University of Warsaw
Faculty of Mathematics, Informatics and Mechanics

Architecture of large projects in bioinformatics (ADP)

AlphaFold 3

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Warsaw, 2024

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nature

Article | Published: 08 May 2024

Accurate structure prediction of biomolecular interactions with AlphaFold 3

Josh Abramson, Jonas Adler, Jack Dunger, Richard Evans, Tim Green, Alexander Pritzel, Olaf Ronneberger, Lindsay Willmore, Andrew J. Ballard, Joshua Bambrick, Sebastian W. Bodenstein, David A. Evans, Chia-Chun Hung, Michael O'Neill, David Reiman, Kathryn Tunyasuvunakool, Zachary Wu, Akvilė Žemgulytė, Eirini Arvaniti, Charles Beattie, Ottavia Bertolli, Alex Bridgland, Alexey Cherepanov, Miles Congreve, … John M. Jumper + Show authors

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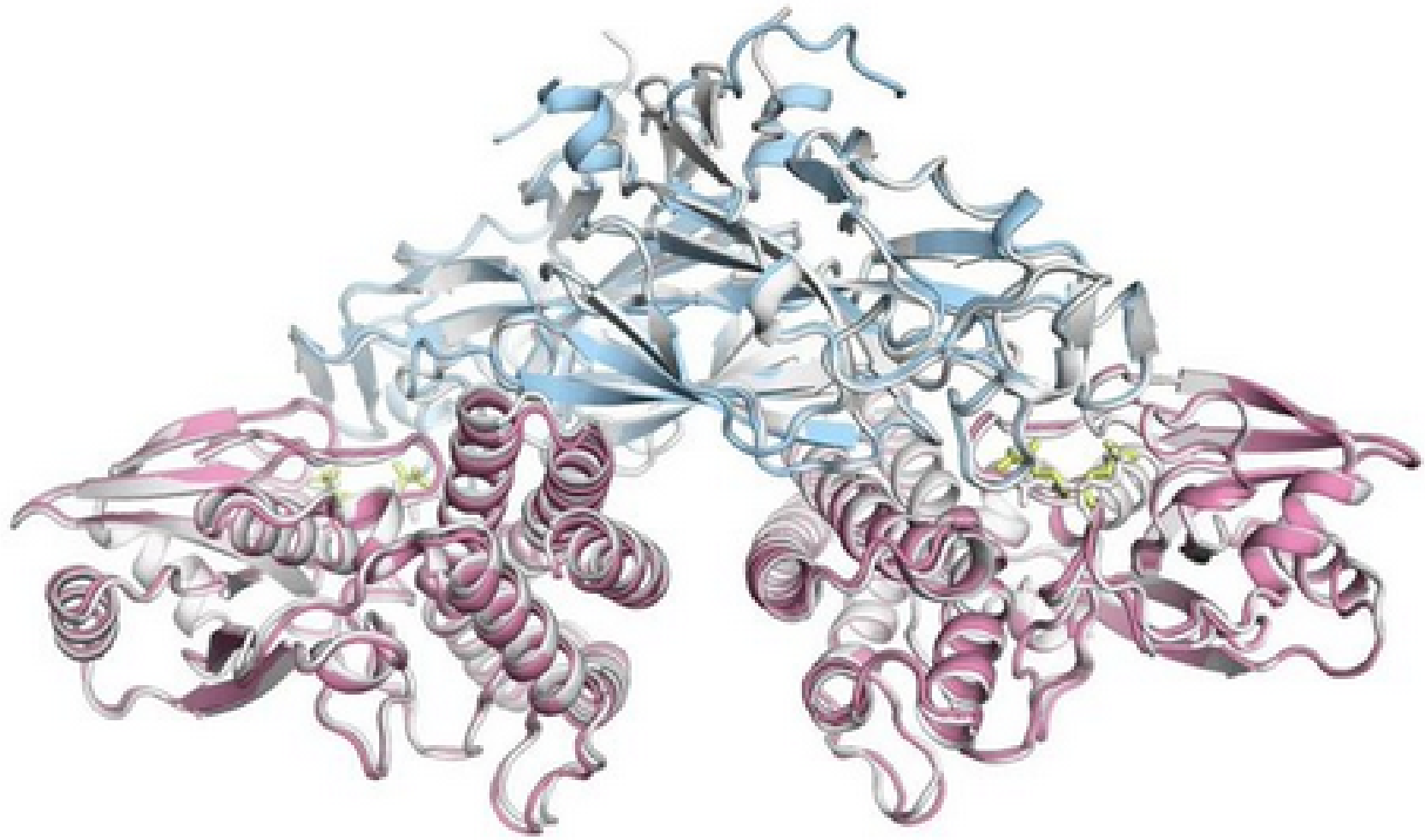
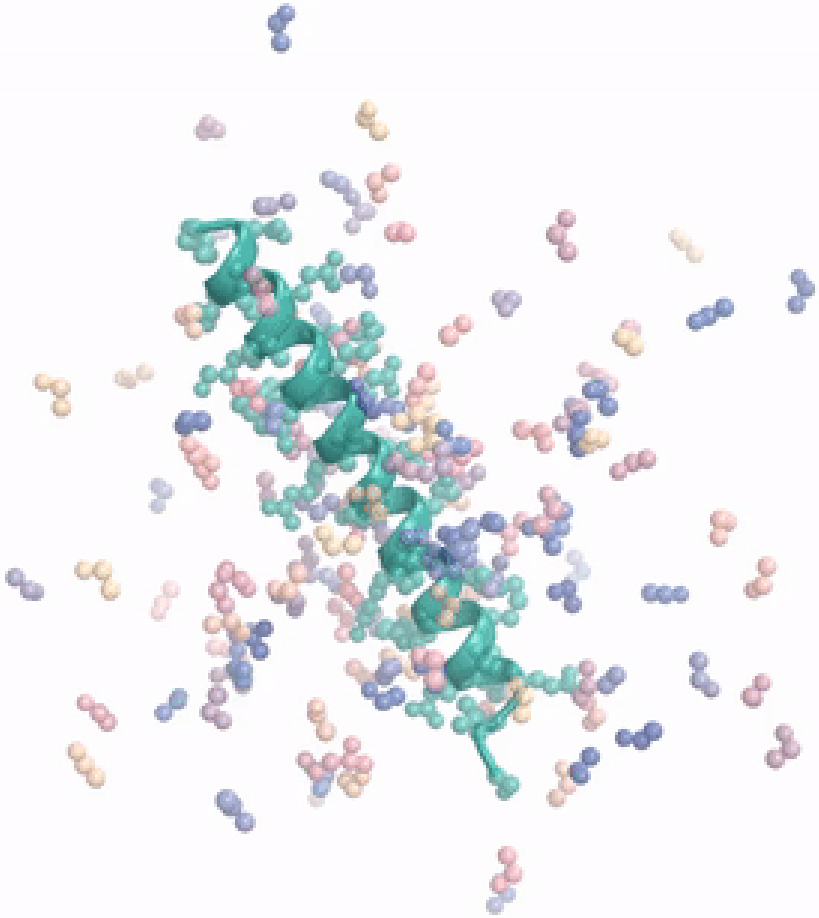
Unlike AF2, which focused on individual proteins, **AF3** embraces complexity of biomolecular interactions. It models diverse entities within a unified framework, highlighting interactions that are crucial for understanding cellular functions, moving toward realistic simulations.



