFT_03104	Parvulin-like peptidyl-prolyl isomerase(EC:5.2.1.8)	201.1	204.1	191.6	175.8	223.6	185.5	0.98	8.7E-01
B035DRAFT_03105	inosine-5''-monophosphate dehydrogenase(EC:1.1.1.205)	1126.2	1223.4	1175.0	1200.8	1241.6	1090.8	1.00	9.9E-01
B035DRAFT_03106	Lysophospholipase L1 and related esterases (CE3)	29.4	26.1	27.4	26.1	31.1	26.4	1.01	9.6E-01
B035DRAFT_03107	Antirepressor regulating drug resistance, predicted signal transduction N-terminal membrane component	101.3	97.8	106.5	122.3	116.7	92.4	1.08	6.5E-01
B035DRAFT_03108	Predicted transcriptional regulator	112.6	106.2	91.5	111.6	121.4	115.2	1.13	3.4E-01
B035DRAFT_03109	ATP-dependent DNA helicase RecQ(EC:3.6.4.12)	677.1	641.2	617.7	608.7	675.4	684.9	1.02	8.6E-01
B035DRAFT_03110	endopeptidase Clp ATP-binding regulatory subunit (clpX)	673.3	638.0	667.4	583.8	639.6	673.9	0.96	5.9E-01
B035DRAFT_03111	Protease subunit of ATP-dependent Clp proteases(EC:3.4.21.92)	742.1	678.2	691.6	652.0	704.8	755.0	1.00	9.9E-01
B035DRAFT_03112	trigger factor	1555.3	1601.7	1367.2	1287.3	1436.9	1566.4	0.95	6.9E-01
B035DRAFT_03113	hypothetical protein	13862.3	14929.7	16669.1	20112.8	11843.4	14675.8	1.00	9.9E-01
B035DRAFT_03114	RNA-binding proteins (RRM domain)	16345.5	19536.1	20602.4	23771.5	14848.4	19115.7	1.01	9.8E-01
B035DRAFT_03115	ABC-type (unclassified) transport system, ATPase component(EC:3.6.3.)	146.4	176.1	158.5	215.8	189.9	174.9	1.21	2.5E-01
B035DRAFT_03116	ABC-type transport system involved in resistance to organic solvents, permease component	275.8	300.7	292.8	255.3	248.9	297.4	0.92	4.5E-01
B035DRAFT_03117	ABC-type transport system involved in resistance to organic solvents, ATPase component	184.4	197.6	196.0	177.8	205.5	237.5	1.07	6.8E-01
B035DRAFT_03118	hypothetical protein	78.0	115.8	110.7	93.5	87.4	101.4	0.94	8.0E-01
B035DRAFT_03119	ribosome-associated GTPase EngA	890.3	887.7	821.0	731.2	887.5	877.2	0.96	7.3E-01
B035DRAFT_03120	GTP-binding protein Era	971.4	963.8	905.4	809.1	916.5	1054.1	0.97	8.6E-01
B035DRAFT_03121	3-oxoacyl-(acyl-carrier-protein) synthase III(EC:2.3.1.180)	2533.9	2655.5	2514.1	2270.9	2362.7	2847.3	0.97	8.0E-01
B035DRAFT_03122	ribosomal protein L32	3551.0	4302.0	3402.7	4022.1	3516.2	3748.9	1.01	9.7E-01
B035DRAFT_03123	Predicted metal-binding, possibly nucleic acid-binding protein	1247.6	1506.6	1296.1	1281.1	1167.7	1350.7	0.94	6.3E-01

B035DRAFT_03124	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.8E-01
B035DRAFT_03125	(rRNA)	897.0	1338.4	1075.0	1026.1	1182.8	1554.6		6.8E-01
B035DRAFT_03126	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03127	hypothetical protein	37.2	47.2	50.8	72.6	65.3	78.0	1.61	8.0E-02
B035DRAFT_03128	Predicted P-loop ATPase and inactivated derivatives	95.5	94.8	84.2	102.1	110.4	98.6	1.13	2.3E-01
B035DRAFT_03129	Predicted thioesterase	143.9	120.4	144.8	155.4	157.2	80.1	0.92	8.5E-01
B035DRAFT_03130	Glycoside hydrolase (GH110)	27.3	26.0	29.9	26.7	34.4	31.3	1.11	5.1E-01
B035DRAFT_03131	Beta-galactosidase (GH35)	9.2	9.5	9.4	10.8	10.7	10.9	1.15	2.8E-03
B035DRAFT_03132	Beta-galactosidase/beta-glucuronidase (GH2)	5.5	5.0	5.5	5.0	5.3	5.7	1.00	9.7E-01
B035DRAFT_03133	Beta-galactosidase/beta-glucuronidase (GH2)	5.3	6.0	5.0	4.5	5.8	4.1	0.87	5.2E-01
B035DRAFT_03134	hypothetical protein	5.1	2.4	2.5	2.2	0.9	1.9	0.50	3.1E-01
B035DRAFT_03135	hypothetical protein	52.5	62.8	61.3	65.6	76.4	69.9	1.20	2.1E-01
B035DRAFT_03136	aconitate hydratase, mitochondrial(EC:4.2.1.3)	962.1	552.9	427.5	518.5	359.1	430.1	0.71	4.6E-01
B035DRAFT_03137	Isocitrate dehydrogenases(EC:1.1.1.42)	655.1	327.6	232.5	279.6	221.4	220.0	0.65	4.5E-01
B035DRAFT_03138	Citrate synthase(EC:2.3.3.1)	688.9	353.1	209.7	224.9	228.7	266.7	0.65	4.9E-01
B035DRAFT_03139	Predicted membrane protein(EC:1.3.99.5)	289.7	159.7	119.8	119.2	157.5	161.1	0.82	6.9E-01
B035DRAFT_03140	NADH:flavin oxidoreductases, Old Yellow Enzyme family	125.8	61.0	60.1	57.0	66.0	50.4	0.74	5.2E-01
B035DRAFT_03141	Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases)	176.0	129.1	146.6	100.9	105.5	96.3	0.68	8.6E-02
B035DRAFT_03142	Predicted permeases	70.2	63.4	64.1	67.9	67.9	59.2	0.99	9.0E-01
B035DRAFT_03143	hypothetical protein	141.2	158.1	132.8	156.2	204.7	212.0	1.32	2.1E-01
B035DRAFT_03144	hypothetical protein	139.5	150.0	147.5	136.0	143.3	166.9	1.02	8.9E-01
B035DRAFT_03145	Predicted membrane protein	486.5	519.6	523.4	417.3	293.8	398.9	0.72	1.7E-01
B035DRAFT_03146	haloacid dehalogenase superfamily, subfamily IA, variant 1 with third motif having Dx(3-4)D or Dx(3-4)E(EC:3.1.3.18)	51.1	52.8	46.7	63.9	60.9	57.8	1.21	8.9E-02
B035DRAFT_03147	Nitroreductase	38.8	42.7	44.7	54.7	58.7	52.7	1.32	5.9E-02
B035DRAFT_03148	hypothetical protein	11.0	7.7	8.9	12.3	11.9	15.3	1.44	1.8E-01
B035DRAFT_03149	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, gamma subunit(EC:4.1.1.3)	144.1	152.7	146.8	182.8	174.4	165.7	1.18	6.5E-02
B035DRAFT_03150	Pyruvate/oxaloacetate carboxyltransferase(EC:6.4.1.1)	172.6	158.6	164.0	168.5	201.2	156.7	1.06	6.9E-01
B035DRAFT_03151	sodium ion-translocating decarboxylase, beta subunit(EC:4.1.1.3)	210.3	206.7	206.1	177.1	235.6	252.6	1.06	7.9E-01
B035DRAFT_03152	Enoyl-[acyl-carrier-protein] reductase (NADH)(EC:1.3.1.9)	825.7	848.6	839.5	646.0	679.4	755.1	0.83	9.0E-02
B035DRAFT_03153	hypothetical protein	538.2	540.0	496.0	386.1	400.9	424.2	0.77	3.5E-02
B035DRAFT_03154	Predicted methyltransferases(EC:2.1.1.198)	203.2	212.0	212.3	140.5	170.5	162.2	0.75	7.0E-02
B035DRAFT_03155	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	134.5	137.2	137.2	109.1	143.1	148.9	0.97	8.8E-01
B035DRAFT_03156	hypothetical protein	13.7	16.4	14.9	14.9	9.2	17.8	0.90	7.8E-01
B035DRAFT_03157	hypothetical protein	8.8	9.1	10.2	7.9	12.3	12.6	1.14	6.4E-01
B035DRAFT_03158	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03159	Uncharacterized conserved protein	164.8	182.3	178.1	220.2	213.1	261.2	1.32	9.8E-02
B035DRAFT_03160	hypothetical protein	64.8	88.4	104.5	87.4	93.2	103.6	1.12	6.7E-01
B035DRAFT_03161	Site-specific recombinase XerD	14.5	16.8	17.1	14.4	17.9	19.1	1.05	7.8E-01
B035DRAFT_03162	Uncharacterized conserved protein	46.4	48.1	44.0	53.4	53.4	65.4	1.24	1.7E-01
B035DRAFT_03163	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	43.6	49.7	44.5	38.8	45.2	51.4	0.98	9.0E-01
B035DRAFT_03164	cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases	40.7	35.5	39.7	24.0	27.2	38.7	0.76	3.3E-01
B035DRAFT_03165	Acetyltransferases	59.8	80.0	71.8	89.7	78.3	110.9	1.31	2.9E-01
B035DRAFT_03166	hypothetical protein	67.3	71.6	73.5	89.8	93.6	117.6	1.41	1.0E-01
B035DRAFT_03167	hypothetical protein	51.1	58.5	70.0	73.6	79.6	100.5	1.41	2.0E-01
B035DRAFT_03168	hypothetical protein	40.6	54.7	58.6	66.6	54.7	77.6	1.29	3.6E-01
B035DRAFT_03169	hypothetical protein	22.1	28.1	19.6	24.7	18.8	26.2	1.00	1.0E+00

B035DRAFT_03170	hypothetical protein	25.3	22.0	22.0	18.2	20.4	30.0	0.97	9.2E-01
B035DRAFT_03171	hypothetical protein	22.8	32.4	24.1	14.4	19.3	20.7	0.69	2.3E-01
B035DRAFT_03172	hypothetical protein	40.6	44.5	40.5	31.1	36.4	27.1	0.75	1.5E-01
B035DRAFT_03173	Relaxase/Mobilisation nuclease domain.	32.6	22.2	26.1	21.0	28.4	12.0	0.72	5.2E-01
B035DRAFT_03174	Bacterial mobilisation protein (MobC).	20.7	10.7	26.2	14.4	15.6	6.4	0.63	5.1E-01
B035DRAFT_03175	DNA primase (bacterial type)	36.4	29.7	31.3	28.3	34.9	23.2	0.88	5.9E-01
B035DRAFT_03176	hypothetical protein	47.7	42.1	40.4	40.2	40.1	27.7	0.82	4.2E-01
B035DRAFT_03177	DNA binding domain, excisionase family	45.8	51.1	40.7	37.0	50.5	36.2	0.89	6.2E-01
B035DRAFT_03178	hypothetical protein	68.9	76.9	84.3	60.3	64.2	82.6	0.89	5.8E-01
B035DRAFT_03179	(tRNA)	64.1	128.7	186.7	167.6	86.2	30.0	0.66	7.0E-01
B035DRAFT_03180	Mannose-1-phosphate guanylyltransferase(EC:2.7.7.22)	173.1	205.0	180.2	223.3	260.2	346.0	1.46	1.9E-01
B035DRAFT_03181	Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT family hydrolases	931.8	986.9	1094.9	1210.3	1037.5	1329.2	1.18	3.1E-01
B035DRAFT_03182	transcription elongation factor GreA	1440.4	1484.3	1415.0	1750.3	1636.6	1663.3	1.16	4.2E-02
B035DRAFT_03183	Glutathione peroxidase	140.8	173.3	145.4	168.1	176.6	206.0	1.20	2.9E-01
B035DRAFT_03184	polyribonucleotide nucleotidyltransferase(EC:2.7.7.8)	1778.4	1693.3	1644.6	1744.0	1666.7	1795.4	1.02	7.7E-01
B035DRAFT_03185	Rubredoxin	324.5	367.7	246.7	396.6	371.2	277.3	1.12	7.1E-01
B035DRAFT_03186	Site-specific recombinase XerD	17.6	12.3	16.2	15.0	15.4	7.4	0.79	6.2E-01
B035DRAFT_03187	hypothetical protein	12.8	8.7	13.6	8.1	9.9	4.0	0.60	3.7E-01
B035DRAFT_03188	DNA binding domain, excisionase family	13.9	5.8	10.9	12.9	11.9	2.0	0.71	7.8E-01
B035DRAFT_03189	hypothetical protein	3.6	2.2	2.5	2.2	3.3	0.7	0.64	6.1E-01
B035DRAFT_03190	hypothetical protein	6.6	2.3	3.2	5.0	4.5	0.9	0.74	8.0E-01
B035DRAFT_03191	Topoisomerase IA(EC:5.99.1.2)	6.0	3.5	6.6	7.0	5.8	1.7	0.78	8.0E-01
B035DRAFT_03192	Domain of unknown function (DUF1896).	27.0	20.6	33.1	37.3	30.9	11.0	0.88	8.8E-01
B035DRAFT_03193	Helicase conserved C-terminal domain./SNF2 family N-terminal domain./N-6 DNA Methylase.	8.5	5.2	8.8	10.1	9.0	3.2	0.90	9.0E-01
B035DRAFT_03194	hypothetical protein(EC:5.3.3.1)	98.5	117.4	112.0	146.8	154.7	178.7	1.46	6.8E-02
B035DRAFT_03195	Acetyltransferases	38.5	51.4	48.5	56.8	59.2	81.8	1.42	2.3E-01
B035DRAFT_03196	small GTP-binding protein domain	89.8	93.5	88.8	93.2	93.6	108.1	1.08	4.1E-01
B035DRAFT_03197	Signal transduction histidine kinase	73.9	58.8	64.0	70.0	71.4	52.8	0.98	9.4E-01
B035DRAFT_03198	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	64.2	50.5	60.5	57.1	49.5	23.6	0.70	4.8E-01
B035DRAFT_03199	ribosomal protein S20	5896.4	8782.4	6976.7	5458.2	4080.4	4330.5	0.64	1.6E-01
B035DRAFT_03200	(tRNA)	221.4	338.0	221.9	88.7	89.2	53.3	0.29	5.2E-02
B035DRAFT_03201	DNA repair protein RecO	54.2	60.6	65.7	74.2	62.4	57.3	1.07	6.9E-01
B035DRAFT_03202	Uncharacterized conserved protein	889.7	813.4	740.5	952.0	849.7	613.7	0.97	9.3E-01
B035DRAFT_03203	cell division protein FtsZ	225.7	211.5	193.6	206.5	231.1	176.2	0.97	8.6E-01
B035DRAFT_03204	cell division protein FtsA	214.7	199.3	182.7	207.3	223.2	219.4	1.09	3.7E-01
B035DRAFT_03205	hypothetical protein	172.8	179.9	149.8	170.4	177.6	199.7	1.09	5.1E-01
B035DRAFT_03206	UDP-N-acetylmuramate--alanine ligase(EC:6.3.2.8)	226.5	235.4	230.4	222.1	243.3	271.7	1.06	5.8E-01
B035DRAFT_03207	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase(EC:2.4.1.227) (GT28)	190.1	218.8	192.8	215.2	215.9	199.7	1.05	6.0E-01
B035DRAFT_03208	Bacterial cell division membrane protein	271.5	282.7	285.5	309.7	289.8	309.0	1.08	1.7E-01
B035DRAFT_03209	UDP-N-acetylmuramoylalanine--D-glutamate ligase(EC:6.3.2.9)	251.4	264.3	239.0	235.4	267.8	288.4	1.05	7.1E-01
B035DRAFT_03210	phospho-N-acetylmuramoyl-pentapeptide-transferase(EC:2.7.8.13)	230.6	245.7	224.8	246.9	245.8	289.6	1.11	3.4E-01
B035DRAFT_03211	UDP-N-acetylmuramyl-tripeptide synthetase(EC:6.3.2.13)	269.2	266.5	261.2	303.5	297.1	334.0	1.17	8.5E-02
B035DRAFT_03212	Cell division protein FtsI/penicillin-binding protein 2(EC:2.4.1.129)	171.9	187.6	168.1	201.7	199.3	212.1	1.16	9.9E-02
B035DRAFT_03213	hypothetical protein	116.2	125.2	102.2	136.9	145.4	175.9	1.33	1.7E-01
B035DRAFT_03214	S-adenosyl-methyltransferase MraW(EC:2.1.1.199)	261.8	264.2	250.7	328.1	316.3	318.5	1.24	1.1E-02
B035DRAFT_03215	Uncharacterized protein conserved in bacteria	250.3	282.5	243.6	328.5	333.6	283.6	1.22	1.8E-01
B035DRAFT_03216	Putative hemolysin	276.4	310.7	286.6	224.5	237.3	253.4	0.82	9.2E-02

