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## BLAST Results

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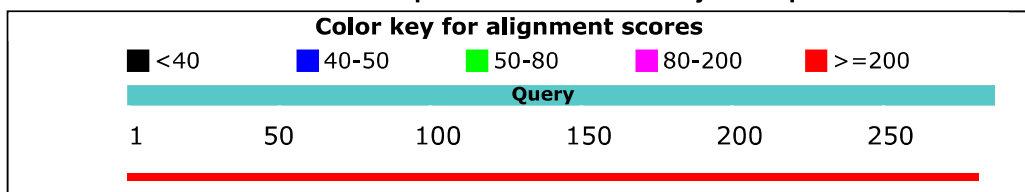
### Blast 2 sequences

Job title: Consensus sdm dupla

<b>RID</b>	<a href="#">BDUSSDC611R</a> (Expires on 04-18 17:00 pm)	<b>Subject ID</b>	Ic Query_49443
<b>Query ID</b>	Ic Query_49441	<b>Description</b>	EC-071 sat
<b>Description</b>	Consensus sdm dupla		<a href="#">See details</a>
<b>Molecule type</b>	dna	<b>Molecule type</b>	dna
<b>Query Length</b>	280	<b>Subject Length</b>	3888
		<b>Program</b>	BLASTN 2.9.0+

## Graphic Summary

### Distribution of the top 1 Blast Hits on 1 subject sequences



## Dot Matrix View



## Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
EC-071 sat	507	507	100%	2e-147	99.29%	Query_49443

## Alignments

EC-071 sat

Sequence ID: Query\_49443 Length: 3888 Number of Matches: 1  
Range 1: 643 to 922

Score	Expect	Identities	Gaps	Strand	Frame
507 bits(274)	2e-147()	278/280(99%)	0/280(0%)	Plus/Plus	

Features:

Query	1	AATT CAGCATATAGCCATGATCTGTTAAGTGC TAGTCTATTTGAGGTCACCCAATGGGAC	60
Sbjct	643	AATT CAGCATATAGCCATGATCTGTTAAGTGC TAGTCTATTTGAGGTCACCCAATGGGAC	702
Query	61	TCATACGGCATGATGATTTATAAAAAATGATAAAACATTTGTAATCTTGAAATATTCGGA	120
Sbjct	703	TCATACGGCATGATGATTTATAAAAAATGATAAAACATTTGTAATCTTGAAATATTCGGA	762
Query	121	GACATCGGCGCTGGAGCATACTTATATGATAACAACTAGAAAAATGGGTATTAGTCGGA	180
Sbjct	763	GACATCGGCGCTGGAGCATACTTATATGATAACAACTAGAAAAATGGGTATTAGTCGGA	822
Query	181	ACAACCCATGGTATTGCCAGCGTTAATGGTGACCAACTGACATGGATAACAAAATACAAT	240
Sbjct	823	ACAACCCATGGTATTGCCAGCGTTAATGGTGACCAACTGACATGGATAACAAAATACAAT	882
Query	241	GATAAACTGGTTAGTGAGTTAAAAGATACCTATAGTCATA	280
Sbjct	883	GATAAACTGGTTAGTGAGTTAAAAGATACCTATAGTCATA	922

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