A protein folding prediction in response to a small molecule generated by AlphaFold 3. ISOMORPHIC LABS

ADP



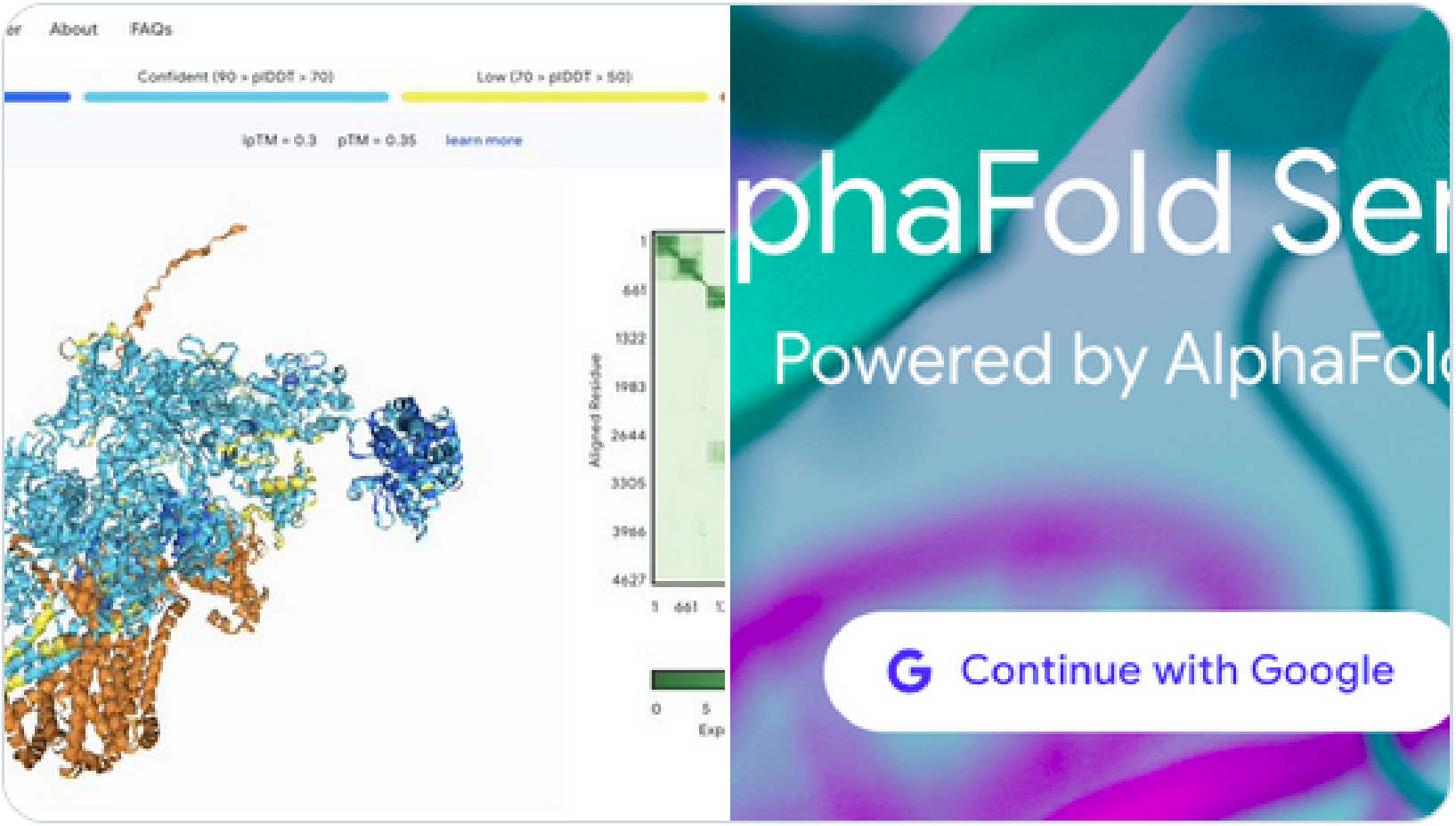
https://golgi.sandbox.google.com

ADP

Sergey Ovchinnikov @sokrypton · 16 g.

