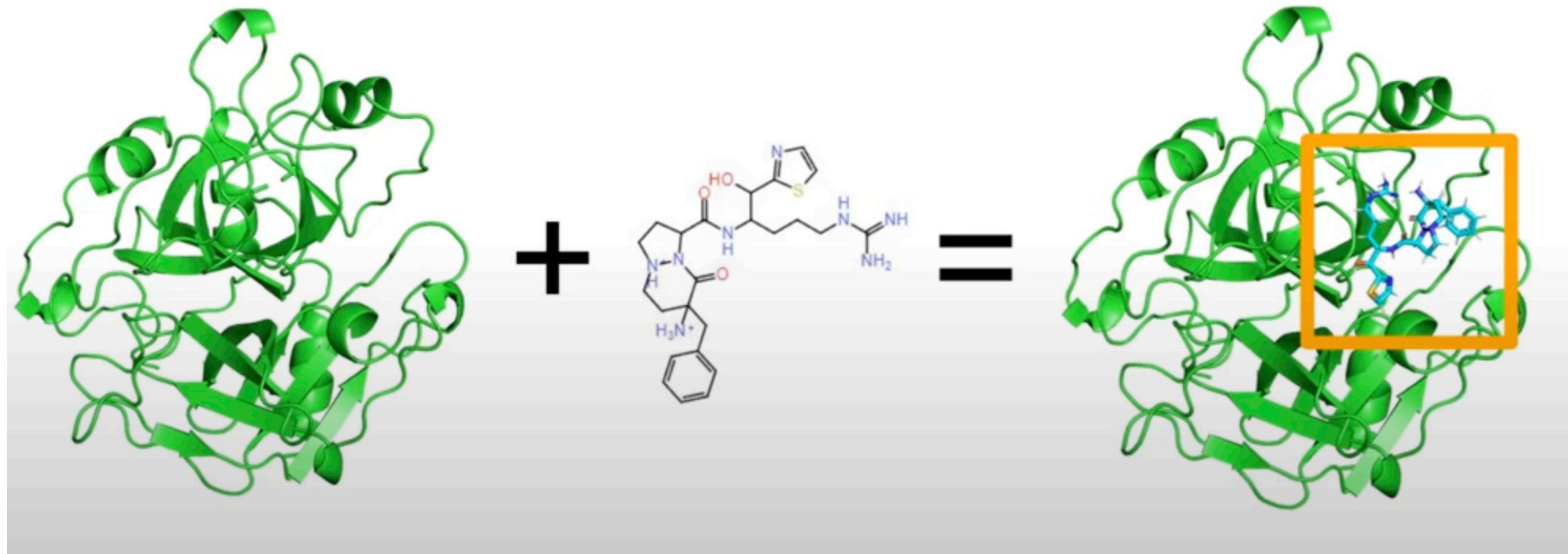


EQUIBIND: Geometric Deep Learning for Drug Binding Structure Prediction

HannesStärk*¹ Octavian-EugenGanea*¹ LagnajitPattanaik¹ ReginaBarzilay¹ TommiJaakkola¹

