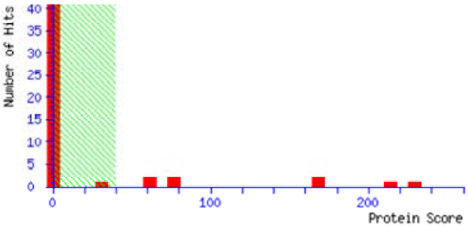
Mascot Search Results

User	: **JPROS**
Email	: **pro@jbios.co.jp**
Search title	: **D:\JPROS\L015\c(x10)_6micro.wiff (sample number 1)**
MS data file	: **mas90F.tmp**
Database	: **NCBIprot 20180429 (152462470 sequences; 55858910152 residues)**
Taxonomy	: **Homo sapiens (human) (327411 sequences)**
Timestamp	: **14 Feb 2019 at 06:30:53 GMT**
Protein hits	: **EAW48850.1** RNA U, small nuclear RNA export adaptor (phosphorylation regulated), partial [Homo sapiens]
	NP_004631.1 spliceosome RNA helicase DDX39B [Homo sapiens]
	AAH00151.1 Chromosome 22 open reading frame 28 [Homo sapiens]
	BAB15509.1 unnamed protein product [Homo sapiens]
	BAH14636.1 unnamed protein product [Homo sapiens]
	NP_000414.2 keratin, type II cytoskeletal 2 epidermal [Homo sapiens]
	NP_006112.3 keratin, type II cytoskeletal 1 [Homo sapiens]
	NP_000412.3 keratin, type I cytoskeletal 10 [Homo sapiens]
	Q6PEY2.2 RecName: Full=Tubulin alpha-3E chain; AltName: Full=Alpha-tubulin 3E; Contains: RecName: Full=Detyrosina

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 39 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary | Help
Significance threshold p< 0.05 | Max. number of hits AUTO
Standard scoring ○ MudPIT scoring ● | Display non-significant matches ☑ | Show sub-sets 0
Show pop-ups ● Suppress pop-ups ○ | Sort unassigned Decreasing Score | Require bold red ☐
Preferred taxonomy All entries

Select All | Select None | Search Selected | ☐ **Error tolerant**

1. EAW48850.1 **Mass:** 46023 **Score:** 229 **Matches:** 18(5) **Sequences:** 10(5) **emPAI:** 0.47
RNA U, small nuclear RNA export adaptor (phosphorylation regulated), partial [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	263	**468.7125**	**935.4104**	**935.4712**	**-0.0609**	**0**	**(31)**	**0.55**	**1**	**U**	**K.VADEISFR.L**
☑	264	**468.7136**	**935.4126**	**935.4712**	**-0.0587**	**0**	**(31)**	**0.49**	**1**	**U**	**K.VADEISFR.L**
☑	265	**468.7168**	**935.4190**	**935.4712**	**-0.0522**	**0**	**52**	**0.0036**	**1**	**U**	**K.VADEISFR.L**
☑	266	**468.7171**	**935.4196**	**935.4712**	**-0.0516**	**0**	**(11)**	**50**	**1**	**U**	**K.VADEISFR.L**
☑	267	**468.7238**	**935.4331**	**935.4712**	**-0.0382**	**0**	**(23)**	**2.9**	**1**	**U**	**K.VADEISFR.L**
☑	268	**468.7303**	**935.4460**	**935.4712**	**-0.0253**	**0**	**(20)**	**6.7**	**1**	**U**	**K.VADEISFR.L**
☑	269	**468.7304**	**935.4463**	**935.4712**	**-0.0250**	**0**	**(19)**	**8.4**	**1**	**U**	**K.VADEISFR.L**
☑	341	**579.8120**	**1157.6094**	**1157.6808**	**-0.0715**	**0**	**77**	**1.6e-05**	**1**	**U**	**R.TPGGVFLNLLK.N**
☑	343	**585.2586**	**1168.5026**	**1168.5764**	**-0.0739**	**0**	**36**	**0.18**	**1**	**U**	**K.DIFYIENQK.E**
	373	**623.2650**	**1244.5154**	**1244.6248**	**-0.1094**	**0**	**(1)**	**5.5e+02**	**6**	**U**	**K.NTPSISEEQIK.D**
☑	374	**623.2676**	**1244.5206**	**1244.6248**	**-0.1042**	**0**	**38**	**0.12**	**1**	**U**	**K.NTPSISEEQIK.D**
☑	375	**623.2742**	**1244.5339**	**1244.6248**	**-0.0909**	**0**	**(30)**	**0.71**	**1**	**U**	**K.NTPSISEEQIK.D**
☑	419	**656.7584**	**1311.5022**	**1311.5830**	**-0.0808**	**0**	**44**	**0.018**	**1**	**U**	**R.YEITAEDSQEK.V**
☑	424	**665.2975**	**1328.5804**	**1328.6612**	**-0.0808**	**0**	**54**	**0.0025**	**1**	**U**	**R.QSETYNYLLAK.K**
☑	449	**713.7594**	**1425.5042**	**1425.6008**	**-0.0966**	**0**	**63**	**0.00014**	**1**	**U**	**K.SLNFQEDDDTSR.E**
☑	462	**509.2150**	**1524.6232**	**1524.7056**	**-0.0824**	**1**	**28**	**0.99**	**1**	**U**	**K.GRYEITAEDSQEK.V**
☑	486	**555.8904**	**1664.6495**	**1664.7352**	**-0.0857**	**1**	**35**	**0.13**	**1**	**U**	**K.DLDKELDEYMHGGK.K + Oxidation (M)**
☑	501	**598.5956**	**1792.7651**	**1792.8315**	**-0.0664**	**0**	**33**	**0.24**	**1**	**U**	**R.AFQNTATACAPVSHYR.A + Carbamidomethyl (C)**

Proteins matching the same set of peptides:
NP_115553.2 **Mass:** 44375 **Score:** 229 **Matches:** 18(5) **Sequences:** 10(5)
phosphorylated adapter RNA export protein [Homo sapiens]

2. NP_004631.1 **Mass:** 48960 **Score:** 218 **Matches:** 22(8) **Sequences:** 14(7) **emPAI:** 0.79
spliceosome RNA helicase DDX39B [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	249	**453.7154**	**905.4162**	**905.4607**	**-0.0445**	**0**	**33**	**0.36**	**2**		**R.DVQEIFR.M**
☑	262	**468.2757**	**934.5368**	**934.5124**	**0.0245**	**0**	**16**	**21**	**1**		**R.ELAFQISK.E**
☑	285	**486.7459**	**971.4773**	**971.5036**	**-0.0263**	**0**	**46**	**0.019**	**1**		**K.ILNDVQDR.F**

