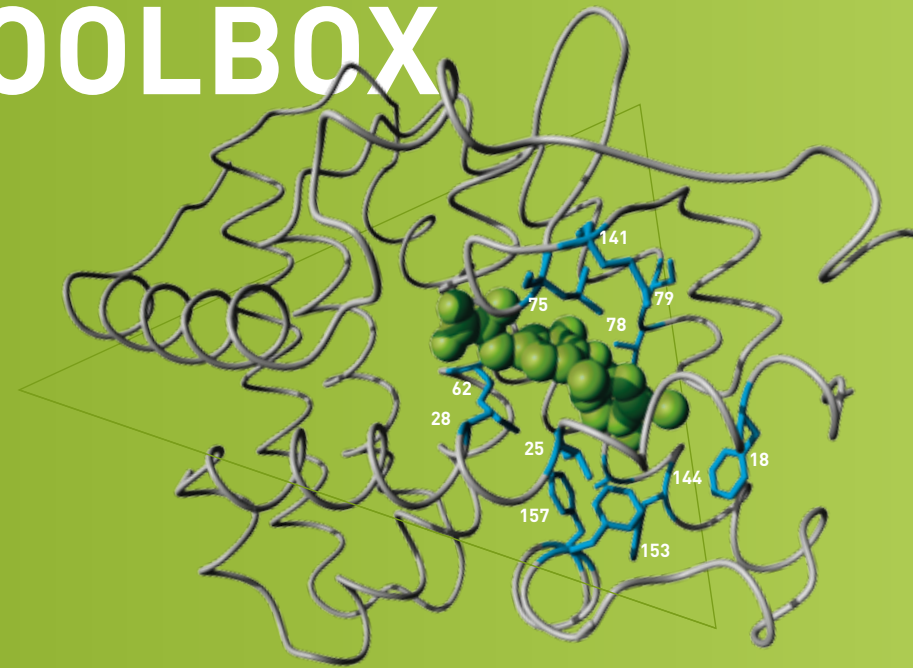


3DM TOOLBOX



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TOOLS FOR
PANEL DESIGN
PATENT ANALYSIS
PROTEIN OPTIMISATION



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.

3DM relieves many of the burdens that researchers face in dealing with the growing amounts and complexity of biomedical data. For each protein family a large amount of information extracted from protein structures, alignments and scientific literature, among others, is available. All this information is integrated and validated, and can be analysed via a number of different methods and tools. We highlight tools in 3DM that give researchers the functionalities they need to design novel enzymes through all the stages of target selection, enzyme optimisation and exploration of the patent landscape:

PANEL DESIGN & TARGET SELECTION

With 3DM, you can intelligently construct sequence panels with a maximised evolutionary spread. In contrast to existing methods that naively sample the complete sequence space, 3DM allows for limiting the sampled sequence space using information and knowledge specific to your needs. When optimising for specificity this allows a focus on specificity hotspots (e.g. positions in proximity of the binding site), thus capturing the most relevant aspects of evolution regarding binding, ignoring irrelevant positions. With the panel design tool you can select proteins that are likely expressible and thereby greatly increase your success rate.

Patented proteins

Panel members

PATENT LANDSCAPE ANALYSIS

Patent data can be explored for a complete protein family and visualised on phylogenetic trees to analyse freedom to operate. Patented sequences, mutations and claimed sequence space are available for analysis and can be projected on both the complete protein family as well as selected individual proteins. The freedom to operate can be used to guide the design of enzyme selection panels.

PROTEIN OPTIMISATION

3DM provides a number of complementary methods to compose sets of mutations to introduce. In a series of optimisation rounds, substitutions are systematically introduced so that covariation between amino acid substitutions are minimised. This enables capturing and quantifying the relative functional contributions of the introduced amino acid substitutions for each round. Mutations can be analysed in the context of known data and structure, allowing you to design novel rounds using acquired knowledge.



These tools are tightly interconnected and integrated with 3DM superfamily data. Comparisons with random designed libraries show that using the 3DM tools results in high quality libraries reducing not only the number of clones that need to be screened but also increases the chance of finding an enzyme with the desired properties. Initial results from partners show that expression levels of enzymes are structurally much higher compared to conventional methods. This demonstrates the opportunities that integrated knowledge databases offer, combined with the right tools that enable researchers to intelligently select proteins, residues and mutations.