Существует 3 подхода к предсказанию пространственной структуры белков.

1. Предсказание структуры методом поиска сходства с известными структурами белков **по гомологии** (сравнительное моделирование).
2. Тридинг (protein threading, распознавание фолда) - моделирование на основе слабой гомологии. Главное отличие от моделирования по гомологии - поиск наилучшей структуры осуществляется с помощью выравнивания последовательности со структурой (SCOP2), а не с последовательностью. При этом используется специальным образом определенная весовая функция
3. ***Ab initio*** (или ***de novo***) моделирование.

CASP, which stands for Critical Assessment of Techniques for Protein Structure Prediction, is a community-wide experiment for protein structure prediction taking place every two years since 1994. CASP provides with an opportunity to assess the quality of available human, non-automated methodology (human category) and automatic servers for protein structure prediction (server category, introduced in the CASP7).[

**Краткое знакомство с моделированием белков**

https://habr. com/ru/companies/timeweb/articles/594859/

Cравнительное моделирование

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| --- | --- | --- |
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| IntFOLD | A unified interface for: Tertiary structure prediction/3D modelling, 3D model quality assessment, Intrinsic disorder prediction, Domain prediction, Prediction of protein-ligand binding residues | Automated webserver and some downloadable programs |
| RaptorX | remote homology detection, protein 3D modeling, binding site prediction | Automated webserver and Downloadable program |
| Biskit | wraps external programs into automated workflow | BLAST search, T-Coffee alignment, and MODE |
| ESyPred3D | Template detection, alignment, 3D modeling | Automated webserver |
| FoldX | Energy calculations and protein design | Downloadable program |
| Phyre and Phyre2 | Remote template detection, alignment, 3D modeling, multi-templates, ab initio | Webserver with job manager, automatically updated fold library, genome searching and other facilities |
| HHpred | Template detection, alignment, 3D modeling | Interactive webserver with help facility |
| MODELLER | Satisfaction of spatial restraints | Standalone program mainly in Fortran and Python |
| CONFOLD | Satisfaction of contact and distance restraints | Standalone program mainly in Fortran and Perl |
| MOE (Molecular Operating Environment) | Template identification, use of multiple templates and accounting for other environments (e.g. excluded ligand volumes), loop modelling, rotamer libraries for sidechain conformations, relaxation using MM forcefields. | Proprietary platform, supported on Windows, Linux and Mac |
| ROBETTA | Rosetta homology modeling and ab initio fragment assembly with Ginzu domain prediction | Webserver |
| BHAGEERATH-H | Combination of ab initio folding and homology methods | Protein tertiary structure predictions |
| SWISS-MODEL | Local similarity/fragment assembly | Automated webserver (based on ProModII) |
| Yasara | Detection of templates, alignment, modeling incl. ligands and oligomers, hybridization of model fragments | Graphical interface or text mode (clusters) |
| AWSEM-Suite | Molecular dynamics simulation based on template-guided, coevolutionary-enhanced optimized folding landscapes | Automated webserver |

Тридинг

|  |  |  |
| --- | --- | --- |
| IntFOLD | A unified interface for: Tertiary structure prediction/3D modelling, 3D model quality assessment, Intrinsic disorder prediction, Domain prediction, Prediction of protein-ligand binding residues | Automated webserver and some downloadable programs |
| RaptorX | Remote template detection, single-template and multi-template threading, totally different from and much better than the old program RAPTOR designed by the same group | Webserver with job manager, automatically updated fold library |
| HHpred | Template detection, alignment, 3D modeling | Interactive webserver with help facility |
| Phyre and Phyre2 | Remote template detection, alignment, 3D modeling, multi-templates, ab initio | Webserver with job manager, automatically updated fold library, genome searching and other facilities |
| I-TASSER | Threading fragment structure reassembly | On-line server for protein modeling |

Ab initio (или de novo) моделирование

|  |  |  |
| --- | --- | --- |
| trRosetta | trRosetta is an algorithm for fast and accurate de novo protein structure prediction. It builds the protein structure based on direct energy minimizations with a restrained Rosetta. The restraints include inter-residue distance and orientation distributions, predicted by a deep residual neural network. | Webserver and source codes. It takes about one hour to fold proteins with ~300 AAs |
| ROBETTA | Rosetta homology modeling and ab initio fragment assembly with Ginzu domain prediction | Webserver |
| Rosetta@home | Distributed-computing implementation of Rosetta algorithm | Downloadable program |
| Abalone | Molecular Dynamics folding | Program |
| C-QUARK | C-QUARK is a method for ab initio protein structure prediction. Based on deep-learning based contact-map predictions into the fragment assembly simulations. | Webserver |

**CASP - конкурс методов предсказания структуры белков**

**Highly accurate protein structure prediction with AlphaFold.**/ Nature | Vol 596 | 26 August 2021. https://www.nature.com/articles/s41586-021-03819-2