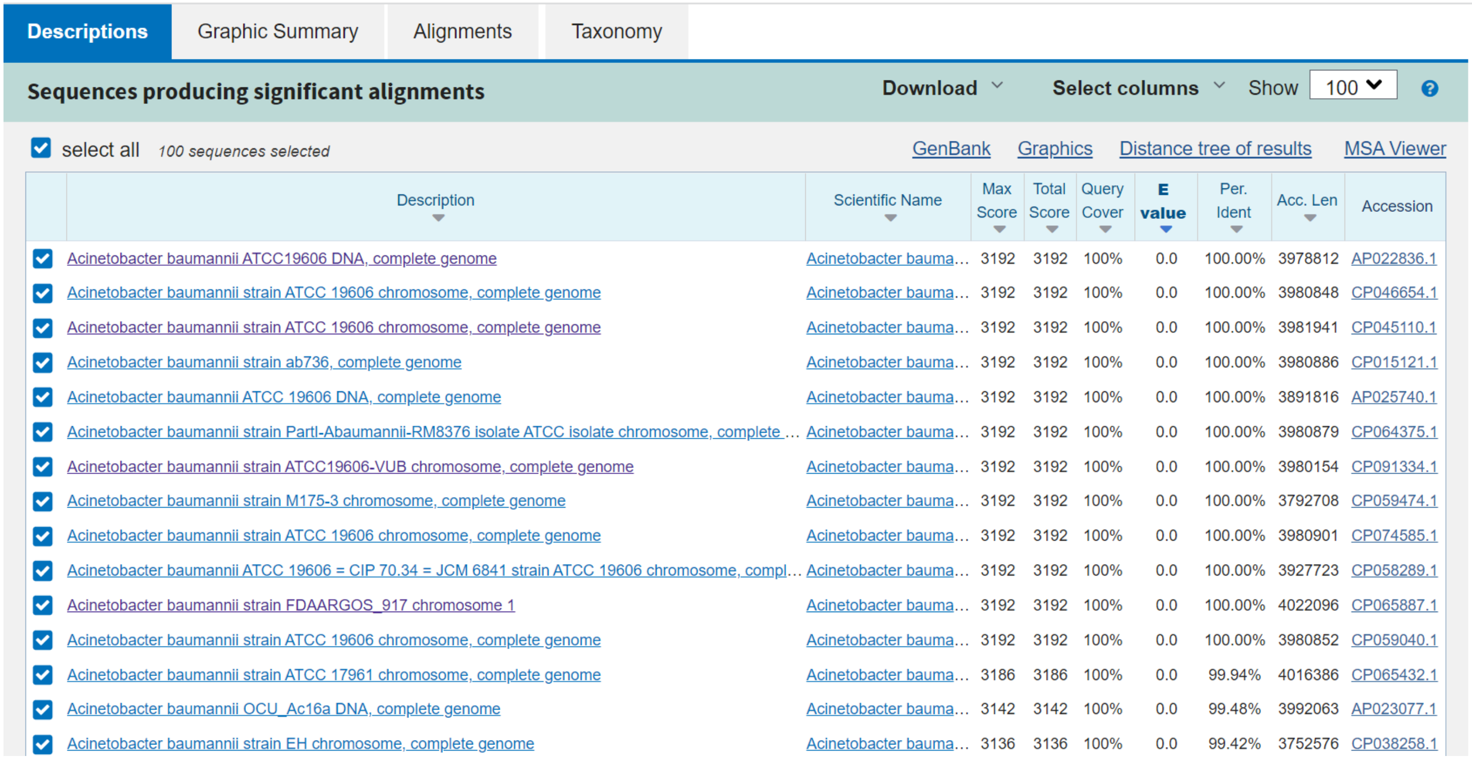
