BV-BRC Test Report

D9. Proteins (Features) Data Tab

Item to test	**Proteins (Features) Data Tab**
URL	https://www.bv-brc.org/view/Taxonomy/194#view_tab=features
Prerequisites	None
References	https://www.bv-brc.org/docs/quick_references/organisms_taxon/proteins.html
Tester(s)	Rebecca Wattam, Christian Zmasek, Anna Niewiadomska, Ron Kenyon
Test date	6-Jan-2022 and 4-Feb-22 (original – passed), 9-May-2022 (follow-up-passed)
Test result	**Passed** (1 minor issue reported)

Overview

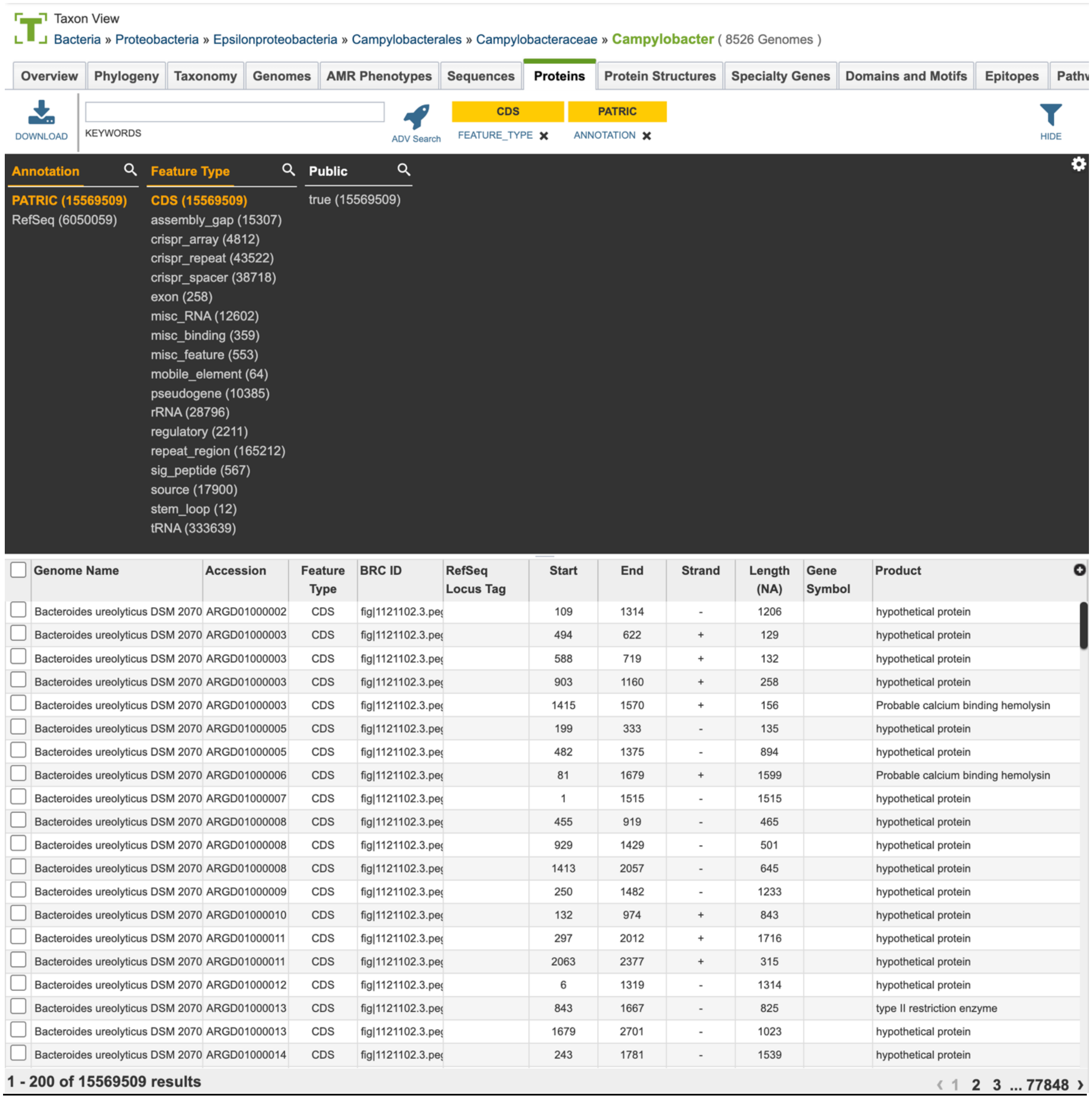
- Test the Proteins Tab with example bacterial and viral data.
- Verify appropriate genomes.
- Test Genome action button.
- Test FASTA action buttons.
- Test ID Map.
- Test MSA.

Test Results

- Test results were verified by examination of returned data via inspection and filters.
- All operations performed as expected, with exception of ID map action button.
    - Issue: ID Mapping button from action bar not working.
    - Resolution: The bug has been identified and being fixed. It will be deployed to production in the next release.

