MASCOT Search Results

User: pbm
E-mail:
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-6SA4
MS data file: G:\PRESTATIONS\Labos académiques\Internationalux\États Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR__2068.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:09:01 GMT

Not what you expected? Try the peptide summary.

Search parameters
Type of search: MS/MS Ion Search
Enzyme: Trypsin
Variable modifications: Carbamidomethyl (C), Oxidation (M)
Mass values: Monoisotopic
Protein mass: Unrestricted
Peptide mass tolerance: ± 1.6 Da
Fragment mass tolerance: ± 0.8 Da
Max missed cleavages: 3
Instrument type: ESI-TRAP
Number of queries: 496

Score distribution
Peptide score distribution. Ions score is $-10 \log(P)$, where $P$ is the probability that the observed match is a random event. There are 8 peptide matches above identity threshold and 11 matches above homology threshold for 496 queries. On average, individual ions scores > 45 (beyond green shading) indicate identity or extensive homology ($p<0.05$).

Protein Family Summary
Significance threshold $p< 0.05$
Display non-sig. matches
Preferred taxonomy

Protein families 1–5 (out of 5)

| Protein | Score | Mass | Matches | Sequences | emPAI |
|---------|-------|------|---------|-----------|-------|
| P55260.3 | 167   | 35826| 4 (4)   | 4 (4)     | 0.62  |

1 peptide matches (4 non-duplicate, 0 duplicate)

| Query Dups | Observed Mr (exact) | Observed Mr (calc) | Delta M | Score | Expect | Rank | U | Peptide |
|------------|---------------------|--------------------|---------|-------|--------|------|---|---------|
| 196        | 574.2400            | 1146.4654          | 1146.5881 | -0.1226 | 72     | 2.9e-05 | U | K.GLOTOSTILR.V |
| 324        | 700.0300            | 1398.0454          | 1397.6688 | 0.3767  | 56     | 8e-05   | U | R.INGYGGQRG.G |
| 326        | 775.2800            | 1548.5454          | 1548.7532 | -0.2078 | 86     | 2e-07   | U | K.AASOFMATEAQVLR.K |
| 338        | 833.3600            | 1664.7054          | 1665.8461 | -1.1407 | 44     | 0.00048 | U | K.SETSGSFEVALLAYV.C |
| # | Accession   | Score | Description                                                                                     | Species                  |
|---|-------------|-------|-------------------------------------------------------------------------------------------------|--------------------------|
| 2 | NP_036767.1 | 132   | anionic trypsin-1 precursor [Rattus norvegicus]                                                   |                          |
| 3 | XP_008763925.1 | 70   | PREDICTED: keratin, type II cytoskeletal 73 isoform X1 [Rattus norvegicus]                      |                          |
| 4 | NP_001008825.1 | 61   | keratin, type II cytoskeletal cochlear [Rattus norvegicus]                                      |                          |
| 5 | NP_001008751.1 | 57   | keratin, type I cytoskeletal 14 [Rattus norvegicus]                                             |                          |

Not what you expected? Try the peptide summary.

Mascot: [http://www.matrixscience.com/](http://www.matrixscience.com/)
MASCOT Search Results

**Protein View: P55260.3**

ReName: Full=Annexin A4; AltName: Full=36 kDa zymogen granule membrane-associated protein; Short=ZAP36; AltName: Full=Annexin IV; AltName= Full=Annexin-4; AltName= Full=Lipocortin IV

| Database: | NCBIprot |
|-----------|-----------|
| Score:    | 167       |
| Monoisotopic mass (Mₐ): | 35826 |
| Calculated pI: | 5.31 |
| Taxonomy: | Rattus norvegicus |

This protein sequence matches the following other entries:
- **P55260.3** from Rattus norvegicus

**Search parameters**
- **MS data file:** G:\PRESTATIONS\Labos académiques\Internationaux\États Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR__2068.mgf
- **Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.
- **Variable modifications:** Carbamidomethyl (C), Oxidation (M)

**Protein sequence coverage:** 16%

**Matched peptides shown in bold red.**

| Query | Start – End | Observed Mr (expt) | Mr (calc) | Delta M | Score | Expect | Rank |
|-------|-------------|-------------------|-----------|---------|-------|--------|------|
| 1     | 10 – 24     | 775.2800          | 1548.5454 | -0.2078 | 86    | 2e-07  | 1    |
| 2     | 124 – 134   | 700.0300          | 1398.0454 | 0.3767  | 56    | 8e-05  | 1    |
| 3     | 134 – 144   | 833.3600          | 1664.7054 | 1.1407  | 44    | 7e-06  | 1    |
| 4     | 196 – 270   | 574.2400          | 1146.4654 | -0.1226 | 72    | 2.9e-05| 1    |

**Unformatted sequence string:** 319 residues (for pasting into other applications).

**SORT** a residue number | Increasing mass | Decreasing mass
---|---|---
**Show** matched peptides only | predicted peptides also

**LOCUS** ANXA4_RAT
**DEFINITION** RecName: Full=Annexin A4; AltName: Full=36 kDa zymogen granule membrane-associated protein; Short=ZAP36; AltName: Full=Annexin IV; AltName= Full=Annexin-4; AltName= Full=Lipocortin IV.
**ACCESSION** P55260
**VERSION** P55260.3
**DBSOURCE** UniProtKB: locus ANXA4_RAT, accession P55260; class: standard.
**created:** Oct 1, 1996. sequence updated: Jan 23, 2007.

**REFERENCE** 1 | residues 1 to 319 |
| 1 | residues 1 to 319 |

**KEYWORDS** 3D; Structure; Acetylation; Annexin; Calcium; Calcium/phospholipid-binding; Complete proteome; Phosphoprotein; Reference proteome; Repeat.
REMARK NUCLEOTIDE SEQUENCE [MRNA].

COMMENT On Oct 28, 2003 this sequence version replaced gi:1703320.

[FUNCTION] Calcium/phospholipid-binding protein which promotes membrane fusion and is involved in exocytosis. (ECO:0000250). A pair of annexin repeats may form one binding site for calcium and phospholipid. [MISCELLANEOUS] Seems to bind one calcium ion with high affinity. (ECO:0000250). [SIMILARITY] Belongs to the annexin family. (ECO:0000305).

FEATURES Location/Qualifiers
source 1..319 /organism="Rattus norvegicus" /db_xref="taxon:10116"
gene 1..319 /gene="Anxa4" /gene_synonym="Anx4"
Protein 1..319 /product="Annexin A4" /note="16 kDa zymogen granule membrane-associated protein; Annexin IV; Annexin-4; Lipocortin IV; ZAP36" /UniProtKB_evidence="Evidence at protein level"
Region 1..319 /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="Annexin A4. /PT1G-BQO_0000067485." Site 7 /site_type="phosphorylation" /experiment="experimental evidence, no additional details recorded" /note="Phosphothreonine. (ECO:0000250|UniProtKB:P08132)." Site 12 /site_type="phosphorylation" /experiment="experimental evidence, no additional details recorded" /note="Phosphoserine. (ECO:0000250|UniProtKB:P05261)." Region 16..27 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 19..83 /region_name="Annexin" /note="Annexin; pfam00191" /db_xref="CDD:278615" Region 23..83 /region_name="Repetitive region" /note="Annexin 1." Region 28..31 /region_name="Beta-strand region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 34..41 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 46..60 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 64..71 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 74..84 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 87..99 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 90..155 /region_name="Annexin" /note="Annexin; pfam00191" /db_xref="CDD:278615" Region 95..155 /region_name="Repetitive region" /experiment="experimental evidence, no additional details recorded" /note="Annexin 2." Region 100..112 /region_name="Beta-strand region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 106..115 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 118..132 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 136..143 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)." Region 146..157 /region_name="Helical region" /experiment="experimental evidence, no additional details recorded" /note="(ECO:0000244|PDB:2ZHJ)."
Region          168..181
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          173..239
/region_name="Annexin"
/note="Annexin; pfam00191"
/db_xref="CDD:278615"

Region          179..239
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"
/note="Annexin 3."
Region          182..184
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          185..187
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          190..199
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          202..216
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Site            213
/site_type="acetylation"
/experiment="experimental evidence, no additional details recorded"
/note="N6-acetyllysine. {ECO:0000250|UniProtKB:P09525}."
Region          220..227
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          230..244
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          246..258
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          254..314
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"
/note="Annexin 4."
Region          259..262
/region_name="Beta-strand region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          265..275
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          276..278
/region_name="Hydrogen bonded turn"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Region          280..291
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Site            293
/site_type="acetylation"
/experiment="experimental evidence, no additional details recorded"
/note="N6-acetyllysine. {ECO:0000250|UniProtKB:P09525}."
Region          295..302
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
Site            300
/site_type="acetylation"
/experiment="experimental evidence, no additional details recorded"
/note="N6-acetyllysine. {ECO:0000250|UniProtKB:P09525}."
Region          305..315
/region_name="Helical region"
/experiment="experimental evidence, no additional details recorded"
/note="ECO:0000244|PDB:2ZHJ."
## MASCOT Search Results

**User**: pbm  
**E-mail**:  
**Search title**: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4  
**MS data file**: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1990.mgf  
**Database**: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)  
**Taxonomy**: Rattus (77,467 sequences)  
**Timestamp**: 25 Jan 2019 at 10:26:10 GMT

Not what you expected? Try [the peptide summary](http://mascot2.crihan.fr/mascot/cgi/master_results_2.pl?file=../data/20...1 sur 1 28/01/2019 à 15:10).

### Search parameters
- **Significance threshold p<**: 0.05  
- **Max. number of families**: 20  
- **Display non-sig. matches**:  
- **Dendrograms cut at**: 0  
- **Preferred taxonomy**: All entries

### Protein Family Summary

#### Protein families 1–5 (out of 5)

| Score | Mass | Matches | Sequences | emPAI |
|-------|------|---------|-----------|-------|
| 4.1   | 33171| 1 (1)   | 1 (1)     | 0.14  |

1 peptide matches (1 non-duplicate, 0 duplicate)

| Query | Dupes | Observed | Mr (expt) | Mr (calc) | Delta M | Score | Expect | Rank | Peptide |
|-------|-------|----------|-----------|-----------|---------|-------|--------|------|---------|
| 322   |       | 734.8300 | 1467.6454 | 1467.7358 | -0.0903 | 58    | 0.00045| 1    | K.VAGYAALEQYQR.A |

2 similar to mKIAA0664 protein (predicted), isoform CRA_b, partial [Rattus norvegicus]

322

### Not what you expected? Try [the peptide summary](http://www.matrixscience.com/).
**MASCOT Search Results**

**Protein View: NP_542152.1**

- **Database:** NCBIprot
- **Score:** 58
- **Monoisotopic mass (M_r):** 33171
- **Calculated pI:** 5.30
- **Taxonomy:** Rattus norvegicus

This protein sequence matches the following other entries:

- XP_005086504.1 from *Mesocricetus auratus*
- XP_012980973.1 from *Mesocricetus auratus*
- XP_021074482.1 from *Mus pahari*
- P54921.2 from *Rattus norvegicus*
- CAAN62005.1 from *Rattus norvegicus*
- AAH63156.1 from *Rattus norvegicus*
- EDM08339.1 from *Rattus norvegicus*

Sequence similarity is available as an NCBI BLAST search of NP_542152.1 against nr.

**Search parameters**

- **MS data file:** Gr:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1990.mgf
- **Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.
- **Variable modifications:** Carbamidomethyl (C), Oxidation (M)

**Protein sequence coverage:** 4%

Matched peptides shown in **bold red.**

| Query | Start - End | Observed Mr (expt) | Monoisotopic mass | Delta M | Score | Expect | Rank |
|-------|-------------|---------------------|-------------------|---------|-------|--------|------|
|       | 168 - 180   | 734.8300            | 1467.6454         | 1467.7358 | -0.0903 | 58     | 0.00048 | 1   |

Unformatted sequence string: **295 residues** (for pasting into other applications).

Sort by:
- increasing mass
- decreasing mass

Show:
- matched peptides only
- predicted peptides also

---

**LOCUS** NP 542152
**DEFINITION** alpha-soluble NSF attachment protein [Rattus norvegicus].
**ACCESSION** NP_542152
**VERSION** NP_542152.1
**DBSOURCE** RefSeq: accession NM_080585.1
**KEYWORDS** RefSeq.
**SOURCE** Rattus norvegicus (Norway rat)
**ORGANISM** Rattus norvegicus
  - Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Rodentia; Rattus.
**REFERENCE** 1 (residues 1 to 295)
**AUTHORS** Xi Z, Deng W, Wang L, Xiao F, Li J, Wang Z, Wang X, Mi X, Wang N, and Wang X.
**TITLE** Association of Alpha-Soluble NSF Attachment Protein with Epileptic Seizure
**JOURNAL** J. Mol. Neurosci. 57 (3), 417-425 (2015)
**PUBMED** 26156199
**REMARK** GeneRIF: alphaSNAP expression showed no change in pilocarpine-induced epileptic rats in the acute phase, but in the chronic phase levels were lower. siRNA decreased the time of latency to seizure and increased the incidence of chronic idiopathic epilepsy seizures.
Region 26..287
/region_name="SNAP"
/note="Soluble N-ethylmaleimide-sensitive factor (NSF) Attachment Protein family; cd15832"
/db_xref="CDD:276937"
Site 26
/site_type="other"
/experiment="experimental evidence, no additional details recorded"
/note="N-acetylmethionine. {ECO:0000250|UniProtKB:P54920}; propagated from UniProtKB/Swiss-Prot (P54921.2)"
Site 29
/site_type="other"
/experiment="experimental evidence, no additional details recorded"
/note="Phosphoserine. {ECO:0000250|UniProtKB:Q9DB05}; propagated from UniProtKB/Swiss-Prot (P54921.2)"
Region 37..74
/region_name="TPR repeat"
/note="TPR repeat [structural motif]"
/db_xref="CDD:276937"
Region 78..114
/region_name="TPR repeat"
/note="TPR repeat [structural motif]"
/db_xref="CDD:276937"
Region 117..154
/region_name="TPR repeat"
/note="TPR repeat [structural motif]"
/db_xref="CDD:276937"
Region 158..194
/region_name="TPR repeat"
/note="TPR repeat [structural motif]"
/db_xref="CDD:276937"
Site 195
/site_type="other"
/experiment="experimental evidence, no additional details recorded"
/note="Phosphoserine. {ECO:0000250|UniProtKB:P54920}; propagated from UniProtKB/Swiss-Prot (P54921.2)"
CDS 1..295
/gene="Napa"
/gene_synonym="alpha-SNAP"
/coded_by="NM_080585.1:46..933"
/db_xref="GeneID:140673"
/db_xref="RGD:620855"

Mascot: http://www.matrixscience.com/
MASCOT Search Results

User: pbm
E-mail:
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR__2950.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:12:25 GMT

Not what you expected? Try the peptide summary.