☑	302	518.2139	1034.4132	1034.4889	-0.0757	0	47	0.014	1		K.MLEQLDMR.R
☑	319	526.2008	1050.3871	1050.4838	-0.0967	0	(38)	0.12	1		K.MLEQLDMR.R + Oxidation (M)
	320	526.2169	1050.4192	1050.4838	-0.0646	0	(7)	1.8e+02	2		K.MLEQLDMR.R + Oxidation (M)
☑	323	534.2281	1066.4416	1066.4787	-0.0371	0	(35)	0.32	1		K.MLEQLDMR.R + 2 Oxidation (M)
	332	552.2359	1102.4573	1102.6499	-0.1926	0	(5)	3.3e+02	2		R.ILVATNLFGR.G
☑	333	552.2887	1102.5628	1102.6499	-0.0870	0	(18)	15	1		R.ILVATNLFGR.G
☑	334	552.2981	1102.5816	1102.6499	-0.0683	0	(18)	16	1		R.ILVATNLFGR.G
☑	336	552.3108	1102.6070	1102.6499	-0.0429	0	73	4.4e-05	1		R.ILVATNLFGR.G
☑	340	569.3175	1136.6205	1136.6594	-0.0389	0	43	0.04	1	U	K.VAVFFGGLSIK.K
☑	371	622.3576	1242.7006	1242.7336	-0.0329	0	24	2.4	1		R.DFLLKPELLR.A
☑	379	629.7877	1257.5608	1257.6097	-0.0489	0	60	0.00065	1	U	K.QVMMFSATLSK.E + Oxidation (M)
☑	392	637.7819	1273.5492	1273.6046	-0.0554	0	(46)	0.017	1	U	K.QVMMFSATLSK.E + 2 Oxidation (M)
☑	411	432.8691	1295.5856	1295.6259	-0.0403	0	29	0.78	1	U	K.GSYVSIHSSGFR.D
☑	417	436.2066	1305.5979	1305.6612	-0.0633	0	9	77	1	U	K.NCPHIVVGTPGR.I + Carbamidomethyl (C)
☑	455	488.2490	1461.7251	1461.7980	-0.0729	0	42	0.036	1		K.LTLHGLQQYYVK.L
☑	457	740.3255	1478.6364	1478.7253	-0.0889	0	62	0.00032	1		K.GLAITFVSDENDAK.I
☑	458	740.3494	1478.6842	1478.7253	-0.0411	0	(8)	84	1		K.GLAITFVSDENDAK.I
☑	511	626.2311	1875.6715	1875.7907	-0.1191	0	18	2.2	1	U	K.FMQDPMEIFVDDETK.L + 2 Oxidation (M)
☑	528	668.9311	2003.7715	2003.8856	-0.1141	1	28	0.35	1	U	R.KFMQDPMEIFVDDETK.L + 2 Oxidation (M)

Proteins matching the same set of peptides:
BAF31287.1 **Mass:** 50647 **Score:** 218 **Matches:** 22(8) **Sequences:** 14(7)
BAT1 protein [Homo sapiens]
BAD96632.1 **Mass:** 48988 **Score:** 218 **Matches:** 22(8) **Sequences:** 14(7)
HLA-B associated transcript 1 variant, partial [Homo sapiens]

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3. AAH00151.1 **Mass:** 55209 **Score:** 164 **Matches:** 8(4) **Sequences:** 8(4) **emPAI:** 0.29
Chromosome 22 open reading frame 28 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	288	488.2516	974.4887	974.5219	-0.0332	0	20	8.1	1	U	K.LADMGIAIR.V + Oxidation (M)
☑	338	553.7566	1105.4987	1105.5590	-0.0603	0	33	0.33	1	U	R.GGGVGGFLPAMK.Q + Oxidation (M)
☑	350	603.7683	1205.5220	1205.5928	-0.0709	0	53	0.0031	1	U	R.NLDFQDVLDK.L
☑	354	610.7890	1219.5635	1219.6084	-0.0449	0	66	0.00019	1	U	R.IASPEGQDYLK.G
☑	437	672.7971	1343.5796	1343.6569	-0.0772	0	55	0.0017	1	U	R.TNLDESDVQPVK.E
☑	441	693.2823	1384.5501	1384.6510	-0.1009	0	53	0.0028	1	U	R.SYNDELQFLEK.I
☑	452	482.2528	1443.7366	1443.8310	-0.0944	0	28	0.92	1	U	K.QIGNVAALPGIVHR.S
☑	493	577.2702	1728.7887	1728.8101	-0.0214	0	38	0.089	1	U	K.NVTDVVNTCHDAGISK.K + Carbamidomethyl (C)

Proteins matching the same set of peptides:
CAG33456.1 **Mass:** 55228 **Score:** 164 **Matches:** 8(4) **Sequences:** 8(4)
HSPC117 [Homo sapiens]
NP_055121.1 **Mass:** 55175 **Score:** 164 **Matches:** 8(4) **Sequences:** 8(4)
tRNA-splicing ligase RtcB homolog [Homo sapiens]

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4. BAB15509.1 **Mass:** 52980 **Score:** 163 **Matches:** 16(5) **Sequences:** 9(5) **emPAI:** 0.40
unnamed protein product [Homo sapiens]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
249	453.7154	905.4162	905.4607	-0.0445	0	33	0.36	2		R.DVQEIFR.L
262	468.2757	934.5368	934.5124	0.0245	0	16	21	1		R.ELAFQISK.E
285	486.7459	971.4773	971.5036	-0.0263	0	46	0.019	1		K.ILNDVQDR.F
302	518.2139	1034.4132	1034.4889	-0.0757	0	47	0.014	1		K.MLEQLDMR.R
319	526.2008	1050.3871	1050.4838	-0.0967	0	(38)	0.12	1		K.MLEQLDMR.R + Oxidation (M)
320	526.2169	1050.4192	1050.4838	-0.0646	0	(7)	1.8e+02	2		K.MLEQLDMR.R + Oxidation (M)
323	534.2281	1066.4416	1066.4787	-0.0371	0	(35)	0.32	1		K.MLEQLDMR.R + 2 Oxidation (M)
332	552.2359	1102.4573	1102.6499	-0.1926	0	(5)	3.3e+02	2		R.ILVATNLFGR.G
333	552.2887	1102.5628	1102.6499	-0.0870	0	(18)	15	1		R.ILVATNLFGR.G
334	552.2981	1102.5816	1102.6499	-0.0683	0	(18)	16	1		R.ILVATNLFGR.G
336	552.3108	1102.6070	1102.6499	-0.0429	0	73	4.4e-05	1		R.ILVATNLFGR.G
371	622.3576	1242.7006	1242.7336	-0.0329	0	24	2.4	1		R.DFLLKPELLR.A
390	424.2794	1269.8165	1269.6214	0.1951	0	4	1.7e+02	3	U	K.GSHVSIHSSGFR.D
455	488.2490	1461.7251	1461.7980	-0.0729	0	42	0.036	1		K.LTLHGLQQYYVK.L
457	740.3255	1478.6364	1478.7253	-0.0889	0	62	0.00032	1		K.GLAITFVSDENDAK.I
458	740.3494	1478.6842	1478.7253	-0.0411	0	(8)	84	1		K.GLAITFVSDENDAK.I

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5. BAH14636.1 **Mass:** 46537 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1) **emPAI:** 0.08
unnamed protein product [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	342	580.2948	1158.5750	1158.6219	-0.0469	0	28	1.1	1	U	K.LAVNMVPFPR.L + Oxidation (M)
☑	373	623.2650	1244.5154	1244.5860	-0.0706	0	34	0.29	1	U	R.ISEQFTAMFR.R + Oxidation (M)
☑	413	651.3254	1300.6362	1300.6299	0.0063	0	38	0.098	1	U	R.ISVYYNEATGGK.Y
☑	433	668.3216	1334.6286	1334.6904	-0.0618	0	45	0.018	1	U	R.IMNTFSVVPSPK.V + Oxidation (M)
☑	454	731.8068	1461.5990	1461.6769	-0.0779	0	22	2.9	1	U	K.EVDEQMLNVQNK.N + Oxidation (M)
☑	479	816.3902	1630.7659	1630.8236	-0.0578	0	10	59	1	U	R.AILVDLEPGTMDSVR.S + Oxidation (M)

Proteins matching the same set of peptides:
AAH20946.1 **Mass:** 49640 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1)
Tubulin, beta [Homo sapiens]

NP_035785.1 **Mass:** 49639 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1)
tubulin beta-5 chain [Mus musculus]

pir||I38369 **Mass:** 48848 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1)
beta-tubulin - human (fragment)

AAB59507.1 **Mass:** 49727 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1)
beta-tubulin [Homo sapiens]

BAG63652.1 **Mass:** 52015 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1)
unnamed protein product [Homo sapiens]

NP_001280141.1 **Mass:** 51985 **Score:** 73 **Matches:** 6(1) **Sequences:** 6(1)
tubulin beta chain isoform a [Homo sapiens]

