

Spot S1

MASCOT Mascot Search Results

Protein View

Match to: [gi|256724272](#) Score: **83** Expect: **0.0032**
 hypothetical protein NECHADRAFT_53490 [*Nectria haematococca* mpVI 77-13-4]

Nominal mass (M_r): **13527**; Calculated pI value: **9.60**

NCBI BLAST search of [gi|256724272](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Nectria haematococca mpVI 77-13-4](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

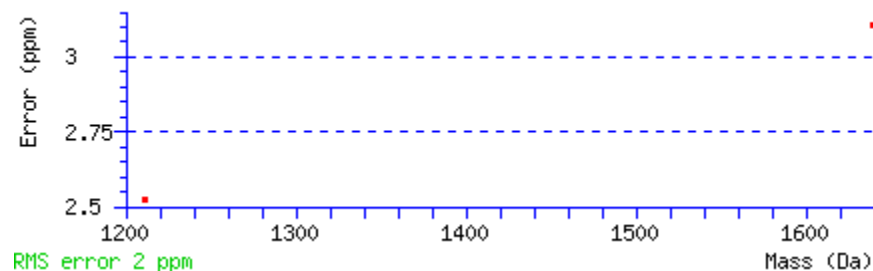
1 MAAPAASSDS VSMMAATPQW TIQGLSRSCD KPDTTCTWNF K**INTGSGAAT**
 51 **ACKYVVK**GKS ASKANGGPAK CGTFTITSGW SGQFGAGKGF TTVSVVSSKK
 101 **QIIYPAYTDK** QLAGGKVVKP DQSYAPAALP

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
42 - 57	1639.8523	1638.8450	1638.8399	3	1	K.INTGSGAATACKYVVK.G (No match)
101 - 110	1211.6337	1210.6264	1210.6234	3	0	K.QIIYPAYTDK.Q (Ions score 72)
101 - 110	1211.6337	1210.6264	1210.6234	3	0	K.QIIYPAYTDK.Q (No match)



LOCUS EEU37643 130 aa linear PLN 30-AUG-2009
 DEFINITION hypothetical protein NECHADRAFT_53490 [Nectria haematococca mpVI 77-13-4].
 ACCESSION EEU37643
 VERSION EEU37643.1 GI:256724272
 DBLINK Project: 16586
 DBSOURCE accession GG698921.1
 KEYWORDS .
 SOURCE Nectria haematococca mpVI 77-13-4
 ORGANISM Nectria haematococca mpVI 77-13-4
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria; Nectria
 haematococca complex.
 REFERENCE 1 (residues 1 to 130)
 AUTHORS Coleman,J.J., Rounsley,S.D., Rodriguez-Carres,M., Kuo,A.,
 Wasmann,C.C., Grimwood,J., Schmutz,J., Taga,M., White,G.J.,
 Zhou,S., Schwartz,D.C., Freitag,M., Ma,L.J., Danchin,E.G.,
 Henrissat,B., Coutinho,P.M., Nelson,D.R., Straney,D., Napoli,C.A.,
 Barker,B.M., Gribskov,M., Rep,M., Kroken,S., Molnar,I., Rensing,C.,
 Kennell,J.C., Zamora,J., Farman,M.L., Selker,E.U., Salamov,A.,
 Shapiro,H., Pangilinan,J., Lindquist,E., Lamers,C., Grigoriev,I.V.,
 Geiser,D.M., Covert,S.F., Temporini,E. and Vanetten,H.D.
 TITLE The genome of Nectria haematococca: contribution of supernumerary
 chromosomes to gene expansion
 JOURNAL PLoS Genet. 5 (8), E1000618 (2009)
 PUBMED 19714214
 REFERENCE 2 (residues 1 to 130)
 AUTHORS Kuo,A., Salamov,A., Grimwood,J., Schmutz,J., Pangilinan,J.,
 Shapiro,H., Lindquist,E., Lucas,S., Pitluck,S., Henrissat,B.,
 Geiser,D.M., Coleman,J.J., Kroken,S., Napoli,C.A., Rep,M.,
 Covert,S.F., Temporini,E., VanEtten,H.D. and Grigoriev,I.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2009) US DOE Joint Genome Institute, 2800
 Mitchell Drive, Walnut Creek, CA 94598-1698, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..130
 /organism="Nectria haematococca mpVI 77-13-4"
 /isolate="77-13-4"
 /culture_collection="FGSC:9596"
 /db_xref="taxon:660122"
 /chromosome="12"
 /country="USA"
 /note="mpVI; mating population VI"
 Protein 1..130
 /product="hypothetical protein"

CDS 1..130
 /locus_tag="NECHADRAFT_53490"
 /coded_by="complement(GG698921.1:41444..41836)"
 /note="expressed hypothetical protein"
 /db_xref="JGIDB:Necha2_53490"

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

Spot S3

MASCOT Mascot Search Results

Protein View

Match to: [gi|256724272](#) Score: **82** Expect: **0.0038**
 hypothetical protein NECHADRAFT_53490 [*Nectria haematococca* mpVI 77-13-4]

Nominal mass (M_r): **13527**; Calculated pI value: **9.60**

NCBI BLAST search of [gi|256724272](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Nectria haematococca mpVI 77-13-4](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

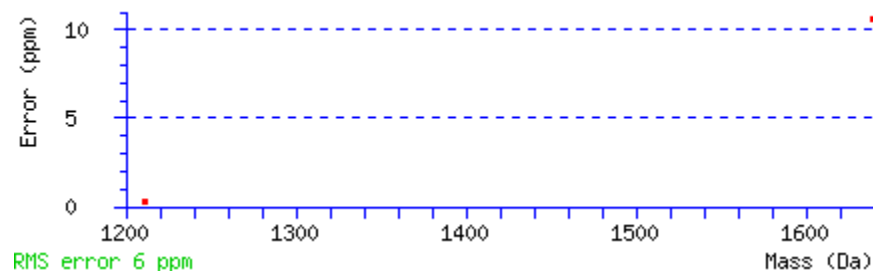
1 MAAPAASSDS VSMMAATPQW TIQGLSRSCD KPDTTCTWNF K**INTGSGAAT**
 51 **ACKYVVK**GKS ASKANGGPAK CGTFTITSGW SGQFGAGKGF TTVSVVSSKK
 101 **QIIYPAYTDK** QLAGGKVVKP DQSYAPAALP

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
42 - 57	1639.8645	1638.8572	1638.8399	11	1	K.INTGSGAATACKYVVK.G (No match)
101 - 110	1211.6310	1210.6237	1210.6234	0	0	K.QIIYPAYTDK.Q (Ions score 71)
101 - 110	1211.6310	1210.6237	1210.6234	0	0	K.QIIYPAYTDK.Q (No match)



LOCUS EEU37643 130 aa linear PLN 30-AUG-2009
 DEFINITION hypothetical protein NECHADRAFT_53490 [Nectria haematococca mpVI 77-13-4].
 ACCESSION EEU37643
 VERSION EEU37643.1 GI:256724272
 DBLINK Project: 16586
 DBSOURCE accession GG698921.1
 KEYWORDS .
 SOURCE Nectria haematococca mpVI 77-13-4
 ORGANISM Nectria haematococca mpVI 77-13-4
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria; Nectria
 haematococca complex.
 REFERENCE 1 (residues 1 to 130)
 AUTHORS Coleman,J.J., Rounsley,S.D., Rodriguez-Carres,M., Kuo,A.,
 Wasmann,C.C., Grimwood,J., Schmutz,J., Taga,M., White,G.J.,
 Zhou,S., Schwartz,D.C., Freitag,M., Ma,L.J., Danchin,E.G.,
 Henrissat,B., Coutinho,P.M., Nelson,D.R., Straney,D., Napoli,C.A.,
 Barker,B.M., Gribskov,M., Rep,M., Kroken,S., Molnar,I., Rensing,C.,
 Kennell,J.C., Zamora,J., Farman,M.L., Selker,E.U., Salamov,A.,
 Shapiro,H., Pangilinan,J., Lindquist,E., Lamers,C., Grigoriev,I.V.,
 Geiser,D.M., Covert,S.F., Temporini,E. and Vanetten,H.D.
 TITLE The genome of Nectria haematococca: contribution of supernumerary
 chromosomes to gene expansion
 JOURNAL PLoS Genet. 5 (8), E1000618 (2009)
 PUBMED 19714214
 REFERENCE 2 (residues 1 to 130)
 AUTHORS Kuo,A., Salamov,A., Grimwood,J., Schmutz,J., Pangilinan,J.,
 Shapiro,H., Lindquist,E., Lucas,S., Pitluck,S., Henrissat,B.,
 Geiser,D.M., Coleman,J.J., Kroken,S., Napoli,C.A., Rep,M.,
 Covert,S.F., Temporini,E., VanEtten,H.D. and Grigoriev,I.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2009) US DOE Joint Genome Institute, 2800
 Mitchell Drive, Walnut Creek, CA 94598-1698, USA
 COMMENT Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..130
 /organism="Nectria haematococca mpVI 77-13-4"
 /isolate="77-13-4"
 /culture_collection="FGSC:9596"
 /db_xref="taxon:660122"
 /chromosome="12"
 /country="USA"
 /note="mpVI; mating population VI"
 Protein 1..130
 /product="hypothetical protein"

CDS 1..130
 /locus_tag="NECHADRAFT_53490"
 /coded_by="complement(GG698921.1:41444..41836)"
 /note="expressed hypothetical protein"
 /db_xref="JGIDB:Necha2_53490"

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

Spot S7

MASCOT Mascot Search Results

Protein View

Match to: [gi|189192036](#) Score: **94** Expect: **0.00026**
hypothetical protein PTRG_02024 [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **22518**; Calculated pI value: **7.63**

NCBI BLAST search of [gi|189192036](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187973963](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

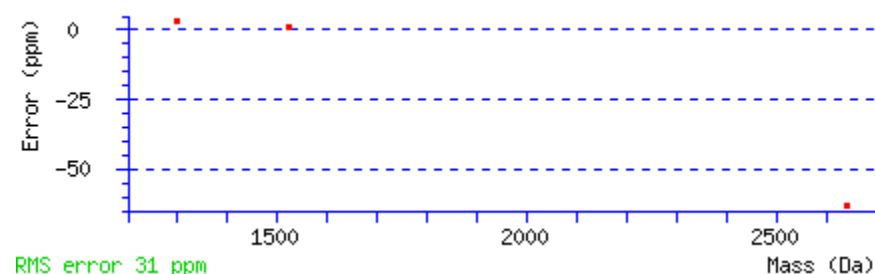
1 MKTSIFIAVA SAALVSAAPA PVSLEARAPP NIPTKATATT LLAGLTVAAQ
 51 GPQDGYSRDL FPHWITQSGT CNTRETVLKR DGTNVVTNDA CASTSGNWLS
 101 PYDGGSWTAA SDVDIDHMVP LSNAWKSGAA AWTTAR**RQAF ANDLTNPQLL**
 151 **AVTDNVNQAK** GDKGPEDWKP PLTSYYCTYS KAWIK**VKSVY SLTITSAEKS**
 201 ALTSMLATCS S

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
137 - 160	2641.2021	2640.1948	2640.3620	-63	1	R.RQAFANDLTNPQLLAVTDNVNQAK.G (No match)
186 - 199	1525.8484	1524.8411	1524.8399	1	1	K.VKSVYSLTITSAEK.S (No match)
188 - 199	1298.6881	1297.6808	1297.6765	3	0	K.SVYSLTITSAEK.S (Ions score 78)
188 - 199	1298.6881	1297.6808	1297.6765	3	0	K.SVYSLTITSAEK.S (No match)



LOCUS XP_001932357 211 aa linear PLN 30-MAY-2008
 DEFINITION hypothetical protein PTRG_02024 [Pyrenophora tritici-repentis Pt-1C-BFP].
 ACCESSION XP_001932357
 VERSION XP_001932357.1 GI:189192036
 DBSOURCE REFSEQ: accession XM_001932322.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 211)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L.,
 Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Genome Sequence of Pyrenophora tritici-repentis
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 211)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7
 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EDU41462.
Method: conceptual translation.

FEATURES Location/Qualifiers
 source 1..211
 /organism="Pyrenophora tritici-repentis Pt-1C-BFP"
 /strain="Pt-1C-BFP"
 /db_xref="taxon:426418"
 Protein 1..211
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 /calculated_mol_wt=22173
 Region 50..200
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 /note="Domain of unknown function (DUF1994); pfam09352"
 /db_xref="CDD:150128"
 CDS 1..211
 /locus_tag="PTRG_02024"
 /coded_by="XM_001932322.1:1..636"
 /db_xref="GeneID:6339539"

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

Spot S9

MASCOT Mascot Search Results

Protein View

Match to: [gi|156061869](#) Score: 77 Expect: 0.012
 hypothetical protein SS1G_03080 [Sclerotinia sclerotiorum 1980]

Nominal mass (M_r): 26879; Calculated pI value: 6.64

NCBI BLAST search of [gi|156061869](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Sclerotinia sclerotiorum 1980 UF-70](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|154700481](#) from [Sclerotinia sclerotiorum 1980 UF-70](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 21%

Matched peptides shown in **Bold Red**

1 **MLFTNTKFLS** **VLAAAAAVKG** APVEGNDIQA RAVVNHDSIN PWPENVPGGA
 51 LGNTLKRFEF YLHIAHCQP YSAVDGYGNT SGGLQDTGNI SAGCR**DQAKG**
 101 **QTYVR**GAWSG **GKYGIMYAWY** **FPKDQPAAGN** **VVGGR**HDWE YVVIWTNNPE
 151 VANPELLGGA ASSHSSNRKS TSIPTQGTRP KVEYFVEFPT NHELQFTNTL
 201 GRDLPMWYD FLPAVSKTAL DNTKFGDANC PFNNANFARK LAEAQI

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 7	854.4020	853.3947	853.4368	-49	0	-.MLFTNTK.F (No match)
1 - 7	854.4020	853.3947	853.4368	-49	0	-.MLFTNTK.F (No match)
1 - 7	870.4010	869.3937	869.4317	-44	0	-.MLFTNTK.F Oxidation (M) (No match)
1 - 19	2011.9583	2010.9510	2011.1176	-83	1	-.MLFTNTKFLSVLAAAAAVK.G Oxidation (M) (No match)
96 - 105	1165.5872	1164.5799	1164.5887	-8	1	R.DQAKGQTYVR.G (No match)
113 - 123	1438.6901	1437.6828	1437.6791	3	0	K.YGIMYAWYFPK.D (Ions score 41)
113 - 123	1438.6901	1437.6828	1437.6791	3	0	K.YGIMYAWYFPK.D (No match)
113 - 123	1454.6866	1453.6793	1453.6740	4	0	K.YGIMYAWYFPK.D Oxidation (M) (No match)
113 - 136	2713.2756	2712.2683	2712.2907	-8	1	K.YGIMYAWYFPKDQPAAGNVVGGR.H Oxidation (M) (No match)
124 - 136	1277.7162	1276.7089	1276.6273	64	0	K.DQPAAGNVVGGR.H (No match)

Error: try setting browser cache to automatic.

LOCUS XP_001596857 246 aa linear PLN 26-FEB-2008
 DEFINITION hypothetical protein SS1G_03080 [Sclerotinia sclerotiorum 1980].
 ACCESSION XP_001596857
 VERSION XP_001596857.1 GI:156061869
 DBSOURCE REFSEQ: accession XM_001596807.1
 KEYWORDS .
 SOURCE Sclerotinia sclerotiorum 1980 UF-70
 ORGANISM Sclerotinia sclerotiorum 1980 UF-70
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Leotiomycetes;
 Helotiales; Sclerotiniaceae; Sclerotinia.
 REFERENCE 1 (residues 1 to 246)
 AUTHORS Birren,B., Galagan,J., Lander,E., Devon,K., Nusbaum,C., Cuomo,C.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Yandava,C., Kodira,C.,
 Zeng,Q., Alvarado,L., O'Leary,S., Dickman,M.B., Kohn,L. and
 Rollins,J.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Sclerotinia sclerotiorum 1980 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 246)
 AUTHORS Lander,E., Birren,B. and Cuomo,C.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (10-JUN-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02142, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from ED000220.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..246
 /organism="Sclerotinia sclerotiorum 1980 UF-70"
 /strain="1980"

Protein	/db_xref="taxon:665079" 1..246 /product="hypothetical protein" /calculated_mol_wt=26594
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CDS	1..246 /locus_tag="SS1G_03080" /coded_by="XM_001596807.1:1..741" /db_xref="GeneID:5492677"

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

Spot S10

Mascot Search Results

Protein View

Match to: [gi|189196154](#) Score: **302** Expect: **4.1e-025**

NADP-specific glutamate dehydrogenase [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **49094**; Calculated pI value: **5.88**

NCBI BLAST search of [gi|189196154](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187980294](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

1 MSEPEFEQAR **KELVSTLEAS SLFSK**NPEYK KALEVVSVP E RIIQFRVWE
51 NDKGECQVQK GYR**VQFNSAL GPYK**GGLRFH **PTVNLSILKF LGFEQIFK**NA
101 LTGLNMGGGK GGCDFDPKGK SDNEIRKFCV AFMRELNK**HI GADTDVPAGD**
151 **IGVGGR**EIGY LFGAYRAER**N RWEGVLTGKG GSWGGS**LIRP **EATGYGLVYY**
201 **VEHMINYASG GKESFAGKRV ALSGSGNVAQ YAALK**IIELG GTVISLSDSK
251 GALIAEDDKG FTPEIINQIA ALKLERKALT ALENHNFKYI EGARPWKEVN
301 KVDVALPSAT QNEVSEDEAK ALIESGAKYI AEGSNMGCTQ EAIEVFEAHR
351 REKKGDAIWY APGK**AANAGG VAVSGLEMAQ NSQR**LSWTAE QVDEKLKGIM
401 KDCFENCLST AKEYFTPAEG EFPSLVGGAN VAGFRKVAAA MHDQGDWW

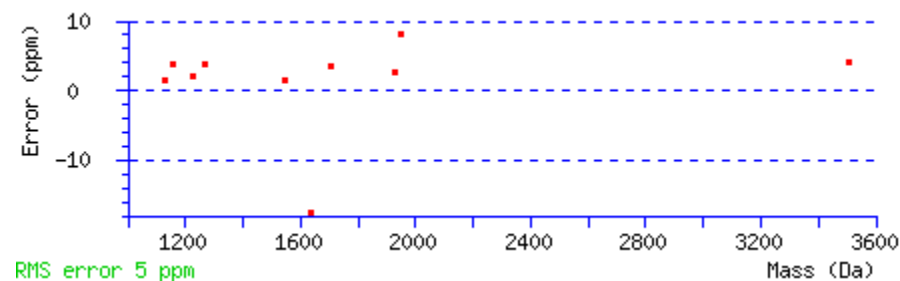
Show predicted peptides also

Sort Peptides By

☒ Residue Number
 ☐ Increasing Mass
 ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
11 - 25	1638.8660	1637.8587	1637.8876	-18	1	R.KELVSTLEASSLFSK.N (No match)
64 - 74	1223.6444	1222.6371	1222.6346	2	0	R.VQFNSALGPYK.G (No match)
79 - 89	1268.7410	1267.7337	1267.7289	4	0	R.FHPTVNLSILK.F (Ions score 73)
79 - 89	1268.7410	1267.7337	1267.7289	4	0	R.FHPTVNLSILK.F (No match)
90 - 98	1128.6104	1127.6031	1127.6015	1	0	K.FLGFEQIFK.N (Ions score 34)
90 - 98	1128.6104	1127.6031	1127.6015	1	0	K.FLGFEQIFK.N (No match)
139 - 156	1706.8516	1705.8443	1705.8384	3	0	K.HIGADTDVPAGDIGVGGR.E (Ions score 114)

139 - 156	1706.8516	1705.8443	1705.8384	3	0	K.HIGADTDVPAGDIGVGGR.E	(No match)
170 - 179	1159.6262	1158.6189	1158.6145	4	1	R.NRWEGLTGK.G	(Ions score 33)
170 - 179	1159.6262	1158.6189	1158.6145	4	1	R.NRWEGLTGK.G	(No match)
180 - 212	3505.6985	3504.6912	3504.6772	4	0	K.GGSWGGSLIRPEATGYGLVYYVEHMINYASGGK.E	Oxidation (M) (No match)
220 - 235	1548.8401	1547.8328	1547.8307	1	0	R.VALSGSGNVAQYAALK.I	(No match)
365 - 384	1930.9451	1929.9378	1929.9326	3	0	K.AANAGGVAVSGLEMAQNSQR.L	(No match)
365 - 384	1946.9508	1945.9435	1945.9276	8	0	K.AANAGGVAVSGLEMAQNSQR.L	Oxidation (M) (No match)



LOCUS XP_001934415 448 aa linear PLN 30-MAY-2008
 DEFINITION NADP-specific glutamate dehydrogenase [Pyrenophora tritici-repentis Pt-1C-BFP].
 ACCESSION XP_001934415
 VERSION XP_001934415.1 GI:189196154
 DBSOURCE REFSEQ: accession XM_001934380.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 448)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C., Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L., Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Genome Sequence of Pyrenophora tritici-repentis
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 448)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,

DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.

CONSRTM The Broad Institute Genome Sequencing Platform

TITLE Direct Submission

JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7
 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from EDU46920.
 Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..448
 /organism="Pyrenophora tritici-repentis Pt-1C-BFP"
 /strain="Pt-1C-BFP"
 /db_xref="taxon:426418"

Protein 1..448
 /product="NADP-specific glutamate dehydrogenase"
 /calculated_mol_wt=48651

Region 3..445
 /region_name="PRK09414"
 /note="glutamate dehydrogenase; Provisional; PRK09414"
 /db_xref="CDD:169848"

Region 39..166
 /region_name="ELFV_dehydrog_N"
 /note="Glu/Leu/Phe/Val dehydrogenase, dimerization domain;
 pfam02812"
 /db_xref="CDD:145786"

Region 177..446
 /region_name="NAD_bind_2_Glu_DH"
 /note="NAD(P) binding domain of glutamate dehydrogenase,
 subgroup 2; cd05313"
 /db_xref="CDD:133455"

Site order(226..228,248..249,309..310,333..335)
 /site_type="other"
 /note="NAD(P) binding site"
 /db_xref="CDD:133455"

CDS 1..448
 /locus_tag="PTRG_04082"
 /coded_by="XM_001934380.1:1..1347"
 /db_xref="GeneID:6342318"

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

Spot S11

MASCOT Mascot Search Results

Protein View

Match to: **gi|171677093** Score: **80** Expect: **0.0072**
unnamed protein product [Podospora anserina]

Nominal mass (M_r): **43049**; Calculated pI value: **8.26**

NCBI BLAST search of [gi|171677093](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Podospora anserina DSM 980](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|170936614](#) from [Podospora anserina](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```

1 MSLKVPQYVF GITEAFKADT FDKKINLGVG AYRDDAGKPY VLPSVRQAE
51 KVIASRLNKE YAGITGVPEF TKAAAVLAYG KDSPALDRVA ITQSISGTGA
101 LRIGGAFLAR FFPGAKTIYI PQPSWANHAA VFKDSGLAVE KYAYYNKETI
151 GLDFEGMIAD INKAPNGSIF LFHACAHNPT GVDPTPEQWK EIEAAVKAKG
201 HYSFFDMAYQ GFASGDIHKD AFAVRHFVAQ GHNVALSQSF AKNMGLYGER
251 IGAFSIVCEN AEEKKRVDSQ IKILVRPMYS NPPIHGARIA AEILNTPALY
301 DQWLVEVKEM ADRIITMRAL LKENLEKLGS KHDWSHITSQ IGMFAYTGLS
351 PEQMDALAKE HSYVATRDGR ISVAGITTGN VGRLEAEIFK VTG

```

Show predicted peptides also

Sort Peptides By



Residue Number

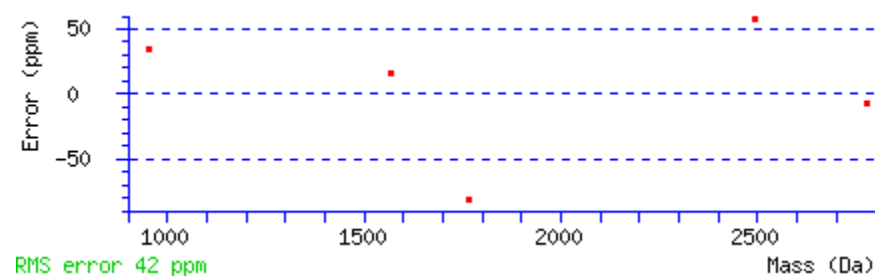


Increasing Mass



Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
57	72	1766.7885	1765.7812	1765.9250	-81	1	R.LNKEYAGITGVPEFTK.A (No match)
198	219	2493.2739	2492.2666	2492.1219	58	1	K.AKGHYSFFDMAYQGFASGDIHK.D Oxidation (M) (No match)
226	250	2777.3384	2776.3311	2776.3504	-7	1	R.HFVAQGHNVALSQSFAKNMGLYGER.I Oxidation (M) (No match)
226	250	2777.3384	2776.3311	2776.3504	-7	1	R.HFVAQGHNVALSQSFAKNMGLYGER.I Oxidation (M) (No match)
243	250	955.4633	954.4560	954.4229	35	0	K.NMGLYGER.I Oxidation (M) (Ions score 54)
243	250	955.4633	954.4560	954.4229	35	0	K.NMGLYGER.I Oxidation (M) (No match)
251	264	1566.7706	1565.7633	1565.7395	15	0	R.IGAFSIVCENAEK.K (No match)



LOCUS XP_001903498 393 aa linear PLN 05-MAY-2010
 DEFINITION hypothetical protein [Podospora anserina S mat+].
 ACCESSION XP_001903498
 VERSION XP_001903498.1 GI:171677093
 DBSOURCE REFSEQ: accession XM_001903463.1
 KEYWORDS .
 SOURCE Podospora anserina S mat+
 ORGANISM Podospora anserina S mat+
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
 REFERENCE 1 (residues 1 to 393)
 AUTHORS Eric,Espagne., Olivier,Lespinet., Fabienne,Malagnac., Corinne
 Da,Silva., Olivier,Jaillon., Betina,M.Porcel., Arnaud,Couloux.,
 Beatrice,Segurens., Julie,Poulain., Veronique,Anthouard.,
 Sandrine,Grossetete., Hamid,Khalili., Evelyne,Coppin.,
 Michelle,Dequard.-Chablat., Marguerite,Picard.,
 Veronique,Contamine., Sylvie,Arnaise., Anne,Bourdais.,
 Veronique,Berteaux.-Lecellier., Daniel,Gautheret.,
 Ronald,Pde.Vries., Evy,Battaglia., Pedro,M.Coutinho.,
 Etienne,G.J.Danchin., Bernard,Henrissat., Riyad El,Khoury.,
 Annie,Sainsard.-Chanet., Antoine,Boivin.,
 Berangere,Pinan.-Lucarre., Carole,H.Sellem., Robert,Debuchy.,
 Patrick,Wincker., Jean,Weissenbach. and Philippe,Silar.
 TITLE The Genome Sequence of the Model Ascomycete Fungus Podospora
 anserina
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 393)
 AUTHORS Genoscope -,C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (25-MAR-2008) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from CAP61273.

FEATURES	Location/Qualifiers
source	1..393 /organism="Podospira anserina S mat+" /db_xref="taxon:515849" /chromosome="3"
Protein	1..393 /product="hypothetical protein" /calculated_mol_wt=42831
Region	25..390 /region_name="AAT_like" /note="Aspartate aminotransferase family. This family belongs to pyridoxal phosphate (PLP)-dependent aspartate aminotransferase superfamily (fold I). Pyridoxal phosphate combines with an alpha-amino acid to form a compound called a Schiff base or aldimine...; cd00609" /db_xref="CDD:99734"
Site	order(96..98,125,178,209,239,241..242,250) /site_type="other" /note="pyridoxal 5'-phosphate binding site" /db_xref="CDD:99734"
Site	order(99,135,202,248..250,286,289) /site_type="other" /note="homodimer interface" /db_xref="CDD:99734"
Site	242 /site_type="other" /note="catalytic residue" /db_xref="CDD:99734"
CDS	1..393 /locus_tag="PODANSg513" /coded_by="XM_001903463.1:1..1182" /note="Predicted CDS Pa_3_11290" /db_xref="GeneID:6187631"

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

Spot 1

MASCOT Mascot Search Results

Protein View

Match to: [gi|238498522](#) Score: **251** Expect: **7.9e-019**
phosphoglycerate kinase PgkA, putative [Aspergillus flavus NRRL3357]

Nominal mass (M_r): **44399**; Calculated pI value: **7.66**

NCBI BLAST search of [gi|238498522](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus flavus NRRL3357](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|220693770](#) from [Aspergillus flavus NRRL3357](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

1 MSLSNK**LAIT** DVDLDKRVL IRVDFNVPLD **ADKKITNNQR** **IVGALPTIKY**
 51 AIENGAK**AVV** **LMSHLGRPDG** KANPKYSLKP VATELEKLLS KSVIFAENCV
 101 GKETEEIVNK **ATGGQVILE** **NLRFHAE**EEG SSKDAEGKKV KADKEKVEEF
 151 RKGLTALGDV YINDAFGTAH RAHSSMVGVD LPQKASGFLV **KKELEYFAKA**
 201 LESPQRPFLA ILGGAKVSDK IQLIDNLLPK **VNSLIITGAM** **AFTFKK**TLEN
 251 VKIGNSLFDE AGSK**IVGDIV** **EKAK**KNNVKI VLPVDYVTAD KFAADAKTGY
 301 ATDADGIPDG YMGLDVGEKS VELYKKTIAE AKTILWNGPP GVFELEPFAN
 351 ATKKTLDAAV AAAQSGSIVI IGGDTATVA AKYGAEAK**LS** **HVSTGGGASL**
 401 **ELLEGVLP****G** **VDALSSK**

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
7 - 15	987.5745	986.5672	986.5648	2	0	K.LAITDVDLK.D	(No match)
23 - 33	1232.6282	1231.6209	1231.6085	10	0	R.VDFNVPLDADK.K	(No match)
23 - 33	1232.6282	1231.6209	1231.6085	10	0	R.VDFNVPLDADK.K	(No match)
34 - 40	873.4912	872.4839	872.4828	1	1	K.KITNNQR.I	(No match)
41 - 49	911.5909	910.5836	910.5851	-2	0	R.IVGALPTIK.Y	(No match)

58 - 71	1479.8085	1478.8012	1478.8028	-1	0	K.AVVLMShLGRPDGK.A	(Ions score 91)
58 - 71	1479.8085	1478.8012	1478.8028	-1	0	K.AVVLMShLGRPDGK.A	(No match)
58 - 71	1495.8011	1494.7938	1494.7977	-3	0	K.AVVLMShLGRPDGK.A	Oxidation (M) (Ions score 38)
58 - 71	1495.8011	1494.7938	1494.7977	-3	0	K.AVVLMShLGRPDGK.A	Oxidation (M) (No match)
111 - 123	1383.8152	1382.8079	1382.7881	14	0	K.ATGGQVILLENLR.F	(Ions score 91)
111 - 123	1383.8152	1382.8079	1382.7881	14	0	K.ATGGQVILLENLR.F	(No match)
192 - 199	1027.5510	1026.5437	1026.5386	5	1	K.KELEYFAK.A	(No match)
193 - 199	899.4527	898.4454	898.4436	2	0	K.ELEYFAK.A	(No match)
231 - 246	1756.9224	1755.9151	1755.9593	-25	1	K.VNSLIITGAMAFKK.T	Oxidation (M) (No match)
265 - 274	1071.5603	1070.5530	1070.6335	-75	1	K.IVGDIWEKAK.K	(No match)
389 - 406	1754.9307	1753.9234	1753.9210	1	0	K.LSHVSTGGGASLELLEK.V	(No match)
407 - 417	1085.5751	1084.5678	1084.6128	-41	0	K.VLPGVDALSSK.-	(No match)

Error: try setting browser cache to automatic.

LOCUS XP_002380496 417 aa linear PLN 19-JAN-2010
 DEFINITION phosphoglycerate kinase PgkA, putative [Aspergillus flavus NRRL3357].
 ACCESSION XP_002380496
 VERSION XP_002380496.1 GI:238498522
 DBSOURCE REFSEQ: accession XM_002380455.1
 KEYWORDS .
 SOURCE Aspergillus flavus NRRL3357
 ORGANISM Aspergillus flavus NRRL3357
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (residues 1 to 417)
 AUTHORS Nierman,W.C.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-2007) J. Craig Venter Institute, 9704 Medical
 Center Drive, Rockville, MD 20850, USA
 REFERENCE 2 (residues 1 to 417)
 AUTHORS Nierman,W.C.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUN-2005) The Institute for Genomic Research, 9712
 Medical Center Drive, Rockville, MD 20850, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from
mrna.AFLA_069370A.
Method: conceptual translation.

FEATURES Location/Qualifiers

source	1..417 /organism="Aspergillus flavus NRRL3357" /strain="NRRL3357" /db_xref="taxon:332952"
Protein	1..417 /product="phosphoglycerate kinase PgkA, putative" /EC_number="2.7.2.3" /calculated_mol_wt=44238
Region	9..416 /region_name="Phosphoglycerate_kinase" /note="Phosphoglycerate kinase (PGK) is a monomeric enzyme which catalyzes the transfer of the high-energy phosphate group of 1,3-bisphosphoglycerate to ADP, forming ATP and 3-phosphoglycerate. This reaction represents the first of the two substrate-level...; cd00318" /db_xref="CDD:29400"
Site	order(24,26,40,64,123) /site_type="other" /note="substrate binding site" /db_xref="CDD:29400"
Site	order(201..204,392..394) /site_type="other" /note="hinge regions" /db_xref="CDD:29400"
Site	order(239,313,337,339,341..344,374..376) /site_type="other" /note="ADP binding site" /db_xref="CDD:29400"
Site	375 /site_type="other" /note="catalytic site" /db_xref="CDD:29400"
CDS	1..417 /locus_tag="AFLA_069370" /coded_by="XM_002380455.1:1..1254" /note="encoded by transcript AFLA_069370A" /db_xref="GeneID:7910479"

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

Spot 2

MASCOT Mascot Search Results

Protein View

Match to: [gi|67903236](#) Score: **219** Expect: **1.3e-015**
hypothetical protein AN8605.2 [Aspergillus nidulans FGSC A4]

Nominal mass (M_r): **17787**; Calculated pI value: **8.86**

NCBI BLAST search of [gi|67903236](#) against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus nidulans FGSC A4](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|40741449](#) from [Aspergillus nidulans FGSC A4](#)

[gi|259483180](#) from [Aspergillus nidulans FGSC A4](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**

1 MSNVFFDITA NGEPLGRVEF KLFDDVVPK ARNFRELATG QHGFYKKGSP
51 FHRVIPQFML QGGDFTRQNG TGGK**SIYGEK FEDENFTLKH** DRPYLLSMAN
101 AGRNTNGSQF FITTVKTSWL DGAHVVFGEV VKQGEVVDAV EKLGSQSGAT
151 KKKVVISNSG TL

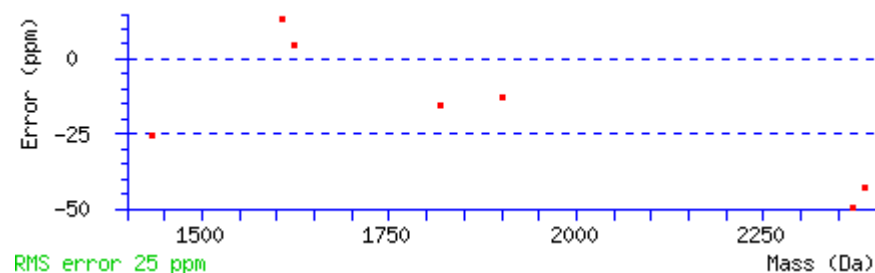
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 21	2371.0571	2370.0498	2370.1678	-50	1	-.MSNVFFDITANGEPLGRVEFK.L (No match)
1 - 21	2387.0676	2386.0603	2386.1627	-43	1	-.MSNVFFDITANGEPLGRVEFK.L Oxidation (M) (No match)
18 - 29	1435.7466	1434.7393	1434.7759	-25	1	R.VEFKLFDDVVPK.T (Ions score 53)
18 - 29	1435.7466	1434.7393	1434.7759	-25	1	R.VEFKLFDDVVPK.T (No match)
54 - 67	1608.8413	1607.8340	1607.8130	13	0	R.VIPQFMLQGGDFTR.Q (Ions score 128)
54 - 67	1608.8413	1607.8340	1607.8130	13	0	R.VIPQFMLQGGDFTR.Q (No match)
54 - 67	1624.8225	1623.8152	1623.8079	4	0	R.VIPQFMLQGGDFTR.Q Oxidation (M) (Ions score 55)
54 - 67	1624.8225	1623.8152	1623.8079	4	0	R.VIPQFMLQGGDFTR.Q Oxidation (M) (No match)
75 - 89	1819.8466	1818.8393	1818.8676	-16	1	K.SIYGEKFEDENFTLK.H (No match)

133 - 151 1902.9520 1901.9447 1901.9694 -13 1 K.GQEVVDAVEKLGSGGATK.K (No match)



LOCUS XP_681874 162 aa linear PLN 09-APR-2008
 DEFINITION hypothetical protein AN8605.2 [Aspergillus nidulans FGSC A4].
 ACCESSION XP_681874
 VERSION XP_681874.1 GI:67903236
 DBSOURCE REFSEQ: accession XM_676782.1
 KEYWORDS .
 SOURCE Aspergillus nidulans FGSC A4
 ORGANISM Aspergillus nidulans FGSC A4
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; Emericella.
 REFERENCE 1 (residues 1 to 162)
 AUTHORS Galagan, J.E., Calvo, S.E., Cuomo, C., Ma, L.J., Wortman, J.R.,
 Batzoglou, S., Lee, S.I., Basturkmen, M., Spevak, C.C., Clutterbuck, J.,
 Kapitonov, V., Jurka, J., Scazzocchio, C., Farman, M., Butler, J.,
 Purcell, S., Harris, S., Braus, G.H., Draht, O., Busch, S., D'Enfert, C.,
 Bouchier, C., Goldman, G.H., Bell-Pedersen, D., Griffiths-Jones, S.,
 Doonan, J.H., Yu, J., Vienken, K., Pain, A., Freitag, M., Selker, E.U.,
 Archer, D.B., Penalva, M.A., Oakley, B.R., Momany, M., Tanaka, T.,
 Kumagai, T., Asai, K., Machida, M., Nierman, W.C., Denning, D.W.,
 Caddick, M., Hynes, M., Paoletti, M., Fischer, R., Miller, B., Dyer, P.,
 Sachs, M.S., Osmani, S.A. and Birren, B.W.
 TITLE Sequencing of Aspergillus nidulans and comparative analysis with A.
 fumigatus and A. oryzae
 JOURNAL Nature 438 (7071), 1105-1115 (2005)
 PUBMED 16372000
 REFERENCE 2 (residues 1 to 162)
 AUTHORS Birren, B., Nusbaum, C., Abebe, A., Abouelleil, A., Adekoya, E.,
 Ait-zahra, M., Allen, N., Allen, T., An, P., Anderson, M., Anderson, S.,
 Arachchi, H., Armbruster, J., Bachantsang, P., Baldwin, J., Barry, A.,
 Bayul, T., Blitshsteyn, B., Bloom, T., Blye, J., Boguslavskiy, L.,
 Borowsky, M., Boukhgalter, B., Brunache, A., Butler, J., Calixte, N.,
 Calvo, S., Camarata, J., Campo, K., Chang, J., Cheshatsang, Y.,

Citroen,M., Collymore,A., Considine,T., Cook,A., Cooke,P.,
 Corum,B., Cuomo,C., David,R., Dawoe,T., Degray,S., Dodge,S.,
 Dooley,K., Dorje,P., Dorjee,K., Dorris,L., Duffey,N., Dupes,A.,
 Elkins,T., Engels,R., Erickson,J., Farina,A., Faro,S., Ferreira,P.,
 Fischer,H., Fitzgerald,M., Foley,K., Gage,D., Galagan,J.,
 Gearin,G., Gnerre,S., Gnirke,A., Goyette,A., Graham,J.,
 Grandbois,E., Gyaltsen,K., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Hatcher,B., Heller,A., Higgins,H., Honan,T., Horn,A.,
 Houde,N., Hughes,L., Hulme,W., Husby,E., Iliev,I., Jaffe,D.,
 Jones,C., Kamal,M., Kamat,A., Kamvysselis,M., Karlsson,E.,
 Kells,C., Kieu,A., Kisner,P., Kodira,C., Kulbokas,E., Labutti,K.,
 Lama,D., Landers,T., Leger,J., Levine,S., Lewis,D., Lewis,T.,
 Lindblad-toh,K., Liu,X., Lokyitsang,T., Lokyitsang,Y., Lucien,O.,
 Lui,A., Ma,L.J., Mabbitt,R., Macdonald,J., Maclean,C., Major,J.,
 Manning,J., Marabella,R., Maru,K., Matthews,C., Mauceli,E.,
 Mccarthy,M., Mcdonough,S., Mcghee,T., Meldrim,J., Meneus,L.,
 Mesirov,J., Mihalev,A., Mihova,T., Mikkelsen,T., Mlenga,V.,
 Moru,K., Mozes,J., Mulrain,L., Munson,G., Naylor,J., Neues,C.,
 Nguyen,C., Nguyen,N., Nguyen,T., Nicol,R., Nielsen,C., Nizzari,M.,
 Norbu,C., Norbu,N., O'donnell,P., Okoawo,O., O'leary,S.,
 Omotosho,B., O'Neill,K., Osman,S., Parker,S., Perrin,D.,
 Phunkhang,P., Piqani,B., Purcell,S., Rachupka,T., Ramasamy,U.,
 Rameau,R., Ray,V., Raymond,C., Retta,R., Richardson,S., Rise,C.,
 Rodriguez,J., Rogers,J., Rogov,P., Rutman,M., Schupbach,R.,
 Seaman,C., Settipalli,S., Sharpe,T., Sheridan,J., Sherpa,N.,
 Shi,J., Smirnov,S., Smith,C., Sougnez,C., Spencer,B., Stalker,J.,
 Stange-thomann,N., Stavropoulos,S., Stetson,K., Stone,C., Stone,S.,
 Stubbs,M., Talamas,J., Tchinga,P., Tenzing,P., Tesfaye,S.,
 Theodore,J., Thoulutsang,Y., Topham,K., Towey,S., Tsamla,T.,
 Tsomo,N., Vallee,D., Vassiliev,H., Venkataraman,V., Vinson,J.,
 Vo,A., Wade,C., Wang,S., Wangchuk,T., Wangdi,T., Whittaker,C.,
 Wilkinson,J., Wu,Y., Wyman,D., Yadav,S., Yang,S., Yang,X.,
 Yeager,S., Yee,E., Young,G., Zainoun,J., Zembeck,L., Zimmer,A.,
 Zody,M. and Lander,E.

TITLE	Direct Submission
JOURNAL	Submitted (26-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02142, USA
COMMENT	PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EAA60639. Method: conceptual translation.
FEATURES	Location/Qualifiers
source	1..162 /organism="Aspergillus nidulans FGSC A4" /strain="FGSC A4" /db_xref="taxon:227321" /chromosome="III"
Protein	1..162

Region	<pre>/product="hypothetical protein" /calculated_mol_wt=17667 2..160 /region_name="cyclophilin_ABH_like" /note="cyclophilin_ABH_like: Cyclophilin A, B and H-like cyclophilin-type peptidylprolyl cis- trans isomerase (PPIase) domain. This family represents the archetypal cystolic cyclophilin similar to human cyclophilins A, B and H. PPIase is an enzyme which...; cd01926" /db_xref="CDD:29397"</pre>
Site	<pre>order(52..53,58,109,111,119) /site_type="active" /db_xref="CDD:29397"</pre>
CDS	<pre>1..162 /locus_tag="AN8605.2" /coded_by="XM_676782.1:1..489" /db_xref="GeneID:2868486"</pre>

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

Spot 3

Mascot Search Results

Protein View

Match to: [gi|169601412](#) Score: **595** Expect: **3.2e-053**
hypothetical protein SNOG_03571 [Phaeosphaeria nodorum SN15]

Nominal mass (M_r): **47405**; Calculated pI value: **5.20**
 NCBI BLAST search of [gi|169601412](#) against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Phaeosphaeria nodorum SN15](#)
 Links to retrieve other entries containing this sequence from NCBI Entrez:
[gi|111067656](#) from [Phaeosphaeria nodorum SN15](#)

Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

1 MAITKIHARS VYDSR**GNPTV EVDIVTETGL HRAIVPSGAS TGSHEACELR**
 51 **DGDK**TKWGGK GVTKAVANVN DTIAPALIKE AIDVKDQSAV DAFLNKLDGT
 101 KNKEKLGANA ILGVSMIAK AAAAEK**GVPL YAHISDLAGT KKPYPVLPVPF**
 151 **QNVLNGGSHA GGR**LAFQEFM IVPSEAPTFS EAMRQGAEVY QKLKSLAKKR
 201 YGQSAGNVGD EGGVAPDIQT PEEALDLITD AIEEAGYTGK IK**IAMDVASS**
 251 **EFYK**TEEK**KY DLDFK**NPDS KSKWLSYEQ L AELYKSLAQK YPIVSIEDPF
 301 AEDDWEAWSY FFK**TSD**FQIV **GDDL**TVTNPE **FIKK**AIELKS CNALLKVNQ
 351 IGTITEAIQA AKDAFGAGWG VMVSHR**SGET EDVTIADIVV GLR**AGQIKTG
 401 APARSERLAK LNQILRIEEE LGDNAIYAGQ NFRTAINL

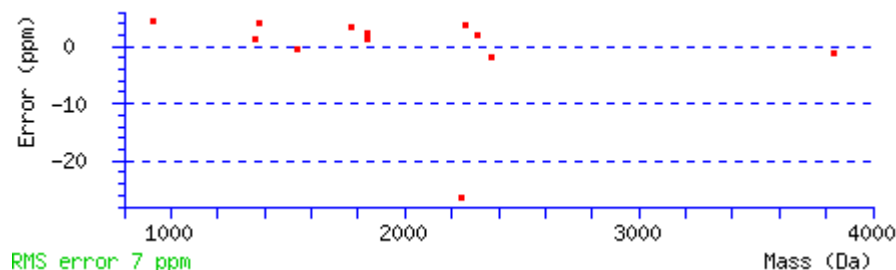
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
16 - 32	1836.9496	1835.9423	1835.9378	2	0	R.GNPTVEVDIVTETGLHR.A (Ions score 124)
16 - 32	1836.9496	1835.9423	1835.9378	2	0	R.GNPTVEVDIVTETGLHR.A (No match)
33 - 50	1841.8832	1840.8759	1840.8737	1	0	R.AIVPSGASTGSHEACELR.D (No match)
33 - 54	2257.0601	2256.0528	2256.0441	4	1	R.AIVPSGASTGSHEACELRDGDK.T (No match)
127 - 141	1541.8315	1540.8242	1540.8249	-0	0	K.GVPLYAHISDLAGTK.K (Ions score 90)

127 - 141	1541.8315	1540.8242	1540.8249	-0	0	K.GVPLYAHISDLAGTK.K	(No match)
127 - 163	3830.0461	3829.0388	3829.0428	-1	1	K.GVPLYAHISDLAGTKKPYVLPVPFQNVNLGGSHAGGR.L	(No match)
142 - 163	2307.2405	2306.2332	2306.2284	2	0	K.KPYVLPVPFQNVNLGGSHAGGR.L	(Ions score 145)
142 - 163	2307.2405	2306.2332	2306.2284	2	0	K.KPYVLPVPFQNVNLGGSHAGGR.L	(No match)
243 - 254	1360.6470	1359.6397	1359.6380	1	0	K.IAMDVASSEFYK.T	(No match)
243 - 254	1376.6459	1375.6386	1375.6329	4	0	K.IAMDVASSEFYK.T	Oxidation (M) (No match)
259 - 265	928.4814	927.4741	927.4702	4	1	K.KYDLDFK.N	(No match)
314 - 333	2239.0540	2238.0467	2238.1056	-26	0	K.TSDFQIVGDDLTVTNPEFIK.K	(No match)
314 - 334	2367.2034	2366.1961	2366.2006	-2	1	K.TSDFQIVGDDLTVTNPEFIKK.A	(No match)
377 - 393	1773.9287	1772.9214	1772.9156	3	0	R.SGETEDVTIADIVVGLR.A	(Ions score 159)
377 - 393	1773.9287	1772.9214	1772.9156	3	0	R.SGETEDVTIADIVVGLR.A	(No match)



LOCUS XP_001794128 438 aa linear PLN 02-APR-2008
 DEFINITION hypothetical protein SNOG_03571 [Phaeosphaeria nodorum SN15].
 ACCESSION XP_001794128
 VERSION XP_001794128.1 GI:169601412
 DBSOURCE REFSEQ: accession XM_001794076.1
 KEYWORDS .
 SOURCE Phaeosphaeria nodorum SN15
 ORGANISM Phaeosphaeria nodorum SN15
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Phaeosphaeriaceae;
 Phaeosphaeria.
 REFERENCE 1 (residues 1 to 438)
 AUTHORS Birren,B., Lander,E., Galagan,J., Devon,K., Nusbaum,C., Jaffe,D.,
 Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Zeng,Q.,
 Yandava,C., Alvarado,L., Oleary,S., Oliver,R.O. and Solomon,P.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Phaeosphaeria nodorum SN15 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 438)

AUTHORS Lander,E. and Birren,B.
CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2008) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
REMARK Direct Submission
REFERENCE 3 (residues 1 to 438)
AUTHORS Oliver,R. and Solomon,P.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2008) Murdoch University, South Street, Perth, WA
6150, Australia
REMARK Direct Submission
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EAT88776.
Method: conceptual translation.
FEATURES
 Location/Qualifiers
 source 1..438
 /organism="Phaeosphaeria nodorum SN15"
 /db_xref="taxon:321614"
 Protein 1..438
 /product="hypothetical protein"
 /calculated_mol_wt=47190
 Region 1..431
 /region_name="PTZ00081"
 /note="enolase (2-phospho-D-glycerate hydrolase);
 Provisional; PTZ00081"
 /db_xref="CDD:173375"
 Region 5..420
 /region_name="enolase"
 /note="Enolase: Enolases are homodimeric enzymes that
 catalyse the reversible dehydration of
 2-phospho-D-glycerate to phosphoenolpyruvate as part of
 the glycolytic and gluconeogenesis pathways. The reaction
 is facilitated by the presence of metal ions; cd03313"
 /db_xref="CDD:48188"
 Site order(7,9..17,21,32,160..162,183..184,187..188,191..192,
 207..208,215,217,379..381,404..406,408..409,412,415..416,
 419)
 /site_type="other"
 /note="dimer interface"
 /db_xref="CDD:48188"
 Site order(40,246,297,322)
 /site_type="metal-binding"
 /db_xref="CDD:48188"
 Site order(159,211,347,375..377,398)
 /site_type="other"
 /note="substrate binding pocket"

CDS

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/coded_by="XM_001794076.1:36..1352"  
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/inference="similar to RNA sequence, EST (same  
species):INSO:DR045144.1"  
/inference="similar to RNA sequence, EST (same  
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species):INSO:EH387450.1"  
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species):INSO:EH400989.1"  
/note="gene prediction version 2"  
/db_xref="GeneID:5970991"
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Mascot: <http://www.matrixscience.com/>

Spot 4

MASCOT Mascot Search Results

Protein View

Match to: **gi|198425409** Score: **88** Expect: **0.015**

PREDICTED: Zn-finger (U1-like)-10 isoform 1 [Ciona intestinalis]

Nominal mass (M_r): **22597**; Calculated pI value: **9.48**

NCBI BLAST search of **gi|198425409** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Ciona intestinalis](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **54%**

Matched peptides shown in **Bold Red**

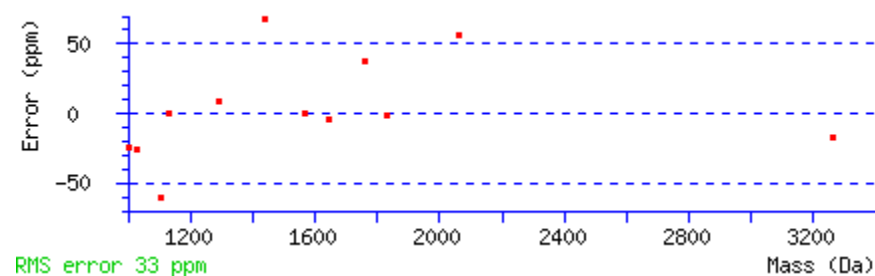
1 MAGRGRGRGW LSK**FESQSKE MKPFEQKTNP VEQK**SNNSNG FMEK**NSTLSK**
51 **LM**AKYNYKAN **PNSPAGFK**EL SIRQSEELFL LSEHKEQPHW WLVRNKAGEE
101 GYSPK**SYLMK METKVASLPW LENK**KTVEIN TKVVPHTVAP KKYVSAYKEN
151 QGK**SDIQWHC DVCNKSFN**GP **HPYN**SHMVSK **AHREEVEVAQ** LYGRM

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
14 - 27	1758.9020	1757.8947	1757.8294	37	1	K.FESQSK EMKPFEQK.T Oxidation (M) (No match)
20 - 34	1832.9186	1831.9113	1831.9138	-1	1	K.EMKPFEQK TNPVEQK.S (No match)
45 - 54	1108.5361	1107.5288	1107.5958	-60	1	K.NSTLSKL MAK.Y Oxidation (M) (No match)
51 - 58	1030.5126	1029.5053	1029.5317	-26	1	K.L MAK YNYK.A (No match)
51 - 58	1030.5126	1029.5053	1029.5317	-26	1	K.L MAK YNYK.A (No match)
55 - 68	1570.7637	1569.7564	1569.7576	-1	1	K.YNYKAN PNSPAGFK.E (No match)
59 - 68	1002.4763	1001.4690	1001.4930	-24	0	K.ANPNS PAGFK.E (No match)
106 - 114	1130.5592	1129.5519	1129.5511	1	1	K.SYLM KMETK.V (No match)
111 - 124	1645.8542	1644.8469	1644.8545	-5	1	K.METK VASLPWLENK.K (No match)
154 - 180	3260.3545	3259.3472	3259.4022	-17	1	K.SDIQ WHCDVCNKSFN GPHYPYNSHMVSK.A Oxidation (M) (No match)
166 - 183	2066.0923	2065.0850	2064.9700	56	1	K.SFN GPHYPYN SHMVSKAHR.E (No match)
184 - 194	1292.6592	1291.6519	1291.6408	9	0	R.EEVEVAQ LYGR.M (No match)
184 - 195	1439.7808	1438.7735	1438.6762	68	1	R.EEVEVAQ LYGRM.- Oxidation (M) (No match)



LOCUS XP_002130942 195 aa linear INV 09-SEP-2008
 DEFINITION PREDICTED: Zn-finger (U1-like)-10 isoform 1 [*Ciona intestinalis*].
 ACCESSION XP_002130942
 VERSION XP_002130942.1 GI:198425409
 DBSOURCE REFSEQ: accession XM_002130906.1
 KEYWORDS .
 SOURCE *Ciona intestinalis*
 ORGANISM *Ciona intestinalis*
 Eukaryota; Metazoa; Chordata; Tunicata; Ascidiacea; Enterogona;
 Phlebobranchia; Cionidae; *Ciona*.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational
 analysis. This record is derived from a genomic sequence
 (NW_001955313) annotated using gene prediction method: GNOMON,
 supported by mRNA and EST evidence.
 Also see:
 Documentation of NCBI's Annotation Process
 COMPLETENESS: full length.
 FEATURES Location/Qualifiers
 source 1..195
 /organism="Ciona intestinalis"
 /db_xref="taxon:7719"
 Protein 1..195
 /product="Zn-finger (U1-like)-10 isoform 1"
 /calculated_mol_wt=22366
 Region 53..108
 /region_name="SH3"
 /note="Src homology 3 domains; SH3 domains bind to
 proline-rich ligands with moderate affinity and
 selectivity, preferentially to PxxP motifs; they play a
 role in the regulation of enzymes by intramolecular
 interactions, changing the subcellular localization...;
 cl09950"
 /db_xref="CDD:158800"
 Region 157..187

CDS

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/region_name="zf-C2H2_jaz"  
/note="Zinc-finger double-stranded RNA-binding; cl09952"  
/db_xref="CDD:158802"  
1..195  
/gene="zf(u1like)-10"  
/coded_by="XM_002130906.1:213..800"  
/db_xref="GeneID:100170048"
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Mascot: <http://www.matrixscience.com/>

Spot 5

MASCOT Mascot Search Results

Protein View

Match to: **gi|156053161** Score: **83** Expect: **0.0036**
hypothetical protein SS1G_06748 [Sclerotinia sclerotiorum 1980]

Nominal mass (M_r): **37910**; Calculated pI value: **8.75**

NCBI BLAST search of [gi|156053161](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Sclerotinia sclerotiorum 1980 UF-70](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|154704526](#) from [Sclerotinia sclerotiorum 1980 UF-70](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

