Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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- Chait Lab

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.2×10^{-16}	gi|38197676|gb|AAH61872.1| Desmin [Rattus norvegicus]	62	5.2	53.46	
-		gi|11968118|ref|NP_071976.1| desmin [Rattus norvegicus]	60	5.2	53.50	
-		gi|40538874|ref|NP_631977.1| nexilin isoform b [Rattus norvegicus]	35	5.0	72.21	
-		gi|6651167|gb|AAF22213.1|AF139494_1 syndapin IIba [Rattus norvegicus]	36	5.1	56.06	
-		gi|22256944|sp|Q9QY17|PACN2_RAT Protein kinase C and casein kinase substrate in neurons 2 protein (Synaptic dynamin-associated protein II) (Syndapin 2) (Syndapin-II) (SdpII)	35	5.0	56.30	
-		gi|51858601|gb|AAH81803.1| Hspa2 protein [Rattus norvegicus]	36	5.5	69.91	
-		gi|56090413|ref|NP_001007661.1| hypothetical protein LOC300359 [Rattus norvegicus]	32	5.3	60.85	
-		gi|3132829|gb|AAC16391.1| nuclear RNA helicase [Rattus norvegicus]	42	5.4	49.58	
-		gi|55926219|ref|NP_446015.2| nuclear RNA helicase, DECD variant of DEAD box family [Rattus norvegicus]	42	5.5	49.61	
-		gi|6651169|gb|AAF22214.1|AF139495_1 syndapin IIbb [Rattus norvegicus]	38	5.3	51.62	
-		gi|6651165|gb|AAF22212.1|AF139493_1 syndapin IIab [Rattus norvegicus]	37	5.2	51.86	
-		gi|47087085|ref|NP_997710.1| type I keratin KA17 [Rattus norvegicus]	43	5.0	48.39	
-		gi|56788780|gb|AAH88424.1| Krt1-19 protein [Rattus norvegicus]	42	5.3	46.68	

-	gi|42409519|ref|NP_955792.1| keratin complex 1, acidic, gene 19 [Rattus norvegicus]	44	5.2	44.62
-	gi|21314404|gb|AAM46928.1| liver regeneration-related protein 2 [Rattus norvegicus]	33	5.2	65.48
-	gi|111518|pir||A37180 chromogranin/secretogranin-like vesicle protein precursor - rat	41	5.3	59.75
-	gi|56090427|ref|NP_001007695.1| interferon-induced protein with tetratricopeptide repeats 3 [Rattus norvegicus]	37	5.5	48.78
-	gi|1857139|gb|AAC53054.1| guanylate kinase associated protein [Rattus norvegicus]	25	5.3	74.96
-	gi|92355|pir||S08211 dnaK-type molecular chaperone hst70 - rat	37	5.4	69.81
-	gi|16758722|ref|NP_446308.1| secretogranin III [Rattus norvegicus]	45	4.9	53.17
-	gi|27659719|ref|NP_659549.2| optineurin [Rattus norvegicus]	32	5.2	67.20
-	gi|52000743|sp||Q63862_2 [Segment 2 of 2] Myosin-11 (Myosin heavy chain, smooth muscle isoform) (SMMHC)	36	5.1	71.76
-	gi|11177910|ref|NP_068635.1| heat shock protein 2 [Rattus norvegicus]	33	5.4	69.80
-	gi|51858922|gb|AAH81736.1| Clcc1 protein [Rattus norvegicus]	19	5.3	62.11
-	gi|19173780|ref|NP_596905.1| Mid-1-related chloride channel 1 [Rattus norvegicus]	18	5.4	62.07
-	gi|203734|gb|AAA19668.1| cytokeratin 8 polypeptide	42	5.5	52.69
-	gi|4079713|gb|AAC98729.1| reggie1-4 [Rattus norvegicus]	49	5.2	41.96
-	gi|13929186|ref|NP_114018.1| flotillin 2 [Rattus norvegicus]	43	5.2	47.55
-	gi|13124119|sp|Q9Z2S9|FLOT2_RAT Flotillin-2 (Reggie-1) (REG-1)	43	5.1	47.42
-	gi|19173762|ref|NP_596893.1| nucleosome assembly protein 1-like 3 [Rattus norvegicus]	22	4.7	61.33
-	gi|34862422|ref|XP_343190.1| PREDICTED: similar to cytoskeleton-associated protein 4 [Rattus norvegicus]	30	5.4	63.59

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A51AD53A-1530-55291B4E

Sequences 20092

Date & Time Mon Jan 22 19:50:45 2007 UTC (Search Time: 0.63 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 40 - 75 kDa

pI Range 4.0 -5.5

Digestion Trypsin

Missed Cuts 2

Modifications +C2H3ON@C(Complete); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 707.397 717.443 729.448 735.451 741.442 743.421 751.433
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954.456 956.536 964.541 967.510 973.545 981.874 989.519
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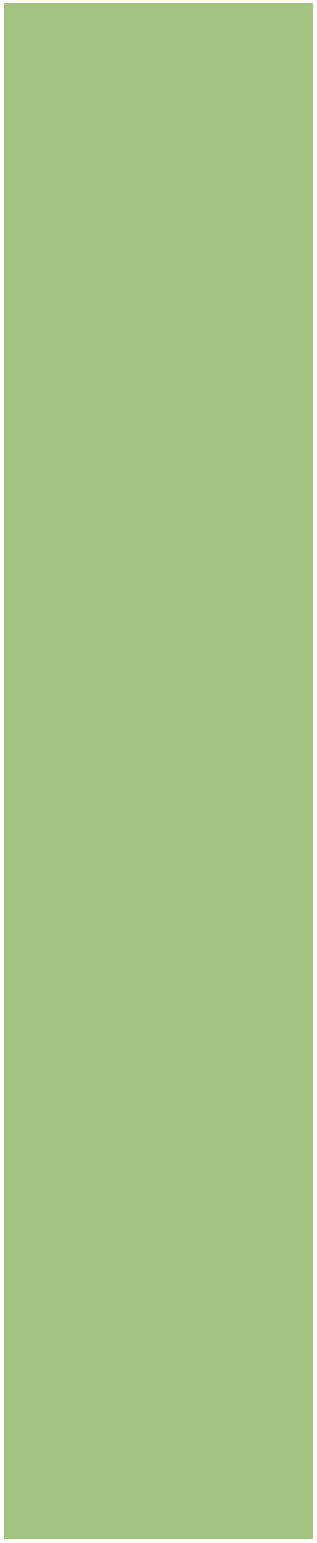

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1490.741	1501.571	1502.615	1515.636	1518.625	1523.718
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1681.805	1682.799	1687.829	1696.801	1699.797	1707.689
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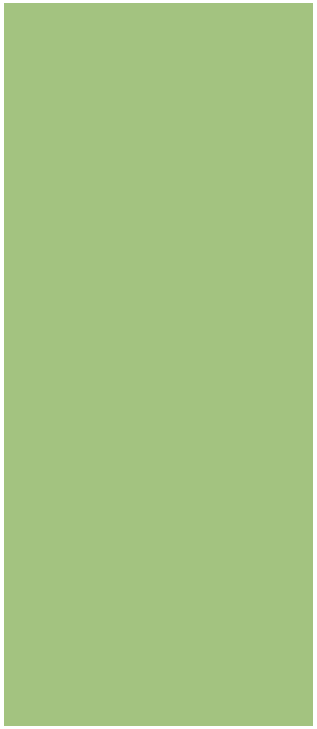

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Tolerance (mon)	52.00 ppm
Number of Peptides	418

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Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.5×10^{-11}	gi|8393910|ref|NP_058932.1| phosphatidylethanolamine binding protein [Rattus norvegicus]	36	5.5	20.90	
2	6.5×10^{-7}	gi|56268897|gb|AAH87105.1| Neurocalcin delta [Rattus norvegicus]	31	5.2	22.34	
3	1.6×10^{-6}	gi|38454238|ref|NP_942044.1| RAB15, member RAS onocogene family [Rattus norvegicus]	25	5.4	24.61	
+4	6.5×10^{-6}	gi|22219117|pdb|1KWZ|A Chain A, Rat Mannose Protein A (H189v) Complexed With Man-A13-Man	20	6.0	16.63	
	-	gi|22219120|pdb|1KX0|A Chain A, Rat Mannose Protein A (H189v I207v) Complexed With Man-A13- Man	20	6.0	16.61	
	-	gi|206553|gb|AAA42006.1| ras protein	16	6.0	22.97	
	-	gi|6531679|gb|AAF15537.1|AF202266_1 unknown [Rattus norvegicus]	19	5.2	25.57	
	-	gi|32492566|gb|AAP85371.1| Aa1114 [Rattus norvegicus]	19	5.5	28.09	
	-	gi|57528169|ref|NP_001009624.1| hypothetical protein LOC287598 [Rattus norvegicus]	40	5.7	16.67	
	-	gi|786459|gb|AAB32798.1| protein tyrosine phosphatase; PTP; CL100; 3CH134 [Rattus sp.]	20	4.9	19.19	
	-	gi|16758368|ref|NP_446041.1| RAB14, member RAS oncogene family [Rattus norvegicus]	18	5.8	24.14	
	-	gi|420272|pir||E42148 GTP-binding protein rab14 - rat	18	5.8	24.08	
	-	gi|13430206|gb|AAK25769.1| non-erythrocyte beta-spectrin [Rattus norvegicus]	25	5.6	23.31	
	-	gi|13559353|dbj|BAB40836.1| h-caldesmon [Rattus norvegicus]	12	5.0	26.62	

-	gi|7441592|pir||S74158 cGMP-gated cation channel protein - rat (fragment)	21	4.8	21.43
-	gi|6940826|gb|AAF31764.1|AF130338_1 beta-1 adducin [Rattus norvegicus]	21	4.9	20.99
-	gi|25282431|ref|NP_742044.1| ELL associated factor 2 [Rattus norvegicus]	22	4.9	29.31

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Mon Jan 22 21:16:13 2007 UTC (Search Time: 0.42 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 15 - 30 kDa

pI Range 4.2 -6.0

Digestion Trypsin

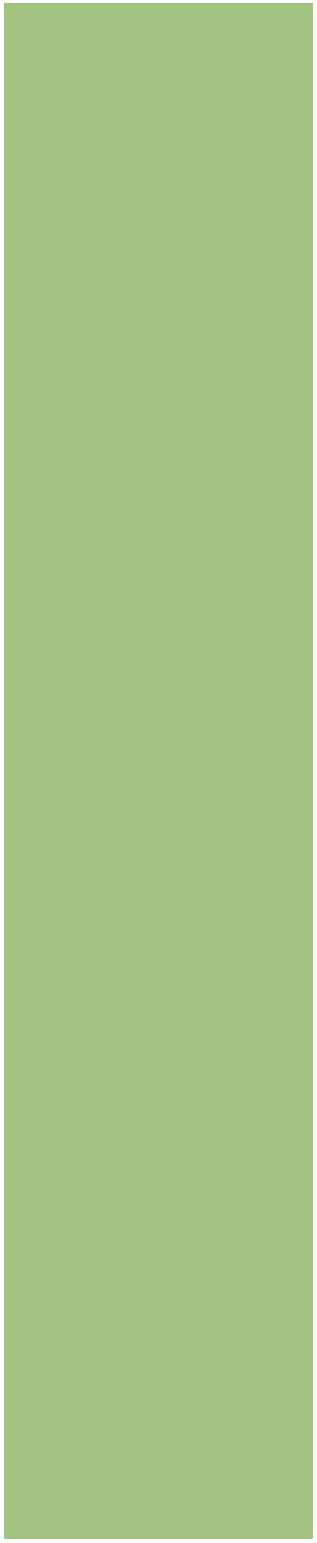
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



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1769.340 1782.335 1786.317 1797.490 1805.778 1814.830
1821.721 1832.255 1838.370 1842.587 1857.300 1865.841
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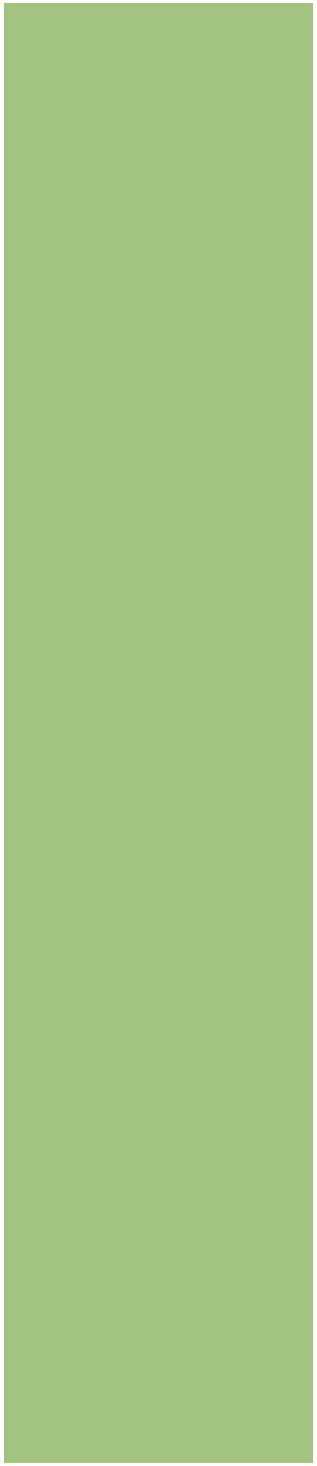

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Tolerance (mon)	12.00 ppm
Number of Peptides	434

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	$9.8?0^{-11}$	gi|45737864|gb|AAS75813.1| mitochondrial aldehyde dehydrogenase precursor [Rattus norvegicus]	53	6.4	56.07	
-		gi|25990263|gb|AAM94394.2| mitochondrial aldehyde dehydrogenase [Rattus norvegicus]	56	5.7	53.83	
-		gi|16073616|gb|AAK57732.1| aldehyde dehydrogenase [Rattus norvegicus]	57	6.1	48.65	
-		gi|55742753|ref|NP_001007002.1| coiled-coil domain containing 2 [Rattus norvegicus]	47	5.7	69.24	
-		gi|755493|gb|AAA96350.1| rbSec1B	47	6.3	69.12	
-		gi|6981602|ref|NP_037170.1| syntaxin binding protein 1 [Rattus norvegicus]	43	6.5	67.95	
-		gi|13592101|ref|NP_112388.1| syntaxin binding protein 2 [Rattus norvegicus]	45	6.3	67.13	
-		gi|50926225|gb|AAH79241.1| Similar to ALS2CR12 gene product [Rattus norvegicus]	54	6.1	48.70	
-		gi|6166127|sp|O88267|ACOT1_RAT Acyl-coenzyme A thioesterase 1 (Acyl-CoA thioesterase 1) (Inducible cytosolic acyl-coenzyme A thioester hydrolase) (Long chain acyl-CoA thioester hydrolase) (Long chain acyl-CoA hydrolase) (CTE-I) (LACH2) (ACH2)	43	6.3	46.22	
-		gi|40786432|ref|NP_955402.1| keratin complex 2, basic, gene 8 [Rattus norvegicus]	38	5.8	54.00	
-		gi|30352203|gb|AAP31862.1| cytokeratin-8 [Rattus sp.]	38	5.8	54.07	
-		gi|8393668|ref|NP_058989.1| KIS [Rattus norvegicus]	39	5.6	47.11	
-		gi|46485098|tpg|DAA02218.1| TPA_exp: type II keratin Kb7 [Rattus norvegicus]	55	5.7	50.69	

-	gi|40018588|ref|NP_954537.1| UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 [Rattus norvegicus]	33	6.4	64.84
-	gi|40254754|ref|NP_112619.2| occludin [Rattus norvegicus]	30	5.9	59.57
-	gi|4126665|dbj|BAA36681.1| occludin [Rattus norvegicus]	30	5.9	59.60
-	gi|40786491|ref|NP_955433.1| cytochrome P450, family 20, subfamily A, polypeptide 1 [Rattus norvegicus]	41	6.3	52.32
-	gi|56090634|ref|NP_001007663.1| archain [Rattus norvegicus]	34	5.9	57.64
-	gi|13929056|ref|NP_113940.1| basal cell adhesion molecule [Rattus norvegicus]	38	5.5	68.29
-	gi|2144059|pir||I56606 estrogen sulfotransferase isoform 3 - rat	55	5.6	35.77
-	gi|50927747|gb|AAH79240.1| Similar to Murine homolog of human ftp-3 [Rattus norvegicus]	37	5.9	49.56
-	gi|32363191|sp|Q63648|MERL_RAT Merlin (Moesin-ezrin-radixin-like protein) (Neurofibromin-2) (Schwannomin)	36	6.2	68.98
-	gi|543840|sp|P36407|ARD1_RAT GTP-binding protein ARD-1 (ADP-ribosylation factor domain protein 1) (Tripartite motif-containing protein 23)	33	5.9	63.71
-	gi|54673782|gb|AAH85124.1| LOC501069 protein [Rattus norvegicus]	37	5.6	68.82
-	gi|21955134|ref|NP_665715.1| dynein, cytoplasmic, light intermediate chain 1 [Rattus norvegicus]	45	6.1	57.00
-	gi|40804381|gb|AAR91694.1| ezrin [Rattus norvegicus]	29	5.8	69.50
-	gi|19705559|ref|NP_599246.1| Hspb associated protein 1 [Rattus norvegicus]	39	6.5	49.75
-	gi|1778213|gb|AAC53362.1| chaperonin 60 [Rattus norvegicus]	33	5.8	61.05
-	gi|1845602|gb|AAC53134.1| outer dense fiber protein [Rattus norvegicus]	32	6.1	69.28
-	gi|21728414|ref|NP_663716.1| protein-tyrosine phosphatase, non-receptor type 7 [Rattus norvegicus]	36	6.4	40.81
-	gi|11560024|ref|NP_071565.1| heat shock protein 1 (chaperonin) [Rattus norvegicus]	33	5.9	61.12

-	gi|51702230|sp|P63039|CH60_RAT 60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa chaperonin) (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein P1) (HSP-65)	33	5.9	61.11
-	gi|34098962|ref|NP_036753.3| 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 1 [Rattus norvegicus]	36	6.3	55.38
-	gi|1711602|sp|P49890|ST1E6_RAT Estrogen sulfotransferase, isoform 6 (EST-6) (Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase)	50	5.6	35.63
-	gi|56485|emb|CAA47838.1| class I MHC [Rattus norvegicus]	46	6.2	40.08
-	gi|56585031|gb|AAH87631.1| TRNA splicing endonuclease 2 homolog (S. cerevisiae) [Rattus norvegicus]	44	5.8	53.39
-	gi|119751|sp|P07953|F261_RAT 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-bisphosphatase]	33	6.3	55.32
-	gi|55824739|gb|AAH86579.1| Akr1c18 protein [Rattus norvegicus]	45	5.6	39.45
-	gi|52138521|ref|NP_062230.1| ezrin [Rattus norvegicus]	29	5.8	69.49
-	gi|14916547|sp|O35824|DNJA2_RAT DnaJ homolog subfamily A member 2 (RDJ2)	43	6.1	46.38
-	gi|56799412|ref|NP_114468.2| DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus]	43	6.1	46.36
-	gi|34872065|ref|XP_239639.2| PREDICTED: similar to Matrix metalloproteinase-17 precursor (MMP-17) (Membrane-type matrix metalloproteinase 4) (MT-MMP 4) (Membrane-type-4 matrix metalloproteinase) (MT4-MMP) [Rattus norvegicus]	24	5.9	65.66
-	gi|6978503|ref|NP_036955.1| Annexin III (Lipocortin III) [Rattus norvegicus]	54	6.0	36.53
-	gi|129372|sp|P10361|P53_RAT Cellular tumor antigen p53 (Tumor suppressor p53)	45	6.2	44.06
-	gi|13591878|ref|NP_112251.1| tumor protein p53 [Rattus norvegicus]	45	6.2	44.09
-	gi|71766|pir||LURT3 annexin III - rat	54	6.0	36.57

-	gi|34852984|ref|XP_231046.2| PREDICTED: similar to Negative elongation factor B (NELF-B) [Rattus norvegicus]	32	5.7	66.24
-	gi|56972637|gb|AAH88184.1| LOC366747 protein [Rattus norvegicus]	44	6.3	65.84
-	gi|1166528|gb|AAC52417.1| ksGC	41	6.2	48.66
-	gi|17902245|gb|AAL47844.1|AF450298_1 EZRIN [Rattus norvegicus]	32	6.2	54.27
-	gi|7434494|pir||S77704 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) clone 5c, skeletal muscle - rat	35	6.4	54.83
-	gi|42476092|ref|NP_446421.2| G protein pathway suppressor 1 [Rattus norvegicus]	34	6.4	53.99
-	gi|2494624|sp|P97834|CSN1_RAT COP9 signalosome complex subunit 1 (Signalosome subunit 1) (SGN1) (JAB1-containing signalosome subunit 1) (G protein pathway suppressor 1) (MFH protein)	34	6.4	53.98
-	gi|1711599|sp|P52844|ST1E1_RAT Estrogen sulfotransferase, isoform 1 (EST-1) (Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase)	40	5.8	35.83
-	gi|13540689|ref|NP_110490.1| moesin [Rattus norvegicus]	26	6.2	67.89
-	gi|57012382|ref|NP_001008811.1| type II keratin Kb25 [Rattus norvegicus]	33	6.3	54.65
-	gi|5030428|gb|AAD01874.2| glial fibrillary acidic protein delta [Rattus norvegicus]	31	5.7	48.82
-	gi|56090198|ref|NP_001007719.1| estrogen sulfotransferase [Rattus norvegicus]	47	5.8	35.69
-	gi|56605726|ref|NP_001008325.1| eukaryotic translation initiation factor 4B [Rattus norvegicus]	33	5.6	69.16
-	gi|56922|emb|CAA33606.1| unnamed protein product [Rattus norvegicus]	34	6.0	52.62
-	gi|1934603|gb|AAB51724.1| RN protein [Rattus norvegicus]	41	6.1	38.05
-	gi|53734490|gb|AAH83578.1| Zinc finger protein 143 [Rattus norvegicus]	25	5.7	68.51
-	gi|33086640|gb|AAP92632.1| Ba1-647 [Rattus norvegicus]	35	6.1	43.08

-	gi|38512106|gb|AAH61756.1| Ribophorin I [Rattus norvegicus]	35	6.1	68.50
-	gi|6981486|ref|NP_037199.1| ribophorin I [Rattus norvegicus]	36	6.1	68.40
-	gi|56605698|ref|NP_001008309.1| hypothetical protein LOC294390 [Rattus norvegicus]	35	6.1	67.02
-	gi|205578|gb|AAA41654.1| cardiac myosin heavy chain 5	30	5.5	47.89
-	gi|55742713|ref|NP_446334.1| extracellular matrix protein 1 [Rattus norvegicus]	30	6.4	64.89
-	gi|13592025|ref|NP_112344.1| protein geranylgeranyltransferase type I, beta subunit [Rattus norvegicus]	33	6.2	43.25
-	gi|56605800|ref|NP_001008363.1| vav-1 interacting Kruppel-like protein [Rattus norvegicus]	28	6.5	64.84
-	gi|55741518|ref|NP_001006987.1| evolutionarily conserved signaling intermediate in Toll pathway [Rattus norvegicus]	24	6.0	49.89

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Tue Jan 23 01:42:50 2007 UTC (Search Time: 0.61 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 35 - 70 kDa

pI Range 5.5 -6.5

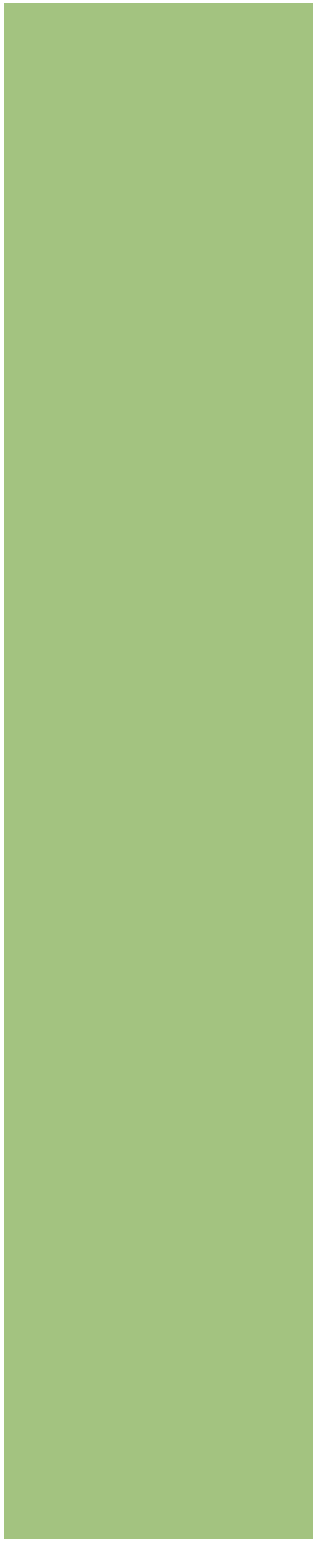
Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)



Tolerance (avg) 1.00 ppm

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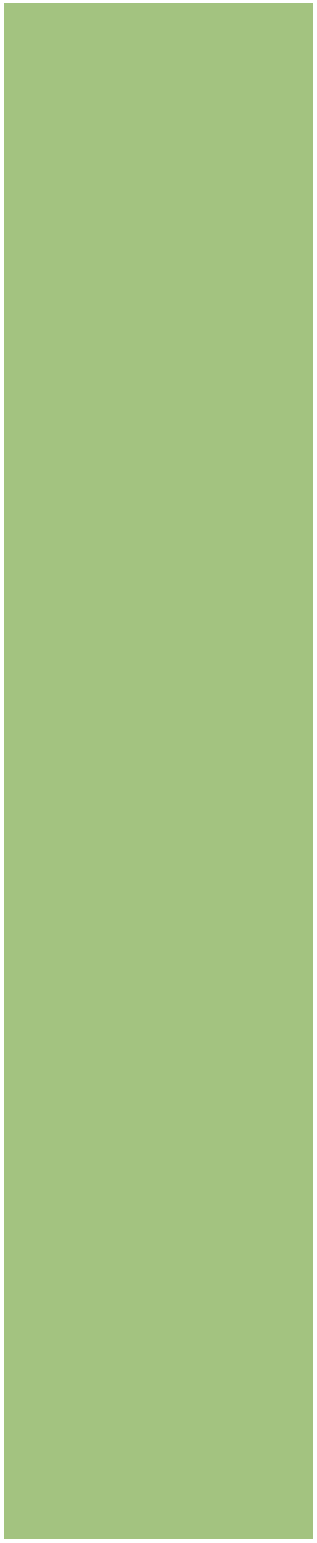

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Tolerance (mon) 38.00 ppm

Number of Peptides 449

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

- PROWL Home
- Chait Lab

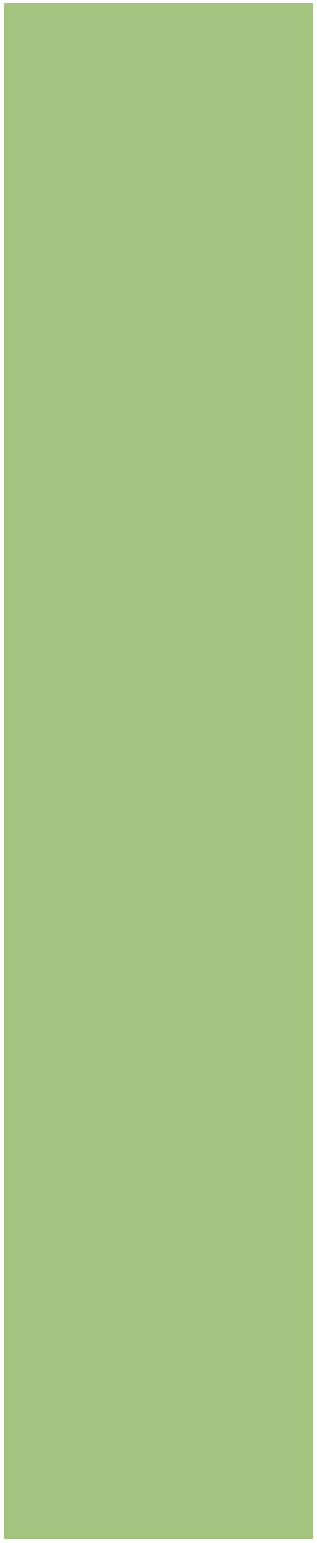
The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	2.5×10^{-9}	gi|33086650|gb|AAP92637.1| Cb1-812 [Rattus norvegicus]	47	6.8	30.53	
	-	gi|12585364|sp|Q9Z0T0|TPMT_RAT Thiopurine S-methyltransferase (Thiopurine methyltransferase)	35	6.3	27.96	
2	2.8×10^{-7}	gi|51980519|gb|AAH82050.1| Nudt18 protein [Rattus norvegicus]	48	6.3	36.48	
	-	gi|25992750|gb|AAN77242.1| immunophilin XAP2 [Rattus norvegicus]	38	6.1	38.05	
	-	gi|56789141|gb|AAH88125.1| Sulfotransferase family, cytosolic, 1C, member 1 [Rattus norvegicus]	48	6.1	35.87	
	-	gi|204655|gb|AAA41348.1| haptoglobin (Hp)	27	6.3	39.11	
	-	gi|38194517|gb|AAR13265.1| GP49B2 [Rattus norvegicus]	44	6.3	38.72	
	-	gi|585574|sp|P37805|TAGL3_RAT Transgelin-3 (Neuronal protein NP25)	53	6.5	24.98	
	-	gi|13929030|ref|NP_113920.1| sulfotransferase family 1A, member 2 [Rattus norvegicus]	41	6.1	35.86	
	-	gi|19550353|gb|AAL91351.1| serum- and glucocorticoid-inducible kinase 2-related [Rattus norvegicus]	35	6.9	34.95	
	-	gi|7245844|pdb|1C9L|A Chain A, Peptide-In-Groove Interactions Link Target Proteins To The B-Propeller Of Clathrin	52	6.5	39.98	
	-	gi|56090453|ref|NP_001007724.1| 5'-nucleotidase, cytosolic III-like [Rattus norvegicus]	34	6.3	33.96	
	-	gi|1351280|sp|P48500|TPIS_RAT Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)	51	6.5	27.42	
	-	gi|38512111|gb|AAH61781.1| Tpi1 protein [Rattus norvegicus]	52	7.1	27.21	



-	gi|27465551|ref|NP_775133.1| prolactin-like protein C related [Rattus norvegicus]	42	6.9	23.93
-	gi|11560081|ref|NP_071598.1| translin-associated factor X [Rattus norvegicus]	41	6.1	33.10
-	gi|420272|pir||E42148 GTP-binding protein rab14 - rat	54	5.8	24.08
-	gi|31324556|ref|NP_852143.1| retinol dehydrogenase 10 (all-trans) [Rattus norvegicus]	32	7.2	38.73
-	gi|57164003|ref|NP_001009175.1| tripartite motif-containing 40 [Rattus norvegicus]	47	6.8	29.11
-	gi|27695760|ref|XP_215692.1| PREDICTED: similar to myozenin 2 [Rattus norvegicus]	35	7.0	29.83
-	gi|123513|sp|P06866|HPT_RAT Haptoglobin precursor [Contains: Haptoglobin alpha chain; Haptoglobin beta chain]	22	6.1	39.04
-	gi|56789734|gb|AAH88443.1| Similar to RAB19, member RAS oncogene family [Rattus norvegicus]	45	6.1	24.66
-	gi|28933457|ref|NP_803175.1| glutathione S-transferase, mu 2 [Rattus norvegicus]	47	6.9	25.86
-	gi|39930501|ref|NP_446228.1| zuotin related factor 2 [Rattus norvegicus]	34	6.2	32.83
-	gi|55670081|pdb|1TZD|A Chain A, Crystal Structure Of The Catalytic Core Of Inositol 1,4,5- Trisphosphate 3-Kinase	24	6.3	30.82
-	gi|13124592|sp|Q9JI51|VTI1A_RAT Vesicle transport through interaction with t-SNAREs homolog 1A (Vesicle transport v-SNARE protein Vti1-like 2) (Vti1-rp2)	52	6.1	26.02
-	gi|46237562|emb|CAE83942.1| proteasome (prosome, macropain) subunit, beta type, 8 [Rattus norvegicus]	46	7.0	30.84
-	gi|2351075|dbj|BAA22048.1| 6-phosphofructo-2-kinase/ fructose-2, 6-bisphosphatase [Rattus norvegicus]	31	6.2	36.58
-	gi|16758368|ref|NP_446041.1| RAB14, member RAS oncogene family [Rattus norvegicus]	47	5.8	24.14
-	gi|38532559|gb|AAR23524.1| triosephosphate isomerase [Rattus norvegicus]	46	6.5	27.31
-	gi|1584427|prf||2123218B corticoliberin-binding protein	31	6.1	36.72

-	gi|14249130|ref|NP_116002.1| LIM and SH3 protein 1 [Rattus norvegicus]	18	6.6	30.35
-	gi|3493247|gb|AAC33331.1| MHC class I antigen [Rattus norvegicus]	21	6.4	39.56
-	gi|16758434|ref|NP_446078.1| D-amino acid oxidase [Rattus norvegicus]	24	6.7	39.14

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Tue Jan 23 15:38:02 2007 UTC (Search Time: 0.55 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 40 kDa

pI Range 5.8 -7.2

Digestion Trypsin

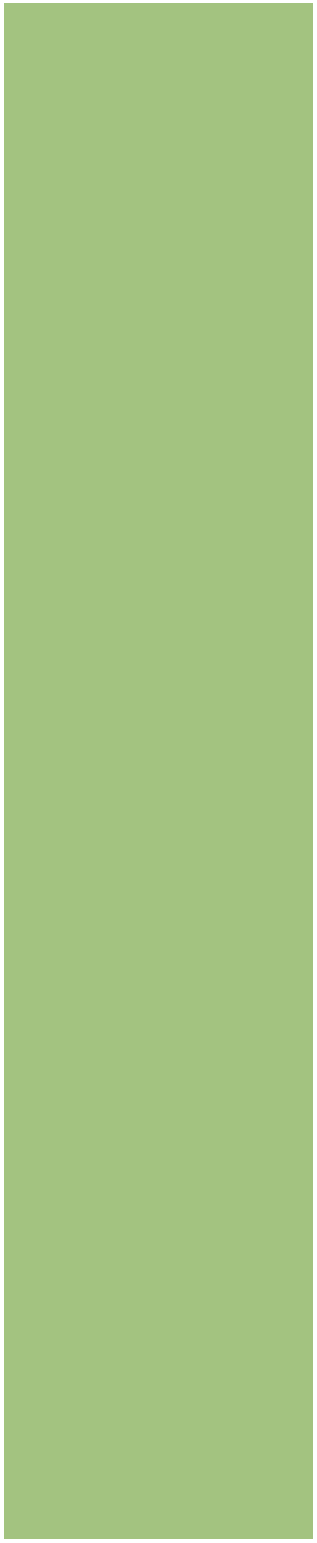
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



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863.502	875.521	881.821	882.620	884.579	887.502	891.474
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934.518	941.606	945.532	948.471	954.572	955.529	962.528
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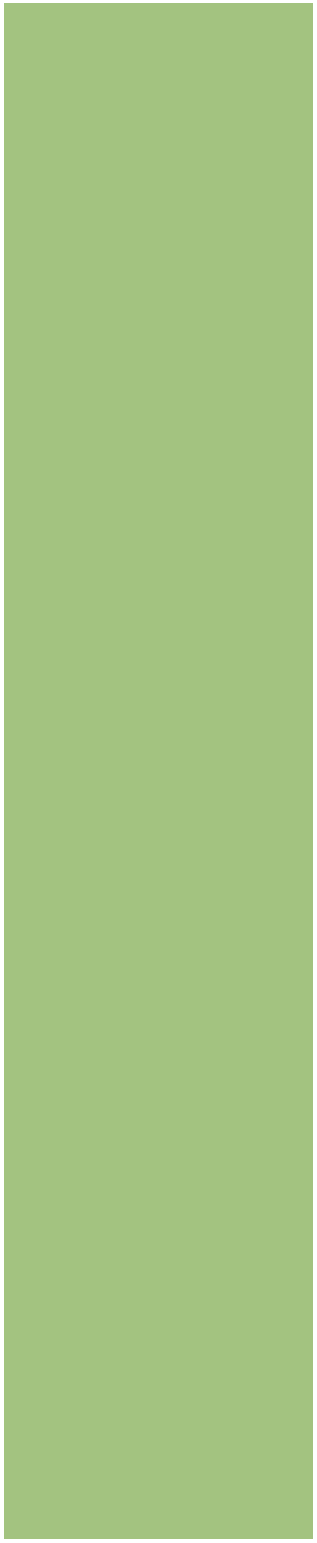
1009.592	1010.576	1017.045	1017.560	1020.524	1025.516	
1032.595	1037.574	1044.172	1053.586	1060.586	1067.609	
1068.577	1075.582	1082.567	1088.597	1089.529	1091.618	
1098.565	1100.573	1104.595	1107.549	1113.558	1125.581	
1126.529	1130.598	1136.625	1141.530	1148.543	1149.593	
1155.624	1164.562	1167.550	1174.642	1177.596	1185.553	
1192.654	1193.630	1194.607	1201.642	1210.569	1213.568	
1221.035	1221.599	1226.591	1231.640	1234.712	1242.006	
1243.619	1254.656	1262.630	1270.678	1277.741	1284.775	
1285.644	1292.651	1300.552	1302.688	1308.671	1312.813	
1320.628	1327.682	1335.639	1337.706	1348.559	1349.548	
1357.720	1366.663	1368.654	1375.685	1377.733	1382.684	
1391.708	1396.685	1405.200	1405.704	1411.666	1419.720	
1427.898	1434.774	1443.507	1450.728	1452.728	1460.229	
1460.744	1463.729	1469.762	1475.807	1482.745	1489.752	
1502.092	1502.771	1515.742	1522.721	1523.772	1529.769	
1537.784	1539.791	1547.090	1547.778	1554.725	1561.794	
1565.840	1568.771	1578.813	1580.740	1586.794	1593.720	
1596.732	1600.824	1608.860	1609.724	1614.861	1624.832	
1634.724	1638.865	1646.887	1650.769	1653.834	1660.796	
1669.642	1675.810	1683.867	1692.775	1700.818	1707.766	
1716.849	1726.011	1727.914	1732.114	1734.862	1742.891	
1751.221	1757.934	1766.922	1772.871	1774.913	1784.058	
1787.814	1791.688	1800.306	1800.877	1803.850	1813.873	
1818.809	1821.912	1830.371	1831.870	1838.908	1847.234	
1847.928	1856.390	1858.073	1864.871	1867.955	1876.988	
1878.855	1887.037	1888.909	1897.289	1905.569	1906.804	
1916.874	1926.852	1936.381	1938.041	1943.559	1947.896	
1957.954	1959.981	1968.876	1971.985	1979.947	1982.945	
1995.981	2004.957	2007.973	2016.371	2018.912	2021.940	



	2032.066 2036.136 2041.001 2048.920 2061.926 2067.925 2076.693 2080.684 2095.641 2106.013 2114.366 2118.518 2122.984 2132.242 2144.575 2154.880 2163.893 2167.780 2174.056 2184.054 2186.509 2191.930 2194.958 2203.992 2207.977 2211.080 2220.909 2222.813 2230.123 2234.005 2242.928 2244.204 2254.681 2262.107 2266.082 2273.012 2283.299 2286.132 2295.804 2309.702 2313.005 2321.110 2330.660 2337.168 2347.338 2350.342 2352.432 2356.092 2367.221 2376.274 2380.282 2383.898 2393.510 2396.082 2398.983 2408.229 2410.147 2419.150 2424.188 2433.881 2436.141 2444.992 2454.260 2465.618 2469.231 2472.781 2479.551 2482.906 2490.496 2502.006 2509.018 2519.150 2524.900 2537.573 2547.082 2556.337 2562.402 2576.058 2580.983 2593.109 2603.684 2606.709 2612.214 2618.000 2627.106 2633.185 2644.256 2657.294 2663.964 2672.174 2682.070 2688.632 2705.140 2717.062 2729.855 2734.079 2740.351 2752.421 2754.612 2759.916 2764.871 2776.072 2786.727 2792.275 2799.254 2809.739 2813.237 2825.251 2838.725 2844.396 2858.563 2869.229 2873.126 2883.530 2889.173 2900.258 2904.247 2929.556 2932.983 2940.498 2950.583 2953.656 2957.170 2968.456 2982.852 2992.934 3006.059 3011.598 3022.691 3032.247 3044.936 3056.089 3062.343 3065.920 3076.812 3088.321 3091.538 3094.608 3098.952 3110.653 3116.361 3124.707 3129.599 3142.412 3145.581 3154.192 3167.357 3179.032 3189.511 3203.053 3209.605 3223.036 3234.657 3243.233 3256.733 3259.804 3271.336 3276.109 3291.836 3303.732 3311.932 3327.277 3338.925 3345.378 3357.290 3363.371 3377.893 3383.523 3395.265 3397.538 3414.567 3429.982 3434.708 3438.649 3443.538 3457.120 3470.411 3481.506 3488.330 3502.314 3515.689 3522.784 3526.375 3531.803 3540.113 3547.312 3557.002 3561.250 3577.785 3590.332 3603.060 3608.302 3626.317 3634.733 3648.510 3656.057 3668.652 3680.209 3693.008 3695.537
Tolerance (mon)	25.00 ppm
Number of Peptides	443

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	5.7×10^{-29}	gi|204499|gb|AAA41285.1| glutathione S-transferase Y-b subunit (EC 2.5.1.18)	26	7.9	22.04	
	-	gi|207692|gb|AAA42351.1| glutathione S-transferase Yb2 subunit	25	7.0	23.01	
	-	gi|28933457|ref|NP_803175.1| glutathione S-transferase, mu 2 [Rattus norvegicus]	22	6.9	25.86	
	-	gi|33356830|pdb|1B4P|A Chain A, Crystal Structures Of Class Mu Chimeric Gst Isoenzymes M1-2 And M2-1	17	8.6	25.86	
2	6.4×10^{-18}	gi|22074155|gb|AAK95857.1| retinol dehydrogenase similar protein [Rattus norvegicus]	20	9.0	20.33	
3	4.2×10^{-12}	gi|554403|gb|AAA79025.1| alpha-1-inhibitor III	24	6.9	16.46	
4	4.6×10^{-11}	gi|27674205|ref|XP_213416.1| PREDICTED: similar to sperm acrosome associated 3 [Rattus norvegicus]	17	6.4	18.86	
5	6.2×10^{-11}	gi|2443209|dbj|BAA22285.1| c-met/hepatocyte growth factor receptor [Rattus norvegicus]	17	8.2	15.34	
6	2.0×10^{-10}	gi|16258813|ref|NP_434688.1| von Hippel-Lindau syndrome homolog [Rattus norvegicus]	12	6.1	21.31	
7	2.5×10^{-10}	gi|32527713|gb|AAP86258.1| Ac2-032 [Rattus norvegicus]	21	8.0	15.94	
8	4.6×10^{-10}	gi|42558275|ref|NP_973717.1| pyroglutamyl-peptidase I [Rattus norvegicus]	12	5.3	23.41	
9	8.7×10^{-10}	gi|41349751|dbj|BAD08305.1| core binding factor alpha1 subunit type I [Rattus norvegicus]	18	6.8	16.62	
10	1.0×10^{-9}	gi|6114760|emb|CAB59427.1| phosphodiesterase I/nucleotide pyrophosphatase [Rattus norvegicus]	17	5.5	17.54	
11	1.3×10^{-9}	gi|16758194|ref|NP_445905.1| regulator of G-protein signaling 2 [Rattus norvegicus]	9	9.2	24.59	

12	1.6×10^{-9}	gi|41349753|dbj|BAD08306.1| core binding factor alpha1 subunit type II [Rattus norvegicus]	17	6.3	18.24
13	2.9×10^{-9}	gi|27687955|ref|XP_225498.1| PREDICTED: similar to isopentenyl-diphosphate delta isomerase 2 [Rattus norvegicus]	11	5.4	26.65
14	7.7×10^{-9}	gi|3687907|gb|AAC78485.1| dlg 3 [Rattus norvegicus]	9	5.4	26.47
15	7.9×10^{-9}	gi|16758202|ref|NP_445911.1| RAB27B, member RAS oncogene family [Rattus norvegicus]	10	5.4	24.83
16	8.1×10^{-9}	gi|19424194|ref|NP_598220.1| RAB3C, member RAS oncogene family [Rattus norvegicus]	10	5.2	26.11
17	1.0×10^{-8}	gi|8394142|ref|NP_059013.1| low Mr GTP-binding protein [Rattus norvegicus]	9	5.1	25.34
18	2.5×10^{-8}	gi|3687905|gb|AAC78484.1| dlg 2 [Rattus norvegicus]	9	5.3	25.45
19	5.5×10^{-8}	gi|27718481|ref|XP_235187.1| PREDICTED: similar to Serine/threonine/tyrosine-interacting protein (Protein tyrosine phosphatase-like protein) (Phosphoserine/threonine/tyrosine interaction protein) [Rattus norvegicus]	14	6.0	25.58
20	4.5×10^{-7}	gi|50925721|gb|AAH79134.1| Ube2e2 protein [Rattus norvegicus]	7	9.4	26.72
21	7.3×10^{-7}	gi|56605730|ref|NP_001008327.1| REX2, RNA exonuclease 2 homolog [Rattus norvegicus]	9	6.7	26.96
22	2.4×10^{-6}	gi|56541165|gb|AAH87584.1| Rab8a protein [Rattus norvegicus]	14	9.5	17.58
23	9.4×10^{-6}	gi|49522647|gb|AAH71176.1| Rab8a protein [Rattus norvegicus]	11	9.3	23.69
24	3.3×10^{-4}	gi|46237565|emb|CAE83945.1| RT1 class II, B beta [Rattus norvegicus]	14	8.0	27.07

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id ADFAB1EA-0BF8-5E6124AA

Sequences 20073

Date & Time Fri Mar 30 17:00:13 2007 UTC (Search Time: 0.38 sec.)

Sample ID 20040813 NIA MRich spot 4216 search 20070330 number 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 15 - 28 kDa

pI Range 5.0 -9.6

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 706.348 711.629 712.257 717.362 718.407 723.389 725.416
730.423 733.370 738.404 739.391 742.411 744.446 749.444
754.422 763.351 765.396 769.438 773.453 779.468 781.440
787.467 788.487 792.419 799.362 801.474 813.474 819.469
825.487 831.449 833.466 836.848 841.485 848.679 850.483
854.508 856.495 863.476 877.545 880.536 884.512 891.467
892.551 903.455 904.406 906.470 916.501 918.396 922.497
933.500 939.490 942.503 948.542 950.574 953.521 956.493
962.515 963.475 969.581 970.587 980.546 988.503 989.519
993.480 996.578 1003.555 1009.574 1010.557 1016.768
1017.541 1023.580 1039.569 1043.520 1051.533 1056.535
1060.562 1066.618 1068.552 1074.499 1078.648 1084.601
1090.569 1094.572 1100.635 1102.555 1105.596 1107.565
1113.799 1114.585 1124.648 1132.560 1138.590 1140.544
1146.665 1148.557 1155.591 1163.564 1173.708 1186.862
1187.581 1194.594 1209.081 1209.642 1210.602 1212.616
1215.594 1222.643 1223.631 1228.674 1231.624 1238.956
1239.619 1242.606 1246.666 1253.709 1254.615 1259.649
1263.665 1270.636 1274.621 1285.118 1285.625 1287.604
1294.666 1301.625 1302.693 1305.512 1312.988 1313.720
1315.648 1327.710 1328.667 1332.595 1339.704 1347.722
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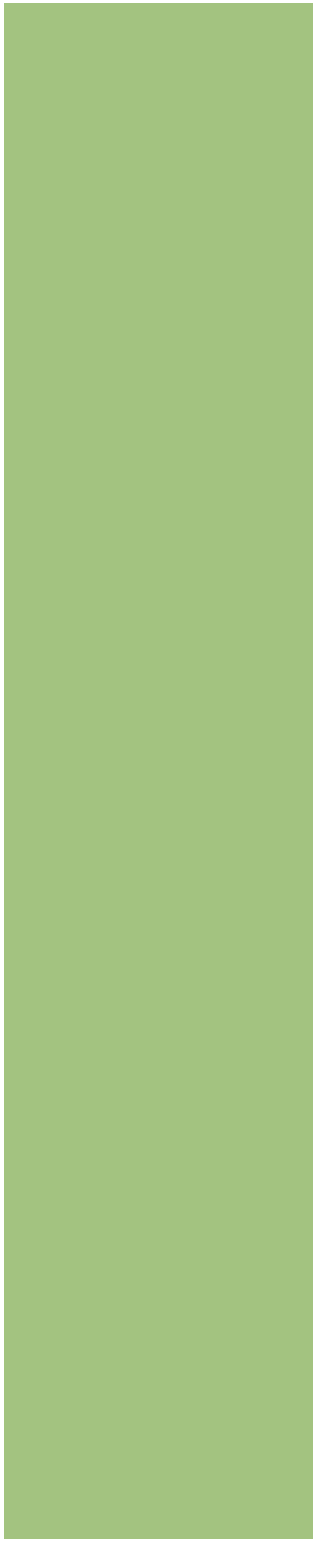

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1517.734	1520.778	1527.716	1534.696	1535.698	1539.737
1543.755	1550.878	1552.787	1555.733	1562.751	1565.732
1568.744	1571.785	1579.160	1579.828	1586.739	1587.812
1595.010	1595.816	1598.883	1605.836	1614.751	1615.806
1619.651	1627.708	1628.821	1636.792	1642.844	1651.779
1654.790	1657.776	1665.790	1666.862	1674.815	1683.781
1693.049	1694.905	1715.673	1725.923	1728.805	1736.961
1743.758	1746.824	1756.940	1765.049	1773.800	1781.863
1783.739	1788.947	1791.881	1801.842	1809.824	1814.783
1819.921	1823.772	1831.976	1853.770	1858.005	1866.810
1870.856	1879.253	1881.034	1889.922	1899.330	1903.000
1911.204	1915.917	1931.688	1940.991	1945.058	1954.960
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2054.141	2064.164	2073.107	2075.868	2085.390	2096.074
2100.948	2104.994	2113.035	2116.100	2120.936	2130.436
2132.022	2141.267	2143.854	2146.443	2150.688	2160.068
2166.018	2183.165	2188.958	2196.148	2206.101	2219.977
2229.920	2233.070	2242.085	2244.892	2258.154	2260.138
2269.208	2270.973	2275.983	2285.052	2294.075	2311.074
2320.083	2321.186	2330.183	2331.874	2346.043	2354.957
2361.073	2366.246	2376.019	2378.154	2395.230	2407.905
2418.228	2423.065	2432.258	2438.340	2448.494	2450.328
2461.276	2472.181	2485.897	2498.102	2504.401	2509.258
2514.996	2524.023	2527.443	2531.168	2542.941	2554.911
2568.889	2574.423	2579.278	2591.265	2595.244	2609.263
2614.943	2617.528	2627.393	2630.432	2635.375	2646.417
2658.976	2671.217	2683.695	2694.524	2697.007	2701.942
2705.094	2715.229	2726.227	2734.005	2746.383	2748.642
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2800.235	2810.654	2820.627	2831.156	2838.437	2843.105
2854.971	2863.329	2875.816	2886.085	2890.466	2903.738
2913.803	2915.040	2919.661	2926.618	2937.161	2941.289
2951.858	2962.740	2972.870	2983.239	2995.174	3008.759
3018.969	3024.672	3036.393	3048.844	3053.571	3066.841
3079.317	3090.395	3092.680	3104.345	3116.935	3121.865
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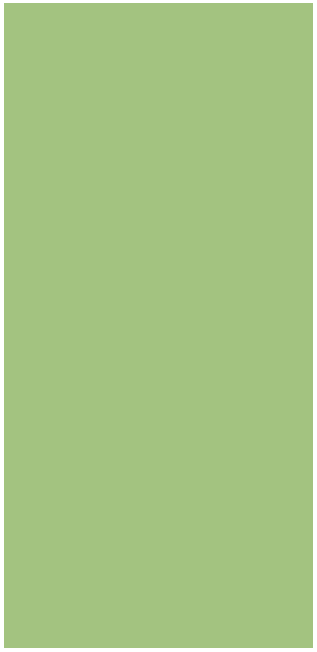

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Tolerance (mon)	8.00 ppm
Number of Peptides	448

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.4×10^{-14}	gi|50925930|gb|AAH79461.1| Similar to RIKEN cDNA C430008C19 [Rattus norvegicus]	44	6.5	23.90	
+2	1.3×10^{-6}	gi|56388776|gb|AAH87696.1| Fgfr1op2 protein [Rattus norvegicus]	19	5.4	25.05	
	-	gi|38426813|gb|AAR20448.1| wound inducible transcript 3.0 alpha [Rattus norvegicus]	16	5.4	25.05	
3	2.7×10^{-6}	gi|46485429|ref|NP_997477.1| glyoxylase 1 [Rattus norvegicus]	23	5.1	20.97	
4	9.5×10^{-6}	gi|4138018|emb|CAA76114.1| metallopeptidase [Rattus norvegicus]	16	6.1	23.12	
5	1.5×10^{-4}	gi|41386755|ref|NP_958824.1| FGFR1 oncogene partner 2 [Rattus norvegicus]	18	5.6	29.53	
6	4.0×10^{-4}	gi|38489091|gb|AAR21241.1| eomesodermin [Rattus norvegicus]	27	6.8	22.10	
7	7.7×10^{-4}	gi|13399989|pdb|1I1A|C Chain C, Crystal Structure Of The Neonatal Fc Receptor Complexed With A Heterodimeric Fc	16	6.8	25.60	
8	8.0×10^{-4}	gi|56388596|gb|AAH87673.1| Lipoma HMGIC fusion partner-like 5 [Rattus norvegicus]	21	6.7	24.68	
9	3.3×10^{-3}	gi|55552|emb|CAA78041.1| 45kDa protein [Rattus norvegicus]	13	6.7	21.26	
10	4.9×10^{-3}	gi|762882|gb|AAA64892.1| glycoprotein P	16	6.5	27.74	
11	5.2×10^{-3}	gi|1658331|gb|AAB18293.1| 5-HT3 receptor subunit A short form	16	6.8	25.81	
12	6.0×10^{-3}	gi|50811823|ref|NP_001002851.1| SCIRP10-related protein [Rattus norvegicus]	20	5.3	18.97	
+13	9.7×10^{-3}	gi|33356831|pdb|1C7Z|A Chain A, Regulatory Complex Of Fructose-2,6-Bisphosphatase	14	5.8	22.48	

	-	gi|2914269|pdb|1TIP|A Chain A, The Bisphosphatase Domain Of The Bifunctional Rat Liver 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase	14	5.7	22.34
	-	gi|2392330|pdb|1FBT|A Chain A, The Bisphosphatase Domain Of The Bifunctional Rat Liver 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase	14	5.8	21.82
14	0.012	gi|3687905|gb|AAC78484.1| dlg 2 [Rattus norvegicus]	14	5.3	25.45
+15	0.034	gi|2145145|gb|AAB58429.1| apolipoprotein A-I [Rattus norvegicus]	20	5.5	29.96
	-	gi|2145143|gb|AAB58428.1| apolipoprotein A-I [Rattus norvegicus]	20	5.5	29.87
16	0.041	gi|8393355|ref|NP_058822.1| ferredoxin 1 [Rattus norvegicus]	20	5.6	20.57
17	0.079	gi|56605778|ref|NP_001008352.1| hypothetical protein LOC309681 [Rattus norvegicus]	10	6.6	28.39
18	0.16	gi|8394513|ref|NP_058884.1| UNC-119 homolog [Rattus norvegicus]	14	5.8	27.20
19	0.19	gi|34871653|ref|XP_343924.1| PREDICTED: similar to retinoic acid, EGF, and NGF upregulated [Rattus norvegicus]	19	6.0	26.38
20	0.19	gi|50925831|gb|AAH79271.1| Similar to Glutathione S-transferase A1 (GTH1) (HA subunit 1) (GST-epsilon) (GSTA1-1) (GST class-alpha) [Rattus norvegicus]	14	5.9	25.79

NOTE:

1. To search again using unmatched masses, click the symbol ◉.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B002E773-09EC-606D26B6

Sequences 20073

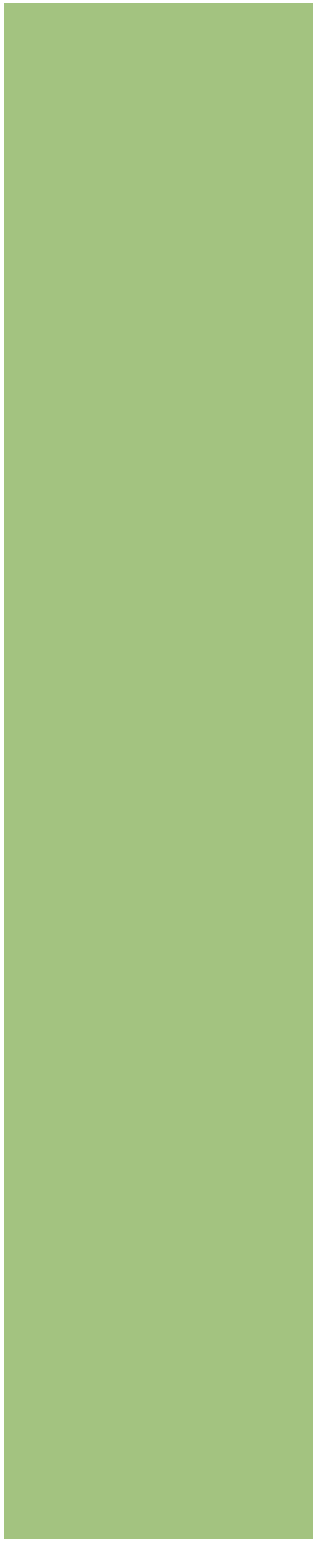
Date & Time Mon Apr 02 14:09:36 2007 UTC (Search Time: 0.42 sec.)

Sample ID 20040813 NIA MRich spot 6308 search 20070402 number 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 15 - 30 kDa



pI Range 5.0 -7.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 709.380 711.387 715.410 720.418 725.425 727.437 732.651
733.415 737.426 742.438 747.429 749.416 752.401 755.465
763.600 764.381 766.502 770.453 776.400 778.481 784.496
785.400 788.456 794.434 796.520 798.514 805.465 810.473
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1359.722 1372.707 1376.700 1390.645 1395.669 1402.643
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1434.737 1441.807 1444.671 1449.792 1453.639 1456.771
1463.665 1464.695 1469.748 1479.726 1487.659 1500.929
1502.755 1506.724 1513.761 1517.718 1523.703 1531.649
1537.714 1545.749 1552.770 1559.754 1564.783 1567.713
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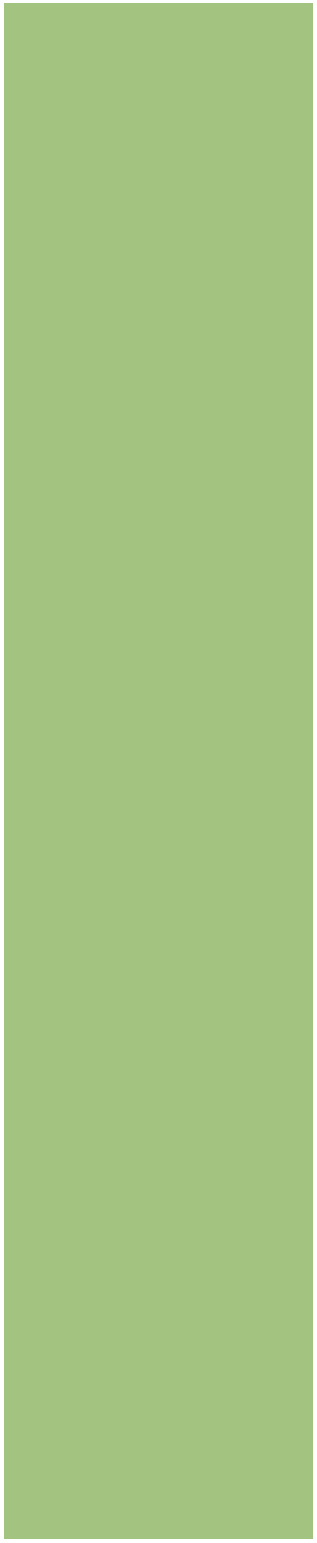

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1694.799	1696.990	1708.240	1708.769	1725.899	1727.718
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1791.941	1794.877	1802.930	1812.004	1819.865	1824.866
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1864.977	1874.206	1877.939	1887.873	1896.718	1899.681
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2092.369	2095.604	2106.068	2114.729	2123.813	2127.197
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2257.213	2263.873	2272.019	2277.062	2287.260	2290.192
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2361.351	2366.066	2368.557	2378.400	2383.394	2393.664
2395.905	2400.589	2409.341	2415.097	2419.037	2428.952
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2571.290	2580.281	2586.237	2599.647	2608.653	2614.918
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2679.726	2684.540	2695.300	2698.098	2708.430	2713.726
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3181.934	3192.776	3201.731	3216.008	3223.120	3234.110
3237.560	3250.726	3254.838	3266.575	3277.909	3284.240
3295.141	3299.863	3305.828	3319.871	3331.103	3335.072
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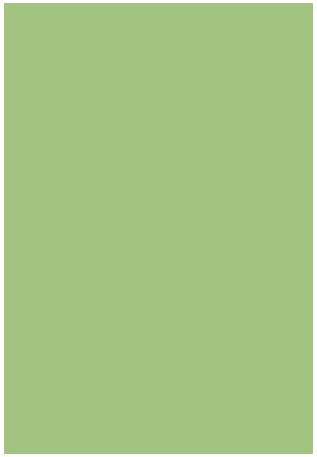

	3399.685 3411.447 3423.110 3427.292 3438.311 3444.045 3453.387 3460.165 3471.673 3482.804 3488.376 3496.423 3511.228 3521.742 3534.677 3540.250 3544.825 3555.873 3567.944 3570.885 3584.556 3596.393 3608.656 3620.737 3629.343 3641.458 3647.320 3661.180 3672.205 3686.644 3692.420 3697.339
Tolerance (mon)	28.00 ppm
Number of Peptides	456

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

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- X! Tandem
- X! Hunter
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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.2×10^{-5}	gi|205486|gb|AAA41623.1| myosin light chain MLC3-f	55	4.6	16.72	
	-	gi|13487933|ref|NP_064489.1| fast myosin alkali light chain 3f [Rattus norvegicus]	47	4.6	16.71	
2	4.4×10^{-4}	gi|34810965|pdb|1NN7|A Chain A, Crystal Structure Of The Tetramerization Domain Of The Shal Voltage-Gated Potassium Channel	46	4.9	12.92	
	-	gi|39654792|pdb|1R13|A Chain A, Carbohydrate Recognition And Neck Domains Of Surfactant Protein A (Sp-A)	23	4.6	16.87	
	-	gi|13591758|gb|AAK31339.1|AAK31339 KIAA1454-like protein [Rattus norvegicus]	30	4.3	17.25	
	-	gi|16758744|ref|NP_446330.1| complexin 2 [Rattus norvegicus]	39	5.1	15.49	
	-	gi|1703700|gb|AAB37711.1| KRP4=kinesin-related protein [rats, testes, Peptide Partial, 153 aa]	48	4.8	17.06	
	-	gi|4096760|gb|AAD10399.1| phosphatidylinositol 4-kinase [Rattus norvegicus]	39	4.7	16.28	
	-	gi|2160456|dbj|BAA03557.1| calcium-binding protein P23K beta [Rattus norvegicus]	45	4.7	16.95	
	-	gi|2956998|emb|CAA76404.1| fractalkine/neuroactin [Rattus norvegicus]	34	4.6	13.77	
	-	gi|1363278|pir||C57233 complexin II - rat	28	5.1	15.39	
	-	gi|49259317|pdb|1UD0|A Chain A, Crystal Structure Of The C-Terminal 10-Kda Subdomain Of Hsc70	27	4.8	11.82	
	-	gi|7547027|gb|AAF63763.1|AF250032_1 agrin precursor [Rattus norvegicus]	19	5.0	16.01	

-	gi|27679694|ref|XP_215044.1| PREDICTED: similar to Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (CI-SDAP) [Rattus norvegicus]	17	4.9	17.78
-	gi|11596861|ref|NP_071620.1| guanylate cyclase activator 2b [Rattus norvegicus]	52	4.7	11.90
-	gi|52695347|pdb|1Q8D|A Chain A, The Crystal Structure Of Gdnf Family Co-Receptor Alpha 1 Domain 3	40	4.7	12.44
-	gi|47058998|ref|NP_997679.1| TOM22 protein [Rattus norvegicus]	19	4.3	15.47

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Thu Jan 25 15:42:03 2007 UTC (Search Time: 0.38 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 10 - 18 kDa

pI Range 4.0 -5.1

Digestion Trypsin

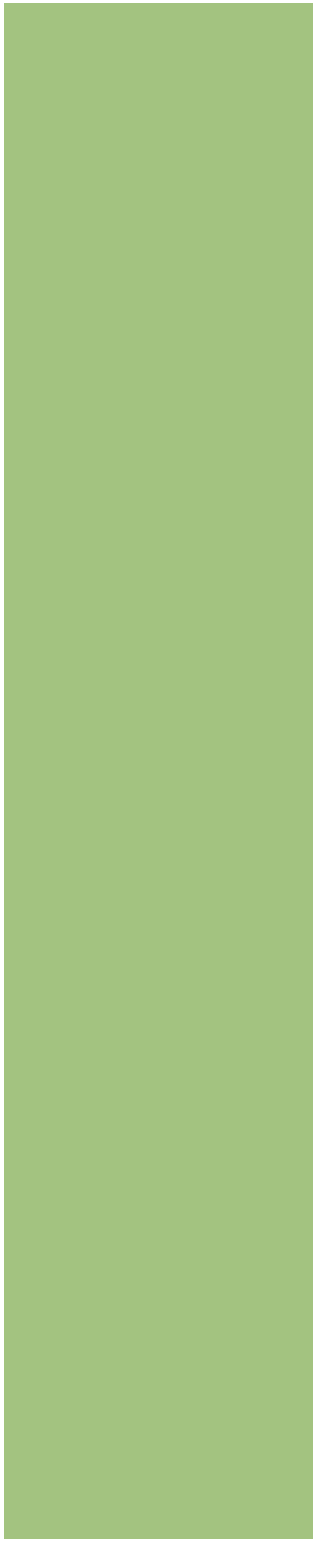
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@TY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

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1328.721 1329.604 1336.657 1337.666 1348.518 1351.659
1364.854 1372.673 1373.621 1380.689 1390.661 1398.578
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1456.712 1463.657 1470.799 1483.034 1483.682 1486.666
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1568.719 1569.760 1576.755 1582.776 1585.750 1592.781
1595.765 1598.778 1606.755 1614.780 1619.598 1627.818
1635.840 1646.777 1649.756 1656.819 1660.822 1668.953
1669.723 1672.806 1676.663 1683.810 1688.870 1697.652
1715.842 1724.918 1725.813 1731.831 1739.770 1744.716
1754.826 1757.845 1762.761 1773.802 1782.917 1785.846
1790.858 1799.816 1802.845 1810.973 1813.839 1819.838
1827.717 1831.778 1847.025 1847.894 1849.891 1858.706
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1900.069 1906.855 1914.950 1924.982 1930.984 1938.893
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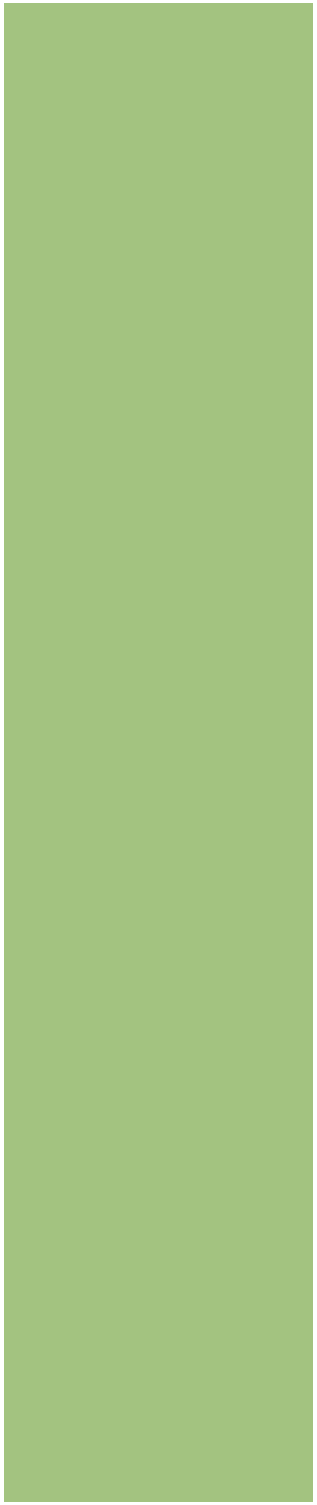

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3139.023	3150.434	3155.693	3160.275	3171.345	3177.419
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3246.227	3249.990	3253.141	3264.372	3278.477	3285.695
3291.761	3303.989	3312.282	3323.459	3326.645	3337.807
3349.222	3353.708	3367.495	3380.684	3386.719	3390.446
3404.269	3413.592	3425.845	3429.592	3438.159	3452.237
3455.167	3466.701	3481.076	3487.796	3492.971	3504.328
3529.379	3541.677	3566.296	3585.391	3589.547	3593.786
3606.721	3609.716	3622.841	3637.615	3648.024	3660.974
3670.232	3682.035	3694.430	3698.936	3701.927	

Tolerance (mon) 19.00 ppm

Number of Peptides 441

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.6×10^{-8}	gi|1363305|pir||S57854 myosin regulatory light chain 2 (clone YU63), brain - rat (fragment)	47	4.2	12.57	
	-	gi|1334227|emb|CAA38437.1| unnamed protein product [Rattus norvegicus]	55	4.6	6.68	
2	3.4×10^{-6}	gi|4322329|gb|AAD16017.1| amiloride-sensitive epithelial sodium channel alpha subunit [Rattus norvegicus]	58	4.6	8.56	
3	5.2×10^{-6}	gi|1881810|gb|AAB49505.1| RET1 alpha subunit [Rattus sp.]	32	4.6	6.91	
	-	gi|1675351|gb|AAB19106.1| inositol monophosphate [Rattus norvegicus]	58	4.9	9.66	
	-	gi|111289|pir||S21218 peptidylprolyl isomerase (EC 5.2.1.8), 22K - rat (fragments)	30	4.4	8.87	
	-	gi|56541036|gb|AAH87583.1| Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11 [Rattus norvegicus]	46	4.6	10.01	
	-	gi|561839|gb|AAB02848.1| guanine nucleotide regulatory protein G alpha q	47	4.7	11.21	
	-	gi|1483586|emb|CAA67567.1| RT6 [Rattus norvegicus]	29	5.0	11.99	
	-	gi|206996|gb|AAA42152.1| senescence marker protein 2B	58	4.9	7.99	
	-	gi|30841840|gb|AAP34393.1| follistatin 288 variant [Rattus norvegicus]	60	4.4	5.85	
	-	gi|56388612|gb|AAH87681.1| Similar to RIKEN cDNA 4933433P14 gene [Rattus norvegicus]	16	4.2	15.71	
	-	gi|56246|emb|CAA29100.1| alpha 2u-globulin [Rattus norvegicus]	30	4.9	7.99	
	-	gi|587518|emb|CAA57204.1| keratin 18 [Rattus norvegicus]	12	4.6	16.94	

-	gi|56540888|gb|AAH87139.1| Atg12 protein [Rattus norvegicus]	16	4.9	15.25
-	gi|92028|pir||C31982 Ca2+-transporting ATPase (EC 3.6.3.8) RB5-10, brain - rat (fragment)	45	4.3	10.50
-	gi|544788|gb|AAB29567.1| platelet-derived growth factor beta-receptor, PDGF beta receptor [rats, Rat-1 cells, Peptide Partial, 102 aa]	34	4.9	11.43
-	gi|21693154|dbj|BAC02713.1| growth and differentiation factor-5 [Rattus norvegicus]	48	4.6	7.70

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AD4C3020-0CFC-5D5D2382

Sequences 20092

Date & Time Wed Jan 24 20:34:43 2007 UTC (Search Time: 0.30 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 5 - 17 kDa

pI Range 4.0 -5.0

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 706.362 711.392 712.253 717.430 720.350 724.525 729.456
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1725.938 1727.505 1735.882 1740.008 1743.801 1752.048
1752.866 1756.843 1779.718 1788.221 1790.785 1794.861
1803.000 1810.956 1817.811 1825.915 1833.951 1834.989
1848.020 1856.046 1856.975 1863.916 1867.929 1876.728
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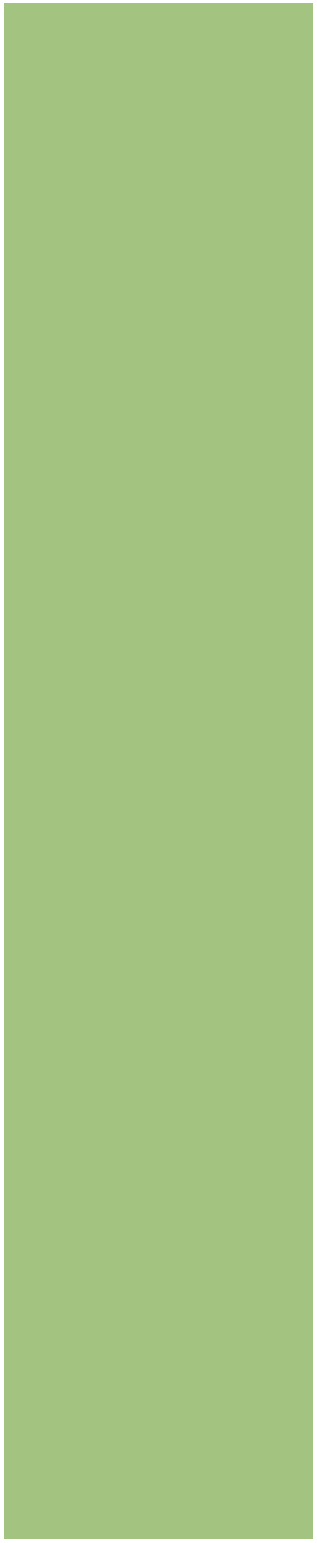

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Tolerance (mon)	11.00 ppm
Number of Peptides	442

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
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The Rockefeller University

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	2.4×10^{-11}	gi|57164117|ref|NP_001009385.1| apolipoprotein N [Rattus norvegicus]	19	5.3	28.50	
2	5.8×10^{-7}	gi|27706430|ref|XP_228520.1| PREDICTED: similar to polycomb group ring finger 6 isoform a [Rattus norvegicus]	17	5.1	25.46	
3	8.0×10^{-7}	gi|34013518|ref|NP_898874.1| RT1 class II, locus DOa [Rattus norvegicus]	14	6.4	28.51	
4	8.0×10^{-7}	gi|9438772|gb|AAB35455.2| major histocompatibility complex class II alpha chain [Rattus sp.]	16	5.8	25.34	
5	9.1×10^{-7}	gi|2499750|sp|Q63340|DUS7_RAT Dual specificity protein phosphatase 7 (Dual specificity protein phosphatase MKP-X)	10	4.9	31.05	
6	9.2×10^{-7}	gi|56404684|sp|Q6QA27|TRI44_RAT Tripartite motif-containing protein 44 (Protein DIPB)	11	4.1	38.70	
7	1.0×10^{-6}	gi|13928892|ref|NP_113834.1| receptor activity modifying protein 2 [Rattus norvegicus]	15	5.0	20.57	
8	1.0×10^{-6}	gi|204044|gb|AAA41120.1| entactin	11	4.3	26.55	
9	2.1×10^{-6}	gi|16758656|ref|NP_446264.1| BCL2-antagonist/killer 1 [Rattus norvegicus]	15	5.5	23.25	
10	5.4×10^{-6}	gi|16758526|ref|NP_446158.1| doublesex and mab-3 related transcription factor 1 [Rattus norvegicus]	9	6.2	39.88	
11	6.2×10^{-6}	gi|128201|sp|P08460|NID1_RAT Nidogen-1 (Entactin)	8	4.6	35.99	
12	9.6×10^{-6}	gi|21667355|gb|AAM74035.1| allantoicase [Rattus norvegicus]	15	5.6	21.40	
13	1.1×10^{-5}	gi|34871770|ref|XP_342933.1| PREDICTED: similar to ATP binding domain 1 family, member B [Rattus norvegicus]	10	4.9	34.83	
14	1.6×10^{-5}	gi|477540|pir||A49183 retinal particulate-guanylate cyclase - rat (fragments)	8	4.9	38.02	
15	1.6×10^{-5}	gi|13928908|ref|NP_113844.1| syntaxin 8 [Rattus norvegicus]	17	4.9	27.12	
16	4.2×10^{-5}	gi|34861797|ref|XP_344982.1| PREDICTED: similar to calcium binding protein 4 [Rattus norvegicus]	7	5.0	30.47	
17	4.8×10^{-5}	gi|19386562|gb|AAL86569.1| vesicular protein vp-165 short isoform [Rattus norvegicus]	8	5.2	38.83	
18	5.1×10^{-5}	gi|55250746|gb|AAH85816.1| WD repeat domain 45 [Rattus norvegicus]	6	6.5	35.31	
19	1.9×10^{-4}	gi|38970029|gb|AAH63148.1| F-box only protein 6b [Rattus norvegicus]	7	6.0	33.17	
20	1.9×10^{-4}	gi|3184552|gb|AAC18967.1| syntaxin 13 [Rattus norvegicus]	10	5.4	30.56	