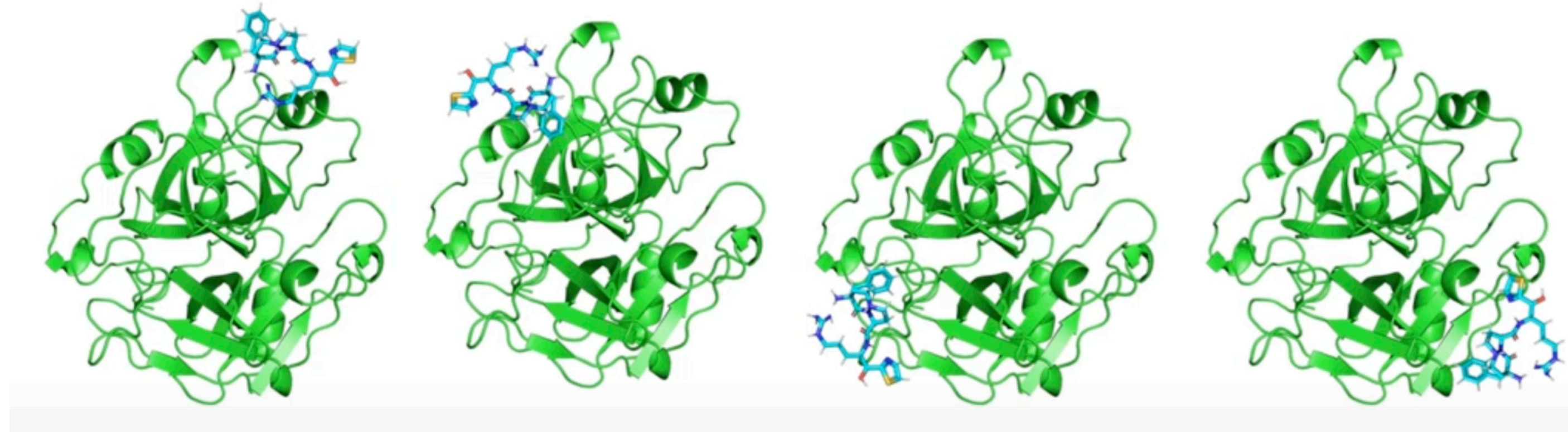
Aditya Bantwal

Introduction



Introduction

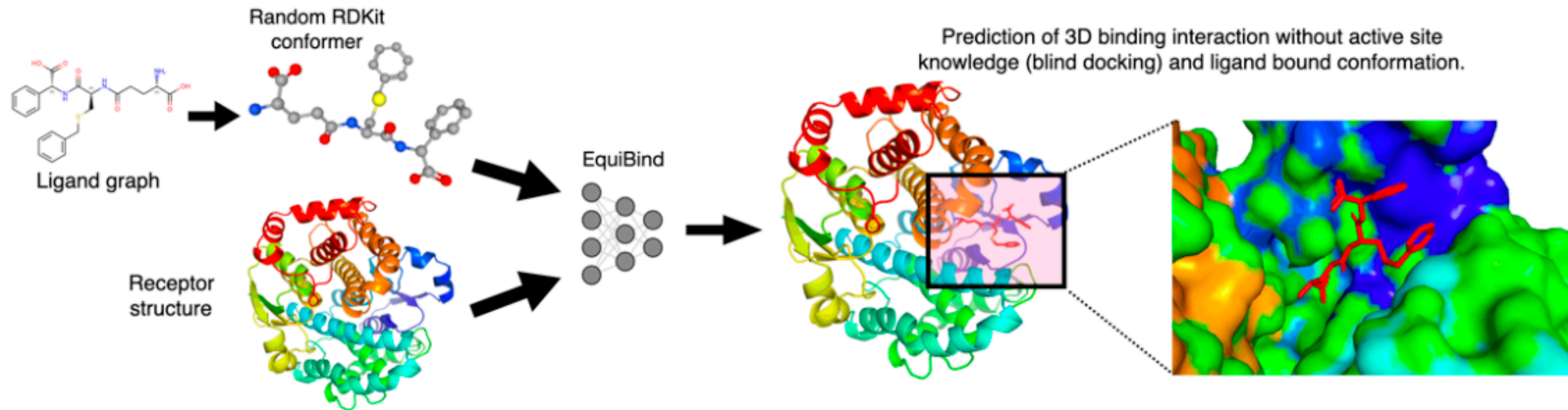
- Existing methods are slow
- Try many different ligand structures and score them



