Table S1

Assembly of the genome of *Leptospirilum* group II from the 5-way CG location of the Richmond Mine (sample collected March 2002, as described by Tyson et al. 2004
The manually curated assembly (columns A to F) is compared with the draft assembly reported by Tyson et al. (column G). Red bars separate genome fragments for
linkage has been established. Blue bars indicate the positions of major strain variant sequences (shown at end).

Main genome path:

contig #	gene #	Locus_Tag	Product description	Length aa	Position on Phrap contig	Gene number (Tyson et al. 2004)
9398	1	CGL2_09398001	Putative cobyrinic acid a,c-diamide synthase	248	157..900	245_GENE_16
9398	2	CGL2_09398002	ParB-like partition protein	313	1047..1985	245_GENE_15
10284	1	CGL2_10284001	Transcriptional regulator, HxlR family	111	complement(680..1012)	245_GENE_14
10284	2	CGL2_10284002	NADPH:quinone reductase 1 (EC 1.6.5.5)	330	1184..2173	245_GENE_12
10284	3	CGL2_10284003	Hypothetical protein	69	2151..2357	245_GENE_11
10284	4	CGL2_10284004	Hypothetical protein	52	2483..2638	245_GENE_10
10284	5	CGL2_10284005	DNA methyltransferase	350	2661..3710	245_GENE_9
10284	6	CGL2_10284006	type II restriction endonuclease	241	3719..4441	245_GENE_8
10284	7	CGL2_10284007	isonitrile hydratase	268	4475..5278	245_GENE_7
10284	8	CGL2_10284008	Hypothetical protein	68	5385..5588	245_GENE_6
10284	9	CGL2_10284009	short-chain dehydrogenase	248	5576..6319	245_GENE_5
10284	10	CGL2_10284010	Putative phospholipid/glycerol acyltransferase	178	complement(6332..6865)	245_GENE_4
10284	11	CGL2_10284011	Probable conjugal transfer protein (TraB)	373	complement(7031..8149)	245_GENE_3
7472	2	CGL2_07472002	Probable conjugal transfer protein (TraF)	175	complement(1816..2340)	245_GENE_2
7472	1	CGL2_07472001	Putative diguanylate phosphodiesterase	256	complement(1040..1807)	245_GENE_1
8228	1	CGL2_08228001	Hypothetical protein	91	40..312	1147_GENE_3a
8228	2	CGL2_08228002	DNA topoisomerase III (EC 5.99.1.2)	684	320..2371	1147_GENE_3
8228	3	CGL2_08228003	Protein of unknown function	139	2334..2750	1147_GENE_2
8228	4	CGL2_08228004	Hypothetical protein	95	2807..3091	1147_GENE_1
8228	5	CGL2_08228005	Single-strand DNA-binding protein	133	3091..3489	
8228	6	CGL2_08228006	Hypothetical protein	16	3531..3578	
6046	1	CGL2_06046001	ssDNA binding protein	139	130..546	751_GENE_1
6046	2	CGL2_06046002	Hypothetical protein	78	609..842	751_GENE_2
6046	3	CGL2_06046003	DNA repair proteins (RadC)	146	829..1266	751_GENE_3
9933	1	CGL2_09933001	Conserved hypothetical protein	298	287..1180	751_GENE_4
9933	2	CGL2_09933002	Protein of unknown function	96	complement(1350..1637)	751_GENE_5
9933	3	CGL2_09933003	Conserved hypothetical protein	368	complement(1867..2970)	751_GENE_6
9207	1	CGL2_09207001	HD-GYP hydrolase domain protein/response regulato	206	116..733	259_GENE_12
9207	3	CGL2_09207003	Hypothetical protein	107	complement(1116..1436)	259_GENE_10

9933	**4**	**CGL2_09933004**	Protein of unknown function	154	complement(2970..3431)	259_GENE_9
9933	**5**	**CGL2_09933005**	Putative conjugal transfer protein (TrbI)	425	complement(3434..4708)	259_GENE_8
9933	**6**	**CGL2_09933006**	Putative conjugal transfer protein (TrbG)	312	complement(4708..5643)	259_GENE_7
9933	**7**	**CGL2_09933007**	Probable conjugal transfer protein (TrbF)	221	complement(5643..6305)	259_GENE_6
9933	**8**	**CGL2_09933008**	Probable conjugal transfer protein (TrbL)	454	complement(6308..7669)	259_GENE_5
8831	**1**	**CGL2_08831001**	Probable conjugal transfer (TrbJ)	288	complement(349..1212)	259_GENE_4
8831	**2**	**CGL2_08831002**	Probable conjugal transfer protein (TrbE)	812	complement(1230..3665)	259_GENE_2
8831	**3**	**CGL2_08831003**	Putative conjugal transfer protein (TrbD)	104	complement(3668..3979)	259_GENE_1
8831	**4**	**CGL2_08831004**	Hypothetical protein	102	complement(3983..4288)	
8831	**5**	**CGL2_08831005**	Putative conjugal transfer protein (TrbB)	168	complement(4288..4791)	440_GENE_3
11226	**1**	**CGL2_11226001**	Putative plasmid transfer factor (TraG)	65	complement(240..434)	440_GENE_5
11226	**2**	**CGL2_11226002**	Hypothetical protein	166	595..1092	582_GENE_1
11226	**3**	**CGL2_11226003**	Hypothetical protein	64	1103..1294	582_GENE_2
11226	**4**	**CGL2_11226004**	Hypothetical protein	141	1294..1716	582_GENE_3
11226	**5**	**CGL2_11226005**	Putative twitching motility protein (PilT)	346	1716..2753	582_GENE_4
11226	**6**	**CGL2_11226006**	Hypothetical protein	438	2753..4066	582_GENE_6
11226	**7**	**CGL2_11226007**	Protein of unknown function	196	4069..4656	582_GENE_7
11226	**8**	**CGL2_11226008**	Hypothetical protein	363	4656..5744	582_GENE_8
11226	**9**	**CGL2_11226009**	Putative type II secretion system protein D	615	5822..7666	
11226	**10**	**CGL2_11226010**	Putative type II secretion system protein E	574	7673..9394	
11226	**11**	**CGL2_11226011**	Conserved protein of unknown function	202	9397..10002	
11226	**12**	**CGL2_11226012**	Hypothetical protein	160	complement(10072..10551)	
11226	**13**	**CGL2_11226013**	Conserved hypothetical protein	101	complement(10734..11036)	784_GENE_6
11226	**14**	**CGL2_11226014**	Conserved hypothetical protein	136	complement(11106..11513)	784_GENE_5
11226	**15**	**CGL2_11226015**	Putative type II secretion system protein F	402	complement(11654..12859)	1145_GENE_1
11226	**16**	**CGL2_11226016**	Hypothetical protein	85	complement(12859..13113)	
11226	**17**	**CGL2_11226017**	Putative phage integrase	346	complement(13238..14275)	784_GENE_2
11226tRNA		**CGL2_11226R001**	TRNA Arg CCG		complement(14411..14488)	
11226	**18**	**CGL2_11226018**	Putative Cl-channel, voltage gated	570	complement(14549..16258)	283_GENE_8
11226	**19**	**CGL2_11226019**	Conserved hypothetical protein	144	complement(16258..16689)	283_GENE_7
11226	**20**	**CGL2_11226020**	Hypothetical protein	78	complement(16881..17114)	283_GENE_6
11226	**21**	**CGL2_11226021**	Protoporphyrinogen oxidase (EC 1.3.3.4)	462	17322..18707	283_GENE_5
11226	**22**	**CGL2_11226022**	Putative metallophosphoesterase	227	complement(18727..19407)	283_GENE_4
11226	**23**	**CGL2_11226023**	Zinc-containing alcohol dehydrogenase superfamily (	333	complement(19436..20434)	283_GENE_3
11226	**24**	**CGL2_11226024**	Putative radical SAM family protein	172	complement(20542..21057)	283_GENE_2
11067	**45**	**CGL2_11067045**	Protein of unknown function	108	complement(53116..53439)	53_GENE_28
11067	**44**	**CGL2_11067044**	Probable signal transduction protein	277	complement(52073..52903)	53_GENE_27
11067	**43**	**CGL2_11067043**	Conserved protein of unknown function	485	complement(50243..51697)	53_GENE_26
11067	**42**	**CGL2_11067042**	Hypothetical protein	496	complement(48607..50094)	53_GENE_24
11067	**41**	**CGL2_11067041**	Conserved protein of unknown function	185	complement(48034..48588)	53_GENE_23
11067	**40**	**CGL2_11067040**	Glucokinase (EC 2.7.1.2)	344	complement(46445..47476)	53_GENE_22

11067	39	CGL2_11067039	6-phosphogluconolactonase (EC 3.1.1.31)	276	complement(45477..46304)	53_GENE_21
11067	38	CGL2_11067038	Transketolase (EC 2.2.1.1)	677	complement(43407..45437)	53_GENE_20
11067	37	CGL2_11067037	Transaldolase	977	complement(40415..43345)	53_GENE_19
11067	36	CGL2_11067036	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49	510	complement(38831..40360)	53_GENE_18
11067	35	CGL2_11067035	Protein of unknown function	582	complement(37072..38817)	53_GENE_17
11067	34	CGL2_11067034	Putative monooxygenase	414	complement(35831..37072)	53_GENE_16
11067	33	CGL2_11067033	Probable trigger factor	467	complement(34231..35631)	53_GENE_15
11067	32	CGL2_11067032	Peptidase S14, ClpP (EC 3.4.21.92)	203	complement(33595..34203)	53_GENE_14
11067	31	CGL2_11067031	ClpX, ATPase regulatory subunit	426	complement(32287..33564)	53_GENE_13
11067	30	CGL2_11067030	Protein of unknown function	217	31634..32284	53_GENE_12
11067	29	CGL2_11067029	Protein of unknown function	442	complement(30241..31566)	53_GENE_11
11067	28	CGL2_11067028	Putative CDP-alcohol phosphatidyltransferase	183	complement(29690..30238)	53_GENE_10
11067	27	CGL2_11067027	Conserved protein of unknown function	462	complement(28288..29673)	53_GENE_9
11067	26	CGL2_11067026	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (	293	complement(27410..28288)	53_GENE_8
11067tRNA		CGL2_11067R006	TRNA Gln TTG		complement(27326..27400)	
11067	25	CGL2_11067025	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	314	complement(26318..27259)	53_GENE_7
11067	24	CGL2_11067024	Ribosomal protein L25	207	complement(25636..26256)	53_GENE_6
11067	23	CGL2_11067023	Peptidyl-tRNA hydrolase (EC 3.1.1.29)	187	complement(25054..25614)	53_GENE_5
11067	22	CGL2_11067022	GTP binding protein	364	complement(23895..24986)	53_GENE_4
11067	21	CGL2_11067021	Ribosomal protein S6	122	complement(23499..23864)	271_GENE_14
11067	20	CGL2_11067020	Single-stranded DNA-binding protein	140	complement(23080..23499)	271_GENE_13
11067	19	CGL2_11067019	Ribosomal protein S18	76	complement(22781..23008)	271_GENE_12
11067	18	CGL2_11067018	Hypothetical protein	289	complement(21810..22676)	271_GENE_11
11067	17	CGL2_11067017	Rare lipoprotein A family protein	263	complement(21080..21868)	271_GENE_10
11067	16	CGL2_11067016	Protein of unknown function	74	complement(20800..21021)	271_GENE_9
11067	15	CGL2_11067015	Conserved hypothetical protein	56	complement(20626..20793)	271_GENE_8
11067	14	CGL2_11067014	Protein of unknown function	151	20162..20614	271_GENE_7
11067	13	CGL2_11067013	RNA modification enzyme, MiaB family	483	complement(18599..20047)	271_GENE_6
11067	12	CGL2_11067012	Hypothetical protein	342	17538..18563	271_GENE_5
11067tRNA		CGL2_11067R005	TRNA Leu TAG		complement(17410..17495)	
11067	11	CGL2_11067011	Putative flavoprotein reductase	379	complement(16112..17248)	271_GENE_3
11067	10	CGL2_11067010	Protein of unknown function	258	complement(15336..16109)	271_GENE_2
11067tRNA		CGL2_11067R004	TRNA Tyr GTA		complement(15070..15155)	
11067tRNA		CGL2_11067R003	TRNA Gly TCC		complement(14959..15033)	
11067tRNA		CGL2_11067R002	TRNA Thr GGT		complement(14860..14935)	
11067	9	CGL2_11067009	Translation elongation factor Tu (EC 2.7.7.4)	399	complement(13549..14745)	137_GENE_1
11067	8	CGL2_11067008	Ribosomal protein L33	49	complement(13372..13518)	137_GENE_1a
11067tRNA		CGL2_11067R001	TRNA Trp CCA		complement(13285..13361)	
11067	7	CGL2_11067007	Preprotein translocase (SecE)	69	complement(13064..13270)	
11067	6	CGL2_11067006	Transcription antitermination protein (NusG)	184	complement(12489..13040)	137_GENE_2
11067	5	CGL2_11067005	Ribosomal protein L11	141	complement(12027..12449)	137_GENE_3

11067	**4**	**CGL2_11067004**	Ribosomal protein L1	232	complement(11286..11981)	137_GENE_4
11067	**3**	**CGL2_11067003**	Ribosomal protein L10	174	complement(10762..11283)	137_GENE_5
11067	**2**	**CGL2_11067002**	Ribosomal protein L7/L12	128	complement(10271..10654)	137_GENE_6
11067	**1**	**CGL2_11067001**	DNA-directed RNA polymerase, beta subunit (EC 2.7	1718	complement(4756..9909)	137_GENE_7
11067	**1a**	**CGL2_11067001a**	DNA-directed RNA polymerase, beta' subunit (EC 2.7	1574	complement(30..4751)	137_GENE_8
11212	**1**	**CGL2_11212001**	Ribosomal protein S12	65	133..327	713_GENE_4
11212	**2**	**CGL2_11212002**	Ribosomal protein S7	157	368..838	713_GENE_3
11212	**3**	**CGL2_11212003**	Translation elongation factor G	692	854..2929	713_GENE_2
11212	**4**	**CGL2_11212004**	Translation elongation factor Tu (EC 2.7.7.4)	399	2952..4148	713_GENE_1
11212	**5**	**CGL2_11212005**	Ribosomal protein S10	101	4185..4487	
11212	**6**	**CGL2_11212006**	Ribosomal protein L3	207	4502..5122	349_GENE_14
11212	**7**	**CGL2_11212007**	Ribosomal protein L4	218	5147..5800	349_GENE_13
11212	**8**	**CGL2_11212008**	Ribosomal protein L23	95	5790..6074	
11212	**9**	**CGL2_11212009**	Ribosomal protein L2	273	6080..6898	349_GENE_12
11212	**10**	**CGL2_11212010**	Ribosomal protein S19	94	6917..7198	349_GENE_11
11212	**11**	**CGL2_11212011**	Ribosomal protein L22	110	7223..7552	349_GENE_10
11212	**12**	**CGL2_11212012**	Ribosomal protein S3	226	7573..8250	349_GENE_9
11212	**13**	**CGL2_11212013**	Ribosomal protein L16/L10E	127	8287..8667	349_GENE_8
11212	**14**	**CGL2_11212014**	Ribosomal protein L29	66	8667..8864	349_GENE_7a
11212	**15**	**CGL2_11212015**	Ribosomal protein S17	95	8860..9144	349_GENE_7
11212	**16**	**CGL2_11212016**	Ribosomal protein L14	122	9182..9547	349_GENE_6
11212	**17**	**CGL2_11212017**	Ribosomal protein L24	117	9564..9914	349_GENE_5a
11212	**18**	**CGL2_11212018**	Ribosomal protein L5	226	9946..10623	349_GENE_5
11212	**19**	**CGL2_11212019**	Ribosomal protein S14	61	10646..10828	349_GENE_4a
11212	**20**	**CGL2_11212020**	Ribosomal protein S8	132	10853..11248	349_GENE_4
11212	**21**	**CGL2_11212021**	Ribosomal protein L6P/L9E	179	11280..11816	349_GENE_3
11212	**22**	**CGL2_11212022**	Ribosomal protein L18	117	11855..12205	349_GENE_2
11212	**23**	**CGL2_11212023**	Ribosomal protein S5	161	12234..12716	349_GENE_1
11212	**24**	**CGL2_11212024**	Ribosomal protein L30	63	12751..12939	88_GENE_20
11212	**25**	**CGL2_11212025**	Ribosomal protein L15	149	12975..13421	88_GENE_19
11212	**26**	**CGL2_11212026**	Preprotein translocase subunit (SecY)	437	13445..14755	88_GENE_18
11212	**27**	**CGL2_11212027**	Adenylate kinase (EC 2.7.4.3)	219	14761..15417	88_GENE_17
11212	**28**	**CGL2_11212028**	Methionine aminopeptidase (EC 3.4.11.18)	252	15423..16178	88_GENE_16
11212	**29**	**CGL2_11212029**	Translation initiation factor 1 (IF-1)	72	16191..16406	88_GENE_16a
11212	**30**	**CGL2_11212030**	Ribosomal protein L36	37	16420..16530	
11212	**31**	**CGL2_11212031**	Ribosomal protein S13	124	16545..16916	
11212	**32**	**CGL2_11212032**	Ribosomal protein S11	128	16970..17353	88_GENE_15a
11212	**33**	**CGL2_11212033**	Ribosomal protein S4 and related proteins	209	17410..18036	88_GENE_15
11212	**34**	**CGL2_11212034**	DNA-directed RNA polymerase, alpha subunit (EC 2.	324	18083..19054	88_GENE_14
11212	**35**	**CGL2_11212035**	Ribosomal protein L17	154	19093..19554	88_GENE_13
11212	**36**	**CGL2_11212036**	Protein of unknown function	143	19579..20007	88_GENE_12

11212	**37**	**CGL2_11212037**	DTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	288	20079..20942	88_GENE_11
11212	**38**	**CGL2_11212038**	Trehalose-6-phosphate phosphatase	285	complement(20962..21816)	88_GENE_10
11212	**39**	**CGL2_11212039**	Alpha,alpha-trehalose-phosphate synthase (UDP-for	500	complement(21785..23284)	88_GENE_8
11212	**40**	**CGL2_11212040**	Putative glycosyl transferase, group 1	361	complement(23326..24408)	88_GENE_7
11212	**41**	**CGL2_11212041**	Putative major facilitator superfamily transporter	428	complement(24414..25697)	88_GENE_6
11212	**42**	**CGL2_11212042**	Probable macrolide-efflux protein	429	complement(25851..27137)	88_GENE_5
11212	**43**	**CGL2_11212043**	ADP-L-glycero-D-mannoheptose-6-epimerase (EC 5.	303	27352..28260	88_GENE_4
11212	**44**	**CGL2_11212044**	Protein of unknown function	610	28241..30070	88_GENE_3
11212	**45**	**CGL2_11212045**	Amidophosphoribosyltransferase (EC 2.4.2.14)	504	complement(30090..31601)	88_GENE_2
11212	**46**	**CGL2_11212046**	Phosphoribosylformylglycinamidine synthase II (EC	737	complement(31607..33817)	88_GENE_1
11212	**47**	**CGL2_11212047**	Phosphoribosylformylglycinamidine synthase I	255	complement(33924..34688)	30_GENE_4
11212	**48**	**CGL2_11212048**	Conserved hypothetical protein	257	34948..35718	30_GENE_5
11212	**49**	**CGL2_11212049**	Protein of unknown function	238	35917..36630	30_GENE_6
11212	**50**	**CGL2_11212050**	Putative transcriptional regulator, TetR family	237	36679..37389	30_GENE_7
11212	**51**	**CGL2_11212051**	Putative outer membrane efflux protein	490	37389..38858	30_GENE_8
11212	**52**	**CGL2_11212052**	Secretion protein (HlyD)	376	38854..39981	30_GENE_9
11212	**53**	**CGL2_11212053**	Putative cation/multidrug efflux pump split	1070	40003..43212	30_GENE_10
11212	**54**	**CGL2_11212054**	Putative transcriptional regulator, LysR family	310	complement(43219..44148)	30_GENE_11
11212	**55**	**CGL2_11212055**	Putative outer membrane efflux protein	474	44343..45764	30_GENE_12
11212	**56**	**CGL2_11212056**	Protein of unknown function	243	45764..46492	30_GENE_13
11212	**57**	**CGL2_11212057**	Protein of unknown function	207	46534..47154	30_GENE_14
11212	**58**	**CGL2_11212058**	ABC transporter, ATPase subunit (EC 3.6.3.29)	256	47150..47917	30_GENE_15
11212	**59**	**CGL2_11212059**	Putative ABC-2 transporter	285	47913..48767	30_GENE_16
11212	**60**	**CGL2_11212060**	Putative oxidoreductase FAD/NAD(P)-binding	257	48821..49591	30_GENE_17
11212	**61**	**CGL2_11212061**	Protein of unknown function	346	49656..50693	30_GENE_18
11212	**62**	**CGL2_11212062**	Putative 3-hydroxybutyryl-coA dehydrogenase	378	50707..51840	30_GENE_19
11212	**63**	**CGL2_11212063**	Protein of unknown function	160	51915..52394	30_GENE_20
11212	**63**	**CGL2_11212063**	Protein of unknown function	160	51915..52394	30_GENE_20
11212	**65**	**CGL2_11212065**	Protein of unknown function	231	52537..53229	30_GENE_21
11212	**66**	**CGL2_11212066**	Putative TPR-domain containing protein	731	53229..55421	30_GENE_22
11212	**67**	**CGL2_11212067**	Putative DegT/DnrJ/EryC1/StrS aminotransferase	391	55443..56615	30_GENE_23
11212	**68**	**CGL2_11212068**	Putative OsmC-like protein (osmotic induced)	173	56615..57133	30_GENE_24
11212	**69**	**CGL2_11212069**	Probable dethiobiotin synthase	237	57085..57795	30_GENE_25
11212	**70**	**CGL2_11212070**	Protein of unknown function	110	complement(57853..58182)	30_GENE_26
11212	**71**	**CGL2_11212071**	Protein of unknown function	68	complement(58263..58466)	30_GENE_27
11212	**72**	**CGL2_11212072**	Protein of unknown function	284	complement(58472..59323)	30_GENE_28
11212	**73**	**CGL2_11212073**	Protein of unknown function	350	complement(59348..60397)	30_GENE_29
11212	**74**	**CGL2_11212074**	Protein of unknown function	107	complement(60412..60732)	30_GENE_30
11212	**75**	**CGL2_11212075**	Multi-sensor signal transduction histidine kinase	596	61548..63335	30_GENE_31
11212	**76**	**CGL2_11212076**	Putative response regulator receiver protein	148	63416..63859	30_GENE_32
11212	**77**	**CGL2_11212077**	Response regulator receiver modulated diguanylate	874	63923..66544	30_GENE_33

11212	**78**	**CGL2_11212078**	Thiamine-phosphate pyrophosphorylase ThiE(EC 2.5.	212	complement(66551..67186)	30_GENE_34
11212	**79**	**CGL2_11212079**	Acetyl-CoA carboxylase, biotin carboxylase (EC 6.3.4	456	complement(67235..68602)	30_GENE_35
11212	**80**	**CGL2_11212080**	Acetyl-CoA biotin carboxyl carrier protein	157	complement(68611..69081)	30_GENE_36
11212	**81**	**CGL2_11212081**	Translation elongation factor P	191	complement(69131..69703)	30_GENE_37
11212	**82**	**CGL2_11212082**	3-dehydroquinate dehydratase, type II (EC 4.2.1.10	149	complement(69771..70217)	30_GENE_38
11212	**83**	**CGL2_11212083**	Putative TPR-domain containing protein	464	complement(70217..71608)	30_GENE_39
11212	**84**	**CGL2_11212084**	DNA/pantothenate metabolism flavoprotein (EC 4.1.	415	complement(71770..73014)	30_GENE_40
11212	**85**	**CGL2_11212085**	Putative DNA-directed RNA polymerase, omega subu	134	complement(73025..73426)	30_GENE_41
11212	**86**	**CGL2_11212086**	Guanylate kinase (EC 2.7.4.8)	243	complement(73426..74154)	30_GENE_42
11212	**87**	**CGL2_11212087**	Conserved protein of unknown function	94	complement(74222..74503)	30_GENE_43
11212	**88**	**CGL2_11212088**	Conserved protein of unknown function	293	complement(74496..75374)	30_GENE_44
11212	**89**	**CGL2_11212089**	Probable amylo-alpha-1,6-glucosidase	725	75575..77749	30_GENE_45
11212	**90**	**CGL2_11212090**	Putative penicillin-binding protein, transpeptidase	468	77964..79367	30_GENE_46
11212	**91**	**CGL2_11212091**	Putative signal-transduction protein with CBS domai	136	79504..79911	317_GENE_7
11212	**92**	**CGL2_11212092**	8-amino-7-oxononanoate synthase (EC 2.3.1.47)	380	complement(80007..81146)	317_GENE_6
11212	**93**	**CGL2_11212093**	6-carboxyhexanoate--CoA ligase (EC 6.2.1.14)	300	complement(81127..82026)	317_GENE_5
11212	**94**	**CGL2_11212094**	Biotin synthetase (EC 2.8.1.6)	346	complement(82026..83063)	317_GENE_4
11212	**95**	**CGL2_11212095**	Diguanylate cyclase	412	83322..84557	317_GENE_3
11212	**96**	**CGL2_11212096**	transposase	124	85643..86014	94_GENE_21
11212	**97**	**CGL2_11212097**	Glycyl-tRNA synthetase, alpha subunit (EC 6.1.1.14)	300	86421..87320	94_GENE_20
11212	**98**	**CGL2_11212098**	Glycyl-tRNA synthetase, beta subunit (EC 6.1.1.14)	739	87320..89536	94_GENE_19
11212	**99**	**CGL2_11212099**	Riboflavin biosynthesis protein RibD (EC 3.5.4.26) (E	388	89539..90702	94_GENE_18
11212	**100**	**CGL2_11212100**	Riboflavin synthase, alpha subunit	210	90709..91338	94_GENE_17
11212	**101**	**CGL2_11212101**	Hypothetical protein	67	91354..91554	94_GENE_16
11212	**102**	**CGL2_11212102**	Cobalt-precorrin-2 C(20)-methyltransferase (EC 2.1.	251	91554..92306	94_GENE_15
11212	**103**	**CGL2_11212103**	Hypothetical protein	179	92306..92842	94_GENE_14
11212	**104**	**CGL2_11212104**	Precorrin-4 C11-methyltransferase (EC 2.1.1.133)	279	92829..93665	94_GENE_13
11212	**105**	**CGL2_11212105**	Protein of unknown function (transcrip reg?)	179	complement(93823..94359)	94_GENE_12
11212	**106**	**CGL2_11212106**	Protein of unknown function	221	complement(94513..95175)	94_GENE_11
11212	**107**	**CGL2_11212107**	Putative radical SAM family protein	476	complement(95203..96630)	94_GENE_10
11212	**108**	**CGL2_11212108**	Cation efflux family protein	315	96844..97788	94_GENE_9
11212	**109**	**CGL2_11212109**	Conserved hypothetical protein	112	complement(97802..98137)	94_GENE_8
11212	**110**	**CGL2_11212110**	Putative DNA recombination protein, RmuC family	477	complement(98137..99567)	94_GENE_7
11212	**111**	**CGL2_11212111**	Dihydroxy-acid dehydratase (EC 4.2.1.9)	557	complement(99607..101277)	94_GENE_6
11212	**112**	**CGL2_11212112**	Protein of unknown function	183	complement(101476..102024)	94_GENE_5
11212	**113**	**CGL2_11212113**	Hypothetical protein	59	complement(102073..102249)	94_GENE_4
11212	**114**	**CGL2_11212114**	Cobyric acid synthase (CobQ)	500	102394..103893	94_GENE_3
11212	**115**	**CGL2_11212115**	Cobalamin biosynthesis protein (CbiB)	338	103893..104906	94_GENE_2
11212	**116**	**CGL2_11212116**	Putative L-threonine-O-3-phosphate decarboxylase	369	104913..106019	94_GENE_1
11212	**117**	**CGL2_11212117**	Fumarate hydratase class II (EC 4.2.1.2)	471	106493..107905	57_GENE_26

11212tRNA		**CGL2_11212R001**	TRNA Pro CGG		108074..108150	
11212	**118**	**CGL2_11212118**	Putative acylphosphatase	99	108264..108560	57_GENE_24
11212	**119**	**CGL2_11212119**	RNA polymerase, RpoD-like sigma subunit	499	108623..110119	57_GENE_23
11212	**120**	**CGL2_11212120**	Conserved protein of unknown function	110	110125..110454	57_GENE_22
11212	**121**	**CGL2_11212121**	Glutamate synthase [NADPH] large subunit (EC 1.4.	1525	complement(110573..115147)	57_GENE_21
11212	**122**	**CGL2_11212122**	Putative metal dependent phosphohydrolase	332	115413..116408	57_GENE_20
11212	**123**	**CGL2_11212123**	D-lactate dehydrogenase (Cytochrome) (EC 1.1.2.4)	945	116408..119242	57_GENE_19
11212	**124**	**CGL2_11212124**	Putative methyl-accepting chemotaxis sensory trans	372	complement(119251..120366)	57_GENE_18
11212	**125**	**CGL2_11212125**	Probable acyl-[acyl-carrier protein] desaturase	286	complement(120700..121557)	57_GENE_17
11212	**126**	**CGL2_11212126**	Exodeoxyribonuclease III (EC 3.1.11.2)	265	complement(121793..122587)	57_GENE_16
11212	**127**	**CGL2_11212127**	Probable cation transport protein	181	complement(122580..123122)	57_GENE_15
11212	**128**	**CGL2_11212128**	3-methyl-2-oxobutanoate hydroxymethyltransferase	287	complement(123127..123987)	57_GENE_14
11212	**129**	**CGL2_11212129**	Putative methylenetetrahydrofolate reductase	289	complement(123993..124859)	57_GENE_13
11212	**130**	**CGL2_11212130**	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9	294	complement(124859..125740)	57_GENE_12
11212	**131**	**CGL2_11212131**	GTP cyclohydrolase I (EC 3.5.4.16)	191	complement(125824..126396)	57_GENE_11
11212	**132**	**CGL2_11212132**	Putative 5-formyltetrahydrofolate cyclo-ligase	206	complement(126377..126994)	57_GENE_10
11212	**133**	**CGL2_11212133**	Probable citrate transporter	633	127016..128914	57_GENE_9
11212	**134**	**CGL2_11212134**	Putative acyltransferase	232	complement(128922..129617)	57_GENE_8
11212	**135**	**CGL2_11212135**	Cytidylate kinase (EC 2.7.4.14)	221	complement(129593..130255)	57_GENE_7
11212	**136**	**CGL2_11212136**	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2	454	complement(130252..131613)	57_GENE_6
11212	**138**	**CGL2_11212138**	Prephenate dehydrogenase (EC 1.3.1.12)	302	complement(131600..132505)	57_GENE_5
11212	**139**	**CGL2_11212139**	Phospho-2-dehydro-3-deoxyheptonate aldolase, sub	340	complement(132505..133524)	57_GENE_4
11212	**140**	**CGL2_11212140**	Prephenate dehydratase (EC 4.2.1.51)	365	complement(133548..134642)	57_GENE_3
11212	**141**	**CGL2_11212141**	Conserved protein of unknown function	252	complement(134731..135486)	57_GENE_2
11212	**142**	**CGL2_11212142**	Probable cytochrome C oxidase mono-heme subunit	176	135909..136436	120_GENE_14
11212	**143**	**CGL2_11212143**	Conserved hypothetical protein	429	136596..137882	120_GENE_13
11212	**144**	**CGL2_11212144**	Glycine oxidase (ThiO)	375	complement(137898..139022)	120_GENE_12
11212	**145**	**CGL2_11212145**	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	443	139252..140580	120_GENE_11
11212	**146**	**CGL2_11212146**	Sugar fermentation stimulation protein	239	140562..141278	120_GENE_10
11212	**147**	**CGL2_11212147**	Putative NAD-dependent epimerase/dehydratase fam	308	141307..142230	120_GENE_9
11212	**148**	**CGL2_11212148**	Conserved hypothetical protein	349	142223..143269	120_GENE_8
11212	**149**	**CGL2_11212149**	Nucleoside-diphosphate kinase (EC 2.7.4.6)	138	143276..143689	120_GENE_7
11212	**150**	**CGL2_11212150**	Protein of unknown function	397	143746..144936	120_GENE_6
11212	**151**	**CGL2_11212151**	Tyrosyl-tRNA synthetase (EC 6.1.1.1)	403	145018..146226	120_GENE_5
11212	**152**	**CGL2_11212152**	Secretion protein HlyD	374	146440..147561	120_GENE_4
11212	**153**	**CGL2_11212153**	Heavy metal efflux pump, CzcA family	1027	147561..150641	120_GENE_3
11212	**154**	**CGL2_11212154**	Putative glutamine amidotransferase class-I	235	150735..151439	120_GENE_2
11212	**155**	**CGL2_11212155**	Transposase	446	151619..152956	120_GENE_1
11233rRNA		**CGL2_11233R001**	16S rRNA		219..1736	
11233tRNA		**CGL2_11233R001**	TRNA Ile GAT		1862..1938	
11233tRNA		**CGL2_11233R002**	TRNA Ala TGC		1944..2019	

11233rRNA		**CGL2_11233R002**	23S rRNA		2347..4992	
11233rRNA		**CGL2_11233R003**	5S rRNA		5220..5283	
11233	**1**	**CGL2_11233001**	Hypothetical protein	49	5616..5762	
11233	**3**	**CGL2_11233003**	NADH dehydrogenase, subunit F (EC 1.6.99.5)	1048	5797..8940	67_GENE_27
11233	**4**	**CGL2_11233004**	Putative endonuclease III	210	complement(8905..9534)	67_GENE_26
11233	**5**	**CGL2_11233005**	Putative transcriptional regulators, TraR/DksA family	136	9653..10060	67_GENE_25
11233	**6**	**CGL2_11233006**	Prolipoprotein diacylglyceryl transferase	272	10091..10906	67_GENE_24
11233	**7**	**CGL2_11233007**	Putative methyl-accepting chemotaxis sensory transc	484	10919..12370	67_GENE_23
11233	**8**	**CGL2_11233008**	Transcriptional regulator, BadM/Rrf2 family	141	12409..12831	67_GENE_22
11233	**9**	**CGL2_11233009**	Hypothetical protein	109	complement(12830..13156)	67_GENE_21
11233	**10**	**CGL2_11233010**	Conserved hypothetical protein	90	13304..13573	67_GENE_20
11233	**11**	**CGL2_11233011**	Conserved protein of unknown function	380	complement(13576..14715)	67_GENE_19
11233	**12**	**CGL2_11233012**	Putative permease	852	complement(14711..17266)	67_GENE_18
11233	**13**	**CGL2_11233013**	ABC transporter, ATP-binding protein (3.6.3.25)	241	complement(17273..17995)	67_GENE_17
11233	**14**	**CGL2_11233014**	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)	292	complement(17995..18870)	67_GENE_16
11233	**15**	**CGL2_11233015**	Hypothetical protein	87	19172..19432	67_GENE_14
11233	**16**	**CGL2_11233016**	Conserved hypothetical protein	97	19435..19725	67_GENE_13
11233	**17**	**CGL2_11233017**	Conserved hypothetical protein	834	19721..22222	67_GENE_12
11233	**18**	**CGL2_11233018**	Hypothetical protein	204	22222..22833	67_GENE_11
11233	**19**	**CGL2_11233019**	Hypothetical protein	410	22845..24074	67_GENE_10
11233	**20**	**CGL2_11233020**	Hypothetical protein	229	24074..24760	67_GENE_9
11233	**21**	**CGL2_11233021**	DNA-dependent RNA polymerase	385	24760..25914	67_GENE_8
11233	**22**	**CGL2_11233022**	Hypothetical protein	316	25919..26866	67_GENE_7
11233	**23**	**CGL2_11233023**	Putative MoxR-like ATPases	282	26866..27711	67_GENE_6
11233	**24**	**CGL2_11233024**	Hypothetical protein	151	complement(27892..28344)	67_GENE_5
11233	**25**	**CGL2_11233025**	Putative oxygen-independent coproporphyrinogen II	389	28602..29768	67_GENE_4
11233	**26**	**CGL2_11233026**	Putative phage integrase family protein	314	complement(29784..30725)	67_GENE_3
11233	**27**	**CGL2_11233027**	Hypothetical protein	390	complement(30742..31911)	67_GENE_2
11233	**28**	**CGL2_11233028**	Protein of unknown function	455	complement(31935..33299)	62_GENE_28
11233	**29**	**CGL2_11233029**	Ferredoxin-nitrite reductase (EC 1.7.7.1)	547	33572..35212	62_GENE_27
11233	**30**	**CGL2_11233030**	Hypothetical protein	63	complement(35224..35412)	62_GENE_26
11233	**31**	**CGL2_11233031**	Conserved protein of unknown function	282	complement(35489..36334)	62_GENE_25
11233	**32**	**CGL2_11233032**	Glycogen synthase (EC 2.4.1.21)	493	36597..38075	62_GENE_24
11233	**33**	**CGL2_11233033**	transposase	133	complement(38375..38773)	62_GENE_23
11233	**34**	**CGL2_11233034**	Hypothetical protein	45	complement(39064..39198)	62_GENE_22
11233	**35**	**CGL2_11233035**	Putative transcriptional regulator, Crp/Fnr family	237	complement(39216..39926)	62_GENE_21
11233	**36**	**CGL2_11233036**	Putative peptidoglycan-binding lytic transglycosylase	473	40318..41736	62_GENE_20
11233	**37**	**CGL2_11233037**	Protein of unknown function	264	complement(41888..42679)	62_GENE_19
11233	**38**	**CGL2_11233038**	Probable ferredoxin	86	complement(42687..42944)	62_GENE_18
11233	**39**	**CGL2_11233039**	NADH dehydrogenase (Quinone) (EC 1.6.99.5)	453	complement(43053..44411)	62_GENE_17
11233	**40**	**CGL2_11233040**	Phosphoribosylaminoimidazole carboxylase, catalytic	175	44665..45189	62_GENE_16

11233	41	CGL2_11233041	Phosphoribosylaminoimidazole carboxylase, ATPase s	382	45189..46334	62_GENE_15
11233	42	CGL2_11233042	Conserved protein of unknown function	221	complement(46352..47014)	62_GENE_14
11233	43	CGL2_11233043	Protein of unknown function	136	complement(47165..47572)	62_GENE_13
11233	44	CGL2_11233044	Putative adenylate/guanylate cyclase	454	complement(48132..49493)	62_GENE_12
11233	45	CGL2_11233045	Hypothetical protein	483	49618..51066	62_GENE_11
11233	46	CGL2_11233046	Conserved protein of unknown function	374	51339..52460	62_GENE_10
11233	47	CGL2_11233047	Conserved hypothetical protein	338	52613..53626	62_GENE_9
11233	48	CGL2_11233048	Conserved hypothetical protein	132	53633..54028	62_GENE_8
11233	49	CGL2_11233049	Protein of unknown function	213	54121..54759	62_GENE_7
11233	50	CGL2_11233050	oxidoreductase/K+-channel protein?	58	54944..55117	62_GENE_6
11233	51	CGL2_11233051	Protein of unknown function	313	complement(55300..56238)	62_GENE_5
11233	52	CGL2_11233052	Putative ABC transporter	304	complement(56238..57149)	62_GENE_4
11233	53	CGL2_11233053	Putative ABC transporter	257	complement(57188..57958)	62_GENE_3
11233	54	CGL2_11233054	Probable ABC transporter, permease protein	261	complement(57981..58763)	62_GENE_2
11233	55	CGL2_11233055	Protein of unknown function	243	complement(58813..59541)	62_GENE_1
11233	57	CGL2_11233057	Cold shock proteins	68	complement(60195..60398)	140_GENE_1
11233	58	CGL2_11233058	Hypothetical protein	205	60718..61332	140_GENE_2
11233	59	CGL2_11233059	Probable general secretion pathway protein I	127	61332..61712	140_GENE_3
11233	60	CGL2_11233060	Probable general secretion pathway protein J	235	61712..62416	140_GENE_4
11233	61	CGL2_11233061	DnaB helicase	463	complement(62454..63842)	140_GENE_5
11233	62	CGL2_11233062	Histidyl-tRNA lygase (EC 6.1.1.21)	437	complement(63849..65159)	140_GENE_6
11233	63	CGL2_11233063	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	535	complement(65159..66763)	140_GENE_7
11233	64	CGL2_11233064	Serine--glyoxylate transaminase (EC 2.6.1.45)	381	complement(66785..67927)	140_GENE_8
11233	65	CGL2_11233065	Putative oligopeptide ABC transporter	533	complement(68134..69732)	140_GENE_9
11233rRNA		CGL2_11233R004	5S rRNA		complement(69908..69971)	
11233rRNA		CGL2_11233R005	23S rRNA		complement(70199..72844)	
11233tRNA		CGL2_11233R003	TRNA Ala TGC		complement(73172..73247)	
11233tRNA		CGL2_11233R004	TRNA Ile GAT		complement(73253..73329)	
11277	2	CGL2_11277002	Protein of unknown function	40	complement(239..358)	42_GENE_2
11277	3	CGL2_11277003	Protein of unknown function (probable hemolysin?)	455	562..1926	42_GENE_3
11277	4	CGL2_11277004	Protein of unknown function	189	1957..2523	42_GENE_4
11277	5	CGL2_11277005	Protein of unknown function	355	2548..3612	42_GENE_5
11277	6	CGL2_11277006	Transcriptional regulator, BadM/Rrf2 family	156	3698..4165	42_GENE_6
11277	7	CGL2_11277007	Cysteine desulfurase (EC 2.8.1.7)	404	4128..5339	42_GENE_7
11277	8	CGL2_11277008	FeS cluster assembly scaffold IscU	137	5380..5790	42_GENE_8
11277	9	CGL2_11277009	Iron-sulfur cluster assembly protein	109	5805..6131	42_GENE_9
11277	10	CGL2_11277010	Putative co-chaperone HscB	225	6228..6902	42_GENE_10
11277	11	CGL2_11277011	Chaperone protein HscA	603	6926..8734	42_GENE_11
11277	12	CGL2_11277012	Putative ferredoxin	103	8754..9062	42_GENE_13
11277	13	CGL2_11277013	Protein of unknown function	67	9098..9298	42_GENE_14

