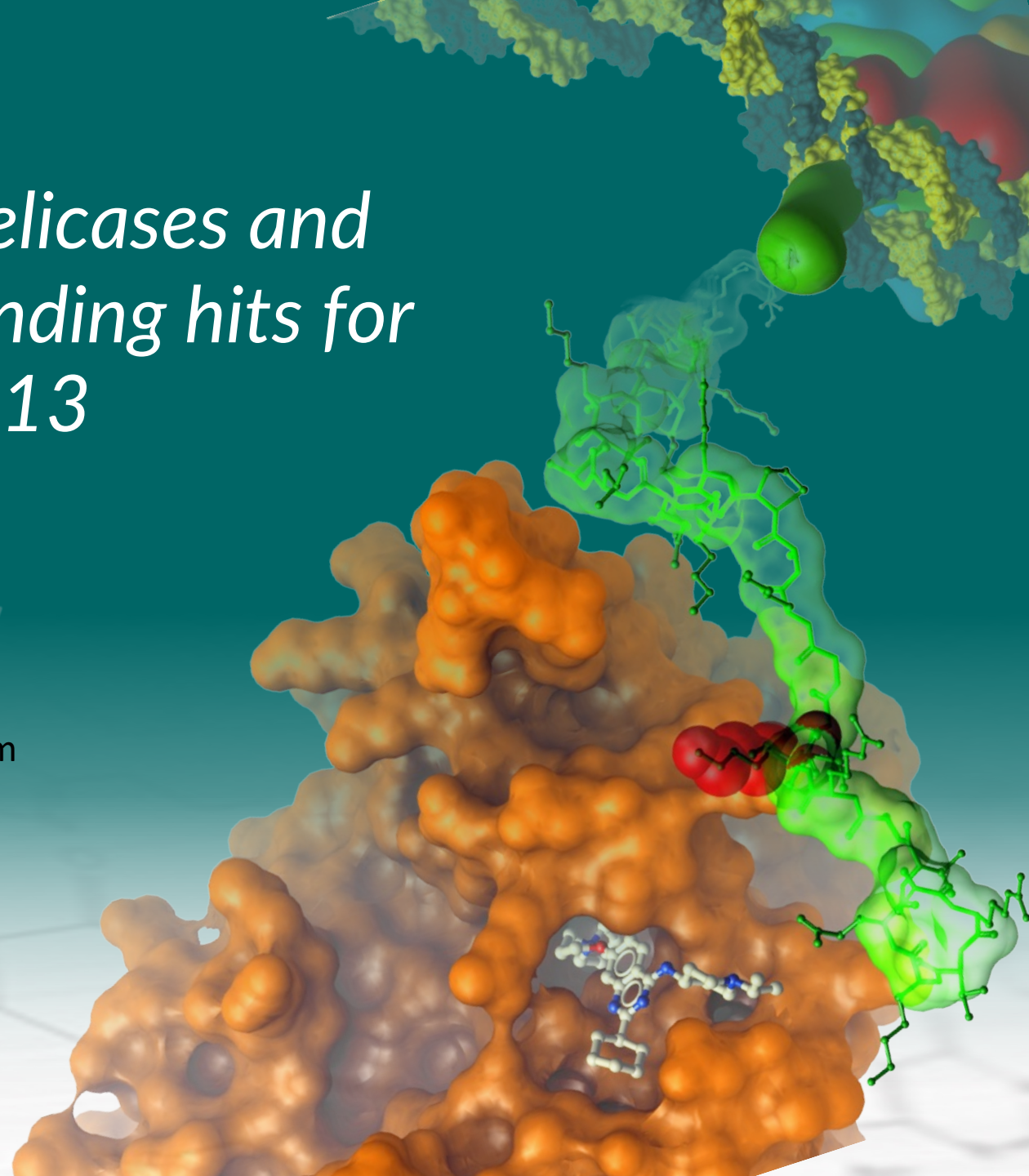




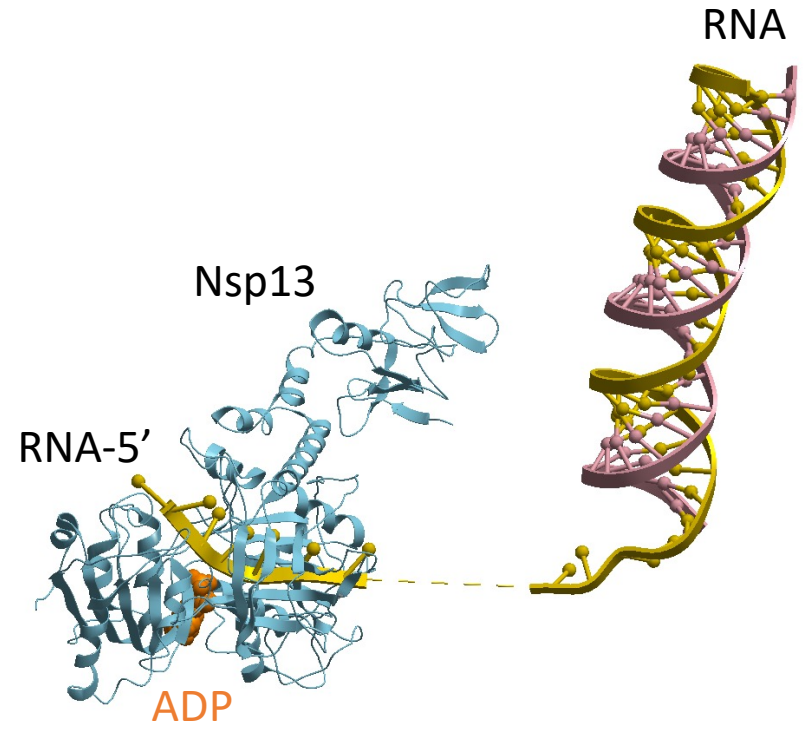
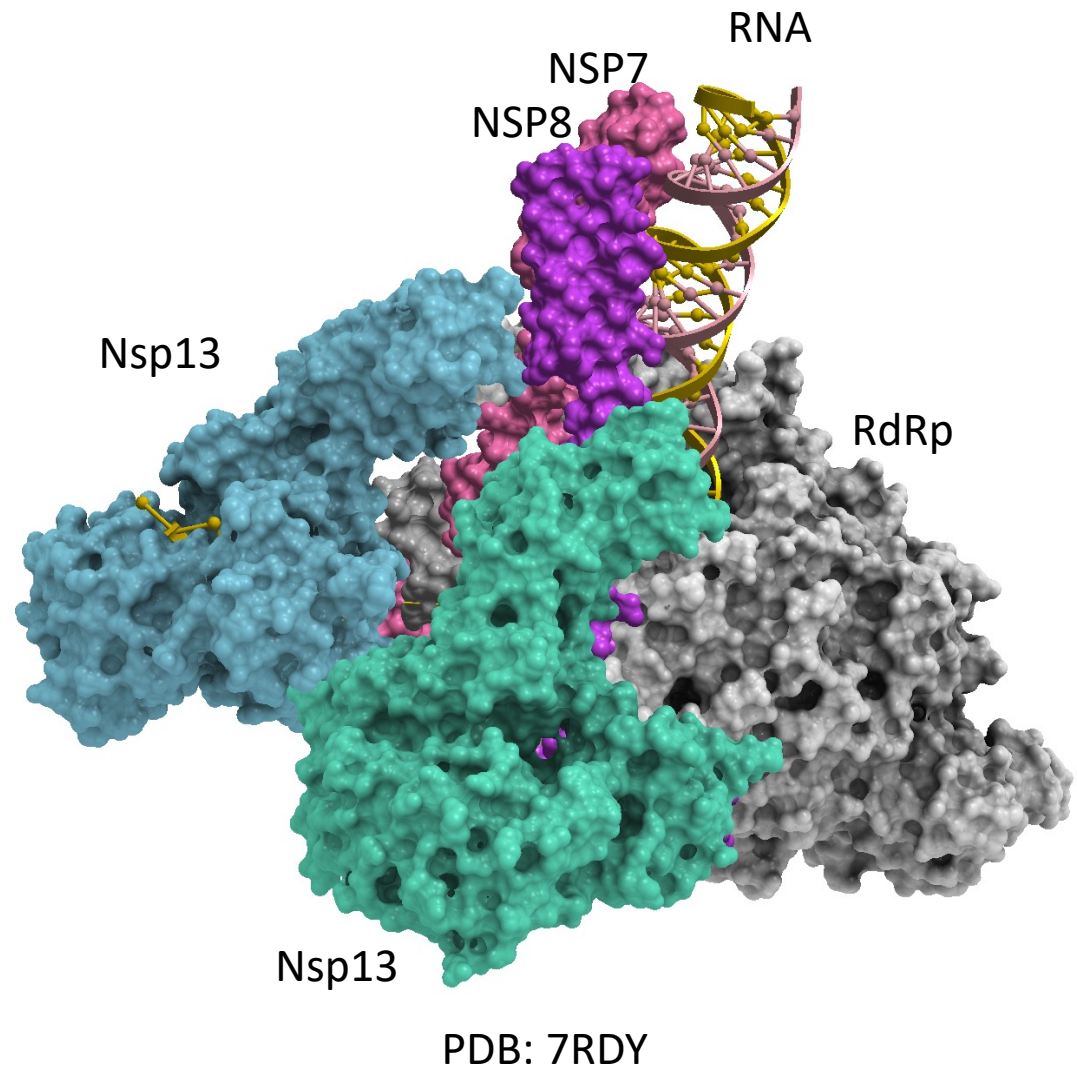
# *Analysis of coronavirus helicases and CACHE Challenge #2 on finding hits for SARS-CoV-2 nsp13*

Matthieu Schapira  
