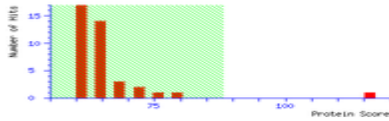


A**Mascot Score Histogram**

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 88 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.	gi 572938662	Mass: 98521	Score: 116	Expect: $9.6e-05$	Matches: 19
	interleukin 17 receptor A [Gallus gallus]				
	gi 515180230	Mass: 93554	Score: 105	Expect: 0.0012	Matches: 18
	PREDICTED: Interleukin-17 receptor A isoform X2 [Gallus gallus]				
	gi 528912380	Mass: 94647	Score: 78	Expect: 0.68	Matches: 18
	PREDICTED: Interleukin-17 receptor A-like [Meleagris gallopavo]				
	gi 489940991	Mass: 41275	Score: 74	Expect: 1.5	Matches: 11
	dTDP-glucose 4,6 dehydratase [Citrobacter]				
	gi 489155940	Mass: 20004	Score: 62	Expect: 25	Matches: 9
	MarR family transcriptional regulator [Comamonas testosteroni]				
	gi 489185455	Mass: 19890	Score: 62	Expect: 25	Matches: 9
	MarR family transcriptional regulator [Comamonas testosteroni]				
	gi 588591022	Mass: 12855	Score: 62	Expect: 27	Matches: 7
	coenzyme F420-dependent N(5),N(10)-methylene tetrahydrodihydropteridine reductase [Nocardia seriolae N-2927]				
	gi 488023558	Mass: 25775	Score: 61	Expect: 28	Matches: 8
	PREDICTED: dual specificity protein phosphatase 15 isoform 2 [Orinus orca]				
2.	gi 490588614	Mass: 85075	Score: 79	Expect: 0.45	Matches: 13
	RNA pseudouridine synthase [Bacillus methanolicus]				

Search Parameters

Type of search : **Peptide Mass Fingerprint**
 Enzyme : **Trypsin**
 Mass values : **Monoisotopic**
 Protein Mass : **Unrestricted**
 Peptide Mass Tolerance : **± 1.2 Da**
 Peptide Charge State : **1+**
 Max Missed Cleavages : **1**
 Number of queries : **26**

B**Protein View: gi|572938662
interleukin 17 receptor A [Gallus gallus]**

```

1  MAGAGRPGLS  PELLFLLVLP  VPPAAAALRL  LLGAAPPFTC  SQPDNLCLVG
51  NSTCIERSWL  QNQTWTPSAP  SSLDVFSDVF  RQTDGELLPV  LRIEWKVATD
101  ASIRYLKGA  LAVMQRVSRN  QICAQFFEQN  NLPLQVRPDT  GRWNFTFNRF
151  EVEPGQTYQV  TVYHLPKLSV  NGDYNFKSVS  LTMPTDQDRTL  MKRTEPCIKT
201  GSLWEPKIQ  RSLDDITLLV  SFNFWREPTR  YQIHVTSFLN  ERKCRMITRD
251  VTEGELQPQA  NVTIRMEKNL  RACCNYKQVI  QFFFAICGTD  CLRHSTFIPC
301  SPAPSVGPS  DMMIWVYWC  TGICVLLVGS  VIAGVICMTK  KRGGHGRGRC
351  SHYDLQTVFP  TDLPLPLKFP  RKVWIVYSAD  HLLYVDVVLK  FAEFLMTVCG
401  TAVALDLED  HQISEFGPLP  WLTRQKKEME  ELSSKIIILC  SRGTQAKWQA
451  MLGSAPVCLK  QDQQKPTGDL  FTPALNLIPL  DFKKPACFGM  YIVCYFDGIS
501  SEKDIPDLFN  VTSRYQLMDK  FEDIYFRIQD  LEKEEPGRIH  RIQEITAENY
551  IDTPSGRKLK  EAIQKFRNWQ  TEHPDWFEAE  SISLDNEEEL  QSLNRESQVD
601  SLLSEPGGIV  KHQLHLREPD  PNCYVINLH  IREGHSRGCK  LQPQLNLCGD
651  PASQTLIDFM  DEAPLVQVVV  PVSFMEDKNI  LGHHVLSNED  CMEGVPLLET
701  SFPMRNNIIL  HDDCDVSAID  EQSFMANLGE  LRHHHLNGLMY  SLYQQSVIPS
751  DFCFCQEEAD  KQHQLIFEDQ  CKDQRQSVQS  DQGYISRCSP  LFPDDFVEEE
801  EEDQENQVVC  HELSPEVLNS  LKSLOQQLFF  QDIQRSSSESG  YPAELMMSF
851  SPDCN

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Figure S1. MALDI-TOF/MS and analysis of peptide sequence. (A) Mascot search result of a spot from lysate of COS-7 cells transfected with chIL-17RA-myc construct. Protein visualized after silver nitrate staining in 2-DE gel was subjected to MALDI-TOF/MS analysis [1]. The peptide fingerprinting data were used to search the NCBI database using the Mascot program (<http://www.matrixscience.com>). Histogram showed the protein score distribution for identified protein (x -axis, Mascot score; y -axis, number of matching). Score that exceeded the shaded area obtained positive identification ($P < 0.05$). (B) The protein sequence coverage and matched peptides in the sequence of chIL-17RA (GenBank accession number: KF743557). The matched peptide sequences are indicated with red characters. [1] **Shevchenko A, Wilm M, Vorm O, Mann M.** 1996. Mass spectrometric sequencing of proteins from silver-stained polyacrylamide gels. *Ana. Chem.* **68**: 850–858.