AF3 server is LIVE! Just tried predicting complex with almost 5K amino acids.

TIP: you need to click "continue with google" to access the server (otherwise the "server" is grayed out). alphafoldserver.com



7 77 324 23 tys.

https://golgi.sandbox.google.com

Use of AlphaFold Server is subject to the Google Terms of Service; and AlphaFold Server Additional Terms of Service

Key things to know

1. AlphaFold Server is **only** available for non-commercial use by individuals and non-commercial organizations (universities, non-profit organizations and research institutes, educational and government bodies), or for journalism.
2. You **must not** use AlphaFold Server or its outputs:
   a. in connection with **any commercial activities, including research on behalf of commercial organizations;**
   b. in **any automated system that predicts the binding or interaction of the protein with ligands or peptides**, such as Glide or AutoDock; or
   c. to **train machine learning models** or related technology for **biomolecular structure prediction** similar to AlphaFold Server.
3. You **can publish, share and adapt** AlphaFold Server output in accordance with our terms, including the requirement to provide clear notice that ongoing use is subject to AlphaFold Server Output Terms of Use and of any modifications you make.

Ajasja @AjasjaLjubetic · 18 g.

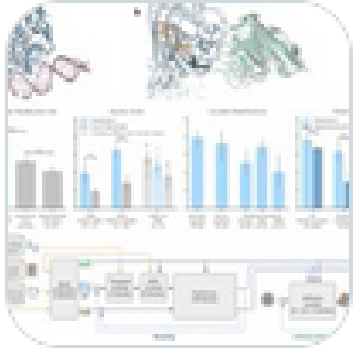
This is super exciting! Although it's a bit sad to see that the source code and weights are not available, even for academic use.

Time will tell if **AF3** will be as widely used and universal as AF2 currently is. Can't wait for this year's CASP :)

Code availability

AlphaFold 3 will be available as a non-commercial usage only server at https://www.alphafoldserver.com, with restrictions on allowed ligands and covalent modifications. Pseudocode describing the algorithms is available in the Supplementary Information. Code is not provided.

Max Jaderberg @maxjaderberg · 19 g.

