

	PROKKA data	Predictor	Type	gene length			Distance to the previous CDS											
1		Prodigal 2.6	CDS	653	456	1109	+		ID=KKBGGML G_00001	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00001	product=rhyoth etical protein		IncRNA (Rfam)	Marmota monax (woodchuck) non-coding RNA	Oncorhynchus mykiss (rainbow trout) incRNA		
2		Prodigal 2.6	CDS	1154	1241	2395	132 -		ID=KKBGGML G_00002	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00002	product=rhyoth etical protein						
3		Prodigal 2.6	CDS	3029	2392	5421	-3 -		ID=KKBGGML G_00003	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00003	product=rhyoth etical protein		BLAST				
4		Prodigal 2.6	CDS	1736	5418	7154	-3 -		ID=KKBGGML G_00004	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00004	product=rhyoth etical protein		type I-LJ CRISPR-associated helicase/endonuclease Cas3 [Bacillus subtilis]				
5	operon1	Prodigal 2.6	CDS	1352	7154	8506	0 -		ID=KKBGGML G_00005	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00005	product=rhyoth etical protein		TPA: type I-LJ CRISPR-associated helicase/endonuclease Cas3 [Polyangia caelestium]				
6		Prodigal 2.6	CDS	1265	8640	9905	134 -		ID=KKBGGML G_00006	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00006	product=rhyoth etical protein						
7		Prodigal 2.6	CDS	350	10005	10355	100 -		ID=KKBGGML G_00007	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00007	product=rhyoth etical protein						
8		Prodigal 2.6	CDS	3398	10382	13780	27 -		ID=KKBGGML G_00008	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00008	product=rhyoth etical protein						
9		Prodigal 2.6	CDS	2825	13783	16608	3 -		ID=KKBGGML G_00009	eC_number=3.6.4.-	Name=rapA	gene=rapA		inference=ab initio prediction: Prodigal 2.6; protein motif: HAMAP MF_01821	locus_tag=KKB GGMLG_00009	product=rRNA polymerase-associated protein RapA		
10		Prodigal 2.6	CDS	5168	16605	21773	-3 -		ID=KKBGGML G_00010	eC_number=3.6.4.13	Name=cshA	gene=cshA		inference=ab initio prediction: Prodigal 2.6; protein motif: HAMAP MF_01493	locus_tag=KKB GGMLG_00010	product=rDEAD-box ATP-dependent RNA helicase CshA		
11		Prodigal 2.6	CDS	134	21827	21961	54 -		ID=KKBGGML G_00011	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00011	product=rhyoth etical protein						
12		Prodigal 2.6	CDS	704	22180	22884	219 -		ID=KKBGGML G_00012	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00012	product=rhyoth etical protein						
13		Prodigal 2.6	CDS	683	23510	24193	626 +		ID=KKBGGML G_00013	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00013	product=rhyoth etical protein						
14		Prodigal 2.6	CDS	125	24633	24758	440 +		ID=KKBGGML G_00014	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00014	product=rhyoth etical protein						
15	operon2	Prodigal 2.6	CDS	1034	24833	25867	75 -		ID=KKBGGML G_00015	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00015	product=rhyoth etical protein						
16		Prodigal 2.6	CDS	353	25821	26174	-46 -		ID=KKBGGML G_00016	inference=ab initio prediction: Prodigal 2.6	locus_tag=KKB GGMLG_00016	product=rhyoth etical protein						
17	also operon2?	Aragorn 1.2	tRNA	74	26314	26388	140 -		ID=KKBGGML G_00017	inference=CODONALTES profile: Aragorn 1.2	locus_tag=KKB GGMLG_00017	product=tRNA-Met(cat)						
18		Prodigal 2.6	CDS	1505	26795	28300	407 +		ID=KKBGGML G_00018	inference=ab initio prediction: Prodigal 2.6	Name=vnfA db_xref=COG:COG3604	gene=vnfA		inference=ab initio prediction: Prodigal 2.6; similar to AA sequence: UniProtKB:P12627	locus_tag=KKB GGMLG_00018	product=Nitrogen fixation protein VnfA		
19		Prodigal 2.6	CDS	1646	28333	29979	33 -		ID=KKBGGML G_00019	inference=ab initio prediction: Prodigal 2.6; similar to AA sequence: UniProtKB:P5981	locus_tag=KKB GGMLG_00019	gene=vnfB		locus_tag=KKB GGMLG_00019	product=UvrABC system protein B			