

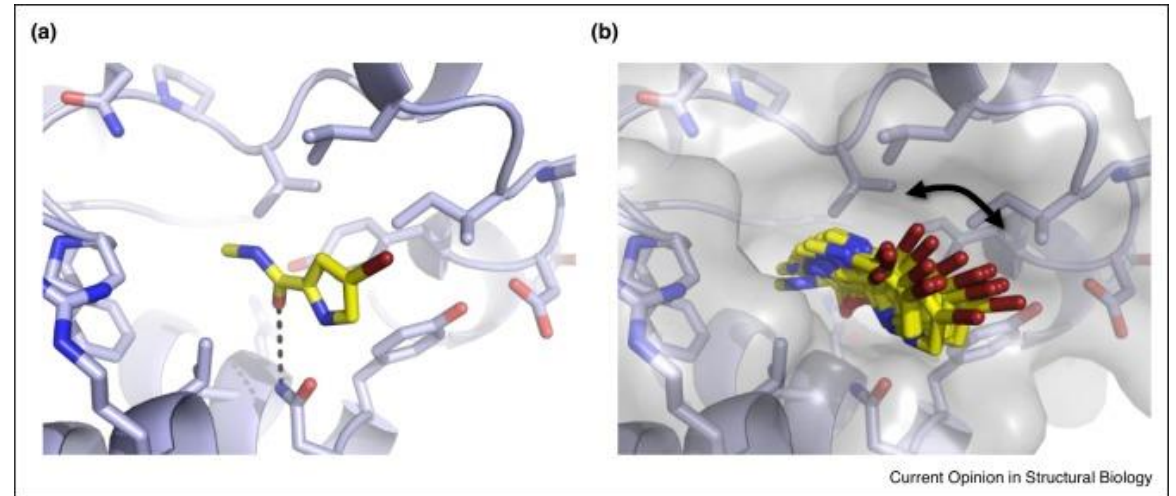


Prediction of protein structures

New AI-prediction system, “*AlphaFold*”

Why protein structure?

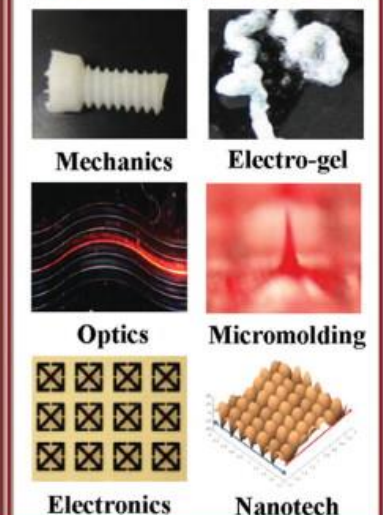
- Drug design
- Material use
- catalysts



Protein Composite Materials

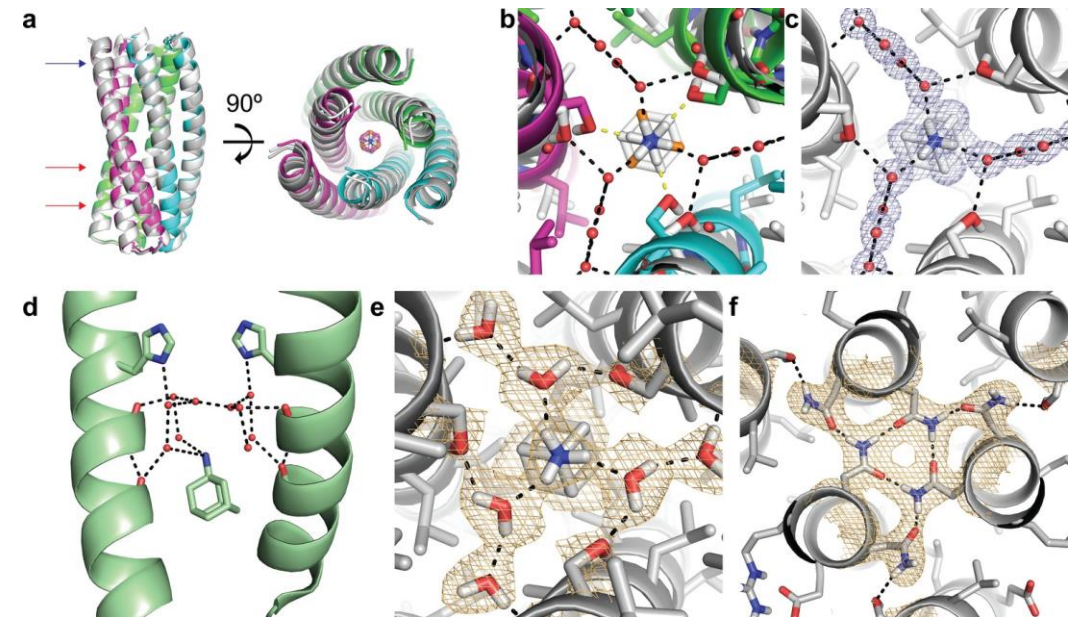
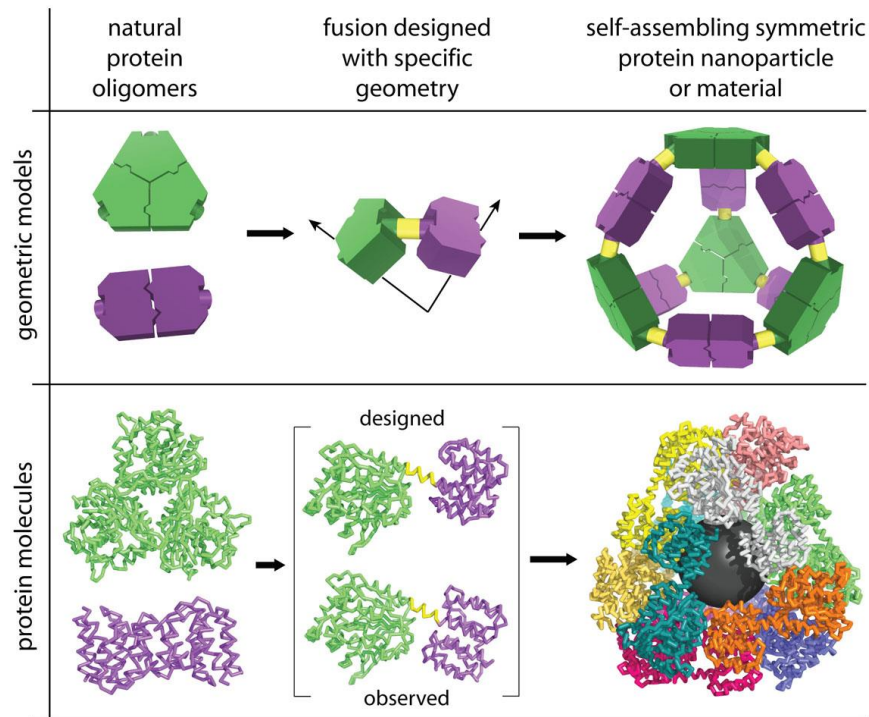