B035DRAFT_03217	hypothetical protein	219.9	272.4	249.3	184.0	203.7	235.7	0.84	3.3E-01
B035DRAFT_03218	deoxyguanosinetriphosphate triphosphohydrolase, putative(EC:3.1.5.1)	59.5	62.7	65.3	68.5	65.0	65.1	1.06	3.4E-01
B035DRAFT_03219	deoxyuridine 5''-triphosphate nucleotidohydrolase (dut)(EC:3.6.1.23)	69.5	84.4	74.7	109.1	115.8	75.9	1.30	3.3E-01
B035DRAFT_03220	hypothetical protein	174.2	179.8	196.2	257.7	241.1	211.0	1.29	1.1E-01
B035DRAFT_03221	hypothetical protein	186.4	183.5	184.0	239.4	233.7	181.7	1.17	3.4E-01
B035DRAFT_03222	Membrane-bound metallopeptidase	135.2	125.0	136.4	161.7	154.7	117.5	1.08	6.7E-01
B035DRAFT_03223	hypothetical protein	39.6	59.0	57.6	65.8	67.5	46.1	1.15	6.7E-01
B035DRAFT_03224	hypothetical protein	53.2	48.5	49.0	55.4	61.4	50.8	1.11	3.7E-01
B035DRAFT_03225	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases(EC:3.5.1.16)	140.8	142.3	130.9	146.6	149.5	151.4	1.08	1.8E-01
B035DRAFT_03226	Long-chain acyl-CoA synthetases (AMP-forming)(EC:6.2.1.3)	434.2	448.1	414.4	338.1	386.5	399.2	0.86	2.0E-01
B035DRAFT_03227	Protein chain release factor B	270.7	265.0	229.6	199.0	245.8	180.0	0.81	3.0E-01
B035DRAFT_03228	hypothetical protein	158.7	154.7	147.9	138.8	187.9	161.7	1.05	7.7E-01
B035DRAFT_03229	Uncharacterized protein conserved in bacteria	61.9	61.0	46.3	59.3	68.3	64.6	1.14	4.7E-01
B035DRAFT_03230	Outer membrane receptor proteins, mostly Fe transport	176.7	191.2	196.1	187.9	237.5	273.8	1.23	3.4E-01
B035DRAFT_03231	RNA polymerase sigma factor, sigma-70 family	2274.4	2610.0	2288.4	2971.9	2346.7	3224.3	1.18	3.9E-01
B035DRAFT_03232	VanZ like family	260.2	265.9	267.7	254.6	210.9	311.8	0.97	8.8E-01
B035DRAFT_03233	Na+-dependent transporters of the SNF family	286.7	291.5	302.7	264.1	235.4	279.4	0.88	2.3E-01
B035DRAFT_03234	hypothetical protein	195.9	218.2	221.4	226.1	181.1	236.8	1.01	9.7E-01
B035DRAFT_03235	Alkaline phosphatase(EC:3.1.3.1)	118.0	123.3	108.6	126.5	126.3	134.3	1.11	2.3E-01
B035DRAFT_03236	hypothetical protein	28.0	34.9	30.8	22.7	30.0	25.7	0.84	3.5E-01
B035DRAFT_03237	hypothetical protein	67.8	66.1	63.6	82.0	72.1	46.7	0.99	9.8E-01
B035DRAFT_03238	hypothetical protein	5.1	3.3	4.1	7.7	5.1	7.2	1.60	2.0E-01
B035DRAFT_03239	(tRNA)	817.2	1324.1	1725.0	1009.3	496.6	296.7	0.43	2.9E-01
B035DRAFT_03240	Predicted esterase of the alpha-beta hydrolase superfamily	9.7	10.6	11.8	17.4	16.5	22.7	1.75	6.4E-02
B035DRAFT_03241	Molecular chaperone, HSP90 family	213.5	205.6	196.2	231.7	235.7	319.9	1.27	2.6E-01
B035DRAFT_03242	ATPases with chaperone activity, ATP-binding subunit	157.0	138.4	141.3	177.1	176.9	214.9	1.30	1.3E-01
B035DRAFT_03243	hypothetical protein	0.0	0.0	1.4	0.0	1.1	1.1	0.75	
B035DRAFT_03244	DNA gyrase, A subunit(EC:5.99.1.3)	509.0	523.4	536.2	516.7	552.4	614.0	1.07	4.7E-01
B035DRAFT_03245	hypothetical protein	1036.6	1118.2	1007.5	916.0	942.1	1233.7	0.97	8.8E-01
B035DRAFT_03246	Universal stress protein UspA and related nucleotide-binding proteins	150.4	163.8	165.1	167.9	145.8	212.2	1.09	6.9E-01
B035DRAFT_03247	hypothetical protein	252.5	310.7	260.5	363.5	422.9	506.1	1.56	1.0E-01
B035DRAFT_03248	Membrane-associated phospholipid phosphatase	115.7	135.6	130.4	142.2	129.3	187.8	1.19	4.3E-01
B035DRAFT_03249	Tetratricopeptide repeat.	265.8	314.2	307.7	354.5	368.6	469.2	1.34	1.8E-01
B035DRAFT_03250	hypothetical protein	229.2	242.5	232.7	278.4	287.0	329.7	1.27	8.2E-02
B035DRAFT_03251	Tetratricopeptide repeat.	233.6	224.9	207.6	251.4	301.9	297.7	1.27	1.2E-01
B035DRAFT_03252	Mg-chelatase subunit ChlD	272.5	274.7	257.6	322.3	339.0	384.9	1.30	7.4E-02
B035DRAFT_03253	Mg-chelatase subunit ChlD	233.7	241.6	249.8	268.3	272.5	290.4	1.15	8.0E-02
B035DRAFT_03254	hypothetical protein	349.6	374.8	383.4	409.1	407.4	449.4	1.14	1.5E-01
B035DRAFT_03255	Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain)	461.7	452.8	487.7	544.3	523.6	564.5	1.16	6.6E-02
B035DRAFT_03256	MoxR-like ATPases(EC:3.6.3.)	575.3	575.7	568.2	709.2	704.3	764.5	1.27	1.9E-02
B035DRAFT_03257	Bacterial nucleoid DNA-binding protein (CBM50)	209.5	213.0	191.8	178.4	203.1	212.8	0.97	7.7E-01
B035DRAFT_03258	Bacterial nucleoid DNA-binding protein	213.5	232.3	211.6	181.7	203.6	231.7	0.93	6.3E-01
B035DRAFT_03259	ribosomal protein S12 methylthiotransferase RimO(EC:2.)	293.2	313.7	305.6	260.6	289.2	312.6	0.94	5.6E-01
B035DRAFT_03260	signal recognition particle-docking protein FtsY	300.5	309.5	277.7	258.3	254.7	287.4	0.90	2.9E-01
B035DRAFT_03261	hypothetical protein	2536.0	3341.9	2698.6	2373.3	2082.9	2826.4	0.85	4.6E-01
B035DRAFT_03262	ribosomal protein L33, bacterial type	5103.5	5797.4	4115.4	4023.2	3711.5	4598.4	0.83	3.8E-01
B035DRAFT_03263	ribosomal protein L28	4669.7	5176.9	3420.4	3673.7	3181.6	3608.1	0.80	3.6E-01
B035DRAFT_03264	competence/damage-inducible protein CinA C-terminal domain	152.4	149.3	125.1	132.4	159.5	140.7	1.01	9.3E-01
B035DRAFT_03265	putative glycoprotease GCP(EC:3.4.24.57)	186.5	201.0	190.6	189.2	191.4	235.7	1.06	6.6E-01

B035DRAFT_03266	methionine aminopeptidase, type I(EC:3.4.11.18)	207.1	209.9	191.4	228.0	231.4	239.7	1.15	8.3E-02
B035DRAFT_03267	Predicted P-loop ATPase and inactivated derivatives	100.0	76.8	101.6	118.0	98.0	44.7	0.87	8.2E-01
B035DRAFT_03268	hypothetical protein	62.1	63.9	76.1	67.2	63.1	73.3	1.01	9.5E-01
B035DRAFT_03269	CRISPR-associated endoribonuclease Cas2	78.4	66.8	55.1	37.3	46.3	65.4	0.73	3.8E-01
B035DRAFT_03270	CRISPR-associated endonuclease Cas1	83.5	71.5	76.8	60.2	63.7	64.5	0.81	8.9E-02
B035DRAFT_03271	CRISPR-associated protein Cas4	92.1	87.6	88.3	83.6	89.2	86.4	0.97	4.6E-01
B035DRAFT_03272	CRISPR-associated protein Cas7/Csd2, subtype I-C/DVULG	101.9	107.5	94.0	92.5	100.7	90.5	0.94	4.7E-01
B035DRAFT_03273	CRISPR-associated protein Cas8c/Csd1, subtype I-C/DVULG	74.5	85.7	75.0	58.4	60.7	78.8	0.84	3.6E-01
B035DRAFT_03274	CRISPR-associated protein Cas5, subtype I-C/DVULG	85.7	91.2	76.7	68.1	77.9	72.4	0.86	2.4E-01
B035DRAFT_03275	CRISPR-associated helicase Cas3/CRISPR-associated endonuclease Cas3-HD	82.7	87.2	79.7	67.4	74.0	79.6	0.88	2.5E-01
B035DRAFT_03276	hypothetical protein	21.0	25.8	25.6	20.6	24.1	20.8	0.91	5.2E-01
B035DRAFT_03277	hypothetical protein	1468.8	1520.1	1357.5	1369.8	1447.6	1631.3	1.02	8.6E-01
B035DRAFT_03278	hypothetical protein	69.2	57.0	62.5	64.7	67.0	45.5	0.93	7.7E-01
B035DRAFT_03279	hypothetical protein	14.1	10.5	5.5	4.7	9.7	6.1	0.70	5.8E-01
B035DRAFT_03280	hypothetical protein	9.9	4.9	6.4	4.8	4.8	3.2	0.62	3.1E-01
B035DRAFT_03281	hypothetical protein	8.4	6.0	5.7	3.0	3.4	2.1	0.42	7.2E-02
B035DRAFT_03282	hypothetical protein	24.3	20.6	21.2	20.4	22.8	17.8	0.92	6.0E-01
B035DRAFT_03283	hypothetical protein	19.9	16.0	19.9	16.5	17.3	12.9	0.83	4.0E-01
B035DRAFT_03284	hypothetical protein	15.2	7.1	9.3	8.8	15.2	8.3	1.04	9.5E-01
B035DRAFT_03285	hypothetical protein	5.7	7.2	4.1	5.5	4.8	6.9	1.03	9.5E-01
B035DRAFT_03286	hypothetical protein	5.3	2.9	4.6	3.2	3.5	2.8	0.76	4.4E-01
B035DRAFT_03287	Rhomboid family	4.6	2.3	4.4	3.1	3.5	4.7	1.05	9.3E-01
B035DRAFT_03288	hypothetical protein	7.8	2.7	5.2	7.0	3.9	6.4	1.16	8.3E-01
B035DRAFT_03289	hypothetical protein	1.9	0.7	0.3	0.9	0.4	0.4	0.71	7.8E-01
B035DRAFT_03290	hypothetical protein	2.2	1.9	2.1	1.1	3.2	1.4	0.81	7.3E-01
B035DRAFT_03291	hypothetical protein	1.7	1.6	1.6	1.1	0.3	0.9	0.41	2.5E-01
B035DRAFT_03292	hypothetical protein	1.3	1.5	0.6	0.3	1.0	0.5	0.46	3.5E-01
B035DRAFT_03293	hypothetical protein	9.2	7.6	8.5	8.7	7.7	5.4	0.84	5.4E-01
B035DRAFT_03294	Phage-related protein	67.1	63.2	59.6	80.9	71.0	73.9	1.19	1.4E-01
B035DRAFT_03295	Predicted transcriptional regulator with C-terminal CBS domains	88.3	90.6	76.4	107.2	105.5	95.0	1.21	1.7E-01
B035DRAFT_03296	Reverse transcriptase (RNA-dependent DNA polymerase).	94.0	91.7	87.4	95.9	92.5	89.9	1.02	7.2E-01
B035DRAFT_03297	hypothetical protein	320.9	318.8	290.7	343.4	376.0	353.9	1.15	1.3E-01
B035DRAFT_03298	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03299	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03300	(tRNA)	341.1	448.8	528.6	473.4	213.8	118.6	0.53	4.1E-01
B035DRAFT_03301	(tRNA)	341.1	448.8	528.6	473.4	213.8	118.6	0.53	4.1E-01
B035DRAFT_03302	Activator of Hsp90 ATPase homolog 1-like protein.	462.9	439.5	395.4	331.9	315.0	349.8	0.77	7.0E-02
B035DRAFT_03303	Predicted permeases	243.2	246.2	239.9	232.4	207.9	244.5	0.94	4.6E-01
B035DRAFT_03304	GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase(EC:4.1.99.12,EC:3.5.4.25)	271.7	279.9	262.9	305.6	310.2	286.8	1.11	1.3E-01
B035DRAFT_03305	Aspartate/tyrosine/aromatic aminotransferase(EC:2.6.1.1)	331.8	414.4	346.7	386.2	433.3	450.0	1.16	3.3E-01
B035DRAFT_03306	hypothetical protein	4961.1	7935.2	8109.6	7300.4	6137.8	7198.2	1.00	9.9E-01
B035DRAFT_03307	Beta-glucosidase-related glycosidases (GH3)	99.3	94.1	101.7	108.9	112.8	91.4	1.06	6.6E-01
B035DRAFT_03308	ribosomal protein L19, bacterial type	6342.3	6755.1	5966.3	6101.3	5452.9	6134.4	0.93	4.3E-01
B035DRAFT_03309	Uncharacterized conserved protein(EC:5.1.3.)	163.7	180.3	164.4	168.7	207.7	189.7	1.11	4.0E-01
B035DRAFT_03310	Transcriptional regulator/sugar kinase(EC:2.7.1.2)	147.3	175.1	174.7	164.6	194.0	192.9	1.11	4.6E-01
B035DRAFT_03311	ABC-type antimicrobial peptide transport system, ATPase component	56.3	55.1	50.2	62.7	71.2	81.5	1.33	1.3E-01
B035DRAFT_03312	ABC-type antimicrobial peptide transport system, permease component	37.3	29.6	32.5	44.1	54.3	48.5	1.48	8.2E-02
B035DRAFT_03313	ABC-type antimicrobial peptide transport system, permease component	28.4	28.5	30.4	40.9	50.7	49.8	1.61	3.6E-02
B035DRAFT_03314	RND family efflux transporter, MFP subunit	30.3	25.6	25.6	45.0	60.0	51.0	1.91	3.8E-02

