

Job Title	BVAB-1_AY724739.1 Uncultured bacterium clone...
RID	PNJ0X2UG016 Search expires on 11-10 04:20 am Download All ▾
Program	BLASTN ? Citation ▾
Database	nt See details ▾
Query ID	lcl Query_40607
Description	BVAB-1_AY724739.1 Uncultured bacterium clone 123-f 57 ...
Molecule type	dna
Query Length	1007
Other reports	Distance tree of results MSA viewer ?

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Organism *only top 20 will appear* exclude

Type common name, binomial, taxid or group name

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Percent Identity to **E value** to **Query Coverage** to

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- Alignments
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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Clostridiales genomosp. BVAB1 isolate UAB071 chromosome, complete genome	Clostridiales genomosp. BVAB1	1860	7431	100%	0.0	100.00%	1649642	CP049781.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1853a08c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1860	1860	100%	0.0	100.00%	1352	JF160899.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone nbu405d06c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1860	1860	100%	0.0	100.00%	1352	GQ037632.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 123-f 57 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1860	1860	100%	0.0	100.00%	1007	AY724739.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone rRNA296 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1860	1860	100%	0.0	100.00%	1507	AY959069.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone nck189a08c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.90%	1352	KF094234.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 23.001-2 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.90%	1377	JX871285.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 22.001-2 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.90%	1377	JX871284.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1854c08c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.90%	1352	JF159358.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone nbw1010h11c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.90%	1352	GQ047285.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone nbu405e02c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.90%	1352	GQ037635.1

Supplemental file 1.1: BLAST alignment analysis of BVAB-1

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Clostridiales genomsp. BVAB1 isolate UAB071 chromosome, complete genome

Sequence ID: [CP049781.1](#) Length: 1649642 Number of Matches: 4

Range 1: 9272 to 10278 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1860 bits(1007)	0.0	1007/1007(100%)	0/1007(0%)	Plus/Plus
Query 1	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGCGAAGAAGT	60		
Sbjct 9272	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGCGAAGAAGT	9331		
Query 61	ATTTCCGGTATGTAAAGCTCTATCAGAAGGGAAGAAAATGACGGTACCTTACTAAGAAGCT	120		
Sbjct 9332	ATTTCCGGTATGTAAAGCTCTATCAGAAGGGAAGAAAATGACGGTACCTTACTAAGAAGCT	9391		
Query 121	CCGGCTAAATACGTGCCAGCAGCCGCGGTAATACGTATGGAGCAAGCGTTATCCGGATTT	180		
Sbjct 9392	CCGGCTAAATACGTGCCAGCAGCCGCGGTAATACGTATGGAGCAAGCGTTATCCGGATTT	9451		
Query 181	ACTGGGTGTAAAGGGAGTGTAGGCGGCACTATAAGTCTGATGTGAAAACCTAAGGCTTAA	240		
Sbjct 9452	ACTGGGTGTAAAGGGAGTGTAGGCGGCACTATAAGTCTGATGTGAAAACCTAAGGCTTAA	9511		
Query 241	CCATAGGATTGCATTGGAAACTGTAGAGCTGGAGTATCGGAGAGGCAAGCGGAATTCCTG	300		
Sbjct 9512	CCATAGGATTGCATTGGAAACTGTAGAGCTGGAGTATCGGAGAGGCAAGCGGAATTCCTG	9571		
Query 301	GTGTAGTGGTGAATACGTAGATATCAGGAAGAACATCGGTGGCGAAGGCGGCTTGCTGG	360		
Sbjct 9572	GTGTAGTGGTGAATACGTAGATATCAGGAAGAACATCGGTGGCGAAGGCGGCTTGCTGG	9631		
Query 361	ACGATAACTGACGCTAAGGCTCGAAAGCGTGGGAAGCGAACAGGATTAGATACCCTGGTA	420		
Sbjct 9632	ACGATAACTGACGCTAAGGCTCGAAAGCGTGGGAAGCGAACAGGATTAGATACCCTGGTA	9691		
Query 421	GTCCACGCTGTAAACGATGAACACTAGGTGTTGGGAGGCTAAGCCTTTTCAGTGCCGCAGC	480		
Sbjct 9692	GTCCACGCTGTAAACGATGAACACTAGGTGTTGGGAGGCTAAGCCTTTTCAGTGCCGCAGC	9751		
Query 481	AAACGCAATAAGTGTTCCACCTGGGGAGTACGTTTCGCAAGAATGAAACTCAAAGGAATTG	540		
Sbjct 9752	AAACGCAATAAGTGTTCCACCTGGGGAGTACGTTTCGCAAGAATGAAACTCAAAGGAATTG	9811		
Query 541	ACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTT	600		