Structural Genomics Consortium  
Dept Pharmacology & Toxicology  
University of Toronto

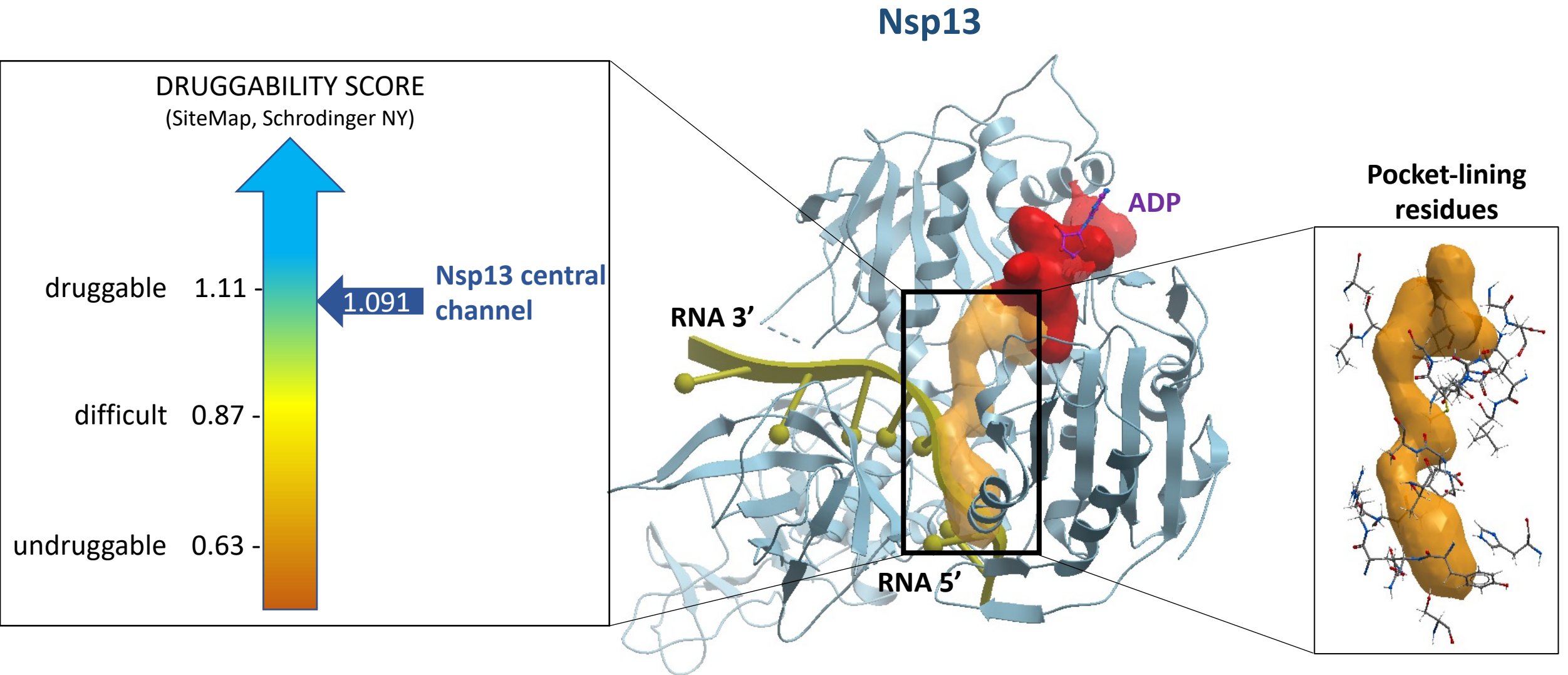
AViDD Open Science Forum  
November 16<sup>th</sup> 2022



