

Sequences Submitted to GenBank

1. Enterococcus faecium strain GR7 16S ribosomal RNA gene, partial sequence

GenBank: KC179714.1

[FASTA Graphics](#)

LOCUS KC179714 1445 bp DNA linear BCT 27-
JAN-2013

DEFINITION Enterococcus faecium strain GR7 16S ribosomal RNA gene,
partial
sequence.

ACCESSION KC179714

VERSION KC179714.1 GI:443298396

KEYWORDS .

SOURCE Enterococcus faecium
ORGANISM [Enterococcus faecium](#)
Bacteria; Firmicutes; Bacilli; Lactobacillales;
Enterococcaceae;
Enterococcus.

REFERENCE 1 (bases 1 to 1445)
AUTHORS Kaur,B. and Kaur,R.
TITLE Isolation, identification and characterization of Enterococcus
faecium isolate GR7 with arginine catabolizing capacity
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1445)
AUTHORS Kaur,B. and Kaur,R.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2012) Department of Biotechnology, Punjabi
University, Patiala, Punjab 147002, India

COMMENT ##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

FEATURES Location/Qualifiers
source 1..1445
/organism="Enterococcus faecium"
/mol_type="genomic DNA"
/strain="GR7"
/isolation_source="lassi"
/db_xref="taxon:[1352](#)"
/country="India: Patiala, Punjab"

rRNA

<1..>1445

/product="16S ribosomal RNA"

ORIGIN

```
1  gacgaacgct ggcggcgtgc ctattacatg caagtcgaac gcttcttttt ccaccggagc
61  ttgctcccc ggaaaaagag gagtggcgaa cgggtgagta acacgtgggt aacctgcca
121 tcagaagggg ataacacttg gaaacaggtg ctaataccgt ataacaatca aaaccgcatg
181 gttttgattt gaaaggggct ttcgggtgtc gctgatggat ggacccgchg tgcattagct
241 agttggtgag gtaacggctc accaaggcca cgatgcatag ccgacctgag agggatgatc
301 gccacattgg gactgagaca cggcccaaac tcctacggga ggcagcagta gggaatcttc
361 ggcaatggac aaaagtctga ccgaacaacg ccgctgagat gaaagaaggt ttcggatcg
421 taaaactctg ttgttagaga agacaaggat gagagtaact gttcatccct tgacggtatc
481 taaccagaaa gccacggcta actacgtgcc agcagccgch gtaatacgtg gttggcaagc
541 gttgtccgga tttattgggc gtaaagcgag cgcagccggt ttcttaagtc tgatgtgaaa
601 gccccgggct caaccgggga gggtcattgg aaactgggag acttgagtgc agaagaggag
661 agtggaatte catgtgtagc ggtgaaatgc gtagatataat ggaggaacac cagtggcgaa
721 ggcggctctc tggctctgta ctgacgctga ggctcgaaag cgtggggagc aacaggatt
781 agataccctg gtagtccacg ccgtaaacga tgagtgctaa gtggtggagg gttccgccc
841 ttctctgctg cttttaacgc attaagcact ccgctgggg agtacgaccg cagggttgaa
901 actcaaggaa ttgacggggg cccgcacaag cggtgagca tgtggtttaa ttcgaagcaa
961 cgcgaagaac cttaccaggt cttgacatcc tttgaccact ctagagatag agcttcccct
1021 tcgggggcaa agtgacaggt ggtgcatggt tgcgctcagc tcgtgctgtg agatgttggg
1081 ttaagtcccg caacgagcgc aacccttatt gttagttgcc atcattcagt tgggcacttt
1141 agcaagactg ccggtgacaa accggaggaa ggtggggatg acgtcaaate atcatgcccc
1201 ttatgacctg ggctacacac gtgttacaat gggaaagtaca acgagttgch aagtcgchag
1261 gttaagttaa ttttttaaag cttttttcag ttcggattgc aggctgcaac tcgctgchag
1321 gaagccggaa tcgttagtaa tcgchgatca gcacccgchg gtgaatacgt tcccggcct
1381 tgtaccacc gcccgcccc ccacgagagt ttgtaacacc cgaagtcggg gaggtaacct
1441 tttgg
```

//

2. Enterococcus faecium carbamate kinase (arcC), ornithine transcarbamylase (arcB), arginine deiminase subunit A2 (arcA2), and arginine deiminase subunit A (arcA) genes, complete cds

GenBank: KC700335.1

[FASTA Graphics](#)

[Go to:](#)

LOCUS KC700335 3906 bp DNA linear BCT 18-

FEB-2015

DEFINITION Enterococcus faecium carbamate kinase (arcC), ornithine transcarbamylase (arcB), arginine deiminase subunit A2 (arcA2), and arginine deiminase subunit A (arcA) genes, complete cds.