Bacteria

Campylobacter:



Annotation
PATRIC (15569509)
RefSeq (6050059)

Feature Type
CDS (15569509)
assembly_gap (15307)
crispr_array (4812)
crispr_repeat (43522)
crispr_spacer (38718)
exon (258)
misc_RNA (12602)
misc_binding (359)
misc_feature (553)
mobile_element (64)
pseudogene (10385)
rRNA (28796)
regulatory (2211)
repeat_region (165212)
sig_peptide (567)
source (17900)
stem_loop (12)
tRNA (333639)

Public
true (15569509)

☐	Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
☐	Bacteroides ureolyticus DSM 2070	ARGD01000002	CDS	fig|1121102.3.pe		109	1314	-	1206		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000003	CDS	fig|1121102.3.pe		494	622	+	129		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000003	CDS	fig|1121102.3.pe		588	719	+	132		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000003	CDS	fig|1121102.3.pe		903	1160	+	258		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000003	CDS	fig|1121102.3.pe		1415	1570	+	156		Probable calcium binding hemolysin
☐	Bacteroides ureolyticus DSM 2070	ARGD01000005	CDS	fig|1121102.3.pe		199	333	-	135		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000005	CDS	fig|1121102.3.pe		482	1375	-	894		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000006	CDS	fig|1121102.3.pe		81	1679	+	1599		Probable calcium binding hemolysin
☐	Bacteroides ureolyticus DSM 2070	ARGD01000007	CDS	fig|1121102.3.pe		1	1515	-	1515		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000008	CDS	fig|1121102.3.pe		455	919	-	465		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000008	CDS	fig|1121102.3.pe		929	1429	-	501		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000008	CDS	fig|1121102.3.pe		1413	2057	-	645		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000009	CDS	fig|1121102.3.pe		250	1482	-	1233		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000010	CDS	fig|1121102.3.pe		132	974	+	843		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000011	CDS	fig|1121102.3.pe		297	2012	+	1716		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000011	CDS	fig|1121102.3.pe		2063	2377	+	315		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000012	CDS	fig|1121102.3.pe		6	1319	-	1314		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000013	CDS	fig|1121102.3.pe		843	1667	-	825		type II restriction enzyme
☐	Bacteroides ureolyticus DSM 2070	ARGD01000013	CDS	fig|1121102.3.pe		1679	2701	-	1023		hypothetical protein
☐	Bacteroides ureolyticus DSM 2070	ARGD01000014	CDS	fig|1121102.3.pe		243	1781	-	1539		hypothetical protein

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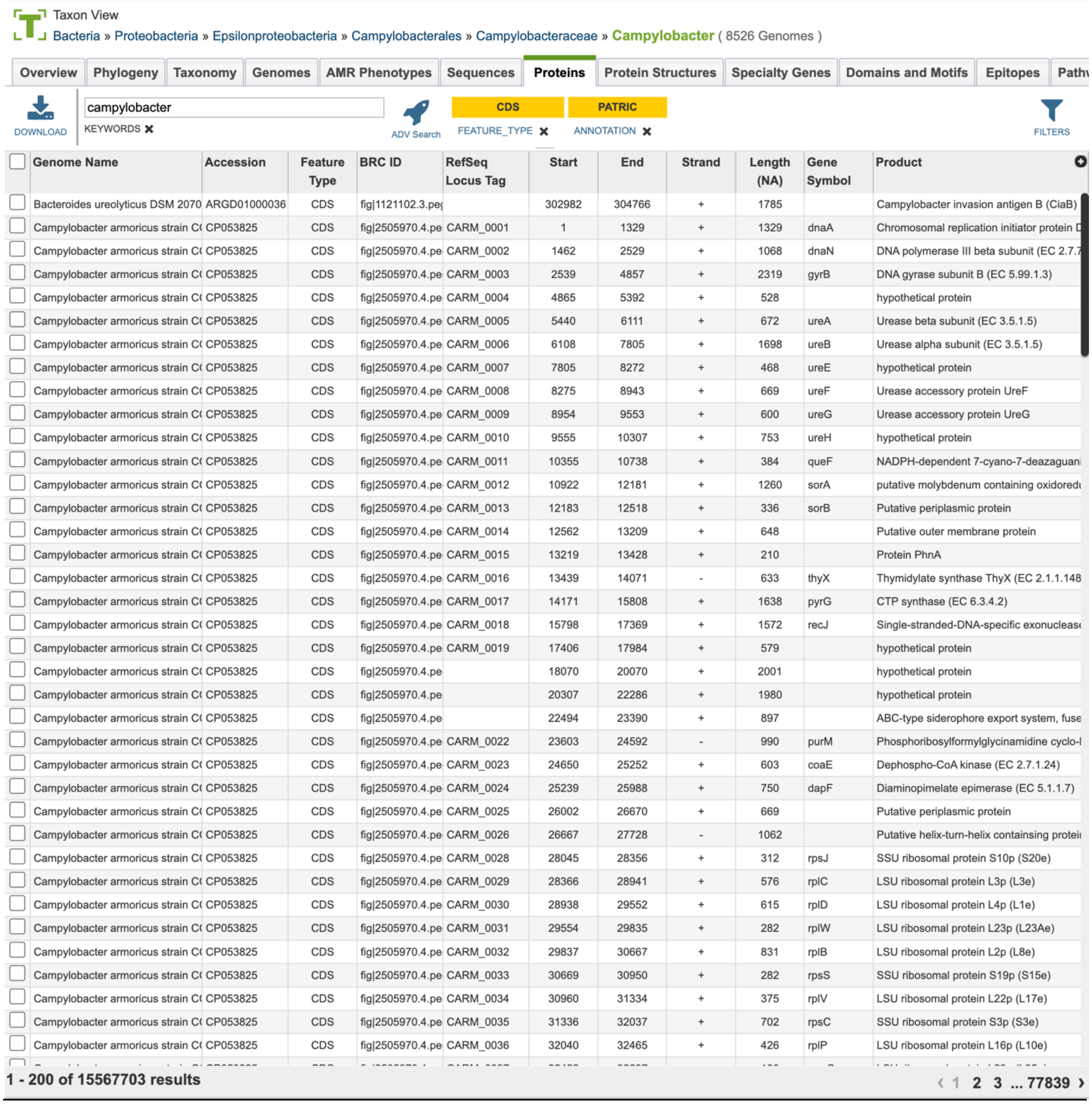
Keyword: Campylobacter