# Nsp13 is an Integrated Component of the Replication Transcription Complex



# RNA Occupies a Druggable Central Channel of Nsp13



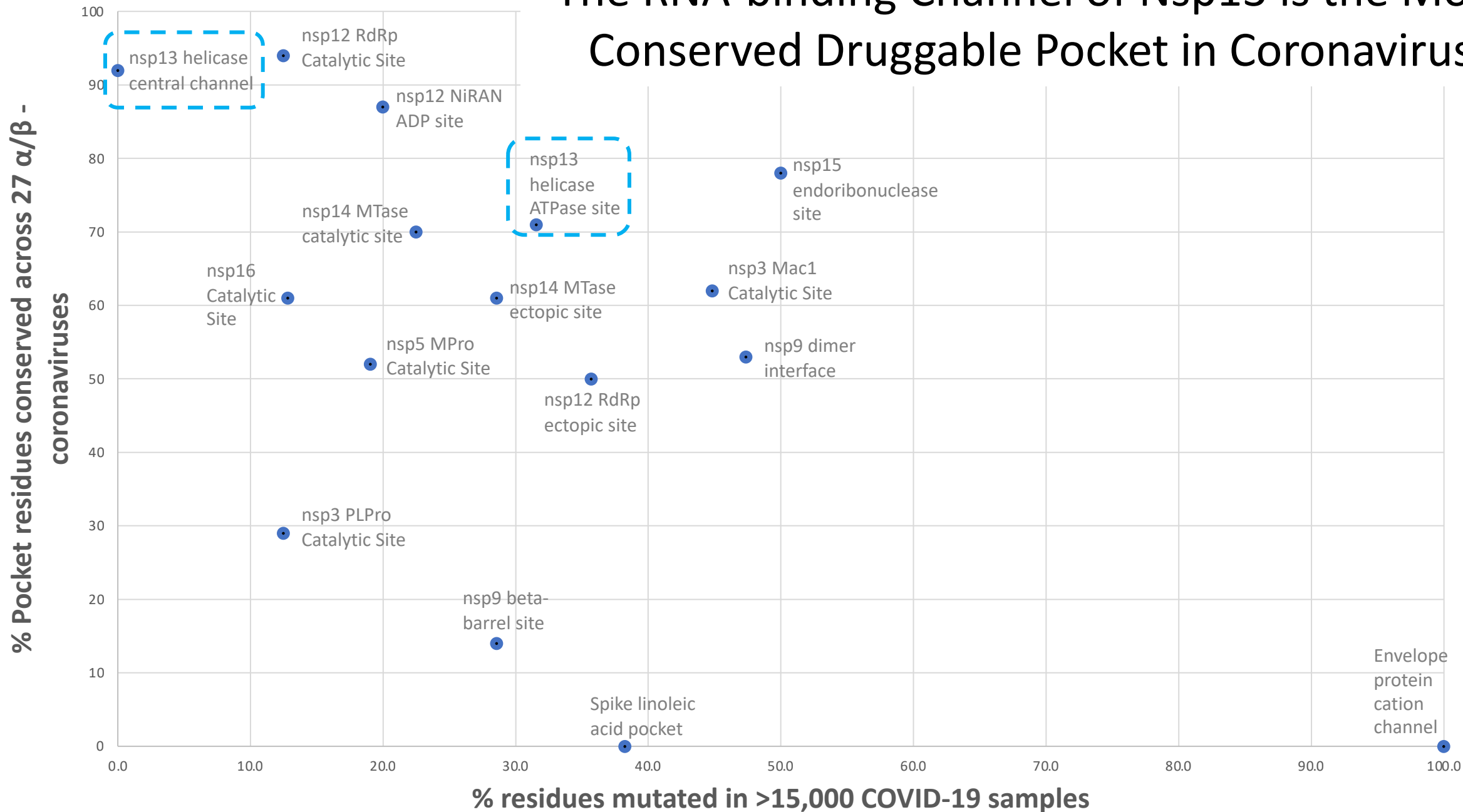
# Residues Lining the Central Channel of Nsp13 Are Highly Conserved in Coronavirus