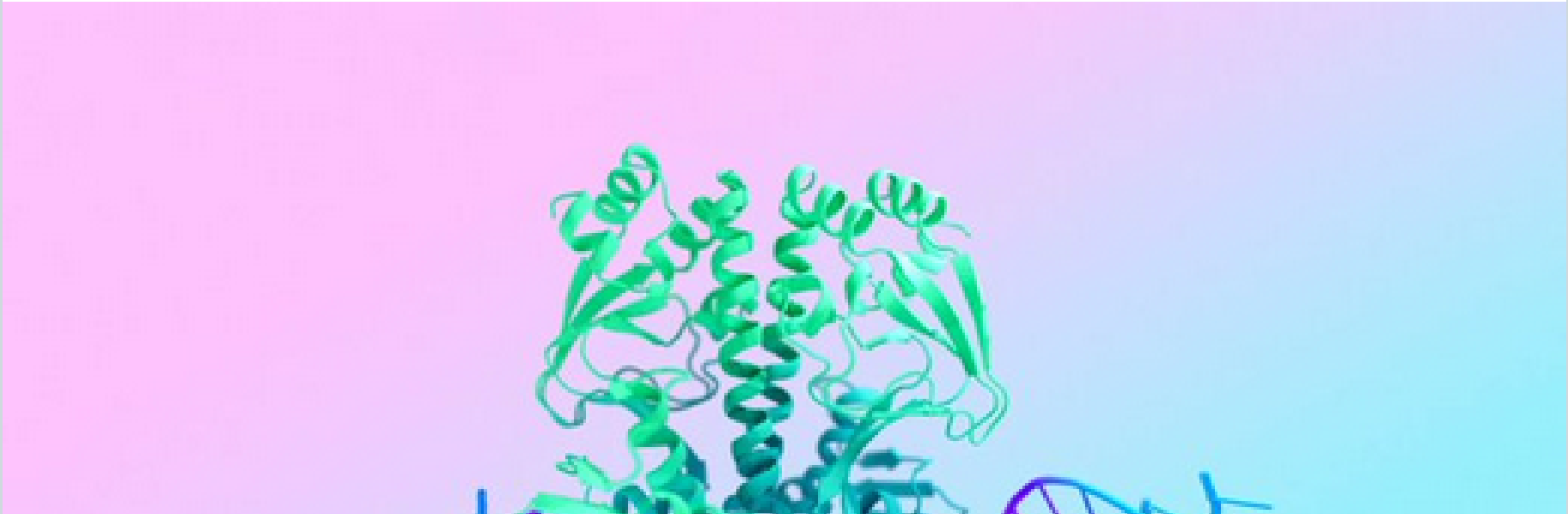


Super excited to be releasing AlphaFold 3 today, developed by @IsomorphicLabs and @GoogleDeepMind: our next generation AI model for predicting the biomolecular structures and interactions of proteins, DNA, RNA, small molecules, and more: bit.ly/44yfaCw...

13 1 tys.

Demis Hassabis @demishassabis · 18 g.

Thrilled to announce AlphaFold 3 which can predict the structures and interactions of nearly all of life's molecules with state-of-the-art accuracy including proteins, DNA and RNA. Biology is a complex dynamical system so modeling interactions is crucial blog.google/technology/ai/...



Roland Dunbrack 🏳️‍🌈 **@rolanddunbrack.bsky.socia** @RolandDunbrack · 16 g. ···

Demis -- I think AlphaFold3 is really exciting. As Reviewer #3, I got great results from the server. I tried hard to get @Nature to urge you to release the code but was unsuccessful. I did not get it for re-review so I don't know if you responded. So why no code? @GoogleDeepMind

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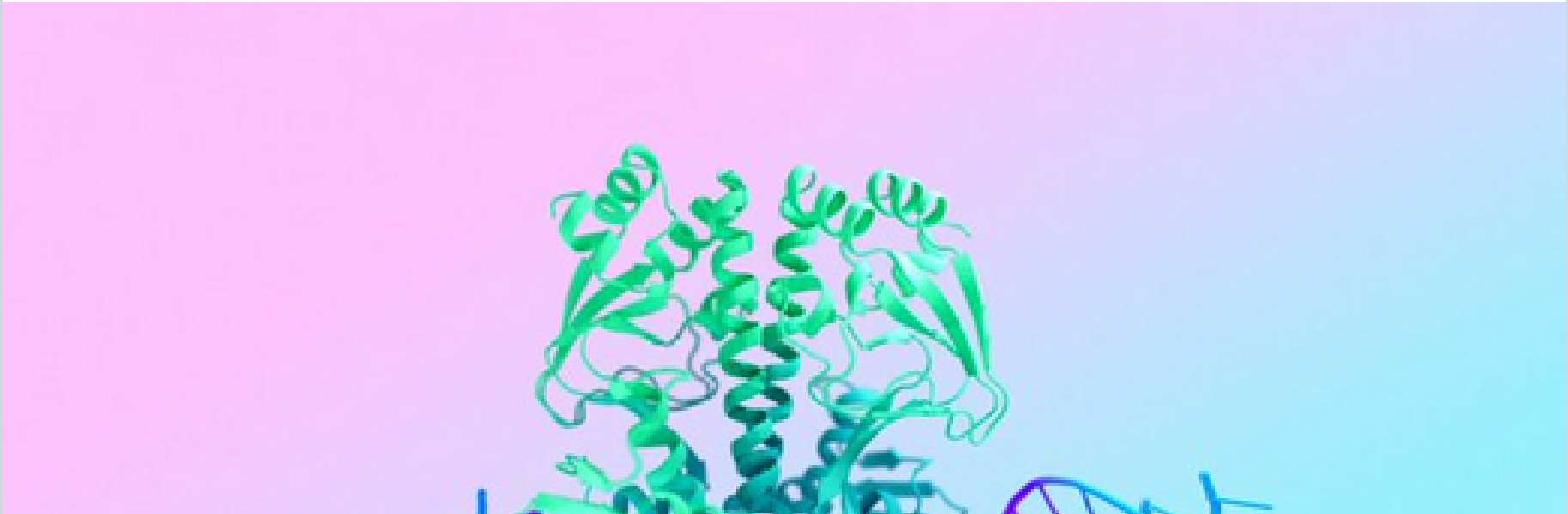