Protein Family Summary

Significance threshold p< 0.05 Max. number of families 20
Display non-sig. matches N
Preferred taxonomy All entries

Sensitivity

Protein families 1–8 (out of 8)

10 per page 1

1  XP_008763925.1  69 PREDICTED: keratin, type II cytoskeletal 73 isoform X1 [Rattus norvegicus]
2  EDM12437.1  61 rCG47227, isoform CRA_a [Rattus norvegicus]

Score Mass Matches Sequences emPAI
61 66079 3 (3) 3 (3) 0.22

2.1  EDM12437.1  rCG47227, isoform CRA_a [Rattus norvegicus]

2  samesets of EDM12437.1

3 peptide matches (3 non-duplicate, 0 duplicate)

Query Dupes Observed Mr(expt) Mr(calc) Delta M Score Expect Rank U Peptide
177  536.3900 1070.7654 1070.6335 0.1319 0 37 0.004 R.XYFQGHRQVYR.G
179  538.6100 1612.8082 1611.7430 1.0652 0 35 0.014 R.XYFQGHRQVYR.G
409  944.4100 1886.8054 1886.9837 -0.1782 0 43 0.0013 R.XYFQGHRQVYR.G

3  NP_036767.1  58 anionic trypsin-1 precursor [Rattus norvegicus]
4  Q62871.1  43 RecName: Full=Cytoplasmic dynein 1 intermediate chain 2; AltName: Full=Cytoplasmic dynein intermediate chain 2; AltName: Full=Dyne...
5  XP_008770740.1  39 PREDICTED: nuclear factor of activated T-cells, cytoplasmic 3 isoform X1 [Rattus norvegicus]
6  NP_01008751.1  38 keratin, type I cytoskeletal 14 [Rattus norvegicus]
7  EDM06524.1  33 similar to hypothetical protein D11Ertd636e (predicted), isoform CRA_a [Rattus norvegicus]
8  Q5SWQ30.1  25 RecName: Full=Neurogenic locus notch homolog protein 2; Short=Notch 2; Contains: RecName: Full=Notch 2 extracellular truncation; C...

10 per page 1

Not what you expected? Try the peptide summary.

Mascot: http://www.matrixscience.com/
MASCOT Search Results

Protein View: NP_446200.1
dipeptidyl peptidase 3 [Rattus norvegicus]

Database: NCBIprot
Score: 61
Monoisotopic mass (M_r): 82987
Calculated pI: 5.12
Taxonomy: Rattus norvegicus

This protein sequence matches the following other entries:
- XP_006230695.1 from Rattus norvegicus
- O55096.2 from Rattus norvegicus
- BAA24608.2 from Rattus norvegicus
- AAI07674.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of NP_446200.1 against nr.

Search parameters
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MRC_2950.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 5%
Matched peptides shown in bold red.

Unformatted sequence string: 738 residues (for pasting into other applications).

Sort by residue number or increasing mass or decreasing mass
Show matched peptides only or predicted peptides also

LOCUS NP_446200 738 aa  Linear  ROD 11-NOV-2018
DEFINITION dipeptidyl peptidase 3 [Rattus norvegicus].
ACCESSION NP_446200 XP_341989
VERSION NP_446200.1
DBSOURCE RefSeq: accession NM_053748.1
KEYWORDS RefSeq.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE 1 (residues 1 to 738)
AUTHORS Hayes JD and Dinkova-Kostova AT.
TITLE The Nrf2 regulatory network provides an interface between redox and intermediary metabolism
JOURNAL Trends Biochem. Sci. 39 (4), 199-218 (2014)
PUBMED 24647116

REFERENCE 2 (residues 1 to 738)
AUTHORS Hirose J, Hata T, Kawaoka C, Ikeura T, Kitahara S, Horii K, Tomida H, Iwamoto H, Ono Y and Fukasawa KM.
TITLE Flexibility of the coordination geometry around the cupric ions in Cu(II)-rat dipeptidyl peptidase III is important for the expression of enzyme activity
JOURNAL Arch. Biochem. Biophys. 525 (1), 71-81 (2012)
PUBMED 22683474

REMARK Review article
REMARK Gene2IF: structure and activity of Cu(II)-rat dipeptidyl peptidase III
MASCOT Search Results

User: pbm
E-mail:
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\États-Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1016.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:14:03 GMT

Not what you expected? Try the peptide summary.

Search parameters
Score distribution
Modification statistics
Legend

Protein Family Summary

Significance threshold p< 0.05
Display non-sig. matches
Max. number of families 20
Preferred taxonomy All entries

Sensitivity

Protein families 1–7 (out of 7)

10 per page 1

1 NP_036767.1 79 anionic trypsin-1 precursor [Rattus norvegicus]
2 XP_008770740.1 40 PREDICTED: nuclear factor of activated T-cells, cytoplasmic isoform X1 [Rattus norvegicus]
3 XP_008759890.2 40 PREDICTED: laminin subunit gamma-3 isoform X1 [Rattus norvegicus]
4 Q9JII4.1 33 RecName: Full=Prolactin-5A1; AltName: Full=Placental prolactin-like protein L; Short=PRL-L; Short=PRL-like protein L; Flags: Precursor
5 Q62871.1 32 RecName: Full=Cytosplasmic dynein 1 intermediate chain 2; AltName: Full=Cytosplasmic dynein intermediate chain 2; AltName: Full=Dynein intermediate chain 2, cytosolic; Short=DM IC-2

Score Mass Matches Sequences emPAI
5.1 Q62871.1 32 71134 1 (1) 1 (1) 0.06

1 peptide matches (1 non-duplicate, 0 duplicate)

Query Duplicates Observed Mr (expt) Mr (calc) Delta M Score Expect Rank U Peptide
6 NP_001008751.1 31 keratin, type I cytoskeletal 14 [Rattus norvegicus]
7 EDM13863.1 30 similar to 2210403N09Rik protein (predicted), isoform CRA_a [Rattus norvegicus]

5 samesets of Q62871.1

Mascot: http://www.matrixscience.com/
**MASCOT Search Results**

**Protein View: Q62871.1**

RecName: Full=Cytoplasmic dynein 1 intermediate chain 2; AltName: Full=Cytoplasmic dynein intermediate chain 2; AltName: Full=Dynein intermediate chain 2, cytosolic; Short=DH IC-2

| Database  | NCBIprot |
|-----------|----------|
| Score     | 32       |
| Monoisotopic mass (M)_i | 71134 |
| Calculated pI | 5.11 |
| Taxonomy  | Rattus norvegicus |

This protein sequence matches the following other entries:
- AAA89163.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of Q62871.1 against nr.

**Search parameters**

- **MS data file:** G:\PRESTATIONS\Labos académiques\Internationala\\Unia\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\VR_1016.mgf
- **Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.
- **Variable modifications:** Carbamidomethyl (C), Oxidation (M)

**Protein sequence coverage:** 3%

Matched peptides shown in **bold red.**

```
1 MSKSELSAE LERSKKRALE IEEKKRRKKE EEEKKETEQK KEAAVSVQER
51 SDLEKREEKAA EALQSSMLT TOSIPPSYER HPPPMVESPS KEVSTPESEAG
101 SGQGQSGQG uartmKTPQ SAQHLQHSGD LUGQVQGQLM AKITQVFQPP
151 REVTTYKT QGTPYQKREE DKEKDIYAPC PREPKKFEE PIILPEYKED
201 SEAFKPFTE EKQXGAIK EKSSQDSS ESRESESLQI SEENRSESGE
251 DLDEEKGQF AQGKLSIAQ SFDQWSKPR HVLASNQDS QELPVAYSYN
301 NEEAPHEPO GVALWKNKDL KSTPQYVFCH SQAVHSSAFI KEFPRFILVG
351 GTYSQYLVND RIKNLQYTVQ QKLLASAAH HPTVYCNVQG QTVANNHSLIS
401 ISTDQISCM SLINSKHLNQG NLMNQHDPQ AVATVQHEPD VQMQNPHVG
451 SEGSSGYTCAL RIKHAGQKGGK RIKLDQGQQSE GYAGWDAQVAG VIKKHHEFSL
501 SFPWMLKPS TKNPRKFS LEISIDYVGD IOSHTPLAF ACTQGGRDLD
551 LMLHNDTVE PSTASVEPHN PALTMRMTHS GREGAVGDE EQVIVMQYGD
601 EQIAVPRNDE WAPFWLGELA IAASRADEDE EAAATRIPE
```

Unformatted sequence string: 638 residues

**Sort by** residue number **increasing mass** decreasing mass

**Show** matched peptides only predicted peptides also

**Query** Start – End **Observed** Mr (expt) **Mr (calc)** Delta M Score Expect Rank

1 432 92 – 112 976.0000 1949.9854 1949.8563 0.1292 32 0.022 1 K.SVSTPESEAGGQSDDQAVGEB.R

**LOCAL** DC1I2_RAT 638 aa linear ROD 16-JAN-2019

**DEFINITION** RecName: Full=Cytoplasmic dynein 1 intermediate chain 2; AltName: Full=Cytoplasmic dynein intermediate chain 2; AltName: Full=Dynein intermediate chain 2, cytosolic; Short=DH IC-2.

**ACCESSION** Q62871

**VERSION** Q62871.1

**DBSOURCE** UniProtKB: locus DC1I2_RAT, accession Q62871; class: standard.

**extra accessions:** Q62872, Q62873

created: Nov 1, 1997.
sequence updated: Nov 1, 1997.
annotation updated: Jan 16, 2019.

**KEYWORDS** 3D-structure; Acetylation; Alternative splicing; Complete proteome; Cytoplasm; Cytoskeleton; Dynein; Motor protein; Phosphoprotein; Reference proteome; Repeat; Transport; WD repeat.

**SOURCE** Rattus norvegicus (Norway rat)

**ORGANISM** Rattus norvegicus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Rodentia; Myomorpha;


**REFERENCE**

1 (residues 1 to 638)  
**AUTHORS** Vaughan,K.T. and Vale,R.B.  
**TITLE** Cytoplasmic dynein binds dynactin through a direct interaction between the intermediate chains and p150glued  
**JOURNAL** J. Cell Biol. 131 (6 Pt 1), 1507-1516 (1995)  
**PUBMED** 8522607  
**REMARK** NUCLEOTIDE SEQUENCE [MRNA] [ISOSFORMS 2A; 2B AND 2C], AND INTERACTION WITH DCTN1.  

2 (residues 1 to 638)  
**AUTHORS** Pfeifer,K.K., Salata,H.W., Dillman,J.F. 3rd, Torres,K. and Vale,R.B.  
**TITLE** Identification and developmental regulation of a neuron-specific subunit of cytoplasmic dynein  
**JOURNAL** Mol. Biol. Cell 7 (2), 331-343 (1996)  
**PUBMED** 8488502  
**REMARK** IDENTIFICATION IN THE CYTOPLASMIC DYNEIN 1 COMPLEX.  

3 (residues 1 to 638)  
**AUTHORS** King,S.M., Barbarese,E., Dillman,J.F. 3rd, Benashski,S.E., Do,K.T., Patel-King,R.B. and Pfeifer,K.K.  
**TITLE** Cytoplasmic dynein contains a family of differentially expressed light chains  
**JOURNAL** Biochemistry 37 (43), 15033-15041 (1998)  
**PUBMED** 9790665  
**REMARK** IDENTIFICATION IN THE CYTOPLASMIC DYNEIN 1 COMPLEX.  

4 (residues 1 to 638)  
**AUTHORS** Tyman,S.H., Gwe,M.A. and Vale,R.B.  
**TITLE** Distinct but overlapping sites within the cytoplasmic dynein heavy chain for dimerization and for intermediate chain and light intermediate chain binding  
**JOURNAL** J. Biol. Chem. 275 (42), 32769-32774 (2000)  
**PUBMED** 10893223  
**REMARK** INTERACTION WITH DYN1HL1.  

5 (residues 1 to 638)  
**AUTHORS** Vaughan,P.S., Lessy,J.D. and Vaughan,K.T.  
**TITLE** Cytoplasmic dynein intermediate chain phosphorylation regulates binding to dynactin  
**JOURNAL** J. Biol. Chem. 276 (28), 26171-26179 (2001)  
**PUBMED** 11340075  
**REMARK** FUNCTION, PHOSPHORYLATION AT SER-90, SUBCELLULAR LOCATION, INTERACTION WITH DCTN1, MUTATION OF SER-90, AND IDENTIFICATION BY MASS SPECTROMETRY.  

6 (residues 1 to 638)  
**AUTHORS** Lo,K.W., Kopyo,J.M., Rasoul,A.A., King,S.M. and Pfeifer,K.K.  
**TITLE** Interaction of the DYNLT (TCTEX1/RP3) light chains and the intermediate chains reveals novel inter-subunit regulation during assembly of the dynein complex  
**JOURNAL** J. Biol. Chem. 282 (51), 36871-36878 (2007)  
**PUBMED** 17279546  
**REMARK** ALTERNATIVE SPLICING, AND INTERACTION WITH DYN1HL1.  

7 (residues 1 to 638)  
**AUTHORS** Myers,K.R., Lo,K.W., Lye,R.J., Kogoy,J.M., Soura,V., Hafezparast,M. and Pfeifer,K.K.  
**TITLE** Intermediate chain subunit as a probe for cytoplasmic dynein function: biochemical analyses and live imaging in PC12 cells  
**JOURNAL** J. Neurosci. Res. 85 (12), 2640-2647 (2007)  
**PUBMED** 17965411  
**REMARK** QUANTITATIVE MAPS OF CYTOPLASMIC PHOSPHORYLATION SITES ACROSS 14 DIFFERENT RAT ORGANS AND TISSUES.  

**REFERENCE**

8 (residues 1 to 638)  
**AUTHORS** Lundby,A., Secher,A., Nordborg,N.M., Dmytriyev,A., Lundby,C. and Olsen,J.V.  
**TITLE** Quantitative maps of cytoplasmic phosphorylation sites across 14 different rat organs and tissues  
**JOURNAL** Nat Commun 3, 876 (2012)  
**PUBMED** 22673903  
**REMARK** ALTERNATIVE SPLICING, AND INTERACTION WITH DYNC1H1.  