campylobacter
KEYWORDS ✖

CDS
FEATURE_TYPE ✖

PATRIC
ANNOTATION ✖

☐	Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
☐	Bacteroides ureolyticus DSM 2070	ARGD01000036	CDS	fig|1121102.3.pe		302982	304766	+	1785		Campylobacter invasion antigen B (CiaB)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0001	1	1329	+	1329	dnaA	Chromosomal replication initiator protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0002	1462	2529	+	1068	dnaN	DNA polymerase III beta subunit (EC 2.7.
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0003	2539	4857	+	2319	gyrB	DNA gyrase subunit B (EC 5.99.1.3)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0004	4865	5392	+	528		hypothetical protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0005	5440	6111	+	672	ureA	Urease beta subunit (EC 3.5.1.5)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0006	6108	7805	+	1698	ureB	Urease alpha subunit (EC 3.5.1.5)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0007	7805	8272	+	468	ureE	hypothetical protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0008	8275	8943	+	669	ureF	Urease accessory protein UreF
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0009	8954	9553	+	600	ureG	Urease accessory protein UreG
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0010	9555	10307	+	753	ureH	hypothetical protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0011	10355	10738	+	384	queF	NADPH-dependent 7-cyano-7-deazaguan
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0012	10922	12181	+	1260	sorA	putative molybdenum containing oxidored
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0013	12183	12518	+	336	sorB	Putative periplasmic protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0014	12562	13209	+	648		Putative outer membrane protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0015	13219	13428	+	210		Protein PhnA
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0016	13439	14071	-	633	thyX	Thymidylate synthase ThyX (EC 2.1.1.148
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0017	14171	15808	+	1638	pyrG	CTP synthase (EC 6.3.4.2)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0018	15798	17369	+	1572	recJ	Single-stranded-DNA-specific exonucleas
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0019	17406	17984	+	579		hypothetical protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe		18070	20070	+	2001		hypothetical protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe		20307	22286	+	1980		hypothetical protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe		22494	23390	+	897		ABC-type siderophore export system, fuse
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0022	23603	24592	-	990	purM	Phosphoribosylformylglycinamidine cyclo-
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0023	24650	25252	+	603	coaE	Dephospho-CoA kinase (EC 2.7.1.24)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0024	25239	25988	+	750	dapF	Diaminopimelate epimerase (EC 5.1.1.7)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0025	26002	26670	+	669		Putative periplasmic protein
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0026	26667	27728	-	1062		Putative helix-turn-helix containsing protei
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0028	28045	28356	+	312	rpsJ	SSU ribosomal protein S10p (S20e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0029	28366	28941	+	576	rplC	LSU ribosomal protein L3p (L3e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0030	28938	29552	+	615	rplD	LSU ribosomal protein L4p (L1e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0031	29554	29835	+	282	rplW	LSU ribosomal protein L23p (L23Ae)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0032	29837	30667	+	831	rplB	LSU ribosomal protein L2p (L8e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0033	30669	30950	+	282	rpsS	SSU ribosomal protein S19p (S15e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0034	30960	31334	+	375	rplV	LSU ribosomal protein L22p (L17e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0035	31336	32037	+	702	rpsC	SSU ribosomal protein S3p (S3e)
☐	Campylobacter armoricus strain C	CP053825	CDS	fig|2505970.4.pe	CARM_0036	32040	32465	+	426	rplP	LSU ribosomal protein L16p (L10e)

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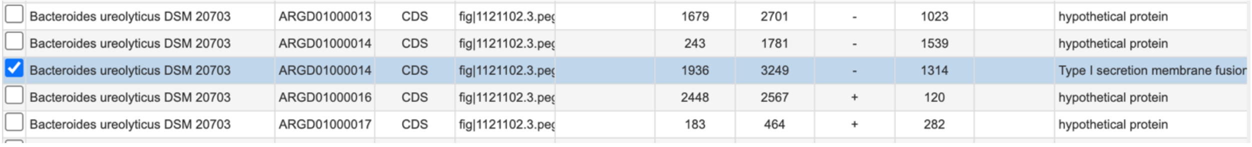
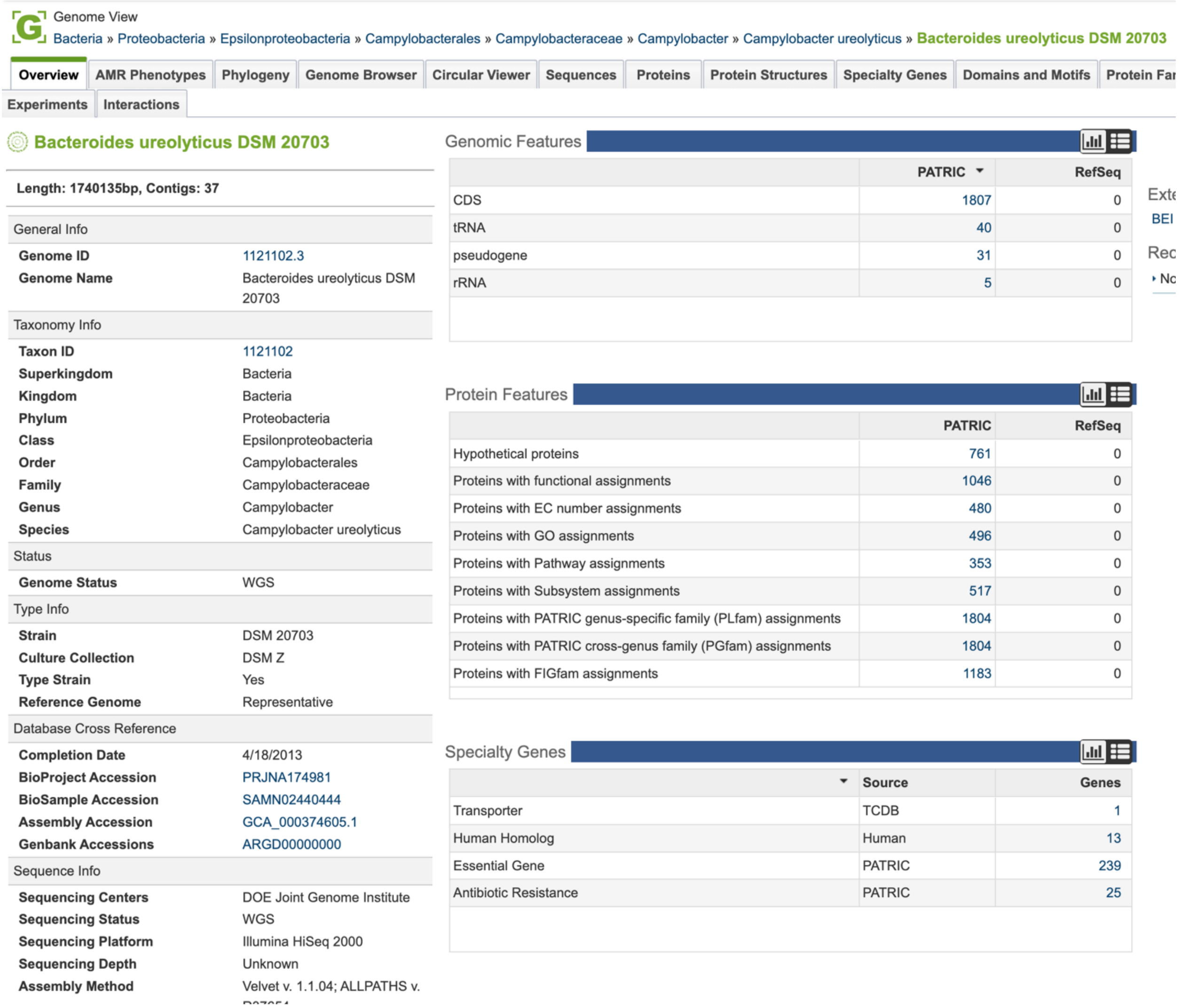
Genome Action Button:



☐	Bacteroides ureolyticus DSM 20703	ARGD01000013	CDS	fig|1121102.3.pe		1679	2701	-	1023		hypothetical protein
☐	Bacteroides ureolyticus DSM 20703	ARGD01000014	CDS	fig|1121102.3.pe		243	1781	-	1539		hypothetical protein
☑	Bacteroides ureolyticus DSM 20703	ARGD01000014	CDS	fig|1121102.3.pe		1936	3249	-	1314		Type I secretion membrane fusio
☐	Bacteroides ureolyticus DSM 20703	ARGD01000016	CDS	fig|1121102.3.pe		2448	2567	+	120		hypothetical protein
☐	Bacteroides ureolyticus DSM 20703	ARGD01000017	CDS	fig|1121102.3.pe		183	464	+	282		hypothetical protein

Result:



Genome View

Bacteria » Proteobacteria » Epsilonproteobacteria » Campylobacterales » Campylobacteraceae » Campylobacter » Campylobacter ureolyticus » **Bacteroides ureolyticus DSM 20703**

Bacteroides ureolyticus DSM 20703

Length: 1740135bp, Contigs: 37

General Info	
Genome ID	1121102.3
Genome Name	Bacteroides ureolyticus DSM 20703
Taxonomy Info	
Taxon ID	1121102
Superkingdom	Bacteria
Kingdom	Bacteria
Phylum	Proteobacteria
Class	Epsilonproteobacteria
Order	Campylobacterales
Family	Campylobacteraceae
Genus	Campylobacter
Species	Campylobacter ureolyticus
Status	
Genome Status	WGS
Type Info	
Strain	DSM 20703
Culture Collection	DSM Z
Type Strain	Yes
Reference Genome	Representative
Database Cross Reference	
Completion Date	4/18/2013
BioProject Accession	PRJNA174981
BioSample Accession	SAMN02440444
Assembly Accession	GCA_000374605.1
Genbank Accessions	ARGD00000000
Sequence Info	
Sequencing Centers	DOE Joint Genome Institute
Sequencing Status	WGS
Sequencing Platform	Illumina HiSeq 2000
Sequencing Depth	Unknown
Assembly Method	Velvet v. 1.1.04; ALLPATHS v.

Genomic Features

	PATRIC	RefSeq
CDS	1807	0
tRNA	40	0
pseudogene	31	0
rRNA	5	0

Protein Features

	PATRIC	RefSeq
Hypothetical proteins	761	0
Proteins with functional assignments	1046	0
Proteins with EC number assignments	480	0
Proteins with GO assignments	496	0
Proteins with Pathway assignments	353	0
Proteins with Subsystem assignments	517	0
Proteins with PATRIC genus-specific family (PLfam) assignments	1804	0
Proteins with PATRIC cross-genus family (PGfam) assignments	1804	0
Proteins with FIGfam assignments	1183	0

Specialty Genes

	Source	Genes
Transporter	TCDB	1
Human Homolog	Human	13
Essential Gene	PATRIC	239
Antibiotic Resistance	PATRIC	25