B035DRAFT_03315	Outer membrane protein	37.0	34.8	33.5	43.8	61.1	66.8	1.61	1.2E-01
B035DRAFT_03316	hypothetical protein	16.0	16.7	16.4	17.8	14.2	16.1	0.98	8.6E-01
B035DRAFT_03317	hypothetical protein	10.3	12.4	13.5	13.4	11.9	9.0	0.94	8.1E-01
B035DRAFT_03318	RNA polymerase sigma factor, sigma-70 family	17.0	17.7	16.3	19.1	17.6	23.0	1.16	3.3E-01
B035DRAFT_03319	hypothetical protein	47.4	45.8	49.1	49.1	44.3	53.5	1.03	8.0E-01
B035DRAFT_03320	Uncharacterized protein conserved in bacteria	302.8	300.2	267.2	287.0	325.5	235.1	0.97	8.7E-01
B035DRAFT_03321	Uncharacterized oxidoreductases, Fe-dependent alcohol dehydrogenase family(EC:1.1.)	433.3	359.6	396.9	564.3	558.3	519.7	1.38	5.4E-02
B035DRAFT_03322	hypothetical protein	547.5	585.6	601.3	742.5	628.0	696.2	1.19	1.6E-01
B035DRAFT_03323	Protein of unknown function (DUF1812).	323.8	301.5	328.8	376.6	343.0	342.7	1.11	2.0E-01
B035DRAFT_03324	ABC-type antimicrobial peptide transport system, ATPase component(EC:3.6.3.)	230.1	233.0	263.2	266.5	220.6	166.8	0.89	6.4E-01
B035DRAFT_03325	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 1	110.7	102.9	106.9	93.2	95.9	68.6	0.80	2.8E-01
B035DRAFT_03326	Kef-type K+ transport systems, membrane components	106.4	101.3	98.8	86.3	103.1	77.5	0.87	3.6E-01
B035DRAFT_03327	aspartate-semialdehyde dehydrogenase (peptidoglycan organisms)(EC:1.2.1.11)	704.4	801.6	778.5	735.2	733.2	759.7	0.98	7.6E-01
B035DRAFT_03328	FKBP-type peptidyl-prolyl cis-trans isomerases 1	1048.0	1089.0	1153.7	1217.5	1168.0	1183.8	1.09	2.0E-01
B035DRAFT_03329	glycyl-tRNA synthetase, dimeric type(EC:6.1.1.14)	668.8	679.6	668.1	715.2	705.8	750.8	1.08	1.1E-01
B035DRAFT_03330	Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit(EC:5.99.1.)	107.5	107.4	106.4	133.2	135.7	152.0	1.31	3.7E-02
B035DRAFT_03331	Protein of unknown function (DUF3316).	73.7	88.4	80.7	83.4	82.2	101.6	1.10	5.4E-01
B035DRAFT_03332	Periplasmic protease	73.8	80.7	79.9	77.7	77.2	96.1	1.07	6.5E-01
B035DRAFT_03333	(tRNA)	164.8	220.3	263.2	321.0	112.0	58.0	0.60	5.9E-01
B035DRAFT_03334	Signal transduction histidine kinase	86.9	88.1	85.7	81.3	78.3	99.3	0.99	9.3E-01
B035DRAFT_03335	AraC-type DNA-binding domain-containing proteins	66.9	77.6	77.2	77.4	77.5	87.9	1.10	4.3E-01
B035DRAFT_03336	membrane protein, MarC family	37.5	46.3	37.6	37.8	39.4	46.4	1.02	9.2E-01
B035DRAFT_03337	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.9E-01
B035DRAFT_03338	**TonB-linked outer membrane protein, SusC/RagA family**	**76.7**	**69.6**	**66.3**	**140.4**	**212.1**	**230.6**	**2.69**	**4.1E-02**
B035DRAFT_03339	SusD family	84.0	89.7	82.5	211.2	315.3	380.2	3.44	3.0E-02
B035DRAFT_03340	alpha-1,2-mannosidase, putative (GH92)	123.6	103.3	117.4	140.2	146.4	117.9	1.17	3.2E-01
B035DRAFT_03341	Peptide-N-glycosidase F, N terminal./Peptide-N-glycosidase F, C terminal.	145.7	127.9	158.9	191.3	140.0	70.3	0.86	7.9E-01
B035DRAFT_03342	hypothetical protein	113.6	121.6	160.3	100.6	112.1	107.8	0.82	3.3E-01
B035DRAFT_03343	glutamate 5-kinase(EC:2.7.2.11)	163.8	118.8	146.5	170.6	156.8	58.7	0.82	7.7E-01
B035DRAFT_03344	gamma-glutamyl phosphate reductase(EC:1.2.1.41)	214.4	160.3	226.4	194.2	150.9	57.3	0.60	4.7E-01
B035DRAFT_03345	Ornithine carbamoyltransferase(EC:2.1.3.11)	285.5	275.2	291.0	281.9	272.1	172.1	0.83	5.2E-01
B035DRAFT_03346	Transposase and inactivated derivatives	53.9	49.9	58.4	47.1	48.3	52.4	0.91	3.7E-01
B035DRAFT_03347	Rhodanese-related sulfurtransferase	104.6	112.2	90.2	107.9	95.9	87.7	0.95	7.6E-01
B035DRAFT_03348	hypothetical protein	278.4	327.6	384.1	483.4	350.7	316.2	1.15	6.2E-01
B035DRAFT_03349	hypothetical protein	76.7	82.6	78.6	75.7	93.8	85.6	1.07	5.8E-01
B035DRAFT_03350	D-alanine--D-alanine ligase(EC:6.3.2.4)	85.2	90.6	80.7	72.0	93.3	97.6	1.02	9.3E-01
B035DRAFT_03351	pseudouridine synthase, RluA family(EC:5.4.99.23)	115.4	118.3	100.7	91.2	112.9	84.2	0.86	4.1E-01
B035DRAFT_03352	Uncharacterized protein conserved in bacteria	104.2	115.6	90.6	80.6	105.9	70.1	0.82	4.3E-01
B035DRAFT_03353	Uncharacterized conserved protein	159.9	149.5	141.9	139.9	144.3	137.1	0.93	3.4E-01
B035DRAFT_03354	Arylsulfatase A and related enzymes	99.5	109.5	105.9	118.7	125.5	146.8	1.24	1.6E-01
B035DRAFT_03355	N-acetyl-beta-hexosaminidase(EC:3.2.1.52) (GH20)	118.8	116.5	107.6	119.8	129.5	95.0	1.00	9.9E-01
B035DRAFT_03356	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	101.5	91.8	93.8	100.6	118.2	91.2	1.07	6.3E-01
B035DRAFT_03357	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	188.1	160.9	168.3	175.6	182.8	132.6	0.94	7.8E-01
B035DRAFT_03358	anaerobic sulfatase-maturating enzyme	90.8	84.1	78.0	92.5	100.2	86.9	1.11	3.7E-01
B035DRAFT_03359	ribosomal protein L34, bacterial type	1249.6	1679.2	1054.1	1463.6	1038.5	1265.6	0.95	8.9E-01
B035DRAFT_03360	hypothetical protein	84.5	134.4	46.9	113.9	69.8	74.1	1.03	9.6E-01

B035DRAFT_03361	translation elongation factor P	972.1	1233.9	1059.7	757.4	676.2	752.2	0.67	6.2E-02
B035DRAFT_03362	Glycosyltransferases, probably involved in cell wall biogenesis (GT2)	124.0	131.7	124.2	127.9	134.1	98.2	0.94	7.4E-01
B035DRAFT_03363	DNA repair protein radc	81.5	79.4	81.3	61.1	73.9	70.1	0.84	1.7E-01
B035DRAFT_03364	Highly conserved protein containing a thioredoxin domain (GH88)	72.5	81.2	81.7	85.7	87.7	86.1	1.10	2.2E-01
B035DRAFT_03365	hypothetical protein	5.4	7.6	9.2	2.3	6.9	4.9	0.59	4.2E-01
B035DRAFT_03366	hypothetical protein	95.1	94.3	92.4	252.2	242.8	271.4	2.72	3.3E-04
B035DRAFT_03367	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03368	Transposase DDE domain.	208.0	227.9	251.6	140.2	128.0	154.4	0.61	4.0E-02
B035DRAFT_03369	hypothetical protein	48.8	51.3	42.5	16.1	18.1	24.1	0.40	3.3E-02
B035DRAFT_03370	Saccharopine dehydrogenase and related proteins	36.5	30.1	27.5	8.4	13.3	12.0	0.35	3.9E-02
B035DRAFT_03371	Saccharopine dehydrogenase and related proteins	20.1	22.6	15.2	8.0	9.0	7.6	0.43	3.5E-02
B035DRAFT_03372	hypothetical protein	11.3	14.1	9.9	2.2	4.2	6.8	0.34	1.5E-01
B035DRAFT_03373	Methylase involved in ubiquinone/menaquinone biosynthesis	17.2	23.0	23.8	7.4	8.9	12.2	0.44	7.4E-02
B035DRAFT_03374	hypothetical protein	13.5	15.1	15.8	7.1	6.1	8.2	0.48	2.6E-02
B035DRAFT_03375	hypothetical protein	6.6	6.5	5.6	4.6	2.9	2.4	0.51	1.3E-01
B035DRAFT_03376	ABC-type multidrug transport system, ATPase and permease components	12.6	15.0	12.6	4.7	5.6	7.2	0.43	4.2E-02
B035DRAFT_03377	ABC-type multidrug transport system, ATPase and permease components	15.1	15.8	16.7	8.9	9.0	9.4	0.57	3.0E-03
B035DRAFT_03378	hypothetical protein	111.8	131.6	131.6	131.7	117.8	169.3	1.11	6.4E-01
B035DRAFT_03379	Predicted ATP-binding protein involved in virulence	211.1	205.1	196.9	225.9	243.6	334.3	1.29	2.8E-01
B035DRAFT_03380	hypothetical protein	9.8	16.5	16.0	10.7	10.6	16.1	0.89	7.7E-01
B035DRAFT_03381	Methylase involved in ubiquinone/menaquinone biosynthesis	43.5	47.0	47.5	41.6	39.8	64.3	1.03	9.2E-01
B035DRAFT_03382	Site-specific recombinase XerD	9.5	7.6	9.8	5.6	6.2	8.3	0.74	2.9E-01
B035DRAFT_03383	DNA primase (bacterial type)	6.1	4.5	4.5	3.5	4.1	3.2	0.72	1.8E-01
B035DRAFT_03384	hypothetical protein	15.1	9.2	16.7	11.1	11.2	9.6	0.80	5.2E-01
B035DRAFT_03385	hypothetical protein	6.7	5.8	4.1	3.5	3.0	6.6	0.76	5.9E-01
B035DRAFT_03386	hypothetical protein	2.9	0.7	2.8	3.0	4.2	1.0	1.35	8.1E-01
B035DRAFT_03387	Orotate phosphoribosyltransferase	5.0	5.2	7.4	7.4	5.5	2.0	0.75	7.1E-01
B035DRAFT_03388	hypothetical protein	5.2	4.7	4.9	3.6	6.3	3.7	0.89	7.3E-01
B035DRAFT_03389	Uncharacterized conserved protein	167.0	134.8	193.6	192.2	150.7	37.5	0.63	6.2E-01
B035DRAFT_03390	PRTRC system ThiF family protein	82.5	69.7	111.9	77.0	68.3	23.5	0.58	4.5E-01
B035DRAFT_03391	hypothetical protein	23.6	22.7	29.3	30.1	18.5	9.8	0.71	5.6E-01
B035DRAFT_03392	hypothetical protein	7.0	4.2	5.9	7.5	5.2	3.2	0.89	8.4E-01
B035DRAFT_03393	PRTRC system protein C	2.3	2.7	0.9	4.8	0.0	0.0	2.71	
B035DRAFT_03394	PRTRC system protein E	5.5	4.8	7.5	4.2	5.6	2.2	0.64	4.2E-01
B035DRAFT_03395	hypothetical protein	34.6	24.3	35.2	28.8	24.1	17.5	0.74	3.9E-01
B035DRAFT_03396	hypothetical protein	42.0	37.8	33.8	35.9	24.4	18.0	0.67	3.1E-01
B035DRAFT_03397	Topoisomerase IA(EC:5.99.1.2)	30.3	16.5	26.2	26.7	20.6	4.6	0.58	6.0E-01
B035DRAFT_03398	hypothetical protein	20.8	12.1	15.6	18.7	11.7	3.9	0.60	5.6E-01
B035DRAFT_03399	hypothetical protein	20.5	14.9	15.9	15.4	14.0	5.9	0.64	4.4E-01
B035DRAFT_03400	hypothetical protein	21.4	19.7	24.8	16.9	16.3	21.2	0.82	3.3E-01
B035DRAFT_03401	Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains	34.2	27.1	31.0	29.8	29.3	15.8	0.78	5.4E-01
B035DRAFT_03402	Signal transduction histidine kinase	37.0	32.5	27.2	26.4	28.0	17.3	0.73	3.5E-01
B035DRAFT_03403	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03404	Laminin G domain.	37.6	36.8	34.1	43.2	48.7	39.2	1.20	2.0E-01
B035DRAFT_03405	DNA/RNA endonuclease G, NUC1	54.7	57.2	46.7	68.8	60.1	42.4	1.06	8.5E-01
B035DRAFT_03406	Alpha-L-fucosidase(EC:3.2.1.51) (GH29)	111.7	96.4	110.9	118.9	127.3	91.0	1.05	8.3E-01
B035DRAFT_03407	Uncharacterized protein conserved in bacteria (CBM9)	175.1	164.1	174.9	181.9	182.0	126.6	0.94	8.0E-01
B035DRAFT_03408	hypothetical protein	41.7	49.3	40.6	45.4	56.1	37.9	1.05	8.5E-01
B035DRAFT_03409	(tRNA)	13.9	21.5	14.1	26.8	23.1	8.4	1.07	9.3E-01
B035DRAFT_03410	Glutamine phosphoribosylpyrophosphate amidotransferase(EC:2.4.2.14)	135.6	110.0	118.4	113.8	135.1	71.1	0.85	6.6E-01