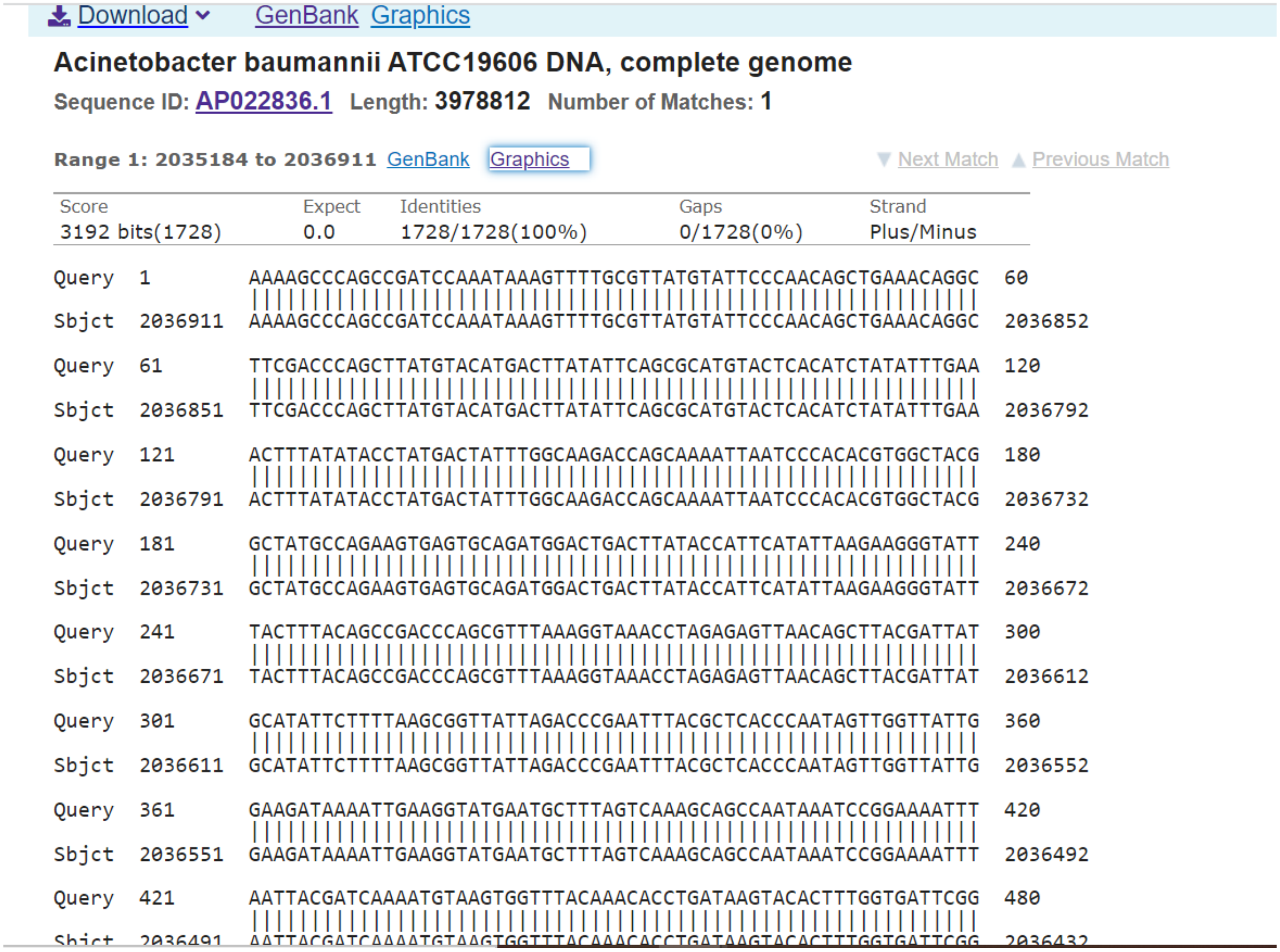