21	1.9×10^{-4}	gi|3213231|gb|AAC23484.1| syntaxin 12 [Rattus norvegicus]	10	5.4	31.21
22	2.2×10^{-4}	gi|51315729|sp|Q923V4|FBX6_RAT F-box only protein 6 (F-box only protein 6b) (F-box/G-domain protein 2)	7	6.4	33.17
23	3.8×10^{-4}	gi|52695718|pdb|1TDQ|A Chain A, Structural Basis For The Interactions Between Tenascins And The C-Type Lectin Domains From Lecticans: Evidence For A Cross-Linking Role For Tenascins	11	4.8	30.28
24	9.3×10^{-4}	gi|9506919|ref|NP_062080.1| neurogenic differentiation 3 [Rattus norvegicus]	12	6.4	26.56
25	2.5×10^{-3}	gi|56971793|gb|AAH88192.1| Angiopoietin-like 3 [Rattus norvegicus]	5	6.1	37.14
26	8.1×10^{-3}	gi|55715651|gb|AAH85739.1| 3-hydroxyanthranilate 3,4-dioxygenase [Rattus norvegicus]	6	5.5	32.82
27	9.6×10^{-3}	gi|9910256|ref|NP_064461.1| 3-hydroxyanthranilate 3,4-dioxygenase [Rattus norvegicus]	6	5.6	32.85

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

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Date & Time Tue Feb 20 17:53:41 2007 UTC (Search Time: 0.33 sec.)
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Taxonomy Rattus
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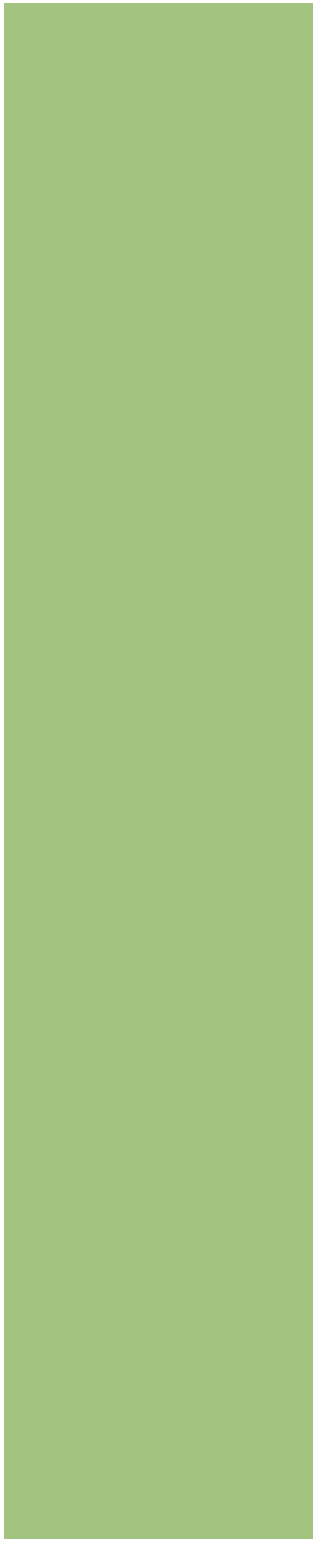
pI Range 4.0 -7.0
Digestion Trypsin
Missed Cuts 0
Modifications +C2H3ON@C(Complete);
Charge State MH+
Masses (avg)
Tolerance (avg) 1.00 ppm



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2113.010 2115.857 2120.071 2129.007 2130.623 2138.834 2143.132 2148.995
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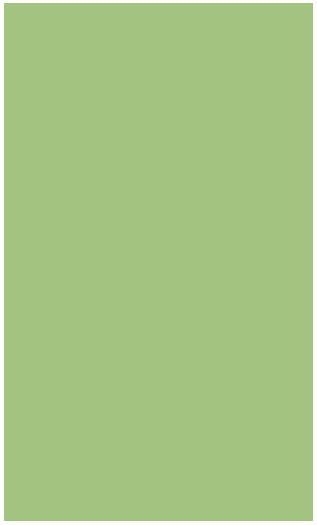

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2994.396	3001.255	3004.724	3015.624	3024.951	3037.447	3041.309	3051.159
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3109.957	3122.890	3139.585	3145.853	3159.428	3173.222	3180.739	3191.611
3197.701	3209.289	3216.007	3228.624	3232.911	3240.229	3250.588	3264.772
3270.393	3281.340	3285.006	3296.093	3307.625	3313.282	3317.703	3321.428
3334.559	3340.395	3347.327	3355.007	3366.212	3372.857	3384.523	3396.444
3400.448	3412.200	3416.567	3422.002	3428.466	3439.949	3449.317	3460.321
3468.367	3479.202	3485.402	3499.728	3508.418	3520.594	3525.191	3532.551
3544.247	3549.902	3562.873	3583.925	3600.350	3612.644	3620.500	3625.566
3637.576	3640.623	3648.021	3661.657	3673.931	3683.161	3695.757	

Tolerance (mon) 19.00 ppm

Number of Peptides 487

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	3.7×10^{-3}	gi|207498|gb|AAA42289.1| embryonic fibroblast tropomyosin 1	20	4.6	33.00	
	-	gi|20178269|sp|P58775|TPM2_RAT Tropomyosin beta chain (Tropomyosin 2) (Beta-tropomyosin)	10	4.7	32.93	
+2	5.5×10^{-3}	gi|2145145|gb|AAB58429.1| apolipoprotein A-I [Rattus norvegicus]	38	5.5	29.96	
	-	gi|2145143|gb|AAB58428.1| apolipoprotein A-I [Rattus norvegicus]	29	5.5	29.87	
+3	0.018	gi|6978515|ref|NP_036870.1| apolipoprotein A-I [Rattus norvegicus]	33	5.5	30.10	
	-	gi|113997|sp|P04639|APOA1_RAT Apolipoprotein A-I precursor (Apo-AI) (ApoA-I)	27	5.5	30.13	
4	0.029	gi|37589620|gb|AAH59151.1| Emd protein [Rattus norvegicus]	32	5.0	29.57	
	-	gi|34863185|ref|XP_234036.2| PREDICTED: similar to expressed sequence AW125753 [Rattus norvegicus]	22	5.4	33.07	
	-	gi|27661844|ref|XP_219510.1| PREDICTED: similar to expressed sequence AI842788 [Rattus norvegicus]	24	5.0	22.46	
	-	gi|25452816|sp|Q63149|CADH4_RAT Cadherin-4 (Retinal-cadherin) (R-cadherin) (R-CAD)	21	4.5	32.89	
	-	gi|18266686|ref|NP_543163.1| thioredoxin-like (32kD) [Rattus norvegicus]	24	4.8	32.63	
	-	gi|1323728|gb|AAB00334.1| phosducin-like protein [Rattus norvegicus]	19	4.9	25.25	
	-	gi|27227451|gb|AAN85424.1| MHC class Ib antigen [Rattus norvegicus]	30	5.1	31.90	

-	gi|9507243|ref|NP_062250.1| tyrosine 3-monooxgenase/ tryptophan 5-monooxgenase activation protein, beta polypeptide [Rattus norvegicus]	18	4.8	28.15
-	gi|40018538|ref|NP_954528.1| androgen-responsive gene encoding an ARD-like protein [Rattus norvegicus]	27	5.3	21.36
-	gi|27680212|ref|XP_219321.1| PREDICTED: similar to synaptonemal complex protein 3 [Rattus norvegicus]	20	5.6	27.44
-	gi|55976166|sp|Q68VK5|TSN5_RAT Tetraspanin-5 (Tspan-5) (Transmembrane 4 superfamily member 9)	29	4.6	30.98
-	gi|14192925|ref|NP_062004.1| tropomyosin 1, alpha isoform f [Rattus norvegicus]	24	4.8	28.91
-	gi|41386755|ref|NP_958824.1| FGFR1 oncogene partner 2 [Rattus norvegicus]	25	5.6	29.53
-	gi|56605828|ref|NP_001008377.1| trafficking protein particle complex 3 [Rattus norvegicus]	17	4.8	20.46
-	gi|8926237|gb|AAF81755.1|AF269283_1 potassium channel auxiliary subunit KCHIP2a [Rattus norvegicus]	17	4.9	31.26
-	gi|8926239|gb|AAF81756.1|AF269284_1 potassium channel auxiliary subunit KCHIP2b [Rattus norvegicus]	18	4.8	29.31
-	gi|3184552|gb|AAC18967.1| syntaxin 13 [Rattus norvegicus]	20	5.4	30.56
-	gi|8394091|ref|NP_058953.1| proteasome activator subunit 2 [Rattus norvegicus]	19	5.5	27.07

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Thu Jan 25 18:48:42 2007 UTC (Search Time: 0.49 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 34 kDa

pI Range 4.5 -5.6

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 706.377 712.358 718.886 719.391 722.370 726.405 728.436
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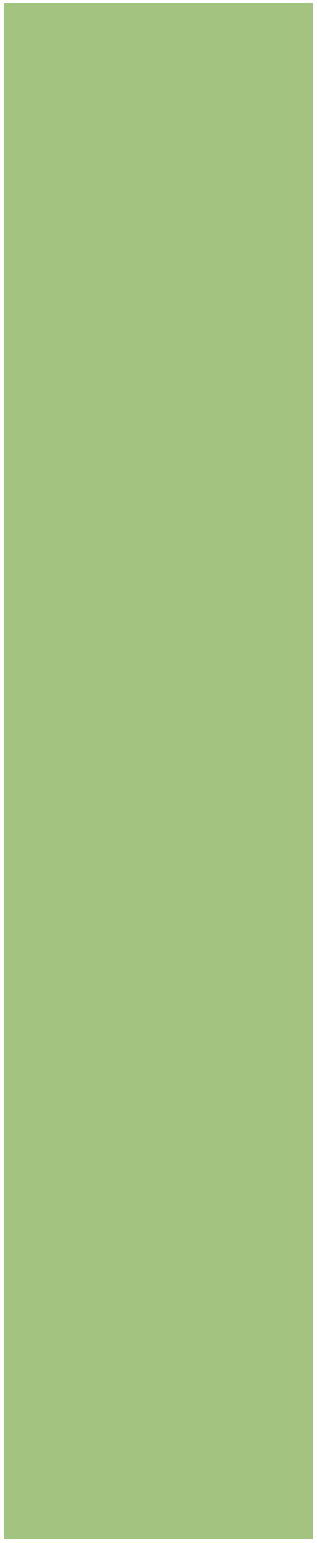

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1737.860	1740.837	1744.800	1752.853	1755.842	1763.891
1783.884	1784.851	1788.835	1791.713	1800.044	1800.815
1802.902	1811.088	1812.836	1821.993	1829.934	1834.920
1847.894	1850.876	1860.884	1863.964	1867.920	1875.873
1877.886	1888.844	1890.952	1897.927	1906.943	1909.885
1918.016	1926.962	1928.913	1937.025	1941.948	1950.950
1955.950	1964.059	1967.971	1976.374	1978.950	1984.946
2003.078	2006.033	2009.050	2011.949	2019.871	2027.900
2031.996	2036.005	2044.126	2046.015	2054.034	2064.027
2069.048	2078.985	2083.010	2093.011	2095.045	2106.961
2115.966	2118.911	2128.035	2138.019	2140.979	2150.057
2160.062	2169.965	2182.029	2184.043	2192.046	2195.074
2204.077	2208.126	2219.915	2229.128	2233.105	2236.129
2245.088	2256.081	2265.047	2268.126	2277.374	2280.139
2283.131	2292.442	2295.119	2309.081	2314.133	2323.475
2326.170	2352.135	2364.238	2367.252	2376.076	2393.281
2399.018	2409.985	2418.292	2424.093	2437.045	2440.238
2450.232	2455.336	2464.290	2468.237	2481.206	2492.427
2500.370	2509.879	2523.126	2527.324	2539.905	2546.427
2552.176	2561.476	2566.217	2577.354	2581.255	2594.381
2600.115	2611.291	2614.012	2625.218	2628.222	2634.339
2645.069	2654.815	2660.302	2666.457	2677.287	2688.594
2695.235	2705.212	2718.123	2728.390	2734.129	2741.179
2753.363	2763.554	2766.423	2776.141	2779.337	2783.353
2793.563	2808.040	2821.409	2826.278	2831.223	2842.420
2853.962	2868.270	2881.456	2888.585	2900.438	2904.395
2917.664	2928.665	2932.495	2944.694	2955.014	2964.471
2972.364	2983.505	2993.340	3002.747	3009.064	3020.273
3029.389	3039.708	3053.691	3067.894	3080.035	3083.476
3092.575	3099.473	3111.601	3124.619	3129.668	3141.515
3149.300	3161.676	3174.533	3177.609	3188.519	3192.667
3203.603	3214.596	3221.705	3227.598	3234.491	3246.688
3250.835	3263.680	3275.700	3288.708	3292.651	3304.415
3312.282	3324.042	3326.761	3338.858	3350.704	3353.824
3366.791	3371.680	3380.841	3392.525	3396.882	3408.280
3420.563	3423.045	3434.763	3445.590	3450.061	3462.220
3467.852	3484.813	3510.512	3514.865	3524.537	3547.211

	3560.103 3571.004 3580.673 3594.998 3608.744 3618.706 3631.604 3650.140 3667.212 3685.592 3690.051
Tolerance (mon)	13.00 ppm
Number of Peptides	429

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- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

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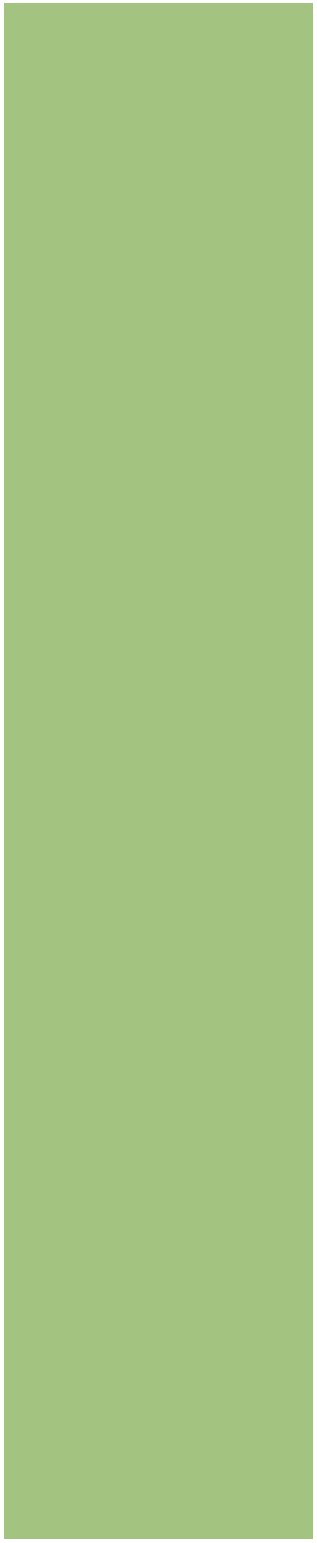
ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	8.3×10^{-36}	gi|57528169|ref|NP_001009624.1| hypothetical protein LOC287598 [Rattus norvegicus]	63	5.7	16.67	
2	1.6×10^{-9}	gi|2145098|gb|AAB63349.1| G-protein coupled inward rectifier potassium channel splice variant Kir3.1b [Rattus norvegicus]	46	5.5	13.58	
3	1.8×10^{-9}	gi|3891677|pdb|1BE9|A Chain A, The Third Pdz Domain From The Synaptic Protein Psd-95 In Complex With A C-Terminal Peptide Derived From Cript.	37	5.1	12.72	
4	2.5×10^{-9}	gi|27664048|ref|XP_213753.1| PREDICTED: similar to DNA-directed RNA polymerase II 13.3 kDa polypeptide (RPB11) [Rattus norvegicus]	28	5.6	13.33	
5	2.8×10^{-7}	gi|51854249|ref|NP_001004095.1| S100 calcium binding protein A11 [Rattus norvegicus]	44	5.6	11.22	
6	8.9×10^{-7}	gi|16758754|ref|NP_446336.1| ATPase, H+ transporting, V1 subunit F [Rattus norvegicus]	48	5.5	13.35	
+7	1.4×10^{-6}	gi|643039|emb|CAA57089.1| variable region-alpha RAV4.25 [Rattus norvegicus]	32	5.0	10.05	
	-	gi|643041|emb|CAA57090.1| variable region-alpha RAV4.26 [Rattus norvegicus]	32	5.3	10.02	
	-	gi|9857600|dbj|BAB11956.1| prepro-des-Gln14-ghrelin [Rattus norvegicus]	34	5.6	13.09	
	-	gi|52695719|pdb|1TDQ|B Chain B, Structural Basis For The Interactions Between Tenascins And The C-Type Lectin Domains From Lecticans: Evidence For A Cross-Linking Role For Tenascins	28	5.0	15.98	
	-	gi|13786138|ref|NP_112608.1| t-complex testis expressed 1 [Rattus norvegicus]	14	5.0	12.66	



-	gi|11067387|ref|NP_067701.1| ghrelin precursor [Rattus norvegicus]	33	5.6	13.22
-	gi|2143802|pir||I57802 Ig lambda2-like chain - rat (fragment)	28	5.1	8.89
-	gi|5830494|emb|CAB54560.1| cysteine sulfinate decarboxylase [Rattus norvegicus]	31	5.6	12.27
-	gi|643047|emb|CAA57093.1| variable region-alpha RAV4.33 [Rattus norvegicus]	22	4.9	10.19
-	gi|47087087|ref|NP_998732.1| zinc ribbon domain containing 1 [Rattus norvegicus]	24	4.9	14.08
-	gi|643027|emb|CAA57083.1| variable region-alpha RAV4.12 [Rattus norvegicus]	19	5.5	9.93
-	gi|643031|emb|CAA57085.1| variable region-alpha RAV4.14 [Rattus norvegicus]	19	5.5	10.01
-	gi|5327243|emb|CAB46337.1| RT1-A [Rattus norvegicus]	24	5.4	8.21
-	gi|19110875|gb|AAL85327.1|AF474162_1 global ischemia induced gene GIIG15B [Rattus norvegicus]	49	4.8	8.36
-	gi|31542843|ref|NP_598305.2| homeobox only domain [Rattus norvegicus]	49	4.8	8.38
-	gi|203355|gb|AAA40888.1| CCAAT binding transcription factor-B subunit	25	4.9	16.51
-	gi|205574|gb|AAA41652.1| myosin heavy chain	18	5.3	15.40
-	gi|643051|emb|CAA57095.1| variable region-alpha RAV4.35 [Rattus norvegicus]	22	5.2	10.24
-	gi|544788|gb|AAB29567.1| platelet-derived growth factor beta-receptor, PDGF beta receptor [rats, Rat-1 cells, Peptide Partial, 102 aa]	36	4.9	11.43
-	gi|53733524|gb|AAH83728.1| Similar to Ubiquitin-like protein SMT3A precursor (Ubiquitin-related protein SUMO-2) [Rattus norvegicus]	11	5.6	12.55
-	gi|13242275|ref|NP_077350.1| myotrophin [Rattus norvegicus]	31	5.3	13.01
-	gi|5852192|gb|AAD53965.1| GTP-binding protein [Rattus norvegicus]	25	5.5	13.18
-	gi|27666688|ref|XP_213616.1| PREDICTED: similar to Stefin homolog [Rattus norvegicus]	25	5.7	11.07

-	gi|688395|gb|AAB31189.1| zinc finger transcription factor; Kid-1 [Rattus sp.]	41	5.4	12.68
-	gi|6685834|sp|Q9WVB1|RAB6A_RAT Ras-related protein Rab-6A (Rab-6)	12	5.3	15.87

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B71C303B-032C-672D2D52

Sequences 20092

Date & Time Wed Jan 24 21:16:08 2007 UTC (Search Time: 0.28 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 8 - 17 kDa

pI Range 4.8 -5.8

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 704.537 710.546 719.427 721.466 724.504 729.544 734.437
737.447 739.475 743.485 748.517 749.455 752.459 757.429
763.585 765.537 768.517 772.567 779.498 781.471 787.498
793.435 794.439 798.519 804.421 805.451 813.487 816.617
822.411 824.534 826.466 832.451 838.516 840.523 848.419
854.542 860.628 866.498 879.454 881.450 883.528 889.476
890.499 899.513 905.515 907.499 913.507 919.738 920.432
922.515 929.494 935.513 937.468 943.450 944.504 947.504
953.518 955.513 961.699 962.555 963.577 969.496 979.555
988.798 989.581 993.521 999.531 1002.510 1018.528
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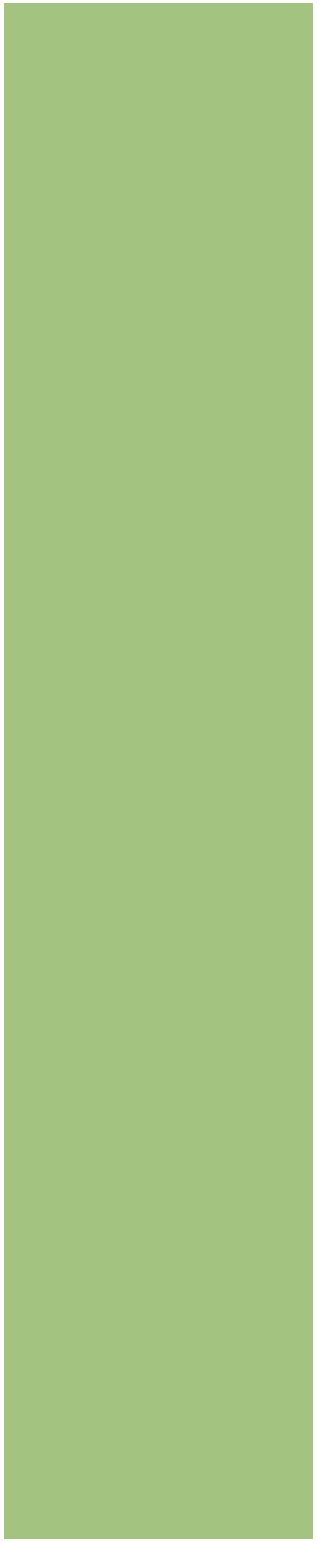

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1147.555	1150.543	1154.541	1156.553	1162.763	1163.589
1173.549	1177.540	1186.632	1187.606	1190.553	1196.644
1203.801	1204.525	1207.632	1211.588	1219.588	1220.599
1228.652	1230.564	1234.627	1238.627	1245.694	1246.597
1251.615	1254.736	1260.631	1268.145	1270.758	1284.614
1291.739	1292.683	1298.666	1301.651	1307.704	1314.795
1317.725	1328.668	1329.674	1336.702	1347.650	1351.655
1364.702	1372.669	1373.717	1381.686	1390.732	1397.769
1400.790	1408.661	1409.671	1415.591	1417.770	1425.103
1427.594	1430.699	1433.756	1436.739	1443.815	1445.759
1450.677	1454.756	1461.722	1462.803	1465.714	1468.781
1482.745	1500.735	1501.831	1504.806	1514.850	1516.684
1522.772	1528.767	1535.723	1543.832	1555.864	1558.733
1566.769	1571.783	1579.719	1583.842	1591.782	1595.840
1599.742	1603.837	1611.828	1613.855	1619.620	1627.786
1628.791	1637.823	1647.592	1648.767	1654.786	1657.800
1665.896	1668.865	1677.071	1677.871	1684.800	1688.920
1696.786	1698.118	1702.810	1724.828	1729.892	1734.684
1742.826	1750.958	1753.804	1762.754	1773.824	1782.625
1784.900	1787.831	1795.868	1796.953	1801.837	1813.803
1823.825	1829.983	1830.876	1848.927	1857.013	1862.879
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1913.849	1919.892	1932.008	1936.895	1940.898	1949.034
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2091.820	2095.147	2101.039	2112.259	2115.944	2120.004
2130.995	2142.014	2146.006	2150.125	2152.000	2161.194
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2282.160	2292.177	2296.145	2308.070	2312.116	2315.161
2320.998	2324.211	2327.070	2338.846	2352.383	2362.390
2367.270	2378.097	2395.207	2399.033	2408.146	2411.056
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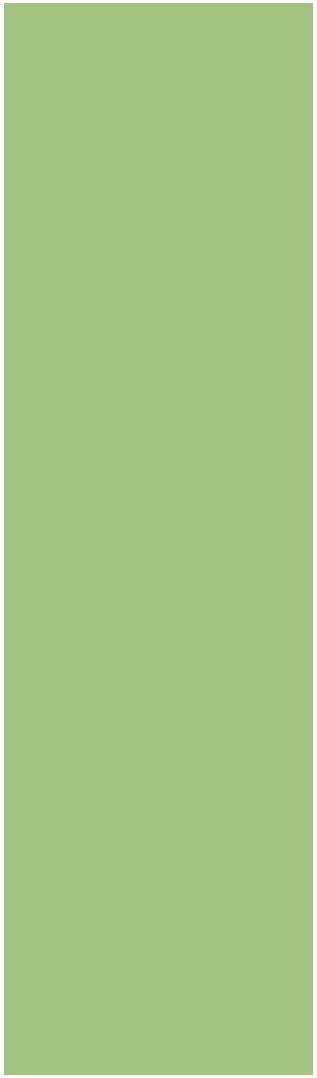

	2522.279	2533.319	2538.169	2549.279	2553.293	2564.197
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	2641.102	2645.362	2652.296	2663.235	2666.608	2677.332
	2689.371	2694.229	2704.168	2707.216	2717.847	2721.465
	2727.302	2741.110	2747.250	2757.180	2767.767	2774.504
	2779.332	2789.356	2800.432	2806.317	2811.280	2824.761
	2831.102	2842.404	2851.103	2861.436	2864.427	2873.304
	2888.273	2895.482	2903.462	2907.384	2918.292	2928.491
	2931.590	2936.662	2946.747	2950.369	2960.587	2968.620
	2979.421	2982.400	2987.332	2991.568	3002.411	3008.283
	3020.601	3030.977	3034.353	3043.860	3054.351	3065.195
	3069.561	3074.751	3091.135	3096.568	3108.539	3111.808
	3115.342	3128.441	3141.342	3145.156	3158.394	3161.386
	3165.062	3177.468	3188.529	3200.333	3204.526	3213.877
	3228.369	3245.234	3248.650	3261.219	3265.606	3276.781
	3279.365	3283.379	3287.280	3292.419	3303.484	3307.591
	3316.236	3330.102	3341.074	3344.698	3349.803	3353.743
	3366.592	3376.019	3380.993	3386.871	3399.626	3409.493
	3423.986	3426.904	3441.354	3457.894	3461.857	3474.117
	3487.393	3507.196	3519.015	3530.576	3535.862	3550.098
	3565.168	3569.031	3574.788	3594.998	3604.255	3618.426
	3638.149	3645.793	3658.292	3662.735	3673.998	

Tolerance (mon)	8.00 ppm
Number of Peptides	440

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Macromolecules

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	6.5×10^{-24}	gi|8248633|gb|AAB29536.2| heat shock protein 27 [Rattus norvegicus]	48	6.1	22.86	
	-	gi|1170367|sp|P42930|HSPB1_RAT Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27)	48	6.1	22.93	
2	1.2×10^{-7}	gi|13592152|ref|NP_112416.1| glutathione S-transferase, mu type 3 [Rattus norvegicus]	20	6.9	25.83	
3	1.3×10^{-4}	gi|40217491|dbj|BAD05179.1| ankyrin repeat small protein [Rattus norvegicus]	14	5.6	25.39	
4	3.0×10^{-4}	gi|11693154|ref|NP_071782.1| platelet-activating factor acetylhydrolase alpha 2 subunit [Rattus norvegicus]	13	5.6	25.73	
5	3.3×10^{-4}	gi|27682181|ref|XP_219746.1| PREDICTED: similar to Three prime repair exonuclease 2 (3-5 exonuclease TREX2) [Rattus norvegicus]	14	5.2	26.45	
6	3.6×10^{-4}	gi|1943431|pdb|6GSU|A Chain A, First-Sphere And Second-Sphere Electrostatic Effects In The Active Site Of A Class Mu Glutathione Transferase	12	8.6	25.91	
7	8.1×10^{-4}	gi|34866849|ref|XP_216949.2| PREDICTED: similar to Exosome complex exonuclease RRP41 (Ribosomal RNA-processing protein 41) (Exosome component 4) (p12A) [Rattus norvegicus]	11	5.7	26.66	
8	2.3×10^{-3}	gi|286206|dbj|BAA03318.1| calcineurin B [Rattus sp.]	12	5.0	25.08	
9	3.4×10^{-3}	gi|19424180|ref|NP_598212.1| preimplantation protein 3 [Rattus norvegicus]	14	5.5	26.53	
10	8.6×10^{-3}	gi|34880612|ref|XP_228900.2| PREDICTED: similar to myosin light chain 1 slow a [Rattus norvegicus]	16	5.8	27.67	
11	0.025	gi|25453412|ref|NP_620430.1| glutathione S-transferase, pi 2 [Rattus norvegicus]	22	6.9	23.65	
12	0.67	gi|16758972|ref|NP_446050.1| nudix-type motif 4 [Rattus norvegicus]	21	6.0	20.35	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Tue Feb 20 18:22:04 2007 UTC (Search Time: 0.39 sec.)

Sample ID 20040813 richardson NIA set 1 spot 2201 CONSENSUS search

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 28 kDa

pI Range 5.0 -9.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 704.671 706.404 710.412 718.895 719.400 725.490 728.463 732.388 737.383
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906.460 917.470 920.487 923.531 932.486 938.493 941.505 944.500 947.438
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1725.809 1731.884 1735.753 1744.375 1745.810 1753.893 1761.825 1773.914
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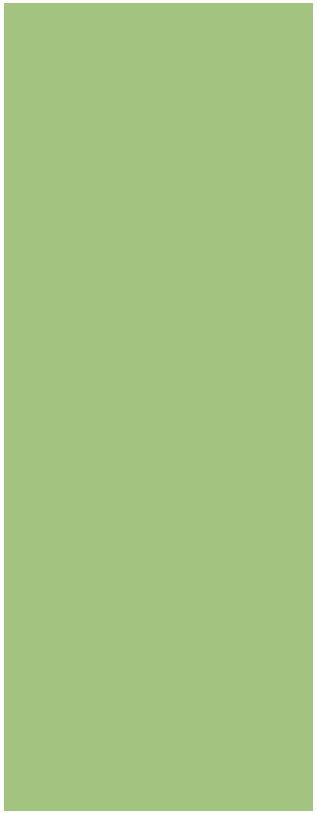
2053.949 2063.055 2065.931 2076.045 2079.146 2090.124 2093.111 2103.107
2107.093 2118.082 2119.943 2126.988 2138.060 2142.048 2150.067 2160.823



2170.007 2183.110 2192.152 2195.086 2204.025 2208.043 2220.181 2223.071
2232.195 2234.104 2237.161 2246.251 2258.142 2265.125 2274.078 2279.156
2282.115 2291.522 2294.102 2311.039 2314.149 2323.231 2327.226 2353.132
2364.190 2366.221 2377.145 2385.001 2397.156 2399.069 2409.177 2418.377
2424.145 2436.100 2440.358 2446.118 2456.124 2470.133 2481.161 2487.239
2501.403 2510.239 2521.795 2524.300 2534.973 2540.199 2546.553 2550.192
2560.374 2565.183 2568.426 2573.174 2590.359 2596.259 2621.242 2630.079
2641.217 2653.454 2664.293 2667.389 2679.163 2691.313 2695.369 2705.242
2717.345 2723.319 2735.393 2742.198 2746.222 2759.230 2763.337 2773.370
2780.400 2784.238 2795.306 2805.753 2809.395 2822.445 2826.348 2831.401
2841.377 2852.449 2859.147 2868.522 2878.454 2884.567 2889.346 2902.217
2904.432 2915.445 2927.573 2937.352 2943.307 2948.646 2951.574 2956.774
2966.859 2970.346 2980.491 2992.347 2995.998 3003.637 3009.364 3019.093
3020.129 3025.612 3035.924 3039.601 3054.032 3065.624 3078.172 3082.584
3088.760 3097.455 3111.984 3117.662 3142.506 3146.322 3157.481 3161.647
3171.126 3177.580 3187.844 3199.343 3204.719 3211.360 3218.657 3230.288
3242.708 3257.728 3262.190 3265.809 3277.410 3288.953 3292.819 3304.854
3315.709 3321.065 3324.910 3336.654 3354.854 3367.667 3380.817 3405.976
3410.499 3429.018 3446.281 3450.989 3466.085 3478.591 3483.998 3493.190
3506.104 3519.480 3530.320 3541.377 3552.853 3558.236 3561.894 3574.933
3578.559 3593.164 3614.517 3627.165 3646.909 3660.632 3674.177 3680.672
3690.692

Tolerance (mon) 19.00 ppm

Number of Peptides 432

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- X! Hunter
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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	5.3×10^{-4}	gi|205595|gb|AAA41657.1| myosin heavy chain	41	5.2	44.90	
+2	1.0×10^{-3}	gi|2507388|sp|P09006|CPI6_RAT Contrapsin-like protease inhibitor 6 precursor (CPI-26) (Serine protease inhibitor 3) (SPI-3) (SPI-2.2)	38	5.3	46.81	
	-	gi|13928716|ref|NP_113719.1| serine protease inhibitor 2c [Rattus norvegicus]	43	5.4	45.65	
	-	gi|3169626|gb|AAC17905.1| 7acomp protein [Rattus sp.]	28	5.9	48.21	
	-	gi|38454312|ref|NP_942084.1| basic leucine zipper and W2 domains 1 [Rattus norvegicus]	32	5.7	48.20	
	-	gi|57012388|ref|NP_001008815.1| type II keratin Kb20 [Rattus norvegicus]	28	5.9	51.05	
	-	gi|16758790|ref|NP_446362.1| pleckstrin homology, Sec7 and coiled/coil domains 1 [Rattus norvegicus]	27	5.5	46.71	
	-	gi|38181888|gb|AAH61542.1| Proteasome (prosome, macropain) 26S subunit, ATPase 2 [Rattus norvegicus]	33	5.7	49.00	
	-	gi|15100181|ref|NP_150239.1| proteasome (prosome, macropain) 26S subunit, ATPase 2 [Rattus norvegicus]	33	5.6	48.96	
	-	gi|19173736|ref|NP_596874.1| serine carboxypeptidase 1 [Rattus norvegicus]	27	5.4	51.44	
	-	gi|56605766|ref|NP_001008345.1| eukaryotic translation termination factor 1 [Rattus norvegicus]	40	5.5	49.24	
	-	gi|37788073|gb|AAO65547.1| brain and heart protein NDRG4-C2 [Rattus norvegicus]	27	5.5	43.30	
	-	gi|18202478|sp|P97738|NPTX2_RAT Neuronal pentraxin-2 precursor (NP2) (Neuronal pentraxin II) (NP-II) (Neuronal activity-regulated pentraxin)	15	5.5	47.81	

NOTE:

1. To search again using unmatched masses, click the symbol ◉.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A32811EF-1720-5339195E

Sequences 20092

Date & Time Wed Jan 24 22:00:17 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 42 - 52 kDa

pI Range 5.0 -6.0

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 706.396 711.373 712.324 714.299 719.322 722.391 726.445
731.310 734.459 739.296 741.382 743.397 748.392 752.408
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786.410 791.302 792.476 798.507 804.333 811.425 817.432
819.414 822.401 825.451 831.471 833.431 836.852 840.494
849.428 854.513 857.484 864.490 878.509 884.500 885.500
890.471 892.499 898.518 904.435 905.447 907.533 916.451
921.508 932.629 939.420 945.471 946.526 952.517 955.509
961.507 964.576 968.529 974.420 977.447 983.556 989.536
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1011.603 1017.818 1018.376 1023.600 1034.499 1038.484
1044.520 1051.512 1055.530 1061.550 1067.565 1079.668
1081.504 1088.551 1091.528 1097.694 1098.608 1100.594
1102.582 1109.586 1113.624 1120.010 1120.551 1123.571
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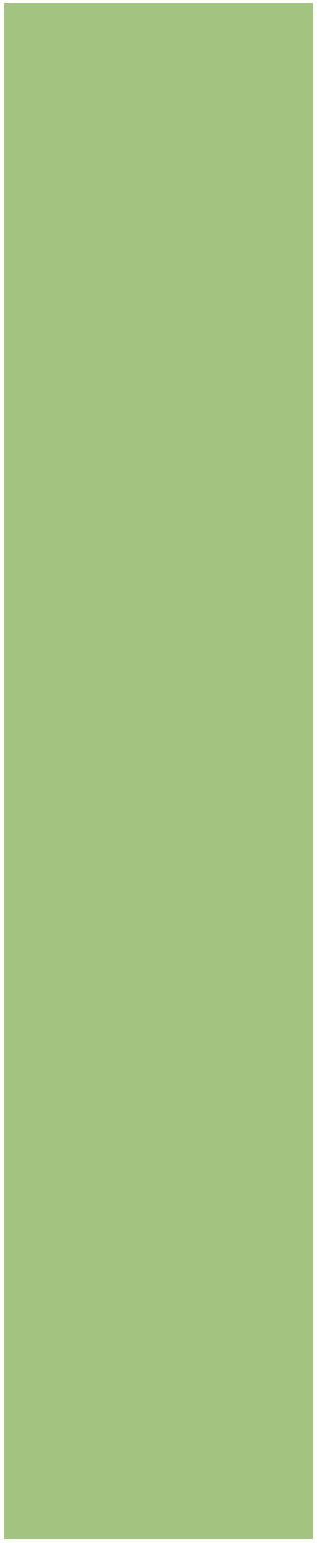

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1254.032	1254.557	1262.626	1267.558	1274.684	1282.650
1291.462	1294.560	1298.729	1303.730	1310.689	1313.639
1326.648	1334.480	1335.709	1341.669	1348.605	1349.792
1352.687	1355.684	1360.769	1362.656	1369.871	1372.289
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1411.714	1418.602	1425.785	1435.256	1436.659	1443.837
1444.553	1451.366	1454.702	1462.801	1466.768	1470.870
1477.693	1484.688	1485.752	1492.740	1497.790	1506.138
1506.765	1515.689	1523.850	1531.797	1534.432	1538.813
1545.687	1552.788	1554.858	1558.709	1565.786	1569.785
1576.834	1584.784	1591.867	1592.834	1599.747	1602.818
1609.915	1612.563	1616.810	1624.806	1628.852	1633.801
1642.711	1651.236	1651.838	1657.616	1665.932	1667.307
1669.754	1673.773	1677.769	1684.754	1692.860	1701.070
1703.820	1711.917	1713.756	1724.644	1725.762	1730.801
1738.793	1742.782	1751.647	1754.805	1757.852	1766.162
1766.784	1770.862	1773.895	1781.958	1782.754	1790.695
1791.891	1800.167	1801.824	1809.635	1812.845	1820.823
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1999.747	2002.669	2009.697	2018.855	2023.941	2031.978
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2089.820	2096.568	2101.042	2104.995	2112.851	2122.023
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2162.985	2170.132	2174.967	2184.998	2188.431	2192.245
2196.063	2206.711	2220.178	2224.179	2233.082	2242.608
2252.219	2254.169	2260.249	2269.192	2271.085	2280.821
2284.232	2295.771	2308.471	2313.231	2317.120	2321.272
2330.692	2339.676	2343.229	2353.085	2362.996	2367.320
2376.177	2386.662	2390.151	2398.985	2408.132	2416.204
2422.068	2431.194	2435.712	2445.029	2446.795	2451.162
2460.775	2468.500	2480.496	2488.117	2498.174	2504.137
2511.153	2519.768	2528.940	2531.108	2541.217	2555.227
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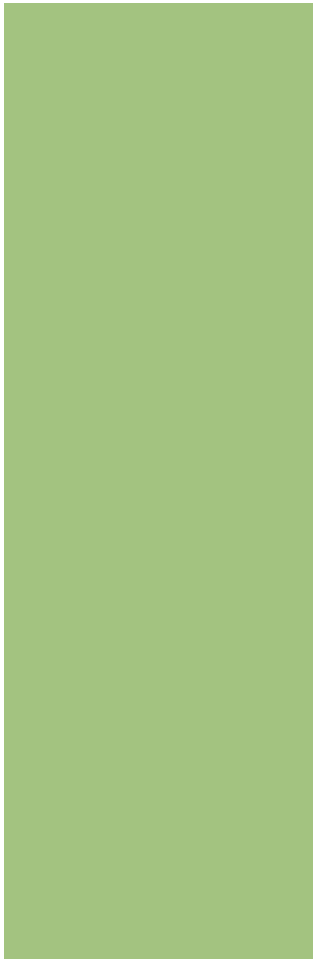

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2818.435	2829.210	2838.858	2848.666	2853.090	2860.472
2870.678	2885.641	2892.883	2905.834	2910.558	2921.253
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2969.149	2974.254	2986.943	2999.291	3012.736	3018.212
3026.286	3037.341	3041.910	3054.147	3068.387	3079.219
3084.568	3096.253	3100.079	3111.117	3122.815	3128.314
3136.233	3142.575	3149.604	3161.601	3164.367	3170.510
3182.814	3188.518	3200.589	3219.370	3230.542	3238.857
3250.870	3255.059	3260.981	3272.380	3283.450	3287.351
3294.656	3305.649	3316.621	3321.744	3334.104	3339.709
3343.564	3356.902	3363.698	3371.557	3383.578	3388.792
3398.487	3407.291	3416.461	3428.996	3440.289	3445.231
3457.224	3468.841	3472.533	3476.504	3489.070	3496.396
3509.915	3515.466	3530.462	3541.640	3544.769	3559.224
3564.613	3581.166	3587.176	3599.090	3602.486	3616.776
3624.114	3638.040	3656.106	3675.441	3683.043	3695.976

Tolerance (mon) 21.00 ppm

Number of Peptides 453

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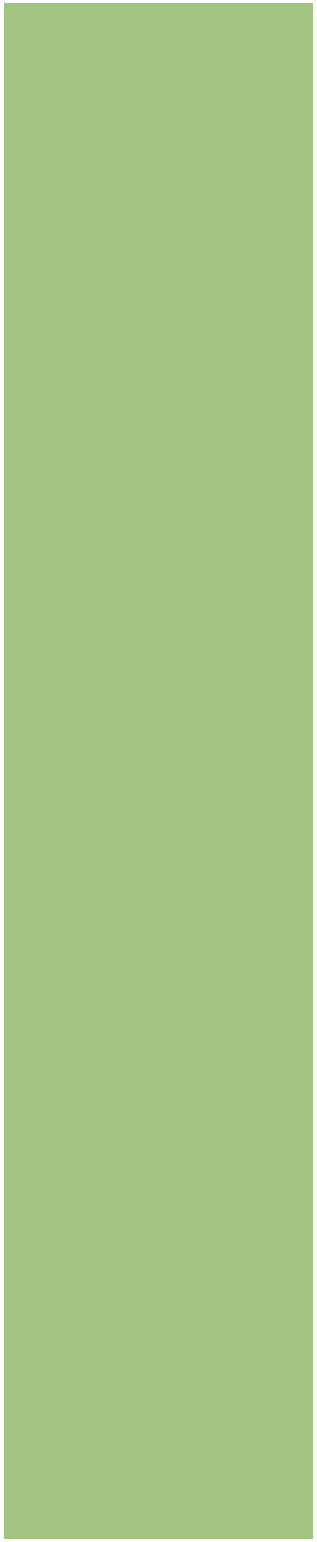
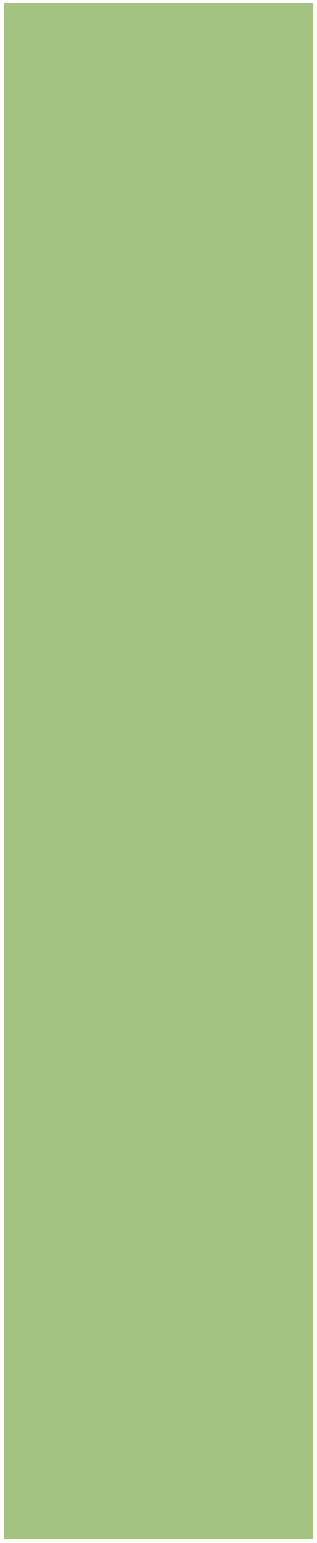
Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	$2.7?0^{-6}$	gi|23463271|ref|NP_695209.1| COP9 (constitutive photomorphogenic) homolog, subunit 2 [Rattus norvegicus]	53	5.4	51.86	
2	$5.0?0^{-5}$	gi|25742837|ref|NP_446009.1| protein arginine N-methyltransferase 3 [Rattus norvegicus]	53	5.0	60.09	
3	$2.5?0^{-4}$	gi|37784494|gb|AAO60218.1| MTSG1 346aa isoform [Rattus norvegicus]	50	5.8	40.19	
4	$3.3?0^{-4}$	gi|5802541|gb|AAD51699.1| calpain isoform Rt88' [Rattus norvegicus]	51	5.5	57.31	
5	$4.2?0^{-4}$	gi|44921592|gb|AAS49162.1| SCI-related protein [Rattus norvegicus]	47	5.3	57.65	
6	$6.7?0^{-4}$	gi|23618920|ref|NP_112339.1| PCTAIRE protein kinase 1 isoform b [Rattus norvegicus]	51	6.3	52.85	
7	$7.3?0^{-4}$	gi|13027473|ref|NP_076491.1| MRS2-like, magnesium homeostasis factor [Rattus norvegicus]	48	6.1	49.63	
8	$1.4?0^{-3}$	gi|56905|emb|CAA30916.1| unnamed protein product [Rattus norvegicus]	40	6.4	57.06	
9	$1.7?0^{-3}$	gi|6714522|dbj|BAA89475.1| dihydropyrimidinase-related protein [Rattus norvegicus]	46	6.5	61.89	
10	$2.1?0^{-3}$	gi|56119147|ref|NP_001007798.1| arrestin domain containing 3 [Rattus norvegicus]	41	6.0	46.85	
11	$2.2?0^{-3}$	gi|27692054|ref|XP_227318.1| PREDICTED: similar to tigger transposable element derived 4 [Rattus norvegicus]	43	5.7	58.06	
12	$3.9?0^{-3}$	gi|17902245|gb|AAL47844.1|AF450298_1 EZRIN [Rattus norvegicus]	43	6.2	54.27	
13	$4.4?0^{-3}$	gi|13242285|ref|NP_077358.1| serine (or cysteine) proteinase inhibitor, clade D, member 1 [Rattus norvegicus]	47	6.5	54.76	



14	4.6?0^{-3}	gi|51890219|ref|NP_001004078.1| chaperonin containing TCP1, subunit 5 (epsilon) [Rattus norvegicus]	40	5.5	59.98
15	4.8?0^{-3}	gi|51854223|ref|NP_001004077.1| glucokinase activity, related sequence 2 [Rattus norvegicus]	38	5.1	61.97
16	4.9?0^{-3}	gi|20302020|ref|NP_620217.1| spermatogenesis-associated protein 7 [Rattus norvegicus]	46	5.8	60.36
+17	5.9?0^{-3}	gi|123513|sp|P06866|HPT_RAT Haptoglobin precursor [Contains: Haptoglobin alpha chain; Haptoglobin beta chain]	46	6.1	39.04
	-	gi|33086640|gb|AAP92632.1| Ba1-647 [Rattus norvegicus]	39	6.1	43.08
	-	gi|204655|gb|AAA41348.1| haptoglobin (Hp)	42	6.3	39.11
18	6.6?0^{-3}	gi|51948518|ref|NP_001004275.1| COP9 signalosome subunit 4 [Rattus norvegicus]	50	5.6	46.56
19	8.9?0^{-3}	gi|34879586|ref|XP_225769.2| PREDICTED: similar to glycerol kinase-like 1 [Rattus norvegicus]	40	5.3	61.09
+20	0.012	gi|34098962|ref|NP_036753.3| 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 1 [Rattus norvegicus]	44	6.3	55.38
	-	gi|119751|sp|P07953|F261_RAT 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 1 (6PF-2-K/Fru-2,6-P2ASE liver isozyme) [Includes: 6-phosphofructo-2-kinase ; Fructose-2,6-bisphosphatase]	44	6.3	55.32
	-	gi|56922|emb|CAA33606.1| unnamed protein product [Rattus norvegicus]	41	6.0	52.62
	-	gi|7434494|pir||S77704 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) clone 5c, skeletal muscle - rat	42	6.4	54.83
	-	gi|55824719|gb|AAH86510.1| Snx25 protein [Rattus norvegicus]	37	5.5	61.42
	-	gi|16758148|ref|NP_445863.1| sorting nexin 1 [Rattus norvegicus]	36	5.2	59.14
	-	gi|27715247|ref|XP_233266.1| PREDICTED: hypothetical protein [Rattus norvegicus]	36	5.1	63.96
	-	gi|21426787|ref|NP_653355.1| calcium activated nucleotidase 1 [Rattus norvegicus]	47	6.2	45.70



-	gi|54035324|gb|AAH83853.1| Crystallin, zeta (quinone reductase)-like 1 [Rattus norvegicus]	44	5.6	39.05
-	gi|56847624|ref|NP_001008753.1| keratin complex 1, acidic, gene 23 [Rattus norvegicus]	39	5.7	48.26
-	gi|13096481|pdb|1D4F|A Chain A, Crystal Structure Of Recombinant Rat-Liver D244e Mutant S- Adenosylhomocysteine Hydrolase	46	6.1	47.92
-	gi|51260613|gb|AAH78681.1| Carboxylesterase-like [Rattus norvegicus]	39	5.9	62.42
-	gi|40786436|ref|NP_955404.1| eukaryotic translation initiation factor 4A, isoform 1 [Rattus norvegicus]	50	5.3	46.36
-	gi|6981416|ref|NP_036765.1| peripherin [Rattus norvegicus]	45	5.4	53.65
-	gi|54673768|gb|AAH85123.1| RGD1309107 protein [Rattus norvegicus]	41	6.4	57.97
-	gi|50401219|sp|P62603|TRI26_RAT Tripartite motif-containing protein 26 (Zinc finger protein 173)	43	5.0	63.53
-	gi|57012378|ref|NP_001008810.1| type II keratin Kb26 [Rattus norvegicus]	50	6.0	58.52
-	gi|585364|sp|P37285|KLC1_RAT Kinesin light chain 1 (KLC 1)	41	5.8	63.69
-	gi|9506963|ref|NP_062245.1| protein phosphatase 2C, magnesium-dependent, catalytic subunit [Rattus norvegicus]	38	6.3	61.76
-	gi|6981396|ref|NP_037313.1| protein kinase, cAMP dependent regulatory, type I, alpha [Rattus norvegicus]	43	5.3	43.31
-	gi|34865922|ref|XP_236627.2| PREDICTED: similar to MON1 homolog A [Rattus norvegicus]	25	5.8	62.48
-	gi|4139571|pdb|1B3R|A Chain A, Rat Liver S-Adenosylhomocystein Hydrolase	39	6.1	47.90
-	gi|8392878|ref|NP_058897.1| S-adenosylhomocysteine hydrolase [Rattus norvegicus]	39	6.1	48.03
-	gi|58000421|ref|NP_001009972.1| gametogenetin-binding protein 1 [Rattus norvegicus]	43	5.8	41.24

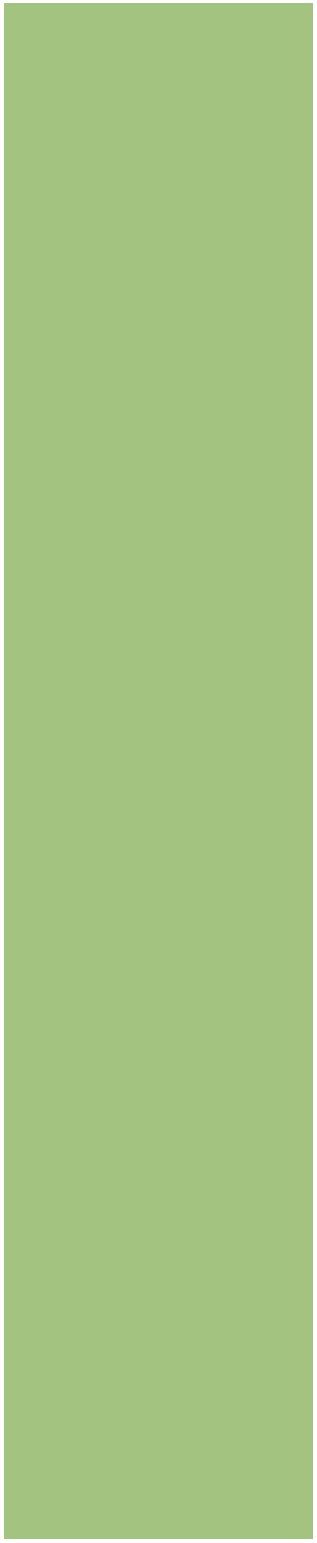
-	gi|34878802|ref|XP_226031.2| PREDICTED: similar to Transcription initiation factor TFIID subunit 7 (Transcription initiation factor TFIID 55 kDa subunit) (TAF(II)55) (TAFII-55) (TAFII55) [Rattus norvegicus]	38	5.2	39.16
-	gi|50925859|gb|AAH79304.1| Tektin 4 [Rattus norvegicus]	49	5.8	52.76
-	gi|34536836|ref|NP_620245.2| EH-domain containing 3 [Rattus norvegicus]	39	6.0	60.83
-	gi|38511542|gb|AAH61802.1| Fibp protein [Rattus norvegicus]	42	6.3	41.50
-	gi|415898|emb|CAA81642.1| heat shock rotein 70 [Rattus rattus]	55	5.6	50.50
-	gi|57012336|ref|NP_001008803.1| type II keratin Kb22 [Rattus norvegicus]	39	5.5	55.72
-	gi|16923972|ref|NP_476464.1| peptidase (prosome, macropain) 26S subunit, ATPase 1 [Rattus norvegicus]	45	5.9	49.34
-	gi|55249675|gb|AAH85725.1| Capn10 protein [Rattus norvegicus]	45	5.6	41.41
-	gi|33086584|gb|AAP92604.1| Ab2-379 [Rattus norvegicus]	37	5.2	62.34
-	gi|18426834|ref|NP_569095.1| coronin, actin binding protein 1A [Rattus norvegicus]	29	6.1	51.73
-	gi|55562834|gb|AAH86371.1| Nedd4l protein [Rattus norvegicus]	42	5.3	52.00
-	gi|3676244|emb|CAA09721.1| DNA polymerase alpha subunit II [Rattus norvegicus]	34	5.8	55.50
-	gi|46237572|emb|CAE83952.1| butyrophilin-like 5 [Rattus norvegicus]	43	5.4	45.67
-	gi|50926983|gb|AAH79135.1| Similar to RIKEN cDNA 1810060J02 [Rattus norvegicus]	35	5.0	50.32
-	gi|20137191|sp|Q91Y80|3BP5_RAT SH3 domain-binding protein 5 (Vascular endothelial cell-specific protein 18)	34	5.3	47.35

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id	A3014387-1748-A3BE7A22
Sequences	20092
Date & Time	Wed Jan 24 00:15:45 2007 UTC (Search Time: 0.61 sec.)
Sample ID	
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	38 - 64 kDa
pI Range	5.0 -6.5
Digestion	Trypsin
Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +HPO3@ST(Partial);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	711.448 719.451 720.425 724.509 729.404 732.421 734.442 740.486 743.416 748.448 751.468 754.420 764.481 765.448 768.502 775.415 778.489 784.448 786.483 793.495 796.510 798.503 804.462 814.449 819.466 822.472 824.498 830.708 831.484 833.483 836.864 841.482 849.480 856.511 862.505 864.482 879.496 882.550 888.515 891.484 903.513 905.476 917.538 921.536 933.499 940.541 942.563 949.556 951.547 955.514 962.555 963.516 968.596 979.576 988.904 989.560 990.597 993.564 996.620 1003.576 1018.528 1020.547 1023.623 1033.872 1034.521 1035.581 1038.528 1044.542 1051.686 1057.847 1059.599 1066.618 1067.695 1074.565 1078.671 1085.620 1088.593 1091.569 1098.627 1104.590 1107.566 1113.867 1114.585 1125.574 1132.877 1133.579 1134.599 1138.614 1141.499 1148.580 1153.648 1164.667 1173.617 1187.627 1190.667 1201.675 1209.666 1211.656 1218.599 1221.631 1226.670 1234.673 1241.705 1243.674 1250.875 1251.613 1254.758 1262.039 1262.636 1263.689 1270.708 1271.692 1285.697 1287.677 1294.738 1298.712 1302.668 1308.699 1315.720 1317.698 1327.734 1332.643 1348.710 1353.707 1372.742 1374.737 1382.734 1390.755



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1463.754	1469.760	1483.780	1500.812	1501.777	1504.804
1514.953	1517.706	1522.771	1530.056	1530.793	1533.771
1541.849	1555.784	1559.769	1567.809	1569.782	1577.767
1581.754	1584.834	1592.777	1596.890	1599.824	1607.750
1609.829	1613.830	1618.891	1623.825	1631.810	1634.912
1647.048	1647.813	1655.858	1658.818	1666.944	1672.832
1681.158	1682.815	1685.827	1688.841	1698.872	1705.789
1716.176	1724.974	1725.896	1730.907	1733.850	1741.905
1742.917	1751.811	1754.884	1763.214	1773.946	1783.032
1786.901	1790.946	1799.904	1801.904	1809.916	1812.897
1821.939	1829.851	1831.897	1846.856	1849.027	1852.909
1861.905	1866.993	1876.053	1880.985	1889.904	1898.138
1900.016	1910.922	1917.050	1922.006	1930.991	1935.966
1939.998	1944.954	1954.023	1962.993	1968.935	1977.041
1978.928	1986.034	1991.981	1995.018	2000.014	2009.089
2016.008	2022.060	2025.059	2033.948	2041.062	2047.974
2057.066	2059.083	2063.945	2072.091	2075.035	2080.991
2091.018	2097.028	2107.032	2109.073	2112.074	2120.967
2127.081	2137.063	2146.195	2148.130	2151.190	2156.066
2166.273	2170.099	2182.132	2185.090	2192.116	2195.082
2203.072	2220.144	2223.033	2232.188	2235.180	2245.093
2257.172	2266.109	2276.251	2280.012	2283.133	2292.250
2296.185	2310.117	2321.201	2326.233	2354.155	2367.278
2381.094	2393.335	2399.039	2409.243	2420.297	2424.143
2435.197	2445.245	2448.344	2454.179	2464.266	2477.255
2493.237	2503.235	2508.326	2517.306	2521.363	2528.300
2538.402	2544.412	2559.109	2562.449	2567.224	2583.150
2595.316	2608.129	2618.181	2623.284	2633.262	2645.164
2651.229	2664.943	2668.177	2678.379	2691.185	2695.239
2706.123	2716.959	2720.049	2723.246	2734.115	2737.214
2748.253	2752.279	2763.135	2766.640	2773.268	2778.234
2788.110	2791.880	2797.256	2807.379	2811.340	2818.414
2825.532	2835.491	2838.252	2841.302	2855.136	2865.543
2869.365	2880.159	2890.394	2896.188	2904.274	2914.805
2918.441	2930.055	2934.028	2942.349	2949.145	2953.351
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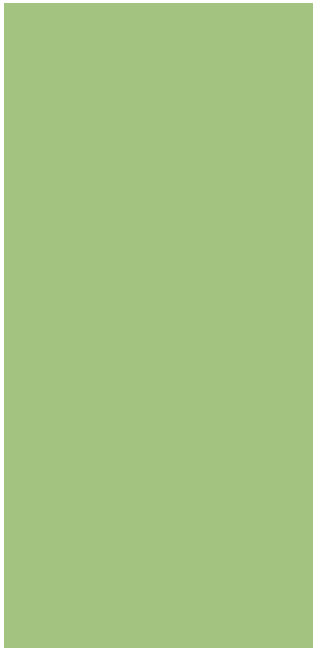

	3068.141 3079.934 3082.923 3093.994 3098.451 3112.215 3116.083 3127.138 3139.004 3148.097 3159.132 3165.224 3176.857 3188.132 3199.197 3202.242 3215.736 3220.240 3238.133 3249.245 3253.541 3264.064 3275.182 3286.086 3292.259 3303.539 3306.981 3312.050 3319.448 3324.915 3336.133 3338.970 3349.861 3353.093 3364.045 3377.946 3380.878 3392.032 3394.774 3398.928 3410.700 3423.436 3438.481 3447.950 3476.116 3487.938 3509.887 3528.310 3537.658 3559.198 3563.369 3566.981 3587.198 3614.576 3625.774 3648.262 3663.942 3668.009 3674.521 3691.928 3698.338
Tolerance (mon)	48.00 ppm
Number of Peptides	423

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New York, NY 10021
(212) 327-8000

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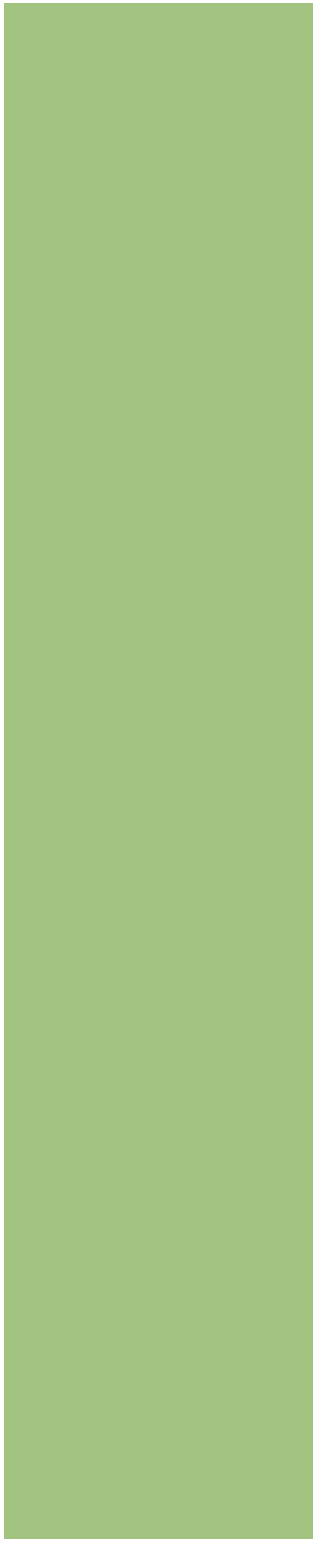
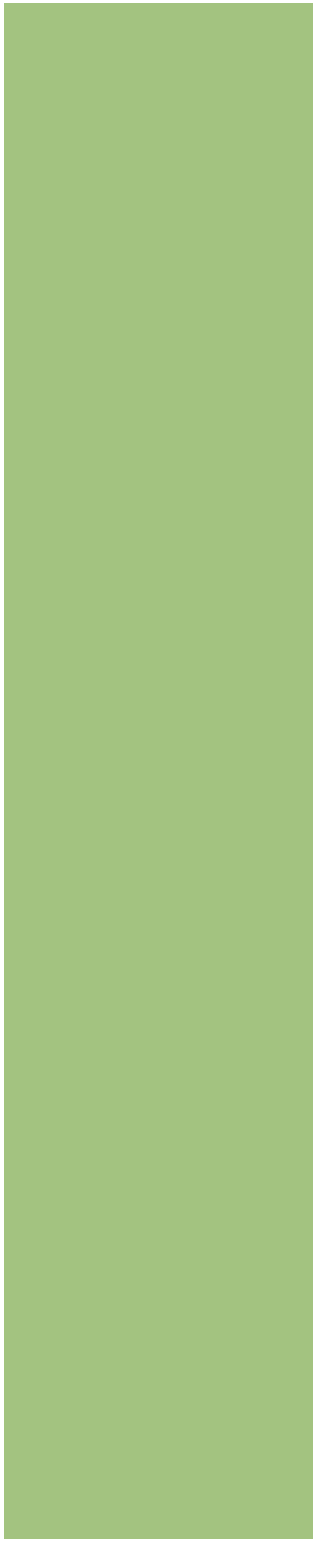
ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	4.2×10^{-12}	gi|205578|gb|AAA41654.1| cardiac myosin heavy chain 5	41	5.5	47.89	
-		gi|223466|prf||0807284A myosin H	28	5.4	49.48	
-		gi|205576|gb|AAA41653.1| cardiac myosin heavy chain 21/26	24	5.4	49.63	
+2	1.8×10^{-11}	gi|204197|gb|AAA41179.1| glucose-6-phosphate dehydrogenase	42	6.2	55.32	
-		gi|8393381|ref|NP_058702.1| glucose-6-phosphate dehydrogenase [Rattus norvegicus]	38	6.0	59.81	
-		gi|56605766|ref|NP_001008345.1| eukaryotic translation termination factor 1 [Rattus norvegicus]	42	5.5	49.24	
-		gi|23463271|ref|NP_695209.1| COP9 (constitutive photomorphogenic) homolog, subunit 2 [Rattus norvegicus]	36	5.4	51.86	
-		gi|50927301|gb|AAH78728.1| Spata7 protein [Rattus norvegicus]	42	5.7	55.86	
-		gi|16758204|ref|NP_445912.1| protein interacting with C kinase 1 [Rattus norvegicus]	33	5.3	47.04	
-		gi|49117334|gb|AAH72689.1| Protein interacting with C kinase 1 [Rattus norvegicus]	33	5.3	47.14	
-		gi|14150695|gb|AAK54603.1|AF373289_1 protein kinase C-binding protein PICK1 [Rattus norvegicus]	33	5.2	47.12	
-		gi|7434494|pir||S77704 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) clone 5c, skeletal muscle - rat	34	6.4	54.83	
-		gi|27465585|ref|NP_775151.1| keratin 20 [Rattus norvegicus]	31	5.3	49.43	
-		gi|57012388|ref|NP_001008815.1| type II keratin Kb20 [Rattus norvegicus]	36	5.9	51.05	



-	gi|6978809|ref|NP_036686.1| enolase 1, alpha [Rattus norvegicus]	35	6.2	47.44
-	gi|56605748|ref|NP_001008336.1| eukaryotic translation initiation factor 4A2 [Rattus norvegicus]	31	5.3	46.61
-	gi|34880703|ref|XP_234142.2| PREDICTED: similar to germ cell-less protein isoform 1 [Rattus norvegicus]	24	5.5	58.92
-	gi|36054040|ref|NP_110468.2| neuronal pentraxin receptor [Rattus norvegicus]	26	5.7	52.70
-	gi|18202030|sp|O35764|NPTXR_RAT Neuronal pentraxin receptor	26	5.8	52.81
-	gi|24308510|ref|NP_714957.1| neuronal pentraxin 1 [Rattus norvegicus]	33	6.3	47.71
-	gi|19924067|ref|NP_612541.1| nucleoside-diphosphate kinase 7 [Rattus norvegicus]	38	6.3	45.09
-	gi|20137191|sp|Q91Y80|3BP5_RAT SH3 domain-binding protein 5 (Vascular endothelial cell-specific protein 18)	27	5.3	47.35
-	gi|34862267|ref|XP_343156.1| PREDICTED: similar to Protein inhibitor of activated STAT protein 4 (Protein inhibitor of activated STAT protein gamma) (PIAS-gamma) (PIASy) [Rattus norvegicus]	28	5.9	56.46
-	gi|56757324|sp|P04764|ENOA_RAT Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	30	6.2	47.45
-	gi|38197558|gb|AAH61764.1| Dnajc3 protein [Rattus norvegicus]	27	6.2	50.68
-	gi|6981442|ref|NP_036769.1| protein tyrosine phosphatase, non-receptor type 1 [Rattus norvegicus]	40	5.8	50.28
-	gi|37805418|gb|AAH60314.1| Non-metastatic cells 7, protein expressed in [Rattus norvegicus]	37	6.3	45.06
-	gi|92459|pir||JC1103 lens fiber cell beaded-filament protein CP94 - rat (fragment)	27	5.4	59.16
-	gi|11560030|ref|NP_071568.1| protein kinase inhibitor p58 [Rattus norvegicus]	23	5.6	58.02



-	gi|56585031|gb|AAH87631.1| TRNA splicing endonuclease 2 homolog (S. cerevisiae) [Rattus norvegicus]	33	5.8	53.39
-	gi|32423788|gb|AAP81281.1| EG3RVC [Rattus norvegicus]	33	6.0	44.20
-	gi|8393340|ref|NP_058839.1| coagulation factor 10 [Rattus norvegicus]	22	5.3	55.62
-	gi|50926203|gb|AAH79267.1| Polymerase (DNA directed), delta 2, regulatory subunit [Rattus norvegicus]	26	5.3	51.96
-	gi|40786436|ref|NP_955404.1| eukaryotic translation initiation factor 4A, isoform 1 [Rattus norvegicus]	31	5.3	46.36
-	gi|6137441|pdb|3BIF|A Chain A, 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase Empty 6-Pf-2k Active Site	28	6.1	54.48
-	gi|46485098|tpg|DAA02218.1| TPA_exp: type II keratin Kb7 [Rattus norvegicus]	27	5.7	50.69
-	gi|2624499|pdb|1BIF| Chain , 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase Bifunctional Enzyme Complexed With Atp-G-S And Phosphate	28	6.1	54.61
-	gi|111518|pir||A37180 chromogranin/secretogranin-like vesicle protein precursor - rat	24	5.3	59.75
-	gi|16758642|ref|NP_446251.1| aspartyl-tRNA synthetase [Rattus norvegicus]	25	6.0	57.56
-	gi|57164007|ref|NP_001009176.1| tripartite motif-containing 10 [Rattus norvegicus]	18	5.7	56.92
-	gi|9506969|ref|NP_062206.1| 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 4 [Rattus norvegicus]	28	6.1	54.76
-	gi|56325|emb|CAA68545.1| unnamed protein product [Rattus norvegicus]	22	6.1	56.30
-	gi|3169626|gb|AAC17905.1| 7acomp protein [Rattus sp.]	24	5.9	48.21
-	gi|51259385|gb|AAH79183.1| Syntaxin 18 [Rattus norvegicus]	25	5.6	38.67
-	gi|39645155|gb|AAH63813.1| Gnn protein [Rattus norvegicus]	31	6.3	46.96
-	gi|5802541|gb|AAD51699.1| calpain isoform Rt88' [Rattus norvegicus]	33	5.5	57.31
-	gi|55583763|sp|Q6AYM2|TEKT2_RAT Tektin-2 (Testicular tektin) (Tektin-t)	30	5.8	50.73

-	gi|6729954|pdb|2BIF|A Chain A, 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase H256a Mutant With F6p In Phosphatase Active Site	26	6.0	54.54
-	gi|23618920|ref|NP_112339.1| PCTAIRE protein kinase 1 isoform b [Rattus norvegicus]	28	6.3	52.85

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AD0D4342-0D3C-B07A137A

Sequences 20092

Date & Time Wed Jan 24 00:59:46 2007 UTC (Search Time: 0.56 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 38 - 60 kDa

pI Range 5.2 -6.6

Digestion Trypsin

Missed Cuts 1

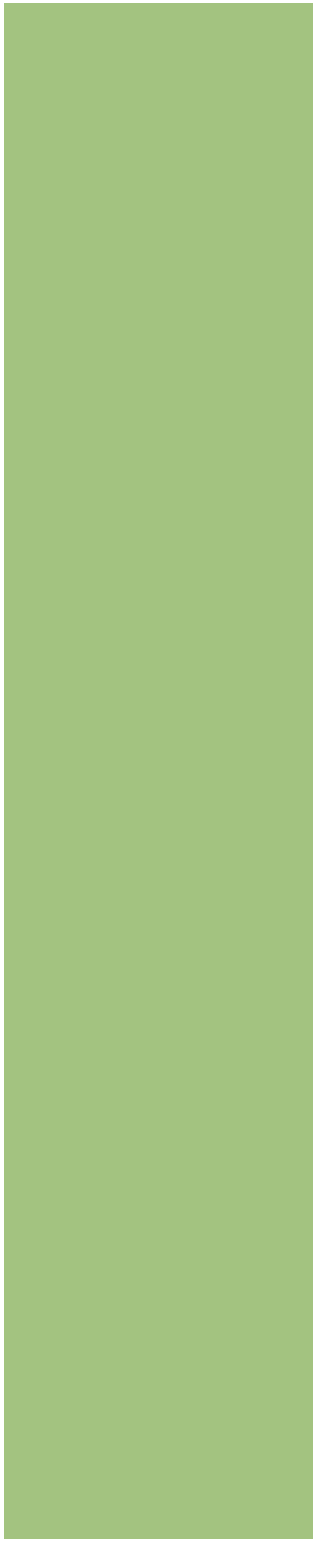
Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 707.395 712.250 717.409 723.418 724.395 726.369 731.415
734.436 739.383 740.261 743.447 749.399 754.414 763.491
764.420 768.423 774.436 778.484 780.436 786.931 787.459
788.441 793.433 796.448 803.428 813.428 819.481 821.427
824.513 830.375 832.430 836.860 840.483 848.437 854.482
858.497 864.498 878.476 882.567 889.454 890.458 893.491
902.500 904.522 906.506 916.497 919.493 922.534 932.490
934.524 940.477 943.532 949.534 952.562 955.513 961.511
963.514 968.532 980.607 986.493 992.588 994.560 997.575
1003.554 1018.570 1021.578 1023.601 1029.528 1034.521