```

1 MFRTLPSAL RTSSRLSQLS SQIQRRSMAS ITTHKLNTGA TIPAIQFGTW
51 QDKDSQEEAV TEALKAGYRH IDTARVYGTE SACGAAIRAS GIPRSELFIT
101 TKLWNNKHKP EDVEPALNES LKDLGLDYVD LYLMHWPSAF KPGDDLFPKV
151 DGKTQTADIS YVNTYKAMEK LIETGKTKAI GISNFSRGEL ENLLKEASIV
201 PAVHQLELHP WLQQTEFCEF NKRKGIHITQ YSPFGNQNEV YDSGKGIGKL
251 MDDPTIVEIG KKYSKSGAQV ALAWGIAHGH SVIPKSKTPS RIKSNLEGDF
301 KLEAEDLKKL DGLDKKLRFN DASASFGYNF YSDLDGKRKN

```

Show predicted peptides also

Sort Peptides By



Residue Number

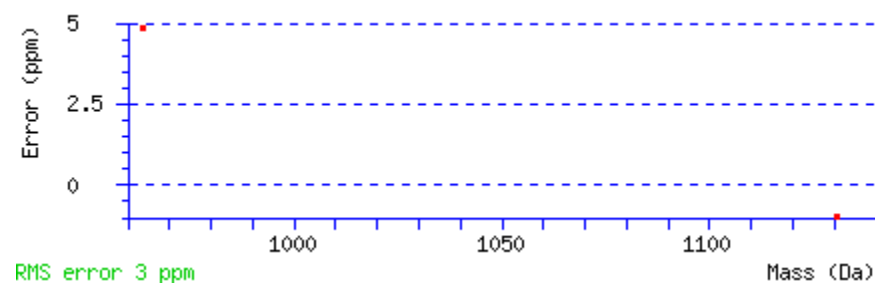


Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
26 - 35	1131.5928	1130.5855	1130.5866	-1	1	R.RSMASITTHK.L	(No match)
179 - 187	964.5257	963.5184	963.5138	5	0	K.AIGISNFSR.G	(Ions score 77)
179 - 187	964.5257	963.5184	963.5138	5	0	K.AIGISNFSR.G	(No match)



LOCUS XP_001592507 340 aa linear PLN 26-FEB-2008
 DEFINITION hypothetical protein SS1G_06748 [Sclerotinia sclerotiorum 1980].
 ACCESSION XP_001592507
 VERSION XP_001592507.1 GI:156053161
 DBSOURCE REFSEQ: accession XM_001592457.1
 KEYWORDS .
 SOURCE Sclerotinia sclerotiorum 1980 UF-70
 ORGANISM Sclerotinia sclerotiorum 1980 UF-70
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Leotiomycetes;
 Helotiales; Sclerotiniaceae; Sclerotinia.
 REFERENCE 1 (residues 1 to 340)
 AUTHORS Birren,B., Galagan,J., Lander,E., Devon,K., Nusbaum,C., Cuomo,C.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Yandava,C., Kodira,C.,
 Zeng,Q., Alvarado,L., O'Leary,S., Dickman,M.B., Kohn,L. and
 Rollins,J.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Sclerotinia sclerotiorum 1980 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 340)
 AUTHORS Lander,E., Birren,B. and Cuomo,C.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (10-JUN-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02142, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from ED004265.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..340
 /organism="Sclerotinia sclerotiorum 1980 UF-70"
 /strain="1980"

Protein	/db_xref="taxon:665079" 1..340 /product="hypothetical protein" /calculated_mol_wt=37689
Region	33..297 /region_name="Aldo_ket_red" /note="Aldo-keto reductases (AKRs) are a superfamily of soluble NAD(P)(H) oxidoreductases whose chief purpose is to reduce aldehydes and ketones to primary and secondary alcohols. AKRs are present in all phyla and are of importance to both health and...; cd06660"
Site	/db_xref="CDD:119408" order(48..50,72,77,102,135..136,183..184,205,231..236,268,283..286,291,294..295) /site_type="active"
Site	/db_xref="CDD:119408" order(72,77,102,135) /site_type="other" /note="catalytic tetrad"
CDS	/db_xref="CDD:119408" 1..340 /locus_tag="SS1G_06748" /coded_by="XM_001592457.1:1..1023" /db_xref="GeneID:5488691"

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

Spot 6

MASCOT Mascot Search Results

Protein View

Match to: [gi|169625443](#) Score: **257** Expect: **2e-019**
 hypothetical protein [SNOG_15994](#) [[Phaeosphaeria nodorum](#) [SN15](#)]

Nominal mass (M_r): **27112**; Calculated pI value: **6.14**

NCBI BLAST search of [gi|169625443](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Phaeosphaeria nodorum](#) [SN15](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|111055453](#) from [Phaeosphaeria nodorum](#) [SN15](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

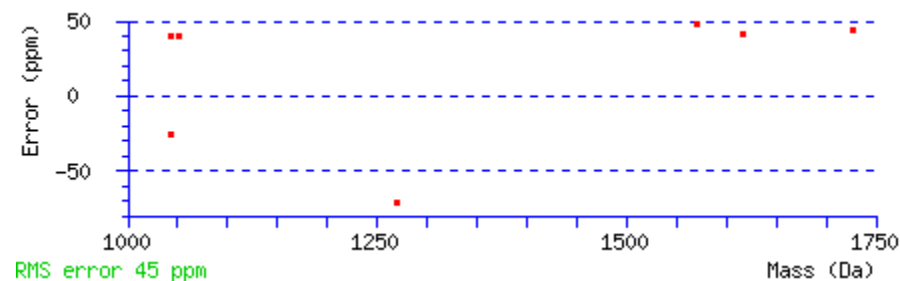
1 **MARQFFVGGN** **FK**MNGTIKSI KEILGHLSQA KLDPNTEVVV APPALYLLLA
 51 REHLRPGLEV AAQNIFDKPS GAFTGEISAD QLK**DSGITWT** **ILGHSERR**TI
 101 LNEDDAFVAS KTKAALDCGL GVILCCGESL EQREANKTIE VVTKQLKAVA
 151 DKVKDWSK**IV** **VAYEPIWAIG** **TGK**VATTEQA QEVHK**AIREW** **LQK**EVSAEAA
 201 EKTR**ILYGGG** **VSEK**NCNELA KQPDIDGFLV GGASLKPAFV DIINAKQA

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
2 - 12	1270.5781	1269.5708	1269.6619	-72	1	M.ARQFFVGGNFK.M (No match)
4 - 12	1043.5726	1042.5653	1042.5236	40	0	R.QFFVGGNFK.M (Ions score 76)
84 - 97	1571.8567	1570.8494	1570.7740	48	0	K.DSGITWTILGHSER.R (Ions score 113)
84 - 97	1571.8567	1570.8494	1570.7740	48	0	K.DSGITWTILGHSER.R (No match)
84 - 98	1727.9580	1726.9507	1726.8751	44	1	K.DSGITWTILGHSERR.T (No match)
159 - 173	1616.9719	1615.9646	1615.8974	42	0	K.IVVAYEPIWAIGTGK.V (Ions score 26)
159 - 173	1616.9719	1615.9646	1615.8974	42	0	K.IVVAYEPIWAIGTGK.V (No match)
186 - 193	1043.5726	1042.5653	1042.5923	-26	1	K.AIREWLQK.E (No match)
205 - 214	1052.6038	1051.5965	1051.5550	40	0	R.ILYGGSVSEK.N (No match)



LOCUS XP_001806125 248 aa linear PLN 02-APR-2008
 DEFINITION hypothetical protein SN0G_15994 [Phaeosphaeria nodorum SN15].
 ACCESSION XP_001806125
 VERSION XP_001806125.1 GI:169625443
 DBSOURCE REFSEQ: accession XM_001806073.1
 KEYWORDS .
 SOURCE Phaeosphaeria nodorum SN15
 ORGANISM Phaeosphaeria nodorum SN15
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Phaeosphaeriaceae;
 Phaeosphaeria.
 REFERENCE 1 (residues 1 to 248)
 AUTHORS Birren,B., Lander,E., Galagan,J., Devon,K., Nusbaum,C., Jaffe,D.,
 Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Zeng,Q.,
 Yandava,C., Alvarado,L., Oleary,S., Oliver,R.O. and Solomon,P.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Phaeosphaeria nodorum SN15 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 248)
 AUTHORS Lander,E. and Birren,B.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-2008) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 REMARK Direct Submission
 REFERENCE 3 (residues 1 to 248)
 AUTHORS Oliver,R. and Solomon,P.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-2008) Murdoch University, South Street, Perth, WA
 6150, Australia
 REMARK Direct Submission

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EAT76573.
Method: conceptual translation.

FEATURES Location/Qualifiers

source	1..248 /organism="Phaeosphaeria nodorum SN15" /db_xref="taxon:321614"
Protein	1..248 /product="hypothetical protein" /calculated_mol_wt=26770
Region	5..244 /region_name="TIM" /note="Triosephosphate isomerase (TIM) is a glycolytic enzyme that catalyzes the interconversion of dihydroxyacetone phosphate and D-glyceraldehyde-3-phosphate. The reaction is very efficient and requires neither cofactors nor metal ions. TIM, usually...; cd00311" /db_xref="CDD:73362"
Site	order(10,12,94,164,170,210,229,231..232) /site_type="other" /note="substrate binding site" /db_xref="CDD:73362"
Site	order(10,13,44..46,48,51,63,81,84..85,96..97) /site_type="other" /note="dimer interface" /db_xref="CDD:73362"
Site	order(12,94,164) /site_type="other" /note="catalytic triad" /db_xref="CDD:73362"
CDS	1..248 /locus_tag="SNOG_15994" /coded_by="XM_001806073.1:64..810" /inference="ab initio prediction:Unveil:1.0" /inference="similar to RNA sequence, EST (same species):INSD:DR045396.1" /inference="similar to RNA sequence, EST (same species):INSD:DR045883.1" /inference="similar to RNA sequence, EST (same species):INSD:EH391712.1" /inference="similar to RNA sequence, EST (same species):INSD:EH395067.1" /inference="similar to RNA sequence, EST (same species):INSD:EH395816.1" /inference="similar to RNA sequence, EST (same species):INSD:EH396096.1" /inference="similar to RNA sequence, EST (same species):INSD:EH396292.1"

/inference="similar to RNA sequence, EST (same species):INSD:EH396491.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH396642.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH397193.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH397293.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH397591.1"
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/inference="similar to RNA sequence, EST (same species):INSD:EH399506.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH399520.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH399782.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH399798.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH400091.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH400187.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH400270.1"
/inference="similar to RNA sequence, EST (same species):INSD:EH401081.1"
/note="gene prediction version 2"
/db_xref="GeneID:5983055"

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

Spot 7

MASCOT Mascot Search Results

Protein View

Match to: [gi|46581334](#) Score: **112** Expect: **6.3e-005**

hypothetical protein DVU2930 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]

Nominal mass (M_r): **16788**; Calculated pI value: **6.30**

NCBI BLAST search of [gi|46581334](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Desulfovibrio vulgaris str. Hildenborough](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|46450756](#) from [Desulfovibrio vulgaris str. Hildenborough](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

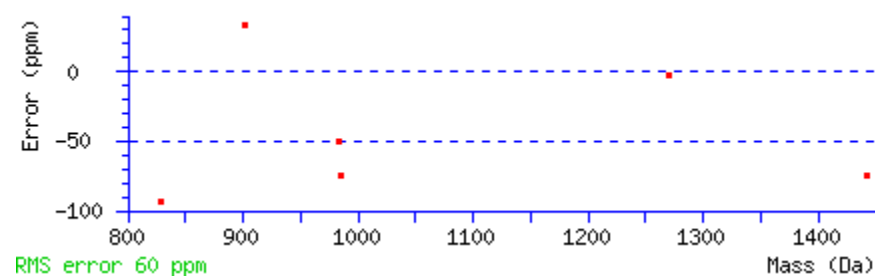
1 MVLRVAVDID DREALNLLR DGAQLKLTLA ATLKRSRTLMPAEEVGVVVA
51 EILMRHDPLT REFEFTSPD LPHRRDRNFN RLMDATLERL RLPLAPAASL
101 AQGESYTVSL TCGLRHTQVP PWLEKTLFFW SWDVVPESTY TQSFTF

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
2 - 12	1270.7087	1269.7014	1269.7041	-2	1	M.VLRVAVDIDDR.E (No match)
2 - 12	1270.7087	1269.7014	1269.7041	-2	1	M.VLRVAVDIDDR.E (No match)
5 - 12	902.4884	901.4811	901.4505	34	0	R.VAVDIDDR.E (No match)
13 - 20	984.5458	983.5385	983.5876	-50	1	R.EALRNLLR.D (No match)
21 - 34	1442.7502	1441.7429	1441.8504	-75	1	R.DGAQLKLTLAATLK.R (No match)
27 - 34	830.4565	829.4492	829.5273	-94	0	K.LTLAATLK.R (Ions score 38)
27 - 35	986.5621	985.5548	985.6284	-75	1	K.LTLAATLK.R.S (Ions score 39)
27 - 35	986.5621	985.5548	985.6284	-75	1	K.LTLAATLK.R.S (No match)



LOCUS YP_012142 146 aa linear BCT 29-MAR-2010
 DEFINITION hypothetical protein DVU2930 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough].
 ACCESSION YP_012142
 VERSION YP_012142.1 GI:46581334
 DBLINK Project: 51
 DBSOURCE REFSEQ: accession NC_002937.3
 KEYWORDS .
 SOURCE Desulfovibrio vulgaris str. Hildenborough
 ORGANISM Desulfovibrio vulgaris str. Hildenborough
 Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
 REFERENCE 1 (residues 1 to 146)
 AUTHORS Heidelberg,J.F., Seshadri,R., Haveman,S.A., Hemme,C.L., Paulsen,I.T., Kolonay,J.F., Eisen,J.A., Ward,N., Methe,B., Brinkac,L.M., Daugherty,S.C., Deboy,R.T., Dodson,R.J., Durkin,A.S., Madupu,R., Nelson,W.C., Sullivan,S.A., Fouts,D., Haft,D.H., Selengut,J., Peterson,J.D., Davidsen,T.M., Zafar,N., Zhou,L., Radune,D., Dimitrov,G., Hance,M., Tran,K., Khouri,H., Gill,J., Utterback,T.R., Feldblyum,T.V., Wall,J.D., Voordouw,G. and Fraser,C.M.
 TITLE The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough
 JOURNAL Nat. Biotechnol. 22 (5), 554-559 (2004)
 PUBMED 15077118
 REFERENCE 2 (residues 1 to 146)
 AUTHORS Heidelberg,J.F., Seshadri,R., Haveman,S.A., Hemme,C.L., Paulsen,I.T., Kolonay,J.F., Eisen,J.A., Ward,N., Methe,B., Brinkac,L.M., Daugherty,S.C., DeBoy,R.T., Dodson,R.J., Durkin,A.S., Madupu,R., Nelson,W.C., Sullivan,S.A., Fouts,D.E., Haft,D.H., Selengut,J., Peterson,J.D., Davidsen,T.M., Zafar,N., Zhou,L., Radune,D., Dimitrov,G., Hance,M., Tran,K., Khouri,H.M., Gill,J., Utterback,T.R., Feldblyum,T.V., Wall,J.D., Voordouw,G. and Fraser,C.M.
 TITLE Direct Submission

JOURNAL Submitted (18-MAR-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA

REFERENCE 3 (residues 1 to 146)

CONSRTM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (15-MAR-2004) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from AAS97402.
Method: conceptual translation.

FEATURES Location/Qualifiers

source	1..146 /organism="Desulfovibrio vulgaris str. Hildenborough" /strain="Hildenborough" /sub_species="vulgaris" /db_xref="taxon:882"
Protein	1..146 /product="hypothetical protein" /calculated_mol_wt=16610
CDS	1..146 /locus_tag="DVU2930" /coded_by="NC_002937.3:3033771..3034211" /inference="non-experimental evidence, no additional details recorded" /transl_table=11 /db_xref="GeneID:2793968"

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

Spot 8

Mascot Search Results**Protein View**

Match to: [gi|189210148](#) Score: **117** Expect: **2e-005**
signal transduction protein [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **14872**; Calculated pI value: **4.85**

NCBI BLAST search of [gi|189210148](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187977499](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

1 MGFWDNKGGEN YDQVYNNDF EENKSSLGHE VIVGGAAFAG FK**AFEDHQR**N
 51 EGKPVSHAFA **KELLAGFAAA EVDKLAETK**G EDWFDREKAK RDAKKHAEQM
 101 YDDHYVDNHG ADQYDPNQYS GPQQFDNRSW

Show predicted peptides also

Sort Peptides By



Residue Number

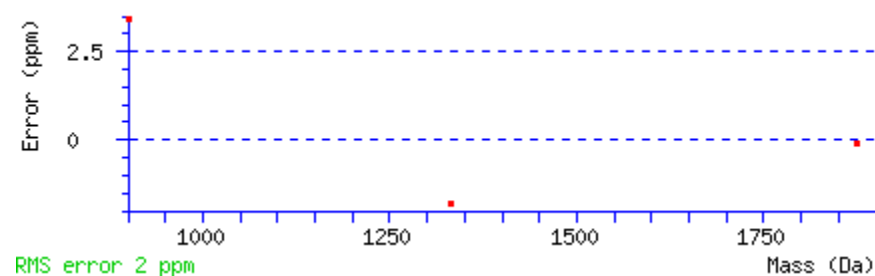


Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
43 - 49	902.4146	901.4073	901.4042	3	0	K.AFEDHQR.N (Ions score 36)
43 - 49	902.4146	901.4073	901.4042	3	0	K.AFEDHQR.N (No match)
62 - 74	1333.6974	1332.6901	1332.6925	-2	0	K.ELLAGFAAAEVDK.L (No match)
62 - 79	1876.0060	1874.9987	1874.9989	-0	1	K.ELLAGFAAAEVDKLAETK.G (Ions score 60)
62 - 79	1876.0060	1874.9987	1874.9989	-0	1	K.ELLAGFAAAEVDKLAETK.G (No match)



LOCUS XP_001941406 130 aa linear PLN 30-MAY-2008
 DEFINITION signal transduction protein [Pyrenophora tritici-repentis
 Pt-1C-BFP].
 ACCESSION XP_001941406
 VERSION XP_001941406.1 GI:189210148
 DBSOURCE REFSEQ: accession XM_001941371.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 130)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L.,
 Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Genome Sequence of Pyrenophora tritici-repentis
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 130)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7
 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EDU44125.
Method: conceptual translation.

FEATURES Location/Qualifiers
 source 1..130
 /organism="Pyrenophora tritici-repentis Pt-1C-BFP"
 /strain="Pt-1C-BFP"
 /db_xref="taxon:426418"
 Protein 1..130
 /product="signal transduction protein"
 /calculated_mol_wt=14750
 Region 9..105
 /region_name="DUF3759"
 /note="Protein of unknown function (DUF3759); pfam12585"
 /db_xref="CDD:153019"
 CDS 1..130
 /locus_tag="PTRG_11075"
 /coded_by="XM_001941371.1:72..464"
 /db_xref="GeneID:6349387"

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

Spot 9

MASCOT Mascot Search Results

Protein View

Match to: [gi|115400267](#) Score: **165** Expect: **3.2e-010**
transaldolase [Aspergillus terreus NIH2624]

Nominal mass (M_r): **35206**; Calculated pI value: **6.16**

NCBI BLAST search of [gi|115400267](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus terreus NIH2624](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|114191388](#) from [Aspergillus terreus NIH2624](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

1 MSSSLEQLKA TGTVVVCD SA IGKYKPQDAT TNPSLILAAS **KKPEYAALID**
 51 **AAVAYGK**QHG KTVDEQVDAT LDR**LLVEFGK** EILK**IIPGKV** **STEVDAR**FSF
 101 DTQASIDKAL HIIKLYEEIG IPKDRI**IKI** **ASTWEGIK**AA QVLQSQHGIN
 151 CNLTLMFSTV QAIAAAEAGA YLISPFVGRI LDWYKAAHKR DYTAQEDPGV
 201 KSVQAIFNYY KKYGYKTIVM GASFRNTGEI TELAGCDYLT ISPNLLEDLY
 251 NSTAAVPKKL DAAAAASQDI PKRSYINDEA LFRFDFNEEA MAVEKLREGI
 301 SK**FAADAVTL** **KDLLK**QKIQA

Show predicted peptides also

Sort Peptides By



Residue Number

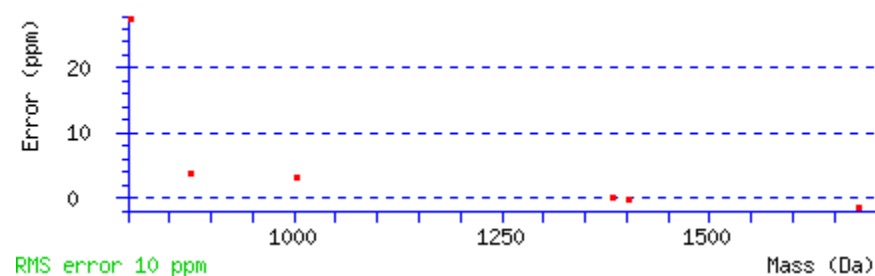


Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
42 - 57	1679.8977	1678.8904	1678.8930	-2	0	K.KPEYAALIDAAVAYGK.Q (Ions score 135)
42 - 57	1679.8977	1678.8904	1678.8930	-2	0	K.KPEYAALIDAAVAYGK.Q (No match)
74 - 80	805.5040	804.4967	804.4745	28	0	R.LLVEFGK.E (No match)
85 - 97	1384.7795	1383.7722	1383.7722	0	1	K.IIPGKVSTEVDAR.F (No match)
90 - 97	876.4454	875.4381	875.4349	4	0	K.VSTEVDAR.F (No match)
130 - 138	1004.5442	1003.5369	1003.5338	3	0	K.IASTWEGIK.A (No match)
303 - 315	1404.8094	1403.8021	1403.8024	-0	1	K.FAADAVTLKDLLK.Q (No match)



LOCUS XP_001215722 320 aa linear PLN 23-APR-2008
 DEFINITION transaldolase [Aspergillus terreus NIH2624].
 ACCESSION XP_001215722
 VERSION XP_001215722.1 GI:115400267
 DBSOURCE REFSEQ: accession XM_001215722.1
 KEYWORDS .
 SOURCE Aspergillus terreus NIH2624
 ORGANISM Aspergillus terreus NIH2624
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (residues 1 to 320)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Henn,M.,
 Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M.,
 Kleber,M., Mauceli,E., Brockman,W., Rounsley,S., Young,S.,
 LaButti,K., Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M.,
 Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L.,
 Luoma,S., White,J., Alvarado,L., Kodira,C., Zeng,Q., Oleary,S.,
 Yandava,C., Denning,D., Nierman,B., Milne,T. and Madden,K.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Aspergillus terreus NIH2624 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 320)
 AUTHORS Birren,B., Lander,E., Galagan,J., Devon,K., Nusbaum,C., Henn,M.,
 Borowsky,M., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S.,
 Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., Rounsley,S.,
 Young,S., LaButti,K., Pushparaj,V., DeCaprio,D., Crawford,M.,
 Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C.,
 Kodira,C., Zeng,Q., Yandava,C., Oleary,S. and Alvarado,L.
 TITLE Direct Submission
 JOURNAL Submitted (02-SEP-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (residues 1 to 320)
 AUTHORS Denning,D. and Anderson,M.
 TITLE Direct Submission

JOURNAL Submitted (02-SEP-2005) The University of Manchester, Oxford Road,
 Manchester M13 9PT, UK
 REFERENCE 4 (residues 1 to 320)
 AUTHORS Nierman,W.C.
 TITLE Direct Submission
 JOURNAL Submitted (02-SEP-2005) The Institute for Genomic Research, 9712
 Medical Center Drive, Rockville, MD 20850, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from EAU33088.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..320
 /organism="Aspergillus terreus NIH2624"
 /strain="NIH2624"
 /db_xref="taxon:341663"
 Protein 1..320
 /product="transaldolase"
 /calculated_mol_wt=34926
 Region 3..314
 /region_name="Transaldolase_TalAB"
 /note="Transaldolases including both TalA and TalB. The
 enzyme catalyses the reversible transfer of a
 dyhydroxyacetone moiety, derived from fructose-6-phosphate
 to erythrose-4-phosphate yielding
 sedoheptulose-7-phosphate and glyceraldehyde-3-phosphate.
 The...; cd00957"
 /db_xref="CDD:29950"
 Site order(18,30,32..33,91,93,129,152,154,174,179)
 /site_type="active"
 /db_xref="CDD:29950"
 Site order(101,280,283,287..288,294,297,301)
 /site_type="other"
 /note="dimer interface"
 /db_xref="CDD:29950"
 Site 129
 /site_type="other"
 /note="catalytic residue"
 /db_xref="CDD:29950"
 CDS 1..320
 /locus_tag="ATEG_06544"
 /coded_by="XM_001215722.1:1..963"
 /db_xref="GeneID:4322187"

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

Spot 10

MASCOT Mascot Search Results

Protein View

Match to: **gi|85107722** Score: **217** Expect: **2e-015**
hypothetical protein NCU07914 [Neurospora crassa OR74A]

Nominal mass (M_r): **45257**; Calculated pI value: **6.17**

NCBI BLAST search of [gi|85107722](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Neurospora crassa OR74A](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|52788211](#) from [Neurospora crassa](#)

[gi|28924036](#) from [Neurospora crassa OR74A](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

1 **MSLSNKL****SIE** **DVDL**KGK**RV**L **IRVDF**N**VPLD** **AEKK**VTNPQR IAGAIPTIKY
51 **ALDHGAK**AVV LMSHLGRPDG KPNPKYSLKP VVPELEKLLG KKVTFAPDCV
101 GPEVEEIVNK ADNGEVILLE NLRFHIEEEG KGTDAGEGNKV KADKAKVEEF
151 RKNLT**LGDV** **YINDAF**G**TAH** **RAHSS**MVGID LPVK**AAGFLM** **KKEL**QYFAKV
201 LESPQRPFSL ILGGAKVSDK IQLIDNLLDK VNTLIVCGGM AFTFKKTLQN
251 MPIGNSLFDE AGAK**IVPDLV** **KKAEK**NNVKL VLPVDFTIAD KFDKDANTGY
301 ATDKDGIPDG WMGLDCGEES VKLFTQAINQ SQTILWNGPA GVFEFDKFAK
351 GTKATLDACV KAAEEGRTVI IGGGDATVA AK**YGVEDKLS** **HVSTG**GGASL
401 **ELLE**GKALPG VVALSERQ

Show predicted peptides also

Sort Peptides By



Residue Number



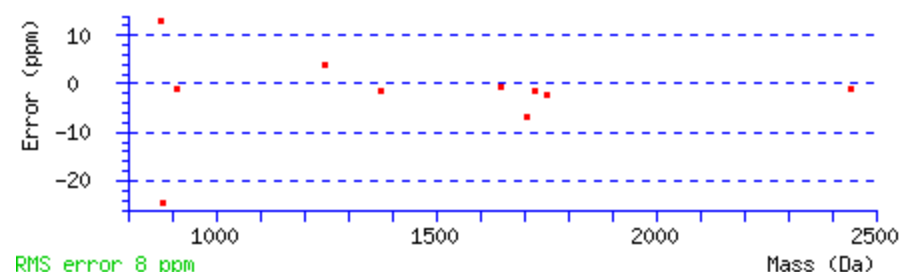
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 15	1707.8717	1706.8644	1706.8760	-7	1	-.MSLSNKL SIEDVDL K.G Oxidation (M) (No match)
19 - 33	1727.9666	1726.9593	1726.9618	-1	1	R.VLIRVDFNVPLDAEK .K (No match)
23 - 33	1246.6361	1245.6288	1245.6241	4	0	R.VDFNVPLDAEK .K (No match)
23 - 34	1374.7245	1373.7172	1373.7191	-1	1	R.VDFNVPLDAEKK .V (No match)
50 - 57	874.4529	873.4456	873.4344	13	0	K.YALDHGAK .A (No match)
157 - 171	1648.8069	1647.7996	1647.8005	-1	0	K.LGDVYINDAFGTAHR .A (Ions score 163)

157 - 171	1648.8069	1647.7996	1647.8005	-1	0	K.LGDVYINDAFGTAHR.A	(No match)
185 - 192	881.4696	880.4623	880.4840	-25	1	K.AAGFLMKK.E	Oxidation (M) (No match)
265 - 272	911.5916	910.5843	910.5851	-1	1	K.IVPDLVKK.A	(No match)
383 - 406	2446.2434	2445.2361	2445.2387	-1	1	K.YGVEDKLSHVSTGGGASLELLEGGK.A	(No match)
389 - 406	1754.9246	1753.9173	1753.9210	-2	0	K.LSHVSTGGGASLELLEGGK.A	(No match)



LOCUS XP_962430 418 aa linear PLN 10-APR-2008
 DEFINITION hypothetical protein NCU07914 [Neurospora crassa OR74A].
 ACCESSION XP_962430
 VERSION XP_962430.1 GI:85107722
 DBSOURCE REFSEQ: accession XM_957337.2
 KEYWORDS .
 SOURCE Neurospora crassa OR74A
 ORGANISM Neurospora crassa OR74A
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (residues 1 to 418)
 AUTHORS Galagan,J.E., Calvo,S.E., Borkovich,K.A., Selker,E.U., Read,N.D.,
 Jaffe,D., FitzHugh,W., Ma,L.J., Smirnov,S., Purcell,S., Rehman,B.,
 Elkins,T., Engels,R., Wang,S., Nielsen,C.B., Butler,J.,
 Endrizzi,M., Qui,D., Ianakiev,P., Bell-Pedersen,D., Nelson,M.A.,
 Werner-Washburne,M., Selitrennikoff,C.P., Kinsey,J.A., Braun,E.L.,
 Zelter,A., Schulte,U., Kothe,G.O., Jedd,G., Mewes,W., Staben,C.,
 Marcotte,E., Greenberg,D., Roy,A., Foley,K., Naylor,J.,
 Stange-Thomann,N., Barrett,R., Gnerre,S., Kamal,M., Kamvysselis,M.,
 Mauceli,E., Bielke,C., Rudd,S., Frishman,D., Krystofova,S.,
 Rasmussen,C., Metzenberg,R.L., Perkins,D.D., Kroken,S., Cogoni,C.,
 Macino,G., Catchside,D., Li,W., Pratt,R.J., Osmani,S.A.,
 DeSouza,C.P., Glass,L., Orbach,M.J., Berglund,J.A., Voelker,R.,
 Yarden,O., Plamann,M., Seiler,S., Dunlap,J., Radford,A.,
 Aramayo,R., Natvig,D.O., Alex,L.A., Mannhaupt,G., Ebbole,D.J.,
 Freitag,M., Paulsen,I., Sachs,M.S., Lander,E.S., Nusbaum,C. and
 Birren,B.
 TITLE The genome sequence of the filamentous fungus Neurospora crassa
 JOURNAL Nature 422 (6934), 859-868 (2003)

PUBMED 12712197
 REFERENCE 2 (residues 1 to 418)
 AUTHORS Galagan,J., Henn,M.R., Hood,H., Radford,A., Collins,R.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Ledlie,T., Kodira,C.,
 Zeng,Q., Yandava,C., Alvarado,L., O'Leary,S., Bowman,B., Colot,H.,
 Ebbole,D., Rasmussen,C., Baker,C., Kalkman,E., Chen,C.-H., Shi,M.,
 Mathur,R., Lambregts,R., mehra,A., Collopy,P., Mehra,A.,
 Schweredtfeger,C., Hong,C., Belden,W., Glass,N.L., Borkovich,K.,
 Dunlap,J., Lander,E., Nusbaum,C., Sachs,M. and Birren,B.
 TITLE Version 3 gene predictions for the *Neurospora crassa* assembly 7
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 418)
 AUTHORS Birren,B., Galagan,J. and Henn,M.R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-2007) Broad Institute of MIT and Harvard, 7
 Cambridge Center, Cambridge, MA 02142, USA
 REFERENCE 4 (residues 1 to 418)
 AUTHORS Birren,B.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02142, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from EAA33194.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..418
 /organism="Neurospora crassa OR74A"
 /strain="OR74A"
 /db_xref="taxon:367110"
 /chromosome="IV"
 Protein 1..418
 /product="hypothetical protein"
 /name="similar to phosphoglycerate kinase 1"
 /calculated_mol_wt=44926
 Region 9..416
 /region_name="Phosphoglycerate_kinase"
 /note="Phosphoglycerate kinase (PGK) is a monomeric enzyme
 which catalyzes the transfer of the high-energy phosphate
 group of 1,3-bisphosphoglycerate to ADP, forming ATP and
 3-phosphoglycerate. This reaction represents the first of
 the two substrate-level...; cd00318"
 /db_xref="CDD:29400"
 Site order(24,26,40,64,123)
 /site_type="other"
 /note="substrate binding site"
 /db_xref="CDD:29400"
 Site order(201..204,392..394)
 /site_type="other"

Site	<pre>/note="hinge regions" /db_xref="CDD:29400" order(239,313,337,339,341..344,374..376) /site_type="other"</pre>
Site	<pre>/note="ADP binding site" /db_xref="CDD:29400" 375 /site_type="other"</pre>
CDS	<pre>/note="catalytic site" /db_xref="CDD:29400" 1..418 /locus_tag="NCU07914" /old_locus_tag="NCU07914.1" /coded_by="XM_957337.2:107..1363" /db_xref="GeneID:3878602"</pre>

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

Spot 11

Mascot Search Results**Protein View**Match to: [gi|120691](#) Score: **334** Expect: **4e-027**

RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase; Short=GAPDH

Nominal mass (M_r): **36641**; Calculated pI value: **6.72**NCBI BLAST search of [gi|120691](#) against nrUnformatted [sequence string](#) for pasting into other applicationsTaxonomy: [Cochliobolus lunatus](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|2601](#) from [Cochliobolus lunatus](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **23%**Matched peptides shown in **Bold Red**

1 MVVKVGINGF GRIGRIVFRN AIEHNDVEIV AVNDPFIEPH YAAAYMLK**YDS**
51 **THGQFKGDIK** VDGNNLTVNG **KTVRFHMEKD** PANIPWSETG AYYVVESTGV
101 FTTTEKAKAH LKGGAKKVVI SAPSADAPMF VMGVNHETYK SDIEVLSNSS
151 CTTNCLAPLA KVIHDKYTII EGLMTTIHSY TATQKVVDGP SAKDWRGGRT
201 AAQNIIPSST GAAKAVGKVI PELNGKLTGM AMRVPTANVS VDLTVRIEK
251 GASYDEIKQA **VKEASEGPLS** **GILGYTEDDI** **VTTDLNGDNR** **SSIFDAK**AGI
301 SLNKNFVK**LV** **SWYDNEWGYS** **RRVLDLLVYI** **AKIDGNA**

Show predicted peptides also

Sort Peptides By



Residue Number



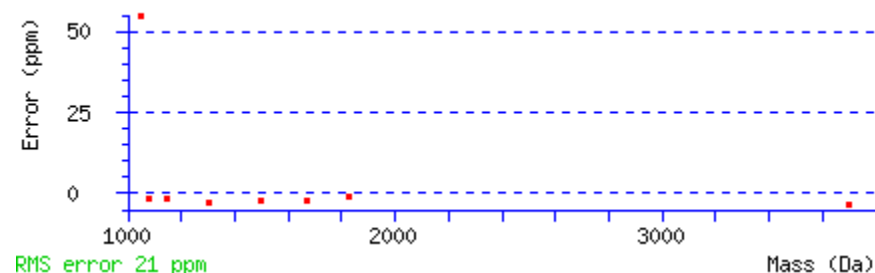
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
48 - 56	1082.4883	1081.4810	1081.4829	-2	0	K.YDSTHGQFK.G (No match)
48 - 60	1495.7140	1494.7067	1494.7103	-2	1	K.YDSTHGQFKGDIK.V (Ions score 75)
48 - 60	1495.7140	1494.7067	1494.7103	-2	1	K.YDSTHGQFKGDIK.V (No match)
72 - 79	1047.5978	1046.5905	1046.5331	55	1	K.TVRFHMEK.D (No match)
72 - 79	1047.5978	1046.5905	1046.5331	55	1	K.TVRFHMEK.D (No match)
263 - 297	3699.7375	3698.7302	3698.7435	-4	1	K.EASEGPLSGILGYTEDDIVTTDLNGDNRSSIFDAK.A (No match)
309 - 321	1674.7506	1673.7433	1673.7474	-2	0	K.LVSWYDNEWGYSR.R (Ions score 108)
309 - 321	1674.7506	1673.7433	1673.7474	-2	0	K.LVSWYDNEWGYSR.R (No match)
309 - 322	1830.8538	1829.8465	1829.8485	-1	1	K.LVSWYDNEWGYSRR.V (Ions score 43)

309 - 322	1830.8538	1829.8465	1829.8485	-1	1	K.LVSWYDNEWGYSRR.V	(No match)
322 - 332	1302.8107	1301.8034	1301.8071	-3	1	R.RVLDLLVYIAK.I	(Ions score 61)
322 - 332	1302.8107	1301.8034	1301.8071	-3	1	R.RVLDLLVYIAK.I	(No match)
323 - 332	1146.7112	1145.7039	1145.7060	-2	0	R.VLDLLVYIAK.I	(No match)



LOCUS G3P_CURLU 337 aa linear PLN 13-JUL-2010
 DEFINITION RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase;
 Short=GAPDH.
 ACCESSION P28844
 VERSION P28844.1 GI:120691
 DBSOURCE UniProtKB: locus G3P_CURLU, accession P28844;
 class: standard.
 created: Dec 1, 1992.
 sequence updated: Dec 1, 1992.
 annotation updated: Jul 13, 2010.
 xrefs: X58718.1, CAA41554.1, DEYDGC
 xrefs (non-sequence databases): SMR:P28844, BRENDA:1.2.1.12,
 GO:0005737, GO:0004365, GO:0051287, GO:0006096, GO:0055114,
 InterPro:IPR020830, InterPro:IPR020829, InterPro:IPR020832,
 InterPro:IPR020831, InterPro:IPR020828, InterPro:IPR000173,
 InterPro:IPR006424, PANTHER:PTHR10836, Pfam:PF02800, Pfam:PF00044,
 PIRSF:PIRSF000149, PRINTS:PR00078, SMART:SM00846,
 TIGRFAMs:TIGR01534, PROSITE:PS00071
 KEYWORDS Cytoplasm; Glycolysis; NAD; Oxidoreductase.
 SOURCE Cochliobolus lunatus (anamorph: Curvularia lunata)
 ORGANISM Cochliobolus lunatus
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Cochliobolus.
 REFERENCE 1 (residues 1 to 337)
 AUTHORS Osiewacz,H.D. and Ridder,R.
 TITLE Genome analysis of imperfect fungi: electrophoretic karyotyping and
 characterization of the nuclear gene coding for
 glyceraldehyde-3-phosphate dehydrogenase (gpd) of Curvularia lunata
 JOURNAL Curr. Genet. 20 (1-2), 151-155 (1991)

PUBMED 1934112
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=AT46
COMMENT On Oct 11, 2005 this sequence version replaced gi:66000.
[CATALYTIC ACTIVITY] D-glyceraldehyde 3-phosphate + phosphate +
NAD(+) = 3-phospho-D-glyceroyl phosphate + NADH.
[PATHWAY] Carbohydrate degradation; glycolysis; pyruvate from
D-glyceraldehyde 3-phosphate: step 1/5.
[SUBUNIT] Homotetramer.
[SUBCELLULAR LOCATION] Cytoplasm.
[SIMILARITY] Belongs to the glyceraldehyde-3-phosphate
dehydrogenase family.

FEATURES Location/Qualifiers

source	1..337 /organism="Cochliobolus lunatus" /db_xref="taxon:5503"
gene	1..337 /gene="GPD"
Protein	1..337 /gene="GPD" /product="Glyceraldehyde-3-phosphate dehydrogenase" /EC_number="1.2.1.12" /note="GAPDH" /UniProtKB_evidence="Inferred from homology"
Region	1..337 /gene="GPD" /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="Glyceraldehyde-3-phosphate dehydrogenase." /FTId=PRO_000014552."
Region	1..334 /gene="GPD" /region_name="PTZ00023" /note="glyceraldehyde-3-phosphate dehydrogenase; Provisional; PTZ00023" /db_xref="CDD:173322"
Region	3..151 /gene="GPD" /region_name="Gp_dh_N" /note="Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain; cl12058" /db_xref="CDD:159718"
Site	12..13 /gene="GPD" /site_type="np-binding" /inference="non-experimental evidence, no additional details recorded" /note="NAD (By similarity)."

Site	34 /gene="GPD" /site_type="binding" /inference="non-experimental evidence, no additional details recorded" /note="NAD (By similarity)."
Site	79 /gene="GPD" /site_type="binding" /inference="non-experimental evidence, no additional details recorded" /note="NAD; via carbonyl oxygen (By similarity)."
Region	150..152 /gene="GPD" /region_name="Region of interest in the sequence" /inference="non-experimental evidence, no additional details recorded" /note="Glyceraldehyde 3-phosphate binding (By similarity)."
Site	151 /gene="GPD" /site_type="active" /inference="non-experimental evidence, no additional details recorded" /note="Nucleophile (By similarity)."
Region	156..313 /gene="GPD" /region_name="Gp_dh_C" /note="Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain; pfam02800" /db_xref="CDD:145777"
Site	178 /gene="GPD" /site_type="other" /inference="non-experimental evidence, no additional details recorded" /note="Activates thiol group during catalysis (By similarity)."
Site	181 /gene="GPD" /site_type="binding" /inference="non-experimental evidence, no additional details recorded" /note="Glyceraldehyde 3-phosphate (By similarity)."
Region	210..211 /gene="GPD" /region_name="Region of interest in the sequence" /inference="non-experimental evidence, no additional details recorded"

Site	<pre>/note="Glyceraldehyde 3-phosphate binding (By similarity)." 233 /gene="GPD" /site_type="binding" /inference="non-experimental evidence, no additional details recorded"</pre>
Site	<pre>/note="Glyceraldehyde 3-phosphate (By similarity)." 315 /gene="GPD" /site_type="binding" /inference="non-experimental evidence, no additional details recorded" /note="NAD (By similarity)."</pre>

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

Spot 12

MASCOT Mascot Search Results

Protein View

Match to: [gi|189204622](#) Score: **156** Expect: **2.5e-009**
fructose-bisphosphate aldolase [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **40217**; Calculated pI value: **5.47**

NCBI BLAST search of [gi|189204622](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187985745](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

