



Foldit and Games for Scientific Discovery

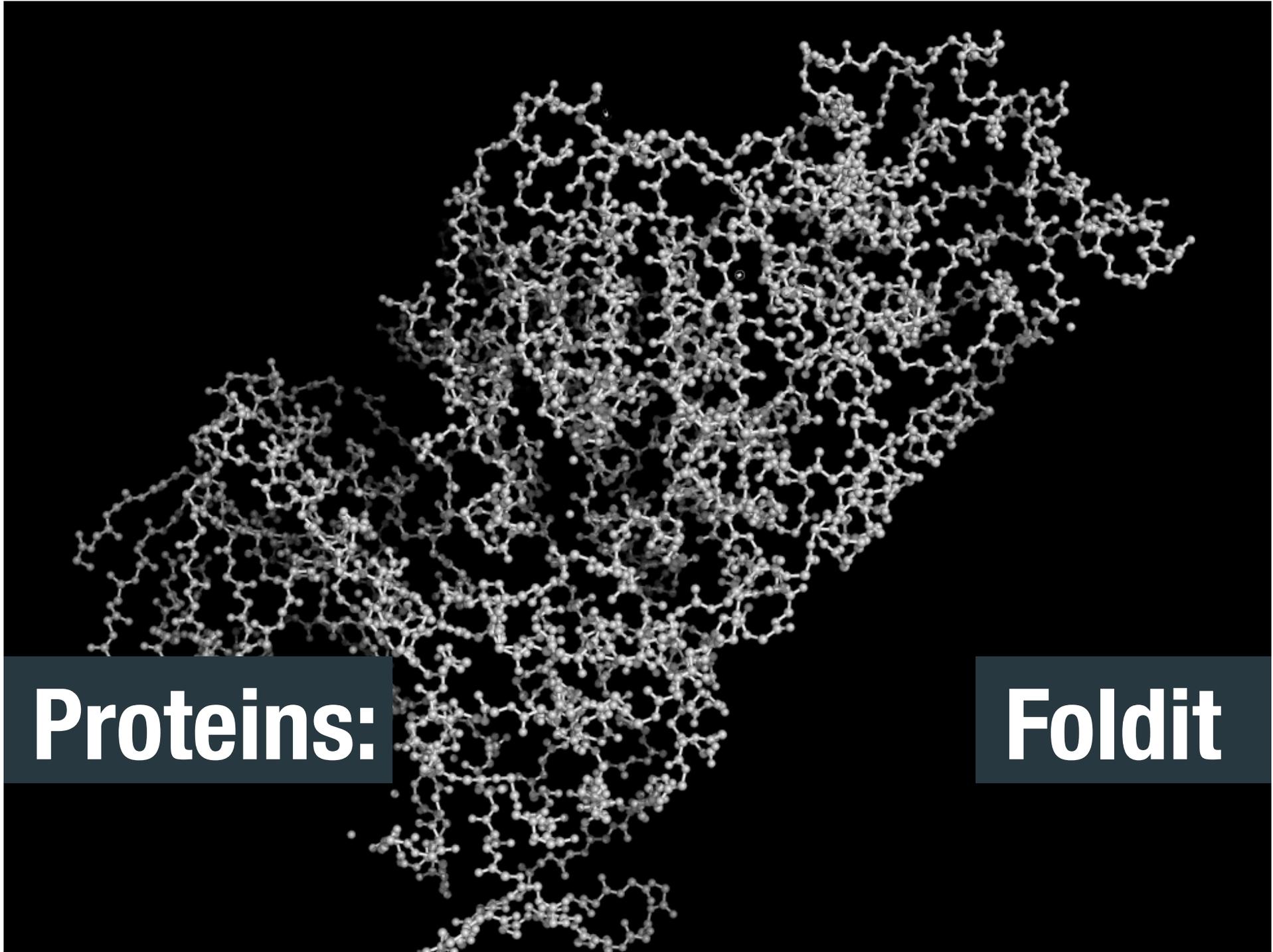
Jeff Flatten

*Center for Game Science
Department of Computer Science
University of Washington*

A photograph of a person with brown hair, seen from the back and side, sitting at a desk and playing a video game. They are holding a black game controller with both hands. In the background, a large television screen displays a game scene with a blue sky and green foliage. The person is wearing a blue t-shirt. The overall scene is brightly lit, suggesting an indoor setting like a living room or a gaming area.

Human Power

Computational Power

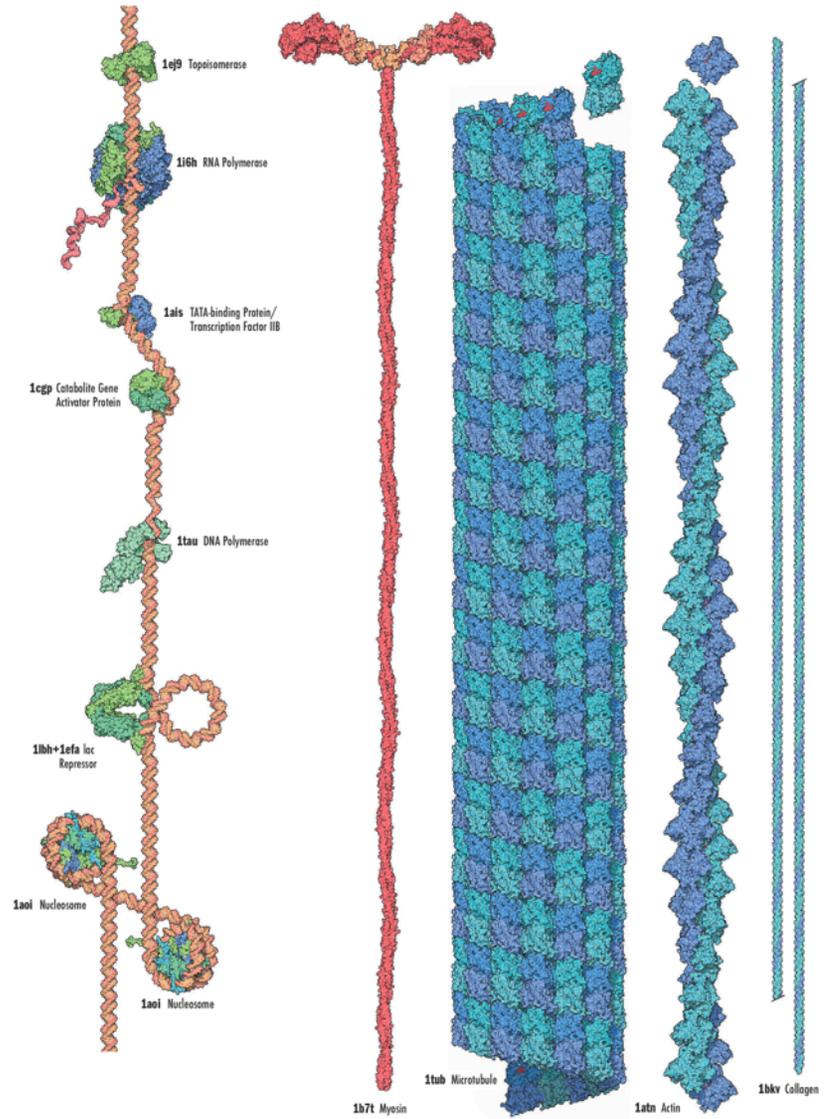
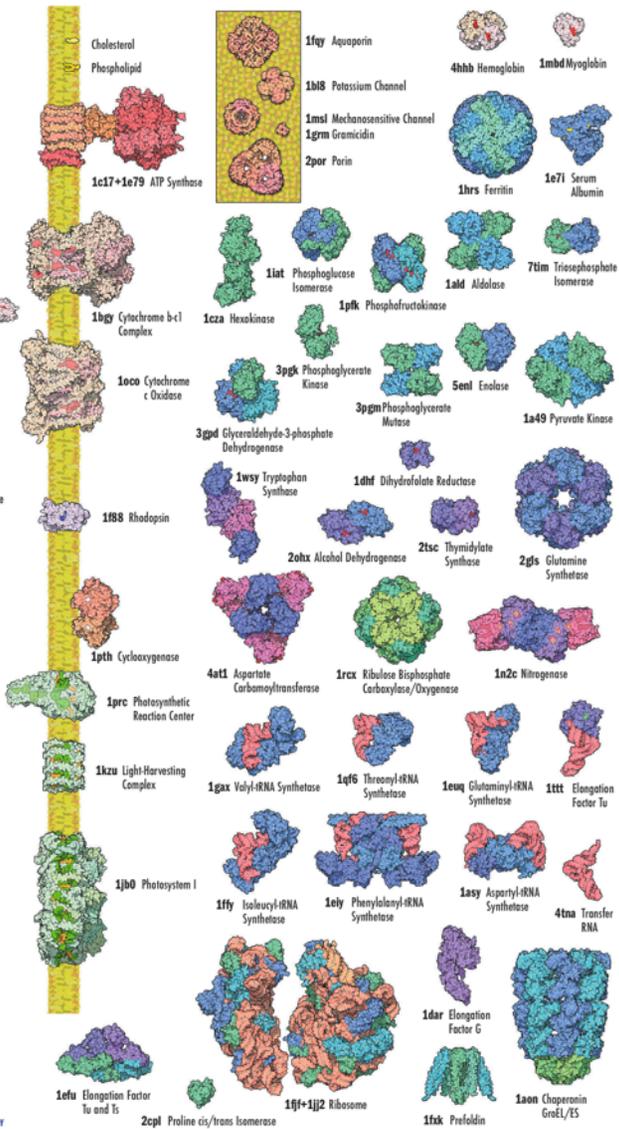
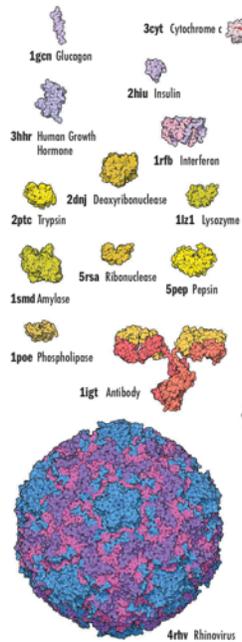


Proteins:

Foldit

Proteins

MOLECULAR MACHINERY: A Tour of the Protein Data Bank



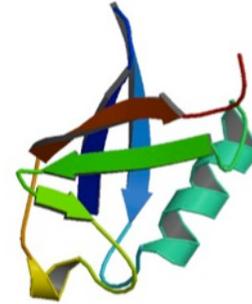
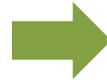
Proteins

MQIFVKTLTGKTILEVEPSDTIE...

Sequence

Proteins

MQIFVKTLTGKTILEVEPSDTIE...

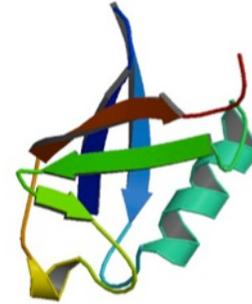


Sequence

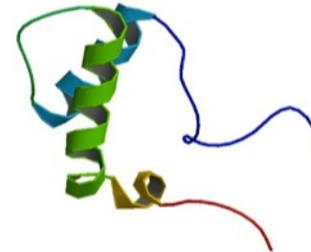
3D Structure

Proteins

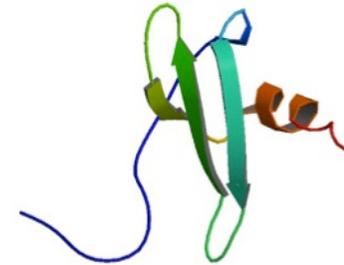
MQIFVKTLTGKTILEVEPSDTIE...



MGKYDKQIDLSTVDLKKLRVKEL...



KPVLSYRCPCRFFESHVARANV...

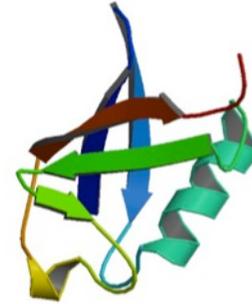


⋮
Sequence

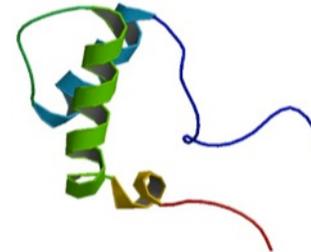
⋮
3D Structure

Proteins

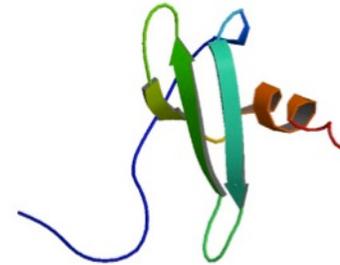
MQIFVKTLTGKTILEVEPSDTIE...



MGKYDKQIDLSTVDLKKLRVKEL...



KPVLSYRCPCRFFESHVARANV...



⋮

Sequence
EASY

⋮

3D Structure
HARD

Proteins

MKTLYDLPIVLRNLPEDLVLEKP...



?

SMSDTAERVKKIVVEHLGVDAK...



?

GPLGSDQYIVVNGAPVIPSAPKVP...



?

⋮

Sequence

EASY

⋮

3D Structure

HARD

Proteins

MKTLYDLPIVLRNLPEDLVLEKP...



?

SMSDTAERVKKIVVEHLGVADK...



?

GPLGSDQYIVVNGAPVIPSAKVP...



?

⋮

Sequence

EASY

⋮

3D Structure

HARD

Proteins

MKTLYDLPIVLRNLPEDLVLEKP...



SMSDTAERVKKIVVEHLGVDAK...



GPLGSDQYIVVNGAPVIPSAKVP...



⋮

Sequence

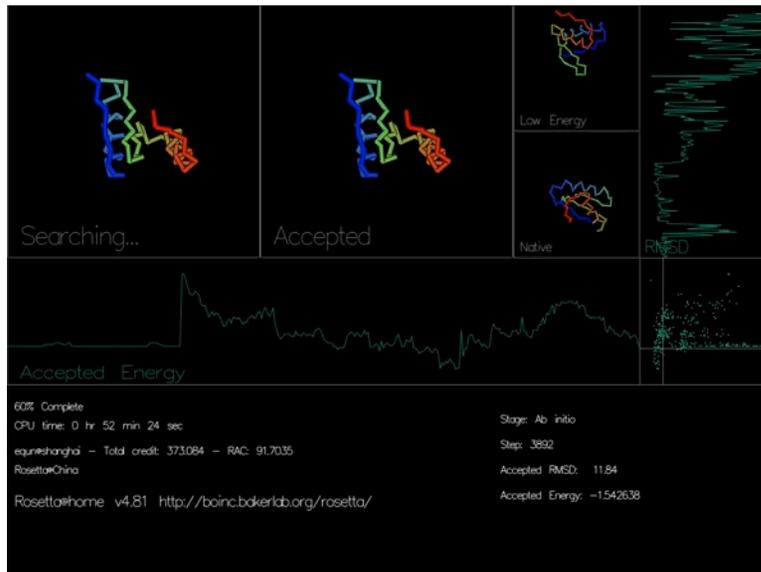
EASY

⋮

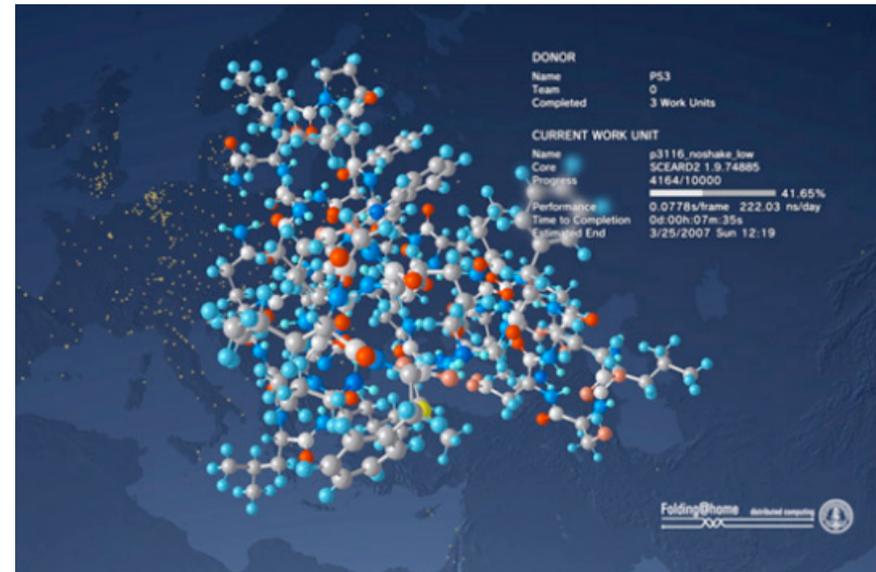
3D Structure

HARD

Distributed computing



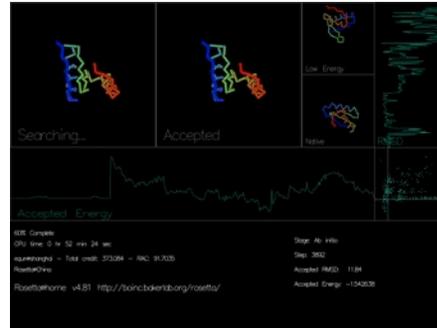
Rosetta@home



Folding@home
(most powerful distributed computing cluster in the world!)

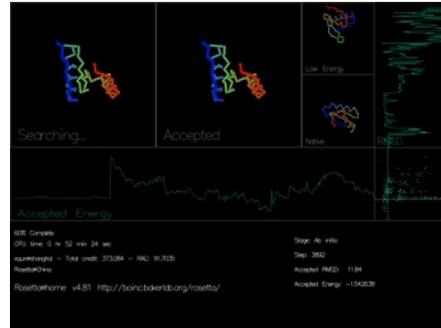
Why a game?

Computationally
Difficult



Why a game?

Computationally
Difficult



Human
Skills

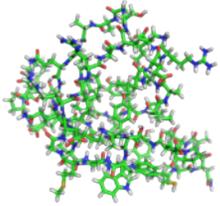


Foldit

The image shows a screenshot of the Foldit game interface. The central focus is a 3D protein structure rendered in a stick-and-ball style, with segments colored in shades of green, tan, and red. The structure is complex and folded. The interface includes several panels:

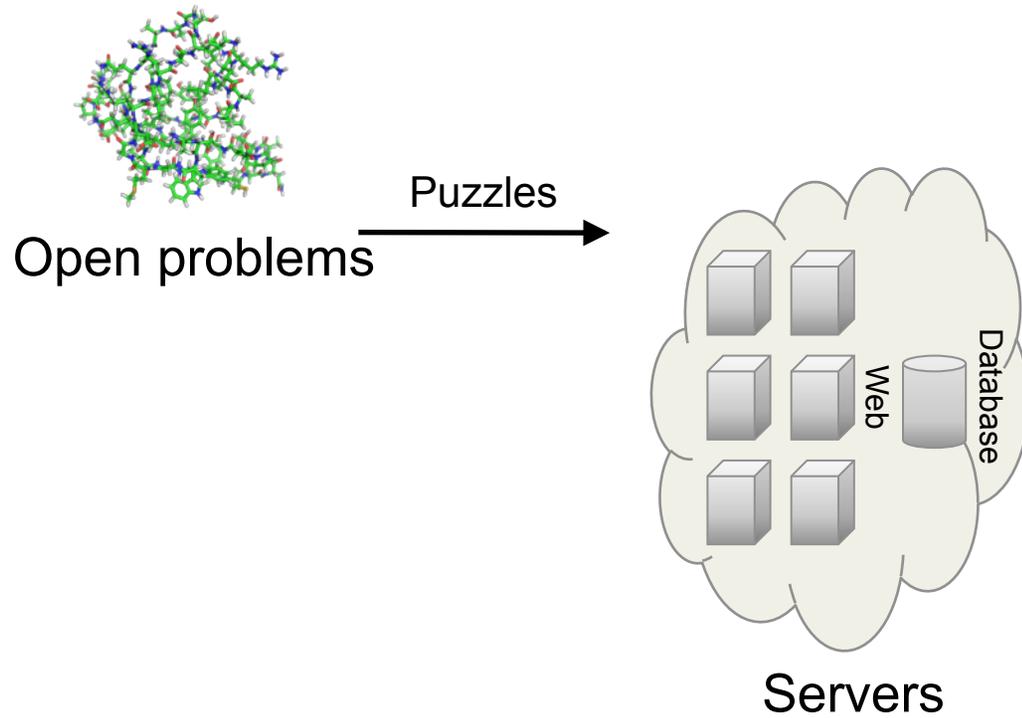
- Top Left:** A button labeled "Pull Mode".
- Top Center:** A panel showing "Rank: -" and "Score: 0" with a small input field. Below this, it says "Soloist" and "BETA Prediction Test" with a sub-option "No bonuses or conditions".
- Top Right:** A panel with two options: "Group Competition" and "Soloist Competition".
- Left Side:** A vertical toolbar with icons for various actions, including a sequence of amino acids: "K O O D R K K O O C".
- Bottom Left:** A navigation bar with buttons for "Actions", "Undo", "Modes", "Behavior", "View", and "Menu".
- Bottom Right:** A panel with three options: "Chat - Puzzle", "Chat - Global", and "Notifications". Each option has a small icon and a toggle switch labeled "auto show".