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1097.336	1098.562	1104.591	1107.545	1113.621	1114.564
1124.515	1133.581	1136.574	1141.479	1148.560	1154.565
1160.586	1162.604	1172.905	1173.574	1176.595	1186.634
1200.629	1209.599	1212.620	1218.556	1225.614	1227.641
1234.653	1241.662	1249.619	1251.666	1254.691	1261.637
1263.694	1270.689	1273.641	1284.979	1285.678	1291.646
1298.645	1299.664	1307.634	1309.728	1311.702	1316.654
1327.667	1329.604	1337.691	1348.667	1351.659	1364.706
1372.824	1373.672	1380.916	1382.717	1389.658	1390.637
1399.612	1402.761	1410.714	1413.724	1417.725	1425.796
1426.787	1428.771	1435.802	1442.773	1449.736	1462.682
1465.695	1472.868	1473.747	1476.746	1479.748	1486.721
1487.734	1500.692	1501.787	1515.698	1516.720	1520.786
1524.779	1531.911	1533.782	1540.803	1554.787	1557.735
1560.765	1567.714	1569.767	1577.753	1579.759	1582.730
1586.777	1594.886	1597.737	1600.860	1607.763	1609.762
1618.796	1621.804	1624.815	1633.864	1634.790	1647.773
1652.860	1658.805	1661.822	1670.011	1670.809	1673.755
1679.793	1684.764	1688.773	1696.834	1706.750	1715.105
1715.802	1725.829	1728.795	1732.885	1740.798	1742.962
1745.802	1753.829	1756.819	1761.846	1773.850	1783.932
1784.899	1790.849	1799.779	1801.865	1810.851	1812.829
1818.941	1827.883	1830.907	1834.943	1848.062	1852.900
1860.995	1864.919	1867.886	1876.073	1876.948	1882.875
1890.919	1895.930	1903.885	1907.883	1913.888	1923.799
1931.871	1934.862	1940.880	1944.887	1953.301	1961.942
1976.854	1980.929	1990.922	2002.086	2013.040	2021.963
2026.993	2036.008	2044.952	2056.053	2058.099	2071.963
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2120.404	2123.041	2126.984	2136.561	2138.087	2147.939
2152.093	2156.125	2166.113	2170.032	2182.349	2184.048
2191.104	2194.069	2204.049	2208.099	2220.141	2221.982
2229.099	2233.076	2238.139	2247.103	2258.163	2267.101
2277.118	2281.169	2290.185	2296.055	2308.141	2311.119
2315.201	2322.174	2331.206	2333.157	2348.082	2353.110
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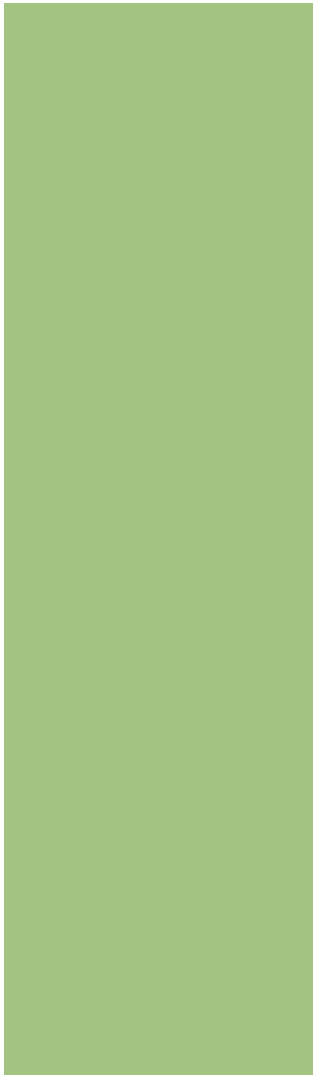
2411.262	2420.299	2424.145	2434.202	2437.128	2441.153



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2538.135	2550.093	2560.067	2568.116	2584.251	2588.052
2597.381	2607.240	2616.155	2622.290	2634.098	2638.247
2646.209	2650.334	2655.364	2661.127	2667.176	2678.387
2689.307	2692.101	2695.212	2705.361	2707.322	2719.917
2723.219	2734.229	2740.113	2752.182	2762.543	2765.198
2773.809	2779.096	2789.329	2796.197	2807.246	2811.065
2822.000	2828.120	2839.196	2849.215	2863.105	2868.223
2883.062	2896.164	2906.354	2910.276	2921.474	2932.291
2937.069	2950.255	2960.210	2965.450	2981.161	2997.061
3008.091	3023.469	3028.134	3032.025	3043.563	3048.541
3052.035	3066.182	3078.494	3092.252	3096.145	3109.830
3121.438	3126.140	3139.361	3143.246	3156.427	3159.680
3173.198	3178.014	3189.253	3202.186	3216.824	3220.145
3225.990	3236.966	3241.140	3247.310	3258.438	3264.047
3276.089	3288.268	3292.088	3303.059	3309.131	3314.744
3319.820	3325.132	3336.778	3347.977	3352.960	3364.927
3376.446	3380.081	3391.351	3397.777	3406.642	3411.471
3422.989	3455.837	3475.627	3503.665	3516.569	3530.813
3560.469	3566.608	3580.549	3592.380	3595.402	3627.302
3634.225	3650.646	3667.755	3674.756	3681.682	3688.777

Tolerance (mon) 18.00 ppm

Number of Peptides 435

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- PepFrag
- X! Tandem
- X! Hunter
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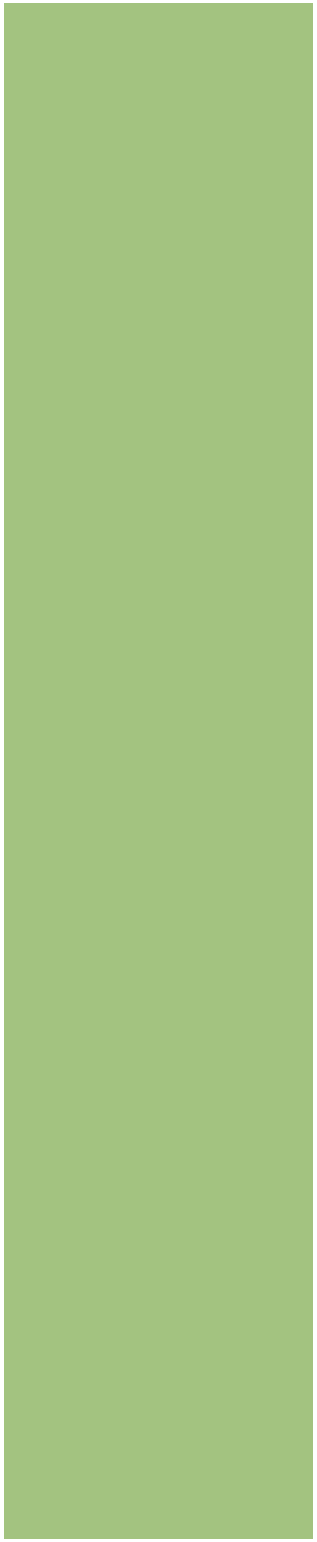
ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.0×10^{-8}	gi|52138739|ref|NP_001004443.1| hexosaminidase A [Rattus norvegicus]	34	6.9	61.09	
2	5.5×10^{-7}	gi|51948406|ref|NP_001004217.1| katanin p60 subunit A 1 [Rattus norvegicus]	52	6.8	56.05	
3	2.0×10^{-6}	gi|48428187|sp|P62024|PHAR1_RAT Phosphatase and actin regulator 1	35	6.6	66.65	
4	3.9×10^{-6}	gi|20302004|ref|NP_620259.1| glutaminase 2 (liver, mitochondrial) [Rattus norvegicus]	37	6.3	60.07	
5	5.4×10^{-6}	gi|48927601|dbj|BAD23895.1| Down-regulated in nephrectomized rat kidney #2 [Rattus norvegicus]	40	6.2	67.27	
6	5.7×10^{-6}	gi|50979280|ref|NP_001003401.1| ectodermal-neural cortex 1 [Rattus norvegicus]	36	6.4	67.31	
+7	9.4×10^{-6}	gi|13751185|emb|CAC37104.1| TA1 KET beta protein [Rattus norvegicus]	30	6.3	61.05	
	-	gi|13751177|emb|CAC37100.1| TA1 KET gamma protein [Rattus norvegicus]	26	6.2	54.07	
	-	gi|13751183|emb|CAC37103.1| TA2 KET beta protein [Rattus norvegicus]	26	6.3	63.21	
	-	gi|13751179|emb|CAC37101.1| TA2 KET gamma protein [Rattus norvegicus]	22	6.2	56.22	
8	1.4×10^{-5}	gi|34098962|ref|NP_036753.3| 6-phosphofructo-2-kinase/ fructose-2,6-biphosphatase 1 [Rattus norvegicus]	40	6.3	55.38	
9	5.1×10^{-5}	gi|21326447|ref|NP_647540.1| EH-domain containing 4 [Rattus norvegicus]	21	6.3	61.68	
10	8.9×10^{-5}	gi|6981372|ref|NP_037226.1| perilipin [Rattus norvegicus]	42	6.4	56.00	



11	9.1×10^{-5}	gi|56268914|gb|AAH87126.1| Similar to KIAA0974 protein [Rattus norvegicus]	41	6.8	53.60
12	1.5×10^{-4}	gi|35902696|ref|NP_037024.2| amiloride-sensitive cation channel 1, neuronal isoform a [Rattus norvegicus]	28	6.7	64.12
-		gi|32527753|gb|AAP86278.1| Ac2-248 [Rattus norvegicus]	28	6.9	67.22
-		gi|51948454|ref|NP_001004241.1| sorting and assembly machinery component 50 homolog [Rattus norvegicus]	29	6.3	52.40
-		gi|56905|emb|CAA30916.1| unnamed protein product [Rattus norvegicus]	30	6.4	57.06
-		gi|19173754|ref|NP_596887.1| testis-specific kinase 2 [Rattus norvegicus]	28	6.5	64.17
-		gi|34871776|ref|XP_232748.2| PREDICTED: similar to CG30497-PA, isoform A [Rattus norvegicus]	27	7.0	47.45
-		gi|28178055|gb|AAC53453.2| hepatic multiple inositol polyphosphate phosphatase [Rattus norvegicus]	27	6.4	55.26
-		gi|50233797|ref|NP_899162.1| keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types) [Rattus norvegicus]	24	6.9	62.08
-		gi|975277|gb|AAA75166.1| p72	22	7.1	69.47
-		gi|458333|gb|AAA19133.1| protein tyrosine phosphatase	26	6.9	68.99
-		gi|18543355|ref|NP_570103.1| cytosolic acetyl-CoA hydrolase [Rattus norvegicus]	21	6.8	62.63
-		gi|32527707|gb|AAP86255.1| Ac1-581 [Rattus norvegicus]	37	6.9	57.34
-		gi|3133137|dbj|BAA28175.1| N-Shc [Rattus rattus]	35	6.9	52.52
-		gi|53733475|gb|AAH83667.1| Polymerase (RNA) III (DNA directed) polypeptide C [Rattus norvegicus]	27	6.6	60.92
-		gi|23618920|ref|NP_112339.1| PCTAIRE protein kinase 1 isoform b [Rattus norvegicus]	28	6.3	52.85
-		gi|51260645|gb|AAH78736.1| Klc3 protein [Rattus norvegicus]	25	6.2	55.87
-		gi|49035970|sp|Q63686|PCTK1_RAT Serine/threonine-protein kinase PCTAIRE-1 (PCTAIRE-motif protein kinase 1)	26	6.9	56.09
-		gi|730311|sp|P38652|PGM1_RAT Phosphoglucomutase-1 (Glucose phosphomutase 1) (PGM 1)	29	6.3	61.67

-	gi|417209|sp|P32577|CSK_RAT Tyrosine-protein kinase CSK (C-SRC kinase)	35	6.6	51.30
-	gi|13592101|ref|NP_112388.1| syntaxin binding protein 2 [Rattus norvegicus]	28	6.3	67.13
-	gi|54400716|ref|NP_001005875.1| proteasome 26S non-ATPase subunit 12 [Rattus norvegicus]	29	7.1	53.32

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Thu Jan 25 20:31:45 2007 UTC (Search Time: 0.58 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 47 - 70 kDa

pI Range 6.2 -7.2

Digestion Trypsin

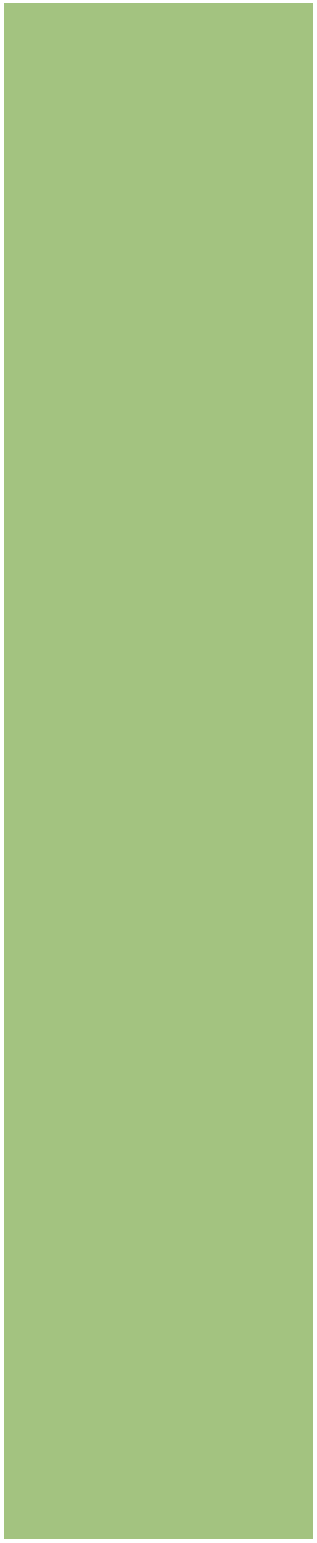
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

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825.511	828.489	832.501	838.664	840.495	848.509	854.436
858.490	863.483	869.443	874.487	880.445	886.883	889.429
895.437	900.415	906.541	907.473	909.480	915.576	916.472
922.509	927.624	933.780	934.932	940.535	942.454	948.598
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980.436	982.438	988.584	990.510	993.540	999.443	1005.706
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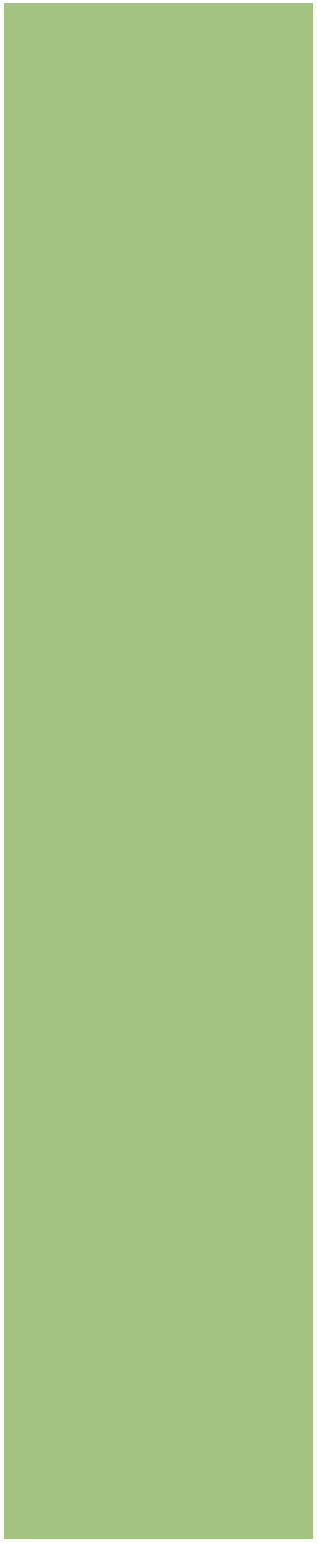

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3657.821 3672.217 3682.348 3696.792

Tolerance (mon)	22.00 ppm
Number of Peptides	477

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- X! Hunter
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New York, NY 10021
(212) 327-8000

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	3.5×10^{-23}	gi|6175089|sp|P12346|TRFE_RAT Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal-binding globulin)	38	7.0	78.57	
2	3.8×10^{-16}	gi|20302047|ref|NP_620231.1| adenosine monophosphate deaminase 1 (isoform M) [Rattus norvegicus]	33	6.5	87.10	
+3	3.7×10^{-14}	gi|205131|gb|AAA41510.1| leukocyte common antigen related protein	30	6.3	99.60	
	-	gi|693993|emb|CAA58537.1| leucocyte common antigen-related protein [Rattus norvegicus]	30	6.5	71.62	
+4	1.1×10^{-10}	gi|51704215|sp|Q01177|PLMN_RAT Plasminogen precursor [Contains: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	18	6.8	93.26	
	-	gi|33086496|gb|AAP92560.1| Ab1-346 [Rattus norvegicus]	16	6.8	88.44	
+5	1.5×10^{-10}	gi|34861509|ref|XP_342003.1| PREDICTED: similar to Glycogen phosphorylase, muscle form (Myophosphorylase) [Rattus norvegicus]	23	6.7	97.78	
	-	gi|1730556|sp|P09812|PYGM_RAT Glycogen phosphorylase, muscle form (Myophosphorylase)	21	6.9	97.77	
	-	gi|204423|gb|AAA41253.1| glycogen phosphorylase	20	6.9	97.64	
	-	gi|2425052|gb|AAB72197.1| dynamin-like protein [Rattus norvegicus]	28	6.6	84.40	
	-	gi|55250424|gb|AAH85843.1| Dynamin 1-like [Rattus norvegicus]	26	6.5	80.45	

-	gi|27685783|ref|XP_214480.1| PREDICTED: similar to Phosphatidylinositol-glycan-specific phospholipase D 1 precursor (PI-G PLD) (Glycoprotein phospholipase D) (Glycosyl-phosphatidylinositol-specific phospholipase D) [Rattus norvegicus]	31	6.2	94.22
-	gi|12621096|ref|NP_075224.1| amiloride binding protein 1 [Rattus norvegicus]	28	6.6	85.40
-	gi|4868358|gb|AAD31278.1| dynamin-like protein DLP1 isoform DLP1-37 [Rattus norvegicus]	24	7.0	80.79
-	gi|27683117|ref|XP_237113.1| PREDICTED: similar to TGF beta receptor associated protein -1 [Rattus norvegicus]	21	6.3	98.53
-	gi|1934981|emb|CAA72938.1| glucocorticoid receptor [Rattus norvegicus]	27	6.2	88.63
-	gi|18766326|gb|AAL78956.1|AF455050_1 glucocorticoid receptor [Rattus norvegicus]	27	6.2	88.41
-	gi|16758126|ref|NP_445852.1| transducin-like enhancer protein 3 [Rattus norvegicus]	18	6.7	83.42
-	gi|18093102|ref|NP_542420.1| dynamin 1 [Rattus norvegicus]	19	6.3	96.25
-	gi|13489067|ref|NP_068516.1| N-ethylmaleimide sensitive fusion protein [Rattus norvegicus]	18	6.6	83.21
-	gi|17388906|gb|AAF80473.2|AF162756_1 cenexin 2 [Rattus norvegicus]	22	6.7	89.88
-	gi|47169484|tpe|CAE48379.1| TPA: glutamine-fructose-6-phosphate transaminase 2 [Rattus norvegicus]	32	6.7	77.80
-	gi|2494044|sp|O09178|AMPD3_RAT AMP deaminase 3 (AMP deaminase isoform E)	24	6.6	88.98
-	gi|31745156|ref|NP_853662.1| F-box only protein 11 [Rattus norvegicus]	21	6.4	95.51
-	gi|53733583|gb|AAH83831.1| Ring finger protein 10 [Rattus norvegicus]	20	6.4	89.48
-	gi|48686585|gb|AAT46048.1| fidgetin-like 1 [Rattus norvegicus]	27	6.6	74.92
-	gi|13928736|ref|NP_113732.1| adenosine monophosphate deaminase 3 [Rattus norvegicus]	23	6.9	92.75

-	gi|13242186|gb|AAK16592.1|AF346902_1 glycogen synthase [Rattus norvegicus]	22	6.6	81.46
-	gi|19424312|ref|NP_598286.1| KH-type splicing regulatory protein [Rattus norvegicus]	25	6.4	74.49
-	gi|1346413|sp|P48679|LMNA_RAT Lamin-A	25	6.5	74.59
-	gi|54312102|ref|NP_001005887.1| itchy homolog E3 ubiquitin protein ligase [Rattus norvegicus]	21	6.3	98.47
-	gi|40786501|ref|NP_955434.1| sperm protein SSP411 [Rattus norvegicus]	23	6.6	89.03
-	gi|22902132|ref|NP_690600.1| RNA binding motif protein 10 [Rattus norvegicus]	19	6.3	94.71
-	gi|6978771|ref|NP_037331.1| dynamin 2 [Rattus norvegicus]	15	7.0	98.55
-	gi|7549773|ref|NP_036873.1| K-kininogen [Rattus norvegicus]	22	6.3	72.00
-	gi|55715908|gb|AAH85700.1| Nibrin [Rattus norvegicus]	13	6.7	84.14
-	gi|20302036|ref|NP_620228.1| nibrin [Rattus norvegicus]	15	6.4	84.31
-	gi|20301994|ref|NP_620205.1| fibroblast activation protein [Rattus norvegicus]	19	6.2	88.51
-	gi|9506961|ref|NP_062205.1| peptidyl arginine deiminase, type I [Rattus norvegicus]	19	6.7	74.58
-	gi|1072002|pir||S27267 lamin A - rat	20	6.3	74.51
-	gi|34870013|ref|XP_344049.1| PREDICTED: similar to DNA replication licensing factor MCM4 (CDC21 homolog) (P1-CDC21) [Rattus norvegicus]	25	6.8	97.24
-	gi|25742586|ref|NP_071622.1| vacuolar protein sorting 33B [Rattus norvegicus]	20	6.4	71.36
-	gi|16758510|ref|NP_446142.1| DnaJ (Hsp40) homolog, subfamily C, member 14 [Rattus norvegicus]	16	7.1	79.65

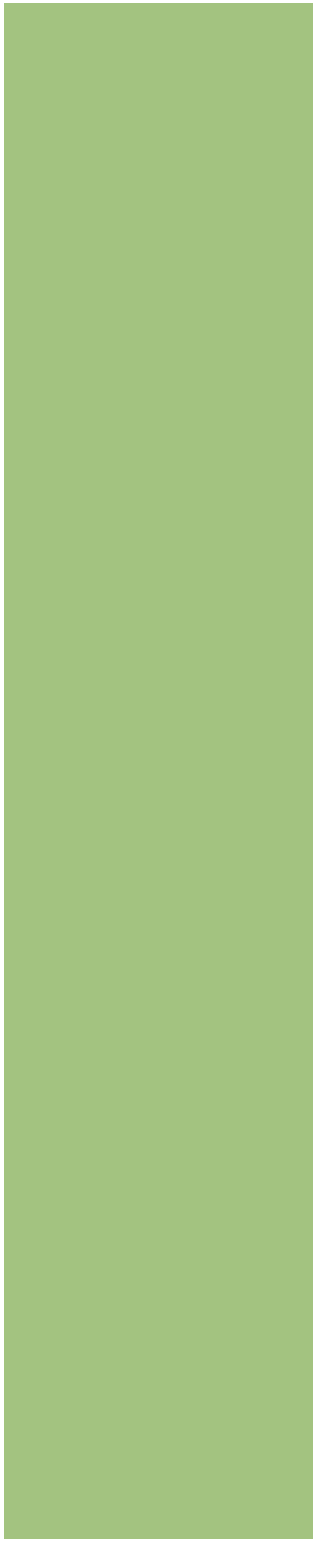
NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AAD6D3BA-0F70-5AE9210E

Sequences	20092
Date & Time	Thu Jan 25 21:10:46 2007 UTC (Search Time: 0.53 sec.)
Sample ID	
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	70 - 100 kDa
pI Range	6.2 -7.2
Digestion	Trypsin
Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	707.374 712.390 717.406 719.424 723.415 726.348 731.413 732.377 737.444 738.430 740.387 745.409 750.392 754.395 764.438 768.404 772.417 778.390 784.462 790.425 791.466 793.397 800.383 804.479 813.412 818.368 824.459 827.513 829.429 835.425 836.437 840.468 849.461 853.426 859.469 860.455 863.456 878.483 885.455 887.437 893.479 903.459 906.495 912.540 913.455 915.489 921.483 922.545 925.530 931.475 935.483 942.512 945.488 949.568 955.526 961.567 963.487 969.740 970.558 979.549 986.510 992.689 993.495 999.505 1001.527 1004.531 1013.529 1017.538 1024.568 1040.523 1051.687 1057.521 1059.578 1061.572 1068.555 1079.514 1080.554 1087.554 1090.574 1096.760 1097.540 1104.551 1105.580 1107.550 1113.694 1114.548 1125.582 1132.569 1135.606 1138.578 1141.486 1147.565 1150.599 1156.564 1163.577 1173.584 1174.645 1186.552 1200.665 1208.630 1216.034 1216.621 1218.547 1226.665 1233.533 1234.668 1241.820 1243.576 1247.566 1254.708 1258.620 1265.650 1269.627 1272.675 1284.708 1285.673 1289.537 1296.628 1300.630 1303.617 1308.628 1316.675 1327.664 1329.651 1336.630 1337.664 1348.665 1355.670 1364.681 1374.670 1380.640 1387.878 1388.781 1390.688 1392.747 1400.696 1406.648 1413.725 1420.770 1423.740 1431.726 1432.745 1440.783 1447.843 1449.688 1451.688 1462.711



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1670.765	1678.755	1681.763	1684.802	1692.881	1695.847
1705.815	1716.232	1725.729	1728.863	1732.813	1744.773
1745.842	1754.885	1756.888	1782.949	1783.632	1791.945
1796.937	1802.850	1811.810	1814.936	1817.806	1820.879
1828.876	1832.794	1835.851	1848.829	1850.827	1859.993
1861.881	1863.858	1872.852	1875.796	1881.868	1890.817
1895.916	1906.928	1919.889	1921.925	1932.953	1940.926
1951.026	1953.883	1971.934	1976.962	1985.925	2003.943
2007.804	2009.947	2023.012	2025.982	2034.023	2037.974
2041.867	2046.983	2056.013	2058.915	2068.032	2076.126
2077.968	2083.006	2093.995	2095.998	2105.815	2108.938
2111.970	2124.959	2128.998	2139.016	2149.028	2151.027
2154.996	2164.073	2165.985	2169.905	2182.159	2183.921
2190.978	2194.069	2203.987	2208.100	2220.906	2230.026
2232.157	2235.118	2238.144	2248.066	2257.082	2266.019
2268.072	2277.031	2279.153	2282.176	2292.131	2308.252
2311.004	2314.114	2324.138	2327.159	2352.086	2361.308
2364.026	2367.106	2377.211	2379.971	2394.289	2396.003
2399.005	2408.749	2410.998	2420.202	2424.048	2433.277
2435.172	2442.025	2448.121	2452.991	2463.445	2470.104
2483.012	2510.076	2522.276	2543.230	2568.298	2578.106
2586.255	2597.231	2600.322	2612.154	2617.184	2629.365
2633.305	2645.247	2652.217	2662.359	2665.454	2668.133
2678.479	2681.339	2685.213	2695.208	2706.168	2716.413
2726.324	2740.344	2750.335	2757.301	2767.323	2772.997
2779.246	2782.372	2792.261	2796.179	2806.486	2811.414
2821.642	2825.222	2830.381	2839.243	2849.305	2853.370
2860.501	2866.126	2876.452	2880.538	2893.318	2899.955
2904.637	2916.197	2932.485	2943.222	2945.819	2950.319
2963.326	2980.113	2985.449	2996.579	3002.003	3005.179
3016.604	3021.343	3029.349	3040.560	3043.422	3061.328
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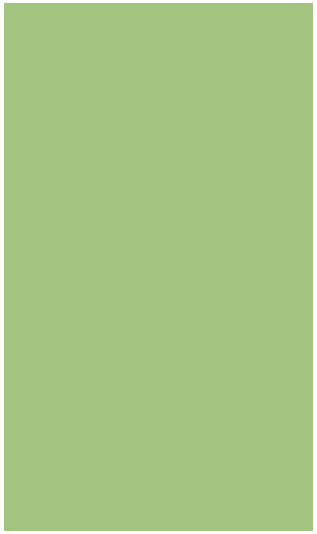

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Tolerance (mon)	38.00 ppm
Number of Peptides	426

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- X! Tandem
- X! Hunter
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Protein Candidates

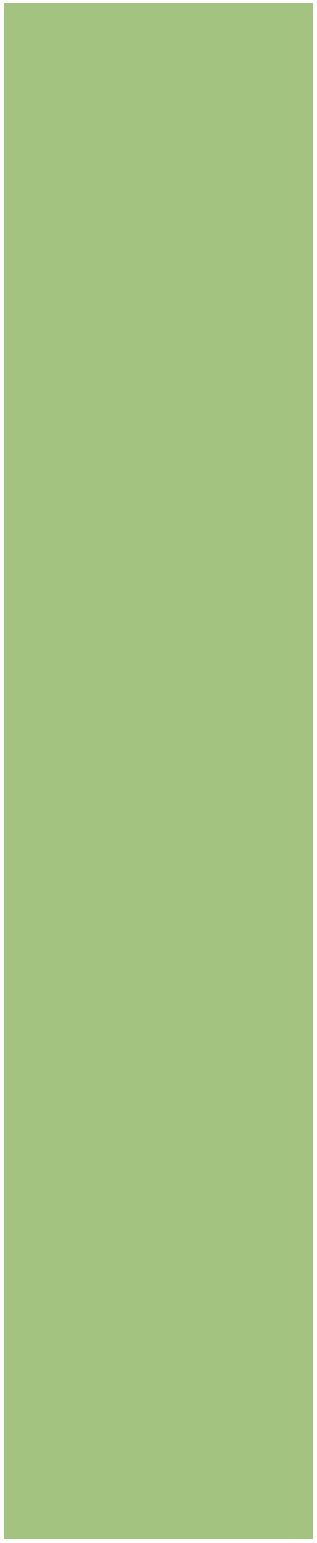
Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	2.4×10^{-4}	gi|51703333|sp|P62989|UBIQ_RAT Ubiquitin	32	6.6	8.55	

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

Search id A7E8D3DE-123C-581D1E65
Sequences 20076
Date & Time Tue Feb 20 15:55:18 2007 UTC (Search Time: 0.19 sec.)
Sample ID 20040813 richardson NIA set 1 spot 6010 CONSENSUS search
Database NCBInr [..\databases\nr]
Taxonomy Rattus
Mass Range 0 - 10 kDa
pI Range 6.4 -8.0
Digestion Trypsin
Missed Cuts 0
Modifications +C2H3ON@C(Complete); +O@M(Partial);
Charge State MH+
Masses (avg)
Tolerance (avg) 1.00 ppm



Masses (mon)

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778.470 781.531 788.427 789.409 796.492 798.505 804.445 813.435 819.469
820.394 825.449 831.411 836.869 841.467 849.446 856.498 862.473 863.481
866.507 877.491 881.480 884.518 891.474 903.463 904.434 917.488 921.466
933.470 940.513 943.548 950.462 952.558 955.508 962.508 964.513 967.544
970.518 971.545 978.519 984.505 990.530 991.525 994.515 999.549 1003.552
1018.999 1019.536 1021.513 1034.542 1037.530 1039.525 1051.556 1052.559
1053.542 1060.586 1065.543 1067.631 1079.558 1081.615 1087.575 1091.551
1097.851 1098.565 1102.605 1106.541 1107.548 1114.568 1124.632 1133.563
1138.576 1145.603 1146.582 1149.592 1156.607 1164.584 1172.613 1175.656
1187.615 1190.632 1209.000 1209.585 1211.599 1218.848 1219.600 1220.610
1227.627 1232.631 1234.687 1242.645 1244.663 1247.632 1255.608 1261.625
1263.658 1271.661 1276.682 1284.630 1285.643 1291.659 1298.659 1299.677
1302.615 1308.670 1316.644 1317.695 1328.712 1329.669 1336.697 1338.691
1347.744 1348.782 1356.704 1364.897 1373.115 1373.689 1381.683 1382.685
1390.705 1398.699 1401.671 1409.721 1411.693 1417.693 1425.688 1432.763
1434.802 1442.768 1444.737 1447.732 1452.679 1463.758 1466.773 1474.750
1477.776 1485.679 1486.743 1501.758 1504.759 1514.751 1519.759 1522.778
1529.774 1534.755 1537.789 1545.163 1545.798 1555.156 1555.819 1562.784
1565.766 1573.074 1573.768 1579.783 1586.775 1590.773 1593.781 1600.777
1607.815 1615.815 1619.688 1627.799 1636.802 1644.793 1647.825 1656.802
1657.816 1666.022 1666.847 1672.817 1680.867 1681.889 1690.819 1699.246
1705.802 1714.824 1725.855 1728.877 1732.854 1735.827 1744.871 1748.867
1757.889 1759.866 1762.833 1771.919 1783.872 1787.884 1791.787 1799.833
1801.948 1809.902 1812.883 1820.919 1822.902 1826.901 1834.911 1847.913
1850.925 1859.045 1860.932 1867.969 1875.893 1879.921 1887.899 1889.919
1894.986 1897.919 1901.911 1907.906 1916.976 1918.982 1924.030 1931.924
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1988.001 1995.996 2004.972 2012.004 2020.017 2022.015 2032.051 2041.959
2049.056 2057.998 2062.002 2065.000 2074.039 2083.065 2092.143 2093.991
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2156.082 2165.255 2168.045 2185.076 2188.099 2195.036 2201.067 2222.066
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2371.173 2380.037 2393.166 2396.199 2399.101 2409.274 2415.262 2424.142
2432.208 2441.119 2448.179 2458.155 2465.106 2474.178 2476.960 2480.347
2484.173 2491.228 2501.190 2509.215 2520.193 2527.266 2538.215 2548.237
2553.204 2564.210 2568.134 2581.192 2586.225 2598.263 2608.369 2612.258
2623.183 2631.194 2643.233 2653.217 2663.115 2666.246 2670.212 2681.259
2687.367 2695.300 2708.151 2719.241 2723.247 2736.446 2740.394 2744.275
2751.196 2757.136 2769.956 2773.432 2776.271 2779.324 2789.563 2802.886
2806.311 2817.278 2822.394 2832.460 2839.385 2851.351 2858.226 2869.294
2873.880 2884.508 2888.417 2904.479 2916.146 2921.023 2933.014 2942.436
2949.273 2959.527 2962.533 2967.339 2970.386 2983.399 2995.850 2999.243
3009.916 3012.319 3016.055 3026.980 3038.482 3045.468 3060.246 3072.222
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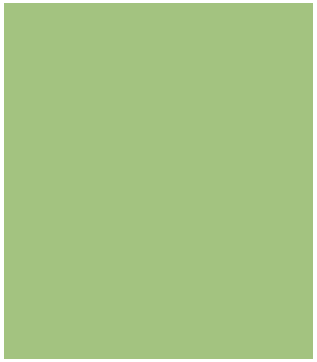

	3151.372 3155.988 3166.974 3177.675 3188.509 3200.123 3202.792 3214.852 3221.999 3232.065 3245.179 3249.172 3267.093 3272.294 3285.759 3301.690 3313.470 3316.535 3330.635 3340.130 3351.470 3364.472 3367.912 3371.588 3375.659 3390.393 3400.680 3410.234 3419.605 3432.344 3443.010 3446.569 3463.083 3475.584 3490.416 3505.240 3508.392 3520.615 3533.179 3537.025 3539.951 3545.004 3553.393 3569.557 3581.443 3596.579 3612.355 3619.851 3631.657 3634.825 3640.027 3654.431 3667.231 3670.333 3684.143 3692.245 3697.323
Tolerance (mon)	10.00 ppm
Number of Peptides	440

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	2.3×10^{-28}	gi|55926145|ref|NP_114021.2| expressed in non-metastatic cells 2 [Rattus norvegicus]	32	6.9	17.38	
	-	gi|206580|gb|AAA42017.1| RBL-NDP kinase 18kDa subunit (p18)	20	6.9	17.47	
2	2.1×10^{-8}	gi|2143727|pir||S62669 folate binding protein I - rat (fragment)	59	6.0	2.55	
3	1.2×10^{-7}	gi|6724099|gb|AAF26845.1|AF196188_1 T cell receptor V delta 1 [Rattus norvegicus]	28	9.5	10.37	
4	2.2×10^{-7}	gi|228110|prf||1717324AA T cell receptor variable region:SUBUNIT=beta: ISOTYPE=19	32	9.5	13.76	
5	2.4×10^{-7}	gi|6724133|gb|AAF26861.1|AF196206_1 T cell receptor V delta 3; delta T cell receptor V delta 3 [Rattus norvegicus]	17	9.5	14.98	
6	1.2×10^{-6}	gi|34875549|ref|XP_344453.1| PREDICTED: similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G [Rattus norvegicus]	23	9.5	11.35	
7	1.5×10^{-6}	gi|902727|emb|CAA61852.1| putative olfactory receptor [Rattus norvegicus]	15	9.2	18.07	
8	1.5×10^{-6}	gi|4102801|gb|AAD01591.1| retinoid X receptor gamma [Rattus norvegicus]	21	8.9	12.41	
9	1.9×10^{-6}	gi|19577318|emb|CAD21563.1| ATPase subunit 8 [Rattus norvegicus]	54	9.3	7.61	
10	2.2×10^{-6}	gi|203022|gb|AAA40773.1| alpha-tropomyosin	25	6.2	4.98	
11	2.8×10^{-6}	gi|55741522|ref|NP_001006961.1| mitochondrial protein, 18 kDa [Rattus norvegicus]	14	9.5	18.41	
12	3.8×10^{-6}	gi|7963642|gb|AAF71299.1|AF213509_1 T cell receptor beta chain variable segment 13 precursor [Rattus norvegicus]	28	6.1	12.81	
13	1.0×10^{-5}	gi|27662826|ref|XP_216691.1| PREDICTED: similar to anterior gradient 2 [Rattus norvegicus]	7	9.0	19.91	
14	1.1×10^{-5}	gi|11066046|gb|AAG28431.1|AF194442_1 SMDF neuregulin beta 4 [Rattus norvegicus]	23	9.6	15.56	
15	2.4×10^{-5}	gi|2896018|gb|AAC03102.1| Axl receptor tyrosine kinase [Rattus norvegicus]	32	9.4	8.88	
16	3.4×10^{-5}	gi|509827|gb|AAA53178.1| T-cell receptor beta-chain V region	16	9.5	9.92	
17	5.4×10^{-5}	gi|543464|pir||B49828 T-cell receptor beta chain V region (Vbeta8.2) - rat	15	9.3	10.61	
18	5.4×10^{-5}	gi|207216|gb|AAA51370.1| T-cell receptor beta	12	9.3	12.84	
19	8.3×10^{-5}	gi|509835|gb|AAA53182.1| T-cell receptor beta-chain V region	16	9.8	9.95	

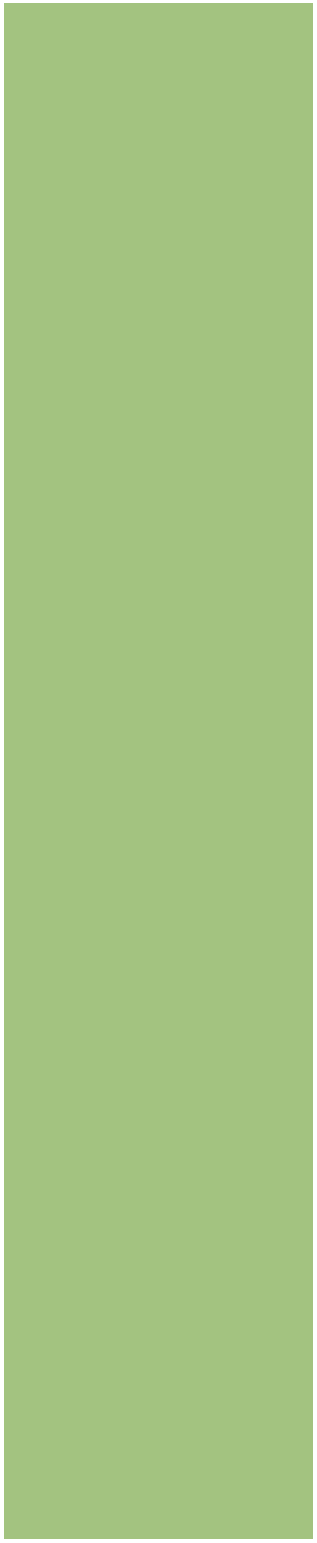
20	8.3×10^{-5}	gi|517184|emb|CAA54957.1| T-cell receptor beta chain, variable region [Rattus norvegicus]	15	9.6	10.60	☐
21	8.3×10^{-5}	gi|112370|pir||B30598 T-cell receptor beta chain precursor V region (Z85) - rat (fragment)	11	9.3	14.50	☐
22	8.3×10^{-5}	gi|999290|gb|AAB34737.1| T-cell receptor av1 V beta chain 8.4 {V-D-J junction} [rats, LER, liver, Peptide Partial, 94 aa]	15	9.6	10.59	☐
23	8.3×10^{-5}	gi|92796|pir||S04542 T-cell receptor beta chain precursor V-J region (Z82) - rat (fragment)	11	9.5	14.61	☐
24	1.2×10^{-4}	gi|207218|gb|AAA51371.1| T-cell receptor beta	12	9.4	12.80	☐
25	1.7×10^{-4}	gi|228121|prf||1717324L T cell receptor variable region:SUBUNIT=beta: ISOTYPE=8.2	11	9.5	13.77	☐
26	1.7×10^{-4}	gi|1438517|emb|CAA66261.1| T-cell receptor beta chain [Rattus norvegicus]	13	9.1	12.08	☐
27	5.9×10^{-4}	gi|92402|pir||A23986 Ig kappa chain precursor V region (IR162) - rat	17	8.8	13.96	☐
28	9.2×10^{-4}	gi|561845|gb|AAA51358.1| This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal	30	6.0	13.14	☐
29	0.94	gi|561849|gb|AAA51363.1| This CDS feature is included to show the translation of the corresponding C_region. Presently translation qualifiers on C_region features are illegal	91	6.7	1.19	☐

NOTE:

1. To search again using unmatched masses, click the symbol ☐.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id	B42CDE18-05F8-64612AA9
Sequences	20076
Date & Time	Tue Feb 20 16:04:00 2007 UTC (Search Time: 0.28 sec.)
Sample ID	20040813 richardson NIA set 1 spot 6110 CONSENSUS search
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	0 - 20 kDa
pI Range	6.0 -10.0
Digestion	Trypsin
Missed Cuts	0
Modifications	+C2H3ON@C(Complete); +O@M(Partial);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm



Masses (mon)

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778.386 784.458 785.400 787.417 790.383 796.425 802.358 804.454 813.674
814.480 820.518 821.462 823.468 827.448 833.767 834.428 835.399 841.846
848.454 849.414 854.519 859.500 865.425 866.474 877.457 881.427 888.490
890.476 899.510 906.443 913.484 915.498 921.532 922.512 932.735 933.536
940.455 944.544 948.496 954.576 960.488 966.669 967.547 968.489 975.473
984.613 991.570 992.523 997.574 1001.551 1018.591 1020.589 1023.579
1029.550 1030.543 1040.588 1041.565 1044.520 1051.490 1057.541 1060.607
1066.685 1067.498 1068.553 1074.544 1076.574 1079.622 1085.599 1088.639
1094.574 1100.570 1102.602 1105.509 1107.545 1114.632 1121.495 1123.546
1130.639 1136.892 1137.573 1140.684 1145.621 1151.618 1154.611 1163.615
1167.681 1174.635 1175.650 1184.620 1187.632 1189.651 1196.600 1197.625
1203.664 1211.615 1213.607 1217.689 1224.814 1225.545 1226.676 1229.647
1232.670 1241.641 1243.704 1250.763 1252.572 1256.672 1260.683 1268.677
1269.660 1275.566 1284.571 1287.660 1295.714 1298.720 1300.734 1308.683
1315.729 1316.534 1326.737 1333.512 1335.749 1339.786 1341.708 1344.767
1352.602 1355.698 1370.757 1377.968 1379.718 1382.794 1384.797 1391.694
1394.759 1398.784 1401.781 1408.669 1409.781 1412.790 1415.726 1424.832
1434.758 1441.829 1448.764 1449.661 1451.635 1458.747 1465.646 1472.792
1479.724 1483.636 1500.824 1503.667 1514.860 1516.826 1521.680 1525.832
1532.834 1534.811 1537.766 1540.803 1548.741 1553.938 1561.270 1562.787
1569.767 1571.795 1580.855 1581.819 1586.696 1594.616 1598.893 1604.875
1611.948 1612.787 1616.871 1619.634 1630.000 1637.892 1646.950 1649.792
1658.829 1660.941 1669.925 1674.798 1682.880 1690.816 1692.893 1701.047
1701.880 1715.852 1724.900 1729.908 1733.859 1737.898 1745.738 1746.892
1751.059 1753.906 1761.810 1763.873 1773.728 1775.940 1783.922 1785.913
1793.918 1795.886 1798.826 1801.912 1810.181 1810.897 1812.846 1815.972
1823.929 1828.936 1837.210 1848.338 1849.901 1852.914 1861.910 1865.689
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1988.255 2003.026 2007.579 2011.141 2020.726 2024.815 2031.031 2037.045
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2220.294 2223.151 2229.983 2234.056 2237.177 2246.297 2255.563 2257.163
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2393.428 2398.901 2408.709 2409.899 2420.160 2423.110 2432.237 2439.384
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2582.277 2593.105 2604.850 2609.218 2614.760 2620.447 2632.357 2644.814
2649.284 2655.147 2660.078 2670.268 2680.721 2687.492 2691.334 2695.215
2706.172 2716.204 2722.527 2732.836 2744.258 2749.412 2759.949 2772.988
2781.188 2791.785 2802.937 2808.290 2813.326 2824.056 2830.360 2833.084
2844.319 2857.628 2867.901 2881.879 2887.669 2895.421 2906.742 2911.793
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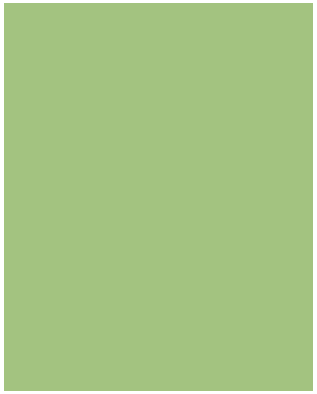

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3292.517	3304.551	3317.228	3328.258	3329.501	3340.552	3353.765	3367.240
3380.507	3394.034	3398.236	3411.091	3419.674	3425.981	3441.220	3450.277
3454.394	3474.897	3479.704	3493.668	3507.421	3521.121	3525.920	3537.050
3548.078	3559.284	3570.548	3575.340	3583.160	3591.836	3607.520	3613.835
3616.550	3631.841	3644.114	3651.601	3665.375	3676.969	3687.967	3700.375

Tolerance (mon) 9.00 ppm

Number of Peptides 455

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.6×10^{-16}	gi|6900621|emb|CAB71407.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	62	8.9	11.11	
2	4.8×10^{-10}	gi|1438517|emb|CAA66261.1| T-cell receptor beta chain [Rattus norvegicus]	44	9.1	12.08	
3	2.3×10^{-8}	gi|7673574|gb|AAF66932.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	38	9.0	11.23	
4	2.8×10^{-8}	gi|1166514|gb|AAC52369.1| RGS8	55	8.3	7.85	
5	7.0×10^{-8}	gi|23477207|emb|CAD38515.1| neuron-specific protein PEP-19 [Rattus norvegicus]	28	8.8	10.88	
6	2.8×10^{-5}	gi|6900569|emb|CAB71379.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	25	8.9	12.38	
7	7.1×10^{-5}	gi|8825628|gb|AAF80146.1| T cell receptor [Rattus norvegicus]	19	8.3	11.46	
8	7.4×10^{-5}	gi|46237624|emb|CAE84001.1| leukocyte specific transcript 1 [Rattus norvegicus]	28	8.0	13.69	
9	8.2×10^{-5}	gi|6900892|emb|CAB71543.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	35	8.2	10.71	
10	8.3×10^{-5}	gi|12018330|ref|NP_072156.1| leucocyte specific transcript 1 [Rattus norvegicus]	28	8.9	13.71	
11	8.4×10^{-5}	gi|7673586|gb|AAF66938.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	29	8.3	10.66	
12	9.5×10^{-5}	gi|12055416|emb|CAC20875.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	40	9.1	9.47	
13	1.0×10^{-4}	gi|27545366|ref|NP_775421.1| defensin NP-4 precursor [Rattus norvegicus]	20	8.1	10.43	
14	2.0×10^{-4}	gi|29243397|gb|AAO66430.1| beta adducin [Rattus norvegicus]	41	9.0	4.61	

15	2.3×10^{-4}	gi|6900732|emb|CAB71463.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	34	8.1	11.40
16	2.8×10^{-4}	gi|37361810|gb|AAQ91018.1| LRRGT00062 [Rattus norvegicus]	38	8.2	11.80
17	4.0×10^{-4}	gi|6900742|emb|CAB71468.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	35	8.1	11.09
18	6.1×10^{-4}	gi|2144049|pir||I56980 arginine decarboxylase - rat (fragment)	20	9.1	9.34
19	1.0×10^{-3}	gi|13928914|ref|NP_113848.1| cyclic AMP phosphoprotein, 19 kDa [Rattus norvegicus]	22	9.1	12.27
20	2.3×10^{-3}	gi|7673582|gb|AAF66936.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	23	9.2	9.29
21	4.8×10^{-3}	gi|5420308|emb|CAB46648.1| MHC class I antigen [Rattus norvegicus]	27	8.3	8.85
22	7.8×10^{-3}	gi|6900762|emb|CAB71478.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	40	8.8	10.65
23	8.9×10^{-3}	gi|6900658|emb|CAB71426.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	37	8.9	11.80
24	0.013	gi|7414613|emb|CAB85952.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	37	9.0	11.53
25	0.75	gi|1352179|sp|P80433|COX82_RAT Cytochrome c oxidase polypeptide VIII-liver (Cytochrome c oxidase subunit 8-2)	16	8.1	5.08

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

Search id AE76B943-0BD0-AF3488CC

Sequences 20092

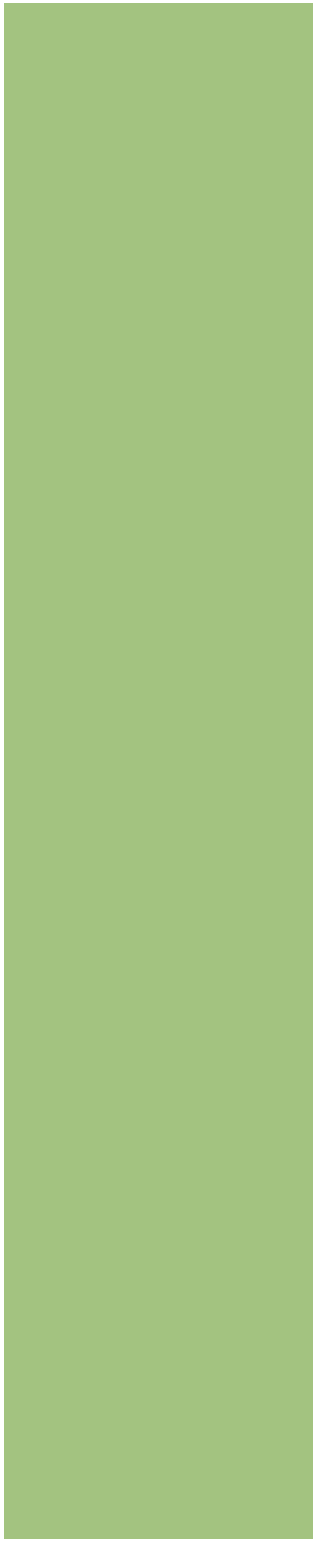
Date & Time Thu Jan 25 23:19:09 2007 UTC (Search Time: 0.28 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 1 - 14 kDa



pI Range 7.8 -9.2

Digestion Trypsin

Missed Cuts 1

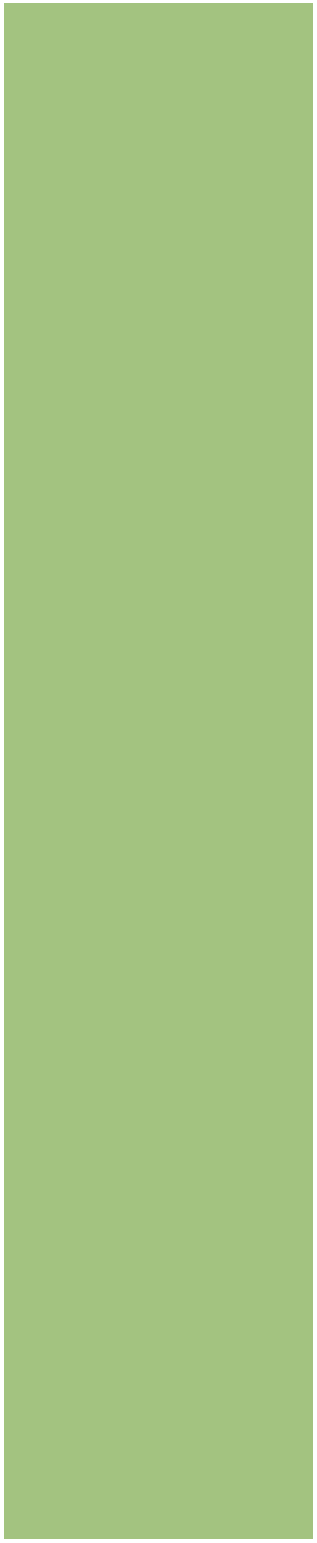
Modifications +C2H3ON@C(Complete); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 710.445 711.342 714.357 719.343 724.383 726.411 730.367
734.388 738.347 742.353 747.436 749.404 752.482 754.401
763.329 768.409 770.386 776.388 778.469 780.403 786.426
792.453 793.381 799.472 801.394 814.410 820.467 824.497
826.449 832.433 834.453 836.844 841.481 849.439 850.420
856.432 857.515 860.451 866.499 876.366 877.482 880.413
882.430 888.794 889.436 895.424 902.643 903.472 904.443
907.480 917.496 918.434 921.494 932.471 938.581 941.468
948.457 949.514 955.493 961.532 962.471 968.533 979.492
980.523 988.460 990.576 993.500 997.554 1004.471 1018.506
1019.516 1023.579 1035.517 1038.506 1044.694 1051.599
1057.563 1062.535 1068.531 1074.521 1077.589 1083.516
1087.617 1091.548 1097.557 1100.614 1104.635 1107.544
1113.598 1115.574 1119.511 1125.710 1132.583 1137.502
1139.568 1145.664 1146.529 1152.643 1163.589 1172.557
1176.570 1186.608 1190.575 1200.626 1208.614 1215.619
1216.698 1224.598 1226.553 1233.728 1235.548 1242.631
1246.548 1253.734 1254.711 1259.602 1267.544 1268.574
1275.583 1282.514 1286.639 1293.455 1294.568 1298.543
1302.668 1306.679 1313.622 1317.552 1323.641 1327.562
1334.707 1339.703 1341.674 1348.487 1355.564 1359.557
1366.688 1373.589 1375.585 1383.084 1387.543 1394.546
1395.703 1401.794 1407.672 1414.777 1419.667 1426.649
1434.770 1442.838 1446.753 1449.673 1462.695 1469.783
1482.713 1486.707 1500.547 1504.669 1514.896 1515.656
1520.718 1527.866 1529.892 1534.635 1540.759 1554.715
1556.786 1564.791 1565.723 1568.654 1576.690 1578.802
1584.639 1591.963 1592.769 1597.743 1604.827 1605.798
1608.875 1613.766 1621.726 1623.706 1631.800 1635.636
1639.914 1642.805 1650.891 1652.724 1660.753 1669.654



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1749.511	1750.835	1758.732	1767.185	1767.722	1783.639
1784.862	1789.871	1793.748	1796.800	1804.886	1805.830
1809.809	1817.896	1819.791	1828.821	1830.895	1835.854
1839.895	1847.817	1855.872	1856.858	1868.075	1871.161
1880.931	1882.917	1890.844	1896.821	1905.923	1914.252
1916.875	1920.916	1929.159	1931.940	1935.967	1940.859
1950.512	1953.904	1960.875	1969.951	1976.591	1986.904
1997.905	2006.885	2010.809	2024.208	2031.790	2041.424
2045.198	2051.904	2054.956	2063.085	2071.106	2074.878
2078.990	2093.910	2096.654	2103.104	2109.007	2118.450
2123.847	2129.096	2137.899	2142.137	2151.061	2153.092
2162.227	2165.171	2170.032	2182.914	2188.047	2195.078
2204.175	2207.781	2221.061	2231.071	2234.062	2237.152
2246.272	2258.067	2267.165	2277.118	2283.487	2293.088
2296.057	2307.949	2311.121	2320.327	2324.092	2333.128
2349.196	2354.259	2363.714	2374.894	2394.368	2397.071
2407.305	2413.159	2416.138	2425.053	2434.483	2436.744
2440.070	2446.996	2455.334	2466.261	2475.335	2479.091
2482.412	2494.274	2497.236	2507.278	2510.044	2517.103
2526.169	2535.116	2539.052	2544.112	2553.295	2563.722
2567.202	2577.384	2580.052	2590.362	2591.631	2597.191
2607.775	2610.598	2614.799	2625.213	2627.906	2634.471
2644.474	2645.825	2655.607	2659.149	2667.285	2677.733
2682.337	2692.396	2696.277	2707.238	2718.959	2723.281
2735.213	2745.370	2748.195	2758.447	2759.438	2764.218
2769.286	2779.648	2791.809	2795.656	2801.144	2811.495
2821.328	2832.791	2843.199	2847.153	2859.497	2865.192
2875.588	2878.624	2882.746	2894.189	2907.398	2915.032
2927.158	2939.529	2949.473	2952.401	2964.495	2968.568
2978.598	2981.173	2986.473	2995.980	3002.622	3012.710
3015.336	3020.110	3024.371	3034.309	3036.907	3040.027
3046.271	3056.470	3060.270	3075.384	3079.309	3092.259
3105.386	3108.992	3120.649	3126.900	3135.044	3145.389
3162.871	3174.705	3177.553	3188.386	3199.810	3204.919
3212.705	3224.325	3231.790	3239.263	3245.325	3256.042
3262.736	3272.865	3276.721	3287.683	3291.973	3303.077
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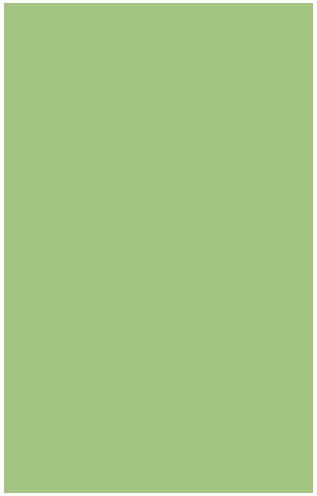

	3365.088 3378.311 3381.836 3390.383 3393.483 3404.087 3417.663 3423.021 3436.357 3442.363 3456.370 3459.857 3465.407 3475.567 3488.368 3498.522 3509.848 3522.032 3527.631 3539.164 3543.654 3556.017 3559.231 3567.154 3574.601 3589.277 3603.416 3607.704 3619.771 3624.069 3628.044 3641.284 3643.317 3658.214 3662.289 3674.814 3679.920 3689.079 3697.840
Tolerance (mon)	16.00 ppm
Number of Peptides	463

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National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	9.5×10^{-7}	gi|223466|prf||0807284A myosin H	12	5.4	49.48	
	-	gi|205576|gb|AAA41653.1| cardiac myosin heavy chain 21/26	12	5.4	49.63	
	-	gi|205578|gb|AAA41654.1| cardiac myosin heavy chain 5	8	5.5	47.89	
+2	6.2×10^{-3}	gi|57178|emb|CAA33412.1| S-antigen [Rattus norvegicus]	10	5.9	45.26	
	-	gi|114219|sp|P15887|ARRS_RAT S-arrestin (Retinal S-antigen) (48 kDa protein) (S-AG) (Rod photoreceptor arrestin)	10	5.7	45.22	
	-	gi|206848|gb|AAA42107.1| S-antigen	10	6.0	45.31	
3	0.010	gi|55778538|gb|AAH86386.1| RGD1359202 protein [Rattus norvegicus]	10	6.9	41.43	
4	0.013	gi|2773249|gb|AAB96759.1| glutamate carboxypeptidase II [Rattus norvegicus]	9	7.4	53.07	
5	0.038	gi|57977291|ref|NP_071599.2| RSD-6 [Rattus norvegicus]	11	4.1	42.29	
6	0.087	gi|56789535|gb|AAH88425.1| Tripartite motif protein 13 [Rattus norvegicus]	9	5.6	47.65	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20073

Date & Time Fri Mar 30 19:35:06 2007 UTC (Search Time: 0.36 sec.)

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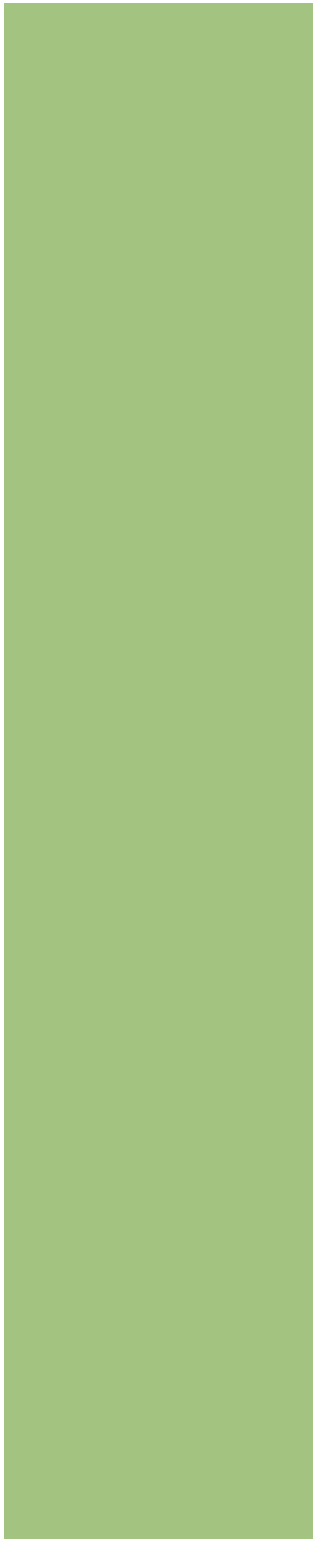
Database NCBInr [..\databases\nr]



Taxonomy Rattus

Mass Range 30 - 55 kDa

pI Range 4.0 -8.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon)

705.523 710.479 718.404 719.540 724.508 733.440 739.406
740.504 743.471 749.460 750.454 752.519 757.470 764.463
767.422 771.470 774.461 780.574 781.439 784.412 786.466
792.456 798.487 804.465 813.609 814.607 818.469 820.491
824.503 825.488 838.505 839.518 841.487 854.551 862.492
864.489 880.482 884.538 890.529 903.483 916.592 920.506
933.490 934.539 943.527 949.570 954.614 961.506 967.607
970.581 980.561 988.667 989.556 1002.784 1003.552
1013.594 1019.557 1022.610 1025.624 1028.556 1040.588
1051.687 1058.615 1060.608 1062.581 1067.675 1086.622
1088.663 1091.551 1097.562 1099.636 1102.516 1106.474
1112.593 1118.526 1124.633 1133.632 1134.516 1146.583
1148.543 1151.715 1154.572 1160.639 1166.722 1169.574
1176.649 1186.550 1200.825 1209.609 1216.665 1221.505
1228.807 1229.633 1231.663 1238.759 1239.659 1242.670
1249.536 1256.731 1258.831 1263.683 1270.726 1273.631
1277.549 1284.631 1290.741 1293.790 1298.708 1305.533
1312.765 1313.765 1320.678 1327.683 1329.694 1333.747
1347.745 1349.599 1354.648 1361.693 1362.636 1368.681
1375.762 1376.611 1380.784 1390.882 1391.610 1399.758
1403.639 1410.936 1412.782 1417.720 1424.749 1425.918
1428.766 1436.767 1438.783 1445.404 1453.861 1455.761
1462.730 1464.635 1471.883 1484.746 1487.705 1494.776
1498.864 1505.726 1515.721 1519.865 1527.775 1529.802
1535.916 1541.726 1543.868 1546.805 1553.776 1555.820
1558.822 1565.980 1567.819 1569.792 1577.056 1581.015
1582.889 1585.837 1592.761 1594.858 1597.816 1599.808
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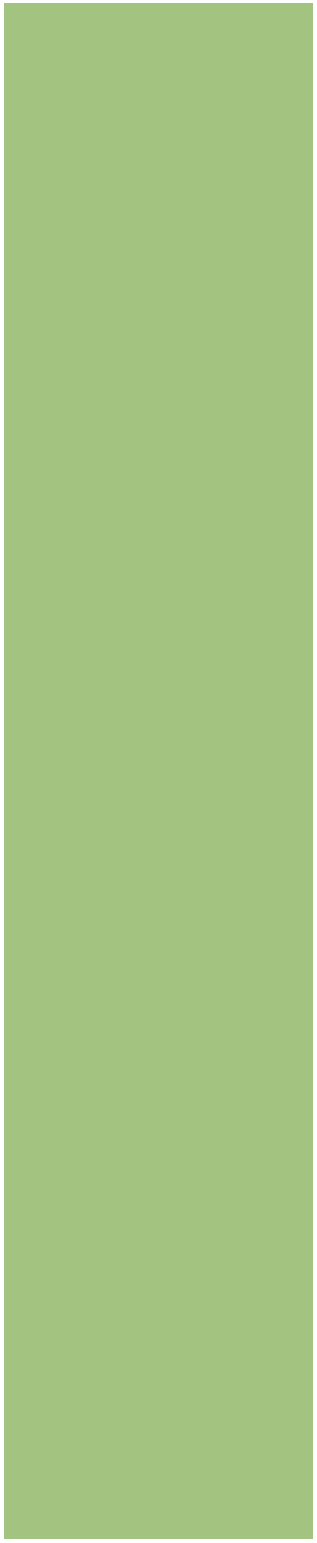

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1697.942	1707.750	1724.904	1731.818	1739.869	1741.021
1744.815	1753.038	1754.842	1756.817	1764.983	1766.765
1771.807	1783.929	1788.767	1797.977	1801.862	1810.390
1810.906	1811.851	1820.000	1824.743	1828.801	1836.902
1839.905	1844.905	1857.914	1859.917	1869.891	1872.862
1881.966	1890.944	1898.947	1916.182	1919.957	1924.769
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1972.121	1982.722	1991.668	1993.922	2006.029	2016.903
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2059.009	2067.820	2072.999	2096.399	2105.073	2112.063
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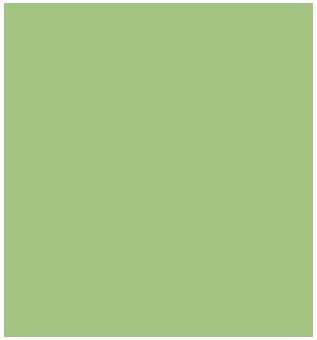
2170.120	2181.776	2184.073	2192.012	2195.009	2201.041
2219.945	2222.199	2231.607	2238.230	2258.030	2260.207
2270.016	2273.066	2282.163	2291.117	2295.149	2309.142
2315.199	2336.216	2346.972	2351.641	2355.071	2357.197
2367.346	2378.469	2388.927	2395.121	2398.979	2409.548
2411.136	2414.974	2420.340	2430.491	2433.148	2440.297
2448.290	2457.297	2471.242	2476.100	2480.023	2493.157
2503.190	2505.954	2509.395	2519.292	2523.250	2529.411
2540.366	2549.406	2554.340	2565.383	2580.315	2585.210
2595.290	2598.964	2612.237	2623.404	2631.968	2640.477
2654.515	2658.404	2666.260	2677.367	2681.028	2692.691
2696.118	2705.220	2716.480	2723.119	2734.169	2737.340
2746.441	2758.847	2764.477	2768.338	2775.893	2783.743
2793.633	2795.841	2801.258	2814.216	2821.547	2825.019
2833.225	2839.360	2851.974	2863.030	2876.816	2882.383
2890.490	2903.398	2913.317	2920.994	2936.452	2941.967
2951.915	2955.869	2966.757	2976.599	2987.193	2997.401
3002.789	3006.223	3016.278	3027.684	3037.886	3040.931
3050.263	3062.666	3065.313	3076.363	3080.325	3091.289
3093.837	3096.760	3107.491	3110.609	3122.003	3126.635
3137.719	3143.722	3153.020	3164.378	3172.986	3178.528
3187.574	3201.433	3206.428	3220.404	3231.346	3234.525
3238.396	3243.726	3255.284	3259.244	3263.784	3275.609
3279.735	3292.632	3304.122	3315.554	3318.386	3329.765
3341.085	3345.720	3354.648	3367.692	3374.692	3384.952
3392.244	3408.505	3414.289	3428.629	3442.209	3454.747



	3470.323 3474.570 3487.246 3499.706 3512.906 3524.292 3532.774 3545.875 3594.808 3609.602 3621.182 3636.598 3651.679 3656.116 3674.584 3692.280 3699.731
Tolerance (mon)	10.00 ppm
Number of Peptides	426

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	5.9×10^{-21}	gi|21730241|pdb|1GVE|B Chain B, Aflatoxin Aldehyde Reductase (Akr7a1) From Rat Liver	20	6.6	37.08	
	-	gi|433611|emb|CAA52740.1| aflatoxin B1 aldehyde reductase [Rattus norvegicus]	20	6.8	37.12	
	-	gi|21730240|pdb|1GVE|A Chain A, Aflatoxin Aldehyde Reductase (Akr7a1) From Rat Liver	20	7.2	37.21	
	-	gi|7106240|ref|NP_037347.1| aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase) [Rattus norvegicus]	20	6.8	37.13	
	-	gi|51261212|gb|AAH78872.1| Afar protein [Rattus norvegicus]	14	6.8	39.16	
2	2.2×10^{-16}	gi|56605744|ref|NP_001008334.1| hypothetical protein LOC302032 [Rattus norvegicus]	22	6.4	24.13	
+3	7.3×10^{-16}	gi|1584427|prf||2123218B corticoliberin-binding protein	13	6.1	36.72	
	-	gi|117444|sp|P24388|CRHBP_RAT Corticotropin-releasing factor-binding protein precursor (CRF-binding protein) (CRF-BP) (Corticotropin-releasing hormone-binding protein) (CRH-BP)	13	6.1	36.73	
	-	gi|21070952|ref|NP_631922.1| corticotropin releasing hormone binding protein [Rattus norvegicus]	13	6.1	36.76	
4	9.0×10^{-16}	gi|57114348|ref|NP_001008877.1| Ac1254 [Rattus norvegicus]	9	5.2	34.82	
5	2.1×10^{-14}	gi|13540671|ref|NP_110481.1| leukocyte cell derived chemotaxin 1 [Rattus norvegicus]	14	6.0	38.00	
6	6.4×10^{-14}	gi|35215315|ref|NP_877400.1| putative C3orf6 protein [Rattus norvegicus]	10	6.4	35.31	
7	7.2×10^{-14}	gi|50927559|gb|AAH78713.1| Cyp4f6 protein [Rattus norvegicus]	12	5.8	40.34	
+8	3.0×10^{-11}	gi|56789141|gb|AAH88125.1| Sulfotransferase family, cytosolic, 1C, member 1 [Rattus norvegicus]	13	6.1	35.87	

	-	gi|13929030|ref|NP_113920.1| sulfotransferase family 1A, member 2 [Rattus norvegicus]	13	6.1	35.86
9	4.9×10^{-11}	gi|34875668|ref|XP_237115.2| PREDICTED: similar to non-catalytic region of tyrosine kinase adaptor protein 2 [Rattus norvegicus]	7	6.5	43.12
10	4.2×10^{-9}	gi|395067|emb|CAA52117.1| amiloride binding protein (short form) [Rattus norvegicus]	12	5.9	25.56
11	7.0×10^{-9}	gi|49175746|gb|AAT52165.1| fos-related 2 [Rattus norvegicus]	10	7.0	35.41
12	1.8×10^{-8}	gi|2627162|dbj|BAA23524.1| Truncated TSH receptor [Rattus sordidus]	9	7.0	26.66
13	4.0×10^{-8}	gi|38146389|gb|AAR11567.1| cardiotrophin-like cytokine [Rattus norvegicus]	9	6.9	20.63
14	4.5×10^{-8}	gi|47577411|ref|NP_001000290.1| olfactory receptor Olr454 [Rattus norvegicus]	5	5.3	35.27
15	7.1×10^{-8}	gi|8394076|ref|NP_058979.1| proteasome (prosome, macropain) subunit, alpha type 6 [Rattus norvegicus]	9	6.3	27.84
16	7.9×10^{-8}	gi|2582497|gb|AAB82567.1| caspase 2 [Rattus norvegicus]	18	6.0	29.21
17	1.2×10^{-7}	gi|16758368|ref|NP_446041.1| RAB14, member RAS oncogene family [Rattus norvegicus]	13	5.8	24.14
18	1.2×10^{-7}	gi|420272|pir||E42148 GTP-binding protein rab14 - rat	13	5.8	24.08
19	1.4×10^{-7}	gi|554486|gb|AAA41864.1| protein kinase C type III	16	7.3	29.82
20	1.4×10^{-7}	gi|19745164|ref|NP_604444.1| protein kinase C, delta binding protein [Rattus norvegicus]	17	5.8	27.89
21	1.7×10^{-7}	gi|40786457|ref|NP_955411.1| hypothetical protein LOC294311 [Rattus norvegicus]	12	6.3	40.12
22	1.9×10^{-7}	gi|6981322|ref|NP_036853.1| purinergic receptor P2X-like 1 [Rattus norvegicus]	9	6.5	43.12
23	5.0×10^{-7}	gi|33086532|gb|AAP92578.1| Ab2-093 [Rattus norvegicus]	6	6.8	43.57
24	5.1×10^{-7}	gi|31324556|ref|NP_852143.1| retinol dehydrogenase 10 (all-trans) [Rattus norvegicus]	8	7.2	38.73
25	5.4×10^{-7}	gi|51948530|ref|NP_001004280.1| hypothetical protein LOC362134 [Rattus norvegicus]	9	5.1	33.55

26	7.8×10^{-7}	gi|38454226|ref|NP_942039.1| tumor protein D52-like 2 [Rattus norvegicus]	9	5.8	24.03
27	8.9×10^{-7}	gi|2143731|pir||JC4845 G protein-activated inward rectifier potassium channel chain - rat	8	5.2	43.02
28	1.1×10^{-6}	gi|34328540|ref|NP_899159.1| cathepsin Y [Rattus norvegicus]	7	6.8	34.86
29	1.2×10^{-6}	gi|38194517|gb|AAR13265.1| GP49B2 [Rattus norvegicus]	7	6.3	38.72
30	1.4×10^{-6}	gi|54035313|gb|AAH83808.1| Similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-associated Sp100 protein) [Rattus norvegicus]	8	5.3	38.61
31	1.4×10^{-6}	gi|5669929|gb|AAD46521.1|AF154914_1 cyclin H [Rattus norvegicus]	8	7.1	38.05
32	1.6×10^{-6}	gi|19865045|sp|Q9R1A0|CCNH_RAT Cyclin-H	8	6.7	38.05
33	1.8×10^{-6}	gi|31542350|ref|NP_443213.2| cyclin H [Rattus norvegicus]	8	7.1	38.13
34	2.7×10^{-6}	gi|38541353|gb|AAH62058.1| Ckm protein [Rattus norvegicus]	4	6.6	43.26
35	2.8×10^{-6}	gi|9296968|sp|P82471|GNAQ_RAT Guanine nucleotide-binding protein G(q) subunit alpha (Guanine nucleotide-binding protein alpha-q)	9	5.6	41.74
36	3.0×10^{-6}	gi|6978661|ref|NP_036662.1| creatine kinase, muscle [Rattus norvegicus]	4	6.6	43.23
37	3.2×10^{-6}	gi|13591957|ref|NP_112298.1| guanine nucleotide binding protein, alpha q polypeptide [Rattus norvegicus]	9	5.5	42.41
38	3.3×10^{-6}	gi|34873464|ref|XP_213437.2| PREDICTED: similar to Speckle-type POZ protein (PDX-1 C-terminal-interacting factor 1) (PCIF1) [Rattus norvegicus]	8	5.6	42.86
39	3.5×10^{-6}	gi|55742832|ref|NP_077069.3| annexin A4 [Rattus norvegicus]	7	5.4	36.22
40	3.5×10^{-6}	gi|37999910|sp|P55260|ANXA4_RAT Annexin A4 (Annexin IV) (Lipocortin IV) (36 kDa zymogen granule membrane-associated protein) (ZAP36)	7	5.3	36.17
41	3.5×10^{-6}	gi|19705473|ref|NP_599199.1| 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase [Rattus norvegicus]	9	6.0	38.47
42	3.6×10^{-6}	gi|38303943|gb|AAH62016.1| RAB4A, member RAS oncogene family [Rattus norvegicus]	13	5.8	24.68
43	3.8×10^{-6}	gi|27545370|ref|NP_775423.1| preprotrypsinogen IV [Rattus norvegicus]	17	6.4	27.24

44	4.3×10^{-6}	gi|37361894|gb|AAQ91060.1| LRRGT00104 [Rattus norvegicus]	6	6.8	40.22
45	4.5×10^{-6}	gi|19386562|gb|AAL86569.1| vesicular protein vp-165 short isoform [Rattus norvegicus]	11	5.2	38.83
46	5.1×10^{-6}	gi|47168483|pdb|1OT7|A Chain A, Structural Basis For 3-Deoxy-Cdca Binding And Activation Of Fxr	15	5.2	26.87
47	5.8×10^{-6}	gi|8393962|ref|NP_058927.1| phosphatidylinositol transfer protein [Rattus norvegicus]	8	6.0	32.12
48	6.1×10^{-6}	gi|3452564|dbj|BAA32479.1| Vesl-2(delta 11) [Rattus norvegicus]	9	6.0	39.61
49	7.3×10^{-6}	gi|1122946|gb|AAC52330.1| arylalkylamine N-acetyltransferase	21	6.8	20.08
50	7.9×10^{-6}	gi|34866299|ref|XP_232664.2| PREDICTED: similar to p47 protein isoform a [Rattus norvegicus]	9	5.1	37.11
51	1.0×10^{-5}	gi|56090449|ref|NP_001007716.1| RIB43A domain with coiled-coils 1 [Rattus norvegicus]	7	6.5	44.75
52	1.1×10^{-5}	gi|12700185|gb|AAG38402.1| recombination activating protein 1 [Rattus norvegicus]	9	5.7	29.27
53	1.6×10^{-5}	gi|12831221|ref|NP_075589.1| vesicle transport through interaction with t-SNAREs homolog 1A [Rattus norvegicus]	5	6.1	25.14
54	1.6×10^{-5}	gi|13124592|sp|Q9JI51|VTI1A_RAT Vesicle transport through interaction with t-SNAREs homolog 1A (Vesicle transport v-SNARE protein Vti1-like 2) (Vti1-rp2)	5	6.1	26.02
55	1.8×10^{-5}	gi|55778322|gb|AAH86609.1| LOC360912 protein [Rattus norvegicus]	14	5.2	34.41
56	2.4×10^{-5}	gi|25453349|sp|Q8VDA5|ZBP1_RAT Z-DNA-binding protein 1 (Tumor stroma and activated macrophage protein DLM-1)	6	5.3	44.24
57	2.4×10^{-5}	gi|34860868|ref|XP_342595.1| PREDICTED: similar to Z-DNA binding protein 1 (Tumor stroma and activated macrophage protein DLM-1) [Rattus norvegicus]	6	5.3	44.21
58	3.3×10^{-5}	gi|50927681|gb|AAH79000.1| Germ cell associated 1 [Rattus norvegicus]	7	5.7	41.34
59	3.4×10^{-5}	gi|28396191|gb|AAO39003.1| HOMER1G [Rattus norvegicus]	9	5.1	21.97
60	6.7×10^{-5}	gi|33086580|gb|AAP92602.1| Ab2-305 [Rattus norvegicus]	9	6.1	43.78

61	8.7×10^{-5}	gi|57526957|ref|NP_001009603.1| aspartoacylase-3 [Rattus norvegicus]	12	5.4	35.80
62	1.9×10^{-4}	gi|729113|sp|P39948|CCND1_RAT G1/S-specific cyclin-D1	7	5.0	34.26
63	1.9×10^{-4}	gi|31377523|ref|NP_741989.2| cyclin D1 [Rattus norvegicus]	7	5.1	34.20
64	3.0×10^{-4}	gi|3834625|gb|AAC71031.1| homer-1b [Rattus norvegicus]	5	5.3	40.22
65	3.4×10^{-4}	gi|13928988|ref|NP_113895.1| homer homolog 1 [Rattus norvegicus]	5	5.4	41.40
66	3.9×10^{-4}	gi|3452560|dbj|BAA32477.1| Vesl-1L [Rattus norvegicus]	5	5.5	41.44
67	4.4×10^{-4}	gi|48927599|dbj|BAD23894.1| Down-regulated in nephrectomized rat kidney #1 [Rattus norvegicus]	7	7.0	32.27
68	5.3×10^{-4}	gi|18426822|ref|NP_569088.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 7 [Rattus norvegicus]	5	7.1	43.03
69	8.4×10^{-3}	gi|27702700|ref|XP_215785.1| PREDICTED: similar to APAF1 interacting protein [Rattus norvegicus]	13	6.5	27.61

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AF22B88E-0ACC-5F8D25D6

Sequences 20073

Date & Time Mon Apr 02 17:25:57 2007 UTC (Search Time: 0.34 sec.)

Sample ID 20040825 NIA MRich spot 5209 search 20070402 number 2

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 17 - 45 kDa

pI Range 5.0 -7.5

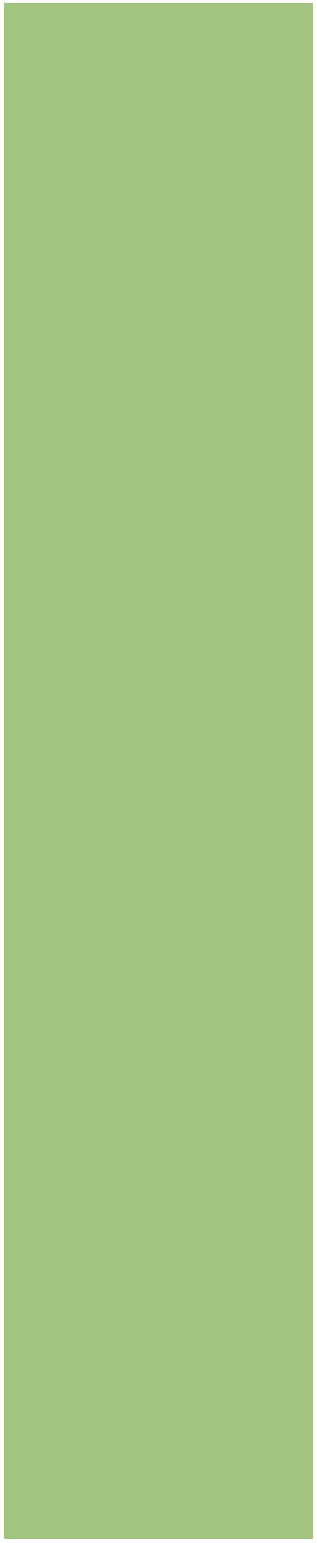
Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial);

Charge State MH+

Masses (avg)



Tolerance (avg) 1.00 ppm

Masses (mon)

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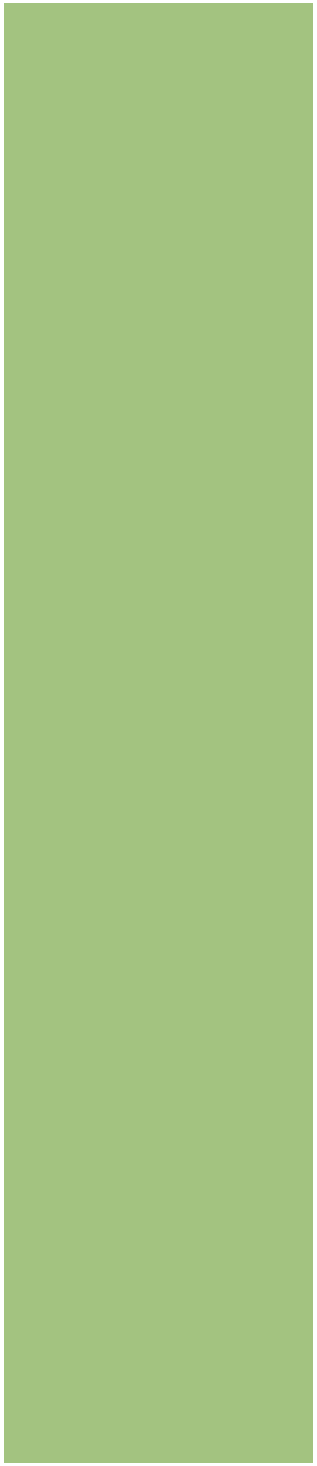

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3404.439	3423.760	3454.327	3462.486	3507.289	3516.626
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Tolerance (mon) 8.00 ppm

Number of Peptides 427

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- X! Hunter
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The Rockefeller University
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New York, NY 10021
(212) 327-8000

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.2×10^{-13}	gi|6940826|gb|AAF31764.1|AF130338_1 beta-1 adducin [Rattus norvegicus]	36	4.9	20.99	
2	7.3×10^{-7}	gi|2144103|pir||I51903 type I interleukin-1 receptor - rat (fragment)	26	4.9	19.74	
+3	1.4×10^{-6}	gi|203361|gb|AAA40891.1| clathryn light chain (LCB3)	14	4.6	23.22	
	-	gi|16758690|ref|NP_446287.1| clathrin, light polypeptide (Lcb) [Rattus norvegicus]	13	4.6	25.21	
4	1.3×10^{-4}	gi|7547027|gb|AAF63763.1|AF250032_1 agrin precursor [Rattus norvegicus]	19	5.0	16.01	
5	4.1×10^{-4}	gi|12964662|dbj|BAB32668.1| branched-chain alpha-keto acid dihydrolipoyl acyltransferase [Rattus norvegicus]	22	5.2	20.82	
6	6.1×10^{-4}	gi|2674183|gb|AAB88701.1| kinesin-related protein KRP4 [Rattus norvegicus]	26	4.9	17.12	
7	9.6×10^{-4}	gi|755583|gb|AAC52590.1| C-CAM4	18	5.6	16.00	
8	9.6×10^{-4}	gi|27545443|ref|NP_775461.1| CEA-related cell adhesion molecule 10 [Rattus norvegicus]	18	5.6	16.10	
9	1.3×10^{-3}	gi|2326257|dbj|BAA21777.1| growth hormone secretagogue receptor type 1a [Rattus norvegicus]	17	5.2	27.31	
10	1.4×10^{-3}	gi|7766811|pdb|1CK4|A Chain A, Crystal Structure Of Rat A1b1 Integrin I-Domain.	17	5.3	22.19	
11	1.4×10^{-3}	gi|30749469|pdb|1MHP|A Chain A, Crystal Structure Of A Chimeric Alpha1 Integrin I-Domain In Complex With The Fab Fragment Of A Humanized Neutralizing Antibody	18	5.6	21.64	
12	1.5×10^{-3}	gi|21930125|gb|AAM82159.1|AF523266_1 osteoclast stimulating factor [Rattus norvegicus]	15	5.3	23.89	
13	1.5×10^{-3}	gi|38382846|gb|AAH62400.1| Osteoclast stimulating factor 1 [Rattus norvegicus]	15	5.4	23.88	
14	1.7×10^{-3}	gi|16758744|ref|NP_446330.1| complexin 2 [Rattus norvegicus]	14	5.1	15.49	
15	1.7×10^{-3}	gi|1363278|pir||C57233 complexin II - rat	14	5.1	15.39	
16	1.9×10^{-3}	gi|12408324|ref|NP_074055.1| complexin 1 [Rattus norvegicus]	14	4.9	15.16	
17	2.1×10^{-3}	gi|13242261|ref|NP_077342.1| neuronal calcium sensor-1 [Rattus norvegicus]	14	4.7	21.92	
18	4.8×10^{-3}	gi|20302119|ref|NP_620270.1| dopamine receptor D1 interacting protein [Rattus norvegicus]	22	5.8	24.99	
19	5.5×10^{-3}	gi|46048487|ref|NP_996833.1| MID1 interacting G12-like protein [Rattus norvegicus]	9	5.4	20.51	

20	6.5×10^{-3}	gi|204128|gb|AAA41153.1| ferritin heavy chain	11	5.9	21.15
21	6.5×10^{-3}	gi|6978859|ref|NP_036980.1| ferritin, heavy polypeptide 1 [Rattus norvegicus]	11	5.6	21.25
22	6.8×10^{-3}	gi|13492652|gb|AAK28292.1|AF345445_1 potassium channel beta subunit KChIP4 variant [Rattus norvegicus]	7	4.7	25.16
23	6.9×10^{-3}	gi|56605760|ref|NP_001008342.1| prolactin-like protein-F beta [Rattus norvegicus]	8	5.4	29.03
24	6.9×10^{-3}	gi|120519|sp|P19132|FRIH_RAT Ferritin heavy chain (Ferritin H subunit)	11	5.9	21.28
25	7.2×10^{-3}	gi|34870715|ref|XP_220404.2| PREDICTED: similar to Keratinocytes-associated transmembrane protein 2 precursor [Rattus norvegicus]	9	5.0	28.42
26	7.3×10^{-3}	gi|51859472|gb|AAH81845.1| Fth1 protein [Rattus norvegicus]	9	6.0	25.22
27	9.0×10^{-3}	gi|56404325|sp|Q6AY91|NRK1_RAT Nicotinamide riboside kinase 1	6	4.7	22.47
28	0.011	gi|34856632|ref|XP_342484.1| PREDICTED: similar to zinc finger, CSL-type containing 3 [Rattus norvegicus]	7	4.7	17.26
29	0.019	gi|20151158|pdb|1L0B|A Chain A, Crystal Structure Of Rat Brca1 Tandem-Brct Region	10	5.2	26.51
30	0.051	gi|27710200|ref|XP_229205.1| PREDICTED: similar to dual specificity phosphatase 21 [Rattus norvegicus]	6	5.9	21.66
31	0.057	gi|7259287|dbj|BAA92743.1| A-type potassium channel modulatory protein 2a [Rattus norvegicus]	10	4.5	25.79

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A79F168E-12A8-57B11DF9

Sequences 20092

Date & Time Thu Jan 25 16:11:53 2007 UTC (Search Time: 0.33 sec.)

Sample ID 20040825 richardson NIA set 1 spot 1111, 20070125, cleaned data #2

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 15 - 30 kDa

pI Range 3.0 -6.0

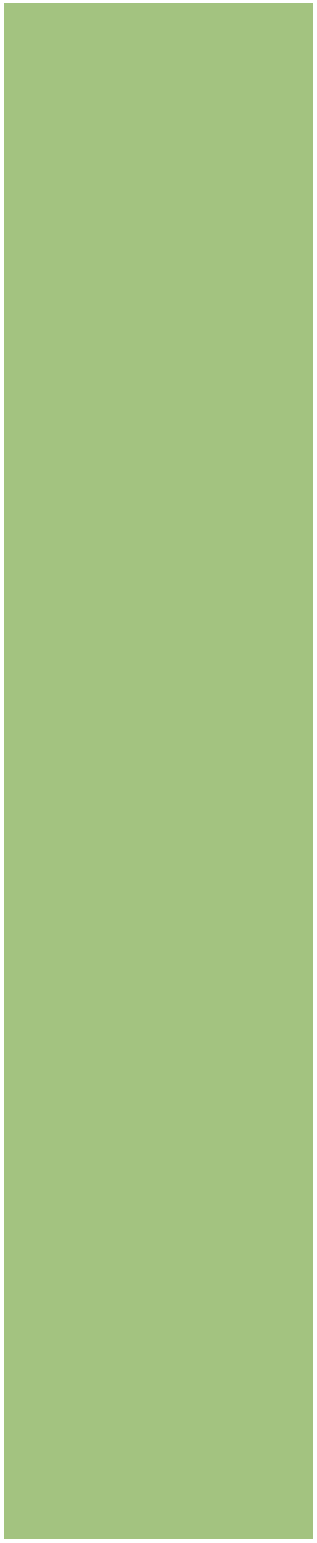
Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +O@M(Partial);

Charge State MH+

Masses (avg)



Tolerance (avg) 1.00 ppm

Masses (mon)

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778.432	780.366	786.445	792.377	798.370	801.451	814.430	820.428	824.498
827.494	833.443	834.473	837.350	840.486	850.557	857.495	858.480	879.456
888.494	891.464	898.506	916.479	923.108	932.471	934.527	946.946	948.479
954.579	956.534	962.535	974.509	979.534	985.523	991.508	992.483	1002.809
1003.448	1004.578	1013.532	1014.517	1020.547	1021.450	1024.462	1027.522	
1033.180	1041.544	1043.564	1051.555	1055.486	1060.563	1064.576	1068.530	
1082.541	1088.637	1091.525	1097.624	1107.565	1113.574	1117.687	1121.581	
1133.601	1139.725	1146.596	1151.705	1153.601	1159.596	1161.636	1172.577	
1176.590	1186.605	1187.602	1191.594	1200.669	1205.524	1207.557	1215.614	
1220.640	1227.632	1228.646	1236.016	1236.702	1237.578	1240.634	1248.586	
1251.751	1256.636	1263.659	1264.664	1271.661	1273.630	1280.796	1281.639	
1284.629	1292.672	1295.675	1301.664	1310.688	1317.591	1320.549	1323.632	
1330.791	1331.675	1336.665	1348.155	1349.588	1353.646	1360.736	1362.698	
1365.582	1372.629	1373.626	1380.469	1381.644	1390.615	1396.720	1404.654	
1407.783	1410.740	1418.105	1418.789	1421.605	1424.728	1432.716	1434.754	
1441.748	1447.632	1453.656	1461.055	1462.728	1464.711	1470.693	1482.823	
1483.627	1488.687	1493.729	1501.673	1503.735	1514.874	1518.701	1527.606	
1529.659	1532.662	1535.720	1543.855	1547.666	1554.956	1557.691	1563.728	
1570.682	1577.412	1580.702	1587.775	1589.707	1596.800	1599.761	1611.683	
1612.791	1621.724	1623.731	1631.715	1635.661	1639.774	1646.760	1651.708	
1659.816	1660.886	1665.855	1672.759	1681.691	1689.706	1698.712	1709.912	
1710.830	1718.804	1727.746	1736.179	1739.716	1748.628	1753.840	1761.828	
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1818.714	1826.820	1828.892	1835.924	1839.850	1849.537	1857.973	1860.935	
1863.578	1872.105	1874.873	1883.805	1886.845	1894.955	1898.797	1907.462	
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1982.530	1983.910	1993.940	2001.886	2009.848	2021.942	2030.277	2038.143	
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2106.473	2120.219	2123.011	2135.908	2146.940	2151.124	2161.382	2186.786	
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2336.510	2338.399	2349.160	2352.001	2362.990	2367.249	2383.203	2394.033	
2397.957	2407.830	2416.928	2419.280	2425.082	2435.210	2439.333	2451.192	
2454.061	2463.213	2465.219	2468.230	2473.253	2478.013	2483.246	2492.150	
2496.086	2510.106	2519.599	2523.287	2527.146	2537.316	2540.031	2553.187	
2555.672	2566.548	2569.108	2579.294	2582.374	2589.191	2593.684	2597.047	
2608.905	2613.070	2620.893	2624.964	2636.228	2641.281	2652.025	2663.730	
2667.139	2677.517	2682.190	2685.331	2696.095	2706.249	2712.315	2726.333	
2736.297	2741.057	2753.274	2761.482	2772.007	2777.650	2781.415	2786.249	
2799.280	2810.448	2819.527	2832.062	2840.279	2852.608	2859.232	2873.083	
2884.542	2891.022	2894.320	2904.441	2913.235	2918.510	2929.403	2939.731	
2944.409	2955.826	2958.390	2970.899	2975.786	2978.505	2988.441	2990.283	
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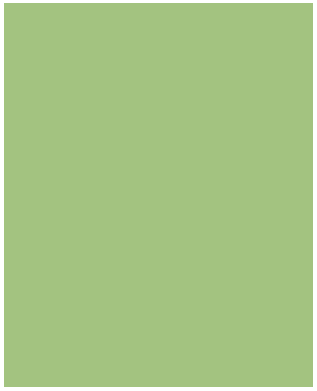

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3153.632	3158.893	3166.128	3173.866	3177.511	3190.397	3202.737	3206.360
3212.581	3221.445	3232.620	3243.391	3249.532	3254.795	3265.834	3270.378
3282.910	3288.470	3299.682	3304.521	3315.682	3323.677	3335.299	3347.524
3359.109	3367.781	3379.283	3385.668	3391.745	3400.577	3409.420	3421.780
3435.741	3450.363	3463.312	3475.688	3479.859	3494.255	3498.875	3514.028
3534.577	3539.543	3551.492	3558.840	3569.614	3574.765	3582.419	3595.893
3599.447	3612.467	3628.510	3635.652	3640.565	3645.198	3667.385	3673.585
3681.792	3694.835	3698.519					

Tolerance (mon) 10.00 ppm

Number of Peptides 433

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

- PROWL Home
- Chait Lab

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.2×10^{-6}	gi|19424194|ref|NP_598220.1| RAB3C, member RAS oncogene family [Rattus norvegicus]	63	5.2	26.11	
	-	gi|51338595|sp|P62824|RAB3C_RAT Ras-related protein Rab-3C	56	5.1	26.08	
+2	1.5×10^{-5}	gi|112442|pir||A39816 tropomyosin 2, fibroblast - rat	38	4.7	32.75	
	-	gi|207502|gb|AAA18097.1| alpha-tropomyosin 3	37	4.7	32.83	
	-	gi|14134107|gb|AAK54243.1|AF372217_1 tropomyosin alpha isoform [Rattus norvegicus]	36	4.8	33.07	
	-	gi|207351|gb|AAA21805.1| non-muscle alpha tropomyosin	36	4.8	32.77	
	-	gi|207353|gb|AAA21802.1| hepatoma alpha tropomyosin	36	4.8	32.85	
	-	gi|207349|gb|AAA21801.1| striated-muscle alpha tropomyosin	32	4.7	32.73	
	-	gi|207352|gb|AAA21803.1| minor striated-muscle alpha tropomyosin	26	4.8	33.93	
	-	gi|207355|gb|AAA42252.1| brain alpha-tropomyosin (TMBr-1)	31	4.7	32.55	
	-	gi|112446|pir||C39816 tropomyosin 5a, fibroblast - rat	35	4.7	28.60	
	-	gi|112447|pir||D39816 tropomyosin 5b, fibroblast - rat	34	4.7	28.68	
	-	gi|112448|pir||A22165 tropomyosin alpha chain, smooth muscle - rat	29	4.9	32.24	
	-	gi|207350|gb|AAA21804.1| smooth-muscle alpha tropomyosin	29	4.7	32.71	
	-	gi|50926969|gb|AAH79119.1| Similar to RIKEN cDNA 5830446M03 [Rattus norvegicus]	49	5.2	32.90	
	-	gi|1098969|gb|AAC53100.1| inositol 1,4,5-trisphosphate receptor	45	5.2	22.58	
	-	gi|38051907|gb|AAH60562.1| Rab3b protein [Rattus norvegicus]	64	5.0	26.12	

-	gi|13592037|ref|NP_112353.1| RAB3B, member RAS oncogene family [Rattus norvegicus]	55	4.9	25.00
-	gi|2981437|gb|AAC06290.1| lipocortin V [Rattus norvegicus]	38	5.0	33.95
-	gi|56649|emb|CAA34347.1| myosin heavy chain (AA 279) [Rattus norvegicus]	40	5.2	31.98
-	gi|9653293|gb|AAB37701.2| tropomyosin 5; TM-5 [Rattus sp.]	31	4.7	29.16
-	gi|56971497|gb|AAH88253.1| Similar to RIKEN cDNA 4933417L10 [Rattus norvegicus]	27	5.2	33.52
-	gi|56388776|gb|AAH87696.1| Fgfr1op2 protein [Rattus norvegicus]	44	5.4	25.05

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Tue Feb 06 02:06:02 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 19 - 34 kDa

pI Range 4.7 -5.8

Digestion Trypsin

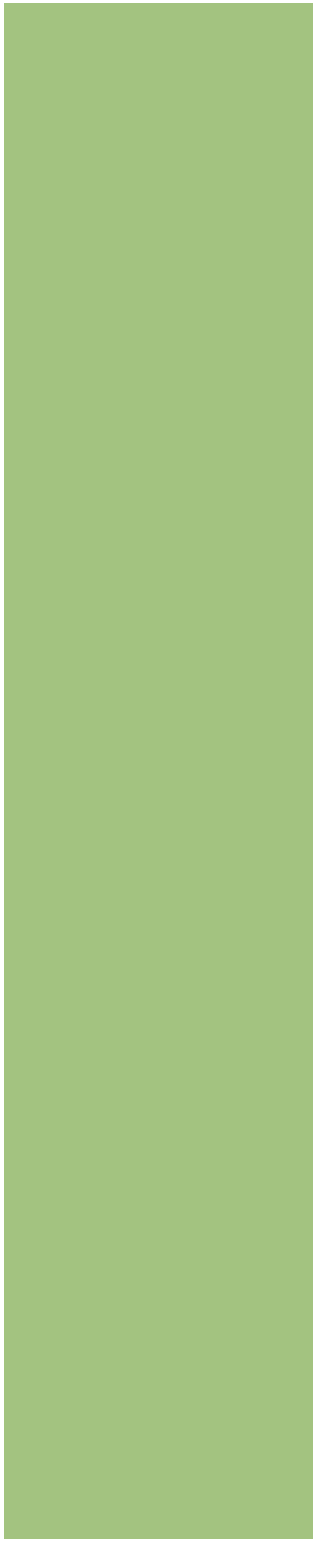
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@SY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

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794.422 797.362 803.449 805.395 813.448 817.404 820.367
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1555.739 1558.740 1563.767 1570.908 1571.842 1579.752
1585.830 1589.827 1596.840 1597.754 1605.782 1608.994
1612.857 1620.788 1621.872 1624.882 1633.985 1635.754
1638.832 1646.799 1654.758 1656.812 1660.760 1664.741
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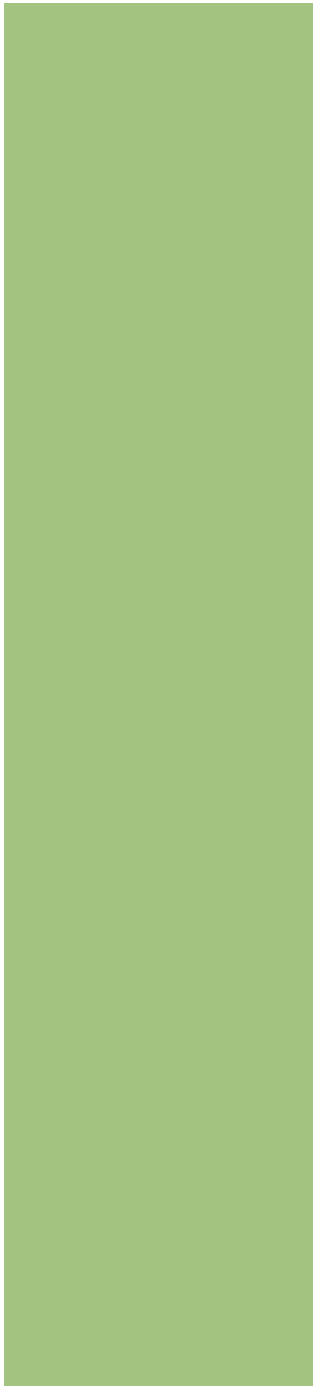

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3256.449 3265.527 3278.086 3282.637 3288.544 3292.330
3304.475 3316.333 3321.377 3329.572 3336.338 3346.499
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3439.587 3446.938 3466.140 3487.145 3525.024 3538.110
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3652.569 3659.896 3672.780 3700.659

Tolerance (mon) 27.00 ppm

Number of Peptides 419

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

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- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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- Chait Lab

The Rockefeller University

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center of Research Resources

National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	8.5×10^{-20}	gi|2914269|pdb|1TIP|A Chain A, The Bisphosphatase Domain Of The Bifunctional Rat Liver 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase	28	5.7	22.34	
	-	gi|33356831|pdb|1C7Z|A Chain A, Regulatory Complex Of Fructose-2,6-Bisphosphatase	28	5.8	22.48	
2	2.7×10^{-9}	gi|3176876|gb|AAC18852.1| ankyrinG [Rattus norvegicus]	34	5.0	15.94	
3	3.7×10^{-8}	gi|34881545|ref|XP_346352.1| PREDICTED: similar to RAB9B, member RAS oncogene family [Rattus norvegicus]	19	4.8	23.04	
4	4.1×10^{-8}	gi|203278|gb|AAA40870.1| clathryn light chain (LCA3)	6	4.4	23.60	
5	6.2×10^{-8}	gi|39654405|pdb|1P1D|A Chain A, Structural Insights Into The Inter-Domain Chaperoning Of Tandem Pdz Domains In Glutamate Receptor Interacting Proteins	15	4.7	21.32	
6	7.2×10^{-8}	gi|56090373|ref|NP_001007648.1| hypothetical protein LOC297337 [Rattus norvegicus]	9	5.7	19.67	
7	7.3×10^{-8}	gi|57863782|ref|NP_001009264.1| T-cell activation protein [Rattus norvegicus]	14	4.7	14.20	
8	1.9×10^{-7}	gi|27708842|ref|XP_216097.1| PREDICTED: similar to replication protein A3 [Rattus norvegicus]	18	4.8	13.79	
9	5.8×10^{-7}	gi|1929922|gb|AAB51478.1| anti-idiotype immunoglobulin M heavy chain [Rattus norvegicus]	28	4.7	19.33	
10	2.1×10^{-6}	gi|207359|gb|AAA42254.1| brain alpha-tropomyosin (TMBr-3)	8	4.6	23.33	
11	3.3×10^{-6}	gi|55831|emb|CAA35499.1| unnamed protein product [Rattus norvegicus]	18	4.6	19.73	
12	4.5×10^{-6}	gi|554472|gb|AAA41539.1| lactase phlorizin hydrolase [Rattus norvegicus]	7	5.4	24.41	
13	4.5×10^{-6}	gi|2392330|pdb|1FBT|A Chain A, The Bisphosphatase Domain Of The Bifunctional Rat Liver 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase	9	5.8	21.82	
14	7.4×10^{-6}	gi|134717|sp|P01244|SOMA_RAT Somatotropin precursor (Growth hormone)	14	5.7	24.92	
15	7.4×10^{-6}	gi|56318|emb|CAA24547.1| unnamed protein product [Rattus norvegicus]	14	5.7	24.89	
16	9.7×10^{-6}	gi|14994701|gb|AAK76996.1| epidermal growth factor receptor [Rattus norvegicus]	3	5.4	20.67	
17	2.4×10^{-5}	gi|6981520|ref|NP_037214.1| syndecan 2 [Rattus norvegicus]	18	4.6	23.26	

18	2.4×10^{-5}	gi|3171996|emb|CAA06509.1| collagen alpha 1 (V) [Rattus norvegicus]	14	4.8	22.73
19	2.2×10^{-4}	gi|2842665|sp|Q64119|MYL6_RAT Myosin light polypeptide 6 (Smooth muscle and nonmuscle myosin light chain alkali 6) (Myosin light chain alkali 3) (Myosin light chain 3) (MLC-3) (LC17)	13	4.5	17.13
20	9.4×10^{-4}	gi|18266698|ref|NP_543171.1| Fas apoptotic inhibitory molecule [Rattus norvegicus]	17	5.3	20.43
21	1.3×10^{-3}	gi|38502804|sp|Q8R5H8|FAIM1_RAT Fas apoptotic inhibitory molecule 1 (rFAIM)	15	4.8	22.86
22	0.64	gi|34873950|ref|XP_213490.2| PREDICTED: similar to Protein C21orf58 [Rattus norvegicus]	16	4.6	20.59

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AA91FA68-0F90-5AC92111

Sequences 20076

Date & Time Thu Feb 22 19:59:04 2007 UTC (Search Time: 0.28 sec.)

Sample ID 20040825 richardson NIA set 1 spot 2112 CONSENSUS search

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 12 - 25 kDa

pI Range 3.0 -6.0

Digestion Trypsin

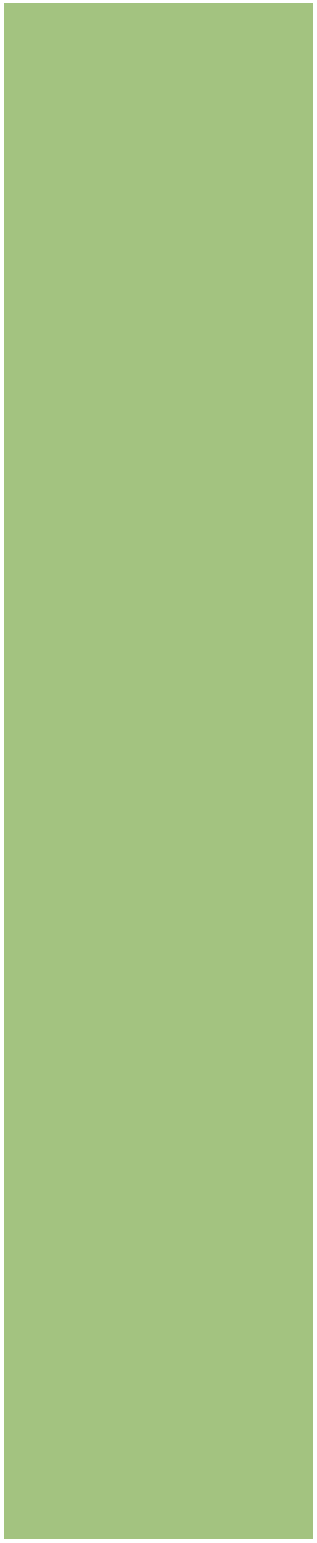
Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@Y(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

710.273	711.295	718.449	719.260	721.353	726.309	731.318	733.374	738.390
740.346	745.422	750.294	755.423	757.402	762.462	766.328	772.371	773.287
778.456	784.471	786.318	789.394	795.414	796.457	802.446	803.456	812.401
818.393	820.317	824.406	827.479	838.542	840.471	850.503	862.272	864.485
876.330	879.479	888.437	889.520	893.416	898.489	904.467	916.380	920.415
932.474	933.481	939.553	941.451	945.459	950.533	954.581	960.451	961.451
965.502	974.490	977.495	988.461	994.541	1002.427	1012.847	1013.490	1016.469
1022.655	1023.537	1025.497	1031.516	1040.741	1041.500	1051.511	1056.513	
1062.557	1068.530	1079.488	1085.531	1086.373	1090.546	1096.531	1097.132	
1098.559	1107.564	1111.531	1117.505	1119.508	1125.617	1132.535	1133.576	
1138.474	1141.473	1147.619	1148.531	1154.513	1157.578	1164.226	1169.558	
1176.656	1187.877	1189.617	1196.799	1197.521	1204.609	1205.637	1208.513	
1215.564	1221.648	1228.642	1229.728	1233.553	1240.606	1243.404	1247.536	
1254.581	1256.441	1261.598	1264.587	1271.584	1272.160	1274.730	1277.566	
1281.610	1288.993	1289.669	1297.656	1304.428	1306.689	1313.631	1320.616	
1326.615	1332.651	1339.735	1347.382	1350.521	1357.628	1362.642	1369.606	
1373.669	1381.587	1385.642	1391.536	1396.712	1403.738	1405.605	1408.584	
1411.718	1418.832	1424.745	1431.917	1433.701	1438.649	1447.597	1448.494	
1451.697	1458.758	1460.275	1463.646	1470.684	1477.764	1479.731	1486.470	
1487.223	1488.755	1492.522	1499.786	1501.663	1509.681	1516.672	1518.638	
1524.808	1529.701	1536.685	1537.345	1541.649	1548.634	1550.939	1553.618	
1557.680	1565.739	1569.764	1574.728	1581.921	1588.702	1593.239	1597.810	
1604.948	1608.834	1616.727	1619.651	1622.796	1630.777	1638.725	1641.724	
1650.026	1651.940	1660.350	1662.518	1666.775	1674.837	1678.751	1687.147	
1689.774	1697.726	1702.861	1710.954	1711.484	1713.935	1716.639	1724.290	
1725.968	1733.864	1735.883	1739.671	1744.814	1753.006	1755.601	1761.727	
1770.809	1782.898	1791.009	1792.805	1796.940	1804.940	1811.926	1819.873	
1821.798	1830.170	1831.812	1843.645	1853.777	1856.909	1862.019	1871.036	
1874.941	1882.996	1886.270	1889.839	1895.698	1904.238	1907.795	1916.038	
1918.043	1922.852	1932.046	1940.697	1950.141	1954.962	1963.695	1971.012	
1976.666	1984.967	1986.407	1991.783	1996.865	2004.756	2009.342	2013.268	
2018.528	2028.979	2032.924	2043.930	2052.708	2058.967	2066.980	2070.349	
2093.702	2096.137	2105.181	2108.581	2111.488	2120.782	2126.803	2137.999	
2147.787	2150.909	2160.102	2163.891	2177.980	2185.971	2194.923	2200.069	
2209.081	2220.238	2222.078	2239.064	2248.092	2257.203	2258.963	2263.927	
2273.166	2276.314	2281.974	2290.669	2295.023	2310.084	2319.060	2338.041	
2348.475	2352.851	2356.119	2365.512	2367.150	2380.046	2390.014	2393.308	
2400.959	2413.021	2415.073	2425.943	2436.206	2437.237	2443.293	2453.759	
2464.147	2466.990	2481.129	2494.098	2499.484	2512.298	2521.354	2531.309	
2535.242	2544.477	2546.108	2557.133	2568.114	2572.109	2584.184	2588.295	
2598.244	2602.916	2613.891	2617.509	2628.964	2633.179	2636.015	2646.090	
2650.216	2661.290	2672.179	2680.962	2691.367	2695.178	2705.295	2712.308	
2722.563	2728.401	2738.898	2743.342	2749.202	2760.093	2766.113	2770.012	
2779.026	2789.156	2798.522	2808.153	2819.732	2826.534	2833.128	2843.393	
2846.771	2851.842	2859.294	2867.225	2872.205	2882.396	2892.823	2897.753	
2908.643	2914.241	2917.552	2928.406	2938.586	2941.143	2951.199	2960.320	
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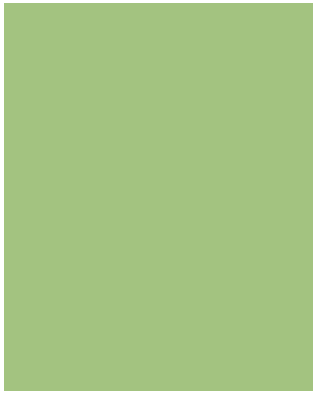


3041.437	3044.187	3054.230	3055.199	3065.448	3067.649	3071.755	3076.087
3087.157	3093.074	3104.475	3108.755	3112.513	3125.418	3136.462	3149.341
3157.550	3169.106	3174.569	3181.405	3187.373	3198.336	3202.604	3215.732
3229.805	3234.860	3245.674	3258.658	3262.581	3271.514	3284.897	3288.643
3298.385	3313.450	3318.764	3330.104	3333.137	3347.229	3358.852	3363.148
3371.903	3385.606	3397.608	3408.570	3421.756	3426.485	3429.561	3440.297
3451.684	3463.327	3469.591	3481.105	3490.409	3501.558	3507.299	3521.311
3526.348	3544.365	3549.379	3563.594	3570.190	3591.303	3595.340	3610.536
3625.804	3629.981	3634.770	3637.855	3650.862	3670.088	3686.583	3699.879

Tolerance (mon) 9.00 ppm

Number of Peptides 455

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.3×10^{-5}	gi|52000743|sp||Q63862_2 [Segment 2 of 2] Myosin-11 (Myosin heavy chain, smooth muscle isoform) (SMMHC)	56	5.1	71.76	◉
+2	2.1×10^{-3}	gi|48734834|gb|AAH72523.1| Anxa6 protein [Rattus norvegicus]	53	5.4	76.14	◉
-		gi|13994159|ref|NP_077070.1| annexin A6 [Rattus norvegicus]	53	5.4	76.14	◉
-		gi|20302073|ref|NP_620244.1| cadherin 13 [Rattus norvegicus]	37	5.0	78.47	◉
-		gi|127572|sp|P18589|MX2_RAT Interferon-induced GTP-binding protein Mx2	45	5.5	75.63	◉
-		gi|127573|sp|P18590|MX3_RAT Interferon-induced GTP-binding protein Mx3	44	5.3	75.56	◉
-		gi|6978647|ref|NP_036658.1| chromogranin B [Rattus norvegicus]	51	5.0	77.49	◉
-		gi|53734296|gb|AAH83905.1| Lrrc43 protein [Rattus norvegicus]	35	5.2	76.55	◉
-		gi|34859658|ref|XP_235782.2| PREDICTED: similar to Kelch repeat and BTB domain-containing protein 3 (BTB and kelch domain-containing protein 3) [Rattus norvegicus]	52	5.6	70.74	◉
-		gi|13928780|ref|NP_113764.1| cytochrome P450 reductase [Rattus norvegicus]	38	5.3	77.34	◉
-		gi|205660|gb|AAA41683.1| NADPH-cytochrome P-450 oxidoreductase	36	5.3	77.32	◉

NOTE:

1. To search again using unmatched masses, click the symbol ◉.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AE3D8DDE-0BFC-B0DDC982

Sequences 20076

Date & Time Sun Feb 04 23:03:01 2007 UTC (Search Time: 0.55 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 69 - 80 kDa

pI Range 4.8 -5.6

Digestion Trypsin

Missed Cuts 1

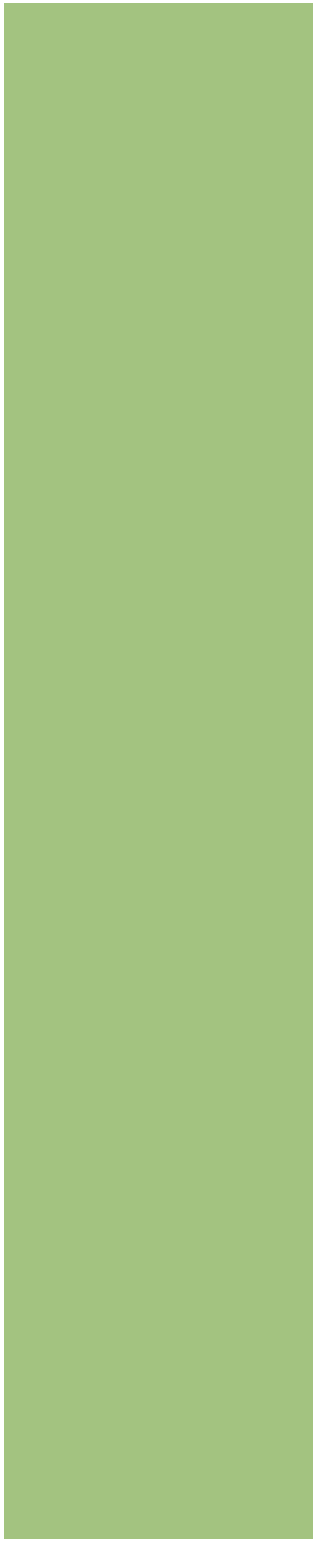
Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 710.379 712.244 717.458 720.469 724.499 740.240 745.426
750.410 751.460 754.431 763.435 767.416 769.429 773.445
780.418 786.498 791.448 797.399 798.482 804.461 813.451
814.430 820.448 824.499 830.477 837.975 839.514 841.484
854.528 862.470 880.480 886.518 888.481 891.491 902.733
903.522 905.464 908.543 916.529 918.505 932.544 938.593
941.522 944.559 950.606 958.712 959.524 966.581 970.580
979.508 988.519 993.538 1003.594 1013.593 1016.551
1022.523 1023.578 1029.570 1033.547 1037.552 1044.564
1051.686 1057.892 1058.636 1060.564 1066.598 1067.675
1085.690 1088.685 1092.552 1098.587 1106.519 1112.548
1113.625 1117.626 1123.956 1124.701 1132.907 1133.564
1138.599 1146.605 1148.543 1151.669 1158.645 1164.608
1173.627 1175.634 1187.686 1188.660 1200.639 1208.790
1209.633 1211.717 1218.661 1220.611 1225.672 1228.689
1236.770 1238.664 1244.616 1249.583 1254.727 1261.650
1263.707 1270.990 1271.710 1273.679 1284.631 1288.807
1291.515 1303.880 1305.533 1312.839 1314.693 1319.529
1327.707 1329.670 1337.486 1338.791 1347.795 1351.751
1354.747 1357.722 1364.824 1365.794 1373.666 1380.710



1381.860	1389.628	1396.612	1399.657	1403.639	1412.732
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1445.430	1453.682	1454.786	1460.774	1467.832	1470.903
1483.191	1483.814	1485.733	1490.719	1497.797	1504.761
1515.697	1519.788	1523.753	1529.540	1537.791	1544.822
1547.760	1555.769	1561.856	1569.021	1570.808	1577.860
1579.679	1584.847	1590.856	1596.984	1604.823	1609.735
1613.925	1617.470	1626.879	1635.172	1637.896	1645.889
1647.993	1656.230	1664.021	1666.631	1674.832	1676.927
1681.782	1686.756	1689.771	1697.835	1707.810	1715.749
1716.920	1725.803	1731.570	1734.794	1743.864	1745.580
1757.613	1765.780	1785.898	1788.944	1797.041	1804.928
1806.960	1815.041	1820.007	1828.866	1837.891	1847.950
1854.817	1857.950	1866.959	1873.978	1881.828	1890.982
1899.161	1907.975	1913.952	1922.948	1924.897	1928.740
1937.890	1944.031	1954.318	1964.871	1976.860	1985.103
1994.024	2002.032	2011.082	2020.032	2029.699	2033.068
2037.109	2046.299	2053.160	2066.947	2078.199	2101.228
2106.233	2111.026	2120.134	2133.272	2136.789	2140.091
2152.041	2161.237	2163.241	2183.431	2186.044	2191.117
2195.092	2204.063	2208.081	2220.410	2222.060	2231.246
2238.251	2247.087	2258.180	2260.325	2270.616	2276.365
2283.184	2292.366	2296.173	2310.300	2315.256	2337.413
2343.083	2353.235	2363.114	2367.307	2376.296	2384.249
2388.132	2394.391	2399.106	2408.652	2420.236	2425.177
2434.474	2436.336	2440.328	2450.955	2455.459	2465.417
2470.169	2480.357	2492.955	2500.326	2509.463	2522.472
2535.448	2545.770	2548.286	2561.123	2571.532	2575.599
2585.181	2596.256	2608.250	2611.451	2617.617	2631.421
2645.471	2657.509	2666.233	2675.982	2679.294	2690.500
2695.499	2706.387	2710.209	2720.741	2723.483	2734.322
2746.454	2762.365	2773.495	2779.494	2782.976	2795.501
2806.447	2810.446	2815.162	2826.183	2831.307	2842.467
2854.764	2857.357	2866.728	2877.559	2888.882	2900.046
2903.421	2915.595	2926.519	2936.551	2950.184	2953.808
2967.078	2979.200	2987.186	2991.495	2997.689	3001.305
3013.571	3021.973	3032.092	3035.729	3047.768	3051.786
3062.216	3075.540	3086.759	3094.699	3105.878	3108.507
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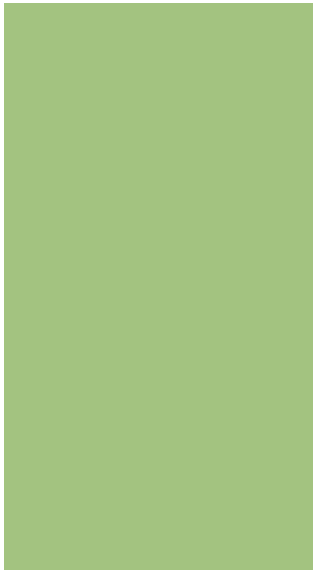

	3164.612	3174.625	3187.658	3199.080	3202.548	3215.066
	3219.804	3225.349	3237.182	3245.467	3252.226	3259.606
	3264.839	3276.320	3289.367	3292.729	3305.615	3318.486
	3326.719	3330.955	3341.850	3345.551	3353.817	3364.827
	3376.795	3382.630	3397.613	3407.594	3420.426	3424.958
	3432.097	3444.184	3459.222	3478.067	3492.423	3502.980
	3506.250	3518.146	3526.741	3537.751	3549.138	3565.287
	3579.579	3589.540	3593.698	3617.317	3620.518	3625.991
	3639.834	3667.151	3677.640	3691.908	3694.610	

Tolerance (mon) 77.00 ppm

Number of Peptides 414

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.2×10^{-5}	gi|1408312|gb|AAB03674.1| dimethylglycine dehydrogenase-like protein	31	5.9	30.09	
2	1.7×10^{-3}	gi|24158900|pdb|1LUF|A Chain A, Crystal Structure Of The Musk Tyrosine Kinase: Insights Into Receptor Autoregulation	23	5.5	39.33	
3	0.021	gi|8547323|gb|AAF76329.1| semaphorin [Rattus norvegicus]	21	6.0	33.89	
+4	0.026	gi|52345435|ref|NP_037027.2| adenosine kinase [Rattus norvegicus]	20	5.8	40.46	
	-	gi|1906013|gb|AAB50236.1| adenosine kinase [Rattus norvegicus]	14	5.8	40.42	
5	0.026	gi|7242211|ref|NP_037178.1| thyrotropin releasing hormone [Rattus norvegicus]	18	5.4	29.44	
6	0.033	gi|11024668|ref|NP_067601.1| aryl hydrocarbon receptor-interacting protein-like 1 [Rattus norvegicus]	12	5.7	38.68	
+7	0.041	gi|34810278|pdb|1OR8|A Chain A, Structure Of The Predominant Protein Arginine Methyltransferase Prmt1	29	5.5	39.77	
	-	gi|31615892|pdb|1ORI|A Chain A, Structure Of The Predominant Protein Arginine Methyltransferase Prmt1	29	5.5	40.13	
	-	gi|53733398|gb|AAH83550.1| Flot2 protein [Rattus norvegicus]	16	5.3	38.81	
	-	gi|4097589|gb|AAD00120.1| R-Reggie-1.1	16	5.3	38.81	
	-	gi|57528160|ref|NP_001009619.1| nucleotide binding protein 1 [Rattus norvegicus]	21	5.7	34.65	
	-	gi|45478210|gb|AAS66276.1| LRRGT00185 [Rattus norvegicus]	16	5.3	29.42	
	-	gi|16758066|ref|NP_445799.1| nuclear distribution gene E homolog 1 [Rattus norvegicus]	17	5.3	38.62	

-	gi|203826|gb|AAA41050.1| cytochrome P-450c17 (EC 1.14.99.9)	35	5.2	26.97	◉

NOTE:

1. To search again using unmatched masses, click the symbol ◉.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A8695475-11D0-A85AF707

Sequences 20076

Date & Time Mon Feb 05 02:43:06 2007 UTC (Search Time: 0.50 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 23 - 41 kDa

pI Range 5.2 -6.1

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 704.586 710.381 718.415 719.479 724.520 739.402 740.481
743.412 748.702 749.475 754.454 763.440 768.465 774.424
777.346 783.452 786.448 792.458 796.381 802.485 804.430
810.661 811.465 817.473 822.461 826.362 833.396 834.367
840.479 848.591 849.394 852.357 859.442 865.526 876.683
878.477 888.494 891.484 897.519 903.495 913.552 919.601
923.460 925.567 931.737 932.497 934.450 942.508 948.486
953.590 959.541 962.523 981.548 987.480 991.522 997.612
1003.570 1013.549 1014.534 1020.673 1022.458 1028.620
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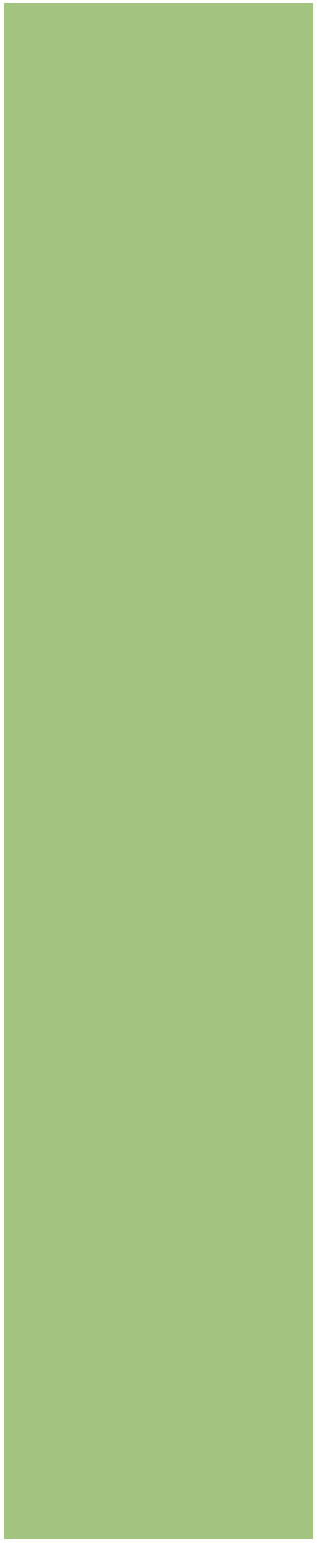

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1219.634	1226.671	1233.776	1235.692	1242.847	1244.413
1245.672	1248.667	1255.645	1256.790	1263.647	1270.667
1285.537	1291.553	1304.331	1305.523	1312.853	1313.805
1320.571	1327.821	1329.686	1336.715	1339.817	1346.700
1353.774	1354.641	1362.083	1362.729	1365.687	1372.711
1379.478	1380.778	1391.027	1391.705	1398.569	1400.811
1402.701	1409.693	1413.790	1417.716	1424.568	1427.720
1431.410	1438.295	1438.806	1441.846	1444.838	1451.832
1454.064	1460.798	1467.727	1469.765	1482.802	1487.783
1491.732	1498.683	1504.709	1515.278	1516.772	1524.175
1524.832	1530.621	1537.846	1539.774	1543.792	1547.762
1555.187	1555.798	1557.657	1560.475	1570.705	1571.692
1579.870	1587.962	1588.767	1597.554	1606.825	1608.823
1613.904	1617.449	1625.881	1631.696	1640.820	1644.749
1653.828	1657.800	1660.872	1670.875	1677.984	1686.075
1688.868	1697.180	1697.762	1707.793	1715.927	1725.032
1732.031	1735.031	1737.921	1745.565	1753.620	1763.871
1765.794	1773.925	1783.865	1789.814	1796.943	1804.802
1812.964	1813.853	1820.973	1829.834	1833.927	1848.201
1851.184	1854.053	1864.885	1874.961	1875.835	1884.040
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1926.073	1932.847	1941.028	1956.696	1968.989	1983.270
1994.022	2004.139	2007.970	2021.998	2033.645	2040.119
2047.061	2055.236	2066.825	2072.187	2094.259	2105.185
2114.621	2120.913	2129.949	2131.877	2137.074	2139.877
2150.078	2160.116	2169.110	2182.683	2184.194	2193.238
2196.046	2205.083	2208.057	2220.514	2222.229	2231.160
2235.235	2238.325	2247.225	2257.199	2267.099	2276.249
2280.268	2283.229	2292.186	2296.057	2308.242	2310.217
2320.167	2323.348	2336.322	2338.081	2343.099	2352.565
2356.324	2365.653	2367.324	2376.773	2379.073	2382.196
2392.103	2399.093	2408.341	2413.931	2420.356	2424.202
2433.498	2435.293	2445.410	2455.248	2466.510	2468.953
2481.320	2495.166	2499.239	2509.286	2519.995	2527.339
2537.306	2550.354	2565.142	2568.248	2582.402	2594.844
2606.079	2617.337	2622.683	2636.156	2641.070	2649.629
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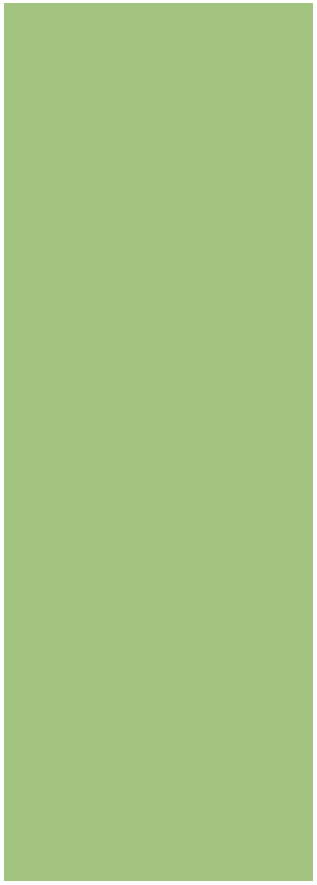

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2758.476	2761.485	2774.529	2783.515	2794.510	2799.213
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2854.162	2866.413	2873.560	2883.464	2888.604	2900.058
2904.450	2914.517	2925.658	2929.486	2942.409	2950.528
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3015.143	3024.548	3036.787	3047.750	3052.737	3064.474
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3177.652	3188.675	3199.870	3214.713	3219.336	3222.127
3234.569	3245.690	3253.564	3266.450	3271.765	3282.873
3286.349	3289.825	3292.763	3304.371	3315.379	3318.715
3324.773	3327.764	3337.838	3347.731	3353.932	3365.060
3368.696	3381.846	3393.178	3397.732	3410.899	3425.788
3429.692	3449.249	3461.525	3473.902	3479.820	3493.105
3506.136	3528.589	3541.165	3555.811	3558.624	3580.113
3627.545	3646.149	3670.715	3687.547	3691.843	

Tolerance (mon) 14.00 ppm

Number of Peptides 421

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

- PROWL Home
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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	8.9×10^{-7}	gi|25282455|ref|NP_741987.1| 3(2),5-bisphosphate nucleotidase [Rattus norvegicus]	30	5.6	33.50	
2	1.5×10^{-6}	gi|1381643|gb|AAB02722.1| cysteine protease p32-beta [Rattus norvegicus]	44	5.7	30.10	
3	1.4×10^{-5}	gi|34859703|ref|XP_215664.2| PREDICTED: similar to Breast carcinoma amplified sequence 2 homolog (DNA amplified in mammary carcinoma 1 protein) [Rattus norvegicus]	42	5.5	26.20	
4	3.0×10^{-5}	gi|547791|sp|P36374|KLK8_RAT Prostatic glandular kallikrein-8 precursor (Tissue kallikrein) (P1 kallikrein) (RGK-8)	35	5.6	29.57	
5	4.1×10^{-5}	gi|12083641|ref|NP_073180.1| synaptosomal-associated protein 23 [Rattus norvegicus]	43	4.8	23.50	
+6	1.2×10^{-4}	gi|3341891|dbj|BAA31863.1| RT1-DOb [Rattus norvegicus]	35	5.0	30.84	
	-	gi|57012350|ref|NP_001008846.1| RT1 class II, locus DOb [Rattus norvegicus]	29	5.0	30.81	
7	1.5×10^{-3}	gi|50925623|gb|AAH79028.1| Leucine rich repeat containing 23 [Rattus norvegicus]	39	5.1	33.76	
+8	2.5×10^{-3}	gi|14192925|ref|NP_062004.1| tropomyosin 1, alpha isoform f [Rattus norvegicus]	24	4.8	28.91	
	-	gi|112448|pir||A22165 tropomyosin alpha chain, smooth muscle - rat	26	4.9	32.24	
9	4.2×10^{-3}	gi|53733481|gb|AAH83676.1| Similar to mage-k1 [Rattus norvegicus]	37	5.5	34.83	
	-	gi|55778318|gb|AAH86598.1| Acyl-Coenzyme A binding domain containing 6 [Rattus norvegicus]	28	4.9	31.25	
	-	gi|16758348|ref|NP_446028.1| peroxiredoxin 6 [Rattus norvegicus]	34	5.6	24.86	

-	gi|13928740|ref|NP_113734.1| regucalcin [Rattus norvegicus]	35	5.3	33.94
-	gi|408807|dbj|BAA07490.1| regucalcin [Rattus norvegicus]	35	5.4	33.94
-	gi|34874480|ref|XP_236938.2| PREDICTED: similar to CG31803-PA [Rattus norvegicus]	33	5.3	31.26
-	gi|56970492|gb|AAH88458.1| Similar to RIKEN cDNA 2700085E05 [Rattus norvegicus]	28	5.1	33.53
-	gi|1711602|sp|P49890|ST1E6_RAT Estrogen sulfotransferase, isoform 6 (EST-6) (Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase)	27	5.6	35.63

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Wed Feb 07 01:38:58 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 23 - 36 kDa

pI Range 4.8 -5.7

Digestion Trypsin

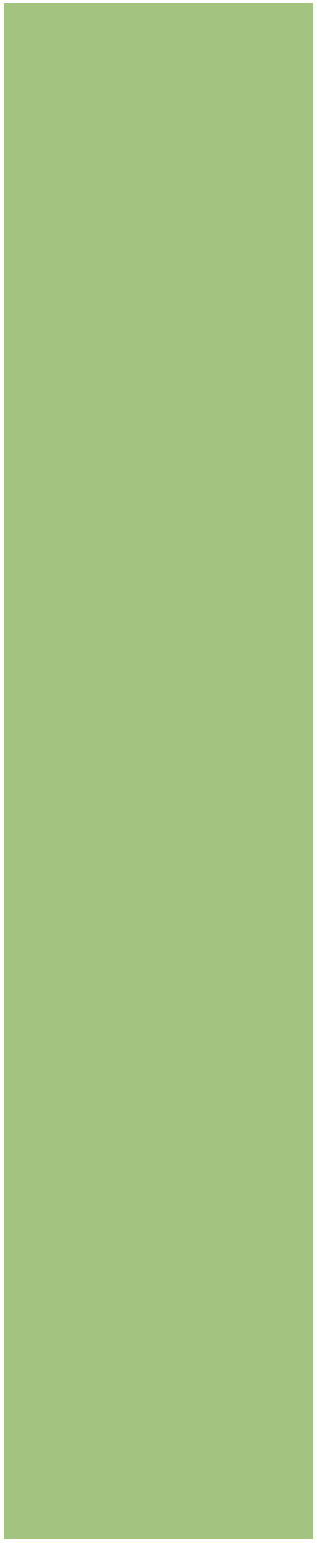
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



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905.470 918.470 932.426 935.509 941.527 942.518 947.563
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1470.893 1479.760 1487.304 1489.616 1497.966 1500.599
1503.834 1515.734 1522.713 1529.049 1535.716 1542.740
1547.715 1556.147 1558.140 1565.242 1566.015 1569.720
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1869.552 1874.825 1882.938 1885.979 1895.934 1905.034
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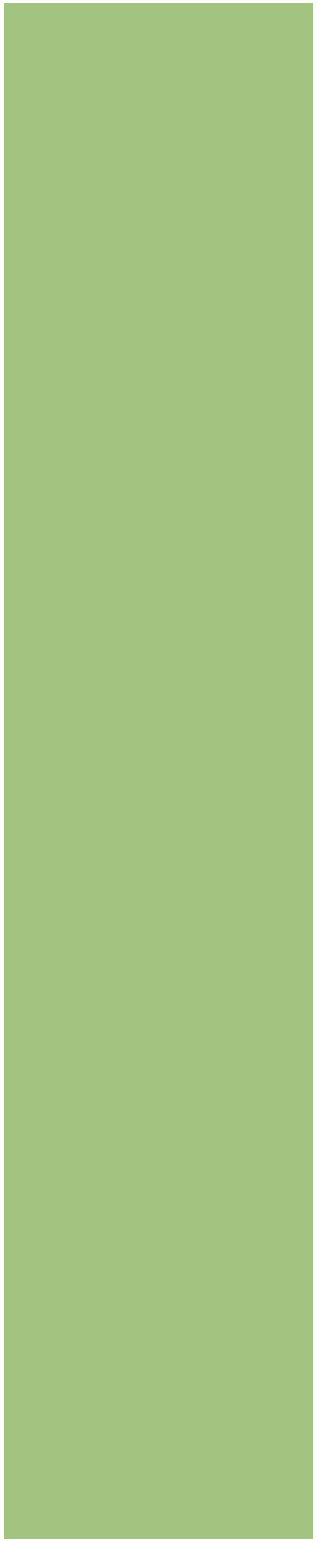

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2247.191	2257.036	2260.077	2269.854	2274.252	2282.161
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2861.524	2868.448	2877.332	2885.469	2896.953	2903.412
2911.514	2921.447	2923.559	2935.301	2941.583	2951.385
2955.412	2964.576	2975.518	2992.374	2995.361	2998.053
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3039.141	3049.885	3054.463	3058.001	3067.210	3078.377
3081.480	3093.722	3105.951	3110.533	3118.429	3125.544
3136.966	3140.703	3145.463	3159.080	3164.497	3177.281
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3241.206	3252.299	3259.526	3266.568	3277.396	3281.871
3294.193	3308.088	3319.877	3332.853	3347.101	3358.100
3365.286	3371.306	3383.677	3391.360	3399.485	3411.867
3416.354	3427.622	3433.698	3445.865	3458.765	3475.978
3483.407	3497.134	3502.752	3505.662	3516.517	3524.828
3534.751	3540.959	3556.806	3560.422	3573.331	3587.717
3590.379	3600.473	3606.780	3620.461	3625.041	3631.327
3648.917	3655.550	3660.314	3670.953	3686.226	3700.054

Tolerance (mon) 24.00 ppm

Number of Peptides 446

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

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- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

- PROWL Home
- Chait Lab

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	6.3×10^{-4}	gi|127764|sp|P04462|MYH8_RAT Myosin-8 (Myosin heavy chain, skeletal muscle, perinatal) (MyHC-perinatal)	61	6.4	29.83	
	-	gi|5802178|gb|AAD51613.1|AF157005_1 type 2X myosin heavy chain [Rattus norvegicus]	50	8.0	21.33	
2	1.7×10^{-3}	gi|50925831|gb|AAH79271.1| Similar to Glutathione S-transferase A1 (GTH1) (HA subunit 1) (GST-epsilon) (GSTA1-1) (GST class-alpha) [Rattus norvegicus]	47	5.9	25.79	
3	2.0×10^{-3}	gi|56789734|gb|AAH88443.1| Similar to RAB19, member RAS oncogene family [Rattus norvegicus]	51	6.1	24.66	
4	2.2×10^{-3}	gi|13124592|sp|Q9JI51|VTI1A_RAT Vesicle transport through interaction with t-SNAREs homolog 1A (Vesicle transport v-SNARE protein Vti1-like 2) (Vti1-rp2)	59	6.1	26.02	
5	5.8×10^{-3}	gi|205755|gb|AAC42095.1| neuronal protein	60	6.5	24.98	
6	5.8×10^{-3}	gi|34871064|ref|XP_220574.2| PREDICTED: similar to Sperm-associated antigen 7 [Rattus norvegicus]	69	6.9	26.12	
7	6.4×10^{-3}	gi|2039340|gb|AAB52995.1| putative RNA binding protein 1 [Rattus norvegicus]	49	6.4	20.68	
	-	gi|34878180|ref|XP_214617.2| PREDICTED: similar to potassium channel tetramerisation domain containing 1 [Rattus norvegicus]	50	6.6	29.70	
	-	gi|203822|gb|AAA41048.1| cytochrome PB24	41	6.1	22.55	
	-	gi|34877568|ref|XP_343617.1| PREDICTED: similar to Eukaryotic translation initiation factor 4E type 3 (eIF4E type 3) (eIF-4E type 3) (mRNA cap-binding protein type 3) (Eukaryotic translation initiation factor 4E-like 3) (eIF4E-like protein 4E-LP) [Rattus norvegicus]	42	6.7	26.58	

-	gi|13592152|ref|NP_112416.1| glutathione S-transferase, mu type 3 [Rattus norvegicus]	56	6.9	25.83
-	gi|50054216|ref|NP_113950.2| cyclin-dependent kinase inhibitor 1B (p27, kip1) [Rattus norvegicus]	61	6.5	22.35
-	gi|56605778|ref|NP_001008352.1| hypothetical protein LOC309681 [Rattus norvegicus]	53	6.6	28.39
-	gi|7767104|pdb|1DVG|A Chain A, Crystal Structure Of Rat Heme Oxygenase-1 In Complex With Heme; Seleleno-Methionine Derivative, Mutated At M51t,M93l, M155l,M191l.	48	6.0	29.89
-	gi|57870410|gb|AAH89059.1| Transmembrane protein 17 [Rattus norvegicus]	28	5.9	22.65
-	gi|2281010|dbj|BAA21561.1| p27 [Rattus norvegicus]	60	6.5	22.32
-	gi|13786152|ref|NP_112618.1| B-cell CLL/lymphoma 10 [Rattus norvegicus]	33	5.9	26.27
-	gi|205630|gb|AAA41670.1| Na,K-ATPase alpha-1 subunit	26	7.0	27.34
-	gi|6093966|sp|P56700|RGS16_RAT Regulator of G-protein signaling 16 (RGS16) (Retinally abundant regulator of G-protein signaling) (RGS-R)	32	8.0	22.61

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Mon Feb 05 03:48:04 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 30 kDa

pI Range 5.8 -8.0

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@SY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon)

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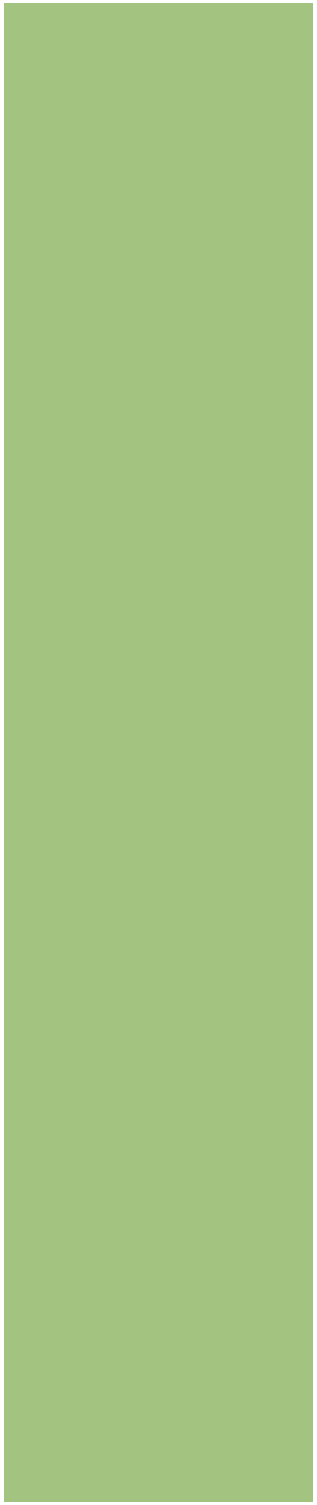

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1895.189 1898.972 1904.639 1915.940 1919.036 1926.891
1931.889 1940.956 1949.985 1973.038 1990.845 1994.001
2004.931 2028.185 2035.926 2058.015 2098.107 2103.972
2108.051 2111.114 2120.065 2125.030 2133.918 2136.003
2139.926 2149.563 2152.125 2161.038 2170.126 2182.159
2185.180 2192.175 2194.951 2204.079 2207.337 2220.964
2229.987 2232.055 2235.206 2245.183 2258.159 2268.124
2277.178 2280.039 2283.192 2292.212 2296.341 2308.201
2317.432 2337.156 2346.314 2350.231 2359.317 2363.114
2367.143 2376.393 2379.185 2382.142 2391.257 2395.146
2404.417 2407.292 2410.234 2420.230 2424.076 2434.234
2443.282 2448.145 2452.146 2455.283 2464.470 2474.143
2477.226 2481.150 2492.302 2495.228 2506.007 2507.255
2510.224 2523.098 2533.361 2537.159 2549.286 2552.280
2562.329 2567.241 2577.320 2591.600 2597.329 2609.944
2623.279 2635.126 2638.412 2651.299 2662.271 2667.348
2678.458 2682.050 2695.288 2707.437 2719.403 2723.233
2734.388 2746.554 2756.660 2773.309 2778.916 2783.464
2796.487 2809.469 2821.228 2825.309 2837.496 2840.224
2852.767 2857.339 2883.360 2895.419 2904.270 2914.626
2925.036 2937.473 2942.185 2960.667 2968.259 2979.905
2983.252 2993.232 3007.807 3021.197 3031.387 3041.707
3048.622 3059.231 3062.884 3066.390 3075.461 3086.529
3089.411 3093.457 3105.120 3108.424 3111.729 3122.712
3124.745 3136.542 3139.637 3143.224 3155.510 3166.607
3171.423 3177.724 3188.783 3201.387 3208.365 3220.281
3232.487 3243.526 3255.007 3264.776 3278.030 3288.799
3292.702 3303.843 3314.383 3325.677 3338.508 3346.920
3353.938 3364.987 3368.661 3381.536 3392.551 3399.067
3410.779 3413.966 3429.411 3444.061 3454.742 3478.298
3509.390 3562.536 3589.076 3614.783 3638.753 3647.655
3653.351

Tolerance (mon) 43.00 ppm

Number of Peptides 405

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.3×10^{-8}	gi|13124118|sp|Q9Z1E1|FLOT1_RAT Flotillin-1 (Reggie-2) (REG-2)	20	6.7	47.77	
	-	gi|40352785|gb|AAH64652.1| Flot1 protein [Rattus norvegicus]	20	6.7	47.78	
	-	gi|38454312|ref|NP_942084.1| basic leucine zipper and W2 domains 1 [Rattus norvegicus]	17	5.7	48.20	
	-	gi|42559550|sp|Q8R5K6|TOB1_RAT Tob1 protein (Transducer of erbB-2 1)	15	6.2	40.56	
	-	gi|16758932|ref|NP_446462.1| neuraminidase 3 [Rattus norvegicus]	17	5.8	48.22	
	-	gi|34857271|ref|XP_214979.2| PREDICTED: similar to alpha/beta hydrolase fold protein [Rattus norvegicus]	13	6.2	49.12	
	-	gi|204052|gb|AAA41123.1| extracellular signal-regulated kinase 1	13	6.0	42.37	
	-	gi|204054|gb|AAA63486.1| extracellular-signal-regulated kinase 1 [Rattus norvegicus]	12	6.0	42.82	
	-	gi|515499|gb|AAA20009.1| microtubule-associated protein-2 kinase	13	6.2	42.46	
	-	gi|8393331|ref|NP_059043.1| protein kinase, mitogen activated 3 (extracellular-signal-regulated kinase 1, ERK1) [Rattus norvegicus]	12	6.0	43.31	
	-	gi|8050445|gb|AAF71666.1|AF155236_1 extracellular signal-regulated kinase 1b [Rattus norvegicus]	11	6.4	46.11	
	-	gi|56090367|ref|NP_001007633.1| activating signal cointegrator 1 complex subunit 1 [Rattus norvegicus]	11	6.0	41.45	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Tue Feb 06 15:13:16 2007 UTC (Search Time: 0.44 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 40 - 52 kDa

pI Range 5.7 -7.0

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon)

702.579	709.274	714.401	716.414	718.286	721.332	729.349
735.387	736.298	740.333	747.243	753.280	755.070	763.477
764.239	770.363	778.574	780.206	786.130	787.110	794.254
798.294	800.213	804.134	805.106	811.201	812.331	816.628
818.107	822.111	827.999	834.064	836.628	844.032	849.940
850.567	856.282	858.013	861.324	864.009	869.729	875.985
880.188	885.961	890.127	891.973	898.047	899.478	904.101
909.992	911.737	918.122	919.936	926.186	931.000	937.164
941.099	943.865	950.133	956.069	958.399	965.113	966.178
972.143	978.253	981.915	986.281	992.118	992.944	1001.990
1005.227	1006.976	1012.873	1016.879	1019.990	1025.796	
1027.843	1033.823	1034.839	1040.796	1047.031	1049.557	
1050.341	1056.015	1056.627	1057.239	1059.733	1064.773	
1070.486	1071.278	1073.282	1076.765	1082.797	1088.935	
1091.244	1092.044	1098.230	1103.943	1106.581	1109.088	
1115.300	1121.822	1131.641	1133.022	1138.983	1145.301	
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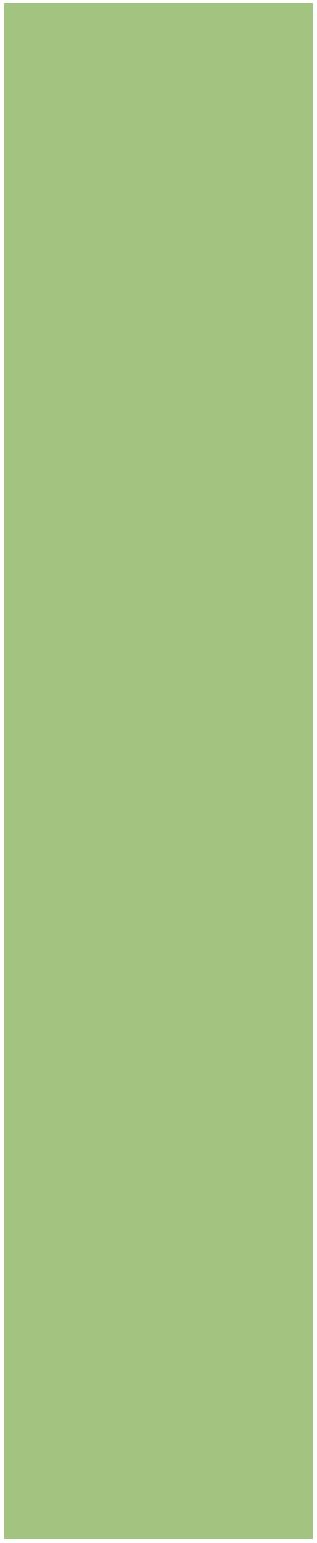

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1246.708	1247.587	1256.130	1257.180	1259.565	1261.524
1265.588	1274.457	1285.285	1287.094	1295.142	1301.104
1303.094	1307.517	1315.019	1317.019	1320.488	1327.561
1335.563	1336.079	1340.509	1344.723	1349.636	1361.524
1370.474	1373.165	1382.928	1392.953	1397.828	1406.114
1413.970	1423.903	1425.554	1427.840	1434.585	1436.420
1443.747	1444.411	1449.734	1457.351	1459.227	1469.009
1473.756	1477.400	1484.624	1486.932	1490.098	1497.482
1504.494	1505.564	1512.411	1514.217	1522.186	1523.104
1525.180	1533.678	1541.275	1545.610	1552.415	1554.430
1558.917	1567.748	1570.067	1572.894	1579.625	1581.177
1585.031	1592.970	1596.006	1599.663	1607.126	1616.094
1624.354	1627.256	1636.661	1638.213	1640.175	1647.922
1655.798	1659.771	1668.582	1670.644	1681.773	1690.642
1696.208	1705.782	1706.727	1714.798	1716.136	1720.711
1728.954	1732.902	1741.372	1749.721	1751.692	1756.145
1764.869	1765.406	1774.040	1779.571	1789.179	1796.987
1799.669	1802.868	1811.851	1819.852	1822.321	1830.115
1838.213	1847.544	1851.306	1856.580	1864.824	1867.440
1875.476	1879.908	1887.912	1890.895	1898.277	1907.466
1914.203	1917.060	1925.467	1930.638	1939.460	1947.144
1960.442	1969.212	1979.290	1987.053	1995.402	1997.777
2007.838	2017.197	2031.490	2034.768	2044.769	2047.265
2058.640	2062.398	2071.272	2074.796	2080.042	2090.338
2091.353	2100.536	2103.128	2110.760	2120.295	2121.720
2126.870	2138.309	2145.536	2153.056	2162.906	2167.291
2176.261	2177.424	2180.346	2189.659	2200.445	2204.867
2215.754	2221.778	2232.324	2234.455	2239.486	2248.733
2251.096	2256.528	2266.420	2271.775	2275.177	2278.357
2290.293	2295.741	2302.260	2305.847	2315.490	2321.454
2333.665	2343.985	2347.571	2357.170	2359.524	2369.279
2379.283	2382.108	2391.843	2401.697	2404.304	2408.630
2413.125	2424.515	2430.187	2437.227	2448.307	2451.706
2462.484	2471.646	2480.892	2485.387	2489.786	2493.415
2504.488	2508.195	2512.647	2524.540	2526.637	2530.056
2542.160	2552.183	2562.328	2566.010	2570.446	2583.193
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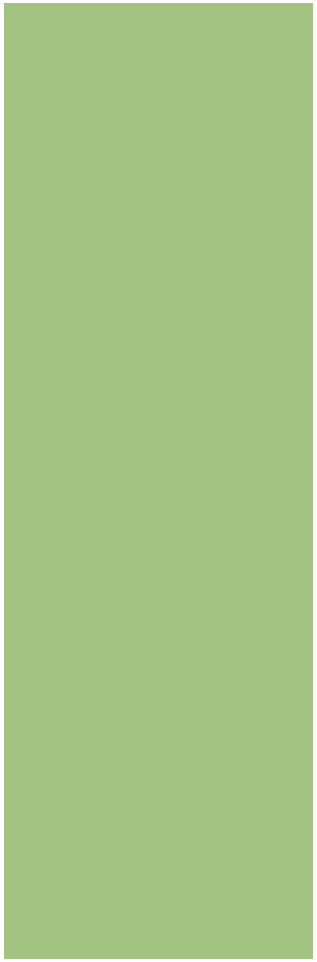

2638.300	2645.325	2659.159	2664.369	2676.058	2680.657
2688.052	2696.646	2709.387	2715.664	2719.068	2723.528
2733.410	2743.874	2746.449	2750.614	2761.041	2767.766
2778.651	2782.592	2790.054	2801.517	2813.111	2818.327
2828.344	2836.657	2851.162	2854.003	2857.708	2870.067
2873.097	2884.476	2888.455	2899.321	2904.761	2919.258
2924.462	2935.176	2939.956	2953.259	2961.313	2972.058
2982.418	2986.390	2991.469	3003.707	3009.614	3020.445
3022.666	3035.375	3045.473	3055.810	3059.719	3070.790
3085.694	3101.608	3113.168	3118.354	3128.625	3149.296
3152.583	3157.953	3169.692	3172.384	3176.746	3191.030
3195.823	3206.526	3215.759	3226.686	3240.123	3250.478
3265.618	3275.936	3284.225	3290.053	3300.951	3311.829
3324.159	3337.408	3348.968	3368.435	3374.298	3385.217
3388.742	3395.407	3398.114	3410.368	3425.637	3437.270
3443.824	3457.861	3468.992	3483.279	3487.134	3496.879
3507.953	3510.385	3522.359	3536.194	3541.840	3553.626
3564.869	3578.385	3585.152	3600.562	3607.148	3622.767
3635.173	3649.186	3654.513	3670.560	3683.701	3688.440

Tolerance (mon) 22.00 ppm

Number of Peptides 460

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New York, NY 10021
(212) 327-8000

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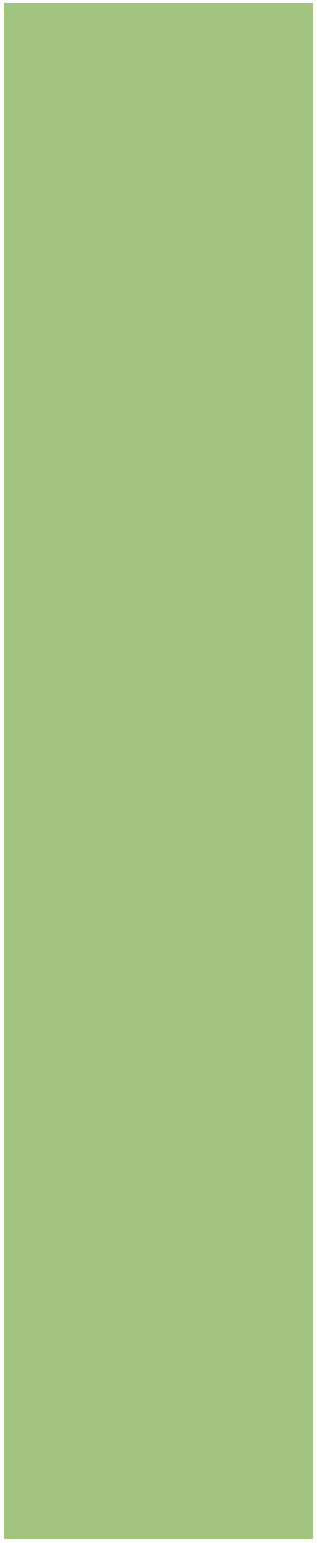
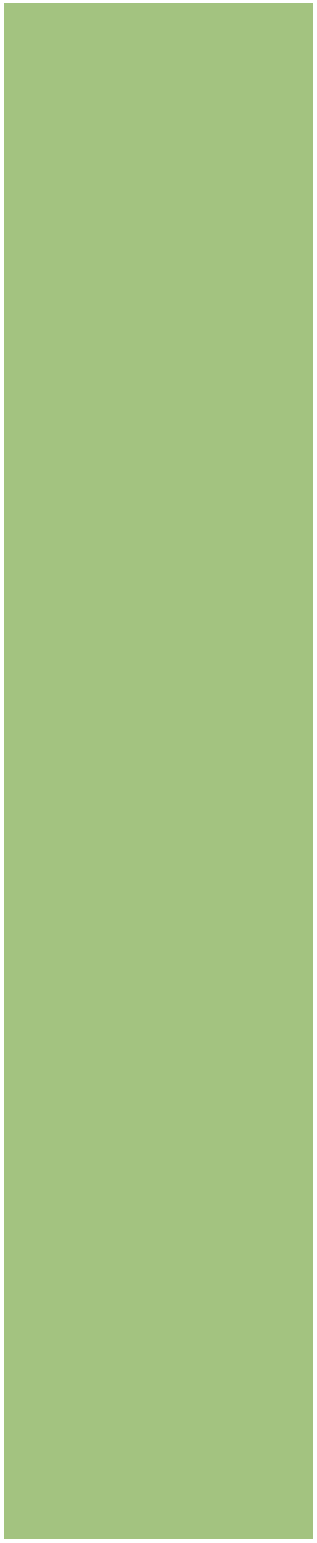
Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.1×10^{-7}	gi|16758678|ref|NP_446279.1| procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 [Rattus norvegicus]	31	6.3	84.16	
+2	2.1×10^{-6}	gi|13489075|ref|NP_071572.1| phosphodiesterase 10A [Rattus norvegicus]	31	6.1	91.51	
	-	gi|6683035|dbj|BAA88997.1| PDE10A3 [Rattus norvegicus]	30	6.1	90.49	
	-	gi|42600939|gb|AAS21246.1| PDE10A14 [Rattus norvegicus]	31	6.7	75.40	
	-	gi|42600937|gb|AAS21245.1| PDE10A13 [Rattus norvegicus]	28	6.3	82.27	
3	3.7×10^{-6}	gi|20301994|ref|NP_620205.1| fibroblast activation protein [Rattus norvegicus]	27	6.2	88.51	
4	4.9×10^{-6}	gi|127570|sp|P18588|MX1_RAT Interferon-induced GTP-binding protein Mx1	27	6.5	75.08	
5	9.2×10^{-6}	gi|55741823|ref|NP_001006977.1| threonyl-tRNA synthetase [Rattus norvegicus]	28	6.5	81.47	
6	1.1×10^{-5}	gi|13489067|ref|NP_068516.1| N-ethylmaleimide sensitive fusion protein [Rattus norvegicus]	27	6.6	83.21	
	-	gi|55250714|gb|AAH85721.1| G elongation factor [Rattus norvegicus]	32	6.4	84.12	
	-	gi|92654|pir||A34337 propionyl-CoA carboxylase (EC 6.4.1.3) alpha chain precursor - rat (fragment)	36	6.3	78.22	
	-	gi|9971583|dbj|BAB12573.1| exchange factor for ARF6 [Rattus norvegicus]	21	7.4	71.14	
	-	gi|9507019|ref|NP_062237.1| sec1 family domain containing 1 [Rattus norvegicus]	26	6.1	72.59	
	-	gi|1144569|gb|AAB08009.1| r-sly1	26	6.0	73.90	
	-	gi|1000686|dbj|BAA06674.1| LIMK-2b [Rattus norvegicus]	29	7.0	71.01	



-	gi|205063|gb|AAA41476.1| ORF with similarities to Kex2 and furin proteins; putative	22	6.0	84.77
-	gi|57977273|ref|NP_996729.1| phosphofructokinase, platelet [Rattus norvegicus]	27	7.0	86.67
-	gi|129684|sp|P14882|PCCA_RAT Propionyl-CoA carboxylase alpha chain, mitochondrial precursor (PCCase subunit alpha) (Propanoyl-CoA:carbon dioxide ligase subunit alpha)	34	6.3	78.32
-	gi|51259466|gb|AAH79391.1| Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) [Rattus norvegicus]	23	6.1	72.68
-	gi|47169484|tpe|CAE48379.1| TPA: glutamine-fructose-6-phosphate transaminase 2 [Rattus norvegicus]	27	6.7	77.80
-	gi|206050|gb|AAA88512.1| alpha-propionyl-CoA carboxylase (EC 6.4.1.3)	33	6.7	80.56
-	gi|48256734|gb|AAT41589.1| acyl-CoA synthetase isoform 6 variant2 [Rattus norvegicus]	26	6.8	79.18
-	gi|20302036|ref|NP_620228.1| nibrin [Rattus norvegicus]	22	6.4	84.31
-	gi|16758432|ref|NP_446077.1| G elongation factor [Rattus norvegicus]	25	7.0	84.55
-	gi|51980333|gb|AAH82049.1| DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Rattus norvegicus]	24	6.8	83.45
-	gi|17388906|gb|AAF80473.2|AF162756_1 cenexin 2 [Rattus norvegicus]	19	6.7	89.88
-	gi|50925505|gb|AAH78857.1| Outer dense fiber of sperm tails 2 [Rattus norvegicus]	23	7.3	74.08
-	gi|56118953|ref|NP_077049.2| LIM motif-containing protein kinase 2 [Rattus norvegicus]	26	7.3	73.55
-	gi|13929158|ref|NP_114002.1| G protein-coupled receptor kinase interactor 1 [Rattus norvegicus]	23	6.5	85.95
-	gi|1517938|gb|AAB48561.1| isoform of PSD-95/SAP90 [Rattus norvegicus]	20	6.4	92.72
-	gi|400195|sp|Q02759|LX12L_RAT Arachidonate 12-lipoxygenase, leukocyte-type (12-LOX)	24	6.1	76.40



-	gi|37361828|gb|AAQ91027.1| LRRGT00071 [Rattus norvegicus]	22	6.3	90.44
-	gi|975277|gb|AAA75166.1| p72	28	7.1	69.47
-	gi|1209468|emb|CAA63043.1| stat5bDelta40C [Rattus norvegicus]	21	6.4	83.65
-	gi|2996000|gb|AAC08408.1| outer dense fiber protein ODF84 [Rattus norvegicus]	22	7.0	74.11
-	gi|51858866|gb|AAH81969.1| Similar to RIKEN cDNA 4921537D05 [Rattus norvegicus]	17	6.2	82.12
-	gi|55715908|gb|AAH85700.1| Nibrin [Rattus norvegicus]	19	6.7	84.14
-	gi|51859211|gb|AAH82042.1| ATP-binding cassette, sub-family F (GCN20), member 3 [Rattus norvegicus]	16	6.1	80.24
-	gi|31542125|ref|NP_112272.2| arachidonate 12-lipoxygenase [Rattus norvegicus]	24	6.2	76.32
-	gi|9507209|ref|NP_062094.1| transformation related protein 63 [Rattus norvegicus]	21	6.2	77.66
-	gi|48686585|gb|AAT46048.1| fidgetin-like 1 [Rattus norvegicus]	26	6.6	74.92
-	gi|18543341|ref|NP_570095.1| acyl-CoA synthetase long-chain family member 6 [Rattus norvegicus]	22	6.6	79.17
-	gi|417242|sp|P33124|ACSL6_RAT Long-chain-fatty-acid--CoA ligase 6 (Long-chain acyl-CoA synthetase 6) (LACS 6) (Long-chain-fatty-acid--CoA ligase, brain isozyme)	22	6.7	79.19
-	gi|13751173|emb|CAC37098.1| TA1 KET alpha protein [Rattus norvegicus]	20	6.2	75.50
-	gi|32264631|gb|AAP78762.1| Ac1288 [Rattus norvegicus]	20	6.4	81.10
-	gi|1845602|gb|AAC53134.1| outer dense fiber protein [Rattus norvegicus]	20	6.1	69.28
-	gi|54035509|gb|AAH83909.1| TNF receptor-associated protein 1 [Rattus norvegicus]	26	6.6	80.67
-	gi|21634411|gb|AAM63551.1| hypertrophied skeletal muscle protein GTF3 [Rattus norvegicus]	19	6.7	93.26
-	gi|51556265|ref|NP_001003957.1| DNA methyltransferase 3A isoform 2 [Rattus norvegicus]	28	6.1	79.29

-	gi|39930373|ref|NP_058867.1| protein kinase C, epsilon [Rattus norvegicus]	24	6.5	84.77
-	gi|34859748|ref|XP_227556.2| PREDICTED: similar to CG10915-PA [Rattus norvegicus]	27	7.2	70.51
-	gi|34858308|ref|XP_232266.2| PREDICTED: similar to Egg-derived tyrosine phosphatase CG6542-PA, isoform A [Rattus norvegicus]	25	6.2	73.40
-	gi|56270161|gb|AAH87149.1| Similar to retinoid x receptor interacting protein [Rattus norvegicus]	17	6.3	81.62

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Wed Feb 07 15:49:01 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 69 - 94 kDa

pI Range 6.0 -7.5

Digestion Trypsin

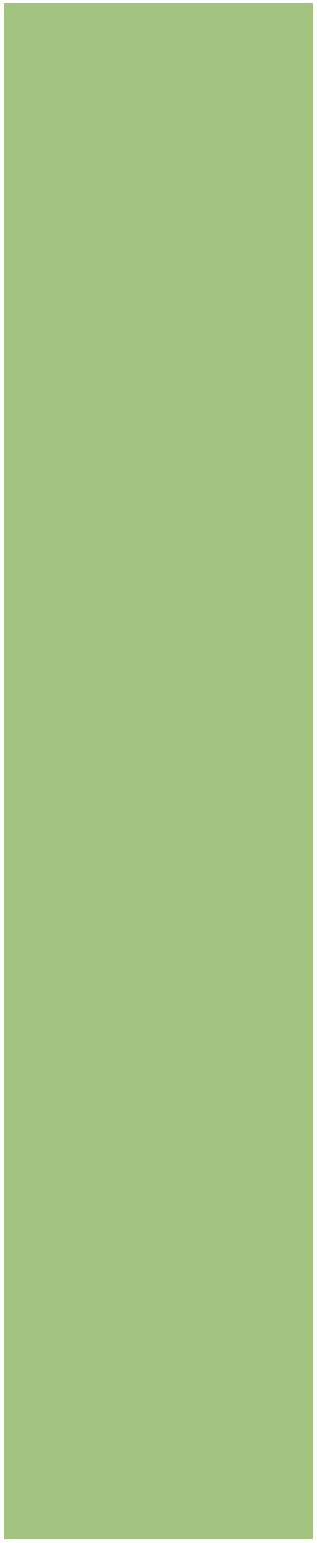
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +O@M(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

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777.355 781.429 783.423 789.438 795.345 798.477 804.264
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941.631 943.490 947.523 954.597 960.634 961.385 967.464
980.038 980.564 983.537 987.486 993.711 994.538 1000.466
1012.824 1013.531 1017.497 1023.643 1024.569 1027.543
1033.525 1040.588 1051.686 1058.504 1061.571 1064.510
1067.696 1085.577 1088.660 1094.596 1100.592 1107.634
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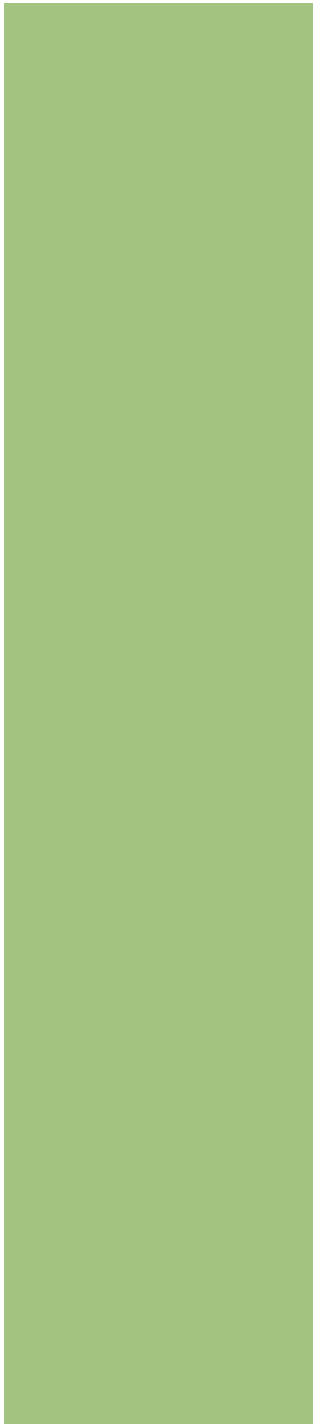

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Tolerance (mon) 35.00 ppm

Number of Peptides 424

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	9.8×10^{-7}	gi|18158453|ref|NP_542961.1| galactose-4-epimerase, UDP [Rattus norvegicus]	62	7.9	38.55	
2	4.1×10^{-5}	gi|16758520|ref|NP_446155.1| mitogen-activated protein kinase kinase 6 [Rattus norvegicus]	63	7.0	37.77	
3	7.7×10^{-4}	gi|45478138|gb|AAS66240.1| LRRGT00149 [Rattus norvegicus]	43	6.6	43.49	
4	1.6×10^{-3}	gi|34869622|ref|XP_214147.2| PREDICTED: similar to proteasome 26S ATPase subunit 6 [Rattus norvegicus]	41	7.8	46.06	
5	6.3×10^{-3}	gi|50925797|gb|AAH79230.1| Similar to actin-like 7-alpha-like protein [Rattus norvegicus]	47	6.9	46.60	
+6	0.018	gi|51980625|gb|AAH81691.1| Sulfotransferase family, cytosolic, 1C, member 2a [Rattus norvegicus]	48	7.0	35.18	
	-	gi|11262122|pir||JC7283 hydroxyarylamine sulfotransferase (EC 2.8.2.-) 2A - rat	38	7.0	35.22	
	-	gi|4689042|emb|CAB41461.1| sulfotransferase K2 [Rattus norvegicus]	38	7.0	35.22	
7	0.026	gi|54035400|gb|AAH83568.1| Phosphoglycerate kinase 2 [Rattus norvegicus]	37	7.7	45.39	
8	0.032	gi|13592141|ref|NP_112411.1| for proteasomal ATPase (SUG1) [Rattus norvegicus]	53	7.1	45.78	
9	0.048	gi|11968124|ref|NP_071979.1| transcobalamin 2 precursor [Rattus norvegicus]	42	7.9	47.86	
10	0.072	gi|34866729|ref|XP_217099.2| PREDICTED: similar to Vacuolar protein sorting 26 homolog (VPS26 protein homolog) [Rattus norvegicus]	53	6.9	39.16	

-	gi|25453414|ref|NP_037289.1| arginosuccinate synthetase [Rattus norvegicus]	45	7.7	46.76
-	gi|1334163|emb|CAA30044.1| unnamed protein product [Rattus norvegicus]	55	6.8	39.60
-	gi|809075|emb|CAA25516.1| cytochrome P-450 [Rattus norvegicus]	37	6.8	42.56
-	gi|4455013|gb|AAD21037.1| G-septin gamma [Rattus norvegicus]	39	7.8	34.56
-	gi|9506591|ref|NP_062111.1| farnesyl diphosphate farnesyl transferase 1 [Rattus norvegicus]	37	6.6	48.72
-	gi|38197390|gb|AAH61877.1| Glutamate oxaloacetate transaminase 1 [Rattus norvegicus]	33	6.7	46.64

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Tue Feb 06 19:40:01 2007 UTC (Search Time: 0.58 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 30 - 50 kDa

pI Range 6.6 -8.3

Digestion Trypsin

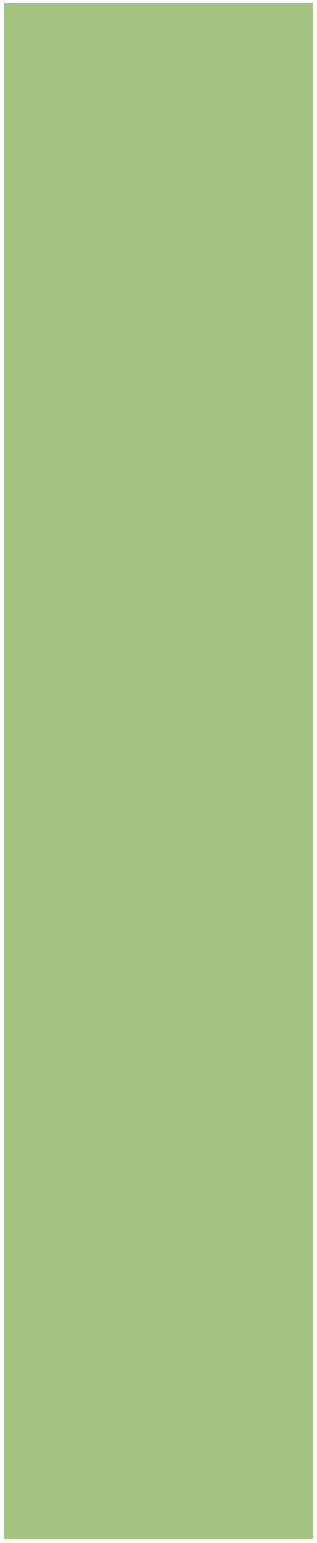
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

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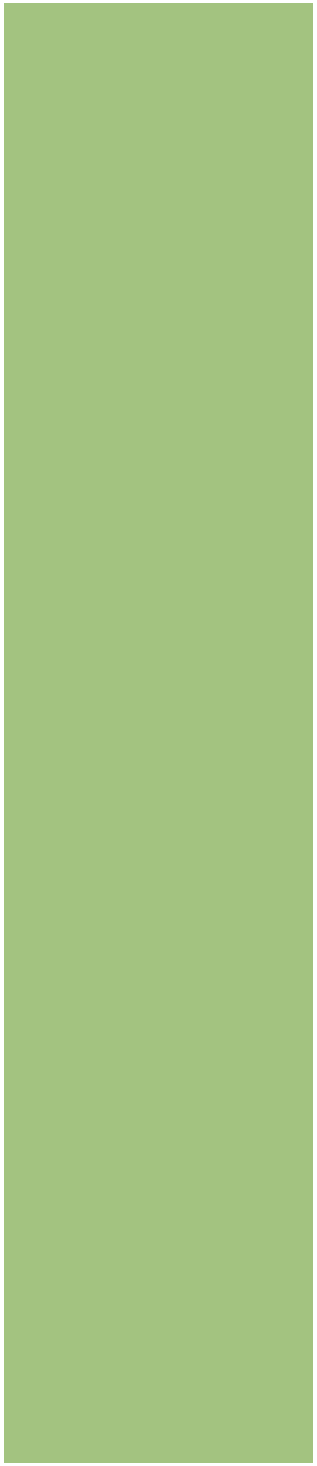

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Tolerance (mon) 34.00 ppm

Number of Peptides 434

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

- PROWL Home
- Chait Lab

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	4.1×10^{-4}	gi|49359177|gb|AAT65503.1| protein kinase C epsilon [Rattus norvegicus]	41	6.6	84.93	◉
	-	gi|39930373|ref|NP_058867.1| protein kinase C, epsilon [Rattus norvegicus]	40	6.5	84.77	◉
+2	5.5×10^{-4}	gi|28557685|ref|NP_787065.1| procollagen lysine, 2-oxoglutarate 5-dioxygenase 2 [Rattus norvegicus]	43	6.3	87.56	◉
	-	gi|28400783|emb|CAD23630.1| procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2, short variant [Rattus norvegicus]	42	6.3	85.15	◉
3	7.7×10^{-4}	gi|48686585|gb|AAT46048.1| fidgetin-like 1 [Rattus norvegicus]	57	6.6	74.92	◉
	-	gi|12083643|ref|NP_073182.1| exocyst complex component 7 [Rattus norvegicus]	36	6.3	75.26	◉
	-	gi|40786501|ref|NP_955434.1| sperm protein SSP411 [Rattus norvegicus]	38	6.6	89.03	◉
	-	gi|34854035|ref|XP_342626.1| PREDICTED: similar to Semaphorin-3D precursor [Rattus norvegicus]	39	6.8	90.66	◉

NOTE:

1. To search again using unmatched masses, click the symbol ◉.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Fri Jan 26 18:46:26 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 73 - 94 kDa

pI Range 6.2 -7.4

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon)

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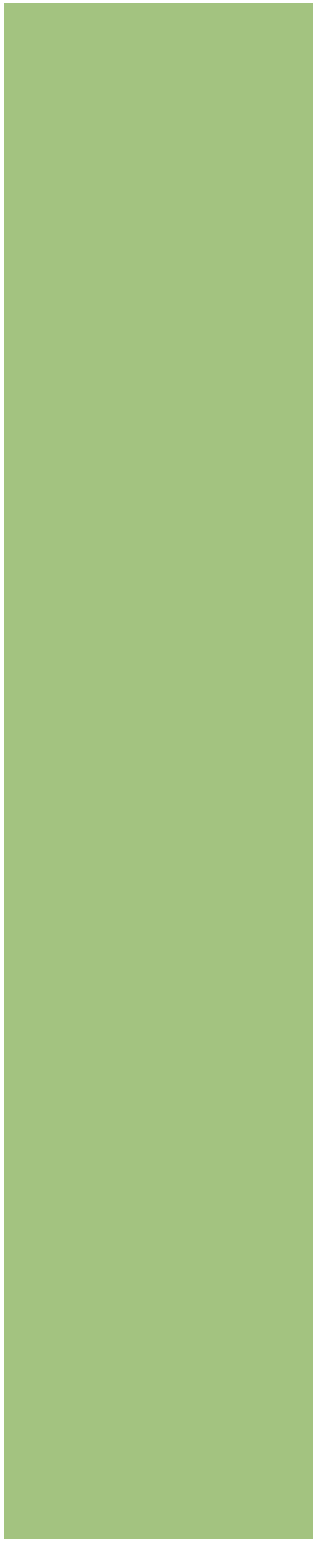

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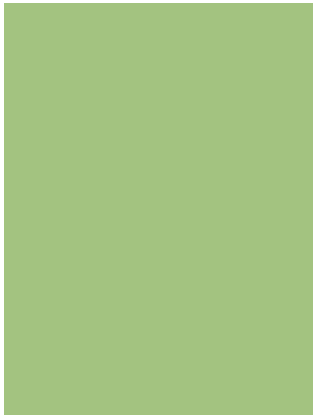
3139.302	3153.514	3161.315	3167.570	3178.464	3191.624
3199.319	3209.161	3223.493	3235.366	3238.050	3248.566
3256.523	3265.529	3277.016	3288.678	3292.738	3304.350
3308.420	3312.182	3323.207	3325.616	3338.650	3350.110
3353.701	3365.343	3369.059	3384.570	3397.563	3410.463



	3414.558 3427.570 3439.578 3451.251 3460.365 3464.213 3479.745 3484.718 3497.146 3505.045 3519.428 3530.516 3534.283 3542.906 3557.368 3563.242 3575.569 3582.305 3599.194 3615.516 3621.437 3637.931 3643.140 3655.034 3666.541 3683.220 3697.272 3701.579
Tolerance (mon)	37.00 ppm
Number of Peptides	433

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- X! Tandem
- X! Hunter
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(212) 327-8000

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.1×10^{-30}	gi|461731|sp|P26772|CH10_RAT 10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (CPN10)	59	8.9	10.88	
	-	gi|6981052|ref|NP_037098.1| heat shock 10 kDa protein 1 [Rattus norvegicus]	59	8.9	10.86	
	-	gi|400542|gb|AAB27570.1| chaperonin 10, cpn10 [Rattus norvegicus=rats, liver, Peptide Mitochondrial, 101 aa]	59	8.9	10.75	
2	3.0×10^{-13}	gi|8825633|gb|AAF80151.1| T cell receptor [Rattus norvegicus]	48	9.0	11.43	
3	2.4×10^{-10}	gi|46015734|pdb|1S6C|B Chain B, Crystal Structure Of The Complex Between Kchip1 And Kv4.2 N1-30	97	9.5	2.95	
4	1.4×10^{-8}	gi|50925829|gb|AAH79266.1| LOC290508 protein [Rattus norvegicus]	63	9.7	7.17	
5	4.6×10^{-8}	gi|1297196|gb|AAC52814.1| RCAT2	51	9.1	4.41	
6	7.9×10^{-8}	gi|41529155|dbj|BAD08448.1| CD89 or IgA Fc receptor isoform 2 [Rattus norvegicus]	35	9.3	12.27	
7	5.2×10^{-7}	gi|12055452|emb|CAC20893.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	44	9.3	9.25	
8	9.6×10^{-7}	gi|114491|sp|P11608|ATP8_RAT ATP synthase protein 8 (ATPase subunit 8) (A6L) (Chargerin II)	37	9.3	7.62	
9	1.0×10^{-6}	gi|6900670|emb|CAB71432.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	38	9.8	11.24	
10	1.6×10^{-6}	gi|6900734|emb|CAB71464.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	36	9.6	10.63	
11	1.8×10^{-6}	gi|7677280|gb|AAF67106.1|AF220557_1 murine complement receptor 1-specific monoclonal antibody Ig light chain variable region [Rattus norvegicus]	25	9.5	12.66	

12	2.7×10^{-6}	gi|6900772|emb|CAB71483.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	40	8.7	11.89
13	2.7×10^{-6}	gi|12055436|emb|CAC20885.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	52	9.4	9.27
14	3.8×10^{-6}	gi|6900790|emb|CAB71492.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	41	9.0	10.71
15	4.8×10^{-6}	gi|984323|gb|AAB17124.1| signal recognition particle 54 kDa subunit	20	9.5	7.98
16	5.2×10^{-6}	gi|6900593|emb|CAB71392.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	42	9.0	11.47
17	5.2×10^{-6}	gi|6900510|emb|CAB71838.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	42	9.3	11.65
18	5.7×10^{-6}	gi|19424244|ref|NP_598245.1| brain protein 44-like [Rattus norvegicus]	31	9.9	12.61
19	5.7×10^{-6}	gi|37361848|gb|AAQ91037.1| LRRGT00081 [Rattus norvegicus]	36	9.6	5.69
20	8.1×10^{-6}	gi|1166518|gb|AAC52371.1| RGS3	31	9.6	7.79
21	5.2×10^{-5}	gi|56799093|dbj|BAD83366.1| myelin protein zero [Rattus norvegicus]	14	8.6	11.78
22	6.6×10^{-5}	gi|6900876|emb|CAB71535.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	20	9.3	11.80
23	1.1×10^{-4}	gi|2253444|gb|AAB62948.1| mucin 1 [Rattus norvegicus]	28	9.1	8.28
24	1.4×10^{-4}	gi|554443|gb|AAA41347.1| heme oxygenase	24	9.3	10.61
25	1.8×10^{-4}	gi|20384773|gb|AAK55112.1| NOVA-1 variant 4 [Rattus norvegicus]	49	9.3	9.46
26	6.4×10^{-4}	gi|818016|emb|CAA25083.1| unnamed protein product [Rattus norvegicus]	22	9.3	10.55
27	6.9×10^{-3}	gi|2570078|emb|CAA05477.1| Immunoglobulin heavy chain [Rattus norvegicus]	34	9.5	9.26

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B12053D2-0918-61412755

Sequences 20076

Date & Time Mon Feb 05 21:35:17 2007 UTC (Search Time: 0.28 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 1 - 13 kDa

pI Range 8.5 -10.0

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 710.424 712.236 717.413 723.368 726.283 731.475 739.425
740.230 746.408 752.446 754.384 763.461 765.358 768.393
774.426 775.399 778.473 784.357 788.431 793.386 799.478
802.409 804.258 811.445 817.395 818.414 820.262 824.486
830.445 838.274 839.462 841.470 854.514 860.422 866.510
880.484 888.486 889.489 902.475 904.436 907.493 913.623
914.477 919.468 921.508 933.493 935.508 941.463 946.486
959.464 960.486 964.514 970.582 976.501 986.322 992.522
995.598 997.594 1003.531 1013.573 1019.557 1023.578
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1132.632 1138.641 1139.595 1145.668 1146.557 1150.616
1156.626 1157.611 1163.663 1169.593 1176.691 1184.622
1191.650 1208.762 1210.658 1218.631 1220.629 1228.683
1231.657 1238.587 1239.629 1241.715 1249.648 1251.719
1259.684 1264.705 1268.585 1275.666 1282.670 1285.733
1292.765 1293.563 1303.725 1305.500 1312.757 1317.638
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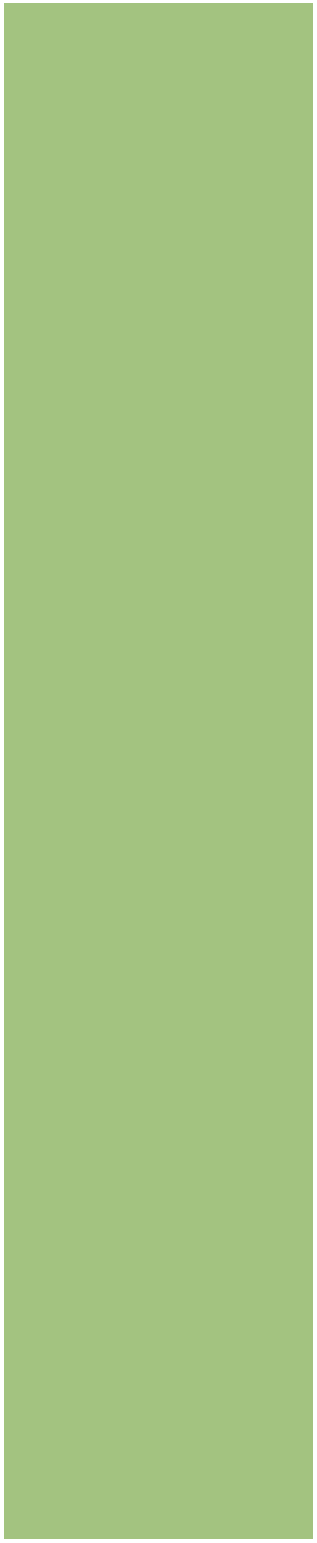

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1519.798	1520.375	1521.740	1526.734	1529.813	1536.956
1537.801	1540.733	1543.773	1547.769	1555.884	1557.797
1564.766	1565.884	1568.683	1575.810	1579.794	1581.427
1584.695	1591.777	1597.665	1605.694	1611.364	1619.617
1620.565	1623.819	1631.886	1635.778	1638.883	1646.933
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1683.887	1684.716	1692.795	1695.732	1705.784	1713.746
1721.838	1722.816	1725.780	1733.788	1734.910	1737.744
1741.760	1749.805	1752.764	1757.757	1765.953	1769.775
1781.606	1790.855	1795.902	1797.900	1801.813	1809.940
1818.429	1819.003	1821.876	1829.875	1830.998	1836.477
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1940.942	1952.976	1956.787	1963.943	1989.091	1993.990
2005.102	2015.036	2030.907	2035.007	2043.096	2054.131
2058.009	2066.144	2074.018	2098.042	2104.154	2111.173
2120.963	2130.993	2136.189	2140.175	2150.282	2152.969
2162.073	2164.077	2170.160	2181.879	2186.096	2192.021
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2450.102	2452.236	2455.339	2466.400	2469.278	2479.297
2481.176	2493.303	2502.495	2509.273	2526.410	2537.223
2550.270	2560.281	2566.011	2568.263	2580.260	2590.159
2597.330	2609.566	2614.283	2626.422	2635.613	2645.479
2653.247	2662.345	2667.179	2679.406	2691.100	2695.365
2707.375	2720.395	2723.277	2737.464	2749.320	2752.323
2765.310	2780.280	2792.691	2795.504	2809.306	2822.283
2833.281	2839.381	2852.534	2866.440	2870.373	2880.489
2886.349	2896.528	2904.474	2914.541	2926.446	2933.776
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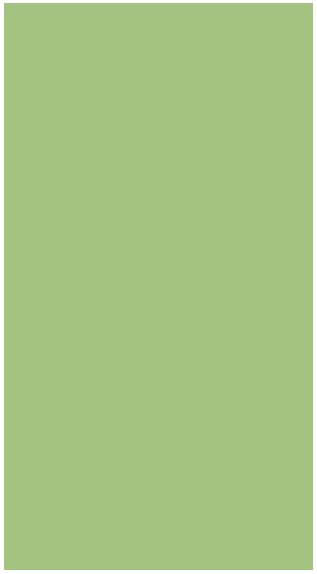

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3171.543	3177.654	3188.677	3199.718	3203.606	3207.688
3218.762	3230.659	3241.543	3247.644	3259.479	3264.635
3277.426	3289.857	3292.717	3304.556	3317.347	3320.840
3325.733	3337.631	3346.550	3353.802	3365.086	3367.744
3378.777	3381.792	3392.809	3396.694	3399.758	3410.725
3424.823	3429.792	3441.518	3456.511	3468.481	3573.716

Tolerance (mon) 13.00 ppm

Number of Peptides 416

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	5.1×10^{-5}	gi|14269568|ref|NP_113843.1| latexin [Rattus norvegicus]	17	5.8	26.36	

NOTE:
1. To search again using unmatched masses, click the symbol .

Input Summary

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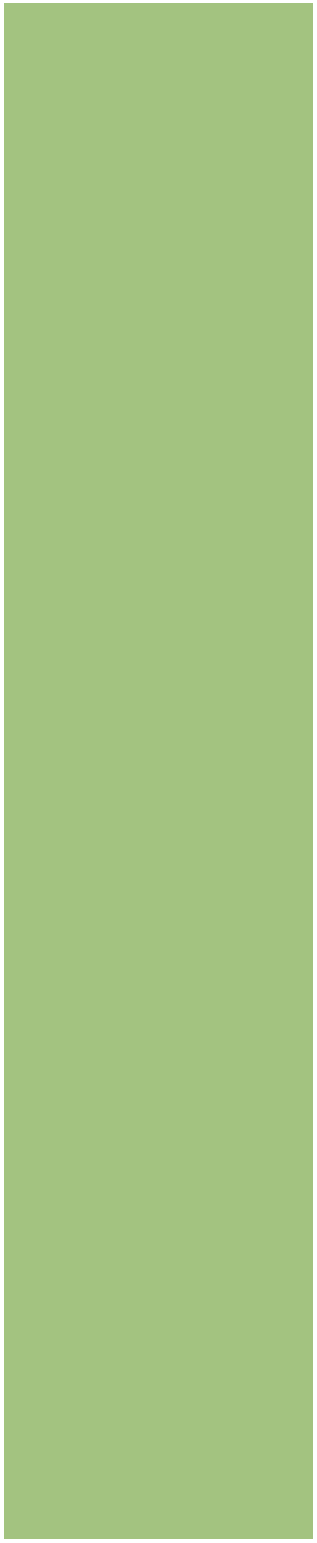
Sequences 20073
Date & Time Fri Mar 30 17:21:36 2007 UTC (Search Time: 0.27 sec.)
Sample ID 20061228 NIA MRich spot 4212 search 20070330 number 1
Database NCBInr [..\databases\nr]
Taxonomy Rattus
Mass Range 15 - 35 kDa
pI Range 4.0 -7.0
Digestion Trypsin
Missed Cuts 0
Modifications +C2H3ON@C(Complete); +CH2N2@K(Complete);
Charge State MH+
Masses (avg)
Tolerance (avg) 1.00 ppm



Masses (mon)

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1838.858 1854.876 1895.880 1929.907 1931.904 1949.902
1957.910 1966.914 1984.930 2006.919 2007.918 2021.936
2024.936 2025.923 2038.952 2039.947 2044.949 2045.967
2047.956 2048.948 2055.958 2056.964 2070.981 2098.992
2120.995 2121.998 2131.008 2150.003 2167.052 2181.047
2209.082 2225.108 2241.133 2242.137 2348.152 2349.149
2364.123 2365.154 2374.167 2375.125 2392.169 2397.135
2398.155 2405.144 2418.155 2435.196 2436.184 2447.143
2448.153 2453.178 2454.156 2460.162 2463.147 2464.198
2479.180 2495.164 2506.148 2507.182 2516.174 2535.146
2536.172 2539.150 2540.189 2550.177 2551.188 2556.193
2557.191 2564.205 2565.184 2575.175 2576.209 2580.200
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2639.211 2650.215 2651.240 2666.219 2668.227 2680.226
2681.237 2687.233 2688.218 2693.228 2700.253 2701.254
2718.262 2719.230 2724.275 2725.236 2731.254 2732.268
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2803.286 2804.267 2818.314 2819.287 2823.300 2824.292
2832.299 2833.295 2838.270 2839.292 2848.282 2849.301
2866.294 2886.372 2895.354 2896.356 2906.356 2914.362
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2962.321 2968.400 2969.349 2981.338 2982.359 2992.359
2993.336 3004.371 3010.338 3011.371 3018.369 3029.428
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3203.463 3212.462 3213.455 3218.479 3228.448 3244.491
3245.466 3262.490 3275.478 3291.459 3301.533 3302.538
3307.453 3308.429 3314.477 3316.501 3327.444 3329.527
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3396.486 3406.535 3407.474 3415.526 3416.518 3422.546
3423.426 3446.530 3447.550 3459.589 3460.491 3465.556
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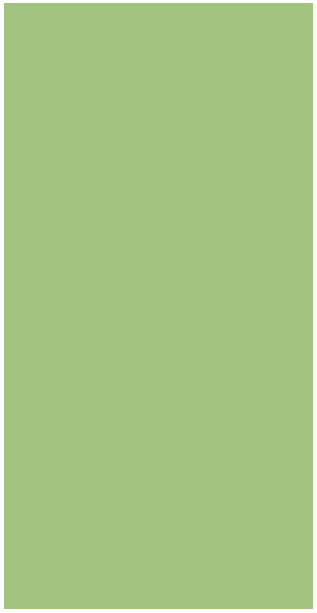

	3570.545 3581.583 3596.548 3603.626 3620.619 3624.675 3638.655 3657.672 3682.656 3695.656 3711.682 3722.703 3742.658 3754.674 3770.676 3781.680 3787.767 3798.716 3803.663 3815.666 3830.698 3847.679 3864.704 3877.703 3889.729 3907.712 3917.709 3923.739 3933.710 3949.781 3970.759 3987.740 4003.829 4010.814 4019.802 4028.768 4034.758 4046.827 4055.821 4066.806 4082.891 4092.734 4100.775 4113.922 4152.871 4185.716 4190.851 4206.879 4218.729 4236.683 4250.442 4278.876 4300.904 4317.274 4644.422
Tolerance (mon)	8.00 ppm
Number of Peptides	290

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	6.5×10^{-8}	gi|11968064|ref|NP_071944.1| parvalbumin [Rattus norvegicus]	38	5.0	12.58	
2	3.4×10^{-5}	gi|6900834|emb|CAB71514.1| immunoglobulin heavy chain variable region [Rattus norvegicus]	46	5.2	11.43	
3	4.0×10^{-5}	gi|205413|gb|AAA41599.1| MHC truncated antigen	27	4.8	12.35	
4	8.2×10^{-5}	gi|27574128|pdb|1N7S|B Chain B, High Resolution Structure Of A Truncated Neuronal Snare Complex	71	4.8	7.99	
5	1.4×10^{-4}	gi|52696058|pdb|1URQ|B Chain B, Crystal Structure Of Neuronal Q-Snares In Complex With R-Snare Motif Of Tomosyn	64	5.1	8.89	
6	1.9×10^{-4}	gi|6729810|pdb|1SFC|B Chain B, Neuronal Synaptic Fusion Complex	58	5.1	9.82	
7	2.9×10^{-4}	gi|15987986|pdb|1G33|A Chain A, Crystal Structure Of Rat Parvalbumin Without The N-Terminal Domain	38	4.6	8.26	
8	5.8×10^{-4}	gi|32185283|gb|AAO64469.1| BCL-WS [Rattus norvegicus]	46	4.9	8.63	
9	7.4×10^{-4}	gi|55669693|pdb|1S3P|A Chain A, Crystal Structure Of Rat Alpha-Parvalbumin S55dE59D MUTANT	26	4.9	12.46	
10	7.4×10^{-4}	gi|494573|pdb|1RTP|1 Chain 1, Alpha-Parvalbumin	26	5.0	12.45	
11	1.3×10^{-3}	gi|205601|gb|AAA41660.1| myosin light chain 2	29	4.7	11.70	
12	1.7×10^{-3}	gi|203239|gb|AAA40853.1| intestinal calcium-binding protein	30	5.0	9.65	
13	6.5×10^{-3}	gi|27545440|ref|NP_775459.1| CaM-kinase II inhibitor alpha [Rattus norvegicus]	29	5.2	8.80	
14	0.013	gi|27065383|pdb|1LJ0|A Chain A, Structure Of Quintuple Mutant Of The Rat Outer Mitocondrial Cytochrome B5.	28	4.8	10.56	
15	0.013	gi|15988286|pdb|1ICC|A Chain A, Rat Outer Mitochondrial Membrane Cytochrome B5	30	4.9	10.14	

16	0.014	gi|27721221|ref|XP_217235.1| PREDICTED: similar to RING-box protein 2 (Rbx2) (RING finger protein 7) (Sensitive to apoptosis gene protein) [Rattus norvegicus]	20	5.2	13.67
17	0.017	gi|56605674|ref|NP_001008279.1| hypothetical protein LOC287278 [Rattus norvegicus]	27	5.1	13.53

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

Search id B109C9CD-0938-61212746

Sequences 20092

Date & Time Mon Jan 29 17:20:58 2007 UTC (Search Time: 0.28 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 4 - 14 kDa

pI Range 4.5 -5.5

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 616.435 640.664 654.687 656.636 668.694 696.734 710.749
719.385 722.748 724.768 725.772 738.785 739.776 740.765
753.802 754.805 766.812 778.813 795.824 797.856 811.868
824.498 850.447 853.410 918.466 920.464 948.524 955.504
990.548 1005.541 1013.522 1028.534 1058.495 1064.528
1087.545 1091.542 1145.567 1177.591 1195.594 1202.566
1217.647 1220.596 1223.605 1233.634 1240.581 1244.598
1248.602 1262.613 1265.633 1268.608 1282.642 1291.616
1329.633 1333.657 1432.738 1456.708 1469.713 1504.710
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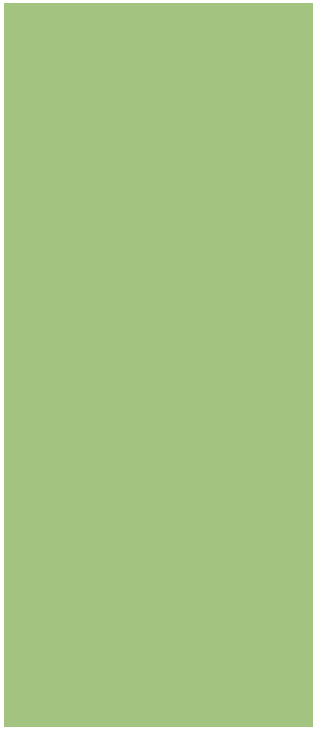
1665.762 1684.763 1713.806 1757.874 1894.891 1928.901



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2408.227	2425.190	2435.111	2448.153	2463.134	2464.196
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3112.469	3135.373	3140.384	3141.430	3190.489	3191.498
3220.525	3232.416	3233.575	3273.463	3274.471	3278.464
3279.435	3281.480	3282.376	3291.521	3316.473	3326.683
3336.515	3337.373	3340.445	3355.515	3369.455	3516.558
3617.587	3704.511	3736.697	3912.638	4183.928	4515.600

Tolerance (mon) 41.00 ppm

Number of Peptides 148

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- PepFrag
- X! Tandem
- X! Hunter
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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	2.7×10^{-9}	gi|554476|gb|AAA41655.1| myosin heavy chain	49	5.3	20.16	
2	7.3×10^{-7}	gi|1065013|pdb|1RSY| Chain , Synaptotagmin I (First C2 Domain) (Calb)	32	5.0	17.69	
3	1.2×10^{-4}	gi|56605732|ref|NP_001008328.1| family with sequence similarity 96, member A [Rattus norvegicus]	48	4.7	18.99	
+4	4.4×10^{-4}	gi|228542|prf||1805343A myosin:SUBUNIT=regulatory light chain	40	4.7	20.32	
	-	gi|2119365|pir||S45709 myosin regulatory light chain 2, brain (clone FY53) - rat	40	4.7	20.45	
	-	gi|27711040|ref|XP_216161.1| PREDICTED: similar to Mitotic spindle assembly checkpoint protein MAD2A (MAD2-like 1) [Rattus norvegicus]	26	5.1	24.24	
	-	gi|2674183|gb|AAB88701.1| kinesin-related protein KRP4 [Rattus norvegicus]	40	4.9	17.37	
	-	gi|47155821|gb|AAT11858.1| dopamine- and cAMP-regulated phosphoprotein DARPP-32 [Rattus norvegicus]	32	4.5	23.29	
	-	gi|56090345|ref|NP_001007739.1| hypothetical protein LOC361744 [Rattus norvegicus]	55	4.9	20.66	
	-	gi|7381175|gb|AAF61422.1|AF136282_1 apoptotic death agonist BID [Rattus norvegicus]	36	4.8	22.57	
	-	gi|12083631|ref|NP_073175.1| BH3 interacting domain death agonist [Rattus norvegicus]	36	4.8	22.54	
	-	gi|554496|gb|AAA41953.1| proline-rich protein	33	5.1	20.37	
	-	gi|34879746|ref|XP_344141.1| PREDICTED: similar to solute carrier family 41, member 1 [Rattus norvegicus]	49	4.6	17.94	

-	gi|57870401|gb|AAH89061.1| Thyroid hormone responsive protein [Rattus norvegicus]	30	4.8	17.48
-	gi|2765346|emb|CAA73919.1| calpastatin [Rattus norvegicus]	35	4.8	19.68
-	gi|7107454|gb|AAF36411.1|AF235993_1 Bax protein splice variant k [Rattus norvegicus]	27	5.1	20.09
-	gi|12964662|dbj|BAB32668.1| branched-chain alpha-keto acid dihydrolipoyl acyltransferase [Rattus norvegicus]	37	5.2	21.49
-	gi|56090259|ref|NP_001007668.1| spermidine/spermine N1-acetyl transferase [Rattus norvegicus]	29	5.2	20.74
-	gi|39654405|pdb|1P1D|A Chain A, Structural Insights Into The Inter-Domain Chaperoning Of Tandem Pdz Domains In Glutamate Receptor Interacting Proteins	32	4.7	21.79
-	gi|1929922|gb|AAB51478.1| anti-idiotype immunoglobulin M heavy chain [Rattus norvegicus]	33	4.7	19.62

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B058773B-09E8-60712696

Sequences 20092

Date & Time Tue Jan 30 17:22:36 2007 UTC (Search Time: 0.33 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 17 - 25 kDa

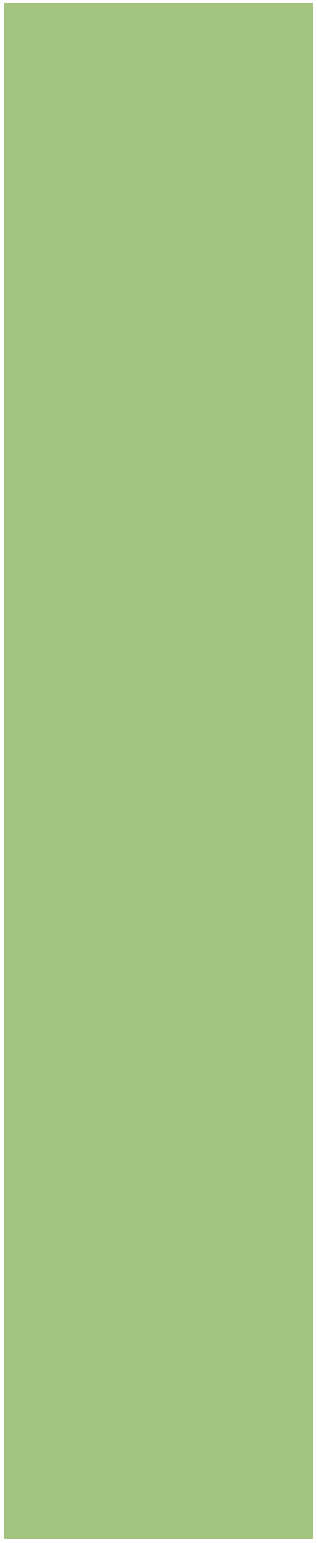
pI Range 4.5 -5.3

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+



Masses (avg)

Tolerance (avg) 1.00 ppm

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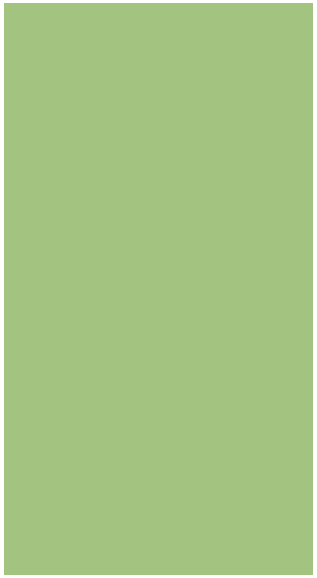

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Tolerance (mon)	15.00 ppm
Number of Peptides	272

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New York, NY 10021
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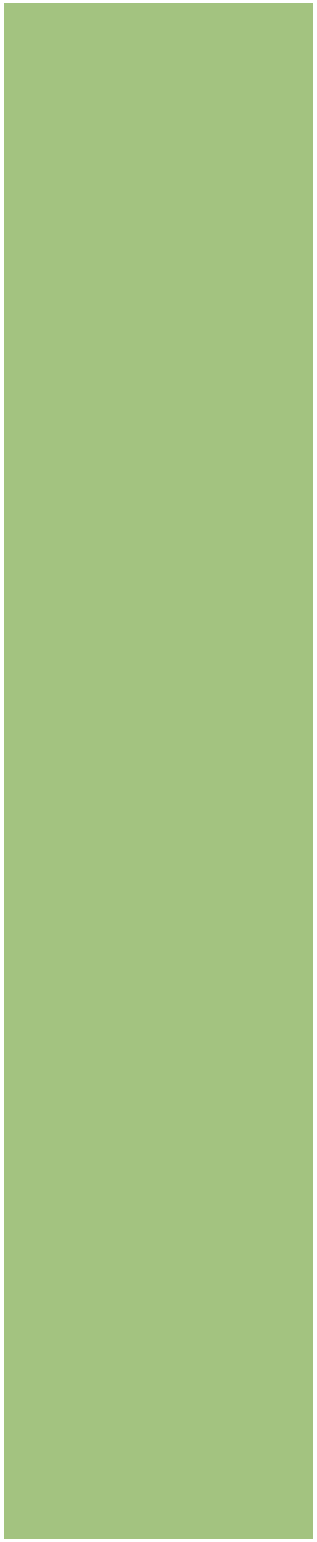
Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.1×10^{-9}	gi|15824045|dbj|BAB68551.1| TAFIIB [Rattus norvegicus]	48	5.5	14.16	
+2	4.8×10^{-8}	gi|45267819|ref|NP_571989.2| caveolin 2 [Rattus norvegicus]	46	5.3	18.81	
	-	gi|38322757|gb|AAR16307.1| caveolin 2 [Rattus norvegicus]	30	5.3	18.78	
3	1.1×10^{-7}	gi|11141738|gb|AAG32053.1| complement component 7 [Rattus norvegicus]	67	5.4	16.33	
4	5.7×10^{-4}	gi|26992096|gb|AAN86738.1| homeobox prot-oncogene [Rattus sp.]	55	5.0	14.75	
5	6.9×10^{-4}	gi|12408324|ref|NP_074055.1| complexin 1 [Rattus norvegicus]	35	4.9	15.92	
6	8.5×10^{-4}	gi|12018254|ref|NP_072115.1| transcription elongation factor B (SIII), polypeptide 1 [Rattus norvegicus]	78	4.7	12.88	
7	1.3×10^{-3}	gi|34856632|ref|XP_342484.1| PREDICTED: similar to zinc finger, CSL-type containing 3 [Rattus norvegicus]	49	4.7	17.85	
8	1.7×10^{-3}	gi|230180|pdb|1MSB|A Chain A, Mannose Binding Protein A (Lectin Domain) Complex With Holmium	38	5.3	13.22	
	-	gi|34858175|ref|XP_227370.2| PREDICTED: similar to Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farnesyl diphosphate synthetase) (Cholesterol-regulated 39 kDa protein) (CR 39) [Rattus norvegicus]	45	5.4	19.48	
	-	gi|56605732|ref|NP_001008328.1| family with sequence similarity 96, member A [Rattus norvegicus]	34	4.7	18.99	
	-	gi|27689593|ref|XP_226974.1| PREDICTED: similar to eukaryotic translation initiation factor 5A2 [Rattus norvegicus]	38	5.4	17.71	
	-	gi|6683092|dbj|BAA89032.1| R-ras GTPase activating protein [Rattus norvegicus]	27	5.4	14.73	
	-	gi|1675351|gb|AAB19106.1| inositol monophosphate [Rattus norvegicus]	49	4.9	9.96	

-	gi|27669100|ref|XP_216785.1| PREDICTED: similar to NADH-ubiquinone oxidoreductase ESSS subunit, mitochondrial precursor (Complex I-ESSS) (CI-ESSS) (Neuronal protein 15.6) (p15.6) (Np15.6) [Rattus norvegicus]	31	5.1	17.78
-	gi|13540630|ref|NP_110459.1| brain lipid binding protein [Rattus norvegicus]	28	5.5	15.64
-	gi|6689091|emb|CAB65384.1| MAp19 protein [Rattus norvegicus]	51	5.0	13.70
-	gi|34855683|ref|XP_214895.2| PREDICTED: similar to DNA-directed RNA polymerase II 14.5 kDa polypeptide (RPB9) (RPB14.5) [Rattus norvegicus]	44	5.0	15.23
-	gi|51980674|gb|AAH82106.1| Similar to RIKEN cDNA 4933415F23 [Rattus norvegicus]	18	4.6	17.16
-	gi|2674183|gb|AAB88701.1| kinesin-related protein KRP4 [Rattus norvegicus]	32	4.9	17.37
-	gi|20302079|ref|NP_620247.1| RS21-C6 protein [Rattus norvegicus]	21	4.8	18.79
-	gi|15826396|pdb|1JEX|A Chain A, Solution Structure Of A67v Mutant Of Rat Ferro Cytochrome B5	41	5.2	11.23
-	gi|6981316|ref|NP_037128.1| oxcytocin [Rattus norvegicus]	44	5.3	14.06
-	gi|27704684|ref|XP_215938.1| PREDICTED: similar to WAP four-disulfide core domain 3 isoform 1 precursor [Rattus norvegicus]	36	5.5	15.70
-	gi|57526823|ref|NP_001009621.1| NudC domain containing 2 [Rattus norvegicus]	34	5.0	18.21
-	gi|34853142|ref|XP_216020.2| PREDICTED: similar to Protein C9orf7 [Rattus norvegicus]	25	5.4	19.01
-	gi|294577|gb|AAB59703.1| cystatin S [Rattus norvegicus]	33	4.7	15.47
-	gi|224985|prf||1205244A cytochrome b5	52	5.4	10.82
-	gi|2914179|pdb|1AW3| Chain , The Solution Nmr Structure Of Oxidized Rat Microsomal Cytochrome B5, Minimized Average Structure	51	5.3	11.08



-	gi|2554670|pdb|1AQA| Chain , Solution Structure Of Reduced Microsomal Rat Cytochrome B5, Nmr, Minimized Average Structure	51	5.2	11.20
-	gi|2098349|pdb|1IEU| Chain , Apocytochrome B5, Ph 6.2, 298 K, Nmr, 10 Structures	49	5.0	11.61
-	gi|3660010|pdb|1BFX| Chain , The Solution Nmr Structure Of The B Form Of Oxidized Rat Microsomal Cytochrome B5, Minimized Average Structure	48	5.0	11.74
-	gi|2257955|gb|AAB67609.1| cytochrome b5 [Rattus norvegicus]	48	5.3	11.81
-	gi|34863048|ref|XP_347100.1| PREDICTED: hypothetical protein [Rattus norvegicus]	40	4.9	13.42
-	gi|11560046|ref|NP_071581.1| cytochrome b-5 [Rattus norvegicus]	36	4.9	15.76
-	gi|45478236|gb|AAS66289.1| LRRGT00198 [Rattus norvegicus]	52	4.9	10.53
-	gi|57012392|ref|NP_001008857.1| RT1 class Ib, locus H2-TL-like (S2) [Rattus norvegicus]	27	5.5	19.59
-	gi|55562787|gb|AAH86338.1| LOC474154 protein [Rattus norvegicus]	22	5.5	16.82
-	gi|758267|emb|CAA26200.1| unnamed protein product [Rattus norvegicus]	27	5.4	18.54
-	gi|92406|pir||A27390 Ig lambda-1 chain C region - rat	39	5.3	12.17
-	gi|204868|gb|AAA41419.1| lambda-chain C1-region	39	5.3	12.16
-	gi|56090411|ref|NP_001007653.1| polymerase (DNA directed), epsilon 3 (p17 subunit) [Rattus norvegicus]	17	4.7	17.44
-	gi|24416601|gb|AAM97286.1| CACNA1I splicing variant b [Rattus norvegicus]	41	4.6	12.66
-	gi|34860679|ref|XP_342576.1| PREDICTED: similar to Seminal vesicle secretory protein 6 precursor (Seminal vesicle secretory protein VI) (SVS VI) (Seminal vesicle protein 6) (SVSP99) [Rattus norvegicus]	34	5.5	11.73
-	gi|34933275|ref|XP_346272.1| PREDICTED: similar to Huntingtin interacting protein M [Rattus norvegicus]	27	5.1	16.93

-	gi|643039|emb|CAA57089.1| variable region-alpha RAV4.25 [Rattus norvegicus]	46	5.0	10.22
-	gi|643041|emb|CAA57090.1| variable region-alpha RAV4.26 [Rattus norvegicus]	46	5.3	10.19
-	gi|1065013|pdb|1RSY| Chain , Synaptotagmin I (First C2 Domain) (Calb)	22	5.0	17.69
-	gi|27672880|ref|XP_213347.1| PREDICTED: similar to MAK31-like protein [Rattus norvegicus]	27	5.3	13.75

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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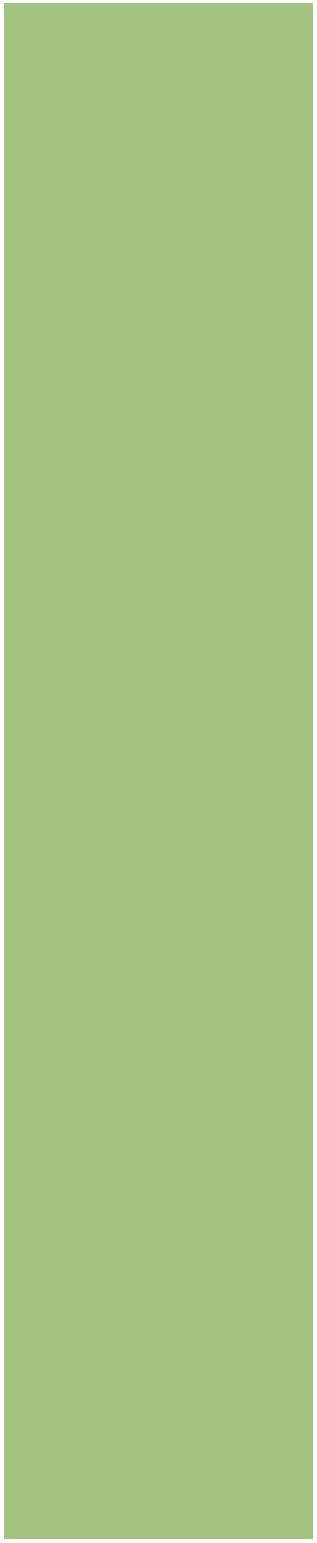
pI Range	4.6 -5.6
Digestion	Trypsin
Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm



Masses (mon) 664.340 791.406 817.420 823.441 848.439 902.463 938.474
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Tolerance (mon)	13.00 ppm
Number of Peptides	241

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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National Center of Research Resources

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	2.5×10^{-23}	gi|56090293|ref|NP_001007621.1| pyruvate dehydrogenase (lipoamide) beta [Rattus norvegicus]	14	6.2	40.11	
2	5.1×10^{-8}	gi|285140|pir||JX0228 proteasome endopeptidase complex (EC 3.4.25.1) delta chain - rat	21	5.0	22.03	
3	7.4×10^{-8}	gi|50925763|gb|AAH79187.1| Similar to hypothetical protein MGC33309 [Rattus norvegicus]	14	6.1	36.45	
4	8.3×10^{-8}	gi|56090624|ref|NP_001007676.1| C1q and tumor necrosis factor related protein 1 [Rattus norvegicus]	14	6.1	33.05	
5	9.2×10^{-8}	gi|47169486|tpe|CAE48380.1| TPA: proteasome subunit beta type 6-like [Rattus norvegicus]	18	4.8	25.68	
6	9.2×10^{-8}	gi|54019419|ref|NP_476440.2| proteasome (prosome, macropain) subunit, beta type 6 [Rattus norvegicus]	18	4.8	25.67	
7	1.3×10^{-7}	gi|19705435|ref|NP_599156.1| alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Rattus norvegicus]	13	6.3	42.05	
8	1.3×10^{-7}	gi|5915678|sp|P41682|ADH7_RAT Alcohol dehydrogenase class 4 mu/sigma chain (Alcohol dehydrogenase class IV mu/sigma chain)	13	6.6	41.98	
9	1.5×10^{-7}	gi|25282455|ref|NP_741987.1| 3(2),5-bisphosphate nucleotidase [Rattus norvegicus]	10	5.6	34.34	
10	2.3×10^{-7}	gi|13928958|ref|NP_113878.1| crystallin, beta B3 [Rattus norvegicus]	11	6.7	24.81	
11	5.4×10^{-7}	gi|299145|gb|AAB26277.1| integrin alpha v subunit [Rattus sp.]	18	5.2	28.46	
12	6.1×10^{-7}	gi|6689087|emb|CAB65382.1| MASP-2 protein [Rattus norvegicus]	5	6.0	38.46	
13	8.1×10^{-7}	gi|57222310|ref|NP_001009491.1| 2'-5' oligoadenylate synthetase 1H [Rattus norvegicus]	6	5.4	44.57	
14	9.0×10^{-7}	gi|6689099|emb|CAB65388.1| MASP-2 protein [Rattus norvegicus]	4	6.2	41.57	
15	2.3×10^{-5}	gi|9506501|ref|NP_062232.1| calponin 3, acidic [Rattus norvegicus]	8	5.5	37.60	
16	3.2×10^{-5}	gi|55778376|gb|AAH86383.1| Eukaryotic translation initiation factor 3, subunit 4 (delta) [Rattus norvegicus]	12	5.7	37.14	
17	1.1×10^{-4}	gi|14091738|ref|NP_114447.1| eukaryotic translation initiation factor 2B, subunit 2 beta [Rattus norvegicus]	6	5.8	39.63	
18	1.1×10^{-4}	gi|47683035|gb|AAH70506.1| Eukaryotic translation initiation factor 2B, subunit 2 beta [Rattus norvegicus]	6	5.7	39.60	

19	1.1×10^{-4}	gi|2149254|gb|AAB58527.1| eukaryotic initiation factor eIF-2B beta subunit [Rattus norvegicus]	6	5.7	39.22

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

Search id B0E30CFE-0954-6105274D

Sequences 20076

Date & Time Tue Feb 06 20:48:45 2007 UTC (Search Time: 0.30 sec.)

Sample ID 20061228 richardson NIA set 1 spot 2403 CONSENSUS search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 45 kDa

pI Range 4.0 -7.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 663.324 718.358 791.411 861.512 902.473 919.455 944.554 991.516 1080.490
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1431.715 1456.709 1486.710 1529.732 1542.755 1559.764 1568.755 1601.792
1664.763 1666.776 1695.792 1699.864 1713.810 1730.839 1745.841 1747.856
1757.865 1763.870 1779.866 1794.883 1801.882 1825.884 1827.870 1851.876
1858.942 1893.892 1904.841 1908.907 1931.911 1953.928 1957.932 1962.908
2001.928 2002.939 2023.940 2033.944 2035.963 2045.954 2046.955 2052.966
2053.953 2062.993 2070.962 2098.993 2122.006 2167.052 2181.061 2209.094
2298.157 2339.153 2341.191 2349.171 2350.170 2367.161 2368.155 2376.176
2377.241 2381.163 2382.168 2392.230 2408.172 2435.237 2450.182 2460.158
2497.189 2498.205 2503.189 2504.154 2514.194 2534.221 2535.194 2553.197
2554.208 2559.208 2560.219 2593.196 2602.228 2603.217 2609.220 2610.214
2633.188 2634.182 2650.220 2651.219 2668.259 2673.254 2674.217 2684.240
2685.260 2691.226 2692.229 2723.271 2724.231 2733.257 2734.246 2746.247
2747.232 2752.279 2753.298 2763.266 2764.234 2775.292 2776.283 2785.276
2786.298 2801.287 2802.297 2820.302 2832.297 2833.274 2837.311 2838.308
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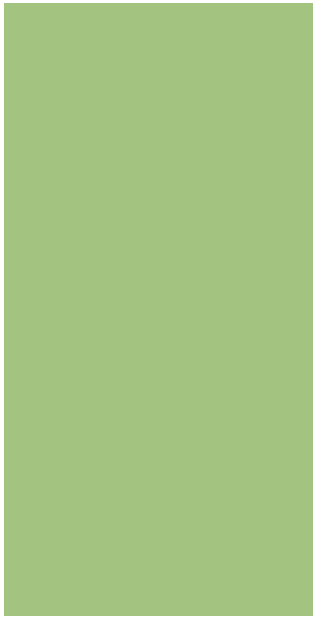

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3203.461 3208.450 3220.468 3228.461 3232.496 3233.479 3245.512 3262.540
3273.488 3281.503 3292.535 3307.556 3308.559 3314.507 3326.535 3342.515
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3398.556 3399.530 3406.547 3407.541 3418.547 3419.572 3434.592 3435.578
3447.596 3448.582 3461.551 3476.591 3478.635 3479.549 3491.629 3492.610
3499.588 3509.578 3519.602 3525.603 3532.619 3548.636 3552.614 3566.617
3581.654 3599.633 3613.637 3622.622 3632.606 3650.655 3665.659 3675.658
3683.646 3695.641 3710.689 3720.674 3727.687 3740.661 3755.744 3766.646
3778.693 3783.707 3792.698 3801.719 3818.737 3835.702 3840.730 3851.822
3861.694 3865.724 3874.753 3884.806 3895.707 3910.765 3920.703 3931.679
3939.788 3948.815 3966.773 3979.763 3987.741 4004.890 4020.866 4036.786
4046.821 4059.886 4080.876 4094.854 4103.912 4114.890 4127.890 4140.892
4147.936 4155.906 4167.855 4190.991 4205.981 4229.838 4458.699 4473.779
4676.501

Tolerance (mon) 9.00 ppm

Number of Peptides 282

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	2.5×10^{-13}	gi|984553|gb|AAC72249.1| G protein beta 1 subunit [Rattus norvegicus]	31	5.5	38.59	
	-	gi|51338711|sp|P54311|GBB1_RAT Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1 (Transducin beta chain 1)	31	5.6	38.58	
	-	gi|34868134|ref|XP_235618.2| PREDICTED: similar to Ankyrin repeat and SOCS box protein 8 (ASB-8) [Rattus norvegicus]	34	5.6	32.78	
	-	gi|24496500|gb|AAN60073.1| RING finger protein MOMO [Rattus norvegicus]	23	4.7	44.83	
	-	gi|51854215|ref|NP_001004075.1| ring finger protein 34 [Rattus norvegicus]	23	4.7	44.82	
	-	gi|13399443|pdb|1CX4|A Chain A, Crystal Structure Of A Deletion Mutant Of The Type Ii Beta Regulatory Subunit Of Camp-Dependent Protein Kinase	25	4.9	35.30	
	-	gi|11120724|ref|NP_068537.1| sulfotransferase family 1D, member 1 [Rattus norvegicus]	25	5.7	37.70	
	-	gi|8926237|gb|AAF81755.1|AF269283_1 potassium channel auxiliary subunit KCHIP2a [Rattus norvegicus]	31	4.9	31.85	
	-	gi|8926239|gb|AAF81756.1|AF269284_1 potassium channel auxiliary subunit KCHIP2b [Rattus norvegicus]	33	4.8	29.90	
	-	gi|27227451|gb|AAN85424.1| MHC class Ib antigen [Rattus norvegicus]	24	5.1	32.36	
	-	gi|50657372|ref|NP_001002821.1| histocompatibility 2, T region locus 18 [Rattus norvegicus]	19	5.3	40.56	
	-	gi|5542343|pdb|1QBQ|A Chain A, Structure Of Rat Farnesyl Protein Transferase Complexed With A Cvim Peptide And Alpha-Hydroxyfarnesylphosphonic Acid	22	5.1	40.44	

-	gi|34881740|ref|XP_215225.2| PREDICTED: similar to UCH37-interacting protein 1 isoform 1 [Rattus norvegicus]	13	4.8	42.39
-	gi|31077142|ref|NP_852030.1| potassium channel interacting protein 4 [Rattus norvegicus]	27	5.1	29.81
-	gi|56585055|gb|AAH87718.1| Ring finger protein 135 [Rattus norvegicus]	14	5.5	47.79
-	gi|40786447|ref|NP_955410.1| craniofacial development protein 1 [Rattus norvegicus]	11	4.8	34.55
-	gi|48843735|ref|NP_001001717.1| RT1 class Ib, locus M2 [Rattus norvegicus]	23	5.7	39.97
-	gi|16758084|ref|NP_445877.1| copper chaperone for superoxide dismutase [Rattus norvegicus]	20	5.8	29.89
-	gi|34878802|ref|XP_226031.2| PREDICTED: similar to Transcription initiation factor TFIID subunit 7 (Transcription initiation factor TFIID 55 kDa subunit) (TAF(II)55) (TAFII-55) (TAFII55) [Rattus norvegicus]	17	5.2	40.68
-	gi|2499601|sp|P70618|MK14_RAT Mitogen-activated protein kinase 14 (Mitogen-activated protein kinase p38 alpha) (MAP kinase p38 alpha) (CRK1)	13	5.6	42.33
-	gi|54035313|gb|AAH83808.1| Similar to Nuclear autoantigen Sp-100 (Speckled 100 kDa) (Nuclear dot-associated Sp100 protein) [Rattus norvegicus]	11	5.3	39.12
-	gi|1916984|gb|AAB51285.1| p38 mitogen activated protein kinase [Rattus norvegicus]	13	5.5	42.22
-	gi|13194758|gb|AAK15541.1|AF346293_1 p38 mitogen-activated protein kinase alpha1 [Rattus norvegicus]	13	5.6	42.34
-	gi|27682039|ref|XP_236922.1| PREDICTED: similar to beta-tubulin cofactor C [Rattus norvegicus]	19	5.1	39.20

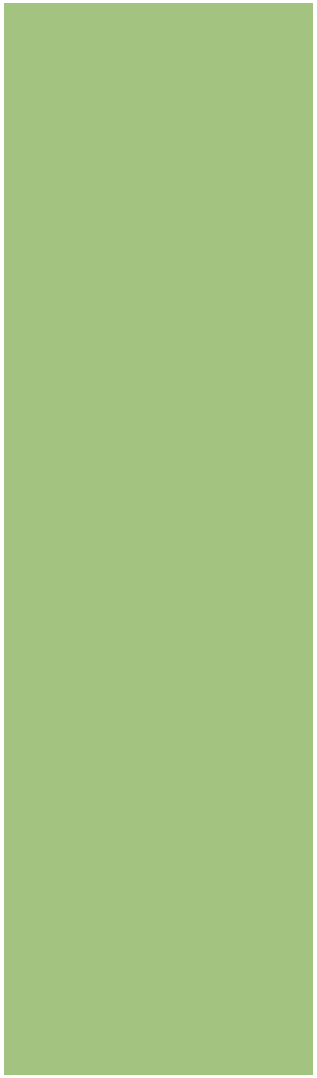
NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B12B2FD8-0914-6145276A

Sequences	20092
Date & Time	Wed Jan 31 16:42:59 2007 UTC (Search Time: 0.41 sec.)
Sample ID	
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	28 - 48 kDa
pI Range	4.7 -5.8
Digestion	Trypsin
Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +CH2N2@K(Complete);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	663.302 849.430 879.433 881.259 899.269 917.276 991.512 1013.529 1177.574 1211.591 1223.608 1224.591 1226.587 1265.616 1267.623 1330.600 1441.714 1529.735 1557.738 1584.791 1630.752 1684.780 1757.849 1762.830 1765.832 1789.833 1837.853 1853.863 1874.898 1887.875 1889.888 1895.881 1904.893 1906.880 1908.888 1932.916 1951.909 1953.919 1962.929 1984.931 2004.927 2022.008 2039.976 2047.979 2048.955 2051.955 2052.956 2057.971 2059.002 2071.003 2100.009 2123.990 2132.013 2150.015 2152.047 2167.034 2183.075 2234.107 2241.129 2242.143 2298.147 2306.147 2341.181 2363.132 2365.150 2376.138 2377.180 2381.142 2382.184 2392.165 2396.151 2397.165 2435.194 2447.148 2448.116 2458.181 2495.185 2507.210 2510.184 2511.203 2537.198 2538.209 2553.221 2562.214 2563.210 2572.231 2583.213 2584.228 2595.204 2596.209 2605.198 2606.239 2611.237 2612.200 2622.240 2625.257 2626.172 2639.265 2640.243 2647.217 2648.242 2668.265 2669.248 2679.227 2680.240 2686.281 2687.240 2690.265 2691.256 2697.309 2698.261 2706.349 2714.258 2715.267 2723.259 2732.308 2733.300 2748.204 2749.334 2751.177 2752.249 2765.304 2776.273 2777.295 2784.369 2785.312 2787.261 2788.320 2795.252 2796.311 2804.208 2805.287 2816.268 2817.295 2821.320 2832.254 2833.282 2839.278 2847.271



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Tolerance (mon)	12.00 ppm
Number of Peptides	268

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Macromolecules

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Protein Candidates

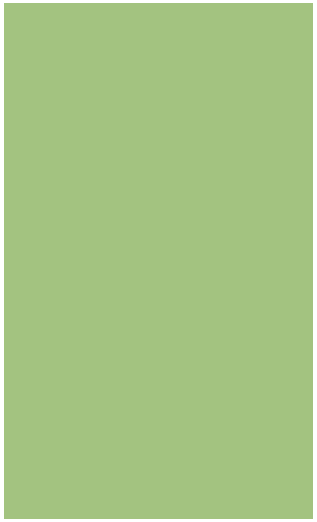
Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	7.2×10^{-30}	gi|818029|emb|CAA29121.1| dismutase [Rattus norvegicus]	38	5.9	16.11	
-		gi|203658|gb|AAA40996.1| Cu-Zn superoxide dismutase (EC 1.15.1.1)	38	5.9	16.24	
-		gi|1213217|emb|CAA79925.1| Cu/Zn superoxide dismutase [Rattus norvegicus]	37	5.7	16.51	
-		gi|8394328|ref|NP_058746.1| superoxide dismutase 1 [Rattus norvegicus]	37	5.9	16.44	
-		gi|27706818|ref|XP_217572.1| PREDICTED: similar to PDZ domain containing 11 [Rattus norvegicus]	47	6.6	16.46	
-		gi|2780953|pdb|1AR0|A Chain A, Nuclear Transport Factor 2 (Ntf2) E42k Mutant	38	5.6	14.93	
-		gi|228123|prf||1717324N T cell receptor variable region:SUBUNIT=beta: ISOTYPE=9	49	6.7	13.28	
-		gi|2058677|gb|AAB53321.1| Kv4.3 [Rattus norvegicus]	38	6.5	17.57	
-		gi|27662982|ref|XP_235505.1| PREDICTED: similar to NADH-ubiquinone oxidoreductase ESSS subunit, mitochondrial precursor (Complex I-ESSS) (CI-ESSS) (Neuronal protein 17.3) (p17.3) (Np17.3) [Rattus norvegicus]	26	6.7	17.78	
-		gi|11560097|ref|NP_071610.1| baculoviral IAP repeat-containing 5 [Rattus norvegicus]	29	5.9	17.56	
-		gi|4928278|gb|AAD33515.1| ephrin A-2 precursor [Rattus norvegicus]	17	6.1	12.12	
-		gi|675469|gb|AAA87728.1| synaptotagmin VIII	23	5.6	15.93	
-		gi|46391590|gb|AAS90843.1| OX2 receptor precursor variant 1 [Rattus norvegicus]	16	5.8	17.14	
-		gi|13516471|dbj|BAB40316.1| beta-actin FE-3 [Rattus norvegicus]	21	5.6	15.43	
-		gi|34869362|ref|XP_221411.2| PREDICTED: similar to stefin A2 [Rattus norvegicus]	7	6.7	12.21	
-		gi|5419945|emb|CAB46528.1| endothelin-converting enzyme-1 b isoform [Rattus norvegicus]	26	6.2	13.65	
-		gi|6114760|emb|CAB59427.1| phosphodiesterase I/nucleotide pyrophosphatase [Rattus norvegicus]	26	5.5	17.83	
-		gi|30387884|gb|AAP32273.1| homeobox Otx1 [Rattus sp.]	22	6.8	15.62	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id	AB7DD259-0EC4-5B9521DD
Sequences	20092
Date & Time	Mon Jan 29 16:20:50 2007 UTC (Search Time: 0.27 sec.)
Sample ID	20061228 richardson NIA set 1 spot 3105, 20070128, cleaned data search 3
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	12 - 18 kDa
pI Range	5.5 -7.0
Digestion	Trypsin
Missed Cuts	0
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +CH2N2@K(Complete);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	605.333 634.274 654.390 660.287 662.302 666.641 668.679 672.396 684.661 719.381 724.767 725.771 753.800 768.381 802.263 804.274 824.497 832.305 854.286 862.286 902.459 904.456 918.458 948.519 955.502 990.543 1005.537 1027.546 1080.480 1091.528 1167.516 1174.568 1179.595 1211.574 1224.565 1233.636 1243.552 1248.597 1262.604 1281.603 1322.657 1330.603 1367.753 1380.699 1408.646 1529.735 1552.760 1666.788 1808.829 1825.828 1837.849 1891.858 1904.846 1908.884 1917.881 1931.916 1949.904 1953.910 1964.908 1986.901 2005.921 2006.927 2015.905 2016.925 2021.936 2025.928 2026.933 2036.947 2037.942 2038.941 2042.953 2046.932 2047.957 2070.957 2098.965 2124.012 2152.048 2183.079 2225.099 2241.116 2242.137 2298.144 2306.146 2366.168 2367.103 2377.151 2378.141 2390.141 2397.156 2398.160 2416.118 2417.143 2430.153 2431.091 2450.172 2455.196 2456.188 2458.158 2465.225 2466.200 2479.184 2498.197 2506.181 2507.187 2512.205 2513.228 2518.166 2519.170 2532.168 2533.193 2543.188 2544.202 2558.185 2559.200 2566.190 2567.138 2591.198 2604.209 2622.208 2627.170 2628.194 2638.221 2639.227 2648.215 2649.227 2668.263 2669.239 2679.264 2686.213 2687.212 2700.220 2701.214 2708.262 2718.230 2719.246 2731.281 2732.254 2743.205 2744.200 2764.299 2765.278 2776.302 2782.247 2784.274 2789.263 2790.251 2800.277 2801.280 2806.291 2807.271 2819.289 2820.282 2834.290 2835.282 2844.275 2845.280 2847.319 2848.298 2862.294 2863.318 2866.318 2893.349 2894.337 2903.314 2914.365 2922.329 2947.336 2958.330 2960.344 2976.320 2977.352 2995.372 2996.375 3001.367 3002.274 3020.336 3033.348 3034.368 3047.420 3048.392 3060.392 3065.390 3066.363 3077.390 3083.380 3084.397 3095.444 3105.425 3114.456 3138.461 3147.456 3148.473 3180.503 3181.469 3187.458



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3583.609	3589.635	3602.569	3613.639	3631.623	3642.667	3653.676	3659.663
3676.684	3692.646	3706.694	3714.707	3724.703	3736.692	3743.689	3757.717
3774.758	3789.665	3806.684	3813.694	3820.787	3834.736	3843.763	3849.729
3860.673	3875.743	3890.743	3907.732	3915.735	3926.754	3931.896	3943.736
3954.776	3963.827	3971.753	3975.781	3984.811	3994.795	4011.821	4022.816
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Tolerance (mon) 38.00 ppm

Number of Peptides 298

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- X! Hunter
- GPMDB

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- Chait Lab

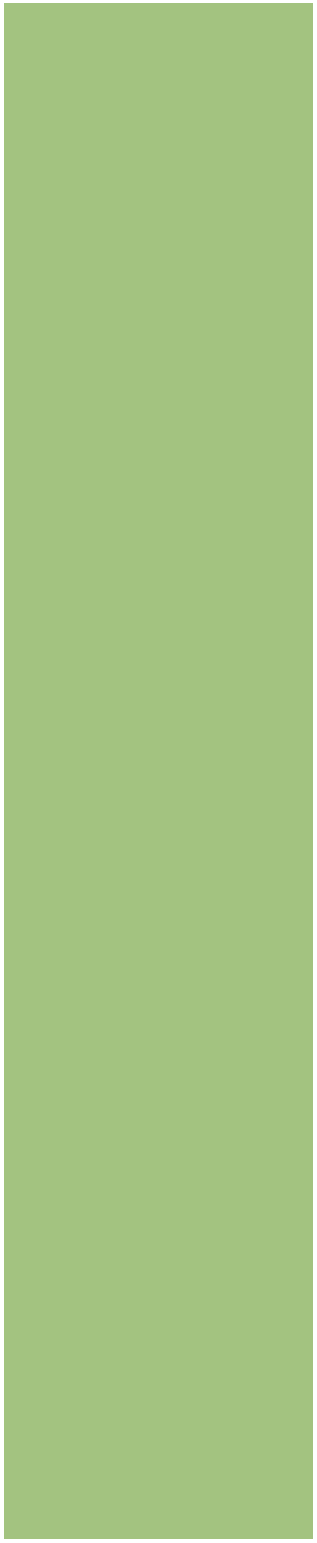
The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.2×10^{-16}	gi|16758348|ref|NP_446028.1| peroxiredoxin 6 [Rattus norvegicus]	29	5.6	25.61	
2	3.3×10^{-9}	gi|46359595|dbj|BAD15354.1| interleukin-1 receptor accessory protein [Rattus norvegicus]	34	6.4	25.13	
3	4.5×10^{-9}	gi|554507|gb|AAA42117.1| stem cell factor	30	5.4	23.43	
+4	1.2×10^{-7}	gi|38426813|gb|AAR20448.1| wound inducible transcript 3.0 alpha [Rattus norvegicus]	26	5.4	25.72	
	-	gi|56388776|gb|AAH87696.1| Fgfr1op2 protein [Rattus norvegicus]	26	5.4	25.72	
	-	gi|6689097|emb|CAB65387.1| MAp19 protein [Rattus norvegicus]	30	5.8	20.85	
	-	gi|16758274|ref|NP_445964.1| peroxiredoxin 4 [Rattus norvegicus]	18	6.2	31.89	
	-	gi|56605786|ref|NP_001008356.1| hypothetical protein LOC312640 [Rattus norvegicus]	26	6.3	30.63	
	-	gi|27465597|ref|NP_775156.1| cytosolic resiniferatoxin-binding protein [Rattus norvegicus]	34	5.9	27.51	
	-	gi|56090405|ref|NP_001007660.1| hypothetical protein LOC300240 [Rattus norvegicus]	20	5.8	25.91	
	-	gi|29293823|ref|NP_808795.1| single-strand selective monofunctional uracil DNA glycosylase [Rattus norvegicus]	18	6.4	31.17	
	-	gi|21245092|ref|NP_640348.1| hypothetical protein LOC246120 [Rattus norvegicus]	26	6.4	24.30	
	-	gi|13591872|ref|NP_112248.1| adenylate kinase 2 isoform a [Rattus norvegicus]	22	6.3	27.49	



-	gi|12585364|sp|Q9Z0T0|TPMT_RAT Thiopurine S-methyltransferase (Thiopurine methyltransferase)	16	6.3	28.76
-	gi|13400108|gb|AAF43717.2| CD40 protein [Rattus norvegicus]	23	5.8	20.06
-	gi|19923695|ref|NP_113908.2| deiodinase, iodothyronine, type II [Rattus norvegicus]	8	6.3	30.49
-	gi|1518958|gb|AAC52767.1| type II iodothyronine deiodinase [Rattus norvegicus]	8	6.3	30.41
-	gi|7436479|pir||T10816 thyroxine deiodinase (EC 3.8.1.4), type II - rat	8	6.3	30.41
-	gi|92444|pir||C27115 K-kininogen, LMW precursor - rat (fragments)	17	6.3	33.24
-	gi|230371|pdb|1TON| Chain , Tonin (E.C. Number Not Assigned)	14	5.8	26.88
-	gi|33086596|gb|AAP92610.1| Ab2-416 [Rattus norvegicus]	24	6.0	21.01
-	gi|112492|pir||S10088 beta-crystallin A3/A1 - rat (fragment)	21	6.4	21.67
-	gi|223879|prf||1003216A tonin	15	6.1	25.02
-	gi|33356831|pdb|1C7Z|A Chain A, Regulatory Complex Of Fructose-2,6-Bisphosphatase	19	5.8	22.85
-	gi|2914269|pdb|1TIP|A Chain A, The Bisphosphatase Domain Of The Bifunctional Rat Liver 6-Phosphofructo-2-KinaseFRUCTOSE-2,6-Bisphosphatase	19	5.7	22.72
-	gi|34853298|ref|XP_341743.1| PREDICTED: similar to histidine triad protein 4 [Rattus norvegicus]	18	6.2	20.66
-	gi|6688729|emb|CAB65248.1| MASP-2 [Rattus norvegicus]	22	6.0	21.79
-	gi|6689093|emb|CAB65385.1| MAp19 protein [Rattus norvegicus]	22	6.0	21.74
-	gi|8394076|ref|NP_058979.1| proteasome (prosome, macropain) subunit, alpha type 6 [Rattus norvegicus]	12	6.3	28.64
-	gi|20385792|gb|AAM21454.1|AF381279_1 parkin isoform [Rattus norvegicus]	13	5.4	23.66
-	gi|19424188|ref|NP_598217.1| CD79B antigen [Rattus norvegicus]	21	5.5	26.69

-	gi|58000409|ref|NP_001009962.1| meteorin, glial cell differentiation regulator [Rattus norvegicus]	9	6.3	32.08
-	gi|56605744|ref|NP_001008334.1| hypothetical protein LOC302032 [Rattus norvegicus]	15	6.4	24.64
-	gi|3769634|gb|AAC64592.1| olfactory receptor [Rattus norvegicus]	17	6.5	25.29
-	gi|3114353|pdb|2KIN|A Chain A, Kinesin (Monomeric) From Rattus Norvegicus	14	5.9	28.08
-	gi|3122309|sp|P56536|KIF5C_RAT Kinesin heavy chain isoform 5C (Kinesin heavy chain neuron-specific 2)	14	5.9	28.22
-	gi|1929920|gb|AAB51477.1| anti-idiotype immunoglobulin M light chain [Rattus norvegicus]	20	5.6	26.19
-	gi|18478866|gb|AAL73348.1|AF343574_1 parkin transcript variant 6 [Rattus norvegicus]	9	6.2	32.77
-	gi|34873023|ref|XP_342995.1| PREDICTED: hypothetical protein [Rattus norvegicus]	24	5.5	20.65
-	gi|47169594|tpe|CAE51906.1| TPA: kallikrein 1 precursor [Rattus norvegicus]	9	6.3	26.13
-	gi|41386755|ref|NP_958824.1| FGFR1 oncogene partner 2 [Rattus norvegicus]	15	5.6	30.21
-	gi|34856053|ref|XP_341851.1| PREDICTED: similar to BCL2-like 12 (proline rich) [Rattus norvegicus]	16	5.7	27.75
-	gi|38454298|ref|NP_942076.1| hypothetical protein LOC362301 [Rattus norvegicus]	19	5.9	21.01

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B469BB3A-05D8-64812AA6

Sequences 20092

Date & Time Mon Jan 29 18:37:33 2007 UTC (Search Time: 0.34 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 34 kDa

pI Range 5.4 -6.5

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon)

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754.805 766.813 767.801 768.797 769.823 795.817 797.854
811.870 813.852 824.498 868.526 888.458 906.466 918.464
920.465 948.524 955.503 976.545 990.546 999.529 1005.538
1009.522 1020.498 1027.552 1058.497 1063.582 1070.554
1076.532 1080.479 1087.543 1089.534 1091.538 1094.510
1099.599 1173.652 1184.637 1191.667 1195.590 1199.621
1217.646 1220.604 1223.612 1233.650 1244.590 1248.613
1262.607 1265.630 1288.602 1291.620 1305.645 1312.628
1322.661 1328.708 1346.642 1352.683 1363.643 1370.733
1377.645 1388.665 1395.652 1432.714 1454.717 1456.716
1481.702 1500.648 1504.720 1529.734 1542.760 1548.754
1551.736 1557.746 1559.778 1568.753 1573.760 1575.732
1584.774 1589.774 1602.807 1616.725 1622.760 1624.750
1632.759 1639.719 1642.739 1653.753 1664.760 1666.772
1683.778 1685.794 1695.790 1713.794 1720.807 1730.770
1745.777 1757.855 1762.847 1779.864 1784.842 1786.873
1828.925 1837.864 1850.899 1855.853 1894.909 1904.809
1914.946 1928.893 1957.951 1962.912 1985.917 1992.926
2000.948 2005.936 2015.847 2016.915 2021.939 2024.956
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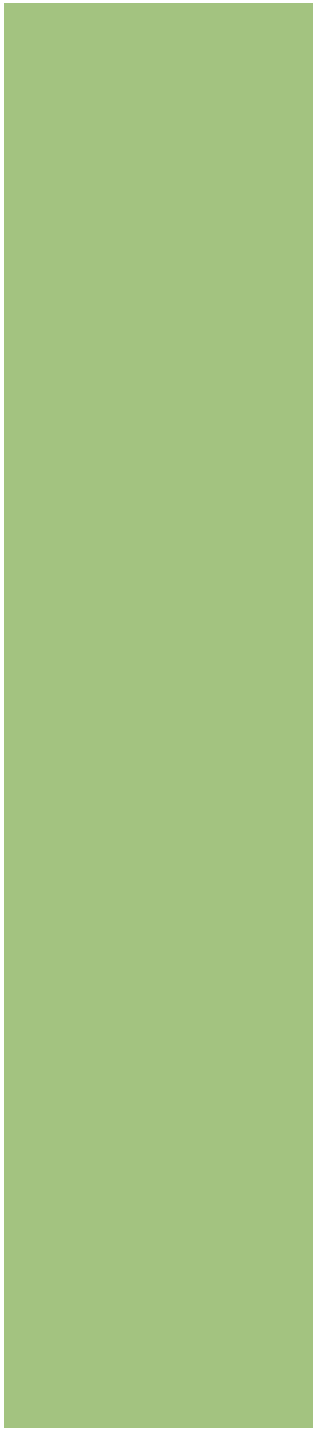

	2448.189 2458.162 2465.201 2466.203 2483.219 2485.211 2497.192 2498.136 2506.126 2513.165 2514.119 2530.176 2531.150 2540.184 2541.200 2554.285 2555.182 2574.169 2591.108 2599.172 2600.181 2604.307 2605.137 2610.246 2611.180 2622.219 2632.158 2633.233 2650.169 2651.221 2667.200 2668.198 2674.232 2676.179 2687.207 2689.175 2704.127 2705.230 2713.206 2714.199 2726.260 2727.250 2733.231 2734.240 2740.317 2742.331 2745.274 2746.166 2749.259 2750.274 2763.212 2765.237 2776.278 2785.281 2786.253 2790.261 2791.239 2801.303 2802.259 2807.290 2818.288 2819.256 2833.293 2834.242 2838.333 2839.292 2852.287 2853.285 2862.306 2863.327 2867.407 2868.406 2885.378 2886.229 2893.223 2894.438 2903.299 2914.335 2916.302 2947.312 2960.241 2963.266 2964.421 2977.349 2978.380 2990.378 2991.401 3001.312 3003.308 3010.334 3011.284 3020.394 3029.355 3030.526 3033.405 3034.351 3046.377 3047.306 3059.355 3061.335 3063.522 3064.407 3077.477 3078.386 3094.384 3105.422 3114.448 3122.392 3135.419 3136.423 3140.364 3141.451 3153.459 3171.487 3172.433 3191.467 3192.451 3210.458 3218.487 3231.509 3232.509 3244.505 3250.485 3260.504 3273.479 3281.481 3316.470 3324.478 3325.475 3339.484 3345.459 3346.427 3355.508 3357.508 3366.572 3367.586 3373.568 3375.514 3382.527 3383.513 3398.560 3403.603 3405.604 3421.612 3422.564 3432.494 3443.544 3448.568 3453.531 3455.454 3460.605 3468.545 3469.566 3472.532 3473.537 3480.815 3484.679 3485.542 3499.542 3506.579 3515.622 3522.605 3543.594 3549.604 3564.719 3567.556 3568.528 3587.641 3595.648 3604.712 3630.678 3665.665 3672.768 3693.691 3707.662 3711.525 3736.634 3744.697 3779.705 3817.679 3849.698 3863.732 3886.779 3892.727 4113.888 4124.926
Tolerance (mon)	16.00 ppm
Number of Peptides	347

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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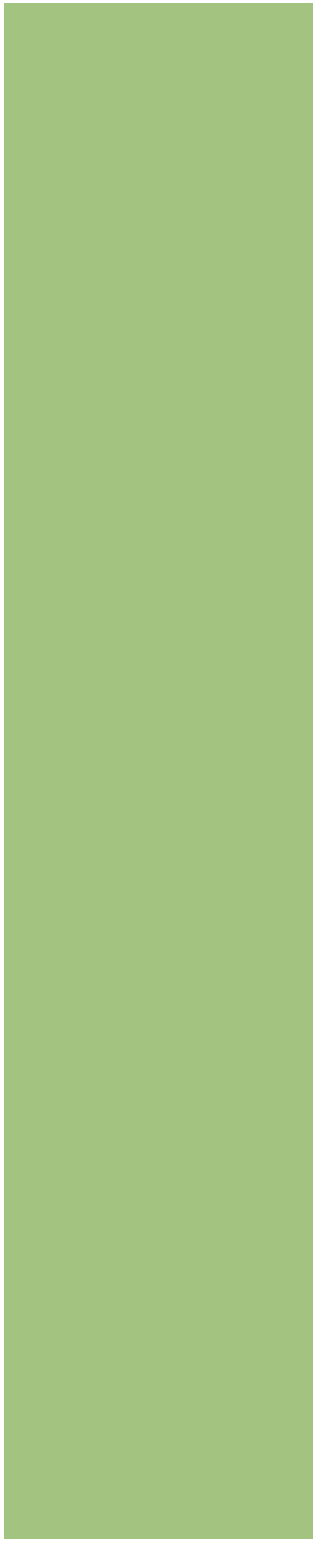
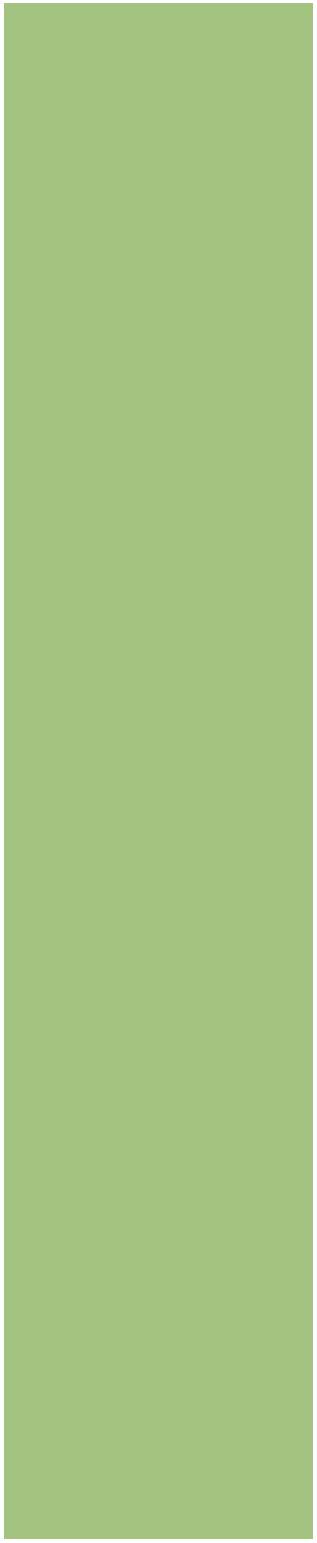
Protein Candidates

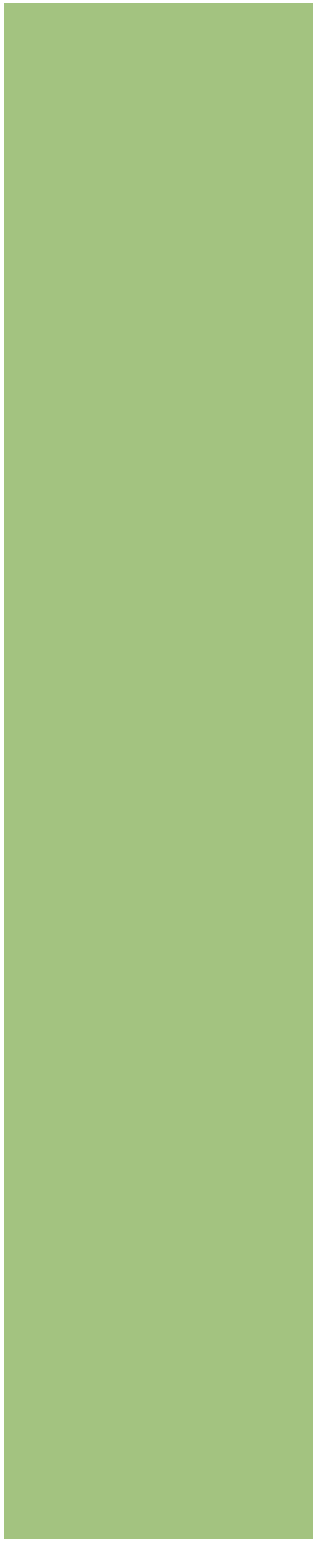
Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.5×10^{-17}	gi|27687455|ref|XP_226755.1| PREDICTED: similar to cytoplasmic beta-actin [Rattus norvegicus]	75	5.3	43.04	
+2	2.3×10^{-15}	gi|51316969|sp|P62738|ACTA_RAT Actin, aortic smooth muscle (Alpha-actin-2)	64	5.2	43.19	
	-	gi|6978441|ref|NP_037025.1| actin, gamma 2 [Rattus norvegicus]	59	5.3	43.06	
	-	gi|54036667|sp|P68035|ACTC_RAT Actin, alpha cardiac muscle 1 (Alpha-cardiac actin)	70	5.2	43.14	
	-	gi|40786499|ref|NP_955437.1| leucine carboxyl methyltransferase 1 [Rattus norvegicus]	42	5.7	39.80	
	-	gi|51036635|ref|NP_036690.2| fructose-1,6- biphosphatase 1 [Rattus norvegicus]	53	5.5	41.06	
	-	gi|310111|gb|AAA41131.1| fructose-biphosphatase	53	5.5	41.03	
	-	gi|21431625|sp||Q9ERB4_1 [Segment 1 of 2] Versican core protein precursor (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP)	57	5.3	40.17	
	-	gi|46237569|emb|CAE83949.1| butyrophilin-like 2 [Rattus norvegicus]	37	5.0	51.58	
	-	gi|40786517|ref|NP_955442.1| WD repeat domain 12 [Rattus norvegicus]	46	5.6	49.36	
	-	gi|1169826|sp|P43424|GALT_RAT Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (UDP-glucose--hexose-1-phosphate uridylyltransferase)	53	6.1	44.24	



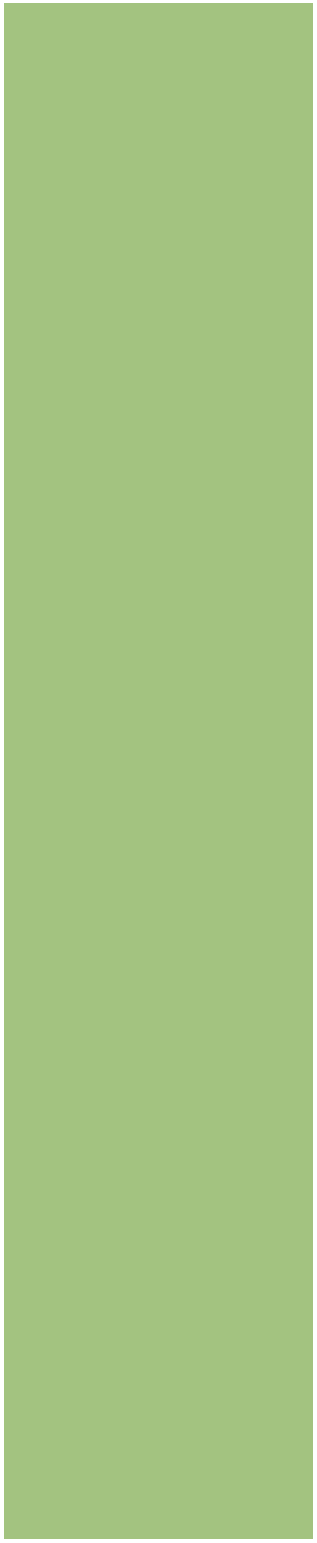
-	gi|9296968|sp|P82471|GNAQ_RAT Guanine nucleotide-binding protein G(q) subunit alpha (Guanine nucleotide-binding protein alpha-q)	44	5.6	42.66
-	gi|13591957|ref|NP_112298.1| guanine nucleotide binding protein, alpha q polypeptide [Rattus norvegicus]	43	5.5	43.34
-	gi|51980596|gb|AAH82087.1| Eukaryotic translation initiation factor 3, subunit 6 [Rattus norvegicus]	49	5.7	53.70
-	gi|1166528|gb|AAC52417.1| ksGC	44	6.2	49.54
-	gi|42476312|ref|NP_714955.2| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10 [Rattus norvegicus]	49	6.2	46.59
-	gi|1711600|sp|P52845|ST1E2_RAT Estrogen sulfotransferase, isoform 2 (EST-2) (Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase)	58	5.6	36.87
-	gi|16758932|ref|NP_446462.1| neuraminidase 3 [Rattus norvegicus]	51	5.8	48.93
-	gi|4433355|dbj|BAA20565.1| carboxyesterase E1 [Rattus norvegicus]	45	5.6	50.03
-	gi|56090198|ref|NP_001007719.1| estrogen sulfotransferase [Rattus norvegicus]	51	5.8	36.86
-	gi|13591874|ref|NP_112249.1| guanine nucleotide-binding protein, beta-1 subunit [Rattus norvegicus]	37	5.5	38.55
-	gi|1711602|sp|P49890|ST1E6_RAT Estrogen sulfotransferase, isoform 6 (EST-6) (Sulfotransferase, estrogen-preferring) (Estrone sulfotransferase)	58	5.6	36.76
-	gi|55250760|gb|AAH85868.1| FK506 binding protein 5 [Rattus norvegicus]	36	5.9	53.70
-	gi|57526868|ref|NP_001009628.1| T-kininogen II precursor [Rattus norvegicus]	44	5.9	50.20
-	gi|50657372|ref|NP_001002821.1| histocompatibility 2, T region locus 18 [Rattus norvegicus]	47	5.3	40.56
-	gi|50925905|gb|AAH79411.1| Ubiquitin-like 1 (sentrin) activating enzyme E1A [Rattus norvegicus]	52	5.0	40.04
-	gi|206150|gb|AAA41856.1| protein kinase type II regulatory subunit (, EC 2.7.1.37)	41	5.0	43.31



-	gi|57012430|ref|NP_001008820.1| keratin complex 1, acidic, gene 2 [Rattus norvegicus]	53	4.9	52.73
-	gi|12666521|emb|CAC28066.1| protein phosphatase 1B2 53 kDa isoform [Rattus norvegicus]	40	4.9	52.46
-	gi|46237572|emb|CAE83952.1| butyrophilin-like 5 [Rattus norvegicus]	46	5.4	46.42
-	gi|50927329|gb|AAH78939.1| Secernin 2 [Rattus norvegicus]	40	5.2	47.39
-	gi|1330250|gb|AAB00808.1| MHC class I antigen [Rattus norvegicus]	47	5.4	41.87
-	gi|40786436|ref|NP_955404.1| eukaryotic translation initiation factor 4A, isoform 1 [Rattus norvegicus]	44	5.3	47.21
-	gi|11120724|ref|NP_068537.1| sulfotransferase family 1D, member 1 [Rattus norvegicus]	53	5.7	37.70
-	gi|57012446|ref|NP_001008816.1| type I keratin KA22 [Rattus norvegicus]	47	5.1	51.29
-	gi|16758340|ref|NP_446020.1| phosphate cytidylyltransferase 2, ethanolamine [Rattus norvegicus]	47	6.2	46.68
-	gi|8393746|ref|NP_058942.1| mitogen activated protein kinase kinase 5 isoform b [Rattus norvegicus]	50	5.9	50.32
-	gi|8393652|ref|NP_058992.1| potassium inwardly-rectifying channel J2 [Rattus norvegicus]	44	5.6	49.91
-	gi|205308|gb|AAA41570.1| alpha-1 major acute phase protein prepeptide	40	6.0	49.77
-	gi|47477878|gb|AAH70884.1| Pgcp protein [Rattus norvegicus]	33	6.0	53.13
-	gi|13928880|ref|NP_113828.1| plasma glutamate carboxypeptidase [Rattus norvegicus]	33	6.1	53.06
-	gi|7108713|gb|AAF36518.1|AF131077_1 liver annexin-like protein [Rattus norvegicus]	33	6.0	53.10
-	gi|47477783|gb|AAH70955.1| Ckb protein [Rattus norvegicus]	48	5.3	45.98
-	gi|1346007|sp|P02680|FIBG_RAT Fibrinogen gamma chain precursor	37	5.4	52.55
-	gi|1183937|emb|CAA29289.1| gamma-fibrinogen [Rattus norvegicus]	40	5.6	51.56



-	gi|769859|gb|AAA69915.1| lamina associated polypeptide 1C	40	5.7	52.92
-	gi|13591934|ref|NP_112285.1| chitobiase, di-N-acetyl- [Rattus norvegicus]	43	5.3	42.91
-	gi|2851391|sp|P16391|HA12_RAT RT1 class I histocompatibility antigen, AA alpha chain precursor	47	5.3	42.52
-	gi|13928776|ref|NP_113761.1| phosphorylase kinase, gamma 1 [Rattus norvegicus]	31	6.1	46.46
-	gi|40786443|ref|NP_955408.1| Sil1 protein [Rattus norvegicus]	37	5.1	53.85
-	gi|940831|emb|CAA62021.1| Mature alpha chain of major histocompatibility complex class I antigen [Rattus norvegicus]	31	5.4	39.67
-	gi|47087085|ref|NP_997710.1| type I keratin KA17 [Rattus norvegicus]	37	5.0	49.32
-	gi|1263200|gb|AAC52551.1| MHC class I RT1.Ac heavy chain precursor	29	5.5	41.85
-	gi|57012370|ref|NP_001008822.1| keratin 25A [Rattus norvegicus]	39	5.0	50.55
-	gi|56270274|gb|AAH87595.1| Similar to RIKEN cDNA 2810428C21 [Rattus norvegicus]	35	6.1	40.22
-	gi|40891590|gb|AAR97521.1| zinc finger protein 183 [Rattus norvegicus]	35	5.9	40.16
-	gi|205578|gb|AAA41654.1| cardiac myosin heavy chain 5	27	5.5	49.78
-	gi|39645155|gb|AAH63813.1| Gnn protein [Rattus norvegicus]	34	6.3	48.18
-	gi|2225995|emb|CAA74333.1| MHC class I alpha chain [Rattus norvegicus]	45	5.2	39.79
-	gi|55778623|gb|AAH86600.1| Inositol polyphosphate-1-phosphatase [Rattus norvegicus]	28	5.0	44.79
-	gi|204050|gb|AAA41122.1| c-erbA-alpha-2 protein	40	5.7	42.82
-	gi|18034777|ref|NP_542143.1| apolipoprotein A-V [Rattus norvegicus]	37	6.0	42.14
-	gi|4103877|gb|AAD01873.1| glial fibrillary acidic protein alpha [Rattus norvegicus]	33	5.4	50.84
-	gi|8393431|ref|NP_058705.1| glial fibrillary acidic protein [Rattus norvegicus]	33	5.4	50.82



-	gi|40018556|ref|NP_954517.1| nin one binding protein [Rattus norvegicus]	27	6.1	47.84
-	gi|14916547|sp|O35824|DNJA2_RAT DnaJ homolog subfamily A member 2 (RDJ2)	38	6.1	47.72
-	gi|51259324|gb|AAH78893.1| Fibrinogen, gamma polypeptide [Rattus norvegicus]	36	5.8	51.56
-	gi|34979829|gb|AAQ83903.1| flavohemoprotein b5/b5R variant [Rattus norvegicus]	30	6.0	51.42
-	gi|27720673|ref|XP_236398.1| PREDICTED: similar to CG11584-PB [Rattus norvegicus]	29	6.0	48.15
-	gi|56799412|ref|NP_114468.2| DnaJ (Hsp40) homolog, subfamily A, member 2 [Rattus norvegicus]	37	6.1	47.70
-	gi|1000514|emb|CAA57986.1| major histocompatibility complex class I [Rattus norvegicus]	47	5.3	41.65
-	gi|25742579|ref|NP_071792.1| heterogeneous nuclear ribonucleoprotein F [Rattus norvegicus]	36	5.3	46.73
-	gi|4930076|pdb|1PHZ|A Chain A, Structure Of Phosphorylated Phenylalanine Hydroxylase	28	5.7	50.72
-	gi|53733952|gb|AAH83669.1| Vacuolar ATPase subunit H [Rattus norvegicus]	37	6.3	52.49
-	gi|22324680|gb|AAM95632.1| FK506 binding protein 4 [Rattus norvegicus]	33	5.7	47.34
-	gi|50925541|gb|AAH78934.1| Protective protein for beta-galactosidase [Rattus norvegicus]	27	5.1	52.72
-	gi|71830|pir||FGRTGB fibrinogen gamma-B chain precursor - rat	28	5.6	52.46
-	gi|5030428|gb|AAD01874.2| glial fibrillary acidic protein delta [Rattus norvegicus]	29	5.7	49.58
-	gi|12711386|emb|CAC28536.1| Ajuba protein [Rattus norvegicus]	29	6.0	42.40
-	gi|2887302|emb|CAA57631.1| RT1.A(u) alpha chain [Rattus norvegicus]	39	5.1	39.48
-	gi|28461157|ref|NP_786933.1| crystallin, lambda 1 [Rattus norvegicus]	26	5.9	36.52

-	gi|1263202|gb|AAC52552.1| MHC class I RT1.Au heavy chain precursor	37	5.3	41.68
-	gi|31581536|ref|NP_787037.2| sequestosome 1 isoform 1 [Rattus norvegicus]	35	5.1	49.29
-	gi|50925859|gb|AAH79304.1| Tektin 4 [Rattus norvegicus]	21	5.8	53.81
-	gi|3150056|gb|AAC26487.1| MHC class Ib RT1.S3 [Rattus norvegicus]	39	5.7	40.71
-	gi|223466|prf||0807284A myosin H	18	5.4	51.50
-	gi|205576|gb|AAA41653.1| cardiac myosin heavy chain 21/26	18	5.4	51.65
-	gi|5912596|emb|CAB56216.1| A2b [Rattus norvegicus]	27	5.6	39.49
-	gi|25742677|ref|NP_476463.1| proteasome 26S ATPase subunit 4 [Rattus norvegicus]	21	5.1	48.72
-	gi|5912590|emb|CAB56213.1| A1k [Rattus norvegicus]	22	5.6	39.69
-	gi|57222292|ref|NP_001009379.1| 2'-5' oligoadenylate synthetase 1D [Rattus norvegicus]	31	6.0	44.30
-	gi|16923954|ref|NP_476449.1| serine (or cysteine) proteinase inhibitor, clade B, member 5 [Rattus norvegicus]	36	5.8	43.99

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A59F0287-14A0-55B91BDE

Sequences 20092

Date & Time Wed Jan 31 19:07:04 2007 UTC (Search Time: 0.55 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 36 - 54 kDa

pI Range 4.9 -6.3

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@TY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 663.345 780.372 832.317 918.466 991.513 1045.526 1064.524
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1226.592 1233.626 1242.595 1258.599 1268.607 1291.615
1313.613 1330.603 1372.660 1441.743 1482.694 1486.706
1504.712 1529.726 1533.723 1543.734 1568.761 1572.744
1584.773 1589.753 1600.756 1602.789 1616.722 1622.732
1624.764 1630.760 1642.767 1653.738 1678.761 1685.790
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1740.825 1743.818 1748.809 1757.861 1766.820 1780.857
1786.836 1790.837 1837.835 1854.849 1871.872 1889.876
1894.872 1904.865 1908.884 1932.891 1954.912 1962.903
1987.920 2004.922 2005.924 2019.917 2020.944 2039.951
2046.950 2047.951 2051.953 2052.942 2056.919 2057.959
2072.986 2091.026 2096.994 2118.987 2124.007 2152.043
2183.056 2209.092 2348.152 2349.143 2364.148 2365.164
2375.145 2376.134 2381.160 2382.146 2397.150 2398.175
2419.144 2420.152 2437.193 2438.169 2447.170 2448.159
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2719.236 2723.255 2724.270 2733.254 2734.244 2741.259
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2768.290 2784.291 2785.368 2789.278 2790.263 2796.291
2797.309 2805.281 2806.269 2817.295 2818.280 2822.295
2823.210 2832.292 2833.233 2837.302 2849.289 2850.306
2868.308 2882.316 2885.323 2886.330 2889.318 2890.305
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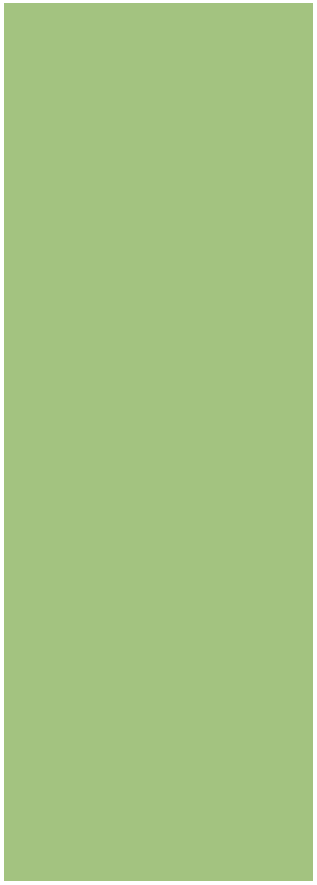

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Tolerance (mon)	36.00 ppm
Number of Peptides	299

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- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
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Macromolecules

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.9×10^{-29}	gi|13592025|ref|NP_112344.1| protein geranylgeranyltransferase type I, beta subunit [Rattus norvegicus]	24	6.2	43.97	
2	2.5×10^{-18}	gi|34860125|ref|XP_345272.1| PREDICTED: similar to Guanine nucleotide-binding protein G(t), alpha-2 subunit (Transducin alpha-2 chain) [Rattus norvegicus]	12	5.2	41.95	
+3	2.7×10^{-12}	gi|25742623|ref|NP_113983.1| UDP-glucose ceramide glucosyltransferase [Rattus norvegicus]	6	8.4	46.27	
	-	gi|2924340|emb|CAA11853.1| ceramide glucosyltransferase [Rattus norvegicus]	6	8.7	46.21	
4	3.7×10^{-12}	gi|34862688|ref|XP_222370.2| PREDICTED: similar to Neurogenic differentiation factor 4 (NeuroD4) (Atonal protein homolog 3) (Helix-loop-helix protein mATH-3) (MATH3) [Rattus norvegicus]	17	6.5	38.40	
5	7.4×10^{-11}	gi|741805|prf||2008147C protein RAKd	17	6.6	38.50	
6	3.7×10^{-10}	gi|48927689|gb|AAT47556.1| UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 [Rattus norvegicus]	15	6.5	41.95	
7	3.9×10^{-10}	gi|29789261|ref|NP_112299.1| guanine nucleotide-binding protein, beta 2 [Rattus norvegicus]	16	5.6	38.39	
8	4.3×10^{-10}	gi|51980596|gb|AAH82087.1| Eukaryotic translation initiation factor 3, subunit 6 [Rattus norvegicus]	12	5.7	53.70	
9	2.9×10^{-9}	gi|16758354|ref|NP_446034.1| lipocalin 7 [Rattus norvegicus]	10	6.5	54.55	
10	3.3×10^{-9}	gi|20301976|ref|NP_620195.1| trans-golgi network protein 1 [Rattus norvegicus]	11	5.0	39.88	
11	4.0×10^{-9}	gi|57351|emb|CAA45884.1| trans golgi network (TGN) specific integral membrane protein TGN38 [Rattus norvegicus]	11	4.9	42.67	
12	4.5×10^{-9}	gi|8895958|gb|AAF81193.1|AF237719_1 PDK2.1 pyruvate dehydrogenase kinase 2 subunit variant p45 [Rattus norvegicus]	11	6.2	44.97	
13	4.9×10^{-9}	gi|9845234|ref|NP_063970.1| annexin A2 [Rattus norvegicus]	13	7.7	40.33	
14	5.5×10^{-9}	gi|9247201|gb|AAB31934.2| annexin II [Rattus sp.]	13	8.3	40.42	
15	7.0×10^{-9}	gi|51948426|ref|NP_001004227.1| RNA terminal phosphate cyclase domain 1 [Rattus norvegicus]	13	7.9	40.63	
16	8.9×10^{-9}	gi|53759105|ref|NP_001005265.1| complement receptor related protein isoform 3 [Rattus norvegicus]	9	5.6	57.36	

17	1.0×10^{-8}	gi|13540705|ref|NP_110499.1| pyruvate dehydrogenase kinase 2 subunit p45 (PDK2) [Rattus norvegicus]	11	6.1	47.16	
18	1.1×10^{-8}	gi|392566|gb|AAC04306.1| LAR receptor-linked tyrosine phosphatase [Rattus norvegicus]	10	7.8	54.44	
19	3.1×10^{-8}	gi|55249723|gb|AAH85801.1| Nucleosome assembly protein 1-like 4 [Rattus norvegicus]	8	4.6	45.56	
20	4.9×10^{-8}	gi|57012884|sp|Q66H86|OLFL1_RAT Olfactomedin-like protein 1 precursor	10	7.2	46.95	
21	6.5×10^{-8}	gi|17105358|ref|NP_476553.1| ubiquitin-activating enzyme E1C [Rattus norvegicus]	6	5.3	53.31	
22	7.2×10^{-8}	gi|11559958|ref|NP_071527.1| synaptotagmin 6 [Rattus norvegicus]	9	8.6	59.37	
23	1.2×10^{-7}	gi|9506451|ref|NP_062166.1| carbonic anhydrase 5 [Rattus norvegicus]	18	9.0	35.33	
24	1.3×10^{-7}	gi|53733416|gb|AAH83587.1| Yip1 domain family, member 2 [Rattus norvegicus]	15	5.5	35.26	
25	1.6×10^{-7}	gi|6978697|ref|NP_036665.1| carboxypeptidase B1 [Rattus norvegicus]	11	5.4	48.78	
26	2.9×10^{-7}	gi|51980318|gb|AAH81983.1| Von Willebrand factor A domain containing 1 [Rattus norvegicus]	10	6.2	45.18	
27	4.4×10^{-7}	gi|226865|prf||1609196A synaptic vesicle protein	7	8.6	50.25	
28	4.4×10^{-7}	gi|92791|pir||S09595 synaptotagmin P65 - rat	7	8.7	50.15	
29	4.4×10^{-7}	gi|57643|emb|CAA36981.1| cellular protein [Rattus rattus]	7	8.7	50.13	
30	4.4×10^{-7}	gi|39918764|emb|CAE85101.1| synaptotagmin 1 [Rattus rattus]	7	8.8	50.08	
31	5.0×10^{-7}	gi|13242310|ref|NP_077373.1| abl-interactor 1 [Rattus norvegicus]	3	6.6	52.64	
32	5.6×10^{-7}	gi|34864886|ref|XP_235164.2| PREDICTED: similar to fibroblast growth factor receptor substrate 2 [Rattus norvegicus]	10	5.8	58.13	
33	5.1×10^{-6}	gi|47577425|ref|NP_001000293.1| olfactory receptor Olr459 [Rattus norvegicus]	17	8.8	36.02	
34	5.9×10^{-6}	gi|27465609|ref|NP_775162.1| guanine nucleotide binding protein, alpha transducing 3 [Rattus norvegicus]	6	5.6	42.05	
35	3.4×10^{-5}	gi|129094|sp|P23272|OLFI9_RAT Olfactory receptor-like protein I9	14	8.6	36.43	
36	3.4×10^{-5}	gi|47575917|ref|NP_001000723.1| olfactory receptor Olr1470 [Rattus norvegicus]	14	8.6	36.39	
37	3.8×10^{-5}	gi|34881317|ref|XP_228523.2| PREDICTED: similar to CG30497-PA, isoform A [Rattus norvegicus]	6	7.8	46.26	
38	2.9×10^{-4}	gi|9910234|ref|NP_064481.1| interferon-induced protein with tetratricopeptide repeats 1 [Rattus norvegicus]	9	5.9	55.20	
39	4.6×10^{-4}	gi|7767180|pdb|1QFC|A Chain A, Structure Of Rat Purple Acid Phosphatase	9	9.0	35.05	
40	4.6×10^{-4}	gi|9506369|ref|NP_062017.1| acid phosphatase 5 [Rattus norvegicus]	9	8.9	37.48	
41	0.84	gi|47576531|ref|NP_001000092.1| olfactory receptor Olr1630 [Rattus norvegicus]	13	8.6	37.22	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Tue Jan 30 18:03:50 2007 UTC (Search Time: 0.30 sec.)

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Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 30 - 60 kDa

pI Range 4.5 -9.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +HPO3@Y(Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 664.343 750.677 841.882 899.271 902.473 917.280 938.478 991.513 1046.511
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2749.267 2764.260 2765.267 2768.268 2769.272 2776.257 2777.265 2784.272
2786.265 2788.284 2789.258 2793.279 2794.281 2801.281 2802.271 2806.281
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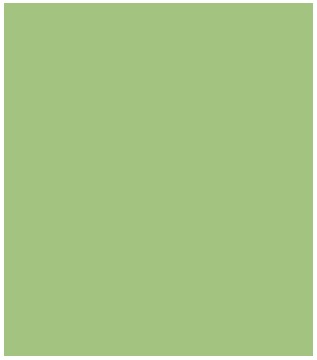

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3465.561	3466.529	3472.717	3473.565	3484.505	3485.511	3499.564	3509.571
3518.573	3525.604	3530.597	3545.543	3556.582	3563.595	3576.659	3586.601
3593.605	3605.672	3614.626	3620.572	3630.618	3638.651	3649.657	3663.663
3678.627	3684.616	3704.608	3708.648	3712.621	3726.685	3739.618	3744.648
3751.691	3758.734	3762.670	3771.675	3783.694	3790.693	3810.701	3822.622
3839.689	4009.826	4281.030	4517.788	4731.618			

Tolerance (mon) 8.00 ppm

Number of Peptides 254

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	9.9×10^{-12}	gi|396270|emb|CAA52328.1| heat shock protein 70 [Rattus norvegicus]	54	5.5	72.29	
	-	gi|407164|emb|CAA53140.1| heat shock protein 70 [Rattus norvegicus]	49	5.5	72.16	
	-	gi|47059179|ref|NP_997669.1| heat shock 70kD protein 1B [Rattus norvegicus]	46	5.6	72.43	
	-	gi|14010867|ref|NP_114177.1| heat shock 70kD protein 1A [Rattus norvegicus]	41	5.5	72.41	
2	5.5×10^{-9}	gi|6980978|ref|NP_036868.1| glycerol-3-phosphate dehydrogenase 2 [Rattus norvegicus]	49	6.2	83.22	
+3	2.8×10^{-8}	gi|28849961|ref|NP_579843.2| calpain 8 [Rattus norvegicus]	39	5.5	82.22	
	-	gi|495222|dbj|BAA03369.1| calpain [Rattus norvegicus]	39	5.5	82.26	
+4	1.6×10^{-7}	gi|47087121|ref|NP_997711.1| heat shock 70kD protein 1-like [Rattus norvegicus]	44	5.9	73.12	
	-	gi|450934|emb|CAA54424.1| heat shock protein 70 [Rattus norvegicus]	44	5.9	73.12	
+5	8.4×10^{-7}	gi|205233|gb|AAA41540.1| lysophospholipase precursor	25	5.3	68.96	
	-	gi|203458|gb|AAB46376.1| cholesterol esterase	26	5.3	69.01	
	-	gi|8393096|ref|NP_058693.1| carboxyl ester lipase [Rattus norvegicus]	26	5.3	68.89	
	-	gi|311386|emb|CAA80460.1| sterol esterase [Rattus norvegicus]	26	5.4	66.81	
6	7.7×10^{-6}	gi|34859658|ref|XP_235782.2| PREDICTED: similar to Kelch repeat and BTB domain-containing protein 3 (BTB and kelch domain-containing protein 3) [Rattus norvegicus]	36	5.6	72.42	
7	9.8×10^{-6}	gi|51858601|gb|AAH81803.1| Hspa2 protein [Rattus norvegicus]	36	5.5	72.10	
+8	3.7×10^{-5}	gi|55716045|gb|AAH85704.1| Pde4b protein [Rattus norvegicus]	29	5.8	84.10	
	-	gi|19923680|ref|NP_058727.2| phosphodiesterase 4B [Rattus norvegicus]	28	5.4	84.38	
9	2.0×10^{-4}	gi|8394033|ref|NP_058738.1| protein phosphatase 3, catalytic subunit, beta isoform [Rattus norvegicus]	37	5.6	60.71	
10	3.8×10^{-4}	gi|50925932|gb|AAH79463.1| Hbs1-like (S. cerevisiae) [Rattus norvegicus]	41	6.2	77.57	
11	1.2×10^{-3}	gi|38304005|gb|AAH62079.1| Signal transducer and activator of transcription 1 [Rattus norvegicus]	24	5.8	85.99	
12	3.6×10^{-3}	gi|21666559|gb|AAM73758.1|AF398465_1 TUC-4b [Rattus norvegicus]	30	6.0	75.98	
+13	4.0×10^{-3}	gi|21630291|ref|NP_037211.1| asparagine synthetase [Rattus norvegicus]	34	6.0	66.39	

	-	gi|51859420|gb|AAH81719.1| Asns protein [Rattus norvegicus]	34	6.0	66.35	☐
+14	5.7×10^{-3}	gi|13994159|ref|NP_077070.1| annexin A6 [Rattus norvegicus]	34	5.4	78.45	☐
	-	gi|48734834|gb|AAH72523.1| Anxa6 protein [Rattus norvegicus]	31	5.4	78.45	☐
15	0.052	gi|13786172|ref|NP_112628.1| calcium/calmodulin-dependent protein kinase 2 beta [Rattus norvegicus]	32	5.6	66.57	☐
16	0.054	gi|21426765|ref|NP_653346.1| G-protein signalling modulator 1 (AGS3-like, C. elegans) [Rattus norvegicus]	34	5.8	73.61	☐
+17	0.068	gi|50927301|gb|AAH78728.1| Spata7 protein [Rattus norvegicus]	37	5.7	57.33	☐
	-	gi|20302020|ref|NP_620217.1| spermatogenesis-associated protein 7 [Rattus norvegicus]	33	5.8	61.96	☐
18	0.11	gi|50927611|gb|AAH78812.1| Ica1 protein [Rattus norvegicus]	38	5.6	57.10	☐
	-	gi|37361834|gb|AAQ91030.1| LRRGT00074 [Rattus norvegicus]	21	6.0	81.65	☐

☐

NOTE:

1. To search again using unmatched masses, click the symbol ☐.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B03F4AD9-09F8-606126A9

Sequences 20076

Date & Time Tue Feb 06 16:22:07 2007 UTC (Search Time: 0.50 sec.)

Sample ID 20061228 richardson NIA set 1 spot 3709 CONSENSUS search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 54 - 86 kDa

pI Range 5.3 -6.2

Digestion Trypsin

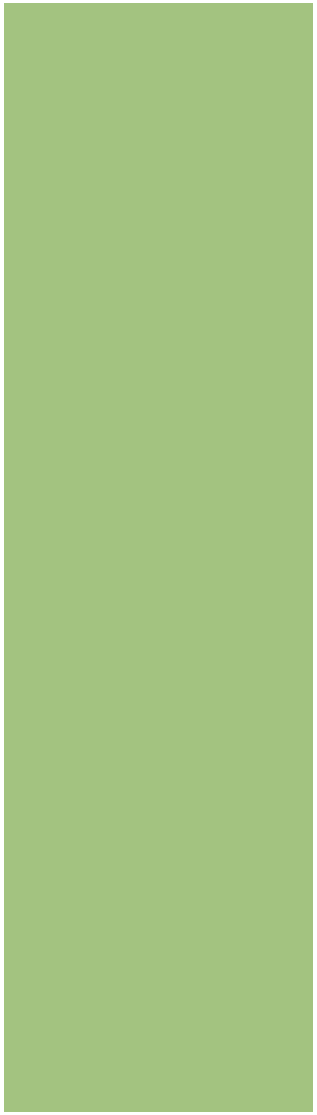
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY(Partial); +CH2N2@K (Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon) 664.338 712.267 768.354 781.839 817.419 832.316 841.478 849.456 902.474
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1195.592 1205.630 1210.586 1247.612 1265.634 1268.619 1283.703 1291.631
1298.680 1314.607 1329.644 1334.651 1347.702 1406.708 1414.689 1438.698
1457.699 1479.792 1511.757 1531.808 1559.773 1567.739 1575.746 1607.735
1663.834 1725.830 1740.824 1779.865 1827.862 1845.875 1880.057 1917.839
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2745.241 2748.247 2749.246 2764.242 2765.260 2777.290 2778.268 2784.267
2785.268 2787.271 2788.273 2800.274 2801.250 2806.279 2807.270 2820.296
2821.294 2832.279 2839.318 2848.301 2849.295 2868.376 2880.320 2881.321
2885.313 2886.330 2895.329 2904.326 2905.349 2915.387 2922.346 2923.333
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2977.368 2994.352 2995.395 3001.385 3003.365 3012.414 3019.387 3020.371
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3065.408 3066.391 3076.444 3077.434 3094.468 3105.424 3106.445 3123.491
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3192.464 3209.463 3210.467 3232.516 3233.495 3265.471 3266.483 3273.486
3274.491 3281.489 3282.513 3293.535 3294.517 3299.493 3300.499 3314.503
3324.516 3325.527 3340.524 3341.500 3356.568 3357.550 3369.601 3372.543
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3407.525 3419.575 3420.557 3439.519 3440.529 3449.606 3450.522 3455.529
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3523.611 3527.597 3544.632 3548.623 3564.602 3581.608 3614.626 3635.665
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3752.702 3759.710 3763.724 3778.713 3794.715 3811.708 3842.747 4021.827
4035.809 4055.791 4072.858 4083.857 4098.717 4102.840 4112.820 4121.868
4127.917 4135.836 4150.729 4166.920 4182.800 4197.904 4223.799 4530.786

Tolerance (mon) 22.00 ppm

Number of Peptides 249

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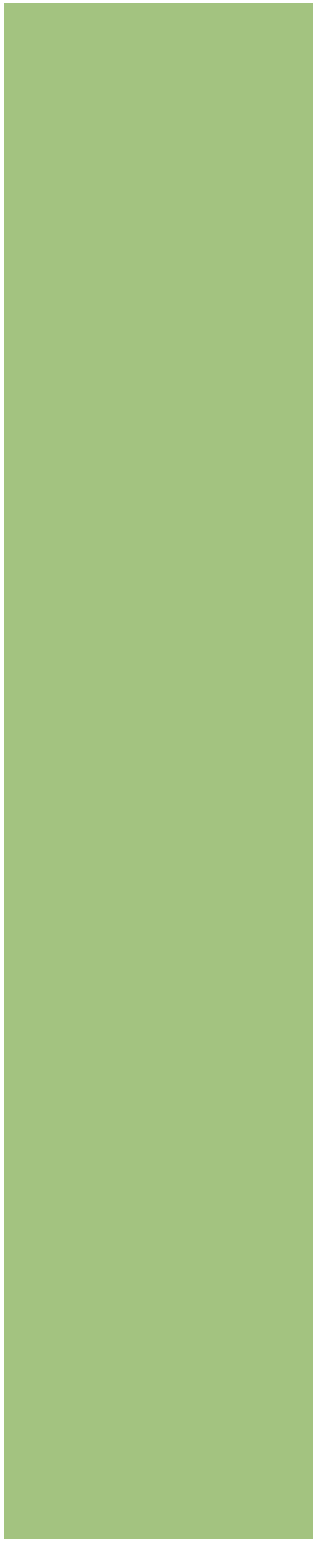
Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.3×10^{-9}	gi|47169594|tpe|CAE51906.1| TPA: kallikrein 1 precursor [Rattus norvegicus]	45	6.3	26.13	
2	4.9×10^{-8}	gi|56676344|ref|NP_001008561.1| ribonuclease A family, member 9 [Rattus norvegicus]	55	5.8	22.33	
3	5.1×10^{-8}	gi|34864887|ref|XP_216890.2| PREDICTED: similar to YEATS domain containing 4 [Rattus norvegicus]	30	6.6	26.92	
4	1.2×10^{-7}	gi|13399990|pdb|1I1A|D Chain D, Crystal Structure Of The Neonatal Fc Receptor Complexed With A Heterodimeric Fc	46	6.3	27.75	
5	5.8×10^{-7}	gi|51247925|pdb|1VG1|A Chain A, Gdp-Bound Rab7	61	6.4	21.84	
6	2.5×10^{-6}	gi|34855419|ref|XP_214868.2| PREDICTED: similar to intersex-like [Rattus norvegicus]	42	5.9	21.81	
7	1.4×10^{-5}	gi|206260|gb|AAB60703.1| plasma membrane calcium ATPase	66	5.8	22.23	
8	2.0×10^{-5}	gi|56090403|ref|NP_001007747.1| hypothetical protein LOC362483 [Rattus norvegicus]	45	6.4	25.12	
9	5.0×10^{-5}	gi|8394513|ref|NP_058884.1| UNC-119 homolog [Rattus norvegicus]	50	5.8	27.71	
10	5.2×10^{-5}	gi|57012386|ref|NP_001008856.1| RT1 class Ib, locus H2-Q-like, grc region [Rattus norvegicus]	54	6.0	21.62	
+11	6.8×10^{-5}	gi|3891675|pdb|1BD7|A Chain A, Circularly Permuted Bb2 - Crystallin	51	6.3	20.73	
	-	gi|6978713|ref|NP_037069.1| crystallin, beta B2 [Rattus norvegicus]	28	6.5	24.02	
12	1.6×10^{-4}	gi|27707658|ref|XP_228699.1| PREDICTED: similar to type 1 protein phosphatase inhibitor [Rattus norvegicus]	52	5.9	21.34	
13	2.2×10^{-4}	gi|45433570|ref|NP_112352.2| RAB1, member RAS oncogene family [Rattus norvegicus]	44	5.9	23.60	



14	5.8×10^{-4}	gi|33086596|gb|AAP92610.1| Ab2-416 [Rattus norvegicus]	39	6.0	21.01
15	1.0×10^{-3}	gi|841426|gb|AAA91987.1| tenascin-X	29	6.4	23.92
16	1.3×10^{-3}	gi|50925930|gb|AAH79461.1| Similar to RIKEN cDNA C430008C19 [Rattus norvegicus]	31	6.5	24.78
17	3.1×10^{-3}	gi|3769634|gb|AAC64592.1| olfactory receptor [Rattus norvegicus]	30	6.5	25.29
18	3.8×10^{-3}	gi|631893|pir||JC2337 T-cell receptor alpha-chain - rat	49	6.0	25.07
+19	6.9×10^{-3}	gi|349083|gb|AAA41479.1| calcium/calmodulin-dependent protein kinase II delta subunit	42	6.0	21.68
	-	gi|2769554|emb|CAA53395.1| calcium/calmodulin dependent protein kinase II subtype delta 2 [Rattus norvegicus]	40	6.2	22.47
	-	gi|2769555|emb|CAA54412.1| calcium/calmodulin dependent protein kinase II subtype delta 3 [Rattus norvegicus]	28	6.0	20.07
	-	gi|20302018|ref|NP_620216.1| prolactin-like protein K [Rattus norvegicus]	31	6.5	26.88
	-	gi|16758778|ref|NP_446355.1| ephrin A5 [Rattus norvegicus]	43	6.1	27.16
	-	gi|122240|sp|P06341|HB2A_RAT RT1 class II histocompatibility antigen, A beta chain	37	6.3	27.37
	-	gi|9506377|ref|NP_062093.1| amino-terminal enhancer of split [Rattus norvegicus]	17	5.9	22.62
	-	gi|48040531|ref|NP_001001517.1| zinc finger protein 313 [Rattus norvegicus]	46	6.4	27.11
	-	gi|257209|gb|AAB23588.1| low M(r) phosphotyrosine protein phosphatase isoenzyme AcP1 [rats, liver, Peptide, 159 aa]	47	6.1	19.15
	-	gi|13928956|ref|NP_113877.1| crystallin, beta A4 [Rattus norvegicus]	32	5.9	22.76
	-	gi|34933260|ref|XP_237746.2| PREDICTED: similar to acid phosphatase 1, soluble [Rattus norvegicus]	35	6.1	22.84
	-	gi|8307696|dbj|BAA96485.1| alpha-2u globulin [Rattus norvegicus]	38	5.9	21.83
	-	gi|51316135|sp|Q8K586|RANT_RAT GTP-binding nuclear protein Ran, testis-specific isoform	30	6.6	25.40

-	gi|10863989|ref|NP_067085.1| acid phosphatase 1, soluble [Rattus norvegicus]	34	6.1	19.05
-	gi|2769556|emb|CAA54413.1| calcium /calmodulin dependent protein kinase II subtype delta 4 [Rattus norvegicus]	32	6.1	23.83

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A25055E4-17F0-5269188E

Sequences 20092

Date & Time Tue Jan 30 18:44:59 2007 UTC (Search Time: 0.39 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 19 - 28 kDa

pI Range 5.8 -6.7

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 876.046 991.515 1046.501 1064.515 1091.535 1177.576
1194.581 1220.597 1223.599 1226.586 1233.626 1268.608
1291.617 1333.656 1475.751 1504.714 1529.731 1601.767
1617.731 1623.738 1631.742 1678.763 1685.790 1695.788
1713.800 1721.794 1743.780 1757.859 1765.815 1784.818
1836.830 1838.855 1853.845 1873.870 1893.865 1904.849
1916.857 1928.889 1932.859 1948.884 1953.902 1962.907
1984.902 2002.890 2003.880 2021.923 2029.894 2030.915
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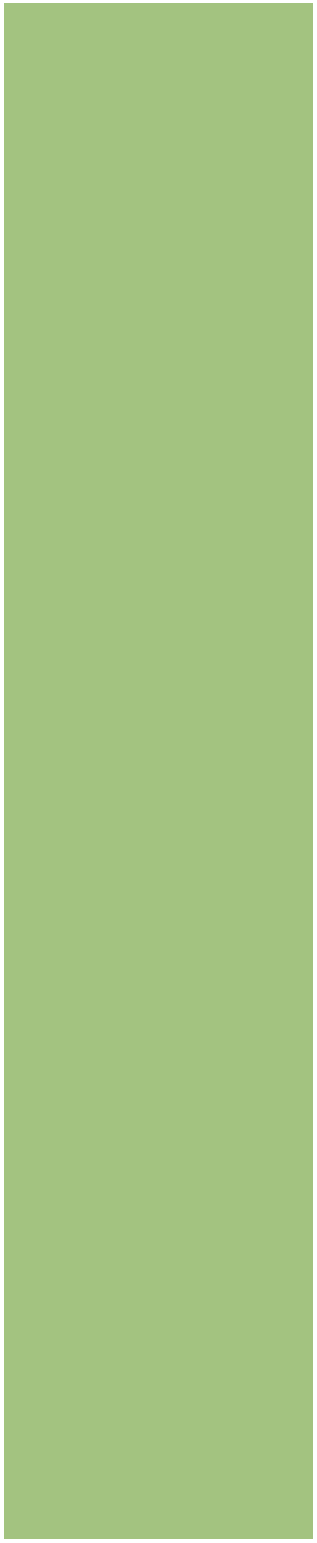

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Tolerance (mon)	28.00 ppm

Number of Peptides 271

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(212) 327-8000

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	3.9×10^{-6}	gi|51948384|ref|NP_001004206.1| proliferation-associated 2G4, 38kDa [Rattus norvegicus]	47	6.4	45.75	
+2	4.2×10^{-4}	gi|203652|gb|AAA40995.1| CTP:phosphocholine cytidylyltransferase	37	6.6	43.38	
	-	gi|430717|gb|AAB60489.1| CTP:phosphocholine cytidylyltransferase	33	6.6	43.25	
	-	gi|53828922|ref|NP_511177.2| phosphate cytidylyltransferase 1, choline, alpha isoform [Rattus norvegicus]	27	6.6	43.28	
3	8.8×10^{-4}	gi|205308|gb|AAA41570.1| alpha-1 major acute phase protein prepeptide	40	6.0	49.77	
4	2.9×10^{-3}	gi|34880908|ref|XP_222911.2| PREDICTED: similar to Pre-B-cell leukemia transcription factor 1 (Homeobox protein PBX1) [Rattus norvegicus]	40	6.5	47.78	
5	0.011	gi|51948372|ref|NP_001004200.1| COP9 constitutive photomorphogenic homolog subunit 3 [Rattus norvegicus]	29	6.2	49.59	
	-	gi|18376837|ref|NP_543166.1| arsenic (+3 oxidation state) methyltransferase [Rattus norvegicus]	42	6.2	42.96	
	-	gi|6015131|sp|Q63199|TNR6_RAT Tumor necrosis factor receptor superfamily member 6 precursor (FASLG receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95 antigen)	29	6.3	39.15	
	-	gi|29293821|ref|NP_808793.1| platelet-activating factor acetylhydrolase 2 [Rattus norvegicus]	35	6.2	44.77	
	-	gi|34858218|ref|XP_227432.2| PREDICTED: similar to TD and POZ domain containing 2 [Rattus norvegicus]	38	6.1	43.14	

-	gi|14916547|sp|O35824|DNJA2_RAT DnaJ homolog subfamily A member 2 (RDJ2)	37	6.1	47.72
-	gi|9507217|ref|NP_062052.1| thymidylate synthase [Rattus norvegicus]	35	6.0	35.96

NOTE:

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Input Summary

Search id A28D8E50-17B4-52A518CA

Sequences 20092

Date & Time Mon Jan 29 20:32:59 2007 UTC (Search Time: 0.50 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 30 - 50 kDa

pI Range 6.0 -7.0

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 605.339 654.392 668.692 692.376 696.736 705.391 719.384
722.746 724.769 725.770 753.803 768.379 791.411 798.484
824.498 852.521 878.440 932.530 948.523 955.509 990.550
1005.535 1027.552 1058.498 1070.510 1113.543 1184.641
1211.592 1217.641 1223.612 1227.625 1241.677 1262.611
1265.638 1276.644 1283.688 1330.615 1349.639 1381.792
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1559.782 1568.748 1601.809 1622.765 1624.758 1632.725
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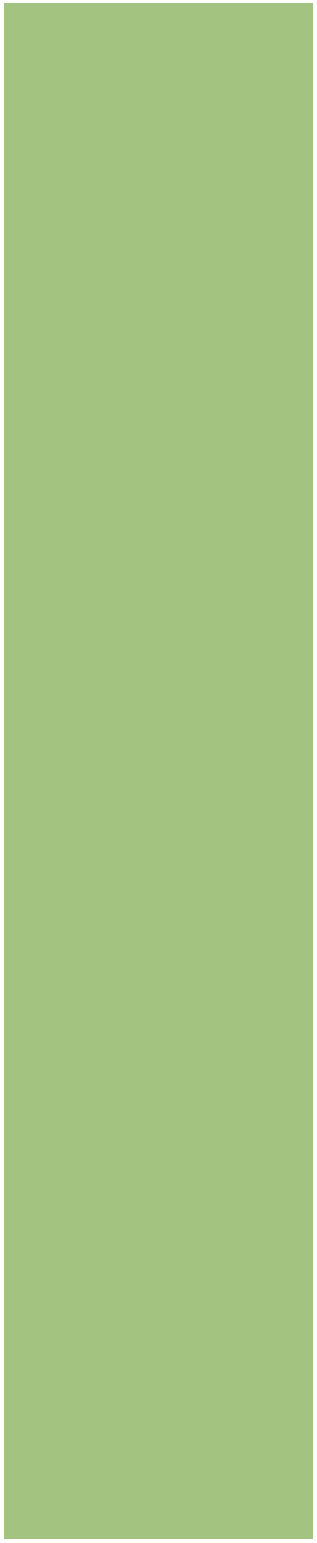

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2435.264	2447.240	2448.218	2458.225	2460.179	2490.178
2492.168	2497.228	2505.145	2516.240	2522.182	2523.109
2534.153	2535.173	2539.251	2540.157	2548.201	2554.200
2555.150	2574.159	2577.175	2589.183	2593.228	2594.191
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3005.351	3010.343	3011.365	3020.375	3033.375	3034.390
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3182.479	3183.357	3189.528	3190.538	3210.450	3221.494
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3313.545	3326.657	3330.489	3331.462	3342.510	3352.456
3353.488	3367.587	3368.607	3374.489	3375.436	3380.422
3381.523	3391.622	3404.600	3408.566	3421.539	3433.650
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3464.616	3465.640	3474.603	3475.488	3480.347	3485.460
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3599.547	3613.721	3627.625	3643.683	3955.670	4223.927