Emerging Materials



Designing protein

- Geometrically assembled protein-based material is expected to be used in various industrial fields.

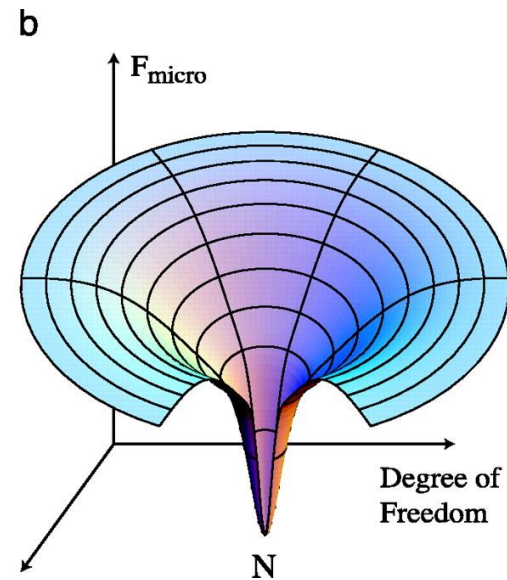
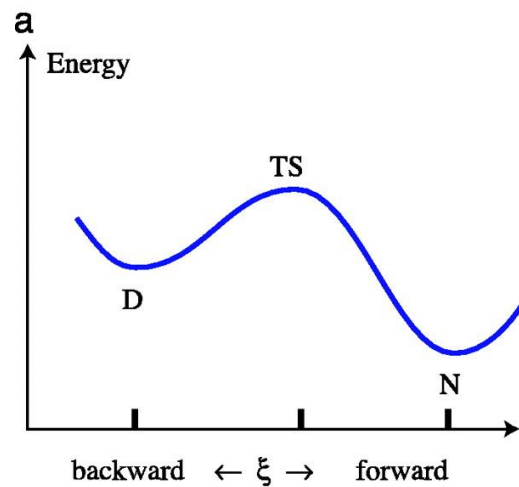