FASTA – DNA:

```
>fig|1121102.3.peg.21|VBIBacUre256426_0021| Type I secretion membrane fusion protein, HlyD [Bacteroides ureolyticus DSM 20703 | 1121102.3]
atgtttaaaatatttaaaaaaataaaagatgattcttatgagtttaaacctgttattatt
gaaatagaagatacccctcaaaacccacttggtagaactattttatatattgtattgtct
ttaataatttttacatttctttggctgtttttagcaaaaatagatattgtagtaagtagc
caaggaaaagttatcccaaatggagagattaaaatcttaaagcctcttgaatcaggtgtt
gtatcaaaaatcttagtaaaagaaggagataaggttttaaaaggcgatactttaatgagt
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aatatgagtataattaggcttagggctttaggaaatgagagtgatttaacaaatgaagag
ctaaatttactaagtaatagtgagttaaatttgtttttaaatcaaaaaaactcttatgat
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aaagatgagataataaggctaaacaatcttttaaataaaaatcaaaatagactaaataga
cttgaaaaagtaaaagacataatatcgcttaaagagtatgatgagcttcaaaaagaggtg
tatgatttaacttctaaattaaatatcgctaaaaataataaaacagcagctataaacaaa
ctaaatgcaacaaaagaagagcttgaagtttttaaacaaaactcaaaaggtaaattccta
gatgaacttatagccaaacaaaaagaggcaaatttaataaaagcagagattaatgcctat
ctttttcaaagcaaacaacaactcattaaaagtcctgttgatggatatgttggaaagctt
ttagtaaatactgaaagtggagttgtaaatagtggggaagctttaataactataattcca
gcaaatgagccacttataataaaagcaacaacgctaaataaagatataggatttttaaaa
gaaggacaaaaagtagctattaaaatagatacttttaactttcaaaaatatggaaaactt
gatggagagttaatacacattgcaaatgatgctatagaagatgaaaaacttggaatagtt
tatgagataaaagtaaaacctttaaaaacaactctaaacatagatggagagataaaaaac
attgagcctggaatgagtgtgatagctgaagtaaaagtaggcaaaagaagagtaattgag
ctatttatctatccaataataaaataccttgatgaggggttaagtgtgaggtaa
```

FASTA – Proteins:

```
>fig|1121102.3.peg.21|VBIBacUre256426_0021| Type I secretion membrane fusion protein, HlyD [Bacteroides ureolyticus DSM 20703 | 1121102.3]
MFKIFKKIKDDSYEFKPVIIEIEDTPQNPLGRTILYIVLSLIIFTFLWLFLAKIDIVVSS
QGKVIPNGEIKILKPLESGVVSKILVKEGDKVLKGDTLMSIDPSVTTVNLQTKENELNNL
NMSIIRLRALGNESDLTNEELNLLSNSELNLFLNQKNSYDNSINQYKFSIEELNFNIESS
KDEIIRLNNLLNKNQNRLNRLEKVKDIISLKEYDELQKEVYDLTSKLNIAKNNKTAAINK
LNATKEELEVFKQNSKGKFLDELIAKQKEANLIKAEINAYLFQSKQQLIKSPVDGYVGKL
LVNTESGVVNSGEALITIIPANEPLIIKATTLNKDIGFLKEGQKVAIKIDTFNFQKYGKL
DGELIHIANDAIEDEKLGIVYEIKVKPLKTTLNIDGEIKNIEPGMSVIAEVKVGKRRVIE
LFIYPIIKYLDEGLSVR
```

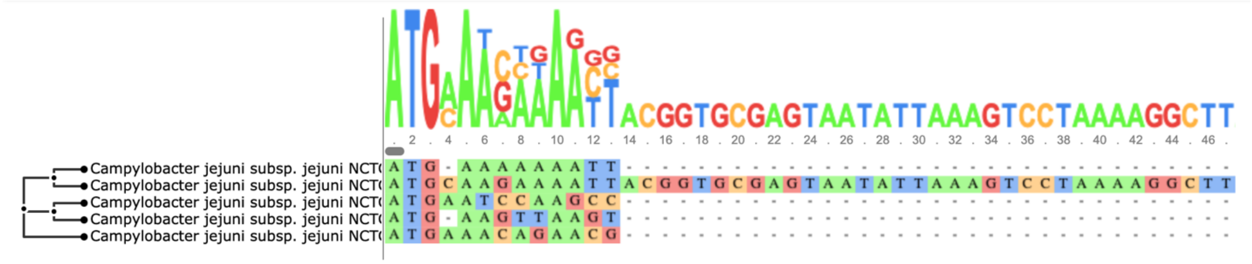
ID Map:

Result: Page never loaded. Tried RefSeq ID, UniProt, and choosing proteins from reference genome

☐	Genome Name	BRC ID	RefSeq Locus Tag	Target	PATRIC Local family	PATRIC Global family	Gene	Product

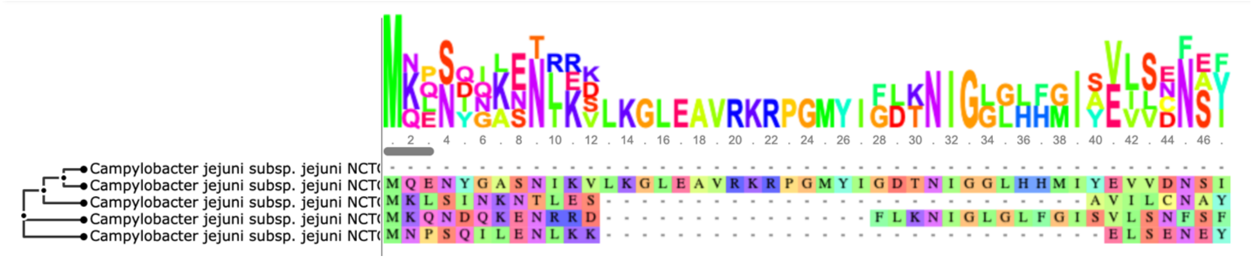
1 - 1 of 0 results

MSA - Nucleotide:



```
Campylobacter jejuni subsp. jejuni NCT( ATG-AAAAAAATT----------------------------------
Campylobacter jejuni subsp. jejuni NCT( ATGCAAGAAAATTACGGTGCGAGTAATATTAAAGTCCTAAAAGGCTT
Campylobacter jejuni subsp. jejuni NCT( ATGAATCCAAGCC----------------------------------
Campylobacter jejuni subsp. jejuni NCT( ATG-AAGTTAAGT----------------------------------
Campylobacter jejuni subsp. jejuni NCT( ATGAAACAGAACG----------------------------------
```