Roland Dunbrack 🏳️‍🌈 **@rolanddunbrack.bsky.socia** @RolandDunbrack · 4 g. •••

Neither @Magda_Skipper (editor of @Nature) nor the handling editor would answer my emails about my concerns. I was not allowed to see any response to the reviews by the AlphaFold3 authors, so I don't know what they think either. Extremely unusual and very disappointing

> **Stephen Curry** @Stephen_Curry · 5 g.
>
> I'd be interested to hear @Nature's and @GoogleDeepMind's responses to this. x.com/rolanddunbrack...

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Altuna Akalin @AltunaAkalin · 1 g.

Reviewer asked @Nature and authors to release **alphafold3** code with no success. Dangerous trend for journals acting as marketing avenues for new tech without reproducibility or code review

> **Roland Dunbrack** 🏳️‍🌈 **@rolanddunbrack.bsky.so** @RolandDunbrac · 17 g.
>
> Demis -- I think AlphaFold3 is really exciting. As Reviewer #3, I got great results from the server. I tried hard to get @Nature to urge you to release the code but was unsuccessful. I did not get it for re-review so I don't know if you responded. So why no code? @GoogleDeepMind x.com/demishassabis/...

Pratyush Tiwary
@tiwarylab

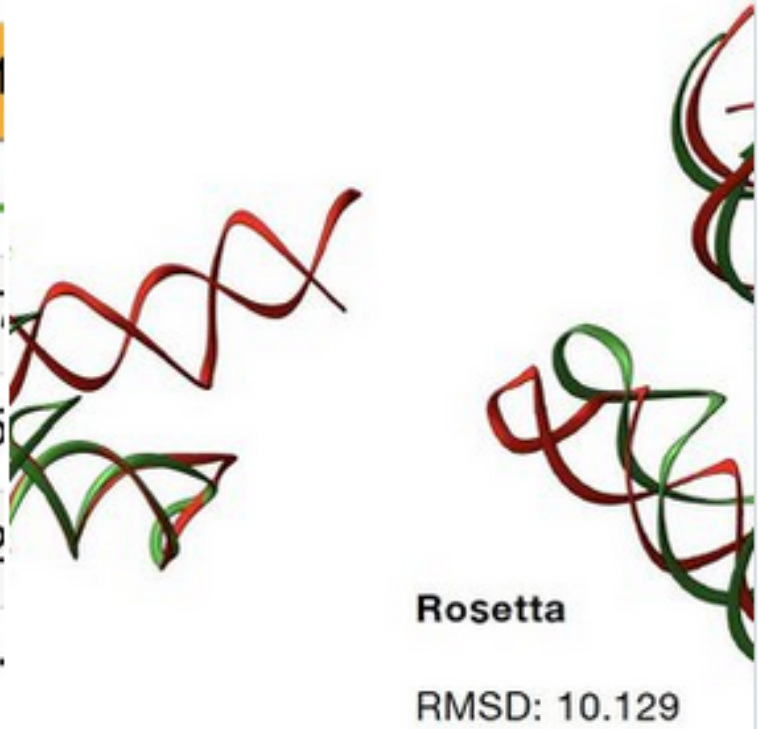
It seems rather convenient that two of the structures* left out in the @Nature paper for AlphaFold3 on RNA by @GoogleDeepMind are ones where it does not well (multiple trials on web server)

* R1149 and R1156 predictioncenter.org/casp15/results...