Supplemental file 1.2: BLAST alignment analysis of BVAB-1

Description BVAB-2_AY724740.1 Uncultured bacterium clone 123-f 23 ...
Molecule type dna
Query Length 1009
Other reports [Distance tree of results](#) [MSA viewer](#) [?](#)

Percent Identity to
E value to
Query Coverage to

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd989g05c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1864	1864	100%	0.0	100.00%	1358	HM334697.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd997d08c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1864	1864	100%	0.0	100.00%	1358	HM332642.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 123-f 23 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1864	1864	100%	0.0	100.00%	1009	AY724740.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone rRNA115 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1864	1864	100%	0.0	100.00%	1513	AY958888.1
<input checked="" type="checkbox"/>	Oscillospiraceae bacterium strain CHIC02 1186E3-8 16S ribosomal RNA gene, partial sequence	Oscillospiraceae...	1858	1858	100%	0.0	99.90%	1450	OP540273.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1058g03c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1858	1858	100%	0.0	99.90%	1358	HM344558.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1008g01c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1858	1858	100%	0.0	99.90%	1358	HM341223.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd988h05c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1858	1858	100%	0.0	99.90%	1358	HM334584.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone rRNA164 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1858	1858	100%	0.0	99.90%	1514	AY958937.1
<input checked="" type="checkbox"/>	Oscillospiraceae bacterium strain UPII 610-J 16S ribosomal RNA gene, partial sequence	Oscillospiraceae...	1855	1855	100%	0.0	99.80%	1455	OP540270.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1060a10c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1853	1853	100%	0.0	99.80%	1358	HM344624.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1005h09c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1853	1853	100%	0.0	99.80%	1358	HM341026.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd998a04c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1853	1853	100%	0.0	99.80%	1358	HM332641.1
<input checked="" type="checkbox"/>	Uncultured bacterium partial 16S rRNA gene, isolate BF0002B065	uncultured bacte...	1853	1853	100%	0.0	99.80%	1490	AM697115.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone nck198e03c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1847	1847	100%	0.0	99.70%	1358	KF094825.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1057f07c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1847	1847	100%	0.0	99.70%	1358	HM340507.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone rRNA351 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1847	1847	100%	0.0	99.70%	1510	AY959124.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone ncd1008a01c1 16S ribosomal RNA gene, partial sequence	uncultured bacte...	1845	1845	100%	0.0	99.70%	1357	HM341161.1

Supplemental file 1.3: BLAST alignment analysis of BVAB-2

Oscillospiraceae bacterium strain CHIC02 1186E3-8 16S ribosomal RNA gene, partial sequence

Sequence ID: [OP540273.1](#) Length: 1450 Number of Matches: 1

Range 1: 358 to 1366 [GenBank](#) [Graphics](#)