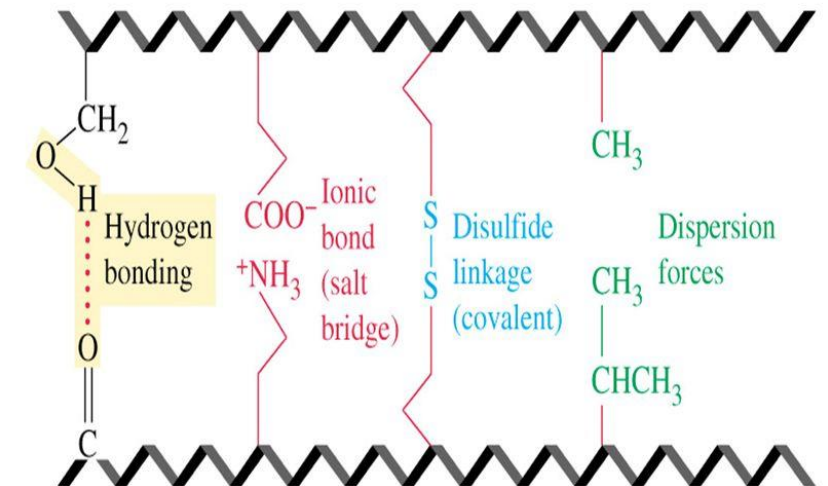
History of protein structure prediction

- Thermodynamics simulation
 - Homology prediction
- 

Thermodynamics simulation: theory

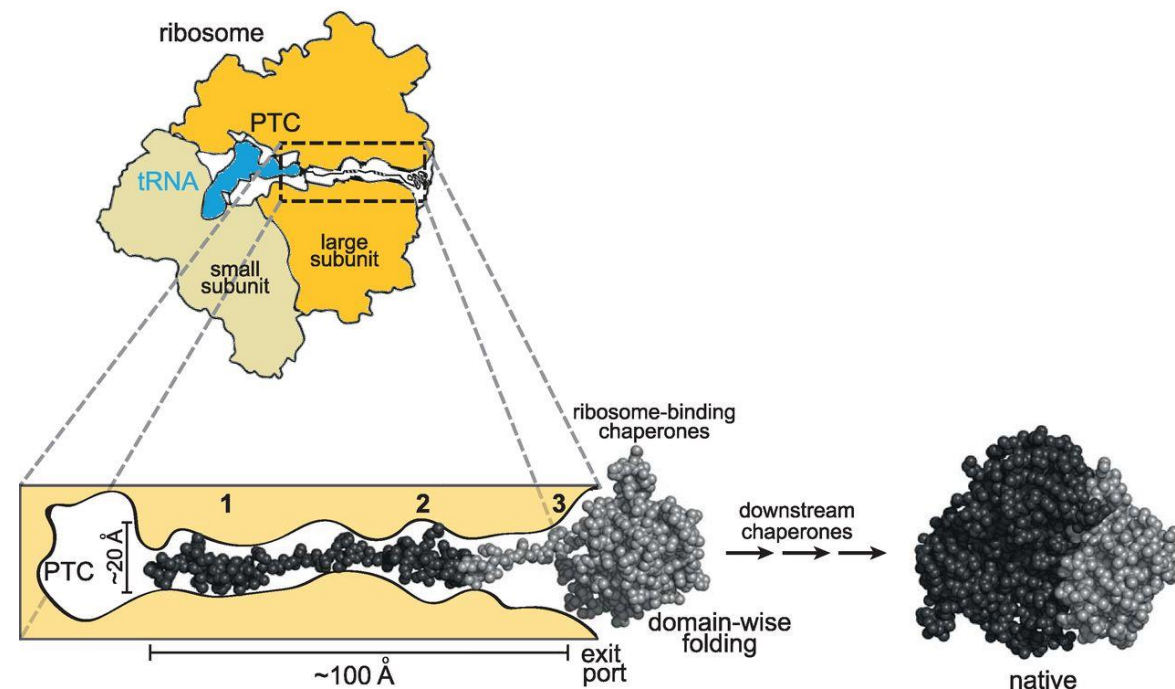
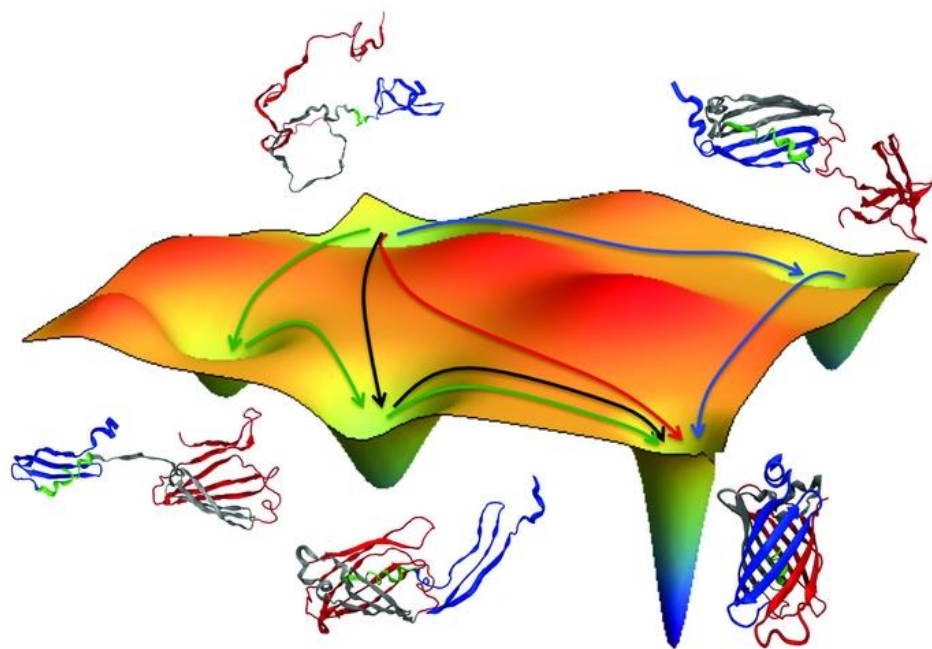