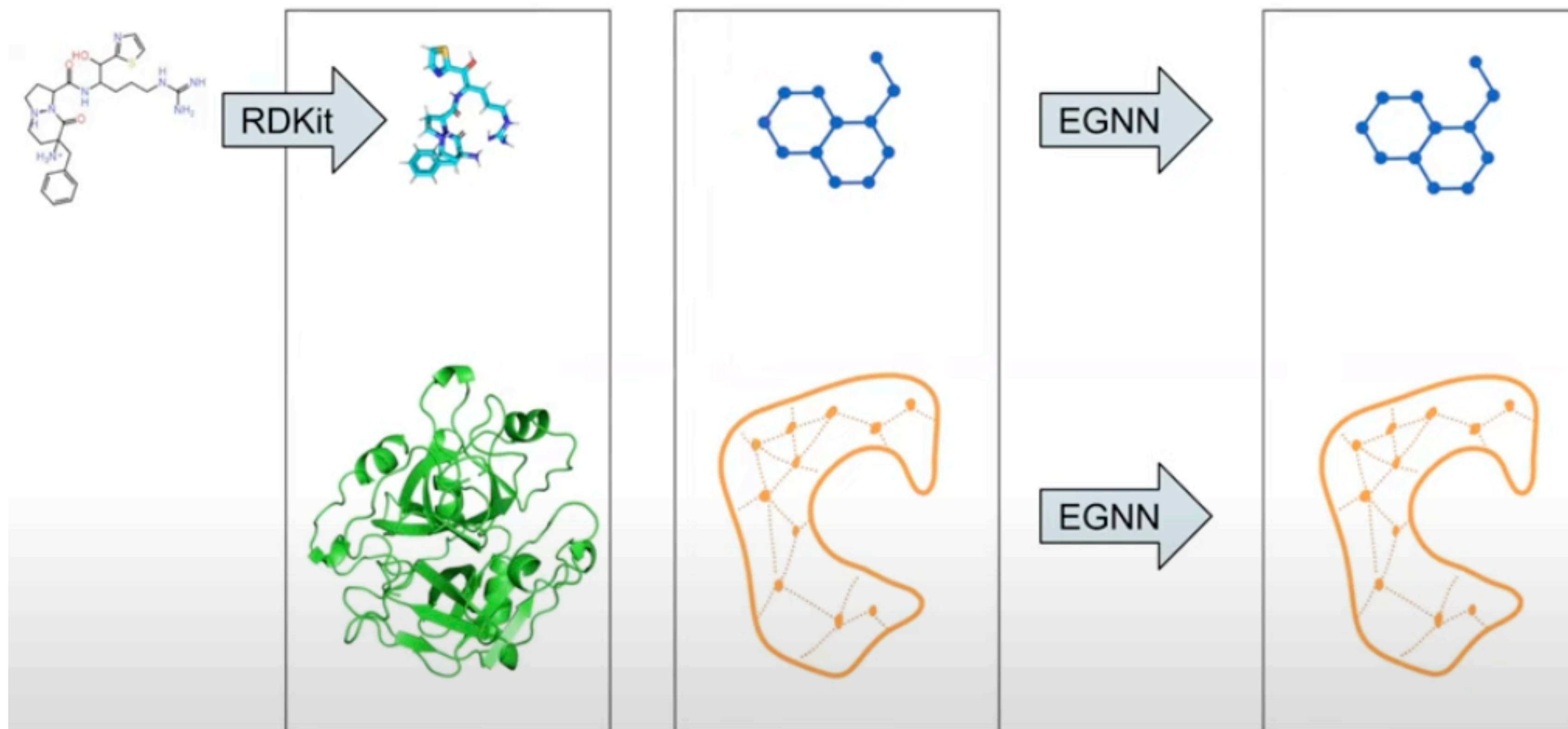
Equibind

- Direct Single forward pass

Equibind



Equibind: Flexible Drug Prediction



Equibind: Flexible Drug Prediction

