Results from MASCOT search

1. Beta-actin-like protein 2

Analysis Information

Protein-Peptide Summary by Spot Analysis Type Combined (MS+MS/MS) Report Type Sample Set Name 2011-05-04 [001300010097-2011-03-18-1] Database SwissProt Analysis Name Khalii-Medicinal Chemistry[Mus Swissprot] Creation Date 05/04/2011 13:12:29 05/04/2011 13:18:54

Last Modified Reported By 05/04/2011 17:22:24 - admin

MS Acq.: Proc. Methods (Unspecified): (Unspecified)

Interpretation Method (Unspecified)

Gel Idx/Pos 325/N3 Plate [#] Name [1] 001300010097 Instr./Gel Orig in Ak115/2011-03-18-1 Instrument Sample Name

gi|81895966|sp|Q8 BFZ3.1|ACTBL_M OUSE RecName: Full=Beta-actin-like protein 2; AltName Full=Kappa-actin

C	Peptide Info	rmation)										
	Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C.1	I. % Modification	Rank	Result Type
	923.5672	923.5939	0.0267	29	330	337	IIAPPERK					Mascot
	1036.6514	1036.6608	0.0094	9	328	336	IKIIAPPER					Mascot
	1232.6569	1232.6783	0.0214	17	30	40	AVFPSMVGRPR			Oxidation (M)[6]		Mascot
	1639.8359	1639.9365	0.1006	61	179	192	LDLAGRDLTDYLMK			Oxidation (M)[13]		Mascot
	1790.892	1790.9762	0.0842	47	240	255	SYELPDGQVITIGNER	131		100		Mascot
	1790.892	1790.9762	0.0842	47	240	255	SYELPDGQVITIGNER					Mascot
	1954.0645	1954.1536	0.0891	46	97	114	VAPDEHPILLTEAPLNPK	63	99.	1.999		Mascot
	1954.0645	1954.1536	0.0891	46	97	114	VAPDEHPILLTEAPLNPK					Mascot

2. Cytochrome b-c1 complex subunit 1

Analysis Information
Report Type Protein-Peptide Summary by Spot Analysis Type Combined (MS+MS/MS) Sample Set Name 2011-05-04 [001300010097-2011-03-18-1] Database SwissProt Khalil-Medicinal Chemistry[Mus Swissprot] Creation Date

Reported By 05/04/2011 17:22:25 - admin 05/04/2011 13:18:54

(Unspecified) : (Unspecified) MS Acq.: Proc. Methods (Unspecified) Interpretation Method

Gel Idx/Pos 327/N5 Plate [#] Name [1] 001300010097 Instr./Gel Origin Instrument Sample Name Ak115/2011-03-18-1 Process Status Analysis Succeeded Spectra 6 Protein Protein Total Ion Total Ion Protein MW P
Score Score Score C. I. % Rank Protein Name

100 53419.7 5.75 A-L-1

Peptide Info	(Peptide Information)										
Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification	Rank	Result Type
912.4396	912,4569	0.0173	19	473	479	SGMFWLR			Oxidation (M)[3]		Mascot
1059,5081	1059.5363	0.0282	27	473	480	SGMFWLRF			Oxidation (M)[3]		Mascot
1100.5735	1100.6115	0.038	35	424	432	IPLAEWESR					Mascot
1110.5426	1110.5802	0.0376	34	214	222	TDLTDYLNR					Mascot
1202,6198	1202.6586	0.0388	32	433	442	IQEVDAQMLR					Mascot
1218.6147	1218.6503	0.0356	29	433	442	IQEVDAQMLR			Oxidation (M)[8]		Mascot
1256.6746	1256.7067	0.0321	26	423	432	RIPLAEWESR	41	99.719)		Mascot
1256.6746	1256.7067	0.0321	26	423	432	RIPLAEWESR					Mascot
1538.7479	1538.8057	0.0578	38	379	392	LCTSATESEVTRGK			Carbamidomethyl (C)[2]		Mascot
1605.7577	1605.7983	0.0406	25	256	269	VYEEDAVPGLTPCR	71	100	Carbamidomethyl (C)[13]		Mascot
1605.7577	1605.7983	0.0406	25	256	269	VYEEDAVPGLTPCR			Carbamidomethyl (C)[13]		Mascot
1646.8132	1646.8577	0.0445	27	112	126	EVESIGAHLNAYSTR					Mascot
2053.9971	2054.0491	0.052	25	397	415	NALVSHLDGTTPVCEDIG R	84	100	Carbamidomethyl (C)[14]		Mascot
2053.9971	2054.0491	0.052	25	397	415	NALVSHLDGTTPVCEDIG R			Carbamidomethyl (C)[14]		Mascot
2602.3259	2602.3831	0.0572	22	112	134	EVESIGAHLNAYSTREHT AYLIK					Mascot