Sequences producing significant alignments

☑ select all *100 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	Acinetobacter baumannii ATCC19606 DNA, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3978812	AP022836.1
☑	Acinetobacter baumannii strain ATCC 19606 chromosome, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3980848	CP046654.1
☑	Acinetobacter baumannii strain ATCC 19606 chromosome, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3981941	CP045110.1
☑	Acinetobacter baumannii strain ab736, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3980886	CP015121.1
☑	Acinetobacter baumannii ATCC 19606 DNA, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3891816	AP025740.1
☑	Acinetobacter baumannii strain PartI-Abaumannii-RM8376 isolate ATCC isolate chromosome, complete …	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3980879	CP064375.1
☑	Acinetobacter baumannii strain ATCC19606-VUB chromosome, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3980154	CP091334.1
☑	Acinetobacter baumannii strain M175-3 chromosome, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3792708	CP059474.1
☑	Acinetobacter baumannii strain ATCC 19606 chromosome, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3980901	CP074585.1
☑	Acinetobacter baumannii ATCC 19606 = CIP 70.34 = JCM 6841 strain ATCC 19606 chromosome, compl…	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3927723	CP058289.1
☑	Acinetobacter baumannii strain FDAARGOS_917 chromosome 1	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	4022096	CP065887.1
☑	Acinetobacter baumannii strain ATCC 19606 chromosome, complete genome	Acinetobacter bauma…	3192	3192	100%	0.0	100.00%	3980852	CP059040.1
☑	Acinetobacter baumannii strain ATCC 17961 chromosome, complete genome	Acinetobacter bauma…	3186	3186	100%	0.0	99.94%	4016386	CP065432.1
☑	Acinetobacter baumannii OCU_Ac16a DNA, complete genome	Acinetobacter bauma…	3142	3142	100%	0.0	99.48%	3992063	AP023077.1
☑	Acinetobacter baumannii strain EH chromosome, complete genome	Acinetobacter bauma…	3136	3136	100%	0.0	99.42%	3752576	CP038258.1

Suppl. Fig. 1. Screenshot of the Description Table of nucleotide BLAST-N results of the cloned sequence of ABC transporter substrate-binding protein of *A. baumannii*. Results confirm identity and sequence of the cloned gene.



Acinetobacter baumannii ATCC19606 DNA, complete genome

Sequence ID: AP022836.1 Length: 3978812 Number of Matches: 1

Range 1: 2035184 to 2036911

Score	Expect	Identities	Gaps	Strand
3192 bits(1728)	0.0	1728/1728(100%)	0/1728(0%)	Plus/Minus

```
Query  1        AAAAGCCCAGCCGATCCAAATAAAGTTTTGCGTTATGTATTCCCAACAGCTGAAACAGGC  60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036911  AAAAGCCCAGCCGATCCAAATAAAGTTTTGCGTTATGTATTCCCAACAGCTGAAACAGGC  2036852

Query  61       TTCGACCCAGCTTATGTACATGACTTATATTCAGCGCATGTACTCACATCTATATTTGAA  120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036851  TTCGACCCAGCTTATGTACATGACTTATATTCAGCGCATGTACTCACATCTATATTTGAA  2036792

Query  121      ACTTTATATACCTATGACTATTTGGCAAGACCAGCAAAATTAATCCCACACGTGGCTACG  180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036791  ACTTTATATACCTATGACTATTTGGCAAGACCAGCAAAATTAATCCCACACGTGGCTACG  2036732

Query  181      GCTATGCCAGAAGTGAGTGCAGATGGACTGACTTATACCATTCATATTAAGAAGGGTATT  240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036731  GCTATGCCAGAAGTGAGTGCAGATGGACTGACTTATACCATTCATATTAAGAAGGGTATT  2036672

Query  241      TACTTTACAGCCGACCCAGCGTTTAAAGGTAAACCTAGAGAGTTAACAGCTTACGATTAT  300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036671  TACTTTACAGCCGACCCAGCGTTTAAAGGTAAACCTAGAGAGTTAACAGCTTACGATTAT  2036612

Query  301      GCATATTCTTTTAAGCGGTTATTAGACCCGAATTTACGCTCACCCAATAGTTGGTTATTG  360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036611  GCATATTCTTTTAAGCGGTTATTAGACCCGAATTTACGCTCACCCAATAGTTGGTTATTG  2036552

Query  361      GAAGATAAAATTGAAGGTATGAATGCTTTAGTCAAAGCAGCCAATAAATCCGGAAAATTT  420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036551  GAAGATAAAATTGAAGGTATGAATGCTTTAGTCAAAGCAGCCAATAAATCCGGAAAATTT  2036492

Query  421      AATTACGATCAAAATGTAAGTGGTTTACAAACACCTGATAAGTACACTTTGGTGATTCGG  480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2036491  AATTACGATCAAAATGTAAGTGGTTTACAAACACCTGATAAGTACACTTTGGTGATTCGG  2036432
```

Suppl. Fig. 2. Screenshot of the sequence alignment of the cloned sequence with *A. baumannii* ABC transporter substrate-binding protein following nucleotide BLAST-N. (https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome)