

Supplementary files

S1 – Consensus sequence, isolated by *Cot*-1, contained in the *pBd*_11 clone and GenBank analysis

> *pBd*_11

```
TTTTGTAAAAACGTACGCCAGTGAATTCGAGCTCGGTACCCGGGGATCCGATATACGATACA
AAATAGAAATAAAATTAGTAAGAAAACGGAGAGACACGATCGGGGAATGACAAGAGGAATG
GAACGGGTTAGAGAAGGGTAAAAATACCGATGAATATTTTATCGAGAACTCGCAAAACTC
CAAGCGCGGTTTGTATCCATTTCAGAGTCTCGGGGACCGTCTTATAGTAAGGCATCCGTCC
GACCTTTGACCTTTGCTCGGTCCGCAATCCATATGACTAGTAGATCCTCTAGAGTCGACCTGC
AGGCATGCAAGCTTCCCTATAGTGAGTCGTATTAGAGCTTGGCGTAATCATGGTCATAGCT
GTTTCCTGA
```

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Nucleotide Sequence (379 letters)

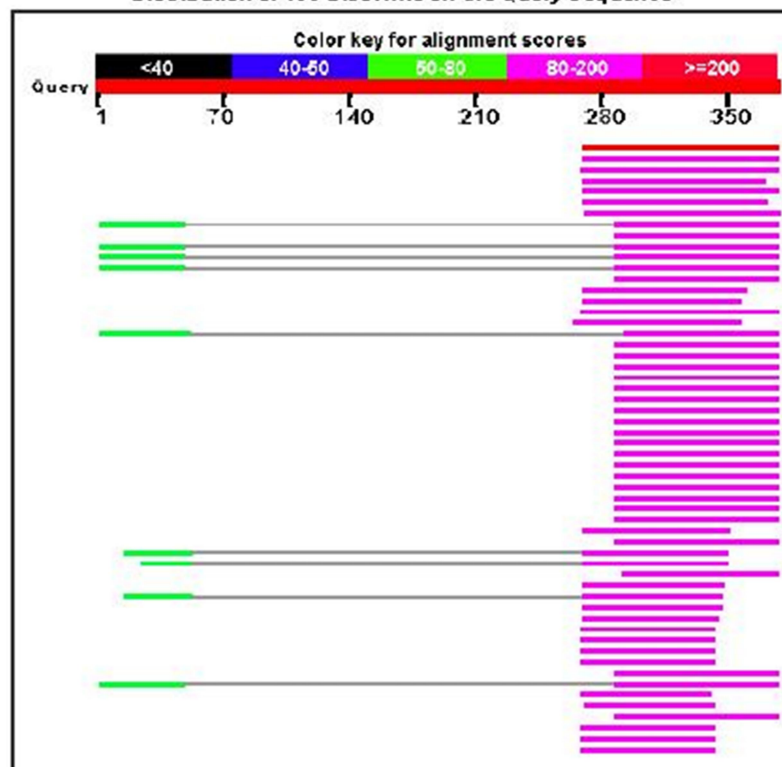
RID [9XC1F0A8014](#) (Expires on 01-21 04:52 am)

Query ID Id|Query_40809
Description None
Molecule type nucleic acid
Query Length 379

Database Name nr
Description Nucleotide collection (nr)
Program BLASTN 2.3.0+

[Graphic Summary](#)

Distribution of 135 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

| Description | Max score | Total score | Query cover | E value | Ident | Accession |
|---|-----------|-------------|-------------|---------|-------|----------------------------|
| S.salar microsatellite DNA, GT-repeat (GT)15 | 200 | 200 | 28% | 2e-47 | 100% | Y11447.1 |
| S.salar microsatellite DNA, GT-repeat (TG)10 | 195 | 195 | 28% | 7e-46 | 99% | Y11449.1 |
| S.salar microsatellite DNA, CAG-repeat (CAG)5 | 193 | 193 | 28% | 3e-45 | 98% | Y11458.1 |
| Uncultured Bacillus sp. gene for 16S rRNA, clone:A01 | 187 | 187 | 26% | 1e-43 | 100% | AB159742.1 |
| Uncultured bacterium gene for 16S rRNA, partial sequence, clone: CN QX1-B18 | 183 | 183 | 28% | 2e-42 | 97% | AB193872.2 |
| Secale cereale DNA, clone: P9, rye chromosome 1 R specific fragment | 182 | 354 | 26% | 6e-42 | 99% | AB669624.1 |
| Uncultured glomeromycete gene for large subunit rRNA, partial sequence, clone: E12_33-1 | 174 | 174 | 28% | 1e-39 | 95% | AB280253.1 |
| Cloning vector pDN19, complete sequence | 169 | 238 | 36% | 5e-38 | 100% | AF327711.1 |
| Escherichia coli pCA4 plasmid microsatellite | 169 | 169 | 24% | 5e-38 | 100% | AJ438270.1 |
| Phagemid cloning vector pTZ19 U, complete sequence | 169 | 238 | 36% | 5e-38 | 100% | Y14836.1 |