**REFERENCE**

9 (residues 1 to 638)  
**AUTHORS** Mezio-Garcia,J., Emara-Carreras,K., Brusa,M. and Rodriguez-Crespo,I.  
**TITLE** Molecular Basis for the Protein Recognition Specificity of the Dynein Light Chain DYN1HL1/Tctex1: CHARACTERIZATION OF THE INTERACTION WITH ACTIVIN RECEPTOR IIB  
**JOURNAL** J. Biol. Chem. 291 (40), 20962-20975 (2016)  
**PUBMED** 27502274  
**REMARK** INTERACTION WITH DYN1HL1.  

**REFERENCE**

10 (residues 1 to 638)  
**AUTHORS** Murdoch,A., Patel-King,R.S. and Pfister,K.K.  
**REFERENCE** 1 (residues 1 to 638)  
**AUTHORS** Pat-R K.K., Thomsen,M., King,S.M. and Pfister,K.K.  
**REFERENCE** 2 (residues 1 to 638)  
**AUTHORS** Salata,H.W., Dillman,J.F. 3rd, Torres,K. and Vale,R.B.  
**REFERENCE** 3 (residues 1 to 638)  
**AUTHORS** King,S.M., Barbarese,E., Dillman,J.F. 3rd, Benashski,S.E., Do,K.T., Patel-King,R.B. and Pfeifer,K.K.  
**REFERENCE** 4 (residues 1 to 638)  
**AUTHORS** Tyman,S.H., Gwe,M.A. and Vale,R.B.  
**REFERENCE** 5 (residues 1 to 638)  
**AUTHORS** Vaughan,P.S., Lessy,J.D. and Vaughan,K.T.  
**REFERENCE** 6 (residues 1 to 638)  
**AUTHORS** Lo,K.W., Kopyo,J.M., Rasoul,A.A., King,S.M. and Pfeifer,K.K.  
**REFERENCE** 7 (residues 1 to 638)  
**AUTHORS** Myers,K.R., Lo,K.W., Lye,R.J., Kogoy,J.M., Soura,V., Hafezparast,M. and Pfeifer,K.K.  
**REFERENCE** 8 (residues 1 to 638)  
**AUTHORS** Lundby,A., Secher,A., Nordborg,N.M., Dmytriyev,A., Lundby,C. and Olsen,J.V.  
**REFERENCE** 9 (residues 1 to 638)  
**AUTHORS** Mezio-Garcia,J., Emara-Carreras,K., Brusa,M. and Rodriguez-Crespo,I.  
**REFERENCE** 10 (residues 1 to 638)  
**AUTHORS** Murdoch,A., Patel-King,R.S. and Pfister,K.K.
Skeletal muscle, testis, kidney, brain, heart, and spleen.

The phosphorylation status of Ser-90 appears to be involved in dynactin-dependent target binding. 

{ECO:0000269|PubMed:11340075}.

Belongs to the dynein intermediate chain family.

{ECO:0000305}.

Protein:

"Cytoplasmic dynein 1 intermediate chain 2"

UniprotKB evidence: Evidence at protein level

Region:

Mature chain

Site:

2

Note:

Cytoplasmic dynein 1 intermediate chain 2.

Site:

51

Note:

Phosphoserine. {ECO:0000244|PubMed:22673903}.

Site:

90

Note:

N-acetylserine. {ECO:0000250|UniProtKB:Q13409}.

Site:

90

Note:

Phosphoserine. {ECO:0000269|PubMed:11340075}.

Region:

Splicing variant

Site:

101

Note:

S->A: No effect on interaction with DCTN1 (mimicks dephosphorylated form). {ECO:0000269|PubMed:11340075}.

Site:

104

Note:

S->D: Impairs interaction with DCTN1 (mimicks phosphorylated form). {ECO:0000269|PubMed:11340075}.

Region:

113..132

Note:

W->H: No effect on interaction with DCTN1 (mimicks dephosphorylated form). {ECO:0000269|PubMed:11340075}.

Region:

133..165

Note:

Interaction with DYNLT1. {ECO:0000269|PubMed:27502274}.

Region:

135..163

Note:

Cytoplasmic dynein 1 intermediate chain 2;

pfam11540

Region:

144..148

Note:

Cytoplasmic dynein 1 intermediate chain 2;

pfam11540

Region:

155..161

Note:

Cytoplasmic dynein 1 intermediate chain 2;

pfam11540

Region:

277..326

Note:

Repeated region

Region:

282..326

Note:

WD 40 repeat
/note="WD40 repeat [structural motif]"
/db_xref="CDD:293791"
Region
329..>599
/region_name="WD40"

/note="WD40 repeat [General function prediction only];
C0G2319"
/db_xref="CDD:225201"
Region
330..370
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"

/note="WD 2."
Region
339..377
/region_name="WD40 repeat"
/note="WD40 repeat [structural motif]"
/db_xref="CDD:293791"
Region
379..420
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"

/note="WD 3."
Region
380..>605
/region_name="WD40"
/note="WD40 domain, found in a number of eukaryotic
proteins that cover a wide variety of functions including
adapter/regulatory modules in signal transduction,
pre-mRNA processing and cytoskeleton assembly; typically
contains a GH dipeptide 11-24 residues from...; cl02567"
/db_xref="CDD:295369"
Region
385..426
/region_name="WD40 repeat"
/db_xref="CDD:293791"
Region
429..469
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"

/note="WD 4."
Region
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/db_xref="CDD:293791"
Region
474..519
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"

/note="WD 5."
Region
489..521
/region_name="WD40 repeat"
/db_xref="CDD:293791"
Region
527..565
/region_name="WD40 repeat"
/db_xref="CDD:293791"
Region
568..607
/region_name="Repetitive region"
/experiment="experimental evidence, no additional details recorded"

/note="WD 6."
Region
573..>599
/region_name="WD40 repeat"
/db_xref="CDD:293791"
MASCOT Search Results

User: pbm
E-mail: 
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1650.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:24:45 GMT

Not what you expected? Try the peptide summary.

Protein Family Summary

Significance threshold p< 0.05
Max. number of families 20
Display non-s. matches
Dendrograms cut at ∞

Preferred taxonomy: All entries

Protein families 1–10 (out of 10)

1
PO2651.2

NP_001008825.1 144 keratin, type II cytoskeletal cochleal [Rattus norvegicus]

2
PO2651.2

P02651.2

Score Mass Matches Sequences emPAI
96 44429 6 (6) 6 (6) 0.79

ReName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor

1 sameset of P02651.2

6 peptide matches (6 non-duplicate, 0 duplicate)

Query Duplicates Observed Mr (exp) Mr (calc) Delta M Score Expect Rank U Peptide
143 573.3800 1144.7454 1144.6088 0.1367 0.014 39 K.VSTHIDQLQK.N
216 656.8500 1311.6854 1311.7034 -0.0180 0.0064 36 K.NLAPLVEDVQSK.L
249 696.0000 2084.9782 2085.0814 -0.1032 0.047 2 39 R.ANELKATIDQNLEDLRSR.L
324 789.3600 1576.7054 1577.7685 -1.0631 0.00082 40 K.LGNINTYADDLQNK.L
343 825.8500 1649.6854 1649.8261 -0.1406 0.0001 55 K.TDVTQQLNTLFQDK.L
424 1009.4200 3025.2382 3025.4372 -0.1991 0.035 40 K.MQTTIQDNVENLQSS.MVPFANELKEK.F + 2 Oxidation (M)

Not what you expected? Try the peptide summary.

Mascot: http://www.matrixscience.com/
MASCOT Search Results

Protein View: P02651.2

RecName: Full=Apolipoprotein A-IV; Short=Apo-AIV; Short=ApoA-IV; AltName: Full=Apolipoprotein A4; Flags: Precursor

Database: NCBIprot
Score: 96
Monoisotopic mass (M,±): 44429
Calculated pI: 5.12
Taxonomy: Rattus norvegicus

This protein sequence matches the following other entries:
- AAA40747.1 from Rattus norvegicus
- AAA40748.1 from Rattus norvegicus
- AAH91159.1 from Rattus norvegicus
- BC091159.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of P02651.2 against nr.

Search parameters
MS data file: G:\PRESTATIONS\Labos académiques\Internationala\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1650.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 24%

Unformatted sequence string: 391 residues (for pasting into other applications).

Sequence similarity is available as an NCBI BLAST search of P02651.2 against nr.
REFERENCE 1 [residues 1 to 391]

AUTHORS Boguski,M.S., Birnbaum,E.H., Elshourbagy,N.A., Taylor,J.M. and Gordon,J.J.

TITLE Evolution of the apolipoproteins. Structure of the rat apo-A-IV and its relationship to the human genes for apo-A-1, C-III, and E

JOURNAL J. Biol. Chem. 261 (14), 6398-6407 (1986)

PUBLISHED 300656

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].

REFERENCE 2 [residues 1 to 391]

AUTHORS Boguski,M.S., Elshourbagy,N., Taylor,J.M. and Gordon,J.J.

TITLE Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-mer segment with amphipathic helical potential

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 81 (16), 5021-5025 (1984)

PUBLISHED 656177

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].

REFERENCE 3 [residues 1 to 391]

AUTHORS Haddad,I.A., Ordovas,J.M., Fitzpatrick,T. and Karathanasis,S.K.

TITLE Linkage, evolution, and expression of the rat apolipoprotein A-1, C-III, and A-IV genes

JOURNAL J. Biol. Chem. 261 (28), 13268-13277 (1986)

PUBLISHED 3500028

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].

REFERENCE 4 [residues 1 to 391]

AUTHORS Gerhard,D.S., Wagner,,., Feingold,E.A., Sherman,C.M., Grouse,L.H., Schuler,G., Klein,S.L., Old,S., Rassenoth,Y., Good,P., Geyer,B., Peck,A.M., Perera,J., Lipman,B., Collinge,J., Jang,W., Sherry,S., Peelo,M., Misquitta,L., Lew,E., Rumihtrovsky,V., Greenhut,S.F., Schauer,C., P. Bourou,B., Bonner,T.J., Nauwasser,D., Renton,J., Kiehahn,H., Purey,Y., Brest,M., Prento,C., Schreiber,Y., Shapiro,M., Bhat,R.K., Hopkins,R.F., Haev,P., Drickoll,T., Soarex,L.B., Casavan,T., Sheets,E., Brownstein,N., Udini,T., Toshiyuki,S., Cazincic,P., Pace,Y., Dudekula,B.S., Ko,M.N., Kewahami,K., Suzuki,Y., Sugino,Y., Gruber,C.E., Smith,M.K., Simons,B., Moore,T., Waterman,R., Johnson,S.L., Ruan,T., Wei,C.L., Mathavan,S., Gunaratne,P.N., Mu,J., Garcia,A.M., Huyk,S.W., Fuh,E., Yuen,Y., Sneed,A., Kowalski,A., Hodgdon,A., Huyng,D., McPherson,J., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Nadan,A., Rodriguez,E., Sanchez,A., Whiting,N., Madari,A., Young,A.C., Wetherby,E.D., Granite,S.J., Kwong,P.N., Brinkley,C.P., Pearson,R.L., Bouffard,G., Blakesley,R.W., Green,E.D., Dickson,H.C., Rodriguez,A.C., Grammond,J., Schowart,J., Myers,R.H., Butterfield,Y.S., Griffith,M., Griffith,G.L., Kunzufi,M., Li,S., Morin,R., Palpegrin,B., Petrisco,A., Skalska,E., Smulski,B.E., Stott,J.M., Schnurch,A., Schein,J.K., Jones,S.J., Holt,R.K., Baross,A., Mars,MA., Clifton,S., Makowski,R.A., Nosale,R., and Malek,J.

CONSRTM MGC Project Team

TITLE The status, quality, and expansion of the NIH full-length cDNA project: the Mammalian Gene Collection (MGC)

JOURNAL Genome Res. 14 (10B), 2121-2127 (2004)

REFERENCE 1 (residues 1 to 391)

AUTHORS Gerhard,D.S., Wagner,L., Feingold,E.A., Shenmen,C.M., Grouse,L.H., Schuler,G., Klein,S.L., Old,S., Rassenoth,Y., Good,P., Geyer,B., Peck,A.M., Perera,J., Lipman,B., Collinge,J., Jang,W., Sherry,S., Peelo,M., Misquitta,L., Lew,E., Rumihtrovsky,V., Greenhut,S.F., Schauer,C., P. Bourou,B., Bonner,T.J., Nauwasser,D., Renton,J., Kiehahn,H., Purey,Y., Brest,M., Prento,C., Schreiber,Y., Shapiro,M., Bhat,R.K., Hopkins,R.F., Haev,P., Drickoll,T., Soarex,L.B., Casavan,T., Sheets,E., Brownstein,N., Udini,T., Toshiyuki,S., Cazincic,P., Pace,Y., Dudekula,B.S., Ko,M.N., Kewahami,K., Suzuki,Y., Sugino,Y., Gruber,C.E., Smith,M.K., Simons,B., Moore,T., Waterman,R., Johnson,S.L., Ruan,T., Wei,C.L., Mathavan,S., Gunaratne,P.N., Mu,J., Garcia,A.M., Huyk,S.W., Fuh,E., Yuen,Y., Sneed,A., Kowalski,A., Hodgdon,A., Huyng,D., McPherson,J., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Nadan,A., Rodriguez,E., Sanchez,A., Whiting,N., Madari,A., Young,A.C., Wetherby,E.D., Granite,S.J., Kwong,P.N., Brinkley,C.P., Pearson,R.L., Bouffard,G., Blakesley,R.W., Green,E.D., Dickson,H.C., Rodriguez,A.C., Grammond,J., Schowart,J., Myers,R.H., Butterfield,Y.S., Griffith,M., Griffith,G.L., Kunzufi,M., Li,S., Morin,R., Palpegrin,B., Petrisco,A., Skalska,E., Smulski,B.E., Stott,J.M., Schnurch,A., Schein,J.K., Jones,S.J., Holt,R.K., Baross,A., Mars,MA., Clifton,S., Makowski,R.A., Nosale,R., and Malek,J.

REFERENCE 2 (residues 1 to 391)

AUTHORS Lundby,A., Secher,A., Lage,K., Nordborg,N.B., Dmitryev,A., Lundby,C. and Olsen,J.V.