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6. NP_000414.2 **Mass:** 65393 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1) **emPAI:** 0.06
keratin, type II cytoskeletal 2 epidermal [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	456	**738.3405**	**1474.6664**	**1474.7780**	**-0.1116**	**0**	**70**	**5.9e-05**	**1**		**R.FLEQQNQVLQTK.W**

Proteins matching the same set of peptides:

AAC83410.1 **Mass:** 65825 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1)
epidermal cytokeratin 2 [Homo sapiens]

XP_011536591.1 **Mass:** 34525 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1)
keratin, type II cytoskeletal 1b isoform X2 [Homo sapiens]

AAI22559.1 **Mass:** 61764 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1)
Keratin 77 [Homo sapiens]

CAD91892.1 **Mass:** 61763 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1)
keratin 1b [Homo sapiens]

EAW96643.1 **Mass:** 61840 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1)
keratin 1B [Homo sapiens]

NP_778253.2 **Mass:** 61864 **Score:** 70 **Matches:** 1(1) **Sequences:** 1(1)
keratin, type II cytoskeletal 1b [Homo sapiens]

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7. NP_006112.3 **Mass:** 65999 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1) **emPAI:** 0.06
keratin, type II cytoskeletal 1 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	386	**633.3139**	**1264.6133**	**1264.6299**	**-0.0166**	**0**	**24**	**2.5**	**1**	**U**	**R.TNAENEFVTIK.K**
☑	440	**692.3119**	**1382.6093**	**1382.6830**	**-0.0737**	**0**	**23**	**2.8**	**1**	**U**	**K.SLNNQFASFIDK.V**
	456	738.3405	1474.6664	1474.7780	-0.1116	0	70	5.9e-05	1		R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:

BAG36698.1 **Mass:** 65980 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
unnamed protein product [Homo sapiens]

AAG41947.1 **Mass:** 66027 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AFA52002.1 **Mass:** 66013 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AFA52003.1 **Mass:** 66029 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AFA52004.1 **Mass:** 65930 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AFA52005.1 **Mass:** 66086 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AFA52006.1 **Mass:** 66026 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AFA52007.1 **Mass:** 66071 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

AAF60327.1 **Mass:** 65978 **Score:** 65 **Matches:** 3(1) **Sequences:** 3(1)
keratin 1 [Homo sapiens]

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8. NP_000412.3 **Mass:** 58766 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2) **emPAI:** 0.13
keratin, type I cytoskeletal 10 [Homo sapiens]
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
☑	330	**545.7244**	**1089.4343**	**1089.5237**	**-0.0893**	**0**	**41**	**0.051**	**1**	**U**	**K.VTMQNLNDR.L**
☑	439	**691.2924**	**1380.5703**	**1380.6408**	**-0.0705**	**0**	**52**	**0.0039**	**1**	**U**	**R.ALEESNYELEGK.I**

Proteins matching the same set of peptides:

P13645.6 **Mass:** 58792 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2)
RecName: Full=Keratin, type I cytoskeletal 10; AltName: Full=Cytokeratin-10; Short=CK-10; AltName: Full=Keratin-10; Short=K10

CAA32649.1 **Mass:** 59492 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2)
unnamed protein product [Homo sapiens]

AAH34697.1 **Mass:** 58792 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2)
Keratin 10 [Homo sapiens]

AAA60544.1 **Mass:** 57213 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2)
keratin 10 [Homo sapiens]

EAW60681.1 **Mass:** 63308 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2)
keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens]

XP_005257400.1 **Mass:** 63308 **Score:** 65 **Matches:** 2(2) **Sequences:** 2(2)
keratin, type I cytoskeletal 10 isoform X1 [Homo sapiens]

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9. Q6PEY2.2 **Mass:** 49827 **Score:** 29 **Matches:** 1(0) **Sequences:** 1(0)

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   RecName: Full=Tubulin alpha-3E chain; AltName: Full=Alpha-tubulin 3E; Contains: RecName: Full=Detyrosinated tubulin alpha-3E cha
 ☐ Check to include this hit in error tolerant search

  Query  Observed   Mr(expt)   Mr(calc)    Delta  Miss Score Expect Rank Unique  Peptide
 ☑  299  508.2534  1014.4922  1014.5709  -0.0787   0    29    0.96   1     U     K.DVNAAIATIK.T


   Proteins matching the same set of peptides:
   AAH11721.1     Mass: 46083     Score: 29     Matches: 1(0)  Sequences: 1(0)
   Tubulin, alpha 3c [Homo sapiens]
   AAH21564.1     Mass: 37194     Score: 29     Matches: 1(0)  Sequences: 1(0)
   TUBA1B protein [Homo sapiens]
   CAA25855.1     Mass: 50126     Score: 29     Matches: 1(0)  Sequences: 1(0)
   alpha-tubulin [Homo sapiens]
   AAH33064.1     Mass: 36625     Score: 29     Matches: 1(0)  Sequences: 1(0)
   TUBA1C protein [Homo sapiens]
   NP_033472.1     Mass: 49928     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-3 chain [Mus musculus]
   AAD33872.1     Mass: 36411     Score: 29     Matches: 1(0)  Sequences: 1(0)
   alpha-tubulin, partial [Homo sapiens]
   NP_035783.1     Mass: 50104     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-1A chain [Mus musculus]
   NP_035784.1     Mass: 50120     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-1B chain [Mus musculus]
   AAC39578.1     Mass: 49797     Score: 29     Matches: 1(0)  Sequences: 1(0)
   alpha tubulin, partial [Homo sapiens]
   BAG51785.1     Mass: 46212     Score: 29     Matches: 1(0)  Sequences: 1(0)
   unnamed protein product [Homo sapiens]
   BAG52918.1     Mass: 46312     Score: 29     Matches: 1(0)  Sequences: 1(0)
   unnamed protein product [Homo sapiens]
   EAW55606.1     Mass: 49868     Score: 29     Matches: 1(0)  Sequences: 1(0)
   hCG1992406, isoform CRA_a [Homo sapiens]
   EAW55607.1     Mass: 42187     Score: 29     Matches: 1(0)  Sequences: 1(0)
   hCG1992406, isoform CRA_b [Homo sapiens]
   BAG56853.1     Mass: 33399     Score: 29     Matches: 1(0)  Sequences: 1(0)
   unnamed protein product [Homo sapiens]
   AAH57810.1     Mass: 49988     Score: 29     Matches: 1(0)  Sequences: 1(0)
   Tubulin, alpha 3d [Homo sapiens]
   BAG60966.1     Mass: 42702     Score: 29     Matches: 1(0)  Sequences: 1(0)
   unnamed protein product [Homo sapiens]
   BAF82043.1     Mass: 50104     Score: 29     Matches: 1(0)  Sequences: 1(0)
   unnamed protein product [Homo sapiens]
   AAA91575.1     Mass: 38102     Score: 29     Matches: 1(0)  Sequences: 1(0)
   alpha-tubulin, partial [Homo sapiens]
   AAA91576.1     Mass: 50120     Score: 29     Matches: 1(0)  Sequences: 1(0)
   alpha-tubulin [Homo sapiens]
   BAD96744.1     Mass: 49791     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha 6 variant, partial [Homo sapiens]
   NP_116093.1     Mass: 49863     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-1C chain isoform c [Homo sapiens]
   NP_997195.1     Mass: 49885     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-3E chain [Homo sapiens]
   NP_001257329.1     Mass: 46268     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-1A chain isoform 2 [Homo sapiens]
   NP_001290043.1     Mass: 57693     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-1C chain isoform a [Homo sapiens]
   NP_001290045.1     Mass: 46028     Score: 29     Matches: 1(0)  Sequences: 1(0)
   tubulin alpha-1C chain isoform b [Homo sapiens]
   XP_004616769.1     Mass: 46284     Score: 29     Matches: 1(0)  Sequences: 1(0)
   PREDICTED: tubulin alpha-1B chain isoform X3 [Sorex araneus]
   XP_012363749.1     Mass: 47819     Score: 29     Matches: 1(0)  Sequences: 1(0)
   PREDICTED: tubulin alpha-1A chain isoform X12 [Nomascus leucogenys]
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Peptide matches not assigned to protein hits: (no details means no match)