Foldit Architecture

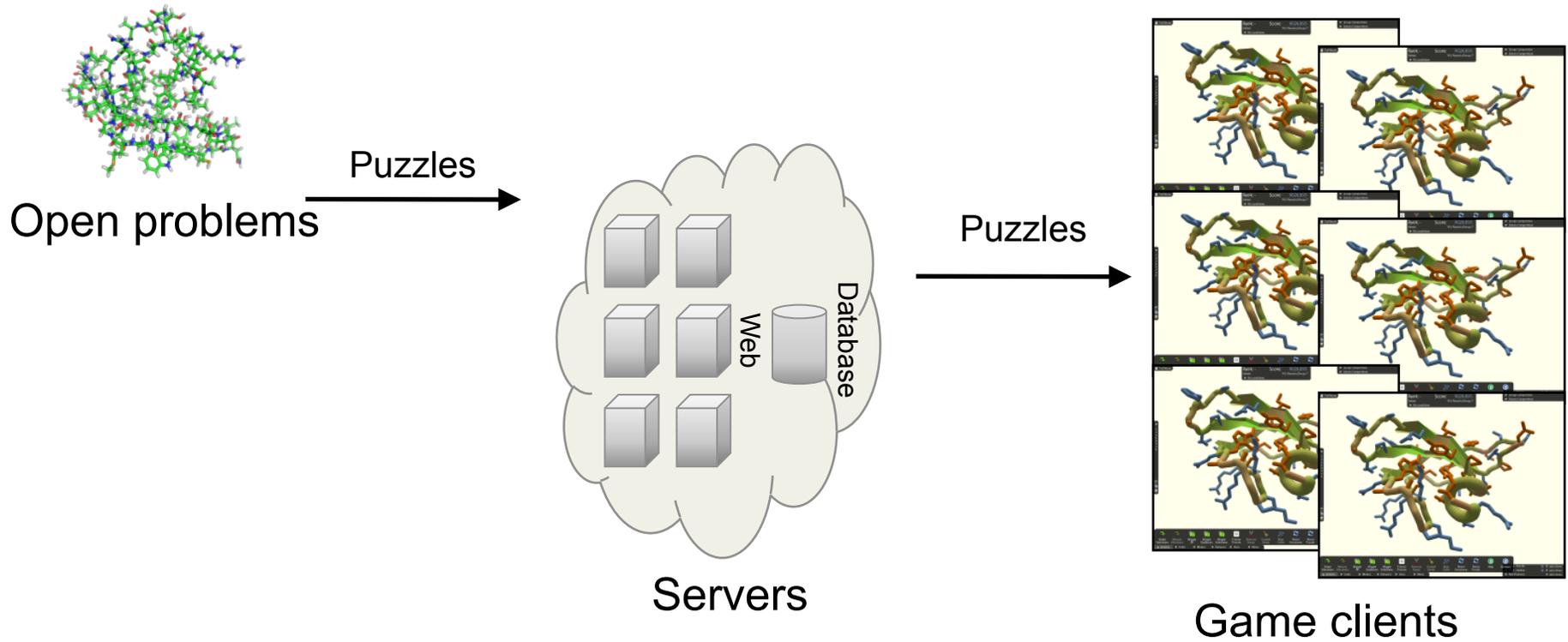


Open problems

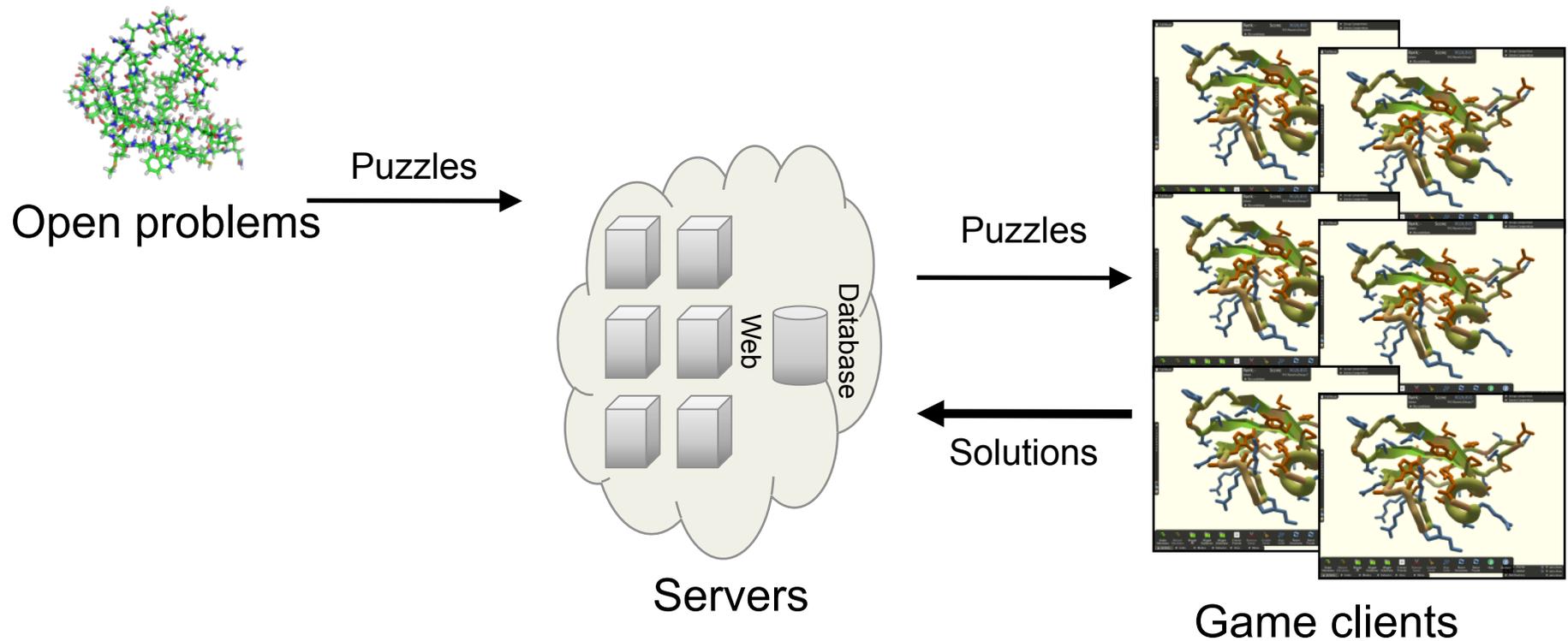
Foldit Architecture



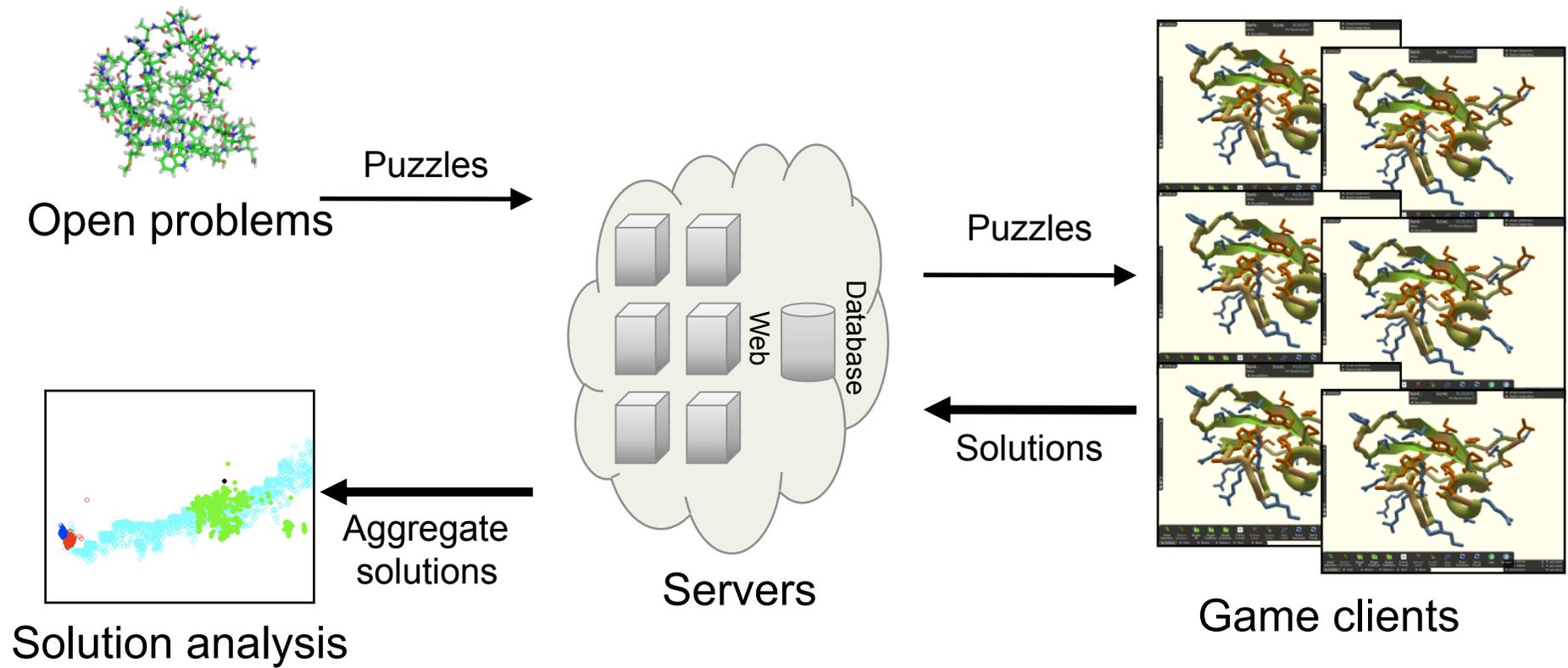
Foldit Architecture



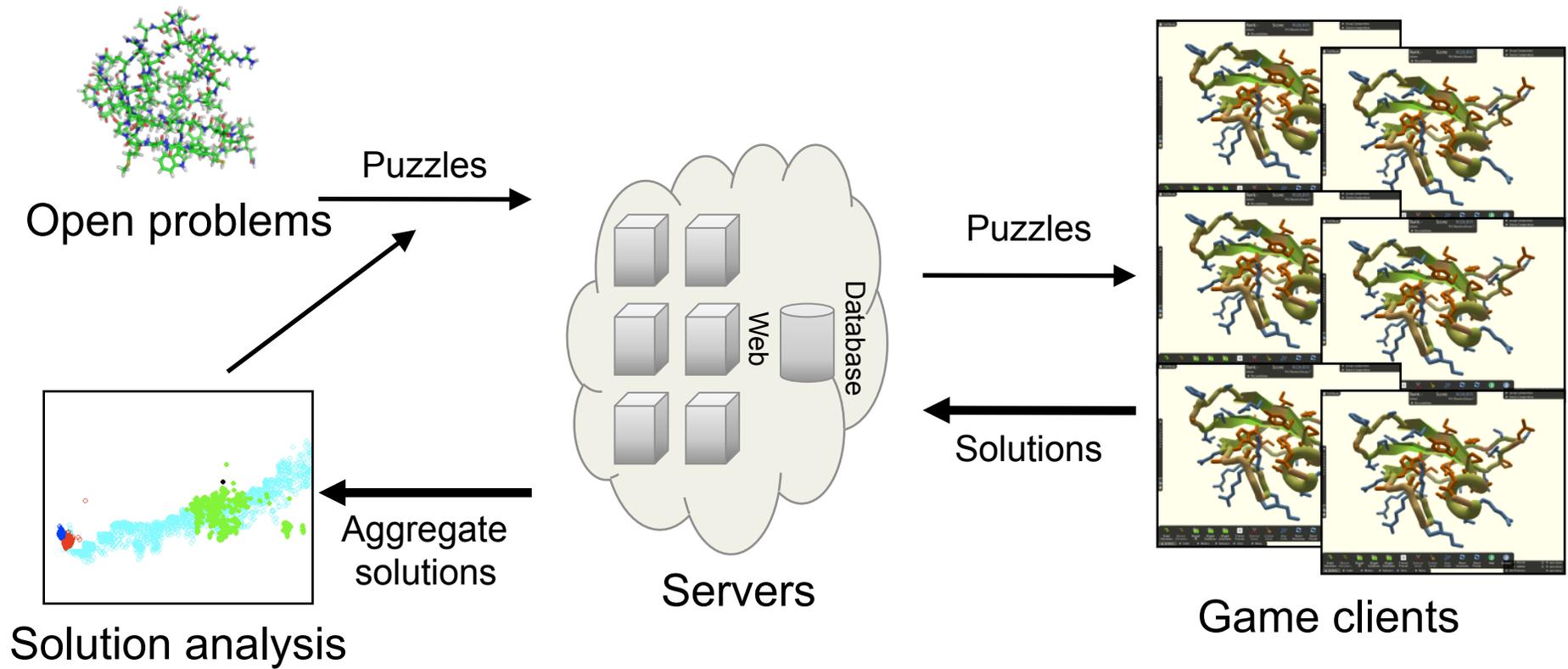
Foldit Architecture



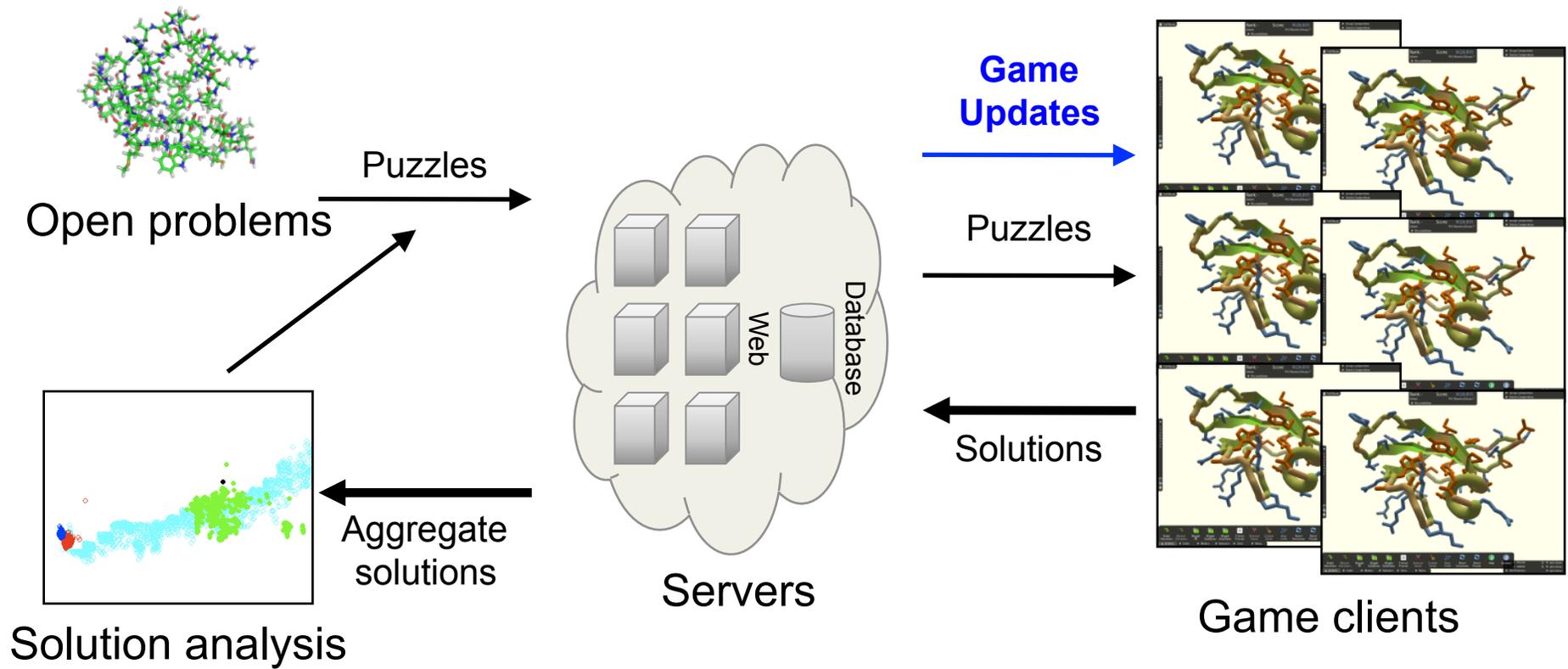
Foldit Architecture



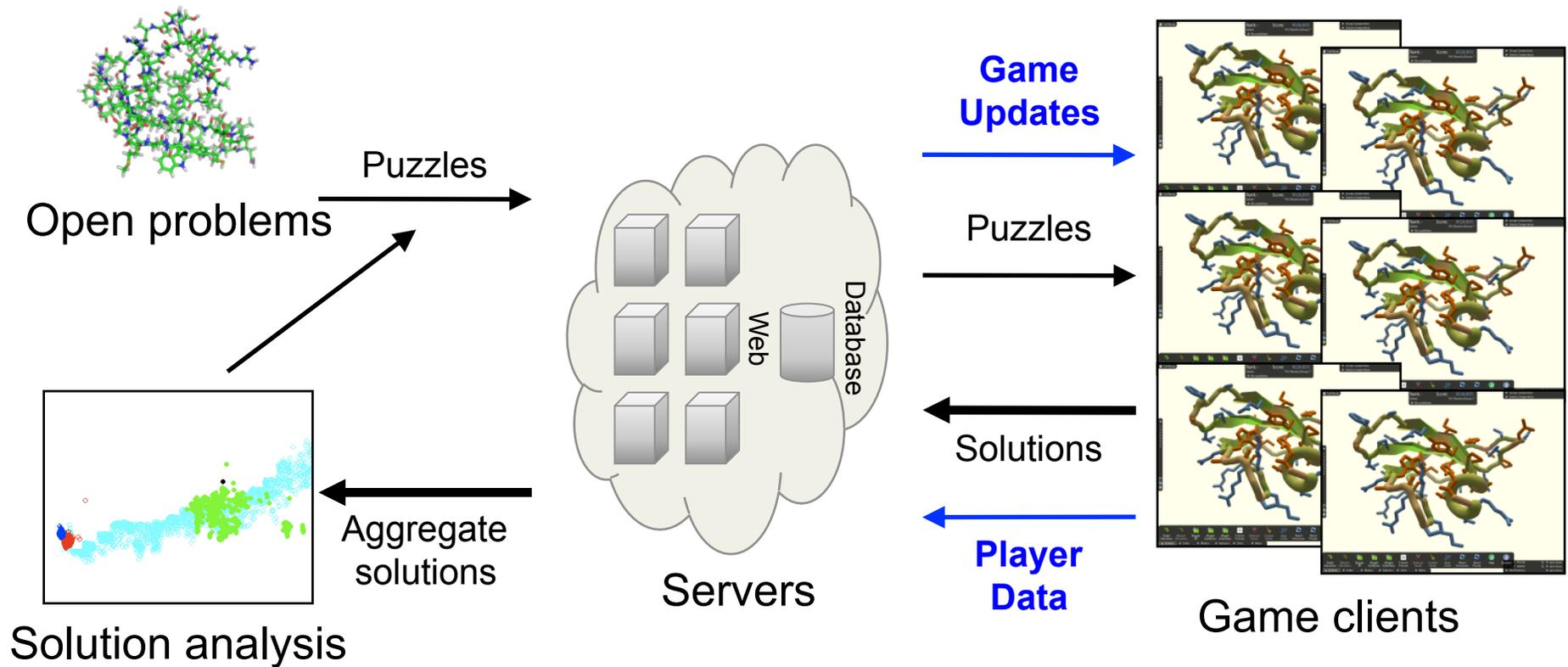
Foldit Architecture



Foldit Architecture



Foldit Architecture



Foldit Scoring

Rank: 436 Score: 7011 
Soloist Beginner Puzzle 20: Alignment Tool
▶ No bonuses or conditions

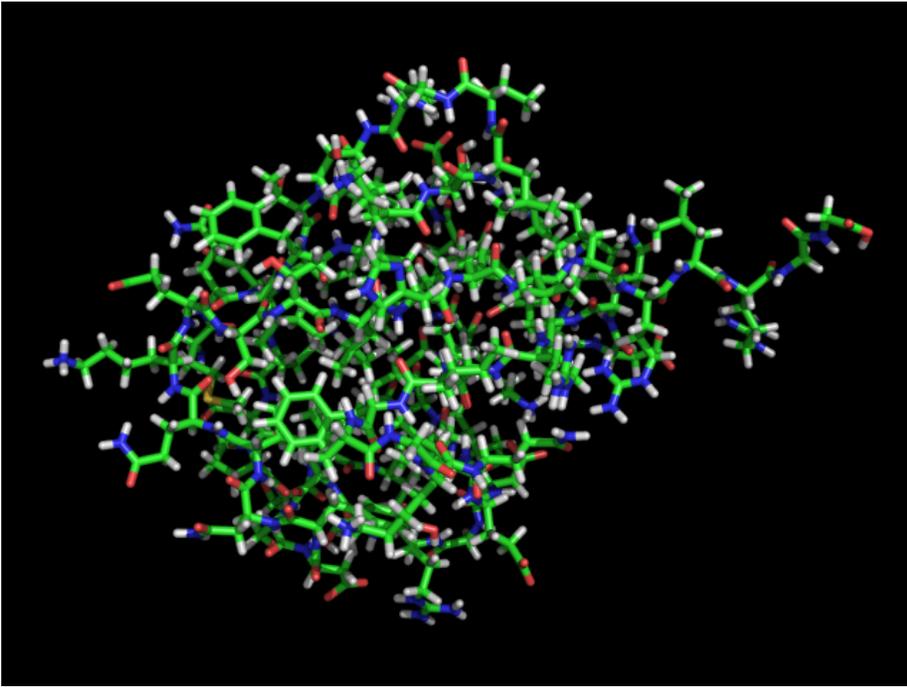
Foldit Scoring

Rank **436** Score: 7011 
Soloist Beginner Puzzle 20: Alignment Tool
▶ No bonuses or conditions