```

1 MVQASEVLSR KTGIVIGDDV YALFKHAQSE GYAIPAINVT SSSTVVASLE
51 AARDSKSPIM LGGAAYFAGK GVDNKDQSAS IQGAIAGAHY IRAIAPAYGI
101 PVILHTDHCA KKLLPWLDGM MDAEAYFKE KGEPLFSSHM IDLSEEPKEW
151 NIATTKKYLQ RAAPMKQLIE MEIGITGEE DGVNNESVDN NSLYTQPEDI
201 FEIYKELSAV SPLFSIAAGF GNDHFHST ALLYITDALS TVHGVYKPGN
251 HQQYVKDQTK SKDDKPVFLV FHGGSGSSVD EFRQAISYGV VKVNLDTDMQ
301 WAYLSGIRDY IQSKSGYLQT QVGNPDGEDK PNKKYYDPRV WVREGEKTMS
351 QRIKTALEDF HAAGKA

```

Show predicted peptides also

Sort Peptides By



Residue Number

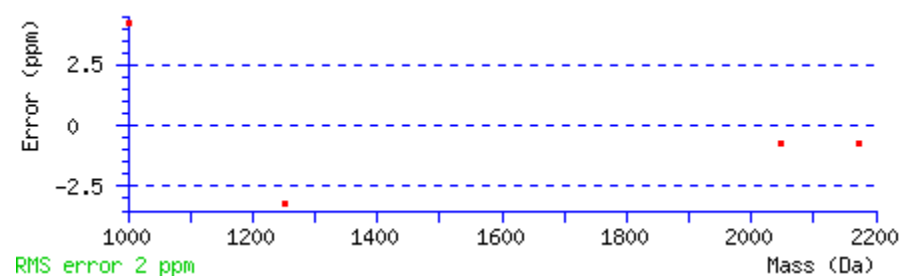


Increasing Mass



Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
93	111	2047.0778	2046.0705	2046.0721	-1	0	R.AIAPAYGIPVILHTDHCAK.K	(Ions score 142)
93	111	2047.0778	2046.0705	2046.0721	-1	0	R.AIAPAYGIPVILHTDHCAK.K	(No match)
93	112	2175.1726	2174.1653	2174.1670	-1	1	R.AIAPAYGIPVILHTDHCAKK.L	(No match)
335	343	1253.6385	1252.6312	1252.6353	-3	1	K.YYDPRVVR.E	(No match)
340	347	1002.5409	1001.5336	1001.5294	4	1	R.VVWREGEK.T	(No match)



LOCUS XP_001938646 366 aa linear PLN 30-MAY-2008
 DEFINITION fructose-bisphosphate aldolase [Pyrenophora tritici-repentis
 Pt-1C-BFP].
 ACCESSION XP_001938646
 VERSION XP_001938646.1 GI:189204622
 DBSOURCE REFSEQ: accession XM_001938611.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 366)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L.,
 Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Genome Sequence of Pyrenophora tritici-repentis
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 366)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7
 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EDU51233.
Method: conceptual translation.

FEATURES Location/Qualifiers

source	1..366 /organism="Pyrenophora tritici-repentis Pt-1C-BFP" /strain="Pt-1C-BFP" /db_xref="taxon:426418"
Protein	1..366 /product="fructose-bisphosphate aldolase" /calculated_mol_wt=40054
Region	17..365 /region_name="FBP_aldolase_IIA" /note="Class II Type A, Fructose-1,6-bisphosphate (FBP) aldolases. The enzyme catalyses the zinc-dependent, reversible aldol condensation of dihydroxyacetone phosphate with glyceraldehyde-3-phosphate to form fructose-1,6-bisphosphate. FBP aldolase is...; cd00946" /db_xref="CDD:29572"
Region	23..366 /region_name="gatY" /note="tagatose-bisphosphate aldolase; Reviewed; PRK09195" /db_xref="CDD:169707"
Site	order(38,107..108,142,172,174,177..180,242..244,246, 272..273,275,294,296..297) /site_type="active" /db_xref="CDD:29572"
Site	order(41..43,46,63,66..68,86,90,93..94,180,297..298, 300..301,304,308,311) /site_type="other" /note="intersubunit interface" /db_xref="CDD:29572"
Site	order(108,142,172,179,243,272) /site_type="other" /note="zinc binding site" /db_xref="CDD:29572"
Site	order(242,244,246,273,275) /site_type="other" /note="Na+ binding site" /db_xref="CDD:29572"
CDS	1..366 /locus_tag="PTRG_08314" /coded_by="XM_001938611.1:1..1101" /db_xref="GeneID:6346595"

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

Spot 13

Mascot Search Results

Protein View

Match to: [gi|189197705](#) Score: **98** Expect: **0.0017**
glycolipid transfer protein HET-C2 [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **24033**; Calculated pI value: **5.78**

NCBI BLAST search of [gi|189197705](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187981138](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

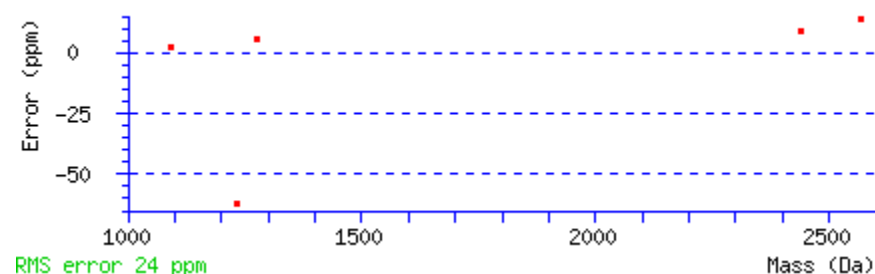
1 MTAEIPPGGT FFDTLKK**SFV DVPIDESK**DS AIPTEFLEA AESLLTLFDV
51 LGSAAFKPVK SDMSGNIKKI RDR**QLEAPAQ SETLQDLVLN ELAEKK**HTAT
101 EGLVWLN**RGL DFTAQALR**HN ISNNEKELAD SFRDAYGNTL KPHHSFIVKP
151 IFSAAMSATP YRRDFYNKLG QDDAKVQAEK VKWLSALEKD VAVLNTFLAK
201 **KEAKWVDWMG** RHCF

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
18 - 28	1235.5391	1234.5318	1234.6081	-62	0	K.SFVDVPIDESK.D (No match)
74 - 95	2439.2832	2438.2759	2438.2540	9	0	R.QLEAPAQSETLQDLVLNELAEK.K (No match)
74 - 96	2567.3911	2566.3838	2566.3490	14	1	R.QLEAPAQSETLQDLVLNELAEKK.H (No match)
109 - 118	1091.5867	1090.5794	1090.5771	2	0	R.GLDFTAQALR.H (Ions score 65)
109 - 118	1091.5867	1090.5794	1090.5771	2	0	R.GLDFTAQALR.H (No match)
202 - 211	1277.6161	1276.6088	1276.6023	5	1	K.EAKWVDWMGR.H (No match)
202 - 211	1277.6161	1276.6088	1276.6023	5	1	K.EAKWVDWMGR.H (No match)



LOCUS XP_001935190 214 aa linear PLN 30-MAY-2008
 DEFINITION glycolipid transfer protein HET-C2 [Pyrenophora tritici-repentis Pt-1C-BFP].
 ACCESSION XP_001935190
 VERSION XP_001935190.1 GI:189197705
 DBSOURCE REFSEQ: accession XM_001935155.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 214)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C., Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L., Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Genome Sequence of Pyrenophora tritici-repentis
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 214)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C., Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EDU47764.
Method: conceptual translation.

FEATURES Location/Qualifiers
 source 1..214
 /organism="Pyrenophora tritici-repentis Pt-1C-BFP"
 /strain="Pt-1C-BFP"
 /db_xref="taxon:426418"
 Protein 1..214
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 /calculated_mol_wt=23860
 Region 31..173
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 /note="Glycolipid transfer protein (GLTP); pfam08718"
 /db_xref="CDD:149696"
 CDS 1..214
 /locus_tag="PTRG_04857"
 /coded_by="XM_001935155.1:73..717"
 /db_xref="GeneID:6343099"

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

Spot 14

MASCOT Mascot Search Results

Protein View

Match to: **gi|126139808** Score: **124** Expect: **4e-006**
hypothetical protein PICST_50942 [Pichia stipitis CBS 6054]

Nominal mass (M_r): **38084**; Calculated pI value: **5.44**

NCBI BLAST search of [gi|126139808](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pichia stipitis CBS 6054](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|126093710](#) from [Pichia stipitis CBS 6054](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```

1  MAPPTRIETT TSVVEVNLAK VSKKSIKLES QADNAEVTFA DWENFKFAPI
51  RESTVSRAMT KRYFADLDKY TESDVVIVGA GSAGLSAAYV LAKNRPNLKI
101 AIIEASVSPG GGCWLGGQLF SAMVLRKPAH LFLDELEIQY DDEGDYVVVK
151 HAALFMSTLL SKVLQFPNVK LFNATAVEDL ITRRDENTGE LRIAGVVTNW
201 TLVALNHDTQ SCMDPNTINC NIVLSTTGHG GPFGAFSAKR LEELGKAPKD
251 ITQGFPRQER AQPVAASADG FQLGGMRGLD MNKAEDAIVK GTREVVPGLV
301 IAGMELAEVD GSNRMGPTFG AMALSGVKA ESVLNAFDLR KKQNETCYGA
351 Q

```

Show predicted peptides also

Sort Peptides By



Residue Number



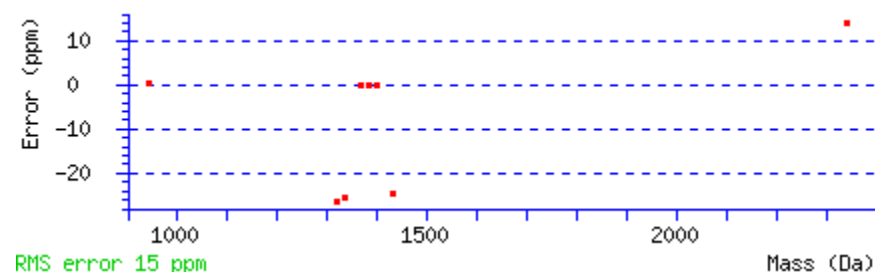
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
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70 - 93	2341.2615	2340.2542	2340.2213	14	0	K.YTESDVVIVGAGSAGLSAAYVLAK.N (No match)
151 - 162	1318.6838	1317.6765	1317.7115	-27	0	K.HAALFMSTLLSK.V (No match)
151 - 162	1334.6796	1333.6723	1333.7064	-26	0	K.HAALFMSTLLSK.V Oxidation (M) (No match)
163 - 170	944.5566	943.5493	943.5491	0	0	K.VLQFPNVK.L (No match)
315 - 328	1366.6854	1365.6781	1365.6785	-0	0	R.MGPTFGAMALSGVK.A (Ions score 86)
315 - 328	1366.6854	1365.6781	1365.6785	-0	0	R.MGPTFGAMALSGVK.A (No match)
315 - 328	1382.6804	1381.6731	1381.6734	-0	0	R.MGPTFGAMALSGVK.A Oxidation (M) (Ions score 49)

315 - 328	1382.6804	1381.6731	1381.6734	-0	0	R.MGPTFGAMALSGVK.A	Oxidation (M) (No match)
315 - 328	1398.6754	1397.6681	1397.6683	-0	0	R.MGPTFGAMALSGVK.A	2 Oxidation (M) (No match)
329 - 341	1433.7393	1432.7320	1432.7674	-25	1	K.AAESVLNAFDLRK.K	(Ions score 14)
329 - 341	1433.7393	1432.7320	1432.7674	-25	1	K.AAESVLNAFDLRK.K	(No match)



LOCUS XP_001386426 351 aa linear PLN 06-JUL-2010
 DEFINITION hypothetical protein PICST_50942 [Scheffersomyces stipitis CBS 6054].
 ACCESSION XP_001386426
 VERSION XP_001386426.1 GI:126139808
 DBSOURCE REFSEQ: accession XM_001386389.1
 KEYWORDS .
 SOURCE Scheffersomyces stipitis CBS 6054 (Pichia stipitis CBS 6054)
 ORGANISM Scheffersomyces stipitis CBS 6054
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Saccharomycotina; Saccharomycetes; Saccharomycetales;
 Debaryomycetaceae; Scheffersomyces.
 REFERENCE 1 (residues 1 to 351)
 AUTHORS Jeffries,T.W., Grigoriev,I.V., Grimwood,J., Laplaza,J.M., Aerts,A.,
 Salamov,A., Schmutz,J., Lindquist,E., Dehal,P., Shapiro,H.,
 Jin,Y.S., Passoth,V. and Richardson,P.M.
 TITLE Genome sequence of the lignocellulose-bioconverting and
 xylose-fermenting yeast Pichia stipitis
 JOURNAL Nat. Biotechnol. 25 (3), 319-326 (2007)
 PUBMED 17334359
 REFERENCE 2 (residues 1 to 351)
 AUTHORS Grigoriev,I., Grimwood,J., Aerts,A., Salamov,A., Zhou,K., Lou,Y.,
 Pitluck,S., Schmutz,J., Myers,R.M., Lucas,S., Detter,J.C., Glavina
 del Rio,T., Jin,Y.-S., Passoth,V., Laplaza,J.M., Jeffries,T.W. and
 Richardson,P.
 CONSRTM US DOE Joint Genome Institute
 TITLE Direct Submission
 JOURNAL Submitted (12-DEC-2006) US DOE Joint Genome Institute, 2800
 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from ABN68397.

Method: conceptual translation.

FEATURES	Location/Qualifiers
source	1..351 /organism="Scheffersomyces stipitis CBS 6054" /strain="CBS 6054" /db_xref="taxon:322104" /chromosome="8"
Protein	1..351 /product="hypothetical protein" /calculated_mol_wt=37749
Region	46..342 /region_name="NADB_Rossmann" /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931" /db_xref="CDD:176428"
Region	56..319 /region_name="Thi4" /note="Thi4 family; pfam01946" /db_xref="CDD:145231"
CDS	1..351 /locus_tag="PICST_50942" /coded_by="XM_001386389.1:1..1056" /transl_table=12 /db_xref="InterPro:IPR002922" /db_xref="GeneID:4840840"

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

Spot 15

MASCOT Mascot Search Results

Protein View

Match to: [gi|212542889](#) Score: **306** Expect: **2.5e-024**
 glycerol dehydrogenase Gcy1, putative [*Penicillium marneffei* ATCC 18224]

Nominal mass (M_r): **33667**; Calculated pI value: **6.02**

NCBI BLAST search of [gi|212542889](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Penicillium marneffei ATCC 18224](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|210066506](#) from [Penicillium marneffei ATCC 18224](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```

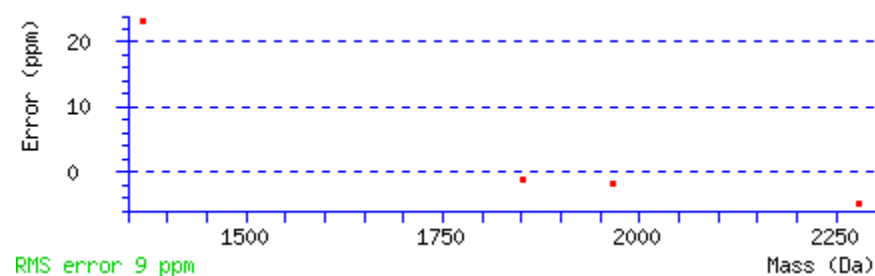
1  MSALEHTKKT FTLNTGDKIP AVGLGTWQSK PNEVREAVKT ALLAGYRHID
51 TALAYGNEHE VGQGIKDSGI PREQIWITTK LDNAWHHRVQ DGINSSLSSL
101 GVDYVDLYLV HWPSSDTPND DMKHLPDWDF IKTWEEIQKL PATGKVRNIG
151 VSNFGIKNLE RLLNAPTTKI VPAVNQIELH PNNPSPKLVE YNVSKGIHCT
201 GYSCLGSTNS PLYKSTLLK MAEKKGKTPQ QLLLAWGVQK GWSVIPKSVS
251 KERIEKNFQL DEWELSAEEL EELSSLKDRF KVCGDDWLPV RVFFGDDE
  
```

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
19 - 35	1852.0052	1850.9979	1851.0003	-1	0	K.IPAVGLGTWQSKPNEVR.E (Ions score 155)
19 - 35	1852.0052	1850.9979	1851.0003	-1	0	K.IPAVGLGTWQSKPNEVR.E (No match)
19 - 39	2279.2395	2278.2322	2278.2433	-5	1	K.IPAVGLGTWQSKPNEVREAVK.T (No match)
158 - 169	1369.8114	1368.8041	1368.7725	23	1	K.NLERLLNAPTTK.I (No match)
170 - 187	1967.0675	1966.0602	1966.0636	-2	0	K.IVPAVNQIELHPNNSPK.L (Ions score 131)
170 - 187	1967.0675	1966.0602	1966.0636	-2	0	K.IVPAVNQIELHPNNSPK.L (No match)



LOCUS XP_002151599 298 aa linear PLN 13-NOV-2008
 DEFINITION glycerol dehydrogenase Gcy1, putative [Penicillium marneffeii ATCC 18224].
 ACCESSION XP_002151599
 VERSION XP_002151599.1 GI:212542889
 DBSOURCE REFSEQ: accession XM_002151563.1
 KEYWORDS .
 SOURCE Penicillium marneffeii ATCC 18224
 ORGANISM Penicillium marneffeii ATCC 18224
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 REFERENCE 1 (residues 1 to 298)
 AUTHORS Fedorova,N.D., Joardar,V., Maiti,R., Schobel,S., Amedeo,P.,
 Galens,K., Inman,J.M., White,O.R., Whitty,B.R., Wortman,J.R. and
 Nierman,W.
 TITLE Direct Submission
 JOURNAL Submitted (03-OCT-2007) J. Craig Venter Institute, 9704 Medical
 Center Drive, Rockville, MD 20850, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from
 mrna.PMAA_044320A.
 Method: conceptual translation.
 FEATURES
 source Location/Qualifiers
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 /strain="ATCC 18224"
 /culture_collection="ATCC:18224"
 /db_xref="taxon:441960"
 Protein 1..298
 /product="glycerol dehydrogenase Gcy1, putative"
 /calculated_mol_wt=33386
 Region 10..259
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 /note="Aldo-keto reductases (AKRs) are a superfamily of

soluble NAD(P)(H) oxidoreductases whose chief purpose is to reduce aldehydes and ketones to primary and secondary alcohols. AKRs are present in all phyla and are of importance to both health and...; cd06660"

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CDS 1..298
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/note="encoded by transcript PMAA_044320A"
/db_xref="GeneID:7029053"

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

Spot 16

MASCOT Mascot Search Results

Protein View

Match to: **gi|67903236** Score: **214** Expect: **4e-015**
hypothetical protein AN8605.2 [Aspergillus nidulans FGSC A4]

Nominal mass (M_r): **17787**; Calculated pI value: **8.86**

NCBI BLAST search of [gi|67903236](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus nidulans FGSC A4](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|40741449](#) from [Aspergillus nidulans FGSC A4](#)

[gi|259483180](#) from [Aspergillus nidulans FGSC A4](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **50%**

Matched peptides shown in **Bold Red**

1 MSNVFFDITA NGEPLGRVEF KLFDDVVPK ARNFR**ELATG QHGFYK**GSP
51 FHRVIPQFML QGGDFTRQNG TGGKSIYGEK FEDENFTLKH **DRPYLLSMAN**
101 AGRNTNGSQF FITTVKTSWL DGAHVVFGEV VKGQEVVDAV EKLGSQSGAT
151 KKKVVISNSG TL

Show predicted peptides also

Sort Peptides By



Residue Number

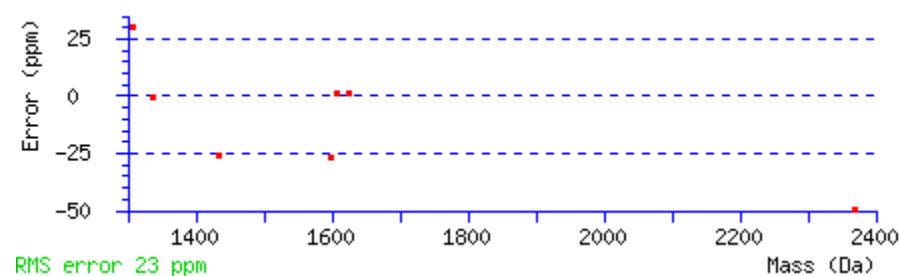


Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 21	2371.0574	2370.0501	2370.1678	-50	1	-.MSNVFFDITANGEPLGRVEFK.L (No match)
18 - 29	1435.7458	1434.7385	1434.7759	-26	1	R.VEFKLFDDVVPK.T (Ions score 59)
18 - 29	1435.7458	1434.7385	1434.7759	-26	1	R.VEFKLFDDVVPK.T (No match)
36 - 47	1307.6772	1306.6699	1306.6306	30	0	R.ELATGQHGFYK.G (No match)
54 - 67	1608.8229	1607.8156	1607.8130	2	0	R.VIPQFMLQGGDFTR.Q (Ions score 107)
54 - 67	1608.8229	1607.8156	1607.8130	2	0	R.VIPQFMLQGGDFTR.Q (No match)
54 - 67	1624.8175	1623.8102	1623.8079	1	0	R.VIPQFMLQGGDFTR.Q Oxidation (M) (Ions score 65)
54 - 67	1624.8175	1623.8102	1623.8079	1	0	R.VIPQFMLQGGDFTR.Q Oxidation (M) (No match)
68 - 80	1338.6637	1337.6564	1337.6575	-1	1	R.QNGTGGKSIYGEK.F (No match)
90 - 103	1600.7590	1599.7517	1599.7940	-26	0	K.HDRPYLLSMANAGR.N (No match)



LOCUS XP_681874 162 aa linear PLN 09-APR-2008
 DEFINITION hypothetical protein AN8605.2 [Aspergillus nidulans FGSC A4].
 ACCESSION XP_681874
 VERSION XP_681874.1 GI:67903236
 DBSOURCE REFSEQ: accession XM_676782.1
 KEYWORDS .
 SOURCE Aspergillus nidulans FGSC A4
 ORGANISM Aspergillus nidulans FGSC A4
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; Emericella.
 REFERENCE 1 (residues 1 to 162)
 AUTHORS Galagan,J.E., Calvo,S.E., Cuomo,C., Ma,L.J., Wortman,J.R.,
 Batzoglou,S., Lee,S.I., Basturkmen,M., Spevak,C.C., Clutterbuck,J.,
 Kapitonov,V., Jurka,J., Scazzocchio,C., Farman,M., Butler,J.,
 Purcell,S., Harris,S., Braus,G.H., Draht,O., Busch,S., D'Enfert,C.,
 Bouchier,C., Goldman,G.H., Bell-Pedersen,D., Griffiths-Jones,S.,
 Doonan,J.H., Yu,J., Vienken,K., Pain,A., Freitag,M., Selker,E.U.,
 Archer,D.B., Penalva,M.A., Oakley,B.R., Momany,M., Tanaka,T.,
 Kumagai,T., Asai,K., Machida,M., Nierman,W.C., Denning,D.W.,
 Caddick,M., Hynes,M., Paoletti,M., Fischer,R., Miller,B., Dyer,P.,
 Sachs,M.S., Osmani,S.A. and Birren,B.W.
 TITLE Sequencing of Aspergillus nidulans and comparative analysis with A.
 fumigatus and A. oryzae
 JOURNAL Nature 438 (7071), 1105-1115 (2005)
 PUBMED 16372000
 REFERENCE 2 (residues 1 to 162)
 AUTHORS Birren,B., Nusbaum,C., Abebe,A., Abouelleil,A., Adekoya,E.,
 Ait-zahra,M., Allen,N., Allen,T., An,P., Anderson,M., Anderson,S.,
 Arachchi,H., Armbruster,J., Bachantsang,P., Baldwin,J., Barry,A.,
 Bayul,T., Blitshsteyn,B., Bloom,T., Blye,J., Boguslavskiy,L.,
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 Corum,B., Cuomo,C., David,R., Dawoe,T., Degray,S., Dodge,S.,

Dooley,K., Dorje,P., Dorjee,K., Dorris,L., Duffey,N., Dupes,A.,
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 Lui,A., Ma,L.J., Mabbitt,R., Macdonald,J., Maclean,C., Major,J.,
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 Norbu,C., Norbu,N., O'donnell,P., Okoawo,O., O'leary,S.,
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 Phunkhang,P., Piquani,B., Purcell,S., Rachupka,T., Ramasamy,U.,
 Rameau,R., Ray,V., Raymond,C., Retta,R., Richardson,S., Rise,C.,
 Rodriguez,J., Rogers,J., Rogov,P., Rutman,M., Schupbach,R.,
 Seaman,C., Settipalli,S., Sharpe,T., Sheridan,J., Sherpa,N.,
 Shi,J., Smirnov,S., Smith,C., Sougnez,C., Spencer,B., Stalker,J.,
 Stange-thomann,N., Stavropoulos,S., Stetson,K., Stone,C., Stone,S.,
 Stubbs,M., Talamas,J., Tchuinga,P., Tenzing,P., Tesfaye,S.,
 Theodore,J., Thoulutsang,Y., Topham,K., Towey,S., Tsamla,T.,
 Tsomo,N., Vallee,D., Vassiliev,H., Venkataraman,V., Vinson,J.,
 Vo,A., Wade,C., Wang,S., Wangchuk,T., Wangdi,T., Whittaker,C.,
 Wilkinson,J., Wu,Y., Wyman,D., Yadav,S., Yang,S., Yang,X.,
 Yeager,S., Yee,E., Young,G., Zainoun,J., Zembeck,L., Zimmer,A.,
 Zody,M. and Lander,E.

TITLE	Direct Submission
JOURNAL	Submitted (26-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02142, USA
COMMENT	PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EAA60639. Method: conceptual translation.
FEATURES	Location/Qualifiers
source	1..162 /organism="Aspergillus nidulans FGSC A4" /strain="FGSC A4" /db_xref="taxon:227321" /chromosome="III"
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Region	2..160 /region_name="cyclophilin_ABH_like"

/note="cyclophilin_ABH_like: Cyclophilin A, B and H-like
cyclophilin-type peptidylprolyl cis- trans isomerase
(PPIase) domain. This family represents the archetypal
cystolic cyclophilin similar to human cyclophilins A, B
and H. PPIase is an enzyme which...; cd01926"
/db_xref="CDD:29397"
Site order(52..53,58,109,111,119)
/site_type="active"
/db_xref="CDD:29397"
CDS 1..162
/locus_tag="AN8605.2"
/coded_by="XM_676782.1:1..489"
/db_xref="GeneID:2868486"

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

Spot 17

MASCOT Mascot Search Results

Protein View

Match to: **gi|70985178** Score: **325** Expect: **3.2e-026**
thiamine biosynthesis protein (Nmt1) [Aspergillus fumigatus Af293]

Nominal mass (M_r): **38583**; Calculated pI value: **6.04**

NCBI BLAST search of [gi|70985178](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus fumigatus Af293](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|55743873](#) from [Aspergillus fumigatus](#)

[gi|66845723](#) from [Aspergillus fumigatus Af293](#)

[gi|159125982](#) from [Aspergillus fumigatus A1163](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

```

1  MSTDKITFLT NWHATPYHAP LYLASHKGFF KEEGLKVAIL EPNDPSDVTE
51 IIGSGKVDMG FKAMIHTLAA KARNFVTSI GSLLDEPFTG VVYLKDSGIT
101 EDFSRLKGKR IGYVGEFGKI QIDELTKYYG MTADDYTAVR CGMNVTKAII
151 RGDIDAGIGL ENVQMVELAE WLASQNRPRD DVQMLRIDQL AELGCCCFCFS
201 ILYIANDAFI AANPDKVQKF MRVAVKRATDY VLAEPKAYE EYIDVKPIMG
251 TPVNRKIFER SFAYFSRDLK NVQRDWAKVT NYGKRLGILD ANFEPNYTNK
301 YLSWDL DADS TDPLGDQKRM AELQKQVAAE GGFKRLHVSA SA
  
