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Visual Guidance

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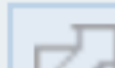
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Categories

- proteomics
- genomics
- structure analysis
- systems biology
- evolutionary biology
- population genetics
- transcriptomics
- biophysics
- imaging
- IT infrastructure
- medicinal chemistry
- glycomics

-  SIB resources
-  External resources - *(No support from the ExPASy Team)*

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 **Phyre2** [Imperial College London]
Categories: proteomics, (protein structure) - Software type(s): website - tool
As with **Phyre**, the new system is designed around the idea that you have a protein sequence/gene and want to predict its three-dimensional (3D) structure. Whereas **Phyre** used a profile-profile alignment algorithm, **Phyre2** uses the alignment of hidden Markov models via HHsearch to significantly improve accuracy of alignment and detection rate.
keywords: hidden markov model (HMM), protein structure prediction, tertiary structure, tertiary structure prediction

 **PhyreRisk** [Imperial College London]
Categories: proteomics, (protein structure), structure analysis - Software type(s): website - database
PhyreRisk is a dynamic web application developed to enable the exploration and mapping of genetic variants onto experimental and predicted structures of proteins and protein complexes. **PhyreRisk** integrates data from several public domain and in-house databases with information about diseases, genetic variation, biological pathways and protein structure and then facilitate the informed analysis by a wide community of users throughout the world.
keywords: disease mutation, protein variation (variant)

Resources A..Z

Links/Documentation