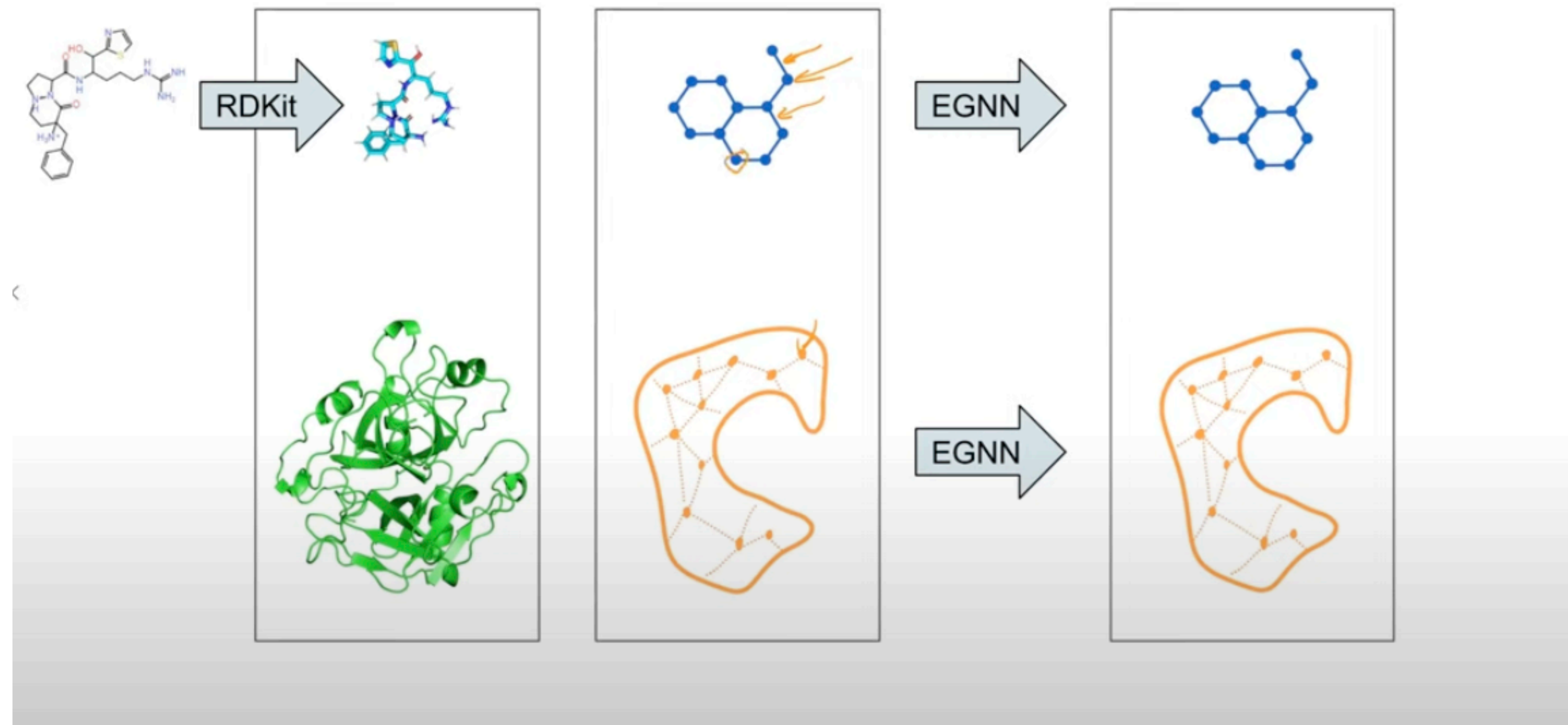


Figure : Equibind Architecture overview. Screenshot from 'Absci Invites: Seminar Series YouTube: <https://www.youtube.com/watch?v=JAvh9e6XEGM&t=2360s>.