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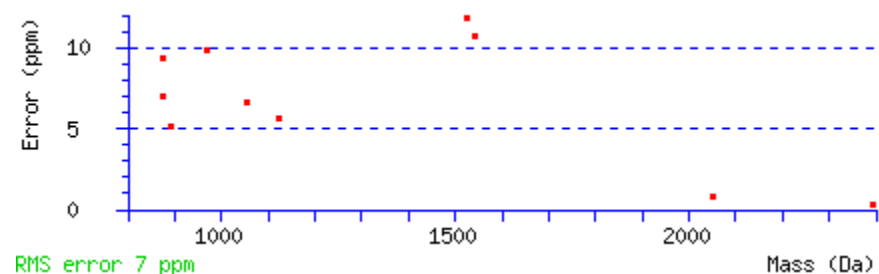
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
28 - 36	1054.5637	1053.5564	1053.5495	7	1	K.GFFKEEGLK.V (Ions score 42)
28 - 36	1054.5637	1053.5564	1053.5495	7	1	K.GFFKEEGLK.V (No match)
37 - 56	2054.0669	2053.0596	2053.0579	1	0	K.VAILEPNDPSDVTEIIGSGK.V (Ions score 35)
37 - 56	2054.0669	2053.0596	2053.0579	1	0	K.VAILEPNDPSDVTEIIGSGK.V (No match)
74 - 95	2396.2756	2395.2683	2395.2675	0	0	R.NFPVTSIGSLLDEPFTGVVYLK.D (Ions score 27)
74 - 95	2396.2756	2395.2683	2395.2675	0	0	R.NFPVTSIGSLLDEPFTGVVYLK.D (No match)
110 - 119	1125.6115	1124.6042	1124.5978	6	1	K.RIGYVGEFGK.I (Ions score 23)

110 - 119	1125.6115	1124.6042	1124.5978	6	1	K.RIGYVGEFGK.I	(No match)
111 - 119	969.5135	968.5062	968.4967	10	0	R.IGYVGEFGK.I	(Ions score 70)
111 - 119	969.5135	968.5062	968.4967	10	0	R.IGYVGEFGK.I	(No match)
128 - 140	1525.6808	1524.6735	1524.6555	12	0	K.YYGMTADDYTAVR.C	(Ions score 30)
128 - 140	1525.6808	1524.6735	1524.6555	12	0	K.YYGMTADDYTAVR.C	(No match)
128 - 140	1541.6741	1540.6668	1540.6504	11	0	K.YYGMTADDYTAVR.C	Oxidation (M) (Ions score 34)
128 - 140	1541.6741	1540.6668	1540.6504	11	0	K.YYGMTADDYTAVR.C	Oxidation (M) (No match)
180 - 186	876.4326	875.4253	875.4171	9	0	R.DDVQMLR.I	(No match)
180 - 186	892.4239	891.4166	891.4120	5	0	R.DDVQMLR.I	Oxidation (M) (No match)
261 - 267	877.4264	876.4191	876.4130	7	0	R.SFAYFSR.D	(Ions score 52)
261 - 267	877.4264	876.4191	876.4130	7	0	R.SFAYFSR.D	(No match)



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

Spot 18

MASCOT Mascot Search Results

Protein View

Match to: [gi|255943905](#) Score: **471** Expect: **7.9e-041**
Pc20g01610 [*Penicillium chrysogenum* Wisconsin 54-1255]

Nominal mass (M_r): **35821**; Calculated pI value: **8.44**

NCBI BLAST search of [gi|255943905](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Penicillium chrysogenum Wisconsin 54-1255](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|211587455](#) from [Penicillium chrysogenum Wisconsin 54-1255](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

1 MFAARRTVNL FQKR**AFSASA INASK**VSVLG AAGGIGQPLS LLLKLNPRVS
 51 **ELALYDIR**GG PGVAADLSHI NTNSTVTGYN PDASGLR**DCL EGSEIILIPA**
 101 **GVPR**KPGMTR **DDL**FNT**NASI VR**DLAKAAAE AAPKAHV LVI ANPVNSTVPI
 151 VAEVYKARNV YDPK**RLF**GV**T TLDVVR**ASRF ISQVQNTNPA GEAVPVVGGH
 201 SGVTIVPLLS QSNHSSIAGQ ARDALVNRIQ FGGDEVVKAK DGAGSATLSM
 251 AMAGAR**FAES LLRAAQ**EGK**G VIEPTFVDSP LYK**DQGIDFF ASRVELGPNG
 301 VEKINSVGEV NEYEQGLLDA CLTDLKKNIQ KGVDFVKANP

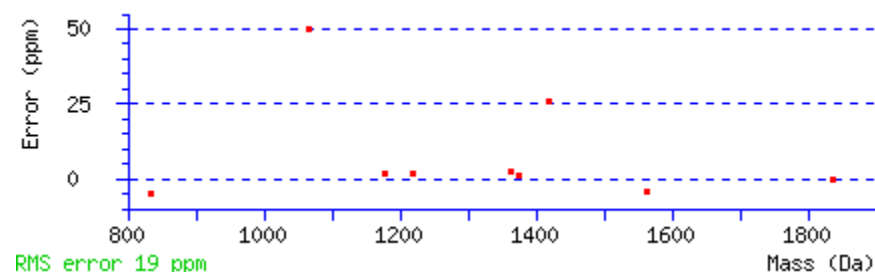
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
15 - 25	1066.6061	1065.5988	1065.5454	50	0	R.AFSASAINASK.V	(No match)
15 - 25	1066.6061	1065.5988	1065.5454	50	0	R.AFSASAINASK.V	(No match)
49 - 58	1178.6432	1177.6359	1177.6343	1	0	R.VSELALYDIR.G	(Ions score 78)
49 - 58	1178.6432	1177.6359	1177.6343	1	0	R.VSELALYDIR.G	(No match)
88 - 104	1838.9681	1837.9608	1837.9608	0	0	R.DCLEGSEIILIPAGVPR.K	(Ions score 48)
88 - 104	1838.9681	1837.9608	1837.9608	0	0	R.DCLEGSEIILIPAGVPR.K	(No match)
111 - 122	1364.6836	1363.6763	1363.6732	2	0	R.DDLFNTNASIVR.D	(Ions score 103)
111 - 122	1364.6836	1363.6763	1363.6732	2	0	R.DDLFNTNASIVR.D	(No match)
165 - 176	1375.8073	1374.8000	1374.7984	1	1	K.RLFGVTTLDVVR.A	(Ions score 81)

165 - 176	1375.8073	1374.8000	1374.7984	1	1	K.RLFGVTTLDVVR.A	(No match)
166 - 176	1219.7064	1218.6991	1218.6972	2	0	R.LFGVTTLDVVR.A	(Ions score 71)
166 - 176	1219.7064	1218.6991	1218.6972	2	0	R.LFGVTTLDVVR.A	(No match)
257 - 263	835.4628	834.4555	834.4599	-5	0	R.FAESLLR.A	(Ions score 37)
257 - 269	1419.7958	1418.7885	1418.7517	26	1	R.FAESLLRAAQGEK.G	(No match)
270 - 283	1564.8185	1563.8112	1563.8185	-5	0	K.GVIEPTFVDSPLYK.D	(No match)



LOCUS XP_002562720 340 aa linear PLN 14-AUG-2009
 DEFINITION Pc20g01610 [Penicillium chrysogenum Wisconsin 54-1255].
 ACCESSION XP_002562720
 VERSION XP_002562720.1 GI:255943905
 DBSOURCE REFSEQ: accession XM_002562674.1
 KEYWORDS .
 SOURCE Penicillium chrysogenum Wisconsin 54-1255
 ORGANISM Penicillium chrysogenum Wisconsin 54-1255
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium;
 Penicillium chrysogenum complex.
 REFERENCE 1 (residues 1 to 340)
 AUTHORS van den Berg,M.A., Albang,R., Albermann,K., Badger,J.H.,
 Daran,J.M., Driessen,A.J., Garcia-Estrada,C., Fedorova,N.D.,
 Harris,D.M., Heijne,W.H., Joardar,V., Kiel,J.A., Kovalchuk,A.,
 Martin,J.F., Nierman,W.C., Nijland,J.G., Pronk,J.T., Roubos,J.A.,
 van der Klei,I.J., van Peij,N.N., Veenhuis,M., von Dohren,H.,
 Wagner,C., Wortman,J. and Bovenberg,R.A.
 TITLE Genome sequencing and analysis of the filamentous fungus
 Penicillium chrysogenum
 JOURNAL Nat. Biotechnol. 26 (10), 1161-1168 (2008)
 PUBMED 18820685
 REFERENCE 2 (residues 1 to 340)
 AUTHORS van den Berg,M.A.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2007) van den Berg M.A., DAI/INNO (624-0270), DSM
 Anti-Infectives, Alexander Fleminglaan 1, Delftn, 2613 AX,
 NETHERLANDS

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence is identical to CAP85490.

FEATURES Location/Qualifiers

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/organism="Penicillium chrysogenum Wisconsin 54-1255"
/strain="Wisconsin 54-1255"
/db_xref="taxon:500485"
/clone="Pc00c20"

Protein 1..340
/product="hypothetical protein"
/name="Pc20g01610"
/calculated_mol_wt=35598

Region 25..337
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/note="malate dehydrogenase, NAD-dependent; TIGR01772"
/db_xref="CDD:130833"

Region 25..336
/region_name="MDH_glyoxysomal_mitochondrial"
/note="Glyoxysomal and mitochondrial malate
dehydrogenases; cd01337"
/db_xref="CDD:133422"

Site order(32..35,56,99,101..102,113,117,120,140,142,169,172,
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/db_xref="CDD:133422"

Site order(37,65..66,68..70,175..176,179,232,235,239..240,
246..249,252)
/site_type="other"
/note="dimerization interface"
/db_xref="CDD:133422"

Site order(104,110,142,176,200,233)
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/note="Substrate binding site"
/db_xref="CDD:133422"

CDS 1..340
/locus_tag="Pc20g01610"
/coded_by="XM_002562674.1:1..1023"
/inference="protein motif:COGS:COG0039"
/inference="protein motif:PFAM:PF00056"
/inference="protein motif:PFAM:PF02866"
/inference="similar to AA sequence:PIR:DEBYMM"
/db_xref="GeneID:8312298"

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

Spot 19

Mascot Search Results

Protein View

Match to: [gi|254583736](#) Score: **161** Expect: **7.9e-010**
ZYR00F05522p [*Zygosaccharomyces rouxii*]

Nominal mass (M_r): **53989**; Calculated pI value: **8.64**

NCBI BLAST search of [gi|254583736](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Zygosaccharomyces rouxii CBS 732](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|238940329](#) from [Zygosaccharomyces rouxii](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

```

1 MFSIRKRQTV VVLLFSLVI YWKHLLMATT RPVVIVGTGL AGLSAGNQLV
51 KHKIPVILLD KASSIGGNSI KASSINGAW TETQKRLNVQ DSPFLFLQDT
101 IRSAGKGGVE PLMEKLTDA ASAIHWLQDE FKLKLDLLMQ IGGQSAPRTH
151 RSSGKLPPGF EIIQSMKAL QAQAEKPSL VKILLESKVV DVSVDGRGKI
201 SGVAYEDSKG NTQKIETDNV IFCSGGFSRS KEMLEEVYPQ YTKIPTTNGE
251 ATTGDGQRIL SKLGADLIDM DQVQLHPTGF IDPNNRDSAW KFLAAEGLRG
301 LGGILINPAT GRRFVDELQT RDYVTNVIRS ECPKDDNKAY LVMSEATYQE
351 FKNMDFYMS KNLLRKVTIE QLVKENNLPV TVAEFVQELK EYSTAKQDKF
401 GRSLVINTFG DQVNPSTEVY LGEVTPVVFH TMGGAQINQQ AQVVGKDNKP
451 LAQGLYAAGE VSGGVHGGNR LGGSSLLECV VYGRAAAKDI AGK
    
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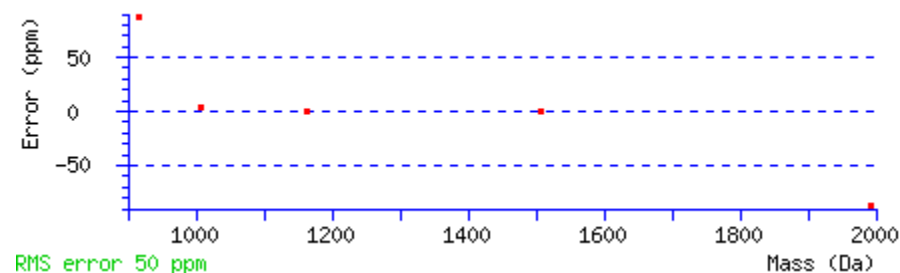
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
8 - 23	1993.9766	1992.9693	1993.1441	-88	0	R.QTVVWVLLFSLVIYWK.H (No match)
108 - 115	918.5399	917.5326	917.4528	87	0	K.GVEPLMEK.L Oxidation (M) (No match)
108 - 115	918.5399	917.5326	917.4528	87	0	K.GVEPLMEK.L Oxidation (M) (No match)
313 - 321	1163.6173	1162.6100	1162.6095	0	1	R.RFVDELQTR.D (Ions score 5)
313 - 321	1163.6173	1162.6100	1162.6095	0	1	R.RFVDELQTR.D (No match)
314 - 321	1007.5192	1006.5119	1006.5084	4	0	R.FVDELQTR.D (Ions score 43)

314 - 321	1007.5192	1006.5119	1006.5084	4	0	R.FVDELQTR.D	(No match)
471 - 484	1509.7740	1508.7667	1508.7657	1	0	R.LGGSSLLECVVYGR.A	(Ions score 100)
471 - 484	1509.7740	1508.7667	1508.7657	1	0	R.LGGSSLLECVVYGR.A	(No match)



LOCUS XP_002497436 493 aa linear PLN 22-JUL-2009
 DEFINITION ZYR00F05522p [Zygosaccharomyces rouxii].
 ACCESSION XP_002497436
 VERSION XP_002497436.1 GI:254583736
 DBSOURCE REFSEQ: accession XM_002497391.1
 KEYWORDS .
 SOURCE Zygosaccharomyces rouxii CBS 732
 ORGANISM Zygosaccharomyces rouxii CBS 732
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Saccharomycotina; Saccharomycetes; Saccharomycetales;
 Saccharomycetaceae; Zygosaccharomyces.
 REFERENCE 1 (residues 1 to 493)
 CONSRTM The Genolevures Consortium
 TITLE Comparative genomics of protoploid Saccharomycetaceae
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 493)
 AUTHORS Genoscope -, C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2009) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from CAR28503.
 FEATURES Location/Qualifiers
 source 1..493
 /organism="Zygosaccharomyces rouxii CBS 732"
 /strain="CBS 732"
 /db_xref="taxon:559307"
 /chromosome="F"
 Protein 1..493
 /product="hypothetical protein"
 /calculated_mol_wt=53721

Region	32..487 /region_name="flavo_cyto_c" /note="flavocytochrome c; TIGR01813" /db_xref="CDD:162543"
Region	33..490 /region_name="NADB_Rossmann" /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931" /db_xref="CDD:176428"
CDS	1..493 /locus_tag="ZYR00F05522g" /old_locus_tag="ZYR0-ORF2942" /coded_by="XM_002497391.1:1..1482" /db_xref="GeneID:8205197"

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

Spot 20

Mascot Search Results**Protein View**

Match to: **gi|154285406** Score: **234** Expect: **4e-017**
nucleoside-diphosphate kinase [Ajellomyces capsulatus NAM1]

Nominal mass (M_r): **16862**; Calculated pI value: **7.77**

NCBI BLAST search of [gi|154285406](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Ajellomyces capsulatus NAM1](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|150407139](#) from [Ajellomyces capsulatus NAM1](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

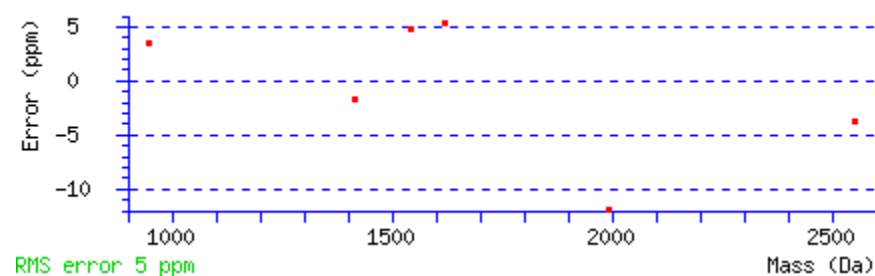
1 MSASEQTFIA IKPDGVQRGL VGPIISRFES RGYKLAAIKL VTPSKEHLEK
51 HYEDLSSKPF FKGLVTYMLS GPICAMWEG RDAVKTGRA**I LGATNPLASA**
101 PGTIRGDFAI DVGRNVCHGS DSVENAKKEI ALWFKPEELV QYQQSQANWV
151 YE

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 18	1993.9775	1992.9702	1992.9939	-12	0	-.MSASEQTFIAIKPDGVQR.G Oxidation (M) (No match)
89 - 105	1622.9312	1621.9239	1621.9151	5	0	R.AILGATNPLASAPGTIR.G (Ions score 115)
89 - 105	1622.9312	1621.9239	1621.9151	5	0	R.AILGATNPLASAPGTIR.G (No match)
89 - 114	2553.3689	2552.3616	2552.3711	-4	1	R.AILGATNPLASAPGTIRGDFRIDVGR.N (No match)
106 - 114	949.4771	948.4698	948.4665	3	0	R.GDFAIDVGR.N (Ions score 69)
106 - 114	949.4771	948.4698	948.4665	3	0	R.GDFAIDVGR.N (No match)
115 - 127	1416.6149	1415.6076	1415.6099	-2	0	R.NVCHGSDSVENAK.K (No match)
115 - 128	1544.7195	1543.7122	1543.7049	5	1	R.NVCHGSDSVENAKK.E (No match)



LOCUS XP_001543498 152 aa linear PLN 26-FEB-2008
 DEFINITION nucleoside-diphosphate kinase [Ajellomyces capsulatus NAM1].
 ACCESSION XP_001543498
 VERSION XP_001543498.1 GI:154285406
 DBSOURCE REFSEQ: accession XM_001543448.1
 KEYWORDS .
 SOURCE Ajellomyces capsulatus NAM1
 ORGANISM Ajellomyces capsulatus NAM1
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Onygenales; Ajellomycetaceae; Ajellomyces.
 REFERENCE 1 (residues 1 to 152)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Henn,M., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M.,
 Kleber,M., Mauceli,E., Brockman,W., Rounsley,S., Young,S.,
 LaButti,K., Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M.,
 Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L.,
 Luoma,S., White,J., Yandava,C., Kodira,C., Zeng,Q., Oleary,S.,
 Alvarado,L., Taylor,J., Sil,A. and Goldman,B.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Ajellomyces capsulatus (Histoplasma capsulatum)
 genome
 JOURNAL Unpublished (2004)
 REFERENCE 2 (residues 1 to 152)
 AUTHORS Birren,B., Ma,L.J., LaButti,K., Lander,E., Taylor,J.,
 Osguthorpe,R., Magrini,V. and Goldman,W.E.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team, The
 Assembly Analysis Team
 TITLE Direct Submission
 JOURNAL Submitted (19-AUG-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from EDN02680.
 Method: conceptual translation.
 FEATURES Location/Qualifiers

source 1..152
/organism="Ajellomyces capsulatus NAM1"
/strain="NAM1"
/db_xref="taxon:339724"

Protein 1..152
/product="nucleoside-diphosphate kinase"
/calculated_mol_wt=16627

Region 5..134
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/note="Nucleoside diphosphate kinase Group I
(NDPk_I)-like: NDP kinase domains are present in a large
family of structurally and functionally conserved proteins
from bacteria to humans that generally catalyze the
transfer of gamma-phosphates of a nucleoside...; cd04413"
/db_xref="CDD:58528"

Site order(12,52,60,88,94,105,115,118,120..121,129)
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Site order(16,21..23,26,29,38..40)
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CDS 1..152
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/coded_by="XM_001543448.1:1..459"
/db_xref="GeneID:5449951"

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

Spot 21

Mascot Search Results

Protein View

Match to: [gi|164429080](#) Score: **252** Expect: **6.3e-019**
adenosine kinase [*Neurospora crassa* OR74A]

Nominal mass (M_r): **49357**; Calculated pI value: **6.02**

NCBI BLAST search of [gi|164429080](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Neurospora crassa OR74A](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|157072401](#) from [Neurospora crassa OR74A](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **12%**

Matched peptides shown in **Bold Red**

```

1 MLLTHPITRP QRLIAGKLES LIGVSYAVGA RRHGQPSAAG ATRCFYSTAP
51 VNPFFAANPS TSNLVRGCDP AVGCFSLAS NLIPVNNSFH TTTPSRFSIR
101 SNPFKMAAT KDYRLLCLEN PLLDIQAFGD EALLEKYGLK ANDAILAEEK
151 HQGLFEDLLQ NYDAKLIAGG AAQNTARGAQ YLLPPNSVVY LGGVGDDKYA
201 AILHDAVKQA GLRVEYRVDP KISTGRCGVV ITGHNSMCT ELGAANHYDL
251 EHLKKPEVWS LVENAEVYV GGYHFTVCP AIMELAKQAA SGNKPFILSL
301 SAPFICQFFK EPLDASAPYW DYVIGNEGEA AAYAESHGLN TTDVKEIAKA
351 LANLPKENTQ RKRVAIITQG TEPTIVAIQG EDEVKEYPVH SIDPAKINDT
401 NGAGDAFAGG FAAGVVEGKS IEESIHMGW LAKLSIQELG PSYFPKQAY
451 PGHN
    
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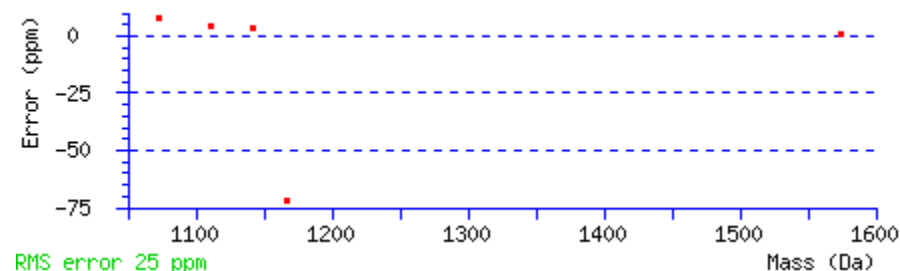
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
141 - 150	1073.5552	1072.5479	1072.5400	7	0	K.ANDAILAEEK.H (No match)
166 - 177	1142.6313	1141.6240	1141.6203	3	0	K.LIAGGAAQNTAR.G (Ions score 80)
166 - 177	1142.6313	1141.6240	1141.6203	3	0	K.LIAGGAAQNTAR.G (No match)
227 - 236	1112.5679	1111.5606	1111.5557	4	0	R.CGVVITGHN.R.S (Ions score 52)
227 - 236	1112.5679	1111.5606	1111.5557	4	0	R.CGVVITGHN.R.S (No match)
346 - 356	1167.6261	1166.6188	1166.7023	-72	1	K.EIAKALANLPK.E (No match)

434 - 447 1575.8433 1574.8360 1574.8344 1 0 K.LSIQELGPSYFPK.Q ([Ions score 105](#))
 434 - 447 1575.8433 1574.8360 1574.8344 1 0 K.LSIQELGPSYFPK.Q ([No match](#))



LOCUS XP_957300 454 aa linear PLN 10-APR-2008
 DEFINITION adenosine kinase [Neurospora crassa OR74A].
 ACCESSION XP_957300
 VERSION XP_957300.2 GI:164429080
 DBSOURCE REFSEQ: accession XM_952207.2
 KEYWORDS .
 SOURCE Neurospora crassa OR74A
 ORGANISM Neurospora crassa OR74A
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (residues 1 to 454)
 AUTHORS Galagan,J.E., Calvo,S.E., Borkovich,K.A., Selker,E.U., Read,N.D.,
 Jaffe,D., FitzHugh,W., Ma,L.J., Smirnov,S., Purcell,S., Rehman,B.,
 Elkins,T., Engels,R., Wang,S., Nielsen,C.B., Butler,J.,
 Endrizzi,M., Qui,D., Ianakiev,P., Bell-Pedersen,D., Nelson,M.A.,
 Werner-Washburne,M., Selitrennikoff,C.P., Kinsey,J.A., Braun,E.L.,
 Zelter,A., Schulte,U., Kothe,G.O., Jedd,G., Mewes,W., Staben,C.,
 Marcotte,E., Greenberg,D., Roy,A., Foley,K., Naylor,J.,
 Stange-Thomann,N., Barrett,R., Gnerre,S., Kamal,M., Kamvysselis,M.,
 Mauceli,E., Bielke,C., Rudd,S., Frishman,D., Krystofova,S.,
 Rasmussen,C., Metzenberg,R.L., Perkins,D.D., Kroken,S., Cogoni,C.,
 Macino,G., Catcheside,D., Li,W., Pratt,R.J., Osmani,S.A.,
 DeSouza,C.P., Glass,L., Orbach,M.J., Berglund,J.A., Voelker,R.,
 Yarden,O., Plamann,M., Seiler,S., Dunlap,J., Radford,A.,
 Aramayo,R., Natvig,D.O., Alex,L.A., Mannhaupt,G., Ebbole,D.J.,
 Freitag,M., Paulsen,I., Sachs,M.S., Lander,E.S., Nusbaum,C. and
 Birren,B.
 TITLE The genome sequence of the filamentous fungus Neurospora crassa
 JOURNAL Nature 422 (6934), 859-868 (2003)
 PUBMED 12712197
 REFERENCE 2 (residues 1 to 454)
 AUTHORS Galagan,J., Henn,M.R., Hood,H., Radford,A., Collins,R.,

DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Ledlie,T., Kodira,C., Zeng,Q., Yandava,C., Alvarado,L., O'Leary,S., Bowman,B., Colot,H., Ebbole,D., Rasmussen,C., Baker,C., Kalkman,E., Chen,C.-H., Shi,M., Mathur,R., Lambreghts,R., Mehra,A., Collopy,P., Mehra,A., Schweredtfeger,C., Hong,C., Belden,W., Glass,N.L., Borkovich,K., Dunlap,J., Lander,E., Nusbaum,C., Sachs,M. and Birren,B.

TITLE Version 3 gene predictions for the *Neurospora crassa* assembly 7
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 454)
 AUTHORS Galagan,J., Henn,M.R., Hood,H., Radford,A., Collins,R., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Ledlie,T., Kodira,C., Zeng,Q., Yandava,C., Alvarado,L., O'Leary,S., Bowman,B., Colot,H., Ebbole,D., Rasmussen,C., Baker,C., Kalkman,E., Chen,C.-H., Shi,M., Mathur,R., Lambreghts,R., mehra,A., Collopy,P., Mehra,A., Schweredtfeger,C., Hong,C., Belden,W., Glass,N.L., Borkovich,K., Dunlap,J., Lander,E., Nusbaum,C., Sachs,M. and Birren,B.

TITLE Version 3 gene predictions for the *Neurospora crassa* assembly 7
 JOURNAL Unpublished
 REFERENCE 4 (residues 1 to 454)
 AUTHORS Birren,B., Galagan,J. and Henn,M.R.

TITLE Direct Submission
 JOURNAL Submitted (06-JUL-2007) Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA

REFERENCE 5 (residues 1 to 454)
 AUTHORS Birren,B.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EAA28064. On Jan 3, 2008 this sequence version replaced gi:85084340. Method: conceptual translation.

FEATURES
 source Location/Qualifiers
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 /strain="OR74A"
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 /chromosome="III"
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 /product="adenosine kinase"
 /calculated_mol_wt=48800
 Region 112..444
 /region_name="adenosine_kinase"
 /note="Adenosine kinase (AK) catalyzes the phosphorylation of ribofuranosyl-containing nucleoside analogues at the 5'-hydroxyl using ATP or GTP as the phosphate donor.The physiological function of AK is associated with the

	regulation of extracellular...; cd01168"
	/db_xref="CDD:29352"
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	/note="substrate binding site"
	/db_xref="CDD:29352"
Site	order(368,370..371,374,389,391,397,400,403..404,407,432, 436)
	/site_type="other"
	/note="ATP binding site"
	/db_xref="CDD:29352"
CDS	1..454
	/locus_tag="NCU00414"
	/old_locus_tag="NCU00414.1"
	/coded_by="XM_952207.2:1..1365"
	/db_xref="GeneID:3873447"

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

Spot 22

MASCOT Mascot Search Results

Protein View

Match to: [gi|242777912](#) Score: **157** Expect: **2e-009**
conserved hypothetical protein [Talaromyces stipitatus ATCC 10500]

Nominal mass (M_r): **42847**; Calculated pI value: **5.79**

NCBI BLAST search of [gi|242777912](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Talaromyces stipitatus ATCC 10500](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|218722748](#) from [Talaromyces stipitatus ATCC 10500](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

1 MSAKPIFVAT HPR**ACSTAFE** RVFMTRR**DSL** **QCIHEPFGDA** **FYFGPER**LSA
 51 RYENDEKAR**L** **DSGFSTSTYK** **TIFDRI**ESET TEGKRIFIKD IIHYLVPPDG
 101 KPASIAPSLF KVK**RGIGTNG** **EINGLTNGHA** **EVNGVTTNGG** **TPVK**AEVPPY
 151 PYPTEAEPGN PTVVPLELLS KFHFTFLIRD PHYSIPSYFR CTIPPLDDVT
 201 GFHEFSPSEA GYDEVRRVFD YLRVGLIGP RVATTTAED TANKQTNGTT
 251 HRHDNGSMGV EICVIDADDL LDNPSLMIES YCKSVGIPFE PEMLRWDTTE
 301 DHAYARAAFE KWKGFHEDAI ASKELKARTH SKSFKSEEEF DAEWREKFGE
 351 KGAKIIRETV NRNMADYHYM KHFALKV

Show predicted peptides also

Sort Peptides By



Residue Number

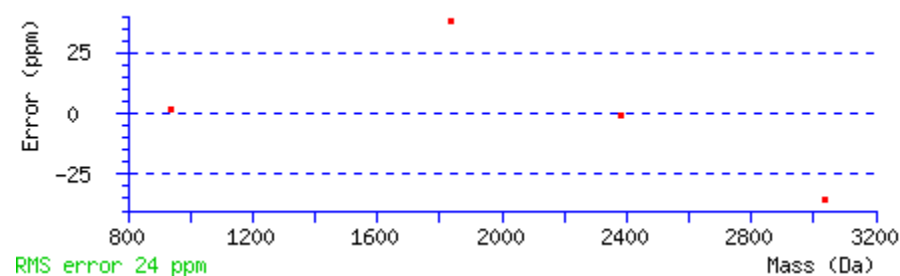


Increasing Mass



Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
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14	21	941.4161	940.4088	940.4073	2	0	R.ACSTAFER.V	(No match)
28	47	2385.0583	2384.0510	2384.0532	-1	0	R.DSLQCIHEPFGDAFYFGPER.L	(Ions score 114)
28	47	2385.0583	2384.0510	2384.0532	-1	0	R.DSLQCIHEPFGDAFYFGPER.L	(No match)
60	75	1837.9657	1836.9584	1836.8894	38	1	R.LDSGFSTSTYKTIFDR.I	(No match)
60	75	1837.9657	1836.9584	1836.8894	38	1	R.LDSGFSTSTYKTIFDR.I	(No match)
114	144	3034.4233	3033.4160	3033.5228	-35	1	K.RGIGTNGEINGLTNGHAEVNGVTTNGGTPVK.A	(No match)



LOCUS XP_002479129 377 aa linear PLN 02-JUL-2009
 DEFINITION conserved hypothetical protein [Talaromyces stipitatus ATCC 10500].
 ACCESSION XP_002479129
 VERSION XP_002479129.1 GI:242777912
 DBSOURCE REFSEQ: accession XM_002479084.1
 KEYWORDS .
 SOURCE Talaromyces stipitatus ATCC 10500
 ORGANISM Talaromyces stipitatus ATCC 10500
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; Talaromyces.
 REFERENCE 1 (residues 1 to 377)
 AUTHORS Fedorova,N.D., Joardar,V., Maiti,R., Schobel,S., Amedeo,P.,
 Galens,K., Inman,J.M., Galinsky,K.J., White,O.R., Whitty,B.R.,
 Wortman,J.R. and Nierman,W.C.
 TITLE Direct Submission
 JOURNAL Submitted (01-OCT-2007) J. Craig Venter Institue, 9704 Medical
 Center Drive, Rockville, MD 20850, USA
 REFERENCE 2 (residues 1 to 377)
 AUTHORS Nierman,W.C.
 TITLE Direct Submission
 JOURNAL Submitted (02-MAY-2007) The Institute for Genomic Research, 9712
 Medical Center Drive, Rockville, MD 20850, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from
 mrna.TSTA_094120A.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..377
 /organism="Talaromyces stipitatus ATCC 10500"
 /strain="ATCC 10500"
 /culture_collection="ATCC:10500"
 /db_xref="taxon:441959"
 Protein 1..377
 /product="hypothetical protein"

CDS /calculated_mol_wt=42458
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 /locus_tag="TSTA_094120"
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 /note="encoded by transcript TSTA_094120A"
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Mascot: <http://www.matrixscience.com/>

Spot 23

Mascot Search Results

Protein View

Match to: [gi|189196154](#) Score: **504** Expect: **4e-044**
NADP-specific glutamate dehydrogenase [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **49094**; Calculated pI value: **5.88**

NCBI BLAST search of [gi|189196154](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187980294](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

```

1 MSEPEFEQAR KELVSTLEAS SLFSKNPEYK KALEVVSVP E RIIQFRVWE
51 NDKGECQVQK GYRVQFNSAL GPYKGGLRFH PTVNLSILKF LGFEQIFKNA
101 LTGLNMGGGK GGCDFFPKGK SDNEIRKFCV AFMRELNKHI GADTDVPAGD
151 IGVGGREIGY LFGAYRAERN RWEGVLTGKG GSWGGSLIRP EATGYGLVYY
201 VEHMINYASG GKESFAGKRV ALSGSGNVAQ YAALKIIELG GTVISLSDSK
251 GALIAEDDKG FTPEIINQIA ALKLERKALT ALENHNFKYI EGARPWKEVN
301 KVDVALPSAT QNEVSEDEAK ALIESGAKYI AEGSNMGCTQ EAIEVFEAHR
351 REKKGDAIWY APGKAANAGG VAVSGLEMAQ NSQRLSWTAE QVDEKLKGIM
401 KDCFENCLST AKEYFTPAEG EFPSLVGGAN VAGFRKVAAA MHDQGDWW
    
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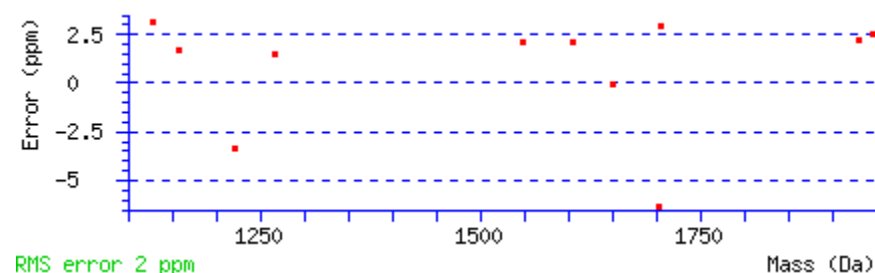
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
64 - 74	1223.6378	1222.6305	1222.6346	-3	0	R.VQFNSALGPYK.G (No match)
64 - 78	1606.8733	1605.8660	1605.8627	2	1	R.VQFNSALGPYKGGLR.F (Ions score 51)
64 - 78	1606.8733	1605.8660	1605.8627	2	1	R.VQFNSALGPYKGGLR.F (No match)
75 - 89	1651.9641	1650.9568	1650.9570	-0	1	K.GGLRFHPTVNLSILK.F (No match)
79 - 89	1268.7380	1267.7307	1267.7289	1	0	R.FHPTVNLSILK.F (Ions score 69)
79 - 89	1268.7380	1267.7307	1267.7289	1	0	R.FHPTVNLSILK.F (No match)
90 - 98	1128.6123	1127.6050	1127.6015	3	0	K.FLGFEQIFK.N (Ions score 69)

90 - 98	1128.6123	1127.6050	1127.6015	3	0	K.FLGFEQIFK.N	(No match)
139 - 156	1706.8507	1705.8434	1705.8384	3	0	K.HIGADTDVPAGDIGVGGR.E	(Ions score 116)
139 - 156	1706.8507	1705.8434	1705.8384	3	0	K.HIGADTDVPAGDIGVGGR.E	(No match)
170 - 179	1159.6238	1158.6165	1158.6145	2	1	R.NRWEGLTGK.G	(Ions score 36)
170 - 179	1159.6238	1158.6165	1158.6145	2	1	R.NRWEGLTGK.G	(No match)
219 - 235	1704.9283	1703.9210	1703.9318	-6	1	K.RVALSGSGNVAQYAALK.I	(No match)
220 - 235	1548.8413	1547.8340	1547.8307	2	0	R.VALSGSGNVAQYAALK.I	(No match)
365 - 384	1930.9442	1929.9369	1929.9326	2	0	K.AANAGGVAVSGLEMAQNSQR.L	(Ions score 108)
365 - 384	1930.9442	1929.9369	1929.9326	2	0	K.AANAGGVAVSGLEMAQNSQR.L	(No match)
365 - 384	1946.9397	1945.9324	1945.9276	2	0	K.AANAGGVAVSGLEMAQNSQR.L	Oxidation (M) (No match)
365 - 384	1946.9397	1945.9324	1945.9276	2	0	K.AANAGGVAVSGLEMAQNSQR.L	Oxidation (M) (No match)



LOCUS XP_001934415 448 aa linear PLN 30-MAY-2008
 DEFINITION NADP-specific glutamate dehydrogenase [Pyrenophora tritici-repentis Pt-1C-BFP].
 ACCESSION XP_001934415
 VERSION XP_001934415.1 GI:189196154
 DBSOURCE REFSEQ: accession XM_001934380.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 448)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C., Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L., Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Genome Sequence of Pyrenophora tritici-repentis
 JOURNAL Unpublished

REFERENCE 2 (residues 1 to 448)

AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C., Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.

CONSRTM The Broad Institute Genome Sequencing Platform

TITLE Direct Submission

JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EDU46920. Method: conceptual translation.

FEATURES

source	Location/Qualifiers
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Protein	1..448
	/product="NADP-specific glutamate dehydrogenase"
	/calculated_mol_wt=48651
Region	3..445
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	/db_xref="CDD:169848"
Region	39..166
	/region_name="ELFV_dehydrog_N"
	/note="Glu/Leu/Phe/Val dehydrogenase, dimerization domain; pfam02812"
	/db_xref="CDD:145786"
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	/note="NAD(P) binding domain of glutamate dehydrogenase, subgroup 2; cd05313"
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CDS	1..448
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	/db_xref="GeneID:6342318"

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

Spot 24

MASCOT Mascot Search Results

Protein View

Match to: [gi|238840987](#) Score: **391** Expect: **7.9e-033**
 eukaryotic translation initiation factor 5A-1 [*Microsporium canis* CBS 113480]

Nominal mass (M_r): **17884**; Calculated pI value: **5.33**

NCBI BLAST search of [gi|238840987](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Microsporium canis CBS 113480](#)

Fixed modifications: Carbamidomethyl (C)

Variable modification: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

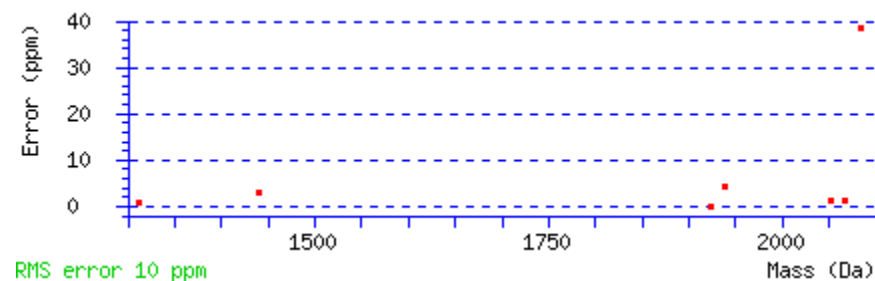
1 MADDEQHNVT FENADAGAST TYPMQCSALR KNGHVVIKGR PCKIVEMSTS
 51 KTGKHGHAK**V HLV**AIIDFTG **KKLEDLSPST HNMDVP**NVR QEYQLVDITD
 101 DGFLNLMKED GTPKDDVKLP DNEVGEEKITK LFKVEEK**DVN VVLTAMGEE**
 151 **CAMDAK**EMAH

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
60 - 71	1312.7632	1311.7559	1311.7551	1	0	K.VHLVAIDIFTGK.K	(Ions score 109)
60 - 71	1312.7632	1311.7559	1311.7551	1	0	K.VHLVAIDIFTGK.K	(No match)
60 - 72	1440.8619	1439.8546	1439.8500	3	1	K.VHLVAIDIFTGKK.L	(Ions score 102)
60 - 72	1440.8619	1439.8546	1439.8500	3	1	K.VHLVAIDIFTGKK.L	(No match)
72 - 89	2052.0205	2051.0132	2051.0106	1	1	K.KLEDLSPSTHNMDVPNVR.R	(Ions score 112)
72 - 89	2052.0205	2051.0132	2051.0106	1	1	K.KLEDLSPSTHNMDVPNVR.R	(No match)
72 - 89	2068.0151	2067.0078	2067.0055	1	1	K.KLEDLSPSTHNMDVPNVR.R	Oxidation (M) (Ions score 50)
72 - 89	2068.0151	2067.0078	2067.0055	1	1	K.KLEDLSPSTHNMDVPNVR.R	Oxidation (M) (No match)
73 - 89	1923.9226	1922.9153	1922.9156	-0	0	K.LEDLSPSTHNMDVPNVR.R	(No match)
73 - 89	1923.9226	1922.9153	1922.9156	-0	0	K.LEDLSPSTHNMDVPNVR.R	(No match)
73 - 89	1939.9261	1938.9188	1938.9105	4	0	K.LEDLSPSTHNMDVPNVR.R	Oxidation (M) (Ions score 36)
73 - 89	1939.9261	1938.9188	1938.9105	4	0	K.LEDLSPSTHNMDVPNVR.R	Oxidation (M) (No match)
138 - 156	2084.0149	2083.0076	2082.9272	39	0	K.DVNVVLTAMGEECAMDAK.E	2 Oxidation (M) (No match)



LOCUS EEQ30649 160 aa linear PLN 03-JUN-2009
 DEFINITION eukaryotic translation initiation factor 5A-1 [*Microsporium canis* CBS 113480].
 ACCESSION EEQ30649
 VERSION EEQ30649.1 GI:238840987
 DBSOURCE accession DS995703.1
 KEYWORDS .
 SOURCE *Arthroderma otae* CBS 113480 (anamorph: *Microsporium canis* CBS 113480)
 ORGANISM *Arthroderma otae* CBS 113480
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Onygenales; Arthrodermataceae; *Arthroderma*.
 REFERENCE 1 (residues 1 to 160)
 AUTHORS Cuomo,C., Henn,M.R., Young,S.K., Kodira,C.D., Zeng,Q., Koehrsen,M., Alvarado,L., Berlin,A., Borenstein,D., Chen,Z., Engels,R., Freedman,E., Gellesch,M., Goldberg,J., Griggs,A., Gujja,S., Heiman,D., Hepburn,T., Howarth,C., Jen,D., Larson,L., Lewis,B., Mehta,T., Park,D., Pearson,M., Roberts,A., Saif,S., Shea,T., Shenoy,N., Sisk,P., Stolte,C., Sykes,S., Walk,T., White,J., Yandava,C., Guigo,R., Borodovsky,M., White,T.C., Oliver,B.G., Graser,Y., Abdel-Rahman,S., Gurr,S.J., Martinez-Rossi,N., Summerbell,R., Lander,E., Nusbaum,C., Galagan,J. and Birren,B.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of *Microsporium canis* strain CBS 113480
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 160)
 AUTHORS Cuomo,C., Henn,M.R., Jaffe,D., Young,S., Gnerre,S., Berlin,A., Heiman,D., Hepburn,T., Sykes,S., Alvarado,L., Kodira,C.D., White,T.C., Oliver,B.G., Graser,Y., Abdel-Rahman,S., Gurr,S.J., Martinez-Rossi,N., Summerbell,R., Lander,E., Nusbaum,C., Galagan,J. and Birren,B.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-2008) Broad Institute of MIT and Harvard, 7

Cambridge Center, Cambridge, MA 02142, USA
COMMENT Method: conceptual translation.
FEATURES Location/Qualifiers
source 1..160
/organism="Arthroderma otae CBS 113480"
/strain="CBS 113480"
/db_xref="taxon:554155"
Protein 1..160
/product="eukaryotic translation initiation factor 5A-1"
Region 18..156
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/note="translation initiation factor eIF-5A; TIGR00037"
/db_xref="CDD:129148"
Region 88..158
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/note="S1_eIF5A: Eukaryotic translation Initiation Factor
5A (eIF5A), S1-like RNA-binding domain. eIF5A is an
evolutionarily conserved protein found in eukaryotes.
eIF5A is the only protein known to have the unusual amino
acid hypusine. Hypusine is essential...; cd04468"
/db_xref="CDD:88433"
Site order(114,142,149..150)
/site_type="other"
/note="RNA binding site"
/db_xref="CDD:88433"
CDS 1..160
/locus_tag="MCG_03468"
/coded_by="join(DS995703.1:1657332..1657349,
DS995703.1:1657493..1657759,DS995703.1:1657827..1657959,
DS995703.1:1658049..1658113)"

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

Spot 25

Mascot Search Results**Protein View**

Match to: **gi|145613040** Score: **306** Expect: **2.5e-024**
conserved hypothetical protein [Magnaporthe grisea 70-15]

Nominal mass (M_r): **25180**; Calculated pI value: **5.73**

NCBI BLAST search of [gi|145613040](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Magnaporthe grisea 70-15](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|145020105](#) from [Magnaporthe grisea 70-15](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

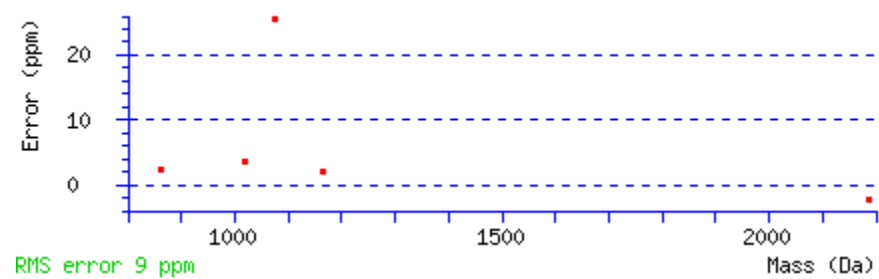
1 MAEEQRPAPL RLGTEAPNFK AETTKGPIDF HEFIGSNWVI LFSHPEDFTP
 51 VCTTELGEFA **RLEPEFTKR**G VKLIGLSANT VGSHDGIWD INDVTGSHVA
 101 FPIIADKERK VAYLYDMLDY QDTTNVDEKG IAFTIRSVFI IDPAKKIR**TI**
 151 **LSYPASTGR**N SAEVLRI**VDS** **LQTGDK**HK**VT** **TPINWVP**G**DD** **VIVHPSIK**DE
 201 QAKDLFPNFR AVKPYLRFTP LPKE

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
62 - 68	863.4529	862.4456	862.4436	2	0	R.LEPEFTK.R (No match)
62 - 69	1019.5555	1018.5482	1018.5447	3	1	R.LEPEFTKR.G (Ions score 68)
62 - 69	1019.5555	1018.5482	1018.5447	3	1	R.LEPEFTKR.G (No match)
149 - 159	1165.6234	1164.6161	1164.6139	2	0	R.TILSYASTGR.N (Ions score 103)
149 - 159	1165.6234	1164.6161	1164.6139	2	0	R.TILSYASTGR.N (No match)
167 - 176	1075.5903	1074.5830	1074.5557	25	0	R.IVDSLQTGDK.H (No match)
179 - 198	2187.1755	2186.1682	2186.1736	-2	0	K.VTTPINWVPGDDVIVHPSIK.D (Ions score 107)
179 - 198	2187.1755	2186.1682	2186.1736	-2	0	K.VTTPINWVPGDDVIVHPSIK.D (No match)



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

Spot 26

Mascot Search Results**Protein View**

Match to: **gi|225877962** Score: **146** Expect: **2.5e-008**
putative saccharopine dehydrogenase (NAD⁺,L-lysine-forming) [Gibberella fujikuroi]

Nominal mass (M_r): **43543**; Calculated pI value: **5.17**

NCBI BLAST search of [gi|225877962](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Gibberella fujikuroi](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **11%**

Matched peptides shown in **Bold Red**

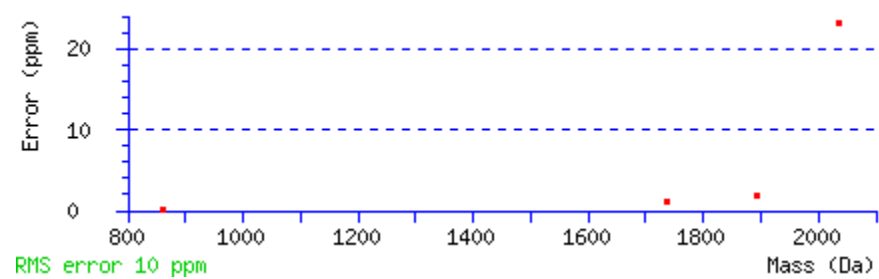
1 MSDYPHILLR AEEKPLEHRS FSPAIIK**TLV DAGYPISVER SSTDPK**FKRI
 51 FEDSEYEAAG ARLVDTGVWP NAEPGTIILG LKELPSEDFP LKNDHITFAH
 101 CYKNQGGWEQ VLGRWARGGS RLYDLEFLVD EQGR**RVSAFG YHAGFAGAAL**
 151 **G**IKTLAHQLQ GSSSKLPSVE TFTDGRGYL NEDELVNQIR EDLAKAEKAL
 201 GRKPTALVLG ALGRCGK**GAV DLFLK**AGMPD DNITRWDLNE TKDRDGPYEE
 251 IAKADVFLNA IYLSKPIPPF INQELLAKQG RNLAVIDVS CDTTNPHNPI
 301 PIYSINTTFE DPTVPVEIKD DQNNLPLSVI SIDHLPSMLP REASEAFSEG
 351 LKESLLTLKD RETSRVWTD A EKLFEKVAL LPEELRTKSV

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
28 - 46	2035.0815	2034.0742	2034.0269	23	1	K.TLV DAGYPISVERS SSTDPK.F	(No match)
135 - 153	1893.0167	1892.0094	1892.0057	2	1	R.RVSAFGYHAGFAGAALGIK.T	(No match)
136 - 153	1736.9139	1735.9066	1735.9046	1	0	R.VSAFGYHAGFAGAALGIK.T	(Ions score 131)
136 - 153	1736.9139	1735.9066	1735.9046	1	0	R.VSAFGYHAGFAGAALGIK.T	(No match)
218 - 225	862.5034	861.4961	861.4960	0	0	K.GAVDLFLK.A	(No match)



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

Spot 27

Mascot Search Results

Protein View

Match to: [gi|194669270](#) Score: 88 Expect: 0.017

PREDICTED: similar to endonuclease reverse transcriptase [Bos taurus]

Nominal mass (M_r): 150298; Calculated pI value: 9.68

NCBI BLAST search of [gi|194669270](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Bos taurus](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 24%

Matched peptides shown in **Bold Red**