		SARS-CoV-2 nsp13 helicase central channel or 5'-RNA site residue numbering																								
		N177	R178	N179	A312	A313	A316	D374	E375	S377	M378	G400	D401	Q404	L405	P408	S486	Y515	N516	T532	D534	S535	Q537	G538	H554	R567
		N	R	N	A	A	A	D	E	S	M	G	D	Q	L	P	S	Y	N	T	D	S	Q	G	H	R
β-coronavirus	SARS2	NRNAAADESMGDQLPSYNTDSQGHR																								
	CVHSA	NRNAAADESMGDQLPSYNTDSQGHR																								
	BCRP3	NRNAAADESMGDQLPSYNTDSQGHR																								
	BC279	NRNAAADESMGDQLPSYNTDSQGHR																								
	BCHK3	NRNAAADESMGDQLPSYNTDSQGHR																								
	BCHK9	NRNAAADESMGDQLPSYNTDSQGHR																								
	CVEMC	NRNAAADESMGDQLPSYNTDSQGHR																								
	BCHK5	NRNAAADESMGDQLPSYNTDSQGHR																								
	BCHK4	NRNAAADESMGDQLPSYNTDSQGHR																								
	BC133	NRNAAADESMGDQLPSYNTDSQGHR																								
	CVHOC	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVBLU	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVBEN	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVBM	NKNAAADESMGDQLPSYNTDSQGHR																								
α-coronavirus	CVBQ	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVMA5	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVMJH	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVM2	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVHN1	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVHN5	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVHN2	NKNAAADESMGDQLPSYNTDSQGHR																								
	CVPPU	NRNAAADESMGDQLPSYNTDSQGHR																								
	FIPV	NRNAAADESMGDQLPSYNTDSQGHR																								
	PEDV7	NRNAASDESMGDQLPSYNTDSQGHR																								
	CVHNL	NRNAASDESMGDQLPSYNTDSQGHR																								
	CVH22	NRNAASDESMGDQLPSYNTDSQGHR																								
	BC512	SRNAASDESMGDQLPSYNTDSQGHR																								

✖ Non-identical residues

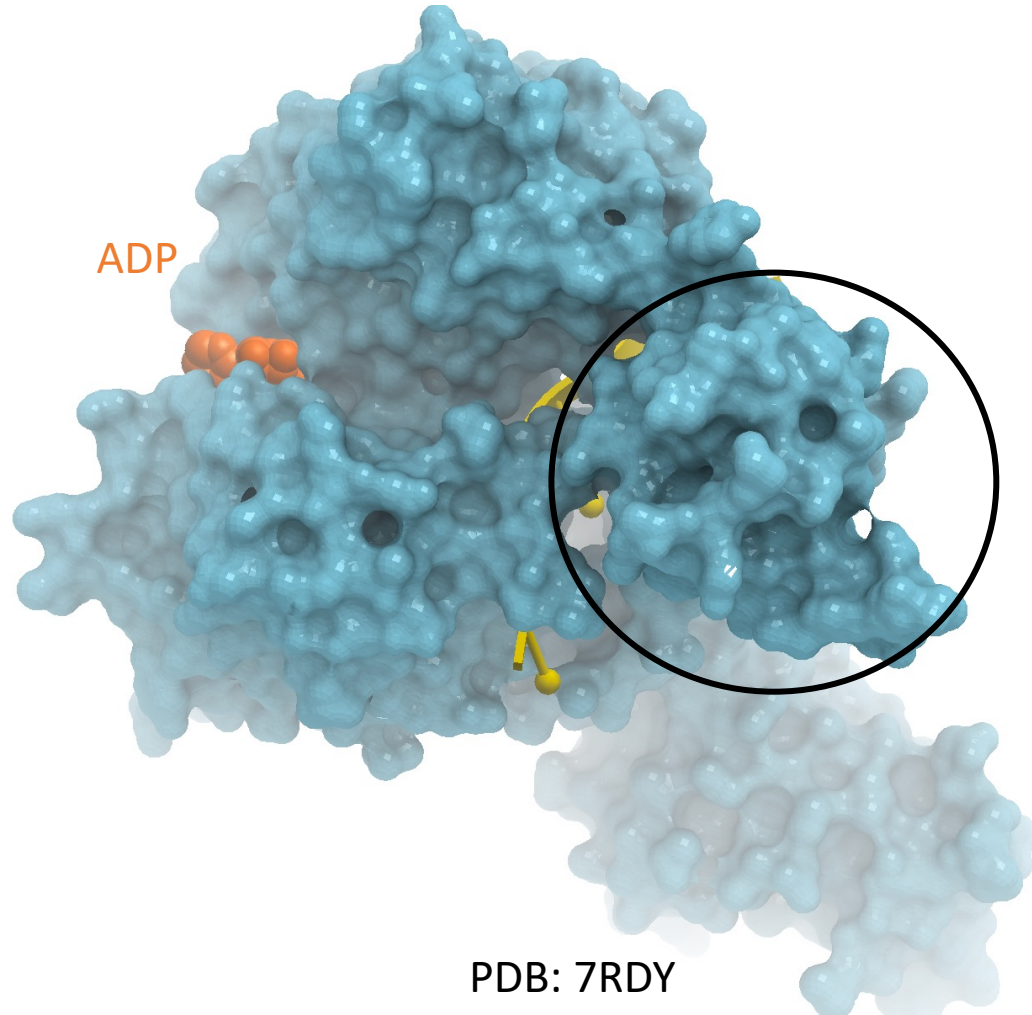
Organism
Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)
Severe acute respiratory syndrome coronavirus (SARS-CoV)
Bat coronavirus Rp3/2004 (BtCoV/Rp3/2004) (SARS-like coronavirus Rp3)
Bat coronavirus 279/2005 (BtCoV) (BtCoV/279/2005)
Bat coronavirus HKU3 (BtCoV) (SARS-like coronavirus HKU3)
Bat coronavirus HKU9 (BtCoV) (BtCoV/HKU9)
Middle East respiratory syndrome-related coronavirus (Human coronavirus EMC)
Bat coronavirus HKU5 (BtCoV) (BtCoV/HKU5/2004)
Bat coronavirus HKU4 (BtCoV) (BtCoV/HKU4/2004)
Bat coronavirus 133/2005 (BtCoV) (BtCoV/133/2005)
Human coronavirus OC43 (HCoV-OC43)
Bovine coronavirus (strain 98TXSF-110-LUN) (BCoV-LUN) (BCV)
Bovine coronavirus (strain 98TXSF-110-ENT) (BCoV-ENT) (BCV)
Bovine coronavirus (strain Mebus) (BCoV) (BCV)
Bovine coronavirus (strain Quebec) (BCoV) (BCV)
Murine coronavirus (strain A59) (MHV-A59) (Murine hepatitis virus)
Murine coronavirus (strain JHM) (MHV-JHM) (Murine hepatitis virus)
Murine coronavirus (strain 2) (MHV-2) (Murine hepatitis virus)
Human coronavirus HKU1 (isolate N1) (HCoV-HKU1)
Human coronavirus HKU1 (isolate N5) (HCoV-HKU1)
Human coronavirus HKU1 (isolate N2) (HCoV-HKU1)
Porcine transmissible gastroenteritis coronavirus (TGEV)
Feline coronavirus (strain FIPV WSU-79/1146) (FCoV)
Porcine epidemic diarrhea virus (strain CV777) (PEDV)
Human coronavirus NL63 (HCoV-NL63)
Human coronavirus 229E (HCoV-229E)
Bat coronavirus 512/2005 (BtCoV) (BtCoV/512/2005)