Equibind: Flexible Drug Prediction

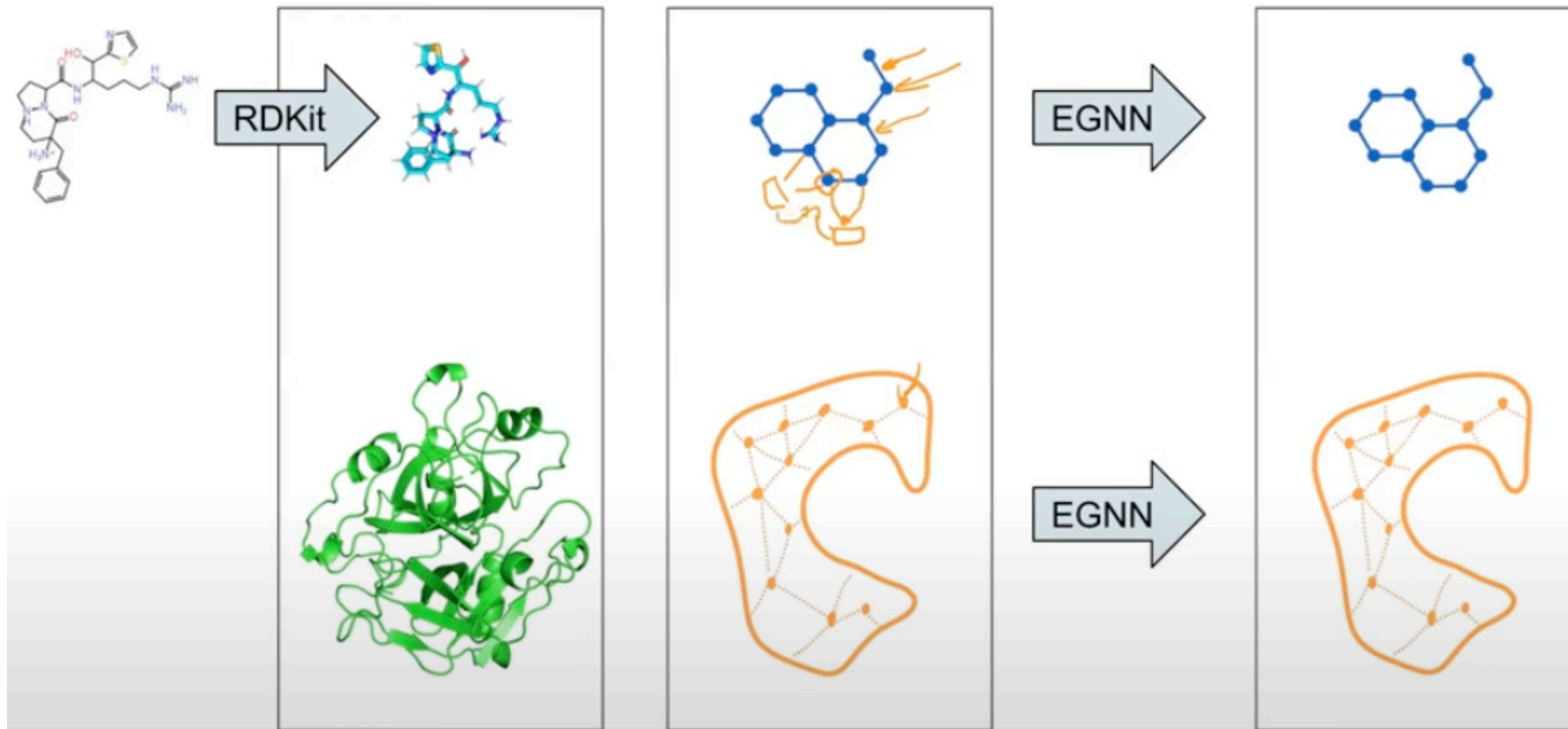


Figure : Equibind Architecture overview. Screenshot from 'Absci Invites: Seminar Series YouTube: <https://www.youtube.com/watch?v=JAvh9e6XEGM&t=2360s>.