ACCESSION KC700335

VERSION KC700335.1 GI:508083229

KEYWORDS .

SOURCE Enterococcus faecium

ORGANISM [Enterococcus faecium](#)

Bacteria; Firmicutes; Bacilli; Lactobacillales;

Enterococcaceae;

Enterococcus.

REFERENCE 1 (bases 1 to 3906)

AUTHORS Kaur,B. and Kaur,R.

TITLE Isolation, identification and genetic organization of the ADI operon in Enterococcus faecium GR7

JOURNAL Ann. Microbiol. (2014) In press

REMARK Publication Status: Available-Online prior to print

REFERENCE 2 (bases 1 to 3906)

AUTHORS Kaur,B. and Kaur,R.

TITLE A Novel Method of Purification of a Dimeric Arginine Deiminase from

Enterococcus faecium GR7 and Study of its Anti-Tumor Activity

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 3906)

AUTHORS Kaur,B. and Kaur,R.

TITLE Direct Submission

JOURNAL Submitted (28-FEB-2013) Department of Biotechnology, Punjabi University, Patiala, Patiala, Punjab 147002, India

REFERENCE 4 (bases 1 to 3906)

AUTHORS Kaur,B. and Kaur,R.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2015) Department of Biotechnology, Punjabi
University, Patiala, Patiala, Punjab 147002, India
REMARK Amino acid sequence updated by submitter
COMMENT ##Assembly-Data-START##
Sequencing Technology :: Sanger dideoxy sequencing
##Assembly-Data-END##

FEATURES Location/Qualifiers
source 1..3906
/organism="Enterococcus faecium"
/mol_type="genomic DNA"
/strain="GR7"
/isolation_source="dairy product"
/db_xref="taxon:[1352](#)"
gene complement(<1..1160)
/gene="arcC"
regulatory complement(<1..185)
/regulatory_class="terminator"
/gene="arcC"
/note="putative"
CDS complement(186..1133)
/gene="arcC"
/codon_start=1
/transl_table=[11](#)
/product="carbamate kinase"
/protein_id="[AGN03851.1](#)"
/db_xref="GI:508083230"

/translation="MVKRKVVVALGGNAILSTDASAKAQQEALTETAKYLVKFIEQGD

ELIISHGNGPQVGNLLIQQAADSEKTPAMPLDTCVAMTEGSIGYWLQNAMGEVLKEK

GIDKDVVSLVTQVIVDENDPSFKNPSKPVGPFYTEEEAKEQMNADSTVTFKEDAGRGW

RKVVASPKPISIKEARVIETLVEQGVITVSVGGGGIPVETATGLEGREAVIDKDFAS

EKLAEIIDADLLIVLTGVDNVYVNYQKPDQKKLETVTVSEMKYIDEKQFAPGSMLPK

VEAAIAFVEAKPNAKAIITSLENIENLLASEEGTIIIVAD"

regulatory complement(1156..1160)
/regulatory_class="ribosome_binding_site"

```

        /gene="arcC"
gene      complement (1161..2281)
        /gene="arcB"
regulatory complement (1161..1246)
        /regulatory_class="terminator"
        /gene="arcB"
        /note="putative"
CDS      complement (1247..2275)
        /gene="arcB"
        /codon_start=1
        /transl_table=11
        /product="ornithine transcarbamylase"
        /protein_id="AGN03852.1"
        /db_xref="GI:508083231"

/translation="MFNMKESVFGQSRLLAEKDFTKHEELQYLIDFSEHLKDLKKGIP
HHYLEGKNIALLFEKTSTRTRSFTTAAIDLGAHPEYLGANDIQLGKKESTEDTAKVL
GRMFDGIEFRGFSQKMVEELAEFSGVPVWNGLTDEWHPTQMIADFLTIQENFGTVEGI
TVAYCGDGRNNMANSLLVTGAILGANMRIVAPKELQPEEEIVKMAEGFAEKSGAQLMI
TDDVDKGVGDADVLYSDVWVSMGEEDKFEERIKLLKPYQINMEMVEKTHNTDRLIFLH
CLPAFHDTNTVYGEQMKERFGITEMEVTDEVFRSKYARQFDQAENRMHSIKAIMAATL
GNLFIPRV"
regulatory complement (2277..2281)
        /regulatory_class="ribosome_binding_site"
        /gene="arcB"
gene      complement (2282..3904)
        /gene="arcA"
        /note="overlapping arcA2/arcA form heterodimer
arginine
        deiminase"
regulatory complement (2282..2546)
        /regulatory_class="terminator"
        /gene="arcA"
        /note="putative"
gene      complement (2547..3872)
        /gene="arcA2"
CDS      complement (2547..3854)
        /gene="arcA2"