11277	**14**	**CGL2_11277014**	Conserved hypothetical protein	155	9298..9762	42_GENE_15
11277	**15**	**CGL2_11277015**	Putative ATP binding protein, Mrp like	358	9855..10928	42_GENE_16
11277	**16**	**CGL2_11277016**	Protein of unknown function	85	10928..11182	42_GENE_17
11277	**17**	**CGL2_11277017**	Pseudouridylate synthase (4.2.1.70)	268	11243..12046	42_GENE_18
11277	**18**	**CGL2_11277018**	Protein of unknown function	103	complement(12064..12372)	42_GENE_19
11277	**19**	**CGL2_11277019**	Glycerol 3-phosphate dehydrogenase (NADP) (1.1.1.	353	complement(12441..13499)	42_GENE_20
11277	**20**	**CGL2_11277020**	Probable phosphoribosyltransferase	223	13734..14402	42_GENE_21
11277	**21**	**CGL2_11277021**	Protein of unknown function	403	14518..15726	42_GENE_22
11277	**22**	**CGL2_11277022**	Putative diguanylate cyclase/phosphodiesterase with	884	complement(15720..18371)	42_GENE_23
11277	**23**	**CGL2_11277023**	Putative phosphatidylethanolamine binding protein	188	complement(18424..18987)	42_GENE_24
11277	**24**	**CGL2_11277024**	Seryl-tRNA synthetase (6.1.1.11)	442	19309..20634	42_GENE_25
11277	**25**	**CGL2_11277025**	Protein of unknown function	123	20634..21002	42_GENE_26
11277	**26**	**CGL2_11277026**	Protein of unknown function	241	20989..21711	42_GENE_27
11277	**27**	**CGL2_11277027**	Hypothetical protein	84	21749..22000	42_GENE_27a
11277	**28**	**CGL2_11277028**	Putative GTP binding protein	518	22111..23664	42_GENE_29
11277	**29**	**CGL2_11277029**	Hypothetical protein	163	23669..24157	42_GENE_30
11277	**30**	**CGL2_11277030**	Hypothetical protein	333	24160..25158	42_GENE_31
11277	**31**	**CGL2_11277031**	Protein of unknown function	140	25253..25672	42_GENE_32
11277	**32**	**CGL2_11277032**	Putative peptidase M16	476	25738..27165	42_GENE_33
11277	**33**	**CGL2_11277033**	Putative peptidase M16	481	27196..28638	42_GENE_34
11277	**34**	**CGL2_11277034**	Hypothetical protein	430	complement(28705..29994)	42_GENE_35
11277	**35**	**CGL2_11277035**	Putative Na+/H+ antiporters	406	complement(30044..31261)	42_GENE_36
11277	**36**	**CGL2_11277036**	Putative metabolite transport protein	429	31715..33001	42_GENE_37
11277	**37**	**CGL2_11277037**	Conserved hypothetical protein	101	complement(33490..33792)	42_GENE_38
11277	**38**	**CGL2_11277038**	Hypothetical protein	102	34138..34443	42_GENE_39
11277	**39**	**CGL2_11277039**	Hypothetical protein	93	34446..34724	42_GENE_40
11277	**40**	**CGL2_11277040**	Hypothetical protein	261	complement(34681..35463)	42_GENE_41
11277	**41**	**CGL2_11277041**	Hypothetical protein	187	complement(35623..36183)	42_GENE_44
11277	**42**	**CGL2_11277042**	Hypothetical protein	111	complement(36183..36515)	42_GENE_45
11277	**43**	**CGL2_11277043**	Conserved hypothetical protein	83	complement(36515..36763)	42_GENE_47
11277	**44**	**CGL2_11277044**	Conserved hypothetical protein	588	complement(36892..38655)	21_GENE_2
11277	**45**	**CGL2_11277045**	Conserved hypothetical protein	307	complement(38648..39568)	21_GENE_3
11277	**46**	**CGL2_11277046**	Hypothetical protein	270	39766..40575	21_GENE_5
11277	**47**	**CGL2_11277047**	Integrase	367	40580..41680	21_GENE_6
11277tRNA		**CGL2_11277R001**	TRNA Arg ACG		complement(41698..41774)	
11277	**48**	**CGL2_11277048**	Leucyl-tRNA synthetase (6.1.1.4)	828	42055..44538	21_GENE_8
11277	**49**	**CGL2_11277049**	Protein of unknown function	239	44538..45254	21_GENE_9
11277	**50**	**CGL2_11277050**	Probable DNA polymerase III, delta subunit	348	45254..46297	21_GENE_10
11277	**51**	**CGL2_11277051**	Ribosomal protein S20	87	complement(46287..46547)	21_GENE_11
11277	**52**	**CGL2_11277052**	Putative virulence factor MVN like	547	46631..48271	21_GENE_12
11277	**53**	**CGL2_11277053**	Probable HNH endonuclease	186	complement(48285..48842)	21_GENE_13

11277	**54**	**CGL2_11277054**	Protein of unknown function	347	complement(48906..49946)	21_GENE_14
11277	**55**	**CGL2_11277055**	Protein of unknown function	163	50116..50604	21_GENE_15
11277	**56**	**CGL2_11277056**	Protein of unknown function	116	50686..51036	21_GENE_16
11277	**57**	**CGL2_11277057**	Probable ATPase, PP-loop superfamily implicat	307	51036..51956	21_GENE_17
11277	**58**	**CGL2_11277058**	Conserved protein of unknown function	324	52008..52979	21_GENE_18
11277	**59**	**CGL2_11277059**	Probable metal-dependent phosphohydrolase	424	complement(52982..54253)	21_GENE_19
11277	**60**	**CGL2_11277060**	Protein of unknown funciton, but transposase (delete	105	54888..55202	21_GENE_20
11277tRNA		**CGL2_11277R002**	TRNA His GTG		complement(55579..55653)	
11277	**62**	**CGL2_11277062**	Anthranilate synthases component I (EC 4.1.3.27)	441	55759..57080	21_GENE_21
11277	**64**	**CGL2_11277064**	Putative branched chain amino acid aminotransferase	295	57072..57956	21_GENE_22
11277	**65**	**CGL2_11277065**	Rubrerythrin	139	58187..58603	21_GENE_23
11277	**66**	**CGL2_11277066**	Ribonucleotide reductase (EC 1.17.4.1)	732	complement(58849..61044)	21_GENE_24
11277	**67**	**CGL2_11277067**	Protein of unknown function	484	complement(61262..62713)	21_GENE_25
11277	**68**	**CGL2_11277068**	Protein of unknown function	205	complement(62854..63468)	21_GENE_26
11277	**69**	**CGL2_11277069**	Putative acriflavin resistance protein	386	complement(63783..64940)	21_GENE_27
11277	**70**	**CGL2_11277070**	Putative acriflavin resistance protein	664	complement(64959..66950)	21_GENE_28
11277tRNA		**CGL2_11277R003**	TRNA Arg TCG		complement(67254..67330)	
11277	**71**	**CGL2_11277071**	Protein of unknown function	152	67577..68032	21_GENE_31
11277tRNA		**CGL2_11277R004**	TRNA Cys GCA		68110..68184	
11277	**72**	**CGL2_11277072**	Putative major facilitator superfamily transporter	487	complement(68293..69753)	21_GENE_32
11277	**73**	**CGL2_11277073**	L-2,4-diaminobutyric acid acetyltransferase	187	70464..71024	21_GENE_34
11277	**74**	**CGL2_11277074**	Diaminobutyrate--pyruvate aminotransferase (EC 2.	425	71048..72322	21_GENE_35
11277	**75**	**CGL2_11277075**	Ectoine synthase	131	72349..72741	21_GENE_36
11277	**76**	**CGL2_11277076**	Ectoine hydroxylase	305	72819..73733	21_GENE_37
11277	**77**	**CGL2_11277077**	Protein of unknown function	147	complement(73776..74216)	21_GENE_38
11277	**78**	**CGL2_11277078**	Hypothetical protein	153	complement(74253..74711)	21_GENE_39
11277	**79**	**CGL2_11277079**	Hypothetical protein	67	74818..75018	21_GENE_40
11277	**80**	**CGL2_11277080**	Probable sodium/calcium exchanger membrane regi	303	75018..75926	21_GENE_41
11277	**81**	**CGL2_11277081**	Probable transporter protein	406	75926..77143	21_GENE_42
11277	**82**	**CGL2_11277082**	Hypothetical protein	214	complement(77134..77775)	21_GENE_43
11277	**83**	**CGL2_11277083**	Putative proteasome component	448	complement(77823..79166)	21_GENE_44
11277	**84**	**CGL2_11277084**	Probable 20S proteasome alpha-subunit	229	complement(79193..79879)	21_GENE_45
11277	**85**	**CGL2_11277085**	Putative 20S proteasome beta-subunit	279	complement(79879..80715)	21_GENE_46
11277	**86**	**CGL2_11277086**	Conserved protein of unknown function	70	complement(80734..80943)	21_GENE_47
11277	**87**	**CGL2_11277087**	Putative proteasome component	505	complement(80969..82483)	21_GENE_48
11277	**88**	**CGL2_11277088**	Vesicle-fusing ATPase (EC 3.6.4.6)	579	complement(82504..84240)	21_GENE_49
11277	**89**	**CGL2_11277089**	Peroxiredoxin	158	complement(84432..84905)	21_GENE_51
11277	**90**	**CGL2_11277090**	Putative band 7 family protein	286	complement(84982..85839)	21_GENE_52
11277	**91**	**CGL2_11277091**	Protein of unknown function	202	complement(85874..86479)	21_GENE_53
11277	**92**	**CGL2_11277092**	Protein of unknown function	93	complement(86487..86765)	21_GENE_54
11277	**93**	**CGL2_11277093**	Protein of unknown function	115	87064..87408	21_GENE_56

11277	**94**	**CGL2_11277094**	Alcohol dehydrogenase (EC 1.1.1.1)	334	complement(87473..88474)	21_GENE_57
11277	**95**	**CGL2_11277095**	Protein of unknown function	72	complement(88519..88734)	21_GENE_58
11277	**96**	**CGL2_11277096**	Putative acriflavin resistance protein	1087	complement(88826..92086)	21_GENE_59
11277	**97**	**CGL2_11277097**	Efflux transporter, RND family, MFP subunit	349	complement(92086..93132)	32_GENE_53
11277	**98**	**CGL2_11277098**	Putative outer membrane efflux protein	472	complement(93193..94608)	32_GENE_52
11277	**99**	**CGL2_11277099**	Putative transcriptional regulator, ArsR family	112	complement(94608..94943)	32_GENE_51
11277	**100**	**CGL2_11277100**	Hypothetical protein	89	95205..95471	32_GENE_50
11277	**101**	**CGL2_11277101**	Exinuclease ABC, B subunit (UvrB)	701	complement(95482..97584)	32_GENE_49
11277	**102**	**CGL2_11277102**	Conserved hypothetical protein	117	complement(97584..97934)	32_GENE_48
11277	**103**	**CGL2_11277103**	Protein of unknown function	239	97991..98707	32_GENE_47
11277	**104**	**CGL2_11277104**	Aminopeptidase N (EC 3.4.11.2)	863	complement(98735..101323)	32_GENE_46
11277	**105**	**CGL2_11277105**	Putative thioredoxin	108	complement(101372..101695)	32_GENE_45
11277	**106**	**CGL2_11277106**	Conserved protein of unknown function	253	101887..102645	32_GENE_44
11277	**107**	**CGL2_11277107**	Protein of unknown function	234	102658..103359	32_GENE_43
11277	**108**	**CGL2_11277108**	Probable cytochrome b561 family	253	103465..104223	32_GENE_42
11277	**109**	**CGL2_11277109**	Putative diguanylate phosphodiesterase	416	complement(104254..105501)	32_GENE_41
11277	**110**	**CGL2_11277110**	Copper translocating P-type ATPase (EC 3.6.3.4)	843	105624..108152	32_GENE_40
11277	**111**	**CGL2_11277111**	Ammonium transporter	435	complement(108233..109537)	32_GENE_39
11277	**112**	**CGL2_11277112**	Nitrogen regulatory protein P-II	112	complement(109608..109943)	32_GENE_38
11277	**113**	**CGL2_11277113**	Ammonium transporter	490	complement(110013..111482)	32_GENE_37
11277	**114**	**CGL2_11277114**	Protein of unknown function	514	complement(111609..113150)	32_GENE_36
11277	**115**	**CGL2_11277115**	Hypothetical protein	154	113548..114009	32_GENE_35
11277	**116**	**CGL2_11277116**	Cystathionine gamma-synthase (EC 2.5.1.48)	401	complement(114028..115230)	32_GENE_34
11277	**117**	**CGL2_11277117**	Protein of unknown function	365	115366..116460	32_GENE_33
11277	**118**	**CGL2_11277118**	Putative oligopeptide ABC transporter	303	complement(116491..117399)	32_GENE_32
11277	**119**	**CGL2_11277119**	Putative oligopeptide ABC transporter	283	complement(117399..118247)	32_GENE_31
11277	**120**	**CGL2_11277120**	Hypothetical protein	90	complement(118250..118519)	32_GENE_29
11277	**121**	**CGL2_11277121**	Protein of unknown function	126	complement(118522..118899)	32_GENE_28
11277	**122**	**CGL2_11277122**	Protein of unknown function	116	complement(118957..119304)	32_GENE_27
11277	**123**	**CGL2_11277123**	Protein of unknown function	208	complement(119294..119917)	32_GENE_26
11277	**124**	**CGL2_11277124**	Putative glycosyl hydrolase, BNR repeat	352	complement(120032..121087)	32_GENE_25
11277	**125**	**CGL2_11277125**	Hypothetical protein	42	complement(121087..121212)	
11277	**126**	**CGL2_11277126**	Hypothetical protein	18	complement(121209..121262)	
11277	**126a**	**CGL2_11277126a**	Transposase	446	complement(121576..122913)	
11277	**127**	**CGL2_11277127**	Protein of unknown function	223	complement(123460..124128)	32_GENE_24
11277	**128**	**CGL2_11277128**	Putative haloacid dehalogenase-like hydrolase	232	complement(124353..125048)	32_GENE_23
11277	**129**	**CGL2_11277129**	Probable hexapeptide transferase family protein	177	125210..125740	32_GENE_22
11277	**130**	**CGL2_11277130**	Putative periplasmic sensor signal transduction histid	546	125800..127437	32_GENE_21
11277	**131**	**CGL2_11277131**	Putative response regulator receiver protein	148	127459..127902	32_GENE_20
11277	**132**	**CGL2_11277132**	Peptidase S1C, Do	500	127946..129445	32_GENE_19
11277	**133**	**CGL2_11277133**	Probable crossover junction endodeoxyribonuclease (	158	129486..129959	32_GENE_18

11277	**134**	**CGL2_11277134**	Probable holliday junction DNA helicase (RuvA)	208	129959..130582	32_GENE_17
11277	**135**	**CGL2_11277135**	Holliday junction DNA helicase (RuvB)	332	130572..131567	32_GENE_16
11277	**136**	**CGL2_11277136**	Protein of unknown function	241	complement(131580..132302)	32_GENE_15
11277	**137**	**CGL2_11277137**	Protein of unknown function	277	132450..133280	32_GENE_14
11277	**138**	**CGL2_11277138**	Protein of unknown function	308	133280..134203	32_GENE_13
11277	**139**	**CGL2_11277139**	Conserved hypothetical protein	51	complement(134216..134368)	32_GENE_12
11277	**140**	**CGL2_11277140**	Conserved hypothetical protein	100	complement(134323..134622)	32_GENE_11
11277	**141**	**CGL2_11277141**	Probable prevent-host-death protein	64	complement(134673..134864)	32_GENE_10
11277	**142**	**CGL2_11277142**	Hypothetical protein	105	135141..135455	32_GENE_9
11277	**143**	**CGL2_11277143**	Putative antibiotic biosynthesis monooxygenase	104	136077..136388	32_GENE_8
11277	**144**	**CGL2_11277144**	Probable thiamine biosynthesis protein	328	136388..137371	32_GENE_7
11277	**145**	**CGL2_11277145**	Probable radical SAM family protein	311	137362..138294	32_GENE_6
11277	**146**	**CGL2_11277146**	Conserved protein of unknown function	109	complement(138672..138998)	32_GENE_5
11277	**147**	**CGL2_11277147**	Probable oxidoreductase FAD/NAD(P)-binding proteir	229	complement(139091..139777)	32_GENE_4
11277	**148**	**CGL2_11277148**	Putative major facilitator superfamily transporter	418	140056..141309	32_GENE_1
11277	**149**	**CGL2_11277149**	Protein of unknown function	244	complement(141338..142069)	
11277	**150**	**CGL2_11277150**	Protein of unknown function	255	142172..142936	630_GENE_3
11277	**151**	**CGL2_11277151**	Transposase	411	143224..144456	630_GENE_4
11277	**153**	**CGL2_11277153**	Protein of unknown function (cyt 572, see full lengt	576	complement(144648..146375)	630_GENE_6
		Strain variant path	**Strain variant path**			**Strain variant path**
11277	**154**	**CGL2_11277154**	Transposase	446	complement(147058..148395)	815_GENE_1
11277tRNA		**CGL2_11277R005**	TRNA Leu CAA		148692..148778	
11277	**155**	**CGL2_11277155**	Integrase	185	149319..149873	815_GENE_2
11277	**156**	**CGL2_11277156**	Hypothetical protein	63	150116..150304	815_GENE_3
11277	**157**	**CGL2_11277157**	Hypothetical protein	60	complement(150474..150653)	815_GENE_4
11277	**158**	**CGL2_11277158**	Protein of unknown function	1140	complement(150680..154099)	815_GENE_5
11277	**159**	**CGL2_11277159**	Hypothetical protein	63	complement(154104..154292)	600_GENE_2
11277	**160**	**CGL2_11277160**	Hypothetical protein	36	complement(154300..154407)	600_GENE_3
11277	**161**	**CGL2_11277161**	Hypothetical protein	150	complement(154407..154856)	600_GENE_4
11277	**162**	**CGL2_11277162**	conjugation TrwB	456	complement(154980..156347)	600_GENE_5
11277	**163**	**CGL2_11277163**	plasmid coupling TrwB	425	complement(156353..157627)	185_GENE_1
11277	**164**	**CGL2_11277164**	Hypothetical protein	138	complement(157645..158058)	185_GENE_2
11277	**165**	**CGL2_11277165**	Hypothetical protein	180	complement(158058..158597)	185_GENE_3
11277	**166**	**CGL2_11277166**	Hypothetical protein	85	complement(158751..159005)	185_GENE_4
11277	**167**	**CGL2_11277167**	Hypothetical protein	75	complement(159005..159229)	185_GENE_5
11277	**168**	**CGL2_11277168**	Hypothetical protein	82	complement(159229..159474)	185_GENE_6
11277	**169**	**CGL2_11277169**	Hypothetical protein	43	complement(159518..159646)	185_GENE_7
11277	**170**	**CGL2_11277170**	Hypothetical protein	104	complement(159661..159972)	185_GENE_8
11277	**171**	**CGL2_11277171**	Protein of unknown function	45	160002..160136	185_GENE_9
11277	**172**	**CGL2_11277172**	Hypothetical protein	43	160097..160225	185_GENE_10
11277	**173**	**CGL2_11277173**	Hypothetical protein	63	160422..160610	185_GENE_12

11277	**174**	**CGL2_11277174**	Protein of unknown function	155	160628..161092	185_GENE_13
11277	**174a**	**CGL2_11277174a**	Hypothetical protein	113	complement(161100..161438)	
11277	**175**	**CGL2_11277175**	Hypothetical protein	302	complement(161562..162467)	185_GENE_14
11277	**176**	**CGL2_11277176**	biopolymer transport, ExbD	147	complement(162562..163002)	185_GENE_15
11277	**177**	**CGL2_11277177**	TonB	509	complement(163575..165101)	185_GENE_16
11277	**178**	**CGL2_11277178**	TolQ	236	complement(165245..165952)	185_GENE_18
11277	**179**	**CGL2_11277179**	Protein of unknown function	500	complement(166046..167545)	185_GENE_19
11277	**180**	**CGL2_11277180**	Hypothetical protein	54	complement(167638..167799)	185_GENE_20
11277	**181**	**CGL2_11277181**	Hypothetical protein	146	complement(167795..168232)	185_GENE_21
11277	**182**	**CGL2_11277182**	Conserved protein of unknown function	577	complement(168204..169934)	185_GENE_22
11277	**183**	**CGL2_11277183**	Probable transposase	213	complement(170344..170982)	173_GENE_16
11277	**184**	**CGL2_11277184**	Transposase	431	complement(170975..172267)	173_GENE_15
11277	**185**	**CGL2_11277185**	Protein of unknown function	620	complement(172511..174370)	173_GENE_14
11277	**186**	**CGL2_11277186**	Conserved hypothetical protein	161	complement(174395..174877)	173_GENE_13
11277	**187**	**CGL2_11277187**	Hypothetical protein	82	complement(174885..175130)	173_GENE_12
11277	**188**	**CGL2_11277188**	IstB helper protein/transposase	259	complement(175186..175962)	173_GENE_11
11277	**189**	**CGL2_11277189**	transposase	440	complement(175965..177284)	173_GENE_10
11277	**189a**	**CGL2_11277189a**	Hypothetical protein	126	complement(177336..177713)	
11277	**190**	**CGL2_11277190**	Conserved protein of unknown function	221	complement(178159..178821)	173_GENE_9
11277	**191**	**CGL2_11277191**	Hypothetical protein	151	complement(179031..179483)	173_GENE_7
11277	**191a**	**CGL2_11277191a**	Hypothetical protein	138	complement(179587..180000)	
11277	**192**	**CGL2_11277192**	transposase	102	complement(180152..180457)	173_GENE_5
11277	**193**	**CGL2_11277193**	transposase	135	complement(180442..180846)	173_GENE_4
11277	**194**	**CGL2_11277194**	Hypothetical protein	225	complement(180864..181538)	173_GENE_3
11277	**195**	**CGL2_11277195**	Hypothetical protein	73	complement(181573..181791)	173_GENE_2
11277	**196**	**CGL2_11277196**	Putative replicative helicase	448	complement(181769..183112)	173_GENE_1
11277	**196a**	**CGL2_11277196a**	Hypothetical protein	75	complement(183112..183336)	
11277	**197a**	**CGL2_11277197a**	Hypothetical protein	110	complement(183336..183665)	
11277	**197**	**CGL2_11277197**	Hypothetical protein	80	complement(183777..184016)	374_GENE_1
11277	**198**	**CGL2_11277198**	Protein of unknown function	231	184124..184816	374_GENE_2
11277	**199**	**CGL2_11277199**	Transposase	146	complement(185024..185461)	374_GENE_3
11277	**200**	**CGL2_11277200**	Probable phage integrase, pseudo	123	185866..186234	374_GENE_4a
11277	**201**	**CGL2_11277201**	Protein of unknown function	113	complement(186368..186706)	374_GENE_5
11277	**202**	**CGL2_11277202**	Protein of unknown function	217	complement(186712..187362)	374_GENE_6
11277	**203**	**CGL2_11277203**	Protein of unknown function	163	complement(187774..188262)	374_GENE_7
11277	**204**	**CGL2_11277204**	Protein of unknown function	371	complement(188410..189522)	374_GENE_8
11277	**205**	**CGL2_11277205**	Conserved hypothetical protein	326	complement(189531..190508)	374_GENE_9
11277	**206**	**CGL2_11277206**	Probable TPR-domain containing protein	176	complement(190718..191245)	374_GENE_10
11277	**207**	**CGL2_11277207**	Conserved protein of unknown function	95	complement(191933..192217)	4_GENE_100
11277	**208**	**CGL2_11277208**	Putative carbon-nitrogen hydrolase	273	complement(192294..193112)	4_GENE_99
11277	**209**	**CGL2_11277209**	Pantoate-beta-alanine ligase (EC 6.3.2.1)	286	193191..194048	4_GENE_98

11277	**210**	**CGL2_11277210**	Putative tetrapyrrole methylase family protein	282	194044..194889	4_GENE_97
11277	**211**	**CGL2_11277211**	Deoxyuridine-triphosphatase (EC 3.6.1.23)	157	complement(194931..195401)	4_GENE_96
11277	**212**	**CGL2_11277212**	Protein of unknown function	156	complement(195401..195868)	4_GENE_95
11277	**213**	**CGL2_11277213**	Acetylglutamate kinase (EC 2.7.2.8)	290	complement(195858..196727)	4_GENE_94
11277	**214**	**CGL2_11277214**	Heat shock protein HslU	444	complement(196784..198115)	4_GENE_93
11277	**215**	**CGL2_11277215**	ATP-dependent protease HslVU (ClpYQ), peptidase s	180	complement(198115..198654)	4_GENE_92
11277	**216**	**CGL2_11277216**	Putative phage integrase family protein	321	complement(198695..199657)	4_GENE_91
11277	**218**	**CGL2_11277218**	Putaive glucose-inhibited division protein A	427	complement(199650..200930)	4_GENE_90
11277	**219**	**CGL2_11277219**	DNA topoisomerase (EC 5.99.1.2)	850	complement(201028..203577)	4_GENE_89
11277	**220**	**CGL2_11277220**	DNA processing protein DprA	306	complement(203549..204466)	4_GENE_88
11277	**221**	**CGL2_11277221**	Protein of unknown function	90	204560..204829	4_GENE_87
11277	**222**	**CGL2_11277222**	Putative ABC transporter ATP-binding protein	160	complement(204832..205311)	4_GENE_86
11277	**223**	**CGL2_11277223**	Sulfate-transporting ATPase (EC 3.6.3.25)	252	complement(205379..206134)	4_GENE_85
11277	**224**	**CGL2_11277224**	Putative transmembrane transporter	577	complement(206130..207860)	4_GENE_84
11277	**225**	**CGL2_11277225**	Protein of unknown function	137	207968..208378	4_GENE_83
11277	**226**	**CGL2_11277226**	Protein of unknown function	107	208414..208734	4_GENE_82
11277	**227**	**CGL2_11277227**	Protein of unknown function	175	complement(208761..209285)	4_GENE_81
11277	**228**	**CGL2_11277228**	Hypothetical protein	362	complement(209466..210551)	4_GENE_80
11277	**229**	**CGL2_11277229**	Putative A/G-specific DNA glycosylase	355	complement(210551..211615)	4_GENE_79
11277	**230**	**CGL2_11277230**	Hypothetical protein	245	complement(211605..212339)	4_GENE_78
11277	**231**	**CGL2_11277231**	Putative 2-amino-4-hydroxy-6-hydroxymethyldihydr	175	complement(212384..212908)	4_GENE_77
11277	**232**	**CGL2_11277232**	Aspartate aminotransferase (EC 2.6.1.1)	394	complement(212911..214092)	4_GENE_76
11277	**233**	**CGL2_11277233**	Hypothetical protein	237	complement(214273..214983)	4_GENE_75
11277	**234**	**CGL2_11277234**	Hypothetical protein	358	complement(215023..216096)	4_GENE_74
11277	**235**	**CGL2_11277235**	Hypothetical protein	149	complement(216216..216662)	4_GENE_73
11277	**236**	**CGL2_11277236**	Hypothetical protein	152	complement(216662..217117)	4_GENE_72
11277	**237**	**CGL2_11277237**	Hypothetical protein	165	complement(217193..217687)	4_GENE_70a
11277	**238**	**CGL2_11277238**	3-oxoacyl-[acyl-carrier-protein] reductase (1.1.1.10	235	217903..218607	4_GENE_70
11277	**239**	**CGL2_11277239**	Probable flagellar biosynthesis protein	100	complement(218585..218884)	4_GENE_69
11277	**240**	**CGL2_11277240**	Hypothetical protein	271	complement(218884..219696)	4_GENE_68
11277	**241**	**CGL2_11277241**	Protein of unknown function	186	complement(219715..220272)	4_GENE_67
11277	**242**	**CGL2_11277242**	Hypothetical protein	96	complement(220305..220592)	4_GENE_66
11277	**243**	**CGL2_11277243**	Putative flagellar motor protein (OmpA/MotB)	261	complement(220616..221398)	4_GENE_65
11277	**244**	**CGL2_11277244**	Putative flagellar motor component (MotA)	260	complement(221410..222189)	4_GENE_64
11277	**245**	**CGL2_11277245**	Putative chemotaxis protein (CheW)	171	complement(222221..222733)	4_GENE_63
11277	**246**	**CGL2_11277246**	Putative methyl-accepting chemotaxis sensory trans	557	complement(222768..224438)	4_GENE_62
11277	**247**	**CGL2_11277247**	Protein-glutamate methylesterase (CheB) (EC 3.1.1.	344	complement(224494..225525)	4_GENE_61
11277	**248**	**CGL2_11277248**	Putative signal transduction histidine kinase (CheA)	646	complement(225538..227475)	4_GENE_60
11277	**249**	**CGL2_11277249**	Putative response regulator receiver protein (CheY)	126	complement(227520..227897)	4_GENE_59
11277	**250**	**CGL2_11277250**	Protein-glutamate O-methyltransferase (CheR) (EC 2	264	complement(228021..228812)	4_GENE_58
11277	**251**	**CGL2_11277251**	Putative RNA polymerase sigma 28 subunit	251	complement(228855..229607)	4_GENE_57

11277	**252**	**CGL2_11277252**	Protein of unknown function	292	complement(229668..230543)	4_GENE_56
11277	**253**	**CGL2_11277253**	flagellar biosynthesis protein FlhF	393	complement(230547..231725)	4_GENE_55
11277	**254**	**CGL2_11277254**	possible flagellar biosynthetic protein FlhA	702	complement(231732..233837)	4_GENE_54
11277	**255**	**CGL2_11277255**	flagellar biosynthesis protein, FlhB	362	complement(233821..234906)	4_GENE_53
11277	**256**	**CGL2_11277256**	flagellar biosynthesis protein, FliR	262	complement(234899..235684)	4_GENE_52
11277	**257**	**CGL2_11277257**	Chemotaxis/flagella (novel lepto genera)	112	complement(235684..236019)	4_GENE_51
11277	**258**	**CGL2_11277258**	Flagellar biosynthesis protein FliP	265	complement(236083..236877)	4_GENE_50
11277	**259**	**CGL2_11277259**	Protein of unknown function	173	complement(236868..237386)	4_GENE_49
11277	**260**	**CGL2_11277260**	flagellar motor switch protein FliN	125	complement(237419..237793)	4_GENE_48
11277	**261**	**CGL2_11277261**	Putative flagellar basal body-associated protein FliL	168	complement(237833..238336)	4_GENE_47
11277	**262**	**CGL2_11277262**	Probable flagellar hook protein FlgE	457	complement(238500..239870)	4_GENE_46
11277	**263**	**CGL2_11277263**	Probable flagellar hook capping protein FlgD	276	complement(239875..240702)	4_GENE_45
11277	**264**	**CGL2_11277264**	Conserved protein of unknown function	494	complement(240733..242214)	4_GENE_44
11277	**265**	**CGL2_11277265**	Protein of unknown function	169	complement(242242..242748)	4_GENE_43
11277	**266**	**CGL2_11277266**	Protein of unknown function	147	complement(242748..243188)	4_GENE_42
11277	**267**	**CGL2_11277267**	Flagellum-specific ATP synthase FliI (EC 3.6.3.14)	462	complement(243191..244576)	4_GENE_41
11277	**268**	**CGL2_11277268**	Protein of unknown function	219	complement(244576..245232)	4_GENE_40
11277	**269**	**CGL2_11277269**	Flagellar motor switch protein FliG	334	complement(245263..246264)	4_GENE_39
11277	**270**	**CGL2_11277270**	Flagellar M-ring protein FliF	531	complement(246292..247884)	4_GENE_38
11277	**271**	**CGL2_11277271**	Flagellar hook-basal body complex protein FliE	109	complement(247936..248262)	4_GENE_37
11277	**272**	**CGL2_11277272**	Flagellar basal-body rod protein FlgC	145	complement(248308..248742)	4_GENE_36
11277	**273**	**CGL2_11277273**	Putative flagellar basal-body rod protein FlgB	144	complement(248748..249179)	4_GENE_35
11277	**274**	**CGL2_11277274**	Putative two component, sigma54 specific, transcript	489	complement(249198..250664)	4_GENE_34
11277	**275**	**CGL2_11277275**	Putative PAS/PAC sensor signal transduction histidine	406	complement(250664..251881)	4_GENE_33
11277	**276**	**CGL2_11277276**	Protein of unknown function	719	complement(251900..254056)	4_GENE_32
11277	**277**	**CGL2_11277277**	Putative sigma54 specific transcriptional regulator, F	344	complement(254233..255264)	4_GENE_31
11277	**278**	**CGL2_11277278**	Probable iron-sulfur cluster binding protein	342	complement(255269..256294)	4_GENE_30
11277	**279**	**CGL2_11277279**	Probable metal dependent phosphohydrolase	281	complement(256294..257136)	4_GENE_29
11277	**280**	**CGL2_11277280**	Probable metal dependent phosphohydrolase	280	complement(257190..258029)	4_GENE_28
11277	**281**	**CGL2_11277281**	Protein of unknown function	110	complement(258070..258399)	4_GENE_27
11277	**282**	**CGL2_11277282**	Probable lipoate protein ligase	209	complement(258399..259025)	4_GENE_26
11277	**283**	**CGL2_11277283**	Glycine dehydrogenase (Decarboxylating) subunit 2	496	complement(259038..260525)	4_GENE_25
11277	**284**	**CGL2_11277284**	Glycine dehydrogenase (Decarboxylating) subunit 1	453	complement(260525..261883)	4_GENE_24
11277	**285**	**CGL2_11277285**	Glycine cleavage system H protein	134	complement(261879..262280)	4_GENE_23
11277	**286**	**CGL2_11277286**	Glycine cleavage system T protein (EC 2.1.2.10)	377	complement(262394..263524)	4_GENE_22
11277	**287**	**CGL2_11277287**	Protein of unknown function	234	264038..264739	4_GENE_21
11277	**288**	**CGL2_11277288**	Putative methyl-accepting chemotaxis sensory transc	454	complement(264821..266182)	4_GENE_20
11277	**289**	**CGL2_11277289**	Putative methyl-accepting chemotaxis sensory transc	158	complement(266088..266561)	4_GENE_19
11277	**290**	**CGL2_11277290**	Protein of unknown function	184	complement(266571..267122)	4_GENE_18
11277	**291**	**CGL2_11277291**	Probable ABC transporter, periplasmic component	339	267338..268354	4_GENE_17
11277	**292**	**CGL2_11277292**	Protein of unknown function	467	268367..269767	4_GENE_16

11277	**293**	**CGL2_11277293**	Putative rhodanese-like domain protein	114	269829..270170	4_GENE_15
11277	**294**	**CGL2_11277294**	Protein of unknown function	101	complement(270246..270548)	4_GENE_14
11277	**295**	**CGL2_11277295**	Putative TRNA (1-methyladenosine) methyltransfera	276	270705..271532	4_GENE_13
11184	**1**	**CGL2_11184001**	Putative methyltransferase	214	complement(73..714)	4_GENE_12
11184	**2**	**CGL2_11184002**	NHL repeat domain protein	494	847..2328	4_GENE_11
11184	**3**	**CGL2_11184003**	Protein of unknown function	436	2404..3711	4_GENE_10
11184	**4**	**CGL2_11184004**	Hypothetical protein	67	3820..4020	4_GENE_9
11184	**5**	**CGL2_11184005**	Diaminopimelate epimerase (EC 5.1.1.7)	290	complement(4043..4912)	4_GENE_8
11184	**6**	**CGL2_11184006**	Protein of unknown function	284	complement(4951..5802)	4_GENE_7
11184	**7**	**CGL2_11184007**	Probable short-chain dehydrogenase/reductase SDR	247	complement(5798..6538)	4_GENE_6
11184	**8**	**CGL2_11184008**	Putative transcriptional regulators, TraR/DksA family	127	complement(6538..6918)	4_GENE_5
11184	**9**	**CGL2_11184009**	Putative catalytic LigB subunit of aromatic ring-openi	291	7054..7926	4_GENE_4
11184	**10**	**CGL2_11184010**	Heavy metal efflux pump (CzcA)	1036	complement(7845..10952)	4_GENE_3
11184	**11**	**CGL2_11184011**	Secretion protein (HlyD)	380	complement(10955..12094)	4_GENE_2
11184	**12**	**CGL2_11184012**	Probable outer membrane efflux protein	458	complement(12109..13482)	59_GENE_29
11184	**13**	**CGL2_11184013**	Protein of unknown function	206	complement(13836..14453)	59_GENE_28
11184	**14**	**CGL2_11184014**	Conserved protein of unknown function	281	complement(14453..15295)	59_GENE_27
11184	**15**	**CGL2_11184015**	Protein of unknown function	402	15515..16720	59_GENE_26
11184	**16**	**CGL2_11184016**	Protein of unknown function	82	16894..17139	59_GENE_24a
11184	**17**	**CGL2_11184017**	Protein of unknown function	100	17174..17473	59_GENE_24
11184	**18**	**CGL2_11184018**	Protein of unknown function	122	17491..17856	59_GENE_23
11184	**19**	**CGL2_11184019**	Protein of unknown function	83	17920..18168	59_GENE_22
11184tRNA		**CGL2_11184R001**	TRNA Ser GGA		18280..18372	
11184	**20**	**CGL2_11184020**	DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	540	18561..20180	59_GENE_21
11184	**21**	**CGL2_11184021**	Protein of unknown function	104	20180..20491	59_GENE_20
11184	**22**	**CGL2_11184022**	Recombination protein RecR	214	20507..21148	59_GENE_19
11184	**23**	**CGL2_11184023**	Peptide chain release factor 3	551	21206..22858	59_GENE_18
11184	**24**	**CGL2_11184024**	Putative mechanosensitive ion channel	313	complement(22805..23743)	59_GENE_17
11184tRNA		**CGL2_11184R002**	TRNA Ser GCT		complement(23816..23908)	
11184tRNA		**CGL2_11184R003**	TRNA Ser TGA		complement(23939..24024)	
11184	**25**	**CGL2_11184025**	Putative TPR-domain containing protein	272	complement(24581..25396)	59_GENE_16
11184	**26**	**CGL2_11184026**	Putative zinc-binding cytidine/deoxycytidylate deami	162	25430..25915	59_GENE_15
11184tRNA		**CGL2_11184R004**	TRNA Ser CGA		25991..26080	
11184	**27**	**CGL2_11184027**	Putative sigma-54 specific transcriptional regulator, I	453	26104..27462	59_GENE_14
11184	**28**	**CGL2_11184028**	Protein of unknown function	45	27707..27841	59_GENE_13
11184	**29**	**CGL2_11184029**	MazG family protein (nucleotide pyrophosphohydrola	301	27947..28849	59_GENE_12
11184	**30**	**CGL2_11184030**	Probable glycosyl transferase family protein	334	28849..29850	59_GENE_11
11184	**31**	**CGL2_11184031**	Probable metal-dependent phosphohydrolase	403	29865..31073	59_GENE_10
11184	**32**	**CGL2_11184032**	Protein of unknown function	80	complement(31072..31311)	59_GENE_9
11184	**33**	**CGL2_11184033**	Protein of unknown function	136	complement(31376..31783)	59_GENE_8
11184	**34**	**CGL2_11184034**	Hypothetical protein	72	31989..32204	59_GENE_7

