

BLAST[®] >> **blastn suite** >> results for RID-BR857EF1016

Your search is limited to records that include: Porcine epidemic diarrhea virus (taxid:28295)

Job Title	F2 ...
RID	BR857EF1016 Search expires on 06-30 08:45 am
Program	BLASTN
Database	ref_viruses_rep_genomes
Query ID	lcl Query_65179
Description	F2 ...
Molecule type	dna
Query Length	32

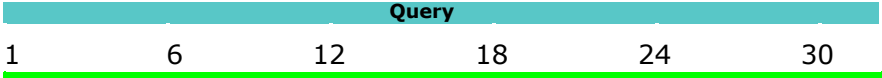
Descriptions

Descriptions

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Porcine epidemic diarrhea virus, complete genome	Porcine epidemic diarrhea virus	63.9	1037	100%	4e-14	100.00%	28033	NC_003436.1

Graphic Summary

Distribution of the top 65 Blast Hits on 1 subject sequences



Alignments

Alignment view

Pairwise

☐ CDS feature

Restore defaults

Porcine epidemic diarrhea virus, complete genome
Sequence ID: **NC_003436.1** Length: 28033 Number of Matches: 65
Range 1: 26049 to 26080

Score	Expect	Identities	Gaps	Strand	Frame
63.9 bits(32)	4e-14()	32/32(100%)	0/32(0%)	Plus/Plus	
Query 1	CTGTGATGGGCCGACAGGTCTGCATTCC				
Sbjct 26049	CTGTGATGGGCCGACAGGTCTGCATTCC				

Range 2: 7086 to 7095

Score	Expect	Identities	Gaps	Strand	Frame
20.3 bits(10)	0.49()	10/10(100%)	0/10(0%)	Plus/Plus	
Query 11	CCGAC				
Sbjct 7086	CCGAC				

Range 3: 7430 to 7438

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	2.0()	9/9(100%)	0/9(0%)	Plus/Minus	
Query 13	GACA				
Sbjct 7438	GACA				

Range 4: 18418 to 18426

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	2.0()	9/9(100%)	0/9(0%)	Plus/Plus	
Query 21	TGCA				
Sbjct 1841	TGCA				

Range 5: 19917 to 19925

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	2.0()	9/9(100%)	0/9(0%)	Plus/Minus	
Query 2	TGTGA				
Sbjct 1992	TGTGA				

Range 6: 20147 to 20155

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	2.0()	9/9(100%)	0/9(0%)	Plus/Plus	
Query 2	TGTGA				
Sbjct 2014					

Range 7: 26528 to 26536

Score	Expect	Identities	Gaps	Strand	Frame
18.3 bits(9)	2.0()	9/9(100%)	0/9(0%)	Plus/Minus	
Query 23	CATT				
Sbjct 2653					

Range 8: 2341 to 2348

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 6	ATGG				
Sbjct 234					

Range 9: 5889 to 5896

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 2	TGT				
Sbjct 589					

Range 10: 5951 to 5958

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 9	GGCC				
Sbjct 595					

Range 11: 6455 to 6462

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 1	CTG				
Sbjct 645					

Range 12: 8544 to 8551

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 19	TCT				
Sbjct 855					

Range 13: 13153 to 13160

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 1	CTG				

Sbjct 131 |||||

Range 14: 15613 to 15620

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 21	TGC				
Sbjct 156					

Range 15: 17070 to 17077

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 2	TGT				
Sbjct 170					

Range 16: 17524 to 17531

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 15	CAG				
Sbjct 175					

Range 17: 18042 to 18049

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 2	TGT				
Sbjct 180					

Range 18: 21081 to 21088

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Plus	
Query 23	CAT				
Sbjct 210					

Range 19: 25731 to 25738

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 24	ATT				
Sbjct 257					

Range 20: 27503 to 27510

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 21	TGC				
Sbjct 275					

Range 21: 27622 to 27629

Score	Expect	Identities	Gaps	Strand	Frame
16.4 bits(8)	7.7()	8/8(100%)	0/8(0%)	Plus/Minus	
Query 23	CAT				
Sbjct 276					