B035DRAFT_03411	carbamoyl-phosphate synthase, small subunit(EC:6.3.5.5)	155.0	150.1	137.8	164.9	182.3	112.6	1.02	9.5E-01
B035DRAFT_03412	carbamoyl-phosphate synthase, large subunit(EC:6.3.5.5)	197.6	192.2	201.5	265.2	279.7	201.5	1.25	2.7E-01
B035DRAFT_03413	PAS domain S-box	83.5	86.6	74.8	93.3	106.7	91.0	1.19	2.0E-01
B035DRAFT_03414	Alpha-glucosidases, family 31 of glycosyl hydrolases (GH31)	369.7	375.9	349.9	277.0	376.4	396.3	0.95	8.0E-01
B035DRAFT_03415	Molecular chaperone (small heat shock protein)	1467.1	1063.3	1144.3	1431.9	1724.7	1688.7	1.33	2.2E-01
B035DRAFT_03416	Alanyl-tRNA synthetase	51.6	52.1	63.3	58.9	45.8	55.7	0.96	8.3E-01
B035DRAFT_03417	Acetyltransferases, including N-acetylases of ribosomal proteins(EC:2.3.1.)	64.0	60.1	58.8	61.2	56.3	60.1	0.97	6.6E-01
B035DRAFT_03418	Penicillin V acylase and related amidases(EC:3.5.1.24)	262.1	215.8	238.5	274.8	243.7	234.3	1.05	7.1E-01
B035DRAFT_03419	hypothetical protein	45.0	38.0	31.5	33.2	30.6	32.8	0.85	4.1E-01
B035DRAFT_03420	hypothetical protein	234.5	265.7	238.3	260.1	231.6	261.2	1.02	8.6E-01
B035DRAFT_03421	HpaII restriction endonuclease.(EC:3.1.21.4)	108.6	120.6	117.0	97.0	101.2	78.1	0.79	2.0E-01
B035DRAFT_03422	Glycoside hydrolase (GH13)	214.1	198.3	204.0	178.7	199.6	185.7	0.91	2.5E-01
B035DRAFT_03423	Predicted esterase of the alpha-beta hydrolase superfamily	112.8	130.9	112.2	116.5	129.6	152.9	1.12	5.1E-01
B035DRAFT_03424	hypothetical protein	232.3	296.5	298.3	265.0	278.2	313.1	1.04	8.4E-01
B035DRAFT_03425	malonyl CoA-acyl carrier protein transacylase(EC:2.3.1.39)	905.6	960.1	859.0	961.4	926.4	801.3	0.98	9.1E-01
B035DRAFT_03426	phosphomethylpyrimidine kinase(EC:2.7.1.49,EC:2.7.4.7)	21.6	24.3	27.3	34.6	36.1	34.6	1.45	5.6E-02
B035DRAFT_03427	Nucleoside-diphosphate-sugar epimerases(EC:4.2.1.46)	112.3	116.3	106.8	105.3	133.1	104.0	1.01	9.3E-01
B035DRAFT_03428	Signal transduction histidine kinase(EC:2.7.13.3)	162.9	149.2	176.1	135.0	161.6	129.7	0.87	3.7E-01
B035DRAFT_03429	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03430	AraC-type DNA-binding domain-containing proteins	14.3	20.8	21.9	12.5	18.3	23.4	0.94	8.8E-01
B035DRAFT_03431	hypothetical protein	62.8	62.5	68.2	35.8	40.3	51.8	0.65	1.1E-01
B035DRAFT_03432	hypothetical protein	13.8	12.4	15.5	13.4	17.3	22.2	1.25	4.4E-01
B035DRAFT_03433	glutaminase A(EC:3.5.1.2)	79.8	98.7	80.9	95.0	106.1	116.1	1.23	2.5E-01
B035DRAFT_03434	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase(EC:1.17.7.1)	123.8	132.9	126.8	148.3	156.2	146.4	1.18	5.0E-02
B035DRAFT_03435	phosphoribosylaminoimidazole carboxylase, PurE protein(EC:5.4.99.18)	496.8	534.8	538.9	441.8	513.1	539.1	0.95	6.6E-01
B035DRAFT_03436	glycine cleavage system H protein	541.8	577.2	547.6	512.5	598.4	701.9	1.08	6.5E-01
B035DRAFT_03437	hypothetical protein	123.7	134.5	137.3	137.5	138.0	167.8	1.12	4.1E-01
B035DRAFT_03438	RNA polymerase sigma-54 factor	97.7	106.0	97.5	118.2	119.4	121.7	1.19	4.2E-02
B035DRAFT_03439	Uridine kinase(EC:2.7.1.48)	86.7	91.8	81.1	162.1	176.9	225.4	2.16	2.8E-02
B035DRAFT_03440	Na/Pi-cotransporter	167.1	185.0	178.3	133.8	148.5	149.6	0.81	8.0E-02
B035DRAFT_03441	Na/Pi-cotransporter	198.0	231.8	232.5	178.1	181.1	199.9	0.85	2.0E-01
B035DRAFT_03442	FKBP-type peptidyl-prolyl cis-trans isomerases 1(EC:5.2.1.8)	1862.7	1827.9	1906.3	1772.9	1581.8	1866.7	0.93	4.3E-01
B035DRAFT_03443	FKBP-type peptidyl-prolyl cis-trans isomerases 1(EC:5.2.1.8)	1139.7	1042.2	967.0	1063.0	1047.5	898.8	0.96	7.3E-01
B035DRAFT_03444	NAD-dependent protein deacetylases, SIR2 family(EC:3.5.1.)	69.8	74.7	74.4	72.0	75.4	69.2	0.99	8.6E-01
B035DRAFT_03445	hypothetical protein	10.0	9.8	10.0	9.9	10.0	6.6	0.87	5.8E-01
B035DRAFT_03446	hypothetical protein	9.6	6.0	6.3	5.4	8.4	5.9	0.91	8.0E-01
B035DRAFT_03447	hypothetical protein	4.6	1.8	3.2	1.6	3.1	4.1	0.92	9.2E-01
B035DRAFT_03448	hypothetical protein	3.2	2.1	2.4	2.9	2.9	1.1	0.83	7.8E-01
B035DRAFT_03449	hypothetical protein	3.4	2.7	3.4	2.3	2.3	1.4	0.62	2.0E-01
B035DRAFT_03450	hypothetical protein	1.3	2.3	4.0	1.7	3.6	1.8	0.97	9.8E-01
B035DRAFT_03451	hypothetical protein	2.9	1.7	3.1	2.7	1.0	2.0	0.70	5.8E-01
B035DRAFT_03452	hypothetical protein	2.1	4.0	2.5	1.4	1.9	1.9	0.63	2.6E-01
B035DRAFT_03453	hypothetical protein	2.2	2.5	3.7	2.0	4.0	2.7	1.02	9.7E-01
B035DRAFT_03454	hypothetical protein	2.7	4.0	3.2	2.4	4.8	2.8	0.98	9.7E-01
B035DRAFT_03455	hypothetical protein	16.6	9.9	17.4	14.2	13.4	6.6	0.76	6.2E-01
B035DRAFT_03456	hypothetical protein	23.3	16.0	15.1	12.9	20.2	7.9	0.72	5.4E-01
B035DRAFT_03457	DNA primase (bacterial type)	29.2	18.6	30.1	21.0	22.2	7.0	0.58	4.6E-01
B035DRAFT_03458	Conjugative transposon protein TraO.	22.3	11.8	15.0	18.7	18.9	3.7	0.69	7.3E-01
B035DRAFT_03459	Bacteroides conjugative transposon TraN protein	32.4	19.6	27.0	23.9	26.7	8.9	0.69	5.9E-01
B035DRAFT_03460	Bacteroides conjugative transposon TraM protein	14.3	5.4	13.6	9.5	8.5	1.5	0.49	5.6E-01

B035DRAFT_03461	hypothetical protein	10.3	7.3	9.6	8.9	11.9	4.3	0.86	8.0E-01
B035DRAFT_03462	Bacteroides conjugative transposon TraK protein	16.6	9.9	14.5	12.8	13.1	5.4	0.72	5.9E-01
B035DRAFT_03463	Bacteroides conjugative transposon TraJ protein	20.4	10.8	18.4	17.3	17.6	5.7	0.75	7.1E-01
B035DRAFT_03464	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.93	
B035DRAFT_03465	(miscRNA)	22.9	12.3	21.4	22.7	25.1	8.6	0.00	9.3E-01
B035DRAFT_03466	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03467	(tRNA)	175.7	130.9	180.9	184.9	91.9	36.8	0.53	4.7E-01
B035DRAFT_03468	3-dehydroquinate synthase(EC:4.2.3.4)	134.5	133.5	117.0	106.9	115.3	130.4	0.91	5.0E-01
B035DRAFT_03469	hypothetical protein	105.4	140.1	143.9	132.5	127.8	154.9	1.07	7.5E-01
B035DRAFT_03470	hypothetical protein	124.8	133.8	135.1	203.3	221.0	193.7	1.57	1.5E-02
B035DRAFT_03471	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes(EC:2.7.8.)	73.0	78.4	83.1	79.8	81.1	94.9	1.09	4.8E-01
B035DRAFT_03472	N6-adenine-specific methylase	245.8	254.1	270.8	237.4	240.1	326.9	1.03	8.8E-01
B035DRAFT_03473	hypothetical protein	158.6	189.9	176.7	154.6	161.9	218.9	1.01	9.7E-01
B035DRAFT_03474	hypothetical protein	1160.3	1291.4	1117.2	1169.5	1300.1	1663.7	1.15	5.0E-01
B035DRAFT_03475	PIF1 helicase.(EC:3.1.11.5)	264.3	216.2	230.5	158.9	123.1	105.3	0.54	7.4E-02
B035DRAFT_03476	hypothetical protein	67.3	60.7	69.0	73.5	71.5	86.5	1.17	2.6E-01
B035DRAFT_03477	alanine--tRNA ligase(EC:6.1.1.7)	285.2	282.5	260.6	240.6	269.5	273.5	0.95	5.3E-01
B035DRAFT_03478	Membrane proteins related to metalloendopeptidases	78.8	90.8	74.7	118.9	129.3	85.1	1.35	2.7E-01
B035DRAFT_03479	Predicted transcriptional regulators	121.4	130.9	122.3	163.0	158.0	154.8	1.27	2.1E-02
B035DRAFT_03480	(p)ppGpp synthetase, RelA/SpoT family(EC:2.7.6.5)	133.8	145.0	138.4	157.5	168.6	188.4	1.23	1.2E-01
B035DRAFT_03481	Soluble lytic murein transglycosylase and related regulatory proteins (some contain LysM/invasin domains)(EC:3.2.1.) (GH23)	119.9	137.5	125.7	150.5	142.0	164.4	1.19	1.6E-01
B035DRAFT_03482	hypothetical protein	215.7	221.7	195.3	248.3	231.8	244.1	1.15	1.5E-01
B035DRAFT_03483	ParB-like partition proteins	204.1	212.8	194.3	235.7	226.9	240.0	1.15	7.7E-02
B035DRAFT_03484	ATPases involved in chromosome partitioning	206.5	238.0	222.4	274.4	245.6	291.9	1.22	1.6E-01
B035DRAFT_03485	5''/3''-nucleotidase SurE(EC:3.1.3.5)	228.5	223.8	208.5	324.9	327.7	284.4	1.42	3.7E-02
B035DRAFT_03486	lipid-A-disaccharide synthase(EC:2.4.1.182) (GT19)	166.0	165.9	171.8	221.0	216.8	234.7	1.33	1.1E-02
B035DRAFT_03487	CDP-diglyceride synthetase(EC:2.7.7.41)	278.3	302.0	286.1	291.7	277.3	337.2	1.04	7.2E-01
B035DRAFT_03488	ATP-dependent metalloprotease FtsH(EC:3.4.24.)	619.1	562.9	594.7	616.5	583.7	551.0	0.99	8.6E-01
B035DRAFT_03489	iojap-like ribosome-associated protein	315.8	360.5	334.0	302.8	249.3	345.0	0.88	4.9E-01
B035DRAFT_03490	hypothetical protein	1.6	1.9	2.9	0.0	1.5	0.7	0.50	3.7E-01
B035DRAFT_03491	(tRNA)	134.7	214.9	186.1	165.8	126.2	87.1	0.70	4.0E-01
B035DRAFT_03492	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03493	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03494	hypothetical protein	125.0	143.4	138.2	74.5	77.7	98.5	0.61	6.1E-02
B035DRAFT_03495	hypothetical protein	10.9	15.0	10.8	32.2	32.2	52.1	3.13	4.5E-02
B035DRAFT_03496	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases (CE1)	147.7	143.1	131.5	138.5	170.6	164.6	1.12	4.0E-01
B035DRAFT_03497	Putative homoserine kinase type II (protein kinase fold)	586.2	577.5	543.2	595.1	674.4	805.0	1.21	2.9E-01
B035DRAFT_03498	Phosphate/sulphate permeases	7.6	6.7	8.2	4.7	4.4	6.0	0.67	1.1E-01
B035DRAFT_03499	AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful)(EC:3.5.4.10,EC:2.1.2.3)	543.9	546.2	513.9	523.1	563.4	513.0	1.00	9.7E-01
B035DRAFT_03500	cell shape determining protein, MreB/Mrl family	363.9	349.7	351.2	325.9	379.9	342.3	0.98	8.5E-01
B035DRAFT_03501	Cell shape-determining protein	244.5	257.9	234.9	238.1	274.5	248.6	1.03	7.4E-01
B035DRAFT_03502	rod shape-determining protein MreD	150.4	159.5	128.0	134.2	141.5	160.3	1.00	9.9E-01
B035DRAFT_03503	penicillin-binding protein 2	147.0	147.0	141.0	121.9	150.5	116.9	0.89	4.2E-01
B035DRAFT_03504	Bacterial cell division membrane protein	88.7	96.2	92.5	90.4	102.5	94.3	1.03	6.7E-01
B035DRAFT_03505	gliding motility-associated lipoprotein GldH	105.1	134.5	131.6	126.5	119.6	109.5	0.96	8.2E-01
B035DRAFT_03506	Uncharacterized homolog of PSP1	189.9	171.6	152.4	186.5	195.8	142.9	1.02	9.5E-01
B035DRAFT_03507	DNA polymerase III, delta'' subunit(EC:2.7.7.7)	177.9	191.5	176.8	188.7	215.7	223.2	1.15	2.3E-01
B035DRAFT_03508	5,10-methylenetetrahydrofolate reductase, prokaryotic form(EC:1.5.1.20)	195.5	205.6	197.8	220.1	215.6	201.8	1.06	2.9E-01

B035DRAFT_03509	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthases and related enzymes	52.0	56.9	53.5	59.4	48.2	61.4	1.04	8.2E-01
B035DRAFT_03510	RND family efflux transporter, MFP subunit	47.6	39.2	44.5	54.3	59.9	40.7	1.17	5.1E-01
B035DRAFT_03511	Cation/multidrug efflux pump	31.6	26.3	24.9	25.2	35.8	21.1	0.97	9.3E-01
B035DRAFT_03512	Outer membrane protein	41.6	45.0	36.1	38.9	46.8	53.3	1.13	5.5E-01
B035DRAFT_03513	hypothetical protein	109.4	134.6	116.4	111.8	133.9	147.7	1.09	6.5E-01
B035DRAFT_03514	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03515	TonB-linked outer membrane protein, SusC/RagA family	33.9	31.8	33.1	23.4	23.8	26.0	0.74	2.2E-02
B035DRAFT_03516	SusD family	34.6	32.4	32.2	27.8	29.3	26.5	0.84	7.6E-02
B035DRAFT_03517	hypothetical protein	8.4	9.2	10.4	3.7	3.0	4.2	0.39	2.2E-02
B035DRAFT_03518	Periplasmic component of the Tol biopolymer transport system	11.1	9.5	11.7	6.4	6.6	6.3	0.60	2.2E-02
B035DRAFT_03519	SusD family	24.3	26.1	22.8	16.9	13.3	20.8	0.69	1.8E-01
B035DRAFT_03520	Ribosomal protein L11 methylase(EC:2.1.1.)	116.4	124.6	115.2	141.5	141.2	186.9	1.31	1.8E-01
B035DRAFT_03521	Glutaredoxin.	84.8	85.0	75.6	119.2	109.7	136.5	1.49	5.7E-02
B035DRAFT_03522	Bacterial nucleoid DNA-binding protein	117.8	92.2	125.2	157.3	118.8	55.4	0.91	8.9E-01
B035DRAFT_03523	hypothetical protein	239.7	216.6	224.3	223.9	299.9	216.9	1.08	7.1E-01
B035DRAFT_03524	hypothetical protein	183.1	175.9	168.2	170.2	236.9	221.9	1.18	3.8E-01
B035DRAFT_03525	hypothetical protein	33.1	33.4	34.4	36.5	39.7	39.1	1.14	7.1E-02
B035DRAFT_03526	Predicted dehydrogenases and related proteins (GH109)	62.5	61.7	59.8	65.0	66.8	70.1	1.10	1.1E-01
B035DRAFT_03527	Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein	55.3	73.6	65.5	77.1	84.8	98.2	1.34	1.9E-01
B035DRAFT_03528	hypothetical protein	104.4	118.7	104.4	125.7	119.2	141.7	1.18	2.2E-01
B035DRAFT_03529	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, gamma subunit(EC:1.2.7.3)	513.6	542.1	541.7	452.6	547.1	497.0	0.93	5.1E-01
B035DRAFT_03530	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, beta subunit(EC:1.2.7.3)	416.8	431.8	378.3	328.8	385.6	330.0	0.85	2.2E-01
B035DRAFT_03531	hypothetical protein	517.8	540.0	480.8	373.6	441.2	562.9	0.88	5.8E-01
B035DRAFT_03532	Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit(EC:1.2.7.3)	562.0	567.3	530.7	470.1	523.9	442.1	0.86	1.9E-01
B035DRAFT_03533	Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits(EC:1.2.7.3)	279.3	311.1	289.2	322.6	300.3	352.9	1.11	3.3E-01
B035DRAFT_03534	Uncharacterized protein conserved in bacteria	445.0	470.1	390.5	467.2	459.9	458.9	1.06	5.3E-01
B035DRAFT_03535	hypothetical protein	149.8	172.0	157.8	227.0	227.8	277.8	1.52	5.5E-02
B035DRAFT_03536	ribose 5-phosphate isomerase B(EC:5.3.1.6)	328.9	380.1	339.8	369.1	364.0	344.5	1.03	7.5E-01
B035DRAFT_03537	Transketolase(EC:2.2.1.1)	515.3	525.8	514.2	482.3	521.9	528.4	0.98	7.8E-01
B035DRAFT_03538	Thiol-disulfide isomerase and thioredoxins	78.1	100.9	82.6	118.0	122.4	134.1	1.44	8.6E-02
B035DRAFT_03539	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03540	hypothetical protein	16.7	14.6	14.4	9.9	13.6	12.2	0.78	2.2E-01
B035DRAFT_03541	Fe2+-dicitrate sensor, membrane component	15.4	12.2	9.9	6.4	14.5	9.3	0.78	6.1E-01
B035DRAFT_03542	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	14.5	17.3	13.2	12.1	14.9	12.4	0.88	4.7E-01
B035DRAFT_03543	hypothetical protein	12.9	15.8	14.1	12.8	20.2	17.6	1.16	5.7E-01
B035DRAFT_03544	Membrane protease subunits, stomatin/prohibitin homologs	7.8	11.2	9.1	14.4	32.5	29.6	2.59	1.3E-01
B035DRAFT_03545	PIF1 helicase./Tetratricopeptide repeat./Helicase.	31.7	35.1	31.0	50.7	52.8	65.9	1.72	4.3E-02
B035DRAFT_03546	Sua5/YciO/YrdC/YwlC family protein	42.2	56.8	42.7	53.5	48.3	69.0	1.20	4.8E-01
B035DRAFT_03547	Small-conductance mechanosensitive channel	227.1	219.7	211.2	203.8	183.2	224.9	0.93	5.1E-01
B035DRAFT_03548	Uncharacterized flavoproteins	244.0	255.0	222.7	182.9	273.8	214.4	0.92	7.1E-01
B035DRAFT_03549	radical SAM protein, TIGR01212 family	139.7	135.1	105.1	88.4	124.8	73.7	0.74	3.7E-01
B035DRAFT_03550	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases(EC:3.4.14.5) (CE1)	78.7	82.1	76.2	68.6	78.1	84.4	0.97	8.2E-01
B035DRAFT_03551	lipoate synthase(EC:2.8.1.8)	40.9	41.6	41.8	42.2	55.0	40.2	1.09	6.1E-01
B035DRAFT_03552	hypothetical protein	128.9	166.3	171.4	169.2	118.0	156.8	0.95	8.5E-01

