

Shigella sp. strain sh.98.R EscN/YscN/HrcN family type III secretion system ATPase (invC) gene, partial cds

GenBank: MN503255.1

[FASTA Graphics](#)[Go to:](#)

LOCUS MN503255 710 bp DNA linear BCT 31-MAY-2020
 DEFINITION Shigella sp. strain sh.98.R EscN/YscN/HrcN family type III secretion system ATPase (invC) gene, partial cds.

ACCESSION MN503255

VERSION MN503255.1

KEYWORDS .

SOURCE Shigella sp.

ORGANISM [Shigella sp.](#)

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella; unclassified Shigella.

REFERENCE 1 (bases 1 to 710)

AUTHORS Teimourpour,R., Sabour,S., Mohammadshahi,J. and Mirzanejad-Asl,H.

TITLE Direct Submission

JOURNAL Submitted (21-SEP-2019) Microbiology, Ardabil University of Medical Science, Ww.Ilamdoc.Ir, Ardabil +98, Iran

COMMENT ##Assembly-Data-START##

Sequencing Technology :: Sanger dideoxy sequencing

##Assembly-Data-END##

FEATURES Location/Qualifiers

source 1..710
 /organism="Shigella sp."
 /mol_type="genomic DNA"
 /strain="sh.98.R"
 /isolation_source="stool"
 /host="Homo sapiens"
 /db_xref="taxon:625"
 /country="Iran"
 gene <1..>710
 /gene="invC"
 CDS <1..>710
 /gene="invC"
 /codon_start=2
 /transl_table=11
 /product="EscN/YscN/HrcN family type III secretion system ATPase"
 /protein_id="QKD77170.1"
 /translation="LYRPVDNAPPLYSERAAIEKPFLTGIKVIDSLLTCGEGQRMGIF
 ASAGCGKTFILMMLIEHSGADIYVIGLIGERGREVTEETVDYLNSEKKNRCVLYVYATS
 DYSSVDRCNAAIATAIAEFFRTEGHKVALFIDSLTRYARALRDVALAAGESPARRGY
 PVSVFDSLPRLLERPGKLGAGGSITAFYTVLLEDDDFADPLAEVRSILDGHIYLSRN
 LAQKGQFPAIDSLKSISR"

ORIGIN

```

1 tctttatcga cctgtagata atgctcctcc gctatatagt gaaagggctg caattgagaa
61 gcctttttta acaggtatta aggttattga ttctttactc acgtgtggtg aaggacagcg
121 aatggggatt tttgcgtcag ctgggttggtg caaaactttt ctcatgaata tgctcattga
181 acatagtggg gctgatatat atgttattgg gttaattggg gagcgaggtc gagaggttac
241 agaaacgggt gattatttga aaaactctga gaaaaaaaaac aggtgtgttt tagtatatgc
301 aacttcggat tactcttcgg ttgatcgttg taatgctgca tatatagcca ctgctatagc
361 cgaatttttt aggactgaag gacataaagt agcgcctttt attgattcat taacaaggta
421 tgccagagca ttacgtgatg tggccttagc cgctggagaa tcacctgcca gaagaggcta
481 tccggtttcg gtttttgata gcttaccag acttcttgaa aggccaggaa agttaaggc
541 aggtggctct attactgcat tttacactgt tcttttgag gatgatgatt ttgctgatcc
601 attagctgaa gaggtaagat ccattttaga tggacatata tatttgagca gaaatctagc
661 ccaaaaagga caatttctg caattgattc ctaaaaaagt ataagcaggg

```

//