```

1  MAMGTYLSVI TLNVGNLNAP TKRQRLAEWI QKQDPYICCL QETHLKTGDT
51 YRLKVKGWKK IFHANRDQKK AGVAILSDK IDFKTKAVKR DKEGHYIMIT
101 GSIQEEDITI INIYAPNTGA PQYVRQLLTS MKGEINNNTI IVGYLNTPLT
151 PMDRSTKQKI NKETQTLNDT IDQLDLIDIY RSFHPKTMNF TFFSSAHGTF
201 SRIDHILGHK ASLGKFKKIE IIPSIFSDHN AVRLDLNYRR KTIKNSNIWR
251 LNNTLLNNQ ITEEIKKEIK ICIETNENEN TTTQNLWDTV KAVLRGKFIA
301 IQAHLKKQEK SQINNLTLHL KQLEKEEMKN PRVSRKEIL KIRAEINAKE
351 TKETIAKINK TKSWFFERIN KIDKPLARLI KKQREKNQIH KVRNQNGEIT
401 RDNTEIQRII RDYYQQLYAN KMDNVEEMDK FLEKYNFPKL DQEEIENLNR
451 PITSTEIETV IKNLPANKSP GPDGFTAEFY QKFREELTPV LLKLFQKIAE
501 EGKLPNSFYE ATITLIPKPD KDPTKKENYR PISLMNIDAK ILNKILAIRI
551 QQHIKKIIHH DQVGFIPGMQ GFFNIRKSVN VIHHINKLKN KNHMIISIDA
601 EKAFDKIQHP FMIKTLQKAG IEGTYLNIK AIYDKPTANI ILNGEKLKAF
651 PLKSGTRQGC PLSPLLFNIV LEVLATAIRA EKEIKGIQIG KEEVKLSLFA
701 DDMILYIENP KESTRKLLEI INDYSKVAGY KINTQKSLAF LYTNEKTER
751 EIKETIPFTI ATERIKYLG YLPKETKDLY IENYKTLVKE IKEDTNRWRN
801 IPCSWIGRIN IVKMSILPKA IYRFNAIPIK LPTVFFTELE QIISQFVWKY
851 KKPRIAKAIL KKKNGTGGIN LPDFRLYYKA TVIKTVWYWH KDRNIDQWNK
901 IESPEINPHT YGHLIFDKGG KNIQWIKDNL FNKWCWENWS TTCKRMKLEH
951 FLTPYTKINS KWIKDLNVRP ETIKLLEENI GKTLSDIHHS RILYDPPPRI
1001 LEIKAKINKW DLINLKSFCT SKETISKVKR QPSEWEKIIA NEATDKQLIS
1051 KIYKQLQLN SRKINDPIKK WAKELNRHFS KKDIQMANKH MKRCSTSLII
1101 REMQIKTTMR YHFTPVRMAA IQKSTNNKCW RGCGEKGTLL HCWWECKLVQ
1151 PLWRTVWRFL KLEIELPYD PAIPLLGIHT EETRRERDTC TPVFITALFI
1201 IARTWKQPRC PSADEWIRKL WYIYTMEYYS AIKKNTFESV LMRWMKLEPI
1251 IQSEVSQKEK HQSILTHIY GI

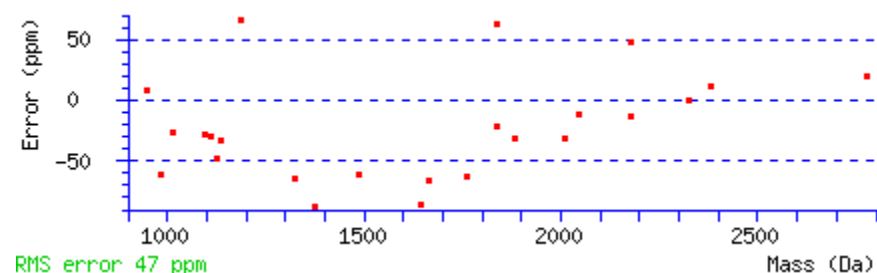
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Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
2 - 22	2177.1362	2176.1289	2176.1562	-13	0	M.AMGTYLSVITLNVNGLNAPTK.R (No match)
61 - 69	1128.5367	1127.5294	1127.5836	-48	1	K.IFHANRDQK.K (No match)
71 - 84	1489.7719	1488.7646	1488.8552	-61	1	K.AGVAILISDKIDFK.T (No match)
133 - 157	2777.4697	2776.4624	2776.4065	20	1	K.GEINNNTIIVGYLNTPLTPMDRSTK.Q Oxidation (M) (No match)
187 - 202	1837.9470	1836.9397	1836.8254	62	0	K.TMNTFFSSAHGTFSR.I (No match)
251 - 266	1884.9423	1883.9350	1883.9952	-32	0	R.LNNTLLNNQQITEEIK.K (No match)
251 - 266	1884.9423	1883.9350	1883.9952	-32	0	R.LNNTLLNNQQITEEIK.K (No match)
251 - 267	2013.0337	2012.0264	2012.0902	-32	1	R.LNNTLLNNQQITEEIKK.E (No match)
463 - 482	2181.1655	2180.1582	2180.0538	48	1	K.NLPANKSPGPDGFTAIFYQK.F (No match)
504 - 521	2047.0862	2046.0789	2046.1037	-12	0	K.LPNSFYEATITLIPKPK.D (No match)
527 - 540	1663.7385	1662.7312	1662.8399	-65	0	K.ENYRPISLMNIDAK.I (No match)
557 - 576	2326.1904	2325.1831	2325.1841	-0	0	K.IIHHDQVGFIPGMQGFNIR.K (No match)
607 - 614	1013.5328	1012.5255	1012.5528	-27	0	K.IQHPPMIK.T (No match)
631 - 646	1759.8478	1758.8405	1758.9516	-63	0	K.AIYDKPTANIILNGEK.L (No match)
631 - 646	1759.8478	1758.8405	1758.9516	-63	0	K.AIYDKPTANIILNGEK.L (No match)
683 - 691	985.5443	984.5370	984.5968	-61	1	K.EIKGIQIGK.E (No match)
683 - 691	985.5443	984.5370	984.5968	-61	1	K.EIKGIQIGK.E (No match)
692 - 711	2383.2380	2382.2307	2382.2028	12	1	K.EEVKLSLFADDMILYIENPK.E Oxidation (M) (No match)
751 - 764	1647.7527	1646.7454	1646.8879	-87	1	R.EIKETIPFTIATER.I (No match)
767 - 777	1324.6663	1323.6590	1323.7438	-64	1	K.YLGIYLPKETK.D (No match)
892 - 900	1188.6536	1187.6463	1187.5683	66	1	K.DRNIDQWNK.I (No match)
1052 - 1062	1375.6859	1374.6786	1374.7983	-87	1	K.IYKQLQLNSR.K (No match)
1082 - 1089	947.5059	946.4986	946.4906	9	1	K.KDIQMANK.H (No match)
1102 - 1110	1137.5371	1136.5298	1136.5682	-34	1	R.EMQIKTTMR.Y (No match)
1102 - 1110	1137.5371	1136.5298	1136.5682	-34	1	R.EMQIKTTMR.Y (No match)
1188 - 1203	1837.9470	1836.9397	1836.9808	-22	0	R.DTCTPVFITALFIIAR.T (No match)
1235 - 1243	1096.5143	1095.5070	1095.5383	-29	0	K.NTFESVLMR.W (No match)
1235 - 1243	1112.5077	1111.5004	1111.5332	-29	0	K.NTFESVLMR.W Oxidation (M) (No match)



LOCUS XP_001790010 1272 aa linear MAM 29-JUL-2008
 DEFINITION PREDICTED: similar to endonuclease reverse transcriptase [Bos taurus].
 ACCESSION XP_001790010
 VERSION XP_001790010.1 GI:194669270
 DBSOURCE REFSEQ: accession XM_001789958.1
 KEYWORDS .
 SOURCE Bos taurus (cattle)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from a genomic sequence (NW_001495409) annotated using gene prediction method: GNOMON, supported by mRNA evidence.
 Also see:
 Documentation of NCBI's Annotation Process
 COMPLETENESS: full length.
 FEATURES Location/Qualifiers
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 /coded_by="XM_001789958.1:1..3819"
 /db_xref="GeneID:100140546"

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

Spot 28

Mascot Search Results**Protein View**

Match to: [gi|169625443](#) Score: 178 Expect: 1.6e-011
 hypothetical protein SNOG_15994 [*Phaeosphaeria nodorum* SN15]

Nominal mass (M_r): 27112; Calculated pI value: 6.14

NCBI BLAST search of [gi|169625443](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Phaeosphaeria nodorum SN15](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|111055453](#) from [Phaeosphaeria nodorum SN15](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 19%

Matched peptides shown in **Bold Red**

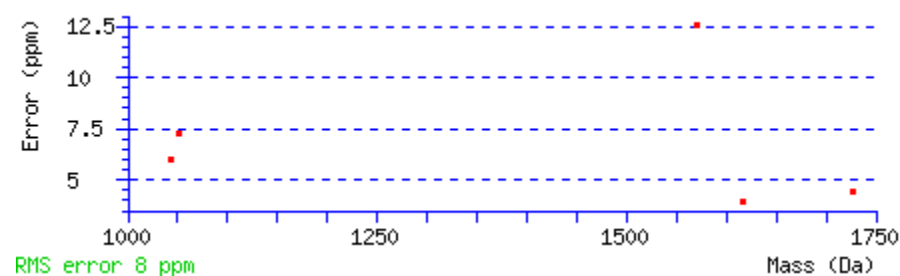
1 MAR**QFFVGGN** FKMNGTIKSI KEILGHLSQA KLDPNTEVVV APPALYLLLA
 51 REHLRPGLEV AAQNIFDKPS GAFTGEISAD QLK**DSGITWT** **ILGHSERR**TI
 101 LNEDDAFVAS KTKAALDCGL GVILCCGESL EQREANKTIE VVTKQLKAVA
 151 DKVKDWSK**IV** **VAYEPIWAIG** **TGK**VATTEQA QEVHKAIREW LQKEVSAEAA
 201 EKTR**ILYGG**S **VSEK**NCNELA KQPDIDGFLV GGASLKPAFV DIINAKQA

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
4 - 12	1043.5372	1042.5299	1042.5236	6	0	R.QFFVGGNFK.M (Ions score 74)
4 - 12	1043.5372	1042.5299	1042.5236	6	0	R.QFFVGGNFK.M (No match)
84 - 97	1571.8010	1570.7937	1570.7740	13	0	K.DSGITWTILGHSER.R (Ions score 79)
84 - 97	1571.8010	1570.7937	1570.7740	13	0	K.DSGITWTILGHSER.R (No match)
84 - 98	1727.8900	1726.8827	1726.8751	4	1	K.DSGITWTILGHSERR.T (No match)
159 - 173	1616.9110	1615.9037	1615.8974	4	0	K.IVVAYEPIWAIGTGK.V (No match)
205 - 214	1052.5699	1051.5626	1051.5550	7	0	R.ILYGGSVSEK.N (No match)



LOCUS XP_001806125 248 aa linear PLN 02-APR-2008
 DEFINITION hypothetical protein SNOG_15994 [Phaeosphaeria nodorum SN15].
 ACCESSION XP_001806125
 VERSION XP_001806125.1 GI:169625443
 DBSOURCE REFSEQ: accession XM_001806073.1
 KEYWORDS .
 SOURCE Phaeosphaeria nodorum SN15
 ORGANISM Phaeosphaeria nodorum SN15
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Phaeosphaeriaceae;
 Phaeosphaeria.
 REFERENCE 1 (residues 1 to 248)
 AUTHORS Birren,B., Lander,E., Galagan,J., Devon,K., Nusbaum,C., Jaffe,D.,
 Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Zeng,Q.,
 Yandava,C., Alvarado,L., Oleary,S., Oliver,R.O. and Solomon,P.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Phaeosphaeria nodorum SN15 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 248)
 AUTHORS Lander,E. and Birren,B.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-2008) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 REMARK Direct Submission
 REFERENCE 3 (residues 1 to 248)
 AUTHORS Oliver,R. and Solomon,P.
 TITLE Direct Submission
 JOURNAL Submitted (05-MAR-2008) Murdoch University, South Street, Perth, WA
 6150, Australia
 REMARK Direct Submission

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from EAT76573.
Method: conceptual translation.

FEATURES Location/Qualifiers

source	1..248 /organism="Phaeosphaeria nodorum SN15" /db_xref="taxon:321614"
Protein	1..248 /product="hypothetical protein" /calculated_mol_wt=26770
Region	5..244 /region_name="TIM" /note="Triosephosphate isomerase (TIM) is a glycolytic enzyme that catalyzes the interconversion of dihydroxyacetone phosphate and D-glyceraldehyde-3-phosphate. The reaction is very efficient and requires neither cofactors nor metal ions. TIM, usually...; cd00311" /db_xref="CDD:73362"
Site	order(10,12,94,164,170,210,229,231..232) /site_type="other" /note="substrate binding site" /db_xref="CDD:73362"
Site	order(10,13,44..46,48,51,63,81,84..85,96..97) /site_type="other" /note="dimer interface" /db_xref="CDD:73362"
Site	order(12,94,164) /site_type="other" /note="catalytic triad" /db_xref="CDD:73362"
CDS	1..248 /locus_tag="SNOG_15994" /coded_by="XM_001806073.1:64..810" /inference="ab initio prediction:Unveil:1.0" /inference="similar to RNA sequence, EST (same species):INSD:DR045396.1" /inference="similar to RNA sequence, EST (same species):INSD:DR045883.1" /inference="similar to RNA sequence, EST (same species):INSD:EH391712.1" /inference="similar to RNA sequence, EST (same species):INSD:EH395067.1" /inference="similar to RNA sequence, EST (same species):INSD:EH395816.1" /inference="similar to RNA sequence, EST (same species):INSD:EH396096.1" /inference="similar to RNA sequence, EST (same species):INSD:EH396292.1"

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/db_xref="GeneID:5983055"

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

Spot 29

MASCOT Mascot Search Results

Protein View

Match to: **gi|255711238** Score: **73** Expect: **0.035**
KLTH0B02596p [*Lachanea thermotolerans*]

Nominal mass (M_r): **16303**; Calculated pI value: **5.43**

NCBI BLAST search of [gi|255711238](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Lachanea thermotolerans CBS 6340](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|238933280](#) from [Lachanea thermotolerans](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **70%**

Matched peptides shown in **Bold Red**

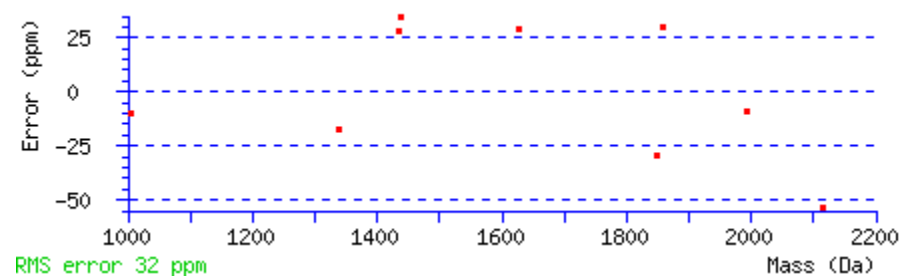
1 MSILVDMDE VRSLAQRHSI EMGLERLRVV GQYVGSWDA GRLRLEFGNV
51 SGLASAGGRA VLDASESALE RVRRARAGLV EGAVCDVRCC VMGR**DVEVME**
101 LRVLTREVQ ALGEFLAGDA GREFMSLSSG ALQHAGHDRR DEDRAR

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 12	1438.7418	1437.7345	1437.6844	35	0	-.MSILVDMDEV.R.S 2 Oxidation (M) (No match)
1 - 17	1993.9860	1992.9787	1992.9972	-9	1	-.MSILVDMDEVRS.LAQR.H 2 Oxidation (M) (No match)
13 - 26	1626.8844	1625.8771	1625.8307	29	1	R.SLAQRHSIEMGLER.L (No match)
18 - 28	1340.6871	1339.6798	1339.7030	-17	1	R.HSIEMGLERLR.V (No match)
29 - 44	1848.8961	1847.8888	1847.9431	-29	1	R.VVGQYVGSWWDAGRLR.L (No match)
45 - 59	1434.7738	1433.7665	1433.7263	28	0	R.LEFGNVSGLASAGGR.A (No match)
45 - 59	1434.7738	1433.7665	1433.7263	28	0	R.LEFGNVSGLASAGGR.A (No match)
95 - 102	1006.4774	1005.4701	1005.4801	-10	0	R.DVEVMELR.V Oxidation (M) (No match)
103 - 122	2115.0432	2114.0359	2114.1484	-53	1	R.VLTREVQALGEFLAGDAGR.E (No match)
103 - 122	2115.0432	2114.0359	2114.1484	-53	1	R.VLTREVQALGEFLAGDAGR.E (No match)
123 - 139	1858.9049	1857.8976	1857.8428	30	0	R.EFMSLSGALQHAGHDR.R Oxidation (M) (No match)



LOCUS XP_002551902 147 aa linear PLN 11-AUG-2009
 DEFINITION KLTH0B02596p [Lachancea thermotolerans].
 ACCESSION XP_002551902
 VERSION XP_002551902.1 GI:255711238
 DBSOURCE REFSEQ: accession XM_002551856.1
 KEYWORDS .
 SOURCE Lachancea thermotolerans CBS 6340 (Kluyveromyces thermotolerans CBS 6340)
 ORGANISM Lachancea thermotolerans CBS 6340
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Saccharomycotina; Saccharomycetes; Saccharomycetales;
 Saccharomycetaceae; Lachancea.
 REFERENCE 1 (residues 1 to 147)
 CONSRTM The Genolevures Consortium
 TITLE Comparative genomics of protoploid Saccharomycetaceae
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 147)
 AUTHORS Genoscope -, C.E.A.
 TITLE Direct Submission
 JOURNAL Submitted (04-JUN-2009) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence is identical to CAR21464.
 FEATURES Location/Qualifiers
 source 1..147
 /organism="Lachancea thermotolerans CBS 6340"
 /strain="CBS 6340"
 /db_xref="taxon:559295"
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 Protein 1..147
 /product="KLTH0B02596p"
 /calculated_mol_wt=16011
 CDS 1..147
 /locus_tag="KLTH0B02596g"

/old_locus_tag="KLTH-ORF15654"
/coded_by="XM_002551856.1:1..444"
/note="conserved hypothetical protein"
/db_xref="GeneID:8290733"

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

Spot 31

Mascot Search Results

Protein View

Match to: [gi|67903236](#) Score: **168** Expect: **1.6e-010**
hypothetical protein AN8605.2 [Aspergillus nidulans FGSC A4]

Nominal mass (M_r): **17787**; Calculated pI value: **8.86**

NCBI BLAST search of [gi|67903236](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus nidulans FGSC A4](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|40741449](#) from [Aspergillus nidulans FGSC A4](#)

[gi|259483180](#) from [Aspergillus nidulans FGSC A4](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

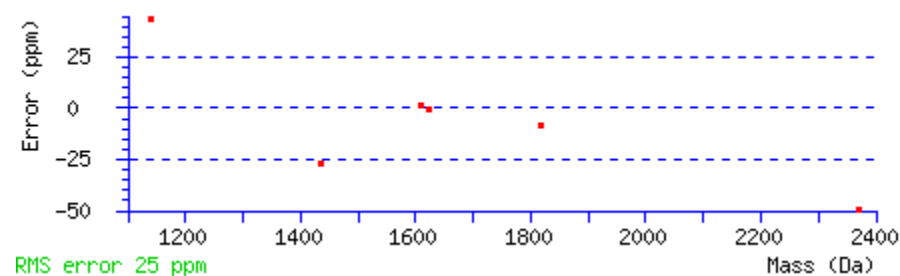
1 MSNVFFDITA NGEPLGRVEF KLFDDVVPK ARNFRELATG QHGFYKGGSP
51 FHRVIPQFML QGGDFTRQNG TGGK**SIYGEK FEDENFTLK**H DRPYLLSMAN
101 AGRNTNGSQF FITTVKTSWL DGAHVVFGEV VKGQEVVDAV EKLGSQSGAT
151 KKKVVISNSG TL

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 21	2371.0581	2370.0508	2370.1678	-49	1	-.MSNVFFDITANGEPLGRVEFK.L (No match)
18 - 29	1435.7448	1434.7375	1434.7759	-27	1	R.VEFKLFDDVVPK.T (Ions score 74)
18 - 29	1435.7448	1434.7375	1434.7759	-27	1	R.VEFKLFDDVVPK.T (No match)
54 - 67	1608.8221	1607.8148	1607.8130	1	0	R.VIPQFMLQGGDFTR.Q (Ions score 58)
54 - 67	1608.8221	1607.8148	1607.8130	1	0	R.VIPQFMLQGGDFTR.Q (No match)
54 - 67	1624.8145	1623.8072	1623.8079	-0	0	R.VIPQFMLQGGDFTR.Q Oxidation (M) (Ions score 58)
54 - 67	1624.8145	1623.8072	1623.8079	-0	0	R.VIPQFMLQGGDFTR.Q Oxidation (M) (No match)
75 - 89	1819.8599	1818.8526	1818.8676	-8	1	K.SIYGEKFEDENFTLK.H (No match)
81 - 89	1142.5856	1141.5783	1141.5291	43	0	K.FEDENFTLK.H (No match)



LOCUS XP_681874 162 aa linear PLN 09-APR-2008
 DEFINITION hypothetical protein AN8605.2 [Aspergillus nidulans FGSC A4].
 ACCESSION XP_681874
 VERSION XP_681874.1 GI:67903236
 DBSOURCE REFSEQ: accession XM_676782.1
 KEYWORDS .
 SOURCE Aspergillus nidulans FGSC A4
 ORGANISM Aspergillus nidulans FGSC A4
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; Emericella.
 REFERENCE 1 (residues 1 to 162)
 AUTHORS Galagan, J.E., Calvo, S.E., Cuomo, C., Ma, L.J., Wortman, J.R.,
 Batzoglou, S., Lee, S.I., Basturkmen, M., Spevak, C.C., Clutterbuck, J.,
 Kapitonov, V., Jurka, J., Scazzocchio, C., Farman, M., Butler, J.,
 Purcell, S., Harris, S., Braus, G.H., Draht, O., Busch, S., D'Enfert, C.,
 Bouchier, C., Goldman, G.H., Bell-Pedersen, D., Griffiths-Jones, S.,
 Doonan, J.H., Yu, J., Vienken, K., Pain, A., Freitag, M., Selker, E.U.,
 Archer, D.B., Penalva, M.A., Oakley, B.R., Momany, M., Tanaka, T.,
 Kumagai, T., Asai, K., Machida, M., Nierman, W.C., Denning, D.W.,
 Caddick, M., Hynes, M., Paoletti, M., Fischer, R., Miller, B., Dyer, P.,
 Sachs, M.S., Osmani, S.A. and Birren, B.W.
 TITLE Sequencing of Aspergillus nidulans and comparative analysis with A.
 fumigatus and A. oryzae
 JOURNAL Nature 438 (7071), 1105-1115 (2005)
 PUBMED 16372000
 REFERENCE 2 (residues 1 to 162)
 AUTHORS Birren, B., Nusbaum, C., Abebe, A., Abouelleil, A., Adekoya, E.,
 Ait-zahra, M., Allen, N., Allen, T., An, P., Anderson, M., Anderson, S.,
 Arachchi, H., Armbruster, J., Bachantsang, P., Baldwin, J., Barry, A.,
 Bayul, T., Blitshsteyn, B., Bloom, T., Blye, J., Boguslavskiy, L.,
 Borowsky, M., Boukhgalter, B., Brunache, A., Butler, J., Calixte, N.,
 Calvo, S., Camarata, J., Campo, K., Chang, J., Cheshatsang, Y.,
 Citroen, M., Collymore, A., Considine, T., Cook, A., Cooke, P.,
 Corum, B., Cuomo, C., David, R., Dawoe, T., Degray, S., Dodge, S.,

Dooley,K., Dorje,P., Dorjee,K., Dorris,L., Duffey,N., Dupes,A.,
 Elkins,T., Engels,R., Erickson,J., Farina,A., Faro,S., Ferreira,P.,
 Fischer,H., Fitzgerald,M., Foley,K., Gage,D., Galagan,J.,
 Gearin,G., Gnerre,S., Gnirke,A., Goyette,A., Graham,J.,
 Grandbois,E., Gyaltsen,K., Hafez,N., Hagopian,D., Hagos,B.,
 Hall,J., Hatcher,B., Heller,A., Higgins,H., Honan,T., Horn,A.,
 Houde,N., Hughes,L., Hulme,W., Husby,E., Iliev,I., Jaffe,D.,
 Jones,C., Kamal,M., Kamat,A., Kamvysselis,M., Karlsson,E.,
 Kells,C., Kieu,A., Kisner,P., Kodira,C., Kulbokas,E., Labutti,K.,
 Lama,D., Landers,T., Leger,J., Levine,S., Lewis,D., Lewis,T.,
 Lindblad-toh,K., Liu,X., Lokyitsang,T., Lokyitsang,Y., Lucien,O.,
 Lui,A., Ma,L.J., Mabbitt,R., Macdonald,J., Maclean,C., Major,J.,
 Manning,J., Marabella,R., Maru,K., Matthews,C., Mauceli,E.,
 Mccarthy,M., Mcdonough,S., Mcghee,T., Meldrim,J., Meneus,L.,
 Mesirov,J., Mihalev,A., Mihova,T., Mikkelsen,T., Mlenga,V.,
 Moru,K., Mozes,J., Mulrain,L., Munson,G., Naylor,J., Neues,C.,
 Nguyen,C., Nguyen,N., Nguyen,T., Nicol,R., Nielsen,C., Nizzari,M.,
 Norbu,C., Norbu,N., O'donnell,P., Okoawo,O., O'leary,S.,
 Omotosho,B., O'neill,K., Osman,S., Parker,S., Perrin,D.,
 Phunkhang,P., Piquani,B., Purcell,S., Rachupka,T., Ramasamy,U.,
 Rameau,R., Ray,V., Raymond,C., Retta,R., Richardson,S., Rise,C.,
 Rodriguez,J., Rogers,J., Rogov,P., Rutman,M., Schupbach,R.,
 Seaman,C., Settipalli,S., Sharpe,T., Sheridan,J., Sherpa,N.,
 Shi,J., Smirnov,S., Smith,C., Sougnez,C., Spencer,B., Stalker,J.,
 Stange-thomann,N., Stavropoulos,S., Stetson,K., Stone,C., Stone,S.,
 Stubbs,M., Talamas,J., Tchuinga,P., Tenzing,P., Tesfaye,S.,
 Theodore,J., Thoulutsang,Y., Topham,K., Towey,S., Tsamla,T.,
 Tsomo,N., Vallee,D., Vassiliev,H., Venkataraman,V., Vinson,J.,
 Vo,A., Wade,C., Wang,S., Wangchuk,T., Wangdi,T., Whittaker,C.,
 Wilkinson,J., Wu,Y., Wyman,D., Yadav,S., Yang,S., Yang,X.,
 Yeager,S., Yee,E., Young,G., Zainoun,J., Zembeck,L., Zimmer,A.,
 Zody,M. and Lander,E.

TITLE	Direct Submission
JOURNAL	Submitted (26-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02142, USA
COMMENT	PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EAA60639. Method: conceptual translation.
FEATURES	Location/Qualifiers
source	1..162 /organism="Aspergillus nidulans FGSC A4" /strain="FGSC A4" /db_xref="taxon:227321" /chromosome="III"
Protein	1..162 /product="hypothetical protein" /calculated_mol_wt=17667
Region	2..160 /region_name="cyclophilin_ABH_like"

/note="cyclophilin_ABH_like: Cyclophilin A, B and H-like
 cyclophilin-type peptidylprolyl cis- trans isomerase
 (PPIase) domain. This family represents the archetypal
 cystolic cyclophilin similar to human cyclophilins A, B
 and H. PPIase is an enzyme which...; cd01926"
 /db_xref="CDD:29397"
 Site order(52..53,58,109,111,119)
 /site_type="active"
 /db_xref="CDD:29397"
 CDS 1..162
 /locus_tag="AN8605.2"
 /coded_by="XM_676782.1:1..489"
 /db_xref="GeneID:2868486"

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

Spot 32

Mascot Search Results

Protein View

Match to: [gi|189196154](#) Score: **541** Expect: **7.9e-048**

NADP-specific glutamate dehydrogenase [Pyrenophora tritici-repentis Pt-1C-BFP]

Nominal mass (M_r): **49094**; Calculated pI value: **5.88**

NCBI BLAST search of [gi|189196154](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|187980294](#) from [Pyrenophora tritici-repentis Pt-1C-BFP](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **29%**

