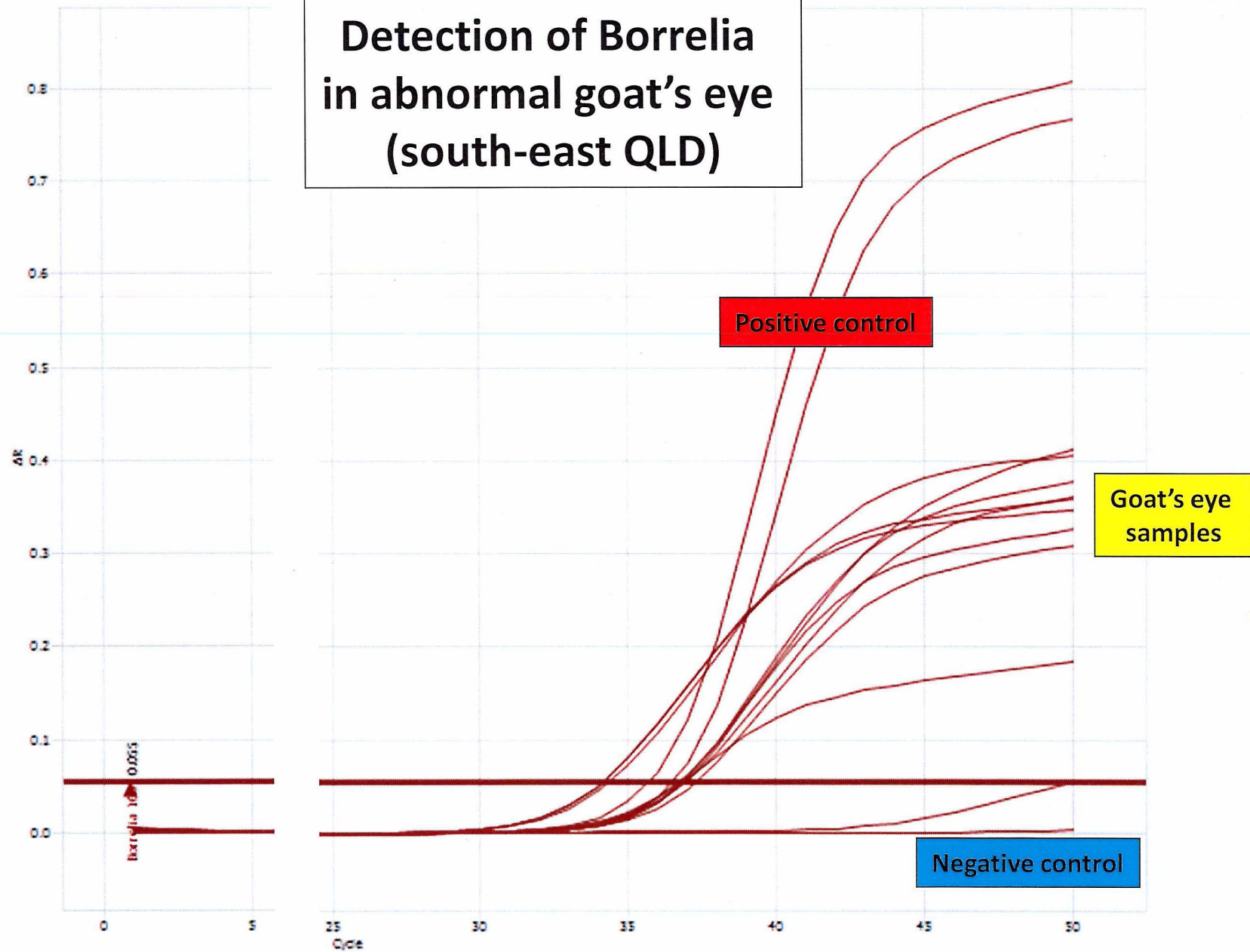


Tabled by Australian Biologies
Ms Jennie Burke
15 April 2016

Detection of *Borrelia* in abnormal goat's eye (south-east QLD)



Results (individual Cq values)

Well	Exclude	Sample Name	Assay Name	Assay Role	Cq
A4		Eye blood vessel	Borrelia 16S	Unknown	34.1
A5		Eye blood vessel	Borrelia 16S	Unknown	34.12
A6		Eye blood vessel	Borrelia 16S	Unknown	34.34
A7		Intraocular flui...	Borrelia 16S	Unknown	36.73
A8		Intraocular flui...	Borrelia 16S	Unknown	36.83
B1		Intraocular flui...	Borrelia 16S	Unknown	36.76
B2		Extraocular tiss...	Borrelia 16S	Unknown	36.66
B3		Extraocular tiss...	Borrelia 16S	Unknown	36.91
B4		Extraocular tiss...	Borrelia 16S	Unknown	37.23
F5		Negative Control	Borrelia 16S	Negative	N/A
F6		Negative Control	Borrelia 16S	Negative	N/A
F7		Positive Control	Borrelia 16S	Positive	35.67
F8		Positive Control	Borrelia 16S	Positive	36.46

Borrelia-associated crystalline keratopathy with intracorneal detection of *Borrelia garinii* by electron microscopy and polymerase chain reaction.

Dietrich T¹, Geissdörfer W, Schlötzer-Schrehardt U, Holbach L, Schoerner C, Seitz B.

Author information

Abstract

First report of a patient with *Borrelia*-associated crystalline keratopathy with intracorneal evidence of *Borrelia garinii* by polymerase chain reaction (PCR) and electron microscopy (EM).

METHODS:

Report of a 67-year-old patient with medical history of recurrent iridocyclitis and arthritis presented with a bilateral, progressive, asymmetric crystalline keratopathy, which was particularly pronounced in the peripheral temporal superior cornea. After penetrating keratoplasty, crystalline keratopathy with stromal haziness recurred. Corneal regrafting was performed. The corneal specimen from the penetrating keratoplasty was examined by light and EM as well as by PCR.

RESULTS:

In the explanted corneal graft, as well as retrospectively in the corneal specimen from the first keratoplasty, spirochetelike bodies and fragments were detected by light and EM. *Borrelia burgdorferi* sensu lato DNA was demonstrated by broad-range (16S rDNA) PCR. A more precise identification as *Borrelia garinii* serotype 5 was possible by analyses of the *flaB* and *ospA* gene sequences. *Borrelia*-specific serological tests showed borderline titers in immunofluorescence and weak reaction in immunoblot, respectively.

CONCLUSIONS:

This case illustrates that borreliae must be considered as a cause of crystalline keratopathy; *Borrelia*-specific serological tests can be false negative; explanted cornea specimens of etiologically unclear crystalline keratopathy should be analyzed by EM or PCR for detection of pathogens; and prolonged antibiotic treatment might be effective to prevent progression or recurrence of the disease.

