

Query: Vibrio cholerae 0395 chromosome 1, complete sequence Query
ID: CP000627.1 Length: 1881

>Vibrio cholerae 01 biovar El Tor str. N16961 genome assembly,
chromosome: 1
Sequence ID: LT906614.1 Length: 2961182
Range 1: 2605627 to 2607507

Score:3267 bits(3622), Expect:0.0,
Identities:1853/1881(99%), Gaps:0/1881(0%), Strand: Plus/Plus

Query 2158781
TTACACCTCTGCCATATCGCCGTTACGTTGCAGCCAAGCTCGGCGGTCATCCGCACGCTT
2158840

|||||
Sbjct 2605627
TTACACCTCTGCCATATCGCCGTTACGTTGCAGCCAAGCTCGGCGGTCATCCGCACGCTT
2605686

Query 2158841
TTTACCCAGCAGCATATCCATCATCTCGTCGGTCGCTTCAGCATCATCAATGGTCAGTTG
2158900

|||||
Sbjct 2605687
TTTACCCAGCAGCATATCCATCATCTCGTCGGTCGCTTCTGCATCATCAATGGTCAGTTG
2605746

Query 2158901
CACCAAGCGGCGAGTGTTGGGATCCATGGTGGTTTCACGCAATTGCAGCGGGTTCATTTT
2158960

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Sbjct 2605747
CACCAAGCGGCGAGTGTTGGGATCCATCGTGGTTTCACGCAATTGCAGCGGGTTCATTTT
2605806

Query 2158961
ACCCAAGCCTTTAAAGCGTTGCACGTTCACTTTGGCTTTTTTCTGGCTCAGACGCTCTAA
2159020

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Sbjct 2605807
ACCCAAGCCTTTAAAGCGTTGCACGTTCACTTTGGCTTTTTTCTGGCTCAGACGCTCTAA
2605866

Query 2159021
CACGCCCTCTTTTCTTGATCATCGAGTGCGTAGAACACCTCTTTACCACAGTCGATGCG
2159080

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Sbjct 2605867
CACGCCCTCTTTCTCTGATCATCGAGTGCGTAGAACACCTCTTTACCACAGTCGATGCG

2605926

Query 2159081

GTAGAGCGGCGGCATGGCAACATAGACGTGACCCGCTTTCACCAGCGCGCGGAAATGGCG
2159140

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Sbjct 2605927

GTAGAGCGGCGGCATAGCAACATAGACGTGACCCGCTTTCACCAGCGCGCGGAAATGGCG
2605986

Query 2159141

GGTAAATAGGGCGCAAAGCAAGGTCGCAATGTGCAGACCATCCGAGTCCGCATCGGCAAG
2159200

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Sbjct 2605987

GGTAAATAGGGCGCAGAGCAAGGTCGCAATGTGCAGACCATCCGAGTCCGCATCCGCAAG
2606046

Query 2159201

GATACAGACCTTGCCGTAACGCAGTGCTTCGAGGTTATCGCTGTCAGGGTCAATCCCCAA
2159260

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Sbjct 2606047

GATACAGACTTTGCCGTAACGCAGTGCTTCGAGGTTATCGCTGTCAGGGTCAATCCCCAA
2606106

Query 2159261

TGCAACTGAGATGTCGTGTAAGCAATACTTGATCGGCAGAACTTCCCA
2159320

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Sbjct 2606107

TGCAACTGAAATATCGTGTACTTCTTGTGAAGCAATACTTGATCGGCAGAACTTCCCA
2606166

Query 2159321

TGTATTGAGGATTTTGCCGCGCAGTGGCATCACCGCTTGGAATTCACGATCCCGCGCTTG
2159380

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Sbjct 2606167

CGTATTGAGGATTTTACCGCGCAGTGGCATCACCGCTTGGAATTCACGATCCCGCGCTTG
2606226

Query 2159381

CTTCGCCGAGCCGCCCGCCGAATCCCCTTCCACCAGGAAGAGTTCGGTGCGGTAAAGGTC
2159440

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Sbjct 2606227

CTTCGCCGAGCCGCCCGCCGAATCCCCTTCCACCAGGAAGAGTTCGGTGCGGTAAAGGTC

2606286

Query 2159441

TTGCACTGTACAGTCGGTTAATTTACCCGGTAAGGCAGGGCCTGAAGCGATCTTCTTACG
2159500

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Sbjct 2606287
TTGCACTGTACAGTCGGTTAATTTACCCGGTAAGGCAGGGCCTGAAGCGATCTTCTTACG
2606346

Query 2159501

TACCACTTTCTTGCTGGCACGCATTCGGCTGTGCGCATTAGCAATACAAACTTCGGCTAA
2159560

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Sbjct 2606347
CACCACTTTCTTGCTGGCACGCATTCGGCTGTGCGCATTAGCAATACAAACTTCGGCTAA
2606406

Query 2159561

CTGCTCTGCCAGTTGTGGTTTTTCGTTAAGCCACAAGCTAAAGGCATCTTTCACCACACC
2159620

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Sbjct 2606407
CTGCTCTGCCAGTTGCGGTTTTTCGTTAAGCCACAAGCTGAAGGCATCTTTCACCACGCC
2606466

Query 2159621

GGAGACAAACGCCCGCGATTGGCGTGAAGATAGGCGCTCTTTGGTTTGGCCAGCAAACCTG
2159680

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Sbjct 2606467
GGAGACAAACGCCCGCGATTGGCGTGAAGAGAGGCGCTCTTTGGTTTGGCCAGCAAACCTG
2606526