B035DRAFT_03553	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	25.5	23.4	23.4	17.0	26.0	13.3	0.75	4.2E-01
B035DRAFT_03554	hypothetical protein	3.6	3.3	6.1	3.0	1.3	0.6	0.33	2.4E-01
B035DRAFT_03555	hypothetical protein	10.1	13.1	15.1	10.7	14.3	14.3	1.03	9.2E-01
B035DRAFT_03556	hypothetical protein	34.9	52.7	43.8	39.0	31.7	40.3	0.85	5.2E-01
B035DRAFT_03557	hypothetical protein	36.2	32.3	27.5	30.2	36.2	34.0	1.05	7.9E-01
B035DRAFT_03558	hypothetical protein	33.4	30.8	26.7	25.6	35.4	37.5	1.07	7.8E-01
B035DRAFT_03559	hypothetical protein	27.5	32.0	24.2	43.1	32.3	46.4	1.45	1.9E-01
B035DRAFT_03560	Predicted P-loop ATPase and inactivated derivatives	98.7	89.5	111.9	98.6	98.4	46.7	0.77	5.8E-01
B035DRAFT_03561	Glycosyltransferase (GT4)	28.0	34.1	33.6	19.2	22.1	30.6	0.74	3.0E-01
B035DRAFT_03562	Ribosomal protein L11 methylase	34.1	30.5	36.9	22.9	23.3	29.7	0.75	1.7E-01
B035DRAFT_03563	Molybdenum cofactor biosynthesis enzyme	37.3	31.5	35.8	24.6	24.6	31.5	0.77	1.9E-01
B035DRAFT_03564	Protein of unknown function (DUF512)./Radical SAM superfamily	35.9	37.7	33.7	25.8	21.3	33.0	0.74	2.4E-01
B035DRAFT_03565	hypothetical protein	39.8	38.0	35.7	29.6	23.9	31.8	0.75	1.5E-01
B035DRAFT_03566	hypothetical protein	18.2	19.3	18.8	12.7	19.2	20.3	0.91	7.3E-01
B035DRAFT_03567	Nucleoside-diphosphate-sugar epimerases(EC:4.2.1.46)	9.7	13.3	13.9	9.7	11.3	12.0	0.90	6.6E-01
B035DRAFT_03568	Fe-S oxidoreductase	11.9	11.0	10.9	9.4	10.6	17.7	1.07	8.6E-01
B035DRAFT_03569	nucleotide sugar dehydrogenase(EC:1.1.1.)	9.0	7.9	9.2	9.4	12.1	13.7	1.34	2.3E-01
B035DRAFT_03570	Predicted transcriptional regulators	3.7	7.8	9.9	5.5	10.7	13.5	1.41	6.4E-01
B035DRAFT_03571	Membrane proteins related to metalloendopeptidases	9.5	7.0	9.4	3.9	2.9	5.4	0.47	1.1E-01
B035DRAFT_03572	hypothetical protein	2.5	2.9	3.0	2.6	2.4	2.2	0.87	3.3E-01
B035DRAFT_03573	hypothetical protein	3.2	3.7	5.9	3.4	2.9	0.7	0.47	4.2E-01
B035DRAFT_03574	hypothetical protein	3.4	2.2	2.3	2.1	2.1	2.1	0.81	4.2E-01
B035DRAFT_03575	hypothetical protein	2.9	2.8	1.3	2.4	2.2	1.9	0.99	9.9E-01
B035DRAFT_03576	Predicted membrane protein	3.1	0.8	1.7	2.5	1.9	1.2	1.13	8.9E-01
B035DRAFT_03577	hypothetical protein	2.2	1.6	2.2	2.1	0.6	0.6	0.47	3.5E-01
B035DRAFT_03578	hypothetical protein	1.4	2.2	2.3	1.0	1.7	0.9	0.59	2.9E-01
B035DRAFT_03579	hypothetical protein	1.7	1.2	0.6	0.3	1.4	1.1	0.69	7.4E-01
B035DRAFT_03580	Membrane proteins related to metalloendopeptidases	2.4	1.7	1.0	1.5	2.2	1.7	1.11	8.5E-01
B035DRAFT_03581	hypothetical protein	2.1	1.7	2.6	0.8	0.0	0.6	0.33	5.2E-02
B035DRAFT_03582	hypothetical protein	2.8	2.3	2.4	2.9	3.0	3.0	1.20	1.7E-01
B035DRAFT_03583	Mismatch repair ATPase (MutS family)	3.3	3.9	3.0	4.7	4.3	4.3	1.31	1.2E-01
B035DRAFT_03584	Muramidase (flagellum-specific) (GH73)	86.1	102.8	102.7	131.0	115.4	149.9	1.36	1.5E-01
B035DRAFT_03585	hypothetical protein	291.8	288.0	262.9	277.0	297.0	246.6	0.97	8.1E-01
B035DRAFT_03586	hypothetical protein	16.4	20.1	20.0	16.1	18.8	16.2	0.91	5.2E-01
B035DRAFT_03587	hypothetical protein	541.1	900.4	837.3	1367.7	882.7	745.1	1.30	5.4E-01
B035DRAFT_03588	hypothetical protein	167.9	229.7	162.9	329.9	305.3	353.4	1.78	6.6E-02
B035DRAFT_03589	radical SAM additional 4Fe4S-binding domain	30.6	37.7	35.2	31.8	33.7	49.1	1.09	7.6E-01
B035DRAFT_03590	Transposase and inactivated derivatives	139.0	115.9	137.2	147.7	143.8	132.8	1.09	5.0E-01
B035DRAFT_03591	DNA replication protein	65.7	53.0	53.9	66.0	66.8	63.8	1.14	3.2E-01
B035DRAFT_03592	DNA binding domain, excisionase family	45.7	35.4	52.8	56.1	46.9	32.5	1.00	1.0E+00
B035DRAFT_03593	hypothetical protein	62.4	34.4	50.7	64.9	51.0	18.1	0.82	8.1E-01
B035DRAFT_03594	hypothetical protein	40.3	35.0	41.8	51.7	48.1	19.0	0.93	9.1E-01
B035DRAFT_03595	hypothetical protein	34.7	19.3	39.4	39.4	34.6	7.7	0.74	7.7E-01
B035DRAFT_03596	hypothetical protein	45.1	22.5	42.3	50.2	33.2	8.8	0.70	7.4E-01
B035DRAFT_03597	hypothetical protein	30.2	15.7	25.3	31.1	23.7	10.0	0.85	8.3E-01
B035DRAFT_03598	hypothetical protein	22.0	26.5	14.1	13.0	11.2	13.1	0.62	2.2E-01
B035DRAFT_03599	Non-ribosomal peptide synthetase modules and related proteins	161.6	153.8	113.0	33.6	60.6	53.1	0.34	6.1E-02
B035DRAFT_03600	hypothetical protein	108.9	127.3	111.0	32.2	34.2	34.0	0.29	7.5E-04
B035DRAFT_03601	Outer membrane cobalamin receptor protein	110.0	125.1	92.7	20.8	29.5	34.4	0.25	2.3E-02
B035DRAFT_03602	hypothetical protein	417.6	475.5	327.9	64.5	77.7	108.7	0.20	2.1E-02
B035DRAFT_03603	Transposase DDE domain.	208.0	227.9	251.6	140.2	128.0	154.4	0.61	4.0E-02

B035DRAFT_03604	hypothetical protein	168.1	172.9	190.2	99.8	119.4	152.6	0.69	1.7E-01
B035DRAFT_03605	hypothetical protein	200.2	210.9	218.2	142.7	141.8	195.2	0.75	2.0E-01
B035DRAFT_03606	Predicted DNA-binding protein with PD1-like DNA-binding motif	223.1	205.9	217.7	173.4	177.8	177.7	0.82	2.3E-02
B035DRAFT_03607	Predicted oxidoreductases (related to aryl-alcohol dehydrogenases)	330.6	255.8	318.9	267.7	244.9	148.3	0.71	3.6E-01
B035DRAFT_03608	hypothetical protein	218.5	197.3	241.1	188.2	175.1	137.4	0.76	2.2E-01
B035DRAFT_03609	Flavodoxins	136.7	125.8	127.9	102.1	99.0	106.9	0.79	3.1E-02
B035DRAFT_03610	hypothetical protein	61.9	57.2	69.0	46.8	36.7	48.3	0.70	1.2E-01
B035DRAFT_03611	hypothetical protein	57.7	43.1	68.2	21.7	18.7	30.0	0.42	7.6E-02
B035DRAFT_03612	Ferritin-like protein	220.9	233.9	213.7	219.3	234.5	290.9	1.11	5.3E-01
B035DRAFT_03613	membrane protein, MarC family	161.4	167.9	181.4	149.3	189.3	223.9	1.09	7.1E-01
B035DRAFT_03614	Ferritin-like protein(EC:1.16.3.1)	326.0	287.8	261.7	279.8	433.7	350.3	1.20	4.7E-01
B035DRAFT_03615	DhnA-type fructose-1,6-bisphosphate aldolase and related enzymes(EC:4.1.2.13)	659.3	587.0	623.5	688.0	895.0	594.8	1.15	5.3E-01
B035DRAFT_03616	phosphoglycerate mutase, BPG-dependent, family 1(EC:5.4.2.1)	516.5	501.1	477.4	524.2	749.5	528.9	1.19	4.3E-01
B035DRAFT_03617	Molecular chaperone (small heat shock protein)	487.9	449.5	383.8	468.4	748.1	702.5	1.43	2.6E-01
B035DRAFT_03618	RNA polymerase sigma factor, sigma-70 family	162.6	156.7	139.7	144.3	222.0	225.9	1.27	4.0E-01
B035DRAFT_03619	6-phosphofructokinase(EC:2.7.1.11)	171.7	146.1	176.9	169.0	207.3	100.2	0.92	8.6E-01
B035DRAFT_03620	Kef-type K+ transport systems, membrane components	212.7	197.7	203.9	223.4	293.0	266.3	1.27	1.7E-01
B035DRAFT_03621	alpha-glucan phosphorylases(EC:2.4.1.1) (GT35)	198.2	185.9	188.0	232.4	252.0	172.2	1.13	5.6E-01
B035DRAFT_03622	Arginase/agmatinase/formimionoglutamate hydrolase, arginase family	136.4	134.9	107.3	119.7	162.4	153.1	1.15	5.3E-01
B035DRAFT_03623	Methylglyoxal synthase(EC:4.2.3.3)	246.6	225.6	213.6	229.8	302.0	378.5	1.30	3.5E-01
B035DRAFT_03624	hypothetical protein	29.6	43.6	36.1	28.1	29.6	31.4	0.82	3.7E-01
B035DRAFT_03625	hypothetical protein	22.2	29.8	22.8	14.4	17.0	20.2	0.69	1.9E-01
B035DRAFT_03626	hypothetical protein	150.4	132.4	171.7	116.5	84.1	115.0	0.69	1.8E-01
B035DRAFT_03627	hypothetical protein	96.3	96.3	104.3	78.4	65.9	84.5	0.77	1.3E-01
B035DRAFT_03628	hypothetical protein	40.6	35.9	42.2	42.7	31.4	20.7	0.77	5.0E-01
B035DRAFT_03629	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase(EC:2.8.1.)	306.9	266.5	253.3	196.2	172.6	134.2	0.60	9.4E-02
B035DRAFT_03630	cysteine synthase A(EC:2.5.1.47)	402.6	297.4	311.1	315.8	220.3	125.9	0.62	3.6E-01
B035DRAFT_03631	Exonuclease III	65.4	67.2	62.0	48.9	75.9	36.5	0.79	5.5E-01
B035DRAFT_03632	FOG: WD40-like repeat	124.5	119.9	123.9	88.0	108.1	98.2	0.80	1.1E-01
B035DRAFT_03633	Superfamily II DNA and RNA helicases(EC:3.6.4.13)	1034.0	1018.8	986.6	1209.4	1211.5	1197.1	1.19	7.4E-03
B035DRAFT_03634	hypothetical protein	505.7	502.2	480.7	506.7	512.1	557.6	1.06	3.7E-01
B035DRAFT_03635	NADH:ubiquinone oxidoreductase 24 kD subunit(EC:1.6.5.3)	23.7	25.5	24.1	22.7	24.4	23.8	0.97	5.4E-01
B035DRAFT_03636	[FeFe] hydrogenase, group A(EC:1.6.5.3)	16.8	16.7	17.6	14.2	15.3	14.8	0.87	5.4E-02
B035DRAFT_03637	NADH:ubiquinone oxidoreductase, NADH-binding (51 kD) subunit(EC:1.6.5.3)	23.0	23.9	21.1	18.5	20.1	22.7	0.90	4.1E-01
B035DRAFT_03638	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	28.1	26.3	24.2	37.5	41.3	43.6	1.56	3.0E-02
B035DRAFT_03639	TonB-linked outer membrane protein, SusC/RagA family	17.2	16.2	17.5	6.1	6.1	8.2	0.40	1.7E-02
B035DRAFT_03640	hypothetical protein	19.5	20.7	19.1	4.9	6.9	8.5	0.33	3.3E-02
B035DRAFT_03641	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03642	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03643	Protein of unknown function (DUF3244).	86.8	105.2	114.6	59.8	56.3	67.4	0.60	6.0E-02
B035DRAFT_03644	Tfp pilus assembly protein PilF	29.6	33.8	30.4	17.8	21.6	21.2	0.65	4.5E-02
B035DRAFT_03645	Cation/multidrug efflux pump	74.4	74.5	69.6	41.3	56.2	49.5	0.67	8.2E-02
B035DRAFT_03646	Outer membrane protein	76.7	80.3	72.6	53.8	63.8	61.2	0.78	8.4E-02
B035DRAFT_03647	Cation/multidrug efflux pump	89.6	89.0	89.9	63.9	78.2	81.5	0.83	2.2E-01
B035DRAFT_03648	RND family efflux transporter, MFP subunit	117.3	101.1	95.9	102.3	124.5	73.9	0.94	8.5E-01
B035DRAFT_03649	Lipid A core - O-antigen ligase and related enzymes	28.6	22.4	34.3	32.7	24.6	9.0	0.69	6.2E-01
B035DRAFT_03650	signal peptidase I, bacterial type(EC:3.4.21.89)	26.0	24.9	19.7	22.5	20.1	12.8	0.77	4.5E-01
B035DRAFT_03651	F5/8 type C domain (CBM62)	33.8	27.5	32.0	25.3	29.6	31.6	0.93	6.4E-01
B035DRAFT_03652	hypothetical protein	14.6	15.7	14.7	13.9	19.6	21.9	1.21	4.6E-01