[▼ Next Match](#) [▲ Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1858 bits(1006)	0.0	1008/1009(99%)	0/1009(0%)	Plus/Plus
Query 1		TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGTGATGAAGG		60
Sbjct 358		TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAGCAACGCCGCGTGAGTGATGAAGG		417
Query 61		CCTTCGGGTTGTAAAACCTTTTGGACAGGGACGAAGAAAGTGACGGTACCTGTAGAACAA		120
Sbjct 418		CCTTCGGGTTGTAAAACCTTTTGGACAGGGACGAAGAAAGTGACGGTACCTGTAGAACAA		477
Query 121		GCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTATCCGGA		180
Sbjct 478		GCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTATCCGGA		537
Query 181		TTTACTGGGCGTAAAGGGCGGTAGGCGGCTAGATAAGTGTGATGTTTTAAATCCAAGGCT		240
Sbjct 538		TTTACTGGGCGTAAAGGGCGGTAGGCGGCTAGATAAGTGTGATGTTTTAAATCCAAGGCT		597
Query 241		TAACCTTGGGGTTCATTACAAACTGTTTAGCTTGAGTGCTGGAGAGGATAGTGGAATTCC		300
Sbjct 598		TAACCTTGGGGTTCATTACAAACTGTTTAGCTTGAGTGCTGGAGAGGATAGTGGAATTCC		657
Query 301		TAGTGTAGCGGTAAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTATCT		360
Sbjct 658		TAGTGTAGCGGTAAAATGCGTAGATATTAGGAGGAACACCGGTGGCGAAGGCGGCTATCT		717
Query 361		GGACAGTAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG		420
Sbjct 718		GGACAGTAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGG		777
Query 421		TAGTCCACGCCGTAAACGATGAATACTAGCTGTAGGAGGTATCGACCCCTTCTGTGGCGC		480
Sbjct 778		TAGTCCACGCCGTAAACGATGAATACTAGCTGTAGGAGGTATCGACCCCTTCTGTGGCGC		837
Query 481		AGTTAACACAATAAGTATTCCGCCCTGGGGAGTACGGCCGCAAGGTTAAAACCTCAAAGGAA		540
Sbjct 838		AGTTAACACAATAAGTATTCCGCCCTGGGGAGTACGGCCGCAAGGTTAAAACCTCAAAGGAA		897
Query 541		TTGACGGGGACCCGCACAAGCAGTGGATTATGTGGTTTAAATTCGAAGCAACGCGAAGAAC		600
Sbjct 898		TTGACGGGGACCCGCACAAGCAGTGGATTATGTGGTTTAAATTCGAAGCAACGCGAAGAAC		957
Query 601		CTTACCAGGACTTGACATCCTCTGACGATTTCAGGAGACTGAATTTTCTCTTCGGAGACAG		660
Sbjct 958		CTTACCAGGACTTGACATCCTCTGACGATTTCAGGAGACTGAATTTTCTCTTCGGAGACAG		1017
Query 661		AGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTGCGTGAGATGTTGGGTTAAGTCCCC		720

Supplemental file 1.4: BLAST alignment analysis of BVAB-2.

Sequences producing significant alignments

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Clostridiales genomosp. BVAB3 16S ribosomal RNA gene, partial sequence	Mageeibacillus indolicus	1866	1866	100%	0.0	100.00%	1382	KC311734.1
<input checked="" type="checkbox"/>	Bacterium BVAB3-Strain 4 16S ribosomal RNA gene, partial sequence	bacterium BVAB3-Strain 4	1866	1866	100%	0.0	100.00%	1480	GQ900634.1
<input checked="" type="checkbox"/>	Mageeibacillus indolicus strain 0009-5 16S ribosomal RNA, partial sequence	Mageeibacillus indolicus	1866	1866	100%	0.0	100.00%	1480	NR_146698.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 1123b-58-f 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1866	1866	100%	0.0	100.00%	1503	GQ900629.1
<input checked="" type="checkbox"/>	Mageeibacillus indolicus UPII9-5 chromosome, complete genome	Mageeibacillus indolicus...	1866	3732	100%	0.0	100.00%	1809746	CP001850.2
<input checked="" type="checkbox"/>	Uncultured bacterium clone nbw1012c09c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1866	1866	100%	0.0	100.00%	1349	GQ043025.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 123f 17 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1866	1866	100%	0.0	100.00%	1010	AY724741.1
<input checked="" type="checkbox"/>	Mageeibacillus indolicus strain 0019-D 16S ribosomal RNA gene, partial sequence	Mageeibacillus indolicus	1862	1862	100%	0.0	99.90%	1480	GQ900633.1
<input checked="" type="checkbox"/>	Mageeibacillus indolicus strain 0004-9 16S ribosomal RNA gene, partial sequence	Mageeibacillus indolicus	1862	1862	100%	0.0	99.90%	1480	GQ900631.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 8.001-2 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1860	1860	100%	0.0	99.90%	1297	JX871279.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone nbu407b07c1 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1855	1855	100%	0.0	99.80%	1349	GQ038494.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone FX93B4-11 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1820	1820	98%	0.0	99.80%	1323	AY995273.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WDoral5F08 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1666	1666	100%	0.0	96.44%	1350	KC259695.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 112Q-85 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1663	1663	89%	0.0	100.00%	900	GQ900636.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone 2BV-25 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1663	1663	89%	0.0	100.00%	900	EU188978.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD9oral2D09 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1350	KC260938.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD9oral2A05 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1350	KC260907.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD2oralAB03 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1350	KC260805.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD9oralEH06 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1350	KC260441.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD1oralAH04 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1351	KC260194.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WDoral5G03 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1351	KC259699.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WDoral3G06 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1661	1661	100%	0.0	96.34%	1350	KC259558.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD9oral2A07 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1655	1655	100%	0.0	96.24%	1350	KC260908.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD2oralBG02 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1655	1655	100%	0.0	96.24%	1350	KC260241.1
<input checked="" type="checkbox"/>	Uncultured bacterium clone WD1oralAD01 16S ribosomal RNA gene, partial sequence	uncultured bacterium	1655	1655	100%	0.0	96.24%	1350	KC260162.1