INTERMOLECULAR FORCES IN PROTEIN STRUCTURE

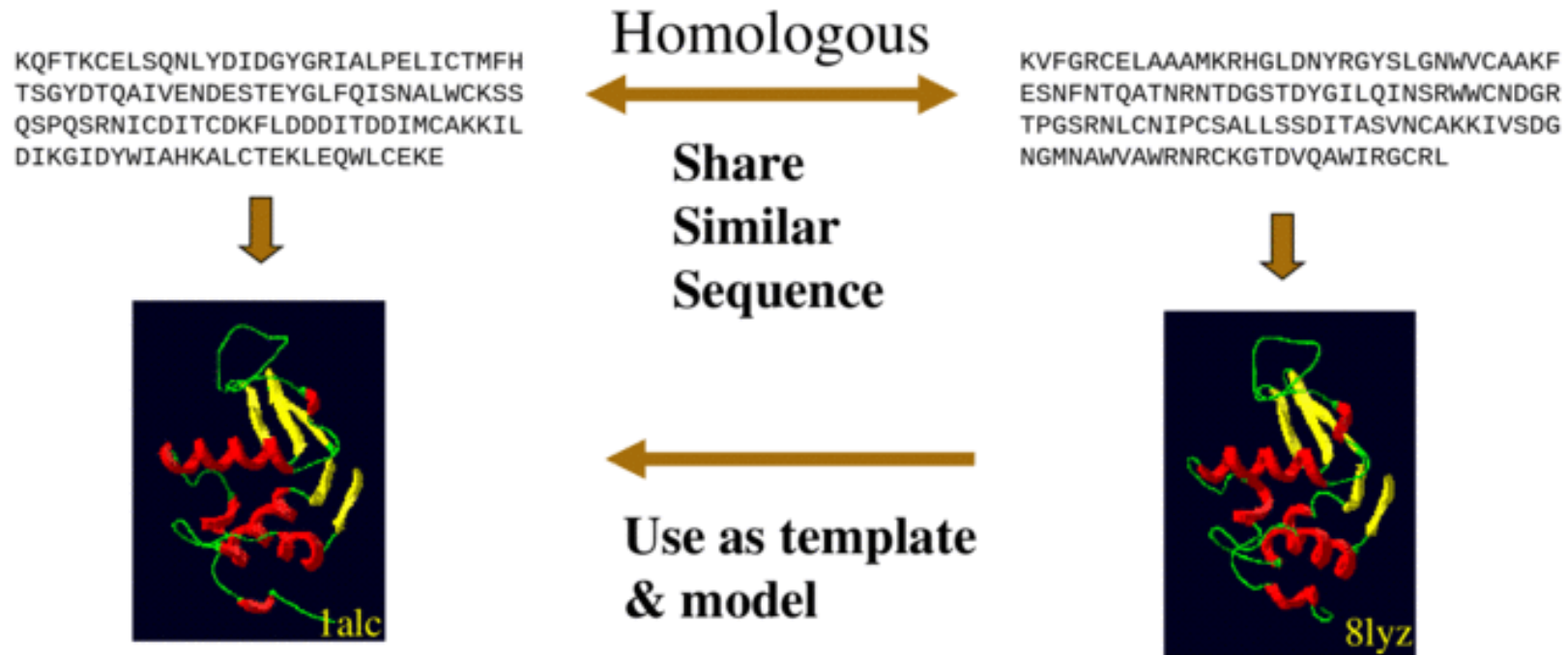


The 4 types of interactions that determine tertiary structure of proteins are shown. Though varying in strength, each set of interactions is significant in the formation of intrachain bonds that fixes the structure of the overall polymer.