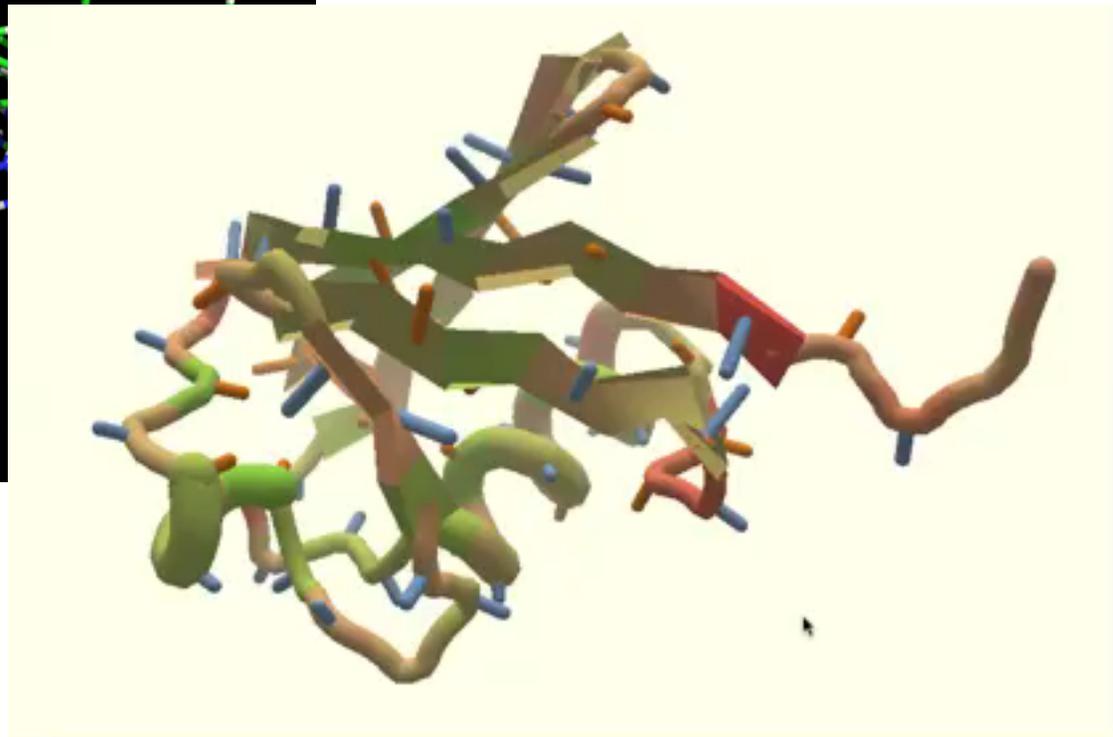
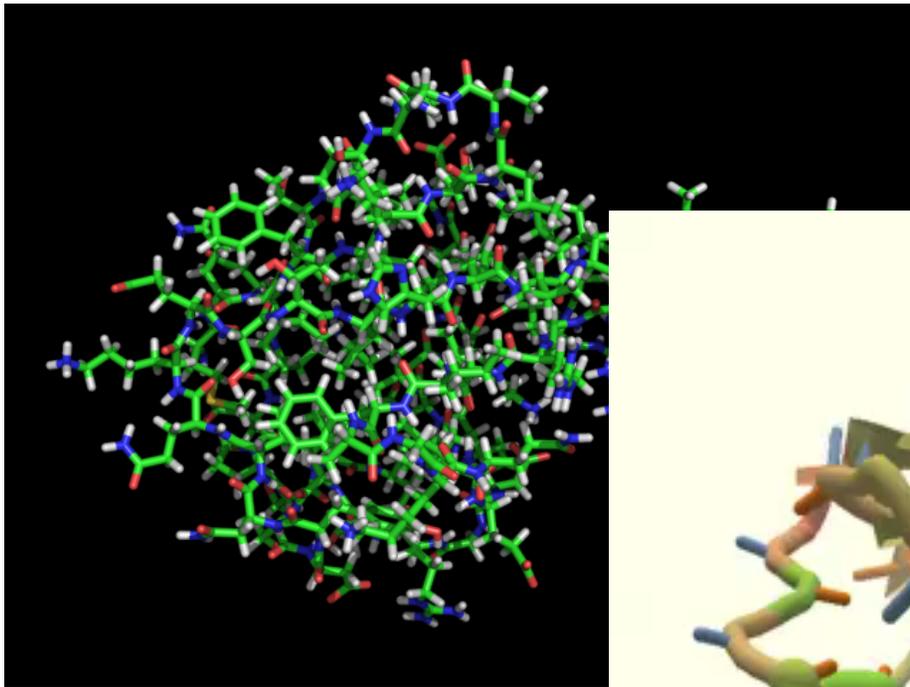
▼ Group Competition		
23	Hungary	8963 ▲
24	Rechenkraft.net	7725
25	Mmm Helix Fries.	7275
26	Leprosorium	7234
27	Cedarburg H.S.	7116
28	Team.Philou.Canailou	7055
29	test_group1	7011
30	Boinc.be	6530 ▼

▼ Soloist Competition		
432	mikeuressner	- 7030 ▲
433	yaDad	- 7029
434	Evil Llama	- 7024
435	tchang	- 7018
436	test_account1	7011 7011
437	xaoren	- 7010
438	lukaszbk	- 7009
439	Coon	- 7006
440	edamrzedniczek	- 7003 ▼