11184	**35**	**CGL2_11184035**	Probable acid phosphatase	329	complement(32217..33203)	59_GENE_6
11184	**36**	**CGL2_11184036**	Protein of unknown function	464	complement(33203..34594)	59_GENE_5
11184	**37**	**CGL2_11184037**	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	462	complement(34642..36027)	59_GENE_4
11184tRNA		**CGL2_11184R005**	TRNA Met CAT		36112..36188	
11184	**38**	**CGL2_11184038**	transposase	479	complement(37465..38901)	333_GENE_1
11184	**39**	**CGL2_11184039**	Hypothetical protein	554	complement(38909..40570)	59_GENE_3
11184	**40**	**CGL2_11184040**	Hypothetical protein	213	complement(40761..41399)	333_GENE_4
11184	**41**	**CGL2_11184041**	Probable transcriptional regulator, LuxR family	358	42029..43102	333_GENE_5
11184	**42**	**CGL2_11184042**	Putative uracil-DNA glycosylase	237	complement(43132..43842)	333_GENE_6
11184	**43**	**CGL2_11184043**	Hypothetical protein	66	complement(43833..44030)	333_GENE_7
11184	**44**	**CGL2_11184044**	Protein of unknown function	404	complement(44030..45241)	333_GENE_8
11184	**45**	**CGL2_11184045**	Protein of unknown function (membrane?)	124	45372..45743	333_GENE_9
11184	**46**	**CGL2_11184046**	Exoribonuclease II (EC 3.1.13.1)	744	complement(45739..47970)	3_GENE_1
11184	**47**	**CGL2_11184047**	Protein of unknown function	160	48741..49220	3_GENE_4
11184	**48**	**CGL2_11184048**	Putative outer membrane protein, OmpA/MotB famil	179	49362..49898	3_GENE_5
11184	**49**	**CGL2_11184049**	Probable OmpA family protein	232	50257..50952	3_GENE_6
11184	**50**	**CGL2_11184050**	Hypothetical protein	161	complement(50891..51373)	3_GENE_7
11184	**51**	**CGL2_11184051**	Thiamine-monophosphate kinase (EC 2.7.4.16)	335	complement(51360..52364)	3_GENE_8
11184	**52**	**CGL2_11184052**	ATP-dependent protease La (EC 3.4.21.53)	816	complement(52357..54804)	3_GENE_9
11184	**53**	**CGL2_11184053**	UTP-glucose-1-phosphate uridylyltransferase (GalU)	297	complement(54811..55701)	3_GENE_10
11184	**54**	**CGL2_11184054**	Dephospho-CoA kinase (EC 2.7.1.24)	204	complement(55723..56334)	3_GENE_11
11184	**55**	**CGL2_11184055**	Hypothetical protein	159	complement(56334..56810)	3_GENE_12
11184	**56**	**CGL2_11184056**	Protein of unknown function	229	complement(56810..57496)	3_GENE_13
11184	**57**	**CGL2_11184057**	DNA polymerase I (EC 2.7.7.7)	872	complement(57530..60145)	3_GENE_14
11184	**58**	**CGL2_11184058**	Branched-chain amino acid aminotransferase (EC 2.	310	complement(60155..61084)	3_GENE_15
11184	**59**	**CGL2_11184059**	Probable membrane protein	234	complement(61126..61827)	3_GENE_16
11184	**60**	**CGL2_11184060**	Hypothetical protein	191	complement(61920..62492)	3_GENE_17
11184	**61**	**CGL2_11184061**	Hypothetical protein	333	complement(62483..63481)	3_GENE_18
11184	**62**	**CGL2_11184062**	Putative transcriptional regulator, LysR family	303	complement(63481..64389)	3_GENE_19
11184	**63**	**CGL2_11184063**	Probable ATP-dependent DNA helicase	737	complement(64411..66621)	3_GENE_20
11184	**64**	**CGL2_11184064**	Conserved hypothetical protein	240	complement(66625..67344)	3_GENE_21
11184	**65**	**CGL2_11184065**	Protein of unknown function	468	complement(67319..68722)	3_GENE_22
11184	**66**	**CGL2_11184066**	Conserved protein of unknown function	185	complement(68725..69279)	3_GENE_23
11184	**67**	**CGL2_11184067**	Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.	230	complement(69263..69952)	3_GENE_25
11184	**68**	**CGL2_11184068**	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)	421	complement(69974..71236)	3_GENE_26
11184	**69**	**CGL2_11184069**	Glutamate 5-kinase (EC 2.7.2.11)	380	complement(71246..72385)	3_GENE_27
11184	**70**	**CGL2_11184070**	Putative GTP binding protein	360	complement(72385..73464)	3_GENE_28
11184	**71**	**CGL2_11184071**	Ribosomal protein L27	92	complement(73492..73767)	3_GENE_29
11184	**72**	**CGL2_11184072**	Ribosomal protein L21	106	complement(73849..74166)	3_GENE_30
11184	**73**	**CGL2_11184073**	Putative ferric uptake regulator, Fur family	153	74477..74935	3_GENE_31
11184	**74**	**CGL2_11184074**	Probable glycosyl hydrolase, BNR repeat	352	complement(74979..76034)	3_GENE_32

11184	**75**	**CGL2_11184075**	transposase	115	complement(76434..76778)	3_GENE_33
11181	**1**	**CGL2_11181001**	Protein of unknown function	332	complement(801..1796)	3_GENE_34
11181	**2**	**CGL2_11181002**	Probable 6-pyruvoyl tetrahydrobiopterin synthase fa	128	2118..2501	3_GENE_36
11181	**3**	**CGL2_11181003**	Oligopeptide/dipeptide ABC transporter, ATP-binding	336	2501..3508	3_GENE_37
11181	**4**	**CGL2_11181004**	ABC phosphate transporter (EC 3.6.3.27)	347	3513..4553	3_GENE_38
11181	**5**	**CGL2_11181005**	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.	519	4581..6137	3_GENE_39
11181	**6**	**CGL2_11181006**	Phenylalanyl-tRNA synthetase beta chain	569	6174..7880	3_GENE_40
11181	**7**	**CGL2_11181007**	Ribosomal protein L20	118	complement(7952..8305)	3_GENE_41
11181	**8**	**CGL2_11181008**	Ribosomal protein L35	65	complement(8390..8584)	3_GENE_42
11181	**9**	**CGL2_11181009**	Translation initiation factor 3 (IF-3)	175	complement(8629..9153)	3_GENE_43
11181	**10**	**CGL2_11181010**	Threonyl-tRNA synthetase (EC 6.1.1.3)	617	complement(9229..11079)	3_GENE_44
11181	**10a**	**CGL2_11181010a**	Putative transpoase	446	complement(11438..12775)	
11181	**11**	**CGL2_11181011**	Putative diguanylate cyclase/phosphodiesterase	1196	complement(12923..16510)	3_GENE_45
11181	**12**	**CGL2_11181012**	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	283	complement(16529..17377)	3_GENE_46
11181	**13**	**CGL2_11181013**	Putative peptidase M23B family protein	296	complement(17383..18270)	3_GENE_47
11181	**14**	**CGL2_11181014**	Thiamine monophosphate synthase (EC 2.5.1.3)	215	complement(18270..18914)	3_GENE_48
11181	**15**	**CGL2_11181015**	Thiazole biosynthesis protein (ThiG)	274	complement(18920..19741)	3_GENE_49
11181	**17**	**CGL2_11181017**	Acetyl-CoA synthetase (EC 6.2.1.1)	641	19983..21905	3_GENE_50
11181	**18**	**CGL2_11181018**	Putative glyoxalase (GloA)	291	21932..22804	3_GENE_51
11181	**19**	**CGL2_11181019**	Hypothetical protein	270	complement(22776..23585)	3_GENE_52
11181	**20**	**CGL2_11181020**	Putative monogalactosyldiacylglycerol synthase	376	23777..24904	3_GENE_53
11181	**21**	**CGL2_11181021**	Putative metallophosphoesterase	311	24904..25836	3_GENE_54
11181	**22**	**CGL2_11181022**	Probable major facilitator superfamily transporter	405	complement(25751..26965)	3_GENE_55
11181	**23**	**CGL2_11181023**	Carboxymethylenebutenolidase (EC 3.1.1.45)	259	complement(27021..27797)	3_GENE_56
11181	**24**	**CGL2_11181024**	Putative outer membrane protein	496	complement(28208..29695)	3_GENE_57
11181	**25**	**CGL2_11181025**	Protein of unknown function	165	complement(29796..30290)	3_GENE_58
11181	**26**	**CGL2_11181026**	Putative periplasmic sensor signal transduction histid	474	complement(30414..31835)	3_GENE_59
11181	**27**	**CGL2_11181027**	Putative two component transcriptional regulator, wi	222	complement(31850..32515)	3_GENE_60
11181	**28**	**CGL2_11181028**	Protein of unknown function	151	complement(32571..33023)	3_GENE_61
11181tRNA		**CGL2_11181R001**	TRNA Pro TGG		complement(33263..33339)	
11181	**29**	**CGL2_11181029**	Protein of unknown function	318	33507..34460	3_GENE_62
11181	**30**	**CGL2_11181030**	Putative beta-lactamase family protein	293	34468..35346	3_GENE_63
11181	**31**	**CGL2_11181031**	ATP synthase F1, epsilon subunit	143	complement(35424..35852)	3_GENE_64
11181	**32**	**CGL2_11181032**	ATP synthase F1, beta subunit (EC 3.6.3.15)	463	complement(35861..37249)	3_GENE_65
11181	**33**	**CGL2_11181033**	ATP synthase F1, gamma subunit (EC 3.6.3.15)	291	complement(37297..38169)	3_GENE_66
11181	**34**	**CGL2_11181034**	ATP synthase F1, alpha subunit (EC 3.6.3.15)	512	complement(38176..39711)	3_GENE_67
11181	**35**	**CGL2_11181035**	Putative ATP synthase F1, delta subunit	189	complement(39711..40277)	3_GENE_68
11181	**36**	**CGL2_11181036**	ATP synthase F0, subunit B	175	complement(40277..40801)	3_GENE_69
11181	**37**	**CGL2_11181037**	ATP synthase F0, subunit C	76	complement(40850..41077)	3_GENE_70
11181	**38**	**CGL2_11181038**	ATP synthase F0, subunit A	244	complement(41111..41842)	3_GENE_71
11181	**39**	**CGL2_11181039**	Hypothetical protein	89	complement(41849..42115)	3_GENE_72

11181	**40**	**CGL2_11181040**	Probable membrane protein	164	42457..42948	3_GENE_73
11181	**41**	**CGL2_11181041**	Phosphoglycolate phosphatase (EC 3.1.3.18)	239	complement(42869..43585)	3_GENE_74
11181	**42**	**CGL2_11181042**	Putative oligopeptide ABC transporter, permease pro	340	complement(43651..44670)	3_GENE_75
11181	**43**	**CGL2_11181043**	Putative oligopeptide ABC transporter, permease pro	324	complement(44670..45641)	3_GENE_76
11181	**44**	**CGL2_11181044**	Transporter (Extracellular solute binding protein fam	534	complement(45641..47242)	3_GENE_77
11181	**45**	**CGL2_11181045**	preprotein translocase, SecG subunit	101	complement(47380..47682)	3_GENE_78
11181	**46**	**CGL2_11181046**	Triosephosphate isomerase (EC 5.3.1.1)	258	complement(47737..48510)	3_GENE_79
11181	**47**	**CGL2_11181047**	Phosphoglycerate kinase (EC 2.7.2.3)	399	complement(48527..49723)	3_GENE_80
11181	**48**	**CGL2_11181048**	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2	342	complement(49723..50748)	3_GENE_81
11181	**49**	**CGL2_11181049**	Peptidoglycan glycosyltransferase (EC 2.4.1.129)	790	complement(50867..53236)	3_GENE_82
11181	**50**	**CGL2_11181050**	Hypothetical protein	70	complement(53463..53672)	3_GENE_84
11181	**51**	**CGL2_11181051**	Orotate phosphoribosyl transferase (EC 2.4.2.10)	212	complement(53820..54455)	3_GENE_85
11181	**52**	**CGL2_11181052**	Putative methyl-accepting chemotaxis sensory trans	368	complement(54660..55763)	3_GENE_86
11181tRNA		**CGL2_11181R002**	TRNA Leu GAG		complement(56130..56213)	
11181	**53**	**CGL2_11181053**	Siroheme synthase, N-terminal	217	complement(56502..57152)	3_GENE_89
11181	**54**	**CGL2_11181054**	Probable DNA uptake lipoprotein	243	complement(57152..57880)	3_GENE_90
11181	**55**	**CGL2_11181055**	3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1	329	57974..58960	3_GENE_91
11181	**56**	**CGL2_11181056**	Putative two component, sigma54 specific, transcript	457	complement(58963..60333)	3_GENE_92
11181	**57**	**CGL2_11181057**	Multi-sensor signal transduction histidine kinase	751	complement(60337..62589)	3_GENE_93
11181	**58**	**CGL2_11181058**	Protein of unknown function	408	complement(62648..63871)	3_GENE_94
11181	**59**	**CGL2_11181059**	Protein of unknown function	222	complement(63878..64543)	3_GENE_95
11181	**60**	**CGL2_11181060**	Probable multiple antibiotic resistance protein (MarC	201	64582..65184	3_GENE_96
11181	**61**	**CGL2_11181061**	Protein of unknown function	144	65289..65720	3_GENE_97
11181	**62**	**CGL2_11181062**	Putative UbiE/COQ5 methyltransferase	279	complement(65732..66568)	3_GENE_98
11181	**63**	**CGL2_11181063**	Putative queuosine biosynthesis protein	385	complement(66568..67722)	3_GENE_99
11181	**64**	**CGL2_11181064**	Putative diguanylate phosphodiesterase	347	67758..68798	3_GENE_100
11181	**65**	**CGL2_11181065**	Protein of unknown function	168	68937..69440	3_GENE_101
11181	**66**	**CGL2_11181066**	Probable lipoprotein	396	69456..70643	3_GENE_102
11181	**67**	**CGL2_11181067**	Putative sulfide-quinone reductase	375	complement(70746..71870)	3_GENE_103
11181	**68**	**CGL2_11181068**	Carbonic anhydrase	193	complement(71985..72563)	147_GENE_15
11181	**69**	**CGL2_11181069**	Diguanylate cyclase	368	72947..74050	147_GENE_14
11181	**70**	**CGL2_11181070**	Protein of unknown function	161	74106..74588	147_GENE_13
11181	**71**	**CGL2_11181071**	Probable helicase	62	74581..74766	147_GENE_11a
11181	**72**	**CGL2_11181072**	Putative helicase	1055	complement(74776..77940)	147_GENE_11
11181	**73**	**CGL2_11181073**	Putative NUDIX hydrolase	134	complement(77930..78331)	147_GENE_10
11181	**74**	**CGL2_11181074**	Putative metal-dependent phosphohydrolase	476	78515..79942	147_GENE_9
11181	**75**	**CGL2_11181075**	Patatin-like phospholipase	330	79948..80937	147_GENE_8
11181	**76**	**CGL2_11181076**	Alcohol dehydrogenase (EC 1.1.1.1)	341	complement(80947..81969)	147_GENE_7
11181	**77**	**CGL2_11181077**	Probable anti-ECFsigma factor (ChrR)	223	complement(81969..82637)	147_GENE_6
11181	**78**	**CGL2_11181078**	Protein of unknown function	268	82811..83614	147_GENE_5
11181	**79**	**CGL2_11181079**	Conserved hypothetical protein	318	83614..84567	147_GENE_4

11181	**80**	**CGL2_11181080**	Protein of unknown function	100	84741..85040	147_GENE_3
11181	**81**	**CGL2_11181081**	Probable transcriptional regulator	97	85040..85330	147_GENE_2
		CGL2_11181CRISPR			85518..89905	
		CGL2_11386CRISPR			36056..37265	
11386	**30**	**CGL2_11386030**	CRISPR-ssociated protein, Cas2	102	35660..35965	26_GENE_2
11386	**29**	**CGL2_11386029**	CRISPR-ssociated protein, Cas1	306	34759..35676	26_GENE_3
11386	**28**	**CGL2_11386028**	CRISPR-ssociated protein, Cas3	218	34110..34763	26_GENE_4
11386	**27**	**CGL2_11386027**	CRISPR-ssociated protein, Cas5	227	33440..34120	26_GENE_5
11386	**26**	**CGL2_11386026**	CRISPR-ssociated protein, Cas4	398	32239..33432	26_GENE_6
11386	**25**	**CGL2_11386025**	CRISPR-ssociated protein, Cas2	171	31727..32239	26_GENE_7
11386	**24**	**CGL2_11386024**	CRISPR-ssociated protein, Cas1	508	30204..31727	26_GENE_8
11386	**23**	**CGL2_11386023**	CRISPR-associated helicase Cas3	880	27565..30204	26_GENE_9
11386	**22**	**CGL2_11386022**	Transposase	455	25968..27332	26_GENE_10
11386	**21**	**CGL2_11386021**	Probable transposase	143	complement(25114..25542)	26_GENE_12
11386	**20**	**CGL2_11386020**	Hypothetical protein	74	complement(24765..24986)	26_GENE_13
11386	**19**	**CGL2_11386019**	Hypothetical protein	43	complement(24580..24708)	26_GENE_14
11386	**18**	**CGL2_11386018**	DNA methyltransferase/helicase	1067	complement(20914..24114)	26_GENE_15
11386	**17**	**CGL2_11386017**	Conserved protein of unknown function	209	complement(20254..20880)	26_GENE_16
11386	**16**	**CGL2_11386016**	Protein of unknown function	229	19380..20066	26_GENE_17
11386	**15**	**CGL2_11386015**	Hypothetical protein	125	18864..19238	26_GENE_18
11386	**14**	**CGL2_11386014**	Conserved hypothetical protein	703	16756..18864	26_GENE_19
		Strain variant path	**Strain variant path**			**Strain variant path**
11386	**13**	**CGL2_11386013**	Conserved hypothetical protein	300	15833..16732	26_GENE_20
11386	**12**	**CGL2_11386012**	phage DNA binding protein	60	15654..15833	26_GENE_21
11386	**11**	**CGL2_11386011**	Hypothetical protein	309	14611..15537	26_GENE_22
11386	**10**	**CGL2_11386010**	integrase INT P4	403	13403..14611	26_GENE_23
11386	**9**	**CGL2_11386009**	SsrA-binding protein	163	12311..12799	26_GENE_24
11386	**8**	**CGL2_11386008**	Leucyl aminopeptidase (EC 3.4.11.1)	532	10649..12244	183_GENE_9
11386	**7**	**CGL2_11386007**	ExsB protein (succinoglycan synthase?)	241	9812..10534	183_GENE_8
11386	**6**	**CGL2_11386006**	Putative radical activating enzyme	212	9171..9806	183_GENE_7
11386	**5**	**CGL2_11386005**	Protein of unknown function	231	8411..9103	183_GENE_6
11386	**4**	**CGL2_11386004**	DNA gyrase, A subunit	816	5860..8307	183_GENE_5
11386	**3**	**CGL2_11386003**	DNA gyrase, B subunit (EC 5.99.1.3)	818	3348..5801	183_GENE_4
11386	**2**	**CGL2_11386002**	DNA polymerase III, beta chain (EC 2.7.7.7)	387	1959..3119	183_GENE_3
11386	**1**	**CGL2_11386001**	Chromosomal replication initiator protein (DnaA) OR	465	543..1937	183_GENE_2
		Strain variant path	**Strain variant path**			**Strain variant path**
11389	**40**	**CGL2_11389040**	Acetolactate synthase, large subunit (EC 2.2.1.6)	581	complement(34161..35903)	26_GENE_33
11389	**39**	**CGL2_11389039**	Acetolactate synthase, small subunit	184	complement(33592..34143)	26_GENE_34
11389	**38**	**CGL2_11389038**	Acetohydroxy acid isomeroreductase (EC 1.1.1.86)	339	complement(32507..33523)	26_GENE_35
11389	**37**	**CGL2_11389037**	Phosphatidylserine decarboxylase (EC 4.1.1.65)	217	complement(31841..32491)	26_GENE_36
11389	**36**	**CGL2_11389036**	CDP-diacylglycerol-serine O-phosphatidyltransferase	278	complement(31036..31869)	26_GENE_37

11389	**35**	**CGL2_11389035**	2-isopropylmalate synthase (EC 2.3.3.13) AA and py	532	complement(29395..30990)	26_GENE_38
11389	**34**	**CGL2_11389034**	3-isopropylmalate dehydrogenase (EC 1.1.1.85) AA	370	complement(28228..29337)	26_GENE_39
11389	**33**	**CGL2_11389033**	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.1	349	complement(27182..28228)	26_GENE_40
11389	**32**	**CGL2_11389032**	Quinolinate synthetase complex, subunit A	316	complement(26215..27162)	26_GENE_41
11389	**31**	**CGL2_11389031**	Conserved hypothetical protein	79	complement(25979..26215)	26_GENE_42
11389	**30**	**CGL2_11389030**	Protein of unknown function	170	25497..26006	26_GENE_43
11389	**29**	**CGL2_11389029**	Putative ferredoxin oxidoreductase	193	24828..25406	26_GENE_44
11389	**28**	**CGL2_11389028**	Putative glyoxalase/bleomycin resistance protein	141	complement(24161..24583)	26_GENE_45
11389	**27**	**CGL2_11389027**	Protein of unknown function	351	23091..24143	26_GENE_46
11389	**26**	**CGL2_11389026**	Conserved hypothetical protein	375	21909..23033	26_GENE_47
11389	**25**	**CGL2_11389025**	Conserved hypothetical protein	191	21350..21922	26_GENE_48
11389	**24**	**CGL2_11389024**	Conserved protein of unknown function	190	20605..21174	80_GENE_26
11389	**23**	**CGL2_11389023**	Cobalamin B12-binding/Radical SAM family protein	517	19008..20558	80_GENE_25
11389	**22**	**CGL2_11389022**	Ribulose-bisphosphate carboxylase (EC 4.1.1.39)	392	complement(17625..18800)	80_GENE_24
11389	**21**	**CGL2_11389021**	Protein of unknown function	283	16774..17622	80_GENE_23
11389	**20**	**CGL2_11389020**	Periplasmic phosphate binding protein	364	15661..16752	80_GENE_22
11389	**19**	**CGL2_11389019**	Protein of unknown function	321	14642..15604	80_GENE_21
11389	**18**	**CGL2_11389018**	Probable 2'-5' RNA ligase	204	14041..14652	80_GENE_20
11389	**17**	**CGL2_11389017**	Protein of unknown function	348	complement(12885..13928)	80_GENE_19
11389	**16**	**CGL2_11389016**	Protein of unknown function	138	complement(12452..12865)	80_GENE_18
11389	**15**	**CGL2_11389015**	Putative ribosomal protein L11 methyltransferase	291	complement(11580..12452)	80_GENE_17
11389	**14**	**CGL2_11389014**	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	251	complement(10828..11580)	80_GENE_16
11389	**13**	**CGL2_11389013**	Peptide deformylase (EC 3.5.1.88)	184	10274..10825	80_GENE_15
11389	**12**	**CGL2_11389012**	Cob(I)alamin adenosyltransferase (EC 2.5.1.17)	179	9735..10271	80_GENE_14
11389	**11**	**CGL2_11389011**	Precorrin-3B methylase (EC 2.1.1.131)	273	8917..9735	80_GENE_13
11389	**10**	**CGL2_11389010**	Putative cobalamin biosynthesis protein (CbiG)	378	7740..8873	80_GENE_12
11389	**9**	**CGL2_11389009**	Precorrin-6B methyltransferase	205	7126..7740	80_GENE_11
11389	**8**	**CGL2_11389008**	Precorrin 6y methyltransferase	210	6466..7095	80_GENE_10
11389	**7**	**CGL2_11389007**	Cobalamin biosynthesis protein (CbiD)	375	5313..6437	80_GENE_9
11389	**6**	**CGL2_11389006**	Conserved hypothetical protein	176	4676..5203	80_GENE_8
11389	**5**	**CGL2_11389005**	Large-conductance mechanosensitive channel	151	complement(3535..3987)	80_GENE_7
11389	**4**	**CGL2_11389004**	transposase	122	2331..2696	80_GENE_6
11389	**3**	**CGL2_11389003**	transposase	79	2107..2343	80_GENE_5
11389	**2**	**CGL2_11389002**	transposase	200	1474..2073	80_GENE_4
11389	**1**	**CGL2_11389001**	transposase	334	complement(405..1406)	80_GENE_3
10706	**8**	**CGL2_10706008**	Hypothetical protein	264	complement(10384..11175)	80_GENE_1
10706	**7**	**CGL2_10706007**	Hypothetical protein	454	8466..9827	
10706	**6**	**CGL2_10706006**	DNA helicase	1573	complement(3543..8261)	214_GENE_4
10706	**5**	**CGL2_10706005**	transposase	78	3207..3440	214_GENE_5
10706	**4**	**CGL2_10706004**	integrase fragment or transposase (Tn domain)	218	2594..3247	214_GENE_6
10706	**3**	**CGL2_10706003**	transposase?	49	complement(1994..2140)	214_GENE_7

10706	**2**	**CGL2_10706002**	Hypothetical protein	81	complement(1752..1994)	214_GENE_8
10706	**1**	**CGL2_10706001**	Hypothetical protein	507	complement(114..1634)	
11172	**1**	**CGL2_11172001**	Ribosomal protein L9	150	873..1322	150_GENE_15
11172	**2**	**CGL2_11172002**	Ribosomal protein L34	44	1415..1546	150_GENE_15a
11172	**3**	**CGL2_11172003**	Protein of unknown function	111	1567..1899	150_GENE_14a
11172	**4**	**CGL2_11172004**	Protein of unknown function	68	1878..2081	150_GENE_13a
11172	**5**	**CGL2_11172005**	Putative inner-membrane protein	511	2128..3660	150_GENE_13
11172	**6**	**CGL2_11172006**	TRNA modification GTPase TrmE	445	3677..5011	150_GENE_12
11172	**7**	**CGL2_11172007**	Glucose-inhibited division protein A	605	5030..6844	150_GENE_11
11172	**8**	**CGL2_11172008**	Putative glucose-inhibited division protein B	210	6852..7481	150_GENE_10
11172	**9**	**CGL2_11172009**	Putative cobyrinic acid a,c-diamide synthase (CbiA)	254	7532..8293	150_GENE_9
11172	**10**	**CGL2_11172010**	ParB-like partition protein	284	8289..9140	150_GENE_8
11172	**11**	**CGL2_11172011**	Protein of unknown function	132	9157..9552	150_GENE_7
11172	**12**	**CGL2_11172012**	tRNA (5-methylaminomethyl-2-thiouridylate)-methyl	361	9570..10652	150_GENE_6
11172	**13**	**CGL2_11172013**	DNA polymerase III, epsilon subunit	265	10652..11446	150_GENE_5
11172	**14**	**CGL2_11172014**	Ribonuclease III (EC 3.1.26.3)	375	11930..13054	150_GENE_4
11172	**15**	**CGL2_11172015**	Transposase	479	13375..14811	150_GENE_1
11172	**16**	**CGL2_11172016**	Protein of unknown function	77	15149..15379	
11172	**17**	**CGL2_11172017**	Ferredoxin	109	complement(15419..15745)	
11172	**18**	**CGL2_11172018**	Protein of unknown function	148	15949..16392	6_GENE_88a
11172	**19**	**CGL2_11172019**	Hypothetical protein	161	16544..17026	6_GENE_88
11172	**20**	**CGL2_11172020**	UDP-3-O-acyl-N-acetylglucosamine deacetylase	298	complement(17057..17950)	6_GENE_87
11172	**21**	**CGL2_11172021**	Hypothetical protein	101	complement(18201..18503)	6_GENE_85
11172	**22**	**CGL2_11172022**	Protein of unknown function	520	complement(18632..20191)	6_GENE_84
11172	**23**	**CGL2_11172023**	Hypothetical protein	180	complement(20252..20791)	6_GENE_83
11172	**24**	**CGL2_11172024**	Inositol monophosphatase (EC 3.1.3.25)	265	21032..21826	6_GENE_82
11172	**25**	**CGL2_11172025**	Putative peptidase M50 family	264	complement(21819..22610)	6_GENE_81
11172	**26**	**CGL2_11172026**	Hypothetical protein	106	complement(22673..22990)	6_GENE_80
11172	**27**	**CGL2_11172027**	Transposase	446	complement(23400..24737)	
11172	**28**	**CGL2_11172028**	Trans-hexaprenyltranstransferase (EC 2.5.1.30)	330	24939..25928	6_GENE_79
11172	**29**	**CGL2_11172029**	Protein of unknown function	426	25980..27257	6_GENE_78
11172	**31**	**CGL2_11172031**	Pseudouridylate synthases, 23S RNA-specific	340	complement(27247..28266)	6_GENE_77
11172	**32**	**CGL2_11172032**	Putative TPR-domain containing protein	327	complement(28279..29259)	6_GENE_76
11172	**33**	**CGL2_11172033**	Signal peptidase II (EC 3.4.23.36)	179	complement(29262..29798)	6_GENE_75
11172	**34**	**CGL2_11172034**	Isoleucyl-tRNA synthetase (EC 6.1.1.5)	976	complement(29798..32725)	6_GENE_74
11172tRNA		**CGL2_11172R001**	TRNA Val CAC		32816..32890	
11172	**35**	**CGL2_11172035**	Transposase	396	complement(33467..34654)	
11172	**36**	**CGL2_11172036**	Hypothetical protein	88	35171..35434	6_GENE_73
11172	**37**	**CGL2_11172037**	Transposase	416	35505..36752	
11172	**38**	**CGL2_11172038**	Conserved hypothetical protein	192	36808..37383	
11172	**39**	**CGL2_11172039**	Hypothetical protein	96	37465..37752	6_GENE_73

11172	**40**	**CGL2_11172040**	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23	291	complement(37655..38527)	6_GENE_72a
11172	**41**	**CGL2_11172041**	Conserved hypothetical protein	343	complement(38650..39678)	48_GENE_37
11172	**42**	**CGL2_11172042**	Putative aminoglycoside phosphotransferase	355	39815..40879	48_GENE_36
11172	**43**	**CGL2_11172043**	Nucleoside-diphosphate-sugar pyrophosphorylase in	240	40914..41633	48_GENE_35
11172	**44**	**CGL2_11172044**	Protein of unknown function	384	complement(41479..42630)	48_GENE_34
11172	**45**	**CGL2_11172045**	GTP-binding protein	212	42767..43402	48_GENE_33
11172	**46**	**CGL2_11172046**	Putative peptidyl-prolyl cis-trans isomerase	340	complement(43411..44430)	48_GENE_32
11172	**47**	**CGL2_11172047**	Putative peptidyl-prolyl cis-trans isomerase	324	complement(44470..45441)	48_GENE_31
11172	**48**	**CGL2_11172048**	Probable peptidil-prolyl cis-trans isomerase	289	complement(45451..46317)	48_GENE_30
11172	**49**	**CGL2_11172049**	Transcription-repair coupling factor	1154	complement(46332..49793)	48_GENE_29
11172	**50**	**CGL2_11172050**	Cytidylyltransferase family protein	179	complement(49793..50329)	48_GENE_28
11172	**51**	**CGL2_11172051**	Phosphoheptose isomerase	203	complement(50322..50930)	48_GENE_27
11172	**52**	**CGL2_11172052**	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.	437	complement(50991..52301)	48_GENE_26
11172	**53**	**CGL2_11172053**	Protein of unknown function	70	52765..52974	48_GENE_24
11172	**54**	**CGL2_11172054**	Protein of unknown function	195	53079..53663	48_GENE_23
11172	**55**	**CGL2_11172055**	Pyruvate synthase alpha subunit (EC 1.2.7.1)	412	53966..55201	48_GENE_21
11172	**56**	**CGL2_11172056**	Pyruvate synthase beta subunit	288	55283..56146	48_GENE_20
11172	**57**	**CGL2_11172057**	Putative ferredoxin oxidoreductase gamma subunit	232	56192..56887	48_GENE_19
11172	**58**	**CGL2_11172058**	Probable ferredoxin oxidoreductase epsilon subunit	101	56918..57220	48_GENE_18
11172	**59**	**CGL2_11172059**	Protein of unknown function	94	57305..57586	48_GENE_17
11172	**60**	**CGL2_11172060**	Protein of unknown function	140	57595..58014	48_GENE_16a
11172	**61**	**CGL2_11172061**	Pyruvate synthase alpha chain (EC 1.2.7.1)	406	58212..59429	48_GENE_16
11172	**62**	**CGL2_11172062**	Putative ferredoxin oxidoreductase beta subunit	296	59425..60312	48_GENE_15
11172	**63**	**CGL2_11172063**	Ferredoxin oxidoreductase gamma subunit	232	60338..61033	48_GENE_13
11172	**64**	**CGL2_11172064**	Protein of unknown function	76	61285..61512	48_GENE_12
11172	**65**	**CGL2_11172065**	Probable ferredoxin oxidoreductase	193	61593..62171	48_GENE_11
11172	**66**	**CGL2_11172066**	Protein of unknown function	133	complement(62234..62632)	48_GENE_10
11172	**67**	**CGL2_11172067**	Conserved hypothetical protein	175	complement(62787..63311)	48_GENE_9
11172	**68**	**CGL2_11172068**	Glutamyl-tRNA synthetase (EC 6.1.1.17)	474	complement(63311..64732)	48_GENE_8
11172	**69**	**CGL2_11172069**	Protein of unknown function	181	65060..65602	48_GENE_7
11172	**70**	**CGL2_11172070**	L-aspartate oxidase (EC 1.4.3.16)	513	65610..67148	48_GENE_6
11172	**71**	**CGL2_11172071**	Putative heat shock protein DnaJ, N-terminal	284	67148..67999	48_GENE_5
11172	**72**	**CGL2_11172072**	Probable heat shock transcription regulator	108	68017..68340	48_GENE_4
11172	**73**	**CGL2_11172073**	Chaperone clpB	866	68430..71027	48_GENE_3
11172	**74**	**CGL2_11172074**	Probable bacterial regulatory protein, Fis family	178	71027..71560	48_GENE_2
11172	**75**	**CGL2_11172075**	Transposase	446	71731..73068	
07502tRNA		CGL2_7502R001	TRNA Val GAC		64..138	
11111	**114**	**CGL2_11111114**	Putative heavy metal efflux pump, CzcA family	1003	complement(116616..119624)	43_GENE_1
11111	**113**	**CGL2_11111113**	Putative secretion protein HlyD	358	complement(115543..116616)	43_GENE_2
11111	**112**	**CGL2_11111112**	Protein of unknown function	230	114799..115488	43_GENE_3
11111	**111**	**CGL2_11111111**	Putative Xaa-Pro aminopeptidase	381	113650..114792	43_GENE_4

11111	**110**	**CGL2_11111110**	Probable O-methyltransferase family protein	220	112988..113647	43_GENE_5
11111	**109**	**CGL2_11111109**	Putative nitrite reductase small subunit	102	complement(112445..112750)	43_GENE_6
11111	**108**	**CGL2_11111108**	Hypothetical protein	75	complement(112137..112361)	43_GENE_7
11111	**107**	**CGL2_11111107**	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.	419	complement(110833..112089)	43_GENE_8
11111	**106**	**CGL2_11111106**	Putative glycoside hydrolase, family 57	717	complement(108683..110833)	43_GENE_9
11111	**105**	**CGL2_11111105**	4-alpha-glucanotransferase (EC 2.4.1.25)	697	complement(106585..108675)	43_GENE_10
11111	**104**	**CGL2_11111104**	Galactose-1-phosphate uridylyltransferase (EC 2.7.7	334	complement(105563..106564)	43_GENE_11
11111	**103**	**CGL2_11111103**	Probable aldolase	460	complement(104127..105506)	43_GENE_12
11111	**102**	**CGL2_11111102**	Putative glycoside hydrolase, family 57	529	complement(102538..104124)	43_GENE_13
11111	**101**	**CGL2_11111101**	Secretion protein HlyD	363	complement(100547..101635)	43_GENE_14
11111	**100**	**CGL2_11111100**	Putative acriflavin resistance protein	1057	complement(97266..100436)	43_GENE_15
11111	**99**	**CGL2_11111099**	Putative aminomethyltransferase	334	96234..97235	43_GENE_16
11111	**98**	**CGL2_11111098**	Putative two component, sigma54 specific, transcript	455	complement(94731..96095)	43_GENE_17
11111	**97**	**CGL2_11111097**	Probable secretion protein HlyD	403	complement(93516..94724)	43_GENE_18
11111	**96**	**CGL2_11111096**	Putative outer membrane efflux protein	490	complement(91979..93448)	43_GENE_19
11111	**95**	**CGL2_11111095**	Thioredoxin reductase (EC 1.8.1.9)	334	complement(90807..91808)	43_GENE_20
11111	**94**	**CGL2_11111094**	Protein of unknown function	168	complement(90304..90807)	43_GENE_21
11111	**93**	**CGL2_11111093**	Protein of unknown function	408	complement(89081..90304)	43_GENE_22
11111	**92**	**CGL2_11111092**	Protein of unknown function	689	complement(86764..88830)	43_GENE_23
11111	**91**	**CGL2_11111091**	Putative carboxylesterase	230	complement(86072..86761)	43_GENE_24
11111	**90**	**CGL2_11111090**	Protein of unknown function	143	complement(85668..86096)	43_GENE_25
11111	**89**	**CGL2_11111089**	Polypeptide deformylase (EC 3.5.1.31)	177	complement(85138..85668)	43_GENE_26
11111	**88**	**CGL2_11111088**	Methionyl-tRNA formyltransferase (EC 2.1.2.9)	319	complement(84189..85145)	43_GENE_27
11111	**87**	**CGL2_11111087**	Putative peptidase, M48 family	295	complement(83251..84135)	43_GENE_28
11111	**86**	**CGL2_11111086**	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	231	complement(82559..83251)	43_GENE_29
11111	**85**	**CGL2_11111085**	Protein of unknown function	149	complement(81973..82419)	43_GENE_30
11111	**84**	**CGL2_11111084**	Putative cell shape determining protein (MreB/Mrl)	343	complement(80891..81919)	277_GENE_2
11111	**83**	**CGL2_11111083**	Putative rod shape-determining protein MreC	281	complement(80012..80854)	277_GENE_3
11111	**82**	**CGL2_11111082**	Hypothetical protein	157	complement(79521..79991)	277_GENE_4
11111	**81**	**CGL2_11111081**	Peptidoglycan glycosyltransferase (EC 2.4.1.129)	644	complement(77527..79458)	277_GENE_5
11111	**80**	**CGL2_11111080**	Putative rod shape-determining protein (RodA)	363	complement(76439..77527)	277_GENE_6
11111	**79**	**CGL2_11111079**	Ribonucleases G and E	526	complement(74756..76333)	277_GENE_7
11111	**78**	**CGL2_11111078**	Hypothetical protein	280	73889..74728	277_GENE_8
11111	**77**	**CGL2_11111077**	Putative dihydroneopterin aldolase	132	73494..73889	277_GENE_9
11111	**76**	**CGL2_11111076**	Protein of unknown function	24	72894..72966	277_GENE_10
11111	**75**	**CGL2_11111075**	Protein of unknown function	181	72952..73494	277_GENE_10
11111	**74**	**CGL2_11111074**	Putative ferredoxin	84	complement(72362..72613)	426_GENE_1
11111	**73**	**CGL2_11111073**	Putative cobalamin B12-binding/Radical SAM family	626	complement(70444..72321)	426_GENE_2
11111	**72**	**CGL2_11111072**	Ribosomal protein L13	151	complement(69959..70411)	426_GENE_3
11111	**71**	**CGL2_11111071**	Ribosomal protein S9	135	complement(69562..69966)	426_GENE_4
11111	**70**	**CGL2_11111070**	N-acetyl-gamma-glutamyl-phosphate reductase (EC	343	complement(68451..69479)	426_GENE_5