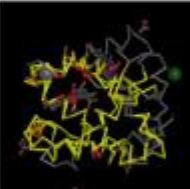




Thermodynamics simulation: problems

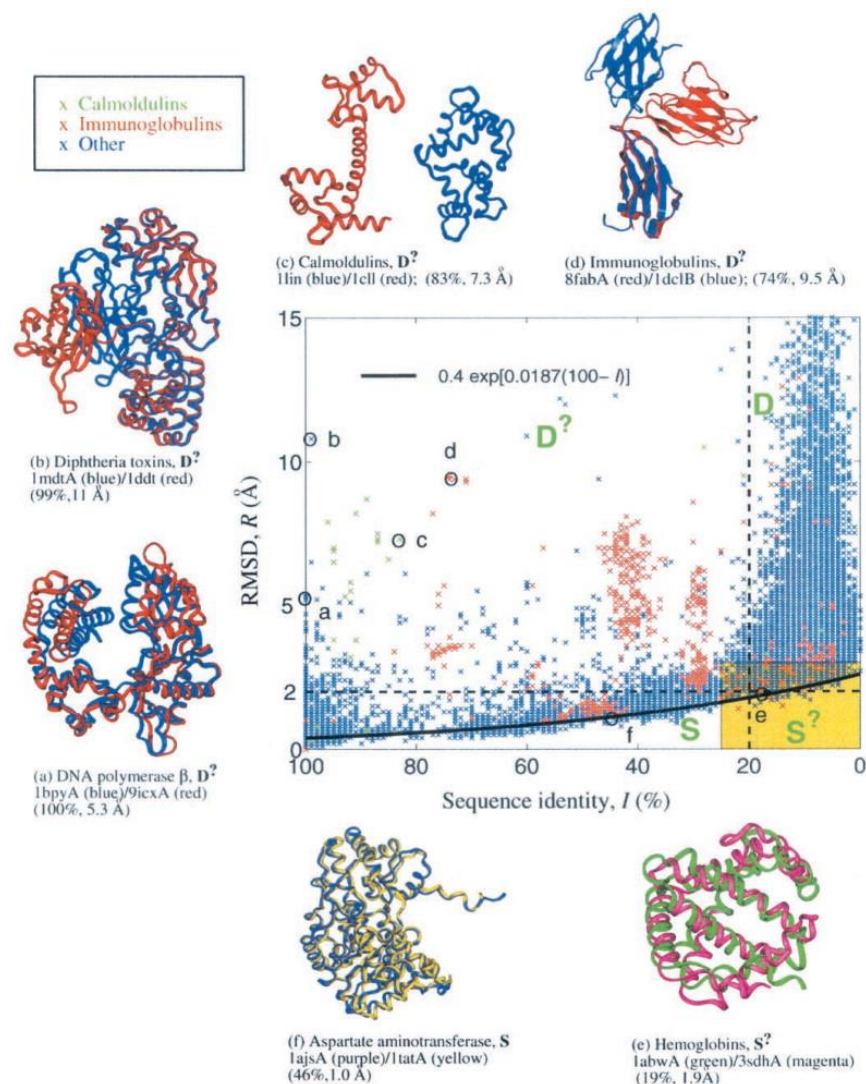


Homology prediction: theory



Homology prediction: problems

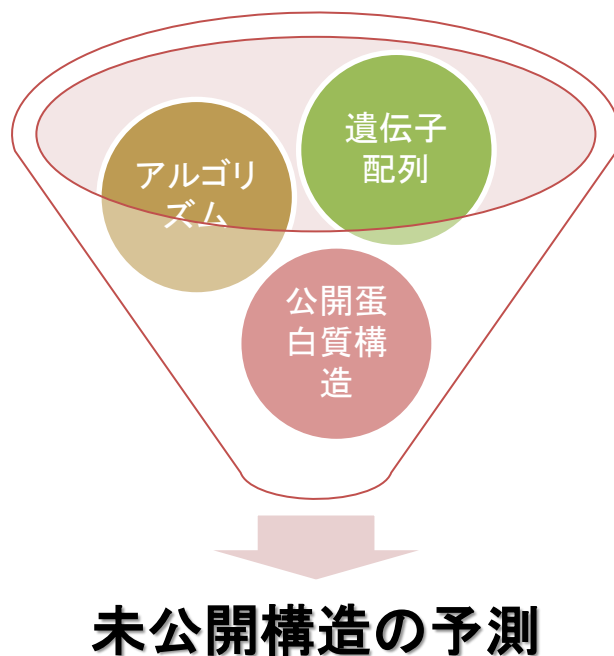
PDB # - Function	RMSD - % Identity	Images from PyMOL and Cn3D		References
Example 1 <ul style="list-style-type: none"> 2GTL_Chain A: <i>Lumbricus terrestris</i> (annelide) hemoglobin part of a 3.6million Dalton protein. Transports oxygen. 1H97_Chain A: <i>Paramphistomum epiclitum</i> (trematode) monomeric hemoglobin. High affinity to oxygen. 	RMSD: 2.3 Identity: 12.1%			24, 25
Example 2 <ul style="list-style-type: none"> 2GNW_Chain B: Found in plants. Its role is not yet determined. <i>Oryza sativa</i>. 2W31_Chain A: detects oxygen and transmits signal. <i>Geobacter sulfurreducens</i>. 	RMSD: 3.2 Identity: 13.4%			27, 28
Example 3 <ul style="list-style-type: none"> 2GLN_Chain A: nitric oxide scavenging. <i>Mycobacterium tuberculosis</i>. 2ZS1_Chain A: extracellular giant Hb. Cooperative oxygen binding via inorganic cations. <i>Oligobranchia mashikoi</i>. 	RMSD: 2.4 Identity: 6.7%			28, 29
Example 4 <ul style="list-style-type: none"> 1KN1_Chain A: allophycocyanin, absorbs light, part of phycobilisomes and phycobilisome structural family. <i>Pyropia yezoensis</i>. 2BNL_Chain C: Non heme, regulates s factor after environmental stress. <i>Bacillus subtilis</i> 	RMSD: 2.9 Identity: 11.4%			30, 31
Example 5 <ul style="list-style-type: none"> 2VEB_Chain A: Found in archae, role is not yet determined. <i>Methanosarcina acetivorans</i>. 1OJ6_Chain A: A neuroglobin found in human brain. Binds to oxygen. <i>Homo sapiens</i>. 	RMSD: 2.9 Identity: 12.7%			32, 33