Visualizations

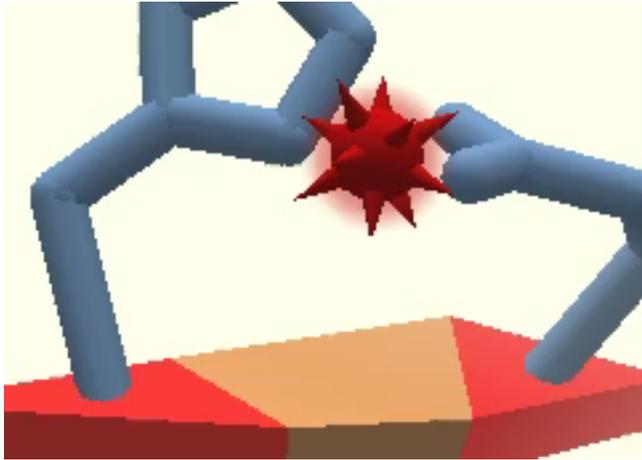


Visualizations



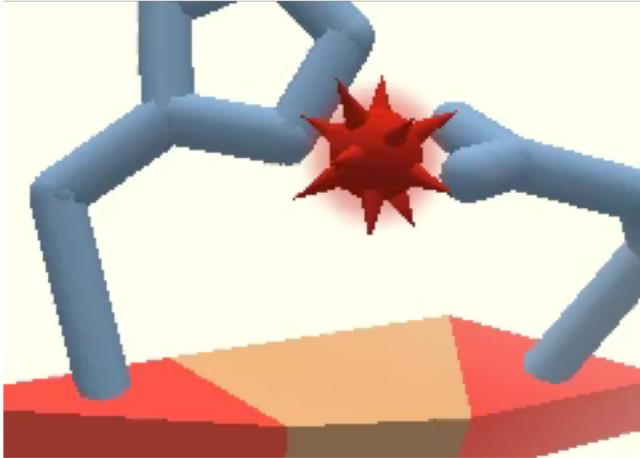
Game Visualization

Visualizations

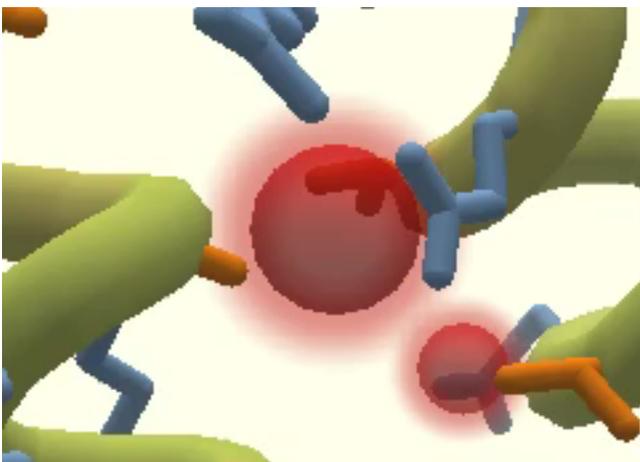


Clashes

Visualizations

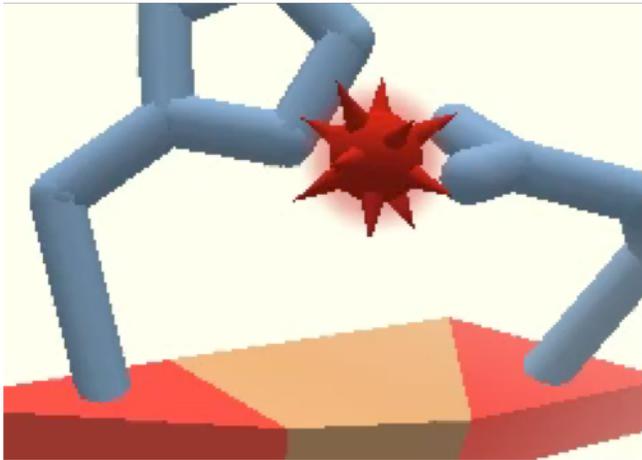


Clashes

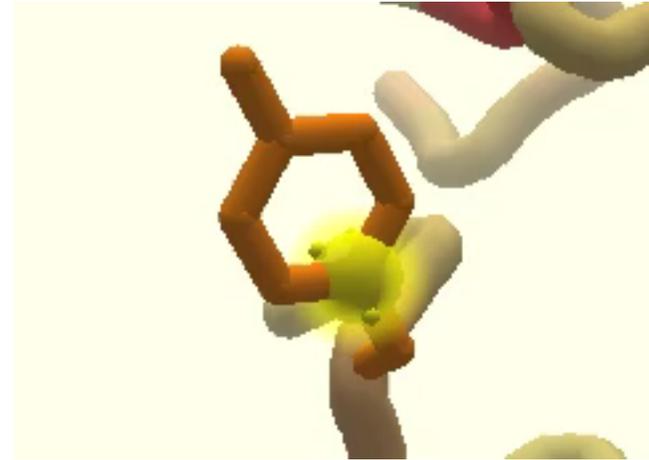


Voids

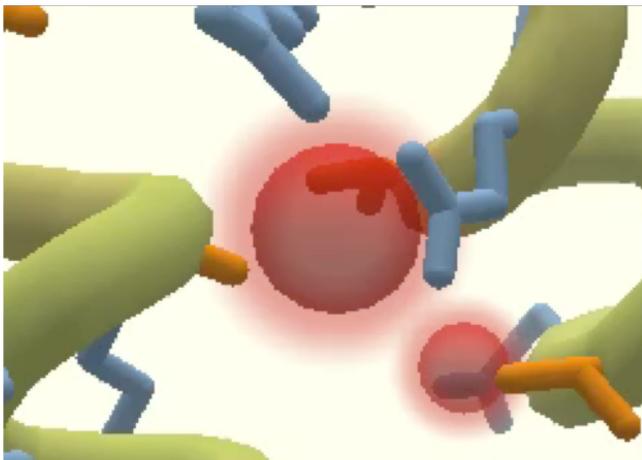
Visualizations



Clashes

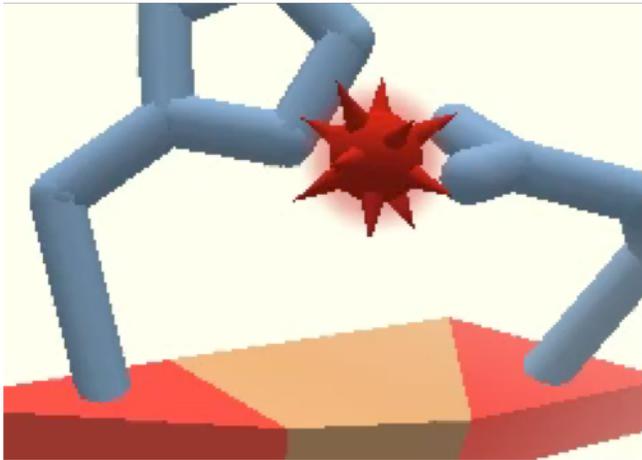


Hydrophobics

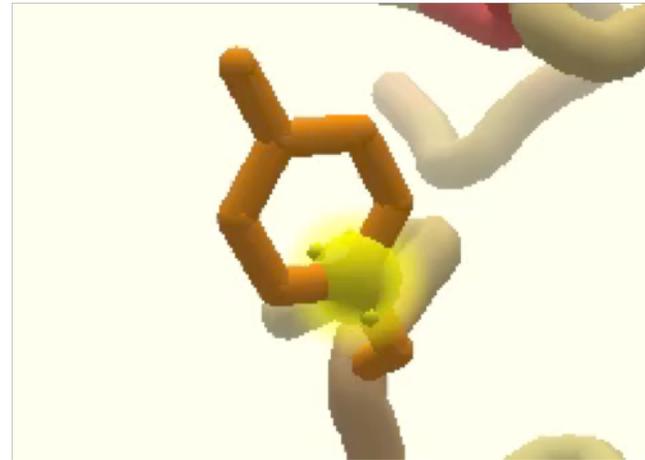


Voids

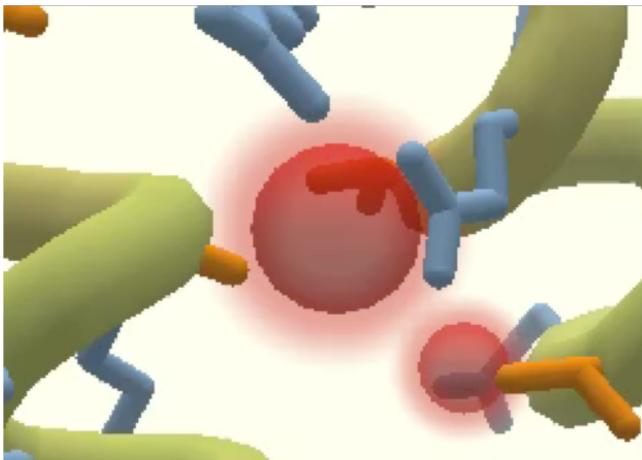
Visualizations



Clashes



Hydrophobics

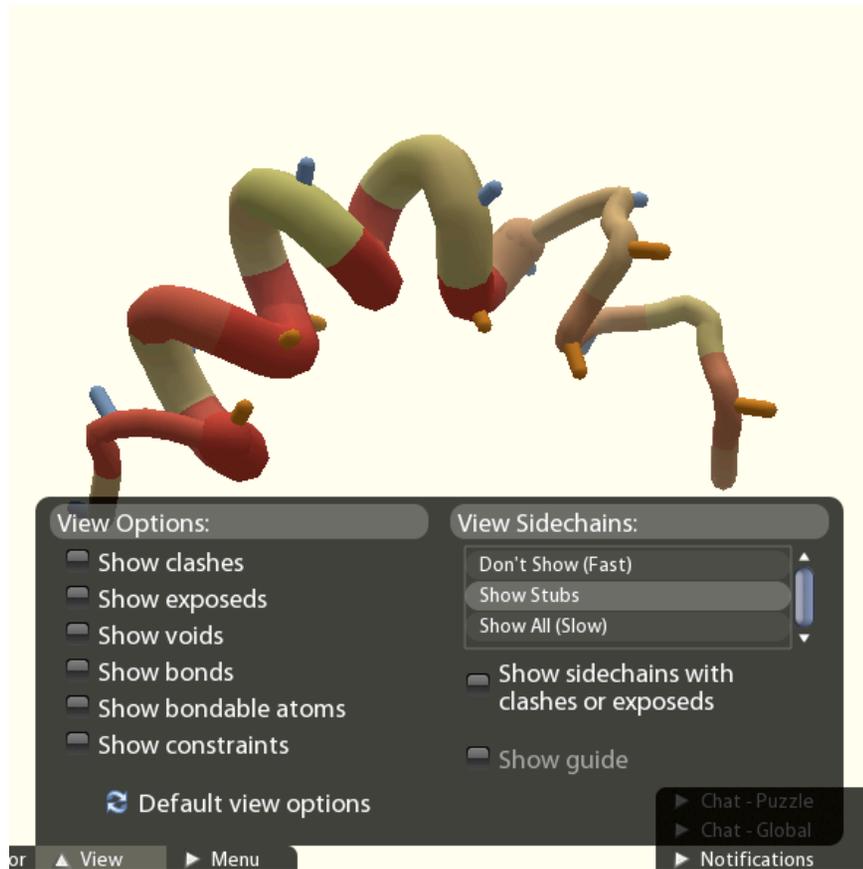


Voids

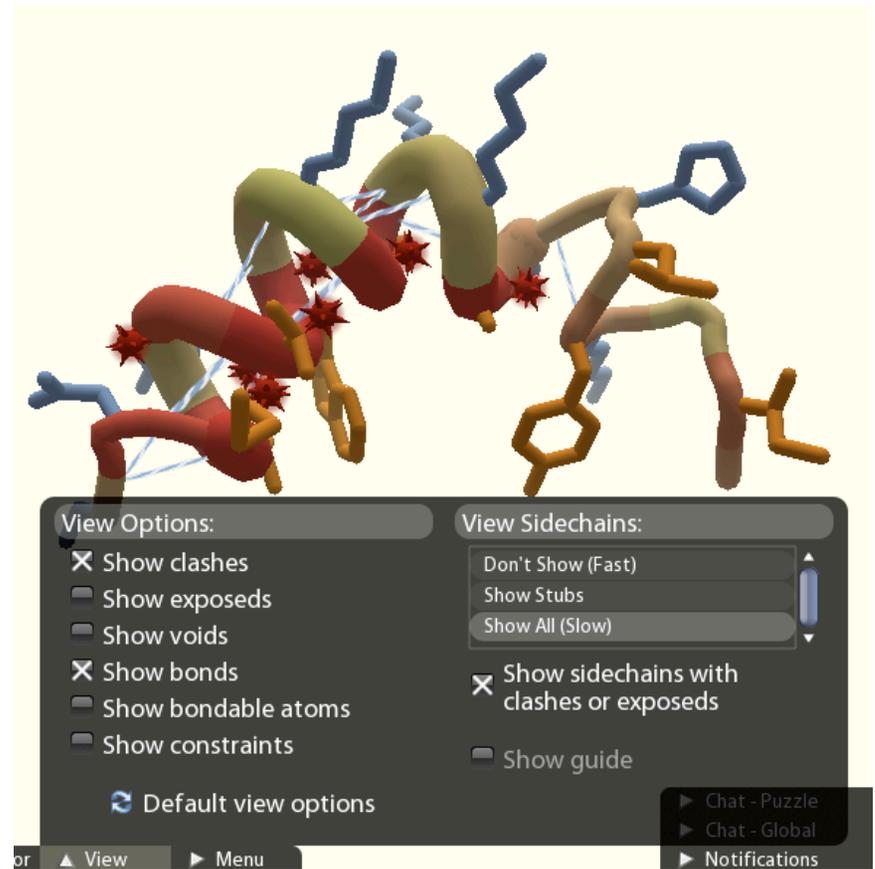


Hydrogen Bonds

Visualizations



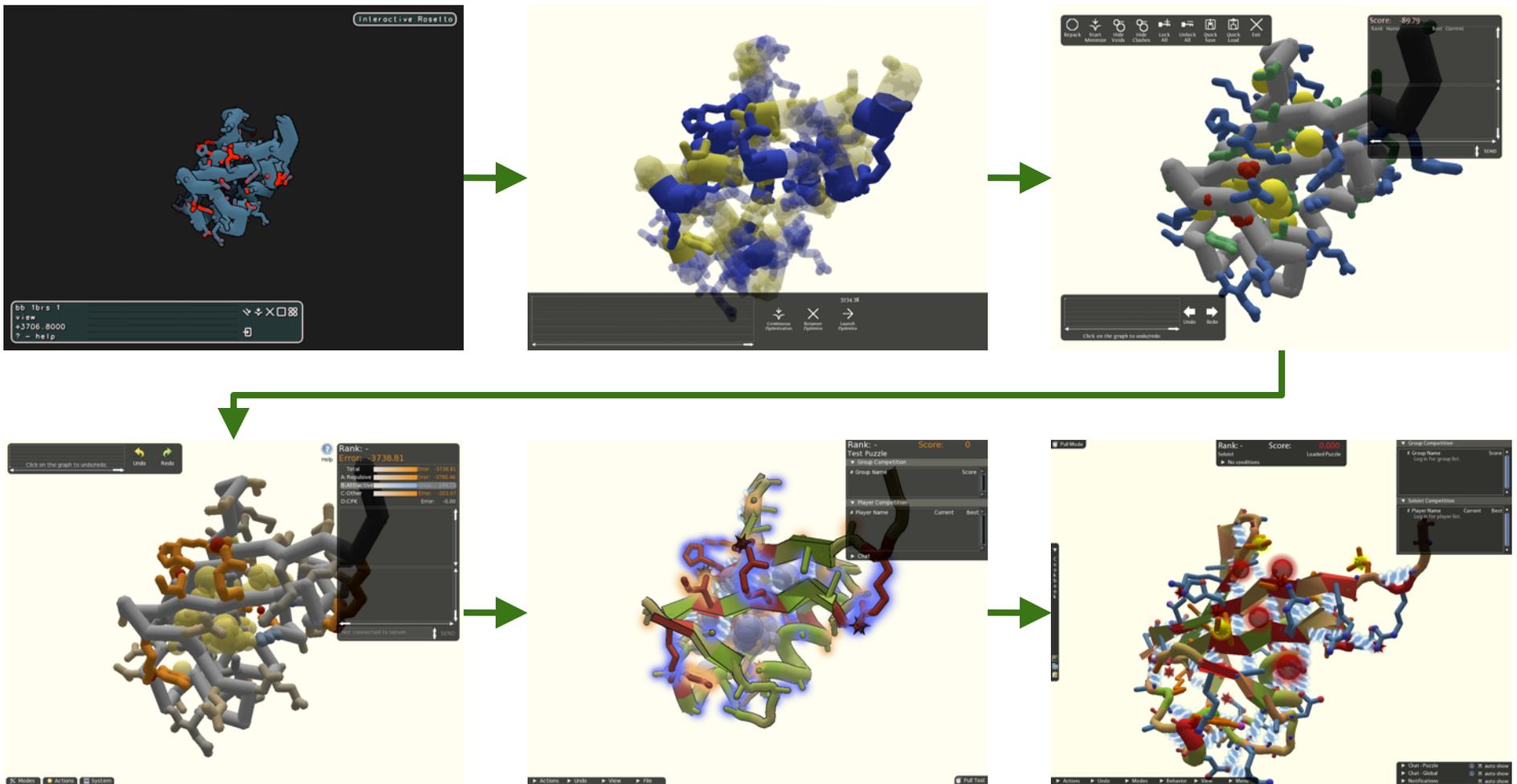
Clashes, hydrogen bonds, sidechains OFF



Clashes, hydrogen bonds, sidechains ON

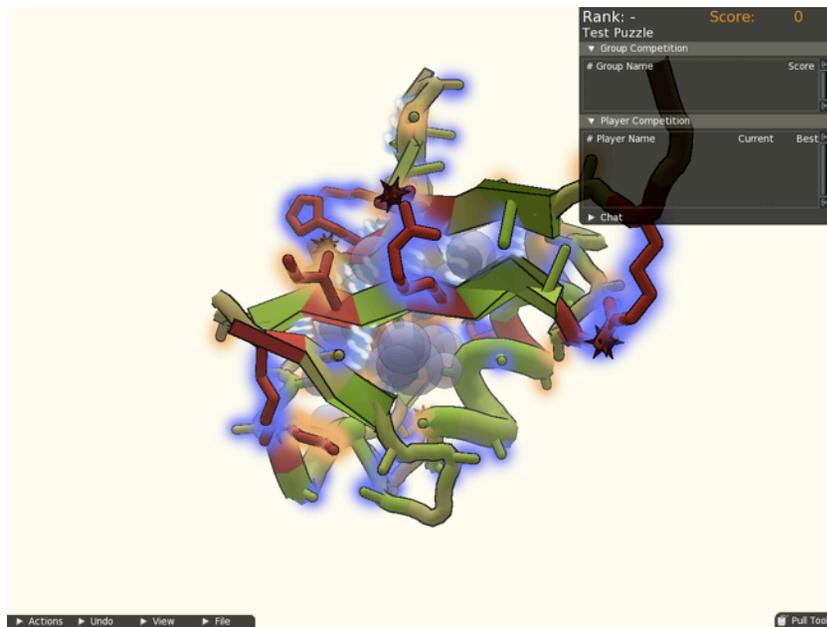
Visualizations

refinement



Visualizations

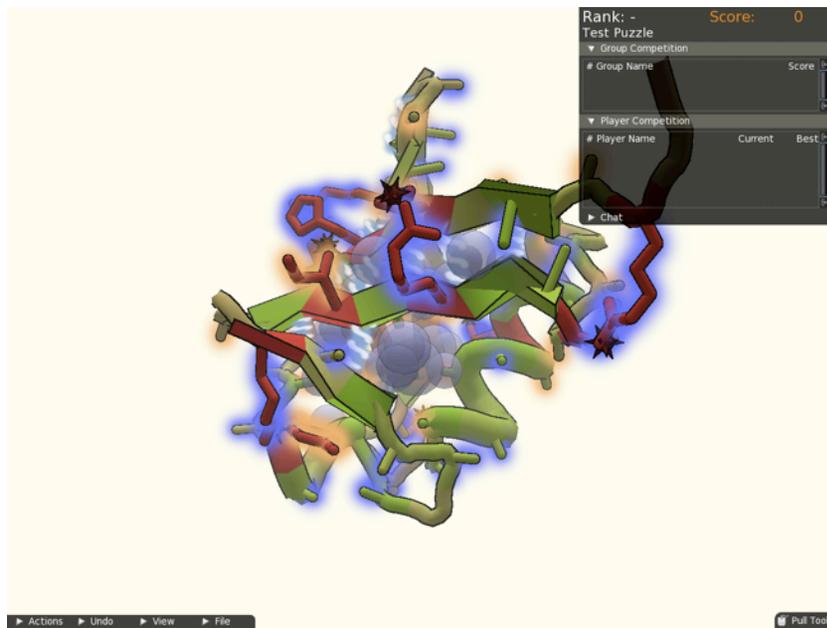
refinement



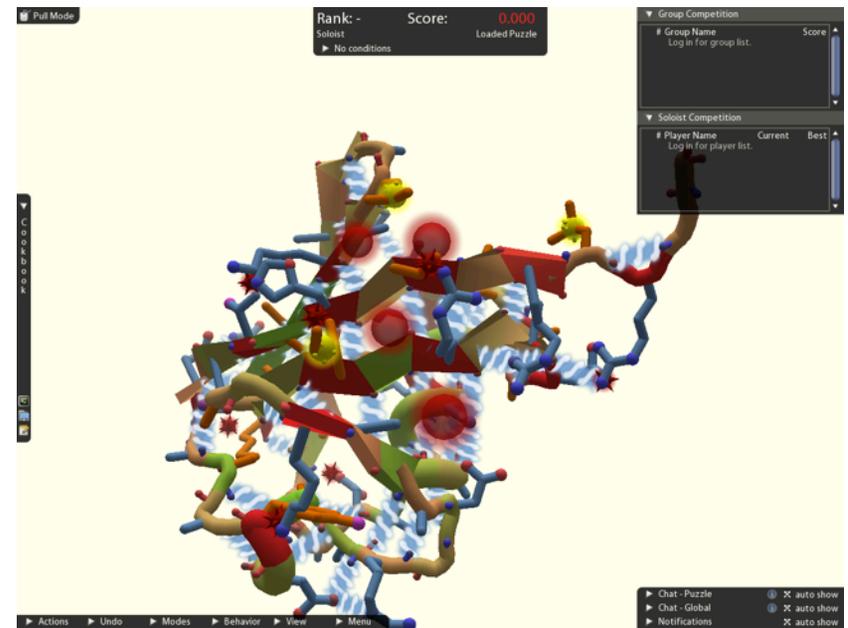
Older Version

Visualizations

refinement

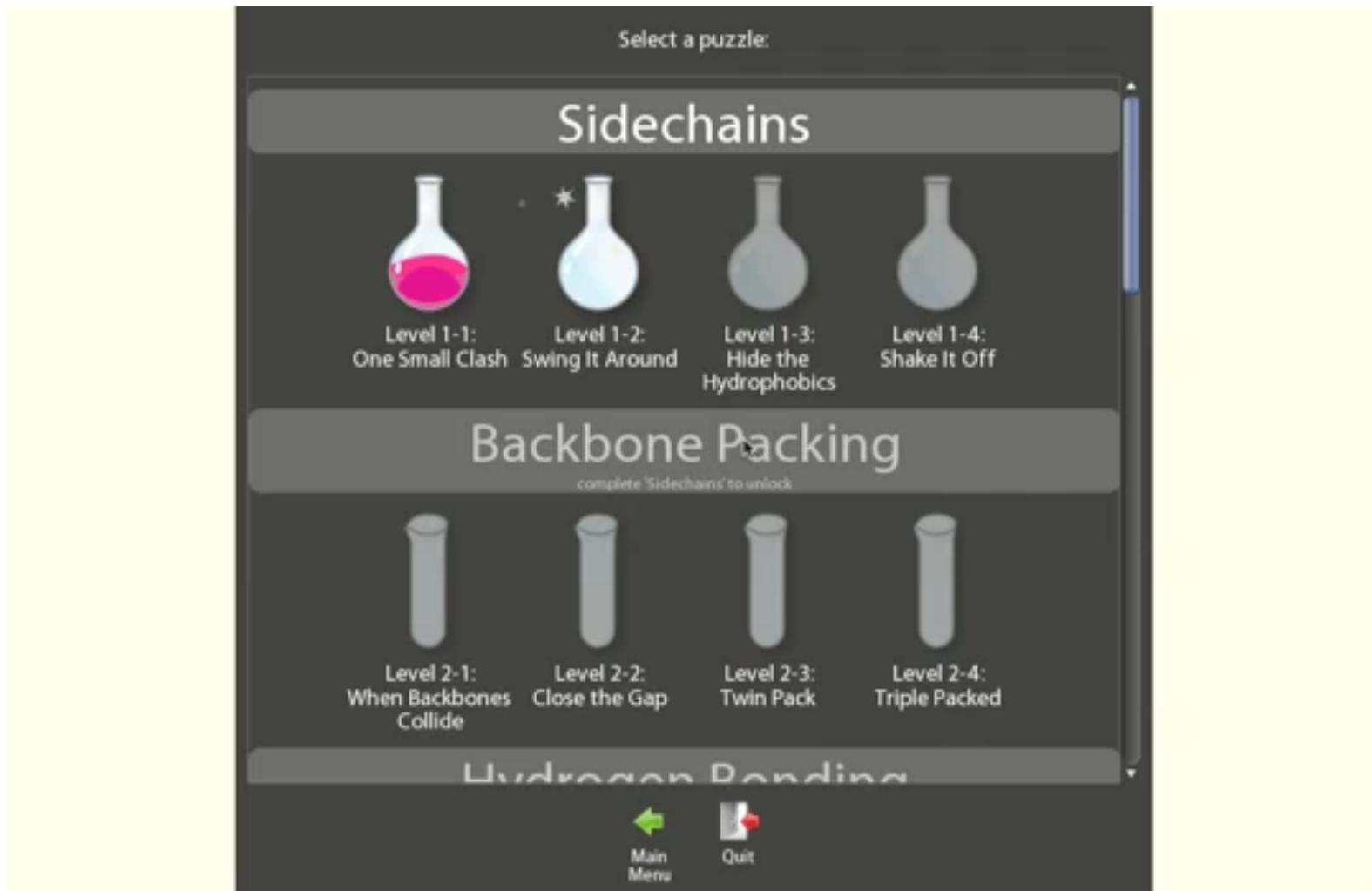


Older Version



Newer Version

Introductory Levels

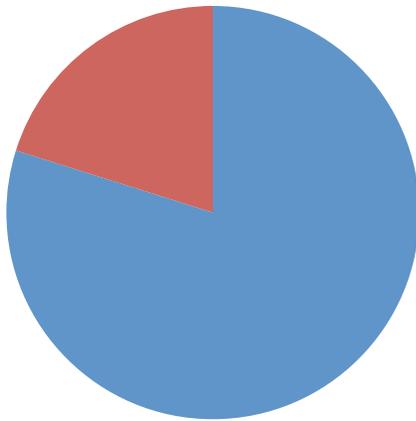


What have we found so far?

Very broad appeal

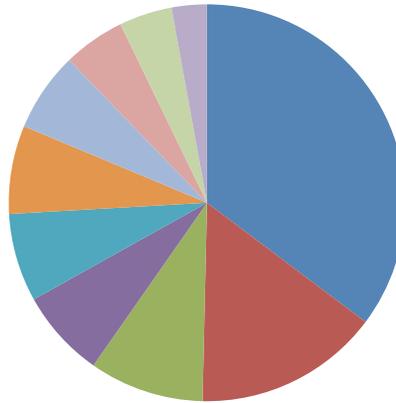
Example demographic data

Gender



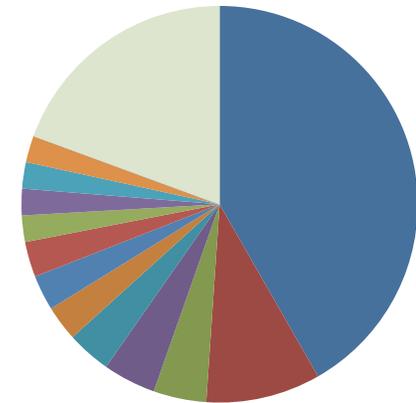
■ Male ■ Female

Occupation



■ Student ■ Computer
■ Labor ■ Unemployed
■ Technical ■ Science
■ Busn./Finan./Legal ■ Art
■ Education ■ Retired

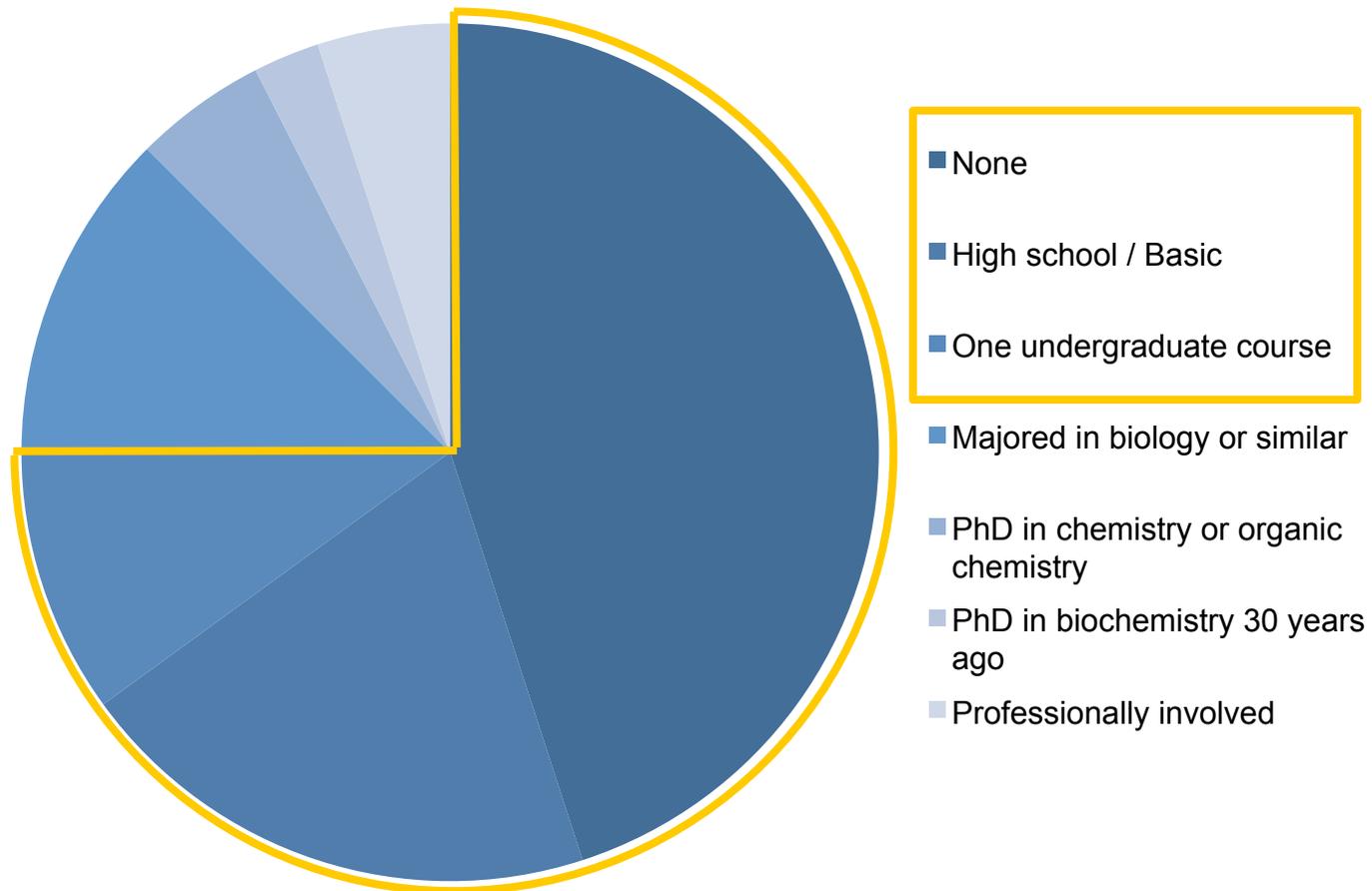
Country



■ USA ■ UK
■ Germany ■ France
■ Poland ■ Sweden
■ Netherlands ■ Australia
■ Russian Federation ■ Portugal
■ New Zealand ■ Argentina
■ Other

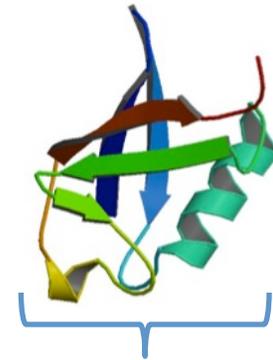
Very broad appeal

Prior knowledge of biochemistry



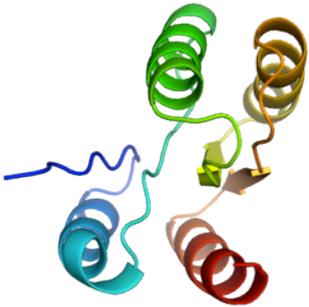
Protein Structure Prediction

MQIFVKTLTGKTILEVEPSDTIE...



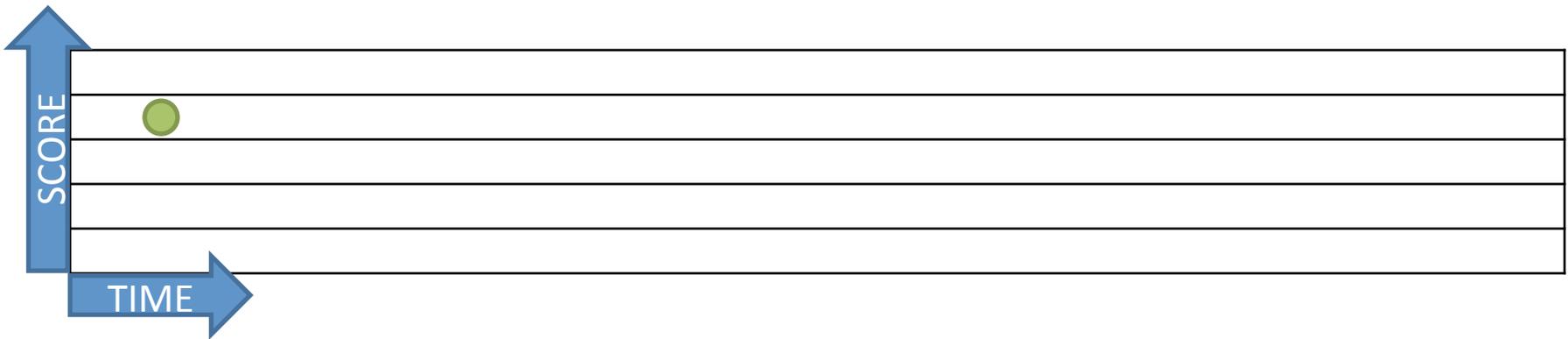
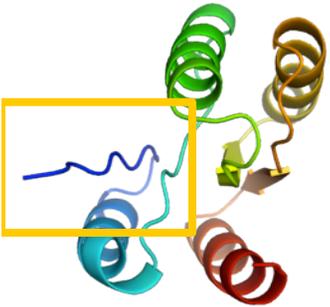
?

