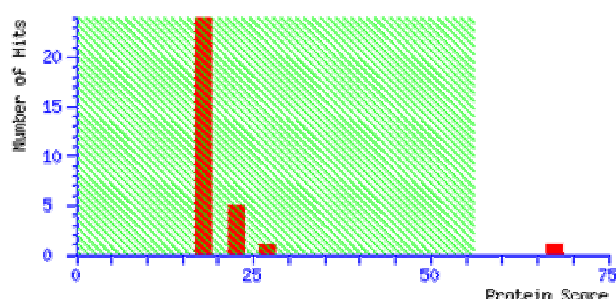


MASCOT Search Results

User : Tosifusa Toda
 Email : ttoda@proteome.jp
 Search title : TIG3-ssp7010
 Database : SwissProt 2017_12 (556388 sequences; 199430408 residues)
 Taxonomy : Homo sapiens (human) (20245 sequences)
 Timestamp : 27 Dec 2017 at 04:33:56 GMT
 Top Score : 68 for **NDKA_HUMAN**, Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 56 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As	Concise Protein Summary	Help
Significance threshold p<	0.05	Max. number of hits
Preferred taxonomy	All entries	
Re-Search All	Search Unmatched	

1.	NDKA_HUMAN	Mass: 17309	Score: 68	Expect: 0.0036	Matches: 6
	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1				
	NDKB_HUMAN	Mass: 17401	Score: 36	Expect: 5.2	Matches: 4
	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1				
	NDK8_HUMAN	Mass: 15690	Score: 26	Expect: 54	Matches: 3
	Putative nucleoside diphosphate kinase OS=Homo sapiens GN=NME2P1 PE=5 SV=1				
	TOM6_HUMAN	Mass: 7997	Score: 22	Expect: 1.2e+02	Matches: 2
	Mitochondrial import receptor subunit TOM6 homolog OS=Homo sapiens GN=TOMM6 PE=1 SV=1				
	CH058_HUMAN	Mass: 39978	Score: 20	Expect: 2.2e+02	Matches: 3
	Uncharacterized protein C8orf58 OS=Homo sapiens GN=C8orf58 PE=2 SV=2				
	PHF1_HUMAN	Mass: 63378	Score: 19	Expect: 2.4e+02	Matches: 4
	PHD finger protein 1 OS=Homo sapiens GN=PHF1 PE=1 SV=3				
	PTCD1_HUMAN	Mass: 79433	Score: 18	Expect: 3.2e+02	Matches: 4
	Pentatricopeptide repeat-containing protein 1, mitochondrial OS=Homo sapiens GN=PTCD1 PE=1 SV=2				
	ARP5L_HUMAN	Mass: 16931	Score: 17	Expect: 3.8e+02	Matches: 2
	Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens GN=ARPC5L PE=1 SV=1				
2.	GIPR_HUMAN	Mass: 53978	Score: 25	Expect: 67	Matches: 4
	Gastric inhibitory polypeptide receptor OS=Homo sapiens GN=GIPR PE=1 SV=1				

Search Parameters

Type of search : Peptide Mass Fingerprint
 Enzyme : Trypsin
 Fixed modifications : **Carbamidomethyl (C)**
 Variable modifications : **Oxidation (M)**
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 0.3 Da
 Peptide Charge State : 1+