  Query  Observed   Mr(expt)   Mr(calc)    Delta  Miss Score  Expect Rank Unique  Peptide
 ☑  164  421.7545   841.4945   841.5022  -0.0077   0    36    0.13    1           GITLSVRP
 ☑  249  453.7154   905.4162   905.4607  -0.0445   0    34    0.27    1           DVEQIFR
 ☑  186  428.7487   855.4828   855.5178  -0.0350   0    29    0.71    1           LASIVTPR
 ☑  162  421.7392   841.4639   841.5022  -0.0383   0    24     1.9    1           GITLSVRP
 ☑  156  421.7338   841.4531   841.5022  -0.0491   0    24     1.9    1           GITLSVRP
 ☑  160  421.7378   841.4611   841.5022  -0.0411   0    24     2.2    1           GITLSVRP
 ☑  182  428.7422   855.4699   855.5178  -0.0479   0    24     2.3    1           LASIVTPR
 ☑  185  428.7474   855.4802   855.5178  -0.0376   0    24     2.4    1           LASIVTPR
 ☑  157  421.7367   841.4588   841.5022  -0.0433   0    23     2.3    1           GITLSVRP
 ☑  159  421.7376   841.4607   841.5022  -0.0414   0    23     2.4    1           GITLSVRP
 ☑  187  428.7513   855.4881   855.5178  -0.0296   0    19     6.8    1           LSIIPASR
 ☑  380  420.2127  1257.6163  1257.6201  -0.0037   0    19     9.4    1           AEAGLETESPVR
 ☑  312  523.2616  1044.5087  1044.5564  -0.0477   0    19     9.3    1           LSSDGLQVAR
 ☑  161  421.7384   841.4623   841.5022  -0.0399   0    18     7.6    1           GITLSVRP
 ☑  183  428.7440   855.4735   855.5429  -0.0694   0    18     8.1    1           LVLSSLPK
 ☑  306  523.2526  1044.4907  1044.5564  -0.0656   0    18      11    1           LSSDGLQVAR
 ☑  132  414.1703   826.3261   826.4409  -0.1149   1    18     6.7    1           VRRPGEGG
 ☑  114  409.2251   816.4357   816.4593  -0.0236   0    17      12    1           DLESIIK
 ☑  163  421.7402   841.4658   841.5022  -0.0363   0    17      11    1           GITLSVRP
 ☑  315  523.2650  1044.5155  1044.5716  -0.0561   0    17      14    1           LSSAHVYLR
 ☑  201  435.7468   869.4790   869.4971  -0.0181   0    17      11    1           VVDVSVPR
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☑	307	523.2528	1044.4910	1044.6583	-0.1673	0	17	15	1	LLTTFLPIK
☑	539	737.6635	2209.9686	2210.1041	-0.1356	0	16	9.2	1	FAALLFDMDGTVVNSIAAAER
☑	366	413.1809	1236.5209	1236.6826	-0.1618	0	16	14	1	IGALVITNGDHK
☑	208	435.7573	869.5001	869.4971	0.0030	0	16	14	1	VVDVSVPR
☑	158	421.7374	841.4602	841.4657	-0.0056	0	16	14	1	VAAEPLSR
☑	135	415.5859	829.1573	829.3355	-0.1782	0	16	0.33	1	QSHTWDG
☑	420	656.7870	1311.5594	1311.6897	-0.1303	1	15	15	1	MLFEGKEFLAK
☑	436	672.3348	1342.6551	1342.7820	-0.1269	1	15	17	1	SLALRSELLVDK
☑	309	523.2575	1044.5005	1044.5564	-0.0559	0	15	20	1	LSSDGLQVAR
☑	155	421.2112	840.4078	840.5797	-0.1719	1	15	13	1	AAKVVILK
☑	316	523.2662	1044.5179	1044.6179	-0.1000	0	15	23	1	ILAINSSSLK
☑	308	523.2554	1044.4963	1044.5703	-0.0739	0	14	25	1	LSEDIDLLK
☑	311	523.2596	1044.5047	1044.6179	-0.1131	0	14	27	1	ILAINSSSLK
☑	317	523.2664	1044.5182	1044.6179	-0.0997	0	14	27	1	ILAINSSSLK
☑	367	413.1929	1236.5570	1236.6251	-0.0681	1	14	23	1	LGGGETWFRSK
☑	270	469.2726	936.5307	936.4553	0.0754	0	14	29	1	AVALNTDFS
☑	88	400.2029	798.3913	798.4824	-0.0911	1	14	16	1	RGALLGGR
☑	385	421.2000	1260.5782	1260.7516	-0.1734	0	13	47	1	MAVFVVLLALVA + Oxidation (M)
☑	184	428.7463	855.4780	855.5178	-0.0398	0	13	28	1	LASIVTPR
☑	144	419.2925	836.5705	836.3884	0.1821	0	12	20	1	DMLMGVR + Oxidation (M)
☑	314	523.2638	1044.5130	1044.6179	-0.1049	0	12	45	1	ILAINSSSLK
☑	313	523.2630	1044.5114	1044.6583	-0.1469	0	12	45	1	LLTTFLPIK
☑	461	505.9114	1514.7125	1514.8093	-0.0968	1	12	42	1	LARFVAEGGPELEK
☑	242	450.2625	898.5104	898.3814	0.1290	1	11	41	1	TCSSRSTAS
☑	202	435.7494	869.4842	869.4429	0.0413	0	11	37	1	TPCPSLPR
☑	344	585.2818	1168.5490	1168.6023	-0.0532	1	11	58	1	LTPTHGEMRK
☑	203	435.7521	869.4897	869.5222	-0.0325	0	11	39	1	VVPESLVK
☑	141	419.2916	836.5687	836.3884	0.1802	0	11	30	1	DMLMGVR + Oxidation (M)
☑	181	428.7398	855.4650	855.5178	-0.0527	0	11	44	1	LSIIPASR
☑	213	437.2396	872.4647	872.4603	0.0043	0	11	68	1	VAEGQELK
☑	310	523.2579	1044.5013	1044.5273	-0.0261	1	11	56	1	EMAKASAPQL
☑	152	420.3000	838.5854	838.4436	0.1418	0	11	29	1	GTLVTVYS
☑	205	435.7530	869.4914	869.4494	0.0420	0	11	45	1	EPTPTTPK
☑	128	412.7304	823.4463	823.3898	0.0565	0	11	37	1	MGWISSK + Oxidation (M)
☑	207	435.7548	869.4950	869.4971	-0.0021	0	11	45	1	VVDVSVPR
☑	154	421.2000	840.3854	840.5797	-0.1942	1	11	38	1	AAKVVILK
☑	357	408.2870	1221.8392	1221.7193	0.1199	1	11	16	1	LNPKTINPGLR
☑	126	412.7233	823.4321	823.4664	-0.0343	1	10	39	1	VAPPERR
☑	292	493.2561	984.4975	984.5063	-0.0087	0	10	60	1	SVCPVDLPR
☑	192	432.2059	862.3973	862.4331	-0.0358	1	10	65	1	QQKMGQK + Oxidation (M)
☑	210	437.1848	872.3550	872.5266	-0.1716	1	10	81	1	KLGCLLAR
☑	216	439.1788	876.3430	876.5320	-0.1891	0	10	80	1	LILEYVK
☑	222	441.2969	880.5792	880.4510	0.1282	1	9	56	1	MQKMLSK + Oxidation (M)
☑	320	526.2169	1050.4192	1050.4618	-0.0426	0	9	97	1	DEEIENFR
☑	355	407.8658	1220.5756	1220.6401	-0.0645	1	9	1.1e+02	1	LGQSGIEDFKK
☑	220	441.2606	880.5067	880.4654	0.0413	0	9	66	1	TQAGTYIK
☑	275	475.3757	948.7369	948.5756	0.1613	1	9	12	1	ALLSKYVR
☑	291	491.3096	980.6047	980.5039	0.1008	1	9	72	1	EPAGHSQKK
☑	214	437.3000	872.5854	872.4716	0.1139	1	9	1e+02	1	KQQDVQK
☑	92	402.3000	802.5854	802.4297	0.1557	0	9	63	1	GSGTTRPK
☑	254	459.2343	916.4541	916.5164	-0.0623	0	9	1.1e+02	1	MLVSIQAR
☑	111	409.1532	816.2918	816.4817	-0.1900	1	9	87	1	GIKSSIGR
☑	304	519.2876	1036.5606	1036.5852	-0.0246	1	8	95	1	LQGKVPMHK
☑	226	444.1952	886.3759	886.4872	-0.1113	0	8	1.4e+02	1	VQLTSPSR
☑	329	545.3000	1088.5854	1088.5614	0.0240	1	8	1.1e+02	1	KQWVDQSAK
☑	231	445.1245	888.2345	888.3937	-0.1592	0	8	33	1	GDSGQPSNK
☑	113	409.1945	816.3744	816.5221	-0.1478	1	8	1e+02	1	KPVKAFK
☑	256	459.2382	916.4618	916.4767	-0.0148	0	8	1.2e+02	1	FNHTAISK
☑	229	445.1093	888.2041	888.3937	-0.1896	0	8	10	1	GDSGQPSNK
☑	175	424.2888	846.5631	846.3905	0.1726	0	8	1.2e+02	1	CEPETLR
☑	91	402.1827	802.3508	802.4297	-0.0789	1	8	1e+02	1	KTGNQQK
☑	290	489.3559	976.6973	976.5342	0.1632	0	7	72	1	IHSLPPEGK
☑	109	408.2898	814.5650	814.4912	0.0738	1	7	87	1	ATVTKAPK
☑	108	408.2845	814.5544	814.4912	0.0632	1	7	89	1	ATVTKAPK
☑	179	427.2031	852.3917	852.4271	-0.0354	0	7	86	1	LAIMMMK + Oxidation (M)
☑	531	509.2659	2033.0344	2033.0847	-0.0503	0	7	81	1	ALVETVTAPGFHHPIFAAR
☑	301	517.2901	1032.5657	1032.5638	0.0019	0	7	1.4e+02	1	LMTGAGNILK + Oxidation (M)
☑	206	435.7543	869.4940	869.4607	0.0333	0	7	1e+02	1	VHLSSEAK
☑	287	487.2530	972.4914	972.5253	-0.0339	1	7	1.5e+02	1	RNGVSWVR
☑	200	435.3278	868.6410	868.5607	0.0804	1	7	52	1	LVRLNVR
☑	435	670.2928	1338.5710	1338.6285	-0.0575	1	7	1.2e+02	1	MPHSHCSLAKR + Carbamidomethyl (C); Oxidation (M)
☑	148	419.3000	836.5854	836.3884	0.1970	0	7	68	1	DMLMGVR + Oxidation (M)
☑	502	449.2026	1792.7814	1792.8699	-0.0885	1	7	1e+02	1	QLDKMVLEDNCSLTK + Carbamidomethyl (C)
☑	237	447.3204	892.6263	892.4807	0.1456	1	7	93	1	FWDIKGK
☑	197	433.3131	864.6117	864.4375	0.1743	1	7	93	1	MATAAKEK + Oxidation (M)
☑	243	451.1829	900.3512	900.2888	0.0624	0	7	1.6e+02	1	GMSCCDGR + Carbamidomethyl (C); Oxidation (M)
☑	188	429.1000	856.1854	856.3787	-0.1933	0	6	10	1	NETNHSR
☑	89	400.2324	798.4502	798.3000	0.1501	0	6	83	1	MDSMGSR + Oxidation (M)
☑	224	442.3004	882.5862	882.4671	0.1191	1	6	1.5e+02	1	GSKEGLHR
☑	170	424.2621	846.5097	846.3719	0.1378	0	6	1.7e+02	1	EAEDVER
☑	174	424.2791	846.5436	846.4382	0.1054	0	6	1.7e+02	1	VATAQMAR
☑	390	424.2794	1269.8165	1269.6929	0.1237	1	6	97	1	VEIERTVAAPSV
☑	332	552.2359	1102.4573	1102.4172	0.0401	0	6	2.5e+02	1	NFASCMGDSR + Oxidation (M)
☑	253	459.2327	916.4508	916.5164	-0.0656	0	6	2e+02	1	AIIMAVQR + Oxidation (M)
☑	204	435.7522	869.4899	869.4971	-0.0072	0	6	1.4e+02	1	VVDVSVPR
	346	593.2000	1184.3854	1184.5067	-0.1212	0	6	1.1e+02	1	GSQFGQSCCLR

