

spot: 2



Mascot Search Results

Protein View

Match to: **A0090003001112** Score: 80
acyl-CoA synthetase

Nominal mass (M_r): **74750**; Calculated pI value: **5.83**

NCBI BLAST search of [A0090003001112](#) against nr

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

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  MADGNVMPK  PSVLEAHEV  DTFHVPKAFY  EKHTPTGTHLK  DLDEYKKLYD
51  ESIRSPQTFW  ARMARELLSF  DKDFQTTHTG  SLENGDSAWF  VEGRLNAAYN
101  CVDRHALKNP  DKVALIYEAD  EPNEGRTITY  GELLREVSrv  AWWLKKQGVK
151  KGDTVAIYLP  MIPEAVVAF  ACSRIGAIHS  VVFAGFSSDS  LRDRVIDAGS
201  KVVITDDEGK  RGGKVIKTR  IVDEALKQCP  DVTSVLVYKR  TGTEVPWTQG
251  RDVWWHEEVE  KYPNYFPPES  VSSEDPLFLL  YTSGSTGPK  GVMHTTAGYL
301  LGAAMTGK  YV  FDIHDDDRFF  CGGDVGWITG  HTYVVYAPLL  LGCSTVVFES
351  TPAYPNFSRY  WDVIEKHQVT  QFYVAPTALR  LLKRAGDEHI  HHKMAHLRIL
401  GSVGEPIAAE  VWKWFYFEKV  KEEAHICD  TY  WQTETGSNVI  TPLGGITPTK
451  PGSASLPFFG  IEPALIDPVS  GEEISGNDVE  GVLAFKQPWP  SMARTVWGAH
501  KRYMDTYLNV  YKGYFTGDG  AGRDHDGYW  IRGRVDDVVN  VSGHRLSTAE
551  IEAALLEHHM  VAEAAVVGIA  DELTGQAVNA  FVSLKEGNET  NEQVRKDLVM
601  QVRKSIGPFA  APKAVFVDD  LPKTRSGKIM  RRILRKILSG  EEDSLGDTST
651  LSDPSVVDKI  IETVHTARGK

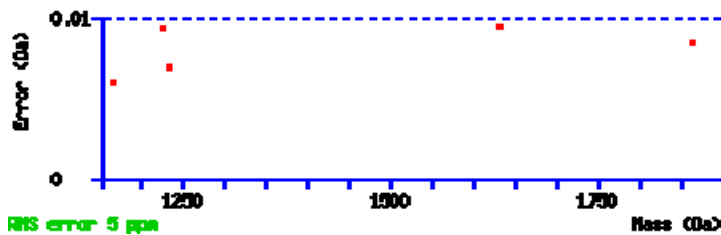
```

Show predicted peptides also

Sort Peptides By

Residue Number Increasing Mass Decreasing Mass

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
175 - 192	1862.9843	1861.9770	1861.9686	0.0085	0	IGAIHSVVFAGFSSDSL R (Ions score)
241 - 251	1231.6135	1230.6062	1230.5993	0.0070	0	TGTEVPWTQGR (Ions score 7)
367 - 380	1630.8795	1629.8722	1629.8627	0.0096	0	HQVTQFYVAPTALR (Ions score 24)
513 - 523	1163.5176	1162.5103	1162.5043	0.0061	0	GYFTGDGAGR (Ions score 5)
524 - 532	1224.5526	1223.5453	1223.5359	0.0094	0	DHDGYWIR (Ions score 26)



No report text found using parse rule 9

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