Alignments

S.salar microsatellite DNA, GT-repeat (GT)15

Sequence ID: emb|Y11447.1| Length: 313 Number of Matches: 1

Range 1: 149 to 256

| Score | Expect | Identities | Gaps | Strand | Frame |
|----------------|---------|---------------|-----------|-----------|-------|
| 200 bits (108) | 2e-47() | 108/108(100%) | 0/108(0%) | Plus/Plus | |

Features:

| | | | |
|-------|-----|--|-----|
| Query | 271 | AATCCATATGACTAGTAGATCCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTTCCTATA | 338 |
| Sbjct | 149 | AATCCATATGACTAGTAGATCCCTCTAGAGTCGACCTGCAGGCATGCAAGCTTTCCTATA | 208 |
| Query | 331 | GTGAGTCGTAATTAGAGCTGGCGTAATCATGGTCATAGCTGTTCCTG | 378 |
| Sbjct | 209 | GTGAGTCGTAATTAGAGCTGGCGTAATCATGGTCATAGCTGTTCCTG | 256 |

S2 – Consensus sequence of 18S rDNA contained in the p*Bh*_18S_c2 clone and GenBank analysis

>p*Bh*_18S_c2

GAGTCTCGTTCGTTATCGGAATTAACCAGACAAATCGTTCCACCAACTAAGAACGGCCATGC
ACCACTATCCATTGAATCAAGAGAGAGCTATCAATCTGTCAATCCTTCCAATGTCCGGGCCT
GATGAGGTTCCCCGTGTTGAGTCAAATTAAGCCGCAGGCTCCACTCCTGGTGGTGCCCTTCC
GTCAATTCTTTAAGTTTCAGCTTTGCAACCATACTTCCCCGGAACCCAAAAGCTTTGGTTT
CCCGGAAGCTGCCCCGCCGAGTCATCGGAGGAACATCGGCGGATCGCTGGCTGGCATCGTTTA
TGGTTAGAACTAGGGCGGTATCTGATCGCCTTCGAACCTCTAACTTTCGTTCTTGATCAACTA
AGACATACTTGGCAAATGCTTTCGCTTTAGTGCGTCTTGCGACGATCCAAGAATTTACCTCT
AACGCCGCAATACGAATGCCCCGCCTGTCCATATTGATCATTACCTCGGGTCCGAAAAACC
AACAAAATAGAACCGAGGTCCTATTCAATTATTCCATGCACCACTATTTCAGGCTGAGCTCAG
CCTGCTTTGAGCACTCTAATTTGTTCAAAGTAAACGTGCCGGGCCACCTCGACACTCAGTTA
AGAGCACCGCGGGGATTAGATAGGCGACCGCGGATCCCGGGGGGGAGCTTCGGACCCG
TTCCGGGTCTTACGCCCCGCCGCCGGGCCGCGGCCGCCACCGGCAGGACATCCCACGGCGT
GCCAGTTGCACCGACAGGCGGTGAACCGACAGCGTGGGACGCAGGACCAACTACGAGCTTT
TTAACCGCAACAACCTTAATATACGCCATTGGAGCTGGAATTACCGCGGCTGCTGGCACCAG
ACTTGCCCTCCAATAGGTACTTGTAAATGATTTAGAGTGTGCTCATTCCGATTACGGGGCCT
CGGATGAGTCCCGTATCGTTATTTTTTGTCACTACCTCCCCGTGCCGGGAGTGGGTAATGTGC
GTGCCTGCTGCCTTCCTTG

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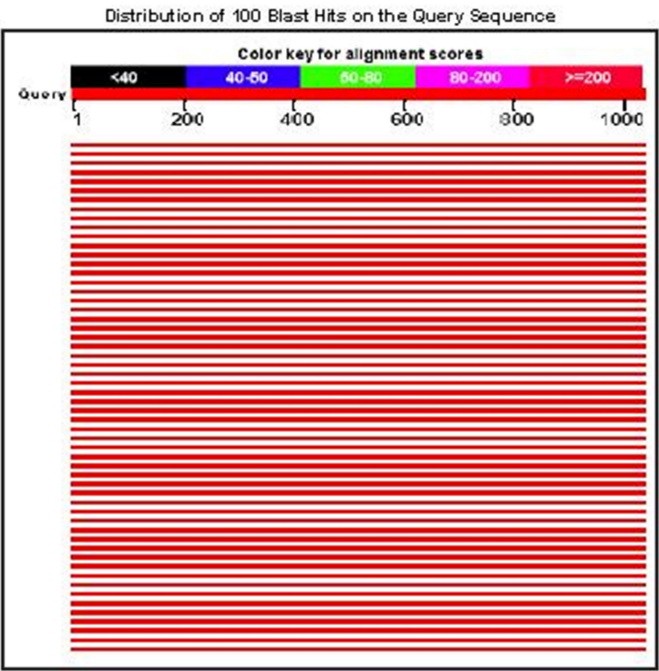
18s_Bh_c2