PMID:

18434857

[PubMed - indexed for MEDLINE]

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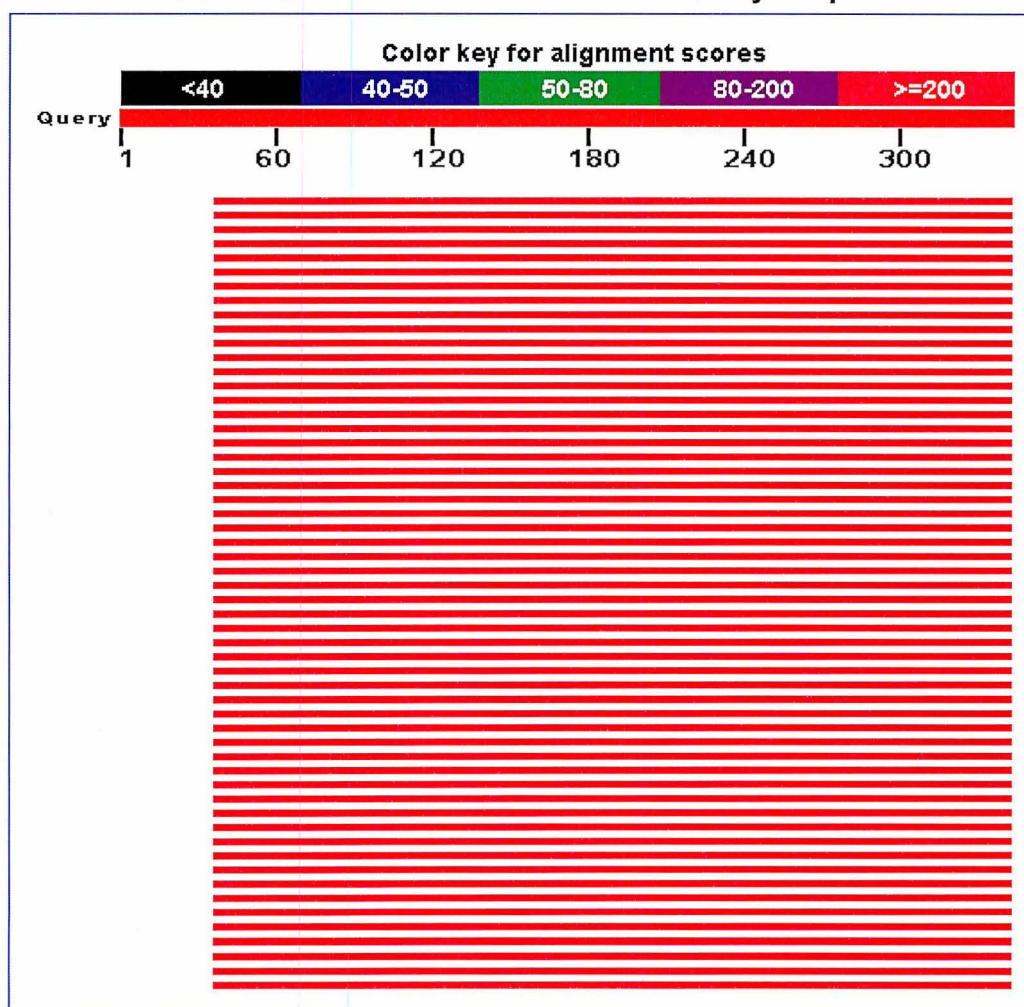
CF0046

Query ID |cl|997
Description None
Molecule type nucleic acid
Query Length 342

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.27+

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Description	Max score	Total score	Query cover	E value	Max ident	Accession
Borrelia burgdorferi N40, complete genome	544	544	89%	2e-151	99%	CP002228.1
Borrelia burgdorferi JD1, complete genome	544	544	89%	2e-151	99%	CP002312.1
Borrelia americana strain SCW-30h 16S ribosomal RNA gene, partial sequence	544	544	89%	2e-151	99%	HM802226.1
Borrelia americana strain SCW-30f 16S ribosomal RNA gene, partial sequence	544	544	89%	2e-151	99%	HM802225.1
Borrelia sp. SCW-30d 16S ribosomal RNA gene, partial sequence	544	544	89%	2e-151	99%	HM802224.1
Borrelia sp. SCW-30c 16S ribosomal RNA gene, partial sequence	544	544	89%	2e-151	99%	HM802223.1
Borrelia sp. SCW-30b 16S ribosomal RNA gene, partial sequence	544	544	89%	2e-151	99%	HM802222.1
Borrelia sp. SCW-30a 16S ribosomal RNA gene, partial sequence	544	544	89%	2e-151	99%	HM802221.1
Borrelia americana strain SCW-42c 16S ribosomal RNA (rrs) gene, partial sequence	544	544	89%	2e-151	99%	EU081288.1
Borrelia americana strain SCW-42b 16S						