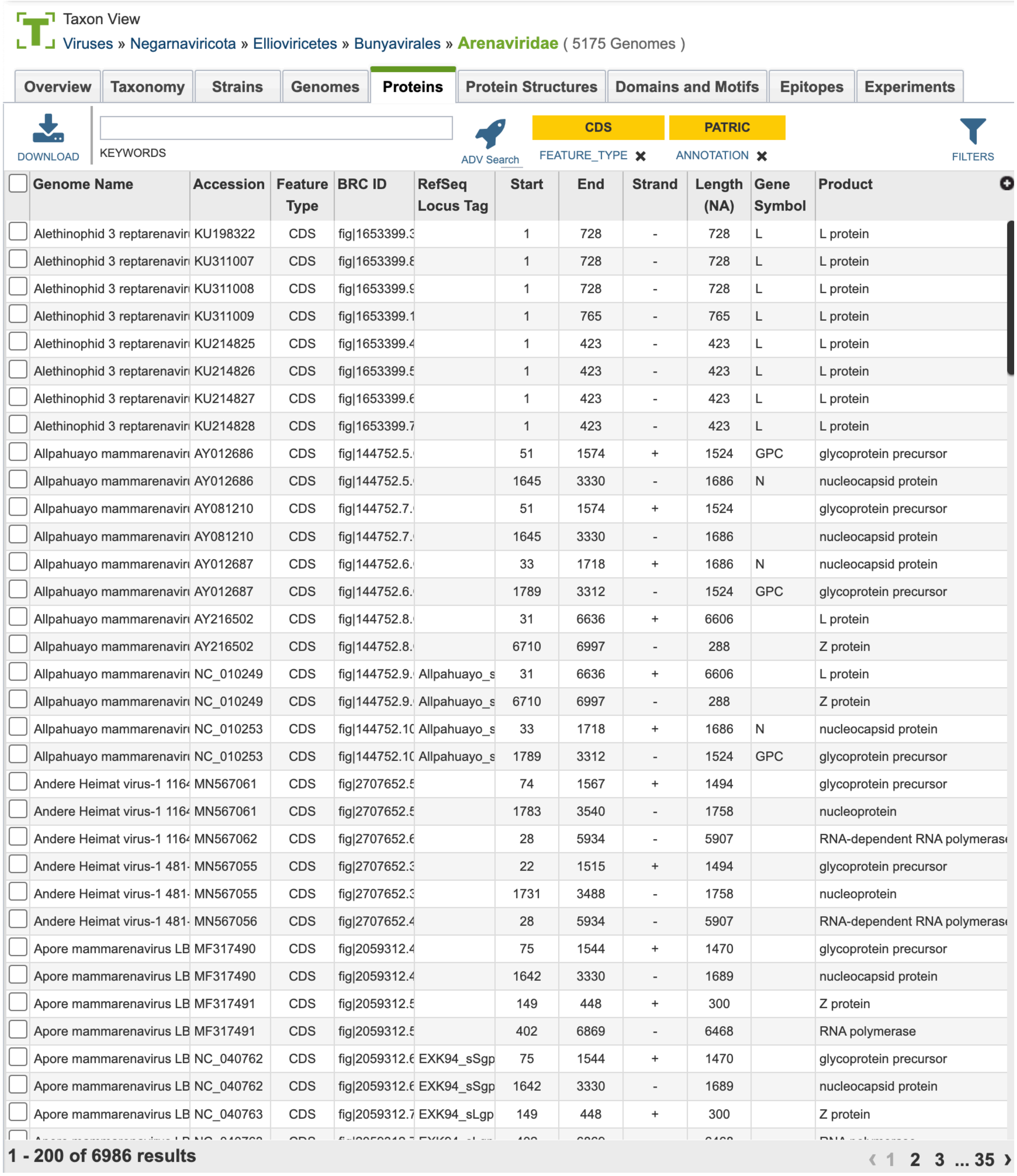
MSA - Amino Acid:



```
Campylobacter jejuni subsp. jejuni NCT( -----------------------------------------------
Campylobacter jejuni subsp. jejuni NCT( MQENYGASNIKVLKGLEAVRKRPGMYIGDTNIGGLHHMIYEVVDNSI
Campylobacter jejuni subsp. jejuni NCT( MKLSINKNTLES---------------------------AVILCNAY
Campylobacter jejuni subsp. jejuni NCT( MKQNDQKENRRD---------------FLKNIGLGLFGISVLSNFSF
Campylobacter jejuni subsp. jejuni NCT( MNPSQILENLKK----------------------------ELSENEY
```

Virus

Arenaviridae:



☐	Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
☐	Alethinophid 3 reptarenavir	KU198322	CDS	fig|1653399.3		1	728	-	728	L	L protein
☐	Alethinophid 3 reptarenavir	KU311007	CDS	fig|1653399.8		1	728	-	728	L	L protein
☐	Alethinophid 3 reptarenavir	KU311008	CDS	fig|1653399.9		1	728	-	728	L	L protein
☐	Alethinophid 3 reptarenavir	KU311009	CDS	fig|1653399.1		1	765	-	765	L	L protein
☐	Alethinophid 3 reptarenavir	KU214825	CDS	fig|1653399.4		1	423	-	423	L	L protein
☐	Alethinophid 3 reptarenavir	KU214826	CDS	fig|1653399.5		1	423	-	423	L	L protein
☐	Alethinophid 3 reptarenavir	KU214827	CDS	fig|1653399.6		1	423	-	423	L	L protein
☐	Alethinophid 3 reptarenavir	KU214828	CDS	fig|1653399.7		1	423	-	423	L	L protein
☐	Allpahuayo mammarenavir	AY012686	CDS	fig|144752.5.		51	1574	+	1524	GPC	glycoprotein precursor
☐	Allpahuayo mammarenavir	AY012686	CDS	fig|144752.5.		1645	3330	-	1686	N	nucleocapsid protein
☐	Allpahuayo mammarenavir	AY081210	CDS	fig|144752.7.		51	1574	+	1524		glycoprotein precursor
☐	Allpahuayo mammarenavir	AY081210	CDS	fig|144752.7.		1645	3330	-	1686		nucleocapsid protein
☐	Allpahuayo mammarenavir	AY012687	CDS	fig|144752.6.		33	1718	+	1686	N	nucleocapsid protein
☐	Allpahuayo mammarenavir	AY012687	CDS	fig|144752.6.		1789	3312	-	1524	GPC	glycoprotein precursor
☐	Allpahuayo mammarenavir	AY216502	CDS	fig|144752.8.		31	6636	+	6606		L protein
☐	Allpahuayo mammarenavir	AY216502	CDS	fig|144752.8.		6710	6997	-	288		Z protein
☐	Allpahuayo mammarenavir	NC_010249	CDS	fig|144752.9.	Allpahuayo_s	31	6636	+	6606		L protein
☐	Allpahuayo mammarenavir	NC_010249	CDS	fig|144752.9.	Allpahuayo_s	6710	6997	-	288		Z protein
☐	Allpahuayo mammarenavir	NC_010253	CDS	fig|144752.10	Allpahuayo_s	33	1718	+	1686	N	nucleocapsid protein
☐	Allpahuayo mammarenavir	NC_010253	CDS	fig|144752.10	Allpahuayo_s	1789	3312	-	1524	GPC	glycoprotein precursor
☐	Andere Heimat virus-1 116	MN567061	CDS	fig|2707652.5		74	1567	+	1494		glycoprotein precursor
☐	Andere Heimat virus-1 116	MN567061	CDS	fig|2707652.5		1783	3540	-	1758		nucleoprotein
☐	Andere Heimat virus-1 116	MN567062	CDS	fig|2707652.6		28	5934	-	5907		RNA-dependent RNA polymeras
☐	Andere Heimat virus-1 481-	MN567055	CDS	fig|2707652.3		22	1515	+	1494		glycoprotein precursor
☐	Andere Heimat virus-1 481-	MN567055	CDS	fig|2707652.3		1731	3488	-	1758		nucleoprotein
☐	Andere Heimat virus-1 481-	MN567056	CDS	fig|2707652.4		28	5934	-	5907		RNA-dependent RNA polymeras
☐	Apore mammarenavirus LB	MF317490	CDS	fig|2059312.4		75	1544	+	1470		glycoprotein precursor
☐	Apore mammarenavirus LB	MF317490	CDS	fig|2059312.4		1642	3330	-	1689		nucleocapsid protein
☐	Apore mammarenavirus LB	MF317491	CDS	fig|2059312.5		149	448	+	300		Z protein
☐	Apore mammarenavirus LB	MF317491	CDS	fig|2059312.5		402	6869	-	6468		RNA polymerase
☐	Apore mammarenavirus LB	NC_040762	CDS	fig|2059312.6	EXK94_sSgp	75	1544	+	1470		glycoprotein precursor
☐	Apore mammarenavirus LB	NC_040762	CDS	fig|2059312.6	EXK94_sSgp	1642	3330	-	1689		nucleocapsid protein
☐	Apore mammarenavirus LB	NC_040763	CDS	fig|2059312.7	EXK94_sLgp	149	448	+	300		Z protein

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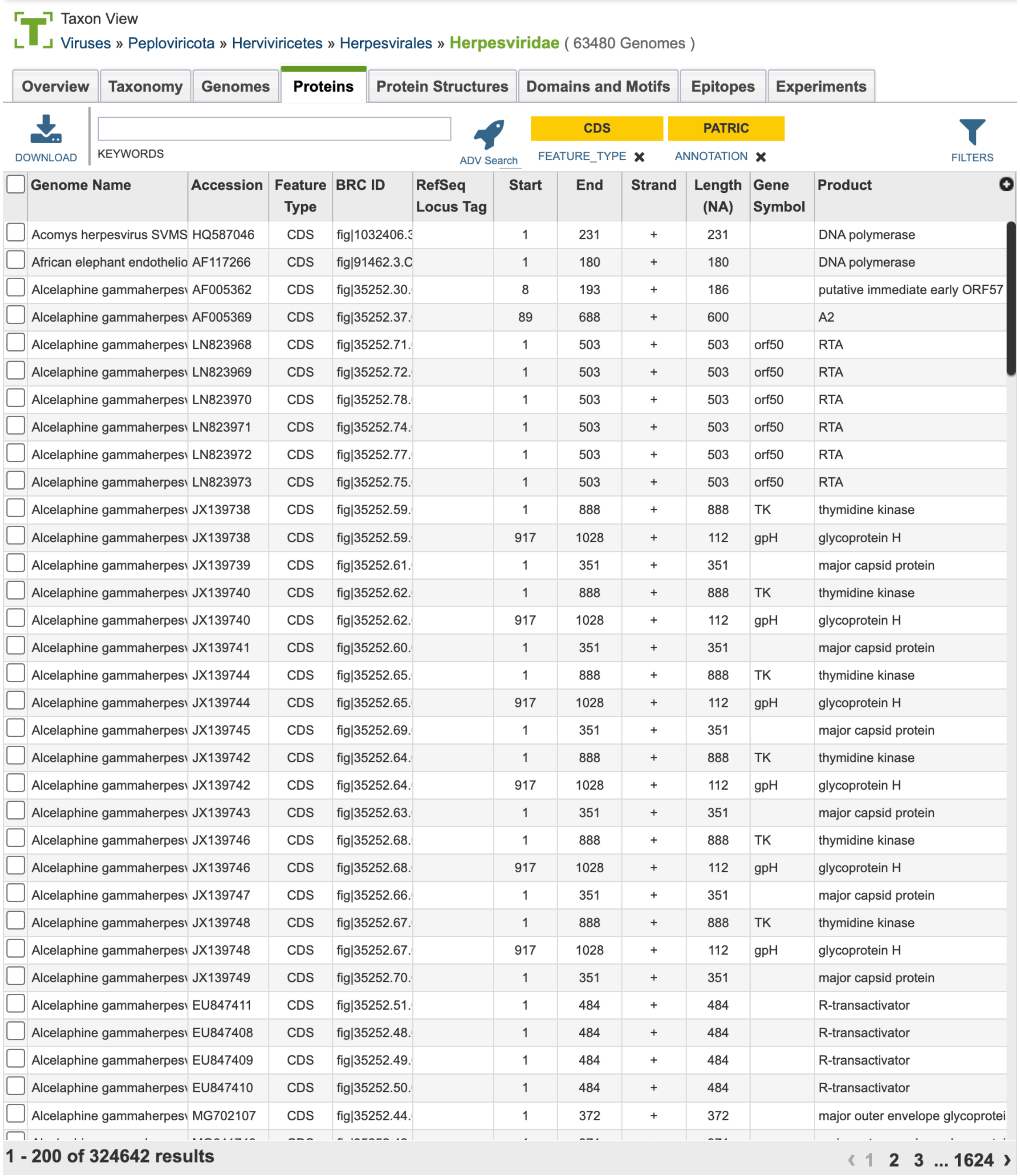
‹ 1 2 3 ... 35 ›