RID [X9J0KJ85D16](#) (Expires on 08-21 02:16 am)

Query ID [k|Query_2.2579](#)
Description 18s_Bh_c2
Molecule type nucleic acid
Query Length 1037

Database Name nt
Description Nucleotide collection (nt)
Program BLASTN 2.2.32+

Graphic Summary



Descriptions

Sequences producing significant alignments:

| Description | Max score | Total score | Query cover | E value | Ident | Accession |
|--|-----------|-------------|-------------|---------|-------|----------------------------|
| <i>Belostoma flumineum</i> 18S ribosomal RNA gene, partial sequence | 1653 | 1653 | 99% | 0.0 | 95% | AY252132.1 |
| <i>Raia taenioides</i> 18S ribosomal RNA gene, partial sequence | 1605 | 1605 | 99% | 0.0 | 95% | FJ372644.1 |
| <i>Raia taenioides</i> sp. QX-2006 small subunit ribosomal RNA gene, complete sequence | 1574 | 1574 | 99% | 0.0 | 94% | DQ610778.1 |
| <i>Coniidae</i> sp. QX-2006 small subunit ribosomal RNA gene, complete sequence | 1515 | 1515 | 99% | 0.0 | 93% | DQ610774.1 |
| <i>Stegana</i> sp. YT-2009 18S ribosomal RNA gene, partial sequence | 1513 | 1513 | 99% | 0.0 | 93% | FJ372642.1 |
| <i>Blepharodon</i> sp. MRN-1996 18S ribosomal RNA gene, partial sequence | 1482 | 1482 | 99% | 0.0 | 93% | U65120.1 |
| <i>Notonecta chelon</i> 18S ribosomal RNA gene, partial sequence | 1474 | 1474 | 99% | 0.0 | 93% | FJ372643.1 |
| <i>Petroleophilus</i> sp. JL-2010 18S ribosomal RNA gene, partial sequence | 1421 | 1421 | 99% | 0.0 | 92% | GQ405938.1 |
| <i>Leptaspis</i> sp. JL-2010 18S ribosomal RNA gene, partial sequence | 1415 | 1415 | 99% | 0.0 | 91% | GQ406034.1 |

Alignments

Belostoma flumineum 18S ribosomal RNA gene, partial sequence
Sequence ID: db|AY252132.1| Length: 1047 Number of Matches: 1
Range 1: 1 to 1047

| Score | Expect | Identity | Gaps | Strand | Frame |
|-----------------|--------|----------------|--------------|------------|-------|
| 1653 bits (95%) | 0.00 | 999/1050 (95%) | 17/1050 (1%) | Plus/Minus | |
| Features: | | | | | |
| Query 1 | 60 | 60 | | | |
| Subject 1047 | 988 | 988 | | | |
| Query 61 | 120 | 120 | | | |
| Subject 987 | 928 | 928 | | | |
| Query 121 | 180 | 180 | | | |
| Subject 927 | 868 | 868 | | | |
| Query 181 | 240 | 240 | | | |
| Subject 867 | 808 | 808 | | | |
| Query 241 | 300 | 300 | | | |
| Subject 807 | 748 | 748 | | | |
| Query 301 | 360 | 360 | | | |
| Subject 747 | 688 | 688 | | | |
| Query 361 | 420 | 420 | | | |
| Subject 687 | 628 | 628 | | | |
| Query 421 | 467 | 467 | | | |
| Subject 627 | 569 | 569 | | | |
| Query 468 | 527 | 527 | | | |
| Subject 568 | 509 | 509 | | | |
| Query 528 | 587 | 587 | | | |
| Subject 508 | 449 | 449 | | | |
| Query 588 | 647 | 647 | | | |
| Subject 448 | 389 | 389 | | | |
| Query 648 | 706 | 706 | | | |
| Subject 388 | 330 | 330 | | | |
| Query 707 | 766 | 766 | | | |
| Subject 329 | 270 | 270 | | | |
| Query 767 | 826 | 826 | | | |
| Subject 289 | 211 | 211 | | | |
| Query 827 | 886 | 886 | | | |
| Subject 210 | 151 | 151 | | | |
| Query 887 | 946 | 946 | | | |
| Subject 150 | 91 | 91 | | | |
| Query 947 | 1006 | 1006 | | | |
| Subject 90 | 31 | 31 | | | |
| Query 1007 | 1036 | 1036 | | | |
| Subject 30 | 1 | 1 | | | |