3. ATP synthase subunit alpha

nalysis Informa	tion													
Report Type	Protein-f	Peptide	Summa	ry by Sp	pot	Ana	lysis Ty	ype		Com	bined (MS+M	ISMS)		
Sample Set Name	2011-05	-04 [001	300010	097-201	11-03-18	3-1] Data	abase			Swis	sProt			
Analysis Name	Khalil-Me	Khalil-Medicinal Chemistry[Mus Swissprot]					Creation Date 05/				1/2011 13:12:	29		
Reported By 05/04/2011 17:				22:26 - admin				Last Modified			1/2011 13:18:	54		
MS Acq.: Pro	c. Methods	ds (Unspecified): (Unspecified)				cified)								
Interpretation	Method		(Unspec			,								
Idx/Pos 328/No te [#] Name [1] 001						Instr./Gel O			Ak115/2011-0	3-18-1		Process Status Spectra	Analysis Succeede	d
nk Protein Name					Accessio			Protein	Total Ion Score	Total Ion C. I. %	Protein MW P	rotein Spot Name Pl	Pep. User name Count	Departmen
RecName: Full=A	TP synthase s	uhunit ak	nha	ai	il416677l	knlO032	130	100	97	100	598296	9 22 4-1-2	10 Kha	Madicinal
RecName: Full=A mito chondrial; Fla	gs: Precursor			ě.		A_MOUS	139	100	97	100	59829.6	9.22 A-L-2	10 Kha 🖬	Medicinal Chemistry
mitochondrial; Fla	gs: Precursor		pha, ±ppm	6	5.1 ATPA		139	100	97 Ion Score	n C.I.	59829.6 % Modificatio		10 Kha li Rank Resu	Chemistry
mitochondrial; Fla	gs: Precursor			Start	End S	A_MOUS	139	100	loi	n C.I.				Chemistry It Type
Peptide Inform	gs: Precursor nation Obsrv. Mass	± da	±ppm	Start Seq.	End Seq.	A_MOUS Sequence	139	100	loi	n C.I.			Rank Resu	Chemistry It Type
Peptide Inform Calc. Mass C	gs: Precursor nation Obsrv. Mass	± da	± ppm	Start Seq.	End : Seq.	A_MOUS Sequence		100	loi	n C.I.			Rank Resu	Chemistry It Type
Peptide Inform Calc. Mass C	nation Dbsrv. Mass 1000.6279 1026.6487	± da 0.0243 0.0545	±ppm 24 53	Start Seq.	End : Seq. 132 L 204 /	A_MOUS Sequence LIKEGDVVK AVDSLVPIGR	1	100	loi	n C.I.			Rank Resu Maso Maso	Chemistry It Type
Peptide Inform Calc. Mass C 1000.6036 1026.5942 1120.7201	nation) 0bsrv. Mass 1000.6279 1026.6487 1120.7817	± da 0.0243 0.0545 0.0616	±ppm 24 53 55	Start Seq. 124 195 172	5.1 ATPA	A_MOUS Sequence LIKEGDVVK AVDSLVPKGR VGLKAPGIIPR	1	100	loi	n C.I.			Rank Resu Maso Maso Maso	Chemistry It Type
Peptide Inform Calc. Mass C 1000.6036 1026.5942 1120.7201 1229.8848	nation Obsrv. Mass 1000.6279 1026.6487 1120.7817 1229.7469	± da 0.0243 0.0545 0.0616 0.0621	±ppm 24 53 55 51	Start Seq. 124 195 172 208	End : Seq. : 132 L 204 A 182 V 218 E	A_MOUS Sequence LIKEGDVVK AVDSLVPIGR VGLKAPGIIPR ELIIGDRQTGK	t K	100	loi	n C.I.		n	Rank Resu Maso Maso Maso	Chemistry It Type ot ot ot ot ot ot