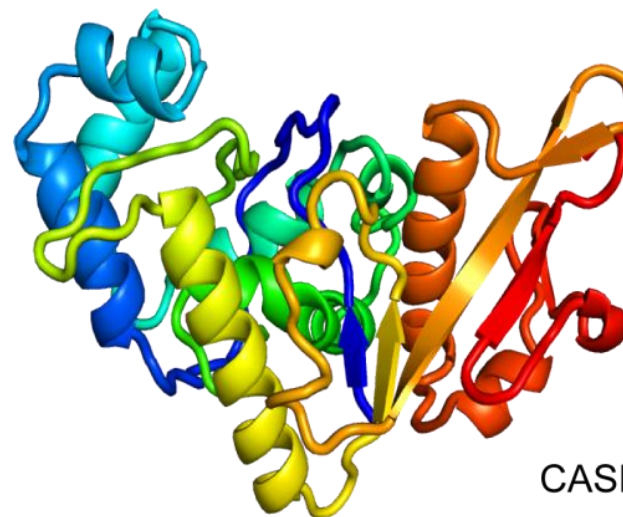
Critical Assessment of protein Structure Prediction



タンパク質構造予測精密評価 (Critical Assessment of protein Structure Prediction、略称: CASP) は、1994年から2年ごとに行われているタンパク質構造予測のための世界的な実験である。

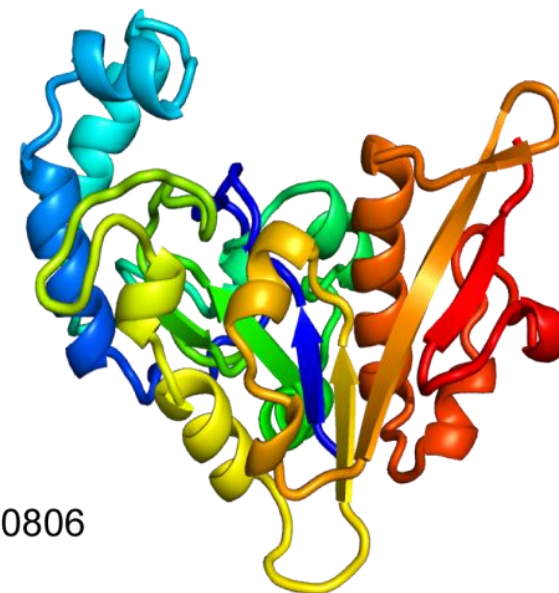


Prediction



CASP11 T0806

Crystal structure

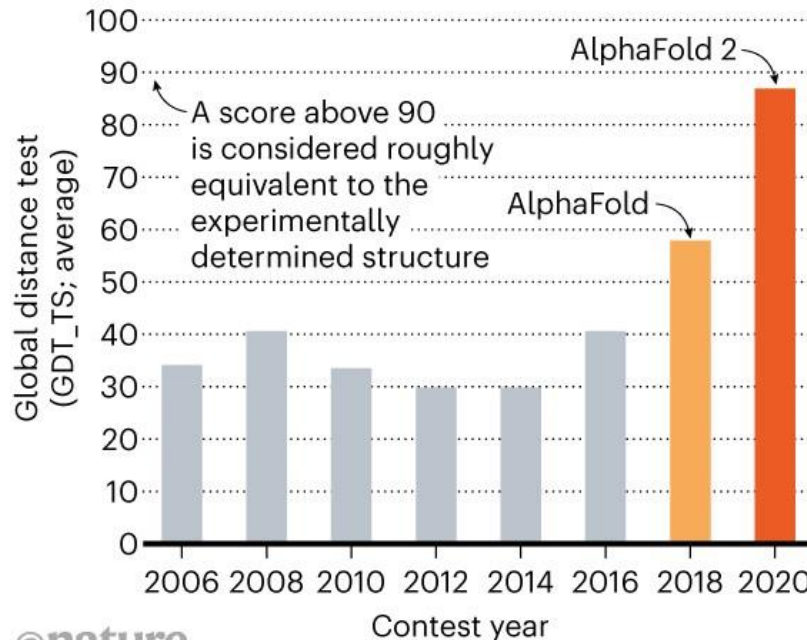


Revolutionary algorithm: AlphaFold

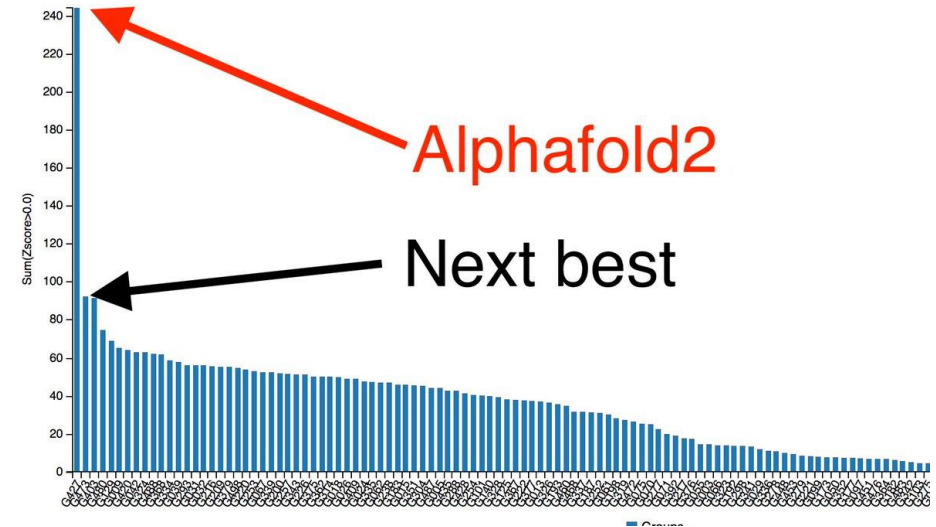
The champion Algorithm in CASP13&14 (2018 & 2020)

STRUCTURE SOLVER

DeepMind's AlphaFold 2 algorithm significantly outperformed other teams at the CASP14 protein-folding contest — and its previous version's performance at the last CASP.