REFERENCE 3 (residues 1 to 391)

AUTHORS Haddad,I.A., Ordovas,J.M., Fitzpatrick,T. and Karathanasis,S.K.

REFERENCE 4 (residues 1 to 391)

AUTHORS Boguski,M.S., Birnbaum,E.H., Elshourbagy,N.A., Taylor,J.M. and Gordon,J.J.

REFERENCE 5 [residues 1 to 391]

AUTHORS Lundby,A., Secher,A., Lage,K., Nordborg,N.B., Dmitryev,A., Lundby,C. and Olsen,J.V.

REFERENCE 6 [residues 1 to 391]

AUTHORS Biocca,B., Shimizu,S., Hasegawa,Y., Koizumi,Y., Taniguchi,A., Kikuchi,M., Obata,H., Ogata,Y., Yamada,K., Ikeda,K., Matsumoto,M. and Fauser,B.W.

REFERENCE 7 [residues 1 to 391]

AUTHORS Lundby,A., Secher,A., Lage,K., Nordborg,N.B., Dmitryev,A., Lundby,C. and Olsen,J.V.

REFERENCE 8 [residues 1 to 391]

AUTHORS Biocca,B., Shimizu,S., Hasegawa,Y., Koizumi,Y., Taniguchi,A., Kikuchi,M., Obata,H., Ogata,Y., Yamada,K., Ikeda,K., Matsumoto,M. and Fauser,B.W.

REFERENCE 9 [residues 1 to 391]

AUTHORS Lundby,A., Secher,A., Lage,K., Nordborg,N.B., Dmitryev,A., Lundby,C. and Olsen,J.V.

REFERENCE 10 [residues 1 to 391]

AUTHORS Biocca,B., Shimizu,S., Hasegawa,Y., Koizumi,Y., Taniguchi,A., Kikuchi,M., Obata,H., Ogata,Y., Yamada,K., Ikeda,K., Matsumoto,M. and Fauser,B.W.

REFERENCE 11 [residues 1 to 391]

AUTHORS Lundby,A., Secher,A., Lage,K., Nordborg,N.B., Dmitryev,A., Lundby,C. and Olsen,J.V.

REFERENCE 12 [residues 1 to 391]

AUTHORS Biocca,B., Shimizu,S., Hasegawa,Y., Koizumi,Y., Taniguchi,A., Kikuchi,M., Obata,H., Ogata,Y., Yamada,K., Ikeda,K., Matsumoto,M. and Fauser,B.W.

REFERENCE 13 [residues 1 to 391]

AUTHORS Lundby,A., Secher,A., Lage,K., Nordborg,N.B., Dmitryev,A., Lundby,C. and Olsen,J.V.

REFERENCE 14 [residues 1 to 391]

AUTHORS Biocca,B., Shimizu,S., Hasegawa,Y., Koizumi,Y., Taniguchi,A., Kikuchi,M., Obata,H., Ogata,Y., Yamada,K., Ikeda,K., Matsumoto,M. and Fauser,B.W.
## MASCOT Search Results

**User**: pbm

**Search title**: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4

**MS data file**: G:\PRESTATIONS\Labos académiques\Interina\(Etats Uni\|\Martina Rosenberg)\Data pour publi M Rosenberg\Identifications Mascot\MR_1409.mgf

**Database**: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)

**Taxonomy**: Rattus (77,467 sequences)

**Timestamp**: 25 Jan 2019 at 10:21:39 GMT

Not what you expected? Try the peptide summary.

### Protein Family Summary

#### Sensitivity

Protein Family Summary

| Score | Mass | Matches | Sequences | emPAI |
|-------|------|---------|-----------|-------|
| 355   | 50775| 13 (13) | 11 (11)   | 1.55  |

1.1 XP_003754401.1  keratin, type II cytoskeletal 7 [Rattus norvegicus]

1.2 EDL86881.1  keratin, type II cytoskeletal 1 [Rattus norvegicus]

Threshold (0):

#### Threshold (0): 0

### 16 peptide matches (15 non-duplicate, 1 duplicate)

| Query Dopes | Observed | Me (avg) | Me (cal) | Delta M | Score | Expect | Rank | Peptide |
|-------------|----------|----------|----------|---------|-------|--------|------|---------|
| 81          | 455.0500 | 1362.1282| 1361.7554| -0.3727 | 39    | 0.028  |      | R.TAANEFVILK. D |
| 113         | 508.8500 | 1015.6854| 1015.5550| -0.1305 | 42    | 0.019  |      | L.QAEIDTVK. N  |
| 134         | 541.7800 | 1081.5454| 1081.5920| -0.0466 | 70    | 0.00018|      | K.FASFIDKVR. F |
| 139         | 546.7300 | 1091.4454| 1091.5611| -0.1157 | 39    | 0.0021 |      | R.FETLQAQGKR K |
| 148         | 555.4400 | 1103.6654| 1103.5724| 0.0931  | 0     | 4.9e-05| 2    | R.SAYGUPVGCIR K |
| 196         | 559.4700 | 1116.9254| 1116.6291| 0.2963  | 0     | 8.4e-05| 2    | R.IFEAQIAGLR. Q |
| 209         | 564.7800 | 1127.7024| 1127.6738| -0.0902 | 3     | 0.00018|      | R.AKLARVESLK. A |
| 233         | 571.8400 | 1136.6654| 1136.7554| -0.0902 | 78    | 2.3e-06|      | R.TAANEFVILK. D |
| Query | Dupes | Observed | Mr (expt) | Mr (calc) | Delta M | Score | Expect | Rank | U | 1 | 2 | 3 | Peptide |
|-------|-------|----------|----------|----------|---------|-------|--------|------|---|---|---|---|---------|
| 243   |       | 707.8400 | 1413.6654| 1413.7576| -0.0921 | 85    | 7.2e-06| 1    | U | U | - | K.LQAEITVEKQR.A |
| 253   |       | 719.9300 | 2156.7682| 2156.0723| 0.6989  | 57    | 0.00013| 2    | U | U | K.PETLQAGKRGLGTLTNR.N |
| 262   |       | 738.3600 | 1474.7054| 1474.7780| -0.0725 | 58    | 0.00029| 3    | U | U | R.FLEQQRQLTQR.W |
| 291   |       | 786.6800 | 2357.0182| 2357.2074| -0.1892 | 62    | 8.6e-05| 1    | U | U | R.AKLESIAAXEKEQHIALEDAR.A |
| 316   |       | 819.8800 | 1637.7454| 1638.8729| -1.1275 | 40    | 0.0018 | 2   | U | U | K.SJQKTSFIDYKR.F |

6 subsets and intersections (20 subset proteins in total)

Not what you expected? Try [the peptide summary](http://www.matrixscience.com/).

Mascot: [http://www.matrixscience.com/](http://www.matrixscience.com/)
MASCOT Search Results

Protein View: XP_003754401.1

PREDICTED: keratin, type II cytoskeletal 7 [Rattus norvegicus]

- Database: NCBIprot
- Score: 355
- Monoisotopic mass (Mr): 50775
- Calculated pI: 5.67
- Taxonomy: Rattus norvegicus

This protein sequence matches the following other entries:
- XP_003750455.1 from Rattus norvegicus
- XP_017459005.1 from Rattus norvegicus
- XP_017450823.1 from Rattus norvegicus
- EDL86895.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of XP_003754401.1 against nr.

Search parameters
- MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1409.mgf
- Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
- Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 26%

Unformatted sequence string: 457 residues (for pasting into other applications).

Sort by: residue number □ increasing mass □ decreasing mass
Show □ matched peptides only □ predicted peptides also

| Query Start - End | Observed Mr (expr) | Observed Mr (calc) | Delta Mr | Score | Expect | Rank |
|-------------------|--------------------|--------------------|----------|-------|--------|------|
| 44                | 47 - 58            | 552.8400           | 1103.5724 | 0.0931 | 0       | 60   |
| 101               | 96 - 104           | 541.7800           | 1081.5454 | 0.0931 | 0       | 63   |
| 138               | 134 - 143          | 559.7000           | 1116.6291 | 0.2963 | 0       | 70   |
| 19        | 182 - 189          | 681.8400           | 1361.5954 | 0.00018 | 1     | 61   |
| 201               | 182 - 193          | 455.0500           | 900.5920  | 0.0466  | 1      | 78   |
| 235               | 248 - 259          | 630.1500           | 1257.6186 | 0.6038  | 0      | 86   |
| 297               | 281 - 299          | 719.9300           | 2156.7523 | 0.1187  | 0      | 39   |
| 324               | 312 - 320          | 508.8500           | 1015.5610 | 0.3727  | 0      | 42   |
| 351               | 324 - 345          | 707.8400           | 1413.7567 | 0       | 0      | 85   |
| 371               | 346 - 357          | 664.7800           | 1327.7347 | 0.1892  | 1      | 56   |
| 411               | 251                | 630.1500           | 1257.6186 | 0.6038  | 0      | 86   |

LOCUS       XP_003754401             457 aa            linear   ROD 26-JUL-2016
DEFINITION  PREDICTED: keratin, type II cytoskeletal 7 [Rattus norvegicus].
ACCESSION   XP_003754401
VERSION     XP_003754401.1
DBLINK
DBSOURCE   refseq accession XM_003754353.4
KEYWORDS    Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.
COMMENT    This record is predicted by automated computational analysis. This record is derived from a genomic sequence (AC_000075.1) annotated using gene prediction method: Gnomon, supported by EST evidence.

Also see: Documentation of NCBI's Annotation Process

#Genome-Annotation-Data-START#
Annotation Provider :: NCBI
Annotation Status :: Full annotation
Annotation Version :: Rattus norvegicus Annotation Release 106
##Genome-Annotation-Data-END##

**COMPLETENESS:** full length.

**FEATURES**

- **source**
  
  `organism="Rattus norvegicus"`  
  `/strain="BN; Sprague-Dawley"`  
  `/chromosome="7"`

- **Protein**
  
  `1..457`  
  `/product="keratin, type II cytoskeletal 7"`  
  `/calculated_mol_wt=50675`

- **Region**
  
  `5..81`  
  `/region_name="Keratin_2_head"`  
  `/note="Keratin type II head; pfam16208"`  
  `/db_xref="CDD:293926"`

  `84..396`  
  `/region_name="Filament"`  
  `/note="Intermediate filament protein; pfam0038; CDD:278467"`

  `<104..220`  
  `/region_name="GBP_C"`  
  `/note="Guanylate-binding protein, C-terminal domain; cl20817; CDD:303769"`

  `189..200`  
  `/region_name="coiled coil"`  
  `/db_xref="CDD:293879"`

  `209..220`  
  `/region_name="coiled coil"`  
  `/note="coiled coil [structural motif]; CDD:293879"`

- **CDS**
  
  `1..457`  
  `/gene="Krt7"`  
  `/coded_by="XM_003754353.4:565..1938"`  
  `/db_xref="GeneID:300242; RGID:1310865"`

**Mascot:** [http://www.matrixscience.com/](http://www.matrixscience.com/)
MASCOT Search Results

User: pbm
E-mail: 
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1069B.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:15:33 GMT

Not what you expected? Try the peptide summary.

Search parameters
Score distribution
Modification statistics
Legend

Protein Family Summary

| Significance threshold p< | Max. number of families |
|--------------------------|-------------------------|
| 0.05                     | 20                      |

Display non-sig. matches
Dendrograms cut at □
Preferred taxonomy: All entries

Sensitivity

Protein families 1–5 (out of 5)

10 per page 1

1

pir|S31716 125

| Score | Mass | Matches | Sequences | emPAI |
|-------|------|---------|-----------|--------|
| 125   | 70884| 6 (6)   | 5 (5)     | 0.36   |

dnaI-type molecular chaperone hsp72-ps1 - rat

3 subsets and intersections (2 subset proteins in total)

1 peptides matches (5 non-duplicate, 1 duplicate)

Query Duplicates | Observed Mr (cal): | Mr (expt): | Delta M | Score | Expect | Rank | Peptide |
|-----------------|-------------------|-----------|---------|-------|--------|------|---------|
| 198             | 600.360 1198.7054 | 1198.6670 | 0.0385  | 49    | 0.0044 | 1    | K.DAGTIAGLNLR.A |
| 272             | 659.600 1317.1854 | 1318.5863 | -1.4009 | 52    | 0.0024 | 1    | K.KSLEYVAFMK.A + Oxidation (M) |
| 343             | 835.780 1665.5654 | 1664.7828 | 0.7826  | 40    | 0.0018 | 1    | K.NVAMKEHPYFPK.R + Oxidation (M) |
| 400             | 947.450 2839.3282 | 2839.5443 | -0.2161 | 42    | 0.0056 | 1    | K.DAGTIAGLNLR5INEPTAAIAAYGLDEK.K |
| 425             | 990.2700 2967.782 | 2967.6393 | 0.1489  | 52    | 0.0012 | 1    | K.DAGTIAGLNLR5INEPTAAIAAYGLDEK.V |

2 subsets and intersections (2 subset proteins in total)

1 XP_008763925.1 58 PREDICTED: keratin, type II cytoskeletal 73 isoform X1 [Rattus norvegicus]

2 Q6P6Q2.1 57 ReName: Full=Keratin, type II cytoskeletal 5; AltName: Full=Cytokeratin-5; Short=CK-5; AltName: Full=Keratin-5; Short=K5; AltName...

4 NP_036767.1 54 anionic trypsin-1 precursor [Rattus norvegicus]

6 CAB94693.1 36 immunoglobulin heavy chain variable region, partial [Rattus norvegicus]

10 per page 1

Not what you expected? Try the peptide summary.

Mascot: http://www.matrixscience.com/
MASCOT Search Results

Protein View: pir||S31716
dnaK-type molecular chaperone hsp72-ps1 - rat

Database: NCBIprot
Score: 125
Monoisotopic mass (Mr): 70884
Calculated pI: 5.43
Taxonomy:

This protein sequence matches the following other entries:
- CAA49670.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of pir||S31716 against nr.

Search parameters

MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1069B.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 8%

Matched peptides shown in bold red.

Unformatted sequence string: 646 residues (for pasting into other applications).