Matched peptides shown in **Bold Red**

```

1 MSEPEFEQAR KELVSTLEAS SLFSKNPEYK KALEVVSVP E RIIQFRVWE
51 NDKGECQVQK GYRVQFNSAL GPYKGGLRFH PTVNLSILKF LGFEQIFKNA
101 LTGLNMGGGK GGCDFFPKGK SDNEIRKFCV AFMRELNKHI GADTDVPAGD
151 IGVGGREIGY LFGAYRAERN RWEGVLTGKG GSWGGSLIRP EATGYGLVYY
201 VEHMINYASG GKESFAGKRV ALSGSGNVAQ YAALKIIELG GTVISLSDSK
251 GALIAEDDKG FTPEIINQIA ALKLERKALT ALENHNFKYI EGARPWKEVN
301 KVDVALPSAT QNEVSEDEAK ALIESGAKYI AEGSNMGCTQ EAIEVFEAHR
351 REKKGDAIWY APGKAANAGG VAVSGLEMAQ NSQRLSWTAE QVDEKLKGIM
401 KDCFENCLST AKEYFTPAEG EFPSLVGGAN VAGFRKVAAA MHDQGDWW
    
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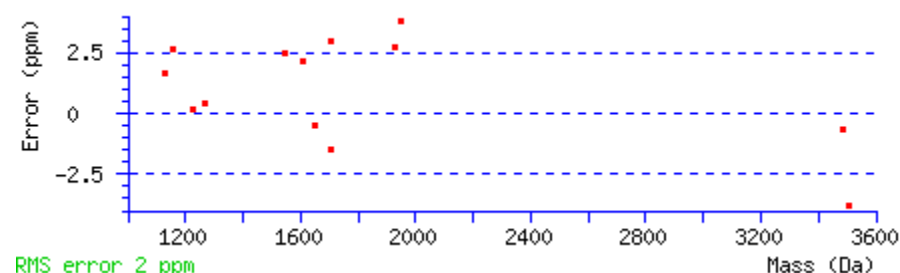
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
64 - 74	1223.6421	1222.6348	1222.6346	0	0	R.VQFNSALGPYK.G (Ions score 54)
64 - 74	1223.6421	1222.6348	1222.6346	0	0	R.VQFNSALGPYK.G (No match)
64 - 78	1606.8735	1605.8662	1605.8627	2	1	R.VQFNSALGPYKGGLR.F (No match)
75 - 89	1651.9634	1650.9561	1650.9570	-1	1	K.GGLRFHPTVNLSILK.F (No match)
79 - 89	1268.7367	1267.7294	1267.7289	0	0	R.FHPTVNLSILK.F (Ions score 83)
79 - 89	1268.7367	1267.7294	1267.7289	0	0	R.FHPTVNLSILK.F (No match)
90 - 98	1128.6107	1127.6034	1127.6015	2	0	K.FLGFEQIFK.N (Ions score 60)

90 - 98	1128.6107	1127.6034	1127.6015	2	0	K.FLGFEQIFK.N	(No match)
139 - 156	1706.8507	1705.8434	1705.8384	3	0	K.HIGADTDVPAGDIGVGGR.E	(Ions score 120)
139 - 156	1706.8507	1705.8434	1705.8384	3	0	K.HIGADTDVPAGDIGVGGR.E	(No match)
170 - 179	1159.6249	1158.6176	1158.6145	3	1	R.NRWEGLVTGK.G	(Ions score 58)
170 - 179	1159.6249	1158.6176	1158.6145	3	1	R.NRWEGLVTGK.G	(No match)
180 - 212	3489.6873	3488.6800	3488.6823	-1	0	K.GGSWGGSLIRPEATGYGLVYYVEHMINYASGGK.E	(No match)
180 - 212	3505.6711	3504.6638	3504.6772	-4	0	K.GGSWGGSLIRPEATGYGLVYYVEHMINYASGGK.E	Oxidation (M) (No matc
219 - 235	1704.9366	1703.9293	1703.9318	-1	1	K.RVALSGSGNVAQYAALK.I	(No match)
220 - 235	1548.8418	1547.8345	1547.8307	2	0	R.VALSGSGNVAQYAALK.I	(No match)
365 - 384	1930.9451	1929.9378	1929.9326	3	0	K.AANAGGVAVSGLEMAQNSQR.L	(Ions score 98)
365 - 384	1930.9451	1929.9378	1929.9326	3	0	K.AANAGGVAVSGLEMAQNSQR.L	(No match)
365 - 384	1946.9423	1945.9350	1945.9276	4	0	K.AANAGGVAVSGLEMAQNSQR.L	Oxidation (M) (Ions score 59)
365 - 384	1946.9423	1945.9350	1945.9276	4	0	K.AANAGGVAVSGLEMAQNSQR.L	Oxidation (M) (No match)



LOCUS XP_001934415 448 aa linear PLN 30-MAY-2008
 DEFINITION NADP-specific glutamate dehydrogenase [Pyrenophora tritici-repentis Pt-1C-BFP].
 ACCESSION XP_001934415
 VERSION XP_001934415.1 GI:189196154
 DBSOURCE REFSEQ: accession XM_001934380.1
 KEYWORDS .
 SOURCE Pyrenophora tritici-repentis Pt-1C-BFP
 ORGANISM Pyrenophora tritici-repentis Pt-1C-BFP
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
 Pyrenophora.
 REFERENCE 1 (residues 1 to 448)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C., Guigo,R., Borodovsky,M., Zeng,Q., O'Leary,S., Alvarado,L., Pandelova,I. and Ciuffetti,L.
 CONSRTM The Broad Institute Genome Sequencing Platform

TITLE Genome Sequence of *Pyrenophora tritici-repentis*
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 448)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., MacCallum,I.A., Young,S., LaButti,K.,
 DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P.,
 Pearson,M., Howarth,C., Larson,L., White,J., Yandava,C., Kodira,C.,
 Zeng,Q., O'Leary,S., Alvarado,L., Ciuffetti,L. and Pandelova,I.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (16-MAR-2007) Broad Institute of MIT and Harvard, 7
 Cambridge Center, Cambridge, MA 02142, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from EDU46920.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
 source 1..448
 /organism="Pyrenophora tritici-repentis Pt-1C-BFP"
 /strain="Pt-1C-BFP"
 /db_xref="taxon:426418"
 Protein 1..448
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 /calculated_mol_wt=48651
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 /note="glutamate dehydrogenase; Provisional; PRK09414"
 /db_xref="CDD:169848"
 Region 39..166
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 /note="Glu/Leu/Phe/Val dehydrogenase, dimerization domain;
 pfam02812"
 /db_xref="CDD:145786"
 Region 177..446
 /region_name="NAD_bind_2_Glu_DH"
 /note="NAD(P) binding domain of glutamate dehydrogenase,
 subgroup 2; cd05313"
 /db_xref="CDD:133455"
 Site order(226..228,248..249,309..310,333..335)
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 /note="NAD(P) binding site"
 /db_xref="CDD:133455"
 CDS 1..448
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 /coded_by="XM_001934380.1:1..1347"
 /db_xref="GeneID:6342318"

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

Spot 33

MASCOT Mascot Search Results

Protein View

Match to: **gi|145613040** Score: **305** Expect: **3.2e-024**
conserved hypothetical protein [Magnaporthe grisea 70-15]

Nominal mass (M_r): **25180**; Calculated pI value: **5.73**

NCBI BLAST search of [gi|145613040](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Magnaporthe grisea 70-15](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|145020105](#) from [Magnaporthe grisea 70-15](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

1 MAEEQRPAPL RLGTEAPNFK AETTKGPIDF HEFIGSNWVI LFSHPEDFTP
 51 VCTTELGEFA **RLEPEFTKR**G VKLIGLSANT VGSHDGIWD INDVTGSHVA
 101 FPIIADKERK VAYLYDMLDY QDTTNVDEKG IAFTIR**SVFI IDPAKKIRTI**
 151 **LSYPASTGR**N SAEVLRIVDS LQTGDKHK**VT TPINWVP**GDD **VIVHPSIK**DE
 201 QAKDLFPNFR AVKPYLRFTP LPKE

Show predicted peptides also

Sort Peptides By



Residue Number

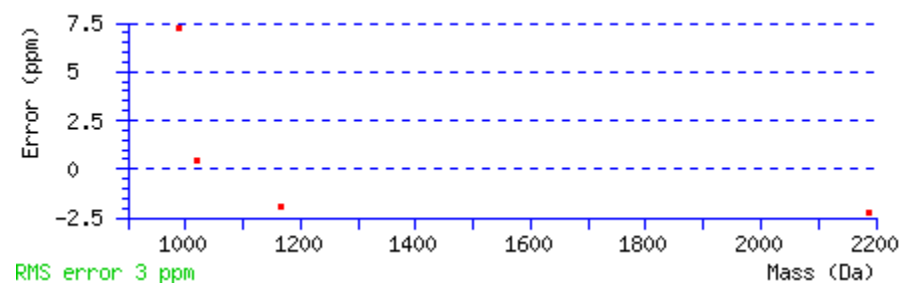


Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
62 - 69	1019.5524	1018.5451	1018.5447	0	1	R.LEPEFTKR.G (Ions score 56)
62 - 69	1019.5524	1018.5451	1018.5447	0	1	R.LEPEFTKR.G (No match)
137 - 145	989.5738	988.5665	988.5593	7	0	R.SVFIIDPAK.K (No match)
149 - 159	1165.6189	1164.6116	1164.6139	-2	0	R.TILSYASTGR.N (Ions score 95)
149 - 159	1165.6189	1164.6116	1164.6139	-2	0	R.TILSYASTGR.N (No match)
179 - 198	2187.1760	2186.1687	2186.1736	-2	0	K.VTTPINWVP GDD VIVHPSIK.D (Ions score 133)
179 - 198	2187.1760	2186.1687	2186.1736	-2	0	K.VTTPINWVP GDD VIVHPSIK.D (No match)



LOCUS XP_362792 224 aa linear PLN 17-MAY-2010
 DEFINITION conserved hypothetical protein [Magnaporthe oryzae 70-15].
 ACCESSION XP_362792
 VERSION XP_362792.2 GI:145613040
 DBSOURCE REFSEQ: accession XM_362792.2
 KEYWORDS .
 SOURCE Magnaporthe oryzae 70-15
 ORGANISM Magnaporthe oryzae 70-15
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Magnaporthales; Magnaporthaceae; Magnaporthe.
 REFERENCE 1 (residues 1 to 224)
 AUTHORS Dean,R.A., Talbot,N.J., Ebbole,D.J., Farman,M.L., Mitchell,T.K.,
 Orbach,M.J., Thon,M., Kulkarni,R., Xu,J.R., Pan,H., Read,N.D.,
 Lee,Y.H., Carbone,I., Brown,D., Oh,Y.Y., Donofrio,N., Jeong,J.S.,
 Soanes,D.M., Djonovic,S., Kolomiets,E., Rehmeier,C., Li,W.,
 Harding,M., Kim,S., Lebrun,M.H., Bohnert,H., Coughlan,S.,
 Butler,J., Calvo,S., Ma,L.J., Nicol,R., Purcell,S., Nusbaum,C.,
 Galagan,J.E. and Birren,B.W.
 TITLE The genome sequence of the rice blast fungus Magnaporthe grisea
 JOURNAL Nature 434 (7036), 980-986 (2005)
 PUBMED 15846337
 REFERENCE 2 (residues 1 to 224)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Jaffe,D.,
 Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Yandava,C.,
 Zeng,Q., Alvarado,L., O'Leary,S., Dean,R., Mitchell,T., Brown,D.,
 Pan,H., Thon,M., Zhu,H. and Blackmon,B.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission
 JOURNAL Submitted (26-SEP-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02142, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final

NCBI review. The reference sequence was derived from EDK04333.
On Apr 23, 2007 this sequence version replaced gi:39946510.
Method: conceptual translation.

FEATURES	Location/Qualifiers
source	1..224 /organism="Magnaporthe oryzae 70-15" /strain="70-15" /db_xref="taxon:242507" /chromosome="I"
Protein	1..224 /product="hypothetical protein" /calculated_mol_wt=25008
Region	9..203 /region_name="AhpC" /note="Peroxiredoxin [Posttranslational modification, protein turnover, chaperones]; COG0450" /db_xref="CDD:30799"
Region	12..220 /region_name="PRX_1cys" /note="Peroxiredoxin (PRX) family, 1-cys PRX subfamily; composed of PRXs containing only one conserved cysteine, which serves as the peroxidatic cysteine. They are homodimeric thiol-specific antioxidant (TSA) proteins that confer a protective role in cells by...; cd03016" /db_xref="CDD:48565"
Site	order(12,50,53..55,58,90,93,116,134,148..150,152..154,156..161,163,166,170..171,180..181,183..184,215,218) /site_type="other" /note="dimer interface" /db_xref="CDD:48565"
Site	order(24,78..80,82..83,85..86,88..89,98,107..108,118,132..133,196,213) /site_type="other" /note="decamer (pentamer of dimers) interface" /db_xref="CDD:48565"
Site	order(49,52,136) /site_type="other" /note="catalytic triad" /db_xref="CDD:48565"
CDS	1..224 /locus_tag="MGG_08256" /old_locus_tag="MG08256.4" /coded_by="XM_362792.2:1..675" /db_xref="GeneID:2678602"

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

Spot 34

Mascot Search Results

Protein View

Match to: [gi|156057169](#) Score: **98** Expect: **0.0016**
ATP sulfurylase [Sclerotinia sclerotiorum 1980]

Nominal mass (M_r): **64159**; Calculated pI value: **6.55**

NCBI BLAST search of [gi|156057169](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Sclerotinia sclerotiorum 1980 UF-70](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|154702101](#) from [Sclerotinia sclerotiorum 1980 UF-70](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **22%**

Matched peptides shown in **Bold Red**

1 **MANSPHGGVL KDLLAR**DLPR HNELSAEAET LPAIVLTER**Q LCDLELILSG**
51 **GFSPLEGFMN EKDYNGVVEN** NRLADGNVFS MPITLDVSKE QIEQLGIKEG
101 VRITIRDFRD DRNLAIINVE DVYKPNKEKE AKEVFGGDVD HPAVKYLYNT
151 AAEFYVGSKI DAINRLEHYD YVALRYTPAE MRLHFDKLGW SKVVAFQTRN
201 PMHRAHRELT VRAARAR**QAN VLIHPVVGLT KPGDIDHFTR VRVYQALLPR**
251 **YPNGMAVLGL LPLAMR**MGGP REAVWHAI**IR KNYGATHFIV** GRDHAGPGKN
301 SKGEFFYGPY DAQYAVEKFK DELGIEVVPF QMMTYLPDSD EYRPKDEVPO
351 GTR**TLDISGT ELRSRLRSGR** EIPWFSSYPE VVRVLRESHP PRSAQGFTVF
401 LTGYHSSGKD AIARALQTTL NQQGGR**SVSL LLGETVRAEL** SSELGFSRAD
451 RTRNIGR**IAF VASELTR**SGA AVIAAPIAPY EDARKHAREM VEKYGDFYLV
501 HVATSLEHSE KIDKKGVYAK ARNGEIKGFT GVDDPYEVPA KADFTVDIEK
551 TSVRNAVHSI ILMLESAGLL DRL

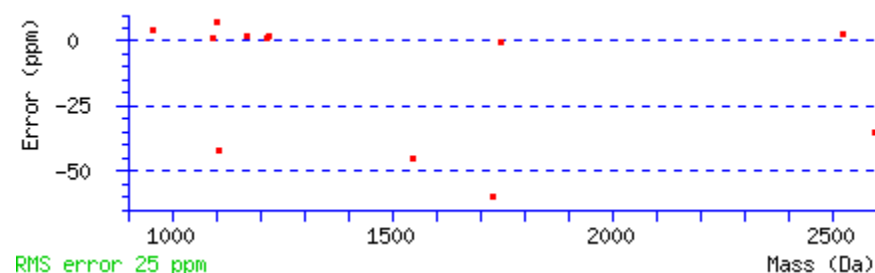
Show predicted peptides also

Sort Peptides By

☒ Residue Number
 ☐ Increasing Mass
 ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
2 - 16	1547.7948	1546.7875	1546.8580	-46	1	M.ANSPHGGVLKDLLAR.D (No match)
40 - 62	2597.1714	2596.1641	2596.2553	-35	0	R.QLCDLELILSGGFSPLEGFMNEK.D (No match)
218 - 240	2527.3840	2526.3767	2526.3707	2	0	R.QANVLIHPVVGLTKPGDIDHFTR.V (No match)
241 - 250	1214.7379	1213.7306	1213.7295	1	1	R.VRVYQALLPR.Y (No match)

243 - 250	959.5714	958.5641	958.5600	4	0	R.VYQALLPR.Y	(Ions score 48)
243 - 250	959.5714	958.5641	958.5600	4	0	R.VYQALLPR.Y	(No match)
251 - 266	1731.8242	1730.8169	1730.9211	-60	0	R.YPNGMAVLGLLPLAMR.M	Oxidation (M) (No match)
251 - 266	1747.9231	1746.9158	1746.9161	-0	0	R.YPNGMAVLGLLPLAMR.M	2 Oxidation (M) (No match)
251 - 266	1747.9231	1746.9158	1746.9161	-0	0	R.YPNGMAVLGLLPLAMR.M	2 Oxidation (M) (No match)
272 - 280	1094.6117	1093.6044	1093.6032	1	0	R.EAVWHAIR.K	(No match)
272 - 281	1222.7073	1221.7000	1221.6982	1	1	R.EAVWHAIRK.N	(No match)
354 - 363	1104.5975	1103.5902	1103.5822	7	0	R.TLDISGTEL.R.S	(No match)
427 - 437	1173.6858	1172.6785	1172.6765	2	0	R.SVSLLLGETVR.A	(No match)
458 - 467	1106.5741	1105.5668	1105.6131	-42	0	R.IAFVASELTR.S	(No match)



LOCUS XP_001594508 573 aa linear PLN 26-FEB-2008
 DEFINITION ATP sulfurylase [Sclerotinia sclerotiorum 1980].
 ACCESSION XP_001594508
 VERSION XP_001594508.1 GI:156057169
 DBSOURCE REFSEQ: accession XM_001594458.1
 KEYWORDS .
 SOURCE Sclerotinia sclerotiorum 1980 UF-70
 ORGANISM Sclerotinia sclerotiorum 1980 UF-70
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Leotiomycetes;
 Helotiales; Sclerotiniaceae; Sclerotinia.
 REFERENCE 1 (residues 1 to 573)
 AUTHORS Birren,B., Galagan,J., Lander,E., Devon,K., Nusbaum,C., Cuomo,C.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Yandava,C., Kodira,C.,
 Zeng,Q., Alvarado,L., O'Leary,S., Dickman,M.B., Kohn,L. and
 Rollins,J.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Sclerotinia sclerotiorum 1980 genome
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 573)
 AUTHORS Lander,E., Birren,B. and Cuomo,C.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team

TITLE Direct Submission
 JOURNAL Submitted (10-JUN-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02142, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from ED001840.
 Method: conceptual translation.
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 source Location/Qualifiers
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 /strain="1980"
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 Protein 1..573
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 /calculated_mol_wt=64011
 Region 4..572
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 /note="bifunctional sulfate adenylyltransferase subunit 1/adenylylsulfate kinase protein; Validated; PRK05537"
 /db_xref="CDD:168090"
 Region 31..388
 /region_name="ATPS"
 /note="ATP-sulfurylase; cd00517"
 /db_xref="CDD:173895"
 Site order(196..200,206,291..292,294..295,332..333)
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 /db_xref="CDD:173895"
 Site 228..238
 /site_type="other"
 /note="flexible loop"
 /db_xref="CDD:173895"
 Region 398..547
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 /db_xref="CDD:30200"
 Site order(405..406,408..411,437,446,451,454,477..479,512,529..530)
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 /note="ligand-binding site"
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 /coded_by="XM_001594458.1:1..1722"
 /db_xref="GeneID:5490580"

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

Spot 35

MASCOT Mascot Search Results

Protein View

Match to: [gi|169596136](#) Score: 271 Expect: 7.9e-021
 hypothetical protein SNOG_00819 [*Phaeosphaeria nodorum* SN15]

Nominal mass (M_r): 58359; Calculated pI value: 5.71

NCBI BLAST search of [gi|169596136](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Phaeosphaeria nodorum SN15](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|111071194](#) from [Phaeosphaeria nodorum SN15](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: 28%

Matched peptides shown in **Bold Red**

```

1  MANALDHLNA GRTRIEWLSQ LNTEYHPAKE YRRTSIIGTI GPKTNSAEKM
51  NALRRAGLNV VRMNFSGSY EYHQSVIDNA REAEKQSGR PLAIALDTKG
101 PEIRTGNTVG DADIPIKAGT ELNITDDAY ATKCDDKNMY VDYKNITKVI
151 EVGRTIYVDD GVLSFEVLEV VDDQTLRVKC VNNGKISSKK GVNLPKTDID
201 LPPLSEKDKA DLKFGVKNKV DMVFASFIRR GSDITAIREV LGEEGKDIQI
251 IAKVENQQGV NNFDDILKET DGVMVARGDL GIEIPPSQVF IAQKMMITKC
301 NIAGKPVICA TQMLSEMTYN PRPTRAEVSD VGNAVLDGAD CVMLSGETAK
351 GDYPVEAVTM MHETCLLAEV AIPYVNAFDE LRKLAPVPCP TTETCMAAAV
401 SASLEQNAGA ILVLTTSGTT ARLVSKYRPV CPIIMVTRNA SASRYSHLYR
451 GVYPFYFAEE KPDFKAAPWQ EDVDRRLKWG IMNAIKLGVL EKGAPVICVQ
501 GWRGGMGHTN TLRIVPATED LGLDQEA
  
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Show predicted peptides also

Sort Peptides By



Residue Number



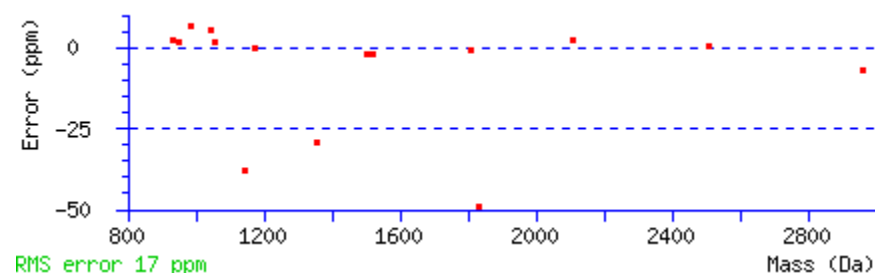
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
33 - 43	1142.6462	1141.6389	1141.6819	-38	1	R.RTSIIGTIGPK.T	(Ions score 7)
33 - 43	1142.6462	1141.6389	1141.6819	-38	1	R.RTSIIGTIGPK.T	(No match)
34 - 43	986.5948	985.5875	985.5808	7	0	R.TSIIGTIGPK.T	(Ions score 28)
34 - 43	986.5948	985.5875	985.5808	7	0	R.TSIIGTIGPK.T	(No match)
105 - 133	2965.4426	2964.4353	2964.4564	-7	1	R.TGNTVGDA DIPIKAGTELNITDDAYATK.C	(No match)

105 - 133	2965.4426	2964.4353	2964.4564	-7	1	R.TGNTVGDAIPIKAGTELNITDDAYATK.C	(No match)
191 - 207	1835.9216	1834.9143	1835.0040	-49	1	K.GVNLPKTDIDLPLSEK.D	(No match)
191 - 207	1835.9216	1834.9143	1835.0040	-49	1	K.GVNLPKTDIDLPLSEK.D	(No match)
220 - 230	1356.6699	1355.6626	1355.7020	-29	1	K.VDMVFASFIRR.G	Oxidation (M) (No match)
220 - 230	1356.6699	1355.6626	1355.7020	-29	1	K.VDMVFASFIRR.G	Oxidation (M) (No match)
278 - 294	1811.9882	1810.9809	1810.9829	-1	0	R.GDLGIEIPPSQVFIAQK.M	(Ions score 62)
278 - 294	1811.9882	1810.9809	1810.9829	-1	0	R.GDLGIEIPPSQVFIAQK.M	(No match)
326 - 350	2508.1599	2507.1526	2507.1520	0	0	R.AEVSDVGNAVLDGADCVMLSGETAK.G	(No match)
326 - 350	2508.1599	2507.1526	2507.1520	0	0	R.AEVSDVGNAVLDGADCVMLSGETAK.G	(No match)
427 - 438	1504.8096	1503.8023	1503.8054	-2	0	K.YRPVCPIMVTR.N	(Ions score 40)
427 - 438	1504.8096	1503.8023	1503.8054	-2	0	K.YRPVCPIMVTR.N	(No match)
427 - 438	1520.8043	1519.7970	1519.8003	-2	0	K.YRPVCPIMVTR.N	Oxidation (M) (Ions score 12)
427 - 438	1520.8043	1519.7970	1519.8003	-2	0	K.YRPVCPIMVTR.N	Oxidation (M) (No match)
427 - 444	2107.0947	2106.0874	2106.0826	2	1	K.YRPVCPIMVTRNASASR.Y	Oxidation (M) (No match)
427 - 444	2107.0947	2106.0874	2106.0826	2	1	K.YRPVCPIMVTRNASASR.Y	Oxidation (M) (No match)
477 - 486	1173.6812	1172.6739	1172.6740	-0	1	R.LKWGIMNAIK.L	(No match)
477 - 486	1173.6812	1172.6739	1172.6740	-0	1	R.LKWGIMNAIK.L	(No match)
479 - 486	932.5044	931.4971	931.4949	2	0	K.WGIMNAIK.L	(Ions score 45)
479 - 486	932.5044	931.4971	931.4949	2	0	K.WGIMNAIK.L	(No match)
479 - 486	948.4987	947.4914	947.4899	2	0	K.WGIMNAIK.L	Oxidation (M) (Ions score 28)
479 - 486	948.4987	947.4914	947.4899	2	0	K.WGIMNAIK.L	Oxidation (M) (No match)
504 - 513	1043.5105	1042.5032	1042.4978	5	0	R.GGMGHTNTRL.I	(Ions score 11)
504 - 513	1043.5105	1042.5032	1042.4978	5	0	R.GGMGHTNTRL.I	(No match)
504 - 513	1059.5015	1058.4942	1058.4927	1	0	R.GGMGHTNTRL.I	Oxidation (M) (Ions score 21)
504 - 513	1059.5015	1058.4942	1058.4927	1	0	R.GGMGHTNTRL.I	Oxidation (M) (No match)



LOCUS XP_001791492 527 aa linear PLN 02-APR-2008
 DEFINITION hypothetical protein SNOG_00819 [Phaeosphaeria nodorum SN15].
 ACCESSION XP_001791492
 VERSION XP_001791492.1 GI:169596136
 DBSOURCE REFSEQ: accession XM_001791440.1
 KEYWORDS .
 SOURCE Phaeosphaeria nodorum SN15
 ORGANISM Phaeosphaeria nodorum SN15
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyces; Dothideomycetes;

Pleosporomycetidae; Pleosporales; Pleosporineae; Phaeosphaeriaceae; Phaeosphaeria.

REFERENCE 1 (residues 1 to 527)

AUTHORS Birren,B., Lander,E., Galagan,J., Devon,K., Nusbaum,C., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M., Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K., Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Zeng,Q., Yandava,C., Alvarado,L., Oleary,S., Oliver,R.O. and Solomon,P.

CONSRTM The Broad Institute Genome Sequencing Platform

TITLE Annotation of the Phaeosphaeria nodorum SN15 genome

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 527)

AUTHORS Lander,E. and Birren,B.

CONSRTM The Genome Sequencing Platform, The Genome Assembly Team

TITLE Direct Submission

JOURNAL Submitted (05-MAR-2008) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA

REMARK Direct Submission

REFERENCE 3 (residues 1 to 527)

AUTHORS Oliver,R. and Solomon,P.

TITLE Direct Submission

JOURNAL Submitted (05-MAR-2008) Murdoch University, South Street, Perth, WA 6150, Australia

REMARK Direct Submission

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EAT92314.
Method: conceptual translation.

FEATURES Location/Qualifiers

source 1..527
/organism="Phaeosphaeria nodorum SN15"
/db_xref="taxon:321614"

Protein 1..527
/product="hypothetical protein"
/calculated_mol_wt=57694

Region 31..517
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/note="Pyruvate kinase (PK): Large allosteric enzyme that regulates glycolysis through binding of the substrate, phosphoenolpyruvate, and one or more allosteric effectors. Like other allosteric enzymes, PK has a high substrate affinity R state and a low...; cd00288"
/db_xref="CDD:29370"

Region 32..514
/region_name="pyruv_kin"
/note="pyruvate kinase; TIGR01064"
/db_xref="CDD:162184"

Site order(33..34,91,93,101..104,192..193,199,202..206,221,229,236,247,283,301..302,306,338,340,369,371..372,426,428,430,

Site	441,444..445,447,449..451) /site_type="other" /note="domain interfaces" /db_xref="CDD:29370"
CDS	order(62,64,97,227,253,255,279,311) /site_type="active" /db_xref="CDD:29370" 1..527 /locus_tag="SNOG_00819" /coded_by="XM_001791440.1:1..1584" /inference="ab initio prediction:Unveil:1.0" /inference="similar to RNA sequence, EST (same species):INSD:EH389286.1" /inference="similar to RNA sequence, EST (same species):INSD:EH389713.1" /inference="similar to RNA sequence, EST (same species):INSD:EH390034.1" /inference="similar to RNA sequence, EST (same species):INSD:EH390088.1" /note="gene prediction version 2" /db_xref="GeneID:5967717"

Mascot: http://www.matrixscience.com/
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Spot 36

MASCOT Mascot Search Results

Protein View

Match to: **gi|145239481** Score: **136** Expect: **2.5e-007**
hypothetical protein An08g02700 [Aspergillus niger]

Nominal mass (M_r): **42273**; Calculated pI value: **5.70**

NCBI BLAST search of [gi|145239481](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus niger CBS 513.88](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|134076898](#) from [Aspergillus niger](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

1 MGSVANGSTF LFTSESVGEG HPDKIADQVS DAILDACLA E DPLSKVACET
51 ATKTMGMVMVF GEITTQAKLD YQKVIRGAIQ DIGYDASEKG FDYKTCNVLV
101 AIEQQSPDIA QGLHYEEALE KLGAGDQGIM FGYATDETPE LLPLTVVLSH
151 KLNKAMTDAR **KNGTIPWLRP** DTKTQVTIEY AHDNGAVKPL RVDIVISAQ
201 HSDDVTTEEL RKVLKEQIIK **SVIPANLLDD** RTVYHLQPSG RFVIGGPQGD
251 AGLTGR**KIIV** **DTYGGWGAHG** **GGAFGSGKDYS** KVDRAAYVA RWIAKSLINA
301 GLARRALVQL SYAIGVAEPL SIFVETYGTS SK**TSDELVQI** **IRNNFDLRPG**
351 **VIVK**ELDLAK PIYFKTAKNG HFTNQEFSEW KPKALKF

Show predicted peptides also

Sort Peptides By



Residue Number



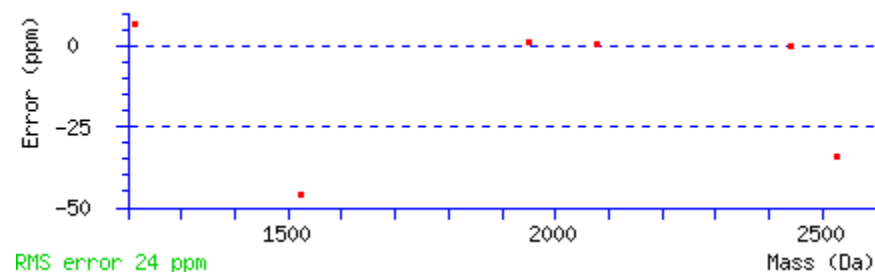
Increasing Mass



Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
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161	173	1525.7782	1524.7709	1524.8412	-46	1	R.KNGTIPWLRPDTK.T (No match)
221	231	1212.6659	1211.6586	1211.6510	6	0	K.SVIPANLLDDR.T (No match)
257	277	2078.0459	2077.0386	2077.0381	0	1	R.KIIVDTYGGWGAHGGGAFSGK.D (Ions score 50)
257	277	2078.0459	2077.0386	2077.0381	0	1	R.KIIVDTYGGWGAHGGGAFSGK.D (No match)
258	277	1949.9519	1948.9446	1948.9432	1	0	K.IIVDTYGGWGAHGGGAFSGK.D (No match)
258	277	1949.9519	1948.9446	1948.9432	1	0	K.IIVDTYGGWGAHGGGAFSGK.D (No match)
258	281	2443.1670	2442.1597	2442.1604	-0	1	K.IIVDTYGGWGAHGGGAFSGKDYSK.V (No match)

333 - 354 2526.3167 2525.3094 2525.3966 -35 1 K.TSDELVQIIRNFDLRPGVIVK.E ([No match](#))



LOCUS XP_001392387 387 aa linear PLN 28-MAR-2008
 DEFINITION hypothetical protein An08g02700 [Aspergillus niger].
 ACCESSION XP_001392387
 VERSION XP_001392387.1 GI:145239481
 DBSOURCE REFSEQ: accession XM_001392350.1
 KEYWORDS .
 SOURCE Aspergillus niger CBS 513.88
 ORGANISM Aspergillus niger CBS 513.88
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (residues 1 to 387)
 AUTHORS Pel,H.J., de Winde,J.H., Archer,D.B., Dyer,P.S., Hofmann,G.,
 Schaap,P.J., Turner,G., de Vries,R.P., Albang,R., Albermann,K.,
 Andersen,M.R., Bendtsen,J.D., Benen,J.A., van den Berg,M.,
 Breestraat,S., Caddick,M.X., Contreras,R., Cornell,M.,
 Coutinho,P.M., Danchin,E.G., Debets,A.J., Dekker,P., van
 Dijck,P.W., van Dijk,A., Dijkhuizen,L., Driessen,A.J., d'Enfert,C.,
 Geysens,S., Goosen,C., Groot,G.S., de Groot,P.W., Guillemette,T.,
 Henrissat,B., Herweijer,M., van den Hombergh,J.P., van den
 Hondel,C.A., van der Heijden,R.T., van der Kaaij,R.M., Klis,F.M.,
 Kools,H.J., Kubicek,C.P., van Kuyk,P.A., Lauber,J., Lu,X., van der
 Maarel,M.J., Meulenbergh,R., Menke,H., Mortimer,M.A., Nielsen,J.,
 Oliver,S.G., Olsthoorn,M., Pal,K., van Peij,N.N., Ram,A.F.,
 Rinas,U., Roubos,J.A., Sagt,C.M., Schmoll,M., Sun,J., Ussery,D.,
 Varga,J., Vervecken,W., van de Vondervoort,P.J., Wedler,H.,
 Wosten,H.A., Zeng,A.P., van Ooyen,A.J., Visser,J. and Stam,H.
 TITLE Genome sequencing and analysis of the versatile cell factory
 Aspergillus niger CBS 513.88
 JOURNAL Nat. Biotechnol. 25 (2), 221-231 (2007)
 PUBMED 17259976
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from CAK45307.
 FEATURES Location/Qualifiers

source 1..387
 /organism="Aspergillus niger CBS 513.88"
 /db_xref="taxon:425011"
 /clone="An08"
 Protein 1..387
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 /calculated_mol_wt=41997
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 /note="S-adenosylmethionine synthetase; Provisional;
 PTZ00104"
 /db_xref="CDD:173396"
 Region 10..107
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 /note="S-adenosylmethionine synthetase, N-terminal domain;
 pfam00438"
 /db_xref="CDD:144142"
 Region 120..242
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 /note="S-adenosylmethionine synthetase, central domain;
 pfam02772"
 /db_xref="CDD:145757"
 Region 244..381
 /region_name="S-AdoMet_synt_C"
 /note="S-adenosylmethionine synthetase, C-terminal domain;
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 /db_xref="CDD:111646"
 CDS 1..387
 /locus_tag="An08g02700"
 /coded_by="XM_001392350.1:1..1164"
 /inference="profile:COGS:COG0192"
 /inference="profile:PFAM:PF00438"
 /inference="profile:PFAM:PF02772"
 /inference="profile:PFAM:PF02773"
 /inference="similar to AA sequence:PIR:S65800"
 /note="Catalytic activity: methionine adenosyltransferases
 convert ATP and L-methionine and H(2)O to phosphate and
 diphosphate and S-adenosyl-L-methionine.;
 Function: adenosylmethionine is an important methyl donor
 in most transmethylation reactions and is also the
 propylamino donor in the biosynthesis of polyamines.;
 Phenotype: mutations of the human adenosylmethionine can
 result in an autosomal recessive disorder, the
 hypermethioninemia.;
 Title: strong similarity to S-adenosylmethionine synthase
 eth-1 - Neurospora crassa"
 /citation=[PUBMED 8849888]
 /db_xref="GOA:A2QQJ1"
 /db_xref="GeneID:4982584"

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

Spot 37

MASCOT Mascot Search Results

Protein View

Match to: **gi|148361511** Score: **115** Expect: **3.2e-005**
vacuolar serine protease [Cladosporium cladosporioides]

Nominal mass (M_r): **41006**; Calculated pI value: **5.80**

NCBI BLAST search of [gi|148361511](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Cladosporium cladosporioides](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

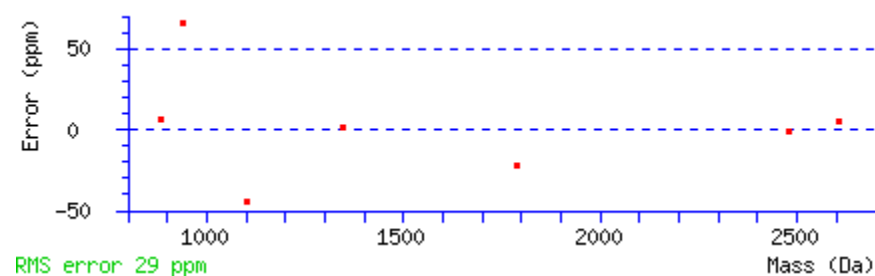
1 DQEVHVLKSE SEVEK**NAPWG LAR**ISHRDSL SFGTFNKYLY TEDGGEGVDV
 51 YVVDGTGTVND HVDFEGRASW GK**TIPQGDAD EDGNHGTHC SGT**VAGKKY
 101 VAKKAHVAV KVLRSNGSGS MSDVVKVEY AAESHLEQVS IAKKGKRGKF
 151 KGSTANMSLG GKGSPILDKA VNAAVDAGIH FAVAAGNDNA DSCNYSPAAA
 201 ENAVTVGAST LSDERAYFSN YGKCNDIFAP GLNIQSTWIG SKYAVNTISG
 251 TSMASPHVAG LLAYLLSLQP AK**DSAF**AVAD **ISP**KKLKANL ISIAITVGALT
 301 DVPSNTANIL AWNGGGESNY SAIVEKGGYK **AAVRPTMLEE IESEAK**VASK
 351 KVYSEGDELA KKVAELTEK**I EDLISGDLKD MFRDLK**RE

Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
16 - 23	884.4792	883.4719	883.4664	6	0	K.NAPWGLAR.I (Ions score 57)
16 - 23	884.4792	883.4719	883.4664	6	0	K.NAPWGLAR.I (No match)
73 - 97	2481.0664	2480.0591	2480.0623	-1	0	K.TIPQGDAD EDGNHGTHCSGT VAGK.K (Ions score 23)
73 - 97	2481.0664	2480.0591	2480.0623	-1	0	K.TIPQGDAD EDGNHGTHCSGT VAGK.K (No match)
73 - 98	2609.1775	2608.1702	2608.1572	5	1	K.TIPQGDAD EDGNHGTHCSGT VAGKK.Y (No match)
273 - 285	1348.7119	1347.7046	1347.7034	1	1	K.DSAFAVAD ISP KK.L (No match)
331 - 346	1789.8601	1788.8528	1788.8927	-22	0	K.AAVRPTMLEE IESEAK.V Oxidation (M) (No match)
370 - 379	1102.5500	1101.5427	1101.5917	-44	0	K.IEDLISGDLK.D (No match)
370 - 379	1102.5500	1101.5427	1101.5917	-44	0	K.IEDLISGDLK.D (No match)
380 - 386	940.5173	939.5100	939.4484	66	1	K.DMFRDLK.R Oxidation (M) (No match)



LOCUS ABQ59329 388 aa linear PLN 17-JUL-2009
 DEFINITION vacuolar serine protease [Cladosporium cladosporioides].
 ACCESSION ABQ59329
 VERSION ABQ59329.1 GI:148361511
 DBSOURCE accession EF407520.1
 KEYWORDS .
 SOURCE Cladosporium cladosporioides
 ORGANISM Cladosporium cladosporioides
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
 Dothideomycetidae; Capnodiales; Davidiellaceae; mitosporic
 Davidiellaceae; Cladosporium.
 REFERENCE 1 (residues 1 to 388)
 AUTHORS Chou,H., Tam,M.F., Lee,L.H., Chiang,C.H., Tai,H.Y., Panzani,R.C.
 and Shen,H.D.
 TITLE Vacuolar serine protease is a major allergen of Cladosporium
 cladosporioides
 JOURNAL Int. Arch. Allergy Immunol. 146 (4), 277-286 (2008)
 PUBMED 18362473
 REFERENCE 2 (residues 1 to 388)
 AUTHORS Shen,H.-D. and Lee,L.-H.
 TITLE Direct Submission
 JOURNAL Submitted (29-JAN-2007) Medical Research and Education, Taipei
 Veterans General Hospital, No. 201, Shih-pai Road, Section 2,
 Taipei, Taiwan 11217, R.O.C.
 FEATURES Location/Qualifiers
 source 1..388
 /organism="Cladosporium cladosporioides"
 /db_xref="taxon:29917"
 Protein <1..388
 /product="vacuolar serine protease"
 Region 19..296
 /region_name="Peptidases_S8_PCSK9_ProteinaseK_like"
 /note="Peptidase S8 family domain in ProteinaseK-like
 proteins; cd04077"

Site	/db_xref="CDD:173790" order(22,25..26) /site_type="other" /note="calcium binding site 2"
Site	/db_xref="CDD:173790" order(54,86,159..160,187,249,252) /site_type="active"
Site	/db_xref="CDD:173790" order(54,86,252) /site_type="other" /note="catalytic triad"
Site	/db_xref="CDD:173790" order(201,203,226) /site_type="other" /note="calcium binding site 1"
CDS	/db_xref="CDD:173790" 1..388 /coded_by="EF407520.1:<1..1167"

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

Spot 38

Mascot Search Results

Protein View

Match to: [gi|85094513](#) Score: **222** Expect: **6.3e-016**
hypothetical protein NCU02252 [Neurospora crassa OR74A]

Nominal mass (M_r): **57010**; Calculated pI value: **5.36**

NCBI BLAST search of [gi|85094513](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Neurospora crassa OR74A](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|28921353](#) from [Neurospora crassa OR74A](#)

[gi|40804637](#) from [Neurospora crassa](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```

1 MAPEHKACLI VIDGWGIPSE ESPKNGDAIA AAETPVMDL SKSATGFSEL
51 EASSLAVGLP EGLMGNSEVG HLNIGAGRVV WQDVVRIDQT IKKGELSQNE
101 VIKATFERAK NGNGRLHLCG LVSHGGVHSK QTHLYALLKA AKEAGVPKVF
151 IHFFGDGRDT DPKSGAGYMQ ELLDTIKEIG IGELATVVGR YYAMDRDKRW
201 ERVEVALKGM ILGEGEESTD PVKTIKERYE KGENDEFKLP IVVGGDERRI
251 KEDDTVFFFN YRSDRVQIT QLMGGVDRSP LPDFPFPNIK LVTMTQYKLD
301 YPFDVAFKPQ QMDNVLAEWL GKQGVKQVHI AETEKYAHVT FFFNGGVEKV
351 FPLETRDESQ DLVPSNKSVA TYDKAPEMSA DGVANQVVKR LGEQEFPFVM
401 NNFAPPDMVG HTGVYEAIV GCAATDKAIG KILEGCKKEG YILFITSDHG
451 NAEEMKFPDG KPKTSHTTNK VPFIMANPE GWSLKKEGGV LGDVAPTILA
501 AMGLPQAEM TGQNLLVKA
    
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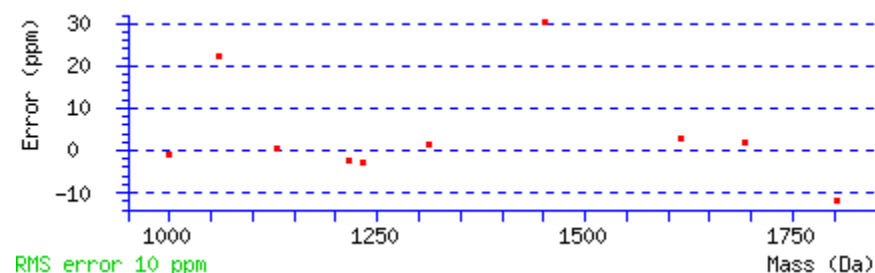
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
79 - 86	1000.5567	999.5494	999.5502	-1	0	R.VVWQDVVR.I (Ions score 51)
79 - 86	1000.5567	999.5494	999.5502	-1	0	R.VVWQDVVR.I (No match)
178 - 190	1313.7440	1312.7367	1312.7351	1	0	K.EIGIGELATVVGR.Y (Ions score 76)
178 - 190	1313.7440	1312.7367	1312.7351	1	0	K.EIGIGELATVVGR.Y (No match)

191 - 198	1061.4958	1060.4885	1060.4648	22	1	R.YYAMDRDK.R	(No match)
200 - 208	1129.6368	1128.6295	1128.6291	0	1	R.WERVEALK.G	(Ions score 17)
200 - 208	1129.6368	1128.6295	1128.6291	0	1	R.WERVEALK.G	(No match)
250 - 262	1693.8256	1692.8183	1692.8148	2	1	R.IKEDDTVFFFNYR.S	(Ions score 37)
250 - 262	1693.8256	1692.8183	1692.8148	2	1	R.IKEDDTVFFFNYR.S	(No match)
252 - 262	1452.6869	1451.6796	1451.6358	30	0	K.EDDTVFFFNYR.S	(No match)
268 - 278	1217.6276	1216.6203	1216.6234	-3	0	R.QITQLMGGVDR.S	(No match)
268 - 278	1233.6219	1232.6146	1232.6183	-3	0	R.QITQLMGGVDR.S	Oxidation (M) (Ions score 9)
268 - 278	1233.6219	1232.6146	1232.6183	-3	0	R.QITQLMGGVDR.S	Oxidation (M) (No match)
336 - 349	1615.7952	1614.7879	1614.7831	3	0	K.YAHVTFFFNGGVEK.V	(No match)
471 - 486	1803.9244	1802.9171	1802.9389	-12	1	K.VPFIMANAPEGWSLKK.E	Oxidation (M) (No match)
471 - 486	1803.9244	1802.9171	1802.9389	-12	1	K.VPFIMANAPEGWSLKK.E	Oxidation (M) (No match)



LOCUS XP_959896 519 aa linear PLN 10-APR-2008
 DEFINITION hypothetical protein NCU02252 [Neurospora crassa OR74A].
 ACCESSION XP_959896
 VERSION XP_959896.1 GI:85094513
 DBSOURCE REFSEQ: accession XM_954803.2
 KEYWORDS .
 SOURCE Neurospora crassa OR74A
 ORGANISM Neurospora crassa OR74A
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (residues 1 to 519)
 AUTHORS Galagan,J.E., Calvo,S.E., Borkovich,K.A., Selker,E.U., Read,N.D.,
 Jaffe,D., FitzHugh,W., Ma,L.J., Smirnov,S., Purcell,S., Rehman,B.,
 Elkins,T., Engels,R., Wang,S., Nielsen,C.B., Butler,J.,
 Endrizzi,M., Qui,D., Ianakiev,P., Bell-Pedersen,D., Nelson,M.A.,
 Werner-Washburne,M., Selitrennikoff,C.P., Kinsey,J.A., Braun,E.L.,
 Zelter,A., Schulte,U., Kothe,G.O., Jedd,G., Mewes,W., Staben,C.,
 Marcotte,E., Greenberg,D., Roy,A., Foley,K., Naylor,J.,
 Stange-Thomann,N., Barrett,R., Gnerre,S., Kamal,M., Kamvysselis,M.,
 Mauceli,E., Bielke,C., Rudd,S., Frishman,D., Krystofova,S.,
 Rasmussen,C., Metzenberg,R.L., Perkins,D.D., Kroken,S., Cogoni,C.,
 Macino,G., Catcheside,D., Li,W., Pratt,R.J., Osmani,S.A.,

DeSouza,C.P., Glass,L., Orbach,M.J., Berglund,J.A., Voelker,R., Yarden,O., Plamann,M., Seiler,S., Dunlap,J., Radford,A., Aramayo,R., Natvig,D.O., Alex,L.A., Mannhaupt,G., Ebbole,D.J., Freitag,M., Paulsen,I., Sachs,M.S., Lander,E.S., Nusbaum,C. and Birren,B.