Peptide Inform Calc. Mass C 1000.8036 1026.5942 1120.7201 1229.8848 1358.7461	nation Dbsrv. Mass 1000.6279 1026.6487 1120.7817 1229.7469 1358.8114	± da 0.0243 0.0545 0.0616 0.0621 0.0653	±ppm 24 53 55 51 48	Start Seq. 124 195 172 208 183	End : Seq. 132 L 204 / 182 \ 218 E 194 I	Sequence LIKEGDVVK AVDSLVPIGR VGLKAPGIIPR ELHIGDRQTGK SVREPMQTG	ł C SIK	100	loi	n C.I.	% Modificatio	n	Rank Resu Maso Maso Maso Maso	Chemistry It Type ot ot ot ot ot ot
Peptide Inform Calc. Mass C 1000.6036 1026.5942 1120.7201 1229.6848 1358.7461	nation) Diserv. Mass 1000.6279 1026.6487 1120.7817 1229.7469 1358.8114 1374.8071	± da 0.0243 0.0545 0.0616 0.0621 0.0653 0.0661	±ppm 24 53 55 51 48 48	Start Seq. 124 195 172 208 183 183	End : Seq	Sequence LIKEGDVVK AVDSLVPIGR VGLKAPGIIPR ELIIGDRQTGK ISVREPMQTG	t (iik iik	100	loi	n C.I.	% Modificatio	n (7)	Rank Resu Maso Maso Maso Maso Maso	Chemistry It Type ot
Peptide Inform Calc. Mass C 1000.6036 1026.5942 1120.7201 1229.8848 1358.7461 1374.741	nation))bsrv. Mass 1000.6279 1026.6487 1120.7817 1229.7469 1358.8114 1374.8071 1438.9028	± da 0.0243 0.0545 0.0616 0.0621 0.0663 0.0661 0.0539	±ppm 24 53 55 51 48 48 37	Start Seq. 124 195 172 208 183 183 403	5.1 ATPA	Sequence LIKEGDVVK AVDSLVPIGR VGLKAPGIIPR ELIIGDRQTGK ISVREPMQTG SVREPMQTG GIRPAINVGLS	t (ilk ilk ivsr	100	loi	n C.I.º	Modificatio Modificatio Oxidation (M) Oxidation (M)	n (7)	Rank Resu Maso Maso Maso Maso Maso Maso	Chemistry It Type st s
Peptide Inform Calc. Mass C 1000.6036 1026.5942 1122.7201 1229.6848 1356.7461 1374.741 1438.8499	1000.6279 1026.6487 1120.7817 1229.7459 1358.8114 1374.8071 1438.9028 1439.8993	± da 0.0243 0.0545 0.0616 0.0621 0.0663 0.0661 0.0539 0.0629	±ppm 24 53 55 51 48 48 37 44	Start Seq. 124 195 172 208 183 183 403 323	End : Seq. 132 L 204 / 182 \ 218 E 194 I 194 I 416 (334 (Sequence LIKEGDVVK AVDSLVPIGR VGLKAPGIIPR ELHIGDRQTGK SVREPMQTG SVREPMQTG GIRPAINVGLS QMSLLLRRPP	t K SIK SIVSR VGR HSR	100	loi Scori	n C.I.º	Modificatio Modificatio Oxidation (M) Oxidation (M)	n (7)	Rank Resu Masos Masos Masos Masos Masos Masos	Chemistry It Type of the state of the stat
Peptide Inform Calc. Mass C 1000.6036 1026.5942 1120.7201 1229.6848 1358.7461 1374.741 1438.8499 1438.8394 1553.7383	mation Dbsrv. Mass 1000.8279 1026.6487 1120.7817 1229.7489 1356.8114 1374.8071 1438.9028 1439.8893 1553.8164	± da 0.0243 0.0545 0.0616 0.0621 0.0653 0.0661 0.0539 0.0629 0.0781	±ppm 24 53 55 51 48 48 37 44 50	Start Seq. 124 195 172 208 183 183 403 323 335	End : Seq. 132 L 204 / 182 \ 218 E 194 I 194 I 416 (334 C 347 E 347 E	A_MOUS Sequence LIKEGDVVK AVDSLVPIGR VGLKAPGIIPR ELIKGDRQTGS ISVREPMQTG ISVREPMQTG	t Gilk GIR GR HSR HSR	100	loi Scori	n C.I.º	Modificatio Modificatio Oxidation (M) Oxidation (M)	n (7)	Rank Resu Maso Maso Maso Maso Maso Maso	Chemistry It Type of the state of the stat

