Protein Report

Project Info

Name: UGR_Microbiologia_M.Manzanera **Date:** April 15, 2014

Sample Info & Protocols

Date: April 15, 2014

Name: 140409C

Search Result Info

Search Result	Location	Search Engine	Database	Ident. Compounds
LIFT_NCBI_Viridiplantae_Mascot_2014-04-23 11:46:19	/UGR_Microbiologia_M.Manzanera/140409C/140409/geles ZT/15/CombinedLIFT	Mascot, 2.4.0	NCBInr, NCBInr_20140305.fasta	4/5 (FDR:0.00%)

Protein 1: RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor

Accession: gi|114421 **Score:** 182.08

Database: NCBInr **MW [kDa]:** 59.80

Seq. Coverage [%]: 9.80 % **pI:** 5.92

No. of Peptides: 4

Modification(s): Oxidation

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        10         20         30         40         50         60         70         80         90        100        110        120
MASRRLLASL LRQSAQRGGG LISRSLGNSI PKSASRASSR ASPKGFLLNR AVQYATSAAA PASQPSTPPK SGSEPSGKIT DEFTGAGSIG KVCQVIGAVV DVRFDEGLPP ILTALEVLDN

       130        140        150        160        170        180        190        200        210        220        230        240
QIRLVLEVAQ HLGENMVRTI AMDGTEGLVR GQRVLNTGSP ITVPVGRATL GRIINVIGEA IDERGPITTD HFLPIHREAP AFVEQATEQQ ILVTGIKVVD LLAPYQRGGK IGLFGGAGVG

       250        260        270        280        290        300        310        320        330        340        350        360
KTVLIMELIN NVAKAHGGFS VFAGVGERTR EGNDLYREMI ESGVIKLGEK QSESKCALVY GQMNEPPGAR ARVGLTGLTV AEHFRDAEGQ DVLLFIDNIF RFTQANSEVS ALLGRIPSAV

       370        380        390        400        410        420        430        440        450        460        470        480
GYQPTLATDL GGLQERITTT KKGSITSVQA IYVPADDLTD PAPATTFAHL DATTVLSRQI SELGIYPAVD PLDSTSRMLS PHILGEDHYN TARGVQKVLQ NYKNLQDIIA ILGMDELSED

       490        500        510        520        530        540        550        560        570
DKMTVARARK IQRFLSQPFH VAEVFTGAPG KYVDLKESIN SFQGVLDGKY DDLSEQSFYM VGGIDEVIAK AEKIAKESAA
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Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
	1	1723.9351	11.12	1		29.72		0	124-138	R.LVLEVAQHLGENMVR.T	Oxidation: 13	CID

Cmpd.	No. of Cmpds.	m/z meas.	Δ m/z [ppm]	z	Rt [min]	Score	Site [%]	P	Range	Sequence	Modification	Type
	1	1278.6530	13.45	1		35.90		0	139-150	R.TIAMDGTEGLVR.G	Oxidation: 4	CID
	1	1390.7005	10.29	1		92.62		0	255-268	K.AHGGFSVFAGVGER.T		CID
	1	1492.7936	12.20	1		23.84		0	342-355	R.FTQANSEVSALLGR.I		CID