Sort by residue number increasing mass decreasing mass Show matched peptides only predicted peptides also

Query Start – End Observed Mr(expt) Mr(calc) Delta M Score Expect Rank U Peptide

400 160 – 187 947.4500 2839.3282 2839.5443 -0.2161 1 42 0.0056
1 U K.DAGTIAGLNVLRIINEPTAAAIAYGLDKK.V

http://mascot2.crihan.fr/mascot/cgi/protein_view.pl?file=../data/20190...
Region 1..613
/region_name="PTZ00009"
/note="heat shock 70 kDa protein; Provisional"
/db_xref="CDD:240227"
Region 6..381
/region_name="HSPA1-2_6-8-like_NBD"
/note="Nucleotide-binding domain of HSPA1-A, -B, -L, HSPA-2, -6, -7, -8, and similar proteins; cd10233"
/db_xref="CDD:212675"
Site order(10,12,15,71,147,175,199..204,206,230,231,268,271,273,338,340,342,343,366)
/site_type="other"
/note="nucleotide binding site [chemical binding]"
/db_xref="CDD:212675"
Site order(23,25,27,32,34,36,50,54,57,133..134,175,220,230,231,257,262,264,266,268,286,292,294)
/site_type="other"
/note="NEF/HSP70 interaction site [polypeptide binding]"
/db_xref="CDD:212675"
Site order(33,35,57,61,64,65,77,257,261,262,265,266,268,286,292,294)
/site_type="other"
/note="BAG/HSP70 interaction site [polypeptide binding]"
/db_xref="CDD:212675"
Site order(152,192,213,215,219,220,325)
/site_type="other"
/note="SBD interface [polypeptide binding]"
/db_xref="CDD:212675"
MASCOT Search Results

User: pbm
E-mail: 
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\États-Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1233.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:18:33 GMT

Not what you expected? Try the peptide summary.

Protein Family Summary

Significance threshold p< 0.05
Display non-sig. matches
Preferred taxonomy

Protein families 1–5 (out of 5)

| Query | Peptide | Score | Mass (calc) | Matches | Sequences | emPAI |
|-------|---------|-------|-------------|---------|-----------|-------|
| 1     | NP_034607.3 | 91 60 kDa heat shock protein, mitochondrial [Mus musculus] | 60 kDa heat shock protein, mitochondrial [Mus musculus] | | | |
| 2     | NP_036767.1 | 85 anionic trypsin-1 precursor [Rattus norvegicus] | | | | |
| 3     | XP_006247453.1 | 54 PREDICTED: keratin, type I cytoskeletal 10 isoform X2 [Rattus norvegicus] | | | | |
| 4     | EDL86877.1 | 52 type II keratin Kb1 [Rattus norvegicus] | | | | |
| 5     | Q6P6Q2.1 | 45 ReName: Full=Keratin, type II cytoskeletal 5; AltName: Full=Cytokeratin-5; Short=CK-5; AltName: Full=Keratin-5; Short=K5; AltName... | | | | |

Not what you expected? Try the peptide summary.

Mascot: http://www.matrixscience.com/
MASCOT Search Results

Protein View: CAA38564.1

heat shock protein (hsp60) precursor [Rattus norvegicus]

Database: NCBIprot
Score: 91
Monoisotopic mass (M_r): 60927
Calculated pI: 5.91
Taxonomy: Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of CAA38564.1 against nr.

Search parameters
MS data file: G:\PRESTATIONS\Labsos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1233.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 5%
Matched peptides shown in bold red.

Unformatted sequence string: 573 residues (for pasting into other applications).

Sort by residue number increasing mass decreasing mass
Show matched peptides only predicted peptides also

Query Start – End Observed Mr(expt) Mr(calc) Delta M Score Expect Rank U Peptide
1 407 29 – 58 1035.4500 3103.3282 3103.6046 -0.2764 2 59 0.00013 K.DVKFGADARALMLQGVDLLADAVAVTMGPK.G + 2 Oxidation (M)
2 342 32 – 58 921.5800 2761.7182 2761.4143 0.3039 1 35 0.016 K.FGADARALMLQGVDLLADAVAVTMGPK.G + 2 Oxidation (M)
3 430 38 – 58 1073.5800 2145.1454 2144.1221 1.0233 0 57 6e-05 R.ALMLQGVDLLADAVAVTMGPK.G + 2 Oxidation (M)

LOCUS CAA38564 573 aa linear  ROD 06-MAY-1992
DEFINITION heat shock protein (hsp60) precursor [Rattus norvegicus].
ACCESSION CAA38564
VERSION CAA38564.1
DBSOURCE embl accession X54793.1
KEYWORDS .
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Peralta,D., Hartman,D.J., McIntosh,A.M., Hoogenraad,N.J. and Hoj,P.B.
TITLE cDNA and deduced amino acid sequence of rat liver prehsp60 (chaperonin-60)
JOURNAL Nucleic Acids Res. 18 (23), 7162 (1990)
PUBMED 1979858
REFERENCE 2 (residues 1 to 573)
AUTHORS Hoj,P.B.
TITLE Direct Submission
JOURNAL Submitted (05-OCT-1990) Hoj P.B., Department of Biochemistry, La Trobe University, Bundoora, Victoria, 3083, AUSTRALIA
COMMENT See X53585 for Rat kidney mRNA for heat shock protein (hsp60).
FEATURES Location/Qualifiers
source 1..573 /organism="Rattus norvegicus" /strain="Wistar" /db_xref="taxon:10116" /cell_type="hepatocyte" /tissue_type="liver" /clone_lib="lambda gt10"
Protein 1..573 /product="heat shock protein (hsp60) precursor"
Region 24..555 /region_name="FAVINGAVTLAVDRATGAMKNNLQIKGQKVTAV" /note="Heat shock protein 60; Provisional" /db_xref="CDD:185455"
Region 28..548
Chaperonins are involved in productive folding of proteins. They share a common general morphology, a double toroid of 2 stacked rings, each composed of 7-9 subunits. The symmetry of type I is seven-fold and they are found...; cd03344" 

Site order(28,32,49,60..63,65,70..71,73,83,85,93,97,100,221, 253,281,409,411,484,538,541..547) /site_type="other" /note="ring oligomerisation interface [polypeptide binding]" /db_xref="CDD:239460"

Site order(55..57,111,115,174,423,440,479,518,520) /site_type="other" /note="ATP/Mg binding site [chemical binding]" /db_xref="CDD:239460"

Site order(133,459,477,486,488..489,492) /site_type="other" /note="stacking interactions" /db_xref="CDD:239460"

Site order(165,210,217,400,434..435) /site_type="other" /note="hinge regions" /db_xref="CDD:239460"

CDS 1..573 /coded_by="X54793.1:7..1728" /db_xref="GOA:963039" /db_xref="InterPro:1PR001844" /db_xref="InterPro:1PR002423" /db_xref="InterPro:1PR018310" /db_xref="UniProtKB/Swiss-Prot:963039"

Mascot: http://www.matrixscience.com/
**MASCOT Search Results**

User: pbm
E-mail: 
Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-6SA4
MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1272.mgf
Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)
Taxonomy: Rattus (77,467 sequences)
Timestamp: 25 Jan 2019 at 10:20:08 GMT

Not what you expected? Try the peptide summary.

### Protein Family Summary

| Significance threshold p| Max. number of families |
|-------------------------|-------------------------|
| 0.05                    | 20                      |

Display non-sig. matches

Dendrograms cut at 

Preferred taxonomy

AI entries

---

### Sensitivity

**Protein families 1–5 (out of 5)**

| Score | Mass | Matches | Sequences | emPAI |
|-------|------|---------|-----------|-------|
| 92    | 56554| 6 (6)   | 6 (6)     | 0.59  |

**NP_059015.1** 92 protein disulfide-isomerase A3 precursor [Rattus norvegicus]

| Query | Dupes | Observed | Mr (exp) | Mr (calc) | Delta M | Score | Expect | Rank | U | Peptide |
|-------|-------|----------|----------|-----------|---------|-------|--------|------|---|---------|
| 166   |       | 551.6100 | 1651.8082| 1651.7590 | 0.0491  | 1     | 50     | 0.0011 | U | K.IFRDGEEAGAYDGPR.T |
| 177   |       | 582.9700 | 1745.8882| 1745.9213 | -0.0331 | 1     | 37     | 0.022  | U | K.TFLDAGHKLNFAVASR.K |
| 190   |       | 594.7800 | 1187.5454| 1187.5281 | 0.0173  | 0     | 38     | 0.0099 | U | K.FVMQEEKLFAYAVASR.K |
| 191   |       | 596.2900 | 1190.5654| 1190.5931 | -0.0277 | 0     | 50     | 0.0017 | U | K.LAPEYEAARAT.L |
| 197   |       | 599.3500 | 1196.6854| 1196.7128 | -0.0274 | 42    | 0.011  | U | K.LSKDVPIVIAK.M |
| 271   |       | 698.8200 | 1395.6254| 1395.6882 | -0.0627 | 0     | 42     | 0.024  | U | K.SEPFEPKDEPDYV.P |

**NP_001008825.1** 85 keratin, type II cytoskeletal cochleal [Rattus norvegicus]

**NP_001008802.2** 51 keratin, type II cytoskeletal 1 [Rattus norvegicus]

**NP_036767.1** 62 anionic trypsin-1 precursor [Rattus norvegicus]

**XP_008770740.1** 36 PREDICTED: nuclear factor of activated T-cells, cytoplasmic isoform X1 [Rattus norvegicus]

**NP_001110171.1** 34 suppression of tumorigenicity 5 protein [Rattus norvegicus]

Mascot: [http://www.matrixscience.com/](http://www.matrixscience.com/)
MASCOT Search Results

Protein View: P11598.2

ReName: Full=Protein disulfide-isomerase A3; AltName: Full=58 kDa glucose-regulated protein; AltName: Full=58 kDa microsomal protein; Short=p58; AltName: Full=Disulfide isomerase ER-60; AltName: Full=Endoplasmic reticulum resident protein 57; Short

Database: NCBIprot
Score: 92
Monoisotopic mass (Mr): 56588
Calculated pI: 5.88
Taxonomy: Rattus norvegicus

This protein sequence matches the following other entries:
- AAH62393.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of P11598.2 against nr.

Search parameters

MS data file: G:\PRESTATIONS\Labos académiques\International\Data Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1272.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 14%

Matched peptides shown in bold red.

Unformatted sequence string: 505 residues (for pasting into other applications).

Sort by residue number increasing mass decreasing mass
Show only matched peptides or predicted peptides also

Mascot Search Results: P11598.2
http://mascot2.crihan.fr/mascot/cgi/protein_view.pl?file=../data/20190...
Acetylation; Complete proteome; Direct protein sequencing; Disulfide bond; Endoplasmic reticulum; Isomerase; Methylation; Phosphoprotein; Redox-active center; Reference proteome; Repeat; Signal.

Organism: Rattus norvegicus (Norway rat)
REMARK MUTAGENESIS OF 502-GLN--LEU-505.
REFERENCE 10 (residues 1 to 505)
AUTHORS Urade,R. and Kito,M.
TITLE Inhibition by acidic phospholipids of protein degradation by ER-60
protease, a novel cysteine protease, of endoplasmic reticulum
JOURNAL PERS Lett. 312 (1), 83-86 (1992)
PUBMED 1306485
REMARK INHIBITION BY PHOSPHOLIPIDS.
REFERENCE 11 (residues 1 to 505)
AUTHORS Kameshwari,D.B., Bhande,S., Sundaram,C.S., Rota,V., Sila,A.B., and
Shivaji,S.
TITLE Glucose-regulated protein precursor (GRB78) and tumor rejection
antigen (GP96) are unique to hamster caput epididymal spermatozoa
JOURNAL Asian J. Androl. 12 (3), 344-355 (2010)
PUBMED 20400973
REMARK TISSUE SPECIFICITY.
COMMENT On or before Mar 15, 2005 this sequence version replaced gi:91897,
gi:130233.
[CATALYTIC ACTIVITY] Reaction=Catalyzes the rearrangement of -S-S-
bonds in proteins.; EC=5.3.4.1.
ACTIVITY REGULATION: Seems to be inhibited by acidic phospholipids.
[SUBUNIT] Subunit of the TAP complex, also known as the peptide
loading complex (PLC). Can form disulfide-linked heterodimers with
TAPBP. Interacts with ERK27 and CAMX (By similarity). Interacts
with HER1 in a calcium-dependent manner (By similarity). Interacts
with SERPIN2 and with the S and Z variants of SERPIN1. Interacts
with AYP22 (By similarity). [ECO:0000250|UniProtKB:P27773],
ECO:0000250|UniProtKB:P30101].
[SUBCELLULAR LOCATION] Endoplasmic reticulum
[ECO:0000250|UniProtKB:P30101]. Endoplasmic reticulum lumen
[ECO:0000250]. Melanosome [ECO:0000250|UniProtKB:P30101].
[TISSUE SPECIFICITY] In caput epididymal spermatozoa, detected in
the head, mid and principal pieces. In cauda epididymal spermatozoa
detected only in the acrosome (at protein level).
[ECO:0000269|PubMed:20400973].
[SIMILARITY] Belongs to the protein disulfide isomerase family.
[ECO:0000305].
[CAUTION] Was originally thought to be a phosphatidylinositol
4,5-bisphosphate phosphodiesterase type I (phospholipase C-alpha)
then was thought (PubMed:1321829 and PubMed:1330685) to be a thiol
protease. [ECO:0000305|PubMed:3398923].

FEATURES             Location/Qualifiers
source          1..505
     /organism="Rattus norvegicus"
     /db_xref="taxon:10116"
     gene            1..505
     /gene="Pdia3"
     /gene_synonym="Erp60"
     /gene_synonym="Grp58"
     Protein         1..505
     /product="Protein disulfide-isomerase A3";
     /EC_number="5.3.4.1"
     /note="58 kDa glucose-regulated protein; 58 kDa microsomal
protein; Disulfide isomerase ER-60; Endoplasmic reticulum
resident protein 57; Endoplasmic reticulum lumen
protein 60; Map57t; ERp57; ER
protein 60; Erp58"
     /UniProtKB_evidence="Evidence at protein level"
Region          1..24
     /region_name="Signal"
     /experiment="experimental evidence, no additional details
recorded"
     /note="/EOL:0000269|PubMed:1657921]."
Region          1..13
     /region_name="Conflict"
     /experiment="experimental evidence, no additional details
recorded"
     /note="/PUBSCIGALLOPOVA -> NYSAAABCMEMK (in Ref. 1)."
     /ECO:0000305]."
Region          25..505
     /region_name="Mature chain"
     /experiment="experimental evidence, no additional details
recorded"
     /note="Protein disulfide-isomerase A3."
Region          25..133
     /region_name="Domain"
     /experiment="experimental evidence, no additional details
recorded"
     /note="/Thioredoxin 1."
     /ECO:0000305|PROSITE-ProRule:PRU00691]."
Region          26..487
     /region_name="ER_PDI_fam"
     /note="protein disulfide isomerase, eukaryotic; TIGR01130"
     /db_xref="CDD:273457"
Region          27..131
     /region_name="Thioredoxin"
     /note="Thioredoxin; pfam00085"
     /db_xref="CDD:278513"
Bond            bond(57,60)
     /bond_type="disulfide"
     /experiment="experimental evidence, no additional details
recorded"
     /note="Redox-active."
     /ECO:0000255|PROSITE-ProRule:PRU00691]."
Bond            bond(57)
     /bond_type="disulfide"
     /experiment="experimental evidence, no additional details
recorded"
     /note="/Interchain (with C-115 in TAPBP); in linked form."
     /ECO:0000250]."
Site            57
     /site_type="active"
     /experiment="experimental evidence, no additional details
recorded"
     /note="Protonatable site."
     /ECO:0000250]."
Site            58
     /site_type="other"
     /experiment="experimental evidence, no additional details
recorded"
     /note="Contributes to redox potential value."
     /ECO:0000250]."
Site 60 /site_type="active" /experiment="experimental evidence, no additional details recorded" /note="Contributes to redox potential value. {ECO:0000250}."

