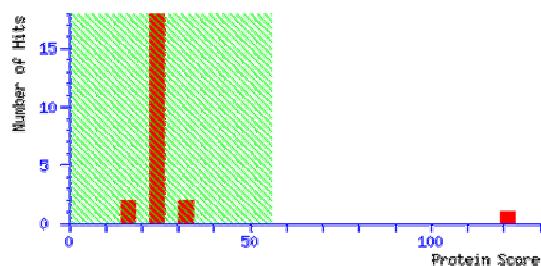


# MASCOT Search Results

User : Tosifusa Toda  
 Email : ttoda@proteome.jp  
 Search title : TIG3-ssp2417  
 Database : SwissProt 2017\_12 (556388 sequences; 199430408 residues)  
 Taxonomy : Homo sapiens (human) (20245 sequences)  
 Timestamp : 25 Dec 2017 at 09:01:51 GMT  
 Top Score : 121 for **GRP78\_HUMAN**, 78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2

## 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="#">GRP78_HUMAN</a>	Mass: 72402	Score: <b>121</b>	Expect: 1.6e-08	Matches: 11
	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2				
	<a href="#">ARAP1_HUMAN</a>	Mass: 163743	Score: 30	Expect: 19	Matches: 6
	Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ARAP1 PE=1 SV=3				
	<a href="#">BICC1_HUMAN</a>	Mass: 105405	Score: 28	Expect: 29	Matches: 5
	Protein bicaudal C homolog 1 OS=Homo sapiens GN=BICC1 PE=1 SV=2				
	<a href="#">CRLD1_HUMAN</a>	Mass: 58277	Score: 27	Expect: 37	Matches: 4
	Cysteine-rich secretory protein LCCL domain-containing 1 OS=Homo sapiens GN=CRISPLD1 PE=2 SV=1				
	<a href="#">MIF4GD_HUMAN</a>	Mass: 25749	Score: 25	Expect: 66	Matches: 3
	MIF4G domain-containing protein OS=Homo sapiens GN=MIF4GD PE=1 SV=1				
	<a href="#">EBP2_HUMAN</a>	Mass: 34887	Score: 24	Expect: 88	Matches: 3
	Probable rRNA-processing protein EBP2 OS=Homo sapiens GN=EBNA1BP2 PE=1 SV=2				
	<a href="#">FLOT2_HUMAN</a>	Mass: 47434	Score: 23	Expect: 97	Matches: 3
	Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2				
	<a href="#">SNP25_HUMAN</a>	Mass: 23528	Score: 23	Expect: 1.1e+02	Matches: 3
	Synaptosomal-associated protein 25 OS=Homo sapiens GN=SNAP25 PE=1 SV=1				
	<a href="#">WNT3_HUMAN</a>	Mass: 40988	Score: 22	Expect: 1.1e+02	Matches: 3
	Proto-oncogene Wnt-3 OS=Homo sapiens GN=WNT3 PE=1 SV=2				
	<a href="#">HDHD1_HUMAN</a>	Mass: 25404	Score: 22	Expect: 1.2e+02	Matches: 3
	Pseudouridine-5'-phosphatase OS=Homo sapiens GN=PUDP PE=1 SV=3				
	<a href="#">FKBP1B_HUMAN</a>	Mass: 11889	Score: 22	Expect: 1.4e+02	Matches: 2
	Peptidyl-prolyl cis-trans isomerase FKBP1B OS=Homo sapiens GN=FKBP1B PE=1 SV=2				
	<a href="#">ALR_HUMAN</a>	Mass: 24004	Score: 21	Expect: 1.5e+02	Matches: 3
	FAD-linked sulphydryl oxidase ALR OS=Homo sapiens GN=GFER PE=1 SV=2				
	<a href="#">RPC9_HUMAN</a>	Mass: 16918	Score: 21	Expect: 1.6e+02	Matches: 2
	DNA-directed RNA polymerase III subunit RPC9 OS=Homo sapiens GN=CRCP PE=1 SV=1				
	<a href="#">FGF13_HUMAN</a>	Mass: 27774	Score: 21	Expect: 1.6e+02	Matches: 3
	Fibroblast growth factor 13 OS=Homo sapiens GN=FGF13 PE=1 SV=1				
	<a href="#">YT014_HUMAN</a>	Mass: 14568	Score: 21	Expect: 1.8e+02	Matches: 2
	Putative uncharacterized protein FLJ40606 OS=Homo sapiens PE=5 SV=1				
	<a href="#">AKND1_HUMAN</a>	Mass: 93833	Score: 20	Expect: 1.8e+02	Matches: 4
	Protein AKNAD1 OS=Homo sapiens GN=AKNAD1 PE=2 SV=3				
	<a href="#">CXL10_HUMAN</a>	Mass: 11216	Score: 20	Expect: 1.8e+02	Matches: 2
	C-X-C motif chemokine 10 OS=Homo sapiens GN=CXL10 PE=1 SV=2				
	<a href="#">BCL3_HUMAN</a>	Mass: 47953	Score: 20	Expect: 1.9e+02	Matches: 3
	B-cell lymphoma 3 protein OS=Homo sapiens GN=BCL3 PE=1 SV=2				
	<a href="#">MTEF4_HUMAN</a>	Mass: 44500	Score: 20	Expect: 1.9e+02	Matches: 3
	Transcription termination factor 4, mitochondrial OS=Homo sapiens GN=MTERF4 PE=1 SV=3				
	<a href="#">PLOD2_HUMAN</a>	Mass: 85373	Score: 20	Expect: 2.1e+02	Matches: 4