Players can solve structures

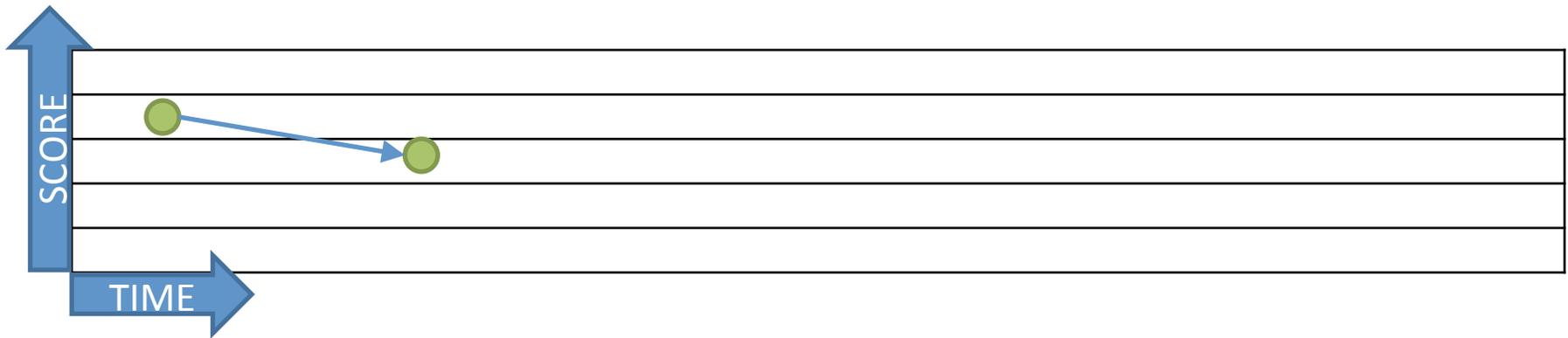
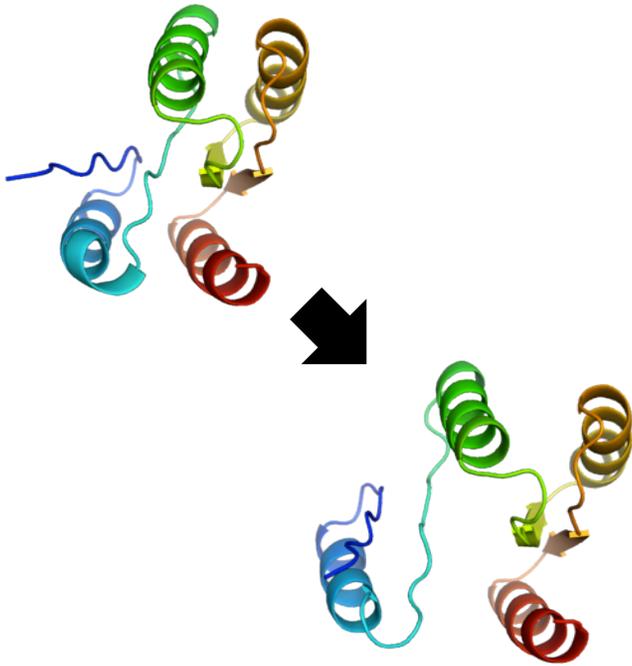


- Fix incorrectly folded proteins
- Move through worse scores to find better ones
- Outperform computational methods

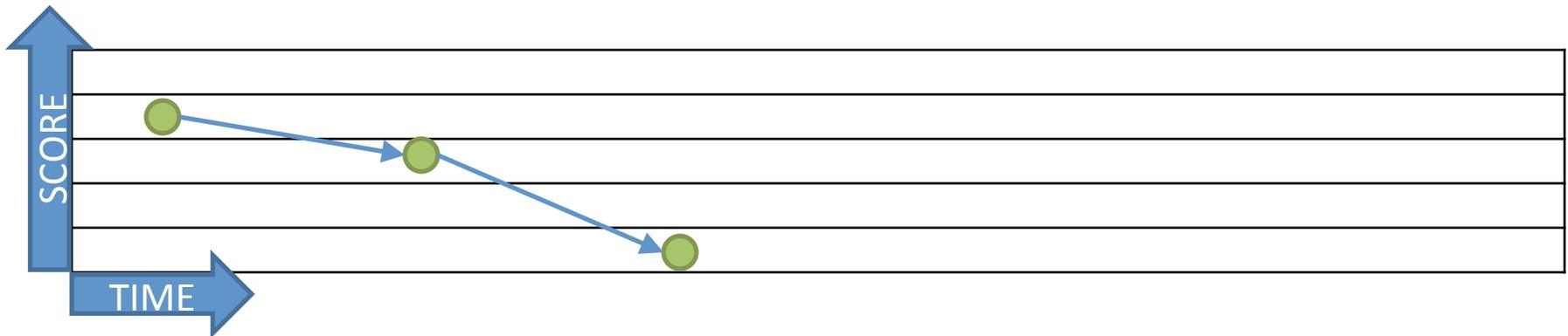
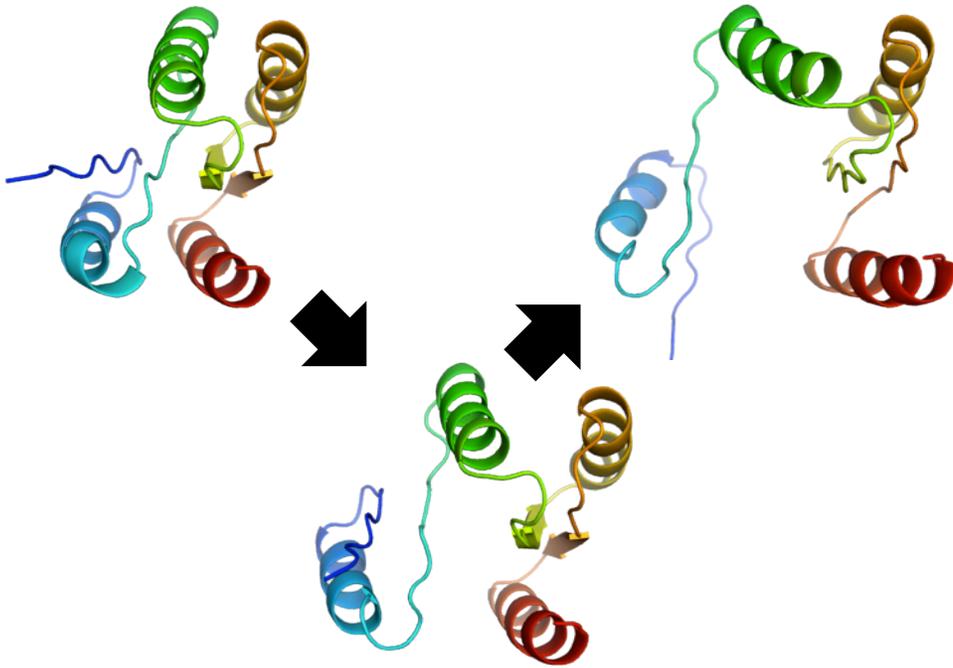
Players can solve structures



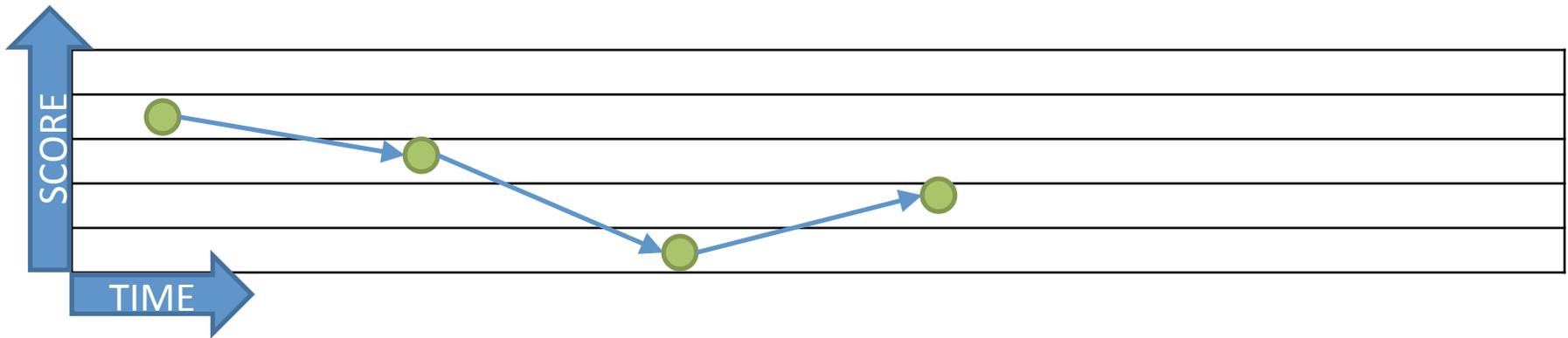
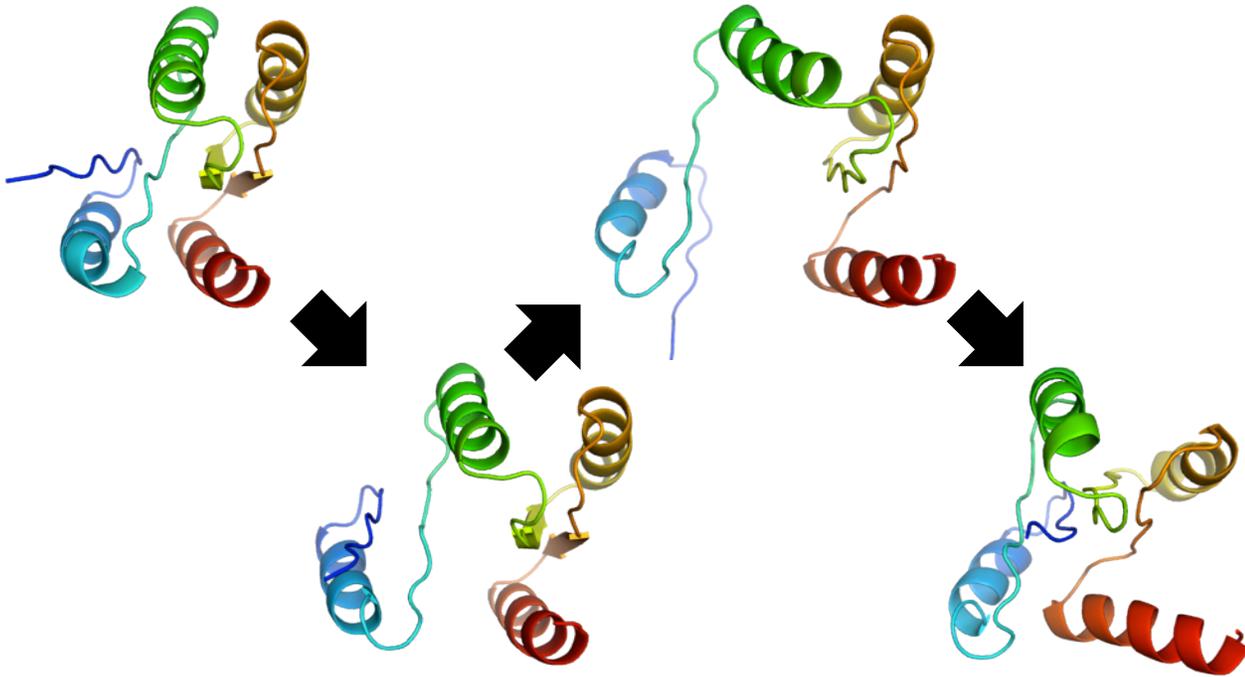
Players can solve structures



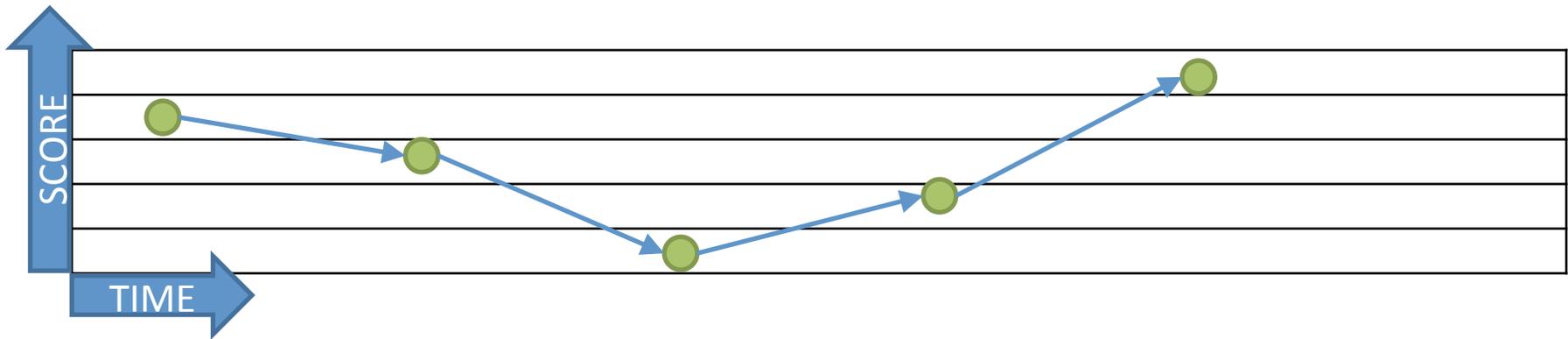
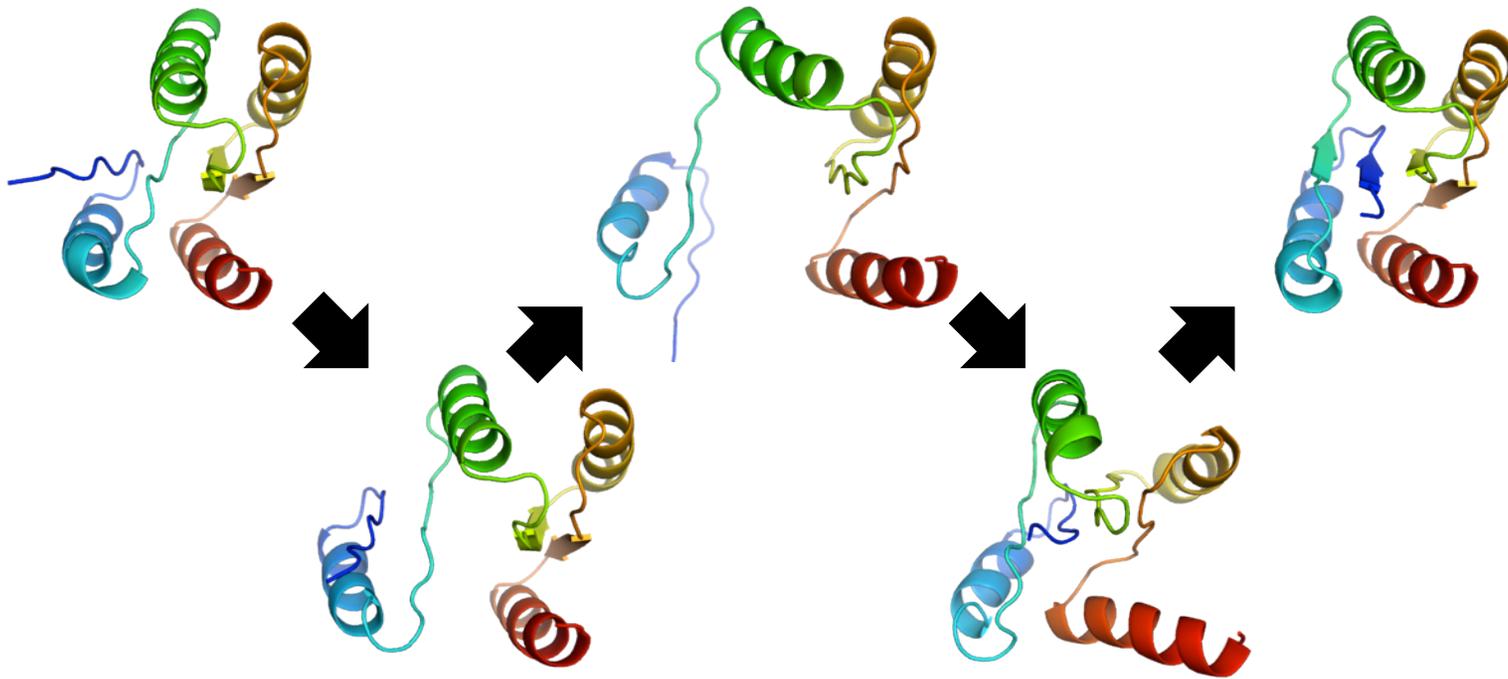
Players can solve structures



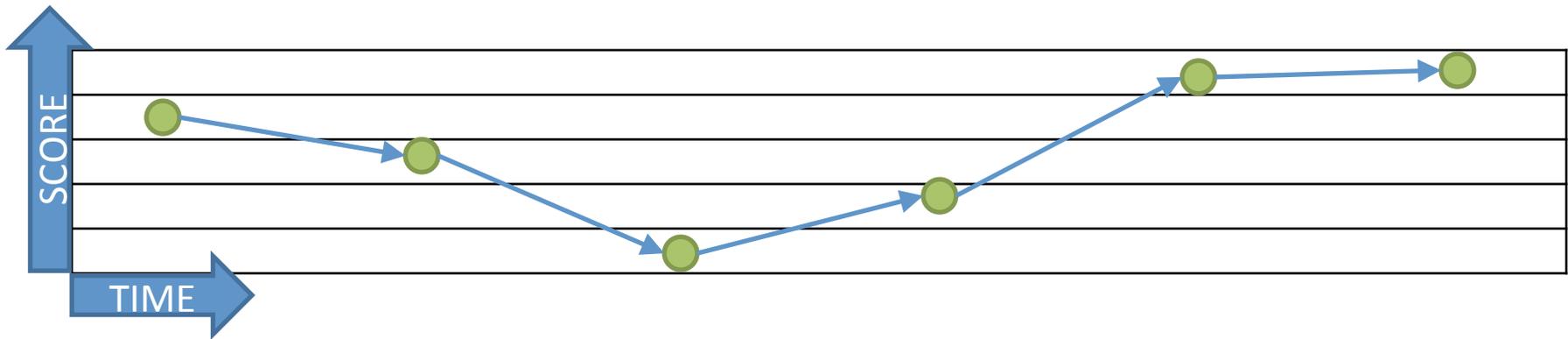
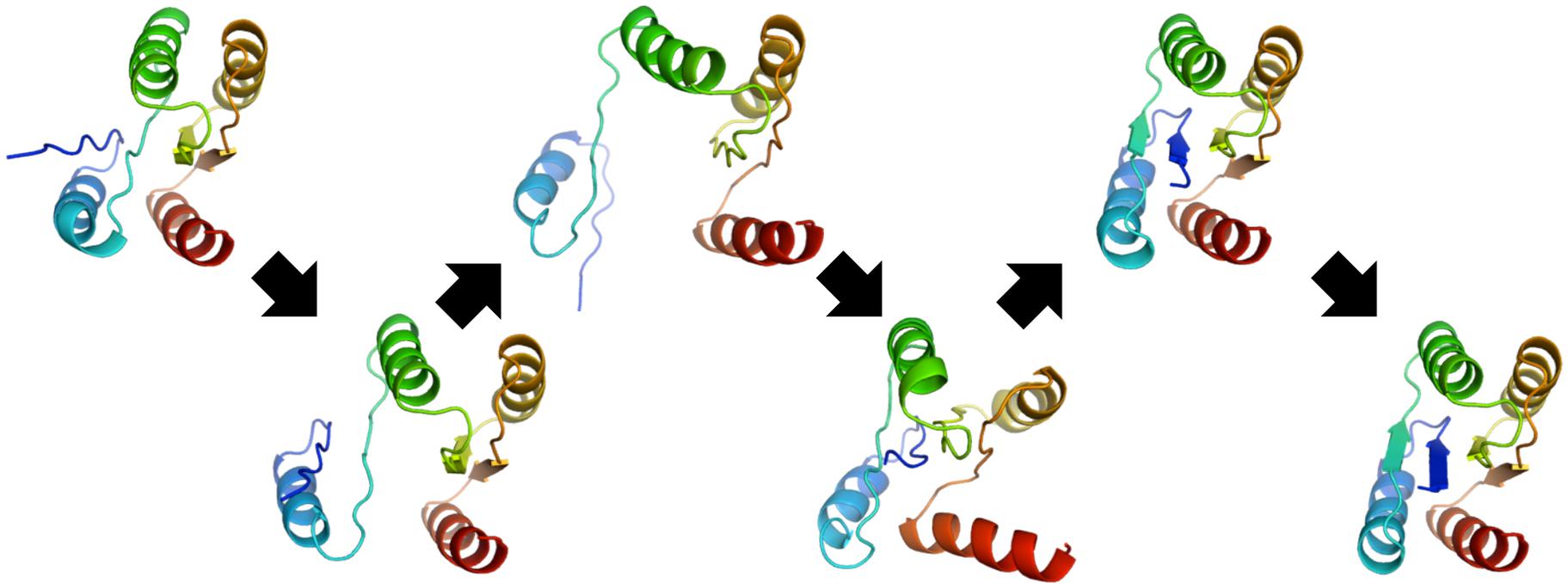
Players can solve structures