Site 61 /site_type="methylolation" /experiment="experimental evidence, no additional details recorded" /note="N6-methyllysine. {ECO:0000250|UniProtKB:P30101}."

Bond /bond_type="disulfide" /experiment="experimental evidence, no additional details recorded" /note="N6-succinyllysine. {ECO:0000250|UniProtKB:P27773}."

Region /region_name="Conflict" /experiment="experimental evidence, no additional details recorded" /note="S -> T (in Ref. 1; CAA30916). {ECO:0000305}."

Site 119 /site_type="other" /experiment="experimental evidence, no additional details recorded" /note="Lowers pKa of C-terminal Cys of first active site. {ECO:0000250}."

Site 129 /site_type="modified" /experiment="experimental evidence, no additional details recorded" /note="N6-succinyllysine. {ECO:0000250|UniProtKB:P27773}."

Region /region_name="PDI_b_ERp57" /note="PDIb family, ERp57 subfamily, first redox inactive TRX-like domain b; ERp57 exhibits both disulfide oxidase and reductase functions like PDI, by catalyzing the formation of disulfide bonds of newly synthesized polypeptides in the ER and acting...; cd03069" /db_xref="CDD:239367"

Site 152 /site_type="acetylation" /experiment="experimental evidence, no additional details recorded" /note="N6-acetyllysine. {ECO:0000250|UniProtKB:P27773}."

Site 218 /site_type="modified" /experiment="experimental evidence, no additional details recorded" /note="N6-succinyllysine. {ECO:0000250|UniProtKB:P27773}."

Region /region_name="PDI_b'_ERp72_ERp57" /note="PDIb' family, ERp72 and ERp57 subfamily, second redox inactive TRX-like domain b'; ERp72 and ER57 are involved in oxidative protein folding in the ER, like PDI. They exhibit both disulfide oxidase and reductase functions, by catalyzing the formation of...; cd03073" /db_xref="CDD:239371"

Site 252 /site_type="acetylation" /experiment="experimental evidence, no additional details recorded" /note="N6-acetyllysine. {ECO:0000250|UniProtKB:P27773}."

Site 319 /site_type="phosphorylation" /experiment="experimental evidence, no additional details recorded" /note="Phosphothreonine. {ECO:0000250|UniProtKB:P30101}."

Region /region_name="Domain" /note="Thioredoxin 2. {ECO:0000255|PROSITE-ProRule:PRU00691}."

Site 362 /site_type="acetylation" /experiment="experimental evidence, no additional details recorded" /note="N6-acetyllysine. {ECO:0000250|UniProtKB:P27773}."

Region /region_name="PDI_a_PDI_a'_C" /note="PDIa family, C-terminal TRX domain (a') subfamily; composed of the C-terminal redox active a' domains of PDI, ERp72, ERp57 (or ERp60) exhibits both disulfide oxidase and reductase functions like PDI. They exhibit both disulfide oxidase and reductase functions, by catalyzing the formation of...; cd02995" /db_xref="CDD:239293"

Site 406 /site_type="active" /note="Nucleophile. {ECO:0000250}."
### MASCOT Search Results

**User**: pbm  
**E-mail**:  
**Search title**: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4  
**MS data file**: G:\PRESTATIONS\Labos académiques\Internationaux\États Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_1193.mgf  
**Database**: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)  
**Taxonomy**: Rattus (77,467 sequences)  
**Timestamp**: 25 Jan 2019 at 10:17:00 GMT

Not what you expected? Try the peptide summary.

#### Search parameters

#### Score distribution

#### Modification statistics

#### Protein Family Summary

| Significance threshold p< | Max. number of families | 0.05 | 20 |
|---------------------------|-------------------------|------|----|
| Display non-sig. matches  | Dendrograms cut at      |      |    |
| Preferred taxonomy        | AI entries              |      |    |

#### Sensitivity

#### Protein families 1–6 (out of 6)

| Score | Mass | Matches | Sequences | emPAI |
|-------|------|---------|-----------|-------|
| 1.1   | 76   | 60565   | 2 (2)     | 2 (2) | 0.15 |

#### 1 peptide matches (2 non-duplicate, 0 duplicate)

| Query Dupos | Observed | Mr (wept) | Mr (calc) | Delta M | Score | Expect | Rank | Peptide |
|-------------|----------|-----------|-----------|---------|-------|--------|------|---------|
| 352         | 742.9700 | 1483.9254 | 1482.7024 | 1.2230  | 46    | 0.0073 |      |         |
| 366         | 845.8300 | 1689.6454 | 1689.8243 | -0.1789 | 67    | 7e-05  |      | K. KIELLOQTVDFSK + Oxidation (M) |

Not what you expected? Try the peptide summary.

---

**Mascot**: [http://www.matrixscience.com/](http://www.matrixscience.com/)
MASCOT Search Results

Protein View: NP_034249.1

EH domain-containing protein 1 [Mus musculus]

Database: NCBIprot
Score: 76
Monoisotopic mass (M_r): 60565
Calculated pI: 6.35
Taxonomy: Mus musculus

This protein sequence matches the following other entries:

- **NP_001011939.1** from Rattus norvegicus
- **XP_021008206.1** from Mus caroli
- **Q641Z6.1** from Mus musculus
- **Q9WVK4.1** from Mus musculus
- **AAD45423.1** from Mus musculus
- **AAH38956.1** from Mus musculus
- **AAH32742.1** from Mus musculus
- **BAE43067.1** from Mus musculus
- **BAE35499.1** from Mus musculus
- **AAH54828.2** from Rattus norvegicus
- **EDL33231.1** from Mus musculus
- **EDM12590.1** from Rattus norvegicus
- **EDL33232.1** from Mus musculus
- **EMD25901.1** from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of NP_034249.1 against nr.

Search parameters

- **MS data file:** G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publ M Rosenberg\Identifications Mascot\VM11_03.rpf
- **Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.
- **Variable modifications:** Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 5%

Matched peptides shown in **bold red**.

| Query | Start – End | Observed Mr(wt) | Observed Mr(calc) | Delta M | Score | Expect | Rank | UniProtID | Peptide |
|-------|-------------|-----------------|-------------------|---------|-------|--------|------|-----------|---------|
| U     | 302 – 359   | 742.9700        | 1483.9254         | 1482.7024 | 1.2230 | T      | 46   | 0.0073    | U K. MQELLQTQDFSK.F + Oxidation (M) |
| U     | 366 – 378   | 845.8300        | 1689.6454         | 1689.8243 | -0.1789 | 0      | 67   | 7e-05     | U K. LLDTVDDLANDIAR.L + Oxidation (M) |

Unformatted sequence string: 534 residues (for pasting into other applications).

Sort by: residue number | increasing mass | decreasing mass
Show: matched peptides only | predicted peptides also

**LOCSU** NP_034249 534 aa linear ROD 15-DEC-2018
**DEFINITION** EH domain-containing protein 1 [Mus musculus].
**ACCESSION** NP_034249
**VERSION** NP_034249.1
**DBSOURCE** RefSeq: accession NM_010119.5
**KEYWORDS** RefSeq.
**SOURCE** Mus musculus (house mouse)
**ORGANISM** Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus.

**REFERENCE** 1 (residues 1 to 534)
**AUTHORS** Ikeka FN, Goetz BT, Mushtaq I, An W, Cypher LR, Bielecki TA, Tom EC, Arya P, Bhattacharyya S, Storck MD, Semerad CL, Talmadge JE, Mosley RL, Band V and Band H.
**TITLE** Role of the EHD Family of Endocytic Recycling Regulators for TCR Recycling and T Cell Function
**JOURNAL** J. Immunol. 200 (2), 483-499 (2018)
**PUBMED** 29212907

**REFERENCE** 2 (residues 1 to 534)
AUTHORS Yeow I, Howard G, Chadwick J, Mendosa-Topaz C, Hansen CG, Nichols BJ and Shvets E.

TITLE EHD Proteins Cooperate to Generate Caveolar Clusters and to Maintain Caveolae during Repeated Mechanical Stress

JOURNAL Curr. Biol. 27 (19), 2951-2962 (2017)

PUBMED 28943089

REMARK GeneRIF: EHD1, EHD2, and EHD4 are recruited to caveolae. Recruitment of the other EHDs increases markedly when EHD2, which has been previously detected at caveolae, is absent. Construction of knockout cell lines lacking EHD1, 2, and 4 confirms this apparent functional redundancy.

REFERENCE 3 (residues 1 to 534)

AUTHORS Cypher LR, Bielecki TA, Adepegba O, Huang L, An W, Iseka F, Luan H, Tom E, Storck MD, Hoppe AB, Band V and Band H.

TITLE CSP-1 receptor signaling is governed by pre-requisite EHD1-mediated receptor display on the macrophage cell surface

JOURNAL J. Cell. Signal. 28 (19), 1325-1335 (2016)

PUBMED 27224507

REMARK GeneRIF: These findings reveal a novel and functionally important role for EHD1 in governing CSP-1R signaling via regulation of anterograde transport of CSP-1R to the macrophage cell surface.

REFERENCE 4 (residues 1 to 534)

AUTHORS Bhattacharyya S, Rainey NA, Arya P, Mathapati BC, Mantegi I, Dutta S, George N, Storck MD, McComb RO, McClurk K, Todd GT, Guild R, Datta R, Gelineau-Vella JE, Band V and Band H.

TITLE Endocytic recycling protein EHD1 regulates primary cilium morphogenesis and SHH signaling during neural tube development

JOURNAL Sci Rep 6, 20727 (2016)

PUBMED 26884322

REMARK Erratum:[Sci Rep. 2017 Mar 23;7:42320. PMID: 28332491]

Publication Status: Online-Only

REFERENCE 5 (residues 1 to 534)

AUTHORS Arya P, Rainey NA, Bhattacharyya S, Mathapati BC, George M, Karacha MK, Storck MD, Band V, Govindarajan V and Band H.

TITLE The endocytic recycling regulatory protein EHD1 is required for ocular lens development

JOURNAL Dev. Biol. 408 (1), 41-55 (2015)

PUBMED 26455409

REMARK GeneRIF: these data reveal a unique role for EHD1 in early lens development.

REFERENCE 6 (residues 1 to 534)

AUTHORS Guilherme A, Soriano HA, Fuccinitti PS and Czech NP.

TITLE Role of EHD1 and EHBP1 in perinuclear sorting and insulin-regulated GLUT4 recycling in 3T3-L1 adipocytes

JOURNAL J. Biol. Chem. 279 (38), 40062-40075 (2004)

PUBMED 15247266

REMARK GeneRIF: EHD1 and EHBP1, but not EHD2, are required for perinuclear localization of GLUT4 and reveal that loss of EHBP1 disrupts insulin-regulated GLUT4 recycling in cultured adipocytes.

REFERENCE 7 (residues 1 to 534)

AUTHORS Galperin E, Benjamin S, Rapaport D, Rotem-Yehudar R, Tolchinsky S and Horowitz M.

TITLE EHBP1: a protein that resides in recycling tubular and vesicular membrane structures and interacts with EHD1

JOURNAL Traffic 3 (8), 575-589 (2002)

PUBMED 12121420

REMARK GeneRIF: EHD3: a protein that resides in recycling tubular and vesicular membrane structures and interacts with EHD1.

REFERENCE 8 (residues 1 to 534)

AUTHORS Lin SN, Grant B, Hirsh D and Manfield FR.

TITLE Rme-1 regulates the distribution and function of the endocytic recycling compartment in mammalian cells

JOURNAL Nat. Cell Biol. 3 (6), 567-572 (2001)

PUBMED 11389441

REFERENCE 9 (residues 1 to 534)

AUTHORS Pohl U, Smith JS, Tachibana I, Ueki K, Lee HK, Ramaswamy S, Wu Q, Mohrenweiser HM, Jenkins RB and Louis DN.

TITLE EHBP2, EHBP3, and EHBP4 encode novel members of a highly conserved family of EH domain-containing proteins

JOURNAL Genome 63 (1), 255-262 (2000)

PUBMED 10673336

REFERENCE 10 (residues 1 to 534)

AUTHORS Arya P, Rainey NA, Pasmanik-Chor M, Tulzinsky S, Bromberg Y, Kozak CA, Joyner A, Fein A and Horowitz M.

TITLE EHD3: a protein that resides in recycling tubular and vesicular membrane structures and interacts with EHD1

JOURNAL Genomics 59 (1), 66-76 (1999)

PUBMED 10395801

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBi review. The reference sequence was derived from AC176556.4.

Sequence Note: The RefSeq transcript and protein were derived from genomic sequences to make the sequence consistent with the reference genome assembly. The genomic coordinates used for the transcript record were based on alignments.

Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.

FEATURES Location/Qualifiers

source 1.154 /organism="Mus musculus" /strain="C57BL/6" /db_xref="taxon:10090" /chromosome="19" /map="19 4.4 cm"

Protein 1.154 /product="EHD1 domain-containing protein 1" /note="PAST1; EASH homolog 1" /calculated_mdw="60472"

Site 1 /site_type="other" /experiment="experimental evidence, no additional details recorded" /note="N-acetylmethionine. (ECO:0000250)(UniProtKB:Q9H4M9);"
Peptide Summary Report

User: Mascot Daemon

Email: laurent.coquet@univ-rouen.fr

Search title: Submitted from Martina Rosenberg PC1809 on PBM-IBBR-PERM2

MS data file: P:\Electrophorese\Martina Rosenberg\LCMSMS\090504_CQSM\MR_1412.mgf

Database: MCBInf 20090430 (8483808 sequences, 2914572939 residues)

Taxonomy: Rattus (68467 sequences)

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Individual ions scores > 43 indicate identity or extensive homology (p<0.05).