Tolerance (mon) 22.00 ppm

Number of Peptides 285

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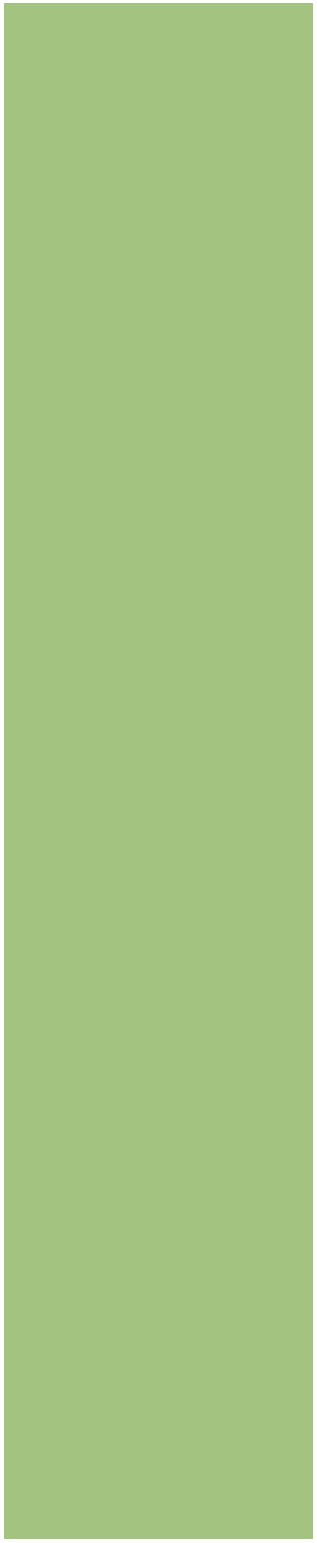
National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	4.1×10^{-16}	gi|13929082|ref|NP_113957.1| pyridoxal (pyridoxine, vitamin B6) kinase [Rattus norvegicus]	72	6.3	35.83	
+2	1.6×10^{-13}	gi|5669929|gb|AAD46521.1|AF154914_1 cyclin H [Rattus norvegicus]	48	7.1	39.10	
	-	gi|19865045|sp|Q9R1A0|CCNH_RAT Cyclin-H	43	6.7	39.10	
	-	gi|204362|gb|AAA41234.1| pot. glutaminase (EC 3.5.1.2); putative	36	5.6	37.58	
	-	gi|20070082|gb|AAM00020.1| kidney-type glutaminase GAC isoform [Rattus norvegicus]	44	5.7	35.00	
	-	gi|6978491|ref|NP_036630.1| aldehyde reductase 1 [Rattus norvegicus]	50	6.3	37.29	
	-	gi|11693178|ref|NP_071799.1| G protein beta subunit-like [Rattus norvegicus]	38	5.5	36.95	
	-	gi|16758944|ref|NP_446045.1| cyclin-dependent kinase 4 [Rattus norvegicus]	58	6.1	34.47	
	-	gi|19386562|gb|AAL86569.1| vesicular protein vp-165 short isoform [Rattus norvegicus]	48	5.2	39.37	
	-	gi|6013133|gb|AAF01254.1|AF109643_1 coxsackie-adenovirus-receptor homolog [Rattus norvegicus]	50	7.0	39.68	
	-	gi|408807|dbj|BAA07490.1| regucalcin [Rattus norvegicus]	56	5.4	34.74	
	-	gi|13928740|ref|NP_113734.1| regucalcin [Rattus norvegicus]	56	5.3	34.74	
	-	gi|1942645|pdb|1MIR|A Chain A, Rat Procathepsin B	49	5.5	37.01	
	-	gi|56605830|ref|NP_001008378.1| hypothetical protein LOC362793 [Rattus norvegicus]	62	5.3	35.74	



-	gi|28948957|pdb|1NL4|A Chain A, Crystal Structure Of Rat Farnesyl Transferase In Complex With A Potent Biphenyl Inhibitor	48	5.3	38.31
-	gi|54780892|gb|AAV40612.1| MHC class II antigen [Rattus norvegicus]	50	7.1	30.66
-	gi|28373971|pdb|1N95|A Chain A, Aryl Tetrahydrophyridine Inhbitors Of Farnesyltranferase: Glycine, Phenylalanine And Histidine Derivatives	48	5.5	38.69
-	gi|50927086|gb|AAH79324.1| LOC361776 [Rattus norvegicus]	42	5.3	32.62
-	gi|11691853|emb|CAC18729.1| metalloprotease/disintegrin [Rattus norvegicus]	47	7.0	35.72
-	gi|55778435|gb|AAH86408.1| LOC246120 protein [Rattus norvegicus]	38	6.5	34.23
-	gi|29468146|gb|AAO85418.1|AF457139_1 MHC class Ib RT1.L [Rattus norvegicus]	40	5.6	37.71
-	gi|8393944|ref|NP_058835.1| proenkephalin 1 [Rattus norvegicus]	55	5.4	32.37
-	gi|11560075|ref|NP_071596.1| caspase 7 [Rattus norvegicus]	51	5.5	35.96
-	gi|53734234|gb|AAH83675.1| Ring finger protein 146 [Rattus norvegicus]	25	5.2	39.48
-	gi|51259507|gb|AAH79425.1| Hypothetical protein LOC654482 [Rattus norvegicus]	49	6.4	32.17
-	gi|53733613|gb|AAH83907.1| Hypothetical protein LOC502372 [Rattus norvegicus]	42	6.0	35.65
-	gi|8394272|ref|NP_058967.1| nuclear distribution gene C homolog [Rattus norvegicus]	40	5.3	39.82
-	gi|8394516|ref|NP_059046.1| plasminogen activator, urokinase receptor [Rattus norvegicus]	40	6.7	37.59
-	gi|16758208|ref|NP_445916.1| spermidine synthase [Rattus norvegicus]	61	5.4	35.18
-	gi|16758442|ref|NP_446086.1| ficolin B [Rattus norvegicus]	46	6.2	35.98
-	gi|5070662|gb|AAD39239.1|AF155822_1 kinesin heavy chain [Rattus norvegicus]	34	5.9	30.77

-	gi|34868134|ref|XP_235618.2| PREDICTED: similar to Ankyrin repeat and SOCS box protein 8 (ASB-8) [Rattus norvegicus]	50	5.6	32.78
-	gi|2145143|gb|AAB58428.1| apolipoprotein A-I [Rattus norvegicus]	43	5.5	30.88
-	gi|2145145|gb|AAB58429.1| apolipoprotein A-I [Rattus norvegicus]	43	5.5	30.97
-	gi|55824680|gb|AAH86587.1| Gs3 protein [Rattus norvegicus]	42	5.6	35.96

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AE01B3E8-0C40-5E19243E

Sequences 20092

Date & Time Mon Jan 29 18:41:27 2007 UTC (Search Time: 0.53 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 30 - 40 kDa

pI Range 5.0 -7.2

Digestion Trypsin

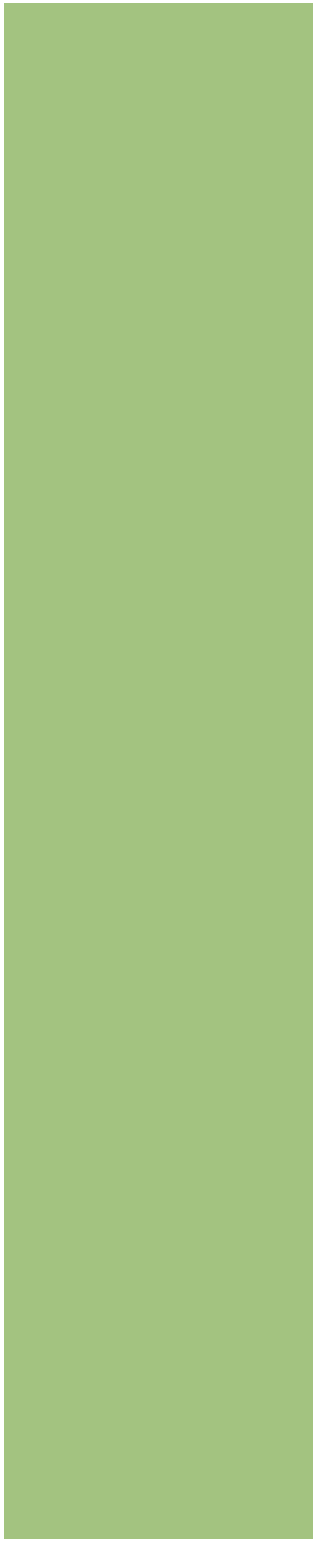
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon)

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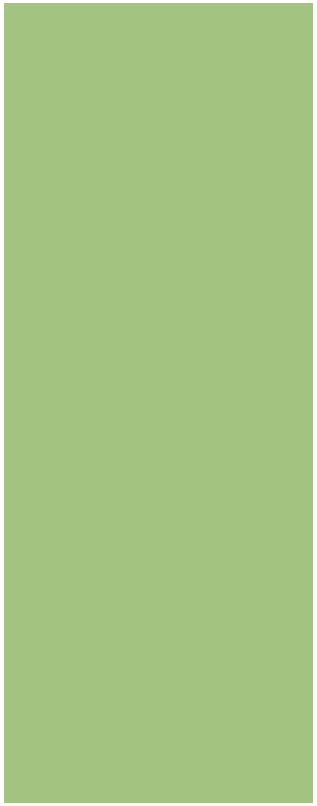
918.468 948.524 990.546 1005.446 1028.522 1030.506
1058.495 1063.512 1076.534 1080.493 1130.589 1177.587
1195.589 1199.638 1215.626 1217.642 1223.599 1227.567
1233.637 1244.589 1250.609 1258.572 1262.606 1268.612
1280.646 1296.617 1305.636 1312.616 1322.678 1330.611
1357.623 1361.622 1371.668 1375.668 1379.665 1388.698
1404.685 1424.676 1432.709 1443.681 1454.702 1456.718
1464.685 1469.710 1482.696 1486.708 1494.711 1501.696
1504.724 1509.714 1520.711 1529.735 1542.767 1553.737
1557.806 1568.762 1584.773 1589.762 1602.806 1616.759
1630.762 1632.770 1639.748 1642.768 1672.774 1678.784
1685.823 1690.779 1695.794 1712.787 1724.805 1730.819
1734.825 1743.815 1757.867 1762.840 1791.821 1827.867
1838.876 1855.875 1893.856 1903.873 1905.891 1929.907
1932.909 1962.922 1987.927 2005.916 2006.936 2017.937
2018.926 2023.955 2031.967 2032.947 2049.969 2050.977
2057.982 2058.975 2070.971 2096.985 2122.009 2152.049
2176.055 2181.056 2209.105 2241.114 2242.124 2265.146
2266.147 2290.151 2291.155 2306.151 2355.146 2363.147
2364.148 2368.146 2369.146 2381.147 2382.145 2390.148
2397.135 2398.191 2408.147 2436.188 2450.188 2458.180
2464.214 2465.256 2495.197 2507.240 2514.214 2531.187
2532.181 2541.208 2542.205 2557.209 2558.208 2572.200
2581.215 2582.226 2590.213 2604.256 2605.228 2622.243
2630.297 2631.181 2638.240 2639.241 2647.241 2648.220
2662.195 2663.223 2668.225 2669.241 2678.221 2679.251
2688.251 2689.250 2695.292 2696.248 2713.262 2714.274
2718.258 2719.260 2727.288 2728.281 2733.295 2741.277
2742.262 2749.313 2765.329 2766.310 2774.331 2775.229
2779.304 2780.289 2789.286 2790.299 2793.281 2794.279
2806.314 2817.293 2818.321 2832.286 2833.317 2836.326
2837.369 2850.322 2851.311 2866.379 2887.326 2888.360
2893.326 2894.389 2906.367 2937.366 2944.329 2945.339
2949.358 2950.349 2962.357 2963.343 2979.405 2994.341
2995.357 2998.338 2999.364 3004.374 3005.276 3011.406
3018.387 3029.404 3030.363 3033.331 3034.374 3048.361
3049.336 3058.384 3059.379 3064.364 3065.402 3077.435



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Tolerance (mon)	33.00 ppm
Number of Peptides	323

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	2.3×10^{-12}	gi|38649320|gb|AAH63174.1| Eno1 protein [Rattus norvegicus]	35	6.7	53.26	
-		gi|56757324|sp|P04764|ENOA_RAT Alpha-enolase (2-phospho-D-glycerate hydro-lyase) (Non-neural enolase) (NNE) (Enolase 1)	32	6.2	48.97	
-		gi|6978809|ref|NP_036686.1| enolase 1, alpha [Rattus norvegicus]	25	6.2	48.95	
-		gi|48686579|gb|AAT46045.1| cyclin A2 variant [Rattus norvegicus]	29	6.9	45.22	
-		gi|2499877|sp|P70645|BLMH_RAT Bleomycin hydrolase (BLM hydrolase) (BMH) (BH)	27	6.0	54.40	
-		gi|115720|sp|P24268|CATD_RAT Cathepsin D precursor [Contains: Cathepsin D 12 kDa light chain; Cathepsin D 9 kDa light chain; Cathepsin D 34 kDa heavy chain; Cathepsin D 30 kDa heavy chain]	20	6.7	46.35	
-		gi|6981296|ref|NP_037123.1| nucleoporin 50 [Rattus norvegicus]	24	6.3	52.15	
-		gi|19705545|ref|NP_599238.1| RAB3A interacting protein (rabin3)-like 1 [Rattus norvegicus]	28	6.1	43.47	
-		gi|28373972|pdb|1N95|B Chain B, Aryl Tetrahydrophyridine Inhbitors Of Farnesyltranferase: Glycine, Phenylalanine And Histidine Derivatives	18	6.1	46.40	
-		gi|28948958|pdb|1NL4|B Chain B, Crystal Structure Of Rat Farnesyl Transferase In Complex With A Potent Biphenyl Inhibitor	18	6.1	46.30	

-	gi|3891484|pdb|1FT2|B Chain B, Co-Crystal Structure Of Protein Farnesyltransferase Complexed With A Farnesyl Diphosphate Substrate	18	6.1	46.25
-	gi|28373970|pdb|1N94|B Chain B, Aryl Tetrahydropyridine Inhbitors Of Farnesyltransferase: Glycine, Phenylalanine And Histidine Derivates	18	6.1	45.90
-	gi|54035288|gb|AAH83566.1| Enolase 3, beta [Rattus norvegicus]	20	7.1	48.94
-	gi|50925459|gb|AAH78772.1| Pcyt2 protein [Rattus norvegicus]	21	6.4	44.89
-	gi|54035294|gb|AAH83724.1| Unknown (protein for IMAGE:7191109) [Rattus norvegicus]	18	6.7	42.14
-	gi|20150494|pdb|1JQI|A Chain A, Crystal Structure Of Rat Short Chain Acyl-Coa Dehydrogenase Complexed With Acetoacetyl-Coa	21	6.4	43.37
-	gi|24987409|pdb|1JQP|A Chain A, Dipeptidyl Peptidase I (Cathepsin C), A Tetrameric Cysteine Protease Of The Papain Family	23	6.9	51.45
-	gi|2500146|sp|P56163|DPF1_RAT Zinc-finger protein neuro-d4 (D4, zinc and double PHD fingers family 1)	23	6.8	47.78
-	gi|27703780|ref|XP_225049.1| PREDICTED: similar to zinc finger protein, subfamily 1A, 5 [Rattus norvegicus]	18	6.6	45.98
-	gi|18034777|ref|NP_542143.1| apolipoprotein A-V [Rattus norvegicus]	22	6.0	42.14
-	gi|56325|emb|CAA68545.1| unnamed protein product [Rattus norvegicus]	15	6.1	57.73

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B1B9B633-0888-61D127F6

Sequences 20092

Date & Time Mon Jan 29 18:47:32 2007 UTC (Search Time: 0.45 sec.)

Sample ID	
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	42 - 58 kDa
pI Range	6.0 -7.2
Digestion	Trypsin
Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	640.662 654.394 668.685 696.737 704.410 710.749 719.383 722.731 724.768 725.771 738.785 753.803 754.805 766.815 767.802 778.814 791.415 795.816 797.852 806.449 811.870 813.854 824.497 832.305 850.429 852.489 857.510 877.416 918.467 920.469 948.522 955.506 990.546 1000.536 1005.532 1037.554 1057.501 1088.540 1194.604 1217.641 1223.607 1233.640 1244.591 1247.617 1262.613 1265.629 1280.640 1312.601 1322.684 1329.627 1347.640 1455.723 1481.755 1529.732 1542.773 1560.790 1624.750 1675.833 1713.797 1757.857 1779.861 1804.934 1828.868 1846.909 1922.926 1929.943 2002.926 2003.934 2144.017 2241.123 2242.139 2291.137 2339.175 2341.201 2373.135 2374.175 2382.212 2392.227 2434.297 2492.136 2532.115 2533.165 2556.145 2611.190 2702.208 2746.209 3004.357 3022.432 3029.525 3047.591 3063.581 3064.558 3075.346 3077.497 3105.424 3112.523 3113.561 3146.452 3147.517 3154.409 3173.489 3174.458 3190.518 3191.458 3210.459 3220.490 3233.459 3234.477 3262.450 3272.556 3273.486 3281.520 3292.599 3293.646 3316.495 3324.450 3325.490 3335.549 3336.565 3342.679 3355.570 3367.670 3382.651 3383.521 3398.500 3404.495 3410.560 3418.654 3433.564 3444.543 3663.721 3691.753 3881.815 4109.070 4458.692 4500.278 4534.361
Tolerance (mon)	26.00 ppm

Number of Peptides 137

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	9.2×10^{-14}	gi|417220|sp|P80204|TGFR1_RAT TGF-beta receptor type-1 precursor (TGF-beta receptor type I) (TGFR-1) (TGF-beta type I receptor) (Transforming growth factor-beta receptor type I) (TbetaR-I) (Serine/threonine-protein kinase receptor R4) (SKR4)	13	7.3	58.22	
	-	gi|56540874|gb|AAH87035.1| Transforming growth factor, beta receptor 1 [Rattus norvegicus]	13	7.3	57.83	
2	8.7×10^{-9}	gi|27716061|ref|XP_233452.1| PREDICTED: similar to zinc finger protein 691 [Rattus norvegicus]	21	8.9	33.69	
3	6.5×10^{-8}	gi|56090624|ref|NP_001007676.1| C1q and tumor necrosis factor related protein 1 [Rattus norvegicus]	20	6.1	33.05	
4	9.1×10^{-7}	gi|1932801|gb|AAB51686.1| synaptotagmin X [Rattus norvegicus]	8	8.3	58.73	
5	9.9×10^{-7}	gi|39930465|ref|NP_113854.1| synaptotagmin X [Rattus norvegicus]	8	8.4	61.39	
6	2.2×10^{-6}	gi|16758014|ref|NP_445770.1| hemopexin [Rattus norvegicus]	12	7.9	53.02	
7	2.3×10^{-6}	gi|54035429|gb|AAH83903.1| Kelch-like 7 (Drosophila) [Rattus norvegicus]	7	6.2	68.73	
8	6.4×10^{-6}	gi|41054868|ref|NP_955788.1| fucose-1-phosphate guanylyltransferase [Rattus norvegicus]	9	7.0	68.14	
9	1.8×10^{-5}	gi|53850644|ref|NP_001005558.1| hypothetical protein LOC313430 [Rattus norvegicus]	9	6.3	68.41	
10	2.8×10^{-5}	gi|6978449|ref|NP_036623.1| adducin 2 (beta) [Rattus norvegicus]	8	6.1	64.40	
11	6.9×10^{-5}	gi|1552374|emb|CAA69358.1| 2-arylpropionyl-CoA epimerase [Rattus norvegicus]	12	6.1	40.75	
12	3.6×10^{-4}	gi|24987409|pdb|1JQP|A Chain A, Dipeptidyl Peptidase I (Cathepsin C), A Tetrameric Cysteine Protease Of The Papain Family	7	6.9	51.45	
13	1.1×10^{-3}	gi|7106246|ref|NP_037191.1| alkaline phosphatase, tissue-nonspecific [Rattus norvegicus]	9	6.5	59.30	
14	1.1×10^{-3}	gi|130751|sp|P08289|PPBT_RAT Alkaline phosphatase, tissue-nonspecific isozyme precursor (AP-TNAP) (Liver/bone/kidney isozyme) (TNSALP)	9	6.4	59.25	
15	1.7×10^{-3}	gi|91940|pir||S00289 alkaline phosphatase (EC 3.1.3.1), hepatic precursor - rat	9	6.3	59.51	
16	4.7×10^{-3}	gi|223231|prf||0610238A amylase	11	8.7	58.16	
17	4.7×10^{-3}	gi|67373|pir||ALRTP alpha-amylase (EC 3.2.1.1) precursor, pancreatic - rat (fragment)	11	8.7	58.23	

18	4.7×10^{-3}	gi|13928684|ref|NP_113690.1|	amylase 2, pancreatic [Rattus norvegicus]	11	8.9	58.89

NOTE:

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Input Summary

Search id B44455F9-05FC-645D2AA5

Sequences 20092

Date & Time Tue Jan 30 20:01:14 2007 UTC (Search Time: 0.28 sec.)

Sample ID 20061228 richardson NIA set 1 spot 4704, 20070130, cleaned data search 2

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 30 - 70 kDa

pI Range 6.0 -9.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 841.471 848.445 1064.521 1203.536 1211.585 1242.571 1268.616 1305.647
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2125.014 2152.048 2183.085 2209.084 2241.125 2242.141 2298.152 2365.173
2366.185 2376.151 2377.170 2390.177 2398.149 2399.166 2420.163 2435.196
2448.177 2460.160 2506.164 2507.194 2514.186 2533.160 2534.136 2536.181
2538.190 2547.193 2548.196 2557.199 2558.196 2562.195 2563.197 2593.200
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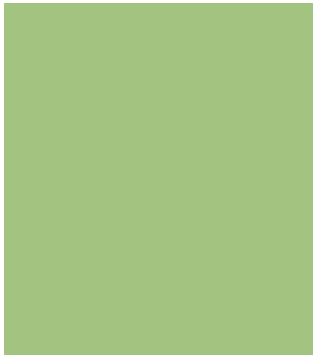
2669.241 2675.247 2676.203 2680.237 2681.244 2687.221 2688.226 2694.260
2700.333 2701.245 2705.247 2722.228 2723.283 2733.276 2734.258 2742.251
2743.261 2749.197 2750.259 2762.279 2763.267 2767.275 2768.347 2772.261
2773.273 2783.270 2784.297 2789.260 2790.260 2801.291 2802.305 2819.309
2820.312 2832.320 2837.313 2838.288 2849.299 2850.294 2865.298 2879.307
2893.359 2894.317 2915.403 2916.494 2935.359 2936.330 2949.344 2959.311
2960.344 2965.315 2977.332 2978.259 2982.416 2983.344 2995.375 2996.336
3003.367 3010.332 3011.329 3020.356 3029.452 3033.376 3034.366 3047.502
3048.503 3065.392 3066.379 3094.461 3105.391 3147.428 3148.456 3180.486
3181.478 3185.440 3187.449 3198.489 3211.469 3212.457 3218.448 3228.454
3244.485 3245.464 3262.478 3272.451 3273.492 3283.453 3284.498 3298.490
3314.485 3329.474 3330.548 3357.506 3358.501 3371.531 3372.551 3384.527



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Tolerance (mon)	8.00 ppm
Number of Peptides	220

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center for Research Resources
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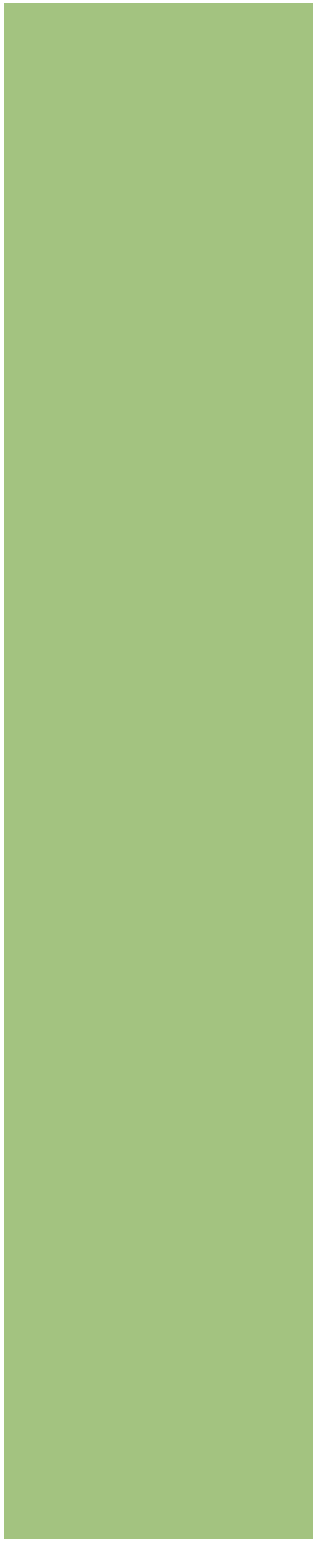
Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	6.4×10^{-11}	gi|6978605|ref|NP_037054.1| caspase 3 [Rattus norvegicus]	40	5.9	32.81	
2	6.8×10^{-10}	gi|57164143|ref|NP_001009268.1| ARP2 actin-related protein 2 homolog [Rattus norvegicus]	31	6.3	46.05	
3	2.9×10^{-8}	gi|24987409|pdb|1JQP|A Chain A, Dipeptidyl Peptidase I (Cathepsin C), A Tetrameric Cysteine Protease Of The Papain Family	30	6.9	51.45	
4	2.4×10^{-7}	gi|55669578|pdb|1QX4|A Chain A, Structrue Of S127p Mutant Of Cytochrome B5 Reductase	28	7.2	32.21	
5	1.6×10^{-6}	gi|225691|prf||1310344A decarboxylase,uroporphyrinogen	28	6.5	41.62	
6	2.2×10^{-6}	gi|56922|emb|CAA33606.1| unnamed protein product [Rattus norvegicus]	24	6.0	53.67	
7	2.4×10^{-6}	gi|17943396|pdb|1IB0|A Chain A, Crystal Structure Of Rat B5r In Complex With Fad And Nad	24	7.2	32.20	
8	3.5×10^{-6}	gi|1167999|gb|AAB35050.1| spermidine synthase, putrescine aminopropyltransferase, PAPT {EC 2.5.1.6} [rats, Peptide, 297 aa]	33	6.5	35.05	
9	3.8×10^{-6}	gi|56971338|gb|AAH88271.1| Similar to Ig gamma-1, chain C region [Rattus norvegicus]	25	7.2	53.56	
+10	1.0×10^{-5}	gi|19924067|ref|NP_612541.1| nucleoside-diphosphate kinase 7 [Rattus norvegicus]	18	6.3	46.02	
	-	gi|37805418|gb|AAH60314.1| Non-metastatic cells 7, protein expressed in [Rattus norvegicus]	18	6.3	45.99	
11	1.3×10^{-5}	gi|1169826|sp|P43424|GALT_RAT Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (UDP-glucose--hexose-1-phosphate uridylyltransferase)	34	6.1	44.24	

+12	1.4×10^{-5}	gi|7001384|gb|AAF34874.1|AF168004_1 Parkin [Rattus norvegicus]	26	6.7	53.81
	-	gi|20385790|gb|AAM21453.1|AF381278_1 parkin isoform [Rattus norvegicus]	21	6.6	51.83
	-	gi|20385796|gb|AAM21456.1|AF381281_1 parkin isoform [Rattus norvegicus]	16	6.8	51.45
13	2.0×10^{-5}	gi|3133137|dbj|BAA28175.1| N-Shc [Rattus rattus]	17	6.9	53.57
14	1.0×10^{-4}	gi|416892|sp|P32362|DCUP_RAT Uroporphyrinogen decarboxylase (URO-D) (UPD)	22	6.4	41.35
+15	1.3×10^{-4}	gi|228136|prf||1717354A Gln synthetase	22	6.4	41.88
	-	gi|204349|gb|AAC42038.1| glutamine synthetase	21	6.8	43.81
	-	gi|38181948|gb|AAH61559.1| Glul protein [Rattus norvegicus]	21	6.5	43.79
	-	gi|121376|sp|P09606|GLNA_RAT Glutamine synthetase (Glutamate--ammonia ligase) (GS)	21	6.6	43.79
16	2.0×10^{-4}	gi|21105476|gb|AAM34681.1|AF508019_1 arginase-related protein [Rattus norvegicus]	26	6.1	38.59
+17	2.9×10^{-4}	gi|50925537|gb|AAH78930.1| Acy1 protein [Rattus norvegicus]	26	6.0	46.83
	-	gi|52851387|ref|NP_001005383.1| aminoacylase 1 [Rattus norvegicus]	26	5.9	46.93
18	2.9×10^{-4}	gi|27703780|ref|XP_225049.1| PREDICTED: similar to zinc finger protein, subfamily 1A, 5 [Rattus norvegicus]	19	6.6	45.98
	-	gi|50925641|gb|AAH79049.1| Calreticulin 3 [Rattus norvegicus]	28	6.0	45.92
	-	gi|34858816|ref|XP_215857.2| PREDICTED: similar to CG8067-PA [Rattus norvegicus]	24	6.0	38.97
	-	gi|51948384|ref|NP_001004206.1| proliferation-associated 2G4, 38kDa [Rattus norvegicus]	22	6.4	45.75
	-	gi|8394193|ref|NP_059037.1| lipase, gastric [Rattus norvegicus]	24	6.1	45.72
	-	gi|15420315|gb|AAK97344.1| interleukin-5 receptor alpha [Rattus norvegicus]	16	6.9	48.75
	-	gi|16758704|ref|NP_446297.1| ureidopropionase, beta [Rattus norvegicus]	23	6.5	45.35



-	gi|57012410|ref|NP_001008849.1| RT1 class I, M1, gene 2 [Rattus norvegicus]	17	6.8	40.27
-	gi|53850618|ref|NP_001005545.1| MYG1 protein [Rattus norvegicus]	25	6.0	43.75
-	gi|27706912|ref|XP_228584.1| PREDICTED: similar to HIN-6 protease [Rattus norvegicus]	17	7.2	34.65
-	gi|14389301|ref|NP_112650.1| sphingomyelin phosphodiesterase 2, neutral [Rattus norvegicus]	19	6.6	49.42
-	gi|7839599|gb|AAF70344.1| p47phox [Rattus norvegicus]	28	7.1	36.82
-	gi|56605708|ref|NP_001008315.1| makorin, ring finger protein, 2 [Rattus norvegicus]	25	7.3	49.32
-	gi|347021|pir||S29690 Ig heavy chain VDJ region - rat (fragment)	24	6.5	32.67
-	gi|4379409|emb|CAA48681.1| Ig heavy chain VDJh2 region [Rattus norvegicus]	24	6.4	32.69
-	gi|50925654|gb|AAH79068.1| DTW domain containing 1 [Rattus norvegicus]	22	6.6	36.27
-	gi|34866113|ref|XP_343235.1| PREDICTED: similar to Tetratricopeptide repeat protein KIAA0103 [Rattus norvegicus]	25	6.4	35.91
-	gi|47606369|ref|NP_001001278.1| olfactory receptor Olr382 [Rattus norvegicus]	23	6.3	36.30
-	gi|42476312|ref|NP_714955.2| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 10 [Rattus norvegicus]	17	6.2	46.59
-	gi|16758340|ref|NP_446020.1| phosphate cytidylyltransferase 2, ethanolamine [Rattus norvegicus]	15	6.2	46.68
-	gi|50925459|gb|AAH78772.1| Pcyt2 protein [Rattus norvegicus]	16	6.4	44.89
-	gi|21311520|gb|AAM46762.1|AF458414_1 flavin-containing monooxygenase 2 [Rattus norvegicus]	14	7.2	50.95
-	gi|50925581|gb|AAH78977.1| Phytanoyl-CoA hydroxylase interacting protein-like [Rattus norvegicus]	16	6.9	39.12
-	gi|27692997|ref|XP_227419.1| PREDICTED: similar to Pygopus homolog 2 [Rattus norvegicus]	27	6.9	42.01

-	gi|37222638|gb|AAQ90023.1| estrogen receptor-related receptor gamma [Rattus norvegicus]	19	6.0	53.65
-	gi|50400205|sp|P62510|ERR3_RAT Estrogen-related receptor gamma (Estrogen receptor-related protein 3)	19	6.0	53.57
-	gi|56972083|gb|AAH88196.1| Similar to KTI12 homolog, chromatin associated [Rattus norvegicus]	24	7.0	39.06

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20076

Date & Time Sat Feb 03 18:30:46 2007 UTC (Search Time: 0.44 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 32 - 54 kDa

pI Range 5.9 -7.3

Digestion Trypsin

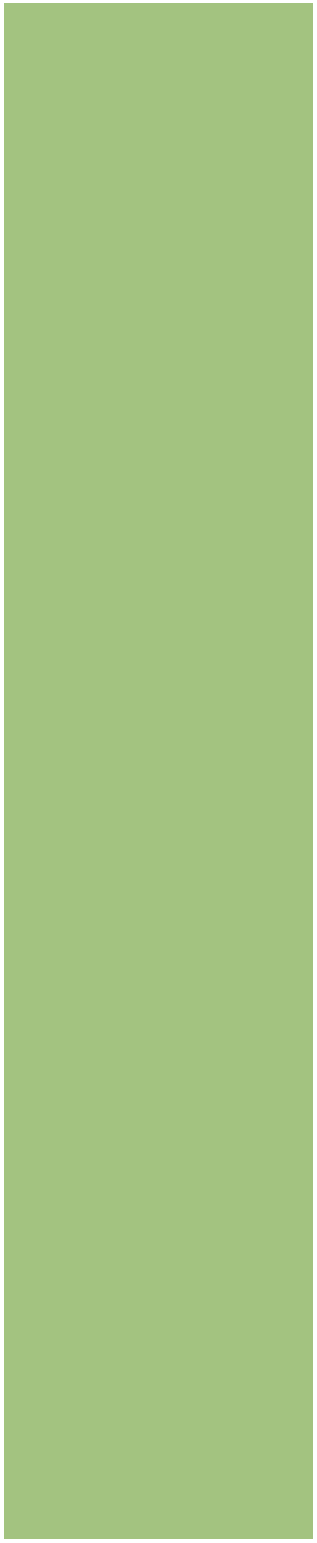
Missed Cuts 1

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +O@M (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



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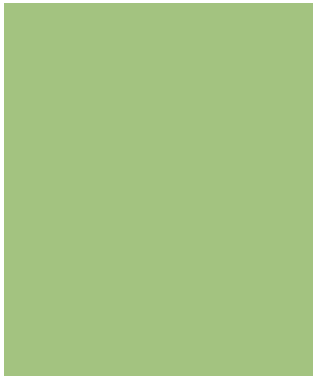

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Tolerance (mon)	18.00 ppm
Number of Peptides	258

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National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	2.1×10^{-12}	gi|54035509|gb|AAH83909.1| TNF receptor-associated protein 1 [Rattus norvegicus]	32	6.6	82.61	
2	6.8×10^{-12}	gi|20302047|ref|NP_620231.1| adenosine monophosphate deaminase 1 (isoform M) [Rattus norvegicus]	35	6.5	89.24	
3	1.4×10^{-9}	gi|57528264|ref|NP_001009653.1| methylcrotonoyl-Coenzyme A carboxylase 1 (alpha) [Rattus norvegicus]	42	6.7	81.36	
+4	2.7×10^{-9}	gi|6683035|dbj|BAA88997.1| PDE10A3 [Rattus norvegicus]	34	6.1	92.38	
	-	gi|13489075|ref|NP_071572.1| phosphodiesterase 10A [Rattus norvegicus]	30	6.1	93.40	
	-	gi|42600937|gb|AAS21245.1| PDE10A13 [Rattus norvegicus]	31	6.3	83.86	
	-	gi|42600939|gb|AAS21246.1| PDE10A14 [Rattus norvegicus]	26	6.7	76.95	
5	4.9×10^{-9}	gi|13929158|ref|NP_114002.1| G protein-coupled receptor kinase interactor 1 [Rattus norvegicus]	40	6.5	87.72	
	-	gi|6981002|ref|NP_037221.1| glycogen synthase 2 [Rattus norvegicus]	36	6.5	82.81	
	-	gi|6685708|sp|P97570|PA2G6_RAT 85 kDa calcium-independent phospholipase A2 (iPLA2) (CaI-PLA2) (Group VI phospholipase A2) (GVI PLA2)	36	6.3	86.11	
	-	gi|29789297|ref|NP_445812.1| SH3 domain-containing adapter protein [Rattus norvegicus]	37	6.2	76.00	
	-	gi|12621082|ref|NP_075216.1| midline 1 [Rattus norvegicus]	29	6.3	78.54	
	-	gi|55250418|gb|AAH85814.1| Special AT-rich sequence binding protein 1 [Rattus norvegicus]	24	6.1	88.10	
	-	gi|53733599|gb|AAH83876.1| Pleckstrin homology domain containing, family C (with FERM domain) member 1 [Rattus norvegicus]	35	6.3	81.09	

-	gi|42407285|dbj|BAD10852.1| TAP-Like isoform C3 [Rattus norvegicus]	32	6.2	77.68
-	gi|13242186|gb|AAK16592.1|AF346902_1 glycogen synthase [Rattus norvegicus]	36	6.6	83.06
-	gi|16758678|ref|NP_446279.1| procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1 [Rattus norvegicus]	28	6.3	85.80
-	gi|52695822|pdb|1TLL|A Chain A, Crystal Structure Of Rat Neuronal Nitric-Oxide Synthase Reductase Module At 2.3 A Resolution.	31	6.3	80.31
-	gi|38512106|gb|AAH61756.1| Ribophorin I [Rattus norvegicus]	35	6.1	70.18
-	gi|6981486|ref|NP_037199.1| ribophorin I [Rattus norvegicus]	35	6.1	70.08
-	gi|16758262|ref|NP_445954.1| ATP-binding cassette, sub-family G (WHITE), member 1 [Rattus norvegicus]	28	6.7	76.18
-	gi|55741823|ref|NP_001006977.1| threonyl-tRNA synthetase [Rattus norvegicus]	26	6.5	83.87
-	gi|11560034|ref|NP_071574.1| ATP-binding cassette, sub-family B (MDR/TAP), member 9 [Rattus norvegicus]	28	7.0	85.47
-	gi|42407287|dbj|BAD10853.1| TAP-Like isoform C4 [Rattus norvegicus]	28	6.1	79.10
-	gi|1531647|gb|AAB40718.1| C2-HC type zinc finger protein r-MyT2 [Rattus norvegicus]	27	7.0	94.61
-	gi|9506955|ref|NP_062204.1| proprotein convertase subtilisin/kexin type3 [Rattus norvegicus]	25	6.1	89.00
-	gi|38197562|gb|AAH61791.1| Phosphofructokinase, liver, B-type [Rattus norvegicus]	23	6.9	87.63
-	gi|47169484|tpe|CAE48379.1| TPA: glutamine-fructose-6-phosphate transaminase 2 [Rattus norvegicus]	40	6.7	79.61
-	gi|13929146|ref|NP_113996.1| calpain 6 [Rattus norvegicus]	33	6.9	77.18
-	gi|18034779|ref|NP_542144.1| nuclear protein localization 4 [Rattus norvegicus]	40	6.0	70.56
-	gi|13591987|ref|NP_112314.1| mitochondrial intermediate peptidase [Rattus norvegicus]	31	6.1	83.07

-	gi|13786188|ref|NP_112637.1| peroxisome proliferative activated receptor, gamma, coactivator 1 alpha [Rattus norvegicus]	31	6.1	93.92
-	gi|12083643|ref|NP_073182.1| exocyst complex component 7 [Rattus norvegicus]	30	6.3	77.53
-	gi|6978671|ref|NP_037060.1| cyclic nucleotide gated channel 4 [Rattus norvegicus]	26	6.3	78.51
-	gi|16758638|ref|NP_446249.1| crooked neck protein [Rattus norvegicus]	23	6.5	86.25
-	gi|53733406|gb|AAH83567.1| Ring finger protein 190 [Rattus norvegicus]	29	6.8	90.54
-	gi|23305781|gb|AAN17280.1| testicular angiotensin-1 converting enzyme [Rattus norvegicus]	26	6.6	90.42
-	gi|47059181|ref|NP_997631.1| B-factor, properdin [Rattus norvegicus]	27	6.6	88.83
-	gi|1083665|pir||S51635 fibroblast growth factor receptor 2b, keratinocyte growth factor receptor - rat	30	6.5	82.10
-	gi|49359177|gb|AAT65503.1| protein kinase C epsilon [Rattus norvegicus]	21	6.6	87.28
-	gi|204158|gb|AAA41168.1| fibronectin 3	32	6.4	77.14
-	gi|204157|gb|AAA41167.1| fibronectin 2	28	6.4	87.73
-	gi|204156|gb|AAA41166.1| fibronectin 1	27	6.1	90.44
-	gi|13929022|ref|NP_113915.1| LIM motif-containing protein kinase 1 [Rattus norvegicus]	29	6.4	75.39
-	gi|1209468|emb|CAA63043.1| stat5bDelta40C [Rattus norvegicus]	27	6.4	85.37
-	gi|25742638|ref|NP_114012.1| CCCTC-binding factor [Rattus norvegicus]	22	6.5	88.13
-	gi|38257802|sp|P59996|PCSK9_RAT Proprotein convertase subtilisin/kexin type 9 precursor (Proprotein convertase PC9) (Subtilisin/kexin-like protease PC9) (Neural apoptosis-regulated convertase 1) (NARC-1)	25	6.5	76.92
-	gi|551274|emb|CAA84511.1| fibroblast growth factor receptor 2b, keratinocyte growth factor receptor [Rattus rattus]	28	6.8	78.33

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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Sequences 20092

Date & Time Wed Jan 31 19:37:46 2007 UTC (Search Time: 0.47 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 69 - 95 kDa

pI Range 6.0 -7.1

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

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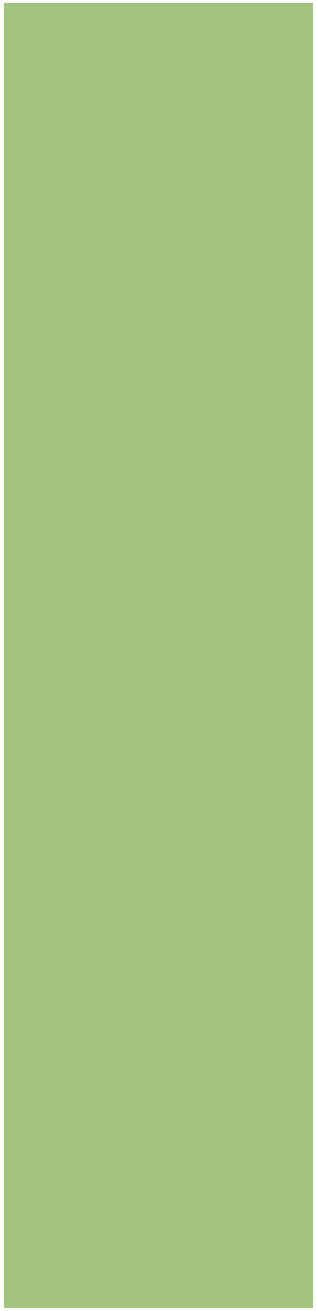

2555.176 2560.194 2561.171 2567.183 2568.208 2586.230
2593.178 2601.209 2602.218 2605.200 2606.188 2610.184
2611.243 2634.175 2635.188 2649.225 2650.214 2666.224
2667.221 2673.260 2674.204 2689.223 2690.218 2714.240
2715.263 2723.219 2724.219 2731.211 2732.244 2742.264
2743.247 2747.233 2748.239 2752.271 2762.253 2763.237
2771.277 2772.268 2786.302 2787.267 2805.265 2818.283
2819.269 2836.285 2837.287 2847.283 2849.295 2866.328
2882.327 2887.337 2894.244 2895.328 2906.353 2914.348
2922.358 2949.331 2953.338 2954.339 2963.306 2964.328
2978.319 2980.316 3000.434 3001.422 3012.319 3020.376
3029.458 3047.471 3052.331 3053.338 3060.376 3061.393
3068.359 3069.335 3075.380 3083.350 3084.344 3092.396
3102.383 3103.401 3111.372 3112.357 3134.415 3135.412
3154.412 3172.464 3173.422 3182.450 3183.435 3187.445
3198.464 3208.429 3220.470 3230.483 3244.472 3245.462
3262.497 3266.415 3267.448 3276.467 3277.475 3281.485
3292.503 3314.488 3326.496 3327.520 3342.521 3355.521
3356.456 3372.534 3373.491 3383.491 3384.516 3393.548
3409.532 3419.547 3423.431 3424.490 3430.553 3433.574
3434.550 3444.501 3445.523 3452.554 3463.519 3464.578
3470.560 3471.571 3478.517 3479.542 3490.668 3491.517
3507.569 3526.564 3532.583 3539.609 3546.639 3553.619
3566.602 3574.608 3583.650 3594.673 3601.594 3614.616
3620.628 3635.621 3648.645 3653.599 3666.648 3677.609
3695.652 3710.667 3724.682 3741.708 3753.661 3774.662
3784.705 3799.721 3815.737 3831.691 3843.726 3860.704
3877.754 4113.796

Tolerance (mon) 26.00 ppm

Number of Peptides 255

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- X! Hunter
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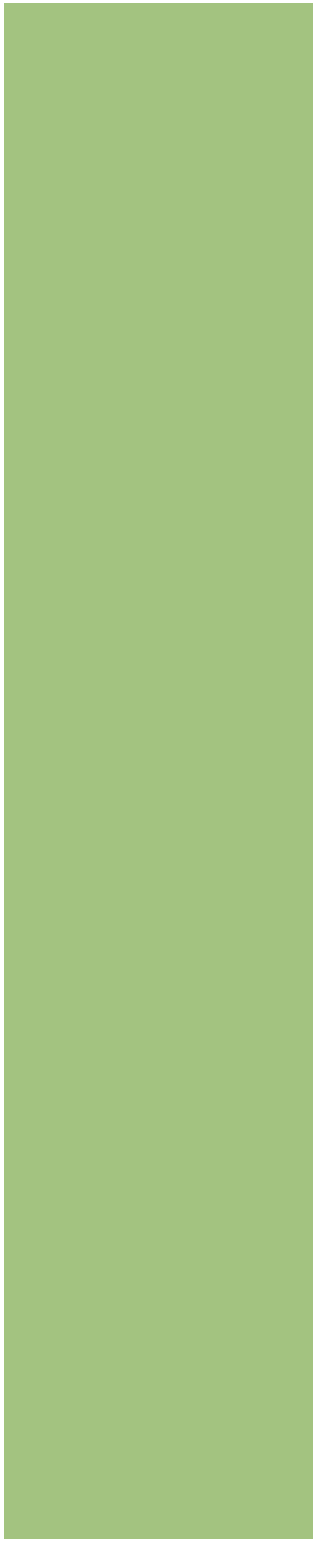
Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	3.7×10^{-8}	gi|48927601|dbj|BAD23895.1| Down-regulated in nephrectomized rat kidney #2 [Rattus norvegicus]	31	6.2	68.99	
+2	6.9×10^{-7}	gi|204576|gb|AAA41312.1| tyrosine kinase	31	6.8	59.02	
	-	gi|34734058|ref|NP_037317.2| hemopoietic cell kinase [Rattus norvegicus]	30	7.2	61.27	
	-	gi|57582|emb|CAA44218.1| protein-tyrosine kinase [Rattus rattus]	26	6.8	58.95	
	-	gi|349096|gb|AAA42095.1| transcription factor	41	7.0	57.21	
	-	gi|693993|emb|CAA58537.1| leucocyte common antigen-related protein [Rattus norvegicus]	35	6.5	72.71	
	-	gi|16758070|ref|NP_445802.1| alkyl-dihydroxyacetonephosphate synthase precursor [Rattus norvegicus]	35	7.0	73.87	
	-	gi|91940|pir||S00289 alkaline phosphatase (EC 3.1.3.1), hepatic precursor - rat	32	6.3	59.51	
	-	gi|51980290|gb|AAH81791.1| Leucine rich repeat protein 3, neuronal [Rattus norvegicus]	28	6.8	81.74	
	-	gi|117230|sp|P20814|CP2CD_RAT Cytochrome P450 2C13, male-specific (CYPIIC13) (P450-G) (P-450g) (UT-5)	35	6.8	57.70	
	-	gi|37727814|gb|AAO45419.1| EG1RVC [Rattus norvegicus]	31	6.2	79.94	
	-	gi|25453406|ref|NP_612523.1| cytochrome P450 2c13 [Rattus norvegicus]	38	6.7	57.68	
	-	gi|11890719|gb|AAG41192.1| inhibitor of apoptosis protein 3 [Rattus norvegicus]	25	6.1	58.96	
	-	gi|458333|gb|AAA19133.1| protein tyrosine phosphatase	31	6.9	70.80	



-	gi|13540675|ref|NP_110483.1| leucine rich repeat protein 3, neuronal [Rattus norvegicus]	23	6.7	81.80
-	gi|55741778|ref|NP_001006998.1| sphingomyelin phosphodiesterase 1, acid lysosomal [Rattus norvegicus]	29	7.1	71.51
-	gi|50927382|gb|AAH79245.1| Similar to RIKEN cDNA 3010001K23 gene [Rattus norvegicus]	25	6.6	56.78
-	gi|2117406|pir||I52410 cytochrome P450 IIC13 - rat	32	6.7	57.70
-	gi|13592023|ref|NP_112343.1| 3-phosphoinositide dependent protein kinase-1 [Rattus norvegicus]	31	6.7	65.76
-	gi|56905|emb|CAA30916.1| unnamed protein product [Rattus norvegicus]	28	6.4	59.12
-	gi|11890721|gb|AAG41193.1| inhibitor of apoptosis protein 3 [Rattus norvegicus]	20	6.1	58.99
-	gi|10765281|gb|AAG22969.1|AF183429_1 inhibitor of apoptosis protein 3 [Rattus norvegicus]	20	6.1	58.47
-	gi|11560028|ref|NP_071567.1| baculoviral IAP repeat-containing 4 [Rattus norvegicus]	20	6.1	58.43
-	gi|56611129|gb|AAH87741.1| Glucosamine (N-acetyl)-6-sulfatase [Rattus norvegicus]	23	6.3	59.72
-	gi|6981444|ref|NP_037220.1| protein tyrosine phosphatase, non-receptor type 11 [Rattus norvegicus]	27	6.9	70.48
-	gi|6978607|ref|NP_036652.1| catalase [Rattus norvegicus]	35	7.1	61.34
-	gi|29293813|ref|NP_808789.1| pre-B-cell colony enhancing factor 1 [Rattus norvegicus]	30	6.7	57.64
-	gi|7434494|pir||S77704 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) clone 5c, skeletal muscle - rat	19	6.4	56.01
-	gi|125552|sp|P05696|KPCA_RAT Protein kinase C alpha type (PKC-alpha) (PKC-A)	27	6.6	80.40
-	gi|34880864|ref|XP_222803.2| PREDICTED: similar to zinc finger and BTB domain containing 37 [Rattus norvegicus]	25	6.2	57.46
-	gi|55154558|gb|AAH85333.1| Coiled-coil domain containing 67 [Rattus norvegicus]	22	6.6	70.56

-	gi|12711692|ref|NP_075412.1| dihydropyrimidinase-like 5 [Rattus norvegicus]	18	6.6	63.40
-	gi|56971844|gb|AAH88305.1| Protein disulfide isomerase-associated 5 [Rattus norvegicus]	21	7.0	62.23
-	gi|6978747|ref|NP_036862.1| cytochrome P450, family 2, subfamily d, polypeptide 26 [Rattus norvegicus]	19	6.8	57.90
-	gi|117242|sp|P10634|CP2DQ_RAT Cytochrome P450 2D26 (CYPIID26) (P450-DB2) (P450-CMF2) (Debrisoquine 4-hydroxylase)	19	7.0	57.90
-	gi|19343354|gb|AAB88700.2| kinesin-related protein 3A [Rattus norvegicus]	27	6.1	57.15
-	gi|6714522|dbj|BAA89475.1| dihydropyrimidinase-related protein [Rattus norvegicus]	25	6.5	63.15

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B4B7FA09-0584-B5806257

Sequences 20076

Date & Time Sat Feb 03 03:24:35 2007 UTC (Search Time: 0.44 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 56 - 83 kDa

pI Range 6.1 -7.2

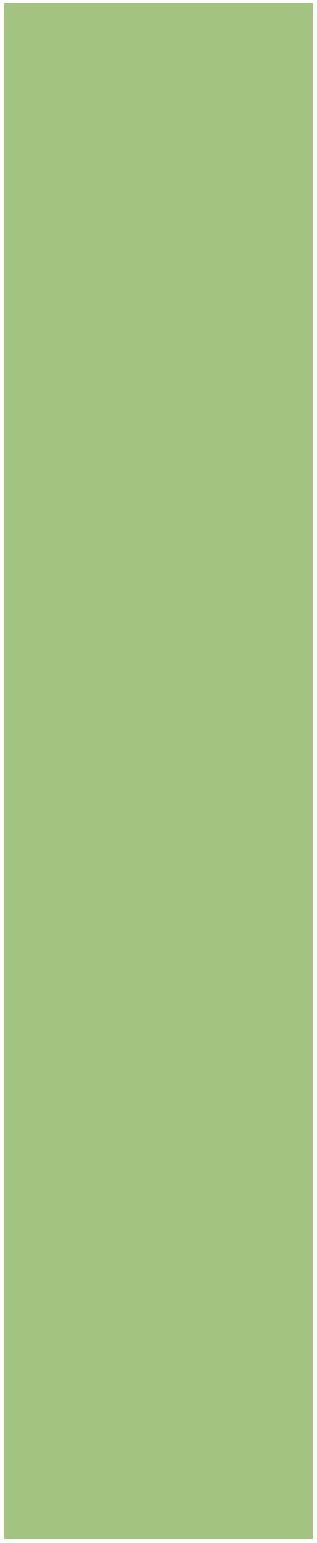
Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)



Tolerance (avg) 1.00 ppm

Masses (mon)

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1322.669	1330.605	1895.870	1904.886	1908.898	1932.901
2012.947	2017.928	2018.931	2023.944	2036.952	2037.952
2115.981	2124.004	2135.019	2150.016	2183.073	2225.110
2241.122	2242.145	2291.143	2298.140	2306.139	2348.139
2349.130	2367.115	2368.106	2373.147	2374.160	2376.168
2377.174	2390.151	2397.140	2398.148	2433.160	2448.187
2458.164	2464.186	2465.213	2497.202	2505.187	2514.161
2533.181	2534.175	2541.189	2542.189	2554.191	2555.194
2560.207	2561.208	2574.185	2593.188	2602.218	2603.213
2637.224	2638.221	2647.211	2649.229	2652.213	2653.220
2663.221	2680.225	2681.239	2690.236	2701.238	2702.233
2723.250	2732.249	2733.254	2743.252	2744.249	2749.270
2750.265	2765.263	2766.261	2783.286	2784.287	2787.250
2788.263	2792.255	2793.254	2801.277	2802.301	2806.291
2807.276	2819.293	2820.310	2832.287	2837.302	2838.294
2848.306	2849.313	2868.351	2885.322	2886.328	2894.348
2895.337	2906.333	2920.354	2921.331	2944.343	2945.340
2959.346	2960.361	2964.346	2965.330	2978.362	2979.355
2985.380	2986.389	2995.374	2996.379	3002.394	3003.391
3012.432	3018.384	3029.465	3030.531	3048.486	3064.423
3065.415	3075.417	3076.436	3092.434	3107.444	3136.419
3147.446	3148.485	3179.443	3180.465	3191.457	3192.451
3196.442	3210.462	3228.475	3232.498	3233.488	3244.508
3245.504	3262.510	3273.520	3283.523	3294.494	3316.504
3327.540	3328.561	3337.566	3338.564	3342.514	3356.565
3357.538	3368.596	3382.544	3391.551	3402.564	3403.554
3417.496	3418.516	3432.566	3433.559	3441.529	3442.556
3447.540	3448.551	3455.578	3465.561	3470.531	3471.546
3489.597	3494.597	3495.569	3510.597	3517.599	3526.610
3534.614	3545.624	3551.615	3565.636	3577.615	3587.635
3595.643	3603.651	3614.657	3632.665	3638.649	3649.666
3661.645	3677.632	3681.690	3692.642	3708.671	3721.653
3727.671	3739.684	3751.699	3756.698	3762.694	3776.689
3781.668	3794.692	3814.726	3826.743	3835.720	3843.704
4055.855	4084.834	4096.941	4107.760	4127.896	4149.951
4158.885	4187.870	4198.890	4216.711	4229.937	4255.002

	4457.620 4474.910 4500.772 4517.695
Tolerance (mon)	18.00 ppm
Number of Peptides	232

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	6.6×10^{-5}	gi|13929146|ref|NP_113996.1| calpain 6 [Rattus norvegicus]	12	6.9	77.18	◉
+2	6.3×10^{-3}	gi|13242186|gb|AAK16592.1|AF346902_1 glycogen synthase [Rattus norvegicus]	9	6.6	83.06	◉
	-	gi|6981002|ref|NP_037221.1| glycogen synthase 2 [Rattus norvegicus]	6	6.5	82.81	◉
3	7.8×10^{-3}	gi|50233797|ref|NP_899162.1| keratin 5 (epidermolysis bullosa simplex, Dowling-Meara/Kobner/Weber-Cockayne types) [Rattus norvegicus]	11	6.9	63.22	◉
4	0.14	gi|16758432|ref|NP_446077.1| G elongation factor [Rattus norvegicus]	6	7.0	86.48	◉

NOTE:

1. To search again using unmatched masses, click the symbol ◉.
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A2BFF966-177C-A3887EC6
Sequences 20076
Date & Time Sat Feb 03 02:10:38 2007 UTC (Search Time: 0.34 sec.)
Sample ID
Database NCBInr [..\databases\nr]
Taxonomy Rattus
Mass Range 63 - 94 kDa
pI Range 6.5 -7.5
Digestion Trypsin

Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +CH2N2@K(Complete);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	664.342 791.414 823.439 991.520 1046.505 1063.513 1091.541 1113.594 1193.573 1211.587 1220.599 1224.589 1233.639 1241.688 1248.605 1262.621 1280.629 1291.617 1310.631 1323.655 1330.599 1333.641 1456.704 1529.740 1542.761 1560.774 1602.797 1779.860 1808.826 1894.875 1904.806 2191.078 2209.099 2225.110 2291.145 2315.114 2316.123 2364.145 2365.161 2380.166 2381.158 2392.198 2397.162 2398.163 2408.139 2419.163 2420.164 2435.196 2460.165 2466.177 2467.210 2483.208 2484.207 2504.119 2535.171 2536.187 2562.194 2593.174 2610.191 2632.151 2633.156 2650.213 2674.189 2691.215 2692.198 2723.225 2787.254 3052.335 3053.308 3060.388 3061.388 3068.358 3069.334 3077.412 3084.354 3085.342 3092.396 3102.395 3103.398 3111.369 3112.346 3134.402 3135.406 3172.436 3173.425 3210.461 3220.460 3230.495 3265.506 3266.486 3277.473 3283.488 3292.487 3316.498 3329.524 3331.519 3337.438 3338.513 3345.398 3346.504 3353.506 3354.498 3372.487 3373.509 3384.525 3396.453 3398.485 3416.520 3518.623 3635.598 3651.597 3666.633 3677.679 3683.612 3693.624 3708.755 3744.653 3758.694 3800.643
Tolerance (mon)	12.00 ppm
Number of Peptides	119

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	7.7×10^{-30}	gi|13786202|ref|NP_112644.1| voltage-dependent anion channel 2 [Rattus norvegicus]	15	7.7	33.32	
	-	gi|299036|gb|AAB26053.1| B-36 VDAC=36 kda voltage dependent anion channel [rats, hippocampus, Peptide, 295 aa]	15	7.7	33.30	
2	4.7×10^{-14}	gi|1934603|gb|AAB51724.1| RN protein [Rattus norvegicus]	15	6.1	39.40	
+3	2.9×10^{-12}	gi|9845234|ref|NP_063970.1| annexin A2 [Rattus norvegicus]	9	7.7	40.33	
	-	gi|2143593|pir||S55277 annexin II - rat	9	8.3	40.63	
	-	gi|9247201|gb|AAB31934.2| annexin II [Rattus sp.]	9	8.3	40.42	
4	1.1×10^{-11}	gi|13027414|ref|NP_076454.1| glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Rattus norvegicus]	13	8.7	48.43	
5	2.1×10^{-9}	gi|27462661|gb|AAO15540.1|AF459022_1 ZAKI-4 alpha [Rattus norvegicus]	29	6.2	22.83	
6	2.3×10^{-8}	gi|56605708|ref|NP_001008315.1| makorin, ring finger protein, 2 [Rattus norvegicus]	11	7.3	49.32	
7	5.7×10^{-8}	gi|47577209|ref|NP_001000754.1| olfactory receptor Olr363 [Rattus norvegicus]	17	7.9	36.18	
8	9.3×10^{-8}	gi|11693160|ref|NP_071785.1| quinoid dihydropteridine reductase [Rattus norvegicus]	21	7.9	26.39	
9	1.2×10^{-7}	gi|47576063|ref|NP_001000007.1| olfactory receptor Olr1422 [Rattus norvegicus]	16	8.7	36.17	
10	2.4×10^{-7}	gi|16758274|ref|NP_445964.1| peroxiredoxin 4 [Rattus norvegicus]	14	6.2	31.89	
11	3.1×10^{-7}	gi|34932585|ref|XP_214526.2| PREDICTED: similar to zinc binding alcohol dehydrogenase, domain containing 2 [Rattus norvegicus]	12	7.8	41.63	
12	3.4×10^{-7}	gi|22652804|gb|AAN03824.1| aldehyde reductase AFAR2 subunit [Rattus norvegicus]	8	7.9	41.63	
13	4.5×10^{-7}	gi|34881169|ref|XP_223005.2| PREDICTED: similar to degenerative spermatocyte homolog 1 [Rattus norvegicus]	13	7.9	38.83	
14	4.7×10^{-7}	gi|47576395|ref|NP_001000046.1| olfactory receptor Olr1563 [Rattus norvegicus]	18	8.8	36.57	
15	2.4×10^{-6}	gi|6166481|gb|AAF04850.1| claudin-1 [Rattus norvegicus]	7	7.8	23.55	
16	5.5×10^{-6}	gi|226008|prf||1405343A phosphorylase kinase gamma	7	6.1	46.33	

17	5.5×10^{-6}	gi|13928776|ref|NP_113761.1| phosphorylase kinase, gamma 1 [Rattus norvegicus]	7	6.1	46.46	
18	6.9×10^{-6}	gi|6689099|emb|CAB65388.1| MASP-2 protein [Rattus norvegicus]	4	6.2	41.57	
19	8.8×10^{-6}	gi|47168545|pdb|1PK8|A Chain A, Crystal Structure Of Rat Synapsin I C Domain Complexed To Ca.Atp	10	7.9	46.65	
20	1.2×10^{-5}	gi|27689567|ref|XP_213467.1| PREDICTED: similar to CG15735-PA [Rattus norvegicus]	15	7.8	22.68	
21	1.7×10^{-5}	gi|1134884|emb|CAA62607.1| ligand gated ATP receptor [Rattus norvegicus]	6	8.4	45.26	
22	1.7×10^{-5}	gi|1709521|sp|P51577|P2RX4_RAT P2X purinoceptor 4 (ATP receptor) (P2X4) (Purinergic receptor)	6	8.4	45.25	
23	1.7×10^{-5}	gi|13928806|ref|NP_113782.1| purinergic receptor P2X4 [Rattus norvegicus]	6	8.7	45.18	
24	2.0×10^{-5}	gi|56090628|ref|NP_001007667.1| BCS1-like [Rattus norvegicus]	4	8.5	48.09	
25	2.0×10^{-5}	gi|1161345|gb|AAC52380.1| P2X4 ATP-gated channel subunit	6	8.7	45.33	
26	3.0×10^{-5}	gi|14389301|ref|NP_112650.1| sphingomyelin phosphodiesterase 2, neutral [Rattus norvegicus]	7	6.6	49.42	
27	3.8×10^{-5}	gi|51260852|gb|AAH79474.1| Mamdc2 protein [Rattus norvegicus]	14	6.2	28.89	
28	7.8×10^{-5}	gi|22219456|ref|NP_671746.1| alpha-2u globulin PGCL5 [Rattus norvegicus]	15	6.1	21.76	
29	3.8×10^{-4}	gi|27702700|ref|XP_215785.1| PREDICTED: similar to APAF1 interacting protein [Rattus norvegicus]	15	6.5	28.32	
30	8.4×10^{-4}	gi|2851469|sp|P38406|GNAL_RAT Guanine nucleotide-binding protein G(olf) subunit alpha (Adenylate cyclase-stimulating G alpha protein, olfactory type)	6	6.2	45.92	
31	8.4×10^{-4}	gi|235879|gb|AAB19866.1| lipocortin I [Rattus sp.]	5	7.0	40.45	
32	8.4×10^{-4}	gi|6978501|ref|NP_037036.1| annexin 1 [Rattus norvegicus]	5	7.0	40.46	
33	9.2×10^{-4}	gi|5669929|gb|AAD46521.1|AF154914_1 cyclin H [Rattus norvegicus]	10	7.1	39.10	
34	1.1×10^{-3}	gi|19865045|sp|Q9R1A0|CCNH_RAT Cyclin-H	10	6.7	39.10	
35	1.2×10^{-3}	gi|31542350|ref|NP_443213.2| cyclin H [Rattus norvegicus]	10	7.1	39.22	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B199B808-08A8-61B127F9

Sequences 20092

Date & Time Mon Jan 29 18:39:11 2007 UTC (Search Time: 0.34 sec.)

Sample ID 20061228 richardson NIA set 1 spot 6312, 20070128, cleaned data search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 50 kDa

pI Range 6.0 -9.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 605.335 654.392 662.306 678.347 719.383 722.778 724.771 734.377 753.802
791.407 797.854 824.493 832.307 866.484 913.458 948.524 955.505 976.497
990.545 999.546 1005.530 1009.439 1058.606 1071.564 1113.597 1137.557
1145.558 1219.613 1224.582 1262.605 1280.631 1323.652 1330.599 1335.667
1357.611 1470.708 1482.747 1529.738 1543.735 1559.766 1601.772 1624.761
1630.752 1642.777 1695.787 1713.813 1751.837 1756.838 1779.866 1790.815
1795.860 1808.814 1836.865 1856.865 1893.880 1904.822 1908.887 1920.876
1930.916 1935.892 1947.930 1957.939 1962.906 1965.909 2012.934 2021.937
2036.968 2037.977 2045.963 2046.972 2051.956 2062.984 2096.968 2121.989
2124.019 2173.032 2179.058 2180.066 2191.088 2209.092 2251.154 2314.120
2315.105 2324.163 2339.176 2341.192 2348.171 2349.181 2365.172 2366.169
2376.199 2377.214 2390.208 2392.229 2408.148 2419.186 2420.185 2433.192
2448.143 2460.170 2467.191 2481.168 2482.177 2487.235 2497.184 2504.159
2505.124 2536.169 2544.207 2545.173 2552.197 2553.177 2560.207 2562.205
2577.229 2593.191 2610.203 2611.163 2631.200 2632.175 2649.215 2650.186
2656.218 2657.153 2666.214 2667.194 2673.243 2674.178 2680.231 2681.222
2691.200 2692.201 2700.219 2701.226 2712.243 2713.234 2723.232 2724.232
2732.230 2733.244 2743.278 2744.252 2759.201 2760.263 2776.258 2777.314
2785.301 2786.292 2800.284 2801.287 2804.246 2805.271 2816.252 2818.279
2832.259 2833.286 2837.291 2838.307 2848.294 2849.295 2868.358 2884.325
2885.304 2896.324 2905.404 2914.355 2922.347 2948.345 2949.338 2964.231
2965.315 2977.355 2978.330 2994.271 2995.346 2999.305 3000.426 3011.325
3012.334 3020.390 3028.352 3029.566 3047.570 3052.323 3054.335 3061.397
3068.366 3069.343 3084.364 3085.365 3092.350 3102.399 3103.411 3111.382
3112.371 3172.443 3173.426 3181.450 3182.438 3198.491 3211.469 3220.456
3228.486 3233.441 3234.475 3244.481 3245.499 3250.457 3260.479 3276.492
3277.456 3292.439 3301.533 3307.497 3308.506 3313.443 3314.491 3329.542
3330.555 3342.503 3347.567 3356.531 3357.522 3372.487 3373.504 3378.413
3379.494 3390.531 3395.553 3396.525 3408.518 3410.471 3417.451 3418.571
3431.542 3432.571 3440.583 3445.551 3446.492 3462.650 3463.501 3469.475
3470.559 3477.500 3486.590 3487.643 3509.638 3520.635 3524.625 3534.636
3539.563 3548.616 3554.580 3567.646 3579.568 3584.608 3618.618 3638.622
3651.635 3665.623 3679.609 3698.654 3709.744 3725.649 3730.697 3739.706
3751.648 3756.703 3768.670 3773.746 3780.748 3787.732 3800.726 3817.705
3825.712 3834.617 3860.734 3884.813 4095.872 4226.614

Tolerance (mon) 15.00 ppm

Number of Peptides 280

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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- X! Hunter
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New York, NY 10021
(212) 327-8000

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	2.0×10^{-8}	gi|458333|gb|AAA19133.1| protein tyrosine phosphatase	36	6.9	70.80	
	-	gi|6981444|ref|NP_037220.1| protein tyrosine phosphatase, non-receptor type 11 [Rattus norvegicus]	36	6.9	70.48	
2	3.7×10^{-8}	gi|50926240|gb|AAH79209.1| Coronin, actin binding protein 2A [Rattus norvegicus]	34	7.0	61.59	
	-	gi|29293813|ref|NP_808789.1| pre-B-cell colony enhancing factor 1 [Rattus norvegicus]	41	6.7	57.64	
	-	gi|16758354|ref|NP_446034.1| lipocalin 7 [Rattus norvegicus]	37	6.5	54.55	
	-	gi|53850604|ref|NP_001005540.1| protein phosphatase 2C zeta [Rattus norvegicus]	30	7.2	56.46	
	-	gi|1708153|sp|P50545|HCK_RAT Tyrosine-protein kinase HCK (p56-HCK) (Hemopoietic cell kinase)	30	6.8	59.02	
	-	gi|57582|emb|CAA44218.1| protein-tyrosine kinase [Rattus rattus]	30	6.8	58.95	
	-	gi|34734058|ref|NP_037317.2| hemopoietic cell kinase [Rattus norvegicus]	29	7.2	61.27	
	-	gi|55741778|ref|NP_001006998.1| sphingomyelin phosphodiesterase 1, acid lysosomal [Rattus norvegicus]	24	7.1	71.51	
	-	gi|52138739|ref|NP_001004443.1| hexosaminidase A [Rattus norvegicus]	33	6.9	62.06	
	-	gi|202553|gb|AAA40622.1| 60 kDa protein	30	6.6	61.40	
	-	gi|349096|gb|AAA42095.1| transcription factor	28	7.0	57.21	
	-	gi|48686583|gb|AAT46047.1| hypothetical protein [Rattus norvegicus]	22	6.5	66.74	

-	gi|41054868|ref|NP_955788.1| fucose-1-phosphate guanylyltransferase [Rattus norvegicus]	25	7.0	68.14
-	gi|34932038|ref|XP_225891.2| PREDICTED: similar to chloride ion pump-associated 55 kDa protein [Rattus norvegicus]	26	7.2	55.67
-	gi|56789277|gb|AAH88187.1| Coagulation factor XII (Hageman factor) [Rattus norvegicus]	23	7.2	69.99
-	gi|16757994|ref|NP_445749.1| pyruvate kinase, muscle [Rattus norvegicus]	33	6.6	59.83
-	gi|47933915|gb|AAT39522.1| ankyrin repeat and SOCS box-containing protein 4 [Rattus norvegicus]	24	7.1	50.34
-	gi|203695|gb|AAA41007.1| cytochrome P450	34	7.2	59.00
-	gi|206205|gb|AAB93667.1| M2 pyruvate kinase [Rattus norvegicus]	27	7.2	59.89
-	gi|92061|pir||A31948 carnitine octanoyltransferase, hepatic - rat	23	6.8	62.57
-	gi|2493792|sp|Q63514|C4BP_RAT C4b-binding protein alpha chain precursor (C4bp)	13	7.2	65.82
-	gi|16758600|ref|NP_446216.1| regulator of G-protein signaling 14 [Rattus norvegicus]	22	7.2	61.16
-	gi|48428187|sp|P62024|PHAR1_RAT Phosphatase and actin regulator 1	21	6.6	68.21
-	gi|38328492|gb|AAH62243.1| LOC303057 protein [Rattus norvegicus]	22	7.0	61.33
-	gi|42627865|ref|NP_976081.1| estrogen-related receptor gamma [Rattus norvegicus]	13	6.7	50.73

NOTE:

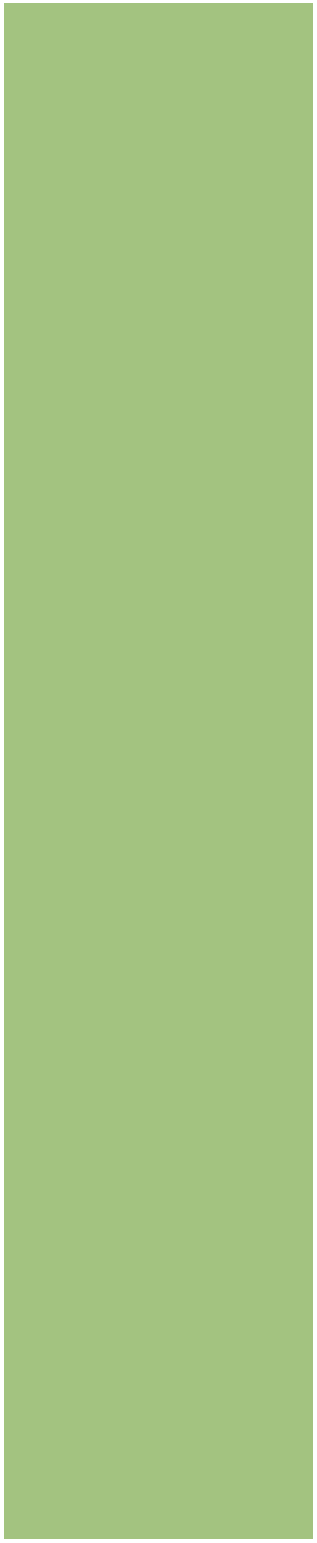
1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

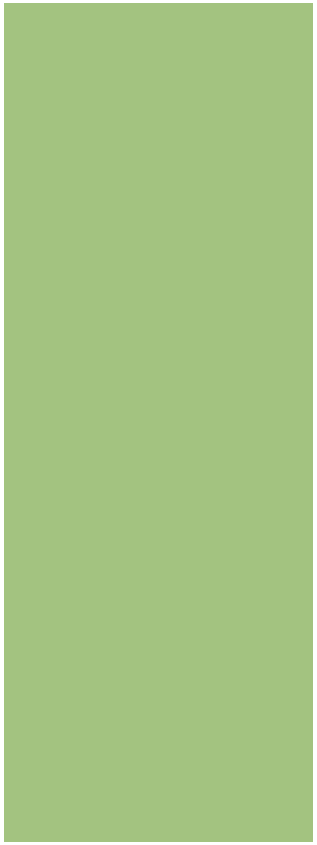
Search id AA174277-1028-5A312056

Sequences 20092

Date & Time Wed Jan 31 14:53:20 2007 UTC (Search Time: 0.49 sec.)