Supplemental file 1.5: BLAST alignment analysis of BVAB-3

Mageeibacillus indolicus UPII9-5 chromosome, complete genome

Sequence ID: [CP001850.2](#) Length: 1809746 Number of Matches: 2

Range 1: 255893 to 256902 [GenBank](#) [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Gaps	Strand
1866 bits(1010)	0.0	1010/1010(100%)	0/1010(0%)	Plus/Plus
Query 1		TGGGGAATATTGGGCAATGGGGCGAAAGCCTGACCCAGCAACGCCGCGTGAAGTATGAAGG		60
Sbjct 255893		TGGGGAATATTGGGCAATGGGGCGAAAGCCTGACCCAGCAACGCCGCGTGAAGTATGAAGG		255952
Query 61		CCTTCGGGTTGTAAACTTCTTTGATCAGGGAAGAAACAAATGACGGTACCTGAAAAACAA		120
Sbjct 255953		CCTTCGGGTTGTAAACTTCTTTGATCAGGGAAGAAACAAATGACGGTACCTGAAAAACAA		256012
Query 121		GCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTATCCGGA		180
Sbjct 256013		GCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCGAGCGTTATCCGGA		256072
Query 181		TTTACTGGGTGTAAAGGGCGTGCAGGCGGGCTGATAAGTCAGATGTGAAATCCCCGAGCT		240
Sbjct 256073		TTTACTGGGTGTAAAGGGCGTGCAGGCGGGCTGATAAGTCAGATGTGAAATCCCCGAGCT		256132
Query 241		TAACTCGGGAAC TGCATCTGATACTGTTGGTCTTGAGTGCTGGAGAGGATAGTGGAATTC		300
Sbjct 256133		TAACTCGGGAAC TGCATCTGATACTGTTGGTCTTGAGTGCTGGAGAGGATAGTGGAATTC		256192
Query 301		CTAGTG TAGCGGTA AAAATGCGCAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTATC		360
Sbjct 256193		CTAGTG TAGCGGTA AAAATGCGCAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTATC		256252
Query 361		TGGACAGTA AACTGACGCTGAGGCGCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTG		420
Sbjct 256253		TGGACAGTA AACTGACGCTGAGGCGCGAAAGCGTGGGTAGCAAACAGGATTAGATACCCTG		256312
Query 421		GTAGTCCACGCCGTA AACGATGATTACTAGGTGTAGGAGGTATCGACCCCTTCTGTGCCG		480
Sbjct 256313		GTAGTCCACGCCGTA AACGATGATTACTAGGTGTAGGAGGTATCGACCCCTTCTGTGCCG		256372
Query 481		GAGTTAACACAATAAGTAATCCACCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGA		540
Sbjct 256373		GAGTTAACACAATAAGTAATCCACCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGA		256432
Query 541		ATTGACGGGGGCGCCGCA AAGCAGTGGAGTATGTGGTTTAAATTCGACGCAACGCGAAGAA		600
Sbjct 256433		ATTGACGGGGGCGCCGCA AAGCAGTGGAGTATGTGGTTTAAATTCGACGCAACGCGAAGAA		256492
Query 601		CCTTACCAGGGTTTGACATCCCTTGAACGATGTAGAGATACATAATTCCCTTCGGGGACA		660
Sbjct 256493		CCTTACCAGGGTTTGACATCCCTTGAACGATGTAGAGATACATAATTCCCTTCGGGGACA		256552
Query 661		AGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTGTCGTGAGATGTTGGGTTAAGTCCC		720

Supplemental file 1.6: BLAST alignment analysis of BVAB-3