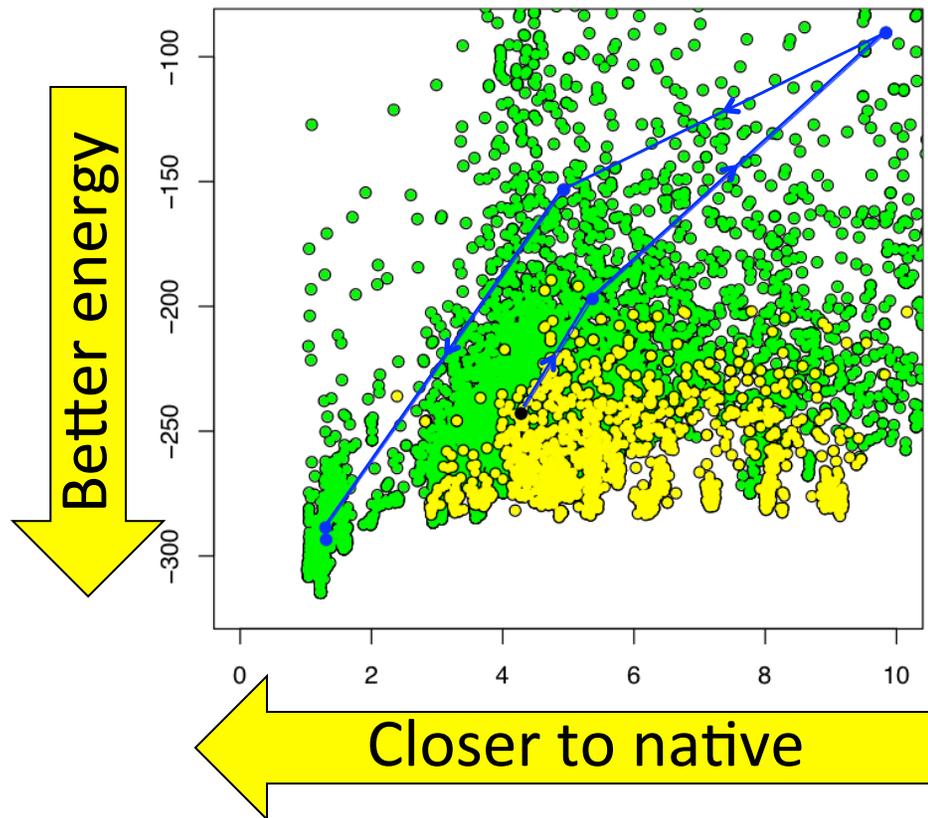
Players can solve structures



Players can solve structures

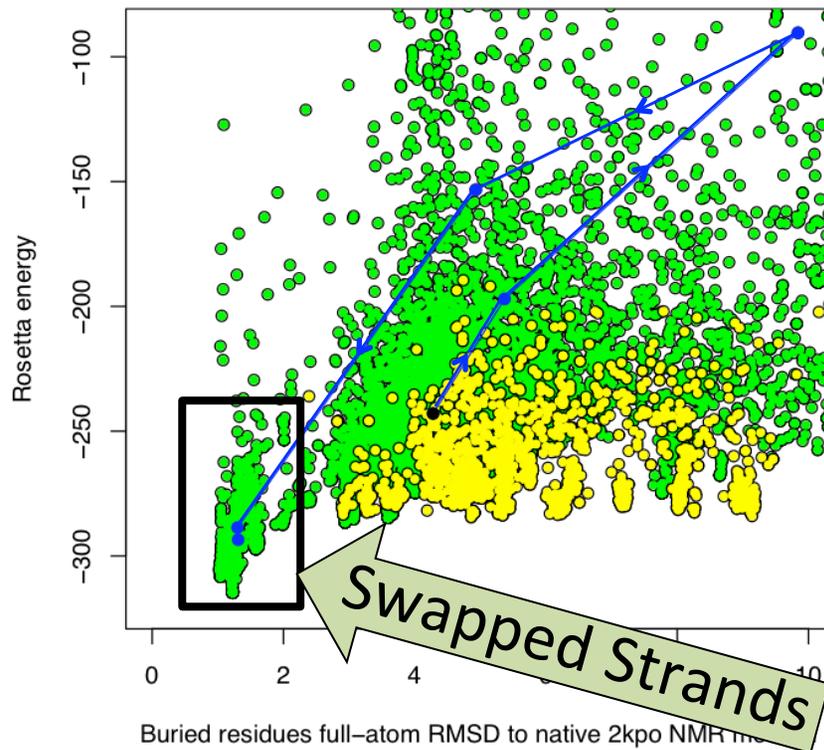


Comparison to Algorithm



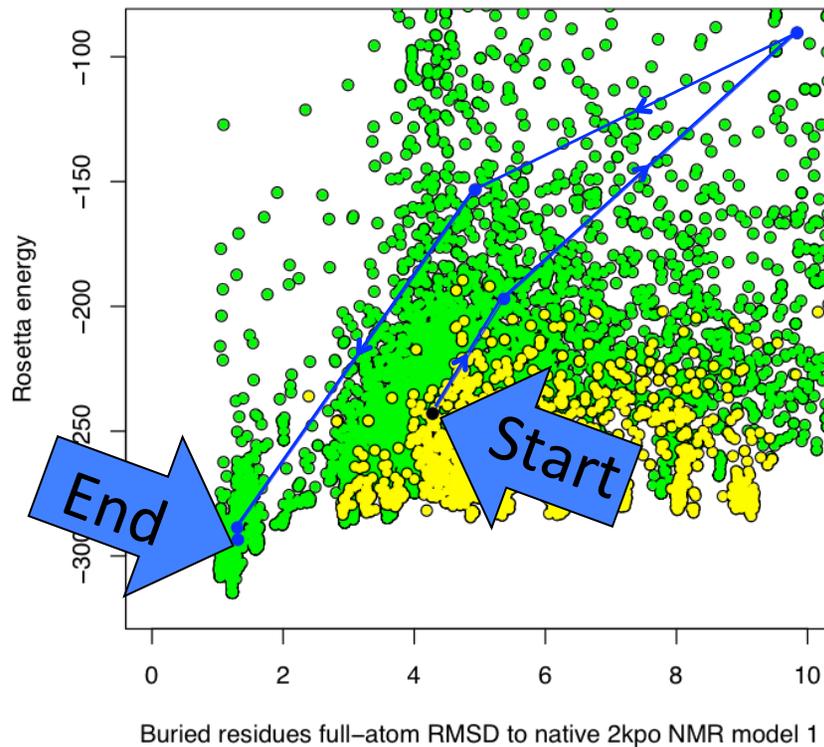
Player solutions
Top player path
Algorithm solutions

Comparison to Algorithm



Player solutions
Top player path
Algorithm solutions

Comparison to Algorithm



Player solutions
Top player path
Algorithm solutions

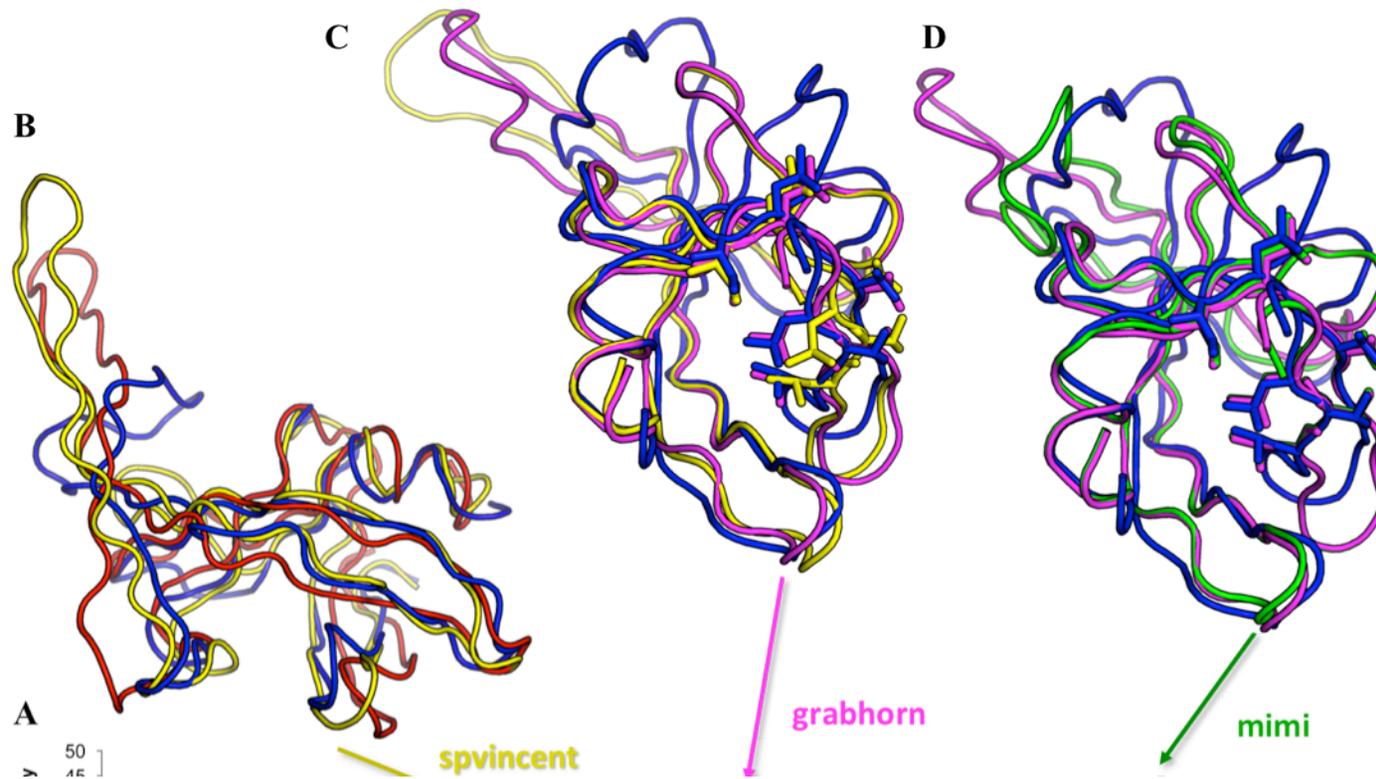
Experimental Structure Solved

- Mason-Pfizer Monkey Virus
Retroviral Protease (MPMV PR)
- Plays a role in AIDS in monkeys
- Experimentalists worked on for ~15
years
- Computational methods failed to solve
- Gave to players for 3 weeks

Experimental Structure Solved

Starting structure

Native

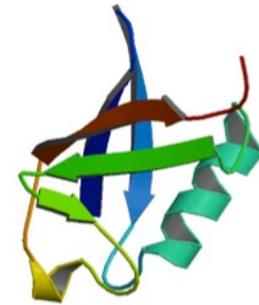


Algorithm Discovery

MQIFVKTLTGKTILEVEPSDTIE...



?



Players develop strategies

Strategy - FoldIt Wiki - a Wikia Gaming wiki

http://foldit.wikia.com/wiki/Strategy

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Strategy

[Dell Efficient Enterprise](#)
Unlocking Growth and Innovation With Dell's IT Efficiency Solutions
www.EfficientEnterprise.com

Ads by Google

Most folders seem to agree that FoldIt strategy is still in its infancy. Much remains to be discovered. With that said, here are some of the goals and methods that have often been found to be helpful.

First, there are several goals to pursue that will increase a fold's [score](#). They include the following:

- [Compactness](#)
- [Hydrophobic Hiding](#)
- [Hydrogen Bond](#)
- [Sidechain Position](#)

These goals should be considered at all stages of the game, from the [opening](#) to the [midlegame](#) to the [endgame](#).

Questions about strategy should be directed (for now) to [the Big Question Page](#). As new strategies are explored, they can get spinoff pages of their own.

Contents [\[show\]](#)

Tips

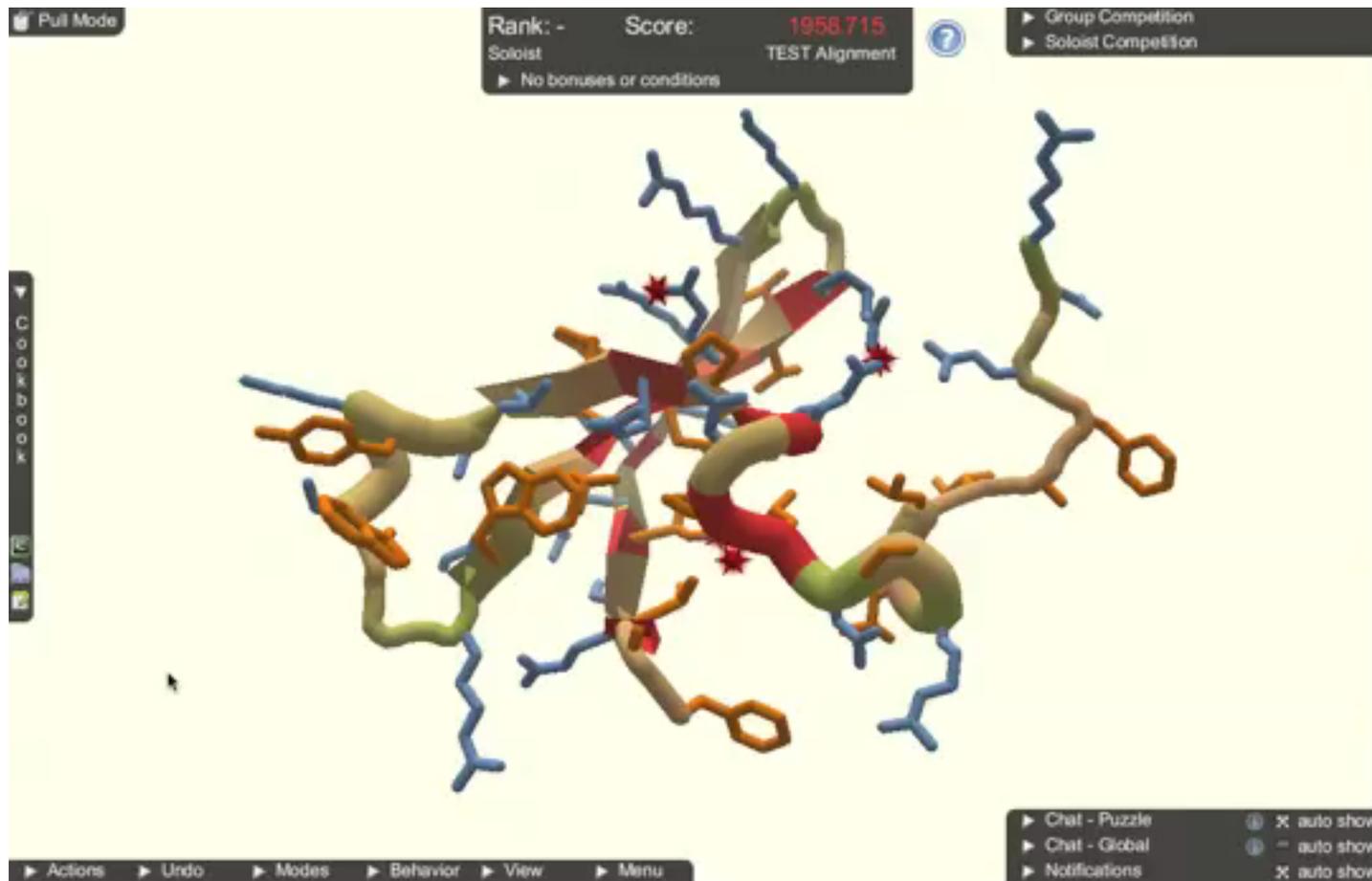
Several strategic tips that may prove useful include the following:

- Use [rubber bands](#) to pull together widely spaced structures.

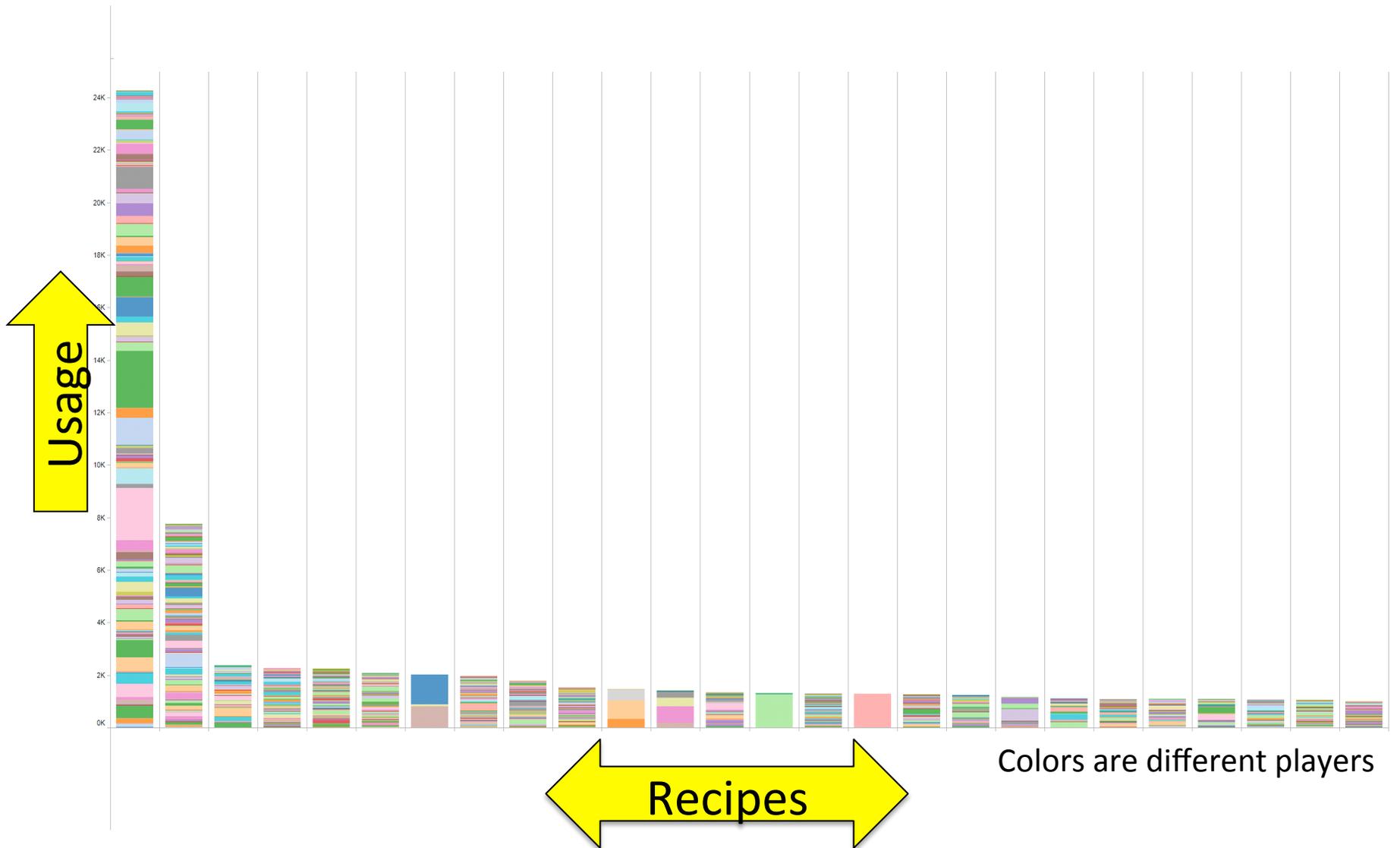
114 articles on this wiki

edit

Players develop strategies

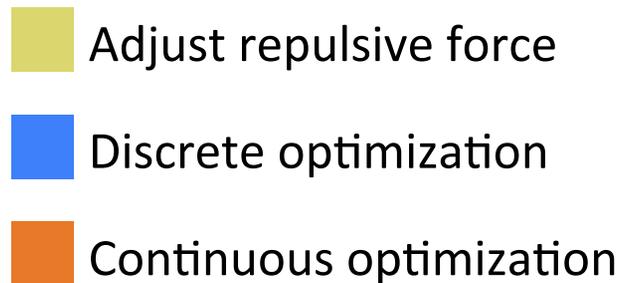
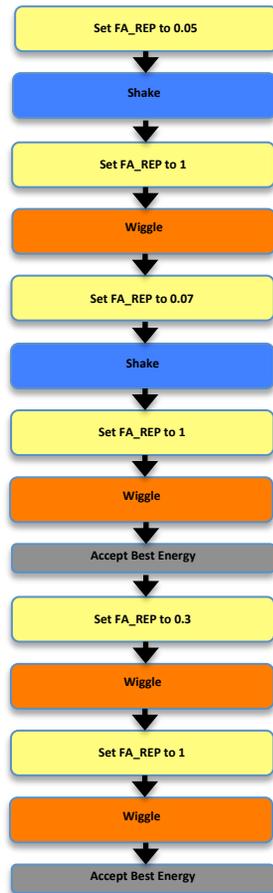


Top Cookbook Recipes



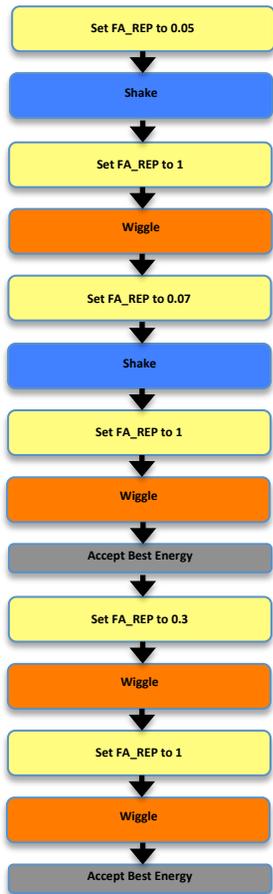
Algorithm Comparison

Player
Algorithm
(Blue Fuse v1.1)

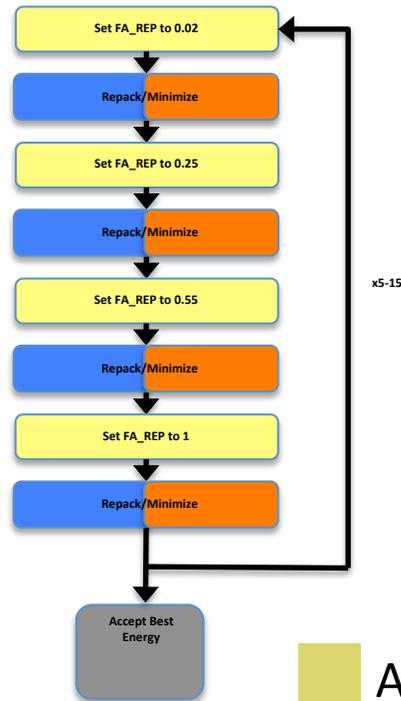


Algorithm Comparison

Player Algorithm
(Blue Fuse v1.1)



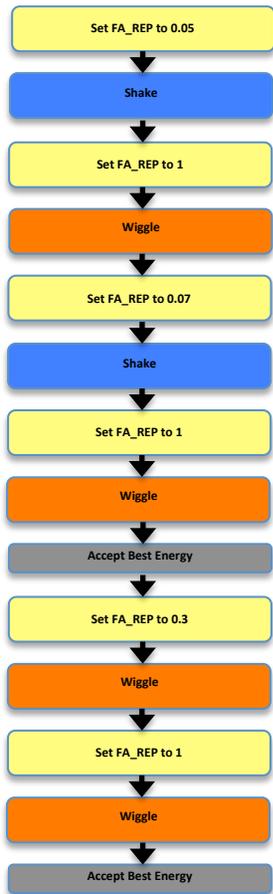
Scientist Algorithm
(Fast Relax)