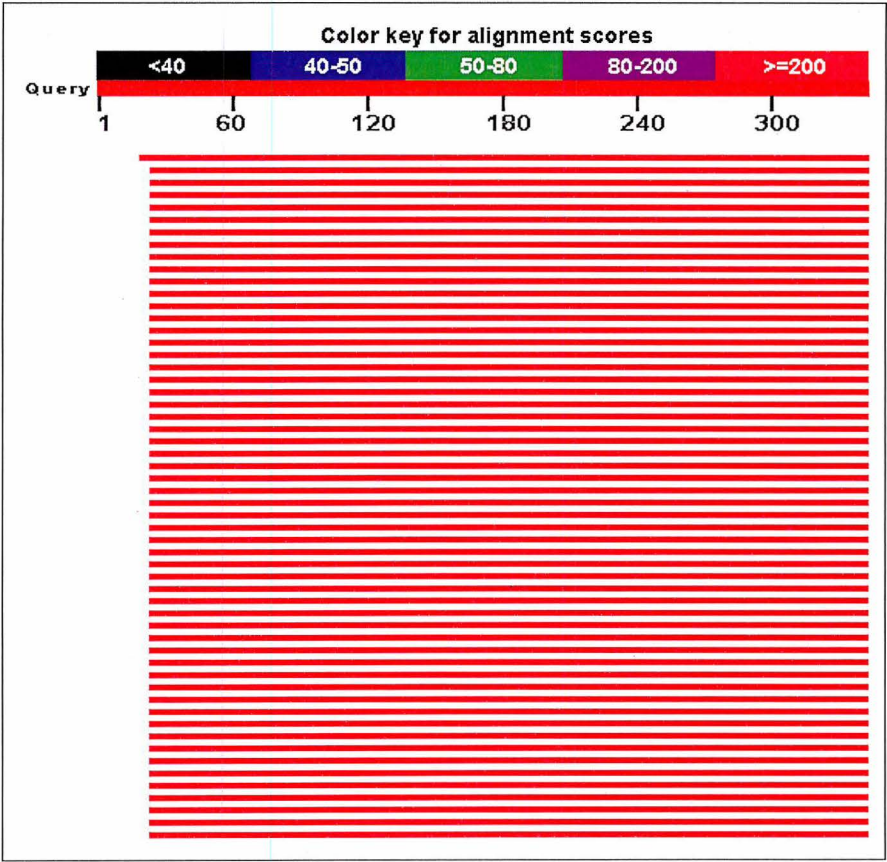
BLAST Results

CF98

RID	GVH53U5M014 (Expires on 04-14 12:01 pm)		
Query ID	Id Query_243679	Database Name	nr
Description	CF98	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.3.1+
Query Length	344		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
<i>Borrelia burgdorferi</i> sensu lato, 16S rRNA gene, isolate CA2	595	595	94%	2e-166	99%	AJ224136.1
<i>Borrelia burgdorferi</i> strain B31, complete genome	592	592	93%	2e-165	100%	CP009656.1
<i>Borrelia burgdorferi</i> CA382, complete genome	592	592	93%	2e-165	100%	CP005925.1
<i>Borrelia burgdorferi</i> N40 strain N40 16S ribosomal RNA, complete sequence	592	592	93%	2e-165	100%	NR_103929.1
<i>Borrelia bavariensis</i> strain PBi 16S ribosomal RNA, complete sequence	592	592	93%	2e-165	100%	NR_074854.1
<i>Borrelia burgdorferi</i> N40, complete genome	592	592	93%	2e-165	100%	CP002228.1
<i>Borrelia burgdorferi</i> JD1, complete genome	592	592	93%	2e-165	100%	CP002312.1
<i>Borrelia americana</i> strain SCW-30h 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	HM802226.1
<i>Borrelia</i> sp. SCW-30d 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	HM802224.1
<i>Borrelia</i> sp. SCW-30b 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	HM802222.1
<i>Borrelia</i> sp. SCW-30a 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	HM802221.1
<i>Borrelia americana</i> strain SCW-42c 16S ribosomal RNA (rrs) gene, partial sequence	592	592	93%	2e-165	100%	EU081288.1
<i>Borrelia americana</i> strain SCW-42b 16S ribosomal RNA (rrs) gene, partial sequence	592	592	93%	2e-165	100%	EU081287.1
<i>Borrelia americana</i> strain SCW-33 16S ribosomal RNA (rrs) gene, partial sequence	592	592	93%	2e-165	100%	EU081286.1
<i>Borrelia americana</i> strain SCW-41 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	NR_116166.1
<i>Borrelia burgdorferi</i> strain SCCH5 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	EF015630.1
<i>Borrelia burgdorferi</i> ZS7, complete genome	592	592	93%	2e-165	100%	CP001205.1
<i>Borrelia yangtzensis</i> strain QTMP2 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	EU135597.1
<i>Borrelia yangtzensis</i> strain QSYSP3 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	EU135595.1
<i>Borrelia burgdorferi</i> isolate BUL-1 16S ribosomal RNA (rrs) gene, partial sequence	592	592	93%	2e-165	100%	EU014796.1
<i>Borrelia</i> sp. Ir-3519 partial 16S rRNA gene, isolate Ir-3519	592	592	93%	2e-165	100%	AM418456.1
<i>Borrelia garinii</i> partial 16S rRNA gene, isolate Ir-2200	592	592	93%	2e-165	100%	AM418453.1
<i>Borrelia garinii</i> PBi, complete genome	592	592	93%	2e-165	100%	CP000013.1
<i>Borrelia garinii</i> strain K48 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	AY342032.1
<i>Borrelia garinii</i> strain Sika1 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	AY342029.1
<i>Borrelia burgdorferi</i> strain IP2 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	AY342028.1
<i>Borrelia</i> sp. SCGT-10 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	AF467970.1
<i>Borrelia</i> sp. MI-9 16S ribosomal RNA gene, partial sequence	592	592	93%	2e-165	100%	AF467968.1

BLAST Results

CF109

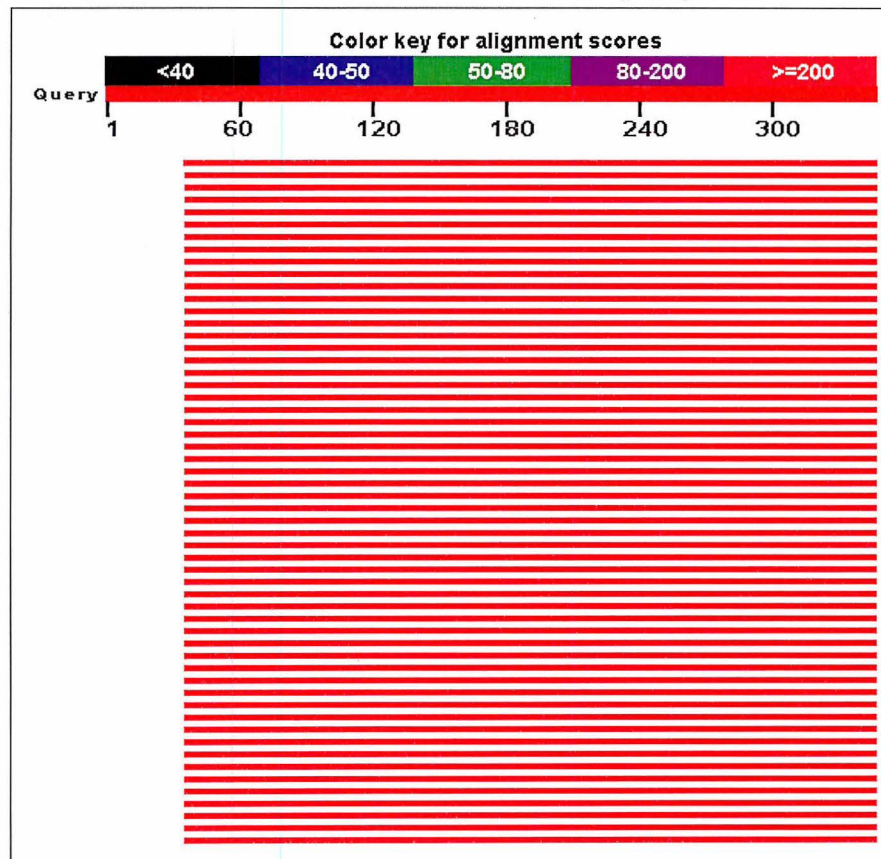
RID [GVHC456001R](#) (Expires on 04-14 12:05 pm)

Query ID Id|Query_7529
Description CF109
Molecule type nucleic acid
Query Length 345