☑										
☑	504	897.8746	1793.7346	1793.8843	-0.1496	1	6	1.1e+02	1	MQGTLGASQGGLSYPRR + Oxidation (M)
☑	489	425.2052	1696.7918	1696.7078	0.0840	0	5	1.4e+02	1	GDDSNGYGDIWGQGTR
☑	145	419.2931	836.5716	836.3923	0.1794	1	5	1e+02	1	MGRSSQR + Oxidation (M)
☑	104	407.1792	812.3439	812.5120	-0.1681	1	5	1e+02	1	NIPKLTK
☑	199	435.3109	868.6072	868.4079	0.1993	0	5	1e+02	1	VFEGDFR
☑	127	412.7280	823.4414	823.5280	-0.0866	0	5	1.3e+02	1	VVLPQLR
☑	381	420.3000	1257.8782	1257.6929	0.1853	0	5	75	1	VTAVDGISLDIR
☑	289	488.2578	974.5010	974.4781	0.0229	1	5	2.3e+02	1	AAEGESRQK
☑	335	552.3042	1102.5938	1102.6386	-0.0448	1	5	3e+02	1	FTPTPATIKK
☑	537	537.2643	2145.0281	2145.0854	-0.0573	1	5	1.3e+02	1	SYTLNGTKTWITNSLAYGR
☑	532	515.2615	2057.0169	2057.0905	-0.0736	1	5	1.4e+02	1	FIANSQEPEIRLTSSLPR
☑	195	433.1925	864.3704	864.4341	-0.0638	1	5	2e+02	1	VEGKTNAF
☑	93	402.3000	802.5854	802.4661	0.1194	1	5	1.6e+02	1	RVLSSGGK
☑	180	427.2164	852.4183	852.4453	-0.0270	0	5	1.6e+02	1	LDALEHR
☑	190	430.2354	858.4563	858.4559	0.0004	0	5	2.8e+02	1	AVAELSNR
☑	525	499.2451	1992.9513	1993.1207	-0.1694	1	5	1.6e+02	1	ILNLEIADRTPQELLQK
☑	286	487.2483	972.4821	972.5716	-0.0895	1	5	2.5e+02	1	LIATGRTNK
☑	79	631.2000	630.1927	630.3337	-0.1410	0	5	8.3	1	GATPGTK
☑	211	437.2232	872.4318	872.5080	-0.0762	0	4	3e+02	1	VTSLLGAGR
☑	353	406.2591	1215.7554	1215.6183	0.1371	1	4	2.1e+02	1	HICGRLFGEK + Carbamidomethyl (C)
☑	517	477.2332	1904.9036	1904.9315	-0.0279	1	4	1.9e+02	1	YQACRFGQVPDQPAGLR
☑	356	408.2848	1221.8325	1221.6717	0.1608	1	4	83	1	ARIEDVPPPTK
☑	247	453.2292	904.4438	904.5238	-0.0800	0	4	2.8e+02	1	MLMILIR + Oxidation (M)
☑	244	451.2203	900.4260	900.4487	-0.0227	0	4	2.8e+02	1	TIMEHVR + Oxidation (M)
☑	218	441.2347	880.4548	880.3926	0.0622	0	4	2.2e+02	1	EYEIDGR
☑	232	445.1926	888.3707	888.4123	-0.0417	0	4	3.3e+02	1	MQEVPNR + Oxidation (M)
☑	112	409.1620	816.3094	816.4341	-0.1247	0	4	2.6e+02	1	SGEVLNAK
☑	147	419.3000	836.5854	836.4868	0.0986	0	4	1.3e+02	1	APQPVVAR
☑	331	547.2745	1092.5345	1092.5564	-0.0218	0	4	2.6e+02	1	FGGTSVADIAR
☑	297	502.7738	1003.5331	1003.5233	0.0098	1	4	3.2e+02	1	CQLQKATR + Carbamidomethyl (C)
☑	176	425.1932	848.3718	848.4352	-0.0634	1	4	2.6e+02	1	EAATKSSR
☑	149	419.3006	836.5867	836.4868	0.0998	0	4	1.4e+02	1	APQPVVAR
☑	257	459.2436	916.4727	916.4436	0.0291	0	4	3.3e+02	1	SQPQGCLGK
☑	478	408.2865	1629.1167	1628.9250	0.1917	1	4	16	1	FAELLDRLVLTPSR
☑	142	419.2924	836.5702	836.4868	0.0834	0	4	1.6e+02	1	APQPVVAR
☑	118	411.1516	820.2886	820.3861	-0.0975	0	4	2.1e+02	1	NGSLSMGR
☑	139	419.2884	836.5623	836.3923	0.1700	1	3	1.7e+02	1	MGRSSQR + Oxidation (M)
☑	146	419.2934	836.5723	836.3923	0.1800	1	3	1.6e+02	1	MGRSSQR + Oxidation (M)
☑	143	419.2925	836.5705	836.4868	0.0837	0	3	1.6e+02	1	APQPVVAR
☑	228	445.1015	888.1884	888.3825	-0.1941	0	3	18	1	GDQEEPSK
☑	123	411.3000	820.5854	820.3861	0.1993	1	3	1.7e+02	1	GARQDMK + Oxidation (M)
☑	271	471.2000	940.3854	940.4866	-0.1011	0	3	2.5e+02	1	EDLVSPPGK
☑	151	420.2951	838.5757	838.4773	0.0984	1	3	1.7e+02	1	APRVGSPR
☑	298	503.2550	1004.4954	1004.5576	-0.0622	0	3	3.3e+02	1	LITVTAMEK
☑	125	412.7033	823.3921	823.4916	-0.0995	0	3	2e+02	1	IPGTAPLR
☑	194	433.1890	864.3634	864.4561	-0.0927	1	3	3e+02	1	LLNKMCK + Oxidation (M)
☑	230	445.1163	888.2180	888.3937	-0.1757	0	3	52	1	GDSGQPSNK
☑	412	433.2174	1296.6304	1296.7085	-0.0781	1	3	3.2e+02	1	LLGCGRALGAPGR + Carbamidomethyl (C)
☑	209	436.2506	870.4866	870.4559	0.0307	0	3	3.2e+02	1	SAPGSTPVR
☑	150	420.2874	838.5602	838.4773	0.0829	1	3	2e+02	1	PARTAPAR
☑	432	445.2000	1332.5782	1332.6285	-0.0503	1	3	3.1e+02	1	RTTSTCGFFWK
☑	337	553.3210	1104.6274	1104.5855	0.0419	0	3	3.5e+02	1	LAFLYTYSK
☑	140	419.2912	836.5679	836.3923	0.1756	1	3	1.9e+02	1	MGRSSQR + Oxidation (M)
☑	284	484.3960	966.7774	966.6226	0.1548	1	3	15	1	LGALGLAPKK
☑	444	702.3703	1402.7260	1402.6155	0.1104	1	3	3.1e+02	1	MNARTYMDVMR + Oxidation (M)
☑	293	494.2667	986.5188	986.3990	0.1198	0	3	3.8e+02	1	CCPYGYPK + Carbamidomethyl (C)
☑	377	419.3054	1254.8942	1254.7044	0.1898	1	3	76	1	GAQTAAATAPRIK
☑	387	633.4339	1264.8533	1264.6696	0.1837	1	3	96	1	KEMSSIISLNK + Oxidation (M)
☑	384	631.2000	1260.3854	1260.5557	-0.1703	1	3	2.2e+02	1	RMDGSVDFYR + Oxidation (M)
☑	173	424.2736	846.5327	846.4092	0.1235	1	3	3.7e+02	1	QCPPMKK + Oxidation (M)
☑	446	471.2000	1410.5782	1410.6424	-0.0643	0	3	2.4e+02	1	YAMTWVCQAPGK + Carbamidomethyl (C)
☑	97	405.1669	808.3192	808.3616	-0.0424	0	3	2.1e+02	1	GGNYGWR
☑	550	815.1613	3256.6159	3256.5482	0.0677	1	2	1.4e+02	1	EKPMWLHKGWQPCMYISFLDMALFNR + Oxidation (M)
☑	130	413.2245	824.4344	824.3408	0.0936	0	2	2.3e+02	1	DLLSCSM + Carbamidomethyl (C)
☑	98	405.1869	808.3593	808.3935	-0.0342	1	2	2.2e+02	1	IMKNCGK + Oxidation (M)
☑	480	545.3000	1632.8782	1632.8545	0.0237	0	2	3.3e+02	1	MLGSAFPETVNNLLK
☑	252	455.2457	908.4769	908.4790	-0.0021	1	2	3.7e+02	1	MPKVQYK + Oxidation (M)
☑	235	445.3149	888.6153	888.4818	0.1335	1	2	4.4e+02	1	DPRGFAVK
☑	530	509.2539	2032.9865	2033.0905	-0.1040	1	2	2.6e+02	1	ALGAQKEAISPPDAASAAPLR
☑	551	817.1543	3264.5882	3264.5213	0.0669	1	2	1.9e+02	1	GSQCQEDRIPQILNMASELEFNLETMPR + Oxidation (M)
☑	359	408.2957	1221.8652	1221.6717	0.1935	1	2	61	1	ARIEDVPPPTK
☑	121	411.2005	820.3864	820.4443	-0.0579	0	2	3.1e+02	1	EVLAAYR
☑	324	535.3000	1068.5854	1068.5426	0.0428	0	2	3.8e+02	1	MTHFVPPPK + Oxidation (M)
☑	236	447.1694	892.3243	892.4212	-0.0968	0	2	4.2e+02	1	EDMLELK + Oxidation (M)
☑	516	631.2000	1890.5782	1890.7730	-0.1948	1	2	14	1	DELCYRDGEEYEWK + Carbamidomethyl (C)
☑	383	630.2000	1258.3854	1258.5836	-0.1982	1	2	86	1	CPPNASGSASRR + Carbamidomethyl (C)
☑	138	419.2785	836.5425	836.3884	0.1540	0	2	2.8e+02	1	DMLMGVR + Oxidation (M)
☑	105	407.1857	812.3569	812.4980	-0.1412	1	2	2.6e+02	1	ARPVRSK
☑	227	445.1000	888.1854	888.3760	-0.1905	0	2	23	1	DGAPGAMDR
☑	518	477.2446	1904.9494	1904.8363	0.1131	0	2	3.6e+02	1	LSSDDTAVYYCAAWQR + Carbamidomethyl (C)
☑	153	420.3070	838.5994	838.4773	0.1221	1	2	2.2e+02	1	PARTAPAR
☑	212	437.2287	872.4429	872.3851	0.0579	0	2	5.9e+02	1	EVLHCSW
☑	119	411.1819	820.3493	820.3749	-0.0256	0	1	3.5e+02	1	ACDTGLNK
☑	503	449.2303	1792.8920	1792.7760	0.1160	0	1	3.8e+02	1	MNSLGTEDTAVFYCAR + Oxidation (M)
	239	449.2000	896.3854	896.5807	-0.1953	1	1	4.1e+02	1	IAKVPITR