TITLE The genome sequence of the filamentous fungus *Neurospora crassa*
 JOURNAL Nature 422 (6934), 859-868 (2003)
 PUBMED 12712197
 REFERENCE 2 (residues 1 to 519)
 AUTHORS Galagan,J., Henn,M.R., Hood,H., Radford,A., Collins,R., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L., White,J., Ledlie,T., Kodira,C., Zeng,Q., Yandava,C., Alvarado,L., O'Leary,S., Bowman,B., Colot,H., Ebbole,D., Rasmussen,C., Baker,C., Kalkman,E., Chen,C.-H., Shi,M., Mathur,R., Lambregts,R., mehra,A., Collopy,P., Mehra,A., Schweredtfeger,C., Hong,C., Belden,W., Glass,N.L., Borkovich,K., Dunlap,J., Lander,E., Nusbaum,C., Sachs,M. and Birren,B.

TITLE Version 3 gene predictions for the *Neurospora crassa* assembly 7
 JOURNAL Unpublished
 REFERENCE 3 (residues 1 to 519)
 AUTHORS Birren,B., Galagan,J. and Henn,M.R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUL-2007) Broad Institute of MIT and Harvard, 7 Cambridge Center, Cambridge, MA 02142, USA

REFERENCE 4 (residues 1 to 519)
 AUTHORS Birren,B.
 TITLE Direct Submission
 JOURNAL Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EAA30660.
 Method: conceptual translation.

FEATURES Location/Qualifiers
 source 1..519
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 /strain="OR74A"
 /db_xref="taxon:367110"
 /chromosome="VII"
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 /db_xref="CDD:175217"
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 /region_name="GpmI"
 /note="Phosphoglyceromutase [Carbohydrate transport and

CDS metabolism]; COG0696"
/db_xref="CDD:31040"
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/db_xref="GeneID:3876059"

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

Spot 39

Mascot Search Results

Protein View

Match to: **gi|145232889** Score: **123** Expect: **5e-006**
hypothetical protein An02g06820 [Aspergillus niger]

Nominal mass (M_r): **62977**; Calculated pI value: **6.29**

NCBI BLAST search of [gi|145232889](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus niger CBS 513.88](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|134056738](#) from [Aspergillus niger](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

```

1  MATDIATRDL RKPTTVAEYL FRRLHEVGVR SVHGVPGDYN LAALDYLPKC
51 GLHWVGNCNE LNAGYAADGY ARVNGIGALI TTFGVGELSA LNAIGASYSE
101 FVPVVHIVGQ PNTKSQKDGM LLHHTLGNGD FNVFAKMSAG ISCTLGRLNE
151 TLEAATLIDN AIRECWIRSR PVYISLPTDM IVKQIEGDRL DKPLDLSLPA
201 NDPEKEDYVV DVVLKYLHAA KKPVILVDAC AIRHRVLDEV HDLMEASGLP
251 TFVAPMGKGA VDETRPNYGG VYAGTGSNAG VREQVESSDL ILSIGAIKSD
301 FNTSGFSYHI GQLNTIDFHS TYVRVRYSEY PEINMKGVLR KVIQRMGAVN
351 AAPVPHLSNT LPESEKSSSS QEITHDWLWP NVGQWLKEND IVITETGTAN
401 FGIWETRFPA NVTASQVLW GSIGYSVGAC QGAALAAKEL GNRRTVLFVG
451 DGSLQLTVQE LSTMIRNNLN PIIFVICNNG YTIERYIHGW DESYNDIQPW
501 DIEGLPRVFG AKDKYGYKV KTRDELRLQF ANQEFASAPY LQFTCLVMML
551 PPRXKSRLRR LPPGTSK
    
```

Show predicted peptides also

Sort Peptides By



Residue Number



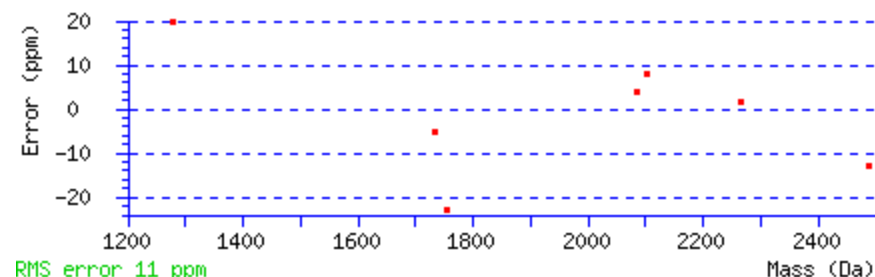
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 11	1278.6725	1277.6652	1277.6398	20	1	-.MATDIATRD L.R K Oxidation (M) (No match)
118 - 136	2086.0256	2085.0183	2085.0102	4	0	K.DGMLLHHTLGNGDFNVFAK.M (No match)
118 - 136	2086.0256	2085.0183	2085.0102	4	0	K.DGMLLHHTLGNGDFNVFAK.M (No match)
118 - 136	2102.0295	2101.0222	2101.0051	8	0	K.DGMLLHHTLGNGDFNVFAK.M Oxidation (M) (No match)

148 - 163	1756.9041	1755.8968	1755.9366	-23	0	R.LNETLEAATLIDNAIR.E	(No match)
169 - 183	1734.9370	1733.9297	1733.9386	-5	0	R.SRPVYISLPTDMIVK.Q	Oxidation (M) (No match)
236 - 258	2488.1782	2487.1709	2487.2026	-13	0	R.VLDEVHDLMEASGLPTFVAPMGK.G	2 Oxidation (M) (No match)
388 - 407	2266.1021	2265.0948	2265.0913	2	0	K.ENDIVITETGTANFGIWETR.F	(Ions score 101)
388 - 407	2266.1021	2265.0948	2265.0913	2	0	K.ENDIVITETGTANFGIWETR.F	(No match)



LOCUS XP_001399817 567 aa linear PLN 28-FEB-2008
 DEFINITION hypothetical protein An02g06820 [Aspergillus niger].
 ACCESSION XP_001399817
 VERSION XP_001399817.1 GI:145232889
 DBSOURCE REFSEQ: accession XM_001399780.1
 KEYWORDS .
 SOURCE Aspergillus niger CBS 513.88
 ORGANISM Aspergillus niger CBS 513.88
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (residues 1 to 567)
 AUTHORS Pel,H.J., de Winde,J.H., Archer,D.B., Dyer,P.S., Hofmann,G.,
 Schaap,P.J., Turner,G., de Vries,R.P., Albang,R., Albermann,K.,
 Andersen,M.R., Bendtsen,J.D., Benen,J.A., van den Berg,M.,
 Breestraat,S., Caddick,M.X., Contreras,R., Cornell,M.,
 Coutinho,P.M., Danchin,E.G., Debets,A.J., Dekker,P., van
 Dijck,P.W., van Dijk,A., Dijkhuizen,L., Driessen,A.J., d'Enfert,C.,
 Geysens,S., Goosen,C., Groot,G.S., de Groot,P.W., Guillemette,T.,
 Henrissat,B., Herweijer,M., van den Hombergh,J.P., van den
 Hondel,C.A., van der Heijden,R.T., van der Kaaij,R.M., Klis,F.M.,
 Kools,H.J., Kubicek,C.P., van Kuyk,P.A., Lauber,J., Lu,X., van der
 Maarel,M.J., Meulenberg,R., Menke,H., Mortimer,M.A., Nielsen,J.,
 Oliver,S.G., Olsthoorn,M., Pal,K., van Peij,N.N., Ram,A.F.,
 Rinas,U., Roubos,J.A., Sagt,C.M., Schmoll,M., Sun,J., Ussery,D.,
 Varga,J., Vervecken,W., van de Vondervoort,P.J., Wedler,H.,
 Wosten,H.A., Zeng,A.P., van Ooyen,A.J., Visser,J. and Stam,H.
 TITLE Genome sequencing and analysis of the versatile cell factory
 Aspergillus niger CBS 513.88
 JOURNAL Nat. Biotechnol. 25 (2), 221-231 (2007)

PUBMED 17259976
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from CAK44227.

FEATURES Location/Qualifiers

source 1..567
/organism="Aspergillus niger CBS 513.88"
/db_xref="taxon:425011"
/clone="An02"

Protein 1..567
/product="hypothetical protein"

Region 12..548
/region_name="COG3961"
/note="Pyruvate decarboxylase and related thiamine
pyrophosphate-requiring enzymes [Carbohydrate transport
and metabolism / Coenzyme metabolism / General function
prediction only]; COG3961"
/db_xref="CDD:33742"

Region 18..178
/region_name="TPP_PYR_PDC_IPDC_like"
/note="Pyrimidine (PYR) binding domain of pyruvate
decarboxylase (PDC), indolepyruvate decarboxylase (IPDC)
and related proteins; cd07038"
/db_xref="CDD:132921"

Site order(36..37,45,48,58..59,85,92,123..124,126,137,140)
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/note="dimer interface"
/db_xref="CDD:132921"

Site order(36..37,45,48,53,56..59,62,65..66,68,70,72..74,85,92,
96,100,123..124)
/site_type="other"
/note="PYR/PP interface"
/db_xref="CDD:132921"

Site order(36,60,85,124)
/site_type="other"
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Region 210..>307
/region_name="TPP_enzyme_M"
/note="Thiamine pyrophosphate enzyme, central domain;
pfam00205"
/db_xref="CDD:143962"

Region 373..537
/region_name="TPP_PDC_IPDC"
/note="TPP-binding module; composed of proteins similar to
pyruvate decarboxylase (PDC) and indolepyruvate
decarboxylase (IPDC). PDC, a key enzyme in alcoholic
fermentation, catalyzes the conversion of pyruvate to
acetaldehyde and CO2. It is able to utilize...; cd02005"
/db_xref="CDD:48168"

Site order(398,421,423,450..453,478,480..484)
 /site_type="other"
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Site order(419..421,455..456,459,462,466,484,488,493..494,498,
 500..501,508..509)
 /site_type="other"
 /note="dimer interface"
 /db_xref="CDD:48168"
CDS 1..567
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 /coded_by="XM_001399780.1:1..1700"
 /inference="profile:COGS:COG0028"
 /inference="profile:PFAM:PF00205"
 /inference="profile:PFAM:PF02775"
 /inference="profile:PFAM:PF02776"
 /inference="similar to AA sequence:UniProtKB:AF098293.1"
 /exception="reasons given in citation"
 /note="Catalytic activity: a 2-oxo acid = an aldehyde +
 CO2 ; pyruvate = acetaldehyde + CO2.;
 Pathway: glycolysis / gluconeogenesis.;
 Remark: PDC levels are a major determinant of ethanol
 production.;
 Similarity: belongs to the thiamine-diphosphate protein
 family.;
 Title: strong similarity to pyruvate decarboxylase pdcA -
 Aspergillus oryzae;
 putative sequencing error"
 /citation=[PUBMED 9210590]
 /db_xref="GeneID:4979172"

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

Spot 40

MASCOT Mascot Search Results

Protein View

Match to: **gi|116196014** Score: **369** Expect: **1.3e-030**
hypothetical protein CHGG_04605 [Chaetomium globosum CBS 148.51]

Nominal mass (M_r): **68195**; Calculated pI value: **5.57**

NCBI BLAST search of [gi|116196014](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Chaetomium globosum CBS 148.51](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|88180518](#) from [Chaetomium globosum CBS 148.51](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

```

1 MMATRLSRAV STTNSAVAIM EGKTPKIIEN AEGARTTPSV VAFAEDGERL
51 VGVAAKRQAV VNPENTLFAT KRLIGRKFTD AEVQRDIKEV PYKIVQHTNG
101 DAWVESRGQK YSPSQIGGFV LNKMKETA EA YLSKPIKNAV VTVPAYFNDS
151 QRQATKDAGQ ISGLNVLRVV NEPTAAALAY GLEKEADRVV AVYDLGGGTF
201 DISILEIQNG VFEVKSTNGD THLGGEDFDI HLVRHFVQQF KKESGIDLSG
251 DRMAIQRIE AAEKAKIELS SSLQTDINLP FITADAGGPK HINSKLTRAQ
301 LEAMVDPLIS KTIEPVRKAL KDAGLQAKDI QEVILVGGMT RMPKVSESVK
351 SIFGRDPAKS VNPDEAVAIG AAVQGAVLSG EVKDLLLLDV TPLSLGIETL
401 GGVFTRLINR NTTIPTKKSQ VFSTAADFQT AVEIKVYQGE RELVRDNKLL
451 GNFQLVGIPP AHRGVPQVEV TFDIDADSIV HVHAKDKSTN KDQSITIASG
501 SGLSDAEIQQ MVEESEKYAE SDKERKAVIE TANRADSVVN DTEKALNEHA
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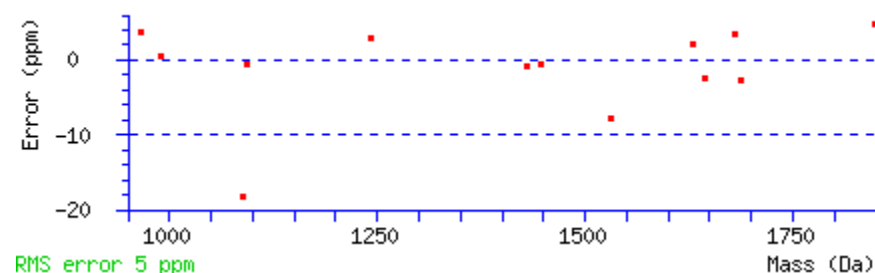
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
58 - 71	1531.7997	1530.7924	1530.8042	-8	0	R.QAVVNPENTLFATK.R	(No match)
58 - 72	1687.9081	1686.9008	1686.9053	-3	1	R.QAVVNPENTLFATKR.L	(No match)
77 - 85	1093.5629	1092.5556	1092.5564	-1	1	R.KFTDAEVQR.D	(No match)

78 - 85	965.4722	964.4649	964.4614	4	0	K.FTDAEVQR.D	(No match)
138 - 152	1680.8400	1679.8327	1679.8267	4	0	K.NAVVTVPAYFNSQR.Q	(Ions score 68)
138 - 152	1680.8400	1679.8327	1679.8267	4	0	K.NAVVTVPAYFNSQR.Q	(No match)
157 - 168	1242.6836	1241.6763	1241.6728	3	0	K.DAGQISGLNVLR.V	(Ions score 66)
157 - 168	1242.6836	1241.6763	1241.6728	3	0	K.DAGQISGLNVLR.V	(No match)
169 - 184	1645.8757	1644.8684	1644.8723	-2	0	R.VVNEPTAAALAYGLEK.E	(No match)
329 - 341	1430.7661	1429.7588	1429.7599	-1	0	K.DIQEVILVGGMTR.M	(Ions score 91)
329 - 341	1430.7661	1429.7588	1429.7599	-1	0	K.DIQEVILVGGMTR.M	(No match)
329 - 341	1446.7612	1445.7539	1445.7548	-1	0	K.DIQEVILVGGMTR.M	Oxidation (M) (Ions score 26)
329 - 341	1446.7612	1445.7539	1445.7548	-1	0	K.DIQEVILVGGMTR.M	Oxidation (M) (No match)
351 - 359	990.5372	989.5299	989.5294	1	1	K.SIFGRDPAK.S	(Ions score 14)
351 - 359	990.5372	989.5299	989.5294	1	1	K.SIFGRDPAK.S	(No match)
449 - 463	1631.9414	1630.9341	1630.9307	2	0	K.LLGNFQLVGIPPAHR.G	(Ions score 75)
449 - 463	1631.9414	1630.9341	1630.9307	2	0	K.LLGNFQLVGIPPAHR.G	(No match)
556 - 564	1089.5336	1088.5263	1088.5462	-18	1	K.TEADQIREK.I	(No match)
589 - 604	1849.9631	1848.9558	1848.9469	5	1	K.EKTDELQVASLNLFDK.M	(No match)



LOCUS XP_001223819 629 aa linear PLN 09-APR-2008
 DEFINITION hypothetical protein CHGG_04605 [Chaetomium globosum CBS 148.51].
 ACCESSION XP_001223819
 VERSION XP_001223819.1 GI:116196014
 DBSOURCE REFSEQ: accession XM_001223818.1
 KEYWORDS .
 SOURCE Chaetomium globosum CBS 148.51
 ORGANISM Chaetomium globosum CBS 148.51
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Sordariales; Chaetomiaceae; Chaetomium.
 REFERENCE 1 (residues 1 to 629)
 AUTHORS Birren,B., Lander,E., Galagan,J., Devon,K., Nusbaum,C., Ma,L.-J.,
 Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Yandava,C.,
 Zeng,Q., Alvarado,L., O'leary,S. and Untereiner,W.
 CONSRTM The Broad Institute Genome Sequencing Platform

TITLE Annotation of the Chaetomium globosum CBS 148.51 Genome
 JOURNAL Unpublished (2004)
 REFERENCE 2 (residues 1 to 629)
 AUTHORS Lander,E., Birren,B. and Ma,L.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (10-MAR-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (residues 1 to 629)
 AUTHORS Untereiner,W.
 TITLE Direct Submission
 JOURNAL Submitted (10-MAR-2005) Brandon University, 270-18th, Brandon, MB
 R7A-6A9, Canada
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from EAQ87986.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /strain="CBS 148.51"
 /db_xref="taxon:306901"
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 /name="similar to heat shock protein 70Kda"
 /calculated_mol_wt=68105
 Region 12..625
 /region_name="dnaK"
 /note="molecular chaperone DnaK; Provisional; PRK00290"
 /db_xref="CDD:166891"
 CDS 1..629
 /locus_tag="CHGG_04605"
 /coded_by="XM_001223818.1:1..1890"
 /db_xref="GeneID:4392109"

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

Spot 41

MASCOT Mascot Search Results

Protein View

Match to: [gi|258575103](#) Score: **335** Expect: **3.2e-027**
3'(2'),5'-bisphosphate nucleotidase [Uncinocarpus reesii 1704]

Nominal mass (M_r): **38061**; Calculated pI value: **5.03**

NCBI BLAST search of [gi|258575103](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Uncinocarpus reesii 1704](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|237901999](#) from [Uncinocarpus reesii 1704](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

1 MSYQKELLVA QLAVQR**ASIL TQNVFHEKAK** GTLSKDDFSP VTKGDFGAQA
 51 LIIQAIRTNF PEDEIVAEAE ASSLRENDL **RNEMWNLVKD IKLTDDESDR**
 101 ILGGPLK**NET EMLEALDGGK** SEG GPK**GRIW ALDPIDGTKG** FLRGQYAVC
 151 LGLIVDGDVK VGVIGCPNLP LSDSATLSAE IGQSGAADAEG TGVLFSAVKG
 201 QGATSRPLSQ GALPEGKAIS MRPVTDISQA CFCEGVEAGH SAQDDNAEVA
 251 RRLGITSPSV RLDSQAKYCS IAR**GAGDIYL RLPVK**ADYQE K**IWDHAAGDL**
 301 **LVREAGGDVT DITGKRLDFS IGR**KLSGNKG VVAAPKPIFE QVINAVRAVY
 351 **AAKASI**

Show predicted peptides also

Sort Peptides By



Residue Number



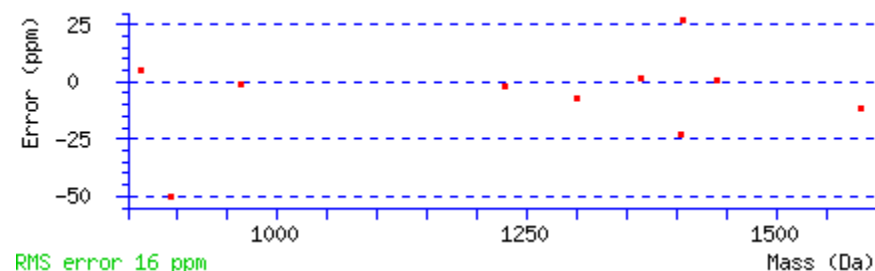
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
17 - 30	1585.8514	1584.8441	1584.8624	-12	1	R.ASILTQNVFHEKAK.G (No match)
82 - 92	1405.6826	1404.6753	1404.7071	-23	1	R.NEMWNLVKDIK.L Oxidation (M) (No match)
108 - 120	1406.6847	1405.6774	1405.6395	27	0	K.NETEMLEALDGGK.S (No match)
127 - 139	1441.7802	1440.7729	1440.7725	0	1	K.GRIWALDPIDGTK.G (Ions score 43)
127 - 139	1441.7802	1440.7729	1440.7725	0	1	K.GRIWALDPIDGTK.G (No match)
129 - 139	1228.6548	1227.6475	1227.6499	-2	0	R.IWALDPIDGTK.G (Ions score 42)
129 - 139	1228.6548	1227.6475	1227.6499	-2	0	R.IWALDPIDGTK.G (No match)
274 - 281	864.4617	863.4544	863.4501	5	0	R.GAGDIYLR.L (Ions score 38)

274 - 281	864.4617	863.4544	863.4501	5	0	R.GAGDIYLR.L	(No match)
274 - 285	1301.7482	1300.7409	1300.7503	-7	1	R.GAGDIYLR.LPVK.A	(No match)
292 - 303	1365.7291	1364.7218	1364.7201	1	0	K.IWDHAAGDLLVR.E	(Ions score 95)
292 - 303	1365.7291	1364.7218	1364.7201	1	0	K.IWDHAAGDLLVR.E	(No match)
316 - 323	963.5363	962.5290	962.5298	-1	1	K.RLDFSIGR.K	(Ions score 56)
316 - 323	963.5363	962.5290	962.5298	-1	1	K.RLDFSIGR.K	(No match)
348 - 356	893.4642	892.4569	892.5018	-50	1	R.AVYAAKASI.-	(No match)



LOCUS XP_002541733 356 aa linear PLN 16-SEP-2009
 DEFINITION 3'(2'),5'-bisphosphate nucleotidase [Uncinocarpus reesii 1704].
 ACCESSION XP_002541733
 VERSION XP_002541733.1 GI:258575103
 DBSOURCE REFSEQ: accession XM_002541687.1
 KEYWORDS .
 SOURCE Uncinocarpus reesii 1704
 ORGANISM Uncinocarpus reesii 1704
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Onygenales; Onygenaceae; Uncinocarpus.
 REFERENCE 1 (residues 1 to 356)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Henn,M., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M.,
 Kleber,M., Mauceli,E., Brockman,W., Rounsley,S., Young,S.,
 LaButti,K., Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M.,
 Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L.,
 Luoma,S., White,J., O'Leary,S., Kodira,C., Zeng,Q., Yandava,C.,
 Alvarado,L., Taylor,J. and Johannesson,H.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Uncinocarpus reesii strain 1704 genome
 JOURNAL Unpublished (2004)
 REFERENCE 2 (residues 1 to 356)
 AUTHORS Taylor,J. and Johannesson,H.
 TITLE Direct Submission
 JOURNAL Submitted (12-AUG-2005) Department of Plant and Microbial Biology,
 UC-Berkeley, 111 Koshland Hall, Berkeley, CA 94720-3102, USA
 REFERENCE 3 (residues 1 to 356)

AUTHORS Lander,E., Birren,B. and Ma,L.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence is identical to EEP76400.
 Method: conceptual translation.
 FEATURES Location/Qualifiers
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 /strain="1704"
 /db_xref="taxon:336963"
 Protein 1..356
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 /calculated_mol_wt=37668
 Region 6..348
 /region_name="PAP_phosphatase"
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 member of the inositol monophosphatase family, and
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 Saccharomyces cerevisiae, HAL2 (MET22) is involved in
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 /note="putative lithium-binding site"
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 Site order(240,267,281,290,294)
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 /note="substrate binding site"
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 CDS 1..356
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 /db_xref="GeneID:8444609"

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

Spot 42

Mascot Search Results

Protein View

Match to: [gi|258577135](#) Score: **396** Expect: **2.5e-033**
rab GDP dissociation inhibitor alpha [Uncinocarpus reesii 1704]

Nominal mass (M_r): **52040**; Calculated pI value: **5.66**

NCBI BLAST search of [gi|258577135](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Uncinocarpus reesii 1704](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|237903015](#) from [Uncinocarpus reesii 1704](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

```

1 MDDIAPEYDV VVLGTGLTEC VLSGVLVSKG QKVLHIDRND HYGAEAAASVN
51 IETLFKKFGN LKPGEEPWK YGRVNDWNVD LVPKLLMSNG ELTNILVSTD
101 VTTRYLEFRQI AGSYVQQGSG SKAMVAKVPS DAGEALRSSL MGLFEKRRAK
151 KFLEWVGFEF EKNPSTHQGL NMANCTMKEV YDKFGLEDST RDFVGHSMAL
201 YQSDGYIGVP GGASETVNRI RLYVNSMARY GKSPYIPLY GLGELPQGFA
251 RLSAIYGGTY MLNTDVDEIL YENGKVSIGK ATMKEKGEPG PGMRFITTKTK
301 KIIADPSYFP GKVRVTGYLL KAICILNHPI DKTDGSDSLQ LIIPQSQIGR
351 KHDVYIAMVS SAHNVCCKGY YVAIVSTIAE NEANHHLELE PGFQRLGKIE
401 EKFMGPPIPL YEPIDSGVED NIYISKSYDA TSHFETTTDD IRDIYKRAEG
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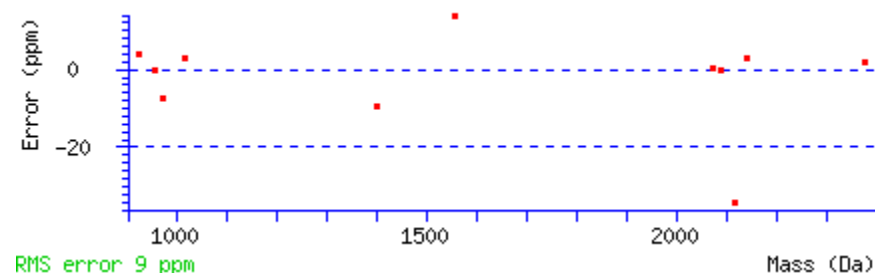
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
58 - 69	1401.7026	1400.6953	1400.7088	-10	0	K.FGNLKPGEEPWK.K (No match)
85 - 103	2076.1011	2075.0938	2075.0932	0	0	K.LLMSNGELTNILVSTDVTR.Y (Ions score 110)
85 - 103	2076.1011	2075.0938	2075.0932	0	0	K.LLMSNGELTNILVSTDVTR.Y (No match)
85 - 103	2092.0947	2091.0874	2091.0882	-0	0	K.LLMSNGELTNILVSTDVTR.Y Oxidation (M) (Ions score 20)
85 - 103	2092.0947	2091.0874	2091.0882	-0	0	K.LLMSNGELTNILVSTDVTR.Y Oxidation (M) (No match)
104 - 122	2117.9885	2116.9812	2117.0542	-34	1	R.YLEFRQIAGSYVQQGSGSK.A (No match)

128 - 137	1014.5245	1013.5172	1013.5142	3	0	K.VPSDAGEALR.S	(Ions score 35)
128 - 137	1014.5245	1013.5172	1013.5142	3	0	K.VPSDAGEALR.S	(No match)
179 - 191	1558.7596	1557.7523	1557.7311	14	1	K.EVYDKFGLEDSTR.D	(No match)
184 - 191	924.4459	923.4386	923.4349	4	0	K.FGLEDSTR.D	(No match)
222 - 229	953.4872	952.4799	952.4800	-0	0	R.LYVNSMAR.Y	(Ions score 41)
222 - 229	953.4872	952.4799	952.4800	-0	0	R.LYVNSMAR.Y	(No match)
222 - 229	969.4752	968.4679	968.4749	-7	0	R.LYVNSMAR.Y	Oxidation (M) (No match)
233 - 251	2141.1133	2140.1060	2140.0993	3	0	K.SPYIYPLYGLGELPQGFAR.L	(Ions score 113)
233 - 251	2141.1133	2140.1060	2140.0993	3	0	K.SPYIYPLYGLGELPQGFAR.L	(No match)
427 - 446	2378.0828	2377.0755	2377.0710	2	1	K.SYDATSHFETTTDDIRDIYK.R	(Ions score 54)
427 - 446	2378.0828	2377.0755	2377.0710	2	1	K.SYDATSHFETTTDDIRDIYK.R	(No match)



LOCUS XP_002542749 468 aa linear PLN 16-SEP-2009
 DEFINITION rab GDP dissociation inhibitor alpha [Uncinocarpus reesii 1704].
 ACCESSION XP_002542749
 VERSION XP_002542749.1 GI:258577135
 DBSOURCE REFSEQ: accession XM_002542703.1
 KEYWORDS .
 SOURCE Uncinocarpus reesii 1704
 ORGANISM Uncinocarpus reesii 1704
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Onygenales; Onygenaceae; Uncinocarpus.
 REFERENCE 1 (residues 1 to 468)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Ma,L.-J.,
 Henn,M., Jaffe,D., Butler,J., Alvarez,P., Gnerre,S., Grabherr,M.,
 Kleber,M., Mauceli,E., Brockman,W., Rounsley,S., Young,S.,
 LaButti,K., Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M.,
 Engels,R., Montgomery,P., Pearson,M., Howarth,C., Larson,L.,
 Luoma,S., White,J., O'Leary,S., Kodira,C., Zeng,Q., Yandava,C.,
 Alvarado,L., Taylor,J. and Johannesson,H.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Annotation of the Uncinocarpus reesii strain 1704 genome
 JOURNAL Unpublished (2004)
 REFERENCE 2 (residues 1 to 468)
 AUTHORS Taylor,J. and Johannesson,H.

TITLE Direct Submission
 JOURNAL Submitted (12-AUG-2005) Department of Plant and Microbial Biology,
 UC-Berkeley, 111 Koshland Hall, Berkeley, CA 94720-3102, USA
 REFERENCE 3 (residues 1 to 468)
 AUTHORS Lander,E., Birren,B. and Ma,L.
 CONSRTM The Genome Sequencing Platform, The Genome Assembly Team
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2005) Broad Institute of MIT and Harvard, 320
 Charles Street, Cambridge, MA 02141, USA
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence is identical to EEP77416.
 Method: conceptual translation.
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 /calculated_mol_wt=51714
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 /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931"
 /db_xref="CDD:176428"
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 /locus_tag="UREG_02265"
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 /db_xref="GeneID:8441543"

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

Spot 43

Mascot Search Results

Protein View

Match to: [gi|255936655](#) Score: **107** Expect: **0.0002**
Pc13g09300 [[Penicillium chrysogenum Wisconsin 54-1255](#)]

Nominal mass (M_r): **63252**; Calculated pI value: **5.65**

NCBI BLAST search of [gi|255936655](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Penicillium chrysogenum Wisconsin 54-1255](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|211583974](#) from [Penicillium chrysogenum Wisconsin 54-1255](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

```

1 MATTDIATRE LKNPVDVAEY LFRRLHEVGI RSLHGVPGDY NLAALDYVSK
51 CGINWVGNCN ELNAGYAADG YARVNGISAL VTTFGVGELS ALNAIAGAYS
101 EFVPVVIHVG QPTTQSQKDG MLLHHTLGNG DFNVFTKMSE GISCYVARLN
151 EPHDAATLID SAIREECWIRS RPVYITLPTD IVAAKVNGDR LKTPIDLSP
201 KNDPEKEDYV VGVVLKYLHA AKNPVILVDA CSIRHRVLEE VRDLVEKSGL
251 PTFVTPMGKG AVNETHKNFG GYAGNGSNV GVSEAVESSD LILSIGAIKS
301 DFNTTGFTYR VGQLNTIDFH STFVRVRYSE YPDINMKGVL RKVIERMNPL
351 TPAPTPQITN RLPSEETSS DQTITHKWLW PIVGQWLKEK DIVLTETGTA
401 NFGIWDTRFP ANVTAVSQVL WGSIGYSMGA CQGAALAAKE QEDRRITLFI
451 GDGSIQLTVQ ELSTILKNKL NPIVFVICND GYTIERYIHG WDAAYNDIQP
501 WDFANIPKVF GAKDNYQGYR IKTRDELNKL FAEDDFNASD KLRLVEVYMP
551 REDAPAGLKL TAEAAAQRNK
    
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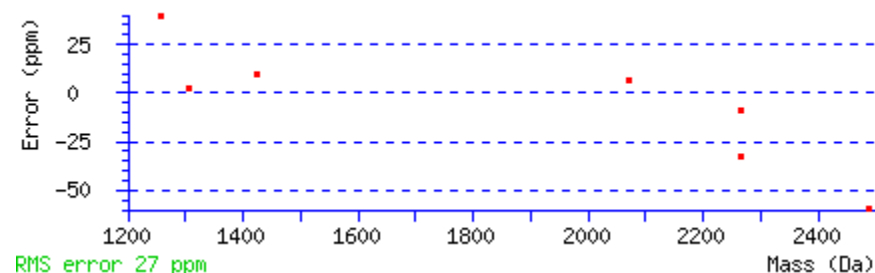
Show predicted peptides also

Sort Peptides By

☒ Residue Number ☐ Increasing Mass ☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
165 - 185	2488.1902	2487.1829	2487.3308	-59	1	R.ECWIRSRPVYITLPTDIVAAK.V (No match)
248 - 267	2071.0776	2070.0703	2070.0568	7	1	K.SGLPTFVTPMGKGAVNETHK.N (No match)
300 - 310	1308.5881	1307.5808	1307.5782	2	0	K.SDFNTTGFTYR.V (Ions score 80)
300 - 310	1308.5881	1307.5808	1307.5782	2	0	K.SDFNTTGFTYR.V (No match)

328 - 337	1259.6108	1258.6035	1258.5540	39	0	R.YSEYPDINMK.G	(No match)
378 - 388	1425.8173	1424.8100	1424.7969	9	0	K.WLWPIVGQWLK.E	(No match)
378 - 388	1425.8173	1424.8100	1424.7969	9	0	K.WLWPIVGQWLK.E	(No match)
389 - 408	2266.1145	2265.1072	2265.1277	-9	1	K.EKDIVLTETGTANFGIWDTR.F	(No match)
468 - 486	2265.0947	2264.0874	2264.1623	-33	1	K.NKLNPIVFVICNDGYTIER.Y	(No match)
468 - 486	2265.0947	2264.0874	2264.1623	-33	1	K.NKLNPIVFVICNDGYTIER.Y	(No match)



LOCUS XP_002559354 570 aa linear PLN 14-AUG-2009
 DEFINITION Pc13g09300 [Penicillium chrysogenum Wisconsin 54-1255].
 ACCESSION XP_002559354
 VERSION XP_002559354.1 GI:255936655
 DBSOURCE REFSEQ: accession XM_002559308.1
 KEYWORDS .
 SOURCE Penicillium chrysogenum Wisconsin 54-1255
 ORGANISM Penicillium chrysogenum Wisconsin 54-1255
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium;
 Penicillium chrysogenum complex.
 REFERENCE 1 (residues 1 to 570)
 AUTHORS van den Berg,M.A., Albang,R., Albermann,K., Badger,J.H.,
 Daran,J.M., Driessen,A.J., Garcia-Estrada,C., Fedorova,N.D.,
 Harris,D.M., Heijne,W.H., Joardar,V., Kiel,J.A., Kovalchuk,A.,
 Martin,J.F., Nierman,W.C., Nijland,J.G., Pronk,J.T., Roubos,J.A.,
 van der Klei,I.J., van Peij,N.N., Veenhuis,M., von Dohren,H.,
 Wagner,C., Wortman,J. and Bovenberg,R.A.
 TITLE Genome sequencing and analysis of the filamentous fungus
 Penicillium chrysogenum
 JOURNAL Nat. Biotechnol. 26 (10), 1161-1168 (2008)
 PUBMED 18820685
 REFERENCE 2 (residues 1 to 570)
 AUTHORS van den Berg,M.A.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2007) van den Berg M.A., DAI/INNO (624-0270), DSM
 Anti-Infectives, Alexander Fleminglaan 1, Delftn, 2613 AX,
 NETHERLANDS

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence is identical to CAP91999.

FEATURES

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	/name="Pc13g09300"
	/calculated_mol_wt=62761
Region	12..570
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	/db_xref="CDD:33742"
Region	19..179
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	/note="Pyrimidine (PYR) binding domain of pyruvate decarboxylase (PDC), indolepyruvate decarboxylase (IPDC) and related proteins; cd07038"
	/db_xref="CDD:132921"
Site	order(37..38,46,49,59..60,86,93,124..125,127,138,141)
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	/note="dimer interface"
	/db_xref="CDD:132921"
Site	order(37..38,46,49,54,57..60,63,66..67,69,71,73..75,86,93,97,101,124..125)
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	/note="TPP binding site"
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acetaldehyde and CO₂. It is able to utilize...; cd02005"
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Site order(399,422,424,451..454,479,481..485)
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/inference="similar to AA sequence:TREMBL:AF098293.1"
/db_xref="GeneID:8316057"

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

Spot 44

Mascot Search Results

Protein View

Match to: [gi|114321348](#) Score: **93** Expect: **0.0052**
peptidoglycan synthetase FtsI [Alkalilimnicola ehrlichii MLHE-1]

Nominal mass (M_r): **62727**; Calculated pI value: **7.96**

NCBI BLAST search of [gi|114321348](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Alkalilimnicola ehrlichii MLHE-1](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|114227742](#) from [Alkalilimnicola ehrlichii MLHE-1](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

```

1  MSRRAQKTAM PQVAGWRLGV VALVFFLLVG ALMWRAVELQ VLDRQFLQTQ
51 GEARQMRTRA MPAHRGVITD RHGEPLAISS PVDSVWADPG QLLDHPEAVT
101 ALAELVGMPR ARLQRRLEAR PGSEFAWVRR QVSPEQAEAV RRAALPGVAL
151 QQEYRRFYPS GEVSAHLLGF TNIDDQGQEG LELTYDAWLR GEPGRKRVIQ
201 DRLGRVVEDV ELLREPRAGR DLALSIDRRL QYLAYRELKA AVREHDARGG
251 SLVLLDVESG EVLAMVNQPG FNPHRRNEIG NGVQRNRRAII DAYEPGSLIK
301 PFTVLAALRE GVVPRPETSLS TSPGTLRVGR HTIRDIRDYG EIDVTLLQK
351 SSNVGAVRLA LEMEPDALWG LLEMGFGAS TFGVFQGEAT GRVSSMPPRD
401 EVQRATLSFG YGLTATPLQI ARAYATLAAA GVQRPVSLLH RNGQPPPESEE
451 QVLDPALSRQ VLEMLETVTQ PGGTGTAAV PGYRVAGKTG TVRKAGPTGY
501 GEDDGYIAMF AGVAPVSRPR LAMAVLVDGP RGDEYYGGQV AAPVFGQVMA
551 GALRLMNIAP DGDALPSGLI VAGGEGRP
    
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Show predicted peptides also

Sort Peptides By



Residue Number



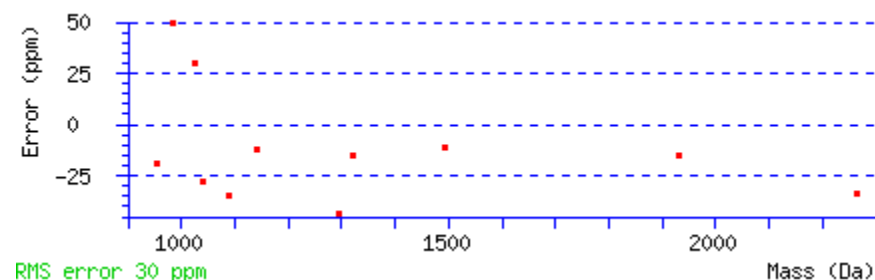
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
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58 - 65	955.4713	954.4640	954.4818	-19	1	R.TRAMPAHR.G Oxidation (M) (No match)
60 - 71	1323.6753	1322.6680	1322.6877	-15	1	R.AMPAHRGVITDR.H (Ions score 13)
60 - 71	1323.6753	1322.6680	1322.6877	-15	1	R.AMPAHRGVITDR.H (No match)

230 - 239	1296.6749	1295.6676	1295.7237	-43	1	R.LQYLAYRELK.A	(No match)
240 - 248	1024.5590	1023.5517	1023.5210	30	1	K.AAVREHDAR.G	(No match)
240 - 248	1024.5590	1023.5517	1023.5210	30	1	K.AAVREHDAR.G	(No match)
276 - 285	1142.5887	1141.5814	1141.5952	-12	1	R.RNEIGNGVQR.N	(No match)
277 - 285	986.5504	985.5431	985.4941	50	0	R.NEIGNGVQR.N	(Ions score 31)
277 - 285	986.5504	985.5431	985.4941	50	0	R.NEIGNGVQR.N	(No match)
338 - 350	1494.7522	1493.7449	1493.7613	-11	0	R.DYGEIDVTLLQK.S	(No match)
338 - 358	2265.0959	2264.0886	2264.1648	-34	1	R.DYGEIDVTLLQKSSNVGAVR.L	(No match)
460 - 477	1932.9397	1931.9324	1931.9623	-15	0	R.QVLEMLETVTPGGTGTR.A	Oxidation (M) (No match)
478 - 488	1088.5837	1087.5764	1087.6138	-34	1	R.AAVPGYRVAGK.T	(No match)



