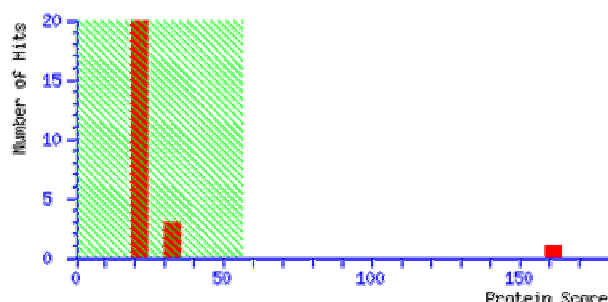


MASCOT Search Results

User : Tosifusa Toda
 Email : ttoda@proteome.jp
 Search title : TIG3-ssp1319
 Database : SwissProt 2017_12 (556388 sequences; 199430408 residues)
 Taxonomy : Homo sapiens (human) (20245 sequences)
 Timestamp : 25 Dec 2017 at 04:57:28 GMT
 Top Score : 161 for **VIME_HUMAN**, Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, 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	
<input type="button" value="Re-Search All"/> <input type="button" value="Search Unmatched"/>		

1.	VIME_HUMAN	Mass: 53676	Score: 161	Expect: 1.6e-12	Matches: 15
	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4				
	CBX3_HUMAN	Mass: 20969	Score: 26	Expect: 56	Matches: 4
	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4				
	NDUA5_HUMAN	Mass: 13507	Score: 25	Expect: 69	Matches: 3
	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3				
	PLIN3_HUMAN	Mass: 47217	Score: 24	Expect: 82	Matches: 4
	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3				
	RGS20_HUMAN	Mass: 44291	Score: 24	Expect: 88	Matches: 4
	Regulator of G-protein signaling 20 OS=Homo sapiens GN=RGS20 PE=1 SV=4				
	BBIP1_HUMAN	Mass: 10557	Score: 23	Expect: 97	Matches: 3
	BBSome-interacting protein 1 OS=Homo sapiens GN=BBIP1 PE=1 SV=2				
	FEZF2_HUMAN	Mass: 50034	Score: 23	Expect: 99	Matches: 4
	Fez family zinc finger protein 2 OS=Homo sapiens GN=FEZF2 PE=2 SV=2				
	HAGHL_HUMAN	Mass: 32278	Score: 23	Expect: 99	Matches: 4
	Hydroxyacylglutathione hydrolase-like protein OS=Homo sapiens GN=HAGHL PE=2 SV=1				
	RTF2_HUMAN	Mass: 34549	Score: 23	Expect: 1.1e+02	Matches: 4
	Protein RTF2 homolog OS=Homo sapiens GN=RTFDC1 PE=1 SV=3				
	CC152_HUMAN	Mass: 30131	Score: 22	Expect: 1.2e+02	Matches: 4
	Coiled-coil domain-containing protein 152 OS=Homo sapiens GN=CCDC152 PE=2 SV=3				
	NSF_HUMAN	Mass: 83055	Score: 22	Expect: 1.4e+02	Matches: 5
	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3				
	CX7B2_HUMAN	Mass: 9129	Score: 21	Expect: 1.6e+02	Matches: 2
	Cytochrome c oxidase subunit 7B2, mitochondrial OS=Homo sapiens GN=COX7B2 PE=3 SV=2				
	KCTD1_HUMAN	Mass: 29671	Score: 21	Expect: 1.6e+02	Matches: 3
	BTB/POZ domain-containing protein KCTD1 OS=Homo sapiens GN=KCTD1 PE=1 SV=1				
	ZSC31_HUMAN	Mass: 48233	Score: 21	Expect: 1.6e+02	Matches: 4
	Zinc finger and SCAN domain-containing protein 31 OS=Homo sapiens GN=ZSCAN31 PE=1 SV=2				
	FUT8_HUMAN	Mass: 66930	Score: 20	Expect: 1.8e+02	Matches: 4
	Alpha-(1,6)-fucosyltransferase OS=Homo sapiens GN=FUT8 PE=1 SV=2				