```

/codon_start=1
/transl_table=11
/product="arginine deiminase subunit A2"
/protein_id="AJM87489.1"
/db_xref="GI:756772494"

/translation="MRQNYESDYKRRI SYTCNQKEGVQHNMDKPIHVFSEIGKLT
LKRPGQEVENTLTPDIMDRLLFDDIPYLP
IAQEEHDNFAKTLQNEG
VETLYLEKLA
AEA
IDAGNVKEQFLNKMLDESHIASNAVRDGLHEFLLSMETQEMVDKIMAGV
RTKDIEVRS
SSLYDLSADDDYPFYMDPMPNLYFTRDPSASMGNGMTVNKMTFEARRRE
SMFTEYILK
HHPRFANKGIEVWLDRENPDHIEGGDELILSDKVVAVGISQRTNAKALE
KLARHPFAK
NSGF
EKVLAIKIPNNRAMMHLDTVFTMVDHDKFTIHPAIQSKDGKMDVFTIE
PDGDDI
KITHSDNLHETMKAALGLDDLVL
IPTGNGDEIVAPREQW
DGSNTLAIAPGVVVTYNR

NYVSNELLRSYGIKVLEINSS
ELSRGGRGGPRC
MSQPLVREDLK"
CDS complement (2547..3776)
/gene="arcA"
/codon_start=1
/transl_table=11
/product="arginine deiminase subunit A"
/protein_id="AGN03853.1"
/db_xref="GI:508083232"

/translation="MDKPIHVFSEIGKLT
VLLKRP
GQEVENTLTPDIMDRLLFDDIPY
LP
IAQEEHDNFAKTLQNEG
VETLYLEKLA
AEA
IDAGNVKEQFLNKMLDESHIASNAVR
DGLHEFLLSMETQEMVDKIMAGV
RTKDIEVRS
SSLYDLSADDDYPFYMDPMPNLYFTR
DPSASMGNGMTVNKMTFEARRRE
SMFTEYILK
HHPRFANKGIEVWLDRENPDHIEGGD
ELILSDKVVAVGISQRTNAKALE
KLARHPFAKNSGF
EKVLAIKIPNNRAMMHLDTVFT
MVDHDKFTIHPAIQSKDGKMDVFTIE
PDGDDIKITHSDNLHETMKAALGLDDL
VL
IPTGNGDEIVAPREQW
DGSNTLAIAPGVVVTYNR
NYVSNELLRSYGIKVLEINSS
ELSRG

RGGPRC
MSQPLVREDLK"
regulatory complement (3788..3792)

```

        /regulatory_class="ribosome_binding_site"
        /gene="arcA"
regulatory complement (3869..3872)
        /regulatory_class="ribosome_binding_site"
        /gene="arcA2"
regulatory complement (3875..3881)
        /regulatory_class="minus_10_signal"
        /gene="arcA"
        /note="putative"
regulatory complement (3898..3904)
        /regulatory_class="minus_35_signal"
        /gene="arcA"
        /note="putative"