☑										
☑	529	505.2559	2016.9945	2016.8391	0.1554	1	1	3.4e+02	1	DMGRGGHESGSHPAGCPHR + Carbamidomethyl (C); Oxidat:
☑	295	499.3000	996.5854	996.5604	0.0251	1	1	4.5e+02	1	QLPSAEPKK
☑	527	667.1135	1998.3188	1998.1262	0.1926	1	1	13	1	NEPALVPPILPPVTTERR
☑	272	472.2000	942.3854	942.5433	-0.1578	1	1	4.5e+02	1	ALAPRLMR + Oxidation (M)
☑	421	657.4000	1312.7854	1312.7900	-0.0046	1	1	4.2e+02	1	LKPLKSCLNIK + Carbamidomethyl (C)
☑	273	472.2695	942.5244	942.4415	0.0828	1	1	4.9e+02	1	CTYGIKCR
☑	276	477.2350	952.4554	952.4726	-0.0172	1	1	4.7e+02	1	YSQKSQGR
☑	177	426.2045	850.3945	850.4218	-0.0273	0	1	4.4e+02	1	LLSMTDR + Oxidation (M)
☑	178	426.2681	850.5216	850.4120	0.1096	0	1	4.5e+02	1	GFIQACR + Carbamidomethyl (C)
☑	481	549.2728	1644.7965	1644.7236	0.0730	0	1	5.3e+02	1	DNSQNMLYLQMTR + 2 Oxidation (M)
☑	499	445.3000	1777.1709	1776.9743	0.1966	1	1	37	1	VMPCLAPIAAKVGSVGHK
☑	101	406.2091	810.4036	810.4058	-0.0022	0	1	2.6e+02	1	MGIVYGR + Oxidation (M)
☑	241	450.2327	898.4509	898.4409	0.0100	0	1	4.8e+02	1	QAPWAGNR
☑	261	467.2434	932.4722	932.4352	0.0370	0	1	6.2e+02	1	AAPEDFAGR
☑	107	408.2817	814.5488	814.4185	0.1303	1	1	4.4e+02	1	DKEAPQK
☑	459	499.3000	1494.8782	1494.8783	-0.0001	1	0	4.1e+02	1	HHILNVKSGILHK
☑	300	509.4000	1016.7854	1016.5879	0.1975	1	0	77	1	RKPFSINR
☑	117	411.1314	820.2482	820.3497	-0.1015	0	0	3.8e+02	1	MAANQDR + Oxidation (M)
☑	358	408.2889	1221.8449	1221.7193	0.1256	1	0	1.5e+02	1	LNPKTINPGLR
☑	171	424.2624	846.5102	846.4811	0.0291	0	0	6.3e+02	1	TISQLASK
☑	95	404.6290	807.2435	807.3949	-0.1514	0	0	3.1e+02	1	MQPAFAK + Oxidation (M)
☑	423	441.2821	1320.8246	1320.8493	-0.0247	1	0	4.2e+02	1	LLPVVSSLPKLR
☑	248	453.2309	904.4473	904.5052	-0.0579	1	0	7e+02	1	VAMKEALK + Oxidation (M)
☑	87	400.1911	798.3676	798.4348	-0.0672	1	0	3.4e+02	1	RQLPTGQ
☑	487	419.9957	1675.9535	1675.7584	0.1951	1	0	4.7e+02	1	LGAEEAARAVDDGGCSR
☑	322	531.2396	1060.4646	1060.5587	-0.0941	0	0	6.6e+02	1	MATAATSPALK
☑	172	424.2718	846.5291	846.4487	0.0804	0	0	6.8e+02	1	EDIPVFK
☑	549	926.1864	2775.5372	2775.4490	0.0882	0	0	1.8e+02	1	VSQMLILTPFQGQGHGAQLLETVHR + Oxidation (M)
☑	1	*401.3000*	*400.2927*							
☑	2	*402.3000*	*401.2927*							
☑	3	*402.3000*	*401.2927*							
☑	4	*403.3000*	*402.2927*							
☑	5	*405.1000*	*404.0927*							
☑	6	*405.1810*	*404.1738*							
☑	7	*405.2073*	*404.2000*							
☑	8	*405.2075*	*404.2002*							
☑	9	*405.2077*	*404.2005*							
☑	10	*405.2107*	*404.2035*							
☑	11	*406.2088*	*405.2016*							
☑	12	*407.2045*	*406.1972*							
☑	13	*408.2157*	*407.2084*							
☑	14	*409.1000*	*408.0927*							
☑	15	*409.2152*	*408.2079*							
☑	16	*410.2206*	*409.2134*							
☑	17	*410.2227*	*409.2154*							
☑	18	*410.2293*	*409.2220*							
☑	19	*411.1735*	*410.1662*							
☑	20	*411.3000*	*410.2927*							
☑	21	*412.2044*	*411.1971*							
☑	22	*412.3000*	*411.2927*							
☑	23	*413.2248*	*412.2175*							
☑	24	*413.4000*	*412.3927*							
☑	25	*415.2013*	*414.1941*							
☑	26	*415.3000*	*414.2927*							
☑	27	*416.2019*	*415.1946*							
☑	28	*416.2026*	*415.1953*							
☑	29	*416.2083*	*415.2011*							
☑	30	*417.2046*	*416.1973*							
☑	31	*419.2933*	*418.2861*							
☑	32	*419.2955*	*418.2882*							
☑	33	*419.2968*	*418.2896*							
☑	34	*420.2888*	*419.2815*							
☑	35	*420.3000*	*419.2927*							
☑	36	*421.2000*	*420.1927*							
☑	37	*422.2291*	*421.2218*							
☑	38	*423.4000*	*422.3927*							
☑	39	*423.4000*	*422.3927*							
☑	40	*426.4000*	*425.3927*							
☑	41	*426.4000*	*425.3927*							
☑	42	*427.2250*	*426.2178*							
☑	43	*429.1000*	*428.0927*							
☑	44	*429.1000*	*428.0927*							
☑	45	*430.1000*	*429.0927*							
☑	46	*430.2113*	*429.2040*							
☑	47	*431.2120*	*430.2047*							
☑	48	*432.2124*	*431.2051*							
☑	49	*432.4000*	*431.3927*							
☑	50	*433.2153*	*432.2080*							
☑	51	*433.2186*	*432.2113*							
☑	52	*436.2015*	*435.1942*							
☑	53	*437.4000*	*436.3927*							
☑	54	*445.1000*	*444.0927*							
☑	55	*445.2000*	*444.1927*							
☑	56	*449.1266*	*448.1193*							
	57	*449.2000*	*448.1927*							