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
B.burgdorferi 16S ribosomal RNA	573	573	89%	8e-160	100%	M60967.1
Borrelia burgdorferi strain B31, complete genome	571	571	89%	3e-159	100%	CP009656.1
Borrelia burgdorferi CA382, complete genome	571	571	89%	3e-159	100%	CP005925.1
Borrelia burgdorferi N40 strain N40 16S ribosomal RNA, complete sequence	571	571	89%	3e-159	100%	NR_103929.1
Borrelia bavariensis strain PBI 16S ribosomal RNA, complete sequence	571	571	89%	3e-159	100%	NR_074854.1
Borrelia burgdorferi N40, complete genome	571	571	89%	3e-159	100%	CP002228.1
Borrelia burgdorferi JD1, complete genome	571	571	89%	3e-159	100%	CP002312.1
Borrelia americana strain SCW-30h 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	HM802226.1
Borrelia sp. SCW-30d 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	HM802224.1
Borrelia sp. SCW-30b 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	HM802222.1
Borrelia sp. SCW-30a 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	HM802221.1
Borrelia americana strain SCW-42c 16S ribosomal RNA (rrs) gene, partial sequence	571	571	89%	3e-159	100%	EU081288.1
Borrelia americana strain SCW-42b 16S ribosomal RNA (rrs) gene, partial sequence	571	571	89%	3e-159	100%	EU081287.1
Borrelia americana strain SCW-33 16S ribosomal RNA (rrs) gene, partial sequence	571	571	89%	3e-159	100%	EU081286.1
Borrelia americana strain SCW-41 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	NR_116166.1
Borrelia burgdorferi strain SCCH5 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	EF015630.1
Borrelia burgdorferi ZS7, complete genome	571	571	89%	3e-159	100%	CP001205.1
Borrelia yangtzensis strain QTMP2 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	EU135597.1
Borrelia yangtzensis strain QSYSP3 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	EU135595.1
Borrelia burgdorferi isolate BUL-1 16S ribosomal RNA (rrs) gene, partial sequence	571	571	89%	3e-159	100%	EU014796.1
Borrelia sp. Ir-3519 partial 16S rRNA gene, isolate Ir-3519	571	571	89%	3e-159	100%	AM418456.1
Borrelia garinii partial 16S rRNA gene, isolate Ir-2200	571	571	89%	3e-159	100%	AM418453.1
Borrelia garinii PBI, complete genome	571	571	89%	3e-159	100%	CP000013.1
Borrelia garinii strain K48 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	AY342032.1
Borrelia garinii strain Sika1 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	AY342029.1
Borrelia burgdorferi strain IP2 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	AY342028.1
Borrelia sp. SCGT-10 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	AF467970.1
Borrelia sp. MI-9 16S ribosomal RNA gene, partial sequence	571	571	89%	3e-159	100%	AF467968.1

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CF398

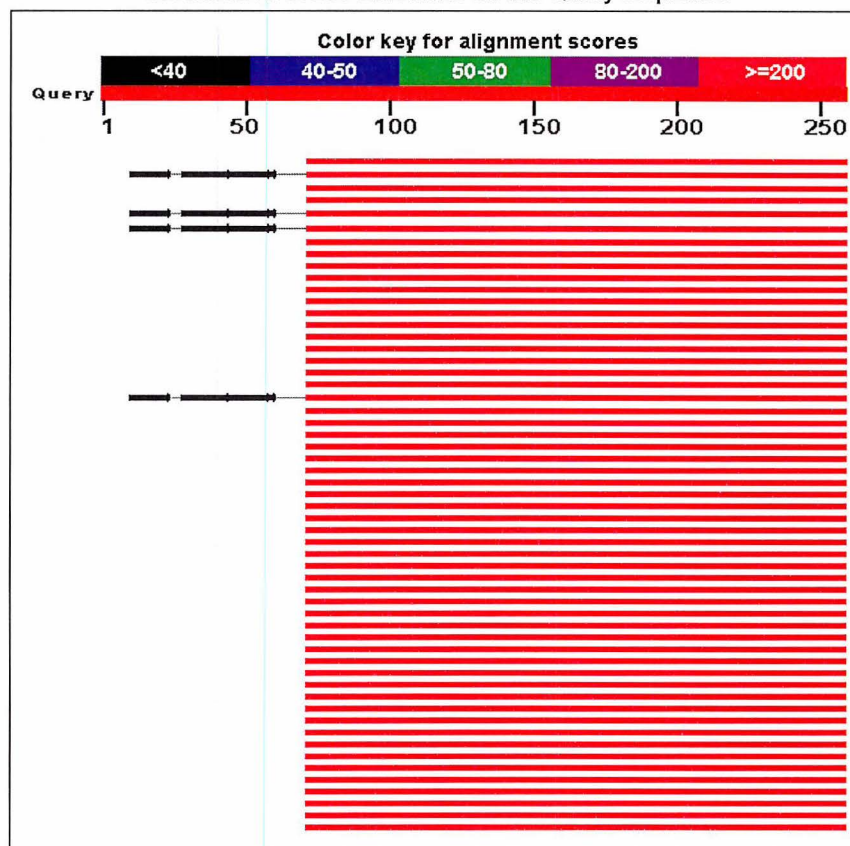
RID [YGA9EHB014](#) (Expires on 08-12 10:23 am)

Query ID |cl|25279
Description None
Molecule type nucleic acid
Query Length 258

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.29+

Graphic Summary

Distribution of 220 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Borrelia burgdorferi strain ATCC 35210 16S ribosomal RNA gene, complete sequence	371	371	72%	2e-102	100%	NR_044732.2
Borrelia burgdorferi CA382, complete genome	371	983	90%	2e-102	100%	CP005925.1
Borrelia burgdorferi N40 strain N40 16S ribosomal RNA, complete sequence	371	371	72%	2e-102	100%	NR_103929.1
Borrelia garinii PBi strain PBi 16S ribosomal RNA, complete sequence	371	371	72%	2e-102	100%	NR_074854.1
Borrelia burgdorferi N40, complete genome	371	1026	90%	2e-102	100%	CP002228.1
Borrelia burgdorferi JD1, complete genome	371	1032	90%	2e-102	100%	CP002312.1
Borrelia americana strain SCW-30h 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	HM802226.1
Borrelia sp. SCW-30d 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	HM802224.1
Borrelia sp. SCW-30b 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	HM802222.1
Borrelia sp. SCW-30a 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	HM802221.1
Borrelia burgdorferi strain CA8 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	GQ247740.1
Borrelia americana strain SCW-42c 16S ribosomal RNA (rrs) gene, partial sequence	371	371	72%	2e-102	100%	EU081288.1
Borrelia americana strain SCW-42b 16S ribosomal RNA (rrs) gene, partial sequence	371	371	72%	2e-102	100%	EU081287.1
Borrelia americana strain SCW-33 16S ribosomal RNA (rrs) gene, partial sequence	371	371	72%	2e-102	100%	EU081286.1
Borrelia americana strain SCW-41 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	NR_116166.1
Borrelia americana strain SCW-32 16S ribosomal RNA (rrs) gene, partial sequence	371	371	72%	2e-102	100%	EU081284.1
Borrelia americana strain SCW-30g 16S ribosomal RNA (rrs) gene, partial sequence	371	371	72%	2e-102	100%	EU081283.1
Borrelia americana strain SCW-30e 16S ribosomal RNA (rrs) gene, partial sequence	371	371	72%	2e-102	100%	EU081282.1
Borrelia burgdorferi strain SCCH5 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	EF015630.1
Borrelia burgdorferi ZS7, complete genome	371	983	90%	2e-102	100%	CP001205.1
Borrelia sp. SCW-42a 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	EF570073.1
Borrelia sp. SCCH-5 16S ribosomal RNA gene, partial sequence	371	371	72%	2e-102	100%	EF570071.1