11111	**69**	**CGL2_11111069**	Arginine biosynthesis protein (ArgJ) (EC 2.3.1.35)	404	complement(67201..68412)	426_GENE_6
11111	**68**	**CGL2_11111068**	Ribosomal protein S2	274	complement(66212..67033)	13_GENE_68
11111	**67**	**CGL2_11111067**	Elongation factor Ts (EF-Ts)	198	complement(65550..66143)	13_GENE_67
11111	**66**	**CGL2_11111066**	Uridylate kinase	236	complement(64840..65547)	13_GENE_66
11111	**65**	**CGL2_11111065**	Ribosome recycling factor	184	complement(64252..64803)	13_GENE_65
11111	**64**	**CGL2_11111064**	Alanine racemase (EC 5.1.1.1)	406	complement(63015..64232)	13_GENE_64
11111	**63**	**CGL2_11111063**	Putative integral membrane protein	255	complement(62248..63012)	13_GENE_63
11111	**62**	**CGL2_11111062**	ABC transporter ATP-binding protein (EC 3.6.3.25)	264	complement(61466..62257)	13_GENE_62
11111	**61**	**CGL2_11111061**	Putative ABC transporter	518	complement(59841..61394)	13_GENE_61
11111	**60**	**CGL2_11111060**	ResB-like family protein (poss cyt biosyn)	513	complement(58137..59675)	13_GENE_60
11111	**59**	**CGL2_11111059**	Putative cytochrome c biogenesis protein	283	complement(57130..57978)	13_GENE_59
11111	**58**	**CGL2_11111058**	Putative cytochrome c biogenesis protein	199	complement(56521..57117)	13_GENE_58
11111	**57**	**CGL2_11111057**	Putative thioredoxin family protein	171	complement(55998..56510)	13_GENE_57
11111	**56**	**CGL2_11111056**	Putative cytochrome c biogenesis protein (CcdA)	249	complement(55204..55950)	13_GENE_56
11111	**55**	**CGL2_11111055**	Geranylgeranyl reductase family protein	416	complement(53919..55166)	13_GENE_55
11111	**54**	**CGL2_11111054**	Probable protease family protein	402	complement(52714..53919)	13_GENE_54
11111	**53**	**CGL2_11111053**	Primosomal protein N' (PriA)	661	50781..52763	13_GENE_53
11111	**52**	**CGL2_11111052**	Regulatory protein	155	50317..50781	13_GENE_52
11111	**51**	**CGL2_11111051**	Glycine hydroxymethyltransferase (EC 2.1.2.1)	414	49048..50289	13_GENE_51
11111	**50**	**CGL2_11111050**	Ribose/galactose isomerase (EC 5.3.1.26)	158	48544..49017	13_GENE_50
11111	**49**	**CGL2_11111049**	Protein of unknown function	181	complement(47916..48458)	13_GENE_49
11111	**48**	**CGL2_11111048**	Thymidylate kinase	229	complement(47107..47793)	13_GENE_48
11111	**47**	**CGL2_11111047**	Thymidylate kinase (EC 2.7.4.9)	217	complement(46457..47107)	13_GENE_47
11111	**46**	**CGL2_11111046**	Putative Ppx/GppA phosphatase family protein	518	44901..46454	13_GENE_46
11111	**45**	**CGL2_11111045**	Protein of unknown function	431	complement(43510..44802)	13_GENE_45
11111	**44**	**CGL2_11111044**	Ubiquinone/menaquinone biosynthesis methyltransfe	259	complement(42687..43463)	13_GENE_44
11111	**43**	**CGL2_11111043**	Putative radical SAM family protein	530	complement(41093..42682)	13_GENE_43
11111	**42**	**CGL2_11111042**	Protein of unknown function	170	complement(40580..41089)	13_GENE_42
11111	**41**	**CGL2_11111041**	Putative 4-hydroxybenzoate polyprenyl transferase	287	complement(39720..40580)	13_GENE_41
11111	**40**	**CGL2_11111040**	Hypothetical protein	38	complement(39348..39461)	13_GENE_39
11111	**39**	**CGL2_11111039**	Hypothetical protein	85	39100..39354	13_GENE_39a
11111	**38**	**CGL2_11111038**	Putative major facilitator superfamily transporter	459	complement(37599..38975)	13_GENE_37
11111	**37**	**CGL2_11111037**	Putative potassium channel protein	347	complement(36548..37588)	13_GENE_36
11111	**36**	**CGL2_11111036**	Acetylornithine aminotransferase (EC 2.6.1.11)	390	complement(35308..36477)	13_GENE_35
11111	**35**	**CGL2_11111035**	Ornithine carbamoyltransferase (EC 2.1.3.3)	309	complement(34379..35305)	13_GENE_34
11111	**34**	**CGL2_11111034**	Argininosuccinate synthase (EC 6.3.4.5)	408	complement(33146..34369)	13_GENE_33
11111	**33**	**CGL2_11111033**	Argininosuccinate lyase (EC 4.3.2.1)	467	complement(31743..33143)	13_GENE_32
11111	**32**	**CGL2_11111032**	Diaminopimelate decarboxylase (EC 4.1.1.20)	414	complement(30307..31548)	13_GENE_31
11111	**31**	**CGL2_11111031**	Protein of unknown function	165	complement(29817..30311)	13_GENE_30
11111	**30**	**CGL2_11111030**	Dihydrodipicolinate synthase (EC 4.2.1.52)	295	complement(28886..29770)	13_GENE_29
11111	**29**	**CGL2_11111029**	Dihydrodipicolinate reductase (EC 1.3.1.26)	265	complement(28083..28877)	13_GENE_28

11111	**28**	**CGL2_11111028**	5-carboxymethyl-2-hydroxymuconate delta-isomeras	267	complement(27283..28083)	13_GENE_27
11111	**27**	**CGL2_11111027**	Putative flagellar basal body rod protein	267	complement(26200..27000)	13_GENE_26
11111	**26**	**CGL2_11111026**	Flagellar basal body rod protein	261	complement(25392..26174)	13_GENE_25
11111	**25**	**CGL2_11111025**	Hypothetical protein	212	complement(24742..25377)	13_GENE_24
11111	**24**	**CGL2_11111024**	Protein of unknown function	208	complement(24129..24752)	13_GENE_23
11111	**23**	**CGL2_11111023**	Putative flagellar P-ring protein	354	complement(23068..24129)	13_GENE_22
11111	**22**	**CGL2_11111022**	Conserved hypothetical protein	121	complement(22706..23068)	13_GENE_21
11111	**21**	**CGL2_11111021**	Putative flagellin	286	complement(21816..22673)	13_GENE_20
11111	**20**	**CGL2_11111020**	Protein of unknown function	119	complement(21336..21692)	13_GENE_19
11111	**19**	**CGL2_11111019**	Protein of unknown function	164	complement(20802..21293)	13_GENE_18
11111	**18**	**CGL2_11111018**	Flagellar hook-associated protein (FlgK)	561	complement(19114..20796)	13_GENE_17
11111	**17**	**CGL2_11111017**	Flagellar hook-associated protein (FlgL)	312	complement(18148..19083)	13_GENE_16
11111	**16**	**CGL2_11111016**	Putative carbon storage regulator (CsrA)	80	complement(17841..18080)	13_GENE_15
11111	**15**	**CGL2_11111015**	Protein of unknown function	143	complement(17413..17841)	13_GENE_14
11111	**14**	**CGL2_11111014**	Putative flagellin	275	complement(16416..17240)	13_GENE_13
11111	**13**	**CGL2_11111013**	Putative flagellar hook-associated protein (FliD)	479	complement(14878..16314)	13_GENE_12
11111	**12**	**CGL2_11111012**	Flagellar protein (FliS)	152	complement(14398..14853)	13_GENE_11
11111	**11**	**CGL2_11111011**	Hypothetical protein	114	complement(14049..14390)	13_GENE_10
11111	**10**	**CGL2_11111010**	Conserved protein of unknown function	326	complement(12893..13870)	13_GENE_9
11111	**9**	**CGL2_11111009**	Putative SAM-dependent methyltransferases	780	complement(10573..12912)	13_GENE_8
11111	**8**	**CGL2_11111008**	Putative heptosyltransferase family protein	519	complement(9002..10558)	13_GENE_7
11111	**6**	**CGL2_11111006**	Conserved hypothetical protein	599	complement(7213..9009)	13_GENE_6
11111	**5**	**CGL2_11111005**	Probable heptosyltransferase family protein	595	complement(5429..7213)	13_GENE_5
11111	**4**	**CGL2_11111004**	Hypothetical protein	217	complement(4779..5429)	13_GENE_4
11111	**2**	**CGL2_11111002**	Probable TonB dependent receptor	861	complement(1953..4535)	13_GENE_3
11111	**2**	**CGL2_11111002**	Probable TonB dependent receptor	861	complement(1953..4535)	13_GENE_3
11111	**1**	**CGL2_11111001**	transposase	360	complement(734..1813)	13_GENE_1
11195	**47**	**CGL2_11195047**	Protein of unknown function	139	complement(54662..55078)	22_GENE_48
11195	**46**	**CGL2_11195046**	Protein of unknown function	206	complement(53810..54427)	22_GENE_46
11195	**45**	**CGL2_11195045**	Inorganic diphosphatase (EC 3.6.1.1)	182	complement(53169..53714)	22_GENE_45
11195	**44**	**CGL2_11195044**	ABC transporter ATP-binding protein (EC 3.6.3.25)	234	complement(52439..53140)	22_GENE_44
11195	**43**	**CGL2_11195043**	Putative ABC transporter, permease protein	402	complement(51234..52439)	22_GENE_43
11195	**42**	**CGL2_11195042**	Secretion protein HlyD	380	complement(50072..51211)	22_GENE_42
11195	**41**	**CGL2_11195041**	Flagellar motor switch protein FliM)	338	complement(48917..49930)	22_GENE_41
11195	**40**	**CGL2_11195040**	Transcriptional regulator, NifA, Fis Family	550	complement(47082..48731)	22_GENE_39
11195	**39**	**CGL2_11195039**	NADH dehydrogenase (Quinone) precursor (EC 1.6.9	584	complement(45113..46864)	22_GENE_38
11195	**38**	**CGL2_11195038**	Probable NADH dehydrogenase I, M subunit	437	complement(43807..45117)	22_GENE_37
11195	**37**	**CGL2_11195037**	Protein of unknown function	1139	complement(40391..43807)	22_GENE_36
11195	**36**	**CGL2_11195036**	Probable nitrogen regulatory protein P-II	114	complement(40059..40400)	22_GENE_35
11195	**35**	**CGL2_11195035**	Putative major facilitator superfamily transporter	265	39251..40045	22_GENE_34
11195	**34**	**CGL2_11195034**	transposase	420	37992..39251	

11195	**33**	**CGL2_11195033**	Putative major facilitator superfamily transporter	159	37448..37924	22_GENE_34
11195	**32**	**CGL2_11195032**	Probable cellulose synthase operon protein C	964	complement(34438..37329)	22_GENE_33
11195	**31**	**CGL2_11195031**	glycosyltransferase	714	complement(32307..34448)	22_GENE_32
11195	**30**	**CGL2_11195030**	cyclic di-GMP binding protein	737	complement(30097..32307)	22_GENE_31
11195	**29**	**CGL2_11195029**	Endoglucanase (EC 3.2.1.4)	366	complement(29000..30097)	22_GENE_30
11195tRNA		**CGL2_11195R001**	TRNA Gln CTG		28853..28926	
11195	**27**	**CGL2_11195027**	Peptidoglycan glycosyltransferase (EC 2.4.1.129)	756	26508..28775	22_GENE_29
11195	**26**	**CGL2_11195026**	Protein of unknown function	125	complement(26027..26401)	22_GENE_28
11195	**25**	**CGL2_11195025**	Putative outer membrane protein	512	complement(24378..25913)	22_GENE_27
11195	**24**	**CGL2_11195024**	Protein of unknown function	247	complement(23602..24342)	22_GENE_26
11195	**23**	**CGL2_11195023**	Hypothetical protein	227	complement(22935..23615)	22_GENE_25
11195	**22**	**CGL2_11195022**	DNA repair protein (RadC)	237	complement(22096..22806)	22_GENE_24
11195	**21**	**CGL2_11195021**	ABC1 family transporter	557	20394..22064	22_GENE_23
11195	**20**	**CGL2_11195020**	Protein of unknown function	523	18783..20351	22_GENE_22
11195	**19**	**CGL2_11195019**	Protein of unknown function	212	complement(17924..18559)	22_GENE_21
11195	**18**	**CGL2_11195018**	Adenylosuccinate synthase (EC 6.3.4.4)	432	16650..17945	22_GENE_20
11195	**17**	**CGL2_11195017**	Protein of unknown function	104	16198..16509	22_GENE_19
11195	**16**	**CGL2_11195016**	Protein of unknown function	547	complement(14171..15811)	22_GENE_18
11195	**15**	**CGL2_11195015**	Putative two component transcriptional regulator, wi	259	complement(13236..14012)	22_GENE_17
11195	**14**	**CGL2_11195014**	Hypothetical protein	112	complement(12901..13236)	22_GENE_15
11195	**13**	**CGL2_11195013**	Periplasmic phosphate binding protein	372	complement(11721..12836)	22_GENE_14
11195	**12**	**CGL2_11195012**	Phosphate ABC transporter, permease protein (PstC)	340	complement(10497..11516)	22_GENE_12
11195	**11**	**CGL2_11195011**	Phosphate transport system permease protein 2	303	complement(9581..10489)	22_GENE_11
11195	**10**	**CGL2_11195010**	Phosphate import ATP-binding protein (PstB) (EC 3.6	250	complement(8801..9550)	22_GENE_10
11195	**9**	**CGL2_11195009**	Phosphate uptake regulator (PhoU)	217	complement(8122..8772)	22_GENE_9
11195	**8**	**CGL2_11195008**	Thymidylate synthase (ThyX)	272	6933..7748	22_GENE_8
11195	**7**	**CGL2_11195007**	Protein of unknown function	419	5429..6685	22_GENE_7
11195	**6**	**CGL2_11195006**	Aldehyde dehydrogenase (EC 1.2.1.3)	502	complement(3768..5273)	22_GENE_6
11195	**5**	**CGL2_11195005**	Hypothetical protein	52	3603..3758	22_GENE_5
11195	**4**	**CGL2_11195004**	Fructose-1,6-bisphosphatase (EC 3.1.3.11)	335	2480..3484	22_GENE_4
11195	**3**	**CGL2_11195003**	Hypothetical protein	139	1993..2409	22_GENE_3a
11195	**2**	**CGL2_11195002**	Protein of unknown function	150	1544..1993	22_GENE_3
11195	**1**	**CGL2_11195001**	Probable histone deacetylase family protein	322	541..1506	22_GENE_2
11364	**1**	**CGL2_11364001**	Transcription termination factor Rho	416	455..1702	174_GENE_2
11364	**2**	**CGL2_11364002**	Ribosomal protein L31	68	1766..1969	174_GENE_3
11364	**3**	**CGL2_11364003**	Peptide chain release factor 1	361	1982..3064	174_GENE_4
11364	**4**	**CGL2_11364004**	Modification methylase (HemK)	293	3064..3942	174_GENE_5
11364	**5**	**CGL2_11364005**	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	442	3951..5276	174_GENE_6
11364	**6**	**CGL2_11364006**	ATP phosphoribosyltransferase (EC 2.4.2.17)	205	5324..5938	174_GENE_7
11364	**7**	**CGL2_11364007**	Histidinol dehydrogenase (EC 1.1.1.23) (HDH)	445	5975..7309	174_GENE_8
11364	**8**	**CGL2_11364008**	Histidinol-phosphate aminotransferase (EC 2.6.1.9)	359	7309..8385	174_GENE_9

11364	**9**	**CGL2_11364009**	Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.	210	8385..9014	174_GENE_10
11364	**10**	**CGL2_11364010**	Imidazole glycerol phosphate synthase, glutamine ar	211	9014..9646	174_GENE_11
11364	**11**	**CGL2_11364011**	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)me	247	9627..10367	174_GENE_12
11364	**12**	**CGL2_11364012**	Histidine biosynthesis protein (HisF) (EC 5.3.1.16)	255	10360..11124	174_GENE_13
11364	**13**	**CGL2_11364013**	Putative histidine biosynthesis bifunctional protein (H	233	11124..11822	174_GENE_14
11364	**14**	**CGL2_11364014**	Putative histidine triad (HIT) protein	118	11822..12175	174_GENE_15
11364	**15**	**CGL2_11364015**	Putative histone-like DNA-binding protein	102	complement(12204..12509)	174_GENE_16
11364	**16**	**CGL2_11364016**	Ribosomal protein S21	65	12847..13041	
11364	**17**	**CGL2_11364017**	Conserved protein of unknown function	139	13104..13520	224_GENE_1
11364	**18**	**CGL2_11364018**	DNA primase	461	13789..15171	224_GENE_3
11364	**19**	**CGL2_11364019**	RNA polymerase, sigma 38 subunit, RpoS	598	15232..17025	224_GENE_4
11364tRNA		**CGL2_11364R001**	TRNA Met CAT		17030..17104	
11364	**20**	**CGL2_11364020**	Conserved protein of unknown function	262	17153..17938	224_GENE_5
11364	**21**	**CGL2_11364021**	Putative ribonuclease H	134	17938..18339	224_GENE_6
11364	**22**	**CGL2_11364022**	Putative metal dependent phosphohydrolase	467	18765..20165	224_GENE_7
11364	**23**	**CGL2_11364023**	Protein of unknown function	110	20322..20651	224_GENE_8
11364	**24**	**CGL2_11364024**	Putative transglycosylase	220	complement(20568..21227)	224_GENE_9
11364	**25**	**CGL2_11364025**	Protein of unknown function	298	21408..22301	224_GENE_10
11364	**26**	**CGL2_11364026**	Putative heat shock protein Hsp20	152	22401..22856	288_GENE_9
11364	**27**	**CGL2_11364027**	ATPase components of ABC transporters wi	643	23133..25061	288_GENE_8
11364	**28**	**CGL2_11364028**	Probable phosphohydrolase	298	25169..26062	288_GENE_7
11364	**29**	**CGL2_11364029**	Ribonuclease PH (EC 2.7.7.56)	245	26163..26897	288_GENE_6
11364	**30**	**CGL2_11364030**	Putative Ham1-like protein	198	26897..27490	288_GENE_5
11364	**31**	**CGL2_11364031**	Beta-N-acetylhexosaminidase (EC 3.2.1.52)	342	27490..28515	288_GENE_4
11364	**32**	**CGL2_11364032**	Glutamate racemase (EC 5.1.1.3)	314	28515..29456	288_GENE_3
11364	**33**	**CGL2_11364033**	Putative peptidase C26	239	complement(29329..30045)	288_GENE_2
11364	**34**	**CGL2_11364034**	Putative ATP-dependent RNA helicase	444	complement(30035..31366)	288_GENE_1
11364	**35**	**CGL2_11364035**	Hypothetical protein	32	31851..31946	175_GENE_1
11364	**36**	**CGL2_11364036**	Conserved protein of unknown function	165	32123..32617	175_GENE_2
11364	**37**	**CGL2_11364037**	Hypothetical protein	53	complement(32842..33000)	175_GENE_3
11364	**38**	**CGL2_11364038**	Phosphoglycerate mutase (EC 5.4.2.1)	223	complement(33000..33668)	175_GENE_4
11364	**39**	**CGL2_11364039**	Lipoate synthase	316	complement(33777..34724)	175_GENE_5
11364	**40**	**CGL2_11364040**	Mutative metal dependent phosphohydrolase	413	complement(34808..36046)	175_GENE_6
11364	**41**	**CGL2_11364041**	Glycogen debranching enzyme GlgX (EC 3.2.1.68)	714	36540..38681	175_GENE_8
11364	**42**	**CGL2_11364042**	Protein of unknown function	143	38744..39172	175_GENE_9
11364	**43**	**CGL2_11364043**	Putative major facilitator superfamily transporter	420	complement(39227..40486)	175_GENE_10
11364	**44**	**CGL2_11364044**	Putative beta-lactamase family protein	290	complement(40595..41464)	175_GENE_11
11364	**45**	**CGL2_11364045**	Hypothetical protein	135	41533..41937	175_GENE_12
11364	**46**	**CGL2_11364046**	Protein of unknown function	398	42122..43315	175_GENE_13
11364	**47**	**CGL2_11364047**	Conserved protein of unknown function	657	complement(43598..45568)	294_GENE_2
11364	**48**	**CGL2_11364048**	Protein of unknown function	281	complement(45602..46444)	294_GENE_3

11364	**49**	**CGL2_11364049**	Hypothetical protein	108	46617..46940	294_GENE_4
11364	**50**	**CGL2_11364050**	Hypothetical protein	81	46928..47170	294_GENE_5
11364	**51**	**CGL2_11364051**	Probable DNA helicase	455	47170..48534	294_GENE_6
11364	**52**	**CGL2_11364052**	Hypothetical protein	316	48494..49441	170_GENE_15
11364	**53**	**CGL2_11364053**	Conserved hypothetical protein	466	complement(49749..51146)	170_GENE_14
11364	**54**	**CGL2_11364054**	Hypothetical protein	106	51487..51804	170_GENE_13
11364	**55**	**CGL2_11364055**	Hypothetical protein	162	51855..52340	170_GENE_12
11364	**56**	**CGL2_11364056**	Protein of unknown function	204	52363..52974	170_GENE_10
11364	**57**	**CGL2_11364057**	Hypothetical protein	73	52974..53192	170_GENE_9
11364	**58**	**CGL2_11364058**	Hypothetical protein	197	53384..53974	170_GENE_8
11364	**59**	**CGL2_11364059**	Probable TrwB protein	672	53980..55995	170_GENE_7
11364	**60**	**CGL2_11364060**	Hypothetical protein	59	55995..56171	170_GENE_6
11364	**61**	**CGL2_11364061**	Probable TrwC protein	1128	56174..59557	170_GENE_5
11364	**62**	**CGL2_11364062**	Hypothetical protein	60	59578..59757	170_GENE_4
10641	**21**	**CGL2_10641021**	Putative transcriptional activator	80	13143..13382	5-way_CG_LeptoII_sc
10641	**20**	**CGL2_10641020**	Probable transposase	162	complement(13425..13910)	5-way_CG_LeptoII_sc
10641	**19**	**CGL2_10641019**	Hypothetical protein	85	complement(12759..13013)	170_GENE_1a
10641	**17**	**CGL2_10641017**	Probable conujugal transfer protein TraB	434	complement(11387..12688)	170_GENE_1
10641	**17**	**CGL2_10641017**	Probable conujugal transfer protein TraB	434	complement(11387..12688)	170_GENE_1
10641	**16**	**CGL2_10641016**	Hypothetical protein	204	complement(10760..11371)	5-way_CG_LeptoII_sc
10641	**15**	**CGL2_10641015**	Conserved protein of unknown function	153	complement(10284..10742)	5-way_CG_LeptoII_sc
10641	**14**	**CGL2_10641014**	Putative phage integrase	325	9275..10249	5-way_CG_LeptoII_sc
10641tRNA		**CGL2_10641R001**	TRNA Leu TAA		9088..9146	
10641	**13**	**CGL2_10641013**	Putative metallophosphoesterase	251	8064..8816	212_GENE_14
10641	**12**	**CGL2_10641012**	N-6 DNA methylase	524	complement(6361..7932)	212_GENE_12
10641	**11**	**CGL2_10641011**	Hypothetical protein	95	complement(6084..6368)	212_GENE_11
10641	**10**	**CGL2_10641010**	Hypothetical protein	74	complement(5863..6084)	212_GENE_10
10641	**9**	**CGL2_10641009**	Hypothetical protein	77	complement(5626..5856)	212_GENE_9
10641	**8**	**CGL2_10641008**	Hypothetical protein	133	complement(4951..5349)	212_GENE_8
10641	**7**	**CGL2_10641007**	Hypothetical protein	116	complement(4448..4795)	212_GENE_7
10641	**6**	**CGL2_10641006a**	Hypothetical protein	98	complement(3943..4236)	
10641	**6**	**CGL2_10641006**	Putative nucletidyltransferase	132	complement(3495..3890)	212_GENE_6
10641	**5**	**CGL2_10641005**	Putative Type I restriction modification system, speci	533	complement(1904..3502)	212_GENE_5
10641	**4**	**CGL2_10641004**	Hypothetical protein	73	complement(1547..1765)	212_GENE_4
10641	**3**	**CGL2_10641003**	Putative DNA damage inducible protein J	78	complement(1263..1496)	212_GENE_3
10641	**2**	**CGL2_10641002**	Hypothetical protein	130	complement(827..1216)	212_GENE_2
10641	**1**	**CGL2_10641001**	Hypothetical protein	106	complement(532..849)	212_GENE_1
11346	**1**	**CGL2_11346001**	ABC transporter, ATP-binding subunit	239	complement(594..1310)	232_GENE_1
11346	**2**	**CGL2_11346002**	Conserved hypothetical protein	222	complement(1332..1997)	232_GENE_2
11346	**3**	**CGL2_11346003**	Hypothetical protein	188	complement(3384..3947)	232_GENE_3
11346	**4**	**CGL2_11346004**	ABC transporter, ATP-binding subunit	389	complement(3957..5123)	232_GENE_4

11346	**5**	**CGL2_11346005**	Hypothetical protein	94	complement(5303..5584)	232_GENE_5
11346	**6**	**CGL2_11346006**	Hypothetical protein	344	5713..6744	232_GENE_6
11346	**7**	**CGL2_11346007**	Hypothetical protein	233	6957..7655	232_GENE_6a
11346	**8**	**CGL2_11346008**	Conserved hypothetical protein	93	complement(7652..7930)	232_GENE_8
11346	**9**	**CGL2_11346009**	Conserved hypothetical protein	98	complement(7937..8230)	232_GENE_9
11346	**10**	**CGL2_11346010**	transposase	313	8499..9437	579_GENE_7
11346	**11**	**CGL2_11346011**	Hypothetical protein	148	9684..10127	232_GENE_12
11346	**12**	**CGL2_11346012**	Hypothetical protein	223	complement(10375..11043)	
11346	**13**	**CGL2_11346013**	transposase	374	complement(11114..12235)	579_GENE_3
11346	**14**	**CGL2_11346014**	transposase	315	12265..13209	579_GENE_2
11346	**15**	**CGL2_11346015**	transposase	153	12951..13409	579_GENE_2
11346	**16**	**CGL2_11346016**	Hypothetical protein	138	13409..13822	579_GENE_1
11346	**16a**	**CGL2_11346016a**	Hypothetical protein	118	complement(13811..14164)	
11346	**17**	**CGL2_11346017**	Protein of unknown function	146	complement(14167..14604)	27_GENE_52
11346	**18**	**CGL2_11346018**	Protein of unknown function	84	complement(14607..14858)	27_GENE_51
11346	**19**	**CGL2_11346019**	Hypothetical protein	92	complement(14976..15251)	27_GENE_50
11346	**20**	**CGL2_11346020**	Conserved protein of unknown function	156	complement(15301..15768)	27_GENE_49
11346	**21**	**CGL2_11346021**	Conserved hypothetical protein	127	complement(16120..16500)	27_GENE_48
11346	**22**	**CGL2_11346022**	Putative helicase	1625	complement(16487..21361)	27_GENE_47
11346	**22**	**CGL2_11346022**	Putative helicase	1625	complement(16487..21361)	27_GENE_47
11346	**24**	**CGL2_11346024**	Protein of unknown function	268	complement(21476..22279)	27_GENE_46
11346	**25**	**CGL2_11346025**	Probable phage integrase	105	complement(22282..22596)	27_GENE_45a
11346	**26**	**CGL2_11346026**	Probable phage integrase CG confirms was misssem	146	complement(22394..22831)	27_GENE_45
11346	**27**	**CGL2_11346027**	integrase	127	22955..23335	27_GENE_44
11346	**28**	**CGL2_11346028**	Protein of unknown function	193	complement(23537..24115)	27_GENE_43
11346	**29**	**CGL2_11346029**	Conserved hypothetical protein	359	complement(24115..25191)	27_GENE_42
11346	**30**	**CGL2_11346030**	Conserved protein of unknown function	423	complement(25194..26462)	27_GENE_41
11346	**31**	**CGL2_11346031**	Putative phage shock protein A (PspA)	225	complement(26465..27139)	27_GENE_40
11346	**32**	**CGL2_11346032**	Protein of unknown function	218	complement(27185..27838)	27_GENE_39
11346	**33**	**CGL2_11346033**	Conserved protein of unknown function	188	28016..28579	27_GENE_38
11346	**34**	**CGL2_11346034**	HAD-superfamily hydrolase, subfamily IA	230	complement(28558..29247)	27_GENE_37
11346tRNA		**CGL2_11346R001**	TRNA Glu CTC		complement(29317..29392)	
11346	**35**	**CGL2_11346035**	Protein of unknown function	148	29468..29911	27_GENE_36
11346	**36**	**CGL2_11346036**	Protein of unknown function	151	complement(29907..30359)	27_GENE_35
11346	**37**	**CGL2_11346037**	Protein of unknown function	536	30492..32099	27_GENE_34
11346	**38**	**CGL2_11346038**	Putative LD-carboxypeptidase family protein	319	complement(32110..33066)	27_GENE_33
11346	**39**	**CGL2_11346039**	Protein of unknown function	89	complement(33036..33302)	27_GENE_32
11346	**40**	**CGL2_11346040**	Putative cobyrinic acid a,c-diamide synthase	208	complement(33308..33931)	27_GENE_31
11346	**41**	**CGL2_11346041**	Putative creatininase	251	complement(33951..34703)	27_GENE_30
11346	**42**	**CGL2_11346042**	Putative phytoene synthase	320	34825..35784	27_GENE_29
11346	**43**	**CGL2_11346043**	Putative amine oxidase	491	35780..37252	27_GENE_28

11346	**44**	**CGL2_11346044**	Putative phytoene synthase	317	37252..38202	27_GENE_27
11346	**45**	**CGL2_11346045**	Putative beta-lactamase family protein	352	complement(38166..39221)	27_GENE_26
11346	**46**	**CGL2_11346046**	Putative peptidase U62, modulator of DNA gyrase	485	39408..40862	27_GENE_25
11346	**47**	**CGL2_11346047**	Putative peptidase U62, modulator of DNA gyrase	452	40862..42217	27_GENE_24
11346	**48**	**CGL2_11346048**	Putative decarboxylase family protein	214	42217..42858	27_GENE_23
11346	**49**	**CGL2_11346049**	Protein of unknown function	247	complement(42877..43617)	27_GENE_22
11346	**50**	**CGL2_11346050**	DNA repair protein RadA	461	43753..45135	27_GENE_21
11346	**51**	**CGL2_11346051**	Probable glycoprotein endopeptidase	215	45135..45779	27_GENE_20
11346	**52**	**CGL2_11346052**	Ribosomal-protein-alanine acetyltransferase	204	45763..46374	27_GENE_19
11346	**53**	**CGL2_11346053**	Protein of unknown function	78	46477..46710	27_GENE_18
11346	**54**	**CGL2_11346054**	Probable twin-arginine translocation protein (TatA/E)	99	46716..47012	27_GENE_17
11346	**55**	**CGL2_11346055**	Sec-independent protein translocase	252	47005..47760	27_GENE_16
11346	**56**	**CGL2_11346056**	Putative undecaprenol kinase	285	47857..48711	27_GENE_15
11346	**57**	**CGL2_11346057**	Formate--tetrahydrofolate ligase (EC 6.3.4.3)	557	48859..50529	27_GENE_14
11346	**58**	**CGL2_11346058**	Protein of unknown function	642	50529..52454	27_GENE_13
11346	**59**	**CGL2_11346059**	Di-trans-poly-cis-decaprenylcistransferase (EC 2.5.1.	264	52460..53251	27_GENE_12
11346	**60**	**CGL2_11346060**	Putative phosphatidate cytidylyltransferase	279	53251..54087	27_GENE_11
11346	**61**	**CGL2_11346061**	1-deoxy-D-xylulose 5-phosphate reductoisomerase (	393	54112..55290	27_GENE_10
11346	**62**	**CGL2_11346062**	Peptidase M50, putative membrane-associated zinc r	354	55317..56378	27_GENE_9
11346	**63**	**CGL2_11346063**	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synth	377	56444..57574	27_GENE_8
11346	**64**	**CGL2_11346064**	Prolyl-tRNA synthetase	422	57591..58856	27_GENE_7
11346	**65**	**CGL2_11346065**	Conserved hypothetical protein	164	58863..59354	27_GENE_6
11346	**66**	**CGL2_11346066**	Ribosomal protein S32	37	59409..59519	27_GENE_5
11346	**67**	**CGL2_11346067**	Ribosomal protein S32	23	59519..59587	27_GENE_5
11346	**68**	**CGL2_11346068**	Fatty acid/phospholipid synthesis protein (PlsX)	331	59603..60595	27_GENE_4
11346	**69**	**CGL2_11346069**	3-oxoacyl-(Acyl-carrier-protein) synthase III (EC 2.3	341	60595..61617	27_GENE_3
11346	**70**	**CGL2_11346070**	Malonyl CoA-acyl carrier protein transacylase (EC 2.	314	61617..62558	27_GENE_2
11346	**71**	**CGL2_11346071**	Malonyl CoA-acyl carrier protein transacylase (EC 2.	251	62558..63310	27_GENE_1
11346	**72**	**CGL2_11346072**	Acyl carrier protein (ACP)	76	63392..63619	295_GENE_10
11346	**73**	**CGL2_11346073**	3-oxoacyl-(Acyl-carrier-protein) synthase II (EC 2.3.	419	63622..64878	295_GENE_9
11346	**74**	**CGL2_11346074**	Ribonuclease III (EC 3.1.26.3)	247	64979..65719	295_GENE_8
11346	**75**	**CGL2_11346075**	hypothetical protein predicted by Glimmer/Critic	382	complement(65748..66893)	295_GENE_7
11346	**76**	**CGL2_11346076**	Hypothetical protein	354	complement(66911..67972)	295_GENE_6
11346	**77**	**CGL2_11346077**	Phosphoribosylformylglycinamidine cyclo-ligase (EC	350	68302..69351	295_GENE_5
11346	**78**	**CGL2_11346078**	Phosphoribosylglycinamide formyltransferase (EC 2.1	207	69338..69958	295_GENE_4
11346tRNA		**CGL2_11346R002**	TRNA Ala CGC		70039..70114	
11346	**79**	**CGL2_11346079**	Hypothetical protein	69	complement(70138..70344)	295_GENE_3
11346	**80**	**CGL2_11346080**	6-phosphogluconate dehydrogenase (decarboxylatin	339	70440..71456	135_GENE_12
11346	**81**	**CGL2_11346081**	Glucose-6-phosphate dehydrogenase (EC 1.1.1.49)	468	71461..72864	135_GENE_11
11346	**82**	**CGL2_11346082**	Serine 3-dehydrogenase (EC 1.1.1.276)	247	72942..73682	135_GENE_10
11346	**83**	**CGL2_11346083**	Conserved protein of unknown function	344	73748..74779	135_GENE_9

11346	**84**	**CGL2_11346084**	Methyl-accepting chemotaxis sensory transducer	577	complement(74814..76544)	135_GENE_8
11346	**85**	**CGL2_11346085**	Amino-acid N-acetyltransferase (EC 2.3.1.1)	448	76933..78276	135_GENE_6
11346	**86**	**CGL2_11346086**	Protein of unknown function	207	78770..79390	135_GENE_5
11346	**87**	**CGL2_11346087**	Putative response regulator receiver protein	322	79589..80554	135_GENE_4
11346	**88**	**CGL2_11346088**	Phosphoenolpyruvate synthase (EC 2.7.9.2)	799	80931..83327	135_GENE_3
11346	**89**	**CGL2_11346089**	GTP-binding protein (EngA)	469	complement(83398..84804)	135_GENE_2
11346	**90**	**CGL2_11346090**	Protein of unknown function	230	complement(84804..85493)	135_GENE_1
11346	**92**	**CGL2_11346092**	Probable purine-cytosine permease	477	85875..87305	14_GENE_68
11346	**93**	**CGL2_11346093**	NADH dehydrogenase (EC 1.6.99.3)	452	87301..88656	14_GENE_67
11346	**94**	**CGL2_11346094**	Putative amino acid permease	651	complement(88659..90611)	14_GENE_66
11346	**95**	**CGL2_11346095**	Hypothetical protein	519	complement(90800..92356)	14_GENE_65
11346	**96**	**CGL2_11346096**	Hypothetical protein	175	complement(92416..92940)	14_GENE_64
11346	**97**	**CGL2_11346097**	Hypothetical protein	54	complement(93068..93229)	14_GENE_63
11346	**98**	**CGL2_11346098**	Hypothetical protein	98	complement(93300..93593)	14_GENE_62
11346	**99**	**CGL2_11346099**	Hypothetical protein	332	complement(93714..94709)	14_GENE_61
11346	**100**	**CGL2_11346100**	Putative amino acid permease	476	complement(94788..96215)	14_GENE_60
11346	**101**	**CGL2_11346101**	Conserved protein of unknown function	176	complement(96288..96815)	14_GENE_59
11346	**102**	**CGL2_11346102**	Putative acetyltransferase	164	complement(96867..97358)	14_GENE_58
11346	**103**	**CGL2_11346103**	Deoxyribonuclease, TatD family	263	complement(97361..98149)	14_GENE_57
11346	**104**	**CGL2_11346104**	Methionyl-tRNA synthetase (EC 6.1.1.10)	673	complement(98157..100175)	14_GENE_56
11346	**105**	**CGL2_11346105**	Conserved protein of unknown function	240	complement(100214..100933)	14_GENE_55
11346	**106**	**CGL2_11346106**	DNA polymerase III (EC 2.7.7.7)	343	complement(101001..102029)	14_GENE_54
11346	**107**	**CGL2_11346107**	Thymidylate kinase (EC 2.7.4.9)	220	complement(102029..102688)	14_GENE_53
11346	**108**	**CGL2_11346108**	Hypothetical protein	43	complement(102857..102985)	14_GENE_52
11346	**109**	**CGL2_11346109**	Putative ferric uptake regulator, Fur family	155	103267..103731	14_GENE_51
11346	**110**	**CGL2_11346110**	Cytochrome c peroxidase (EC 1.11.1.5)	338	103757..104770	14_GENE_50
11346	**111**	**CGL2_11346111**	Putative alkyl hydroperoxide reducatase	200	104922..105521	14_GENE_49
11346	**112**	**CGL2_11346112**	Putative acireductone dioxygenase	186	105580..106137	14_GENE_48
11346	**113**	**CGL2_11346113**	Ribulose-bisphosphate carboxylase (EC 4.1.1.39)	389	106140..107306	14_GENE_47
11346	**114**	**CGL2_11346114**	Putative hydrolase, haloacid dehalogenase-like famil	216	107306..107953	14_GENE_46
11346	**115**	**CGL2_11346115**	Putative aldolase class II	200	107949..108548	14_GENE_45
11346	**116**	**CGL2_11346116**	Transcriptional regulator, MarR family	159	108707..109183	14_GENE_44
11346	**117**	**CGL2_11346117**	Conserved hypothetical protein	150	109215..109664	14_GENE_43
11346	**118**	**CGL2_11346118**	Conserved protein of unknow function	76	109766..109993	14_GENE_42
11346	**119**	**CGL2_11346119**	Putative silent information regulator protein, Sir2 fa	279	complement(110082..110918)	14_GENE_41
11346	**120**	**CGL2_11346120**	Hypothetical protein	125	111491..111865	14_GENE_39
11346	**121**	**CGL2_11346121**	Putative transcriptional regulator, ArsR family	117	112055..112405	14_GENE_38
11346	**122**	**CGL2_11346122**	Glyoxalase family protein	146	112405..112842	14_GENE_37
11346	**123**	**CGL2_11346123**	Hypothetical protein	285	complement(112871..113725)	14_GENE_36
11346	**124**	**CGL2_11346124**	Conserved protein of unknown function	222	113943..114608	14_GENE_35
11346	**125**	**CGL2_11346125**	Glucosamine-1-phosphate n-acetyltransferase] (EC	469	114601..116007	14_GENE_34

11346	**126**	**CGL2_11346126**	Glucosamine--fructose-6-phosphate aminotransferas	605	116012..117826	14_GENE_33
11346	**127**	**CGL2_11346127**	Protein of unknown function	439	117865..119181	14_GENE_32
11346	**128**	**CGL2_11346128**	Putative ATP-dependent DNA helicase, UvrD/REP fam	746	119181..121418	14_GENE_31
11346	**129**	**CGL2_11346129**	Glutamyl-tRNA(Gln) amidotransferase, C subunit	99	121565..121861	14_GENE_30
11346	**130**	**CGL2_11346130**	Aspartate 1-decarboxylase (EC 4.1.1.11	121	121869..122231	14_GENE_29
11346	**131**	**CGL2_11346131**	Glutamyl-tRNA(Gln) amidotransferase A subunit / Am	492	122231..123706	14_GENE_28
11346	**132**	**CGL2_11346132**	Glutamyl-tRNA(Gln) amidotransferase B subunit	490	123706..125175	14_GENE_27
11346	**133**	**CGL2_11346133**	Protein of unknown function	227	125175..125855	14_GENE_26
11346	**134**	**CGL2_11346134**	Probable Cytochrome c, NapC/NirT family	166	125871..126368	14_GENE_25
11346	**135**	**CGL2_11346135**	Enolase (EC 4.2.1.11)	427	126381..127661	14_GENE_24
11346	**136**	**CGL2_11346136**	Hypothetical protein	113	127672..128010	14_GENE_23
11346	**137**	**CGL2_11346137**	Protein of unknown function	146	complement(128038..128475)	14_GENE_22
11346	**138**	**CGL2_11346138**	Probable cytochrome c, class I	185	129079..129633	14_GENE_20
11346	**139**	**CGL2_11346139**	Putative sigma54 specific transcriptional regulator, F	463	130191..131579	14_GENE_19
11346	**140**	**CGL2_11346140**	Hypothetical protein	168	132055..132558	14_GENE_18
11346	**141**	**CGL2_11346141**	Hypothetical protein	121	132641..133003	14_GENE_17
11346	**142**	**CGL2_11346142**	Putative peptidase, C39 family	279	133087..133923	14_GENE_16
11346	**143**	**CGL2_11346143**	Hypothetical protein	246	133957..134694	14_GENE_15
11346	**144**	**CGL2_11346144**	Conserved hypothetical protein	375	135338..136462	14_GENE_14
11346	**145**	**CGL2_11346145**	Putative Outer membrane protein, OmpAfamily	521	136474..138036	14_GENE_13
11346	**146**	**CGL2_11346146**	Protein of unknown function	292	complement(138057..138932)	14_GENE_12
11346	**147**	**CGL2_11346147**	Flavin oxidoreductase/NADH oxidase (EC 1.6.99.1)	367	complement(139106..140206)	14_GENE_11
11346	**148**	**CGL2_11346148**	Putative transcriptional regulator, BadM/Rrf2 family	159	complement(140289..140765)	14_GENE_10
11346	**149**	**CGL2_11346149**	Phosphoglucosamine mutase (EC 5.4.2.10)	457	140920..142290	14_GENE_8
11346	**150**	**CGL2_11346150**	Competence protein (ComEC)	482	142566..144011	14_GENE_7
11346	**151**	**CGL2_11346151**	Putative DNA methylase N-4/N-6	453	complement(143987..145345)	14_GENE_6
11346	**152**	**CGL2_11346152**	Hypothetical protein	46	145522..145659	14_GENE_5
11346	**153**	**CGL2_11346153**	Protein of unknown function	207	complement(145672..146292)	14_GENE_4
11346	**154**	**CGL2_11346154**	NADH dehydrogenase (Quinone) (EC 1.6.99.5)	634	146431..148332	14_GENE_3
11346	**154a**	**CGL2_11346154a**	transposase	446	148469..149806	
11346tRNA		**CGL2_11346R003**	TRNA Lys CTT		150149..150224	
11346	**155**	**CGL2_11346155**	Diguanylate cyclase with GAF sensor	322	150471..151436	14_GENE_2
11346	**156**	**CGL2_11346156**	Conserved hypothetical protein	262	151662..152447	51_GENE_7
11346	**157**	**CGL2_11346157**	Protein of unknown function	409	152512..153738	51_GENE_8
11346	**158**	**CGL2_11346158**	Secretion protein (HlyD)	385	complement(153802..154956)	51_GENE_9
11346	**159**	**CGL2_11346159**	Hydrophobe/amphiphile efflux family protein	1042	complement(155012..158137)	51_GENE_10
11346	**160**	**CGL2_11346160**	RND efflux system, outer membrane lipoprotein (Noc	500	complement(158198..159697)	51_GENE_11
11346	**161**	**CGL2_11346161**	Hypothetical protein	63	complement(159841..160029)	51_GENE_12
11346	**162**	**CGL2_11346162**	Putative transcriptional regulator, MarR family	181	160165..160707	51_GENE_13
11346	**163**	**CGL2_11346163**	Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195)	334	160786..161787	51_GENE_14
11346	**164**	**CGL2_11346164**	Putative exodeoxyribonuclease V, gamma subunit	1095	161852..165136	51_GENE_15