Probability Based Mowse Score

Ions score is \(-10 \log(P)\), where \(P\) is the probability that the observed match is a random event.

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Peptide Summary Report

| Query | Observed Mr (exp) | Observed Mr (calc) | Delta Mass Score | Expect Rank | Peptide |
|-------|------------------|--------------------|------------------|-------------|---------|
| 1     | 542.2800         | 1082.5654         | 530.2854        | 0.9534      | 1 4  K.RASKIDEBR.F |
|       | 554.3500         | 1107.0854         | 551.7354        | 0.5135      | 1 32  2  K.AQSTAEK.R |
| 2     | 590.3400         | 1178.6654         | 578.3254        | 0.0723      | 0 61  0.00084  1  R.YEELQITAGR.H |
| 3     | 652.3500         | 1302.6854         | 640.3354        | 0.9776      | 0 87  1.9e-06  1  R.SLQDSS1AEK.V.A |

Proteins matching the same set of peptides:

gi|109482941

Mass: 59393
Score: 117
Queries matched: 4
emPAI: 0.18

gi|109498009

Mass: 59213
Score: 117
Queries matched: 4
emPAI: 0.12

gi|109466098

Mass: 58060
Score: 92
Queries matched: 3
emPAI: 0.12

Proteins matching the same set of peptides:

gi|114031961

Mass: 54499
Score: 92
Queries matched: 3

rcO50520

Mass: 58060
Score: 92
Queries matched: 3
Protein Summary Report (Submitted from Martina Rosenberg PC1809... file:///G:/PRESTATIONS/Labos académiques/Internationaux/Etats Un...
### Table 11: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 11.   | 452.2800 | 1082.5454 | 1081.5920 | 0.9534     | 41    | 0.0755 | 1    | K.FAS FDVR.F |
|       | 554.5500 | 1107.0854 | 1106.5720 | 0.5153     | 34    | 0.4819 | 1    | R.AQ YEA.R.

Check to include this hit in error tolerant search or archive report.

### Table 12: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 11.   | 388.2700 | 1161.7882 | 1162.5652 | -0.7770    | 1     | 2.6e+02 | 8    | R.KLLEOR.E. + Carboxymethyl (C) |
|       | 738.4100 | 1474.8054 | 1475.7620 | -0.9565    | 0     | 0.432   | 2    | R.FLEQIQKQLETK.W |

### Table 13: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 11.   | 542.2800 | 1082.5454 | 1081.5920 | 0.9534     | 41    | 0.0755 | 1    | K.FAS FDVR.F |
|       | 738.4100 | 1474.8054 | 1475.7620 | -0.9565    | 0     | 0.432   | 2    | R.FLEQIQKQLETK.W |

Check to include this hit in error tolerant search or archive report.

### Table 14: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 12.   | 466.7000 | 1028.9254 | 1028.5866 | 0.3388     | 9     | 0.5     | 1    | R.VLDCILR.I |
|       | 539.9700 | 1063.9225 | 1063.0206 | 0.3229     | 34    | 0.41    | 1    | R.LASTLDEY.A |
|       | 651.3500 | 1300.6854 | 1299.6670 | 0.9534     | 0     | 0.075   | 1    | R.AWYAEIARK.S |

Check to include this hit in error tolerant search or archive report.

### Table 15: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 13.   | 515.4200 | 1028.5454 | 1028.5126 | 0.0028     | 0     | 9.5     | 1    | R.LISQDGWAVGSSFSGAAVR.A + Carboxymethyl (C) |
|       | 539.9700 | 1063.9225 | 1063.0206 | 0.3229     | 34    | 0.41    | 1    | R.LASTLDEY.A |
|       | 651.3500 | 1300.6854 | 1299.6670 | 0.9534     | 0     | 0.075   | 1    | R.AWYAEIARK.S |

Check to include this hit in error tolerant search or archive report.

### Table 16: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 14.   | 388.2700 | 1161.7882 | 1162.5652 | -0.7770    | 1     | 2.6e+02 | 8    | R.KLLEOR.E. + Carboxymethyl (C) |
|       | 738.4100 | 1474.8054 | 1475.7620 | -0.9565    | 0     | 0.432   | 2    | R.FLEQIQKQLETK.W |

Check to include this hit in error tolerant search or archive report.

### Table 17: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 15.   | 515.4200 | 1028.9254 | 1028.5866 | 0.3388     | 9     | 0.5     | 1    | R.VLDCILR.I |
|       | 539.9700 | 1063.9225 | 1063.0206 | 0.3229     | 34    | 0.41    | 1    | R.LASTLDEY.A |
|       | 651.3500 | 1300.6854 | 1299.6670 | 0.9534     | 0     | 0.075   | 1    | R.AWYAEIARK.S |

Check to include this hit in error tolerant search or archive report.

### Table 18: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 16.   | 388.2700 | 1161.7882 | 1162.5652 | -0.7770    | 1     | 2.6e+02 | 8    | R.KLLEOR.E. + Carboxymethyl (C) |
|       | 738.4100 | 1474.8054 | 1475.7620 | -0.9565    | 0     | 0.432   | 2    | R.FLEQIQKQLETK.W |

Check to include this hit in error tolerant search or archive report.

### Table 19: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 17.   | 388.2700 | 1161.7882 | 1162.5652 | -0.7770    | 1     | 2.6e+02 | 8    | R.KLLEOR.E. + Carboxymethyl (C) |
|       | 738.4100 | 1474.8054 | 1475.7620 | -0.9565    | 0     | 0.432   | 2    | R.FLEQIQKQLETK.W |

Check to include this hit in error tolerant search or archive report.

### Table 20: Peptide Summary Report

| Query | Observed | Mr (expt) | Mr (calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|-----------|-----------|------------|-------|--------|------|---------|
| 18.   | 388.2700 | 1161.7882 | 1162.5652 | -0.7770    | 1     | 2.6e+02 | 8    | R.KLLEOR.E. + Carboxymethyl (C) |
|       | 738.4100 | 1474.8054 | 1475.7620 | -0.9565    | 0     | 0.432   | 2    | R.FLEQIQKQLETK.W |

Check to include this hit in error tolerant search or archive report.
| Query | Observed | Mr(calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|----------|------------|-------|--------|------|---------|
| 22 | 744.8400 | 2231.4982 | 2321.1178 | 0.3804 | 1 | 26 | 2.4 | - KMEAAGGPGLRVAIVTFPETG.D + 2 Oxidation (M) |
| 19 | 388.2700 | 1161.7892 | 1162.5329 | -0.7447 | 0 | 10 | 1.1e+02 | 2 K.SPEAQTQYK.T + Oxidation (M) |
| 20 | 429.8400 | 857.6654 | 856.5130 | 1.1524 | 1 | 29 | 1.3 | A.SGAAKKEP |
| 25 | 690.5200 | 1383.0254 | 1381.7129 | 1.3125 | 7 | 2.2 | A.EAILFACHI |
| 30 | 20.4500 | 63.88 | 63.7999 | -0.9944 | 26 | 2.1 | CFDQ |
| 31 | 309.0400 | 924.0992 | 925.5960 | -1.4979 | 33 | 3.1 | LLAIGLALK |
| 32 | 429.5400 | 1258.0454 | 1256.6561 | -0.3893 | 20 | 3.6 | CMQLAQNVR + Oxidation (M) |
| 33 | 1023.2600 | 2040.5004 | 2040.0561 | 1.1443 | 12 | 3.4 | R.MLRLMQTRPEDAGQYT |
| 34 | 444.5500 | 1330.6200 | 1329.5962 | -0.9860 | 25 | 3.6 | VMQGCVSASSPCSTARKFPLMR + Oxidation (M); Carbamidomethyl (C); Oxidation (M) |
| 35 | 656.5400 | 1946.5992 | 1947.0054 | -0.4062 | 24 | 4.3 | SVMVDDTTSPELAAPASER |
| 36 | 435.9300 | 1332.6692 | 1332.6292 | 1.1700 | 19 | 1.1 | 143.82 QMGLMQACQ + Oxidation (M) |
| 37 | 431.9500 | 1332.6692 | 1332.7088 | 1.1193 | 10 | 7.1 | RVQVTQVL |
| 38 | 758.0100 | 2271.0054 | 2270.2188 | 0.7864 | 27 | 6.8 | SANCLEGS |
| 39 | 733.4100 | 2197.2082 | 2197.0083 | 1.2099 | 29 | 1.1 | KQ QESA + Oxidation (M) |
| 40 | 959.1700 | 2839.3782 | 2839.3782 | 1.2099 | 22 | 1.1 | LVVAMQ + Oxidation (M) |
| 41 | 448.7700 | 1343.2882 | 1343.5454 | -1.2672 | 11 | 2.6 | MFMGSLH |
| 42 | 444.3000 | 1330.6200 | 1329.5962 | -0.9860 | 25 | 3.6 | VMQGCVSASSPCSTARKFPLMR + Oxidation (M); Carbamidomethyl (C); Oxidation (M) |
| 43 | 598.1700 | 1791.4882 | 1790.9163 | 0.5719 | 0 | 21 | 8.3 | DLTAVSAGLSCPE |
| 44 | 611.3200 | 1831.3354 | 1831.3354 | 0.0000 | 1 | 26 | 2.4 | - KMEAAGGPGLRVAIVTFPETG.D + 2 Oxidation (M) |
| 45 | 532.4000 | 1595.8712 | 1595.8712 | 0.0000 | 1 | 26 | 2.4 | - KMEAAGGPGLRVAIVTFPETG.D + 2 Oxidation (M) |
| 46 | 550.2900 | 1648.8461 | 1648.8461 | -0.9979 | 19 | 1.1 | FKPRKLK |

### Peptide Summary Report

**Proteins matching the same set of peptides:**

| Query | Observed | Mr(calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|----------|------------|-------|--------|------|---------|
| 22 | 744.8400 | 2231.4982 | 2321.1178 | 0.3804 | 1 | 26 | 2.4 | - KMEAAGGPGLRVAIVTFPETG.D + 2 Oxidation (M) |
| 19 | 388.2700 | 1161.7892 | 1162.5329 | -0.7447 | 0 | 10 | 1.1e+02 | 2 K.SPEAQTQYK.T + Oxidation (M) |

**Proteins matching the same set of peptides:**

| Query | Observed | Mr(calc) | Delta Miss | Score | Expect | Rank | Peptide |
|-------|----------|----------|------------|-------|--------|------|---------|
| 22 | 744.8400 | 2231.4982 | 2321.1178 | 0.3804 | 1 | 26 | 2.4 | - KMEAAGGPGLRVAIVTFPETG.D + 2 Oxidation (M) |
| 19 | 388.2700 | 1161.7892 | 1162.5329 | -0.7447 | 0 | 10 | 1.1e+02 | 2 K.SPEAQTQYK.T + Oxidation (M) |

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**PREDICTED:** similar to High Incidence of Males (increased X chromosome loss) family member (him-4) [Rattus norvegicus]
| Peptide | Charge | MW | Precursor Mass | Observed Mass | Delta | Retention Time | PEP | Oxidation | Carbamidomethylation | Carboxymethylation |
|---------|--------|----|---------------|--------------|-------|----------------|-----|-------------|---------------------|-------------------|
| MGKSQLCSAGTVHGR + Oxidation (M) | 800.56 | 1847.04 | 1847.33 | 0.2972 | 1690.7596 | 15.73 | 1 | 1 | 1 |
| MNFSWR + Carbamidomethyl (C); Oxidation (M) | 581.86 | 1161.7054 | 1161.4617 | -0.2348 | 1690.9292 | 23.74 | 1 | 1 | 1 |
| CLPK + Carbamidomethyl (C); Oxidation (M) | 388.69 | 777.38 | 776.56 | -0.82 | 1738.1918 | 1.07 | 1 | 1 | 1 |
| CVVRFWAEEDGPFP | 604.35 | 1201.70 | 1201.54 | -0.16 | 2079.9524 | 1.92 | 1 | 1 | 1 |
| CMPGVGYTIIPAQ | 556.51 | 1113.02 | 1113.02 | 0 | 2079.9524 | 1.92 | 1 | 1 | 1 |
| CV | 426.21 | 852.42 | 852.42 | 0 | 1738.1918 | 1.07 | 1 | 1 | 1 |
| MNFSWR | 581.86 | 1161.7054 | 1161.4617 | -0.2348 | 1690.9292 | 23.74 | 1 | 1 | 1 |
| CLPK | 388.69 | 777.38 | 776.56 | -0.82 | 1738.1918 | 1.07 | 1 | 1 | 1 |
| CV | 426.21 | 852.42 | 852.42 | 0 | 1738.1918 | 1.07 | 1 | 1 | 1 |
| CV | 426.21 | 852.42 | 852.42 | 0 | 1738.1918 | 1.07 | 1 | 1 | 1 |

**Summary Report (Submitted from Martina Rosenberg PC1809... file:///G:/PRESTATI ONS/Labos académiques/Internationaux/Etats Un...**
# MASCOT Search Results

**User**: pbm  
**E-mail**:  
**Search title**: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-6SA4  
**MS data file**: G:\PRESTATIONS\Labos académiques\Internationaux\États Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR__2116.mgf  
**Database**: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)  
**Taxonomy**: Rattus (77,467 sequences)  
**Timestamp**: 25 Jan 2019 at 10:10:45 GMT

Not what you expected? Try the peptide summary.