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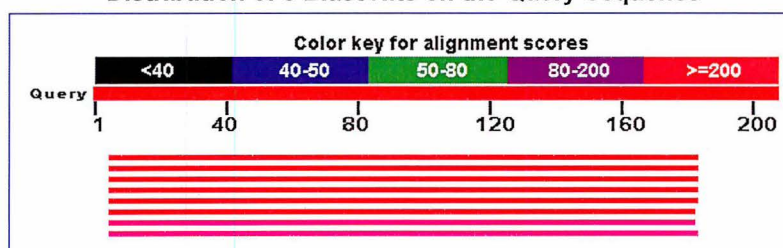
CF0544

Query ID lc|18917
Description None
Molecule type nucleic acid
Query Length 207

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.27+

Graphic Summary

Distribution of 8 Blast Hits on the Query Sequence



Descriptions

Description	Max score	Total score	Query cover	E value	Max ident	Accession
Borrelia burgdorferi N40, complete genome	243	243	85%	5e-61	91%	CP002228.1
Borrelia burgdorferi ZS7, complete genome	243	243	85%	5e-61	91%	CP001205.1
Borrelia burgdorferi B31, complete genome	243	243	85%	5e-61	91%	AE000783.1
Borrelia burgdorferi JD1, complete genome	237	237	85%	2e-59	91%	CP002312.1
Borrelia bissetii DN127, complete genome	204	204	85%	2e-49	87%	CP002746.1
Borrelia garinii BgVir chromosome linear, complete sequence	202	202	85%	9e-49	87%	CP003151.1
Borrelia garinii NMJW1, complete genome	196	196	85%	4e-47	87%	CP003866.1
Borrelia garinii PBi, complete genome	193	193	85%	5e-46	86%	CP000013.1

Alignments

Borrelia burgdorferi N40, complete genome

Sequence ID: [gb|CP002228.1|](#) Length: 902191 Number of Matches: 1
Range 1: 396834 to 397013

Score	Expect	Identities	Gaps	Strand	Frame
243 bits(131)	5e-61()	164/180(91%)	2/180(1%)	Plus/Minus	
Features:					
Query 6	TTTAAATC-CTTCAAAAAGGT-AAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAA	63			
Sbjct 397013	TTTAAATCAATTCAAAAAGGTAAAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAA	396954			
Query 64	CATAAGCATTATATTaaaaaaaGAAAACATCTTTGGTTAGAGATGGAGATGTTGTACCC	123			
Sbjct 396953	CATAAGCATTATATTCCAGCTGGAACATCTTTGGTTAGAGATGGAGATGTTGTAAAA	396894			
Query 124	CCAGGAGACATGCTTTGTGATGGTAGAATCAATCCTCATGATGTCTTGAAATTTAGGT	183			
Sbjct 396893	GCAGGAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGTGCTTGAAATTTAGGT	396834			

Borrelia burgdorferi ZS7, complete genome

Sequence ID: [gb|CP001205.1|](#) Length: 906707 Number of Matches: 1
Range 1: 397347 to 397526

Score	Expect	Identities	Gaps	Strand	Frame
243 bits(131)	5e-61()	164/180(91%)	2/180(1%)	Plus/Minus	
Features:					
Query 6	TTTAAATC-CTTCAAAAAGGT-AAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAA	63			
Sbjct 397526	TTTAAATCAATTCAAAAAGGTAAAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAA	397467			
Query 64	CATAAGCATTATATTaaaaaaaGAAAACATCTTTGGTTAGAGATGGAGATGTTGTACCC	123			
Sbjct 397466	CATAAGCATTATATTCCAGCTGGAACATCTTTGGTTAGAGATGGAGATGTTGTAAAA	397407			
Query 124	CCAGGAGACATGCTTTGTGATGGTAGAATCAATCCTCATGATGTCTTGAAATTTAGGT	183			
Sbjct 397406	GCAGGAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGTGCTTGAAATTTAGGT	397347			

Borrelia burgdorferi B31, complete genome

Sequence ID: [gb|AE000783.1|](#) Length: 910724 Number of Matches: 1
Range 1: 398009 to 398188

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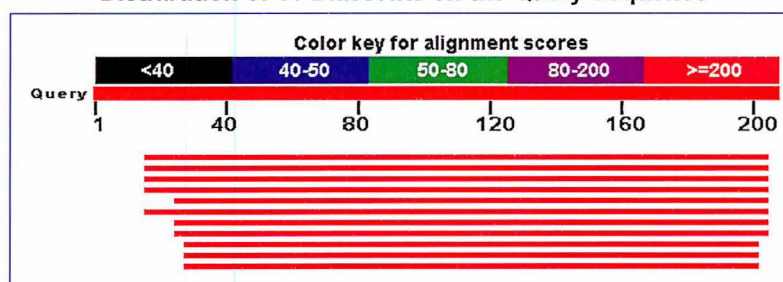
CF0618

Query ID lc|18593
Description None
Molecule type nucleic acid
Query Length 208

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.27+

Graphic Summary

Distribution of 11 Blast Hits on the Query Sequence



Descriptions

Description	Max score	Total score	Query cover	E value	Max ident	Accession
Borrelia burgdorferi N40, complete genome	289	289	90%	7e-75	94%	CP002228.1
Borrelia burgdorferi ZS7, complete genome	289	289	90%	7e-75	94%	CP001205.1
Borrelia burgdorferi B31, complete genome	289	289	90%	7e-75	94%	AE000783.1
Borrelia burgdorferi JD1, complete genome	283	283	90%	3e-73	94%	CP002312.1
Borrelia garinii BgVir chromosome linear, complete sequence	244	244	86%	1e-61	91%	CP003151.1
Borrelia bissettii DN127, complete genome	244	244	90%	1e-61	90%	CP002746.1
Borrelia garinii NMJW1, complete genome	239	239	86%	7e-60	91%	CP003866.1
Borrelia garinii PBi, complete genome	239	239	86%	7e-60	91%	CP000013.1
Borrelia afzelii HLJ01, complete genome	233	233	83%	3e-58	91%	CP003882.1
Borrelia afzelii PKo, complete genome	233	233	83%	3e-58	91%	CP002933.1
Borrelia afzelii PKo, complete genome	233	233	83%	3e-58	91%	CP000395.1

Alignments

Borrelia burgdorferi N40, complete genome

Sequence ID: [gb|CP002228.1|](#) Length: 902191 Number of Matches: 1

Range 1: 396810 to 396999

Score	Expect	Identities	Gaps	Strand	Frame
289 bits(156)	7e-75()	180/191(94%)	3/191(1%)	Plus/Minus	

Features:

Query	17	AAAGGGT-ATAGGCTTATT-ATATTTTAGATGAGTATGGGGTTGAACATAAGCATTATAT	74
Sbjct	396999	AAAAGGTAAAAGGCTTATTAATATTTTAGATGAGTATGGGGTTGAACATAAGCATTATAT	396940
Query	75	TCCAGAGGGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAATCATGAGATATGC	134
Sbjct	396939	TCCAG-CTGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAGCAGGAGATATGC	396881
Query	135	TTTGTGATGGTAGAATTAACTCATGATGTGCTTGAAATTTTAGGTGGGATTAGTTTAC	194
Sbjct	396880	TTTGTGATGGTAGAATTAACTCATGATGTGCTTGAAATTTTAGGTGGGATTAGTTTAC	396821
Query	195	AATATTTTCTG 205	
Sbjct	396820	AAGAATTTCTG 396810	

Borrelia burgdorferi ZS7, complete genome

Sequence ID: [gb|CP001205.1|](#) Length: 906707 Number of Matches: 1

Range 1: 397323 to 397512

Score	Expect	Identities	Gaps	Strand	Frame
289 bits(156)	7e-75()	180/191(94%)	3/191(1%)	Plus/Minus	

Features:

Query	17	AAAGGGT-ATAGGCTTATT-ATATTTTAGATGAGTATGGGGTTGAACATAAGCATTATAT	74
Sbjct	397512	AAAAGGTAAAAGGCTTATTAATATTTTAGATGAGTATGGGGTTGAACATAAGCATTATAT	397453
Query	75	TCCAGAGGGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAATCATGAGATATGC	134
Sbjct	397452	TCCAG-CTGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAGCAGGAGATATGC	397394

BLAST Results

CF275

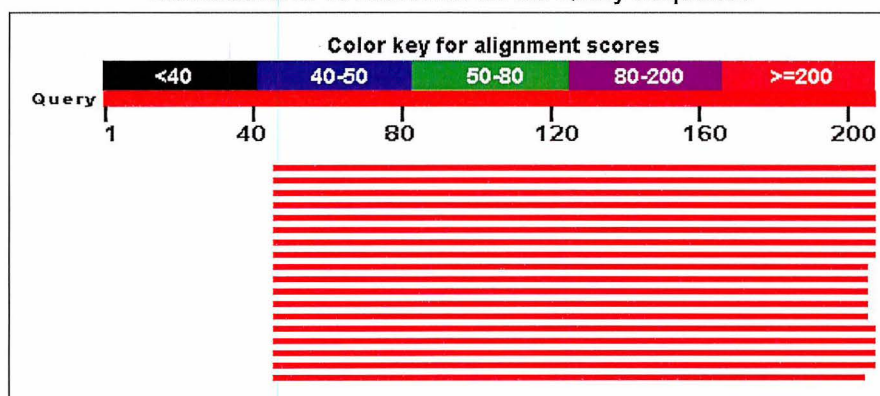
RID [GVHMTSGK01R](#) (Expires on 04-14 12:10 pm)

Query ID lcl|Query_213699
Description CF275
Molecule type nucleic acid
Query Length 207

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.3.1+

Graphic Summary

Distribution of 18 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Borrelia burgdorferi strain B31, complete genome	292	292	77%	1e-75	99%	CP009656.1
Borrelia burgdorferi CA382, complete genome	292	292	77%	1e-75	99%	CP005925.1
Borrelia burgdorferi N40, complete genome	292	292	77%	1e-75	99%	CP002228.1
Borrelia burgdorferi ZS7, complete genome	292	292	77%	1e-75	99%	CP001205.1
Borrelia burgdorferi B31, complete genome	292	292	77%	1e-75	99%	AE000783.1
Borrelia burgdorferi JD1, complete genome	287	287	77%	6e-74	99%	CP002312.1
Borrelia chilensis strain VA1, complete genome	248	248	77%	3e-62	94%	CP009910.1
Borrelia bissetii DN127, complete genome	243	243	77%	1e-60	94%	CP002746.1
Borrelia afzelii K78, complete genome	239	239	76%	2e-59	94%	CP009058.1
Borrelia afzelii Tom3107, complete genome	239	239	76%	2e-59	94%	CP009212.1
Borrelia afzelii HLJ01, complete genome	239	239	76%	2e-59	94%	CP003882.1
Borrelia afzelii PKo, complete genome	239	239	76%	2e-59	94%	CP002933.1
Borrelia afzelii PKo, complete genome	239	239	76%	2e-59	94%	CP000395.1
Borrelia garinii BgVir chromosome linear, complete sequence	237	237	77%	6e-59	93%	CP003151.1
Borrelia garinii SZ, complete genome	231	231	77%	3e-57	93%	CP007564.1
Borrelia garinii NMJW1, complete genome	231	231	77%	3e-57	93%	CP003866.1
Borrelia garinii PBi, complete genome	231	231	77%	3e-57	93%	CP000013.1
Borrelia valaisiana Tom4006, complete genome	215	215	76%	3e-52	91%	CP009117.1

Alignments

Borrelia burgdorferi strain B31, complete genome

Sequence ID: [gb|CP009656.1](#) | Length: 910687 Number of Matches: 1

Range 1: 397951 to 398111

Score	Expect	Identities	Gaps	Strand	Frame
292 bits(158)	1e-75()	160/161(99%)	0/161(0%)	Plus/Minus	
Features:					
Query 47		GATGATTATGGGGTTGAACATAAGCATTATATTCAGCTGGAAAACATCTTTGGTTAGA			106
Sbjct 398111		GATGAGTATGGGGTTGAACATAAGCATTATATTCAGCTGGAAAACATCTTTGGTTAGA			398052
Query 107		GATGGAGATGTTGTAAAAGCAGGAGATATGCTTTGTGATGGTAGAATTAATCCTCATGAT			166
Sbjct 398051		GATGGAGATGTTGTAAAAGCAGGAGATATGCTTTGTGATGGTAGAATTAATCCTCATGAT			397992
Query 167		GTGCTTGAAATTTTAGGTGGGATTAGTTTACAAGAATTCT		207	
Sbjct 397991		GTGCTTGAAATTTTAGGTGGGATTAGTTTACAAGAATTCT		397951	