11346	**165**	**CGL2_11346165**	Putative exodeoxyribonuclease V, beta subunit	1095	165136..168420	51_GENE_16
11346	**166**	**CGL2_11346166**	Exodeoxyribonuclease V, alpha subunit (EC 3.1.11.5	575	168420..170144	51_GENE_17
11346	**167**	**CGL2_11346167**	Conserved protein of unknow function	364	complement(170172..171263)	51_GENE_18
11346	**168**	**CGL2_11346168**	Putative two component transcriptional regulator, wi	253	complement(171263..172021)	51_GENE_19
11346	**169**	**CGL2_11346169**	Protein of unknown function	144	complement(172379..172810)	51_GENE_20
11346	**170**	**CGL2_11346170**	Probable TonB-like protein	216	complement(172824..173471)	51_GENE_21
11346	**171**	**CGL2_11346171**	Putative biopolymer transport protein	139	complement(173471..173887)	51_GENE_22
11346	**172**	**CGL2_11346172**	Putative biopolymer transport protein	234	complement(173954..174655)	51_GENE_23
11346	**173**	**CGL2_11346173**	Probable TonB-dependent receptor	974	complement(174823..177744)	51_GENE_24
11346	**174**	**CGL2_11346174**	Conserved protein of unknown function	238	178026..178739	51_GENE_26
11346	**175**	**CGL2_11346175**	Protein of unknown function	147	179281..179721	51_GENE_27
11346	**175a**	**CGL2_11346175a**	Conserved hypothetical protein	213	complement(179805..180443)	
11346	**176**	**CGL2_11346176**	Transposase	416	complement(180436..181683)	
11346	**177**	**CGL2_11346177**	Hypothetical protein	2132	complement(181919..188314)	
11346	**178**	**CGL2_11346178**	Putative Type I Restriction modification system, S su	360	complement(188806..189885)	
11346	**179**	**CGL2_11346179**	Putative Type I Restriction modification system, M su	549	complement(189885..191531)	
11346	**180**	**CGL2_11346180**	Putative DEAD/DEAH box helicase	756	complement(191575..193842)	
11346	**181**	**CGL2_11346181**	Conserved hypothetical protein	317	complement(193870..194820)	
11346	**182**	**CGL2_11346182**	Hypothetical protein	144	complement(194866..195297)	
11346	**183**	**CGL2_11346183**	Hypothetical protein	164	complement(195704..196195)	265_GENE_7
11346	**184**	**CGL2_11346184**	Probable XRE family transcriptional regulator	175	complement(196188..196712)	265_GENE_6
11346	**185**	**CGL2_11346185**	Conserved hypothetical protein	119	complement(196728..197084)	
11346	**186**	**CGL2_11346186**	Putative mobilization protein TraA	899	complement(197283..199979)	219_GENE_18
11346	**8**	**CGL2_11346008**	Conserved protein of unknow function	93	complement(7652..7930)	232_GENE_8
11346	**9**	**CGL2_11346009**	Conserved protein of unknow function	98	complement(7937..8230)	232_GENE_9
9314	**5**	**CGL2_09314005**	Putative phage integrase	330	complement(2687..3676)	219_GENE_5
9314	**4**	**CGL2_09314004**	Conserved protein of unknown function	73	complement(2385..2603)	219_GENE_4
9314	**3**	**CGL2_09314003**	Probable plasmid stabilization system protein	100	complement(2083..2382)	219_GENE_3
9314	**2**	**CGL2_09314002**	Hypothetical protein	145	complement(1424..1858)	
9314	**1**	**CGL2_09314001**	Hypothetical protein	226	complement(736..1413)	
11185	**11**	**CGL2_11185011**	Protein of unknown function	240	8393..9112	
11346	**187**	**CGL2_11346187**	Hypothetical protein	110	complement(199930..200259)	219_GENE_17
11346	**188**	**CGL2_11346188**	mobilization protein, MobE	210	complement(200263..200892)	219_GENE_16
11346	**189**	**CGL2_11346189**	mobilization protein, MobD	132	complement(200892..201287)	219_GENE_15
11346	**190**	**CGL2_11346190**	Conserved hypothetical protein	111	complement(201218..201550)	219_GENE_14
11346	**191**	**CGL2_11346191**	Protein of unknown function	163	complement(201578..202066)	219_GENE_13
11346	**192**	**CGL2_11346192**	Hypothetical protein	138	complement(202318..202731)	219_GENE_12
11346	**193**	**CGL2_11346193**	Hypothetical protein	430	complement(202860..204149)	219_GENE_10
11346	**194**	**CGL2_11346194**	Hypothetical protein	62	complement(204154..204339)	219_GENE_9
11346	**195**	**CGL2_11346195**	Hypothetical protein	236	204449..205156	219_GENE_8
11346	**196**	**CGL2_11346196**	Integrase	388	205199..206362	219_GENE_7

11346tRNA		**CGL2_11346R004**	TRNA Gly GCC		complement(206302..206376)	
11346	**197**	**CGL2_11346197**	Probable outer membrane lipoprotein	173	complement(206523..207041)	219_GENE_6
		Strain variant path	Strain variant path			Strain variant path
10850	**18**	**CGL2_10850018**	Putative pirin protein	301	complement(19392..20294)	98_GENE_19
10850	**17**	**CGL2_10850017**	Putative potassium channel protein	421	complement(17862..19124)	98_GENE_18
10850	**16**	**CGL2_10850016**	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	534	16247..17848	98_GENE_17
10850	**15**	**CGL2_10850015**	Protein of unknown function	276	complement(15086..15913)	98_GENE_16
10850	**14**	**CGL2_10850014**	Putative secretion protein (HlyD)	299	14139..15035	98_GENE_15
10850	**13**	**CGL2_10850013**	Conserved hypothetical protein	68	13936..14139	98_GENE_14
10850	**12**	**CGL2_10850012**	Putative fusaric acid resistance protein	682	11891..13936	98_GENE_13
10850	**11**	**CGL2_10850011**	Protein of unknown function	240	10986..11705	98_GENE_12
10850	**10**	**CGL2_10850010**	Protein of unknown function	386	9698..10855	98_GENE_11
10850	**9**	**CGL2_10850009**	Protein of unknown function	214	9028..9669	98_GENE_10
10850	**8**	**CGL2_10850008**	a+/H+ antiporter	535	7213..8817	98_GENE_9
10850	**7**	**CGL2_10850007**	Putative transcriptional regulator, TetR family	219	6352..7008	98_GENE_8
10850	**6**	**CGL2_10850006**	Putative isochorismatase hydrolase	188	complement(5681..6244)	98_GENE_7
10850	**5**	**CGL2_10850005**	Putative ammonia monooxygenase	345	complement(4543..5577)	98_GENE_6
10850tRNA		**CGL2_10850R001**	TRNA Asn GTT		4384..4459	
10850	**4**	**CGL2_10850004**	Conserved protein of unknown function	235	3574..4278	98_GENE_4
10850	**3**	**CGL2_10850003**	Conserved protein of unknown function	293	2696..3574	98_GENE_3
10850	**2**	**CGL2_10850002**	Dihydropteroate synthase (EC 2.5.1.15)	283	1843..2691	98_GENE_2
10850	**1**	**CGL2_10850001**	Peptidase M41, FtsH (EC 3.6.4.6)	592	78..1853	98_GENE_1
11247	**23**	**CGL2_11247023**	Hypoxanthine phosphoribosyl transferase (EC 2.4.2.	176	24189..24716	76_GENE_1
11247	**22**	**CGL2_11247022**	TRNA(Ile)-lysidine synthetase	504	22702..24213	76_GENE_2
11247	**21**	**CGL2_11247021**	Riboflavin kinase / FAD synthase (RibC) (EC 2.7.7.2)	319	21771..22727	76_GENE_3
11247	**20**	**CGL2_11247020**	Porphobilinogen synthase (EC 4.2.1.24)	326	20743..21720	76_GENE_4
11247	**19**	**CGL2_11247019**	Uroporphyrin-III C-methyltransferase / synthase (EC	513	19166..20704	76_GENE_5
11247	**18**	**CGL2_11247018**	Porphobilinogen deaminase (EC 2.5.1.61)	314	17662..18603	76_GENE_6
11247	**17**	**CGL2_11247017**	Glutamyl-tRNA reductase	452	16304..17659	76_GENE_7
11247	**16**	**CGL2_11247016**	Putative Cytochrome c assembly protein	269	15425..16231	76_GENE_8
11247	**15**	**CGL2_11247015**	Protein of unknown function	515	complement(13749..15293)	76_GENE_9
11247	**14**	**CGL2_11247014**	Lysine 2,3-aminomutase	383	complement(12597..13745)	76_GENE_10
11247	**13**	**CGL2_11247013**	Nitroreductase	249	complement(11824..12570)	76_GENE_11
11247	**12**	**CGL2_11247012**	Putative 2-deoxycytidine 5-triphosphate deaminase	366	complement(10736..11833)	76_GENE_12
11247	**11**	**CGL2_11247011**	Putative AAA-family ATPase	575	complement(8846..10570)	76_GENE_13
11247	**10**	**CGL2_11247010**	Putative proteasome component	511	complement(7314..8846)	76_GENE_14
11247	**9**	**CGL2_11247009**	Protein of unknown function	64	complement(7103..7294)	76_GENE_15
11247	**8**	**CGL2_11247008**	Putative 20S proteasome beta-subunit	265	complement(6301..7095)	76_GENE_16
11247	**7**	**CGL2_11247007**	Probable 20S proteasome alpha-subunit	251	complement(5553..6305)	76_GENE_17
11247	**6**	**CGL2_11247006**	Conserved protein of unknown function	502	complement(4120..5625)	76_GENE_18
11247	**5**	**CGL2_11247005**	Dihydroorotate dehydrogenase (EC 1.3.3.1)	368	3014..4117	76_GENE_19

11247	**4**	**CGL2_11247004**	Homoserine kinase (EC 2.7.1.39)	331	2041..3033	76_GENE_20
11247	**3**	**CGL2_11247003**	Probable ferredoxin	112	1710..2045	76_GENE_21
11247	**1**	**CGL2_11247001**	Conserved hypothetical protein	239	791..1507	76_GENE_22
11077	**1**	**CGL2_11077001**	Hypothetical protein	37	42..152	
11077	**2**	**CGL2_11077002**	Hypothetical protein	66	215..412	25_GENE_1
11077	**3**	**CGL2_11077003**	Probable cytochrome C oxidase mono-heme subunit	176	477..1004	25_GENE_2
11077	**4**	**CGL2_11077004**	Protein of unknown function	110	1117..1446	25_GENE_3
11077	**5**	**CGL2_11077005**	Hypothetical protein	68	1716..1919	25_GENE_4
11077	**6**	**CGL2_11077006**	Protein of unknown function	143	1934..2362	25_GENE_5
11077	**7**	**CGL2_11077007**	Protein of unknown function	68	2402..2605	25_GENE_6
11077	**8**	**CGL2_11077008**	Protein of unknown function	155	2628..3092	25_GENE_7
11077	**9**	**CGL2_11077009**	Probable cytochrome-c oxidase	185	3092..3646	25_GENE_8
11077	**10**	**CGL2_11077010**	Conserved protein of unknown function	362	3646..4731	25_GENE_9
11077	**11**	**CGL2_11077011**	Probable cytochrome C oxidase	188	4770..5333	25_GENE_10
11077	**12**	**CGL2_11077012**	Hypothetical protein	89	5338..5604	25_GENE_11
11077	**13**	**CGL2_11077013**	Probable iron-sulfur protein	442	5692..7017	25_GENE_12
11077	**14**	**CGL2_11077014**	Protein of unknown function	155	7096..7560	25_GENE_13
11077	**15**	**CGL2_11077015**	Hypothetical protein	108	7544..7867	25_GENE_13a
11077	**16**	**CGL2_11077016**	Conserved hypothetical protein	202	7887..8492	25_GENE_15
11077	**17**	**CGL2_11077017**	Putative ADP-ribose pyrophosphatase	198	8482..9075	25_GENE_16
11077	**18**	**CGL2_11077018**	Probable ferredoxin	63	9106..9294	25_GENE_17
11077	**19**	**CGL2_11077019**	Sigma54 specific transcriptional regulator, Fis family	473	9301..10719	25_GENE_18
11077	**20**	**CGL2_11077020**	Anthranilate synthase component I (EC 4.1.3.27)	501	10719..12221	25_GENE_19
11077	**21**	**CGL2_11077021**	Anthranilate synthase component II (EC 4.1.3.27)	198	12212..12805	25_GENE_20
11077	**22**	**CGL2_11077022**	Anthranilate phosphoribosyltransferase (EC 2.4.2.18	341	12805..13827	25_GENE_21
11077	**23**	**CGL2_11077023**	Indole-3-glycerol phosphate synthase (EC 4.1.1.48)	274	13797..14618	25_GENE_22
11077	**24**	**CGL2_11077024**	Phosphoribosylanthranilate isomerase (EC 5.3.1.24)	212	14611..15246	25_GENE_23
11077	**25**	**CGL2_11077025**	Tryptophan synthase, beta subunit (EC 4.2.1.20)	412	15236..16471	25_GENE_24
11077	**26**	**CGL2_11077026**	Tryptophan synthase, alpha chain (EC 4.2.1.20)	264	16471..17262	25_GENE_25
11077	**27**	**CGL2_11077027**	Acetyl-CoA carboxylase carboxyltransferase, beta su	304	17318..18229	25_GENE_26
11077	**28**	**CGL2_11077028**	Folylpolyglutamate synthase (EC 6.3.2.17)	444	18233..19564	25_GENE_27
11077	**29**	**CGL2_11077029**	Probable organic solvent tolerance protein (OstA)	767	19564..21864	25_GENE_28
11077	**30**	**CGL2_11077030**	Conserved protein of unknown function	266	complement(21891..22688)	25_GENE_29
11077	**31**	**CGL2_11077031**	NAD(+) kinase (EC 2.7.1.23)	305	complement(22753..23667)	25_GENE_30
11077	**32**	**CGL2_11077032**	Glutamate synthase, small subunit (EC 1.4.1.13)	613	24161..25999	25_GENE_31
11077	**33**	**CGL2_11077033**	Putative rieske iron-sulfur family protein	206	25999..26616	25_GENE_32
11077	**34**	**CGL2_11077034**	Putative cytochrome b/b6, N-terminal	253	26795..27553	25_GENE_33
11077	**35**	**CGL2_11077035**	Probable cytochrome b/b6, C-terminal	276	27611..28438	25_GENE_34
11077	**36**	**CGL2_11077036**	Protein of unknown function	72	28540..28755	25_GENE_35
11077	**37**	**CGL2_11077037**	Probable cytochrome c, class I	321	28755..29717	25_GENE_36

11077	**38**	**CGL2_11077038**	Daunorubicin resistance ABC transporter ATP-binding	327	29802..30782	25_GENE_37
11077	**39**	**CGL2_11077039**	Putative ABC-2 type transporter	273	30782..31600	25_GENE_38
11077	**40**	**CGL2_11077040**	Conserved protein of unknown function	164	31704..32195	25_GENE_39
11077	**40**	**CGL2_11077040**	Conserved protein of unknown function	164	31704..32195	25_GENE_39
11077	**42**	**CGL2_11077042**	Signal peptide peptidase, SppA	349	32210..33256	25_GENE_40
11077	**43**	**CGL2_11077043**	Protein of unknown function	119	complement(33223..33579)	25_GENE_41
11077	**44**	**CGL2_11077044**	Putative hydroxypyruvate reductase/glycerate kinase	431	complement(33579..34871)	25_GENE_42
11077	**45**	**CGL2_11077045**	Hypothetical protein	87	complement(34879..35139)	25_GENE_43
11077	**46**	**CGL2_11077046**	Conserved protein of unknown function	359	35184..36260	25_GENE_44
11077	**47**	**CGL2_11077047**	Protein of unknown function	115	complement(36277..36621)	25_GENE_45
11079	**1**	**CGL2_11079001**	Protein of unknown function	220	complement(739..1398)	25_GENE_46
11079	**2**	**CGL2_11079002**	Protein of unknown function	115	complement(1478..1822)	25_GENE_47
11079	**3**	**CGL2_11079003**	Conserved hypothetical protein	168	1908..2411	25_GENE_48
11079	**4**	**CGL2_11079004**	Putative major facilitator superfamily transporter	404	2386..3597	25_GENE_49
11080	**1**	**CGL2_11080001**	Putative CBS domain containing membrane protein	152	1065..1520	25_GENE_50
11080	**2**	**CGL2_11080002**	Conserved protein of unknown function	175	1510..2034	25_GENE_51
11080	**3**	**CGL2_11080003**	Putative histidine triad (HIT) protein	179	2048..2584	25_GENE_52
11080	**4**	**CGL2_11080004**	Protein of unknown function	231	2602..3294	25_GENE_53
11080	**5**	**CGL2_11080005**	Uracil phosphoribosyltransferase (EC 2.4.2.9)	199	3354..3950	25_GENE_54
11080	**6**	**CGL2_11080006**	Aspartate carbamoyltransferase (EC 2.1.3.2)	308	3950..4873	25_GENE_55
11080	**7**	**CGL2_11080007**	Dihydroorotase (EC 3.5.2.3)	438	4906..6219	25_GENE_56
11080	**8**	**CGL2_11080008**	Carbamoyl-phosphate synthase, small subunit (EC 6	365	6219..7313	25_GENE_57
11080	**9**	**CGL2_11080009**	Putative radical SAM family protein	332	7306..8301	25_GENE_58
11080	**10**	**CGL2_11080010**	Carbamoyl-phosphate synthase, large subunit (EC 6.	1080	8297..11536	25_GENE_59
11080	**11**	**CGL2_11080011**	Putative transcription elongation factor GreA	160	11616..12095	25_GENE_60
11080	**12**	**CGL2_11080012**	Hypothetical protein	41	12133..12255	25_GENE_61
11080	**13**	**CGL2_11080013**	Hypothetical protein	25	12437..12511	
11390	**1**	**CGL2_11390001**	Putative lytic transglycosylase	185	163..717	1108_GENE_3
11390	**2**	**CGL2_11390002**	Hypothetical protein	298	840..1733	483_GENE_1
11390	**3**	**CGL2_11390003**	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	461	complement(1764..3146)	483_GENE_2
11390	**4**	**CGL2_11390004**	Putative diguanylate cyclase/phosphodiesterase with	1157	complement(3277..6747)	483_GENE_3
11390	**5**	**CGL2_11390005**	Glutamine synthetase, type I (EC 6.3.1.2)	470	7377..8786	23_GENE_3
11390	**6**	**CGL2_11390006**	Aspartyl-tRNA synthetase (EC 6.1.1.12)	584	complement(8907..10658)	23_GENE_4
11390	**7**	**CGL2_11390007**	Pseudouridine synthase, Rsu	583	complement(10673..12421)	23_GENE_4a
11390	**8**	**CGL2_11390008**	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2)	516	complement(12427..13974)	23_GENE_6
11390	**9**	**CGL2_11390009**	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1	489	complement(14017..15483)	23_GENE_7
11390	**10**	**CGL2_11390010**	Conserved protein of unknown function	173	complement(15583..16101)	23_GENE_8
11390	**11**	**CGL2_11390011**	Probable AAA ATPase superfamily	300	complement(16097..16996)	23_GENE_9
11390	**12**	**CGL2_11390012**	Putative Lon family ATP-dependent protease	218	complement(17020..17673)	23_GENE_10
11390	**13**	**CGL2_11390013**	Protein of unknown function	133	complement(17703..18101)	23_GENE_11
11390	**14**	**CGL2_11390014**	Probable N-acetyltransferase family protein	167	18242..18742	23_GENE_12

11390	**15**	**CGL2_11390015**	DNA ligase (EC 6.5.1.1)	603	complement(18784..20592)	23_GENE_13
11390	**16**	**CGL2_11390016**	Hypothetical protein	155	20772..21236	23_GENE_14
11390	**17**	**CGL2_11390017**	Protein of unknown function	179	complement(21286..21822)	23_GENE_15
11390	**18**	**CGL2_11390018**	Apolipoprotein N-acyltransferase	491	22155..23627	23_GENE_16
11390	**19**	**CGL2_11390019**	Peptide chain release factor 2	370	23667..24776	23_GENE_17
11390	**20**	**CGL2_11390020**	Putative heat shock protein (Hsp20)	147	24833..25273	23_GENE_18
11390	**21**	**CGL2_11390021**	ATP-dependent protease La (EC 3.4.21.53)	813	25269..27707	23_GENE_19
11390	**22**	**CGL2_11390022**	Endonuclease III/Nth	241	27652..28374	23_GENE_20
11390	**23**	**CGL2_11390023**	Conserved hypothetical protein	69	28518..28724	23_GENE_21
11390	**24**	**CGL2_11390024**	Aldo/keto reductase (EC 1.1.1.65)	335	complement(28761..29765)	23_GENE_22
11390	**25**	**CGL2_11390025**	Putative transcriptional regulator, AraC family	315	29953..30897	23_GENE_23
11390	**26**	**CGL2_11390026**	Putative glycoside hydrolase, family 15	684	complement(30969..33020)	23_GENE_24
11390	**28**	**CGL2_11390028**	Histidyl-tRNA synthetase (EC 6.1.1.21)	437	complement(33041..34351)	23_GENE_25
11390	**29**	**CGL2_11390029**	Putative glycoside hydrolase, family 15	659	34579..36555	23_GENE_27
11390	**31**	**CGL2_11390031**	GTP-binding protein (lepA)	609	37020..38846	23_GENE_28
11390	**32**	**CGL2_11390032**	Signal peptidase I (EC 3.4.21.89)	223	38891..39559	23_GENE_29
11390	**33**	**CGL2_11390033**	Carbohydrate kinase, PfkB	352	39587..40642	23_GENE_30
11390	**34**	**CGL2_11390034**	3-deoxy-D-manno-octulosonate cytidylyltransferase	277	40642..41472	23_GENE_31
11390	**35**	**CGL2_11390035**	CTP synthase (EC 6.3.4.2)	545	41463..43097	23_GENE_32
11390	**36**	**CGL2_11390036**	2-Dehydro-3-deoxyphosphooctonate aldolase (EC 4.	289	43097..43963	23_GENE_33
11390	**37**	**CGL2_11390037**	Sugar isomerase, KpsF/GutQ family (EC 5.3.1.13)	332	43963..44958	23_GENE_34
11390	**38**	**CGL2_11390038**	Phosphatase kdsC	182	44961..45506	23_GENE_35
11390	**39**	**CGL2_11390039**	CDP-diacylglycerol--glycerol-3-phosphate 3-phospha	189	45506..46072	23_GENE_36
11390	**40**	**CGL2_11390040**	Conserved hypothetical protein	206	46092..46709	23_GENE_37
11390	**41**	**CGL2_11390041**	Putative peptidase, M23B family	327	46855..47835	23_GENE_39
11390	**42**	**CGL2_11390042**	Putative periplasmic sensor signal transduction histid	506	47955..49472	23_GENE_40
11390	**43**	**CGL2_11390043**	Protein of unknown function	176	49472..49999	23_GENE_41
11390	**44**	**CGL2_11390044**	Putative two component, sigma54 specific, transcript	458	49999..51372	23_GENE_42
11390	**45**	**CGL2_11390045**	Conserved hypothetical protein	256	complement(51412..52179)	23_GENE_43
11390	**46**	**CGL2_11390046**	Hypothetical protein	359	complement(52217..53293)	23_GENE_44
11390	**47**	**CGL2_11390047**	Conserved protein of unknown function	327	complement(53375..54355)	23_GENE_45
11390	**48**	**CGL2_11390048**	Protein of unknown function	102	54439..54744	23_GENE_46
11390	**49**	**CGL2_11390049**	Putative phosphoesterase, PAP2 family	211	54832..55464	23_GENE_47
11390	**50**	**CGL2_11390050**	Putative radical SAM family protein	379	55442..56578	23_GENE_48
11390	**51**	**CGL2_11390051**	Hypothetical protein	105	56548..56862	23_GENE_49
11390	**52**	**CGL2_11390052**	Putative catalytic LigB subunit of aromatic ring-openi	264	complement(56888..57679)	23_GENE_50
11390	**53**	**CGL2_11390053**	Probable methyltransferase	388	complement(57735..58898)	23_GENE_51
11390	**54**	**CGL2_11390054**	Hypothetical protein	77	complement(59023..59253)	23_GENE_52
11390	**55**	**CGL2_11390055**	Putative cytochrome c oxidase, subunit I	479	59439..60875	33_GENE_1
11390	**56**	**CGL2_11390056**	Twin-arginine translocation protein TatA/E	73	61085..61303	33_GENE_4
11390	**57**	**CGL2_11390057**	Protein of unknown function	143	complement(61360..61788)	33_GENE_5

11390	**58**	**CGL2_11390058**	Putative FAD dependent oxidoreductase	413	complement(61788..63026)	33_GENE_6
11390	**60**	**CGL2_11390060**	Conserved hypothetical protein	303	complement(63128..64036)	33_GENE_7
11390	**61**	**CGL2_11390061**	NADH-flavin oxidoreductase/NADH oxidase	354	complement(64103..65164)	33_GENE_8
11390	**62**	**CGL2_11390062**	Putative major facilitator superfamily transporter	496	complement(65312..66799)	33_GENE_9
11390	**63**	**CGL2_11390063**	Hypothetical protein	85	complement(66799..67053)	33_GENE_10
11390	**64**	**CGL2_11390064**	Protein of unknown function	420	complement(67237..68496)	33_GENE_11
11390	**65**	**CGL2_11390065**	Conserved hypothetical protein	195	68836..69420	33_GENE_12
11390	**66**	**CGL2_11390066**	Protein of unknown function	273	69648..70466	33_GENE_14
11390	**67**	**CGL2_11390067**	Probable PAS/PAC sensor protein	218	70493..71146	33_GENE_15
11390	**68**	**CGL2_11390068**	Diguanylate cyclase	426	71221..72498	33_GENE_16
11390	**70**	**CGL2_11390070**	Hypothetical protein	258	72781..73554	33_GENE_17
11390	**71**	**CGL2_11390071**	Hypothetical protein	147	complement(73698..74138)	33_GENE_18
11390	**72**	**CGL2_11390072**	Protein of unknown function	345	74395..75429	33_GENE_19
11390	**73**	**CGL2_11390073**	Protein of unknown function	493	75429..76907	33_GENE_20
11390	**74**	**CGL2_11390074**	Putative nodulation efficiency protein D	465	77161..78555	33_GENE_21
11390	**75**	**CGL2_11390075**	Band 7 family protein	252	78555..79310	33_GENE_22
11390	**76**	**CGL2_11390076**	Putative carboxymuconolactone decarboxylase	146	complement(79331..79768)	33_GENE_23
11390	**77**	**CGL2_11390077**	Protein of unknown function	175	complement(79768..80292)	33_GENE_24
11390	**78**	**CGL2_11390078**	Putative 3-hydroxyisobutyrate dehydrogenas	308	80505..81428	33_GENE_25
11390	**79**	**CGL2_11390079**	Probable hydrolase	277	81424..82254	33_GENE_26
11390	**79**	**CGL2_11390079**	Probable hydrolase	277	81424..82254	33_GENE_26
11390	**81**	**CGL2_11390081**	Protein of unknown function	150	complement(82423..82872)	33_GENE_27
11390	**82**	**CGL2_11390082**	Hypothetical protein	126	complement(82968..83345)	33_GENE_28
11390	**83**	**CGL2_11390083**	Hypothetical protein	101	83398..83700	33_GENE_29
11390	**84**	**CGL2_11390084**	Putative two component, sigma54 specific, transcript	489	complement(83935..85401)	33_GENE_30
11390	**85**	**CGL2_11390085**	Multi-sensor signal transduction histidine kinase	660	complement(85401..87380)	33_GENE_31
11390	**86**	**CGL2_11390086**	Conserved protein of unknown function	826	complement(87548..90025)	33_GENE_32
11390	**87**	**CGL2_11390087**	NADH dehydrogenase (Quinone) (EC 1.6.99.5)	555	complement(90025..91689)	33_GENE_33
11390	**88**	**CGL2_11390088**	Hypothetical protein	112	91972..92307	33_GENE_33a
11390	**89**	**CGL2_11390089**	Dihydroxy-acid dehydratase (EC 4.2.1.9)	561	92432..94114	33_GENE_36
11390	**90**	**CGL2_11390090**	SUA5/yciO/yrdC family	339	complement(94206..95222)	33_GENE_37
11390	**91**	**CGL2_11390091**	Dihydroxy-acid dehydratase (EC 4.2.1.9)	558	complement(95296..96969)	33_GENE_38
11390	**92**	**CGL2_11390092**	Conserved protein of unknown function	288	complement(97064..97927)	33_GENE_39
11390	**93**	**CGL2_11390093**	Conserved protein of unknown function	823	complement(98122..100590)	33_GENE_41
11390	**94**	**CGL2_11390094**	NADH dehydrogenase (Quinone) (EC 1.6.99.5)	553	complement(100590..102248)	33_GENE_42
11390	**95**	**CGL2_11390095**	Hypothetical protein	99	102681..102977	33_GENE_42a
11390	**96**	**CGL2_11390096**	Probable PilT protein-like	105	complement(103189..103503)	33_GENE_44
11390	**97**	**CGL2_11390097**	Probable transcriptional regulator (AbrB)	88	complement(103503..103766)	33_GENE_45
11390	**98**	**CGL2_11390098**	Putative glycosyltransferase	362	104057..105142	33_GENE_47
11390	**98**	**CGL2_11390098**	Putative glycosyltransferase	362	104057..105142	33_GENE_47
11390	**100**	**CGL2_11390100**	Putative glycosyl transferase, group 1	401	105224..106426	33_GENE_48

11390	**101**	**CGL2_11390101**	Undecaprenyl-phosphate galactose phosphotransfera	503	106419..107927	369_GENE_7
11390	**102**	**CGL2_11390102**	ABC transporter permease protein	264	107969..108760	369_GENE_8
11390	**103**	**CGL2_11390103**	ABC transporter ATP-binding protein	181	108773..109315	369_GENE_9
11390	**104**	**CGL2_11390104**	Putative glycosyltransferase	380	110083..111222	
9490	**1**	**CGL2_09490001**	Hypothetical protein	116	674..1021	318_GENE_1
9490	**2**	**CGL2_09490002**	Conserved hypothetical protein	87	1283..1543	318_GENE_2
9490	**3**	**CGL2_09490003**	Probable CopG family protein	79	1536..1772	318_GENE_3
9490	**3**	**CGL2_09490003**	Probable CopG family protein	79	1536..1772	318_GENE_3
9490	**5**	**CGL2_09490005**	Probable transposase	220	complement(2157..2816)	318_GENE_4
9490	**5**	**CGL2_09490005**	Probable transposase	220	complement(2157..2816)	318_GENE_4
9921	**4**	**CGL2_09921004**	Methylated-DNA-[protein]-cysteine S-methyltransfer	164	3045..3536	318_GENE_5
9921	**3**	**CGL2_09921003**	Putative Ada DNA repair protein and transcriptional r	475	1598..3022	318_GENE_6
9921	**2**	**CGL2_09921002**	Protein of unknown function	108	1087..1410	318_GENE_7
9921	**1**	**CGL2_09921001**	Hypothetical protein	142	412..837	318_GENE_8
11284	**2**	**CGL2_11284002**	Putative transposase	182	complement(598..1143)	318_GENE_9
11284	**3**	**CGL2_11284003**	Probable monooxygenase	420	complement(1470..2729)	191_GENE_2
11284	**4**	**CGL2_11284004**	Protein of unknown function	585	complement(2729..4483)	191_GENE_3
11284	**5**	**CGL2_11284005**	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49	495	complement(4498..5982)	191_GENE_4
11284	**6**	**CGL2_11284006**	Transaldolase	974	complement(6319..9240)	191_GENE_5
11284	**7**	**CGL2_11284007**	Transketolase (EC 2.2.1.1)	475	complement(9296..10720)	191_GENE_6
9975	**1**	**CGL2_09975001**	6-phosphogluconolactonase (EC 3.1.1.31)	19	complement(41..97)	511_GENE_9
9975	**2**	**CGL2_09975002**	Glucokinase (EC 2.7.1.2)	347	complement(348..1388)	511_GENE_8
9975	**3**	**CGL2_09975003**	Hypothetical protein	92	complement(1500..1775)	511_GENE_7
9975	**4**	**CGL2_09975004**	Hypothetical protein	61	complement(1796..1978)	511_GENE_5a
9975	**5**	**CGL2_09975005**	Protein of unknown function	185	complement(2110..2664)	511_GENE_5
9975	**6**	**CGL2_09975006**	Protein of unknown function	492	complement(2682..4157)	511_GENE_4
9975	**7**	**CGL2_09975007**	Protein of unknown function	487	complement(4360..5820)	511_GENE_2
10139	**1**	**CGL2_10139001**	Conserved protein of unknown function	241	complement(44..766)	736_GENE_4
10139	**2**	**CGL2_10139002**	DNA/RNA helicase, SNF2 family	263	complement(766..1554)	736_GENE_2
10139	**3**	**CGL2_10139003**	DNA/RNA helicase, SNF2 family	631	complement(1520..3412)	736_GENE_2
10139	**4**	**CGL2_10139004**	Probable transposase	458	3592..4965	412_GENE_6
10139	**5**	**CGL2_10139005**	Transposase	352	complement(5307..6362)	412_GENE_5
10139	**7**	**CGL2_10139007**	Diguanylate cyclase/phosphodiesterase with PAS/PA	250	6459..7208	412_GENE_4
10139	**7**	**CGL2_10139007**	Diguanylate cyclase/phosphodiesterase with PAS/PA	250	6459..7208	412_GENE_4
6867	**4**	**CGL2_06867004**	RNA-directed DNA polymerase (EC 2.7.7.49)	195	complement(2032..2616)	NOTE: see end of file-
6867	**3**	**CGL2_06867003**	Hypothetical protein	155	complement(1166..1630)	
6867	**2**	**CGL2_06867002**	Hypothetical protein	213	complement(116..754)	
11284	**8**	**CGL2_11284008**	Putative transposase	146	10780..11217	191_GENE_7
11284	**9**	**CGL2_11284009**	RNA-directed DNA polymerase (EC 2.7.7.49)	501	11597..13099	73_GENE_33
11284	**10**	**CGL2_11284010**	Probable nucleotidyltransferase superfamily protein	99	complement(13299..13595)	gap between gene 73_
11284	**10**	**CGL2_11284010**	Probable nucleotidyltransferase superfamily protein	99	complement(13299..13595)	73_GENE_31

11284	**12**	**CGL2_11284012**	Hypothetical protein	129	complement(13774..14160)	73_GENE_29a
11284	**13**	**CGL2_11284013**	Conserved protein of unknown function	502	14459..15964	73_GENE_29
11284	**14**	**CGL2_11284014**	3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)	311	16469..17401	73_GENE_27
11284	**15**	**CGL2_11284015**	Probable alpha/beta fold family protein	268	17401..18204	73_GENE_26
11284	**16**	**CGL2_11284016**	Conserved protein of unknown function	157	18365..18835	73_GENE_25
11284	**17**	**CGL2_11284017**	Protein of unknown function	85	complement(18949..19203)	73_GENE_23a
11284	**18**	**CGL2_11284018**	Hypothetical protein	85	complement(19362..19616)	73_GENE_23
11284	**19**	**CGL2_11284019**	Putative transposase	290	complement(19609..20478)	73_GENE_22
11284	**20**	**CGL2_11284020**	Putative transposase	96	complement(20451..20738)	73_GENE_21
11284	**21**	**CGL2_11284021**	Hypothetical protein	66	20895..21092	73_GENE_19
11284	**22**	**CGL2_11284022**	Probable PilT protein, N-terminal	128	complement(21183..21566)	73_GENE_18
11284	**23**	**CGL2_11284023**	Prevent-host-death family protein	79	complement(21624..21860)	73_GENE_17
11284	**24**	**CGL2_11284024**	Hypothetical protein	96	complement(21878..22165)	73_GENE_16
11284	**25**	**CGL2_11284025**	Plasmid maintenance system antidote protein, XRE fa	96	complement(22443..22730)	73_GENE_14
11284	**26**	**CGL2_11284026**	Plasmid maintenance system killer	93	complement(22749..23027)	73_GENE_13
11284	**27**	**CGL2_11284027**	Probable transposase	160	23491..23970	73_GENE_12
11284	**28**	**CGL2_11284028**	Probable transposase	170	24030..24539	73_GENE_11
11284	**29**	**CGL2_11284029**	Probable ATPase protein	159	24945..25421	73_GENE_9
11284	**30**	**CGL2_11284030**	Transposase	380	25456..26595	73_GENE_8
11284	**31**	**CGL2_11284031**	ATPase	135	26674..27078	73_GENE_7
11284	**32**	**CGL2_11284032**	Hypothetical protein	82	complement(27392..27637)	73_GENE_6
11284	**33**	**CGL2_11284033**	Probable transposase	335	complement(27738..28742)	73_GENE_5
11284	**34**	**CGL2_11284034**	Putative glycosyl transferase, group 1	357	29579..30649	73_GENE_4
11284	**35**	**CGL2_11284035**	Putative glycosyl transferase, group 1	431	30699..31991	627_GENE_2
11284	**36**	**CGL2_11284036**	Undecaprenyl-phosphate galactose phosphotransfera	502	31991..33496	73_GENE_1
11284	**37**	**CGL2_11284037**	Putative ABC transporter permease protein	229	33526..34212	627_GENE_4
11284	**40**	**CGL2_11284040**	Teichoic-acid-transporting ATPase (EC 3.6.3.40)	201	34442..35044	955_GENE_4
11284	**42**	**CGL2_11284042**	Probable transposase	133	35177..35575	659_GENE_7
11284	**43**	**CGL2_11284043**	Transposase	314	complement(35582..36523)	659_GENE_6
11284	**44**	**CGL2_11284044**	Probable transposase	180	36657..37196	659_GENE_5
11284	**46**	**CGL2_11284046**	Conserved hypothetical protein	189	complement(37491..38057)	659_GENE_3
11284	**47**	**CGL2_11284047**	Hypothetical protein	109	complement(38060..38386)	659_GENE_2
11284	**48**	**CGL2_11284048**	Putative glycosyl transferase, family 2	568	38669..40372	659_GENE_1
11284	**49**	**CGL2_11284049**	Putative glycosyl transferase, family 2	1023	40459..43527	
11284	**50**	**CGL2_11284050**	Conserved hypothetical protein	441	complement(43627..44949)	
10601	**1**	**CGL2_10601001**	Conserved hypothetical protein	50	complement(312..462)	985_GENE_3
10601	**2**	**CGL2_10601002**	Hypothetical protein	86	787..1044	985_GENE_4
10601	**3**	**CGL2_10601003**	Putative metallo-beta-lactamase family protein	243	1234..1962	178_GENE_1
10601	**4**	**CGL2_10601004**	Probable transcriptional regulator, ArsR family	119	1988..2344	178_GENE_2
10601	**5**	**CGL2_10601005**	Putative major facilitator superfamily transporter	442	2344..3669	178_GENE_3
10601	**6**	**CGL2_10601006**	Hypothetical protein	53	complement(3900..4058)	178_GENE_4