4. ATP synthase subunit beta

Analysis Information

Report Type Protein-Peptide Summary by Spot Analysis Type Combined (MS+MS/MS)

 Sample Set Name
 2011-05-04 [001300010097-2011-03-18-1]
 Database
 SwissProt

 Analysis Name
 Khalil-Medicinal Chemistry[Mus Swissprot]
 Creation Date
 05/04/2011 13:12:29

 Reported By
 05/04/2011 17:22:26 - admin
 Last Modified
 05/04/2011 13:18:54

MS Acq.: Proc. Methods (Unspecified): (Unspecified)

Interpretation Method (Unspecified)

Gel Idx/Pos	328/N6	Ins	str./Gel Origin		Ak115/2011-	03-18-1		Process Status	Analysis Succeeded	i
Plate [#] Name	[1] 00 13000 10097	Ins	strument Sample	Name				Spectra	6	
Rank Protein N	ame Ad	ccession		Proteir Score C. I. %	Score	Total Ion C. I. %	Protein MW Prote	in Spot Name Pl	Pep. User name Count	Department

RecName: Full=ATP synthase subunit beta, gil[20455479[sp]P5 485 100 367 100 56265.5 5.19 A-L-2 15 Khalil Medicinal mitochondrial; Rags: Precursor USE Chemistry

Peptide Information Ion C.I. % Modification Score Calc. Mass Obsrv. Mass ± da ±ppm Start End Sequence Rank Result Type 121 TIAMDGTEGLVR 1262,6409 1262,7026 0.0617 1385.7094 1385.7786 0.0692 155 IMNVIGEPIDER 50 144 Mascot 1401.7753 0.0711 1401.7042 51 144 155 IMNVIGEPIDER Oxidation (M)[2] Mascot 239 AHGGYSVFAGVGER 1406.681 1406.7507 0.0697 226 100 Mascot 1406.7507 1435.7539 1435.8242 0.0703 324 FTQAGSEVSALLGR 1439.7893 1439.8893 0.1 294 VALTGLTVAEYFR 1601.8104 1601.886 0.0756 47 265 279 VALVYGQMNEPPGAR 1601.8104 1601.886 0.0756 47 265 279 VALVYGQMNEPPGAR 1617.8053 1617.8818 0.0765 47 265 279 VALVYGOMNEPPGAR Mascot 1650.9174 1650.9941 0.0767 95 109 LVLEVAQHLGESTVR 100 Mascot 1650.9174 1650,9941 0.0767 46 95 109 LVLEVAQHLGESTVR Mascot 159 IMNVIGEPIDERGPIK 1780,9625 1781.047 0.0845 47 144 Mascot 144 159 IMNVIGEPIDERGPIK 1796.9575 1797.0184 0.0609 34 Oxidation (M)[2] Mascot 422 IMDPNIVGNEHYDVAR 1842.9714 0.0912 407 1842,8802 49 Mascot 1858.8752 1858.9777 422 IMDPNIVGNEHYDVAR 0.1025 Oxidation (M)[2] Mascot 143 VLDSGAPIKIPVGPETLG

5. Trifunctional enzyme subunit beta

Analysis Information

 Report Type
 Protein-Peptide Summary by Spot
 Analysis Type
 Combined (MS+MSMS)

 Sample Set Name
 2011-05-04 [001300010097-2011-03-18-1]
 Database
 SwissProt

 Analysis Name
 Khalil-Medicinal Chemistry[Mus Swissprot]
 Creation Date
 05/04/2011 13:12:29

 Reported By
 05/04/2011 17:22:26 - admin
 Last Modified
 05/04/2011 13:18:54

MS Acq. : Proc. Methods (Unspecified) : (Unspecified)

Interpretation Method (Unspecified)

2 RecName: Full=Trifunctional enzyme subunit beta, gij51316075|sp|C9 91 99.999 27 94.125 51638.5 9.43 A-L-1 11 Khali Medicinal mitochondrial; ARName: Full=Tr-beta; Includes: Re 9JY0.1|ECHB_MO Chemistry

Analysis Information

 Report Type
 Protein-Peptide Summary by Spot
 Analysis Type
 Combined (MS+MSMS)

 Sample Set Name
 2011-05-04 [00130001097-2011-03-18-1]
 Database
 SwissProt

 Analysis Name
 Khalif-Medicinal Chemistry[Mus Swissprot]
 Creation Date
 05/04/2011 13:12:29

 Reported By
 05/04/2011 17:22:25 - admin
 Last Modified
 05/04/2011 13:18:54

MS Acq.: Proc. Methods (Unspecified): (Unspecified)

Interpretation Method (Unspecified)

Peptide Information Ion C.I. % Modification Rank Result Type 905.5203 905.5383 0.018 20 231 239 LAAAFAVSR 27 94,125 937,5577 937,5787 0.021 22 83 91 AALSGLLHR Mascot 937.5577 937.5787 0.021 91 AALSGLLHR 22 83 Mascot 984.5836 984.6089 0.0253 62 NIVVVEGVR Mascot 1055,6095 1055.5413 -0.0682 1154,5146 1154.5502 1170.5095 1170.5463 0.0368 240 248 MEQDEYALR Oxidation (M)[1] 1545.7689 1545.8134 0.0445 292 DNGIRPSSLEQMAK 1561,7639 1561.8085 0.0446 29 279 292 DNGIRPSSLEQMAK Oxidation (M)[12] Mascot 1683.8701 1683 9056 0.0355 21 255 269 KAODEGHI SDIVPEK Mascot 1691,6941 1691,743 0.0489 29 393 406 AMDSDWFAQNYMGR Mascot 17148799 1714.9293 0.0494 29 336 349 AYLRDFIYVSQDPK Mascot 1777,8538 1777.902 0.0482 27 240 254 MEQDEYALRSHSLAK Mascot 1868.0786 1867.9825 -0.0961 -51 62 TLAKPNMKNIVVVEGVR Mascot