

Protein View: [gi|26106455](#)

Aconitate hydratase 2 [Escherichia coli CFT073]

Database: NCBIInr
Score: 50
Nominal mass (M_r): 100033
Calculated pI: 5.78
Taxonomy: Escherichia coli

This protein sequence matches the following other entries:

- [gi|191070760](#) from **Escherichia coli UTI89**
- [gi|115511529](#) from **Escherichia coli APEC O1**
- [gi|190905486](#) from **Escherichia coli F11**
- [gi|226902186](#) from **Escherichia sp. 3_2_53FAA**
- [gi|355418535](#) from **Escherichia coli str. 'clone D i2'**
- [gi|355423455](#) from **Escherichia coli str. 'clone D i14'**
- [gi|641682693](#) from **Escherichia coli ST131**

Sequence similarity is available as [an NCBI BLAST search of qi|26106455 against nr.](#)

Search parameters

MS data file: 1-2.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)

Protein sequence coverage: 2%

Matched peptides shown in **bold red**.

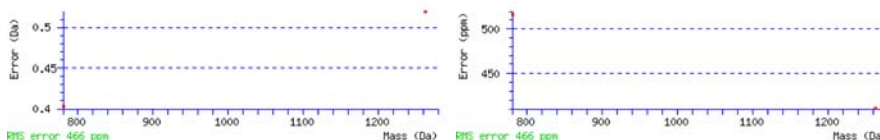
1	MLFLCKQJINT	SKSKCSYASC	GTGHLEPYKLL	SHRSVKRPA	RTMTMRARRL
51	VLEEYERKGVH	AERAEAGTAP	KPLDANQKAA	LVELLNKPAA	GEFEFLFLLD
101	TRNRVPKGVH	AAYYKAGFLA	AVANQMAASP	LTLPKEALIE	LGTMQGGYNI
151	HLFLDALDIA	KLAPIAAKAL	SHVLLMDFNF	YDVPEAKKAG	NEYAKVQKMS
201	WADAEAFNLR	PALAEKLFNR	FHTLVKGTENT	LDLSPADPAM	SRPDJPLHALS
251	AMLKNAEAGI	EDPDQGVGVP	IKQICLAEQO	GFFPLAYGVD	VGTGSSRKSA
301	TSNVLVFMFG	DIPHVNKVRP	GLKGLGKITA	PIFNFTMDIA	GALPVEEIVD
351	NLMDGVDIV	YPYKVEVRNF	ETGELLEATF	LKTFDLIDEV	RAGGER PLII
401	GRGLT KDARE	ALVGSFSDNF	RQAKDVAESD	RKGFSLAQKM	GRACGVKQIR
451	PAYCEPKMT	SVGQSDDTGP	TRMDREKLDA	CLGSLADLDA	QSFCHTAAGP
501	KPVDVNTHTH	LTDFIMNRGG	VSRLRGDGVFI	HSWNLNRNFI	DMVTGTDGSHS
551	TRFFIGISFV	AGSLVAFAA	ATPGPMVSL	ESLVIRFFKG	PDQTGTLRSD
601	VHAIPLAYLA	GLTKVTEKK	KNNISFGRIL	ETIEGLPDYK	EQEAFDTLAS
651	AERSAAGCTI	KLNKEPIETI	KLNIISVLLK	MAIEAGLVR	TLLRITQGBE
701	KWANPELLE	ADADAEEYAA	IDIDLADIKE	PILCAANDRD	DARPLSAVQGD
751	EKIDIEVIGS	CGMNI G HFA	AGKLMDAHKG	GLPTLRWPAV	PTMRDAQLGT
801	EEGYYSVFGK	SATRIEIPGC	SLCMGNQAGV	ADGATVTS	TRNFN NRNLT
851	GANVFLASAE	LAALVAALIG	LTPEETEEQY	VAQVDKTAVD	TRYRLNFDQL
901	SOYTEKADGV	IFOTAV			

Unformatted sequence string: **916 residues** (for pasting into other applications).

Sort peptides by ☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

☐ Show predicted peptides also

Query	Start - End	Observed	Mr(expt)	Mr(calc)	Delta M	Score	Expect	Rank	U	Peptide
32	396 - 402	391.4700	780.9254	780.5221	0.4033	0	12	90	<u>1</u>	U R.IPLIIGR.G
42	830 - 842	632.5900	1263.1654	1262.6467	0.5188	0	38	0.72	<u>1</u>	U R.VADGATVSVSTR.N



LOCUS	AE016751.141	916 aa	linear	BCT 31-JAN-2014
DEFINITION	Aconitate hydratase 2 [Escherichia coli CFT073].			
ACCESSION	AA078641			
VERSION	AA078641.1			
DBLINK	BioProject: PRJNA313			
	BioSample: SAMN02604094			
DBSOURCE	accession AE014075.1			
KEYWORDS	.			
SOURCE	Escherichia coli CFT073			
ORGANISM	Escherichia coli CFT073			
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Escherichia.			
REFERENCE	1 (residues 1 to 916)			
AUTHORS	Welch,R.A., Burland,V., Plunkett,G. III, Redford,P., Roesch,P., Rasko,D., Buckles,E.L., Liou,S.R., Boutin,A., Hackett,J., Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C., Perna,N.T., Mobley,H.L., Donnenberg,M.S. and Blattner,F.R.			
TITLE	Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)			
PUBMED	12471157			
REFERENCE	2 (residues 1 to 916)			
AUTHORS	Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P., Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J., Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C., Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.			
TITLE	Direct Submission			
JOURNAL	Submitted (20-JUN-2002) Genetics Laboratory, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA			
COMMENT	Method: conceptual translation.			
FEATURES	Location/Qualifiers			
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	2/2-methylisocitrate dehydratase; Validated"			
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	/locus_tag="c0147"			