10601	**7**	**CGL2_10601007**	Hypothetical protein	76	4109..4336	178_GENE_4a
10601	**8**	**CGL2_10601008**	Hypothetical protein	152	4463..4918	178_GENE_5
10601	**9**	**CGL2_10601009**	Probable outer membrane efflux protein	481	4994..6436	178_GENE_6
10601	**10**	**CGL2_10601010**	Secretion protein (HlyD)	419	6429..7685	178_GENE_7
10601	**11**	**CGL2_10601011**	Heavy metal efflux pump, CzcA family	1061	7685..10867	178_GENE_8
10601	**12**	**CGL2_10601012**	Conserved protein of unknown function	134	10885..11286	178_GENE_9
10799	**26**	**CGL2_10799026**	Hypothetical protein	479	complement(18611..20047)	178_GENE_10
10799	**25**	**CGL2_10799025**	Putative IstB-like ATP-binding protein	260	17590..18369	321_GENE_1
10799	**24**	**CGL2_10799024**	Probable transposase	284	16742..17593	321_GENE_2
10799	**23**	**CGL2_10799023**	Putative transposase	351	15580..16632	321_GENE_3
10799	**22**	**CGL2_10799022**	Probable transposase	175	complement(14810..15334)	321_GENE_4
10799	**21**	**CGL2_10799021**	Probable transposase	489	complement(13150..14616)	321_GENE_5
10799	**20**	**CGL2_10799020**	Putative IstB-like ATP-binding protein	252	complement(12395..13150)	321_GENE_6
10799	**19**	**CGL2_10799019**	Hypothetical protein	70	complement(12159..12368)	321_GENE_7
10799	**18**	**CGL2_10799018**	Putative transposase	384	complement(10981..12132)	321_GENE_8
10799	**17**	**CGL2_10799017**	Putative IstB-like ATP-binding protein	292	complement(10133..11008)	581_GENE_8
10799	**16**	**CGL2_10799016**	Probable transposase	161	9670..10152	
10799	**15**	**CGL2_10799015**	Conserved protein of unknown function	360	8366..9445	45_GENE_46
10799	**14**	**CGL2_10799014**	Protein of unknown function	120	7891..8250	45_GENE_45a
10799	**13**	**CGL2_10799013**	Putative transcriptional regulator, TetR family	219	7222..7878	45_GENE_45
10799	**12**	**CGL2_10799012**	Conserved hypothetical protein	117	complement(6469..6819)	45_GENE_43
10799	**11**	**CGL2_10799011**	Putative metal dependent phosphohydrolase	254	complement(5091..5852)	45_GENE_41
10799	**10**	**CGL2_10799010**	Conserved protein of unknown function	188	3936..4499	45_GENE_40
10799	**9**	**CGL2_10799009**	Hypothetical protein	79	3570..3806	45_GENE_39
10799	**8**	**CGL2_10799008**	Probable transposase	105	complement(3021..3335)	45_GENE_38
10799	**7**	**CGL2_10799007**	Probable transposase	115	complement(2658..3002)	45_GENE_37
10799	**6**	**CGL2_10799006**	Conserved hypothetical protein	62	complement(2394..2579)	45_GENE_36
10799	**5**	**CGL2_10799005**	Putative PilT protein, N-terminal	140	1946..2365	45_GENE_35
10799	**4**	**CGL2_10799004**	Probable plasmid stability protein	84	1695..1946	45_GENE_34
10799	**3**	**CGL2_10799003**	Conserved protein of unknown function	165	948..1442	45_GENE_33
10799	**2**	**CGL2_10799002**	Conserved hypothetical protein	137	578..988	45_GENE_32
10799	**1**	**CGL2_10799001**	Probable PilT protein, N-terminal	133	172..570	45_GENE_31
11391	**30**	**CGL2_11391030**	Prevent-host-death protein	81	26362..26604	45_GENE_30
11391	**29**	**CGL2_11391029**	Hypothetical protein	49	complement(26133..26279)	45_GENE_29
11391	**28**	**CGL2_11391028**	Conserved hypothetical protein	92	complement(25809..26084)	45_GENE_28
11391	**27**	**CGL2_11391027**	Conserved hypothetical protein	129	complement(25445..25831)	
11391	**26**	**CGL2_11391026**	Hypothetical protein	77	25000..25230	45_GENE_27
11391	**25**	**CGL2_11391025**	Protein of unknown function	119	24550..24906	45_GENE_26
11391	**24**	**CGL2_11391024**	Probable cyclic nucleotide-binding protein	249	23259..24005	45_GENE_25
11391	**23**	**CGL2_11391023**	Conserved hypothetical protein	428	complement(21577..22860)	45_GENE_24
11391	**22**	**CGL2_11391022**	Putative NADH ubiquinone oxidoreductase, 20 kDa su	169	21041..21547	45_GENE_23

11391	**21**	**CGL2_11391021**	Putative NADH-ubiquinone oxidoreductase, 49 kDa s	499	19523..21019	45_GENE_22
11391	**20**	**CGL2_11391020**	NADH dehydrogenase (Quinone) (EC 1.6.99.5)	485	17998..19452	45_GENE_21
11391	**19**	**CGL2_11391019**	Probable hydrogenase 4 membrane component	220	17331..17990	45_GENE_20
11391	**18**	**CGL2_11391018**	Putative formate hydrogenlyase subunit 4	320	16368..17327	45_GENE_19
11391	**17**	**CGL2_11391017**	NADH dehydrogenase (Quinone) (EC 1.6.99.5)	686	14300..16357	45_GENE_18
11391	**16**	**CGL2_11391016**	Plasmid maintenance system antidote protein, XRE fa	116	13943..14290	45_GENE_17
11391	**15**	**CGL2_11391015**	Hypothetical protein	297	12918..13808	45_GENE_16
11391	**14**	**CGL2_11391014**	Conserved protein of unknown function	218	12108..12761	45_GENE_15
11391	**13**	**CGL2_11391013**	Conserved protein of unknown function	483	complement(10047..11495)	45_GENE_13
11391	**12**	**CGL2_11391012**	Conserved protein of unknown function	358	complement(8989..10062)	45_GENE_12
11391	**11**	**CGL2_11391011**	Conserved protein of unknown function	251	complement(8014..8766)	45_GENE_11
11391	**10**	**CGL2_11391010**	DNA-3-methyladenine glycosylase (EC 3.2.2.21)	211	complement(7382..8014)	45_GENE_10
11391	**9**	**CGL2_11391009**	Protein of unknown function	137	complement(6852..7262)	45_GENE_9
11391	**8**	**CGL2_11391008**	Conserved hypothetical protein	211	complement(5782..6414)	45_GENE_8
11391	**7**	**CGL2_11391007**	Conserved protein of unknown function	173	complement(5140..5658)	45_GENE_7
11391	**6**	**CGL2_11391006**	Conserved hypothetical protein	363	complement(3967..5055)	45_GENE_6
11391	**5**	**CGL2_11391005**	Methylated-DNA-[protein]-cysteine S-methyltransfer	164	3485..3976	45_GENE_5
11391	**4**	**CGL2_11391004**	Putative Ada DNA repair protein and transcriptional r	477	2055..3485	45_GENE_4
11391	**3**	**CGL2_11391003**	Aldo/keto reductase (EC 1.1.1.91)	357	complement(824..1894)	45_GENE_3
11391	**2**	**CGL2_11391002**	Hypothetical protein	97	496..786	45_GENE_2
11391	**1**	**CGL2_11391001**	Protein of unknown function	112	44..379	45_GENE_1
9831	**1**	**CGL2_09831001**	Conserved hypothetical protein	333	370..1368	454_GENE_3
9831	**2**	**CGL2_09831002**	Hypothetical protein	44	1721..1852	454_GENE_4
9831	**3**	**CGL2_09831003**	Hypothetical protein	53	complement(2219..2377)	454_GENE_5
9831	**4**	**CGL2_09831004**	Methyl-accepting chemotaxis sensory transducer with	231	complement(2591..3283)	454_GENE_6
9831	**5**	**CGL2_09831005**	transposase	140	3291..3710	454_GENE_8
11278	**42**	**CGL2_11278042**	Putative methyl-accepting chemotaxis protein	247	29709..30449	81_GENE_5
11278	**41**	**CGL2_11278041**	Hypothetical protein	77	complement(29322..29552)	81_GENE_6
11278	**40**	**CGL2_11278040**	Hypothetical protein	142	28412..28837	81_GENE_7
11278	**39**	**CGL2_11278039**	Hypothetical protein	152	27954..28409	81_GENE_8
11278	**38**	**CGL2_11278038**	Hypothetical protein	187	complement(26885..27445)	81_GENE_9
11278	**37**	**CGL2_11278037**	Hypothetical protein	50	26513..26662	81_GENE_10
11278	**36**	**CGL2_11278036**	Hypothetical protein	71	complement(26146..26358)	81_GENE_11
11278	**35**	**CGL2_11278035**	Hypothetical protein	86	25771..26028	81_GENE_12
11278	**33**	**CGL2_11278033**	Putative phage integrase	106	25429..25746	81_GENE_14
11278	**32**	**CGL2_11278032**	Putative phage integrase	248	24690..25433	81_GENE_14
11278	**30**	**CGL2_11278030**	Hypothetical protein	108	24045..24368	75_GENE_30
11278	**29**	**CGL2_11278029**	Hypothetical protein	72	complement(23675..23890)	75_GENE_28a
11278	**28**	**CGL2_11278028**	Putative phage protein Gp37/Gp68	240	22928..23647	75_GENE_28
11278	**27**	**CGL2_11278027**	Conserved hypothetical protein	371	21809..22921	75_GENE_27
11278	**26**	**CGL2_11278026**	Protein of unknown function	149	21363..21809	75_GENE_26

11278	**25**	**CGL2_11278025**	Hypothetical protein	291	20467..21339	75_GENE_25
11278	**24**	**CGL2_11278024**	Hypothetical protein	133	20069..20467	75_GENE_24
11278	**23**	**CGL2_11278023**	Probable O-methyltransferase	199	19442..20038	75_GENE_23
11278	**22**	**CGL2_11278022**	Conserved hypothetical protein	224	18465..19136	75_GENE_22
11278	**21**	**CGL2_11278021**	Conserved hypothetical protein	162	complement(17717..18202)	75_GENE_21
11278	**20**	**CGL2_11278020**	Putative metallo-beta-lactamase family protein	259	complement(16938..17714)	75_GENE_20
11278	**19**	**CGL2_11278019**	Diguanylate cyclase/phosphodiesterase	720	complement(14778..16937)	75_GENE_19
11278	**17**	**CGL2_11278017**	Probable methyl-accepting chemotaxis sensory trans	275	complement(13712..14536)	75_GENE_18
11278	**16**	**CGL2_11278016**	Probable methyl-accepting chemotaxis sensory trans	119	complement(13340..13696)	75_GENE_17
11278	**15**	**CGL2_11278015**	Putative metallo-beta-lactamase family protein	248	complement(12560..13303)	75_GENE_16
11278	**14**	**CGL2_11278014**	Probable methyl-accepting chemotaxis sensory trans	232	complement(11849..12544)	75_GENE_15
11278	**13**	**CGL2_11278013**	Hypothetical protein	47	complement(11102..11242)	75_GENE_13
11278	**12**	**CGL2_11278012**	Probable transposase	87	complement(10666..10926)	75_GENE_12
11278	**11**	**CGL2_11278011**	Conserved hypothetical protein	139	10163..10579	75_GENE_11
11278	**10**	**CGL2_11278010**	Hypothetical protein	210	9465..10094	75_GENE_10
11278	**9**	**CGL2_11278009**	Probable transposase	56	complement(9086..9253)	75_GENE_9
11278	**8**	**CGL2_11278008**	Putative O-methyltransferase, family 3	236	8314..9021	75_GENE_8
11278	**7**	**CGL2_11278007**	Conserved hypothetical protein	231	7529..8221	75_GENE_7
11278	**6**	**CGL2_11278006**	Conserved hypothetical protein	104	7166..7477	75_GENE_6
11278	**5**	**CGL2_11278005**	Hypothetical protein	57	6719..6889	
11278	**4**	**CGL2_11278004**	Protein of unknown function	176	6107..6634	75_GENE_5
11278	**3**	**CGL2_11278003**	DNA helicase	1602	1228..6033	75_GENE_4
11278	**2**	**CGL2_11278002**	Putative putative phage repressor	224	320..991	75_GENE_2
11278	**1**	**CGL2_11278001**	Hypothetical protein	72	complement(18..233)	75_GENE_1
4377	**1**	**CGL2_04377001**	Hypothetical protein	204	557..1168	
4377	**2**	**CGL2_04377002**	Conserved hypothetical protein	60	1175..1354	
2657	**1**	**CGL2_02657001**	Protein of unknown function	104	88..399	
02657tRNA		**CGL2_02657R001**	TRNA Ser CGA		587..677	
2657	**2**	**CGL2_02657002**	Hypothetical protein	60	732..911	376_GENE_1a
7140	**1**	**CGL2_07140001**	Hypothetical protein	79	70..306	376_GENE_1
7140	**2**	**CGL2_07140002**	Conserved hypothetical protein	98	773..1066	376_GENE_3
8598	**2**	**CGL2_08598002**	Hypothetical protein	192	complement(1181..1756)	376_GENE_5
8598	**1**	**CGL2_08598001**	Hypothetical protein	123	907..1275	376_GENE_6
8982	**7**	**CGL2_08982007**	Hypothetical protein	34	complement(3294..3395)	376_GENE_7
8982	**6**	**CGL2_08982006**	Hypothetical protein	61	complement(3112..3294)	376_GENE_8
8982	**5**	**CGL2_08982005**	Hypothetical protein	64	complement(2928..3119)	376_GENE_9
8982	**4a**	**CGL2_08982004a**	Hypothetical protein	84	complement(2680..2928)	
8982	**4**	**CGL2_08982004**	Hypothetical protein	120	complement(2330..2689)	376_GENE_10
8982	**3**	**CGL2_08982003**	Putative phage replisome organizer, N-terminal regic	328	complement(1279..2262)	376_GENE_11
8982	**2**	**CGL2_08982002**	Hypothetical protein	181	complement(731..1273)	376_GENE_12
8982	**1**	**CGL2_08982001**	Hypothetical protein	62	complement(395..580)	376_GENE_12a

8581	**3**	**CGL2_08581003**	Hypothetical protein	541	complement(2408..4030)	376_GENE_14
8581	**2**	**CGL2_08581002**	Hypothetical protein	427	complement(1092..2372)	376_GENE_15
8581	**1**	**CGL2_08581001**	Hypothetical protein	53	complement(931..1089)	
5939	**1**	**CGL2_05939001**	Hypothetical protein	88	complement(458..721)	
5939	**2**	**CGL2_05939002**	Hypothetical protein	175	complement(736..1260)	
10965	**24**	**CGL2_10965024**	Putative adenylylsulfate reductase, subunit A	524	complement(18938..20509)	303_GENE_1
10965	**23**	**CGL2_10965023**	Probable adenylylsulfate reductase, subunit B	114	complement(18610..18951)	303_GENE_2
10965	**22**	**CGL2_10965022**	Sulfate adenylyltransferase (EC 2.7.7.4)	393	complement(17359..18537)	303_GENE_3
10965	**21**	**CGL2_10965021**	Putative transcriptional regulator, XRE family	121	16859..17221	303_GENE_4
10965	**20**	**CGL2_10965020**	Conserved hypothetical protein	64	complement(16608..16799)	303_GENE_5
10965	**19**	**CGL2_10965019**	Putative radical SAM superfamily transporter	445	complement(14911..16245)	303_GENE_6
10965	**18**	**CGL2_10965018**	Putative transport protein	506	complement(13352..14869)	303_GENE_7
10965	**17**	**CGL2_10965017**	Hypothetical protein	65	complement(13158..13352)	303_GENE_9
10965tRNA		**CGL2_10965R001**	TRNA Met CAT		complement(13089..13164)	
10965	**16**	**CGL2_10965016**	transposase	476	11276..12703	303_GENE_10
7414	**1**	**CGL2_07414001**	Hypothetical protein	130	262..651	539_GENE_9
07414tRNA		**CGL2_07414R001**	TRNA Met CAT		55..130	
7414	**2**	**CGL2_07414002**	Hypothetical protein	149	complement(730..1176)	539_GENE_8
7414	**3**	**CGL2_07414003**	Hypothetical protein	91	complement(1179..1451)	539_GENE_7
9479	**2**	**CGL2_09479002**	Hypothetical protein	134	2537..2938	539_GENE_4
9479	**1**	**CGL2_09479001**	Phage/plasmid primase P4, C-terminal	730	366..2555	539_GENE_3
10305	**1**	**CGL2_10305001**	Hypothetical protein	149	complement(1119..1565)	
10305	**2**	**CGL2_10305002**	Hypothetical protein	226	complement(1568..2245)	
10305	**3**	**CGL2_10305003**	Conserved hypothetical protein	229	complement(2921..3607)	
10305	**4**	**CGL2_10305004**	DNA primase	717	complement(3607..5757)	
10305	**5**	**CGL2_10305005**	Hypothetical protein	64	complement(5772..5963)	51_GENE_2
10305	**6**	**CGL2_10305006**	Hypothetical protein	259	complement(6104..6880)	798_GENE_3
10305	**7**	**CGL2_10305007**	Conserved protein of unknown function	69	complement(6912..7118)	798_GENE_4
10305	**8**	**CGL2_10305008**	Conserved hypothetical protein	67	complement(7118..7318)	798_GENE_5
10305	**9**	**CGL2_10305009**	Putative phage integrase	161	complement(7353..7835)	
10965	**15**	**CGL2_10965015**	transposition helper protein, IstB	97	complement(10987..11277)	443_GENE_2
10965	**14**	**CGL2_10965014**	integrase Rci fragment (partial domain)	155	10438..10902	443_GENE_3
10965	**13**	**CGL2_10965013**	Hypothetical protein	72	complement(10199..10414)	443_GENE_4
10965	**12**	**CGL2_10965012**	Hypothetical protein	38	complement(10086..10199)	443_GENE_5
10965	**11**	**CGL2_10965011**	Hypothetical protein	151	9541..9993	443_GENE_6
10965	**10**	**CGL2_10965010**	Hypothetical protein	71	8861..9073	443_GENE_7
10965	**9**	**CGL2_10965009**	transposase	209	complement(8174..8800)	443_GENE_8

10965	**8**	**CGL2_10965008**	transposase	175	complement(7650..8174)	443_GENE_9
10965	**7**	**CGL2_10965007**	Hypothetical protein	224	6745..7416	443_GENE_10
10965	**6**	**CGL2_10965006**	Hypothetical protein	126	6368..6745	
10965	**5**	**CGL2_10965005**	Protein of unknown function	238	complement(5135..5848)	41_GENE_1
10965	**4**	**CGL2_10965004**	Putative sigma54 specific transcriptional regulator, F	454	3651..5012	41_GENE_2
10965	**3**	**CGL2_10965003**	Cytochrome bd ubiquinol oxidase, subunit I	534	complement(1859..3460)	41_GENE_4
10965	**2**	**CGL2_10965002**	Cytochrome bd ubiquinol oxidase, subunit II	379	complement(727..1863)	41_GENE_5
10965	**1**	**CGL2_10965001**	Cyd operon protein (YbgT)	43	complement(556..684)	41_GENE_6
10961	**1**	**CGL2_10961001**	Putative sulfide-quinone reductase	424	457..1728	41_GENE_7
10961	**2**	**CGL2_10961002**	Putative radical SAM superfamily protein	366	complement(1768..2865)	41_GENE_8
10961	**3**	**CGL2_10961003**	Conserved protein of unknown function	150	complement(2902..3351)	41_GENE_9
10961	**4**	**CGL2_10961004**	Conserved hypothetical protein	103	complement(3441..3749)	41_GENE_10
10961	**5**	**CGL2_10961005**	Probable major facilitator superfamily transporter	430	complement(3733..5022)	41_GENE_11
10961	**6**	**CGL2_10961006**	Putative glycosyl transferase, family 9	423	complement(5022..6290)	41_GENE_12
10961	**7**	**CGL2_10961007**	Putative two component transcriptional regulator, Lu	211	complement(6413..7045)	41_GENE_13
10961	**8**	**CGL2_10961008**	Putative periplasmic sensor signal transduction histid	532	complement(7045..8640)	41_GENE_14
10961	**9**	**CGL2_10961009**	Putative amino acid permease	665	complement(8612..10606)	41_GENE_15
10961	**10**	**CGL2_10961010**	Conserved protein of unknown function	482	complement(10712..12157)	41_GENE_16
10961	**11**	**CGL2_10961011**	Potassium-transporting ATPase, C subunit (EC 3.6.3.	205	complement(12266..12880)	41_GENE_17
10961	**12**	**CGL2_10961012**	Potassium-transporting ATPase, A subunit (EC 3.6.3.	567	complement(12939..14639)	41_GENE_18
10961	**13**	**CGL2_10961013**	Potassium-translocating P-type ATPase, B subunit (E	670	complement(14860..16869)	41_GENE_19
10961	**14**	**CGL2_10961014**	Protein of unknown function	202	complement(17129..17734)	41_GENE_20
10961	**15**	**CGL2_10961015**	Hypothetical protein	212	complement(17883..18518)	41_GENE_21
10961	**16**	**CGL2_10961016**	Hypothetical protein	199	complement(18784..19380)	41_GENE_22
10961	**17**	**CGL2_10961017**	Protein of unknown function	214	complement(19725..20366)	41_GENE_24
10961	**18**	**CGL2_10961018**	Putative osmosensitive K+ channel signal transducti	741	20561..22783	41_GENE_25
10961	**19**	**CGL2_10961019**	Hypothetical protein	192	22925..23500	41_GENE_26
10961	**20**	**CGL2_10961020**	Protein of unknown function	309	23535..24461	41_GENE_27
10961	**21**	**CGL2_10961021**	Putative NAD-binding 6-phosphogluconate dehydrog	307	complement(24476..25396)	41_GENE_28
10961	**22**	**CGL2_10961022**	Putative peroxiredoxin	191	complement(25396..25968)	41_GENE_29
10961	**23**	**CGL2_10961023**	Probable Dyp-type peroxidase	295	complement(26137..27021)	41_GENE_30
10961	**24**	**CGL2_10961024**	Putative CoA-binding protein	148	complement(27114..27557)	41_GENE_31
10961	**25**	**CGL2_10961025**	Probable ferredoxin	420	27772..29031	41_GENE_33
10961	**27**	**CGL2_10961027**	Conserved protein of unknown function	197	29119..29709	41_GENE_34
10961	**28**	**CGL2_10961028**	Cysteine desulfurase (EC 2.8.1.7)	390	29705..30874	41_GENE_35
10961	**29**	**CGL2_10961029**	Putative NAD-dependent epimerase/dehydratase	298	30915..31808	41_GENE_36
10961tRNA		**CGL2_10961R001**	TRNA Leu CAG		complement(32176..32261)	
10961tRNA		**CGL2_10961R002**	TRNA Arg TCT		complement(32500..32576)	
10961	**30**	**CGL2_10961030**	Hypothetical protein	68	complement(32609..32812)	287_GENE_8
10961	**31**	**CGL2_10961031**	Putative glutaredoxin	129	complement(32898..33284)	287_GENE_7
10961	**32**	**CGL2_10961032**	Protein of unknown function	450	33491..34840	287_GENE_6

10961	**33**	**CGL2_10961033**	Hypothetical protein	551	34846..36498	287_GENE_5
10961	**34**	**CGL2_10961034**	Protein of unknown function	206	36552..37169	287_GENE_4
10961	**35**	**CGL2_10961035**	Peptide methionine sulfoxide reductase (EC 1.8.4.6)	185	complement(37167..37721)	287_GENE_3
10961	**36**	**CGL2_10961036**	Diguanylate cyclase/phosphodiesterase	702	38235..40340	287_GENE_2
10961	**37**	**CGL2_10961037**	Protein of unknown function	206	40754..41371	86_GENE_19
10961	**38**	**CGL2_10961038**	Conserved hypothetical protein	63	41554..41742	86_GENE_18
10961	**39**	**CGL2_10961039**	Protein of unknown function	356	41864..42931	86_GENE_17
10961	**40**	**CGL2_10961040**	Protein of unknown function	215	42988..43632	86_GENE_16
10961tRNA		**CGL2_10961R003**	TRNA Lys TTT		complement(44332..44407)	
10961	**41**	**CGL2_10961041**	Conserved hypothetical protein	361	complement(44444..45526)	86_GENE_14
10961	**42**	**CGL2_10961042**	3-isopropylmalate dehydratase small subunit (EC 4.2	208	complement(45591..46214)	86_GENE_13
10961	**43**	**CGL2_10961043**	3-isopropylmalate dehydratase large subunit (EC 4.2	465	complement(46251..47645)	86_GENE_12
10961	**44**	**CGL2_10961044**	DTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	357	47836..48906	86_GENE_11
10961	**45**	**CGL2_10961045**	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.	299	48906..49802	86_GENE_10
10961	**47**	**CGL2_10961047**	DTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.	183	49802..50350	86_GENE_9
10961	**48**	**CGL2_10961048**	Putative major facilitator superfamily transporter	425	complement(50382..51656)	86_GENE_8
10961	**49**	**CGL2_10961049**	Conserved protein of unknown function	316	51803..52750	86_GENE_7
10961	**50**	**CGL2_10961050**	Diguanylate cyclase/phosphodiesterase with PAS/PA	878	52830..55463	86_GENE_6
10961	**51**	**CGL2_10961051**	Putative phosphoglycerate mutase	156	55498..55965	86_GENE_5
10961	**52**	**CGL2_10961052**	Glutamate decarboxylase (EC 4.1.1.15)	457	complement(56012..57382)	86_GENE_4
10961	**53**	**CGL2_10961053**	Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.1	637	57614..59524	86_GENE_3
10961	**54**	**CGL2_10961054**	Malto-oligosyltrehalose synthase (EC 5.4.99.15)	965	59524..62418	86_GENE_2
10961	**55**	**CGL2_10961055**	Trehalose synthase (EC 5.4.99.16)	556	62418..64085	213_GENE_8
10961	**56**	**CGL2_10961056**	Trehalose synthase (EC 5.4.99.16)	559	64085..65761	213_GENE_7
10961	**57**	**CGL2_10961057**	Putative fatty acid desaturase	338	complement(65872..66885)	213_GENE_6
10961	**58**	**CGL2_10961058**	Diguanylate cyclase	386	complement(67097..68254)	213_GENE_5
10961	**59**	**CGL2_10961059**	Hypothetical protein	280	69037..69876	213_GENE_4
10961	**60**	**CGL2_10961060**	Diguanylate cyclase	380	complement(69911..71050)	213_GENE_3
10961	**61**	**CGL2_10961061**	Protein of unknown function	211	complement(71244..71876)	206_GENE_8
10961	**62**	**CGL2_10961062**	Hypothetical protein	67	complement(71932..72132)	206_GENE_7
10954	**1**	**CGL2_10954001**	Putative alpha amylase, catalytic region	663	1250..3238	206_GENE_6
10954	**2**	**CGL2_10954002**	Probable alpha amylase, catalytic region	523	3238..4806	206_GENE_5
10954	**3**	**CGL2_10954003**	Zinc-containing alcohol dehydrogenase superfamily (	347	5003..6043	206_GENE_4
10954	**4**	**CGL2_10954004**	Hypothetical protein	107	6396..6716	206_GENE_3
10954	**5**	**CGL2_10954005**	Diguanylate cyclase with PAS/PAC sensor	1029	6892..9978	206_GENE_2
10954	**6**	**CGL2_10954006**	Putative enoyl-CoA hydratase/isomerase	288	complement(10723..11586)	206_GENE_1
10954	**7**	**CGL2_10954007**	Putative multi-sensor hybrid histidine kinase	849	complement(11980..14526)	7_GENE_62
10954	**8**	**CGL2_10954008**	Putative response regulator receiver modulated meta	376	complement(14619..15746)	7_GENE_61
10954	**9**	**CGL2_10954009**	Hypothetical protein	231	complement(16126..16818)	7_GENE_59
10954	**10**	**CGL2_10954010**	Hypothetical protein	295	complement(17224..18108)	7_GENE_58
10954	**11**	**CGL2_10954011**	Hypothetical protein	505	complement(18543..20057)	7_GENE_57

10954	**12**	**CGL2_10954012**	Probable TPR-domain containing protein	1076	complement(20057..23284)	7_GENE_56
10954	**13**	**CGL2_10954013**	Methyltransferase, FkbM family	262	complement(23911..24696)	7_GENE_54
10954	**14**	**CGL2_10954014**	Putative ABC transporter, ATP-binding protein	609	complement(24824..26650)	7_GENE_53
10954	**15**	**CGL2_10954015**	Hypothetical protein	299	complement(26650..27546)	7_GENE_52
10954	**16**	**CGL2_10954016**	SAM-dependent methyltransferase	286	complement(27894..28751)	7_GENE_51
10954	**17**	**CGL2_10954017**	Probable glycosyl transferase	439	complement(28918..30234)	7_GENE_50
10954	**18**	**CGL2_10954018**	Putative glycosyl transferase, family 2	364	complement(30285..31376)	7_GENE_49
10954	**19**	**CGL2_10954019**	Protein of unknown function	351	complement(31418..32470)	7_GENE_48
10954	**20**	**CGL2_10954020**	Putative glycosyl transferase, family 2	367	complement(32530..33630)	7_GENE_47
10954	**21**	**CGL2_10954021**	Probable glycosyl transferase, family 2	625	complement(33764..35638)	7_GENE_46
10954	**22**	**CGL2_10954022**	Protein of unknown function	681	complement(35644..37686)	7_GENE_45
10954	**23**	**CGL2_10954023**	Putative two component, sigma54 specific, transcript	471	complement(37766..39178)	7_GENE_44
10954	**24**	**CGL2_10954024**	Conserved hypothetical protein	237	complement(39178..39888)	7_GENE_43
10954	**25**	**CGL2_10954025**	Eight transmembrane protein (EpsH)	276	complement(39881..40708)	7_GENE_42
10954	**26**	**CGL2_10954026**	UTP-glucose-1-phosphate uridylyltransferase (EC 2.7	307	complement(40698..41618)	7_GENE_41
10954	**27**	**CGL2_10954027**	Putative periplasmic sensor signal transduction histid	704	complement(42142..44253)	7_GENE_39
10954	**28**	**CGL2_10954028**	Putative glycosyl transferase, family 2	329	44593..45579	7_GENE_38
10954	**29**	**CGL2_10954029**	Putative glycosyl transferase, family 2	336	complement(45689..46696)	7_GENE_37
10954	**30**	**CGL2_10954030**	Hypothetical protein	621	47061..48923	7_GENE_36
10954	**31**	**CGL2_10954031**	O-antigen polymerase	503	48994..50502	7_GENE_35
10954	**32**	**CGL2_10954032**	Putative glycosyl transferase, group 1	374	50502..51623	7_GENE_34
10954	**33**	**CGL2_10954033**	Putative polysaccharide deacetylase	653	51619..53577	7_GENE_33
10954	**34**	**CGL2_10954034**	Putative glycosyl transferase, group 1	394	53577..54758	7_GENE_32
10954	**35**	**CGL2_10954035**	Probable glycosyltransferase	381	54752..55894	7_GENE_31
10954	**36**	**CGL2_10954036**	Putative polysaccharide deacetylase	269	55882..56688	7_GENE_30
10954	**37**	**CGL2_10954037**	Conserved hypothetical protein	504	56688..58199	7_GENE_29
10954	**38**	**CGL2_10954038**	Putative polysaccharide export protein	285	58366..59220	7_GENE_28
10954	**39**	**CGL2_10954039**	Putative glycosyltransferase	447	59257..60597	7_GENE_27
10954	**40**	**CGL2_10954040**	Probable lipopolysaccharide biosynthesis protein	660	60620..62599	7_GENE_26
10954	**41**	**CGL2_10954041**	Conserved hypothetical protein	128	complement(62821..63204)	7_GENE_25
10954	**42**	**CGL2_10954042**	Conserved hypothetical protein	75	complement(63204..63428)	7_GENE_24
10954	**43**	**CGL2_10954043**	Hypothetical protein	99	complement(63468..63764)	7_GENE_23
10954	**44**	**CGL2_10954044**	Hypothetical protein	170	complement(63772..64281)	7_GENE_21a
10954	**45**	**CGL2_10954045**	Conserved hypothetical protein	85	64627..64881	7_GENE_21
10954	**46**	**CGL2_10954046**	RNA polymerase sigma factor	193	64881..65459	7_GENE_20
10954	**47**	**CGL2_10954047**	Hypothetical protein	153	65590..66048	7_GENE_19
10954	**48**	**CGL2_10954048**	Mercuric reductase (EC 1.16.1.1)	557	66148..67818	7_GENE_18
10954	**48**	**CGL2_10954048**	Mercuric reductase (EC 1.16.1.1)	557	66148..67818	7_GENE_18
10954	**50**	**CGL2_10954050**	Putative transcriptional regulator, MerR family	135	67864..68268	7_GENE_17
10954	**51**	**CGL2_10954051**	Putative mechanosensitive ion channel (MscS)	365	complement(68413..69507)	7_GENE_16
10954	**52**	**CGL2_10954052**	Diguanylate cyclase	371	complement(69689..70801)	7_GENE_15

10954	**53**	**CGL2_10954053**	Hypothetical protein	108	71327..71650	7_GENE_14
10954	**54**	**CGL2_10954054**	DNA adenine methylase (EC 2.1.1.72)	634	71980..73881	7_GENE_13
10954	**55**	**CGL2_10954055**	UDP-galactopyranose mutase (EC 5.4.99.9)	367	complement(74009..75109)	7_GENE_12
10954	**56**	**CGL2_10954056**	UDP-glucuronate 5'-epimerase (EC 5.1.3.12)	341	complement(75173..76195)	7_GENE_11
10954	**58**	**CGL2_10954058**	Probable adenylate cyclase	1202	complement(76310..79915)	7_GENE_10
10954	**59**	**CGL2_10954059**	Putative sigma54 specific transcriptional regulator, F	518	80349..81902	7_GENE_9
10954	**60**	**CGL2_10954060**	Glucosamine--fructose-6-phosphate aminotransferas	615	83321..85165	7_GENE_8
10954	**61**	**CGL2_10954061**	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	433	85205..86503	7_GENE_7
10954	**62**	**CGL2_10954062**	Protein of unknown function	170	86533..87042	7_GENE_6
10954	**63**	**CGL2_10954063**	UDP-glucose 4-epimerase (EC 5.1.3.2)	316	87101..88048	7_GENE_5
10954	**64**	**CGL2_10954064**	Putative sigma54 specific transcriptional regulator, F	475	complement(88049..89473)	7_GENE_4
10954	**65**	**CGL2_10954065**	Putative protein-tyrosine-phosphatase	189	89750..90316	7_GENE_3
10954	**66**	**CGL2_10954066**	Diguanylate cyclase/phosphodiesterase with PAS/PA	747	90463..92703	7_GENE_2
10954	**67**	**CGL2_10954067**	Hypothetical protein	213	complement(93158..93796)	7_GENE_1
10954	**68**	**CGL2_10954068**	transposase	117	complement(94809..95159)	2_GENE_128
		Strain variant path	Strain variant path			Strain variant path
11068tRNA		**CGL2_11068R002**	TRNA Glu TTC		135482..135559	
11068	**123**	**CGL2_11068123**	Succinyl-CoA synthetase, beta subunit	416	complement(133987..135234)	2_GENE_126
11068	**122**	**CGL2_11068122**	Succinyl-CoA synthetase, alpha subunit (EC 6.2.1.5)	328	complement(132956..133939)	2_GENE_123
11068	**121**	**CGL2_11068121**	Hypothetical protein	50	complement(132772..132921)	2_GENE_122
11068	**120**	**CGL2_11068120**	Aconitate hydratase (EC 4.2.1.3)	641	complement(130542..132464)	2_GENE_121
11068	**119**	**CGL2_11068119**	Probable citrate synthase	269	complement(129639..130445)	2_GENE_120
11068	**118**	**CGL2_11068118**	Conserved hypothetical protein	200	complement(128965..129564)	2_GENE_119
11068	**117**	**CGL2_11068117**	Probable ferredoxin	228	complement(128170..128853)	2_GENE_118
11068	**116**	**CGL2_11068116**	L-aspartate oxidase (EC 1.4.3.16)	540	complement(126551..128170)	2_GENE_117
11068	**115**	**CGL2_11068115**	Succinyl-CoA synthetase, beta subunit (EC 6.2.1.5)	396	complement(125285..126472)	2_GENE_116
11068	**114**	**CGL2_11068114**	Succinyl-CoA synthetase, alpha subunit (EC 6.2.1.5)	305	complement(124371..125285)	2_GENE_115
11068	**113**	**CGL2_11068113**	Putative thioredoxin peroxidase	153	complement(123798..124256)	2_GENE_114
11068	**112**	**CGL2_11068112**	Protein of unknown function	180	123103..123642	2_GENE_113
11068	**111**	**CGL2_11068111**	Conserved hypothetical protein	80	122758..122997	2_GENE_111a
11068	**110**	**CGL2_11068110**	Conserved protein of unknown function	148	complement(122091..122534)	2_GENE_111
11068	**109**	**CGL2_11068109**	S-adenosyl-methyltransferase (MraW)	307	complement(121153..122073)	2_GENE_110
11068	**108**	**CGL2_11068108**	Hypothetical protein	91	complement(120888..121160)	2_GENE_109
11068	**107**	**CGL2_11068107**	Peptidoglycan glycosyltransferase (EC 2.4.1.129)	578	complement(119060..120793)	2_GENE_108
11068	**106**	**CGL2_11068106**	UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-dia	509	complement(117484..119010)	2_GENE_107
11068	**105**	**CGL2_11068105**	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alani	495	complement(116000..117484)	2_GENE_106
11068	**104**	**CGL2_11068104**	Phospho-N-acetylmuramoyl-pentapeptide-transferas	357	complement(114927..115997)	2_GENE_105
11068	**103**	**CGL2_11068103**	UDP-N-acetylmuramoylalanine--D-glutamate ligase (	487	complement(113429..114889)	2_GENE_104
11068	**102**	**CGL2_11068102**	Putative cell division protein (FtsW)	396	complement(112242..113429)	2_GENE_103
11068	**101**	**CGL2_11068101**	N-acetylglucosaminyltransferase, MurG (EC 2.4.1.22	371	complement(111130..112242)	2_GENE_102
11068	**100**	**CGL2_11068100**	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.	464	complement(109615..111006)	2_GENE_101

11068	**99**	**CGL2_11068099**	UDP-N-acetylenolpyruvoylglucosamine reductase (EC	304	complement(108704..109615)	2_GENE_100
11068	**98**	**CGL2_11068098**	D-alanine--D-alanine ligase (EC 6.3.2.4)	303	complement(107742..108650)	2_GENE_99
11068	**97**	**CGL2_11068097**	Protein of unknown function	286	complement(106879..107736)	2_GENE_98
11068	**96**	**CGL2_11068096**	Cell division protein (FtsA)	442	complement(105459..106784)	2_GENE_97
11068	**95**	**CGL2_11068095**	Cell division protein (FtsZ)	390	complement(104238..105407)	2_GENE_96
11068	**94**	**CGL2_11068094**	Conserved hypothetical protein	216	complement(103587..104234)	2_GENE_95
11068	**93**	**CGL2_11068093**	Conserved protein of unknown function	230	complement(102887..103576)	2_GENE_94
11068	**92**	**CGL2_11068092**	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	288	complement(102019..102882)	2_GENE_93
11068	**91**	**CGL2_11068091**	Conserved hypothetical protein	72	complement(101796..102011)	2_GENE_92
11068	**90**	**CGL2_11068090**	Probable cell-division initiation protein	175	complement(101221..101745)	2_GENE_91
11068	**89**	**CGL2_11068089**	Conserved hypothetical protein	102	complement(100897..101202)	2_GENE_90
11068	**88**	**CGL2_11068088**	Protein of unknown function	199	100298..100894	2_GENE_89
11068	**87a**	**CGL2_11068087a**	Probable transposase	197	99506..100096	
11068	**87**	**CGL2_11068087**	Squalene-hopene cyclase (EC 5.4.99.17)	683	complement(96980..99028)	2_GENE_87
11068	**86**	**CGL2_11068086**	Protein of unknown function	262	complement(96195..96980)	2_GENE_86
11068	**85**	**CGL2_11068085**	Conserved protein of unknown function	446	complement(94858..96195)	2_GENE_85
11068	**84**	**CGL2_11068084**	Protein of unknown function	232	94211..94906	2_GENE_84
11068	**83**	**CGL2_11068083**	Dihydroflavonol 4-reductase (EC 1.1.1.219)	336	complement(93047..94054)	2_GENE_83
11068	**82**	**CGL2_11068082**	4-hydroxy-3-methylbut-2-enyl diphosphate reductas	302	complement(92054..92959)	2_GENE_82
11068	**81**	**CGL2_11068081**	Putative radical SAM family protein	479	complement(90578..92014)	2_GENE_81
11068	**80**	**CGL2_11068080**	Ceramide glucosyltransferase (EC 2.4.1.80)	412	complement(89327..90562)	2_GENE_80
11068	**79**	**CGL2_11068079**	Conserved hypothetical protein	97	complement(88941..89231)	2_GENE_79
11068	**78**	**CGL2_11068078**	Conserved hypothetical protein	257	complement(88143..88913)	2_GENE_78
11068	**77**	**CGL2_11068077**	Putative cobalamin (Vitamin B12) biosynthesis (CbiX	276	complement(87206..88033)	2_GENE_77
11068	**76**	**CGL2_11068076**	Uroporphyrinogen decarboxylase (EC 4.1.1.37)	356	complement(86136..87203)	2_GENE_76
11068	**75**	**CGL2_11068075**	Oxygen-independent coproporphyrinogen III oxidase	459	complement(84684..86060)	2_GENE_75
11068	**74**	**CGL2_11068074**	Protein of unknown function	126	84204..84581	2_GENE_74
11068tRNA		**CGL2_11068R001**	TRNA Ala GGC		complement(83757..83832)	
11068	**73**	**CGL2_11068073**	S-adenosylmethionine synthetase (EC 2.5.1.6)	404	complement(82156..83367)	2_GENE_72
11068	**72**	**CGL2_11068072**	Adenosylhomocysteinase (EC 3.3.1.1)	418	complement(80813..82066)	2_GENE_71
11068	**71**	**CGL2_11068071**	Thiamine biosynthesis protein (ThiS)	76	complement(80579..80806)	2_GENE_70
11068	**70**	**CGL2_11068070**	Cysteine synthase (EC 2.5.1.47)	312	complement(79663..80598)	2_GENE_69
11068	**69**	**CGL2_11068069**	Putative ThiF family protein	270	complement(78814..79623)	2_GENE_68
11068	**68**	**CGL2_11068068**	Threonine synthase (EC 4.2.3.1)	407	complement(77571..78791)	2_GENE_67
11068	**67**	**CGL2_11068067**	Putative ThiS family protein	93	complement(77268..77546)	2_GENE_66
11068	**66**	**CGL2_11068066**	Conserved protein of unknown function	80	complement(77029..77268)	2_GENE_65
11068	**65**	**CGL2_11068065**	Putative molybdopterin biosynthesis protein	267	complement(76201..77001)	2_GENE_64
11068	**64**	**CGL2_11068064**	Conserved protein of unknown function	142	complement(75773..76198)	2_GENE_63
11068	**63**	**CGL2_11068063**	Putative two component transcriptional regulator, wi	231	complement(75078..75770)	2_GENE_62
11068	**62**	**CGL2_11068062**	Putative multi-sensor signal transduction histidine ki	453	complement(73706..75064)	2_GENE_61
11068	**61**	**CGL2_11068061**	UDP-glucose 4-epimerase (EC 5.1.3.2)	323	72739..73707	2_GENE_60

11068	**60**	**CGL2_11068060**	Apurinic endonuclease (APN1) (EC 3.1.21.2)	318	complement(71466..72419)	2_GENE_59
11068	**59**	**CGL2_11068059**	Probable ABC transporter, permease	251	complement(70688..71440)	2_GENE_58
11068	**58**	**CGL2_11068058**	ABC transporter, ATP-binding protein (EC 3.6.3.25)	240	complement(69969..70688)	2_GENE_57
11068	**57**	**CGL2_11068057**	Conserved protein of unknown function	325	complement(68948..69922)	2_GENE_56
11068	**56**	**CGL2_11068056**	Putative metallophosphoesterase	385	complement(67767..68921)	2_GENE_55
11068	**55**	**CGL2_11068055**	Protein of unknown function	226	66933..67610	2_GENE_54
11068	**54**	**CGL2_11068054**	Diguanylate cyclase/phosphodiesterase with PAS/PA	1139	63393..66809	2_GENE_53
11068	**53**	**CGL2_11068053**	4-hydroxythreonine-4-phosphate dehydrogenase (E	344	61971..63002	2_GENE_52
11068	**52**	**CGL2_11068052**	Cation efflux system protein	302	61091..61996	2_GENE_51
11068	**51**	**CGL2_11068051**	Excinuclease ABC, A subunit (UvrA)	935	58287..61091	2_GENE_50
11068	**50**	**CGL2_11068050**	Probable outer membrane lipoprotein carrier protein	238	57571..58284	2_GENE_49
11068	**49**	**CGL2_11068049**	Putative cell division protein (FtsK)	758	55308..57581	2_GENE_48
11068	**48**	**CGL2_11068048**	Metallo-beta-lactamase family protein	562	53608..55293	2_GENE_47
11068	**47**	**CGL2_11068047**	Putative dimethyladenosine transferase	256	52841..53608	2_GENE_46
11068	**46**	**CGL2_11068046**	Putative TonB protein	367	complement(51509..52609)	2_GENE_45
11068	**45**	**CGL2_11068045**	Putative lytic transglycosylase	686	complement(49462..51519)	2_GENE_44
11068	**44**	**CGL2_11068044**	Protein of unknown function	91	complement(49181..49453)	2_GENE_43
11068	**43**	**CGL2_11068043**	Protein of unknown function	111	complement(48865..49197)	2_GENE_42
11068	**42**	**CGL2_11068042**	Probable ATPase, AAA family	444	complement(47299..48630)	2_GENE_41
11068	**41**	**CGL2_11068041**	Metal dependent phosphohydrolase	521	complement(45531..47093)	2_GENE_40
11068	**40**	**CGL2_11068040**	Conserved protein of unknown function	284	complement(44696..45547)	2_GENE_39
11068	**39**	**CGL2_11068039**	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6	503	complement(43181..44689)	2_GENE_38
11068	**38**	**CGL2_11068038**	Exodeoxyribonuclease VII small subunit	97	complement(42885..43175)	2_GENE_37
11068	**37**	**CGL2_11068037**	Geranyltranstransferase (EC 2.5.1.10)	303	complement(41932..42840)	2_GENE_36
11068	**36**	**CGL2_11068036**	Deoxyxylulose-5-phosphate synthase (EC 2.2.1.7)	630	complement(40040..41929)	2_GENE_35
11068	**35**	**CGL2_11068035**	Hemolysin A	251	complement(39265..40017)	2_GENE_34
11068	**34**	**CGL2_11068034**	DTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	313	complement(38317..39255)	2_GENE_33
11068	**33**	**CGL2_11068033**	Putative divalent-cation tolerance protein (CutA)	113	complement(37979..38317)	2_GENE_32
11068	**32**	**CGL2_11068032**	Putative peptidase, M23B family	316	complement(37032..37979)	2_GENE_31
11068	**31**	**CGL2_11068031**	Preprotein translocase SecA subunit	908	complement(34290..37013)	2_GENE_30
11068	**30**	**CGL2_11068030**	Putative NADH dehydrogenase (ubiquinone), subunit	123	complement(33727..34095)	2_GENE_29
11068	**29**	**CGL2_11068029**	NADH dehydrogenase (ubiquinone), B subunit (EC 1.	178	complement(33200..33733)	2_GENE_28
11068	**28**	**CGL2_11068028**	NADH dehydrogenase (quinone), chain C (EC 1.6.99	184	complement(32639..33190)	2_GENE_27
11068	**27**	**CGL2_11068027**	NADH dehydrogenase (ubiquinone), D subunit (EC 1	423	complement(31307..32575)	2_GENE_26
11068	**26**	**CGL2_11068026**	Putative NADH dehydrogenase (ubiquinone), E subur	168	complement(30653..31156)	2_GENE_25
11068	**25**	**CGL2_11068025**	NADH dehydrogenase (quinone) (EC 1.6.99.5)	617	complement(28689..30539)	2_GENE_24
11068	**24**	**CGL2_11068024**	NADH dehydrogenase (quinone), chain G (EC 1.6.99	903	complement(25957..28665)	2_GENE_23
11068	**23**	**CGL2_11068023**	NADH dehydrogenase (ubiquinone), H subunit	337	complement(24865..25875)	2_GENE_22
11068	**22**	**CGL2_11068022**	NADH dehydrogenase, chain I (EC 1.6.99.3)	186	complement(24279..24836)	2_GENE_21
11068	**21**	**CGL2_11068021**	Putative NADH dehydrogenase (ubiquinone), chain J	169	complement(23761..24267)	2_GENE_20
11068	**20**	**CGL2_11068020**	Putative NADH dehydrogenase (ubiquinone), chain 4	100	complement(23399..23698)	2_GENE_19

11068	**19**	**CGL2_11068019**	NADH dehydrogenase (quinone), chain L (EC 1.6.99.	639	complement(21455..23371)	2_GENE_18
11068	**18**	**CGL2_11068018**	NADH dehydrogenase (quinone), chain M (EC 1.6.99	500	complement(19910..21409)	2_GENE_17
11068	**17**	**CGL2_11068017**	NADH dehydrogenase (quinone), chain N (EC 1.6.99	481	complement(18424..19866)	2_GENE_16
11068	**16**	**CGL2_11068016**	LexA repressor (EC 3.4.21.88)	222	complement(17729..18394)	2_GENE_15
11068	**15**	**CGL2_11068015**	Conserved protein of unknown function	156	complement(17268..17735)	2_GENE_14
11068	**14**	**CGL2_11068014**	Ammonium transporter	505	complement(15508..17022)	2_GENE_13
11068	**13**	**CGL2_11068013**	Putative nitrogen regulatory protein P-II	112	complement(15173..15508)	2_GENE_12
11068	**12**	**CGL2_11068012**	Putative helicase, Snf2 family	1049	complement(11956..15102)	2_GENE_11
11068	**11**	**CGL2_11068011**	Probable proline dehydrogenase	270	complement(11116..11925)	2_GENE_10
11068	**10**	**CGL2_11068010**	Conserved protein of unknown function	80	10838..11077	2_GENE_9
11068	**9**	**CGL2_11068009**	Transposase	479	complement(9122..10558)	2_GENE_8
11068	**8**	**CGL2_11068008**	Hypothetical protein	157	complement(8533..9003)	2_GENE_7
11068	**7**	**CGL2_11068007**	Diguanylate cyclase/phosphodiesterase with PAS/PA	1035	5408..8512	2_GENE_6
11068	**5**	**CGL2_11068005**	Conserved protein of unknown function	346	4239..5276	2_GENE_5
11068	**4**	**CGL2_11068004**	Protein of unknown function	215	3508..4152	2_GENE_4
11068	**3**	**CGL2_11068003**	Conserved hypothetical protein	499	1968..3464	2_GENE_3
11068	**2**	**CGL2_11068002**	Putative TPR domain containing protein	125	1594..1968	2_GENE_2
11068	**1**	**CGL2_11068001**	Diguanylate cyclase	393	complement(266..1444)	2_GENE_1
10822	**1**	**CGL2_10822001**	Putative TPR domain containing protein	204	complement(826..1437)	186_GENE_13
10822	**2**	**CGL2_10822002**	Putative general secretion pathway protein K	346	complement(1542..2579)	186_GENE_11
10822	**3**	**CGL2_10822003**	Hypothetical protein	196	complement(2557..3144)	186_GENE_10
10822	**4**	**CGL2_10822004**	Protein of unknown function	452	complement(3140..4495)	186_GENE_9
10822	**5**	**CGL2_10822005**	Protein of unknown function	290	complement(4506..5375)	186_GENE_8
10822	**6**	**CGL2_10822006**	General secretion pathway protein G	159	complement(5553..6029)	186_GENE_7
10822	**7**	**CGL2_10822007**	Putative general secretion pathway protein F	400	complement(6067..7266)	186_GENE_6
10822	**8**	**CGL2_10822008**	General secretion pathway protein E	571	complement(7290..9002)	186_GENE_5
10822	**9**	**CGL2_10822009**	Putative general secretion pathway protein D	555	complement(9010..10674)	186_GENE_4
10822	**10**	**CGL2_10822010**	Probable general secretion pathway protein C	323	complement(10674..11642)	186_GENE_3
10822	**11**	**CGL2_10822011**	Thiamine biosynthesis protein (ThiS)	70	11796..12005	186_GENE_2
10822tRNA		**CGL2_10822R001**	TRNA Gly CCC		12087..12161	
10822	**14**	**CGL2_10822014**	Hypothetical protein	97	complement(12331..12621)	710_GENE_6
10822	**17**	**CGL2_10822017**	replication protein A	455	12952..14316	710_GENE_3
10822	**18**	**CGL2_10822018**	replication protein C	335	14270..15274	710_GENE_2
10822	**19**	**CGL2_10822019**	Hypothetical protein	44	15252..15383	710_GENE_1
8970	**2**	**CGL2_08970002**	Probable cytochrome C, class I	269	1992..2798	46_GENE_28
8970	**1**	**CGL2_08970001**	Probable cytochrome C, class I	269	1118..1924	46_GENE_27
11238	**109**	**CGL2_11238109**	Probable cytochrome C, class I	225	118679..119353	46_GENE_26
11238	**108**	**CGL2_11238108**	Diguanylate cyclase/phosphodiesterase with GAF ser	988	115484..118447	46_GENE_25
11238	**107**	**CGL2_11238107**	Conserved hypothetical protein	173	complement(114772..115290)	46_GENE_24
11238	**106**	**CGL2_11238106**	Probable phytoene dehydrogenase	496	113294..114781	46_GENE_23
11238	**105**	**CGL2_11238105**	Hypothetical protein	351	112205..113257	46_GENE_22

11238	**104**	**CGL2_11238104**	Protein of unknown function	556	110490..112157	46_GENE_21
11238	**103**	**CGL2_11238103**	Probable cellulose synthase subunit C	335	109270..110274	46_GENE_20
11238	**102**	**CGL2_11238102**	Probable cellulose synthase regulatory subunit	755	107006..109270	46_GENE_19
11238	**101**	**CGL2_11238101**	Cellulose synthase catalytic subunit (UDP-forming) (I	714	104865..107006	46_GENE_18
11238	**100**	**CGL2_11238100**	Putative cytochrome C, class I	223	complement(103674..104342)	46_GENE_17
11238	**99**	**CGL2_11238099**	Putative cytochrome C, class I	272	complement(102794..103609)	46_GENE_16
11238	**98**	**CGL2_11238098**	DNA polymerase family B	736	100584..102791	46_GENE_15
11238	**97**	**CGL2_11238097**	Conserved hypothetical protein	87	100346..100606	46_GENE_14
11238	**96**	**CGL2_11238096**	Hypothetical protein	179	99807..100343	46_GENE_13
11238	**95**	**CGL2_11238095**	LexA repressor (EC 3.4.21.88)	205	99187..99801	46_GENE_12
11238	**94**	**CGL2_11238094**	Glucose-6-phosphate isomerase (EC 5.3.1.9)	548	97426..99069	46_GENE_11
11238	**93**	**CGL2_11238093**	Conserved protein of unknown function	238	96657..97370	46_GENE_10
11238	**92**	**CGL2_11238092**	Hypothetical protein	125	96254..96628	46_GENE_7a
11238	**91**	**CGL2_11238091**	Putative acriflavin resistance protein	1036	92842..95949	46_GENE_7
11238	**90**	**CGL2_11238090**	Protein of unknown function	211	92089..92721	46_GENE_6
11238	**89**	**CGL2_11238089**	Protein of unknown function	200	91251..91850	46_GENE_5
11238	**88**	**CGL2_11238088**	Protein of unknown function	103	90729..91037	46_GENE_4
11238	**87**	**CGL2_11238087**	Arsenical pump membrane protein	439	89215..90531	46_GENE_3
11238	**86**	**CGL2_11238086**	Putative transcriptional regulator, ArsR family	269	88402..89208	46_GENE_2
11238	**84**	**CGL2_11238084**	transposase	479	86625..88061	297_GENE_3
11238	**83**	**CGL2_11238083**	Protein of unknown function	168	86040..86543	297_GENE_4
11238	**82**	**CGL2_11238082**	Protein of unknown function	231	complement(85079..85771)	297_GENE_5
11238	**81**	**CGL2_11238081**	Putative Kelch domain-containing protein	392	83931..85106	297_GENE_6
11238	**80**	**CGL2_11238080**	Conserved hypothetical protein	125	83020..83394	297_GENE_7
11238	**79**	**CGL2_11238079**	Putative iron permease, FTR1 family	292	82145..83020	297_GENE_8
11238	**78**	**CGL2_11238078**	Putative metallo-beta-lactamase family protein	479	complement(80493..81929)	66_GENE_28
11238	**77**	**CGL2_11238077**	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)	900	complement(77771..80470)	66_GENE_27
11238	**76**	**CGL2_11238076**	Hypothetical protein	209	77156..77782	66_GENE_26
11238	**75**	**CGL2_11238075**	Transcriptional regulator, BadM/Rrf2 family	169	complement(76403..76909)	66_GENE_24
11238	**74**	**CGL2_11238074**	Conserved hypothetical protein	76	complement(76132..76359)	66_GENE_23
11238	**73**	**CGL2_11238073**	Probable oxidoreductase FAD/NAD(P)-binding	248	75285..76028	66_GENE_22
11238	**72**	**CGL2_11238072**	Putative cytochrome c	120	complement(74647..75006)	66_GENE_21
11238	**71**	**CGL2_11238071**	Conserved protein of unknown function	64	complement(74338..74529)	66_GENE_20
11238	**70**	**CGL2_11238070**	Putative flavohemoprotein	133	73794..74192	66_GENE_19
11238	**69**	**CGL2_11238069**	Phosphomannomutase (EC 5.4.2.8)	467	72203..73603	66_GENE_18
11238	**68**	**CGL2_11238068**	Mannose-1-phosphate guanylyltransferase (EC 2.7.7	491	70731..72203	66_GENE_17
11238	**67**	**CGL2_11238067**	Hypothetical protein	90	complement(69993..70262)	66_GENE_15
11238	**66**	**CGL2_11238066**	Protein of unknown function	245	complement(69190..69924)	66_GENE_14
11238	**65**	**CGL2_11238065**	Putative short-chain dehydrogenase	277	68334..69164	66_GENE_13
11238	**64**	**CGL2_11238064**	GTP-binding protein (Era)	312	complement(67283..68218)	66_GENE_12
11238	**63**	**CGL2_11238063**	Recombination protein O (RecO)	246	complement(66530..67267)	66_GENE_11

11238	**62**	**CGL2_11238062**	Hypothetical protein	191	65903..66475	66_GENE_10
11238	**61**	**CGL2_11238061**	Protein of unknown function	332	64620..65615	66_GENE_9
11238	**60**	**CGL2_11238060**	Conserved protein of unknown function	391	complement(63115..64287)	66_GENE_8
11238	**59**	**CGL2_11238059**	GTP-binding protein (TypA)	623	complement(61090..62958)	66_GENE_7
11238	**58**	**CGL2_11238058**	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	218	complement(60423..61076)	66_GENE_6
11238	**57**	**CGL2_11238057**	Putative metallo-beta-lactamase family protein	262	complement(59570..60355)	66_GENE_5
11238	**56**	**CGL2_11238056**	5-methyltetrahydrofolate--homocysteine methyltrans	815	57123..59567	66_GENE_4
11238	**55**	**CGL2_11238055**	Conserved protein of unknown function	282	56278..57123	66_GENE_3
11238	**54**	**CGL2_11238054**	Thiamine biosynthesis protein (ThiC)	468	54838..56241	134_GENE_2
11238	**53**	**CGL2_11238053**	Probable ATP-dependent Clp protease	1026	51541..54618	134_GENE_3
11238	**52**	**CGL2_11238052**	Excinuclease ABC, C subunit (UvrC)	632	49646..51541	134_GENE_4
11238	**51**	**CGL2_11238051**	Hypothetical protein	84	complement(49298..49549)	134_GENE_5
11238	**50**	**CGL2_11238050**	Shikimate 5-dehydrogenase (EC 1.1.1.25)	290	complement(48387..49256)	134_GENE_6
11238	**49**	**CGL2_11238049**	Cell division protein (FtsY)	309	47434..48360	134_GENE_7
11238	**48**	**CGL2_11238048**	Conserved protein of unknown function	169	46893..47399	134_GENE_8
11238	**47**	**CGL2_11238047**	Metal dependent phosphohydrolase	501	45398..46900	134_GENE_9
11238	**46**	**CGL2_11238046**	Putative phosphate starvation-inducible protein (Pho	331	44374..45366	134_GENE_10
11238	**45**	**CGL2_11238045**	Probable universal stress protein (UspA)	178	43838..44371	134_GENE_11
11238	**44**	**CGL2_11238044**	Putative type IV prepilin peptidase	263	42887..43675	410_GENE_2
11238	**43**	**CGL2_11238043**	Protein of unknown function	105	42412..42726	410_GENE_3
11238	**42**	**CGL2_11238042**	Putative polyphosphate kinase (PPK2)	275	41539..42363	410_GENE_4
11238	**41**	**CGL2_11238041**	Probable oxidoreductase	254	40731..41492	410_GENE_5
11238tRNA		**CGL2_11238R001**	TRNA Thr TGT		complement(40186..40261)	
11238	**40**	**CGL2_11238040**	Putative response regulator receiver protein	326	complement(38975..39952)	410_GENE_6
11238	**39**	**CGL2_11238039**	Conserved protein of unknown function	200	complement(38170..38769)	410_GENE_7
11238	**38**	**CGL2_11238038**	Protein of unknown function	74	complement(37914..38135)	410_GENE_8
11238	**37**	**CGL2_11238037**	Conserved protein of unknown function	167	complement(37308..37808)	467_GENE_5a
11238	**36**	**CGL2_11238036**	Transcription termination factor (NusA)	452	complement(35915..37270)	467_GENE_5
11238	**35**	**CGL2_11238035**	Translation initiation factor IF-2	874	complement(33257..35878)	467_GENE_4
11238	**34**	**CGL2_11238034**	Conserved protein of unknown function	99	complement(32938..33234)	467_GENE_3
11238	**33**	**CGL2_11238033**	Probable ribosome-binding factor A	131	complement(32543..32935)	467_GENE_2
11238	**32**	**CGL2_11238032**	TRNA pseudouridine synthase B (EC 4.2.1.70)	325	complement(31569..32543)	467_GENE_1
11238	**31**	**CGL2_11238031**	Ribosomal protein S15	89	complement(31242..31508)	71_GENE_25
11238	**30**	**CGL2_11238030**	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8	713	complement(28969..31107)	71_GENE_24
11238	**29**	**CGL2_11238029**	Hypothetical protein	39	complement(28811..28927)	71_GENE_23
11238	**28**	**CGL2_11238028**	Processing peptidase (EC 3.4.24.64)	411	complement(27357..28589)	71_GENE_22
11238	**27**	**CGL2_11238027**	Putative pyridoxal phosphate biosynthesis protein	255	complement(26593..27357)	71_GENE_21
11238	**26**	**CGL2_11238026**	Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7)	133	complement(26195..26593)	71_GENE_20
11238	**25**	**CGL2_11238025**	Carbohydrate kinase family protein	518	complement(24642..26195)	71_GENE_19
11238	**24**	**CGL2_11238024**	Uracil-DNA glycosylase, family 4	245	complement(23835..24569)	71_GENE_18
11238	**23**	**CGL2_11238023**	Hypothetical protein	85	complement(23581..23835)	71_GENE_17

11238	**22**	**CGL2_11238022**	DNA mismatch repair protein (MutS)	843	complement(21057..23585)	71_GENE_16
11238	**21**	**CGL2_11238021**	Protein of unknown function	381	complement(19796..20938)	71_GENE_15
11238	**20**	**CGL2_11238020**	Protein of unknown function	390	complement(18605..19774)	71_GENE_14
11238	**19**	**CGL2_11238019**	Enoyl-(Acyl-carrier-protein) reductase (EC 1.3.1.9)	265	complement(17770..18564)	71_GENE_13
11238	**18**	**CGL2_11238018**	Probable rieske iron-sulfur family protein	309	complement(16788..17714)	71_GENE_12
11238	**17**	**CGL2_11238017**	Putative cytochrome b/b6, N-terminal	459	complement(15390..16766)	71_GENE_11
11238	**16**	**CGL2_11238016**	Probable thioredoxin	83	15106..15354	71_GENE_10
11238	**15**	**CGL2_11238015**	Hypothetical protein	62	complement(14770..14955)	71_GENE_8a
11238	**14**	**CGL2_11238014**	Endoribonuclease L-PSP	128	complement(14394..14777)	71_GENE_8
11238	**13**	**CGL2_11238013**	Ribosomal protein L28	63	14158..14346	71_GENE_7a
11238	**12**	**CGL2_11238012**	Putative ATP-dependent DNA helicase (RecG)	713	complement(11869..14007)	71_GENE_7
11238	**11**	**CGL2_11238011**	Protein of unknown function	119	complement(11528..11884)	71_GENE_6
11238	**10**	**CGL2_11238010**	Ppx/GppA phosphatase (EC 3.6.1.11)	315	complement(10578..11522)	71_GENE_5
11238	**9**	**CGL2_11238009**	Protein of unknown function	587	8839..10599	71_GENE_4
11238	**8**	**CGL2_11238008**	Putative polyA polymerase family protein	419	complement(7472..8728)	71_GENE_3
11238	**7**	**CGL2_11238007**	Protein of unknown function	166	6882..7379	71_GENE_2
11238	**6**	**CGL2_11238006**	Putative acriflavin resistance protein	1027	complement(3665..6745)	428_GENE_7
11238	**5**	**CGL2_11238005**	Protein of unknown function	206	complement(2986..3603)	428_GENE_6
11238	**4**	**CGL2_11238004**	Putative ferric uptake regulator, Fur family	146	complement(2468..2905)	428_GENE_5
11238	**3**	**CGL2_11238003**	Protein of unknown function	154	complement(1923..2384)	428_GENE_3
11238	**2**	**CGL2_11238002**	Conserved protein of unknown function	261	1114..1896	428_GENE_2
11238	**1**	**CGL2_11238001**	Protein of unknown function	305	186..1100	428_GENE_1
10665	**1**	**CGL2_10665001**	Ribosomal protein S1	591	23..1795	274_GENE_1
10665	**2**	**CGL2_10665002**	Peptidase S49 (SppA)	295	1859..2743	274_GENE_2
10665	**3**	**CGL2_10665003**	Putative integration host factor, beta-subunit	98	2772..3065	274_GENE_2a
10665	**4**	**CGL2_10665004**	Signal recognition particle protein	444	3068..4399	274_GENE_3
10665	**5**	**CGL2_10665005**	Ribosomal protein S16	81	4448..4690	274_GENE_4
10665	**6**	**CGL2_10665006**	Conserved protein of unknown function	76	4741..4968	274_GENE_5
10665	**7**	**CGL2_10665007**	Hypothetical protein	108	5199..5522	274_GENE_5a
10665	**8**	**CGL2_10665008**	tRNA (guanine-N(1)-)-methyltransferase (EC 2.1.1.3	241	5495..6217	274_GENE_6
10665	**9**	**CGL2_10665009**	Ribosomal protein L19	118	6286..6639	274_GENE_7
10665	**10**	**CGL2_10665010**	Ribonuclease HII (EC 3.1.26.4)	228	6656..7339	274_GENE_8
10665	**11**	**CGL2_10665011**	Hypothetical protein	301	7352..8254	274_GENE_9
10665	**12**	**CGL2_10665012**	Putative peptidase M23B family protein	398	8227..9420	274_GENE_10
10776	**10**	**CGL2_10776010**	Chaperonin GroEL	204	complement(11391..12002)	
10776	**9**	**CGL2_10776009**	Thioredoxin	110	complement(10919..11248)	222_GENE_9
10776	**8**	**CGL2_10776008**	Putative DNA repair protein (RecN)	564	complement(9089..10780)	222_GENE_7
10776	**7**	**CGL2_10776007**	Conserved protein of unknown function	915	6268..9012	222_GENE_6
10776	**6**	**CGL2_10776006**	Arginine decarboxylase (EC 4.1.1.19)	489	4753..6219	222_GENE_5
10776	**5**	**CGL2_10776005**	Spermidine synthase (EC 2.5.1.16)	306	3821..4738	222_GENE_4

10776	**4**	**CGL2_10776004**	Putative S-adenosylmethionine decarboxylase	154	3391..3852	222_GENE_3
10776	**3**	**CGL2_10776003**	Diguanylate cyclase	740	830..3049	222_GENE_2
10776	**2**	**CGL2_10776002**	Protein of unknown function	183	81..629	222_GENE_1
10933	**1**	**CGL2_10933001**	Protein of unknown function	247	456..1196	44_GENE_1
10933	**2**	**CGL2_10933002**	Putative phosphatidylglycerophosphatase A	180	1186..1725	44_GENE_2
10933	**3**	**CGL2_10933003**	RecA protein	360	1837..2916	44_GENE_3
10933	**4**	**CGL2_10933004**	Alanyl-tRNA synthetase (EC 6.1.1.7)	891	3000..5672	44_GENE_4
10933	**5**	**CGL2_10933005**	Protein of unknown function	94	5672..5953	44_GENE_5
10933	**6**	**CGL2_10933006**	Putative holliday junction resolvase YqgF	171	5973..6485	44_GENE_6
10933	**7**	**CGL2_10933007**	Aminodeoxychorismate lyase	341	6517..7539	44_GENE_7
10933	**8**	**CGL2_10933008**	Valyl-tRNA synthetase (EC 6.1.1.9)	904	7571..10282	44_GENE_8
10933	**9**	**CGL2_10933009**	Nicotinate-nucleotide pyrophosphorylase (EC 2.4.2.1	292	10282..11157	44_GENE_9
10933	**10**	**CGL2_10933010**	Biotin--acetyl-CoA-carboxylase ligase	255	11157..11921	44_GENE_10
10933	**11**	**CGL2_10933011**	Transcriptional acitvator, Baf family	259	11921..12697	44_GENE_11
10933	**12**	**CGL2_10933012**	Hypothetical protein	60	complement(12739..12918)	44_GENE_12
10933	**13**	**CGL2_10933013**	Diguanylate cyclase/phosphodiesterase with PAS/PAC	1449	complement(12985..17331)	44_GENE_13
10933	**13**	**CGL2_10933013**	PAS/PAC sensor protein	1449	complement(12985..17331)	44_GENE_13
10933	**15**	**CGL2_10933015**	check gene	91	complement(18072..18344)	44_GENE_14
10933	**16**	**CGL2_10933016**	Probable secretion protein (HlyD)	329	18642..19628	44_GENE_15
10933	**17**	**CGL2_10933017**	Putative outer membrane efflux protein	417	19748..20998	44_GENE_16
10933	**18**	**CGL2_10933018**	Malate dehydrogenase (EC 1.1.1.27)	320	21209..22168	44_GENE_17
10933	**19**	**CGL2_10933019**	Protein of unknown function	195	22249..22833	44_GENE_18
10933	**20**	**CGL2_10933020**	Protein of unknown function	209	22826..23452	44_GENE_19
10933	**21**	**CGL2_10933021**	ABC transporter, ATP-binding protein (EC 3.6.3.25)	248	23460..24203	44_GENE_20
10933	**22**	**CGL2_10933022**	RNA polymerase, sigma 54 subunit, RpoN	486	24203..25660	44_GENE_21
10933	**23**	**CGL2_10933023**	Sigma 54 modulation protein/ribosomal protein S30E	176	25707..26234	44_GENE_22
10933	**24**	**CGL2_10933024**	Putative P-loop ATPase protein family	288	26262..27125	44_GENE_23
10933	**25**	**CGL2_10933025**	Protein of unknown function	195	27128..27712	44_GENE_24
10933	**26**	**CGL2_10933026**	Chorismate synthase (EC 4.2.3.5)	401	27752..28954	44_GENE_25
10933	**27**	**CGL2_10933027**	Shikimate kinase (EC 2.7.1.71)	183	28947..29495	44_GENE_26
10933	**28**	**CGL2_10933028**	3-dehydroquinate synthetase (EC 4.2.3.4)	364	29535..30626	44_GENE_27
10933	**29**	**CGL2_10933029**	Putative GAF sensor protein	421	30658..31920	44_GENE_28
10933	**30**	**CGL2_10933030**	Hypothetical protein	123	31966..32334	44_GENE_29
10933	**31**	**CGL2_10933031**	Conserved protein of unknown function	260	32340..33119	44_GENE_30
10933	**32**	**CGL2_10933032**	Probable acetyltransferase	134	33160..33561	44_GENE_31
10933	**33**	**CGL2_10933033**	Putative GTP cyclohydrolase I	149	complement(33626..34072)	44_GENE_32
10933	**34**	**CGL2_10933034**	transposase	173	34165..34683	44_GENE_33
10933tRNA		**CGL2_10933R001**	TRNA Val TAC		complement(34822..34897)	
10933	**35**	**CGL2_10933035**	4-hydroxybenzoyl-CoA thioesterase	148	complement(34891..35334)	44_GENE_34
10933tRNA		**CGL2_10933R002**	TRNA Asp GTC		35492..35568	
10933	**36**	**CGL2_10933036**	Putative MotA/TolQ/ExbB proton channel	223	35891..36559	96_GENE_3

10933	**37**	**CGL2_10933037**	Putative biopolymer transport protein ExbD/TolR	148	36550..36993	96_GENE_4
10933	**38**	**CGL2_10933038**	Probable TonB family protein	278	37003..37836	96_GENE_5
10933	**39**	**CGL2_10933039**	Putative TolB protein	447	37829..39169	96_GENE_6
10933	**40**	**CGL2_10933040**	Putative TPR-domain containing protein	274	39214..40035	96_GENE_7
10933	**41**	**CGL2_10933041**	DNA mismatch repair protein MutL	634	40102..42003	96_GENE_8
10933	**42**	**CGL2_10933042**	tRNA delta(2)-isopentenylpyrophosphate transferase	294	41988..42869	96_GENE_9
10933	**43**	**CGL2_10933043**	Methylthioadenosine phosphorylase (EC 2.4.2.28)	300	43012..43911	96_GENE_10
10933	**44**	**CGL2_10933044**	Putative carbohydrate kinase, PfkB family	313	43940..44878	96_GENE_11
10933	**45**	**CGL2_10933045**	Putative TPR-domain containing protein	254	44890..45651	96_GENE_12
10933	**46**	**CGL2_10933046**	Conserved protein of unknown function	335	45707..46711	96_GENE_13
10933	**47**	**CGL2_10933047**	Protein of unknown function	335	46757..47761	96_GENE_14
10933tRNA		**CGL2_10933R003**	TRNA Thr CGT		47852..47926	
10933	**48**	**CGL2_10933048**	Hypothetical protein	412	complement(47999..49234)	96_GENE_15
		Strain variant path	**Strain variant path**			**Strain variant path**
11276	**210**	**CGL2_11276210**	Probable Holliday junction resolvase	450	complement(229981..231330)	96_GENE_16
11276	**210a**	**CGL2_11276210a**	Hypothetical protein	115	complement(229625..229969)	
11276	**209a**	**CGL2_11276209a**	Hypothetical protein	126	complement(229169..229546)	
11276	**209**	**CGL2_11276209**	Hypothetical protein	89	complement(228885..229151)	
11276	**208**	**CGL2_11276208**	Hypothetical protein	242	complement(228142..228867)	
11276	**207**	**CGL2_11276207**	Hypothetical protein	220	complement(227480..228139)	
		Strain variant path	**Strain variant path**			**Strain variant path**
11276	**206**	**CGL2_11276206**	Conjugal transfer protein, TraA	976	complement(224503..227430)	81_GENE_26
11276	**205**	**CGL2_11276205**	Hypothetical protein	134	223999..224400	81_GENE_25
11276	**204**	**CGL2_11276204**	Hypothetical protein	129	223451..223837	81_GENE_24
11276	**203**	**CGL2_11276203**	Hypothetical protein	132	222865..223260	81_GENE_22
11276	**202**	**CGL2_11276202**	Putative heavy metal efflux protein, CzcA	1060	219665..222844	81_GENE_21
11276	**201**	**CGL2_11276201**	Putative heavy metal efflux protein, CzcB	419	218409..219665	81_GENE_20
11276	**200**	**CGL2_11276200**	Putative heavy metal efflux protein, CzcC	408	217193..218416	81_GENE_19
11276	**199**	**CGL2_11276199**	Hypothetical protein	67	216013..216213	81_GENE_17
11276	**198**	**CGL2_11276198**	Hypothetical protein	103	215717..216025	81_GENE_16
11276	**197**	**CGL2_11276197**	Putative integrase	388	214554..215717	
10580	**1**	**CGL2_10580001**	Conserved protein of unknown function	106	423..740	527_GENE_7
10580	**2**	**CGL2_10580002**	Conserved protein of unknown function	129	complement(746..1132)	527_GENE_6
10580	**3**	**CGL2_10580003**	Hypothetical protein	67	1101..1301	527_GENE_5a
10580	**4**	**CGL2_10580004**	Hypothetical protein	81	complement(1295..1537)	527_GENE_4a
10580	**5**	**CGL2_10580005**	Putative phage integrase	345	complement(1555..2589)	527_GENE_4
10580	**6**	**CGL2_10580006**	transposase	346	3050..4087	527_GENE_3
10580	**7**	**CGL2_10580007**	integrase fragment, INT 22C	474	4580..6001	527_GENE_2
11276	**196**	**CGL2_11276196**	Conserved protein of unknown function	322	complement(213327..214292)	6_GENE_66

11276	**195**	**CGL2_11276195**	Hypothetical protein	49	complement(213095..213241)	6_GENE_65
11276	**194**	**CGL2_11276194**	Putative peptidase, M23B family	332	complement(211567..212562)	6_GENE_64
11276	**193**	**CGL2_11276193**	Putative ATP-dependent Clp protease, ATPase subun	813	complement(208771..211209)	6_GENE_62
11276	**192**	**CGL2_11276192**	O-sialoglycoprotein endopeptidase (EC 3.4.24.57)	345	complement(207711..208745)	6_GENE_61
11276	**191**	**CGL2_11276191**	Arginyl-tRNA synthetase (EC 6.1.1.19)	595	complement(205810..207594)	6_GENE_60
11276	**190**	**CGL2_11276190**	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)	378	complement(204672..205805)	6_GENE_59
11276	**189**	**CGL2_11276189**	Preprotein translocase, YajC subunit	96	complement(204385..204672)	6_GENE_58
11276	**188**	**CGL2_11276188**	SecD export membrane protein	524	complement(202762..204333)	6_GENE_57
11276	**187**	**CGL2_11276187**	SecF export membrane protein	321	complement(201742..202704)	6_GENE_56
11276	**186**	**CGL2_11276186**	Hypothetical protein	37	complement(201613..201723)	6_GENE_55
11276	**185**	**CGL2_11276185**	Putative RecJ exonuclease	549	complement(199953..201599)	6_GENE_54
11276	**184**	**CGL2_11276184**	GTP pyrophosphokinase (EC 2.7.6.5)	762	complement(197708..199993)	6_GENE_53
11276	**183**	**CGL2_11276183**	Probable formate dehydrogenase accessory protein	302	complement(196799..197704)	6_GENE_52
11276	**182**	**CGL2_11276182**	Hypothetical protein	83	complement(196515..196763)	6_GENE_51
11276	**181**	**CGL2_11276181**	Putative transcriptional regulator, TetR family	231	complement(195720..196412)	6_GENE_50
11276	**180**	**CGL2_11276180**	Probable cytochrome c-554	200	complement(195121..195720)	6_GENE_49
11276	**179**	**CGL2_11276179**	Putative secretion protein HlyD	317	complement(194171..195121)	6_GENE_48
11276	**178**	**CGL2_11276178**	Drug resistance transporter, EmrB/QacA family	527	complement(192588..194168)	6_GENE_47
11276	**177**	**CGL2_11276177**	Putative outer membrane efflux protein	464	complement(191197..192588)	6_GENE_46
11276	**176**	**CGL2_11276176**	Putative secretion protein HlyD	330	complement(190143..191132)	6_GENE_45
11276	**175**	**CGL2_11276175**	Drug resistance transporter, EmrB/QacA family	540	complement(188514..190133)	6_GENE_44
11276	**174**	**CGL2_11276174**	Heat-inducible transcription repressor HrcA	352	complement(187240..188295)	6_GENE_43
11276	**173**	**CGL2_11276173**	Putative GrpE protein	189	complement(186661..187227)	6_GENE_42
11276	**172**	**CGL2_11276172**	Chaperone DnaK	640	complement(184649..186568)	6_GENE_41
11276	**171**	**CGL2_11276171**	Chaperone DnaJ	372	complement(183376..184491)	6_GENE_40
11276	**170**	**CGL2_11276170**	Conserved protein of unknown function	287	complement(182506..183366)	6_GENE_39
11276	**169**	**CGL2_11276169**	Protein of unknown function	148	complement(182058..182501)	6_GENE_38
11276	**168**	**CGL2_11276168**	Putative thiopurine S-methyltransferase	201	complement(181422..182024)	6_GENE_37
11276	**167**	**CGL2_11276167**	Putative cobalbumin biosynthesis enzyme	179	complement(180872..181408)	6_GENE_36
11276	**166**	**CGL2_11276166**	Nicotinate-nucleotide--dimethylbenzimidazole phospl	363	complement(179724..180812)	6_GENE_35
11276	**165**	**CGL2_11276165**	Putative cobalamin-5-phosphate synthase (CobS)	260	complement(178945..179724)	6_GENE_34
11276	**164**	**CGL2_11276164**	Conserved hypothetical protein	136	178477..178884	6_GENE_33
11276	**163**	**CGL2_11276163**	Conserved hypothetical protein	84	178226..178477	6_GENE_32
11276	**162**	**CGL2_11276162**	Protein of unknown function	128	177856..178239	6_GENE_31
11276	**161**	**CGL2_11276161**	Hypothetical protein	148	177351..177794	6_GENE_30
11276	**160**	**CGL2_11276160**	Hypothetical protein	108	177008..177331	6_GENE_29
11276	**159**	**CGL2_11276159**	Aldo/keto reductase (EC 1.1.1.65)	337	175692..176702	6_GENE_27
11276	**158**	**CGL2_11276158**	Putative phosphoglycerate mutase family protein	222	complement(174799..175464)	6_GENE_26
11276	**157**	**CGL2_11276157**	Cobyrinic acid a,c-diamide synthase (CbiA)	471	complement(173391..174803)	6_GENE_25
11276	**156**	**CGL2_11276156**	Putative precorrin-8X methylmutase (CbiC)	334	complement(172337..173338)	6_GENE_24
11276	**155**	**CGL2_11276155**	Isocitrate dehydrogenase (NAD+) (EC 1.1.1.41)	336	complement(170991..171998)	6_GENE_23