```

ORIGIN

```

1 gccagaatg atacaagtac tctcttgttc acaaatctt aatcttatta aactttcttg
61 aattcagaaa aaaaaacgaa aggctagtcg tttctaataa aaaaaacaat ccagatggcc
121 taaaggagaa gaaataccac ctggatagtt ataaatcatt tcgtaaatac gaaagactta
181 acaaattaat cagctacgat aatcgttcct tcttcagaag ctaaaagatt ttcgatattt
241 tctaaagaag tgatgattgc ctagcgttc ggttttgctt caacaaatgc aatggctgct
301 tctactttcg gaagcatgct tcttgagcgc aactgttttt catcaatgta ttgtttcatt
361 tctgaaacag taacagtttc tagtttcttt tgatccggtt tttggtaatt gacatacaca
421 ttgtctacac ctgtcaatac gatgagcaaa tctgcatcga tgatttcggc taatttttct
481 gaagcaaaat ctttatcgat cacggcttct cgccttcta atccggtcgc tgtttctaca
541 acaggaatcc cgccaccgcc gacagacacc gtgataactc cttgttcgac tagcgtttcg
601 atgacacgtg cttctttgat cgagattggt ttaggggaag cgactacttt tctccatcca
661 cgtccagcgt cttctttgaa tgtcacagta gaatcagcat tcatttgttc tttcgcttct
721 tcttccgtgt agaatgggcc gactggttta cttggatttt tgaaggaagg atcattttca
781 tccacaataa cttgagtgc taaagaaact acatctttat cgatcccttt ttccttcagt
841 acttcaacca tcgcttttg gagccagtag ccgattgacc cttccgtcat tgcgacacat
901 gtatctaaag gcattgctgg tgttttctca gaatcagcag cttgctgctg aatcaatagg
961 ttgccgactt gcggaccatt tccgtgagag atgattagtt catctccttg ttcgataaat
1021 ttcactaaat actttgctgt ttccgttaac gcttcttggt gggcttttgc acttgcattc
1081 gtagacaaga tggcattgcc tcctaaagcg acaactactt ttogtttgac catttcattc
1141 gtcctttctt cagttctcct gaattttcta gataacaaaa cgagccagcg ttttgtgatt
1201 ttccctcaat gctgactcgt tttttcgtga gatgaatgtg gttatgtaa acgcgagggga
1261 taaacaagtt acctaagtgt gctgccatga ttgctttgat tgaatgcata cgattttctg
1321 cttgggtcaaa ttgacgagca tatttgctgc ggaatacttc atctgttact tccatttcag
1381 tgatgccaaa gcgttctttc atttgttcac cgtaaacagt gtttgtatca tggaaagctg
1441 gtaagcagtg caagaagatc aaacgatctg tattgtgtgt tttttctacc atttccatat
1501 tgatttggtgta aggtttcaac aatttgatcc gttcttcaaa tttatcttct tcaccattg
1561 ataccatac atcagaataa agcacgtctg ctccgtctac acctttatca acatcgtcgg

```

1621 taatcatcaa ttgtgccctt gatttttcag caaaaccttc tgccattttg acgatttctt
1681 cttcaggttg taattccttt ggtgcaacaa tacgcatggt tgctcccaaa attgcacctg
1741 ttactaataa agagtttagc atattgtttc gaccatctcc acagtatgca acagtgatac
1801 cttctacagt tccaaagttt tcttgatag ttaaaaagtc agcgatcatt tgtgttggat
1861 gccattcgtc agtcaaacca ttccaaactg gaacgccaga gaattctgct agttcctcta
1921 ccattttttg actgaatcca cggaattcga ttccgtcaaa catacgacct aacactttag
1981 ctgtatcttc tgttgattct tttttaccta attggatgtc atttgcacct aggtattcag
2041 gatgtgcacc tagatcgatt gctgcagtgg taaatgcaga acgagtacgt gtagatgttt
2101 tttcaaataa aagtgcgata ttttttcctt ctatagatg atgtgggatc ccacgttttt
2161 tcaagtcttt caagtgttct gaaaaatcga tcaaataattg taactcttct tttgtaaaat
2221 ctttttctgc taataaactt cttccttggg aactgattc tttcatatta aacattctcc
2281 ttttagattgt ttttatttaa gattaaagag gaaatcctga cgacagctga cagtaagact
2341 gtcgtcaggt tataaactac ttcaagtctt cacggacaag tggttggctc atacaacgtg
2401 gaccgccacg acctcgtgac aattcactag aattgatttc caacactttg ataccatagc
2461 tacgaagcaa ttcgttcgat acgtaattcc gattgtaagt gactacacac ggggaagccg
2521 attgaagact gccgtcagga aacaaattac ttcaagtctt cacggacaag tggttggctc
2581 atacaacgtg gaccgccacg acctcgtgac aattcactag aattgatttc caacactttg
2641 ataccatagc tacgaagcaa ttcgttcgat acgtaattcc gattgtaagt gactacgaca
2701 cctggagcga ttgccaatgt attggatccg tcattccatt gttctctagg ggcaacgatc
2761 tcatcccat taccagttgg aatcaatata agatcatcta atccaagagc agctttcatc
2821 gtttcgtgta agttatctga atgagtgatc ttgatatcat caccatctgg ttcgatcgta
2881 aagacatcca tcttaccgtc tttactttgg attgctggat ggatagtga tttgtcatga
2941 tctaccattg tgaatacggg gtccagatgc atcattgcac ggttgttcgg gattttgatt
3001 gctaatactt tttcaaatcc tgaatTTTTT gcgaatggat ggcgtgctaa tttttctaaa
3061 gcttttgcac ttgttcgttg agaaatccca actgctacta ctttgcgct taagattaat
3121 tcatctccac cttcgatatg atcaggattt tcacgatcca accatacttc gatcccttta
3181 ttggcaaatc ttggatgatg tttcaaaaata tattctgtaa acatcgattc acgacgacgt
3241 gcttcaaaaag tcatcttatt gacggtcatt ccatttcca ttgatgcgga agggtcgcgt
3301 gtaaagtaca agtttggcat tgggtccatg taaaatggat agtcgtcgtc tgctgaaaga
3361 tcatacaagc tgctagaacg tacttogaata tcttttgtac gaacccagc catgatttta
3421 tctaccattt cttgtgtttc cattgataga aggaactcat gaagaccatc tcttactgca
3481 ttcgatgcga tatgagattc atccaacatt ttattcaaga attgttcttt gacgttgcc
3541 gcgtcaatcg cttctgctgc taatTTTTTc aagtaaagag tttcgacgcc ttcgTTTTTg
3601 aaggTctttg caaagtTgtc atgctcttct tgagcaatcg gaagatatgg aatatcatcg
3661 aacaacagac gatccataat atctggtgtc aaatTTTcca cttcttggcc aggcggtttc
3721 agtaaaaactg tctttaattt ccctatttca gagaaaacgt gaataggttt atccatgttg
3781 tgttgactc cttctttttg attacatgta taggatatcc tctttttgta atcactttca
3841 taatTTTgtc tcattcaaaa tgagacattc ctcacattaa tattccgagc taattaaata
3901 attaaa