©nature



Revolutionary algorithm: AlphaFold



Demis Hassabis



*Subsidiary of Alphabet (google)

ブルフロッグ・プロダクションとライオンヘッド・スタジオでAIプログラマーとしてのキャリアを積んだのちにゲーム開発会社**エリクサー・スタジオ**を設立。売却後、新しいAIアルゴリズムのインスピレーションを求めて**ロンドン大学で認知神経科学の研究**を行い、優れた業績を納める。研究の合間に企業の準備を行い、2010年に**DeepMind technologies** を設立、CEOを務める。2014年にDeepMind社がGoogleに6億2500万ドルで買収され、エンジニアリング担当副社長になる。開発したプログラム**AlphaGo**で世界最高ランクの囲碁棋士である李世乜に5試合中4試合に勝利した。2018年には開発した**AlphaFold**で蛋白質構造予測で世界トップを取得。2020年には改良を加えた**AlphaFold2**で予測精度の歴史を塗り替えた。

Revolutionary algorithm: AlphaFold

Nature 2021.08.26 (last week!)

Article

Highly accurate protein structure prediction with AlphaFold

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 Check for updates

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Publish AlphaFold algorithm

Article

Highly accurate protein structure prediction for the human proteome

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Extend human proteome

Revolutionary algorithm: AlphaFold

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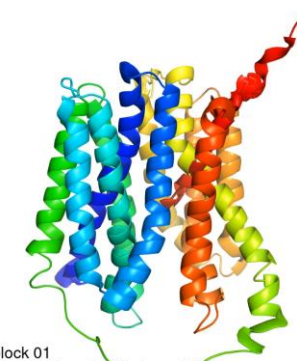
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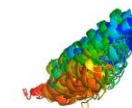
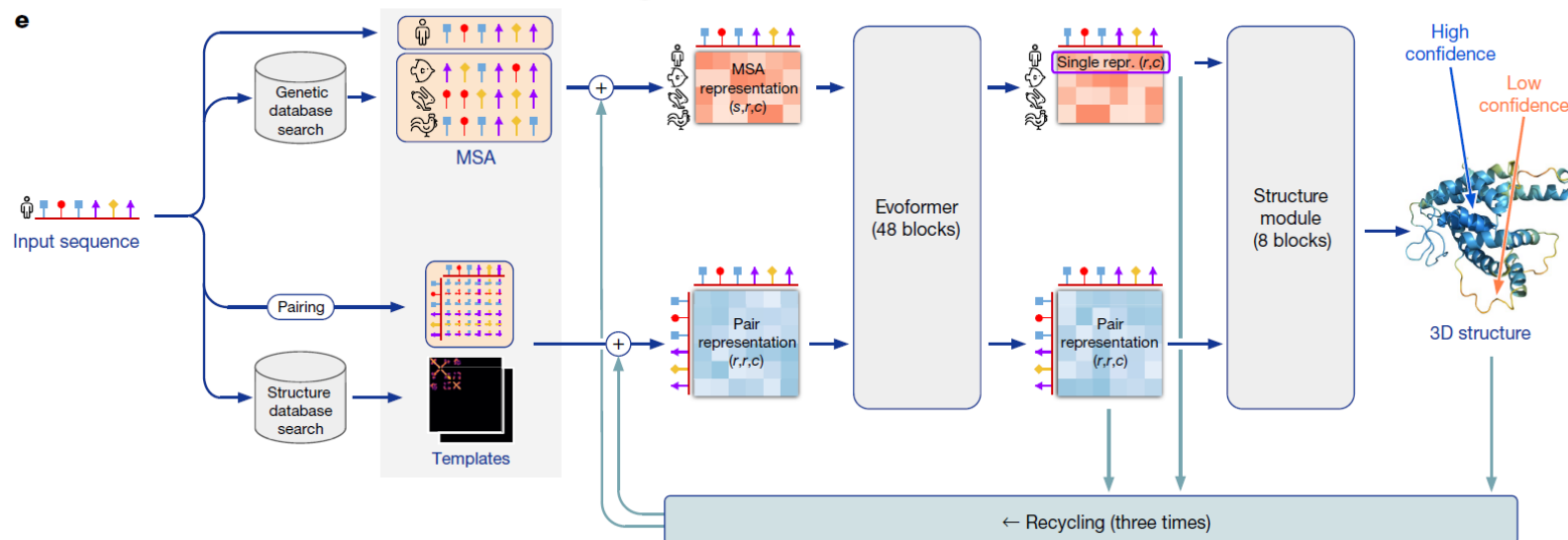
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Recycling iteration 0, block 01
Secondary structure assigned from the final prediction

based on the evolutionary, physical and geometric constraints



Recycling iteration 0, block 01
Secondary structure assigned from the final prediction