Herpesviridae:



☐	Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
☐	Acomys herpesvirus SVMS	HQ587046	CDS	fig|1032406.3		1	231	+	231		DNA polymerase
☐	African elephant endothelio	AF117266	CDS	fig|91462.3.C		1	180	+	180		DNA polymerase
☐	Alcelaphine gammaherpes	AF005362	CDS	fig|35252.30.		8	193	+	186		putative immediate early ORF57
☐	Alcelaphine gammaherpes	AF005369	CDS	fig|35252.37.		89	688	+	600		A2
☐	Alcelaphine gammaherpes	LN823968	CDS	fig|35252.71.		1	503	+	503	orf50	RTA
☐	Alcelaphine gammaherpes	LN823969	CDS	fig|35252.72.		1	503	+	503	orf50	RTA
☐	Alcelaphine gammaherpes	LN823970	CDS	fig|35252.78.		1	503	+	503	orf50	RTA
☐	Alcelaphine gammaherpes	LN823971	CDS	fig|35252.74.		1	503	+	503	orf50	RTA
☐	Alcelaphine gammaherpes	LN823972	CDS	fig|35252.77.		1	503	+	503	orf50	RTA
☐	Alcelaphine gammaherpes	LN823973	CDS	fig|35252.75.		1	503	+	503	orf50	RTA
☐	Alcelaphine gammaherpes	JX139738	CDS	fig|35252.59.		1	888	+	888	TK	thymidine kinase
☐	Alcelaphine gammaherpes	JX139738	CDS	fig|35252.59.		917	1028	+	112	gpH	glycoprotein H
☐	Alcelaphine gammaherpes	JX139739	CDS	fig|35252.61.		1	351	+	351		major capsid protein
☐	Alcelaphine gammaherpes	JX139740	CDS	fig|35252.62.		1	888	+	888	TK	thymidine kinase
☐	Alcelaphine gammaherpes	JX139740	CDS	fig|35252.62.		917	1028	+	112	gpH	glycoprotein H
☐	Alcelaphine gammaherpes	JX139741	CDS	fig|35252.60.		1	351	+	351		major capsid protein
☐	Alcelaphine gammaherpes	JX139744	CDS	fig|35252.65.		1	888	+	888	TK	thymidine kinase
☐	Alcelaphine gammaherpes	JX139744	CDS	fig|35252.65.		917	1028	+	112	gpH	glycoprotein H
☐	Alcelaphine gammaherpes	JX139745	CDS	fig|35252.69.		1	351	+	351		major capsid protein
☐	Alcelaphine gammaherpes	JX139742	CDS	fig|35252.64.		1	888	+	888	TK	thymidine kinase
☐	Alcelaphine gammaherpes	JX139742	CDS	fig|35252.64.		917	1028	+	112	gpH	glycoprotein H
☐	Alcelaphine gammaherpes	JX139743	CDS	fig|35252.63.		1	351	+	351		major capsid protein
☐	Alcelaphine gammaherpes	JX139746	CDS	fig|35252.68.		1	888	+	888	TK	thymidine kinase
☐	Alcelaphine gammaherpes	JX139746	CDS	fig|35252.68.		917	1028	+	112	gpH	glycoprotein H
☐	Alcelaphine gammaherpes	JX139747	CDS	fig|35252.66.		1	351	+	351		major capsid protein
☐	Alcelaphine gammaherpes	JX139748	CDS	fig|35252.67.		1	888	+	888	TK	thymidine kinase
☐	Alcelaphine gammaherpes	JX139748	CDS	fig|35252.67.		917	1028	+	112	gpH	glycoprotein H
☐	Alcelaphine gammaherpes	JX139749	CDS	fig|35252.70.		1	351	+	351		major capsid protein
☐	Alcelaphine gammaherpes	EU847411	CDS	fig|35252.51.		1	484	+	484		R-transactivator
☐	Alcelaphine gammaherpes	EU847408	CDS	fig|35252.48.		1	484	+	484		R-transactivator
☐	Alcelaphine gammaherpes	EU847409	CDS	fig|35252.49.		1	484	+	484		R-transactivator
☐	Alcelaphine gammaherpes	EU847410	CDS	fig|35252.50.		1	484	+	484		R-transactivator
☐	Alcelaphine gammaherpes	MG702107	CDS	fig|35252.44.		1	372	+	372		major outer envelope glycoprotei

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