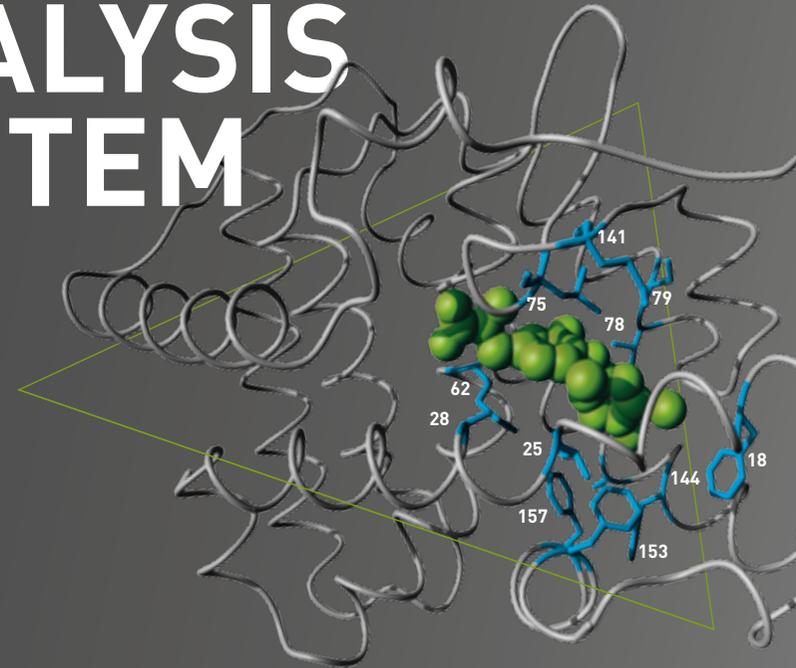


# PROTEIN SUPER-FAMILY ANALYSIS SYSTEM



Curious? Visit our website

[www.bio-product.nl](http://www.bio-product.nl) or contact us at [info@bio-product.nl](mailto:info@bio-product.nl)

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**ACCURATE MUTATION  
PREDICTION FOR  
DRUG DESIGN  
PROTEIN ENGINEERING  
DNA DIAGNOSTICS**



BIO-PRODUCT IS FOCUSED ON DELIVERING SOLUTIONS FOR GUIDING SCIENTIFIC RESEARCH IN THE FIELD OF PROTEIN ENGINEERING, MOLECULAR DESIGN AND DNA DIAGNOSTICS. WE APPLY NOVEL APPROACHES TO DATA MINING, STORAGE AND ANALYSIS OF PROTEIN-(SUPERFAMILY) DATA AND COMBINE THESE WITH STATE-OF-THE ART ANALYSIS METHODS AND VISUALIZATION TOOLS.

Over the years, our software solutions have proven to be powerful instruments for understanding many of the complex aspects involved in protein function and mutation effect prediction. Years of experience in software design, structural biology and the analysis of protein super-family data make Bio-Product your choice for protein-related data analysis and software design. Our team members are all specialized in different (bio)-informatics areas, which make us your perfect partner for outsourcing any of your bio-informatics projects.

We have released a special version of the 3DM protein superfamily analysis suite that is tailored toward DNA Diagnostics. 3DM for DNA Diagnostics provides predictions about the pathogenicity of variants and helps you deal with the growing amounts and complexity of biomedical data. Curious? Find out more at [www.3DM.bio-product.nl](http://www.3DM.bio-product.nl).

## TECHNOLOGY

The main products of Bio-Product are 3DM information systems. 3DM information systems are protein super-family platforms that collect, combine and integrate many different types of protein-related data. 3DM systems are designed to facilitate the exploration of sequence-structure-function relations, and have successfully been used many times to elucidate the function of individual amino acids, predict the effects of mutations, among others. We have a number of publicly available information systems that you can try out at [www.3DM.bio-product.nl](http://www.3DM.bio-product.nl).

## DATA MANAGEMENT

For any one protein family there is already an overwhelming amount of data available. Managing and integrating all this data can be a daunting task; studies that involve carrying over information from one protein to the other seem simple at a first glance, however, the amount of data that needs to be collected from heterogeneous sources, converted to syntactic and semantic homogeneity, validated, curated, stored and indexed, is enormous. To manage the increasing amounts of protein-related data Bio-Product has developed

3DM: systems that can automatically collect, store and connect many different super-family data types from various sources. Examples of data types that are used by 3DM are sequences, structural information, protein-ligand and protein-protein contact information, mutational data (which is automatically retrieved from literature), and information extracted from multiple sequence alignments (correlated mutations, amino acid conservation patterns, subfamily specific residues, etc). All these different data types are stored in specialized protein super-family system that are centered around a structure based multiple sequence alignment.

## DATA INTEGRATION

3DM applies a unified numbering scheme to the alignment, the sequences, and the structures. This numbering scheme makes it easy to visualize and integrate all different data types in the alignment, in the structures and in relation to each other, enabling easy detection of correlations between the different data types. Using a common numbering scheme for all proteins in the system allows for the easy transfer of information between proteins. 3DM super-family systems have a highly flexible setup making it easy to implement in-house data (such as mutational information).

3DM is tightly integrated with the state of the art molecular graphics and modeling software YASARA, which makes it easy to project the different data types on a protein structures and visualize trends extracted from the 3DM systems in a structural context. The use of YASARA, winner of the CASP8 refinement section, to build 3DM-based homology models ensures that you get the highest quality models possible.

Relating information between databases and literature has become increasingly difficult with the growing quantities of data and documents available. With the goal of bridging the gap between data and scientific articles, we have fully integrated the Utopia Documents PDF reader and the 3DM information systems. The software presents you with current, integrated, validated, internally consistent data and information in the context of literature being read. The annotations provided are extensive and detailed, and offer one-click access to related literature and sequential and structural information. 3DM offers full-circle data integration; you can navigate seamlessly between sequential data, protein structures and literature.

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