## Search parameters

- **Modification statistics**
- **Protein Family Summary**
- **Legend**

### Protein Family Summary

| Significance threshold | Max. number of families |
|------------------------|-------------------------|
| 0.05                   | 20                      |

Display non-sig. matches: Dendrograms cut at: All entries

### Sensitivity

Protein families 1–8 (out of 8)

| Protein Family | Description | Score | Mass | Matches | Sequences | emPAI |
|----------------|-------------|-------|------|---------|-----------|-------|
| 1              | NP_036767.1 | 111 anionic trypsin-1 precursor [Rattus norvegicus] |       |         |           |       |
| 2              | NP_001009542.1 | programmed cell death protein 10 [Rattus norvegicus] | 103   | 24340   | 4 (4)     | 4 (4)  | 1.04  |

### Peptide matches (4 non-duplicate, 0 duplicate)

| Query          | Dupes | Observed Mr (expt) | Observed Mr (calc) | Delta Mr | Score | Expect | Rank | Score | Peptide |
|----------------|-------|--------------------|--------------------|----------|-------|--------|------|-------|---------|
| XP_008774848.1  | 101   | 536.8200           | 1071.6254          | 1071.6036 | 0.0218 | 64     | 5.3e-05 | U     | R.VNLSAAQTL.A  |
| XP_001008751.1  | 59    | 552.8300           | 1103.6454          | 1103.6087 | 0.0367 | 45     | 0.0043 | U     | K.AINVFISANR.L  |
| NP_001008802.2  | 52    | 784.7100           | 1567.4054          | 1567.9086 | -0.5032 | 41     | 0.0022 | U     | R.LINQXNILIQTPF.T  |
| XP_006247453.1  | 50    | 977.2700           | 2928.7882          | 2929.2633 | -0.4751 | 50     | 0.0017 | U     | R.MAADOVEETIEMPIERPEPQOLNEK.A  |

Not what you expected? Try the peptide summary.

Mascot: [http://www.matrixscience.com/](http://www.matrixscience.com/)
**MASCOT Search Results**

**Protein View: NP_001009542.1**

**programmed cell death protein 10 [Rattus norvegicus]**

- **Database:** NCBIpro
- **Score:** 103
- **Monoisotopic mass (Mr):** 24340
- **Calculated pI:** 6.78
- **Taxonomy:** Rattus norvegicus

This protein sequence matches the following other entries:
- XP_006232563.1 from Rattus norvegicus
- Q6NX65.1 from Rattus norvegicus
- AAH67245.1 from Rattus norvegicus
- EDM00884.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of NP_001009542.1 against nr.

**Search parameters**
- **MS data file:** G:\PRESTATIONS\Labor académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR__2116.mgf
- **Enzyme:** Trypsin: cuts C-term side of KR unless next residue is P.
- **Variable modifications:** Carbamidomethyl (C), Oxidation (M)

**Protein sequence coverage:** 27%

Matched peptides shown in **bold red.**

Unformatted sequence string: **210 residues** (for pasting into other applications).

Sort by residue number **increasing mass decreasing mass**

| Query | Start - End | Observed Mr (exact) | Mr (calc) | Delta Mr | Score | Expect | Rank | U | Peptide |
|-------|-------------|---------------------|-----------|----------|-------|--------|------|---|---------|
| 1     | 34 - 43     | 536.8200            | 1071.6254 | 1071.6036 | 0.0218 | 64     | 5.3e-05 | 1 | R.VNLSAQTLR.A |
| 2     | 105 - 109   | 977.2700            | 2928.7882 | 2929.2633 | -0.4751 | 50     | 6.9e-05 | 1 | R.WAADOVERKIERPEPEQYQLEK.A + 2 Oxidation (M) |
| 3     | 185 - 194   | 552.8300            | 1103.6454 | 1103.6087 | 0.0367 | 45     | 0.0043 | 1 | R.K.AIYFPISANE.L |
| 4     | 195 - 207   | 784.7100            | 1567.4054 | 1567.9086 | -0.5032 | 41     | 0.0022 | 1 | R.LIHQNLILIQTPR.T |

**LOCUS** NP_001009542
**DEFINITION** programmed cell death protein 10 [Rattus norvegicus].
**ACCESSION** NP_001009542
**VERSION** NP_001009542.1
**DBSOURCE** REFSEQ: accession NM_001009542.2
**KEYWORDS** RefSeq.
**SOURCE** Rattus norvegicus (Norway rat)
**ORGANISM** Rattus norvegicus

**REFERENCE 1** (residues 1 to 210)
- **AUTHORS** Mardakheh FK, Self A and Marshall CJ.
- **TITLE** RHO binding to FAM65A regulates Golgi reorientation during cell migration
- **JOURNAL** J. Cell. Sci. 129 (24), 4466-4479 (2016)
- **PUBMED** 27807006

**REFERENCE 2** (residues 1 to 210)
- **AUTHORS** Zhang M, Dong L, Shi Z, Jiao S, Zhang Z, Zhang W, Liu G, Chen C, Feng M, Hao Q, Wang W, Yin M, Zhao Y, Zhang L and Zhou Z.
- **TITLE** Structural mechanism of CCM3 heterodimerization with GCKIII kinases
- **JOURNAL** Structure 21 (4), 680-688 (2013)
- **PUBMED** 23541896

**REFERENCE 3** (residues 1 to 210)
- **AUTHORS** You C, Sandalcioglu IE, Dammann P, Felbor U, Sure U and Zhu Y.
- **TITLE** Loss of CCM3 impairs DLL4-Notch signalling: implication in endothelial angiogenesis and in inherited cerebral cavernous malformations
- **JOURNAL** J. Cell. Mol. Med. 17 (3), 407-418 (2013)
- **PUBMED** 23888056

**REFERENCE 4** (residues 1 to 210)
- **AUTHORS** Kim HW, Mallick P, Durani S, Ashraf M, Jiang S and Haider RH.
- **TITLE** Concomitant activation of miR-107/PODC10 and hypoxamir-210/Casp8ap2 and their role in cytoprotection during ischemic preconditioning of stem cells
- **JOURNAL** Antioxid. Redox Signal. 17 (8), 1053-1065 (2012)
- **PUBMED** 2282882

**REMARK** GeneSilF: The ischemic preconditioning (IPC) enhances stem cell survival via the combined participation of hypoxia responsive miR-107 and miR-210 via their respective putative target genes Pdcd10 and Casp8ap2.
MASCOT Search Results

User: pbm
E-mail:

Search title: Submitted from MRosenberg Data2009 by Mascot Daemon on SCT-14-65A4

MS data file: G:\PRESTATIONS\Labos académiques\Internationaux\Etats Unis\Martina Rosenberg\Data pour publi M Rosenberg\Identifications Mascot\MR_2944.mgf

Database: NCBIprot 20171205 (139,213,787 sequences; 51,013,024,959 residues)

Taxonomy: Rattus (77,467 sequences)

Timestamp: 25 Jan 2019 at 10:27:41 GMT

Not what you expected? Try the peptide summary.

Protein Family Summary

Significance threshold p< 0.05
Max. number of families 20
Display non-sig. matches
Dendrograms cut at 0
Preferred taxonomy All entries

Sensitivity

Protein families 1–5 (out of 5)

10 per page 1

1

| Score | Mass | Matches | Sequences | emPAI |
|-------|------|---------|-----------|-------|
| 1     | NP_001008825.1 | 67 keratin, type II cytoskeletal cochleal (Rattus norvegicus) | 56 rCG50690, partial (Rattus norvegicus) |
| 2     | EDL86882.1 | 61 anionic trypsin-1 precursor (Rattus norvegicus) |
| 3     | NP_036767.1 | 59 dihydropyrimidinase-related protein 2 (Mus musculus) |
| 4     | NP_034085.2 | 59 dihydropyrimidinase-related protein 2 (Mus musculus) |
| 5     | NP_034085.2 | 59 dihydropyrimidinase-related protein 2 (Mus musculus) |

1 peptide matches (1 non-duplicate, 0 duplicate)

Query Duplicates Observed Mr (expt) Mr (calc) Delta M Score Expect Rank U Peptide
114 508.2400 1014.4654 1014.5458 -0.0803 0 59 0.0023 2 K.SAEVIAQR.K

AAI28704.1

Pgm1 protein, partial (Rattus norvegicus)

XP_006247453.1

PREDICTED: keratin, type I cytoskeletal 10 isoform X2 (Rattus norvegicus)

Mascot: http://www.matrixscience.com/
Protein View: NP_034085.2
dihydropyrimidinase-related protein 2 [Mus musculus]

Database: NCBIprot
Score: 59
Monoisotopic mass (Mr): 62239
Calculated pI: 5.95
Taxonomy: Mus musculus

This protein sequence matches the following other entries:
- NP_001099187.1 from Rattus norvegicus
- XP_002031364.1 from Castor canadensis
- XP_002103697.1 from Mus caroli
- P47461.1 from Rattus norvegicus
- O08553.2 from Mus musculus
- CAA66968.1 from Rattus norvegicus
- AAU62995.1 from Mus musculus
- EDL35988.1 from Rattus norvegicus

Sequence similarity is available as an NCBI BLAST search of NP_034085.2 against nr.

Search parameters
MS data file: G:\PRESTATIONS\Labos académiques\ Internationaux\ Etats Unis\ Martina Rosenberg\ Data pour publi M Rosenberg\ Identifications Mascot\ MR_2944.mgf
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Variable modifications: Carbamidomethyl (C), Oxidation (M)

Protein sequence coverage: 1%

Matched peptides shown in bold red.

| Start - End | Observed Mr (expt) | Mr (calc) | Score Expect | Rank |
|-------------|--------------------|-----------|--------------|------|
| 114 - 259   | 508.2400           | 1014.4654 | 1014.5458    | -0.0803 | 0 | 59 | 0.0023 | 1 | K.SAAEVIAQAR.K |

Unformatted sequence string: 572 residues (for pasting into other applications).

Sort by residue number, increasing mass, decreasing mass
Show matched peptides only, predicted peptides also

LOCUS: NP_034085
DEFINITION: dihydropyrimidinase-related protein 2 [Mus musculus].
ACCESSION: NP_034085
VERSION: NP_034085.2
SOURCE: accession NM_009955.3
KEYWORDS: RefSeq.
SOURCE: Mus musculus (house mouse)
ORGANISM: Mus musculus

REFERENCE 1 [residues 1 to 572]
AUTHORS: Abe H, Jitsuki S, Nakajima W, Murata Y, Jitsuki-Takahashi A, Katsuno Y, Tada H, Sano A, Suyama K, Mochizuki N, Komori T, Masuyama H, Okuda T, Goshima Y, Higo N and Takahashi T.
TITLE: CRMP2-binding compound, edonerpic maleate, accelerates motor function recovery from brain damage
JOURNAL: Science 360 (6384), 50-57 (2018)
PUBMED: 29622647

REFERENCE 2 [residues 1 to 572]
AUTHORS: Dufrêne ET, Perez-Miller S, Francois-Moutal L, Moutal A, Khanna M and Khanna R.
TITLE: A single structurally conserved SUMOylation site in CRMP2 controls NaV1.7 function
JOURNAL: Channels (Austin) 11 (4), 316-328 (2017)
PUBMED: 28277040

REMARK: Gene2LIF: postulate that this state forces CRMP2 toward a monomer, exposing the SUMO site and consequently, resulting in constitutive regulation of NaV1.7.
REFERENCE 3 (residues 1 to 572)
AUTHORS Sarhan AR, Zyroka J, Begum S, Tomlinson MG, Hotchin NA, Heath JK and Cunningham DL.
TITLE Quantitative Phosphoproteomics Reveals a Role for Collapsin Response Mediator Protein 2 in PDGF-Induced Cell Migration
JOURNAL Sci Rep 7 (1), 3970 (2017)
PUBMED 28638064
REMARK GeneRIF: Results show that collapsin response mediator protein 2 is required for platelet derived growth factor-directed cell migration in vitro.
Publication Status: Online-Only
REFERENCE 4 (residues 1 to 572)
AUTHORS Wang Y, Wang XL, Xie GL, Li HY and Wang YL.
TITLE Collapsin Response Mediator Protein-2-induced Retinal Ischemic Injury in a Novel Mice Model of Ocular Ischemia Syndrome
JOURNAL Chin. Med. J. 130 (11), 1342-1351 (2017)
PUBMED 28524835
REMARK GeneRIF: These results revealed that bilateral ligation of the internal carotid artery causes retinal ischemia in mice. Moreover, CRMP2 might play a pivotal role during the ischemic injury in the retina and inhibit the cleavage of CRMP2 can ameliorate the IH injury.
REFERENCE 5 (residues 1 to 572)
AUTHORS Yamane M, Yamashita N, Hida T, Kamiya Y, Nakamura F, Kolattukudy P and Goshima Y.
TITLE A functional coupling between CRMP1 and Nav1.7 for retrograde propagation of Semaphorin3A signaling
JOURNAL J. Cell. Sci. 130 (8), 1393-1403 (2017)
REFERENCE 6 (residues 1 to 572)
AUTHORS Fukada M, Watakabe I, Yuasa-Kawada J, Kawachi H, Kuroiwa A, Matsuda Y and Noda M.
TITLE Molecular characterization of CRMP5, a novel member of the collapsin response mediator protein family
JOURNAL J. Biol. Chem. 275 (48), 37957-37965 (2000)
REFERENCE 7 (residues 1 to 572)
AUTHORS Inagaki H, Kato Y, Hamajima N, Nonaka M, Sasaki M and Eimoto T.
TITLE Differential expression of dihydropyrimidinase-related protein genes in developing and adult enteric nervous system
JOURNAL Histochem. Cell Biol. 113 (1), 37-41 (1998)
REFERENCE 8 (residues 1 to 572)
AUTHORS Byk T, Csan Z and Rubel A.
TITLE The Ulip family phosphoproteins--common and specific properties
JOURNAL Eur. J. Biochem. 254 (1), 14-24 (1998)
REFERENCE 9 (residues 1 to 572)
AUTHORS Hamajima N, Matsuda K, Sakata S, Tamaki H, Sasaki M and Nonaka M.
TITLE A novel gene family defined by human dihydropyrimidase and three related proteins with differential tissue distribution
JOURNAL Gene 180 (1-2), 157-163 (1996)
COMMENT VALIDATED REFSEQ: This record has undergone validation or preliminary review. The reference sequence was derived from BC062955.1 and AC154693.2.
On Dec 20, 2003 this sequence version replaced NP_034085.1.
Publication Note: This RefSeq record includes a subset of the publications that are available for this gene. Please see the Gene record to access additional publications.
Site 555
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/note="Phosphothreonine, by ROCK2.
(ECO:0000250|UniProtKB:O02675); propagated from
UniProtKB/Swiss-Prot (O08553.2)"

Site 565
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/note="Asymmetric dimethylarginine.
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UniProtKB/Swiss-Prot (O08553.2)"

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/db_xref="GeneID:12934"
/db_xref="MGI:MGI:1349763"

Mascot: http://www.matrixscience.com/