

Nº of gene	Operons with two or more genes	Predictor	Type	gene length	Start	Stop	Distance to the previous CDS	Strand	ID	PROKKA annotation additional info				Alignment info
1		Prodigal:2.6	CDS	653	456	1109		+	ID=KKBGGMLG_00001	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00001	product=hypothetical protein		IncRNA (Rfam) - high e-value
2		Prodigal:2.6	CDS	1154	1241	2395	132	-	ID=KKBGGMLG_00002	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00002	product=hypothetical protein		
3		Prodigal:2.6	CDS	3029	2392	5421		-3	ID=KKBGGMLG_00003	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00003	product=hypothetical protein		BLAST (without two known proteins)
4		Prodigal:2.6	CDS	1736	5418	7154		-3	ID=KKBGGMLG_00004	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00004	product=hypothetical protein		type I-U CRISPR-associated helicase/endonuclease Cas3 [Isosphaera pallida]
5		Prodigal:2.6	CDS	1352	7154	8506		0	ID=KKBGGMLG_00005	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00005	product=hypothetical protein		TPA: type I-U CRISPR-associated helicase/endonuclease Cas3 [Polyangiaceae bacterium]
6		Prodigal:2.6	CDS	1265	8640	9905	134	-	ID=KKBGGMLG_00006	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00006	product=hypothetical protein		
7		Prodigal:2.6	CDS	350	10005	10355	100	-	ID=KKBGGMLG_00007	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00007	product=hypothetical protein		
8		Prodigal:2.6	CDS	3398	10382	13780		27	ID=KKBGGMLG_00008	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00008	product=hypothetical protein		
9		Prodigal:2.6	CDS	2825	13783	16608		3	ID=KKBGGMLG_00009	inference=ab initio prediction: Prodigal:2.6, protein motif: HAMAP: MF_01821	locus_tag=KKBGGMLG_00009	product=RNA polymerase-associated protein RapA		
10		Prodigal:2.6	CDS	5168	16608	21773		-3	ID=KKBGGMLG_00010	inference=ab initio prediction: Prodigal:2.6, protein motif: HAMAP: MF_01493	locus_tag=KKBGGMLG_00010	product=DEAD-box ATP-dependent RNA helicase CshA		
11		Prodigal:2.6	CDS	134	21827	21961		54	ID=KKBGGMLG_00011	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00011	product=hypothetical protein		
12		Prodigal:2.6	CDS	704	22180	22884	219	-	ID=KKBGGMLG_00012	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00012	product=hypothetical protein		
13		Prodigal:2.6	CDS	683	23510	24193	626	+	ID=KKBGGMLG_00013	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00013	product=hypothetical protein		high e-value scores with different types of RNA
14		Prodigal:2.6	CDS	125	24633	24758	440	+	ID=KKBGGMLG_00014	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00014	product=hypothetical protein		
15		Prodigal:2.6	CDS	1034	24833	25867	75	-	ID=KKBGGMLG_00015	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00015	product=hypothetical protein		
16		Prodigal:2.6	CDS	353	25821	26174		-46	ID=KKBGGMLG_00016	inference=ab initio prediction: Prodigal:2.6	locus_tag=KKBGGMLG_00016	product=hypothetical protein		
17		Aragorn:1.2	tRNA	74	26314	26388		140	ID=KKBGGMLG_00017	inference=COORDINATES: profile Aragorn:1.2	locus_tag=KKBGGMLG_00017	product=tRNA-Met(cat)		
18		Prodigal:2.6	CDS	1505	26795	28300		407	ID=KKBGGMLG_00018	inference=ab initio prediction: Prodigal:2.6, similar to AA sequence: UniProtKB: P12627	locus_tag=KKBGGMLG_00018	product=UvrAB C system protein B		
19		Prodigal:2.6	CDS	1646	28333	29979		33	ID=KKBGGMLG_00019	inference=ab initio prediction: Prodigal:2.6, similar to AA sequence: UniProtKB: P59981	locus_tag=KKBGGMLG_00019	product=UvrAB C system protein B		