

=/SCRIPT>

Mascot Search Results

User : =/B>
Email :
Search title :
Database : NCBInrEukaryote 23022011 (2385481 sequences; =81413870 residues)
Taxonomy : Eukaryota (eucaryotes) (1305516 =equences)
Timestamp : 29 Jun 2012 at 04:06:04 GMT
Enzyme : Trypsin
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.5 Da
Fragment Mass Tolerance : ± 0.5 Da
Max Missed Cleavages : 0
Instrument type : MALDI-TOF-TOF
Number of queries : 1180
Protein =its : gi|125307 RecName: Full=Creatine kinase =-type; AltName: Full=Creatine kinase M chain; AltName: =ull=M-CK
gi|125304 RecName: Full=Creatine kinase =-type; AltName: Full=Creatine kinase M chain; AltName: =ull=M-CK
gi|125310 RecName: Full=Creatine kinase =-type; AltName: Full=Creatine kinase M chain; AltName: Full=M-CK; =ltName: Full=NU-2 protein
gi|125293 RecName: Full=Creatine kinase =-type; AltName: Full=B-CK; AltName: Full=Creatine kinase B =hain
gi|3183536 RecName: Full=Creatine kinase =-type, mitochondrial; AltName: Full=Basic-type mitochondrial creatine =inase; Short=Mib-CK; AltName: Full=Sarcomeric mitochondrial =reatine kinase; Sho:

../data/20120629/F10720

Select Summary Report

Format As Select Summary (protein hits) Help
Significance threshold p< Max. number of hits AUTO
Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets 0
Show pop-ups Suppress pop-ups scoredown Require bold red

=INPUT value=MIS type=hidden name=SEARCH> Monoisotopic 0.5 0.5 ../data/20120629/F10720 =INPUT value=OFF type=hidden name=OVERVIEW> =INPUT value="Eukaryota (eucaryotes)" type=hidden name=TAXONOMY>

Re-Search All =ueries Unassigned = Below =omology threshold Below =density threshold

1.	gi 125307	Mass: 43=85	Score: 1106	Ma=ches: 263(101)	Sequences: 20(10)	&n=sp;emPAI: 2.40
RecName: Full=Creatine kinase M-type; AltName: Full=Creatine kinase M chain; AltName: =ull=M-CK						
Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss Score	Expect Rank Unique Peptide
113	759.3526	758.3453	758.3347	0.0106	0 36	0.4 1 R.DWPDAR.G
149	778.4458	777.4385	777.4272	0.0113	0 25	4.4 1 K.IEEIFK.K 147 148
175	794.4398	793.4325	793.4156	0.0169	0 28	1.8 1 U R.FCVGLQK.I 163 164 165 167 169 171 172 178 179
450	879.4307	878.4235	878.4241	-0.0007	0 20	12 1 K.LMVEMEK.K 453
515	907.4846	906.4773	906.4811	-0.0037	0 37	0.22 1 U K.FEELTR.L 516 517 519 520 521 523 525 526 530 531 532 533 536 538 540 543 545
557	914.4544	913.4471	913.4406	0.0065	0 27	2.4 1 M.PFGNTHNK.Y 561 562
570	948.5413	947.5340	947.5328	0.0013	0 20	12 1 U K.VLTPDLTK.K 571 574
607	983.4736	982.4663	982.4621	0.0042	0 43	0.047 1 R.GIWHNDNK.S 608 609 610 611
612	986.5097	985.5024	985.4981	0.0043	0 72	6.1e-005 1 U R.HGGFKPTDK.H 613 614 615
645	1083.5530	1082.5457	1082.5356	0.0101	0 30	0.86 1 K.TDLNHENLK.G 644
671	1130.5419	1129.5346	1129.5339	0.0007	0 37	0.2 1 U K.GYTLPPhCSR.G 672 673 676 677 678 679 680 681 683 687 691 694
729	1196.5387	1195.5314	1195.5244	0.0070	0 51	0.0072 1 U K.SEEEYPDLSK.H 728 730 731
749	1231.6428	1230.6355	1230.6245	0.0111	0 67	0.0002 1 U K.DLFDPIIQDR.H 744 745 746 747 748 750 751 752 753 754 755 756 757 758 759 760 761 762 764 765 766 767 768 769 770 771 772 773 774 775 777 778
824	1302.6368	1301.6296	1301.6285	0.0010	0 72	5.9e-005 1 U K.GQSIDDMIPAQK.- 821 825 827
828	1318.6257	1317.6185	1317.6235	-0.0050	0 (21)	7 1 U K.GQSIDDMIPAQK.-
886	1530.7216	1529.7143	1529.7110	0.0032	0 89	7.9e-007 1 U K.GGDDLDPHYVLSSR.V 885 887 888 889 890 891 892 893 894 895 896 897 898 899 900 902 903 904 905 906 907 908 909 910 911 912 913 914 916 917 918 920 9
954	1643.8378	1642.8305	1642.8103	0.0201	0 74	2.1e-005 1 K.SFLVWVNEEDHLR.V 951 952 953 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 975 979 980 981
1027	1785.9600	1784.9527	1784.9520	0.0007	0 99	6.3e-008 1 U R.LGSSEVEQVQLVVDGVK.L <= onmouseover="if (!browser_EXCLUDE) activateEl('Q1028', event)" onmouseout=clearEl() =ref="http://mascot.vuw
1097	2008.9678	2007.9605	2007.9498	0.0107	0 157	8.7e-014 1 U R.GTGGVDTAAVGSVFDISNADR.L <=T>1095 1096 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1117 11
1180	3644.8718	3643.8646	3643.8014	0.0631	0 13	7.1 1 U K.SMTEQEQQQLIDDHFLFDKPVSPLLLASGMAR.D <=TT> 1179