Recycling iteration 0, block 01
Secondary structure assigned from the final prediction

Revolutionary algorithm: AlphaFold

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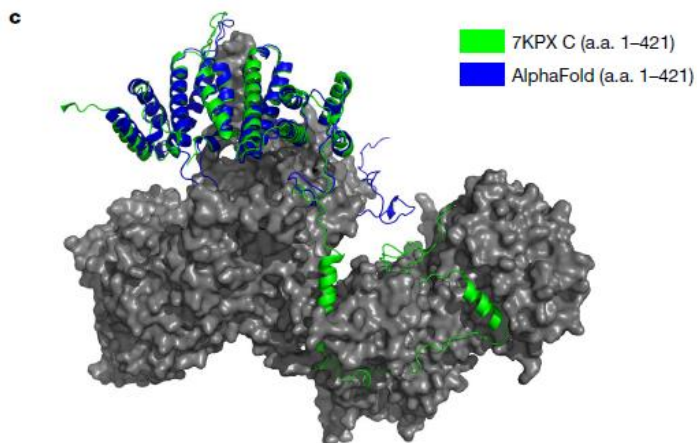
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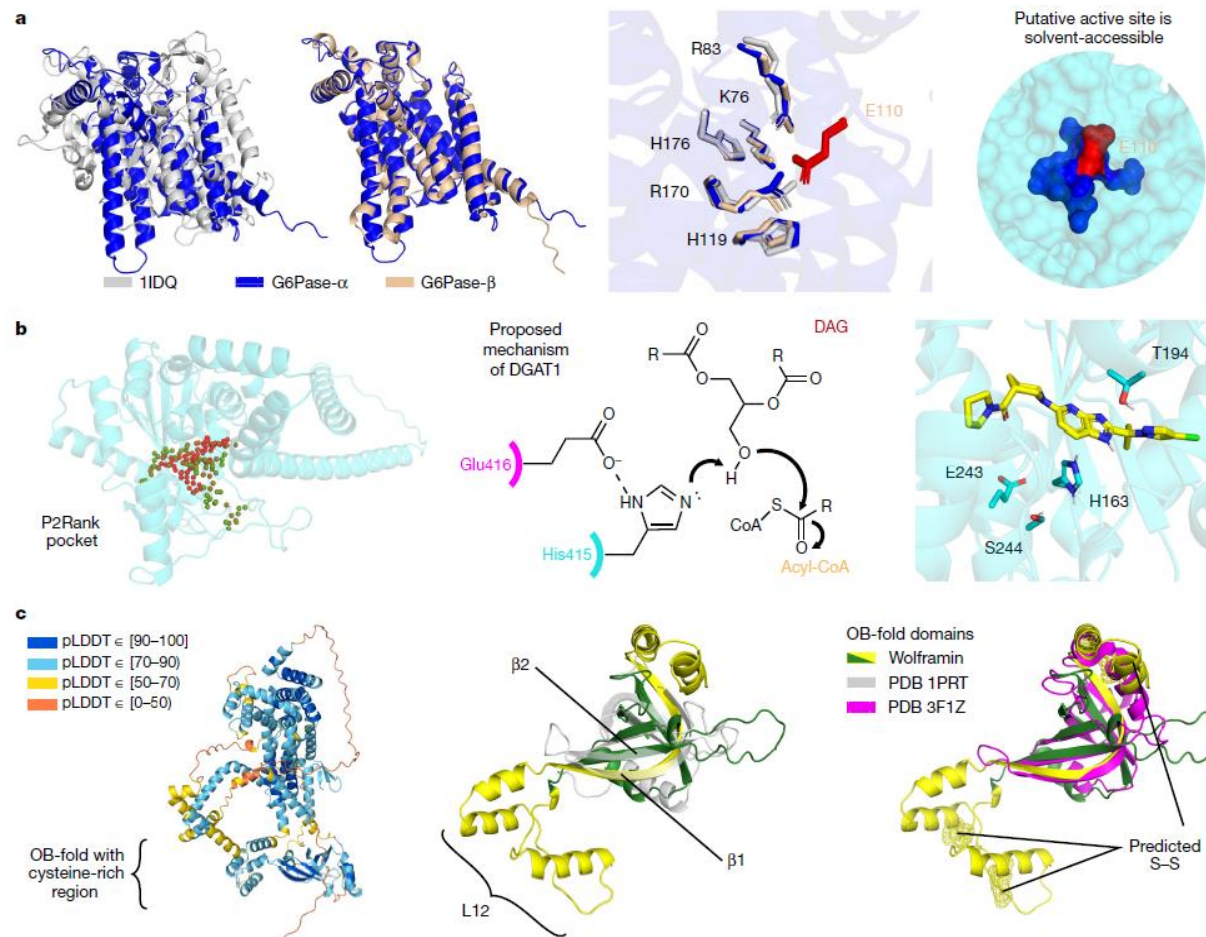
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Problems



Complex structure

Unsolved human protein structures



Summary