Przetłumacz wpis

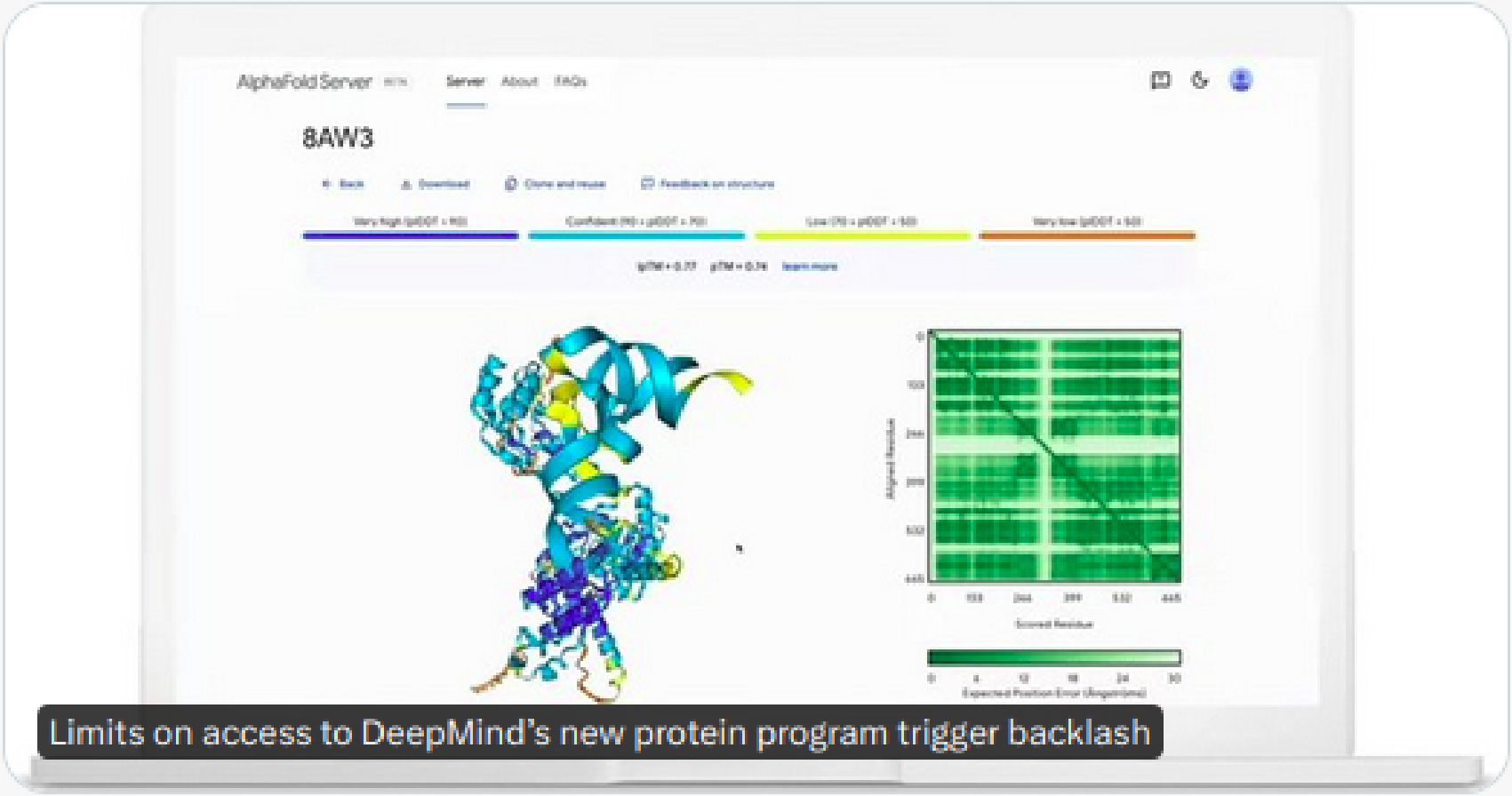
R1107*	R1117	R111
6.513	2.645	15.
9.762	5.102	1
-	0.2225	0.5
-	0.1351	0.2

er form and bound to a protein.