Equibind: Flexible Drug Prediction

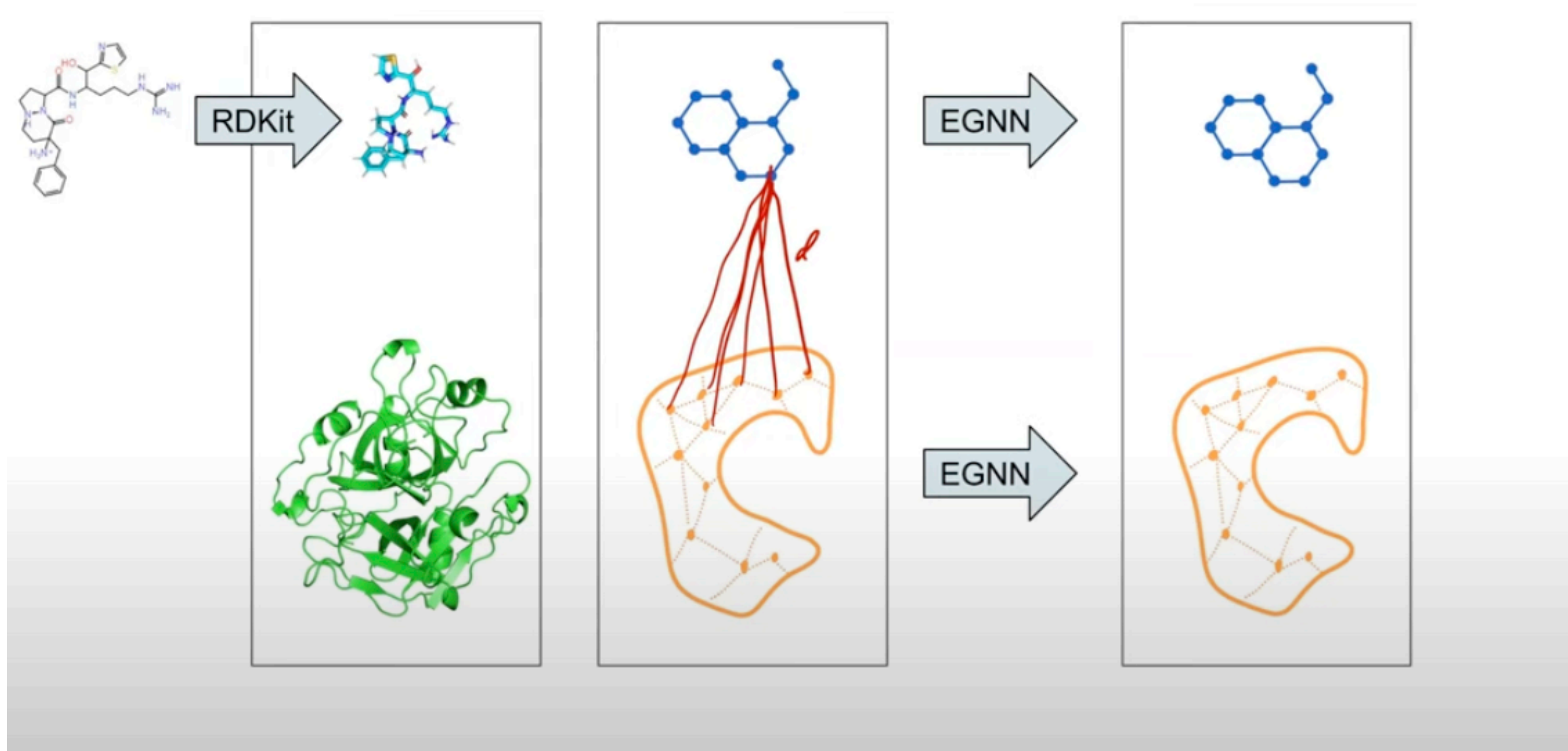


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Equibind: Flexible Drug Prediction