B035DRAFT_03653	hypothetical protein	24.1	26.2	25.1	21.7	27.4	33.9	1.08	7.4E-01
B035DRAFT_03654	hypothetical protein	257.9	337.0	295.2	424.4	429.1	542.7	1.57	9.3E-02
B035DRAFT_03655	Molybdenum cofactor biosynthesis enzyme	15.2	16.5	12.2	8.8	9.8	10.0	0.66	8.5E-02
B035DRAFT_03656	Protein of unknown function (DUF1573).	9.4	10.4	14.0	7.2	5.4	14.3	0.74	6.0E-01
B035DRAFT_03657	Protein of unknown function (DUF1573).	43.7	57.8	51.8	61.0	52.1	51.7	1.08	6.7E-01
B035DRAFT_03658	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03659	Beta-lactamase class A(EC:3.5.2.6)	176.3	184.8	183.4	151.5	150.1	195.3	0.91	5.3E-01
B035DRAFT_03660	hypothetical protein	18.2	24.6	22.8	18.4	19.1	22.1	0.91	6.4E-01
B035DRAFT_03661	hypothetical protein	8.2	4.9	9.8	9.9	12.3	9.4	1.43	3.9E-01
B035DRAFT_03662	RecA-superfamily ATPases implicated in signal transduction	8.5	6.6	9.5	10.7	10.0	10.6	1.29	2.5E-01
B035DRAFT_03663	DNA binding domain, excisionase family	7.2	8.4	9.9	19.0	9.8	6.1	1.24	7.3E-01
B035DRAFT_03664	hypothetical protein	10.6	12.6	10.8	12.9	9.8	12.9	1.04	8.5E-01
B035DRAFT_03665	Site-specific recombinase XerD	13.7	10.7	12.1	12.7	16.0	14.1	1.17	3.8E-01
B035DRAFT_03666	hypothetical protein	5.6	4.6	7.5	3.6	7.7	5.9	0.95	9.2E-01
B035DRAFT_03667	quasi-rSAM protein, GG-Bacteroidales system	4.0	5.5	5.0	2.8	3.2	5.1	0.75	4.3E-01
B035DRAFT_03668	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	4.0	3.0	4.4	2.9	3.1	1.4	0.62	3.6E-01
B035DRAFT_03669	hypothetical protein	1.4	2.2	2.5	0.5	1.4	0.3	0.32	2.3E-01
B035DRAFT_03670	hypothetical protein	1.2	1.0	0.7	1.9	1.6	0.3	0.97	9.8E-01
B035DRAFT_03671	Predicted glycosyltransferase involved in capsule biosynthesis (GT7)	4.2	2.7	3.3	2.4	2.5	1.9	0.67	2.1E-01
B035DRAFT_03672	Glycosyltransferase (GT4)	31.6	23.1	28.0	17.4	16.8	14.9	0.60	6.4E-02
B035DRAFT_03673	hypothetical protein	123.5	112.8	111.6	88.3	78.1	71.3	0.68	5.3E-02
B035DRAFT_03674	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03675	hypothetical protein	51.6	40.4	58.2	38.5	55.3	72.5	1.08	8.5E-01
B035DRAFT_03676	Dimethyladenosine transferase (rRNA methylation)	38.8	48.1	42.2	43.6	39.9	43.0	0.98	9.0E-01
B035DRAFT_03677	Beta-lactamase class D(EC:3.5.2.6)	16.1	16.9	15.6	12.2	13.0	17.9	0.87	5.4E-01
B035DRAFT_03678	Streptomycin adenylyltransferase.(EC:2.7.7.)	36.8	38.4	39.5	49.4	44.3	66.3	1.38	2.0E-01
B035DRAFT_03679	Site-specific recombinase XerD	170.7	155.1	163.2	257.8	206.6	130.3	1.17	6.7E-01
B035DRAFT_03680	Sugar phosphate isomerases/epimerases	172.9	141.0	127.7	181.0	152.8	135.1	1.06	8.0E-01
B035DRAFT_03681	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	57.5	55.1	63.2	66.4	64.3	39.0	0.94	8.6E-01
B035DRAFT_03682	Nucleotidyltransferase/DNA polymerase involved in DNA repair	38.9	33.9	45.2	57.6	46.8	31.0	1.12	7.6E-01
B035DRAFT_03683	SOS-response transcriptional repressors (RecA-mediated autopeptidases)(EC:3.4.21.)	48.2	36.2	48.4	41.9	43.4	21.5	0.77	5.7E-01
B035DRAFT_03684	Uncharacterized protein conserved in bacteria	16.9	19.2	23.0	24.8	22.0	9.2	0.88	8.4E-01
B035DRAFT_03685	hypothetical protein	3.9	3.8	5.4	4.7	7.8	2.7	1.08	9.1E-01
B035DRAFT_03686	hypothetical protein	4.6	1.5	4.0	7.7	6.0	2.4	1.57	6.2E-01
B035DRAFT_03687	hypothetical protein	4.0	4.2	9.2	5.6	6.9	2.4	0.85	8.4E-01
B035DRAFT_03688	hypothetical protein	1.9	1.1	1.7	0.0	2.5	2.1	1.54	2.9E-01
B035DRAFT_03689	hypothetical protein	2.1	1.2	0.0	3.4	1.5	1.9	1.30	7.1E-01
B035DRAFT_03690	hypothetical protein	2.0	0.8	0.8	0.0	3.7	0.0	3.36	
B035DRAFT_03691	Predicted transcriptional regulators	68.1	46.9	62.4	89.4	92.9	96.2	1.59	9.3E-02
B035DRAFT_03692	Type I restriction-modification system methyltransferase subunit(EC:2.1.1.72)	136.3	139.2	147.3	151.6	154.9	165.4	1.12	1.5E-01
B035DRAFT_03693	Site-specific recombinase XerD	137.8	145.5	130.2	123.7	134.2	171.5	1.03	8.9E-01
B035DRAFT_03694	Restriction endonuclease S subunits	106.6	113.7	99.9	95.4	94.4	140.7	1.02	9.6E-01
B035DRAFT_03695	Protein involved in cell division	80.7	91.8	86.6	75.8	80.9	108.7	1.01	9.6E-01
B035DRAFT_03696	Type I restriction modification DNA specificity domain.	36.3	48.6	55.3	38.2	51.0	42.9	0.95	8.6E-01
B035DRAFT_03697	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03698	SusD family	32.9	33.1	36.7	25.4	24.8	32.8	0.80	2.5E-01
B035DRAFT_03699	Domain of unknown function (DUF303) (CE6)	52.0	62.3	60.0	54.8	56.0	76.1	1.06	7.9E-01
B035DRAFT_03700	Arylsulfatase A and related enzymes	103.0	97.8	106.3	108.3	108.2	119.9	1.09	2.7E-01

B035DRAFT_03701	Alpha-L-fucosidase (GH29)	173.8	207.4	199.2	252.6	234.8	217.0	1.21	1.8E-01
B035DRAFT_03702	hypothetical protein	10.0	9.8	10.0	9.9	10.0	6.6	0.87	5.8E-01
B035DRAFT_03703	hypothetical protein	9.6	6.0	6.3	5.4	8.4	5.9	0.91	8.0E-01
B035DRAFT_03704	hypothetical protein	4.6	1.8	3.2	1.6	3.1	4.1	0.92	9.2E-01
B035DRAFT_03705	hypothetical protein	3.2	2.1	2.4	2.9	2.9	1.1	0.83	7.8E-01
B035DRAFT_03706	hypothetical protein	3.4	2.7	3.4	2.3	2.3	1.4	0.62	2.0E-01
B035DRAFT_03707	hypothetical protein	1.3	2.3	4.0	1.7	3.6	1.8	0.97	9.8E-01
B035DRAFT_03708	hypothetical protein	2.9	1.7	3.1	2.7	1.0	2.0	0.70	5.8E-01
B035DRAFT_03709	hypothetical protein	2.1	4.0	2.5	1.4	1.9	1.9	0.63	2.6E-01
B035DRAFT_03710	hypothetical protein	2.2	2.5	3.7	2.0	4.0	2.7	1.02	9.7E-01
B035DRAFT_03711	hypothetical protein	2.7	4.0	3.2	2.4	4.8	2.8	0.98	9.7E-01
B035DRAFT_03712	hypothetical protein	16.6	9.9	17.4	14.2	13.4	6.6	0.76	6.2E-01
B035DRAFT_03713	hypothetical protein	23.3	16.0	15.1	12.9	20.2	7.9	0.72	5.4E-01
B035DRAFT_03714	DNA primase (bacterial type)	29.2	18.6	30.1	21.0	22.2	7.0	0.58	4.6E-01
B035DRAFT_03715	Conjugative transposon protein TraO.	22.3	11.8	15.0	18.7	18.9	3.7	0.69	7.3E-01
B035DRAFT_03716	Bacteroides conjugative transposon TraN protein	32.4	19.6	27.0	23.9	26.7	8.9	0.69	5.9E-01
B035DRAFT_03717	Bacteroides conjugative transposon TraM protein	14.3	5.4	13.6	9.5	8.5	1.5	0.49	5.6E-01
B035DRAFT_03718	hypothetical protein	10.3	7.3	9.6	8.9	11.9	4.3	0.86	8.0E-01
B035DRAFT_03719	Bacteroides conjugative transposon TraK protein	16.6	9.9	14.5	12.8	13.1	5.4	0.72	5.9E-01
B035DRAFT_03720	Bacteroides conjugative transposon TraJ protein	20.4	10.8	18.4	17.3	17.6	5.7	0.75	7.1E-01
B035DRAFT_03721	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.93	
B035DRAFT_03722	(miscRNA)	22.9	12.3	21.4	22.7	25.1	8.6	0.00	9.3E-01
B035DRAFT_03723	Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta)	178.1	157.6	169.2	108.6	166.2	109.0	0.75	3.0E-01
B035DRAFT_03724	Acetyl/propionyl-CoA carboxylase, alpha subunit	163.4	127.1	139.0	92.4	124.9	71.1	0.66	2.4E-01
B035DRAFT_03725	acetyl-CoA carboxylase, biotin carboxylase subunit(EC:6.3.4.14,EC:6.4.1.2)	220.3	204.2	215.8	159.5	187.6	134.7	0.75	1.6E-01
B035DRAFT_03726	Uncharacterized conserved protein	200.6	232.5	181.9	163.5	136.1	154.7	0.74	1.4E-01
B035DRAFT_03727	Sortase and related acyltransferases(EC:2.3.1.183)	67.5	69.1	58.3	95.7	102.4	88.0	1.47	5.1E-02
B035DRAFT_03728	Fe-S oxidoreductase	68.8	78.3	77.7	87.9	87.7	82.0	1.15	1.7E-01
B035DRAFT_03729	Acetyltransferases	30.7	32.5	20.1	32.3	35.7	30.4	1.20	5.1E-01
B035DRAFT_03730	hypothetical protein	29.7	34.9	27.7	33.5	30.1	27.3	0.98	9.3E-01
B035DRAFT_03731	Outer membrane receptor proteins, mostly Fe transport	32.9	34.5	32.6	29.1	34.4	25.4	0.88	4.4E-01
B035DRAFT_03732	Gram-negative bacterial tonB protein.	21.1	25.7	20.7	18.7	20.6	24.6	0.95	7.8E-01
B035DRAFT_03733	hypothetical protein	27.8	34.8	29.2	21.1	22.7	27.1	0.77	2.1E-01
B035DRAFT_03734	hypothetical protein	22.3	24.5	25.2	19.1	16.7	8.6	0.58	2.7E-01
B035DRAFT_03735	hypothetical protein	108.6	125.1	115.0	116.4	96.6	55.7	0.74	4.6E-01
B035DRAFT_03736	hypothetical protein	223.8	264.1	246.7	253.7	256.0	225.4	1.00	9.9E-01
B035DRAFT_03737	hypothetical protein	12.7	18.0	13.0	19.6	18.7	22.0	1.39	1.9E-01
B035DRAFT_03738	Dipeptidyl aminopeptidases/acylaminoacyl-peptidases (CE10)	12.2	14.5	14.3	13.6	14.7	16.8	1.10	5.3E-01
B035DRAFT_03739	Predicted metal-dependent membrane protease	20.1	18.7	21.5	17.1	20.6	23.3	1.01	9.8E-01
B035DRAFT_03740	hypothetical protein	14.3	16.7	14.5	12.9	11.3	14.0	0.84	2.5E-01
B035DRAFT_03741	hypothetical protein	9.6	10.0	9.6	12.3	8.7	12.2	1.12	5.8E-01
B035DRAFT_03742	hypothetical protein	12.1	14.1	17.3	9.0	9.0	9.1	0.63	7.9E-02
B035DRAFT_03743	Predicted transcriptional regulator	11.1	12.9	18.3	18.4	13.7	10.1	0.99	9.8E-01
B035DRAFT_03744	Superfamily II DNA and RNA helicases(EC:3.6.4.13)	879.6	794.8	713.5	835.1	908.1	742.5	1.04	8.0E-01
B035DRAFT_03745	Peptidase S46.	139.6	146.4	142.2	131.3	150.4	149.7	1.01	9.5E-01
B035DRAFT_03746	TIGR00341 family protein	164.0	169.3	158.7	141.3	169.9	168.1	0.97	8.1E-01
B035DRAFT_03747	Membrane protein involved in the export of O-antigen and teichoic acid	160.7	159.8	152.8	133.7	166.8	167.5	0.98	9.2E-01
B035DRAFT_03748	Holliday junction DNA helicase, RuvB subunit(EC:3.6.4.12)	253.0	239.3	265.5	228.5	236.3	157.1	0.81	3.9E-01
B035DRAFT_03749	Site-specific recombinase XerD	262.6	315.8	288.7	244.2	247.3	317.3	0.93	6.9E-01