Query 2159681

CGGATCTTGCATCTTGATCGACAGCACATAAGCACAGCGGTCAAACACGTCCTCGCCTGT
2159740

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Sbjct 2606527
CGGATCTTGCATCTTGATCGACAGTACATAAGCACAGCGATCAAACACGTCCTCGCCTGT
2606586

Query 2159741

CAATTTTACCCCGCGTGGCAGCAGATTGCGGAACTCACAAAACCTCGCGCATCGCATCCAG
2159800

|||||
Sbjct 2606587
CAATTTTACCCCGCGTGGCAGCAGATTGCGGAACTCACAGAACTCGCGCATCGCATCCAG

2606646

Query 2159801

CAAGCCTTGGCGTAAACCGTTGACATGGGTACCACCTTGCGCAGTTGGGATCAGGTTAAC
2159860

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Sbjct 2606647

CAAGCCTTGGCGTAAACCGTTGACATGGGTACCACCTTGCGCGGTTGGGATCAGGTTAAC
2606706

Query 2159861

GTAGCTTTCGGTGATGAGCTCGCCACCTTCGGGTAGCCAAATCACCGCCACGTTGCCGC
2159920

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Sbjct 2606707

GTAGCTTTCGGTGATCAGCTCGCCACCTTCGGGTAGCCAAATCACCGCCACGTTGCCGC
2606766

Query 2159921

TTCGGTTTGCGCAGTAAATTCGCCGGTAAACGGCTCTTCCGGCAGTAAGGTATAACCTTT
2159980

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Sbjct 2606767

TTCGGTTTGCGCAGTAAATTCGCCGGTAAACGGCTCTTCCGGCAGTAAGGTATAACCTTT
2606826

Query 2159981

CACCCCTTCGCCAGATAATCTTTTAGACCATCTTCGTACAACCAGCGGTGCTCGTTGTT
2160040

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Sbjct 2606827

CACACCTTCGCCAGATAATCTTTTAGGCCATCTTCGTACAACCAGCGGTGCTCGTTGTT
2606886

Query 2160041

ATTGACCTTATCGGTAAAGATGATTTCTAAACCGGGCAAAGTACCGCCTTGGCACGCAA
2160100

|||||
Sbjct 2606887

ATTGACCTTATCGGTAAAGATGATTTCTAAACCGGGCAAAGTACCGCCTTGGCACGCAA
2606946

Query 2160101

GTTATTAATCAGGCGGATACGGAGAAATTCGGTGAGTCAAAATATTTGGTGTCTGGCCA
2160160

|||||
Sbjct 2606947

GTTATTAATCAGGCGGATACGGAGAAATTCGGTGAGTCAAAATATTTGGTGTCTGGCCA

2607006

Query 2160161

GAAATGGACGCTAGTACCGGTATTGCGACGGCCGCAAGTCCCCGTAACCGTCAGCTCAGT
2160220

|||||

Sbjct 2607007

GAAATGGACGCTAGTACCGGTATTGCGACGGCCGCAAGTCCCCGTAACCGTCAGCTCAGT
2607066

Query 2160221

CACTTTATCGCCATGTTCAAAGGCAATTCATACACTTGACCATCACGGCGAACCGCCAC
2160280

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Sbjct 2607067

CACTTTATCGCCATGTTCAAAGGCAATTCATACACTTGACCATCACGGCGAACCGCCAC
2607126

Query 2160281

TTCTACCCGTTTGGAGAGCGCATTACCAACCGAAATACCCACCCCATGCAAGCCACCGGA
2160340

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Sbjct 2607127

TTCTACCCGTTTGGAGAGCGCATTACCAACCGAAATACCCACCCCATGCAAGCCACCGGA
2607186

Query 2160341

AAATTGGTAGTTTTTGTGGAAGTACCACCGGCGTGCAGTTTGCACAGGATAAGCTC
2160400

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Sbjct 2607187

AAATTGGTAGTTTTTGTGGAAGTACCACCGGCGTGCAGTTTGCACAGAATAAGCTC
2607246

Query 2160401

CACCCCTGAGACCTTCTCTTCGGGTGAATATCGACGGGCATGCCTCGCCCGTCATCAAT
2160460

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Sbjct 2607247

CACCCCTGAAACCTTCTCTTCAGGTGAATATCGACGGGCATGCCTCGCCCGTCATCAAT
2607306

Query 2160461

CACTTCGAGCGATTGATCGGCATGAAGAATTACCTGAATTTTGGAGGCGTATCCGGCCAG
2160520

|||||

Sbjct 2607307

CACTTCGAGCGATTGATCGGCATGAAGAATTACCTGAATTTTGGAGGCGTATCCGGCCAG

2607366

Query 2160521

CGCTTCATCGACGGAGTTGTCGATCACTTCTTGCCCAAGGTGATTGGGGCGCGTGGTGTC
2160580

|||||
Sbjct 2607367
CGCTTCATCGACGGAGTTGTCGATCACTTCTTGCCCAAGGTGATTGGGGCGCGTGGTGTC
2607426

Query 2160581

GGTATACATTCCCGGTCTGCGACGCACTGGTTCTAAGCCATTGAGAACCTCAATGGCCCC
2160640

|||||
Sbjct 2607427
GGTATACATTCCCGGTCTGCGACGCACTGGTTCTAAGCCATTGAGAACCTCAATGGCCCC
2607486

Query 2160641 AGCATTATATTGTTTCAGTCAT 2160661

|||||
Sbjct 2607487 AGCATTATATTGTTTCAGTCAT 2607507

Figure 8