//

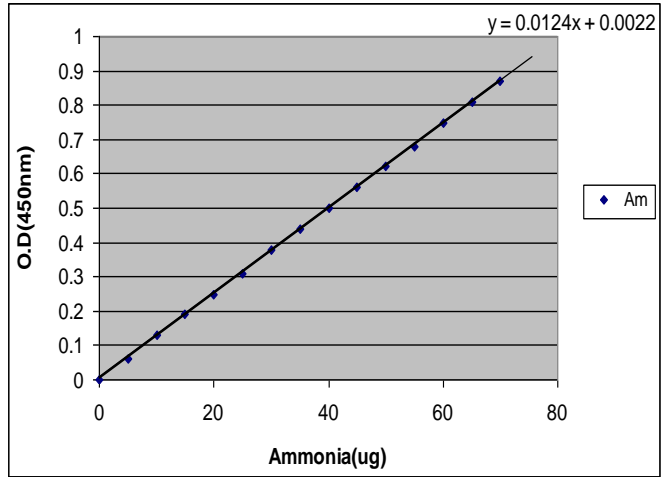


Fig. A1: Standard curve of ammonia

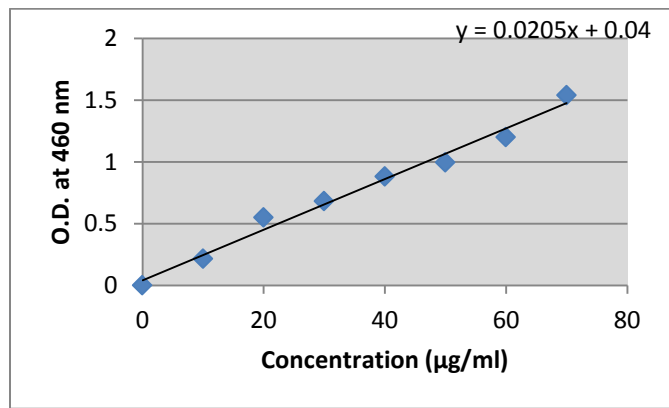


Fig. A2: Standard curve of citrulline

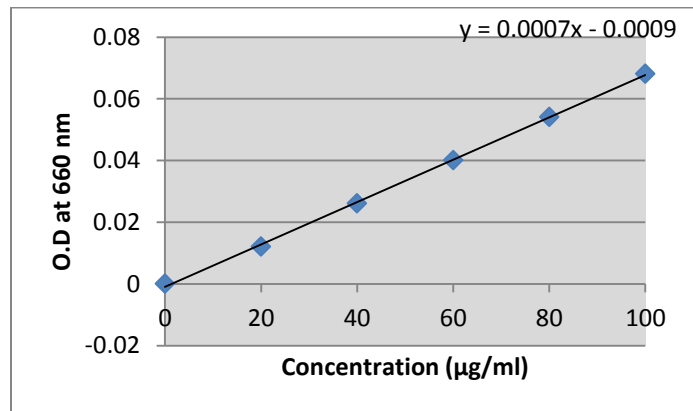


Fig. A3: Standard curve of protein