☑			
☑	58	459.2526	458.2454
☑	59	464.1043	463.0970
☑	60	471.2000	470.1927
☑	61	472.2000	471.1927
☑	62	474.2159	473.2087
☑	63	475.3757	474.3685
☑	64	482.4000	481.3927
☑	65	499.3000	498.2927
☑	66	509.4000	508.3927
☑	67	528.3889	527.3816
☑	68	528.5000	527.4927
☑	69	535.3000	534.2927
☑	70	539.3597	538.3524
☑	71	545.3000	544.2927
☑	72	554.4000	553.3927
☑	73	555.2974	554.2901
☑	74	585.3121	584.3049
☑	75	593.2000	592.1927
☑	76	628.5000	627.4927
☑	77	630.0000	628.9927
☑	78	630.2000	629.1927
☑	80	639.8127	638.8055
☑	81	641.5894	640.5821
☑	82	657.5917	656.5844
☑	83	658.5000	657.4927
☑	84	659.5826	658.5753
☑	85	713.3708	712.3635
☑	86	776.1904	775.1831
☑	90	401.3000	800.5854
☑	94	403.3000	804.5854
☑	96	405.1000	808.1854
☑	99	405.2118	808.4091
☑	100	405.3536	808.6926
☑	102	406.2596	810.5046
☑	103	407.1503	812.2860
☑	106	407.8218	813.6291
☑	110	409.1000	816.1854
☑	115	409.3504	816.6863
☑	116	409.3631	816.7117
☑	120	411.1845	820.3545
☑	122	411.2073	820.4001
☑	124	412.3000	822.5854
☑	129	413.1932	824.3719
☑	131	413.4000	824.7854
☑	133	415.3000	828.5854
☑	134	415.3000	828.5854
☑	136	416.3740	830.7334
☑	137	417.4223	832.8300
☑	165	421.9000	841.7854
☑	166	422.3644	842.7143
☑	167	423.1845	844.3544
☑	168	423.4000	844.7854
☑	169	423.4000	844.7854
☑	189	430.1000	858.1854
☑	191	431.5973	861.1801
☑	193	432.4000	862.7854
☑	196	433.2174	864.4202
☑	198	433.3153	864.6161
☑	215	437.4000	872.7854
☑	217	440.4643	878.9140
☑	219	441.2505	880.4865
☑	221	441.2959	880.5772
☑	223	441.3000	880.5854
☑	225	443.1693	884.3241
☑	233	445.2000	888.3854
☑	234	445.2822	888.5499
☑	238	449.1999	896.3852
☑	240	449.3646	896.7146
☑	245	453.2086	904.4026
☑	246	453.2120	904.4094
☑	250	454.3554	906.6962
☑	251	454.3650	906.7155
☑	255	459.2350	916.4555
☑	258	459.7773	917.5401
☑	259	459.7943	917.5740
☑	260	462.4302	922.8457
☑	274	473.8211	945.6277
☑	277	477.7938	953.5730
☑	278	477.8088	953.6030
☑	279	479.4079	956.8012
☑	280	481.2414	960.4683
☑	281	481.2492	960.4839
☑	282	482.4000	962.7854
☑	283	484.3495	966.6845
	294	499.2737	996.5328