LOCUS YP_743031 578 aa linear BCT 30-MAR-2010
 DEFINITION peptidoglycan synthetase FtsI [Alkalilimnicola ehrlichii MLHE-1].
 ACCESSION YP_743031
 VERSION YP_743031.1 GI:114321348
 DBLINK Project: 15763
 DBSOURCE REFSEQ: accession NC_008340.1
 KEYWORDS .
 SOURCE Alkalilimnicola ehrlichii MLHE-1
 ORGANISM Alkalilimnicola ehrlichii MLHE-1
 Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;
 Ectothiorhodospiraceae; Alkalilimnicola.
 REFERENCE 1 (residues 1 to 578)
 AUTHORS Copeland,A., Lucas,S., Lapidus,A., Barry,K., Detter,J.C., Glavina
 del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Pitluck,S.,
 Sims,D., Brettin,T., Bruce,D., Han,C., Tapia,R., Gilna,P.,
 Schmutz,J., Larimer,F., Land,M., Hauser,L., Kyrpides,N.,
 Mikhailova,N., Oremland,R.S., Hoefl,S.E., Switzer-Blum,J., Kulp,T.,
 King,G., Tabita,R., Witte,B., Santini,J.M., Basu,P.,
 Hollibaugh,J.T., Xie,G., Stolz,J.F. and Richardson,P.
 CONSRTM US DOE Joint Genome Institute
 TITLE Complete sequence of Alkalilimnicola ehrlichei MLHE-1
 JOURNAL Unpublished
 REFERENCE 2 (residues 1 to 578)
 CONSRTM NCBI Genome Project
 TITLE Direct Submission

JOURNAL Submitted (20-SEP-2007) National Center for Biotechnology
Information, NIH, Bethesda, MD 20894, USA
REFERENCE 3 (residues 1 to 578)
AUTHORS Copeland,A., Lucas,S., Lapidus,A., Barry,K., Detter,J.C., Glavina
del Rio,T., Hammon,N., Israni,S., Dalin,E., Tice,H., Pitluck,S.,
Sims,D., Brettin,T., Bruce,D., Han,C., Tapia,R., Gilna,P.,
Schmutz,J., Larimer,F., Land,M., Hauser,L., Kyrpides,N.,
Mikhailova,N., Oremland,R.S., Hoefft,S.E., Switzer-Blum,J., Kulp,T.,
King,G., Tabita,R., Witte,B., Santini,J.M., Basu,P.,
Hollibaugh,J.T., Xie,G., Stolz,J.F. and Richardson,P.
CONSRTM US DOE Joint Genome Institute
TITLE Direct Submission
JOURNAL Submitted (28-AUG-2006) US DOE Joint Genome Institute, 2800
Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
NCBI review. The reference sequence was derived from ABI57541.
Method: conceptual translation.
FEATURES Location/Qualifiers
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/db_xref="taxon:187272"
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protein 2 [Cell envelope biogenesis, outer membrane];
COG0768"
/db_xref="CDD:31111"
Region 62..211
/region_name="PBP_dimer"
/note="Penicillin-binding Protein dimerization domain;
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KEGG: noc:Noc_2867 peptidoglycan glycosyltransferase"
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Mascot: <http://www.matrixscience.com/>

Spot 45

MASCOT Mascot Search Results

Protein View

Match to: **gi|39945784** Score: **344** Expect: **4e-028**
hypothetical protein MGG_08012 [Magnaporthe grisea 70-15]

Nominal mass (M_r): **40874**; Calculated pI value: **5.87**

NCBI BLAST search of [gi|39945784](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Magnaporthe grisea 70-15](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|145019246](#) from [Magnaporthe grisea 70-15](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **15%**

Matched peptides shown in **Bold Red**

```

1 MVRGTVLITG GTGYIGSFTS LALLENDYDV VIVDNLYNSS AVAIDRIELI
51 CGKRPAFHNV DITDEALDK VFDAHPEIDS VIHFAALKAV GESGEIPLEY
101 YRVNVGGSIS LLRSMQKHNV CNIVFSSSAT VYGDATRVPN MIPIPEHCPI
151 GPTNTYGRTK STIEDVISDH VNAQRNNLKK ADKPFDMWNG ALLRYFNPCG
201 AHPSGLMGED PQGVFPNLLP LLGQVATGQR EKLLVFGDDY SSRDGTAIRD
251 YIHVLDLAKG HLAALNYLRD NKPGVKAWNL GSGRGSTVFE MIKAFSSVVG
301 RDLPEYEVPR RQGDVLDLTA NPALANKELG WKTELRMEDA CQDLWKWVKV
351 NPQGYRQDPP QEFVAALKK

```

Show predicted peptides also

Sort Peptides By



Residue Number



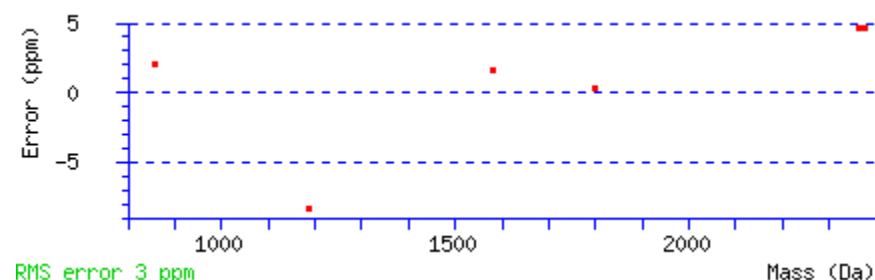
Increasing Mass



Decreasing Mass

Start	End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
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89	102	1582.7773	1581.7700	1581.7675	2	0	K.AVGESGEIPLEYYR.V	(No match)
138	158	2363.1743	2362.1670	2362.1562	5	0	R.VPNMIPIPEHCPIGPTNTYGR.T	(Ions score 89)
138	158	2363.1743	2362.1670	2362.1562	5	0	R.VPNMIPIPEHCPIGPTNTYGR.T	(No match)
138	158	2379.1694	2378.1621	2378.1511	5	0	R.VPNMIPIPEHCPIGPTNTYGR.T	Oxidation (M) (Ions score 57)
138	158	2379.1694	2378.1621	2378.1511	5	0	R.VPNMIPIPEHCPIGPTNTYGR.T	Oxidation (M) (No match)
244	259	1799.9655	1798.9582	1798.9577	0	1	R.DGTAIRDYIHVLDLAK.G	(Ions score 85)
244	259	1799.9655	1798.9582	1798.9577	0	1	R.DGTAIRDYIHVLDLAK.G	(No match)

250 - 259	1186.6367	1185.6294	1185.6394	-8	0	R.DYIHVLDLAK.G	(No match)
277 - 284	860.4391	859.4318	859.4300	2	0	K.AWNLGSGR.G	(Ions score 51)
277 - 284	860.4391	859.4318	859.4300	2	0	K.AWNLGSGR.G	(No match)



LOCUS XP_362429 369 aa linear PLN 17-MAY-2010
 DEFINITION hypothetical protein MGG_08012 [Magnaporthe oryzae 70-15].
 ACCESSION XP_362429
 VERSION XP_362429.1 GI:39945784
 DBSOURCE REFSEQ: accession XM_362429.1
 KEYWORDS .
 SOURCE Magnaporthe oryzae 70-15
 ORGANISM Magnaporthe oryzae 70-15
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Sordariomycetidae; Magnaporthales; Magnaporthaceae; Magnaporthe.
 REFERENCE 1 (residues 1 to 369)
 AUTHORS Dean,R.A., Talbot,N.J., Ebbole,D.J., Farman,M.L., Mitchell,T.K.,
 Orbach,M.J., Thon,M., Kulkarni,R., Xu,J.R., Pan,H., Read,N.D.,
 Lee,Y.H., Carbone,I., Brown,D., Oh,Y.Y., Donofrio,N., Jeong,J.S.,
 Soanes,D.M., Djonovic,S., Kolomiets,E., Rehmeier,C., Li,W.,
 Harding,M., Kim,S., Lebrun,M.H., Bohnert,H., Coughlan,S.,
 Butler,J., Calvo,S., Ma,L.J., Nicol,R., Purcell,S., Nusbaum,C.,
 Galagan,J.E. and Birren,B.W.
 TITLE The genome sequence of the rice blast fungus Magnaporthe grisea
 JOURNAL Nature 434 (7036), 980-986 (2005)
 PUBMED 15846337
 REFERENCE 2 (residues 1 to 369)
 AUTHORS Birren,B., Lander,E., Galagan,J., Nusbaum,C., Devon,K., Jaffe,D.,
 Butler,J., Alvarez,P., Gnerre,S., Grabherr,M., Kleber,M.,
 Mauceli,E., Brockman,W., Rounsley,S., Young,S., LaButti,K.,
 Pushparaj,V., DeCaprio,D., Crawford,M., Koehrsen,M., Engels,R.,
 Montgomery,P., Pearson,M., Howarth,C., Kodira,C., Yandava,C.,
 Zeng,Q., Alvarado,L., O'leary,S., Dean,R., Mitchell,T., Brown,D.,
 Pan,H., Thon,M., Zhu,H. and Blackmon,B.
 CONSRTM The Broad Institute Genome Sequencing Platform
 TITLE Direct Submission

JOURNAL Submitted (26-SEP-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02142, USA

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from EDK03474.
Method: conceptual translation.

FEATURES

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Region	4..133 /region_name="NADB_Rossmann" /note="Rossmann-fold NAD(P)(+)-binding proteins; cl09931" /db_xref="CDD:176428"
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Mascot: <http://www.matrixscience.com/>

Spot 46

MASCOT Mascot Search Results

Protein View

Match to: [gi|145231098](#) Score: **198** Expect: **1.6e-013**
beta-isopropylmalate dehydrogenase A leu2A-Aspergillus niger

Nominal mass (M_r): **38955**; Calculated pI value: **5.39**

NCBI BLAST search of [gi|145231098](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus niger CBS 513.88](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|134055941](#) from [Aspergillus niger](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

```

1 MPAYNIVVFA GDHCGPEVTA EAIKVLRVIE KSRDDITLNL QDHLLGGASI
51 DATGNPLTDE ALAAAKNADA VLLGAIGGPK WGTGAVRPEQ GLLKLRKEMG
101 TFGNLRPCNF AAPSLVEHSP LKASVCEGVD FNIIELTGG IYFGDRKEDD
151 GSGYAMDTEP YSRAEIERIT RLA AHLALQH NPPLPVWSLD KANVLATSRL
201 WRKTVTEIMA KEFPQLKIEH QLIDSAAMIM VKNPRQLNGI IVTSNLFQDI
251 ISDEASVIPG SLGLLPSASL SGIPDGKGRV NGIYEPIHGS APDIAGKGIV
301 NPVAAILSVA MMMQYSFGRF DEARAIEAAV RNVLESGVRT GDIGGKATTS
351 EVGDAVAEL EKLLK

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Show predicted peptides also

Sort Peptides By



Residue Number



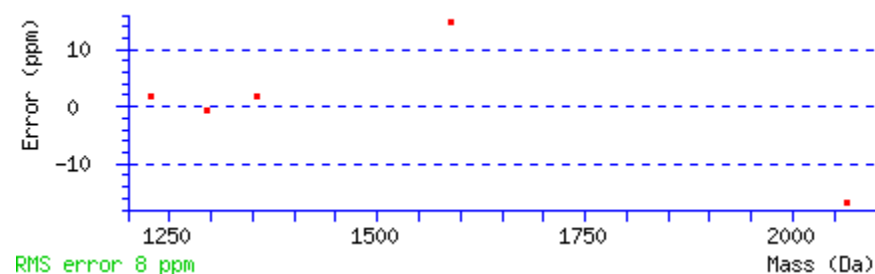
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence	
67 - 80	1295.7308	1294.7235	1294.7245	-1	0	K.NADAVLLGAIGGPK.W	(Ions score 68)
67 - 80	1295.7308	1294.7235	1294.7245	-1	0	K.NADAVLLGAIGGPK.W	(No match)
136 - 146	1227.6025	1226.5952	1226.5932	2	0	R.ELTGGIYFGDR.K	(Ions score 59)
136 - 146	1227.6025	1226.5952	1226.5932	2	0	R.ELTGGIYFGDR.K	(No match)
136 - 147	1355.6980	1354.6907	1354.6881	2	1	R.ELTGGIYFGDRK.E	(Ions score 48)
136 - 147	1355.6980	1354.6907	1354.6881	2	1	R.ELTGGIYFGDRK.E	(No match)
218 - 235	2066.0540	2065.0467	2065.0812	-17	1	K.IEHQLIDSAAMIMVKNPR.Q	(No match)
347 - 362	1590.8090	1589.8017	1589.7784	15	0	K.ATTSEVGDAVAEELEK.L	(Ions score 1)

347 - 362 1590.8090 1589.8017 1589.7784 15 0 K.ATTSEVGDAVAEELEK.L (No match)



LOCUS XP_001389813 365 aa linear PLN 28-FEB-2008
 DEFINITION beta-isopropylmalate dehydrogenase A leu2A-Aspergillus niger.
 ACCESSION XP_001389813
 VERSION XP_001389813.1 GI:145231098
 DBSOURCE REFSEQ: accession XM_001389776.1
 KEYWORDS .
 SOURCE Aspergillus niger CBS 513.88
 ORGANISM Aspergillus niger CBS 513.88
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (residues 1 to 365)
 AUTHORS Pel,H.J., de Winde,J.H., Archer,D.B., Dyer,P.S., Hofmann,G.,
 Schaap,P.J., Turner,G., de Vries,R.P., Albang,R., Albermann,K.,
 Andersen,M.R., Bendtsen,J.D., Benen,J.A., van den Berg,M.,
 Breestraat,S., Caddick,M.X., Contreras,R., Cornell,M.,
 Coutinho,P.M., Danchin,E.G., Debets,A.J., Dekker,P., van
 Dijck,P.W., van Dijk,A., Dijkhuizen,L., Driessen,A.J., d'Enfert,C.,
 Geysens,S., Goosen,C., Groot,G.S., de Groot,P.W., Guillemette,T.,
 Henrissat,B., Herweijer,M., van den Hombergh,J.P., van den
 Hondel,C.A., van der Heijden,R.T., van der Kaaij,R.M., Klis,F.M.,
 Kools,H.J., Kubicek,C.P., van Kuyk,P.A., Lauber,J., Lu,X., van der
 Maarel,M.J., Meulenbergh,R., Menke,H., Mortimer,M.A., Nielsen,J.,
 Oliver,S.G., Olsthoorn,M., Pal,K., van Peij,N.N., Ram,A.F.,
 Rinas,U., Roubos,J.A., Sagt,C.M., Schmoll,M., Sun,J., Ussery,D.,
 Varga,J., Vervecken,W., van de Vondervoort,P.J., Wedler,H.,
 Wosten,H.A., Zeng,A.P., van Ooyen,A.J., Visser,J. and Stam,H.
 TITLE Genome sequencing and analysis of the versatile cell factory
 Aspergillus niger CBS 513.88
 JOURNAL Nat. Biotechnol. 25 (2), 221-231 (2007)
 PUBMED 17259976
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from CAK37418.
 FEATURES Location/Qualifiers

source 1..365
/organism="Aspergillus niger CBS 513.88"
/db_xref="taxon:425011"
/clone="An01"

Protein 1..365
/product="beta-isopropylmalate dehydrogenase A
leu2A-Aspergillus niger"
/EC_number="1.1.1.85"
/calculated_mol_wt=38677

Region 4..363
/region_name="Iso_dh"
/note="Isocitrate/isopropylmalate dehydrogenase; cl00445"
/db_xref="CDD:174206"

Region 6..363
/region_name="PRK06451"
/note="isocitrate dehydrogenase; Validated; PRK06451"
/db_xref="CDD:168554"

CDS 1..365
/gene="leu2A"
/locus_tag="An01g14130"
/coded_by="XM_001389776.1:1..1098"
/inference="profile:COGS:COG0473"
/inference="profile:PFAM:PF00180"
/inference="similar to AA sequence:PIR:S72209"
/note="Catalytic activity:
3-Carboxy-2-hydroxy-4-methylpentanoate + NAD+ =
3-Carboxy-4-methyl-2-oxopentanoate + NADH.;
Gene-ID: leu2A;
Pathway: valine, leucine and isoleucine biosynthesis;
Remark: in A. niger are two highly
divergent,differentially regulated, isozymes for
beta-isopropylmalate dehydrogenase present.;
Remark: the differences in the sequence might be caused by
strain variations or sequencing errors."
/citation=[PUBMED 8781173]
/db_xref="GOA:A2QB74"
/db_xref="GeneID:4977432"

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

Spot 47

MASCOT Mascot Search Results

Protein View

Match to: [gi|74627960](#) Score: **191** Expect: **7.9e-013**

RecName: Full=Mannitol-1-phosphate 5-dehydrogenase; Short=M1PDH; Short=MPDH; Short=MPD

Nominal mass (M_r): **43695**; Calculated pI value: **5.96**NCBI BLAST search of [gi|74627960](#) against nrUnformatted [sequence string](#) for pasting into other applicationsTaxonomy: [Alternaria alternata](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|34329597](#) from [Alternaria alternata](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **17%**Matched peptides shown in **Bold Red**

1 MSYE**KAVHF GGGNIGR**GFV AEFLHNSGYE VVFVDVMSI IESLQTKTKY
51 TVTEIGDDGE **RKFTIDHYR**A INSKHEMDKV VQEIASADV TCAVGPNIKL
101 FVAEPVAKAI EARTLDYPIA VIACENAINA TTTWRGFIES KLSEETKKNI
151 DSKAR**FANSA IDR**IVPQPP NGGLDVVIEK FHEWCVEQKP FENGKKPDV
201 KGIHYVDDLE PYIERKLFTV NTSHATAAYY GHQNKVQYIH EVLHDKKLHD
251 TVRDAVKETA HLIVTKHGV TAEQDAYVEE IIKRISNPVL KDNVERVGRA
301 PLRKLSRKER FIGPAAQLAE **RGEKVDALLG AVEQAYRFQN VEGDEESVEL**
351 **AKILKENSAE EVVT**KVNGIE KGQPLFDRLV AIVKKVQGGG

Show predicted peptides also

Sort Peptides By



Residue Number



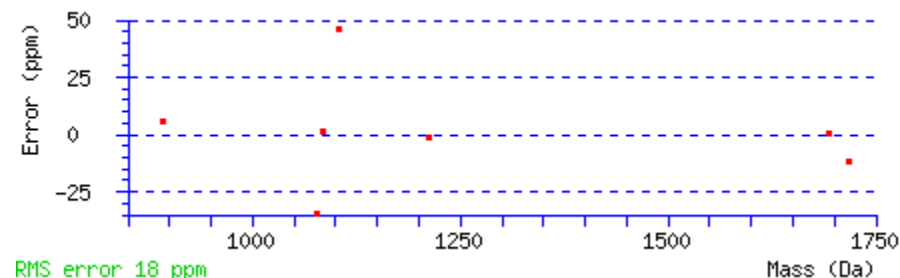
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
6 - 17	1212.6582	1211.6509	1211.6523	-1	1	K.KAVHFGGGNIGR.G (No match)
7 - 17	1084.5658	1083.5585	1083.5574	1	0	K.AVHFGGGNIGR.G (Ions score 87)
7 - 17	1084.5658	1083.5585	1083.5574	1	0	K.AVHFGGGNIGR.G (No match)
62 - 69	1079.5262	1078.5189	1078.5560	-34	1	R.KFTIDHYR.A (No match)
156 - 163	893.4529	892.4456	892.4403	6	0	R.FANSAIDR.I (Ions score 36)
156 - 163	893.4529	892.4456	892.4403	6	0	R.FANSAIDR.I (No match)
322 - 337	1718.8867	1717.8794	1717.8999	-12	1	R.GEKVDALLGAVEQAYR.F (No match)
338 - 352	1693.7928	1692.7855	1692.7842	1	0	R.FQNVEGDEESVELAK.I (Ions score 37)

338 - 352 1693.7928 1692.7855 1692.7842 1 0 R.FQNVEGDEESVELAK.I ([No match](#))
356 - 365 1105.5876 1104.5803 1104.5299 46 0 K.ENSAEEVVTK.V ([No match](#))



LOCUS MTLD_ALTAL 390 aa linear PLN 13-JUL-2010
DEFINITION RecName: Full=Mannitol-1-phosphate 5-dehydrogenase; Short=M1PDH;
Short=MPDH; Short=MPD.
ACCESSION Q6UQ76
VERSION Q6UQ76.1 GI:74627960
DBSOURCE UniProtKB: locus MTLD_ALTAL, accession Q6UQ76;
class: standard.
created: May 5, 2009.
sequence updated: Jul 5, 2004.
annotation updated: Jul 13, 2010.
xrefs: AY364263.1, AAQ63948.1
xrefs (non-sequence databases): SMR:Q6UQ76, GO:0050662, GO:0008926,
GO:0055114, InterPro:IPR008927, InterPro:IPR013328,
InterPro:IPR013118, InterPro:IPR000669, InterPro:IPR013131,
InterPro:IPR016040, Gene3D:G3DSA:3.40.50.720,
Gene3D:G3DSA:1.10.1040.10, Pfam:PF01232, Pfam:PF08125,
PRINTS:PR00084, SUPFAM:SSF48179, PROSITE:PS00974
KEYWORDS NAD; Oxidoreductase.
SOURCE Alternaria alternata
ORGANISM Alternaria alternata
Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
Pezizomycotina; Leotiomyceta; Dothideomyceta; Dothideomycetes;
Pleosporomycetidae; Pleosporales; Pleosporineae; Pleosporaceae;
mitosporic Pleosporaceae; Alternaria; Alternaria alternata group.
REFERENCE 1 (residues 1 to 390)
AUTHORS Velez,H., Glassbrook,N.J. and Daub,M.E.
TITLE Mannitol metabolism in the phytopathogenic fungus Alternaria
alternata
JOURNAL Fungal Genet. Biol. 44 (4), 258-268 (2007)
PUBMED 17092745
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND FUNCTION.
COMMENT [FUNCTION] Catalyzes the NAD(H)-dependent interconversion of
D-fructose 6-phosphate and D-mannitol 1-phosphate in the mannitol

metabolic pathway. Has a strong preference for NADH over NADPH.
 [CATALYTIC ACTIVITY] D-mannitol 1-phosphate + NAD(+) = D-fructose
 6-phosphate + NADH.
 [SUBUNIT] Monomer (By similarity).
 [SIMILARITY] Belongs to the mannitol dehydrogenase family.

FEATURES	Location/Qualifiers
source	1..390 /organism="Alternaria alternata" /db_xref="taxon:5599"
Protein	1..390 /product="Mannitol-1-phosphate 5-dehydrogenase" /EC_number="1.1.1.17" /note="M1PDH; MPDH"
Region	/UniProtKB_evidence="Inferred from homology" 1..390 /region_name="Mature chain" /experiment="experimental evidence, no additional details recorded" /note="Mannitol-1-phosphate 5-dehydrogenase. /FTId=PRO_0000371517."
Region	5..387 /region_name="PRK02318" /note="mannitol-1-phosphate 5-dehydrogenase; Provisional; PRK02318" /db_xref="CDD:167365"
Region	6..126 /region_name="Mannitol_dh" /note="Mannitol dehydrogenase Rossmann domain; pfam01232" /db_xref="CDD:144722"
Site	7..18 /site_type="np-binding" /inference="non-experimental evidence, no additional details recorded" /note="NAD (By similarity)."
Region	156..375 /region_name="Mannitol_dh_C" /note="Mannitol dehydrogenase C-terminal domain; pfam08125" /db_xref="CDD:149275"
Site	216 /site_type="active" /inference="non-experimental evidence, no additional details recorded" /note="By similarity."

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

Spot 48

Mascot Search Results

Protein View

Match to: [gi|255942351](#) Score: **250** Expect: **1e-018**
Pc18g00980 [[Penicillium chrysogenum Wisconsin 54-1255](#)]

Nominal mass (M_r): **57162**; Calculated pI value: **5.62**

NCBI BLAST search of [gi|255942351](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Penicillium chrysogenum Wisconsin 54-1255](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|211586677](#) from [Penicillium chrysogenum Wisconsin 54-1255](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

```

1 MTHPDISVDV LVIGAGPTGL GAAKRLNQIN GPSWMIIDSN ETPGGLASTD
51 VTPEGFLYDV GGHVIFSHYK YFDDCIDEAL PKEEDWYTHE RISYVRCQEQ
101 WVPYPFQNNI SMLPKEEQVK CIDGMIDAAL EARVSNTKPK DFDEWIVRMM
151 GTGIADLFMR PYNYKVVAVP TTKMQCAWL ERVAAPNVKA VTTNVILNKT
201 AGNWGPNATF RFPARDGTGG IWIAVANTIP KENTRYGPKN KVEKVNAVNYK
251 TVTLADGTTI GYGKLVSTMA VDYLAEAMND TELMPLTKQL FYSSTHVIGV
301 GIRGARPDR I GDKCWLYFPE NDCPFYRATI FSNYSPhNQ EASKKLPTIQ
351 LADGSKPKST EPQEGPYWSV MLEVSESSMK PVNNETLLAE SIQGLVNTQM
401 LQPGDEIVST YHRRFDHGYP TPTLEREGAL TQILPKLQEK GIWSRGRFGS
451 WRYEVGNQDH SFMLGVEAVD NIVNGAVELT LNYPDFVNGR QNTERRRLVDG
501 AQIFAKKQ
    
```

Show predicted peptides also

Sort Peptides By



Residue Number



Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
71 - 82	1485.6563	1484.6490	1484.6493	-0	0	K.YFDDCIDEALPK.E (Ions score 61)
71 - 82	1485.6563	1484.6490	1484.6493	-0	0	K.YFDDCIDEALPK.E (No match)
141 - 148	1079.5154	1078.5081	1078.5084	-0	0	K.DFDEWIVR.M (Ions score 53)
141 - 148	1079.5154	1078.5081	1078.5084	-0	0	K.DFDEWIVR.M (No match)
149 - 165	2007.9590	2006.9517	2006.9416	5	0	R.MMGTTGIADLFMRPYNYK.V (No match)

149 - 165	2023.9508	2022.9435	2022.9365	3	0	R.MMGTTGIADLFMRPYNYK.V	Oxidation (M) (No match)
149 - 165	2039.9510	2038.9437	2038.9315	6	0	R.MMGTTGIADLFMRPYNYK.V	2 Oxidation (M) (No match)
166 - 173	901.5137	900.5064	900.5069	-1	0	K.VWAVPTTK.M	(No match)
216 - 231	1612.8663	1611.8590	1611.8621	-2	0	R.DGTGGIWIAVANTIPK.E	(Ions score 34)
216 - 231	1612.8663	1611.8590	1611.8621	-2	0	R.DGTGGIWIAVANTIPK.E	(No match)
242 - 250	1064.5836	1063.5763	1063.5662	10	1	K.VEKVNAYNK.T	(No match)
314 - 327	1966.8308	1965.8235	1965.8178	3	0	K.CWLYFPENDCPFYR.A	(Ions score 32)
314 - 327	1966.8308	1965.8235	1965.8178	3	0	K.CWLYFPENDCPFYR.A	(No match)
328 - 344	1890.9747	1889.9674	1889.8908	41	0	R.ATIFSNYSPHNQPEASK.K	(No match)
437 - 445	1116.5822	1115.5749	1115.6087	-30	1	K.LQEKGIWSR.G	(Ions score 28)
437 - 445	1116.5822	1115.5749	1115.6087	-30	1	K.LQEKGIWSR.G	(No match)

Error: try setting browser cache to automatic.

LOCUS	XP_002561944	508 aa	linear	PLN 14-AUG-2009
DEFINITION	Pc18g00980 [Penicillium chrysogenum Wisconsin 54-1255].			
ACCESSION	XP_002561944			
VERSION	XP_002561944.1 GI:255942351			
DBSOURCE	REFSEQ: accession XM_002561898.1			
KEYWORDS	.			
SOURCE	Penicillium chrysogenum Wisconsin 54-1255			
ORGANISM	Penicillium chrysogenum Wisconsin 54-1255			
	Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;			
	Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;			
	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium;			
	Penicillium chrysogenum complex.			
REFERENCE	1 (residues 1 to 508)			
AUTHORS	van den Berg,M.A., Albang,R., Albermann,K., Badger,J.H.,			
	Daran,J.M., Driessen,A.J., Garcia-Estrada,C., Fedorova,N.D.,			
	Harris,D.M., Heijne,W.H., Joardar,V., Kiel,J.A., Kovalchuk,A.,			
	Martin,J.F., Nierman,W.C., Nijland,J.G., Pronk,J.T., Roubos,J.A.,			
	van der Klei,I.J., van Peij,N.N., Veenhuis,M., von Dohren,H.,			
	Wagner,C., Wortman,J. and Bovenberg,R.A.			
TITLE	Genome sequencing and analysis of the filamentous fungus			
	Penicillium chrysogenum			
JOURNAL	Nat. Biotechnol. 26 (10), 1161-1168 (2008)			
PUBMED	18820685			
REFERENCE	2 (residues 1 to 508)			

AUTHORS van den Berg,M.A.
 TITLE Direct Submission
 JOURNAL Submitted (22-NOV-2007) van den Berg M.A., DAI/INNO (624-0270), DSM
 Anti-Infectives, Alexander Fleminglaan 1, Delftn, 2613 AX,
 NETHERLANDS
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence is identical to CAP94322.
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 /name="Pc18g00980"
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 /db_xref="CDD:176428"
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 COG1232"
 /db_xref="CDD:31425"
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 /inference="protein motif:COGS:COG1233"
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 /db_xref="GeneID:8314645"

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

Spot 49

MASCOT Mascot Search Results

Protein View

Match to: **gi|145232889** Score: **118** Expect: **1.6e-005**
hypothetical protein An02g06820 [Aspergillus niger]

Nominal mass (M_r): **62977**; Calculated pI value: **6.29**

NCBI BLAST search of [gi|145232889](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Aspergillus niger CBS 513.88](#)

Links to retrieve other entries containing this sequence from NCBI Entrez:

[gi|134056738](#) from [Aspergillus niger](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

1 **MATDIATRD**L RKPTTVAEYL FRLHEVGVR SVHGVPDYN LAALDYLPKC
 51 GLHWVGNCNE LNAGYAADGY ARVNGIGALI TTFVGVELSA LNAIGSYSE
 101 FVPVVHIVGQ PNTKSQ**KDGM** **LLHHTLGNGD** **FNVFAK**MSAG ISCTLGR**LNE**
 151 **TLEAATLIDN** AIRECWIR**SR** **PVYISLPTDM** **IVK**QIEGDR LDKPLDLSLPA
 201 NDPEKEDYVV DVVLKYLHAA KKPVILVDAC AIRHR**VLDEV** **HDLMEASGLP**
 251 **TFVAPMGK**GA VDETRPNYGG VYAGTGSNAG VREQVESSDL ILSIGAIKSD
 301 FNTSGFSYHI GQLNTIDFHS TYVRVRYSEY PEINMKGVL R KVIQRMGAVN
 351 AAPVPHLSNT LPESEKSSSS QEITHDWLWP NVGQWL**KEND** **IVITETGTAN**
 401 **FGIWETR**FPA NVTASQVLW GSIGYSVGAC QGAALAAKEL GNRRTVLFVG
 451 DGSLQLTVQE LSTMIRNNLN PIIFVICNNG YTIERYIHGW DESYNDIQPW
 501 DIEGLPRVFG AKDKYGYKV KTRDELRLQF ANQEFASAPY LQFTCLVMML
 551 PPRXKSRLRR LPPGTSK

Show predicted peptides also

Sort Peptides By



Residue Number



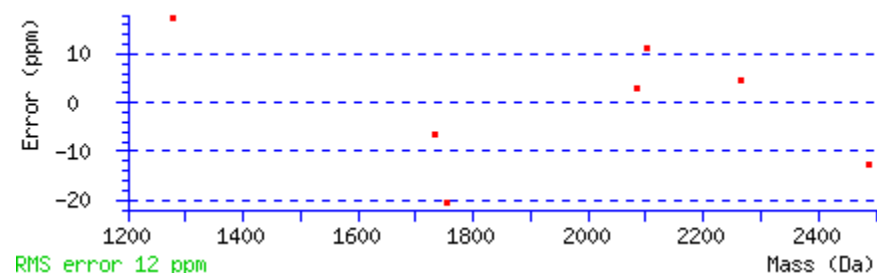
Increasing Mass



Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
1 - 11	1278.6693	1277.6620	1277.6398	17	1	-. MATDIATRD L.R Oxidation (M) (No match)
118 - 136	2086.0234	2085.0161	2085.0102	3	0	K.DGMLLHHTLGNGDFNVFAK.M (No match)
118 - 136	2086.0234	2085.0161	2085.0102	3	0	K.DGMLLHHTLGNGDFNVFAK.M (No match)
118 - 136	2102.0361	2101.0288	2101.0051	11	0	K.DGMLLHHTLGNGDFNVFAK.M Oxidation (M) (No match)

148 - 163	1756.9080	1755.9007	1755.9366	-20	0	R.LNETLEAATLIDNAIR.E	(No match)
148 - 163	1756.9080	1755.9007	1755.9366	-20	0	R.LNETLEAATLIDNAIR.E	(No match)
169 - 183	1734.9344	1733.9271	1733.9386	-7	0	R.SRPVYISLPTDMIVK.Q	Oxidation (M) (No match)
236 - 258	2488.1782	2487.1709	2487.2026	-13	0	R.VLDEVHDLMEASGLPTFVAPMGK.G	2 Oxidation (M) (No match)
388 - 407	2266.1086	2265.1013	2265.0913	4	0	K.ENDIVITETGTANFGIWETR.F	(Ions score 97)
388 - 407	2266.1086	2265.1013	2265.0913	4	0	K.ENDIVITETGTANFGIWETR.F	(No match)



LOCUS XP_001399817 567 aa linear PLN 28-FEB-2008
 DEFINITION hypothetical protein An02g06820 [Aspergillus niger].
 ACCESSION XP_001399817
 VERSION XP_001399817.1 GI:145232889
 DBSOURCE REFSEQ: accession XM_001399780.1
 KEYWORDS .
 SOURCE Aspergillus niger CBS 513.88
 ORGANISM Aspergillus niger CBS 513.88
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Eurotiomycetes; Eurotiomycetidae;
 Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 REFERENCE 1 (residues 1 to 567)
 AUTHORS Pel,H.J., de Winde,J.H., Archer,D.B., Dyer,P.S., Hofmann,G.,
 Schaap,P.J., Turner,G., de Vries,R.P., Albang,R., Albermann,K.,
 Andersen,M.R., Bendtsen,J.D., Benen,J.A., van den Berg,M.,
 Breestraat,S., Caddick,M.X., Contreras,R., Cornell,M.,
 Coutinho,P.M., Danchin,E.G., Debets,A.J., Dekker,P., van
 Dijck,P.W., van Dijk,A., Dijkhuizen,L., Driessen,A.J., d'Enfert,C.,
 Geysens,S., Goosen,C., Groot,G.S., de Groot,P.W., Guillemette,T.,
 Henrissat,B., Herweijer,M., van den Hombergh,J.P., van den
 Hondel,C.A., van der Heijden,R.T., van der Kaaij,R.M., Klis,F.M.,
 Kools,H.J., Kubicek,C.P., van Kuyk,P.A., Lauber,J., Lu,X., van der
 Maarel,M.J., Meulenbergh,R., Menke,H., Mortimer,M.A., Nielsen,J.,
 Oliver,S.G., Olsthoorn,M., Pal,K., van Peij,N.N., Ram,A.F.,
 Rinas,U., Roubos,J.A., Sagt,C.M., Schmoll,M., Sun,J., Ussery,D.,
 Varga,J., Vervecken,W., van de Vondervoort,P.J., Wedler,H.,
 Wosten,H.A., Zeng,A.P., van Ooyen,A.J., Visser,J. and Stam,H.
 TITLE Genome sequencing and analysis of the versatile cell factory
 Aspergillus niger CBS 513.88

JOURNAL Nat. Biotechnol. 25 (2), 221-231 (2007)
 PUBMED 17259976
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from CAK44227.

FEATURES Location/Qualifiers

source	1..567 /organism="Aspergillus niger CBS 513.88" /db_xref="taxon:425011" /clone="An02"
Protein	1..567 /product="hypothetical protein"
Region	12..548 /region_name="COG3961" /note="Pyruvate decarboxylase and related thiamine pyrophosphate-requiring enzymes [Carbohydrate transport and metabolism / Coenzyme metabolism / General function prediction only]; COG3961" /db_xref="CDD:33742"
Region	18..178 /region_name="TPP_PYR_PDC_IPDC_like" /note="Pyrimidine (PYR) binding domain of pyruvate decarboxylase (PDC), indolepyruvate decarboxylase (IPDC) and related proteins; cd07038" /db_xref="CDD:132921"
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Region	210..>307 /region_name="TPP_enzyme_M" /note="Thiamine pyrophosphate enzyme, central domain; pfam00205" /db_xref="CDD:143962"
Region	373..537 /region_name="TPP_PDC_IPDC" /note="TPP-binding module; composed of proteins similar to pyruvate decarboxylase (PDC) and indolepyruvate decarboxylase (IPDC). PDC, a key enzyme in alcoholic fermentation, catalyzes the conversion of pyruvate to acetaldehyde and CO2. It is able to utilize...; cd02005"

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 /inference="profile:PFAM:PF02775"
 /inference="profile:PFAM:PF02776"
 /inference="similar to AA sequence:UniProtKB:AF098293.1"
 /exception="reasons given in citation"
 /note="Catalytic activity: a 2-oxo acid = an aldehyde +
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 Pathway: glycolysis / gluconeogenesis.;
 Remark: PDC levels are a major determinant of ethanol
 production.;
 Similarity: belongs to the thiamine-diphosphate protein
 family.;
 Title: strong similarity to pyruvate decarboxylase pdcA -
 Aspergillus oryzae;
 putative sequencing error"
 /citation=[PUBMED 9210590]
 /db_xref="GeneID:4979172"

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

Spot 50

Mascot Search Results

Protein View

Match to: [gi|256729098](#) Score: **240** Expect: **1e-017**
 predicted protein [[Nectria haematococca mpVI 77-13-4](#)]

Nominal mass (M_r): **37591**; Calculated pI value: **6.39**

NCBI BLAST search of [gi|256729098](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Nectria haematococca mpVI 77-13-4](#)

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

```

1  MAAEIPTTQW AQQVEKNGGP TKYQQVPVRQ PGPDEVLVNV KFSGVCHTDL
51 HAMMGDWPLD TKLPLIGGHE GAGVVVSRGQ LVEDVEIGDY VGIKWLHGSC
101 LQCSFCQTS D EPLCAKALLS GYTVDGSFQQ YAVAKAAHVA RIPKECDLEA
151 ISPILCAGIT VYKGLKESGV KAGQTVAIVG AGGGLGSIAL QYAKAMGIHT
201 IAIDGGDDKK ALCESLGASA FVDFTKSSNL VAEVKAATSD GLGPHAVLLV
251 AVQEKPFQQA TQYVRSRGTV VCIGLPANAS LSAPVFDTVV RMISIKGSYV
301 GNRADTAEAI EFYRRGLIKV PFKTVGLSEL QSVYDLMTAG KIAGRYVVDT
351 SR
  
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Show predicted peptides also

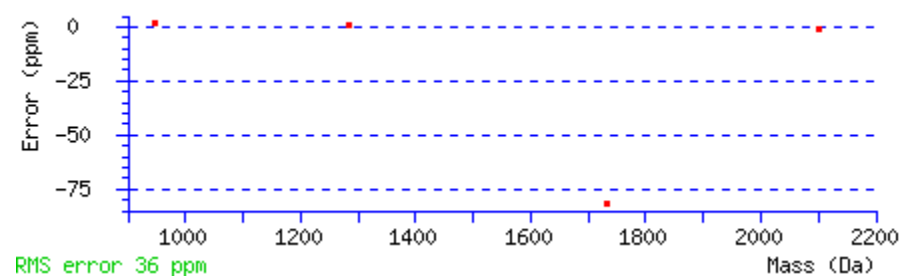
Sort Peptides By

☐ Residue Number

☒ Increasing Mass

☐ Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
79 - 94	1733.7544	1732.7471	1732.8883	-81	0	R.GQLVEDVEIGDYVGIK.W (No match)
172 - 194	2102.1584	2101.1511	2101.1532	-1	0	K.AGQTV AI VGAGGGLGSIALQYAK.A (Ions score 225)
172 - 194	2102.1584	2101.1511	2101.1532	-1	0	K.AGQTV AI VGAGGGLGSIALQYAK.A (No match)
227 - 235	946.5216	945.5143	945.5131	1	0	K.SSNL VAEVK.A (No match)
304 - 314	1285.6066	1284.5993	1284.5986	1	0	R.ADTAE IEFYR.R (No match)



LOCUS EEU42453 352 aa linear PLN 30-AUG-2009
 DEFINITION predicted protein [Nectria haematococca mpVI 77-13-4].
 ACCESSION EEU42453
 VERSION EEU42453.1 GI:256729098
 DBLINK Project: 16586
 DBSOURCE accession GG698905.1
 KEYWORDS .
 SOURCE Nectria haematococca mpVI 77-13-4
 ORGANISM Nectria haematococca mpVI 77-13-4
 Eukaryota; Fungi; Dikarya; Ascomycota; Saccharomyceta;
 Pezizomycotina; Leotiomyceta; Sordariomyceta; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria; Nectria
 haematococca complex.
 REFERENCE 1 (residues 1 to 352)
 AUTHORS Coleman,J.J., Rounsley,S.D., Rodriguez-Carres,M., Kuo,A.,
 Wasmann,C.C., Grimwood,J., Schmutz,J., Taga,M., White,G.J.,
 Zhou,S., Schwartz,D.C., Freitag,M., Ma,L.J., Danchin,E.G.,
 Henrissat,B., Coutinho,P.M., Nelson,D.R., Straney,D., Napoli,C.A.,
 Barker,B.M., Gribskov,M., Rep,M., Kroken,S., Molnar,I., Rensing,C.,
 Kennell,J.C., Zamora,J., Farman,M.L., Selker,E.U., Salamov,A.,
 Shapiro,H., Pangilinan,J., Lindquist,E., Lamers,C., Grigoriev,I.V.,
 Geiser,D.M., Covert,S.F., Temporini,E. and Vanetten,H.D.
 TITLE The genome of Nectria haematococca: contribution of supernumerary
 chromosomes to gene expansion
 JOURNAL PLoS Genet. 5 (8), E1000618 (2009)
 PUBMED 19714214
 REFERENCE 2 (residues 1 to 352)
 AUTHORS Kuo,A., Salamov,A., Grimwood,J., Schmutz,J., Pangilinan,J.,
 Shapiro,H., Lindquist,E., Lucas,S., Pitluck,S., Henrissat,B.,
 Geiser,D.M., Coleman,J.J., Kroken,S., Napoli,C.A., Rep,M.,
 Covert,S.F., Temporini,E., VanEtten,H.D. and Grigoriev,I.
 CONSRTM US DOE Joint Genome Institute (JGI-PGF)
 TITLE Direct Submission
 JOURNAL Submitted (14-JUL-2009) US DOE Joint Genome Institute, 2800
 Mitchell Drive, Walnut Creek, CA 94598-1698, USA

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COMMENT      Method: conceptual translation.
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dehydrogenase activity, zinc-dependent [PMID 8270]"
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 /db_xref="JGIDB:Necha2_69038"

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