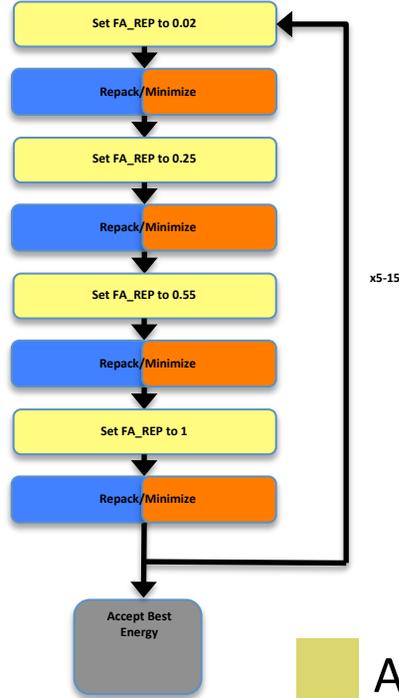
- Adjust repulsive force
- Discrete optimization
- Continuous optimization

Algorithm Comparison

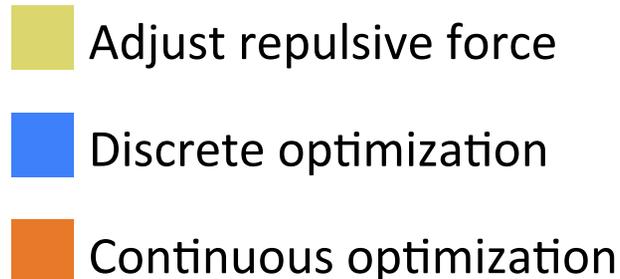
Player Algorithm
(Blue Fuse v1.1)



Scientist Algorithm
(Fast Relax)

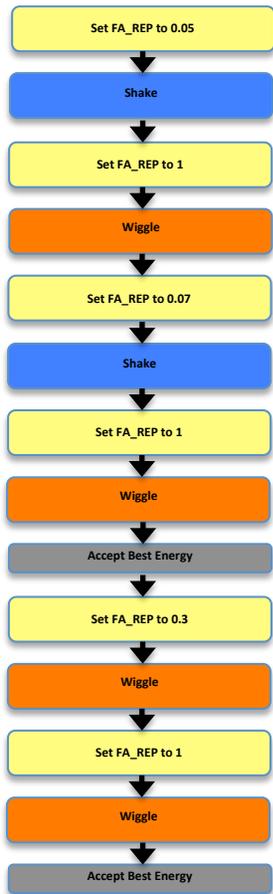


- Independent discovery of scientists' algorithmic techniques

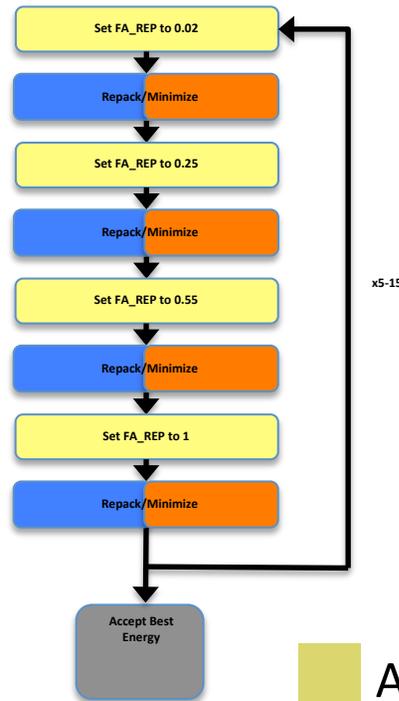


Algorithm Comparison

Player Algorithm
(Blue Fuse v1.1)



Scientist Algorithm
(Fast Relax)



- Adjust repulsive force
- Discrete optimization
- Continuous optimization

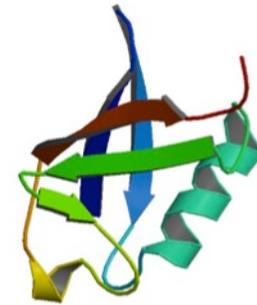
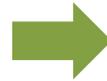
- Independent discovery of scientists' algorithmic techniques
- Improved performance compared to published algorithms

Protein Design

MQIFVKTLTGKTILEVEPSDTIE...



?



Protein Design

Design Mode
Left click: mutate menu
Right (ctrl) or Middle (shift) click: insert/delete menu

Rank: - **Score: 9990** 
Soloist 365: Design the Interface 1
▶ No bonuses or conditions

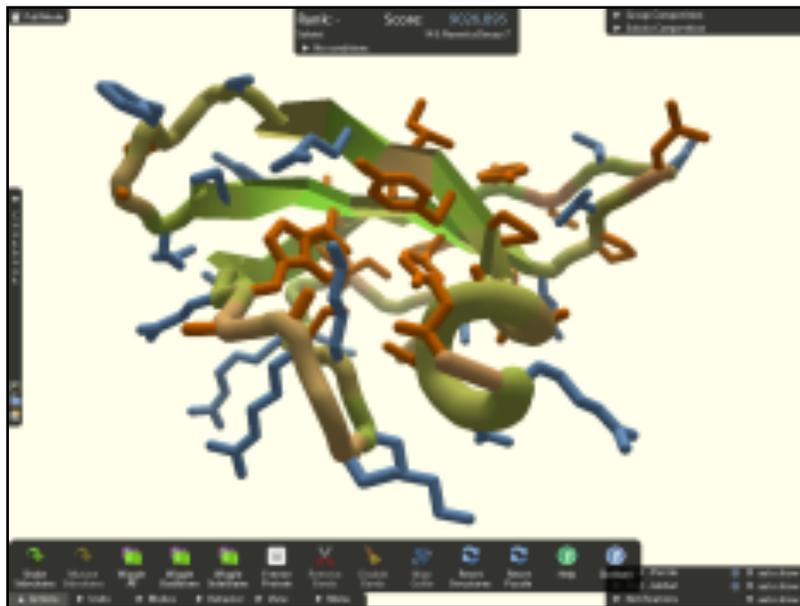
▶ Group Competition
▶ Soloist Competition

Cookbook

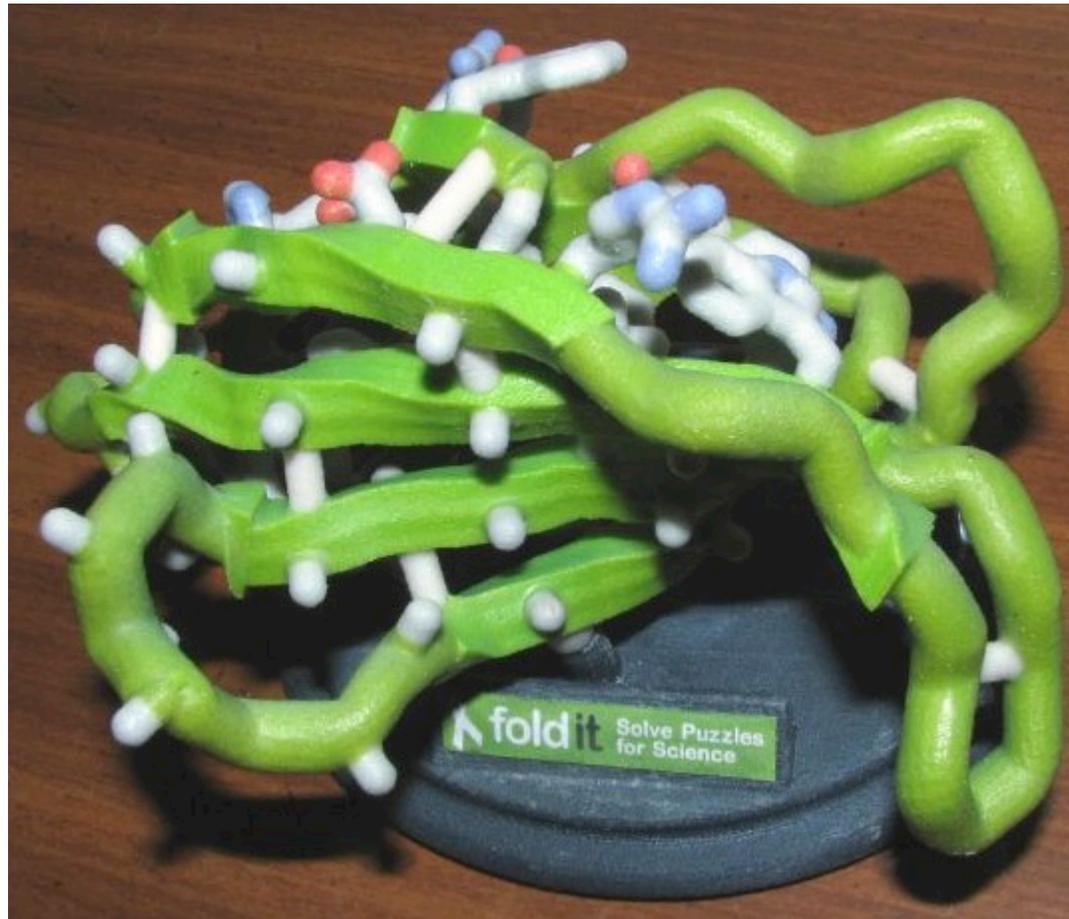
▶ Actions ▶ Undo ▶ Modes ▶ Behavior ▶ View ▶ Menu

▶ Chat - Puzzle ⓘ ✕ auto show
▶ Chat - Global ⓘ ✕ auto show
▶ Notifications ⓘ ✕ auto show

Experimental Validation



Early Player Design

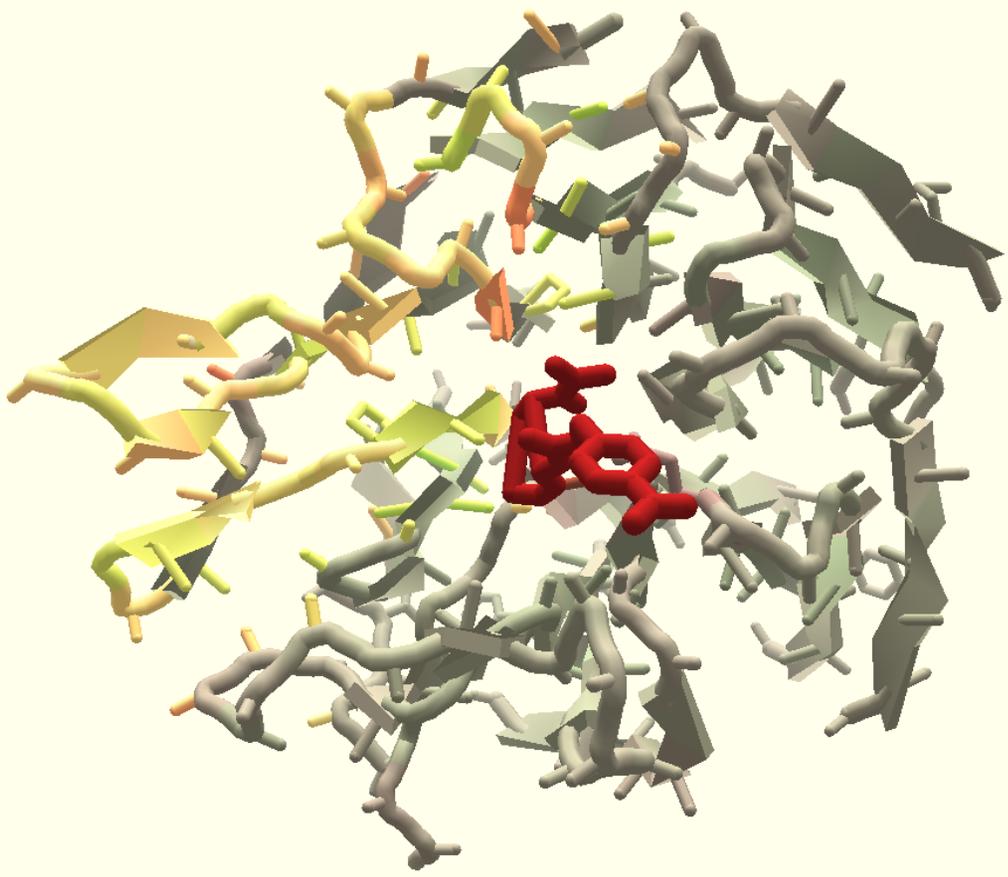


Protein Design

Pull Mode

Rank: - Score: 7510.909
Soloist 192: Cover the Ligand
▶ No bonuses or conditions

▶ Group Competition
▶ Soloist Competition



Looking

▶ Actions ▶ Undo ▶ Modes ▶ Behavior ▶ View ▶ Menu

▶ Chat - Puzzle ⓘ ✕ auto show
▶ Chat - Global ⓘ ✕ auto show
▶ Notifications ⓘ ✕ auto show

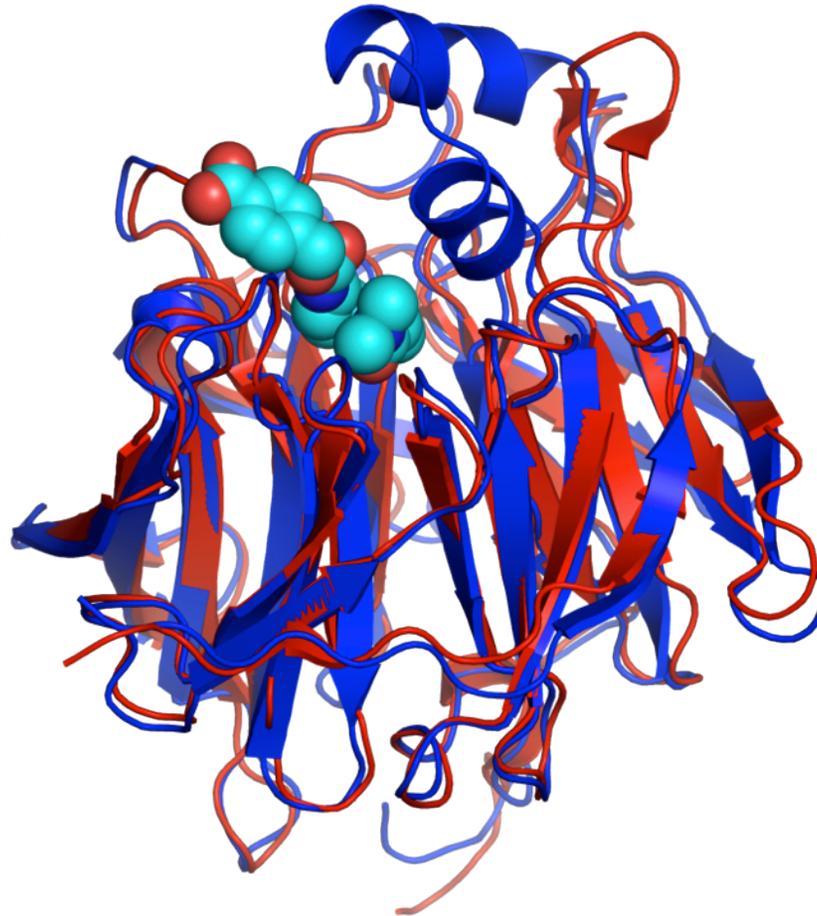
Protein Design

Starting scaffold



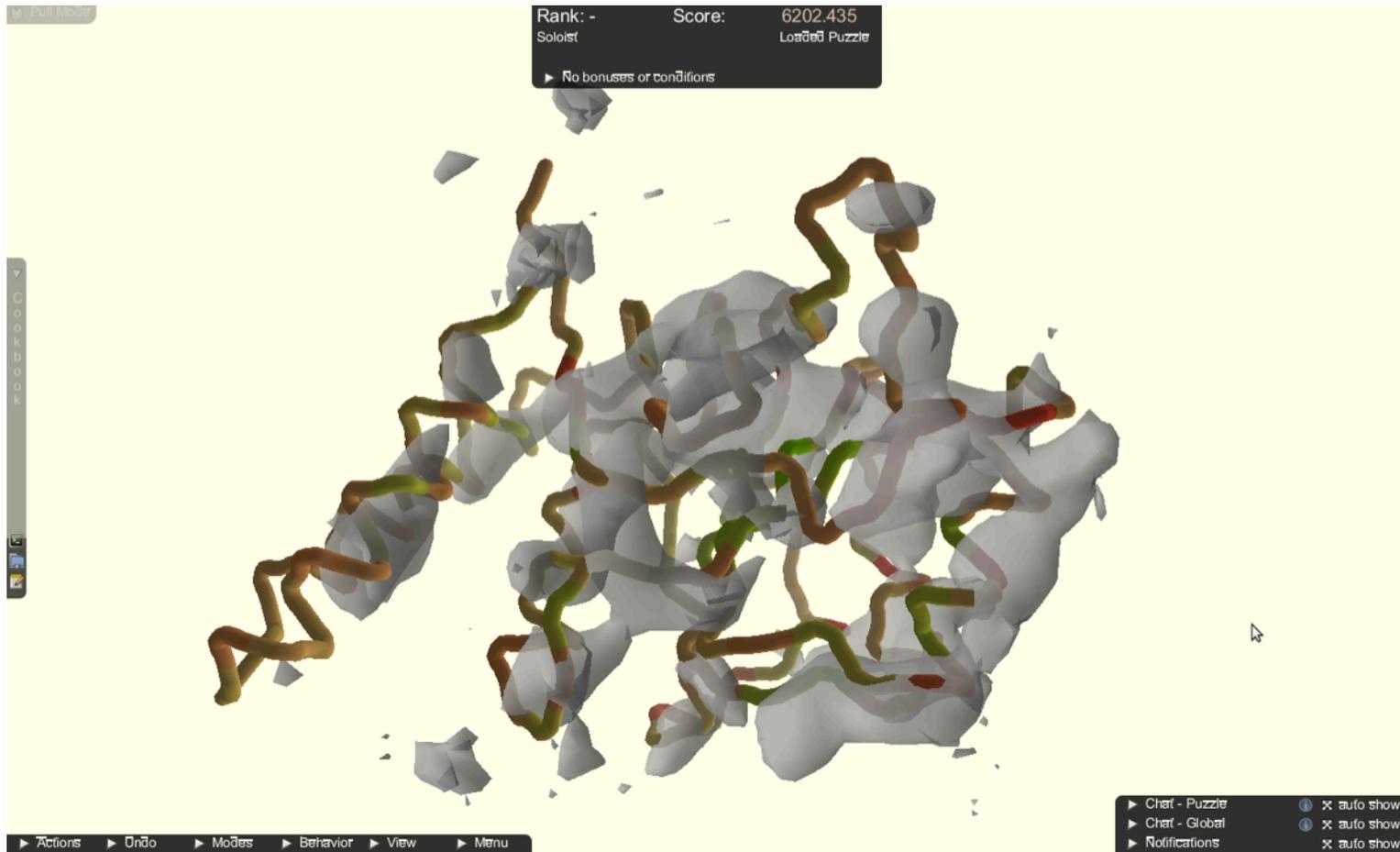
Protein Design

Starting scaffold
Player/scientist design



What's next?

