

1.

Staphylococcus aureus subsp. aureus RN4220 plazmid pRM27, complete sequence

Dizi Kimliği (Erişim numarası) : KT780704.1

Range: 64127

Number of Matches: 31

Score:1.184e+05 bits(64127), Expect:0.0,

Identities:64127/64127(100%), Gaps:0/64127(0%), Strand: Plus/Plus

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Sort by: E value

Staphylococcus aureus subsp. aureus RN4220 plasmid pRM27, complete sequence

Sequence ID: KT780704.1
Length: 64127
Number of Matches: 31

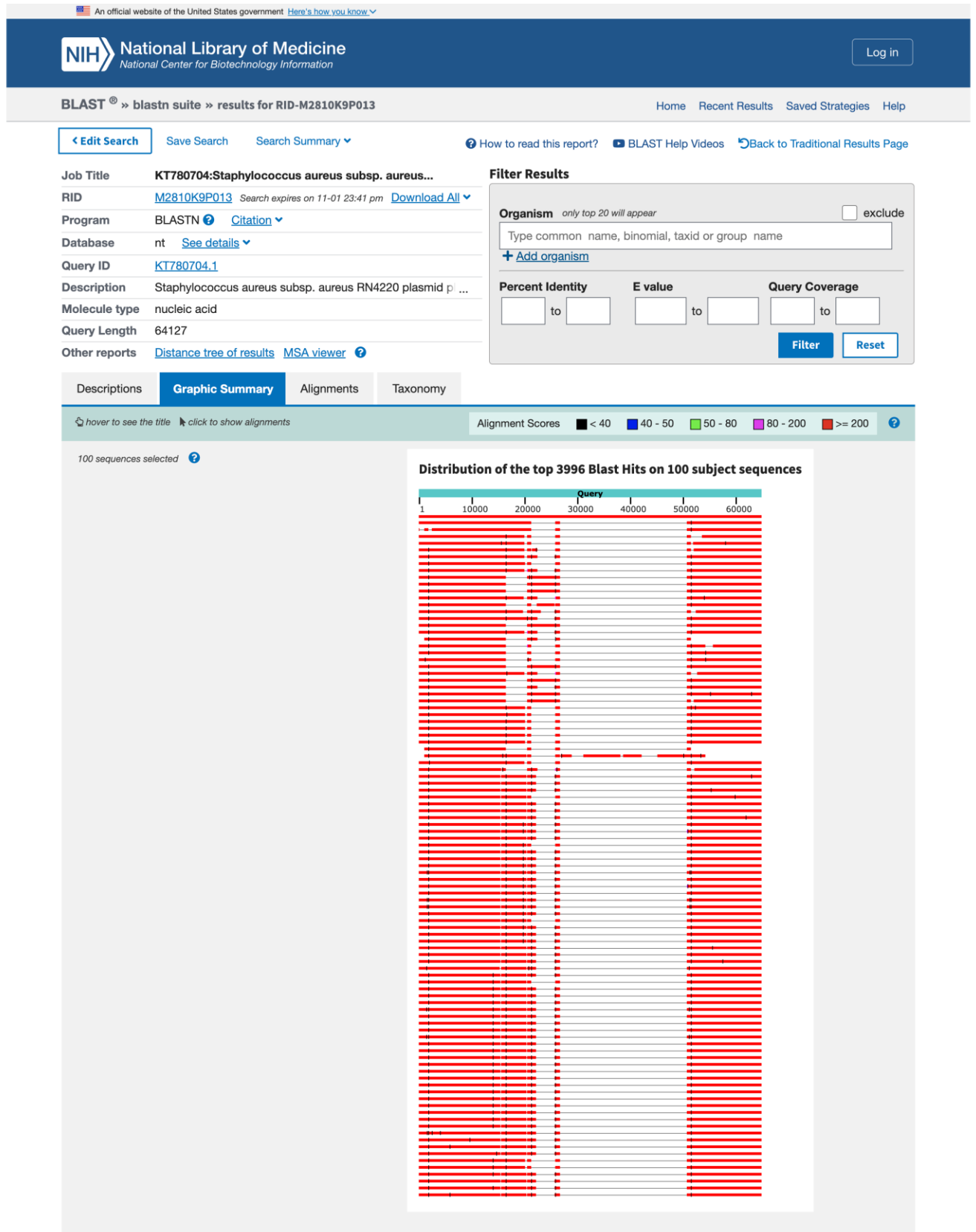
Range 1: 1 to 64127
GenBank
Graphics

Next Match
Previous Match

Score	Expect	Identities	Gaps	Strand
1.184e+05 bits(64127)	0.0	64127/64127(100%)	0/64127(0%)	Plus/Plus
Query 1		ACTTAAACTCCTTAAATATACATTAAAGGAGTTTTTATCATGCTAAACAATTTTTTAC		60
Sbjct 1		ACTTAAACTCCTTAAATATACATTAAAGGAGTTTTTATCATGCTAAACAATTTTTTAC		60
Query 61		AGTAGAAGAAAATTATAAAGAACGCTTTTACCAATTACCTAAAGTATTTTTTACTAATCC		120
Sbjct 61		AGTAGAAGAAAATTATAAAGAACGCTTTTACCAATTACCTAAAGTATTTTTTACTAATCC		120
Query 121		TAATTATAAAGATTATCGAATGACGCTAAATTTGCTTACGCAATATTGAGAGATCGTTT		180
Sbjct 121		TAATTATAAAGATTATCGAATGACGCTAAATTTGCTTACGCAATATTGAGAGATCGTTT		180
Query 181		ACAATTATCTATTAAAAATAACTGGATAGATACAGAAGGTAACATATATTTTCATTTATAC		240
Sbjct 181		ACAATTATCTATTAAAAATAACTGGATAGATACAGAAGGTAACATATATTTTCATTTATAC		240
Query 241		AGTTGCTGATTTAGAAGTGATATTAATTTGTGGGAACaaaaaaaaactcaaaaaattaaaaa		300
Sbjct 241		AGTTGCTGATTTAGAAGTGATATTAATTTGTGGGAACAAAAAAATCCTAAAAATTAATAA		300
Query 301		agaattagaaaatgtagatttactaatccaaaaaaGGCAGGGTTTAAACAAACCAATCT		360
Sbjct 301		AGAATTAGAAAATGTAGATTACTAATCCAAAAAGGCAGGGTTTAAACAAACCAATCT		360
Query 361		ACTTTATTATTAAACCAGCCATACTAAAAATGATATTTATGAAATAGATAAGGCTGA		420
Sbjct 361		ACTTTATTATTAAACCAGCCATACTAAAAATGATATTTATGAAATAGATAAGGCTGA		420
Query 421		AAATGAAGTTGAGGCCTTACAAGACAAGGAAGTGCTAAAAGGACACGTCAGAAATGTCA		480
Sbjct 421		AAATGAAGTTGAGGCCTTACAAGACAAGGAAGTGCTAAAAGGACACGTCAGAAATGTCA		480
Query 481		AAAGGACACGCTAGAAATGTCAAAGGACACGCTAGAAATGTCAAAGGACACACAAA		540
Sbjct 481		AARGGACACGCTAGAAATGTCAAAGGACACGCTAGAAATGTCAAAGGACACACAAA		540
Query 541		TGATACTGATTTTATGTACTGATTTTATTGATACTGAAAGTAATGATATGAATAATAT		600

[Detaylı olarak detaylı1Numara.txt bakabilirsiniz]

Grafik özeti



2.

hypothetical protein L6164_035495 [Bauhinia variegata]

Sequence ID: KAI4295448.1

Length: 207

Number of Matches: 1

Score:413 bits(1061), Expect:3e-145,

Method:Compositional matrix adjust.,

Identities:207/207(100%), Positives:207/207(100%), Gaps:0/207(0%)

hypothetical protein L6164_035495 [Bauhinia variegata]

Sequence ID: [KAI4295448.1](#) Length: 207 Number of Matches: 1

Range 1: 1 to 207 [GenPept](#) [Graphics](#)

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

Score	Expect	Method	Identities	Positives	Gaps
413 bits(1061)	3e-145	Compositional matrix adjust.	207/207(100%)	207/207(100%)	0/207(0%)
Query 1	MTLSTFHERLDHMERTRNERCSSLQAEKELQANKSQVLGSKLANIRTMEQKCLILNQKIA	60			
Sbjct 1	MTLSTFHERLDHMERTRNERCSSLQAEKELQANKSQVLGSKLANIRTMEQKCLILNQKIA	60			
Query 61	SQKFKILAYKSEMENMDMKYEACLHELRLSLQSKIQELEELEKKKDSFYEAQRDLDMIEFKE	120			
Sbjct 61	SQKFKILAYKSEMENMDMKYEACLHELRLSLQSKIQELEELEKKKDSFYEAQRDLDMIEFKE	120			
Query 121	NVDKQVADCMQKQVQNTNRNVNELKSIFIALKSNNKDSNCSEIAAAEMRRSELQALKDNLD	180			
Sbjct 121	NVDKQVADCMQKQVQNTNRNVNELKSIFIALKSNNKDSNCSEIAAAEMRRSELQALKDNLD	180			
Query 181	RKLASKYEIKTQLQKQLQNILMTQTRV	207			
Sbjct 181	RKLASKYEIKTQLQKQLQNILMTQTRV	207			

[Detaylı olarak detayli2Numara.txt bakabilirsiniz]

Grafik özeti



