

A

BLAST® » blastn suite

HomeRecent ResultsSaved StrategiesHelp

blastnblastpblastxtblastntblastx

Standard Nucleotide BLAST

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) Clear

ref|NC_035619

Query subrange

From

To

Or, upload file

选取文件 未选择文件

Job Title

NC_035619-SunNan-Test

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Standard databases (nr etc.) rRNA/ITS databases Genomic + transcript databases Betacoronavirus

RefSeq Genome Database (refseq_genomes)

Organism

Viruses (taxid:10239)

exclude

Add organism

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude

Models (XM/XP) Uncultured/environmental sample sequences

Limit to

Sequences from type material

Entrez Query

Enter an Entrez query to limit search

Program Selection

Optimize for

Highly similar sequences (megablast)

More dissimilar sequences (discontinuous megablast)

Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database refseq_genomes using Megablast (Optimize for highly similar sequences)

Show results in a new window

B

BLAST® » blastn suite » results for RID-3UXHYSZF01R

HomeRecent ResultsSaved StrategiesHelp

Edit Search

Save Search

Search Summary

How to read this report?

BLAST Help Videos

Back to Traditional Results Page

Your search is limited to records that include: Viruses (taxid:10239)

Job Title

NC_035619-SunNan-Test

RID

3UXHYSZF01R

Search expires on 03-26 15:58 pm

Download All

Program

BLASTN

Citation

Database

refseq_genomes (ref_viruses_rep_genomes)

See details

Query ID

NC_035619.1

Description

Odokoileus adenovirus 1, complete genome

Molecule type

nucleic acid

Query Length

30620

Other reports

Distance tree of results

MSA viewer

Filter Results

Organism

only top 20 will appear

exclude

Type common name, binomial, taxid or group name

Add organism

Percent Identity

E value

Query Coverage

Filter

Reset

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download

Select columns

Show

100

select all

4 sequences selected

GenBank

Graphics

Distance tree of results

MSA Viewer

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☒	Odokoileus adenovirus 1, complete genome	Odokoileus adenovirus 1	56538	56688	100%	0.0	100.00%	30620	NC_035619.1
☒	Bovine adenovirus D, complete genome	Bovine adenovirus D	2721	6020	43%	0.0	73.05%	31301	NC_002685.2
☒	Bovine adenovirus 6 strain 671130, complete genome	Bovine adenovirus 6	2691	5621	47%	0.0	72.75%	30024	NC_020074.1
☒	Ovine adenovirus 7, complete genome	Ovine adenovirus 7	2085	3467	25%	0.0	73.76%	29576	NC_004037.2

C

Accession No.	Euclidean dis.	nA	nC	nG	nT	uA	uC	uG	uT	DA	DC	DG	DT	Cov(A,C)	Cov(A,G)	Cov(A,T)	Cov(C,G)	Cov(C,T)	Cov(G,T)																
1	NC_035619	0	10524	5303	4874	9917	15995	78098	16160	73015	14473	50821	14538	61289	251	227073	2562	074722	2509	361931	2550	075425	3556	36061	5397	777822	5062	3814	5078	172535	5360	782019	5396	681189	
2	NC_002685	983	2994623	10318	5857	5149	9977	16443	2548	18260	30186	14850	49	14887	10905	2547	324948	2653	842627	2568	854599	2608	437561	5380	465336	5420	51658	5155	463462	5239	015568	5437	770591	5476	38375
3	NC_020074	1067	668091	9892	5463	5071	9598	15722	95309	15642	69724	14395	81404	14247	40779	2473	272774	2509	422318	2509	814441	2472	209743	5192	980707	5251	350286	4946	061315	5022	701078	5170	087438	5225	481752
4	NC_004037	1372	322754	10180	5374	4564	9458	15482	06906	15425	78936	14240	60955	13944	26718	2449	353633	2467	028342	2411	341657	2451	234495	5163	59653	5272	647616	4903	83435	4899	208891	5111	504953	5203	741247
5	NC_029314	1507	241747	10416	4789	4839	9719	14828	4351	15960	66047	13979	32445	14857	33429	2471	927443	2433	106515	2329	418886	2554	479399	5295	362771	5214	396619	5026	56174	4762	051147	5347	013627	5263	89345
6	NC_034626	1548	085262	10021	4965	5288	9649	15512	34208	15157	46747	14974	29917	14283	12012	2358	170358	2624	921546	2616	577047	2472	656368	5197	855721	5147	016983	4829	525316	5243	838453	5329	964532	5277	1357
7	NC_030860	1586	082317	9765	4848	5273	9695	15364	14798	15416	48288	13994	65598	14334	00251	2348	378978	2542	056545	2539	497403	2467	149704	5124	049047	5061	89747	4815	132601	5085	93256	5286	494765	5218	190957
8	NC_024150	1670	17358	10259	5668	5741	10041	16611	0732	16767	92855	15367	26598	14846	04143	2538	002638	2691	304696	2638	151081	2654	28993	5414	958845	5366	259035	5191	343122	5329	224766	5554	861319	5505	116279
9	NC_035072	1681	333264	9959	4929	5267	9657	15396	24029	15112	53479	15043	02962	14221	81837	2350	914822	2621	483025	2616	403911	2454	800235	5185	928691	5135	419072	4804	685126	5240	589904	5308	89737	5256	217626
10	NC_030874	1845	508421	10007	4483	4655	10017	15020	23334	15303	65983	14045	8073	14068	95158	2341	537692	2448	948939	2407	17175	2492	808345	5137	515938	5074	933843	4834	422184	4856	194657	5364	568648	5297	723245
11	NC_006635	2099	095441	9609	5100	5041	10124	15015	24175	14751	50686	14727	17139	15062	13562	2584	563516	2437	702767	2402	739013	2466	533166	5323	587356	5308	661147	5049	736327	4840	727125	5205	359041	5190	927958