# The RNA-binding Channel of Nsp13 is the Most Conserved Druggable Pocket in Coronavirus

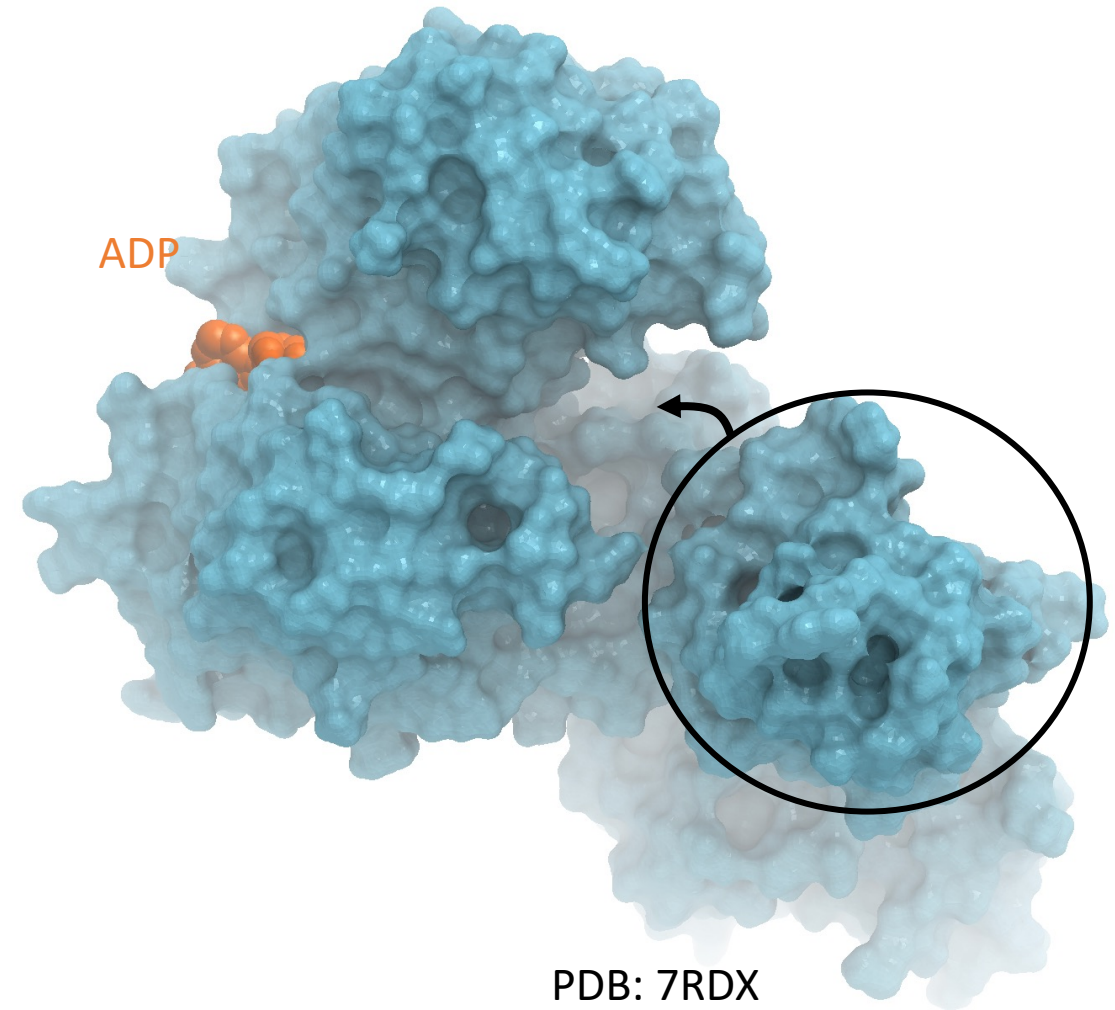


# RNA Engagement is Associated with a Massive Conformational Rearrangement at the Nsp13 Central Channel

RNA-engaged Nsp13

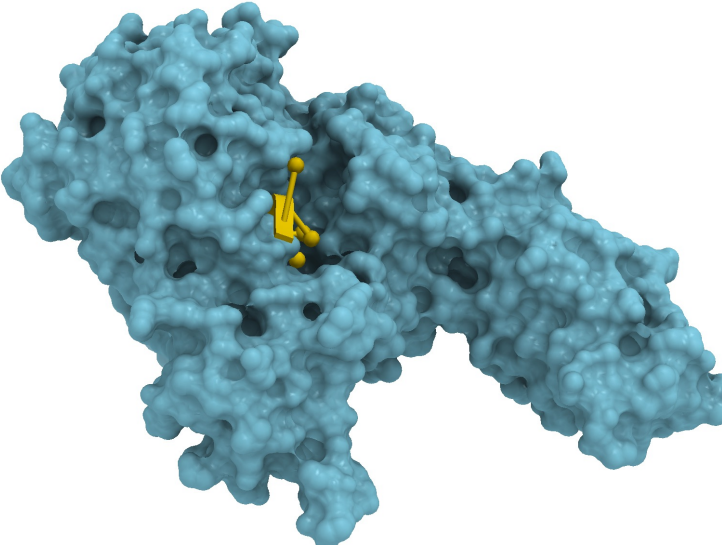


Apo Nsp13

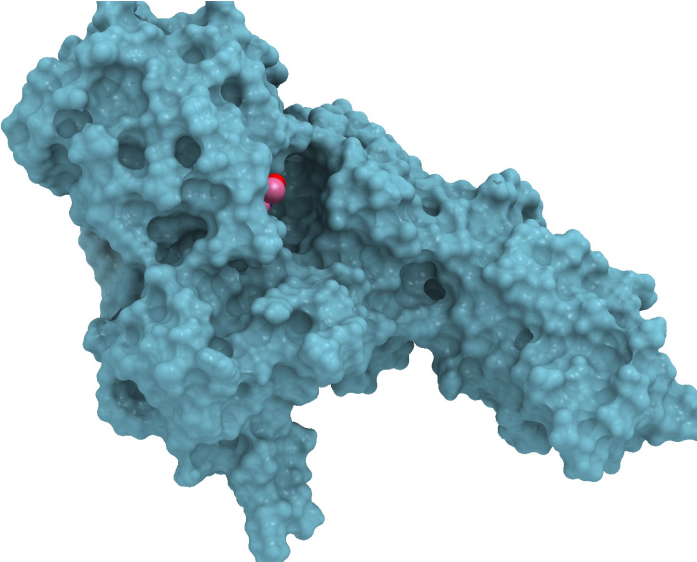


# Fragment-Bound Nsp13 Conformation is Close to the RNA-Engaged State

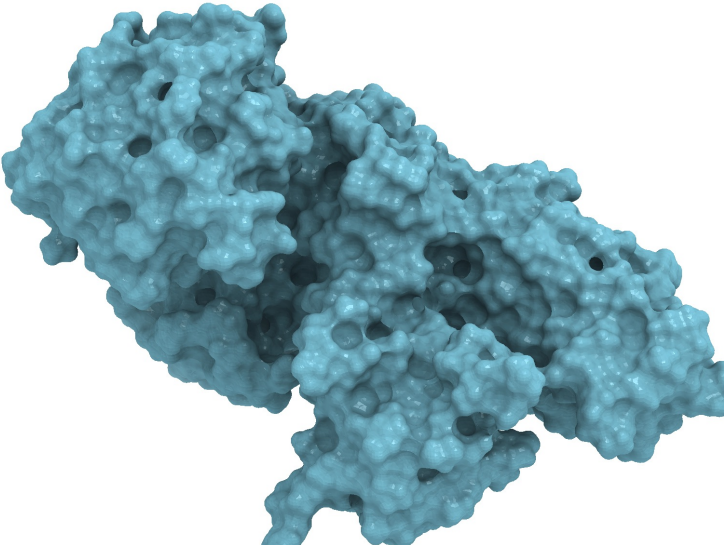
RNA-bound



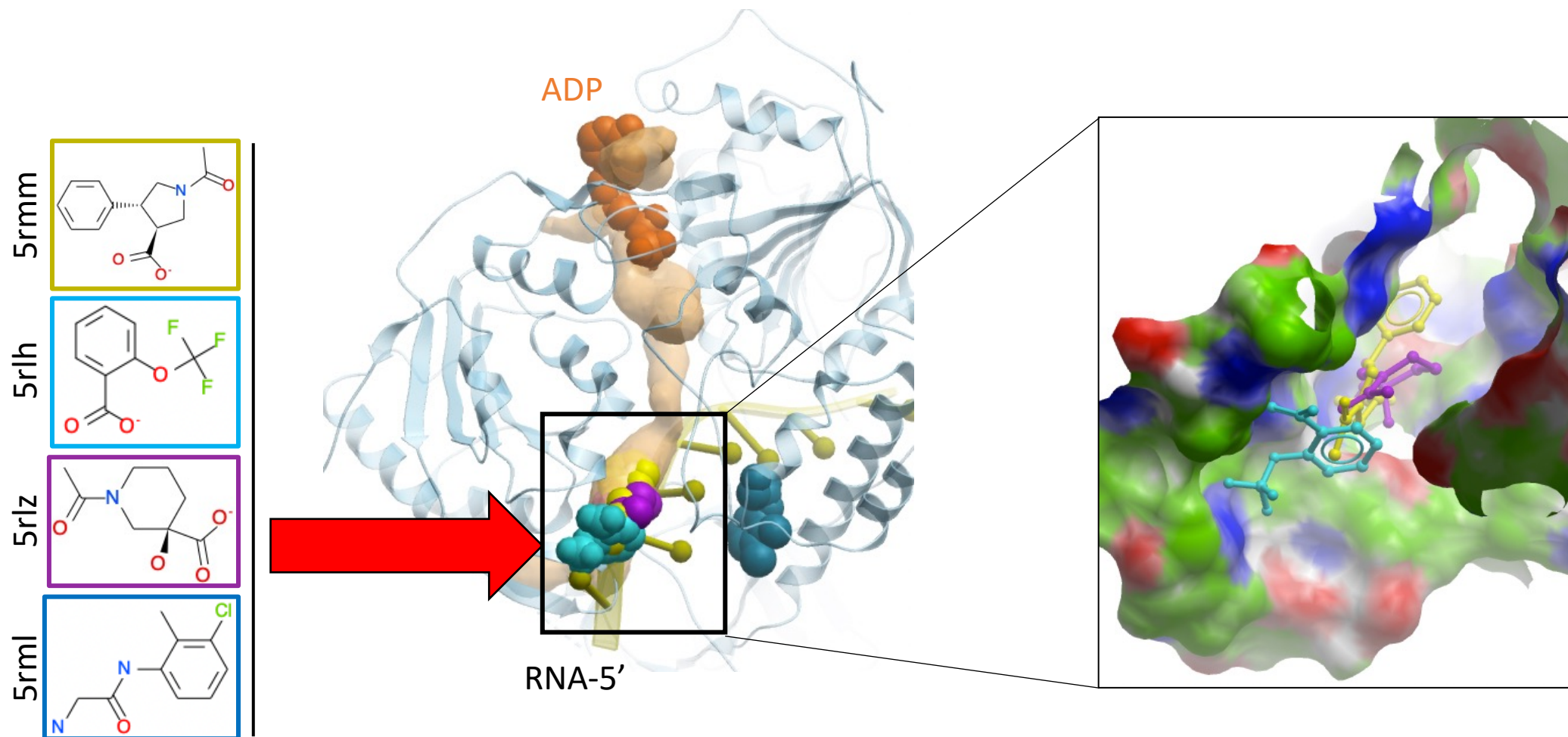
Fragment-bound



Apo



