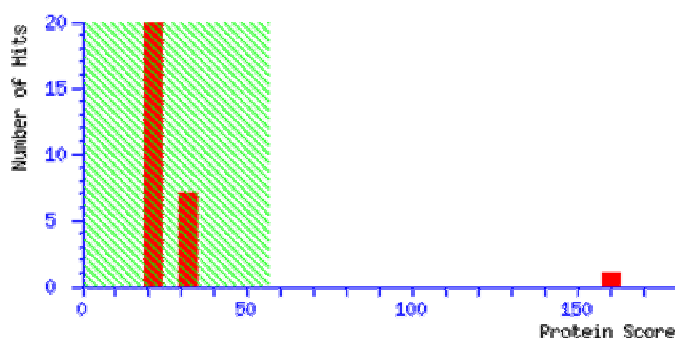


MATRIX SCIENCE Mascot Search Results

User : Tosifusa Toda
 Email : ttoda@proteome.jp
 Search title : TIG3-ssp4312
 Database : SwissProt 2017_12 (556388 sequences; 199430408 residues)
 Taxonomy : Homo sapiens (human) (20245 sequences)
 Timestamp : 26 Dec 2017 at 04:14:21 GMT
 Top Score : 160 for **ACTB_HUMAN**, Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB 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.	ACTB_HUMAN	Mass: 42052	Score: 160	Expect: 2e-12	Matches: 15
	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1				
	ACTG_HUMAN	Mass: 42108	Score: 160	Expect: 2e-12	Matches: 15
	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1				
	ACTC_HUMAN	Mass: 42334	Score: 92	Expect: 1.3e-05	Matches: 11
	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1				
	ACTS_HUMAN	Mass: 42366	Score: 92	Expect: 1.3e-05	Matches: 11
	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1				
	ACTH_HUMAN	Mass: 42249	Score: 78	Expect: 0.00032	Matches: 10
	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN=ACTG2 PE=1 SV=1				
	ACTA_HUMAN	Mass: 42381	Score: 78	Expect: 0.00033	Matches: 10
	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1				
	ACTBL_HUMAN	Mass: 42318	Score: 66	Expect: 0.0054	Matches: 9
	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2				
	SEAS1_HUMAN	Mass: 16430	Score: 26	Expect: 45	Matches: 3
	Putative uncharacterized protein SERTAD4-AS1 OS=Homo sapiens GN=SERTAD4-AS1 PE=5 SV=2				
	MAFB_HUMAN	Mass: 35998	Score: 25	Expect: 70	Matches: 4
	Transcription factor MafB OS=Homo sapiens GN=MAFB PE=1 SV=2				
	SPOPL_HUMAN	Mass: 45302	Score: 24	Expect: 86	Matches: 4
	Speckle-type POZ protein-like OS=Homo sapiens GN=SPOPL PE=1 SV=1				
	MCAT_HUMAN	Mass: 33264	Score: 24	Expect: 90	Matches: 4
	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1				
	RM46_HUMAN	Mass: 31799	Score: 23	Expect: 97	Matches: 4

39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1
[ACTBM_HUMAN](#) **Mass:** 42331 **Score:** 22 **Expect:** 1.1e+02 **Matches:** 4
Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTEKP PE=5 SV=1
[VP26A_HUMAN](#) **Mass:** 38260 **Score:** 22 **Expect:** 1.4e+02 **Matches:** 4
Vacuolar protein sorting-associated protein 26A OS=Homo sapiens GN=VPS26A PE=1 SV=2
[CLC11_HUMAN](#) **Mass:** 36015 **Score:** 21 **Expect:** 1.5e+02 **Matches:** 4
C-type lectin domain family 11 member A OS=Homo sapiens GN=CLEC11A PE=1 SV=1
[ZFY27_HUMAN](#) **Mass:** 46840 **Score:** 21 **Expect:** 1.7e+02 **Matches:** 4
Protrudin OS=Homo sapiens GN=ZFYVE27 PE=1 SV=1
[NEUL3_HUMAN](#) **Mass:** 29626 **Score:** 20 **Expect:** 1.9e+02 **Matches:** 3
E3 ubiquitin-protein ligase NEURL3 OS=Homo sapiens GN=NEURL3 PE=2 SV=2
[RT4I1_HUMAN](#) **Mass:** 43961 **Score:** 20 **Expect:** 1.9e+02 **Matches:** 4
Reticulon-4-interacting protein 1, mitochondrial OS=Homo sapiens GN=RTN4IP1 PE=1 SV=2

2. [NCF1B_HUMAN](#) **Mass:** 45017 **Score:** 32 **Expect:** 13 **Matches:** 6
Putative neutrophil cytosol factor 1B OS=Homo sapiens GN=NCF1B PE=5 SV=2
[NCF1C_HUMAN](#) **Mass:** 42052 **Score:** 28 **Expect:** 32 **Matches:** 5
Putative neutrophil cytosol factor 1C OS=Homo sapiens GN=NCF1C PE=5 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 : ± 0.5 Da
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 20

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