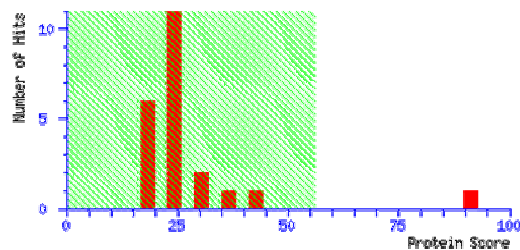


# MATRIX SCIENCE Mascot Search Results

**User** : Tosifusa Toda  
**Email** : ttoda@proteome.jp  
**Search title** : TIG3-ssp2415  
**Database** : SwissProt 2017\_12 (556388 sequences; 199430408 residues)  
**Taxonomy** : Homo sapiens (human) (20245 sequences)  
**Timestamp** : 25 Dec 2017 at 08:49:35 GMT  
**Top Score** : 91 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 **AUTO**  
 Preferred taxonomy **All entries**

Re-Search All Search Unmatched

1.	<a href="#">VIME_HUMAN</a>	Mass: 53676	Score: <b>91</b>	Expect: 1.5e-05	Matches: 9
	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4				
	<a href="#">GG6L2_HUMAN</a>	Mass: 79806	Score: 27	Expect: 42	Matches: 5
	Golgin subfamily A member 6-like protein 2 OS=Homo sapiens GN=GOLGA6L2 PE=1 SV=2				
	<a href="#">GBG5_HUMAN</a>	Mass: 7428	Score: 24	Expect: 79	Matches: 2
	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Homo sapiens GN=GN5 PE=1 SV=3				
	<a href="#">H1FOO_HUMAN</a>	Mass: 35792	Score: 21	Expect: 1.5e+02	Matches: 3
	Histone H1oo OS=Homo sapiens GN=H1FOO PE=2 SV=1				
	<a href="#">PININ_HUMAN</a>	Mass: 81679	Score: 21	Expect: 1.6e+02	Matches: 4
	Pinin OS=Homo sapiens GN=PNN PE=1 SV=4				
	<a href="#">2A5A_HUMAN</a>	Mass: 56500	Score: 21	Expect: 1.7e+02	Matches: 3
	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Homo sapiens GN=PPP2R5A PE=1 SV=1				
	<a href="#">DMRT3_HUMAN</a>	Mass: 51737	Score: 20	Expect: 2e+02	Matches: 3
	Doublesex- and mab-3-related transcription factor 3 OS=Homo sapiens GN=DMRT3 PE=1 SV=1				
	<a href="#">RNA51_HUMAN</a>	Mass: 18089	Score: 20	Expect: 2.1e+02	Matches: 2
	Ribonuclease pancreatic OS=Homo sapiens GN=RNASE1 PE=1 SV=4				
	<a href="#">F90A5_HUMAN</a>	Mass: 50379	Score: 20	Expect: 2.1e+02	Matches: 3
	Putative protein FAM90A5P OS=Homo sapiens GN=FAM90A5P PE=5 SV=1				
	<a href="#">F90A9_HUMAN</a>	Mass: 50277	Score: 20	Expect: 2.1e+02	Matches: 3
	Putative protein FAM90A9P OS=Homo sapiens GN=FAM90A9P PE=5 SV=1				
	<a href="#">F90AE_HUMAN</a>	Mass: 50492	Score: 20	Expect: 2.1e+02	Matches: 3
	Putative protein FAM90A14P OS=Homo sapiens GN=FAM90A14P PE=5 SV=1				
	<a href="#">F90AI_HUMAN</a>	Mass: 50219	Score: 20	Expect: 2.1e+02	Matches: 3
	Putative protein FAM90A18P/FAM90A19P OS=Homo sapiens GN=FAM90A18P PE=5 SV=1				
	<a href="#">F90AJ_HUMAN</a>	Mass: 50434	Score: 20	Expect: 2.1e+02	Matches: 3
	Putative protein FAM90A15P OS=Homo sapiens GN=FAM90A15P PE=5 SV=1				
2.	<a href="#">S31C1_HUMAN</a>	Mass: 131809	Score: 40	Expect: 2.2	Matches: 7
	Spermatogenesis-associated protein 31C1 OS=Homo sapiens GN=SPATA31C1 PE=2 SV=1				
	<a href="#">S31C2_HUMAN</a>	Mass: 125606	Score: 30	Expect: 22	Matches: 6
	Spermatogenesis-associated protein 31C2 OS=Homo sapiens GN=SPATA31C2 PE=2 SV=2				
	<a href="#">RN125_HUMAN</a>	Mass: 27406	Score: 22	Expect: 1.4e+02	Matches: 3
	E3 ubiquitin-protein ligase RNF125 OS=Homo sapiens GN=RNF125 PE=1 SV=4				
	<a href="#">CNTN3_HUMAN</a>	Mass: 113553	Score: 22	Expect: 1.4e+02	Matches: 5
	Contactin-3 OS=Homo sapiens GN=CNTN3 PE=1 SV=3				
	<a href="#">CBX7_HUMAN</a>	Mass: 28437	Score: 20	Expect: 1.9e+02	Matches: 3
	Chromobox protein homolog 7 OS=Homo sapiens GN=CBX7 PE=1 SV=1				
	<a href="#">CP3A7_HUMAN</a>	Mass: 57831	Score: 20	Expect: 2.1e+02	Matches: 3
	Cytochrome P450 3A7 OS=Homo sapiens GN=CYP3A7 PE=1 SV=2				

## Search Parameters