# Fragments in the PDB May be a Starting Point for Inhibitor Design





# CACHE Challenge #2: Asking Participants to Predict Ligands Targeting the RNA-Binding Channel of Nsp13

CACHE is modelled after the protein structure prediction challenge CASP

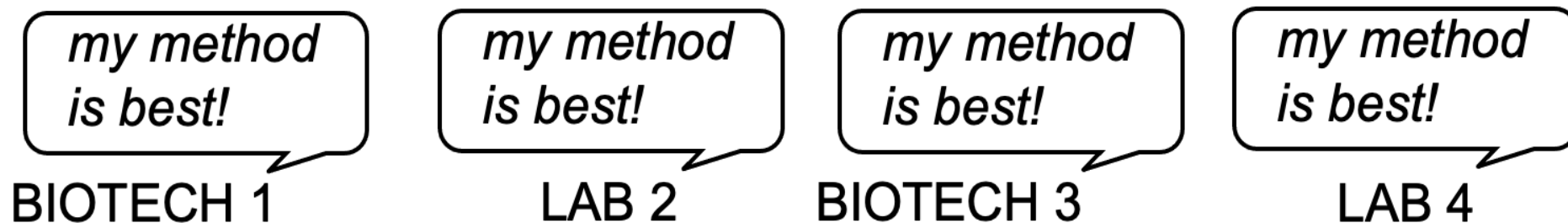
CACHE is a benchmarking initiative to reveal the most efficient computational methods for hit finding and to guide future technological improvement

# CACHE Is a Prospective Hit Finding Competition

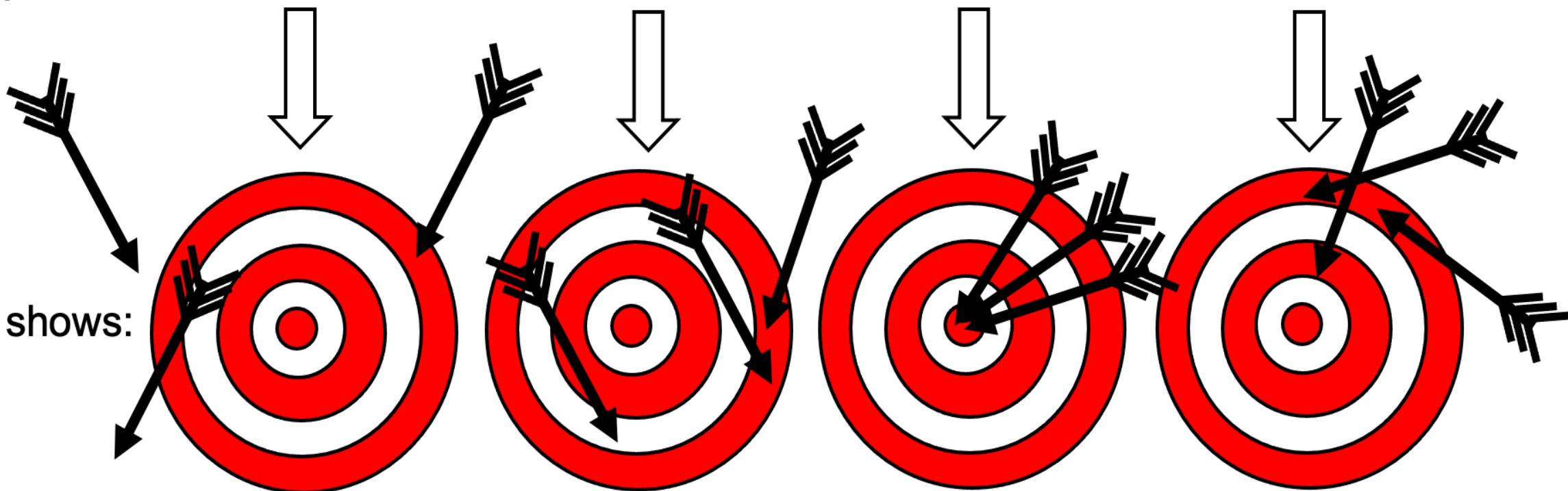
- Participants use their computational method to predict up to 100 hits that are ordered and tested experimentally by CACHE