2. gi|125304 Mass: 43=01 Score: 168 =B>Matches: 15(2) Sequences: 6(1) &n=sp;emPAI: 0.11
RecName: Full=Creatine kinase M-type; AltName: Full=Creatine kinase M chain; AltName: =ull=M-CK

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
113	759.3526	758.3453	758.3347	0.0106	0	36	0.4	1		R.DWPDAR.G
149	778.4458	777.4385	777.4272	0.0113	0	25	4.4	1		K.IEEIFK.K 147 148
450	879.4307	878.4235	878.4241	-0.0007	0	20	12	1		K.LMVEMEK.K 453
607	983.4736	982.4663	982.4621	0.0042	0	43	0.047	1		R.GIWHNDNK.T 608 609 610 611
645	1083.5530	1082.5457	1082.5356	0.0101	0	30	0.86	1		R.TDLNHNELK.G 644
1180	3644.8718	3643.8646	3643.8014	0.0631	0	13	7.1	1	U	K.AMTEQQQLIDDFLFDPVSPLLASGMAR.D<=TT> 1179

3. gi|125310 Mass: 42=47 Score: 153 =B>Matches: 35(11) Sequences: 4(1) &=bsp;emPAI: 0.23
RecName: Full=Creatine kinase M-type; AltName: Full=Creatine kinase M chain; AltName: Full=M-CK; AltName: =ull=NU-2 protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
450	879.4307	878.4235	878.4241	-0.0007	0	20	12	1		K.LMVEMEK.R 453
557	914.4544	913.4471	913.4406	0.0065	0	27	2.4	1		M.PFGNTHNK.W 561 562
609	983.4780	982.4708	982.4621	0.0087	0	31	0.83	2		R.GIWHNDNK.S 607 608 610 611
954	1643.8378	1642.8305	1642.8103	0.0201	0	74	2.1e-005	1		K.SFLVWVNEEDHLR.V 951 952 953 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 975 979 980 981

4. gi|125293 Mass: 42=44 Score: 138 =B>Matches: 12(3) Sequences: 4(2) &n=sp;emPAI: 0.23
RecName: Full=Creatine kinase B-type; AltName: =ull=B-CK; AltName: Full=Creatine kinase B =hain

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
113	759.3526	758.3453	758.3347	0.0106	0	36	0.4	1		R.DWPDAR.G
607	983.4736	982.4663	982.4621	0.0042	0	43	0.047	1		R.GIWHNDNK.T 608 609 610 611
824	1302.6368	1301.6296	1301.6285	0.0010	0	49	0.011	2	U	K.GQSIDDLMPAQK.- 821 825
828	1318.6257	1317.6185	1317.6235	-0.0050	0	(12)	54	4	U	K.GQSIDDLMPAQK.-
1078	1964.9618	1963.9545	1963.9236	0.0309	0	9	53	2	U	R.GTGGVDTAAGGVFVSNADR.L 1079

5. gi|3183536 Mass: 4=054 Score: 68 =nbsp;Matches: 6(0) Sequences: 2(0)
RecName: Full=Creatine kinase S-type, =mitochondrial; AltName: Full=Basic-type mitochondrial creatine kinase; =hort=Mib-CK; AltName: Full=Sarcomeric mitochondrial creatine kinase; =hort=S-MtCK; Flags: Precursor

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
113	759.3526	758.3453	758.3347	0.0106	0	36	0.4	1		R.DWPDAR.G
609	983.4780	982.4708	982.4621	0.0087	0	31	0.83	2		R.GIWHNDNK.T 607 608 610 611

Proteins matching the same set of peptides:
gi|268370038 Mass: =47068 Score: 68 &nbs=; Matches: 6(0) Sequences: 2(0)<=TT>
creatine kinase S-type, mitochondrial [Gallus gallus]

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