☑			
☑	296	499.4420	996.8695
☑	303	519.1087	1036.2029
☑	305	520.1203	1038.2260
☑	318	525.4466	1048.8787
☑	321	528.5000	1054.9854
☑	325	535.4432	1068.8718
☑	326	536.1427	1070.2709
☑	327	537.4900	1072.9655
☑	328	543.2031	1084.3917
☑	339	554.4000	1106.7854
☑	345	593.1584	1184.3022
☑	347	401.3000	1200.8782
☑	348	402.3000	1203.8782
☑	349	402.3000	1203.8782
☑	351	403.3000	1206.8782
☑	352	405.1000	1212.2782
☑	360	612.1356	1222.2567
☑	361	409.1000	1224.2782
☑	362	409.3784	1225.1134
☑	363	411.3000	1230.8782
☑	364	412.3000	1233.8782
☑	365	412.3554	1234.0445
☑	368	413.4000	1237.1782
☑	369	414.7372	1241.1898
☑	370	415.0228	1242.0465
☑	372	415.3000	1242.8782
☑	376	416.3517	1246.0332
☑	378	628.5000	1254.9854
☑	382	630.0000	1257.9854
☑	388	423.4000	1267.1782
☑	389	423.4000	1267.1782
☑	391	425.2984	1272.8734
☑	393	639.4000	1276.7854
☑	394	639.4107	1276.8069
☑	395	639.9000	1277.7854
☑	396	640.7579	1279.5012
☑	397	428.7373	1283.1901
☑	398	428.7383	1283.1932
☑	399	428.7394	1283.1965
☑	400	428.7433	1283.2079
☑	401	428.7433	1283.2080
☑	402	428.7445	1283.2116
☑	403	428.7469	1283.2189
☑	404	428.7481	1283.2226
☑	405	428.7491	1283.2255
☑	406	429.0728	1284.1966
☑	407	429.0781	1284.2124
☑	408	429.1000	1284.2782
☑	409	430.1000	1287.2782
☑	410	432.4000	1294.1782
☑	414	435.3217	1302.9433
☑	415	435.3283	1302.9630
☑	416	435.7535	1304.2386
☑	418	437.4000	1309.1782
☑	422	658.5000	1314.9854
☑	425	667.0986	1332.1825
☑	426	445.0922	1332.2547
☑	427	445.0997	1332.2772
☑	428	445.1000	1332.2782
☑	429	667.1484	1332.2823
☑	430	667.1563	1332.2980
☑	431	445.1091	1332.3053
☑	434	447.0830	1338.2271
☑	438	449.2000	1344.5782
☑	442	463.1015	1386.2827
☑	443	465.0569	1392.1488
☑	445	468.7287	1403.1644
☑	447	472.2000	1413.5782
☑	448	475.3757	1423.1054
☑	450	480.1301	1437.3686
☑	451	480.1317	1437.3732
☑	453	482.4000	1444.1782
☑	460	503.0961	1506.2666
☑	463	509.4000	1525.1782
☑	464	519.1070	1554.2991
☑	465	519.3000	1554.8782
☑	466	521.0865	1560.2377
☑	467	521.0926	1560.2560
☑	468	521.0927	1560.2562
☑	469	528.5000	1582.4782
☑	470	535.3000	1602.8782
☑	471	536.1312	1605.3717
☑	472	537.1176	1608.3310
☑	473	538.1199	1611.3378
	474	538.1208	1611.3405

☑			
☑	475	*538.1309*	*1611.3708*
☑	476	*539.1159*	*1614.3259*
☑	477	*405.3510*	*1617.3747*
☑	482	*554.1362*	*1659.3867*
☑	483	*554.1404*	*1659.3994*
☑	484	*554.1416*	*1659.4029*
☑	485	*554.4000*	*1660.1782*
☑	488	*419.9988*	*1675.9661*
☑	490	*429.0637*	*1712.2257*
☑	491	*429.0649*	*1712.2304*
☑	492	*429.0739*	*1712.2663*
☑	494	*581.2826*	*1740.8260*
☑	495	*445.0947*	*1776.3496*
☑	496	*445.0968*	*1776.3582*
☑	497	*445.0993*	*1776.3683*
☑	498	*593.2000*	*1776.5782*
☑	500	*447.0860*	*1784.3148*
☑	505	*611.1311*	*1830.3713*
☑	506	*612.1298*	*1833.3674*
☑	507	*463.1069*	*1848.3984*
☑	508	*463.1070*	*1848.3989*
☑	509	*463.1112*	*1848.4158*
☑	510	*466.1468*	*1860.5579*
☑	512	*628.1452*	*1881.4137*
☑	513	*628.5000*	*1882.4782*
☑	514	*630.0000*	*1886.9782*
☑	515	*630.2000*	*1887.5782*
☑	519	*479.2084*	*1912.8046*
☑	520	*480.1295*	*1916.4887*
☑	521	*481.2523*	*1920.9800*
☑	522	*482.1240*	*1924.4669*
☑	523	*487.2007*	*1944.7738*
☑	524	*658.5000*	*1972.4782*
☑	526	*499.2466*	*1992.9573*
☑	533	*519.1108*	*2072.4143*
☑	534	*519.1123*	*2072.4202*
☑	535	*521.1240*	*2080.4668*
☑	536	*537.1344*	*2144.5085*
☑	538	*549.2725*	*2193.0607*
☑	540	*554.1522*	*2212.5797*
☑	541	*561.2451*	*2240.9512*
☑	542	*577.2751*	*2305.0713*
☑	543	*581.2973*	*2321.1603*
☑	544	*583.2820*	*2329.0990*
☑	545	*585.2989*	*2337.1664*
☑	546	*615.3141*	*2457.2275*
☑	547	*617.3389*	*2465.3264*
☑	548	*640.4358*	*2557.7140*

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Variable modifications : Carbamidomethyl (C),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 0.2 Da
Fragment Mass Tolerance: ± 0.2 Da
Max Missed Cleavages   : 1
Instrument type        : Default
Number of queries      : 551
```

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