

CytokineDB: a database collecting biological information about the cytokine family

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Motivation

During the past two decades, tumour immunology have showed that chronic inflammation might create favourable condition and promote oncogenesis; occasionally, it participates in cancer rejection. Clinical and experimental observations suggested that the mechanism of this switch recapitulated the events associated with pathogen infection, which stimulated immune cells in order to recognise danger signals and activate immune effector functions. Synthetic molecules have been developed that mimic pathogen invasion at the tumour site. These compounds activate dendritic cells to produce pro-inflammatory cytokines, which in turn trigger cytotoxic mechanisms leading to cancer death. These results suggested the crucial role played by chemokines and cytokines and justify the great interest of the scientific community for these proteins. The aim of this work is that of collecting all the biological information and gene and protein data about all the cytokine family in order to create a complete database useful to understand how the immune networks interact.

Methods

Some databases were used to collect gene and protein data regarding the cytokine family: Pubmed and OMIM for biological activity, ENSEMBL for gene records, SRS retrieval system for searching DNA and protein sequences, PDB for three-dimensional structures, DSSP for secondary structure assignment and CATH, SCOP and PDBsum for structural classification. For the proteins, of which only the sequence is known, the three-dimensional structures will be predict by template-based modelling using Modeller program to build full-atom models and Prosa and Procheck to select the best models in terms of stereo-chemical and energetic quality. All these data were stored in a relational database, called CytokineDB, that is available at the URL: <http://www.cro-m.eu/CytokineDB/>. Search form is based on a CGI script written in PERL language.

Results

The cytokine family was subdivided in 12 sub-families: interleukin, interferon, colony-stimulating factors, tumor necrosis factors, tnf superfamily, transforming growth factors, adipokine, adipose derived hormones, CXC chemokine, C chemokine, CX3 chemokine, CC chemokine. In each subgroup we have inserted all the known cytokines. The user can select a sub-family and choose the protein, of which want have information. The output page for each cytokine reports the cells, on which the protein is located, the target receptors and cells, the main effects, the description of biological activity, the references, EMBL code, Ensembl protein_coding gene, the number of transcripts, associated peptides and exons, the chromosome location, CCDS, RefSeq DNA, RefSeq peptide, Protein ID, UniProt code, amino acid sequence, PDB code, CATH and SCOP classifications, and structural features.

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