

MATRIX
SCIENCE

MASCOT Search Results

Protein View: gi|1311039

Chain A, Dipeptide Binding Protein Complex With Glycyl-L-Leucine

Database: NCBInr
Score: 59
Nominal mass (M_r): 57599
Calculated pI: 5.75
Taxonomy: [Escherichia coli](#)

This protein sequence matches the following other entries:

- [gi|1311041](#) from [Escherichia coli](#)
- [gi|1311043](#) from [Escherichia coli](#)
- [gi|1311045](#) from [Escherichia coli](#)

Sequence similarity is available as [an NCBI BLAST search of gi|1311039 against nr](#).

Search parameters

MS data file: 8-2.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: 3%

Matched peptides shown in **bold red**.

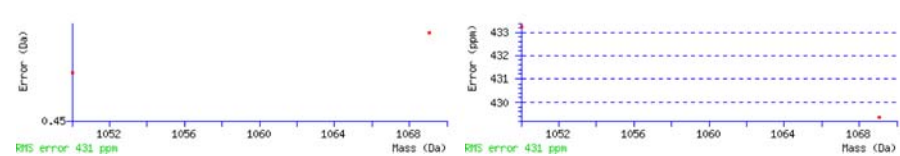
1 KTLVYCSGSG PEGFNPQLFT SGTTYDASSV PLYNRLVEFK IGTTTEVIPGL
51 AEKWEVSEGD KTYTFHLRKG VKWHDNKEFK PTRELNADDV VFSFDRQKNA
101 QNPYHKVSGG SYEYFEGMGL PELISEVKKV DDNTVQFVLT RPEAPFLADL
151 AMDFASILSK EVADAMMKAG TPEKLDLNPI GTGPFQLQQY QKDSRIRYKA
201 FDGYWGTPKQ IDTLVFSITP DASVRYAKLQ KNECQVMYP NPADIARMKQ
251 DKSINLMEMP GLNVGYLSYN VQ**KPLDDVK VR**QALTYAVN KDIIK**AVYQ**
301 **GAGVS**AKNLI PPTMWGYNDQ VQDYTYDPEK AKALLKEAGL EKGFSIDLWA
351 MPVQRPNPN ARMAEMIQA DWAKVGVOAK IVTYEWGEYL KRAKDGEHQT
401 VMWGWTGDNG DPDNFFATLF SCAASEQGSN YSKWCYKPE DLIQPARATD
451 DHNKRVELYK QAVVMHDQA PALIIAHSTV FEPVRKEVKG YVVDPLGKHH
501 FENVSIE

Unformatted sequence string: **507 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
37	274 - 282	357.3700	1069.0882	1068.6291	0.4590	1	13	2.2e+002	8	..	K.KPLDDVKVR.Q
34	297 - 307	526.0100	1050.0054	1049.5506	0.4549	0	47	0.089	2	U	K.AVYQAGVSAS.K



LOCUS 1DPP_A 507 aa linear BCT 10-OCT-2012
DEFINITION Chain A, Dipeptide Binding Protein Complex With Glycyl-L-Leucine.
ACCESSION 1DPP_A
VERSION 1DPP_A
DBSOURCE pdb: molecule 1DPP, chain 65, release Jun 6, 2011;
deposition: Aug 11, 1995;
class: Peptide Binding Protein;
source: Mmdb_id: 71888, Pdb_id 1: 1DPP;
Exp. method: X-Ray Diffraction.
KEYWORDS .
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales;
Enterobacteriaceae; Escherichia.
REFERENCE 1 (residues 1 to 507)
AUTHORS Dunten,P. and Mowbray,S.L.
TITLE Crystal structure of the dipeptide binding protein from Escherichia coli involved in active transport and chemotaxis
JOURNAL Protein Sci. 4 (11), 2327-2334 (1995)
PUBMED 8563629
REFERENCE 2 (residues 1 to 507)
AUTHORS Dunten,P. and Mowbray,S.L.
TITLE Direct Submission
JOURNAL Submitted (11-AUG-1995)
COMMENT 1 Dipeptide Binding Protein.
FEATURES
Location/Qualifiers
source 1..507
/organism="Escherichia coli"
/db_xref="taxon:562"
Region join(1..35,176..241,487..507)
/region name="Domain 1"
/note="NCBI Domains"
SecStr 1..9
/sec_str_type="sheet"
/note="strand 1"
Region 2..491
/region name="PBP2_DppA like"
/note="The substrate-binding component of an ABC-type dipeptide import system contains the type 2 periplasmic binding fold; cd08493"
/db_xref="CDD:173858"
Region 4..507
/region name="PRK15109"
/note="antimicrobial peptide ABC transporter periplasmic binding protein SapA; Provisional"
/db_xref="CDD:185064"
Bond bond(6,234)
/bond_type="disulfide"
SecStr 21..28
/sec_str_type="helix"
/note="helix 1"
SecStr 31..34
/sec_str_type="sheet"
/note="strand 2"
Region join(36..50,143..156)
/region name="Domain 2"
/note="NCBI Domains"
SecStr 37..40
/sec_str_type="sheet"
/note="strand 3"
SecStr 45..48
/sec_str_type="sheet"