@milouness

fold it BETA
Solve Puzzles for Science

12:43:43 GMT

PUZZLES GROUPS PLAYERS RECIPES CONTESTS
BLOG FEEDBACK FORUM WIKI FAQ ABOUT CREDITS

Click to learn how you contribute to science by playing Foldit.

GET STARTED: DOWNLOAD

Win Beta | Mac Beta | Linux Beta

Windows XP/Vista/7 | Intel OSX 10.4 or later | Linux

RECOMMEND FOLDIT

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USER LOGIN

Username: *

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Log in

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What's New

Small Update

We've posted a small update today that should improve some of the introductory levels!

(Sun, 09/25/2011 - 01:25 | **4 comments**)

Puzzle deadlines extended, global chat help

We have extended the deadlines for the Beginner Puzzle and Puzzle 459 by 3 days (due to all the new visitors to the site).

SOLOISTS	EVOLVERS	GROUPS	TOPICS

PLAYER	PUZZLE	SCORE
mottiger 114 309	New Player (<15...le	8,850
mosiac 114 4751	New Player (<15...le	8,868
auntdeen 7 12	New Player Welc...le	9,087

Crystal structure of a monomeric retroviral protease solved by protein folding game players

Firas Khatib[1], Frank DiMaio[1], Foldit Contenders Group, Foldit Void Crushers Group, Seth Cooper[2], Maciej Kazmierczyk[3], Miroslaw Gilski[3,4], Szymon Krzywda[3], Helena Zabranska[5], Iva Pichova[5], James Thompson[1], Zoran Popović[2], Mariusz Jaskolski[3,4] & David Baker[1,6]

Following the failure of a wide range of attempts to solve the crystal structure of M-PMV retroviral protease by molecular replacement, we challenged players of the protein folding game Foldit to produce accurate models of the protein. Remarkably, Foldit players were able to generate models of sufficient quality for successful molecular replacement and subsequent structure determination. The refined structure provides new insights for the design of antiretroviral drugs.

Foldit is a multiplayer online game that enlists players worldwide to solve difficult protein-structure prediction problems. Foldit players leverage human three-dimensional problem-solving skills to interact with protein structures using direct manipulation tools and algorithms from the Rosetta structure prediction methodology[1]. Players collaborate with teammates while competing with other players to obtain the highest-scoring (lowest-energy) models. In proof-of-

Structure Prediction (CASP) experiment was an ideal venue in which to test this. CASP is a biennial experiment in protein structure prediction methods in which the amino acid sequences of structures that are close to being experimentally determined—referred to as CASP targets—are posted to allow groups from around the world to predict the native structure (http://predictioncenter.org/casp9/). Each group taking part in CASP is allowed to submit five different predictions for each sequence. Foldit participated as an independent group during CASP9 and made predictions for the targets with fewer than 165 residues that the CASP organizers did not indicate as oligomeric. For targets with homologs of known structure—the Template-Based Modeling category—Foldit players were given different alignments to templates predicted by the HHpred server[3] via the new Alignment Tool. Despite these new additions to the game, the performance of Foldit players over all CASP9 Template-Based Modeling targets was not as good as those of the best-performing methods, which made better use of information from homologous structures; extensive energy minimization used by Foldit players tended to perturb peripheral portions of the chain away from the conformations present in homologs.

For prediction problems for which there were no identifiable homologous protein structures—the CASP9 Free Modeling category—Foldit players were given the five Rosetta Server CASP9 submissions (which were publicly available to other prediction groups) as starting points, along with the Alignment Tool. Here all five starting models were available, allowing players to use partial threading to combine different features of the Rosetta models. In this Free Modeling

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Lesson 1:

Our ability to understand the world around is a function of the technologies we have for seeing in the world.

Lesson 2:

The best way to understand the future is to observe the present very, very carefully.

Lesson 3:

No matter how sophisticated your sensemaking tools, they will not help you if you have a wrong or inadequate theory.

Lesson 4:

Every great achievement in human knowledge involves breaking through a problem no one else believes can be solved

Lesson 5:

Many great scientific achievements require you to overcome the opposition of the current experts in the field.

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