11276	**154**	**CGL2_11276154**	Probable isocitrate dehydrogenase (NADP)	116	complement(170597..170944)	6_GENE_22
11276tRNA		**CGL2_11276R003**	TRNA Phe GAA		170086..170161	
11276	**153**	**CGL2_11276153**	Putative bacterial surface antigen (D15)	781	complement(167449..169791)	6_GENE_20
11276	**152**	**CGL2_11276152**	Putative outer membrane protein (OmpH)	200	complement(166771..167370)	6_GENE_19
11276	**151**	**CGL2_11276151**	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltr	350	complement(165722..166771)	6_GENE_18
11276	**150**	**CGL2_11276150**	Beta-hydroxyacyl-(Acyl-carrier-protein) dehydratase	173	complement(165235..165753)	6_GENE_17
11276	**149**	**CGL2_11276149**	UDP-N-acetylglucosamine acyltransferase (EC 2.3.1.	287	complement(164375..165235)	6_GENE_16
11276	**148**	**CGL2_11276148**	Conserved protein of unknown function	296	complement(163495..164382)	6_GENE_15
11276	**147**	**CGL2_11276147**	Putative oxidoreductase family protein	321	complement(162539..163501)	6_GENE_14
11276	**146**	**CGL2_11276146**	Lipid A disaccharide synthase (LpxB) (EC 2.4.1.182)	405	complement(161314..162528)	6_GENE_13
11276	**145**	**CGL2_11276145**	glycosyltransferase	357	complement(160204..161274)	6_GENE_12
11276	**144**	**CGL2_11276144**	ABC transporter, ATP-binding protein, MsbA family	600	complement(158351..160150)	6_GENE_11
11276	**143**	**CGL2_11276143**	Putative 3-deoxy-D-manno-octulosonic-acid transfer	457	complement(156981..158351)	6_GENE_10
11276	**142**	**CGL2_11276142**	Tetraacyldisaccharide-1-P 4'-kinase (EC 2.7.1.130)	357	complement(155911..156981)	6_GENE_9
11276	**141**	**CGL2_11276141**	Putative lipid A biosynthesis acyltransferase	309	complement(154985..155911)	6_GENE_8
11276	**140**	**CGL2_11276140**	Hypothetical protein	569	complement(153271..154977)	6_GENE_7
11276	**139**	**CGL2_11276139**	Putative heptosyltransferase family protein	402	complement(152075..153280)	6_GENE_6
11276	**138**	**CGL2_11276138**	Putative heptosyltransferase family protein	371	complement(150967..152079)	6_GENE_5
11276	**137**	**CGL2_11276137**	glycosyltransferase	250	complement(150218..150967)	6_GENE_4
11276	**136**	**CGL2_11276136**	Conserved protein of unknown function	283	complement(149331..150179)	6_GENE_3
11276	**135**	**CGL2_11276135**	transposase	330	complement(148342..149331)	68_GENE_28
11276	**134**	**CGL2_11276134**	Conserved hypothetical protein	273	complement(147388..148206)	68_GENE_27
11276	**133**	**CGL2_11276133**	Putative glycosyl transferase, family 2	343	complement(146173..147201)	68_GENE_26
11276	**132**	**CGL2_11276132**	Lipopolysaccharide heptosyltransferase II	332	complement(145060..146055)	68_GENE_25
11276	**131**	**CGL2_11276131**	Histidinol-phosphate phosphatase	199	complement(144460..145056)	68_GENE_24
11276	**130**	**CGL2_11276130**	Conserved protein of unknown function	61	complement(144285..144467)	68_GENE_23
11276	**129**	**CGL2_11276129**	Probable lipopolysaccharide heptosyltransferase II	344	complement(143227..144258)	68_GENE_22
11276	**128**	**CGL2_11276128**	Putative heptosyltransferase family protein	360	complement(142145..143224)	68_GENE_21
11276	**127**	**CGL2_11276127**	Putative polysaccharide deacetylase	240	complement(141426..142145)	68_GENE_20
11276	**126**	**CGL2_11276126**	Putative glycosyl transferase, family 1	389	complement(140238..141404)	68_GENE_19
11276	**125**	**CGL2_11276125**	Protein of unknown function	95	complement(139954..140238)	68_GENE_18
11276	**124**	**CGL2_11276124**	Probable diacylglycerol kinase	255	139173..139937	68_GENE_17
11276	**123**	**CGL2_11276123**	Protein of unknown function	289	138088..138954	68_GENE_16
11276	**122**	**CGL2_11276122**	Adenosylmethionine--8-amino-7-oxononanoate amin	444	136682..138013	68_GENE_15
11276	**121**	**CGL2_11276121**	Conserved protein of unknown function	295	complement(135687..136571)	68_GENE_14
11276	**120**	**CGL2_11276120**	Putative O-antigen polymerase	453	complement(134251..135609)	68_GENE_12
11276	**119**	**CGL2_11276119**	Putative PilT protein-like	351	complement(133199..134251)	68_GENE_11
11276	**118**	**CGL2_11276118**	2-C-methyl-D-erythritol 4-phosphate cytidylyltransfe	426	complement(131922..133199)	68_GENE_10
11276	**117**	**CGL2_11276117**	Serine O-acetyltransferase (EC 2.3.1.30)	234	complement(131211..131912)	68_GENE_9
11276	**116**	**CGL2_11276116**	Putative phosphoesterase, PA-phosphatase related	183	complement(130645..131193)	68_GENE_8
11276	**115**	**CGL2_11276115**	Conserved protein of unknown function	546	complement(129008..130645)	68_GENE_7

11276	114	CGL2_11276114	Putative glycosyl transferase, family 9	403	complement(127800..129008)	68_GENE_6
11276	113	CGL2_11276113	Putative glycosyl transferase	270	complement(126978..127787)	68_GENE_5
11276	112	CGL2_11276112	Probable glycosyl transferase, family 39	504	complement(125467..126978)	68_GENE_4
11276	111	CGL2_11276111	Phosphoribosylaminoimidazolecarboxamide formyltra	522	complement(123827..125392)	68_GENE_3
11276	110	CGL2_11276110	Phosphoribosylglycinamide synthetase (EC 6.3.4.13)	425	complement(122527..123801)	68_GENE_2
11276	108	CGL2_11276108	Putative translation factor (SUA5)	204	complement(121916..122527)	68_GENE_1
11276	107	CGL2_11276107	Protein of unknown function	117	complement(121357..121707)	8_GENE_1
11276	106	CGL2_11276106	Putative methyltransferase	189	complement(120732..121298)	8_GENE_2
11276	105	CGL2_11276105	Phosphopantetheine adenylyltransferase (EC 2.7.7.3	166	complement(120235..120732)	8_GENE_3
11276	104	CGL2_11276104	Aspartate aminotransferase (EC 2.6.1.1)	403	complement(119027..120235)	8_GENE_4
11276	103	CGL2_11276103	Conserved protein of unknown function	112	complement(118581..118916)	8_GENE_6
11276	102	CGL2_11276102	Putative ABC transporter, ATP-binding protein	247	117833..118573	8_GENE_7
11276	101	CGL2_11276101	Lipoprotein releasing system, transmembrane protei	412	116598..117833	8_GENE_8
11276	100	CGL2_11276100	Lysyl-tRNA synthetase (EC 6.1.1.6)	507	115078..116598	8_GENE_9
11276	99	CGL2_11276099	Translation initiation factor, aIF-2BI/5-methylthiorib	350	114012..115061	8_GENE_10
11276	98	CGL2_11276098	Putative glycogen debranching enzyme	680	111910..113949	8_GENE_11
11276	97	CGL2_11276097	Ferrochelatase (EC 4.99.1.1)	356	110825..111892	8_GENE_12
11276	96	CGL2_11276096	Putative permease, YjgP/YjgQ family	362	109726..110811	8_GENE_13
11276	95	CGL2_11276095	Putative permease, YjgP/YjgQ family	378	108593..109726	8_GENE_14
11276	94	CGL2_11276094	TRNA-i(6)A37 modification enzyme (MiaB)	468	107156..108559	8_GENE_15
11276	93	CGL2_11276093	Protein of unknown function	134	106759..107160	8_GENE_16
11276	92	CGL2_11276092	Putative SAM-dependent methyltransferases	191	106214..106786	8_GENE_17
11276	91	CGL2_11276091	Protein of unknown function	208	105494..106117	8_GENE_18
11276	90	CGL2_11276090	Putative cytochrome c, class I	133	complement(104820..105218)	8_GENE_20
11276	89	CGL2_11276089	transposase	446	complement(103323..104660)	8_GENE_21
11276	88	CGL2_11276088	Aspartate aminotransferase (EC 2.6.1.17)	399	complement(101673..102869)	8_GENE_22
11276	87	CGL2_11276087	Protein of unknown function	215	complement(101029..101673)	8_GENE_23
11276	86	CGL2_11276086	Homoserine dehydrogenase (EC 1.1.1.3)	443	complement(99579..100907)	8_GENE_24
11276	85	CGL2_11276085	Threonine synthase (EC 4.2.3.1)	353	complement(98521..99579)	8_GENE_25
11276	84	CGL2_11276084	Probable phosphoglycerate mutase	400	complement(97297..98496)	8_GENE_26
11276	83	CGL2_11276083	Aspartate kinase (EC 2.7.2.4)	412	complement(96068..97303)	8_GENE_27
11276	82	CGL2_11276082	2-isopropylmalate synthase (EC 2.3.3.13)	544	complement(94444..96075)	8_GENE_28
11276	81	CGL2_11276081	Acyl-(Acyl-carrier-protein)--UDP-N-acetylglucosamin	270	complement(93639..94448)	8_GENE_29
11276	80	CGL2_11276080	Putative integration host factor, alpha subunit HimA	98	complement(93318..93611)	8_GENE_30
11276	79	CGL2_11276079	Putative transcriptional regulator, MerR family	113	complement(92878..93216)	8_GENE_31
11276tRNA		CGL2_11276R002	TRNA Pro GGG		complement(92808..92884)	
11276	78	CGL2_11276078	Acid phosphatase (SurE) (EC 3.1.3.2)	266	complement(91906..92703)	8_GENE_32
11276	77	CGL2_11276077	Protein of unknown function	189	complement(91329..91895)	8_GENE_33
11276	76	CGL2_11276076	Cysteinyl-tRNA synthetase, class Ia (EC 6.1.1.16)	490	complement(89870..91339)	8_GENE_34
11276	75	CGL2_11276075	Putative TRNA/rRNA methyltransferase (SpoU)	192	complement(89139..89714)	8_GENE_35
11276	74	CGL2_11276074	Putative thioredoxin family protein	214	complement(88357..88998)	8_GENE_36

11276	**73**	**CGL2_11276073**	NAD+ synthase (EC 6.3.5.1)	592	complement(86582..88357)	8_GENE_37
11276	**72**	**CGL2_11276072**	3,4-dihydroxy-2-butanone 4-phosphate synthase/GT	400	complement(85328..86527)	8_GENE_38
11276	**71**	**CGL2_11276071**	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.9)	161	complement(84822..85304)	8_GENE_39
11276	**70**	**CGL2_11276070**	Transcription antitermination factor (NusB)	168	complement(84319..84822)	8_GENE_40
11276	**69**	**CGL2_11276069**	Protein of unknown function	166	complement(83822..84319)	8_GENE_41
11276	**68**	**CGL2_11276068**	Adenylosuccinate lyase (EC 4.3.2.2)	437	complement(82418..83728)	8_GENE_42
11276	**67**	**CGL2_11276067**	Phosphoribosylaminoimidazole-succinocarboxamide s	239	complement(81644..82360)	8_GENE_43
11276	**66**	**CGL2_11276066**	Phosphoribosylformylglycinamidine synthetase (PurS	98	complement(81364..81657)	8_GENE_43a
11276	**65**	**CGL2_11276065**	Protein of unknown function	446	complement(80024..81361)	8_GENE_45
11276	**64**	**CGL2_11276064**	Putative asparaginase	308	complement(79087..80010)	8_GENE_46
11276	**63**	**CGL2_11276063**	Acetate kinase (EC 2.7.2.1)	374	77809..78930	8_GENE_47
11276	**62**	**CGL2_11276062**	Putative methyltransferase	224	complement(77008..77679)	8_GENE_48
11276	**61**	**CGL2_11276061**	Hypothetical protein	970	74052..76961	8_GENE_49
11276	**60**	**CGL2_11276060**	TonB protein	222	73316..73981	8_GENE_50
11276	**59**	**CGL2_11276059**	TonB system transport protein, ExbD	137	72884..73294	8_GENE_51
11276	**58**	**CGL2_11276058**	biopolymer transport protein, ExbB	230	72116..72805	8_GENE_52
11276	**57**	**CGL2_11276057**	Putative ABC transporter permease protein	372	70783..71898	8_GENE_53
11276	**56**	**CGL2_11276056**	Putative ABC transporter permease protein	378	69650..70783	8_GENE_54
11276	**55**	**CGL2_11276055**	BC transporter ATP-binding protein (EC 3.6.3.25)	592	67875..69650	8_GENE_55
11276	**54**	**CGL2_11276054**	Secretion protein (HlyD)	301	66983..67885	8_GENE_56
11276	**53**	**CGL2_11276053**	Putative outer membrane efflux protein	483	65508..66956	8_GENE_57
11276	**52**	**CGL2_11276052**	Putative cytochrome c, class I	110	65093..65422	8_GENE_58
11276	**51**	**CGL2_11276051**	Fructose-6-phosphate phosphoketolase (EC 4.1.2.22	788	complement(62484..64847)	8_GENE_59
11276	**50**	**CGL2_11276050**	Fructose-bisphosphate aldolase (EC 4.1.2.13)	305	complement(61517..62431)	8_GENE_60
11276	**49**	**CGL2_11276049**	Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	461	complement(60057..61439)	8_GENE_61
11276	**48**	**CGL2_11276048**	Conserved protein of unknown function	304	59095..60006	8_GENE_62
11276	**47**	**CGL2_11276047**	Glycogen phosphorylase (EC 2.4.1.1)	862	56395..58980	8_GENE_63
11276	**46**	**CGL2_11276046**	Phosphoglucomutase, alpha-D-glucose phosphate-sp	547	54729..56369	8_GENE_64
11276	**45**	**CGL2_11276045**	Putative transposase	362	complement(53117..54202)	8_GENE_65
11276	**44**	**CGL2_11276044**	Probable cytochrome c oxidase, subunit I (cbb-type)	460	complement(51308..52687)	8_GENE_66
11276	**43**	**CGL2_11276043**	Putative major facilitator superfamily protein	510	complement(49355..50884)	8_GENE_67
11276	**42**	**CGL2_11276042**	Hypothetical protein	110	48898..49227	8_GENE_68
11276	**41**	**CGL2_11276041**	ABC transporter, ATP-binding protein	555	47215..48879	8_GENE_69
11276	**40**	**CGL2_11276040**	Conserved protein of unknown function	95	complement(46239..46523)	8_GENE_70
11276	**39**	**CGL2_11276039**	Conserved protein of unknown function	132	complement(45752..46147)	141_GENE_2
11276	**38**	**CGL2_11276038**	Putative OmpA family protein	265	complement(44871..45665)	141_GENE_3
11276	**37**	**CGL2_11276037**	Conserved hypothetical protein	227	43720..44400	141_GENE_5
11276	**36**	**CGL2_11276036**	Putative metallophosphoesterase	251	complement(42818..43570)	141_GENE_6
11276	**35**	**CGL2_11276035**	Conserved hypothetical protein	1175	39220..42744	141_GENE_7
11276	**34**	**CGL2_11276034**	DNA repair exonuclease	410	37991..39220	141_GENE_8
11276	**33**	**CGL2_11276033**	Conserved hypothetical protein	195	37000..37584	141_GENE_10

11276	**32**	**CGL2_11276032**	Conserved hypothetical protein	238	36287..37000	141_GENE_11
11276	**31**	**CGL2_11276031**	Conserved hypothetical protein	390	35111..36280	141_GENE_12
11276	**30**	**CGL2_11276030**	Conserved hypothetical protein	571	33372..35084	141_GENE_13
11276	**29**	**CGL2_11276029**	serine protease	326	32301..33278	141_GENE_14
11276	**28**	**CGL2_11276028**	Protein of unknown function	195	31682..32266	69_GENE_29
11276	**27**	**CGL2_11276027**	Hypothetical protein	406	30404..31621	69_GENE_28
11276	**26**	**CGL2_11276026**	Hypothetical protein	217	29711..30361	69_GENE_26
11276	**25**	**CGL2_11276025**	Protein of unknown function	313	complement(28269..29207)	69_GENE_25
11276	**24**	**CGL2_11276024**	Conserved hypothetical protein	176	complement(27599..28126)	69_GENE_24
11276	**23**	**CGL2_11276023**	Conserved hypothetical protein	267	complement(26722..27522)	69_GENE_21
11276	**22**	**CGL2_11276022**	transposase	316	complement(25796..26743)	69_GENE_20
11276	**21**	**CGL2_11276021**	transposase	138	complement(25402..25815)	69_GENE_19
11276	**20**	**CGL2_11276020**	Conserved hypothetical protein	373	complement(24041..25159)	69_GENE_18
11276	**19**	**CGL2_11276019**	Hypothetical protein	120	complement(23424..23783)	69_GENE_17
11276	**18**	**CGL2_11276018**	Conserved hypothetical protein	59	complement(22360..22536)	69_GENE_15
11276	**17**	**CGL2_11276017**	Conserved hypothetical protein	103	21919..22227	69_GENE_14
11276	**16**	**CGL2_11276016**	universal stress protein	287	21011..21871	69_GENE_13
11276	**15**	**CGL2_11276015**	sulfate permease	491	19521..20993	69_GENE_12
11276	**14**	**CGL2_11276014**	Hypothetical protein	217	complement(18013..18663)	69_GENE_11
		Strain variant path	Strain variant path			Strain variant path
11276	**13a**	**CGL2_11276013a**	Probable transposase	130	complement(17227..17616)	
11276tRNA		**CGL2_11276R001**	TRNA Arg CCT		17023..17099	
11276	**13**	**CGL2_11276013**	Hypothetical protein	56	16792..16959	167_GENE_11
11276	**11**	**CGL2_11276011**	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	437	15391..16701	167_GENE_10
11276	**11**	**CGL2_11276011**	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)	437	15391..16701	167_GENE_10
11276	**10**	**CGL2_11276010**	Conserved protein of unknown function	132	complement(14672..15067)	167_GENE_8
11276	**9**	**CGL2_11276009**	Protein of unknown function	714	complement(12502..14643)	167_GENE_7
11276	**8**	**CGL2_11276008**	Putative peptidase M50	243	complement(11699..12427)	167_GENE_6
11276	**7**	**CGL2_11276007**	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	355	complement(10577..11641)	167_GENE_5
11276	**6**	**CGL2_11276006**	Acetyl-coenzyme A carboxylase carboxyl transferase	296	complement(9579..10466)	167_GENE_4
11276	**5**	**CGL2_11276005**	DNA polymerase III, alpha subunit (EC 2.7.7.7)	1201	5955..9557	167_GENE_3
11276	**4**	**CGL2_11276004**	Putative UvrD/REP helicase	649	3953..5899	167_GENE_2
11276	**3**	**CGL2_11276003**	Conserved hypothetical protein	288	complement(2946..3809)	824_GENE_4
11276	**2**	**CGL2_11276002**	Methyl accepting chemotaxis transducer	714	complement(547..2688)	824_GENE_2
11276	**1**	**CGL2_11276001**	probable transposase	128	complement(40..422)	824_GENE_1

Strain variant contigs:

			Strain variant linked to 11277 at ~142,000			
8975	**2**	**CGL2_08975002**	Protein of unknown function	213	complement(1682..2320)	865_GENE_2

8975	**1 (=Va**	**CGL2_08975001**	Protein of unknown function (cyt 572, full on 7508)	409	46..1272	865_GENE_1
cyt572	**A**	**CGL2_11277153A**	Cyt572 variant			
cyt572	**B**	**CGL2_11277153B**	Cyt572 variant			
cyt572	**C**	**CGL2_11277153C**	Cyt572 variant			
cyt572	**D**	**CGL2_11277153D**	Cyt572 variant			
cyt572	**E**	**CGL2_11277153E**	Cyt572 variant			
			Low depth, links via 7252 to 10391 = 11386 at ~16,000			
7252	**1**	**CGL2_07252001**	Hypothetical protein	126	434..811	
7252	**2**	**CGL2_07252002**	Hypothetical protein	110	811..1140	
7252	**3**	**CGL2_07252003**	Hypothetical protein	69	1140..1346	
7252	**4**	**CGL2_07252004**	Hypothetical protein	195	1524..2108	
7252	**5**	**CGL2_07252005**	Hypothetical protein	70	2068..2278	
8492	**1**	**CGL2_08492001**	Protein of unknown function	366	complement(403..1500)	402_GENE_5
9769	**3**	**CGL2_09769003**	DNA primase	1133	complement(1720..5118)	402_GENE_4
9769	**2**	**CGL2_09769002**	ATPase involved in ABC transporters	221	complement(585..1247)	402_GENE_2
9769	**1**	**CGL2_09769001**	Hypothetical protein	165	complement(58..552)	402_GENE_1
			Strain variant linked to 11386-11389			
11389	**59a**	**CGL2_11389059a**	Hypothetical protein	161	61743..62225	
11389	**58a**	**CGL2_11389058a**	Hypothetical protein	239	61019..61735	
11389	**57a**	**CGL2_11389057a**	putative type III restriction-modification system, Res	939	58210..61026	
11389	**56a**	**CGL2_11389056a**	putative type III restriction-modification system, me	856	55640..58207	
11389	**55a**	**CGL2_11389055a**	Hypothetical protein	241	54708..55430	
11389	**54a**	**CGL2_11389054a**	Hypothetical protein	128	54230..54613	
11389	**53a**	**CGL2_11389053a**	Hypothetical protein	674	52196..54217	
11389	**52a**	**CGL2_11389052a**	Hypothetical protein	301	51267..52169	
11389	**51a**	**CGL2_11389051a**	Hypothetical protein	204	50342..50953	
11389	**50a**	**CGL2_11389050a**	Putative integrase	404	49123..50334	
11389	**49**	**CGL2_11389049**	SsrA-binding protein	163	48031..48519	26_GENE_24
11389	**48**	**CGL2_11389048**	Leucyl aminopeptidase (EC 3.4.11.1)	533	46367..47965	26_GENE_25
11389	**47**	**CGL2_11389047**	ExsB protein (succinoglycan synthase?)	241	45526..46248	26_GENE_26
11389	**46**	**CGL2_11389046**	Putative radical activating enzyme	212	44885..45520	26_GENE_27
11389	**45**	**CGL2_11389045**	Protein of unknown function	231	44144..44836	26_GENE_28
11389	**44**	**CGL2_11389044**	DNA gyrase, A subunit	816	41593..44040	26_GENE_29
11389	**43**	**CGL2_11389043**	DNA gyrase, B subunit (EC 5.99.1.3)	818	39081..41534	26_GENE_30
11389	**42**	**CGL2_11389042**	DNA polymerase III, beta chain (EC 2.7.7.7)	387	37847..39007	26_GENE_31
11389	**41**	**CGL2_11389041**	Chromosomal replication initiator protein (DnaA) OR	465	36431..37825	26_GENE_32
			Strain variant linked to 10851 ~20 kb or 11346 ~21 kb			
11185	**1**	**CGL2_11185001**	Probable Bacterial Conjugative Coupling Protein, Trw	128	complement(311..694)	529 GENE 5
11185	**2**	**CGL2_11185002**	Hypothetical protein	258	complement(1186..1959)	490_GENE_1
11185	**3**	**CGL2_11185003**	Hypothetical protein	75	complement(2248..2472)	490_GENE_2
11185	**4**	**CGL2_11185004**	Hypothetical protein	116	complement(2610..2957)	490_GENE_3

11185	**5**	**CGL2_11185005**	Hypothetical protein	112	3294..3629	490_GENE_5
11185	**6**	**CGL2_11185006**	Transposase	326	complement(3801..4778)	490_GENE_6
11185	**7**	**CGL2_11185007**	Hypothetical protein	46	4924..5061	490_GENE_7
11185	**8**	**CGL2_11185008**	Transposase	267	complement(5328..6128)	
11185	**9**	**CGL2_11185009**	Putative DNA helicase	455	complement(6166..7530)	
11185	**10**	**CGL2_11185010**	Hypothetical protein	107	complement(7530..7850)	
			Strain variant linked to 11068 at ~130,000			
9240	**5**	**CGL2_09240005**	Integrase	316	complement(2150..3097)	435_GENE_1
9240	**4**	**CGL2_09240004**	**Hypothetical protein**	69	complement(1944..2150)	435_GENE_2
9240	**3**	**CGL2_09240003**	**Hypothetical protein**	40	complement(1841..1960)	435_GENE_3
9240	**2**	**CGL2_09240002**	**transcriptional activator**	274	complement(527..1348)	435_GENE_4
9240	**1**	**CGL2_09240001**	**transposase**	59	308..484	435_GENE_5
11402	**1**	**CGL2_11402001**	transcriptional activator	97	427..717	435_GENE_6
6010	**2**	**CGL2_06010002**	autoinducer biosynthetic protein/LuxI-type quorum s	234	complement(403..1104)	435_GENE_7
9250	**1**	**CGL2_09250001**	Conserved hypothetical protein	354	935..1996	435_GENE_8
			Strain variant linked to 9240			
10101	**1**	**CGL2_10101001**	transposase	164	complement(24..515)	234_GENE_9
10101	**2**	**CGL2_10101002**	pyoverdine chromophore precursor synthetase	1125	993..4367	234_GENE_8
10101	**3**	**CGL2_10101003**	transposase (single)	248	complement(4394..5137)	234_GENE_7
10065	**6**	**CGL2_10065006**	Hypothetical protein	180	complement(5248..5787)	234_GENE_6
10065	**5**	**CGL2_10065005**	acetolactate synthase, large subunit	587	complement(3286..5046)	234_GENE_5
10065	**4**	**CGL2_10065004**	acetolactate synthase small subunit	183	complement(2738..3286)	234_GENE_4
10065	**3**	**CGL2_10065003**	Conserved hypothetical protein	137	complement(1862..2272)	234_GENE_3
10065	**2**	**CGL2_10065002**	biotin synthesis protein/methyltransferase	228	complement(1179..1862)	234_GENE_2
10065	**1**	**CGL2_10065001**	DNA binding protein	165	complement(602..1096)	234_GENE_1
			Strain variant linked to 10933 end (alternative to link to end of 11276)			
10608	**11**	**CGL2_10608011**	Hypothetical protein	412	12940..14175	96_GENE_15
10608	**10**	**CGL2_10608010**	Probable Holliday junction resolvase	450	complement(11153..12502)	96_GENE_16
10608	**9**	**CGL2_10608009**	Hypothetical protein	79	complement(10900..11136)	96_GENE_17
10608	**8**	**CGL2_10608008**	Protein of unknown function	127	complement(10524..10904)	96_GENE_18
10608	**7**	**CGL2_10608007**	Probable mobilization protein, MobD	242	complement(9786..10511)	96_GENE_19
10608	**6**	**CGL2_10608006**	Hypothetical protein	215	complement(9138..9782)	637_GENE_2
10608	**5**	**CGL2_10608005**	Conjugal transfer protein, TraA	976	complement(6161..9088)	81_GENE_26
10608	**4**	**CGL2_10608004**	Hypothetical protein	135	5654..6058	81_GENE_25
10608	**3**	**CGL2_10608003**	Hypothetical protein	129	5106..5492	81_GENE_24
10608	**2**	**CGL2_10608002**	Hypothetical protein	132	4520..4915	81_GENE_22
10608	**1**	**CGL2_10608001**	Putative heavy metal efflux protein, CzcA	1060	1320..4499	81_GENE_21
			Unclear how linked except for common (divergent) region to 11276/11608			
11216	**30**	**CGL2_11216030**	ABC transporter, ATP-binding protein (EC 3.6.3.25)	138	31763..32176	115_GENE_22
11216	**29**	**CGL2_11216029**	Hypothetical protein	98	31507..31800	115_GENE_21
11216	**28**	**CGL2_11216028**	Putative resolvase	198	30554..31147	115_GENE_20

11216	**27**	**CGL2_11216027**	transposase	451	complement(29065..30417)	115_GENE_19
11216	**26**	**CGL2_11216026**	Hypothetical protein	108	28621..28944	115_GENE_18
11216	**25**	**CGL2_11216025**	Hypothetical protein	104	28121..28432	115_GENE_17
11216	**24**	**CGL2_11216024**	Hypothetical protein	94	27844..28125	115_GENE_16
11216	**23**	**CGL2_11216023**	Hypothetical protein	57	27647..27817	115_GENE_15
11216	**22**	**CGL2_11216022**	GGDEF/EAL domain-containing protein	404	26334..27545	115_GENE_13
11216	**21**	**CGL2_11216021**	Hypothetical protein	385	25087..26241	115_GENE_11
11216	**20**	**CGL2_11216020**	Hypothetical protein	104	complement(24472..24783)	115_GENE_10
11216	**19**	**CGL2_11216019**	DNA primase	1121	complement(21107..24469)	115_GENE_9
11216	**18**	**CGL2_11216018**	Putative transcriptional regulator	102	20592..20897	115_GENE_8
11216	**17**	**CGL2_11216017**	Hypothetical protein	75	20378..20602	115_GENE_7
11216	**16**	**CGL2_11216016**	Hypothetical protein	135	complement(19888..20292)	115_GENE_6
11216	**15a**	**CGL2_11216015a**	Hypothetical protein	189	complement(19280..19846)	
11216	**15**	**CGL2_11216015**	mobilization protein, MobD	253	complement(18550..19308)	115_GENE_4
11216	**14**	**CGL2_11216014**	Hypothetical protein	237	complement(17780..18490)	115_GENE_3
11216	**13a**	**CGL2_11216013a**	Hypothetical protein	85	complement(17202..17456)	
11216	**13**	**CGL2_11216013**	Conjugal transfer protein, TraB	701	complement(15097..17199)	115_GENE_1
11216	**12**	**CGL2_11216012**	Conjugal transfer protein, TraA	976	complement(12167..15094)	81_GENE_26
11216	**11**	**CGL2_11216011**	Hypothetical protein	135	11660..12064	81_GENE_25
11216	**10**	**CGL2_11216010**	Hypothetical protein	129	11112..11498	81_GENE_24
11216	**9**	**CGL2_11216009**	Hypothetical protein	132	10526..10921	81_GENE_22
11216	**8**	**CGL2_11216008**	Putative heavy metal efflux protein, CzcA	1060	7326..10505	81_GENE_21
11216	**7**	**CGL2_11216007**	Putative heavy metal efflux protein, CzcB	419	6070..7326	81_GENE_20
11216	**6**	**CGL2_11216006**	Putative heavy metal efflux protein, CzcC	408	4854..6077	81_GENE_19
11216	**5**	**CGL2_11216005**	Hypothetical protein	67	3674..3874	81_GENE_17
11216	**4**	**CGL2_11216004**	Hypothetical protein	103	3378..3686	81_GENE_16
11216	**3**	**CGL2_11216003**	Recombinase	373	2260..3378	81_GENE_15
11216	**2**	**CGL2_11216002**	Putative integrase	248	complement(1269..2012)	
11216	**1**	**CGL2_11216001**	Hypothetical protein	86	complement(673..930)	
		Strain variant linked loosely internally to 11276 at ~18,000				
10638	**10**	**CGL2_10638010**	Conserved hypothetical protein	168	complement(19400..19903)	69_GENE_10
10638	**9**	**CGL2_10638009**	transposase	242	complement(18602..19327)	69_GENE_9
10638	**8**	**CGL2_10638008**	restriction endonuclease	285	complement(17519..18373)	69_GENE_8
10638	**7**	**CGL2_10638007**	RNA helicase	1717	complement(12316..17466)	69_GENE_7
10638	**6**	**CGL2_10638006**	Hypothetical protein	59	complement(11945..12121)	69_GENE_5
10638	**5**	**CGL2_10638005**	transposase	254	complement(10886..11647)	69_GENE_4
10638	**4**	**CGL2_10638004**	Hypothetical protein	142	complement(10461..10886)	69_GENE_3
10638	**3**	**CGL2_10638003**	Conserved hypothetical protein	67	complement(9940..10140)	69_GENE_2
10638	**2**	**CGL2_10638002**	Superfamily II DNA/RNA helicases	957	complement(7079..9949)	69_GENE_1
10638	**1**	**CGL2_10638001**	Superfamily II DNA/RNA helicases	1309	complement(3153..7079)	

Small, unplaced genome fragments, likely to be *Leptospirillum* group II:

8298	**6**	**CGL3_08298006**	Hypothetical protein	148	complement(2927..3370)	898_GENE_1
8298	**5**	**CGL3_08298005**	mobilization protein, MobC	146	complement(2155..2592)	898_GENE_2
8298	**4**	**CGL3_08298004**	mobilization protein, MobD	220	complement(1468..2127)	898_GENE_3
8298	**3**	**CGL3_08298003**	mobilization protein MobE	207	complement(848..1468)	898_GENE_5
8298	**2**	**CGL3_08298002**	Hypothetical protein	110	complement(516..845)	898_GENE_6
8298	**1**	**CGL3_08298001**	DNA helicase/TrwC	179	complement(29..565)	898_GENE_7
6909	**5**	**CGU_06909005**	Conserved hypothetical protein	106	complement(1386..1703)	888_GENE_5
6909	**4**	**CGU_06909004**	Hypothetical protein	110	complement(1057..1386)	888_GENE_4
6909	**3**	**CGU_06909003**	Hypothetical protein	157	complement(549..1019)	888_GENE_3
6909	**1**	**CGU_06909001**	Hypothetical protein	153	complement(31..488)	
9588	**1**	**CGLU_09588001**	helicase	844	25..2556	830_GENE_5
9588	**2**	**CGLU_09588002**	Protein of unknown function	136	2691..3098	830_GENE_4
9588	**3**	**CGLU_09588003**	Hypothetical protein	164	complement(3290..3781)	830_GENE_3
9588	**4**	**CGLU_09588004**	Conserved hypothetical protein	383	complement(3808..4956)	830_GENE_2
9588	**5**	**CGLU_09588005**	Hypothetical protein	128	complement(4972..5355)	830_GENE_1
9588	**6**	**CGLU_09588006**	Hypothetical protein	120	complement(5349..5708)	
9588	**7**	**CGLU_09588007**	Hypothetical protein	166	complement(5736..6233)	
9144	**1**	**CGLU_09144001**	RNA helicase	294	complement(78..959)	759_GENE_5
9144	**2**	**CGLU_09144002**	Hypothetical protein	399	complement(1003..2199)	759_GENE_4
9144	**3**	**CGLU_09144003**	Hypothetical protein	87	complement(2306..2566)	759_GENE_2
9144	**4**	**CGLU_09144004**	ATP-dependent protease La	381	complement(2566..3708)	759_GENE_1
9074	**7**	**CGLU_09074007**	Hypothetical protein	84	3258..3508	
9074	**6**	**CGLU_09074006**	thiol-disulfide interchange protein, DsbG	328	1996..2979	728_GENE_6
9074	**5**	**CGLU_09074005**	Hypothetical protein	89	1730..1996	728_GENE_5
9074	**4**	**CGLU_09074004**	Hypothetical protein	99	1327..1623	728_GENE_4
9074	**3**	**CGLU_09074003**	Hypothetical protein	67	1055..1255	728_GENE_3
9074	**2**	**CGLU_09074002**	Conserved hypothetical protein	209	396..1022	728_GENE_2
9074	**1**	**CGLU_09074001**	Conserved hypothetical protein	55	248..412	728_GENE_1
9375	**1**	**CGLU_09375001**	Putative phosphoribulokinase	987	246..3206	745_GENE_2
9375	**2**	**CGLU_09375002**	Hypothetical protein	87	complement(3314..3574)	745_GENE_3
9375	**3**	**CGLU_09375003**	Hypothetical protein	477	complement(3613..5043)	745_GENE_4
8925	**1**	**CGL2_08925001**	Probable plasmid stabilization protein, StbA	332	complement(28..1023)	

8925	**2**	**CGL2_08925002**	DotB (type II secretion)	367	complement(1300..2400)	569_GENE_5
8925	**3**	**CGL2_08925003**	TraI	275	complement(2400..3224)	569_GENE_4
8758	**4**	**CGL2_08758001**	sensory box/GGDEF domain/EAL domain protein	346	558..1595	569_GENE_3
8758	**5**	**CGL2_08758002**	Protein of unknown function	235	1901..2605	569_GENE_2
8758	**6**	**CGL2_08758003**	Putative chemotaxis protein MotB	244	2665..3396	569_GENE_1
9428	**4**	**CGLU_09428004**	Hypothetical protein	300	complement(3206..4105)	
9428	**3**	**CGLU_09428003**	Hypothetical protein	126	complement(2568..2945)	
9428	**2**	**CGLU_09428002**	Putative DNA primase	511	complement(1036..2568)	673_GENE_1
9428	**1**	**CGLU_09428001**	Hypothetical protein	231	complement(1..693)	673_GENE_3
8706	**4**	**CGLU_08706004**	Hypothetical protein	66	complement(3127..3324)	673_GENE_4
8706	**3**	**CGLU_08706003**	Hypothetical protein	100	complement(2377..2676)	673_GENE_5
8706	**3**	**CGLU_08706002**	Putative mobilization relaxase, MobA	272	complement(1562..2377)	673_GENE_6
8706	**1**	**CGLU_08706001**	Putative type IV secretory pathway VirD4	449	complement(161..1507)	
9446	**1**	**CGLU_09446001**	Hypothetical protein	151	complement(70..522)	
9446	**2**	**CGLU_09446002**	Conserved hypothetical protein	114	complement(909..1250)	
9446	**3**	**CGLU_09446003**	Putative hydrolase	281	complement(1373..2215)	
9446	**4**	**CGLU_09446004**	Putative SAM-dependent methyltransferase	227	complement(2251..2931)	
9446	**5**	**CGLU_09446005**	Hypothetical protein	111	complement(2990..3322)	
9446	**6**	**CGLU_09446006**	Hypothetical protein	103	complement(3513..3821)	592_GENE_1
9446	**7**	**CGLU_09446007**	Hypothetical protein	110	complement(4005..4334)	592_GENE_2
9446	**8**	**CGLU_09446008**	Putative N-acetyl transferase	144	complement(4429..4860)	592_GENE_3
8858	**4**	**CGLU_08858004**	Hypothetical protein	170	1298..1807	592_GENE_4
8858	**3**	**CGLU_08858003**	Putative hydrolase	95	949..1233	592_GENE_5
8858	**2**	**CGLU_08858002**	Hypothetical protein	54	677..838	592_GENE_6
8858	**1**	**CGLU_08858001**	Putative N-acetyl transferase	162	192..677	592_GENE_7
9713	**5**	**CGL3_09713005**	Conserved hypothetical protein	517	complement(4991..6541)	
9713	**4**	**CGL3_09713004**	Probable DNA primase	302	complement(3611..4516)	
9713	**3**	**CGL3_09713003**	Hypothetical protein	105	complement(2736..3050)	811_GENE_1
9713	**2**	**CGL3_09713002**	Putative mobilization relaxase, MobA	292	complement(1861..2736)	811_GENE_2
9713	**1**	**CGL3_09713001**	Putative Type IV secretion system, VirD4	599	complement(69..1865)	811_GENE_3
9378	**1**	**CGL2_09378001**	Hypothetical protein	398	complement(502..1695)	684_GENE_1
9378	**2**	**CGL2_09378002**	Hypothetical protein	425	complement(1695..2969)	684_GENE_2
9378	**3**	**CGL2_09378003**	Conserved protein of unknown function	238	complement(2969..3682)	684_GENE_3
9378	**4**	**CGL2_09378004**	Conserved protein of unknown function	161	complement(3682..4164)	684_GENE_4
9378	**5**	**CGL2_09378005**	Conserved protein of unknown function	136	complement(4221..4628)	684_GENE_5
9378	**6**	**CGL2_09378006**	Conserved protein of unknown function	195	complement(4638..5222)	684_GENE_6

9792	**8**	**CGLU_09792008**	Conserved hypothetical protein	71	complement(6197..6409)	478_GENE_8
9792	**7**	**CGLU_09792007**	Hypothetical protein	76	complement(5983..6210)	478_GENE_7
9792	**6**	**CGLU_09792006**	Protein of unknown function	97	complement(5181..5471)	478_GENE_6
9792	**5**	**CGLU_09792005**	Hypothetical protein	93	4893..5171	478_GENE_5
9792	**4**	**CGLU_09792004**	Putative plasmid helicase TrwC	1153	1435..4893	478_GENE_4
9792	**3**	**CGLU_09792003**	Hypothetical protein	64	1239..1430	478_GENE_3
9792	**2**	**CGLU_09792002**	Hypothetical protein	58	1051..1224	478_GENE_2
9792	**1**	**CGLU_09792001**	Hypothetical protein	287	191..1051	478_GENE_1