CytokineDB and CytReD@CROM

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Motivations

The cytokines family is composed by many proteins that need to bind to specific receptors on the cell surface to perform their biological function. This binding can stimulate both the expression of receptors for cytokines and the production of other cytokines that in turn act on other target cells. On the whole, the totality of the cytokines and of their interactions in and around biological cells is defined with the 'cytokinome" term. Often these molecules are involved in cancer-related chronic inflammation and play a pivotal role in promoting tumorigenesis and metastatic processes. Therefore, we have developed i) CytokineDB that is an annotated database that collects biological information regarding the cytokines family in human and ii) CytReD (Cytokine Receptor Database) that collects biological information regarding the human cytokine receptor families and their related ligands and can be used by researchers as well as physicians and clinicians to identify what cytokines are reported in the literature as significant in a given disease.

Methods

Some databases were used to collect gene and protein data regarding the human 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, and FoldIndex for the prediction of disorder propensity of the cytokine receptors. Search form of CytokineDB is based on a CGI script written in PERL language. CytReD is developed using a dynamic content management system Drupal version 6.17 and scripting language PHP version 5.3.2. JMOL visualization package is embedded for cytokine receptors three dimensional structure in detailed information page.

Results

In CytokineDB the human cytokine family was subdivided in 12 sub-families and the user can click on the image near to the name of each cytokine family and have a short description of the structures of these families. In each subgroup, all the known cytokines were inserted. The user can select a sub-family and choose the protein of which want have information. The output page for each cytokine reports the cell type, where the protein is located, Entrez Gene, 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, the number and the code of associated peptides, the number and the code of exons, the chromosome location, CCDS, RefSeq DNA, RefSeq peptide, Protein ID, UniProt code, Sequence isoforms, amino acid sequence, PDB code, CATH and SCOP classifications, and structural features. In CytReD the user can search by selecting from four options: cytokine receptor name, ligands, cytokine Family or disease. The result page is divided into description, sequences and accession codes and other biological information along with the references. Description provides information about the biological description, the name of ligands linked to CytokineDB database, the related synonyms, cell type on which the protein is expressed, the role and the diseases in which it is involved linked to PharmaGKB database. The sequences and accession codes section contains the nucleotide sequence, protein sequence and its isoforms. In particular, the accession codes are linked to the other important databases like Uniprot, Protein Databank, Entrez gene. In the biological information section there are information related to chromosome localization, Ensemble protein coding gene, the codes of transcripts, associated peptides, references, CATH and SCOP classifications, and quantitative analysis like number of residues, isoelectric field, number of positively and negatively charged residues, unfoldability index, and mean hydropathicity value(GRAVY). CytokineDB and CytReD are part of a broader project aimed to develop tools and portals able to be useful supports for a reliable predictive medicine.