- All data is publicly released without restriction on use at the end of each competition

# CACHE Reveals the State-of-The-Art to Scientists, Pharmas, Funders

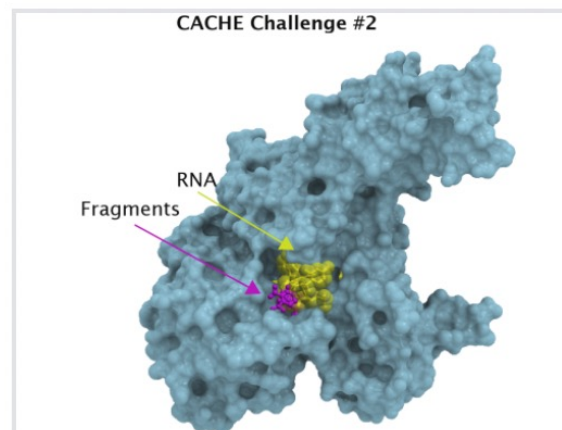
scientists,  
pharmas,  
funders hear  
and see:



CACHE shows:



## CHALLENGE #2



Crystal structures of SARS-CoV-2 NSP13/helicase bound to fragments (5RLH, 5RLZ, 5RML, 5RMM) and RNA (7CXM).

### FINDING LIGANDS TARGETING THE CONSERVED RNA BINDING SITE OF SARS-COV-2 NSP13

The second CACHE Challenge target is the NSP13 helicase of SARS-CoV-2.

Participants are asked to find hits for the RNA-binding site of NSP13. Read more under Details below.