Borrelia burgdorferi CA382, complete genome

Sequence ID: [gb|CP005925.1](#) | Length: 910736 Number of Matches: 1

Range 1: 397995 to 398155

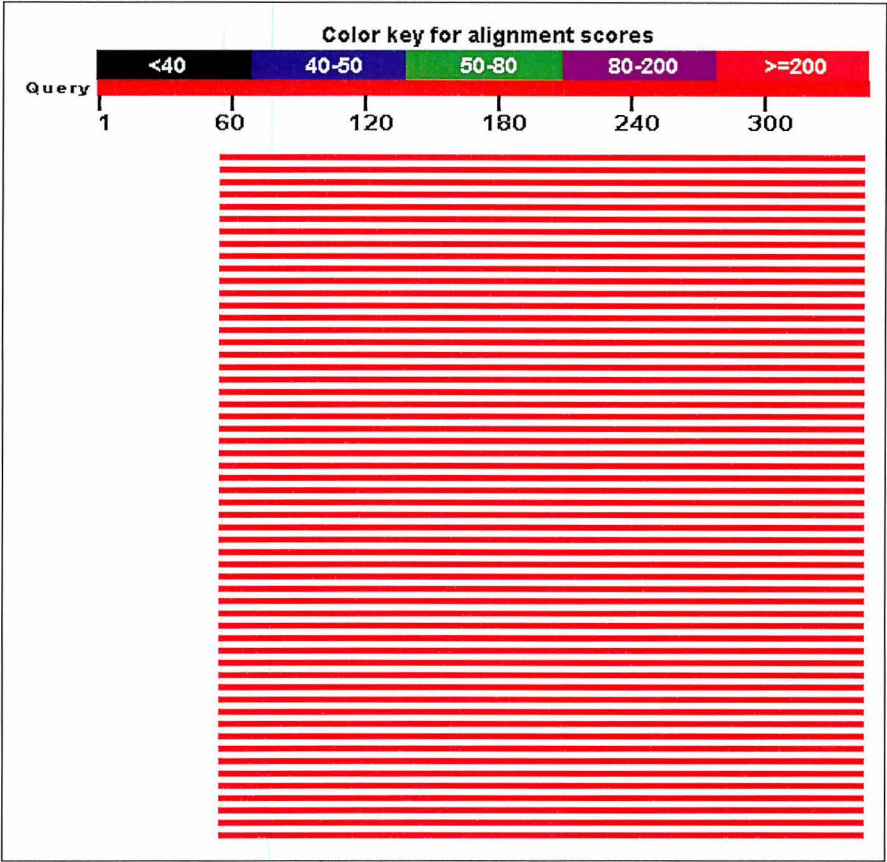
BLAST Results

CF133

RID	GVHFPXEX01R (Expires on 04-14 12:07 pm)		
Query ID	Id Query_181927	Database Name	nr
Description	CF133	Description	Nucleotide collection (nt)
Molecule type	nucleic acid	Program	BLASTN 2.3.1+
Query Length	348		

Graphic Summary

Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
<i>Borrelia burgdorferi</i> strain B31, complete genome	520	520	83%	1e-143	99%	CP009656.1
<i>Borrelia burgdorferi</i> CA382, complete genome	520	520	83%	1e-143	99%	CP005925.1
<i>Borrelia burgdorferi</i> N40 strain N40 16S ribosomal RNA, complete sequence	520	520	83%	1e-143	99%	NR_103929.1
<i>Borrelia bavariensis</i> strain PBi 16S ribosomal RNA, complete sequence	520	520	83%	1e-143	99%	NR_074854.1
<i>Borrelia burgdorferi</i> N40, complete genome	520	520	83%	1e-143	99%	CP002228.1
<i>Borrelia burgdorferi</i> JD1, complete genome	520	520	83%	1e-143	99%	CP002312.1
<i>Borrelia americana</i> strain SCW-30h 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	HM802226.1
<i>Borrelia</i> sp. SCW-30d 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	HM802224.1
<i>Borrelia</i> sp. SCW-30b 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	HM802222.1
<i>Borrelia</i> sp. SCW-30a 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	HM802221.1
<i>Borrelia americana</i> strain SCW-42c 16S ribosomal RNA (rrs) gene, partial sequence	520	520	83%	1e-143	99%	EU081288.1
<i>Borrelia americana</i> strain SCW-42b 16S ribosomal RNA (rrs) gene, partial sequence	520	520	83%	1e-143	99%	EU081287.1
<i>Borrelia americana</i> strain SCW-33 16S ribosomal RNA (rrs) gene, partial sequence	520	520	83%	1e-143	99%	EU081286.1
<i>Borrelia americana</i> strain SCW-41 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	NR_116166.1
<i>Borrelia americana</i> strain SCW-30e 16S ribosomal RNA (rrs) gene, partial sequence	520	520	83%	1e-143	99%	EU081282.1
<i>Borrelia burgdorferi</i> strain SCCH5 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	EF015630.1
<i>Borrelia burgdorferi</i> ZS7, complete genome	520	520	83%	1e-143	99%	CP001205.1
<i>Borrelia yangtzensis</i> strain QTMP2 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	EU135597.1
<i>Borrelia yangtzensis</i> strain QSYSP3 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	EU135595.1
<i>Borrelia burgdorferi</i> isolate BUL-1 16S ribosomal RNA (rrs) gene, partial sequence	520	520	83%	1e-143	99%	EU014796.1
<i>Borrelia</i> sp. Ir-3519 partial 16S rRNA gene, isolate Ir-3519	520	520	83%	1e-143	99%	AM418456.1
<i>Borrelia garinii</i> partial 16S rRNA gene, isolate Ir-2200	520	520	83%	1e-143	99%	AM418453.1
<i>Borrelia garinii</i> PBi, complete genome	520	520	83%	1e-143	99%	CP000013.1
<i>Borrelia garinii</i> strain K48 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	AY342032.1
<i>Borrelia garinii</i> strain Sika1 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	AY342029.1
<i>Borrelia burgdorferi</i> strain IP2 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	AY342028.1
<i>Borrelia</i> sp. SCGT-10 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	AF467970.1
<i>Borrelia</i> sp. MI-9 16S ribosomal RNA gene, partial sequence	520	520	83%	1e-143	99%	AF467968.1

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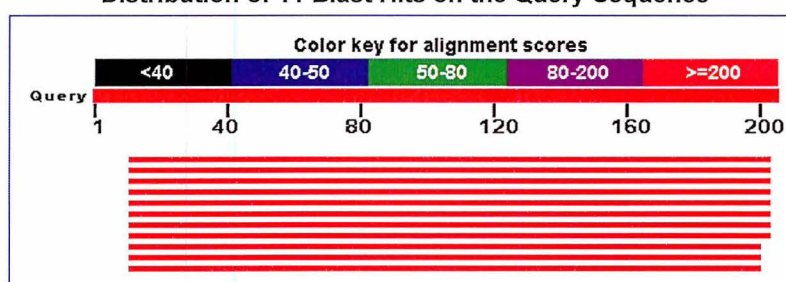
CF0897

Query ID lc|40837
Description None
Molecule type nucleic acid
Query Length 206

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.27+

Graphic Summary

Distribution of 11 Blast Hits on the Query Sequence



Descriptions

Description	Max score	Total score	Query cover	E value	Max ident	Accession
Borrelia burgdorferi N40, complete genome	331	331	93%	1e-87	97%	CP002228.1
Borrelia burgdorferi ZS7, complete genome	331	331	93%	1e-87	97%	CP001205.1
Borrelia burgdorferi B31, complete genome	331	331	93%	1e-87	97%	AE000783.1
Borrelia burgdorferi JD1, complete genome	326	326	93%	5e-86	97%	CP002312.1
Borrelia bissetii DN127, complete genome	281	281	93%	1e-72	93%	CP002746.1
Borrelia garinii BgVir chromosome linear, complete sequence	276	276	93%	5e-71	92%	CP003151.1
Borrelia garinii NMJW1, complete genome	270	270	93%	2e-69	92%	CP003866.1
Borrelia garinii PBi, complete genome	270	270	93%	2e-69	92%	CP000013.1
Borrelia afzelii HLJ01, complete genome	265	265	92%	1e-67	92%	CP003882.1
Borrelia afzelii PKo, complete genome	265	265	92%	1e-67	92%	CP002933.1
Borrelia afzelii PKo, complete genome	265	265	92%	1e-67	92%	CP000395.1

