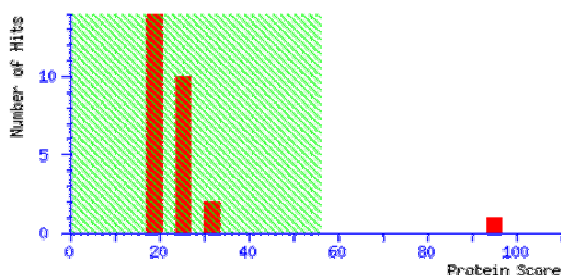


# MATRIX SCIENCE Mascot Search Results

**User** : Tosifusa Toda  
**Email** : ttoda@proteome.jp  
**Search title** : TIG3-ssp1201  
**Database** : SwissProt 2017\_12 (556388 sequences; 199430408 residues)  
**Taxonomy** : Homo sapiens (human) (20245 sequences)  
**Timestamp** : 25 Dec 2017 at 03:51:56 GMT  
**Top Score** : 95 for **RSSA\_HUMAN**, 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4

## 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	<a href="#">Help</a>
Significance threshold p<	0.05	Max. number of hits
Preferred taxonomy	All entries	
Re-Search All	Search Unmatched	

1.	<a href="#">RSSA_HUMAN</a>	Mass: 32947	Score: <b>95</b>	Expect: 6.6e-06	Matches: 8
	40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4				
	<a href="#">UBP21_HUMAN</a>	Mass: 63472	Score: 26	Expect: 51	Matches: 4
	Ubiquitin carboxyl-terminal hydrolase 21 OS=Homo sapiens GN=USP21 PE=1 SV=1				
	<a href="#">CLPX_HUMAN</a>	Mass: 69922	Score: 23	Expect: 1e+02	Matches: 4
	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1 SV=2				
	<a href="#">GEMI7_HUMAN</a>	Mass: 14642	Score: 22	Expect: 1.3e+02	Matches: 2
	Gem-associated protein 7 OS=Homo sapiens GN=GEMIN7 PE=1 SV=1				
	<a href="#">KCD20_HUMAN</a>	Mass: 48020	Score: 21	Expect: 1.6e+02	Matches: 3
	BTB/POZ domain-containing protein KCTD20 OS=Homo sapiens GN=KCTD20 PE=1 SV=1				
	<a href="#">GHDC_HUMAN</a>	Mass: 58058	Score: 20	Expect: 2e+02	Matches: 3
	GH3 domain-containing protein OS=Homo sapiens GN=GHDC PE=1 SV=2				
	<a href="#">ELAF_HUMAN</a>	Mass: 12718	Score: 20	Expect: 2.1e+02	Matches: 2
	Elafin OS=Homo sapiens GN=PI3 PE=1 SV=3				
2.	<a href="#">ZNF81_HUMAN</a>	Mass: 77679	Score: 31	Expect: 15	Matches: 5
	Zinc finger protein 81 OS=Homo sapiens GN=ZNF81 PE=1 SV=3				
	<a href="#">TIM8A_HUMAN</a>	Mass: 11219	Score: 23	Expect: 1e+02	Matches: 2
	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens GN=TIMM8A PE=1 SV=1				
	<a href="#">RHES_HUMAN</a>	Mass: 30745	Score: 21	Expect: 1.7e+02	Matches: 3
	GTP-binding protein Rhes OS=Homo sapiens GN=RASD2 PE=1 SV=1				
	<a href="#">ETV2_HUMAN</a>	Mass: 37294	Score: 20	Expect: 2e+02	Matches: 3
	ETS translocation variant 2 OS=Homo sapiens GN=ETV2 PE=2 SV=2				

## 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** :  $\pm 0.5$  Da  
**Peptide Charge State** : 1+  
**Max Missed Cleavages** : 1  
**Number of queries** : 13