



DisProt



IST

Database of Protein Disorder

The Center for Computational Biology and Bioinformatics at Indiana University is pleased to announce a new release of **DisProt**.

DisProt is a curated online database of disordered proteins, that provides structure and function information about proteins that do not have fixed 3-D structure under putatively native conditions, either in their entirety or in part.

DisProt has become the central repository of disorder-related information. For each disordered protein, the database includes the name of the protein, synonyms, accession numbers, full-length amino acid sequence, functional narrative, location of disordered region(s) and methods used for structural characterization. If the biological function and the functional mode of each disordered region are known it is also included.

DisProt was developed as collaboration between Keith Dunker's group and Zoran Obradovic's group at Temple University.

DisProt Release 3.3 (June 23, 2006) consists of:

- 458 disordered protein entries
- 1096 disordered regions
- Updated disorder functions list with definitions
- Updated detections methods list and descriptions
- Disordered region sequence retrieval by function
- A new FASTA format which includes functions in the header

DisProt 3.3 can be accessed from the web at <http://www.disprot.org>

To facilitate disorder-related research, protein and region information can be downloaded for single proteins or the entire database in XML or FASTA format.

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\* For questions, comments and suggestions about DisProt implementation, please send an email to [disprot@disprot.org](mailto:disprot@disprot.org)

\* For questions, comments and suggestions about DisProt database content, please send an email to [annotator@disprot.org](mailto:annotator@disprot.org)

\* To report technical problems with any of the web pages, please send an email to [webmaster@disprot.org](mailto:webmaster@disprot.org)

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