# Challenge #2: RNA Binding Site of SARS-CoV-2 NSP13

41 Applications, including multiple leaders in the field

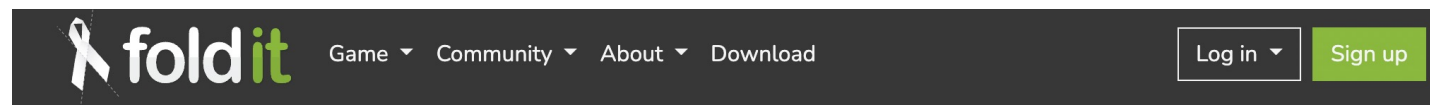
US	11		
UK	5		
China	4		
Canada	3		
Germany	3		
Korea	3		
Brazil	2		
Denmark	1		
India	1		
Ireland	1		
Italy	1		
Japan	1		
Malaysia	1		
So. Africa	1		
Switzerl.	1		
Taiwan	1		
Ukraine	1		
		Academia	28
		Biotech	7
		Electronics giant	1
		Government	2
		Internet giant	1
		Pharma	1
		Independent	1

# CACHE Attracted a Diverse Team of Computational Chemistry and AI Experts to Work on Nsp13

Publications from the 25 selected participants to CACHE #2

JOURNAL	papers since 2020
Any	367
Journal of Chemical Information and Modeling	27
Journal of Medicinal Chemistry	11
Drug Discovery Today	10
Molecules	9
Advances in Neural Information Processing Systems	8
Scientific Reports	8
PLoS Computational Biology	7
Journal of Chemical Theory and Computation	7
European Journal of Medicinal Chemistry	6
Journal of Chemical Physics	6
Nature	5
Science	5

# Drug-it is One of the 25 Participants of CACHE #2. Will Crowd-Sourcing do Better than the Experts?



## Download the Game!

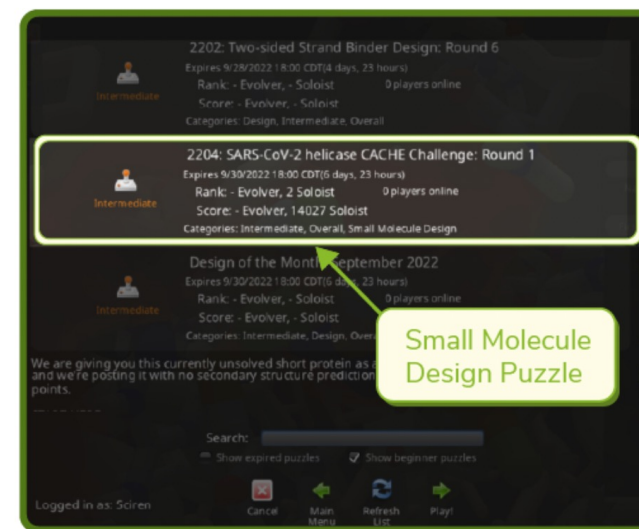
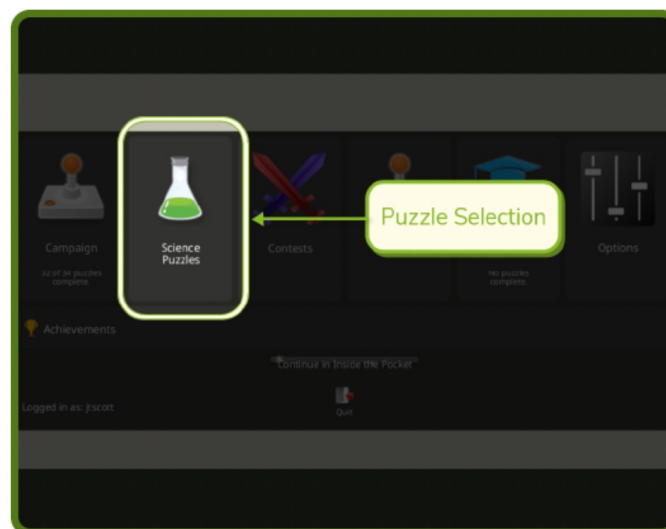
### Current Small Molecule Drug Design Puzzle

- SARS-CoV-2 helicase CACHE Challenge: Round 3

### Finding the Small Molecule Puzzles

- Once the game is running you will be asked to play online or offline.
- Select **Play Online** and sign in.
- Select **Science Puzzles**.
- The current Small Molecule Drug Design Puzzles will automatically appear in your puzzle selection menu shown below:

<https://fold.it/drugit>



## CACHE (Critical Assessment of Computational Hit-finding Experiments): A public-private partnership benchmarking initiative to enable the development of computational methods for hit-finding

**Suzanne Ackloo** University of Toronto & Structural Genomics Consortium,  
**Rima Al-awar** Ontario Institute for Cancer Research & University of Toronto,  
**Rommie E. Amaro** University of California, San Diego,  
**Cheryl H. Arrowsmith** University of Toronto & Structural Genomics Consortium,  
**Hatylas Azevedo** Aché Laboratórios Farmacêuticos,  
**Robert A. Batey** University of Toronto, **Yoshua Bengio** University of Montreal,  
**Ulrich A.K. Betz** Merck Healthcare KGaA,  
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**Johanna M. Jansen** Novartis Institutes for BioMedical Research,  
**Daniel Kuhn** Merck Healthcare KGaA,  
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**Uta Lessel** Boehringer Ingelheim Pharma GmbH & Co. KG,  
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**Patrick Riley** Relay Therapeutics, **Kumar Singh Saikatendu** Takeda California, Inc.,  
**Vijayaratnam Santhakumar** Structural Genomics Consortium & University of Toronto,  
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# ACKNOWLEDGEMENTS

## Nsp13

### **SGC Toronto**

Setayesh Yazdani  
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### **EBI Cambridge**

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## CACHE Experimental Platform

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## FUNDING PARTNERS

The Structural Genomics Consortium is a registered charity (no: 1097737) that receives funds from Bayer AG, Boehringer Ingelheim, Bristol Myers Squibb, Genentech, Genome Canada through Ontario Genomics Institute [OGI-196], EU/EFPIA/OICR/McGill/KTH/Diamond Innovative Medicines Initiative 2 Joint Undertaking [EUbOPEN grant 875510], Janssen, Merck KGaA (aka EMD in Canada and US), Pfizer and Takeda.