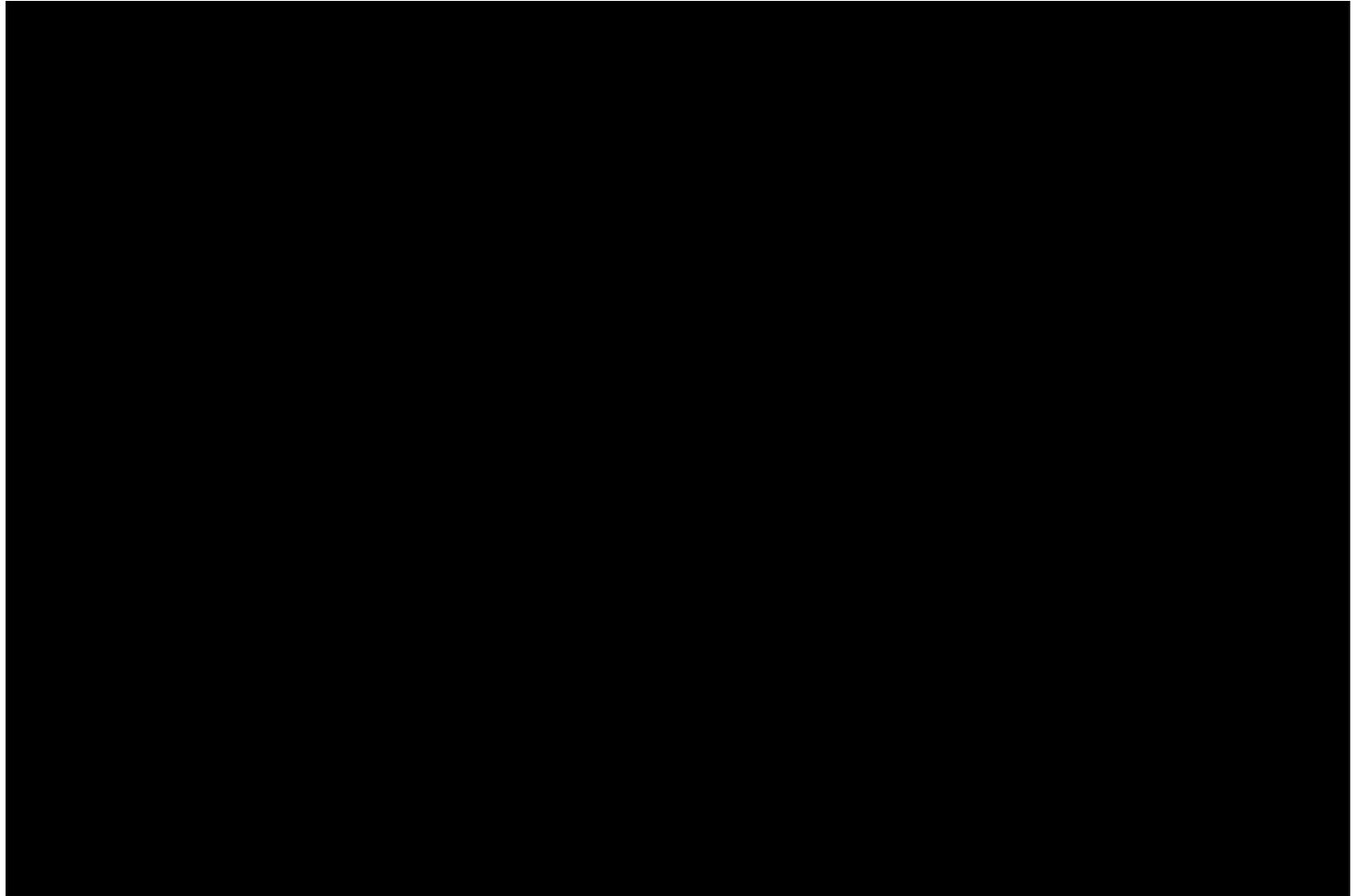
Experimental Density Integration



Tool for Scientists



More Intuitive Interactions



Education

The screenshot shows the Foldit website interface. At the top, there is a green header with the 'foldit BETA' logo and the tagline 'Solve Puzzles for Science'. A navigation menu includes links for 'BLOG', 'PUZZLES', 'RECIPES', 'FORUM', 'WIKI', 'FEEDBACK', 'ABOUT', 'FAQ', and 'CREDITS'. The main content area features a puzzle titled 'Kuhlman Class Puzzle 1' with a status of 'Closed'. A yellow arrow points to the puzzle title. Below the title is a 'Summary' section with details: Name (Kuhlman Class Puzzle 1), Status (Closed), Created (03/11/2009), and Difficulty (Intermediate). A 'Description' follows, explaining it's a homology model. To the right of the puzzle details are sections for 'GET STARTED: DOWNLOAD' (with 'Win Beta' and 'Mac Beta' buttons), 'RECOMMEND FOLDIT' (with a 'Send' button), and 'USER LOGIN' (with fields for 'Username' and 'Password', a 'Log in' button, and links for 'Create new account', 'Request new password', and 'Sign in using Facebook'). At the bottom of the puzzle details is a 'Top Groups' table and a 'Top Evolvers' section.

Kuhlman Class Puzzle 1
Status: Closed

Summary

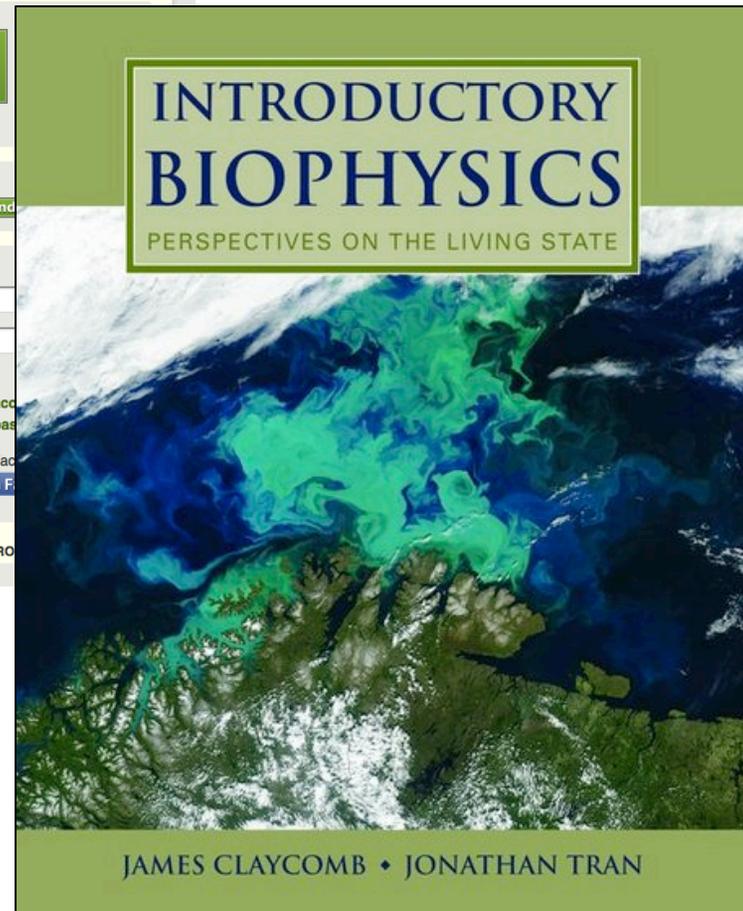
Name: Kuhlman Class Puzzle 1
Status: Closed
Created: 03/11/2009
Difficulty: Intermediate
Description: This is a homology model for Kuhlman's class, though all others are welcome to play. The puzzle will be scored as usual.

Top Groups

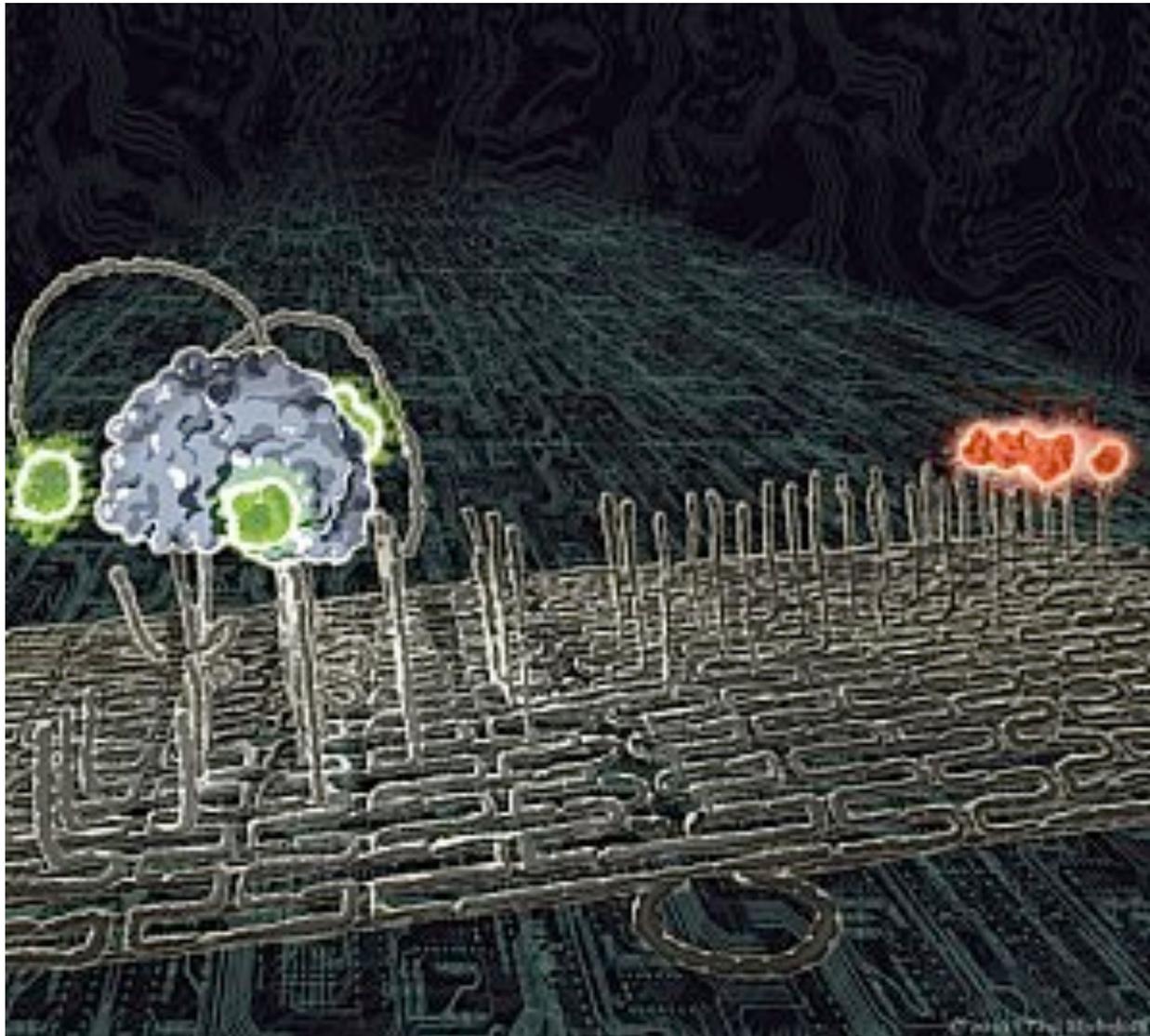
RANK	GROUP	SCORE	POINTS
1	Void Crushers	11,526	100
2	Another Hour Another Point	11,515	87
3	Oma Gawd	11,430	75
4	Richard Dawkins Foundation	11,282	64
5	Pitney Folders	11,138	55

[SHOW ALL >](#)

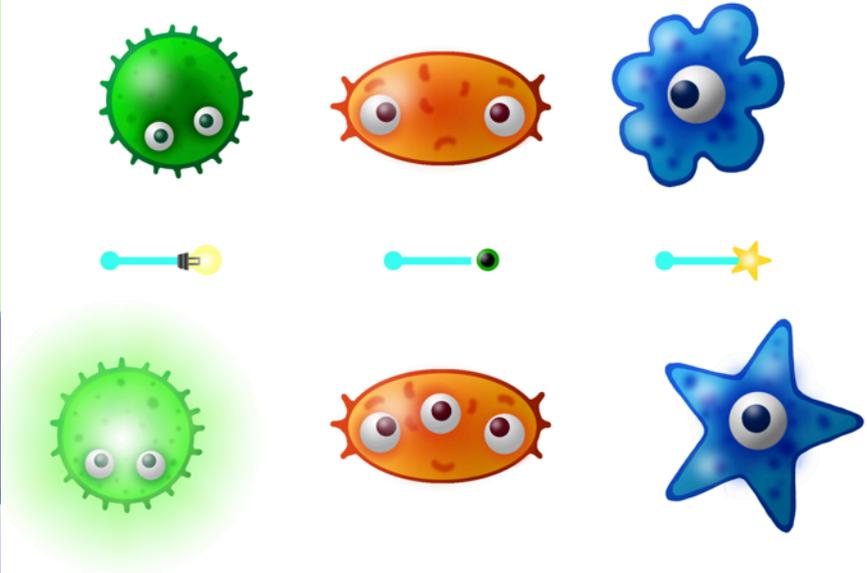
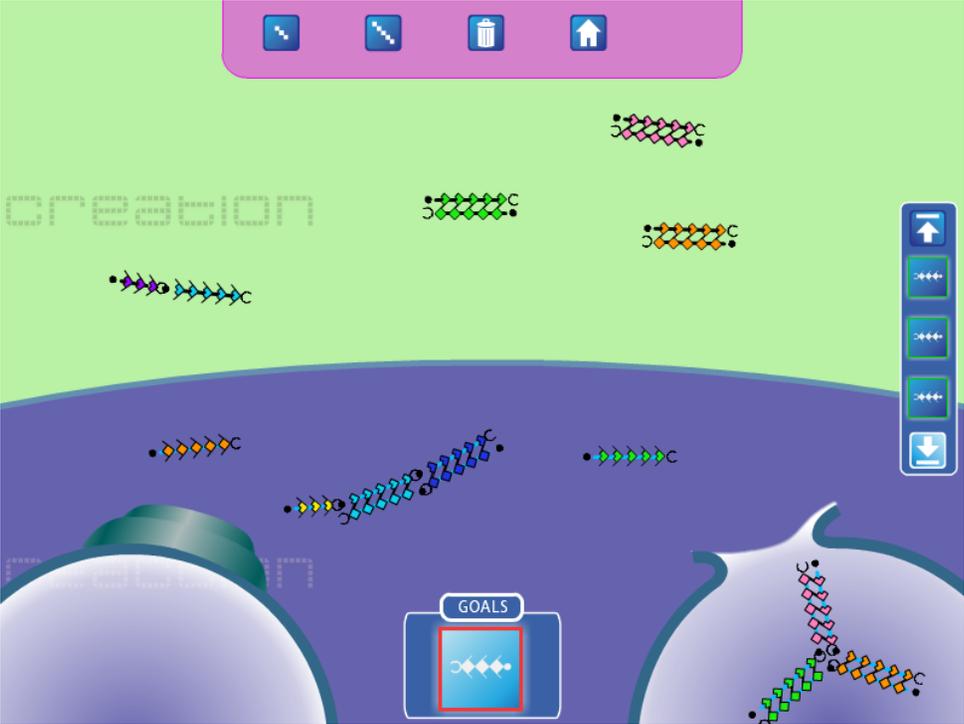
Top Evolvers



Nanotechnology



Nanotechnology





Humans



Computers

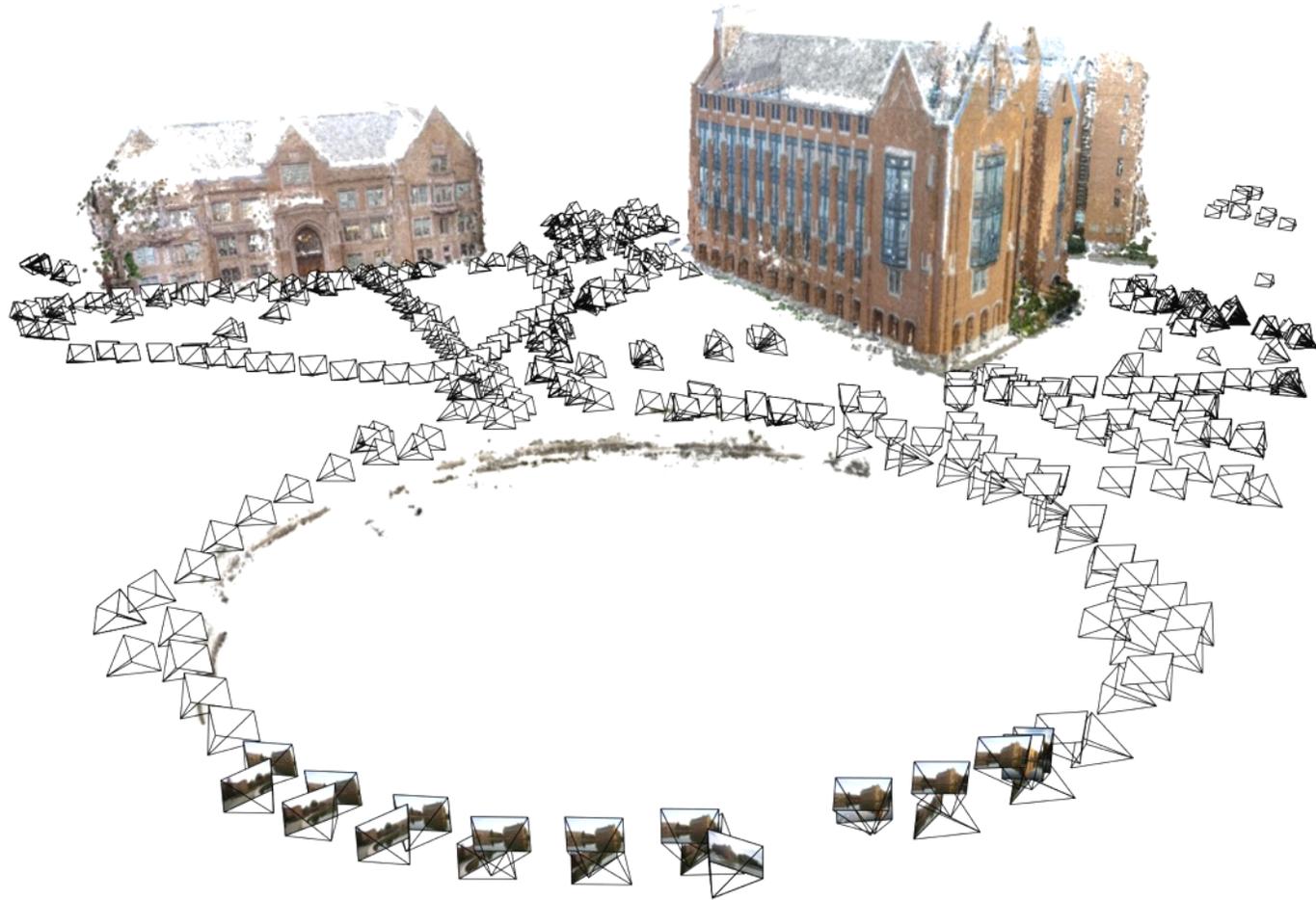
Thank you!

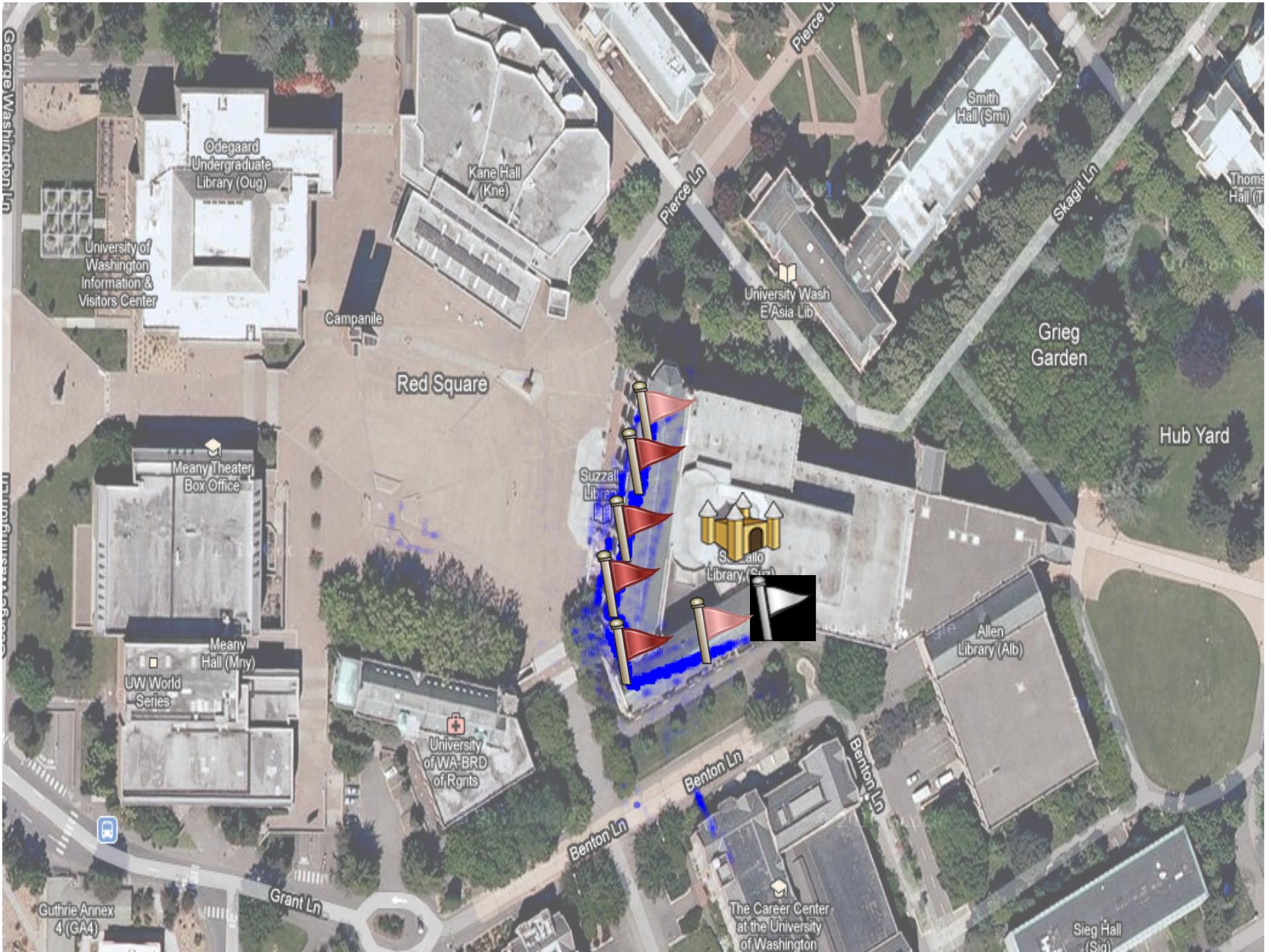
jflat06@cs.washington.edu

Foldit:

<http://fold.it>

Digitizing the World





Odegaard Undergraduate Library (Oug)

Kane Hall (Kne)

Smith Hall (Smi)

University of Washington Information & Visitors Center

Campanile

Red Square

University Wash E/Asia Lib

Greg Garden

Hub Yard

Meany Theater Box Office

Suzzall Library

Suzzallo Library (Suz)

Allen Library (Alb)

Meany Hall (Mny)

UW World Series

University of WA BRD of Rgts

Benton Ln

Benton Ln

Guthrie Annex 4 (GA4)

Grant Ln

The Career Center at the University of Washington

Sieg Hall (Sig)