Roland Dunbrack 🏳️‍🌈 **@rolanddunbrack.bsky.socia** @RolandDunbrack · 19 g. •••

Got interviewed for this article in Science on the release of alphafoldserver.com.



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SCIENCEINSIDER | BIOLOGY

Limits on access to DeepMind's new protein program trigger backlash

Critics accuse *Nature*, which published the research, of failing to meet its own transparency standards

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Critics accuse *Nature*, which published the research, of failing to meet its own transparency standards

AlphaFold 3's code wasn't available during the review process for the *Nature* paper, either. Roland Dunbrack, a computational structural biologist at the Fox Chase Cancer Center and letter co-author, says he received the manuscript without any way to test the program. After contacting the journal, he got access to an early version of the web server, but repeated requests for code in the leadup to publication went unanswered, he says. "I don't understand why [*Nature*'s editors] sent it out for review under those conditions."

The paper doesn't provide a justification, simply noting, "Code is not provided"—an omission that appears to "flagrantly violate" *Nature*'s policies, says James Fraser, a structural biologist at the University of California San Francisco (UCSF) and one of the letter's organizers. *Nature*'s submission guidelines state that custom code supporting a paper's main claims must be made available to referees upon request, and its editorial policies specify that "authors are required to make [code] promptly available to readers without undue qualifications."

Limits on access to DeepMind's new protein program trigger backlash

Critics accuse *Nature*, which published the research, of failing to meet its own transparency standards

Regardless, since the open letter was posted, DeepMind researchers have indicated that more information on AlphaFold 3 is on the way. A DeepMind media representative pointed *Science* to a 13 May social media post in which Kohli, another co-author, announced the increase in the web server's daily request limit to 20. The team is also "working on releasing the AF3 model" for academic use within 6 months, Kohli wrote, a move welcomed by researchers who spoke to *Science*.

Stephanie Wankowicz, a computational structural biologist at UCSF and another of the letter's organizers, says she hopes the episode will encourage the computational biology community to set concrete standards for research communication, particularly given the increasing influence of for-profit companies in this field.

It's also an opportunity for journals to reflect on their role in upholding scientific standards, Fraser says. If they apply standards selectively, "it's like they're the traffic cops that are letting some people speed and pulling other people over for rolling through a stop sign. And that's not fair."

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David Konerding • 3rd+
Principal Engineer at Genentech
1d •

+ Follow

There is a minor controversy over AlphaFold3, DeepMind's latest protein structure prediction model: the paper was published in Nature with insufficient supplementary info to reproduce the results. Even the reviewer was ...see more

Letter to the Editor: AlphaFold3

We are submitting the follow as a Letter to the Editor and will post the text immediately on Zenodo. If you would like to endorse to this letter, please fill out the form below.

Authors:

Stephanie A. Wankowicz, UCSF

Pedro Beltrao, ETH

Benjamin Cravatt, Scripps

Roland Dunbrack, FCCC

Anthony Gitter, UW Madison

Kresten Lindorff-Larsen, Copenhagen

Sergey Ovchinnikov, MIT

Nicholas Polizzi, DFCI/HMS

Brian K. Shoichet, UCSF

James S. Fraser, UCSF

Letter to the Editor: AlphaFold3

Thank you for your time
and
See you at the next lecture

Any other
questions & comments

lukaskoz@mimuw.edu.pl