B035DRAFT_03750	hypothetical protein	350.8	465.5	414.8	345.0	284.3	439.1	0.86	5.8E-01
B035DRAFT_03751	hypothetical protein	177.8	223.5	199.0	205.2	173.8	236.3	1.02	9.3E-01
B035DRAFT_03752	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03753	putative efflux protein, MATE family	29.4	37.1	31.9	17.9	21.6	24.2	0.65	9.8E-02
B035DRAFT_03754	Acetyltransferase (isoleucine patch superfamily)	24.3	22.3	28.6	18.0	20.3	26.4	0.85	5.2E-01
B035DRAFT_03755	hypothetical protein	32.7	41.6	38.1	27.1	37.3	39.3	0.92	7.3E-01
B035DRAFT_03756	Protein of unknown function (DUF3584).	30.5	34.0	28.8	22.9	26.8	29.4	0.85	3.1E-01
B035DRAFT_03757	hypothetical protein	38.3	45.5	34.6	24.5	31.6	36.2	0.77	3.3E-01
B035DRAFT_03758	hypothetical protein	29.4	30.2	28.5	27.9	25.7	34.0	0.99	9.5E-01
B035DRAFT_03759	Predicted transcriptional regulators	27.7	29.5	28.5	22.7	24.2	34.1	0.93	7.7E-01
B035DRAFT_03760	AraC-type DNA-binding domain-containing proteins	31.7	37.2	34.5	39.2	36.2	39.1	1.11	3.1E-01
B035DRAFT_03761	hypothetical protein	6.7	4.7	4.9	8.5	3.6	3.7	0.90	8.6E-01
B035DRAFT_03762	Uncharacterized homolog of gamma-carboxymuconolactone decarboxylase subunit(EC:4.1.1.44)	12.7	9.5	14.0	9.4	9.4	10.8	0.83	4.1E-01
B035DRAFT_03763	Flavodoxins	16.1	19.0	13.4	14.1	15.9	18.4	1.00	9.9E-01
B035DRAFT_03764	hypothetical protein	14.4	15.2	11.2	13.8	11.9	15.5	1.01	9.7E-01
B035DRAFT_03765	Viral (Superfamily 1) RNA helicase.	40.7	34.0	28.9	26.2	30.7	31.5	0.86	4.6E-01
B035DRAFT_03766	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03767	Sulfotransferase domain.	153.1	144.2	148.4	200.5	204.3	199.3	1.36	2.8E-03
B035DRAFT_03768	sulfate adenylyltransferase, large subunit(EC:2.7.7.4)	150.6	134.7	126.3	152.8	188.4	162.2	1.22	2.2E-01
B035DRAFT_03769	sulfate adenylyltransferase, small subunit(EC:2.7.7.4)	96.9	89.6	83.8	100.0	132.3	111.4	1.27	2.1E-01
B035DRAFT_03770	Adenylylsulfate kinase and related kinases(EC:2.7.1.25)	56.6	46.6	46.8	70.3	78.7	59.2	1.38	1.5E-01
B035DRAFT_03771	Di- and tricarboxylate transporters	71.2	67.2	66.8	73.7	87.4	82.4	1.18	1.5E-01
B035DRAFT_03772	3''(2''),5''-bisphosphate nucleotidase, bacterial	97.8	81.5	90.9	92.2	116.5	72.6	1.03	9.3E-01
B035DRAFT_03773	Outer membrane protein/protective antigen OMA87	53.2	56.2	52.3	59.6	71.4	67.3	1.22	1.2E-01
B035DRAFT_03774	hypothetical protein	68.1	63.1	72.4	62.3	62.8	30.7	0.73	4.7E-01
B035DRAFT_03775	Peptidase C10 family	103.7	93.8	108.7	116.9	119.5	60.1	0.93	8.6E-01
B035DRAFT_03776	Two component regulator propeller.	14.2	15.5	16.4	14.0	15.2	19.0	1.04	8.4E-01
B035DRAFT_03777	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03778	TonB-linked outer membrane protein, SusC/RagA family	849.4	836.2	823.5	510.2	713.6	875.9	0.82	4.8E-01
B035DRAFT_03779	SusD family	1108.3	1082.2	969.6	608.0	893.0	1018.3	0.78	4.0E-01
B035DRAFT_03780	Predicted membrane protein	96.1	117.1	107.0	120.5	128.6	135.6	1.20	1.8E-01
B035DRAFT_03781	ABC-type antimicrobial peptide transport system, permease component	24.9	28.8	32.1	31.9	37.6	36.2	1.23	2.3E-01
B035DRAFT_03782	ABC-type antimicrobial peptide transport system, permease component	37.8	38.6	36.6	37.8	41.1	48.0	1.12	4.0E-01
B035DRAFT_03783	Lyzozyme M1 (1,4-beta-N-acetylmuramidase) (GH25)	101.4	114.1	103.7	97.3	111.9	123.4	1.04	8.0E-01
B035DRAFT_03784	diphosphate--fructose-6-phosphate 1-phosphotransferase(EC:2.7.1.90)	1263.7	1332.7	1309.2	1201.3	1410.7	1560.5	1.06	6.7E-01
B035DRAFT_03785	hypothetical protein	1192.0	1283.1	1122.7	1312.6	1138.3	1422.4	1.07	6.0E-01
B035DRAFT_03786	1-acyl-sn-glycerol-3-phosphate acyltransferase	1349.6	1530.1	1376.6	1475.5	1361.7	1665.1	1.06	6.7E-01
B035DRAFT_03787	hypothetical protein	81.7	108.5	92.4	100.6	108.3	133.7	1.21	3.8E-01
B035DRAFT_03788	hypothetical protein	1532.3	1601.1	1570.3	1529.4	1497.1	1556.3	0.97	4.0E-01
B035DRAFT_03789	Galactosyltransferase.	109.3	125.2	136.8	82.8	76.7	103.7	0.71	1.5E-01
B035DRAFT_03790	hypothetical protein	100.8	127.6	117.3	173.4	189.9	191.1	1.61	4.0E-02
B035DRAFT_03791	RNA polymerase sigma-70 factor, Bacteroides expansion family 1	70.1	90.5	81.8	88.0	108.9	113.1	1.28	2.5E-01
B035DRAFT_03792	Fe2+-dicitrate sensor, membrane component	76.2	74.7	75.9	75.5	92.4	79.1	1.08	4.6E-01
B035DRAFT_03793	TonB-linked outer membrane protein, SusC/RagA family	13.8	14.3	12.2	11.4	13.7	14.7	0.98	9.2E-01
B035DRAFT_03794	SusD family	38.8	35.3	34.0	25.4	32.8	31.6	0.83	2.7E-01
B035DRAFT_03795	Predicted phosphohydrolases	49.3	45.5	39.7	40.9	32.8	43.6	0.87	4.7E-01
B035DRAFT_03796	Beta-galactosidase/beta-glucuronidase(EC:3.2.1.23) (GH2)	31.6	28.9	27.0	20.9	23.6	23.8	0.78	9.4E-02
B035DRAFT_03797	hypothetical protein	9.3	10.3	10.8	14.0	6.8	6.9	0.86	7.3E-01
B035DRAFT_03798	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.8E-01

B035DRAFT_03799	Predicted unsaturated glucuronyl hydrolase involved in regulation of bacterial surface properties, and related proteins (GH105)	40.4	40.5	38.9	42.9	52.2	45.4	1.17	2.0E-01
B035DRAFT_03800	TonB-linked outer membrane protein, SusC/RagA family	7.5	6.2	6.7	6.5	8.9	9.4	1.19	4.5E-01
B035DRAFT_03801	F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein)	9.7	8.5	10.8	9.8	9.9	12.0	1.10	6.0E-01
B035DRAFT_03802	His Kinase A (phosphoacceptor) domain./Response regulator receiver domain./Y_Y_Y domain./Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	33.7	43.6	43.0	50.6	54.7	70.2	1.45	1.7E-01
B035DRAFT_03803	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03804	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03805	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.92	
B035DRAFT_03806	(miscRNA)	17.3	12.4	13.4	11.3	13.7	14.6	0.00	7.3E-01
B035DRAFT_03807	Bacteroides conjugative transposon TraJ protein	3.8	2.8	3.0	1.9	2.5	1.0	0.53	2.7E-01
B035DRAFT_03808	Bacteroides conjugative transposon TraK protein	2.4	3.5	3.3	3.1	2.0	2.7	0.84	5.9E-01
B035DRAFT_03809	hypothetical protein	1.8	2.1	6.0	2.6	1.7	0.6	0.47	4.7E-01
B035DRAFT_03810	Bacteroides conjugative transposon TraM protein	2.8	1.8	1.7	3.0	2.1	0.9	0.86	8.5E-01
B035DRAFT_03811	Bacteroides conjugative transposon TraN protein	5.0	3.2	4.7	3.3	6.3	3.0	0.94	9.0E-01
B035DRAFT_03812	Conjugative transposon protein TraO.	3.0	4.2	6.2	3.8	2.2	0.5	0.39	4.0E-01
B035DRAFT_03813	hypothetical protein	10.6	4.1	5.2	6.2	6.7	6.8	1.07	9.0E-01
B035DRAFT_03814	hypothetical protein	8.9	8.6	1.8	1.6	9.4	10.8	1.05	9.8E-01
B035DRAFT_03815	hypothetical protein	6.4	2.8	5.4	7.7	4.9	7.1	1.40	5.1E-01
B035DRAFT_03816	hypothetical protein	1.6	0.0	1.3	3.5	5.0	5.5	3.07	6.4E-02
B035DRAFT_03817	hypothetical protein	0.8	0.0	1.9	1.6	4.9	1.4	1.86	5.8E-01
B035DRAFT_03818	hypothetical protein	1.2	1.1	1.0	0.7	1.4	2.2	1.21	7.7E-01
B035DRAFT_03819	hypothetical protein	0.8	1.4	1.0	1.3	1.8	0.7	1.15	8.1E-01
B035DRAFT_03820	hypothetical protein	1.4	1.6	1.7	2.2	0.0	1.9	1.31	2.2E-01
B035DRAFT_03821	hypothetical protein	0.0	0.0	2.4	0.5	0.5	0.0	0.20	
B035DRAFT_03822	hypothetical protein	1.6	0.9	1.0	2.5	1.5	0.7	1.23	7.9E-01
B035DRAFT_03823	hypothetical protein	32.4	49.1	44.7	66.4	56.6	60.1	1.47	1.7E-01
B035DRAFT_03824	hypothetical protein	48.2	50.8	67.6	56.2	53.7	57.9	1.02	9.3E-01
B035DRAFT_03825	Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain	24.8	29.9	26.1	24.9	21.4	29.8	0.94	7.5E-01
B035DRAFT_03826	hypothetical protein	52.9	43.8	50.2	37.3	32.5	35.7	0.72	7.0E-02
B035DRAFT_03827	hypothetical protein	42.2	45.6	44.2	32.0	27.9	34.2	0.71	5.8E-02
B035DRAFT_03828	hypothetical protein	31.7	43.7	40.5	21.7	33.8	37.6	0.79	5.0E-01
B035DRAFT_03829	hypothetical protein	21.4	22.5	19.4	16.3	20.2	24.0	0.95	8.1E-01
B035DRAFT_03830	hypothetical protein	8.7	7.6	18.4	5.7	17.7	10.8	0.97	9.7E-01
B035DRAFT_03831	hypothetical protein	10.9	10.9	9.5	8.2	5.7	25.6	1.02	9.9E-01
B035DRAFT_03832	hypothetical protein	10.9	10.5	9.8	4.5	7.4	12.3	0.71	5.2E-01
B035DRAFT_03833	hypothetical protein	15.6	33.5	24.7	22.1	26.4	27.4	1.07	8.8E-01
B035DRAFT_03834	hypothetical protein	45.5	41.7	43.5	45.3	48.4	45.1	1.06	3.5E-01
B035DRAFT_03835	hypothetical protein	20.6	19.6	26.0	15.0	22.4	22.6	0.90	7.2E-01
B035DRAFT_03836	hypothetical protein	15.1	15.3	18.7	13.5	14.6	19.6	0.96	8.9E-01
B035DRAFT_03837	hypothetical protein	24.0	29.7	35.6	19.8	37.4	46.4	1.11	8.6E-01
B035DRAFT_03838	Protein of unknown function (DUF1573).	92.7	99.3	101.9	98.5	93.3	101.5	1.00	9.8E-01
B035DRAFT_03839	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03840	hypothetical protein	47.2	41.3	43.3	36.4	36.2	36.3	0.83	6.8E-02
B035DRAFT_03841	hypothetical protein	4.7	6.3	7.1	3.6	3.2	2.5	0.52	9.6E-02
B035DRAFT_03842	hypothetical protein	5.5	5.0	3.7	2.6	2.5	2.1	0.51	7.4E-02
B035DRAFT_03843	VirE N-terminal domain.	1.3	3.1	3.0	0.8	1.2	2.2	0.56	4.3E-01
B035DRAFT_03844	hypothetical protein	1.8	1.0	0.0	2.8	1.6	0.8	1.14	8.9E-01

B035DRAFT_03845	hypothetical protein	8.1	10.3	9.0	10.1	12.0	8.0	1.09	7.3E-01
B035DRAFT_03846	Site-specific DNA methylase	6.5	8.6	8.2	8.8	9.3	6.5	1.06	8.4E-01
B035DRAFT_03847	hypothetical protein	8.9	9.0	12.3	4.1	6.7	9.9	0.65	3.9E-01
B035DRAFT_03848	hypothetical protein	9.1	17.8	9.3	7.0	9.1	8.2	0.71	4.1E-01
B035DRAFT_03849	hypothetical protein	266.4	312.5	267.5	240.5	252.5	347.4	0.98	9.5E-01
B035DRAFT_03850	hypothetical protein	680.3	774.7	728.3	665.5	668.0	965.0	1.04	8.8E-01
B035DRAFT_03851	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03852	hypothetical protein	28.1	25.9	26.8	23.2	24.6	21.3	0.86	1.5E-01
B035DRAFT_03853	AraC-type DNA-binding domain-containing proteins	19.7	17.6	22.2	17.8	20.9	20.3	0.99	9.8E-01
B035DRAFT_03854	3-carboxymuconate cyclase	14.9	12.1	16.3	11.1	11.0	10.5	0.76	1.6E-01
B035DRAFT_03855	Hydrolases of the alpha/beta superfamily	47.0	39.7	46.5	40.9	45.6	39.1	0.94	6.6E-01
B035DRAFT_03856	TonB-linked outer membrane protein, SusC/RagA family	274.0	280.7	262.6	252.5	269.6	282.5	0.98	8.2E-01
B035DRAFT_03857	SusD family	212.7	197.6	214.8	192.5	222.6	198.8	0.98	8.5E-01
B035DRAFT_03858	Cyclic nucleotide-binding domain.	390.8	368.9	352.5	295.4	323.6	349.5	0.87	2.2E-01
B035DRAFT_03859	Type IV secretory pathway, VirD4 components	28.3	26.6	30.3	32.3	32.7	26.2	1.07	6.6E-01
B035DRAFT_03860	Relaxase/Mobilisation nuclease domain.	13.0	9.3	13.0	16.8	14.3	5.6	0.95	9.5E-01
B035DRAFT_03861	hypothetical protein	11.5	11.1	15.0	14.6	11.1	7.2	0.85	7.0E-01
B035DRAFT_03862	ATPases involved in chromosome partitioning	26.4	16.5	27.5	31.0	29.3	10.7	0.93	9.3E-01
B035DRAFT_03863	Protein of unknown function (DUF3408).	14.9	10.2	13.1	24.2	14.9	3.5	0.86	9.0E-01
B035DRAFT_03864	Protein of unknown function (DUF3408).	30.6	16.4	20.1	19.4	14.5	6.2	0.56	4.1E-01
B035DRAFT_03865	hypothetical protein	55.1	23.4	46.8	65.4	41.6	9.7	0.76	8.2E-01
B035DRAFT_03866	hypothetical protein	63.3	40.3	60.6	98.6	99.1	50.7	1.47	4.2E-01
B035DRAFT_03867	hypothetical protein	98.9	63.1	100.6	119.1	132.4	64.1	1.17	7.6E-01
B035DRAFT_03868	Bacteroides conjugation system ATPase, TraG family	71.2	36.6	59.1	65.6	67.5	20.5	0.84	8.4E-01
B035DRAFT_03869	hypothetical protein	52.3	22.2	35.6	51.8	46.2	14.5	0.94	9.5E-01
B035DRAFT_03870	hypothetical protein	41.4	19.8	25.9	43.1	43.3	20.3	1.21	7.6E-01
B035DRAFT_03871	hypothetical protein	256.9	257.1	242.9	256.2	225.6	317.6	1.05	8.2E-01
B035DRAFT_03872	RHS repeat-associated core domain	44.2	35.1	41.4	36.3	33.4	29.9	0.83	2.7E-01
B035DRAFT_03873	Protein of unknown function (DUF877).	3.8	3.3	4.0	4.4	4.0	2.2	0.92	8.5E-01
B035DRAFT_03874	hypothetical protein	3.6	2.5	2.6	3.4	3.9	3.9	1.30	2.7E-01
B035DRAFT_03875	hypothetical protein	2.0	0.6	1.1	1.6	1.9	0.5	1.04	9.8E-01
B035DRAFT_03876	Uncharacterized protein conserved in bacteria	1.4	0.9	1.4	1.4	1.4	1.3	1.13	6.8E-01
B035DRAFT_03877	hypothetical protein	100.8	103.8	113.9	90.9	89.8	79.6	0.82	1.2E-01
B035DRAFT_03878	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03879	hypothetical protein	252.5	308.4	282.4	334.3	294.0	298.8	1.10	4.5E-01
B035DRAFT_03880	(tRNA)	197.4	178.5	181.5	140.9	91.5	45.9	0.45	2.3E-01
B035DRAFT_03881	Putative p-aminobenzoyl-glutamate transporter	51.1	68.8	59.2	56.3	62.3	78.7	1.10	7.0E-01
B035DRAFT_03882	Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain	51.9	58.2	49.3	57.8	58.4	68.7	1.16	3.0E-01
B035DRAFT_03883	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase.	31.4	34.0	33.5	32.4	37.0	43.9	1.14	4.4E-01
B035DRAFT_03884	Histone H1-like protein Hc1.	1650.1	2635.9	2185.6	2646.3	2092.7	2602.1	1.15	6.2E-01
B035DRAFT_03885	L-lactate transport	260.0	255.9	287.6	266.5	173.3	239.2	0.83	4.5E-01
B035DRAFT_03886	hypothetical protein	20.0	23.2	21.5	13.7	16.9	19.1	0.76	2.1E-01
B035DRAFT_03887	Transposase and inactivated derivatives	93.4	112.9	96.4	84.4	93.2	91.1	0.89	3.5E-01
B035DRAFT_03888	hypothetical protein	101.5	114.0	102.8	111.5	111.3	114.9	1.06	3.9E-01
B035DRAFT_03889	hypothetical protein	16.1	15.6	22.8	9.9	8.5	21.9	0.69	5.1E-01
B035DRAFT_03890	hypothetical protein	3.0	3.6	3.0	2.1	2.0	2.4	0.68	7.9E-02
B035DRAFT_03891	hypothetical protein	3.5	2.3	4.2	4.2	5.0	3.2	1.24	5.9E-01
B035DRAFT_03892	Outer membrane protein and related peptidoglycan-associated (lipo)proteins	52.8	22.0	50.7	34.0	21.1	6.4	0.43	4.2E-01
B035DRAFT_03893	hypothetical protein	5.9	2.6	6.9	5.0	3.8	1.3	0.62	6.0E-01