Alignments

Borrelia burgdorferi N40, complete genome

Sequence ID: [gb|CP002228.1|](#) Length: 902191 Number of Matches: 1

Range 1: 396810 to 397004

Score	Expect	Identities	Gaps	Strand	Frame
331 bits(179)	1e-87()	190/195(97%)	2/195(1%)	Plus/Minus	
Features:					
Query 12	ATTC-AAAAGGT-AAAGGCTTATTAATATTTTAGATGAGTATGGGGTTGAACATAAGCAT	69			
Sbjct 397004	ATTCAAAAAGGTAAAAGGCTTATTAATATTTTAGATGAGTATGGGGTTGAACATAAGCAT	396945			
Query 70	TATATTCAGCGGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAAGCATGAGAT	129			
Sbjct 396944	TATATTCAGCTGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAAGCAGGAGAT	396885			
Query 130	ATGCTTTGTGATGGTAGAATTAATCCTCATGATGTGCTTGAAATTTTAGGTGGGATTAAAT	189			
Sbjct 396884	ATGCTTTGTGATGGTAGAATTAATCCTCATGATGTGCTTGAAATTTTAGGTGGGATTAGT	396825			
Query 190	TTACAAGAATTCTG 204				
Sbjct 396824	TTACAAGAATTCTG 396810				

Borrelia burgdorferi ZS7, complete genome

Sequence ID: [gb|CP001205.1|](#) Length: 906707 Number of Matches: 1

Range 1: 397323 to 397517

Score	Expect	Identities	Gaps	Strand	Frame
331 bits(179)	1e-87()	190/195(97%)	2/195(1%)	Plus/Minus	
Features:					
Query 12	ATTC-AAAAGGT-AAAGGCTTATTAATATTTTAGATGAGTATGGGGTTGAACATAAGCAT	69			
Sbjct 397517	ATTCAAAAAGGTAAAAGGCTTATTAATATTTTAGATGAGTATGGGGTTGAACATAAGCAT	397458			
Query 70	TATATTCAGCGGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAAGCATGAGAT	129			
Sbjct 397457	TATATTCAGCTGGAAAACATCTTTTGGTTAGAGATGGAGATGTTGTAAAAGCAGGAGAT	397398			

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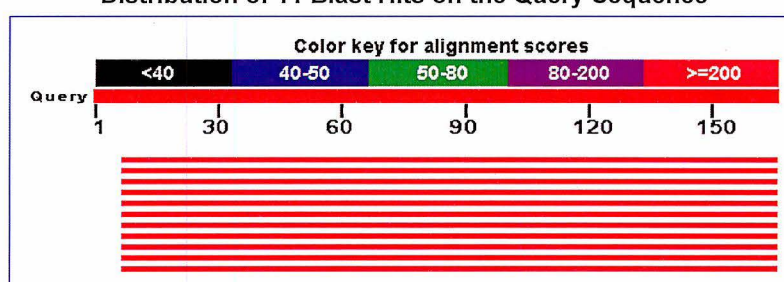
CF0975

Query ID lc|64927
Description None
Molecule type nucleic acid
Query Length 165

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.27+

Graphic Summary

Distribution of 11 Blast Hits on the Query Sequence



Descriptions

Description	Max score	Total score	Query cover	E value	Max ident	Accession
Borrelia burgdorferi N40, complete genome	267	267	95%	2e-68	97%	CP002228.1
Borrelia burgdorferi ZS7, complete genome	267	267	95%	2e-68	97%	CP001205.1
Borrelia burgdorferi B31, complete genome	267	267	95%	2e-68	97%	AE000783.1
Borrelia burgdorferi JD1, complete genome	261	261	95%	1e-66	96%	CP002312.1
Borrelia garinii BgVir chromosome linear, complete sequence	228	228	95%	1e-56	93%	CP003151.1
Borrelia bissettii DN127, complete genome	228	228	95%	1e-56	93%	CP002746.1
Borrelia garinii NMJW1, complete genome	222	222	95%	5e-55	92%	CP003866.1
Borrelia afzelii HLJ01, complete genome	217	217	95%	2e-53	91%	CP003882.1
Borrelia afzelii PKo, complete genome	217	217	95%	2e-53	91%	CP002933.1
Borrelia afzelii PKo, complete genome	217	217	95%	2e-53	91%	CP000395.1
Borrelia garinii PBi, complete genome	217	217	95%	2e-53	91%	CP000013.1

Alignments

Borrelia burgdorferi N40, complete genome

Sequence ID: [gb|CP002228.1](#) Length: 902191 Number of Matches: 1

Range 1: 396850 to 397009

Score	Expect	Identities	Gaps	Strand	Frame
267 bits(144)	2e-68()	155/160(97%)	2/160(1%)	Plus/Minus	
Features:					
Query 8	AATCAGTTC-GAAAGGT-AAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAACATA	65			
Sbjct 397009	AATCAATTCAAAAAGGTAAAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAACATA	396950			
Query 66	AGCATTATATTCAGCAGGAAAACATCTTTGGTTAGAGATGGAGATGTTGTAAAAGCAG	125			
Sbjct 396949	AGCATTATATTCAGCTGGAAAACATCTTTGGTTAGAGATGGAGATGTTGTAAAAGCAG	396890			
Query 126	GAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGT	165			
Sbjct 396889	GAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGT	396850			

Borrelia burgdorferi ZS7, complete genome

Sequence ID: [gb|CP001205.1](#) Length: 906707 Number of Matches: 1

Range 1: 397363 to 397522

Score	Expect	Identities	Gaps	Strand	Frame
267 bits(144)	2e-68()	155/160(97%)	2/160(1%)	Plus/Minus	
Features:					
Query 8	AATCAGTTC-GAAAGGT-AAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAACATA	65			
Sbjct 397522	AATCAATTCAAAAAGGTAAAAGGCTTATTAATATTTAGATGAGTATGGGGTTGAACATA	397463			
Query 66	AGCATTATATTCAGCAGGAAAACATCTTTGGTTAGAGATGGAGATGTTGTAAAAGCAG	125			
Sbjct 397462	AGCATTATATTCAGCTGGAAAACATCTTTGGTTAGAGATGGAGATGTTGTAAAAGCAG	397403			
Query 126	GAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGT	165			
Sbjct 397402	GAGATATGCTTTGTGATGGTAGAATTAATCCTCATGATGT	397363			