Range 22: 334 to 340

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 19	TC				
Sbjct 340					

Range 23: 1817 to 1823

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 7	TGG				
Sbjct 18					

Range 24: 1824 to 1830

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 12	CG				
Sbjct 18					

Range 25: 1985 to 1991

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 21	TG				
Sbjct 19					

Range 26: 3715 to 3721

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 10	GC				
Sbjct 37					

Range 27: 5539 to 5545

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 15	CA				
Sbjct 55					

Range 28: 6529 to 6535

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 16	AG				
Sbjct 65					

Range 29: 6617 to 6623

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 2	TG				
Sbjct 66					

Range 30: 6696 to 6702

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 25	TT				
Sbjct 66					

Range 31: 7236 to 7242

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CT				
Sbjct 72					

Range 32: 7289 to 7295

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 21	TG				
Sbjct 72					

Range 33: 7846 to 7852

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 15	CA				
Sbjct 78					

Range 34: 8498 to 8504

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 18	GT				
Sbjct 84					

Range 35: 8755 to 8761

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 11	CC				
Sbjct 87					

Range 36: 9966 to 9972

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

14.4 bits(7) 30() 7/7(100%) 0/7(0%) Plus/Plus

Query 13 GA
Sbjct 99 |||||||

Range 37: 10088 to 10094

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 19	TC				
Sbjct 10					

Range 38: 10386 to 10392

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 15	CA				
Sbjct 10					

Range 39: 10950 to 10956

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 25	TT				
Sbjct 10					

Range 40: 11542 to 11548

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 21	TG				
Sbjct 11					

Range 41: 12459 to 12465

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 18	GT				
Sbjct 12					

Range 42: 12778 to 12784

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 21	TG				
Sbjct 12					

Range 43: 13391 to 13397

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 24	AT				
Sbjct 13					

Range 44: 15032 to 15038

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 19	TC				
Sbjct 15					

Range 45: 15507 to 15513

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 3	GT				
Sbjct 15					

Range 46: 15885 to 15891

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 17	GG				
Sbjct 15					

Range 47: 18280 to 18286

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 4	TGA				
Sbjct 18					

Range 48: 18550 to 18556

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 20	CT				
Sbjct 18					

Range 49: 20001 to 20007

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 26	TC				
Sbjct 20					

Range 50: 20088 to 20094

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 13	GA				
Sbjct 20					

Range 51: 20388 to 20394

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 1					

Sbjct 20 |||||

Range 52: 21052 to 21058

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 14	AC				
Sbjct 21					

Range 53: 21098 to 21104

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 3	GT				
Sbjct 21					

Range 54: 21117 to 21123

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 10	GC				
Sbjct 21					

Range 55: 22018 to 22024

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 2	TG				
Sbjct 22					

Range 56: 22326 to 22332

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CT				
Sbjct 22					

Range 57: 22373 to 22379

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 13	GA				
Sbjct 22					

Range 58: 22540 to 22546

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 1	CT				
Sbjct 22					

Range 59: 23234 to 23240

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 3	GT				
Sbjct 23					

Range 60: 23308 to 23314

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 16	AG				
Sbjct 23					

Range 61: 24032 to 24038

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 3	GT				
Sbjct 24					

Range 62: 24672 to 24678

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 20	CT				
Sbjct 24					

Range 63: 25414 to 25420

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 20	CT				
Sbjct 25					

Range 64: 26733 to 26739

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Plus	
Query 23	CA				
Sbjct 26					

Range 65: 28006 to 28012

Score	Expect	Identities	Gaps	Strand	Frame
14.4 bits(7)	30()	7/7(100%)	0/7(0%)	Plus/Minus	
Query 15	CA				
Sbjct 28					

Organism	Blast Name	Score	Number of Hits	Description
Porcine epidemic diarrhea virus	viruses	63.9	<u>1</u>	<u>Porcine epidemic diarrhea virus hits</u>

Organism

Description	Score	E value	Accession
Porcine epidemic diarrhea virus [viruses]			
<u>Porcine epidemic diarrhea virus, complete genome</u>	63.9	4e-14	NC_003436

Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
Porcine epidemic diarrhea virus	<u>1</u>	<u>1</u>	<u>Porcine epidemic diarrhea virus hits</u>