B035DRAFT_03894	hypothetical protein	8.5	8.8	9.6	7.2	7.5	6.5	0.79	8.6E-02
B035DRAFT_03895	hypothetical protein	12.8	9.8	11.3	8.0	6.9	7.4	0.66	7.2E-02
B035DRAFT_03896	Transposase and inactivated derivatives, IS30 family	171.5	172.7	151.3	153.0	167.8	111.7	0.86	5.2E-01
B035DRAFT_03897	Bacterial nucleoid DNA-binding protein	81.6	72.7	78.1	73.2	65.3	41.0	0.75	3.9E-01
B035DRAFT_03898	Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen(EC:3.6.4.12)	59.9	60.5	57.3	74.5	80.9	79.3	1.32	1.7E-02
B035DRAFT_03899	DNA primase (bacterial type)	44.9	35.6	46.0	48.7	40.8	27.9	0.91	7.9E-01
B035DRAFT_03900	hypothetical protein	46.4	49.1	40.3	43.6	54.8	47.4	1.07	6.7E-01
B035DRAFT_03901	hypothetical protein	20.3	18.8	20.3	26.3	21.3	19.4	1.12	5.1E-01
B035DRAFT_03902	hypothetical protein	14.1	21.5	18.2	27.8	23.9	18.4	1.30	4.0E-01
B035DRAFT_03903	Predicted transcriptional regulator with C-terminal CBS domains	99.3	97.8	104.1	150.1	111.5	111.4	1.23	2.9E-01
B035DRAFT_03904	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03905	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03906	Transcriptional regulator	104.6	148.1	125.3	96.9	100.6	117.0	0.84	4.0E-01
B035DRAFT_03907	3-oxoacyl-[acyl-carrier-protein] synthase III(EC:2.3.1.180)	208.8	203.6	198.3	187.7	211.4	257.8	1.07	7.1E-01
B035DRAFT_03908	Transcriptional regulator	121.6	119.8	110.2	119.7	144.3	161.4	1.20	3.0E-01
B035DRAFT_03909	hypothetical protein	253.8	255.0	258.4	318.5	323.0	327.2	1.26	6.3E-04
B035DRAFT_03910	hypothetical protein	311.8	267.9	281.9	345.3	359.2	306.8	1.17	2.2E-01
B035DRAFT_03911	hypothetical protein	296.0	280.7	267.3	366.8	391.4	341.7	1.30	5.5E-02
B035DRAFT_03912	hypothetical protein	25.6	20.8	17.6	25.1	21.7	32.6	1.24	4.7E-01
B035DRAFT_03913	hypothetical protein	101.4	107.9	97.4	86.5	100.4	128.4	1.02	9.5E-01
B035DRAFT_03914	hypothetical protein	94.9	107.6	112.1	99.9	100.4	124.3	1.03	8.7E-01
B035DRAFT_03915	Site-specific recombinase XerD	1.6	5.8	3.0	2.8	3.2	2.9	0.99	9.9E-01
B035DRAFT_03916	hypothetical protein	4.7	3.9	6.0	4.5	4.0	3.2	0.81	4.6E-01
B035DRAFT_03917	hypothetical protein	4.7	5.4	6.0	2.9	2.3	3.0	0.51	4.3E-02
B035DRAFT_03918	Site-specific recombinase XerD	13.6	13.1	15.7	10.0	12.4	9.2	0.74	1.8E-01
B035DRAFT_03919	Site-specific recombinase XerD	13.8	9.9	10.1	8.0	11.6	11.5	0.92	7.8E-01
B035DRAFT_03920	hypothetical protein	11.7	3.9	10.8	9.3	14.8	4.6	1.09	9.3E-01
B035DRAFT_03921	Predicted site-specific integrase-resolvase	211.6	192.6	163.6	214.7	234.4	139.1	1.02	9.7E-01
B035DRAFT_03922	hypothetical protein	49.6	61.9	57.9	57.5	61.6	85.2	1.19	4.8E-01
B035DRAFT_03923	hypothetical protein	114.0	128.6	120.3	143.9	129.6	161.1	1.19	2.2E-01
B035DRAFT_03924	hypothetical protein	35.7	34.2	32.7	24.3	25.9	17.6	0.65	1.3E-01
B035DRAFT_03925	hypothetical protein	28.6	31.4	30.6	21.4	19.1	21.0	0.68	2.1E-02
B035DRAFT_03926	hypothetical protein	58.8	54.2	40.4	43.0	20.3	31.1	0.60	2.8E-01
B035DRAFT_03927	hypothetical protein	45.5	46.5	43.0	36.0	45.1	60.4	1.03	9.3E-01
B035DRAFT_03928	hypothetical protein	19.5	29.8	26.7	16.0	18.7	19.8	0.73	2.5E-01
B035DRAFT_03929	hypothetical protein	39.8	25.2	22.2	18.2	13.0	24.0	0.63	3.3E-01
B035DRAFT_03930	hypothetical protein	39.4	41.6	47.3	28.3	29.3	41.6	0.76	3.0E-01
B035DRAFT_03931	hypothetical protein	30.7	45.0	33.2	29.9	32.3	58.0	1.07	8.9E-01
B035DRAFT_03932	hypothetical protein	29.0	30.1	29.7	19.7	19.6	24.5	0.71	7.8E-02
B035DRAFT_03933	hypothetical protein	79.4	87.6	110.6	81.1	75.4	94.0	0.91	6.5E-01
B035DRAFT_03934	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03935	Superfamily I DNA and RNA helicases	151.2	174.2	168.2	156.4	155.8	192.6	1.02	9.1E-01
B035DRAFT_03936	Predicted ATP-dependent endonuclease of the OLD family	176.5	172.0	167.0	143.3	156.8	197.3	0.96	8.1E-01
B035DRAFT_03937	Predicted ATPase (AAA+ superfamily)	249.3	270.3	226.6	228.9	250.5	274.6	1.01	9.5E-01
B035DRAFT_03938	RteC protein.	21.0	17.5	19.0	23.9	23.3	19.6	1.16	3.3E-01
B035DRAFT_03939	Dihydrofolate reductase	146.5	167.0	171.8	181.7	156.8	130.9	0.96	8.5E-01
B035DRAFT_03940	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03941	hypothetical protein	31.6	37.7	43.2	15.4	18.2	21.7	0.49	5.7E-02
B035DRAFT_03942	radical SAM peptide maturase, GG-Bacteroidales family	12.8	13.7	12.6	7.0	6.4	5.8	0.49	7.6E-03

B035DRAFT_03943	hypothetical protein	11.6	13.3	13.6	5.5	4.9	4.7	0.39	5.9E-03
B035DRAFT_03944	natural product precursor, GG-Bacteroidales family	8.7	17.1	14.7	6.4	5.5	7.9	0.50	1.6E-01
B035DRAFT_03945	glycosyltransferase, GG-Bacteroidales peptide system (GT4)	6.7	6.6	8.6	3.9	3.3	4.5	0.54	6.8E-02
B035DRAFT_03946	hypothetical protein	4.9	5.3	6.3	5.8	1.8	2.4	0.53	3.5E-01
B035DRAFT_03947	Protein of unknown function (DUF3244).	13.4	12.0	15.9	14.7	10.1	18.9	1.03	9.5E-01
B035DRAFT_03948	hypothetical protein	7.6	7.9	6.5	4.8	7.2	9.9	0.96	9.2E-01
B035DRAFT_03949	Glycosyltransferase (GT4)	2.4	4.6	3.2	2.1	1.1	3.3	0.60	4.5E-01
B035DRAFT_03950	Protein-disulfide isomerase	3.8	6.9	4.7	2.6	2.6	2.8	0.53	1.2E-01
B035DRAFT_03951	Peroxiredoxin	4.8	8.0	6.0	4.8	2.9	3.9	0.61	2.4E-01
B035DRAFT_03952	hypothetical protein	30.0	29.8	32.0	30.0	39.8	36.6	1.15	3.8E-01
B035DRAFT_03953	ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain	22.5	15.2	19.4	17.5	14.0	7.9	0.66	4.0E-01
B035DRAFT_03954	Galactosyltransferase (GT2)	126.3	118.6	135.8	69.2	85.1	79.2	0.61	3.3E-02
B035DRAFT_03955	hypothetical protein	92.8	104.1	105.9	51.9	60.3	78.5	0.62	1.1E-01
B035DRAFT_03956	hypothetical protein	81.1	86.7	87.1	41.6	44.7	44.9	0.51	1.4E-03
B035DRAFT_03957	natural product precursor, GG-Bacteroidales family	78.8	86.2	95.9	46.0	57.6	60.2	0.63	7.2E-02
B035DRAFT_03958	hypothetical protein	69.3	78.3	87.3	41.3	50.5	63.8	0.65	1.7E-01
B035DRAFT_03959	hypothetical protein	72.9	77.0	92.7	66.2	69.7	74.7	0.87	3.6E-01
B035DRAFT_03960	Lanthionine synthetase C-like protein.	77.8	96.4	97.8	83.4	106.9	123.5	1.14	5.9E-01
B035DRAFT_03961	hypothetical protein	75.5	83.0	58.5	73.7	83.4	101.1	1.19	4.8E-01
B035DRAFT_03962	hypothetical protein	463.3	586.2	539.7	741.3	671.4	763.6	1.37	9.4E-02
B035DRAFT_03963	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03964	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03965	Alkyl hydroperoxide reductase, large subunit	447.8	414.9	435.6	413.4	455.4	257.1	0.84	5.9E-01
B035DRAFT_03966	(tRNA)	663.9	997.1	886.5	700.4	322.7	168.9	0.40	2.8E-01
B035DRAFT_03967	(tRNA)	490.0	1119.5	1241.1	590.6	446.9	447.2	0.56	3.2E-01
B035DRAFT_03968	Sugar kinases, ribokinase family	42.4	46.8	47.3	41.8	52.6	38.4	0.97	8.6E-01
B035DRAFT_03969	C-terminal peptidase (prc)(EC:3.4.21.102)	210.2	212.1	217.6	351.0	334.4	253.2	1.45	1.2E-01
B035DRAFT_03970	hypothetical protein	85.6	94.1	79.9	164.6	161.6	154.6	1.86	7.5E-03
B035DRAFT_03971	hypothetical protein	1828.8	2155.5	1905.4	2377.5	2315.1	2785.1	1.27	1.5E-01
B035DRAFT_03972	hypothetical protein	3581.9	4168.7	3622.1	4673.3	4729.5	5495.4	1.31	1.1E-01
B035DRAFT_03973	hypothetical protein	7.0	4.4	3.4	2.9	3.8	3.8	0.74	4.6E-01
B035DRAFT_03974	hypothetical protein	11.9	13.0	11.7	7.6	9.8	15.3	0.85	6.7E-01
B035DRAFT_03975	Relaxase/Mobilisation nuclease domain.	11.2	10.3	9.1	11.0	11.6	11.8	1.13	3.2E-01
B035DRAFT_03976	hypothetical protein	12.2	10.9	6.5	4.3	11.5	4.1	0.62	4.9E-01
B035DRAFT_03977	Protein of unknown function (DUF3408).	41.9	30.3	27.4	40.8	40.5	24.9	1.06	8.9E-01
B035DRAFT_03978	hypothetical protein	24.1	15.5	17.4	28.6	17.6	12.1	0.98	9.7E-01
B035DRAFT_03979	(rRNA)	6.5	11.9	7.7	4.1	7.9	9.3		6.9E-01
B035DRAFT_03980	Threonine dehydrogenase and related Zn-dependent dehydrogenases	33.1	38.2	29.8	31.0	43.9	36.2	1.09	6.9E-01
B035DRAFT_03981	rRNA methylases	81.1	69.5	83.6	91.7	95.1	75.6	1.12	5.0E-01
B035DRAFT_03982	Viral (Superfamily 1) RNA helicase.	58.4	62.5	56.4	52.6	56.0	74.7	1.02	9.2E-01
B035DRAFT_03983	Small-conductance mechanosensitive channel	246.6	269.9	285.5	265.0	204.2	288.5	0.94	7.6E-01
B035DRAFT_03984	hypothetical protein	73.5	101.8	118.0	110.3	102.1	164.9	1.28	5.0E-01
B035DRAFT_03985	hypothetical protein	217.2	327.3	282.5	382.3	304.2	439.7	1.37	3.1E-01
B035DRAFT_03986	Bacteroides conjugation system ATPase, TraG family	1.4	1.4	1.1	0.5	1.4	0.7	0.59	3.9E-01
B035DRAFT_03987	hypothetical protein	0.0	0.5	0.6	0.5	1.2	0.4	1.16	8.3E-01
B035DRAFT_03988	hypothetical protein	0.7	0.9	0.9	0.8	0.7	0.7	0.85	2.8E-01
B035DRAFT_03989	hypothetical protein	3.5	3.6	4.9	3.3	3.7	4.0	0.92	6.9E-01
B035DRAFT_03990	hypothetical protein	14.3	13.8	20.9	11.2	10.7	5.2	0.53	2.6E-01
B035DRAFT_03991	Relaxase/Mobilisation nuclease domain.	17.4	19.3	17.3	9.8	11.3	12.1	0.61	3.3E-02
B035DRAFT_03992	hypothetical protein	18.6	11.6	17.7	11.0	7.8	8.9	0.58	1.6E-01

B035DRAFT_03993	hypothetical protein	131.0	69.7	92.4	103.1	114.3	123.5	1.20	6.0E-01
B035DRAFT_03994	Retron-type reverse transcriptase	262.5	178.0	236.9	204.0	254.0	328.0	1.15	6.6E-01
B035DRAFT_03995	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03996	(miscRNA)	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_03997	hypothetical protein	1.5	2.1	1.5	2.3	2.8	2.5	1.48	1.6E-01
B035DRAFT_03998	Site-specific recombinase XerD	2.1	2.9	2.8	3.0	4.3	2.9	1.30	3.8E-01
B035DRAFT_03999	Site-specific recombinase XerD	1.8	2.3	2.6	2.1	3.5	3.5	1.32	4.4E-01
B035DRAFT_04000	hypothetical protein	2773.3	2787.9	2735.1	2866.9	2781.2	2519.2	0.98	8.2E-01
B035DRAFT_04001	IS66 Orf2 like protein.	1687.8	1661.4	1634.3	1455.6	1649.3	1785.3	0.98	8.5E-01
B035DRAFT_04002	Transposase IS66 family	2901.8	2502.2	2552.7	2626.1	2730.7	2095.6	0.93	6.8E-01
B035DRAFT_04003	Protein of unknown function (DUF1016).	17.2	17.6	15.0	13.7	14.9	10.0	0.77	3.0E-01
B035DRAFT_04004	Uncharacterized conserved protein	13.0	12.9	12.4	10.8	13.0	11.1	0.90	3.8E-01
B035DRAFT_04005	hypothetical protein	0.0	0.0	0.0	0.0	0.0	0.0	0.00	
B035DRAFT_04006	Transposase domain (DUF772).	223.1	218.2	220.8	243.1	240.5	202.2	1.03	7.8E-01
B035DRAFT_04007	UbiA prenyltransferase family	70.7	78.5	76.1	64.9	64.3	73.9	0.90	3.2E-01
B035DRAFT_04008	Phosphoserine phosphatase	64.0	57.5	58.5	58.7	59.5	69.8	1.04	7.3E-01
B035DRAFT_04009	Transposase DDE domain.	463.6	488.7	506.5	433.3	441.6	499.7	0.94	5.1E-01
B035DRAFT_04010	hypothetical protein	84.7	103.2	78.5	85.0	83.2	105.2	1.03	9.0E-01
B035DRAFT_04011	hypothetical protein	75.1	94.8	82.9	69.9	65.2	93.5	0.90	6.4E-01
B035DRAFT_04012	FOG: Transposase and inactivated derivatives	545.7	573.9	628.7	630.3	547.0	700.6	1.07	6.5E-01
B035DRAFT_04013	hypothetical protein	5.6	3.5	7.1	5.1	5.5	3.6	0.89	8.1E-01
B035DRAFT_04014	Lanthionine synthetase C-like protein.	28.3	45.1	43.3	41.4	36.6	68.1	1.23	6.4E-01
B035DRAFT_04015	Protein of unknown function (DUF3244).	6.4	12.2	9.7	4.8	3.6	13.5	0.68	6.3E-01