Sample ID	
Database	NCBInr [..\databases\nr]
Taxonomy	Rattus
Mass Range	50 - 72 kDa
pI Range	6.5 -7.5
Digestion	Trypsin
Missed Cuts	1
Modifications	+C2H3ON@C(Complete); +O@M(Partial); +HPO3@TY (Partial); +CH2N2@K(Complete);
Charge State	MH+
Masses (avg)	
Tolerance (avg)	1.00 ppm
Masses (mon)	841.459 1091.562 1280.642 1313.624 1756.843 1780.851 1828.868 1837.857 1871.876 1895.879 1904.886 1908.892 1930.913 1934.903 1949.913 1964.913 1983.939 2005.935 2006.937 2017.937 2018.944 2021.939 2035.958 2036.956 2038.948 2039.958 2042.961 2043.971 2046.962 2047.968 2053.968 2054.971 2070.992 2098.996 2116.011 2124.017 2150.026 2183.097 2209.088 2241.127 2242.145 2266.154 2298.154 2306.156 2363.136 2364.130 2373.148 2374.173 2390.145 2397.131 2399.146 2405.150 2435.210 2436.189 2447.166 2448.184 2460.166 2463.186 2464.194 2497.190 2507.197 2514.184 2537.203 2538.202 2547.210 2548.202 2557.195 2558.213 2577.228 2591.213 2594.213 2595.212 2602.239 2603.216 2606.227 2607.235 2613.217 2614.232 2622.220 2638.236 2639.242 2648.235 2649.236 2655.257 2656.236 2667.239 2668.231 2679.256 2685.234 2686.230 2690.266 2691.248 2699.261 2700.260 2714.266 2715.268 2718.252 2719.257 2724.278 2725.269 2732.278 2733.293 2743.288 2744.270 2750.291 2751.309 2756.299 2757.270 2769.310 2770.251 2778.301 2779.290 2784.307 2785.300 2789.277 2790.304 2803.303 2804.284 2819.323 2820.326 2832.317 2839.341 2840.306 2850.326 2866.322 2875.300 2876.301 2882.319 2898.356 2904.337 2914.362 2922.348 2937.371 2949.355 2950.363 2962.372 2963.372 2967.368 2978.369 2979.341 2985.404 2995.418 2996.390 3000.435



	3001.399 3010.391 3011.409 3018.372 3030.493 3047.465 3048.473 3060.423 3065.393 3077.458 3094.472 3095.494 3105.444 3112.442 3138.467 3147.436 3148.469 3179.460 3188.469 3196.455 3202.477 3203.459 3212.488 3214.484 3220.483 3230.491 3244.480 3245.481 3253.464 3260.490 3283.499 3290.497 3291.531 3301.544 3308.536 3309.552 3318.533 3319.510 3328.530 3329.477 3337.562 3347.525 3348.547 3368.583 3384.551 3390.539 3391.552 3398.542 3399.541 3405.564 3417.535 3423.524 3424.541 3428.567 3429.556 3447.540 3448.553 3465.580 3466.569 3474.562 3475.558 3480.588 3481.544 3487.619 3488.580 3493.561 3498.529 3507.606 3516.616 3524.562 3530.586 3536.630 3543.603 3553.598 3563.593 3583.572 3594.646 3601.657 3620.617 3654.615 3662.682 3676.691 3695.660 3718.637 3726.640 3742.690 3986.792 4189.949 4209.995 4219.903 4457.271 4476.357 4501.479
Tolerance (mon)	26.00 ppm
Number of Peptides	237

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

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ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	4.0×10^{-26}	gi|40538860|ref|NP_077374.2| aconitase 2, mitochondrial [Rattus norvegicus]	12	8.2	88.39	
	-	gi|10637996|emb|CAC11018.1| mitochondrial aconitase [Rattus norvegicus]	11	8.2	88.43	
+2	1.2×10^{-10}	gi|34870506|ref|XP_340764.1| PREDICTED: similar to cyclin F [Rattus norvegicus]	9	6.4	90.42	
	-	gi|21311259|gb|AAM46626.1| cyclin F [Rattus norvegicus]	7	6.5	86.70	
3	1.1×10^{-5}	gi|50926941|gb|AAH79073.1| Mitogen-activated protein kinase associated protein 1 [Rattus norvegicus]	9	7.3	61.35	
+4	3.0×10^{-5}	gi|112393|pir||S09178 thyroid hormone receptor alpha - rat	13	8.8	49.36	
	-	gi|55932|emb|CAA31237.1| c-erb-A thyroid hormone receptor [Rattus norvegicus]	14	8.5	47.84	
5	3.8×10^{-5}	gi|55250416|gb|AAH85812.1| Neural precursor cell expressed, developmentally down-regulated gene 9 [Rattus norvegicus]	9	6.0	95.60	
6	7.6×10^{-5}	gi|3493139|gb|AAC33292.1| kinesin-like protein KIF1B [Rattus norvegicus]	8	6.0	80.16	
7	9.1×10^{-5}	gi|55715679|gb|AAH85890.1| Peptidylprolyl isomerase (cyclophilin)-like 2 [Rattus norvegicus]	10	8.9	61.50	
8	9.5×10^{-5}	gi|47605759|sp|Q8R500|MFN2_RAT Transmembrane GTPase MFN2 (Mitofusin-2) (Mitochondrial transmembrane GTPase FZO1A) (Protein HSG)	8	6.5	88.61	
+9	1.0×10^{-4}	gi|206175|gb|AAA41868.1| protein kinase C beta-1	10	6.5	80.45	
	-	gi|55977078|sp|P68403|KPCB_RAT Protein kinase C beta type (PKC-beta) (PKC-B)	10	6.6	80.35	
10	2.0×10^{-4}	gi|41055880|ref|NP_570964.3| hypertension-related protein [Rattus norvegicus]	6	6.4	88.61	
11	2.0×10^{-4}	gi|53850626|ref|NP_001005549.1| tubulointerstitial nephritis antigen [Rattus norvegicus]	8	8.8	56.46	
12	4.2×10^{-4}	gi|13928912|ref|NP_113847.1| transglutaminase type 1 [Rattus norvegicus]	7	6.0	92.80	
13	2.1×10^{-3}	gi|56971343|gb|AAH88275.1| Nucleolar complex associated 4 homolog (S. cerevisiae) [Rattus norvegicus]	12	6.4	60.44	
14	0.034	gi|44890250|gb|AAH66665.1| Transglutaminase 4 (prostate) [Rattus norvegicus]	9	8.5	78.00	

NOTE:

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2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A9C2F862-107C-59DD2025

Sequences 20092

Date & Time Wed Jan 31 20:08:02 2007 UTC (Search Time: 0.38 sec.)

Sample ID 20061228 richardson NIA set 1 spot 6820 , 20070131, cleaned data search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 45 - 100 kDa

pI Range 6.0 -9.0

Digestion Trypsin

Missed Cuts 0

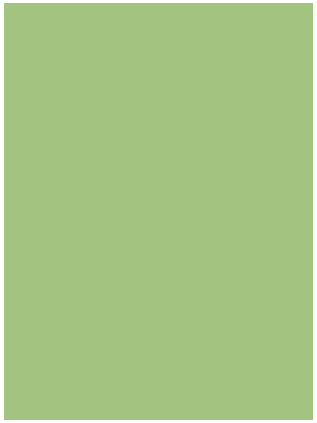
Modifications +C2H3ON@C(Complete); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 648.387 663.329 832.310 991.515 1145.598 1194.589 1199.657 1211.588
1220.599 1224.602 1241.702 1248.613 1257.586 1262.627 1268.617 1277.630
1280.644 1291.616 1310.632 1330.604 1463.726 1500.747 1514.793 1525.751
1530.741 1536.733 1542.777 1547.754 1553.798 1557.775 1568.751 1572.768
1581.737 1589.762 1599.766 1601.784 1630.768 1639.747 1643.779 1653.760
1679.771 1684.808 1695.786 1713.805 1720.819 1744.835 1761.850 1765.837
1779.857 1784.841 1796.882 1803.881 1838.857 1868.905 1879.864 1896.885
1899.904 1908.886 1931.914 1948.926 1957.918 1964.913 2005.937 2006.929
2017.940 2018.938 2023.953 2033.939 2035.966 2038.955 2039.968 2045.968
2046.973 2049.965 2050.962 2072.993 2099.001 2100.004 2125.013 2126.017
2152.051 2183.079 2201.122 2209.089 2242.139 2243.145 2291.154 2306.144
2316.149 2317.151 2364.156 2365.167 2375.161 2381.183 2382.168 2390.161
2401.162 2402.157 2405.170 2419.171 2420.162 2428.169 2429.166 2436.185
2437.196 2446.178 2447.161 2460.170 2479.184 2497.195 2506.171 2507.198
2513.207 2514.190 2533.189 2534.204 2536.212 2537.206 2551.204 2552.218
2556.184 2557.202 2561.221 2562.214 2574.203 2591.193 2604.198 2605.221
2632.234 2633.201 2638.238 2639.239 2647.240 2648.232 2666.215 2668.220
2675.243 2677.235 2678.233 2690.252 2692.260 2718.272 2719.260 2723.266
2724.277 2733.257 2734.267 2743.279 2751.267 2752.303 2762.267 2763.309
2780.395 2786.312 2787.302 2795.285 2804.313 2822.408 2837.326 2849.314
2850.325 2865.351 2866.332 2879.319 2894.371 2906.396 2924.352 2931.364
2937.362 2943.384 2944.404 2959.368 2960.371 2967.354 2977.351 2978.409
2985.404 2986.430 3001.411 3002.407 3010.376 3011.382 3020.368 3030.478
3063.429 3064.396 3077.440 3105.439 3122.433 3136.416 3147.477 3148.479
3180.481 3181.475 3210.463 3211.467 3220.481 3227.465 3243.488 3244.493



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3385.515	3387.517	3399.517	3400.531	3404.543	3405.540	3417.485	3418.533
3433.549	3434.569	3440.490	3441.534	3450.600	3462.580	3464.496	3476.560
3477.559	3481.602	3482.556	3499.571	3510.612	3516.641	3527.594	3540.585
3554.583	3560.635	3564.595	3576.620	3589.696	3597.625	3613.587	3620.595
3634.643	3651.669	3662.641	3667.676	3683.675	3692.671	3696.691	3711.662
3720.675	3728.715	3738.667	3744.720	3756.753	3769.697	3779.705	3790.724
3798.751	3805.757	3822.734	3842.706	3849.729	3871.728	3883.792	4164.883
4174.840	4181.801	4209.980					

Tolerance (mon) 16.00 ppm

Number of Peptides 275

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- PepFrag
- X! Tandem
- X! Hunter
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Macromolecules

ProFound

Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	3.0×10^{-21}	gi|3915863|sp|P52847|ST1B1_RAT Sulfotransferase family cytosolic 1B member 1 (Sulfotransferase 1B1) (DOPA/tyrosine sulfotransferase)	28	8.4	36.39	
	-	gi|11968092|ref|NP_071958.1| sulfotransferase family 1B, member 1 [Rattus norvegicus]	21	8.7	36.32	
2	1.4×10^{-7}	gi|56268926|gb|AAH87146.1| Nit1 protein [Rattus norvegicus]	14	6.6	37.15	
3	1.4×10^{-7}	gi|57164003|ref|NP_001009175.1| tripartite motif-containing 40 [Rattus norvegicus]	11	6.8	29.79	
4	1.9×10^{-7}	gi|34881169|ref|XP_223005.2| PREDICTED: similar to degenerative spermatocyte homolog 1 [Rattus norvegicus]	11	7.9	38.83	
5	9.9×10^{-7}	gi|34870345|ref|XP_233430.2| PREDICTED: similar to T-cell acute lymphocytic leukemia-1 protein homolog (TAL-1 protein) (Stem cell protein) [Rattus norvegicus]	5	8.0	35.13	
6	1.0×10^{-6}	gi|47577415|ref|NP_001000291.1| olfactory receptor Olr455 [Rattus norvegicus]	8	7.8	36.16	
7	1.0×10^{-6}	gi|1228944|dbj|BAA11433.1| protein tyrosine phosphatase epsilon M [Rattus norvegicus]	12	7.0	35.53	
8	1.4×10^{-6}	gi|204456|gb|AAA41269.1| Heymann nephritis antigen gp330	8	7.1	38.84	
9	1.8×10^{-6}	gi|55550|emb|CAA78040.1| 45kDa protein [Rattus norvegicus]	7	6.9	43.31	
10	2.0×10^{-6}	gi|51980664|gb|AAH82020.1| Lrpap1 protein [Rattus norvegicus]	7	6.9	43.61	
11	9.0×10^{-6}	gi|32395723|gb|AAP37958.1| T-cell receptor beta chain [Rattus norvegicus]	9	8.8	34.92	
12	0.42	gi|7637875|gb|AAF65233.1|AF212861_1 membrane interacting protein of RGS16 [Rattus norvegicus]	11	6.4	38.60	

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

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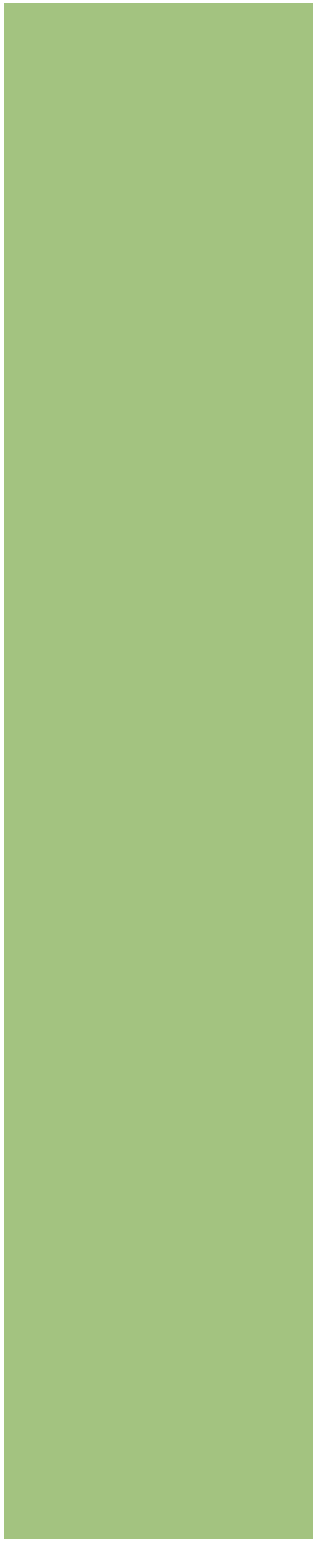
Sequences 20092

Date & Time Mon Jan 29 19:46:06 2007 UTC (Search Time: 0.33 sec.)



Sample ID 20061228 richardson NIA set 1 spot 7403, 20070128, cleaned data search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 25 - 50 kDa

pI Range 6.4 -8.8

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 654.388 719.381 734.378 806.421 824.495 904.440 918.463 948.522 955.496
990.543 1003.552 1058.501 1080.495 1217.637 1219.617 1224.582 1226.586
1244.591 1248.607 1257.751 1262.612 1271.565 1280.612 1290.609 1313.636
1330.600 1357.610 1446.719 1454.731 1529.737 1543.729 1557.776 1602.802
1628.927 1653.924 1670.949 1685.802 1743.794 1751.821 1757.842 1762.810
1765.802 1791.818 1808.834 1837.856 1851.832 1874.872 1880.901 1888.879
1890.860 1897.922 1904.849 1908.883 1913.892 1932.895 1950.916 1959.921
1964.894 1987.931 2000.913 2001.919 2004.895 2005.920 2012.950 2016.909
2017.903 2023.948 2033.924 2034.925 2037.946 2038.957 2050.945 2051.950
2066.000 2070.961 2074.957 2075.963 2099.007 2132.021 2150.030 2159.029
2180.047 2181.070 2234.129 2309.158 2349.137 2351.146 2367.135 2368.128
2382.175 2383.170 2392.158 2397.145 2398.160 2415.114 2416.084 2433.143
2440.166 2441.171 2448.133 2458.132 2466.176 2467.183 2486.167 2497.158
2503.166 2504.134 2517.172 2534.131 2535.174 2547.162 2555.143 2562.169
2574.159 2577.152 2591.177 2610.190 2611.189 2635.185 2636.195 2651.198
2652.203 2664.166 2665.185 2669.222 2670.215 2680.198 2681.203 2689.195
2690.184 2719.226 2721.206 2730.210 2731.209 2744.229 2745.216 2763.241
2764.231 2776.271 2777.261 2785.223 2786.240 2795.254 2796.261 2804.250
2805.246 2818.279 2819.252 2824.174 2825.260 2831.253 2833.246 2836.296
2837.277 2849.261 2850.294 2889.315 2890.307 2906.302 2914.301 2921.304
2950.289 2963.295 2964.301 2980.302 2981.335 3004.348 3011.370 3012.325
3020.345 3029.357 3030.532 3033.369 3034.363 3047.352 3048.492 3053.337
3062.376 3063.381 3077.382 3084.359 3085.354 3092.399 3105.406 3110.392
3111.385 3135.409 3136.422 3147.445 3149.444 3181.442 3182.439 3198.454
3212.469 3213.457 3228.455 3266.451 3275.474 3276.475 3281.460 3292.464
3314.477 3329.580 3340.522 3356.507 3357.481 3373.400 3374.482 3383.500
3396.501 3397.488 3408.499 3409.522 3420.518 3434.517 3435.501 3446.507
3447.512 3449.465 3458.553 3459.528 3464.579 3474.452 3475.529 3486.568
3487.558 3500.571 3510.555 3519.577 3526.578 3536.580 3549.570 3554.584
3558.561 3564.552 3574.607 3590.605 3595.616 3606.565 3611.587 3618.601
3652.608 3663.652 3667.609 3684.617 3698.680 3710.674 3722.640 3729.602
3740.628 3753.670 3761.639 3780.646 3787.720 3801.672 3812.718 3821.638

3837.673 4048.775 4094.747 4109.781

Tolerance (mon) 15.00 ppm

Number of Peptides 261

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- X! Hunter
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The Rockefeller University
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New York, NY 10021
(212) 327-8000

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
+1	1.3×10^{-31}	gi|120707|sp|P04797|G3P_RAT Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (38 kDa BFA-dependent ADP-ribosylation substrate) (BARS-38)	39	8.7	37.24	
	-	gi|8393418|ref|NP_058704.1| glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]	28	8.4	37.19	
	-	gi|56611127|gb|AAH87743.1| Glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]	21	8.4	37.15	
2	6.9×10^{-10}	gi|13027414|ref|NP_076454.1| glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Rattus norvegicus]	12	8.7	48.43	
3	1.0×10^{-9}	gi|51260852|gb|AAH79474.1| Mamdc2 protein [Rattus norvegicus]	17	6.2	28.89	
+4	1.1×10^{-9}	gi|50926816|gb|AAH78833.1| Phosphotriesterase related [Rattus norvegicus]	17	6.4	40.23	
	-	gi|3914481|sp|Q63530|PTER_RAT Phosphotriesterase-related protein (Parathion hydrolase-related protein) (Resiniferotoxin-binding phosphotriesterase-related protein)	17	6.1	40.01	
5	1.2×10^{-9}	gi|10644491|gb|AAG21310.1|AF271037_1 odorant receptor [Rattus norvegicus]	14	8.1	30.91	
6	6.8×10^{-8}	gi|12083663|ref|NP_073192.1| flotillin 1 [Rattus norvegicus]	13	7.1	41.12	
+7	4.4×10^{-7}	gi|38051964|gb|AAH60541.1| Txndc9 protein [Rattus norvegicus]	23	6.3	31.08	
	-	gi|21105482|gb|AAM34684.1|AF508022_1 ES cell-related protein [Rattus norvegicus]	24	6.6	30.32	
8	5.5×10^{-6}	gi|55932|emb|CAA31237.1| c-erb-A thyroid hormone receptor [Rattus norvegicus]	13	8.5	47.84	
9	1.2×10^{-5}	gi|6724176|gb|AAF26878.1|AF196232_1 T cell receptor V delta 6 [Rattus norvegicus]	14	7.8	28.45	
10	3.1×10^{-5}	gi|56789328|gb|AAH88205.1| Dual specificity phosphatase 2 [Rattus norvegicus]	17	6.3	35.43	
11	10.0×10^{-5}	gi|32478176|gb|AAP83441.1| GNAT acetytransferase [Rattus norvegicus]	6	7.2	28.28	
12	1.1×10^{-4}	gi|47577825|ref|NP_001000438.1| olfactory receptor Olr1214 [Rattus norvegicus]	18	7.1	35.65	
13	1.3×10^{-4}	gi|741803|prf||2008147A protein RAKb	13	7.9	38.13	
14	1.5×10^{-4}	gi|56605792|ref|NP_001008359.1| hypothetical protein LOC315286 [Rattus norvegicus]	12	6.3	29.57	

15	1.8×10^{-4}	gi|18041977|gb|AAL57768.1| hypothetical RNA binding protein RDA288 [Rattus norvegicus]	10	8.4	44.44	
16	1.8×10^{-4}	gi|57977275|ref|NP_659554.1| PAI-1 mRNA-binding protein [Rattus norvegicus]	10	8.4	44.41	
+17	1.9×10^{-4}	gi|56555|emb|CAA30528.1| unnamed protein product [Rattus norvegicus]	7	6.0	20.71	
	-	gi|2039340|gb|AAB52995.1| putative RNA binding protein 1 [Rattus norvegicus]	6	6.4	21.64	
18	2.1×10^{-4}	gi|27527649|emb|CAC81080.1| aflatoxin B1 aldehyde reductase [Rattus norvegicus]	9	6.1	38.52	
19	2.1×10^{-4}	gi|16758896|ref|NP_446442.1| protein tyrosine phosphatase, non-receptor type 2 [Rattus norvegicus]	12	8.9	43.53	
20	2.3×10^{-4}	gi|19705537|ref|NP_599234.1| aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase) [Rattus norvegicus]	9	6.3	38.53	
21	2.8×10^{-4}	gi|8393641|ref|NP_058889.1| aminoadipate aminotransferase [Rattus norvegicus]	12	8.4	49.29	
22	3.0×10^{-4}	gi|39930812|sp|Q8CG45|ARK72_RAT Aflatoxin B1 aldehyde reductase member 2 (rAFAR2)	8	8.9	41.66	
23	3.0×10^{-4}	gi|22652804|gb|AAN03824.1| aldehyde reductase AFAR2 subunit [Rattus norvegicus]	8	7.9	41.63	
24	3.2×10^{-4}	gi|12004240|gb|AAG43956.1|AF214647_1 ceramidase [Rattus norvegicus]	8	8.9	45.76	
25	3.2×10^{-4}	gi|40254747|ref|NP_445859.2| N-acylsphingosine amidohydrolase 1 [Rattus norvegicus]	8	8.9	45.83	
26	4.4×10^{-4}	gi|6981406|ref|NP_036762.1| prolactin receptor isoform b [Rattus norvegicus]	15	6.0	36.83	
27	7.9×10^{-4}	gi|2585995|gb|AAC95063.1| stathmin-like-protein splice variant RB3" [Rattus norvegicus]	8	8.6	26.75	
28	1.1×10^{-3}	gi|39930501|ref|NP_446228.1| zuotin related factor 2 [Rattus norvegicus]	11	6.2	33.92	
29	1.2×10^{-3}	gi|46359595|dbj|BAD15354.1| interleukin-1 receptor accessory protein [Rattus norvegicus]	23	6.4	25.13	
30	1.4×10^{-3}	gi|55391506|gb|AAH85357.1| Fgl2 protein [Rattus norvegicus]	5	6.7	49.60	
31	1.6×10^{-3}	gi|21326465|ref|NP_647552.1| UDP-glucuronate decarboxylase 1 [Rattus norvegicus]	6	9.0	48.86	
32	1.7×10^{-3}	gi|9507217|ref|NP_062052.1| thymidylate synthase [Rattus norvegicus]	5	6.0	35.96	
33	2.7×10^{-3}	gi|13925523|gb|AAK49392.1| NHE3 kinase A regulatory protein E3KARP [Rattus norvegicus]	9	6.7	35.76	
34	2.8×10^{-3}	gi|18652302|gb|AAL77056.1| SH2 phosphatase 1 [Rattus norvegicus]	6	9.0	36.97	
35	3.0×10^{-3}	gi|53734236|gb|AAH83684.1| Calcium binding protein 39-like [Rattus norvegicus]	7	8.6	40.87	
36	3.0×10^{-3}	gi|15077853|gb|AAK83379.1|AF395897_1 phosphatidylinositol 3-kinase alpha catalytic subunit [Rattus norvegicus]	5	7.3	35.24	
37	3.0×10^{-3}	gi|38511542|gb|AAH61802.1| Fibp protein [Rattus norvegicus]	9	6.3	42.47	
38	3.2×10^{-3}	gi|18034789|ref|NP_542151.1| phosphorylase kinase, gamma 2 (testis) [Rattus norvegicus]	10	6.4	47.77	

39	3.5×10^{-3}	gi|8393215|ref|NP_058770.1| CTL target antigen [Rattus norvegicus]	14	8.8	45.28
40	3.9×10^{-3}	gi|29293821|ref|NP_808793.1| platelet-activating factor acetylhydrolase 2 [Rattus norvegicus]	12	6.2	44.77
41	4.4×10^{-3}	gi|25992750|gb|AAN77242.1| immunophilin XAP2 [Rattus norvegicus]	7	6.1	39.06
42	6.0×10^{-3}	gi|8394076|ref|NP_058979.1| proteasome (prosome, macropain) subunit, alpha type 6 [Rattus norvegicus]	8	6.3	28.64
43	6.6×10^{-3}	gi|51260799|gb|AAH79367.1| Suclg2 protein [Rattus norvegicus]	4	7.7	48.57
44	9.8×10^{-3}	gi|1168286|sp|P15651|ACADS_RAT Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor (SCAD) (Butyryl-CoA dehydrogenase)	8	8.7	45.96
45	0.010	gi|11968090|ref|NP_071957.1| acyl-coenzyme A dehydrogenase, short chain [Rattus norvegicus]	7	8.7	46.16
46	0.013	gi|33638215|gb|AAQ24208.1| serine/threonine kinase 22A [Rattus norvegicus]	6	7.8	43.15
47	0.013	gi|112412|pir||B39533 transcription factor HNF-3 beta - rat	10	8.9	49.44
48	0.014	gi|57527408|ref|NP_001009599.1| ATP/GTP-binding protein [Rattus norvegicus]	7	6.2	49.06
49	0.025	gi|34853071|ref|XP_345133.1| PREDICTED: similar to C03A3.3 [Rattus norvegicus]	10	6.4	31.69

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id AE91AC89-0BB0-5EA924F1

Sequences 20092

Date & Time Mon Jan 29 19:15:18 2007 UTC (Search Time: 0.36 sec.)

Sample ID 20061228 richardson NIA set 1 spot 7410, 20070128, cleaned data search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 50 kDa

pI Range 6.0 -9.0

Digestion Trypsin

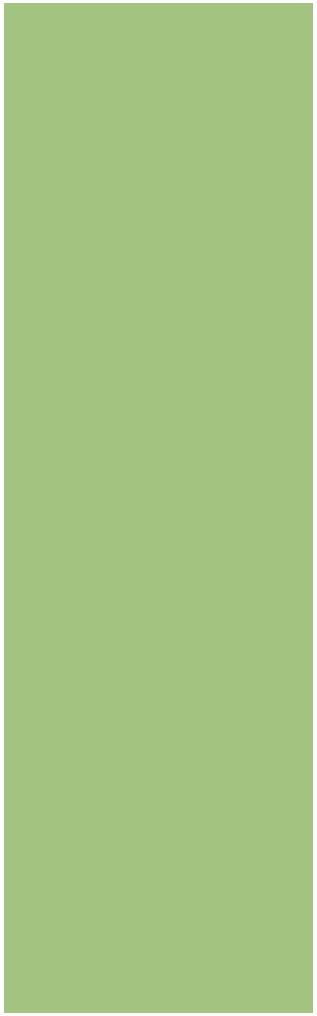
Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon) 632.256 634.272 646.273 654.391 660.288 662.303 677.306 684.283 699.222
719.378 724.766 725.773 747.409 802.260 804.273 811.412 817.420 824.494
830.290 832.305 847.316 854.284 862.282 876.272 884.345 894.224 912.512
918.461 948.521 976.546 990.542 1004.542 1028.540 1058.520 1075.572
1211.575 1215.637 1220.593 1224.580 1230.668 1233.649 1237.616 1239.726
1244.581 1257.751 1262.604 1301.615 1313.626 1316.620 1323.666 1330.600
1411.743 1432.691 1454.762 1497.755 1499.767 1538.780 1543.729 1556.800
1573.778 1610.921 1628.933 1652.937 1670.955 1685.938 1783.801 1791.789
1795.802 1808.804 1862.893 1879.870 1891.845 1897.909 1941.903 2152.047
2159.044 2172.049 2181.081 2222.120 2223.117 2242.136 2243.135 2286.128
2287.111 2306.142 2324.172 2365.133 2366.149 2378.128 2379.159 2392.139
2400.175 2401.172 2417.134 2425.181 2431.139 2432.117 2437.179 2442.184
2443.193 2452.173 2453.186 2460.175 2465.174 2466.175 2479.157 2483.178
2484.217 2502.238 2503.234 2511.266 2512.196 2526.223 2537.173 2538.193
2546.197 2547.232 2555.170 2556.225 2592.261 2593.262 2611.294 2612.336
2622.215 2628.177 2629.256 2635.290 2636.332 2653.352 2668.313 2669.330
2684.299 2685.317 2694.240 2695.237 2711.296 2722.258 2723.240 2733.234
2734.227 2741.247 2764.212 2924.366 2937.278 3028.389 3029.438 3034.365
3035.354 3041.365 3048.394 3049.396 3066.372 3067.379 3077.404 3084.405
3085.425 3095.432 3112.435 3136.459 3147.452 3148.486 3179.463 3187.435
3202.488 3211.481 3212.472 3220.511 3230.520 3242.460 3244.452 3260.501
3273.631 3274.464 3290.715 3297.434 3307.524 3308.579 3314.522 3336.666
3337.661 3353.679 3354.680 3369.585 3383.547 3399.525 3400.550 3417.554
3429.522 3435.592 3446.607 3447.522 3464.579 3465.701 3486.605 3488.572
3512.612 3549.620 3572.646 3726.717 3919.819 3936.791 3944.754 3957.812
3974.833 3985.899 3999.854 4004.776 4017.851 4033.831 4051.788 4057.891
4065.920 4076.891 4094.850 4109.868 4126.994 4138.845 4152.506 4172.142
4186.700 4193.258 4204.042 4504.430 4520.763 4564.889

Tolerance (mon) 22.00 ppm

Number of Peptides 225

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	7.2×10^{-34}	gi|125313|sp|P09605|KCRS_RAT Creatine kinase, sarcomeric mitochondrial precursor (S-MtCK) (Mib-CK) (Basic-type mitochondrial creatine kinase)	12	9.2	48.87	
+2	1.6×10^{-18}	gi|33112416|sp|Q8R415|PKR2_RAT Prokineticin receptor 2 (PK-R2) (G-protein coupled receptor 73-like 1) (G-protein coupled receptor I5E)	12	9.1	45.05	
	-	gi|20376824|ref|NP_620434.1| prokineticin receptor 2 [Rattus norvegicus]	11	8.9	49.38	
3	4.1×10^{-16}	gi|11560103|ref|NP_071613.1| caspase 8 [Rattus norvegicus]	13	5.3	57.68	
4	5.3×10^{-16}	gi|27704688|ref|XP_215924.1| PREDICTED: similar to ubiquitin-conjugating enzyme E2C [Rattus norvegicus]	17	6.8	20.34	
5	7.5×10^{-15}	gi|34857062|ref|XP_227247.2| PREDICTED: similar to protein phosphatase 1 (formerly 2C)-like [Rattus norvegicus]	10	5.6	42.30	
6	1.2×10^{-13}	gi|1587133|prf||2206275A neuronal Glu transporter EAAC1	9	5.8	56.97	
7	9.7×10^{-13}	gi|16758258|ref|NP_445951.1| mitochondrial transcription termination factor 1 [Rattus norvegicus]	9	9.8	44.47	
8	1.7×10^{-12}	gi|56788784|gb|AAH88432.1| Membrane targeting (tandem) C2 domain containing 1 [Rattus norvegicus]	6	9.5	57.38	
9	2.3×10^{-10}	gi|6002248|emb|CAB56708.1| elongation factor [Rattus rattus]	15	6.0	36.27	
10	3.2×10^{-10}	gi|47576821|ref|NP_001000117.1| olfactory receptor Olr19 [Rattus norvegicus]	16	9.7	36.94	
11	4.5×10^{-10}	gi|56057|emb|CAA42519.1| decorin [Rattus norvegicus]	12	9.2	40.09	
12	3.1×10^{-9}	gi|112412|pir||B39533 transcription factor HNF-3 beta - rat	12	8.9	49.44	
13	5.7×10^{-9}	gi|423679|pir||S33175 hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - rat (fragment)	14	9.3	25.96	

14	8.3×10^{-9}	gi|53733823|gb|AAH83596.1| Rexo1 protein [Rattus norvegicus]	11	9.5	58.82
15	8.6×10^{-9}	gi|205224|gb|AAA41535.1| link protein (0.8 kd)	11	9.8	33.86
16	1.4×10^{-8}	gi|55391462|gb|AAH85334.1| Similar to BRI3-binding protein [Rattus norvegicus]	19	9.4	28.72
17	2.2×10^{-8}	gi|15011855|ref|NP_058906.2| deiodinase, iodothyronine, type III [Rattus norvegicus]	15	6.3	32.09
18	2.2×10^{-8}	gi|1708507|sp|P49897|IOD3_RAT Type III iodothyronine deiodinase (Type-III 5' deiodinase) (DIOIII) (Type 3 DI) (5DIII)	15	6.3	32.25
19	2.3×10^{-8}	gi|1346731|sp|P03994|HPLN1_RAT Hyaluronan and proteoglycan link protein 1 precursor (Proteoglycan link protein) (Cartilage link protein) (LP)	13	8.7	41.63
20	2.4×10^{-8}	gi|46577139|sp|Q920M9|SIAH1_RAT E3 ubiquitin-protein ligase SIAH1 (Seven in absentia homolog 1) (Siah-1) (Siah-1a)	10	6.4	32.57
21	3.2×10^{-8}	gi|47577411|ref|NP_001000290.1| olfactory receptor Olr454 [Rattus norvegicus]	14	5.3	35.73
22	3.8×10^{-8}	gi|21542226|sp|Q99MS0|S14L2_RAT SEC14-like protein 2 (Alpha-tocopherol-associated protein) (TAP) (Supernatant protein factor) (SPF) (Squalene transfer protein)	10	7.1	48.08
23	4.7×10^{-8}	gi|53734557|gb|AAH83841.1| Kif2b protein [Rattus norvegicus]	7	9.9	42.74
24	5.1×10^{-8}	gi|16758454|ref|NP_446095.1| phosphatidate cytidylyltransferase 2 [Rattus norvegicus]	9	6.6	52.59
25	5.2×10^{-8}	gi|47168545|pdb|1PK8|A Chain A, Crystal Structure Of Rat Synapsin I C Domain Complexed To Ca.Atp	6	7.9	46.65
26	6.8×10^{-8}	gi|16758340|ref|NP_446020.1| phosphate cytidylyltransferase 2, ethanolamine [Rattus norvegicus]	8	6.2	46.68
27	9.3×10^{-8}	gi|50925459|gb|AAH78772.1| Pcyt2 protein [Rattus norvegicus]	9	6.4	44.89
28	1.1×10^{-7}	gi|51259441|gb|AAH79370.1| LOC498909 protein [Rattus norvegicus]	6	5.5	35.35
29	1.1×10^{-7}	gi|204617|gb|AAA41335.1| hepatic lipase precursor	6	8.9	57.64
30	1.1×10^{-7}	gi|56961643|ref|NP_036729.2| lipase, hepatic [Rattus norvegicus]	6	9.0	57.76

31	1.2×10^{-7}	gi|126310|sp|P07867|LIPC_RAT Hepatic triacylglycerol lipase precursor (Hepatic lipase) (HL) (Lipase member C)	6	8.9	57.59
32	1.4×10^{-7}	gi|27669155|ref|XP_234521.1| PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]	6	9.2	22.72
33	1.4×10^{-7}	gi|34878862|ref|XP_226016.2| PREDICTED: similar to Transcriptional activator protein Pur-alpha (Purine-rich single-stranded DNA-binding protein alpha) [Rattus norvegicus]	12	6.1	35.82
34	1.7×10^{-7}	gi|55250082|gb|AAH85831.1| F-box only protein 9 [Rattus norvegicus]	11	6.7	52.03
35	1.8×10^{-7}	gi|48428498|sp|P61943|SIA10_RAT Type 2 lactosamine alpha-2,3-sialyltransferase (CMP-NeuAc:beta-galactoside alpha-2,3-sialyltransferase VI) (ST3Gal VI) (Sialyltransferase 10)	8	9.7	39.87
36	1.9×10^{-7}	gi|204050|gb|AAA41122.1| c-erbA-alpha-2 protein	8	5.7	42.82
37	2.4×10^{-7}	gi|38454206|ref|NP_942025.1| proteasome, 26S, non-ATPase regulatory subunit 6 [Rattus norvegicus]	10	5.4	46.96
38	2.6×10^{-7}	gi|1085788|pir||S42633 Fit-1M protein - rat	5	9.5	29.34
39	4.0×10^{-7}	gi|55391506|gb|AAH85357.1| Fgl2 protein [Rattus norvegicus]	5	6.7	49.60
40	4.1×10^{-7}	gi|55715693|gb|AAH85942.1| Tripartite motif protein 35 [Rattus norvegicus]	5	6.7	59.65
41	4.8×10^{-7}	gi|54035396|gb|AAH83846.1| Similar to RIKEN cDNA 2310057M21 [Rattus norvegicus]	5	6.5	50.52
42	6.7×10^{-7}	gi|741803|prf||2008147A protein RAKb	12	7.9	38.13
43	7.3×10^{-7}	gi|16758742|ref|NP_446326.1| CAP, adenylate cyclase-associated protein, 2 [Rattus norvegicus]	6	6.7	54.57
44	7.5×10^{-7}	gi|56090443|ref|NP_001007675.1| solute carrier family 25 (mitochondrial deoxynucleotide carrier), member 19 [Rattus norvegicus]	7	9.8	36.69
45	8.4×10^{-7}	gi|27678054|ref|XP_225656.1| PREDICTED: similar to melanoma antigen family A, 10 [Rattus norvegicus]	5	5.1	34.46
46	1.1×10^{-6}	gi|55932|emb|CAA31237.1| c-erb-A thyroid hormone receptor [Rattus norvegicus]	7	8.5	47.84
47	1.2×10^{-6}	gi|112393|pir||S09178 thyroid hormone receptor alpha - rat	7	8.8	49.36
48	1.2×10^{-6}	gi|72121|pir||TVRTAR thyroid hormone receptor alpha-2 - rat	6	6.4	53.06

49	1.3×10^{-6}	gi|45680894|gb|AAS75316.1| non-specific dipeptidase [Rattus norvegicus]	5	5.4	54.69
50	1.3×10^{-6}	gi|226130|prf||1411299A thyroid hormone receptor alpha 1	7	9.2	49.16
51	1.6×10^{-6}	gi|92879|pir||S06907 thyroid hormone receptor alpha-2 (clone rTRalpha2) - rat	6	6.5	57.81
52	1.6×10^{-6}	gi|54035348|gb|AAH83887.1| Similar to RIKEN cDNA 4930563D23 [Rattus norvegicus]	18	9.5	30.61
53	1.7×10^{-6}	gi|226131|prf||1411299B thyroid hormone receptor alpha 2	6	6.3	57.77
54	1.8×10^{-6}	gi|4887597|dbj|BAA77793.1| organic anion transporter-K2 [Rattus norvegicus]	5	9.0	57.87
55	1.8×10^{-6}	gi|204048|gb|AAA41121.1| c-erbA-alpha-2-related protein	6	6.9	57.71
56	1.8×10^{-6}	gi|52001262|sp|P63059|THA_RAT Thyroid hormone receptor alpha (C-erbA-alpha) (c-erbA-1)	6	6.9	57.59
57	2.3×10^{-6}	gi|57526873|ref|NP_001009629.1| replication factor C (activator 1) 3 [Rattus norvegicus]	6	9.3	42.25
58	2.4×10^{-6}	gi|42409519|ref|NP_955792.1| keratin complex 1, acidic, gene 19 [Rattus norvegicus]	5	5.2	45.42
59	2.7×10^{-6}	gi|47576187|ref|NP_001000484.1| olfactory receptor Olr1349 [Rattus norvegicus]	10	9.4	35.56
60	3.0×10^{-6}	gi|56788780|gb|AAH88424.1| Krt1-19 protein [Rattus norvegicus]	5	5.3	47.48
61	4.3×10^{-6}	gi|13540632|ref|NP_110461.1| monocarboxylate transporter [Rattus norvegicus]	3	8.9	51.96
62	8.5×10^{-6}	gi|56268852|gb|AAH87064.1| Cytotoxic granule-associated RNA binding protein 1 [Rattus norvegicus]	7	7.8	42.72
63	9.4×10^{-6}	gi|27465631|ref|NP_775174.1| phosphate cytidylyltransferase 1, choline, beta isoform [Rattus norvegicus]	4	6.0	43.22
64	9.4×10^{-6}	gi|53734533|gb|AAH83705.1| Prohibitin 2 [Rattus norvegicus]	5	9.8	34.09
65	1.3×10^{-5}	gi|47576237|ref|NP_001001087.1| olfactory receptor Olr1318 [Rattus norvegicus]	7	9.1	35.26
66	2.3×10^{-5}	gi|47577743|ref|NP_001000596.1| olfactory receptor Olr1257 [Rattus norvegicus]	7	9.4	36.39

67	3.2×10^{-5}	gi|51858754|gb|AAH82080.1| Fibrous sheath interacting protein 1 [Rattus norvegicus]	5	5.0	51.43
68	3.3×10^{-5}	gi|16757980|ref|NP_445740.1| orosomucoid 1 [Rattus norvegicus]	8	5.6	24.53
69	3.4×10^{-5}	gi|24308492|ref|NP_714948.1| Ly-49 stimulatory receptor 3 [Rattus norvegicus]	6	9.2	34.31
70	3.4×10^{-5}	gi|117465|sp|P02529|CRGC_RAT Gamma crystallin C (Gamma crystallin 2-1)	13	7.9	21.61
71	3.4×10^{-5}	gi|203633|gb|AAA40986.1| gamma-crystallin	13	6.9	20.97
72	3.4×10^{-5}	gi|92259|pir||C24060 gamma-crystallin 2-1 - rat	13	7.9	21.60
73	4.1×10^{-5}	gi|18426866|ref|NP_569117.1| acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) [Rattus norvegicus]	9	8.4	43.22
74	4.1×10^{-5}	gi|56786134|gb|AAW29194.1| Ly49 stimulatory receptor 3 variant [Rattus norvegicus]	6	9.4	35.82
75	4.9×10^{-5}	gi|117463|sp|P10066|CRGB_RAT Gamma crystallin B (Gamma crystallin 1-2)	13	7.9	21.61
76	6.7×10^{-5}	gi|51858723|gb|AAH82012.1| Hypothetical protein LOC690783 [Rattus norvegicus]	5	5.8	35.25
77	6.7×10^{-5}	gi|13592043|ref|NP_112357.1| renin binding protein [Rattus norvegicus]	4	5.6	49.70
78	8.4×10^{-5}	gi|14009486|gb|AAK51627.1|AF255886_1 adapter protein RUK-m1 [Rattus norvegicus]	7	9.1	46.13
79	1.2×10^{-4}	gi|14009488|gb|AAK51628.1|AF255887_1 adapter protein RUK-m3 [Rattus norvegicus]	6	9.0	48.65
80	2.0×10^{-4}	gi|3183109|sp|Q63065|PDK1_RAT [Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial precursor (Pyruvate dehydrogenase kinase isoform 1) (PDK p48)	7	8.4	50.25
81	2.2×10^{-4}	gi|27698122|ref|XP_223674.1| PREDICTED: similar to UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1 [Rattus norvegicus]	8	9.5	47.78
82	2.2×10^{-4}	gi|47577461|ref|NP_001001125.1| olfactory receptor Olr471 [Rattus norvegicus]	7	9.7	36.79

83	4.9×10^{-4}	gi|47576233|ref|NP_001000471.1| olfactory receptor Olr1320 [Rattus norvegicus]	7	9.6	36.56
84	6.8×10^{-4}	gi|12408306|ref|NP_074046.1| casein kinase 1, gamma 3 [Rattus norvegicus]	8	9.4	53.32
85	8.8×10^{-4}	gi|206515|gb|AAA41988.1| quinone reductase (EC 1.6.99.2)	12	6.5	29.50
86	2.7×10^{-3}	gi|206734|gb|AAA42074.1| ribosomal protein L5	4	9.9	35.93
87	2.8×10^{-3}	gi|12621142|ref|NP_075248.1| peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor [Rattus norvegicus]	4	5.2	51.50
88	3.2×10^{-3}	gi|13592051|ref|NP_112361.1| ribosomal protein L5 [Rattus norvegicus]	4	9.9	36.06

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B40485DF-0634-64252A39

Sequences 20076

Date & Time Mon Feb 05 18:14:05 2007 UTC (Search Time: 0.31 sec.)

Sample ID 20061228 richardson NIA set 1 spot 7507 CONSENSUS search 1

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 20 - 60 kDa

pI Range 5.0 -10.0

Digestion Trypsin

Missed Cuts 0

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@Y (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 615.633 626.649 628.603 629.635 654.683 655.682 656.637
657.660 668.681 682.714 684.669 696.736 710.750 719.385
722.753 724.769 725.773 726.774 738.784 739.776 740.764
753.804 766.813 767.799 768.791 769.824 778.813 795.818
797.855 811.870 824.498 852.524 857.893 918.461 920.462
948.524 955.506 990.548 1005.526 1027.551 1057.543
1084.514 1102.527 1107.628 1215.638 1217.641 1220.593
1224.587 1233.647 1244.595 1247.618 1262.611 1280.652
1330.608 1372.687 1375.682 1380.613 1383.724 1388.685
1390.698 1401.747 1432.721 1450.697 1456.723 1482.694
1528.829 1542.788 1547.748 1559.791 1568.770 1584.780
1666.785 1684.827 1735.901 1756.865 1762.835 1779.870
1785.845 1828.876 1892.888 1908.894 1911.892 1927.870
1963.912 2016.919 2017.955 2046.980 2047.986 2052.975
2053.990 2072.995 2091.036 2122.033 2138.041 2183.087
2191.086 2241.123 2242.143 2290.142 2297.174 2324.186
2341.203 2363.160 2364.131 2374.208 2390.186 2398.135
2417.268 2422.219 2435.213 2443.225 2444.174 2458.185
2497.209 2508.238 2514.243 2526.227 2533.229 2534.143
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2639.259 2648.264 2776.263 2817.331 2819.298 2835.269
2894.325 2924.391 2937.396 2938.410 3059.386 3077.516
3095.402 3096.478 3105.484 3114.487 3122.443 3136.466
3179.472 3187.540 3188.479 3202.492 3203.490 3212.465
3213.455 3220.498 3230.529 3244.498 3245.547 3250.483
3261.581 3262.528 3274.486 3275.530 3287.656 3288.539
3298.437 3306.482 3307.432 3316.486 3326.642 3335.496
3336.679 3350.504 3352.472 3366.466 3367.591 3377.551
3385.615 3404.421 3414.660 3426.494 3427.685 3445.594
3455.591 3464.541 3491.590 3614.661 3823.734

Tolerance (mon) 8.00 ppm

Number of Peptides 184

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- X! Hunter
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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	2.0×10^{-9}	gi|29692074|gb|AAO89062.1| phosphoserine aminotransferase [Rattus norvegicus]	13	8.5	41.92	
2	1.1×10^{-5}	gi|47577087|ref|NP_001000765.1| olfactory receptor Olr310 [Rattus norvegicus]	17	8.9	35.35	
3	1.2×10^{-5}	gi|47577593|ref|NP_001000674.1| olfactory receptor Olr529 [Rattus norvegicus]	16	8.9	36.36	
4	1.6×10^{-5}	gi|3915863|sp|P52847|ST1B1_RAT Sulfotransferase family cytosolic 1B member 1 (Sulfotransferase 1B1) (DOPA/tyrosine sulfotransferase)	13	8.4	36.39	
5	2.1×10^{-5}	gi|23096094|dbj|BAC16247.1| histo-blood group ABO transferase [Rattus norvegicus]	15	8.9	41.47	
6	6.2×10^{-5}	gi|741803|prf||2008147A protein RAKb	12	7.9	38.13	
7	7.6×10^{-5}	gi|34867618|ref|XP_217013.2| PREDICTED: similar to Protein PP2447 [Rattus norvegicus]	11	8.8	43.42	
8	8.1×10^{-5}	gi|8392858|ref|NP_058966.1| alcohol dehydrogenase 4 (class II), pi polypeptide [Rattus norvegicus]	13	8.8	42.59	
9	8.2×10^{-5}	gi|27692082|ref|XP_227314.1| PREDICTED: similar to Secreted frizzled-related protein 2 precursor (sFRP-2) (Secreted apoptosis-related protein 1) (SARP-1) (SDF5 protein) [Rattus norvegicus]	12	8.5	35.60	
10	9.3×10^{-5}	gi|34876257|ref|XP_237907.2| PREDICTED: similar to transmembrane 7 superfamily member 1 [Rattus norvegicus]	5	8.9	45.16	
11	9.7×10^{-5}	gi|2499598|sp|Q63454|MK04_RAT Mitogen-activated protein kinase 4 (Extracellular signal-regulated kinase 4) (ERK-4) (MAP kinase isoform p63) (p63-MAPK) (MNK2)	9	8.0	32.21	
12	1.3×10^{-4}	gi|1346731|sp|P03994|HPLN1_RAT Hyaluronan and proteoglycan link protein 1 precursor (Proteoglycan link protein) (Cartilage link protein) (LP)	12	8.7	41.63	
13	1.9×10^{-4}	gi|205390|gb|AAA41592.1| alpha-2-macroglobulin	7	8.8	26.31	
14	2.9×10^{-4}	gi|50925685|gb|AAH79101.1| Ubiquitin specific peptidase 18 [Rattus norvegicus]	7	8.9	43.63	
15	3.2×10^{-4}	gi|19773584|gb|AAL98710.1|AF296761_1 putative blood group A transferase T1 [Rattus norvegicus]	12	8.7	36.71	
16	5.0×10^{-4}	gi|50927021|gb|AAH79217.1| Similar to plasma kallikrein-like protein 4 precursor [Rattus norvegicus]	14	7.9	44.13	

17	5.7×10^{-4}	gi|56090387|ref|NP_001007704.1| hypothetical protein LOC313771 [Rattus norvegicus]	16	7.1	25.10	
18	9.3×10^{-4}	gi|13591949|ref|NP_112293.1| L-arginine: glycine amidinotransferase [Rattus norvegicus]	9	7.2	49.75	
19	2.3×10^{-3}	gi|112412|pir||B39533 transcription factor HNF-3 beta - rat	12	8.9	49.44	
20	0.019	gi|51948426|ref|NP_001004227.1| RNA terminal phosphate cyclase domain 1 [Rattus norvegicus]	13	7.9	40.63	
21	0.93	gi|56961645|ref|NP_112638.2| ficolin A [Rattus norvegicus]	15	7.9	37.87	
22	0.93	gi|13124116|sp|Q9WTS8|FCN1_RAT Ficolin-1 precursor (Ficolin-A) (Ficolin-alpha) (M-ficolin) (Collagen/fibrinogen domain-containing protein 1)	15	7.9	37.89	

NOTE:

1. To search again using unmatched masses, click the symbol .

Input Summary

Search id A7EC8695-1254-58051E4D

Sequences 20092

Date & Time Tue Jan 30 15:41:10 2007 UTC (Search Time: 0.30 sec.)

Sample ID 20061228 richardson NIA set 1 spot 7508, 20070130, cleaned data search 2

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 25 - 52 kDa

pI Range 7.0 -9.0

Digestion Trypsin

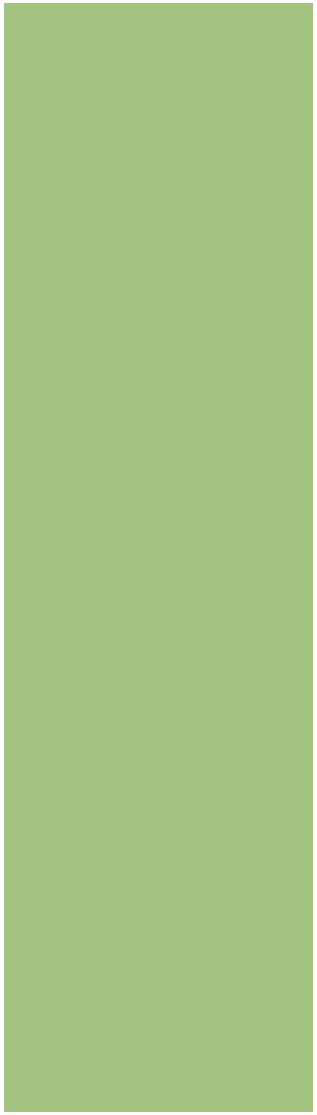
Missed Cuts 0

Modifications +C2H3ON@C(Complete); +NO2-H@Y(Partial); +O@M(Partial); +CH2N2@K (Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm



Masses (mon) 724.766 797.855 817.411 823.451 841.885 848.461 902.463 938.474 1001.367
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1560.784 1584.789 1602.806 1771.871 1779.865 1794.846 1810.906 1837.859
1855.885 1872.947 1896.908 1904.839 1908.910 1914.993 1929.934 1948.925
1957.951 2024.958 2025.974 2047.988 2052.969 2072.990 2098.986 2122.013
2150.030 2179.054 2180.052 2183.057 2191.088 2234.139 2276.149 2339.169
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2382.168 2390.168 2419.177 2420.177 2422.187 2435.241 2450.190 2460.167
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2886.317 2889.310 2890.317 2896.327 2897.330 2906.330 2914.349 2949.362
2959.403 2964.322 2965.365 2977.350 2978.341 2982.363 3001.493 3011.367
3012.319 3018.370 3029.476 3034.374 3047.469 3060.375 3061.405 3075.406
3083.362 3084.349 3092.373 3102.387 3103.400 3111.396 3112.378 3135.421
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3262.457 3274.442 3275.471 3283.493 3309.524 3316.493 3325.480 3342.485
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3419.583 3435.532 3436.524 3447.548 3448.560 3461.562 3462.537 3467.479
3468.572 3482.542 3483.543 3496.552 3497.518 3508.586 3517.594 3526.584
3538.578 3550.593 3567.586 3577.590 3582.583 3593.640 3598.598 3602.606
3614.638 3633.596 3649.610 3662.612 3667.623 3680.667 3698.641 3709.608
3727.697 3742.616 3754.701 3763.697 3772.723 3786.780 3801.758 3811.724
3819.771 3834.717 3843.767 3850.679 3861.742 3869.769 3875.765 3911.667
4099.867 4112.837 4130.884 4149.936 4166.900 4207.943 4220.923 4259.975

Tolerance (mon) 8.00 ppm

Number of Peptides 249

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New York, NY 10021
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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	8.4×10^{-13}	gi|25742635|ref|NP_445768.1| inositol hexaphosphate kinase 1 [Rattus norvegicus]	37	6.8	51.03	
+2	3.2×10^{-6}	gi|204150|gb|AAA41164.1| L-gulono-gamma-lactone oxidase precursor	20	6.8	52.53	
	-	gi|286224|dbj|BAA02232.1| L-gulono-gamma-lactone oxidase [Rattus norvegicus]	20	7.1	52.57	
	-	gi|3171998|emb|CAA06510.1| collagen alpha 1 (III) [Rattus norvegicus]	28	6.7	58.05	
	-	gi|13633872|sp|P97588|SMAD1_RAT Mothers against decapentaplegic homolog 1 (SMAD 1) (Mothers against DPP homolog 1)	17	6.9	54.50	
	-	gi|51948528|ref|NP_001004279.1| peptidylprolyl isomerase D [Rattus norvegicus]	26	6.7	42.83	
	-	gi|16758316|ref|NP_446002.1| phosphatidylinositol-4-phosphate 5-kinase, type II, beta [Rattus norvegicus]	29	7.2	49.20	
	-	gi|50925699|gb|AAH79114.1| Similar to Golgin 45 (Basic leucine zipper nuclear factor 1) [Rattus norvegicus]	25	7.0	46.59	
	-	gi|40254783|ref|NP_037262.2| SMAD, mothers against DPP homolog 1 [Rattus norvegicus]	18	6.9	54.32	
	-	gi|40385881|ref|NP_954700.1| activin A receptor, type 1B [Rattus norvegicus]	16	6.6	58.77	
	-	gi|16758354|ref|NP_446034.1| lipocalin 7 [Rattus norvegicus]	19	6.5	54.55	
	-	gi|12621094|ref|NP_075223.1| DnaJ-like protein 2 [Rattus norvegicus]	31	6.7	47.11	
	-	gi|47933915|gb|AAT39522.1| ankyrin repeat and SOCS box-containing protein 4 [Rattus norvegicus]	22	7.1	50.34	

-	gi|7001384|gb|AAF34874.1|AF168004_1 Parkin [Rattus norvegicus]	23	6.7	53.81
-	gi|6981322|ref|NP_036853.1| purinergic receptor P2X-like 1 [Rattus norvegicus]	18	6.5	43.92
-	gi|6981528|ref|NP_036938.1| mitogen activated protein kinase 10 [Rattus norvegicus]	26	6.4	49.87
-	gi|2507197|sp|P49187|MK10_RAT Mitogen-activated protein kinase 10 (Stress-activated protein kinase JNK3) (c-Jun N-terminal kinase 3) (SAPK-beta) (p54-beta)	23	6.4	54.51
-	gi|18175301|gb|AAK94870.1| IL-13 receptor alpha 1 [Rattus norvegicus]	19	7.1	50.66
-	gi|54400734|ref|NP_001005883.1| phosphatidylinositol 4-kinase type-II beta [Rattus norvegicus]	23	6.4	56.40
-	gi|56605656|ref|NP_001008288.1| downstream neighbor of SON [Rattus norvegicus]	19	6.9	55.52

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id A6B33F1D-1388-A77E7FF2

Sequences 20076

Date & Time Sat Feb 03 15:42:18 2007 UTC (Search Time: 0.50 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 40 - 60 kDa

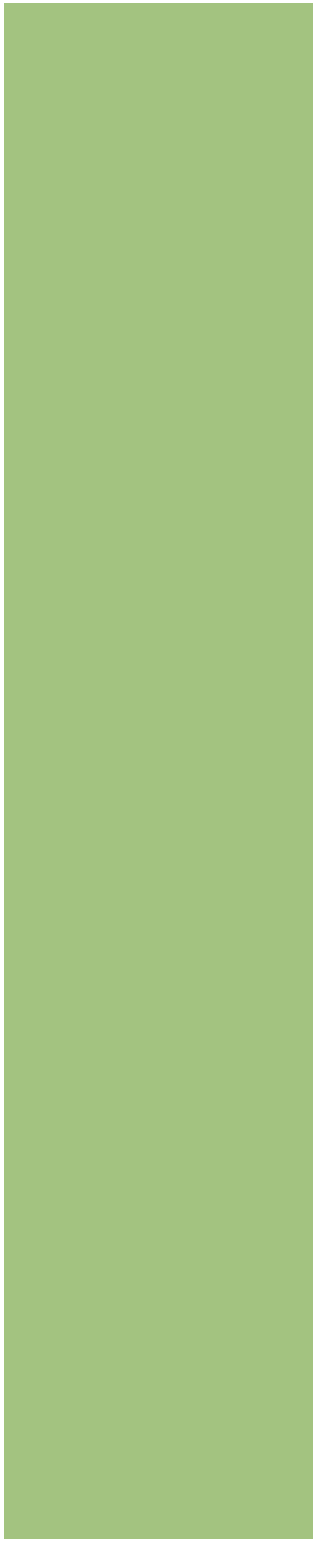
pI Range 6.3 -7.8

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +CH2N2@K(Complete);

Charge State MH+



Masses (avg)

Tolerance (avg) 1.00 ppm

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1631.746 1695.783 1710.821 1736.822 1743.801 1751.829
1756.860 1762.822 1780.856 1785.832 1891.888 1894.892
1922.931 1931.905 1948.913 1964.911 1968.924 2004.920
2005.927 2017.936 2018.937 2021.931 2025.958 2026.955
2038.979 2039.977 2046.948 2047.951 2055.978 2056.960
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2306.135 2365.153 2366.157 2377.201 2382.137 2383.164
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2549.177 2550.197 2559.187 2562.200 2563.217 2577.188
2590.208 2591.183 2606.205 2607.217 2622.219 2630.197
2631.225 2637.229 2638.227 2648.228 2649.231 2662.239
2663.233 2670.236 2671.233 2683.232 2684.228 2690.181
2691.232 2701.307 2702.229 2715.201 2716.260 2720.248
2721.261 2731.217 2732.255 2741.273 2742.272 2749.305
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2778.280 2783.264 2784.253 2795.286 2796.263 2802.295
2808.295 2809.281 2817.282 2832.280 2836.263 2837.297
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2964.349 2965.343 2980.362 2981.348 2995.371 2996.370
3001.414 3003.439 3011.438 3012.309 3020.372 3021.359
3029.544 3048.528 3065.420 3066.352 3077.479 3092.426
3114.432 3149.475 3180.436 3181.466 3185.468 3202.456
3203.456 3213.487 3220.489 3244.480 3245.465 3260.456
3275.476 3276.482 3283.479 3284.500 3292.541 3301.509
3308.483 3309.519 3313.477 3314.446 3326.491 3340.396
3347.527 3348.551 3354.551 3355.538 3369.553 3373.542
3374.532 3384.519 3385.524 3391.543 3392.547 3399.569
3400.560 3408.542 3412.578 3413.530 3423.517 3431.524
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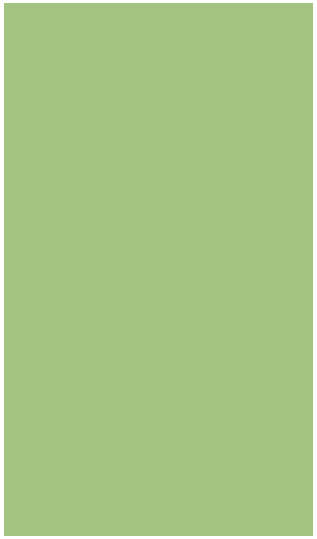

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Tolerance (mon)	36.00 ppm
Number of Peptides	268

Laboratory of Mass Spectrometry and Gaseous Ion Chemistry

PROWL

- *ProFound*
- ProteinInfo
- PeptideMap
- PepFrag
- X! Tandem
- X! Hunter
- GPMDB

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The Rockefeller University

The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

National Center of Research Resources

National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	3.0×10^{-23}	gi|13591997|ref|NP_112319.1| aldehyde dehydrogenase family 6, subfamily A1 [Rattus norvegicus]	10	8.9	59.59	
2	1.2×10^{-8}	gi|21431625|sp||Q9ERB4_1 [Segment 1 of 2] Versican core protein precursor (Large fibroblast proteoglycan) (Chondroitin sulfate proteoglycan core protein 2) (PG-M) (Glial hyaluronate-binding protein) (GHAP)	15	5.3	40.17	
3	1.7×10^{-8}	gi|40254763|ref|NP_075411.2| glycoprotein 50kD [Rattus norvegicus]	12	6.6	49.94	
4	5.3×10^{-8}	gi|21728406|ref|NP_663710.1| mitochondrial Ca2+-dependent solute carrier [Rattus norvegicus]	9	8.9	54.34	
5	5.8×10^{-8}	gi|8394389|ref|NP_058805.1| synapsin 3 [Rattus norvegicus]	10	9.6	64.78	
6	6.2×10^{-8}	gi|125313|sp|P09605|KCRS_RAT Creatine kinase, sarcomeric mitochondrial precursor (S-MtCK) (Mib-CK) (Basic-type mitochondrial creatine kinase)	12	9.2	48.87	
7	6.5×10^{-8}	gi|38541109|gb|AAH62051.1| Bspry protein [Rattus norvegicus]	11	5.7	50.85	
8	9.1×10^{-8}	gi|2507415|sp|P45446|RORB_RAT Nuclear receptor ROR-beta (Nuclear receptor RZR-beta)	11	8.7	54.30	
9	9.2×10^{-8}	gi|11560020|ref|NP_071563.1| amiloride-sensitive cation channel 5, intestinal [Rattus norvegicus]	12	8.7	58.69	
10	1.0×10^{-7}	gi|349096|gb|AAA42095.1| transcription factor	11	7.0	57.21	
11	1.1×10^{-7}	gi|11177872|ref|NP_068613.1| gamma-aminobutyric acid A receptor, alpha 6 [Rattus norvegicus]	8	7.8	52.45	
12	3.7×10^{-7}	gi|3319077|pdb|1TOH| Chain , Tyrosine Hydroxylase Catalytic And Tetramerization Domains From Rat	16	5.5	40.24	
13	3.7×10^{-7}	gi|5822500|pdb|2TOH|A Chain A, Tyrosine Hydroxylase Catalytic And Tetramerization Domains From Rat	16	5.5	40.09	
14	5.2×10^{-7}	gi|13929204|ref|NP_114027.1| cytochrome P450, family 2, subfamily c, polypeptide 23 [Rattus norvegicus]	10	8.7	58.74	
15	9.0×10^{-7}	gi|55778306|gb|AAH86555.1| Platelet-derived growth factor receptor-like [Rattus norvegicus]	10	9.0	43.46	
16	9.4×10^{-7}	gi|50927392|gb|AAH79303.1| Trmt12 protein [Rattus norvegicus]	9	9.0	53.91	
17	1.1×10^{-6}	gi|17865343|ref|NP_446025.1| olfactomedin 1 [Rattus norvegicus]	10	6.5	56.82	
18	2.0×10^{-6}	gi|12018278|ref|NP_072128.1| integrin-linked kinase-associated serine/threonine phosphatase 2C [Rattus norvegicus]	4	6.7	44.47	

19	2.1×10^{-6}	gi|6981652|ref|NP_036872.1| tyrosine hydroxylase [Rattus norvegicus]	11	5.7	57.23	☐
20	2.3×10^{-6}	gi|38541341|gb|AAH62010.1| Integrin-linked kinase-associated serine/threonine phosphatase 2C [Rattus norvegicus]	4	6.7	44.45	☐
21	4.5×10^{-6}	gi|631810|pir||S43845 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II gamma-b chain - rat	9	7.1	60.90	☐
22	5.9×10^{-6}	gi|11560103|ref|NP_071613.1| caspase 8 [Rattus norvegicus]	7	5.3	57.68	☐
23	1.3×10^{-5}	gi|113979|sp|P21396|AOFA_RAT Amine oxidase [flavin-containing] A (Monoamine oxidase type A) (MAO-A)	6	8.5	61.80	☐
24	1.3×10^{-5}	gi|383383|prf||1903159A monoamine oxidase A	6	8.7	61.05	☐
25	1.3×10^{-5}	gi|48425080|pdb|1O5W|A Chain A, The Structure Basis Of Specific Recognitions For Substrates And Inhibitors Of Rat Monoamine Oxidase A	6	8.5	62.82	☐
26	1.3×10^{-5}	gi|220810|dbj|BAA00592.1| monoamine oxidase [Rattus sp.]	6	8.5	61.78	☐
27	1.3×10^{-5}	gi|1658571|gb|AAB18360.1| UGT1A7 [Rattus norvegicus]	8	9.4	61.52	☐
28	2.6×10^{-5}	gi|13242310|ref|NP_077373.1| abl-interactor 1 [Rattus norvegicus]	4	6.6	52.64	☐
29	6.0×10^{-5}	gi|56623|emb|CAA35667.1| unnamed protein product [Rattus norvegicus]	7	9.4	50.85	☐
30	9.5×10^{-5}	gi|525272|emb|CAA52283.1| MAP2d [Rattus norvegicus]	7	9.6	54.46	☐
31	0.31	gi|22761814|dbj|BAC11715.1| centrosomal protein CG-NAP [Rattus norvegicus]	5	5.0	54.11	☐

NOTE:

1. To search again using unmatched masses, click the symbol ☐.

Input Summary

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Sequences 20092
Date & Time Tue Jan 30 19:06:51 2007 UTC (Search Time: 0.31 sec.)
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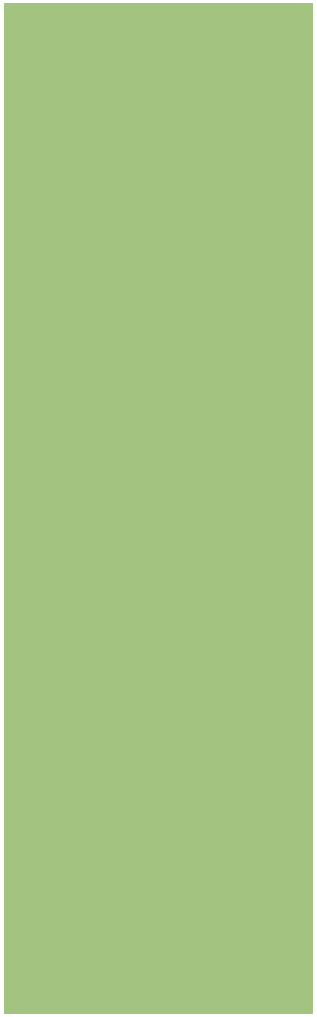
Database NCBInr [..\databases\nr]
Taxonomy Rattus
Mass Range 40 - 65 kDa
pI Range 5.0 -10.0
Digestion Trypsin
Missed Cuts 0
Modifications +C2H3ON@C(Complete); +CH2N2@K(Complete);
Charge State MH+
Masses (avg)
Tolerance (avg) 1.00 ppm



Masses (mon) 767.343 832.376 841.489 902.469 938.478 1013.482 1041.568 1113.602 1214.646
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1720.868 1779.862 1808.823 1887.920 1904.849 1908.884 1911.908 2062.971
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3568.641 3583.649 3599.645 3614.595 3623.676 3634.630 3651.619 3665.625
3667.802 3679.656 3694.693 3699.656 3710.666 3726.614 3742.620 3756.721
3774.733 3781.667 3794.741 3798.675 3813.666 3820.751 3831.685 3839.750
3848.664 3875.744 3891.779 4085.803 4094.891 4115.886 4219.917

Tolerance (mon) 10.00 ppm

Number of Peptides 224

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- X! Tandem
- X! Hunter
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The Rockefeller University
1230 York Avenue,
New York, NY 10021
(212) 327-8000

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National Resource for the Mass Spectrometric Analysis of Biological Macromolecules

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Protein Candidates

Rank	Expectation	Protein Information and Sequence Analyse Tools (T)	%	pI	kDa	R
1	1.1×10^{-8}	gi|53850648|ref|NP_001005560.1| phospholipase A2, group VI [Rattus norvegicus]	49	6.7	92.16	
2	2.9×10^{-6}	gi|17105334|ref|NP_476533.1| folate hydrolase [Rattus norvegicus]	47	7.1	86.73	
3	3.0×10^{-6}	gi|2190301|dbj|BAA20333.1| protein tyrosine phosphatase epsilon C [Rattus norvegicus]	52	7.2	78.91	
4	6.9×10^{-6}	gi|50511338|ref|NP_001002289.1| fucosyltransferase 8 (alpha (1,6) fucosyltransferase) [Rattus norvegicus]	41	7.2	68.52	
5	3.8×10^{-5}	gi|34871240|ref|XP_343881.1| PREDICTED: similar to IL2-inducible T-cell kinase [Rattus norvegicus]	51	7.3	74.62	
+6	1.3×10^{-4}	gi|47575877|ref|NP_757376.2| complement component 2 [Rattus norvegicus]	47	7.1	86.30	
	-	gi|25244377|gb|AAN72414.1| complement component C2 [Rattus norvegicus]	47	7.1	86.41	
	-	gi|47605759|sp|Q8R500|MFN2_RAT Mitofusin-2 (Transmembrane GTPase MFN2) (Mitochondrial transmembrane GTPase FZO1A) (Protein HSG)	41	6.5	88.61	
	-	gi|18426848|ref|NP_569104.1| tripartite motif-containing 9 [Rattus norvegicus]	37	6.6	82.40	
	-	gi|40786501|ref|NP_955434.1| sperm protein SSP411 [Rattus norvegicus]	35	6.6	90.63	
	-	gi|56090285|ref|NP_001007625.1| glutaminyl-tRNA synthetase [Rattus norvegicus]	41	7.0	90.53	
	-	gi|48256734|gb|AAT41589.1| acyl-CoA synthetase isoform 6 variant2 [Rattus norvegicus]	41	6.8	81.07	

-	gi|6980988|ref|NP_036708.1| glucocorticoid receptor [Rattus norvegicus]	36	6.6	90.77
-	gi|47059181|ref|NP_997631.1| B-factor, properdin [Rattus norvegicus]	24	6.6	88.83
-	gi|30060330|gb|AAO89095.1| ARNT2 exon 19 insertion variant; aryl hydrocarbon receptor nuclear translocator 2 splice variant; bHLH/PAS protein [Rattus norvegicus]	48	7.0	77.12
-	gi|13928932|ref|NP_113861.1| calpain 10 [Rattus norvegicus]	35	7.0	76.79
-	gi|32469278|dbj|BAC79049.1| calpain10 [Rattus norvegicus]	35	7.0	76.81
-	gi|40645510|dbj|BAD06361.1| calpain10 [Rattus norvegicus]	35	7.0	76.84
-	gi|417242|sp|P33124|ACSL6_RAT Long-chain-fatty-acid--CoA ligase 6 (Long-chain acyl-CoA synthetase 6) (LACS 6) (Long-chain-fatty-acid--CoA ligase, brain isozyme)	37	6.7	81.04
-	gi|18543341|ref|NP_570095.1| acyl-CoA synthetase long-chain family member 6 [Rattus norvegicus]	37	6.6	81.02
-	gi|49359177|gb|AAT65503.1| protein kinase C epsilon [Rattus norvegicus]	37	6.6	87.28
-	gi|31088216|dbj|BAC76890.1| nuclear protein UKp83 [Rattus norvegicus]	40	6.6	85.77
-	gi|6981002|ref|NP_037221.1| glycogen synthase 2 [Rattus norvegicus]	40	6.5	82.81
-	gi|50927110|gb|AAH79435.1| Zinc finger proliferation 1 [Rattus norvegicus]	34	7.4	66.01
-	gi|23305781|gb|AAN17280.1| testicular angiotensin-1 converting enzyme [Rattus norvegicus]	41	6.6	90.42
-	gi|27704760|ref|XP_230845.1| PREDICTED: similar to zinc finger, SWIM domain containing 3 [Rattus norvegicus]	31	6.8	82.64
-	gi|13928736|ref|NP_113732.1| adenosine monophosphate deaminase 3 [Rattus norvegicus]	36	6.9	94.98

NOTE:

1. To search again using unmatched masses, click the symbol .
2. Highly similar protein sequences were given the same rank (click "+" to expand/contract).

Input Summary

Search id B17C136D-08C0-B24488C2

Sequences 20076

Date & Time Sat Feb 03 01:22:26 2007 UTC (Search Time: 0.52 sec.)

Sample ID

Database NCBInr [..\databases\nr]

Taxonomy Rattus

Mass Range 66 - 95 kDa

pI Range 6.5 -7.7

Digestion Trypsin

Missed Cuts 1

Modifications +C2H3ON@C(Complete); +O@M(Partial); +HPO3@STY (Partial); +CH2N2@K(Complete);

Charge State MH+

Masses (avg)

Tolerance (avg) 1.00 ppm

Masses (mon) 841.481 848.443 902.470 1030.511 1046.496 1064.507
1194.589 1211.585 1247.607 1268.605 1280.623 1330.603
1695.791 1752.840 1780.859 1891.875 1895.882 1905.881
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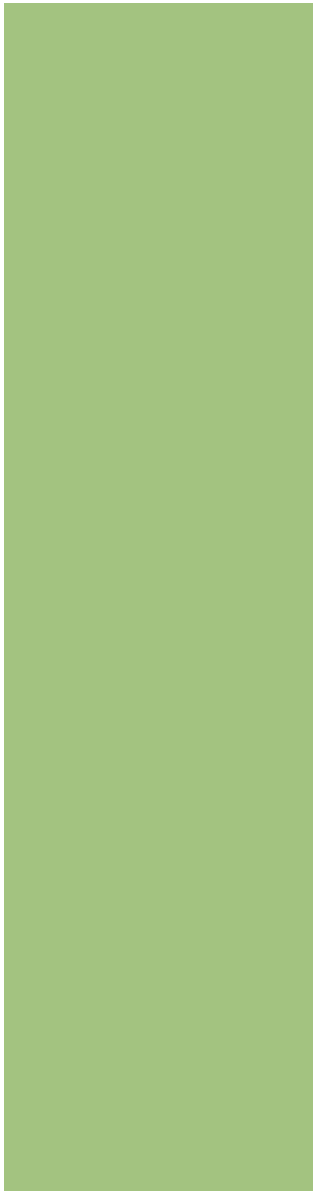

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Tolerance (mon)	39.00 ppm
Number of Peptides	262