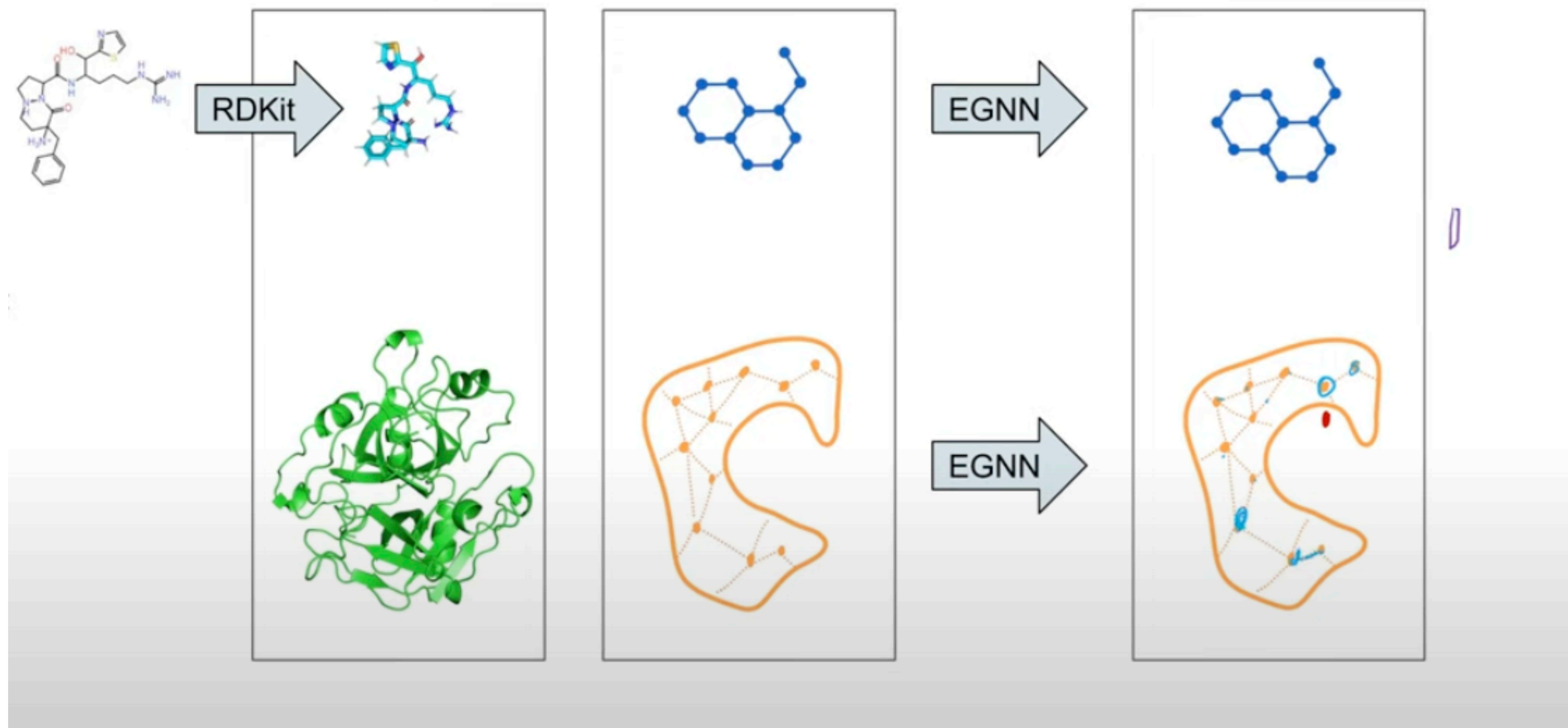


Figure : Equibind Architecture overview. Screenshot from 'Absci Invites: Seminar Series YouTube: <https://www.youtube.com/watch?v=JAvh9e6XEGM&t=2360s>.

Equibind: Flexible Drug Prediction

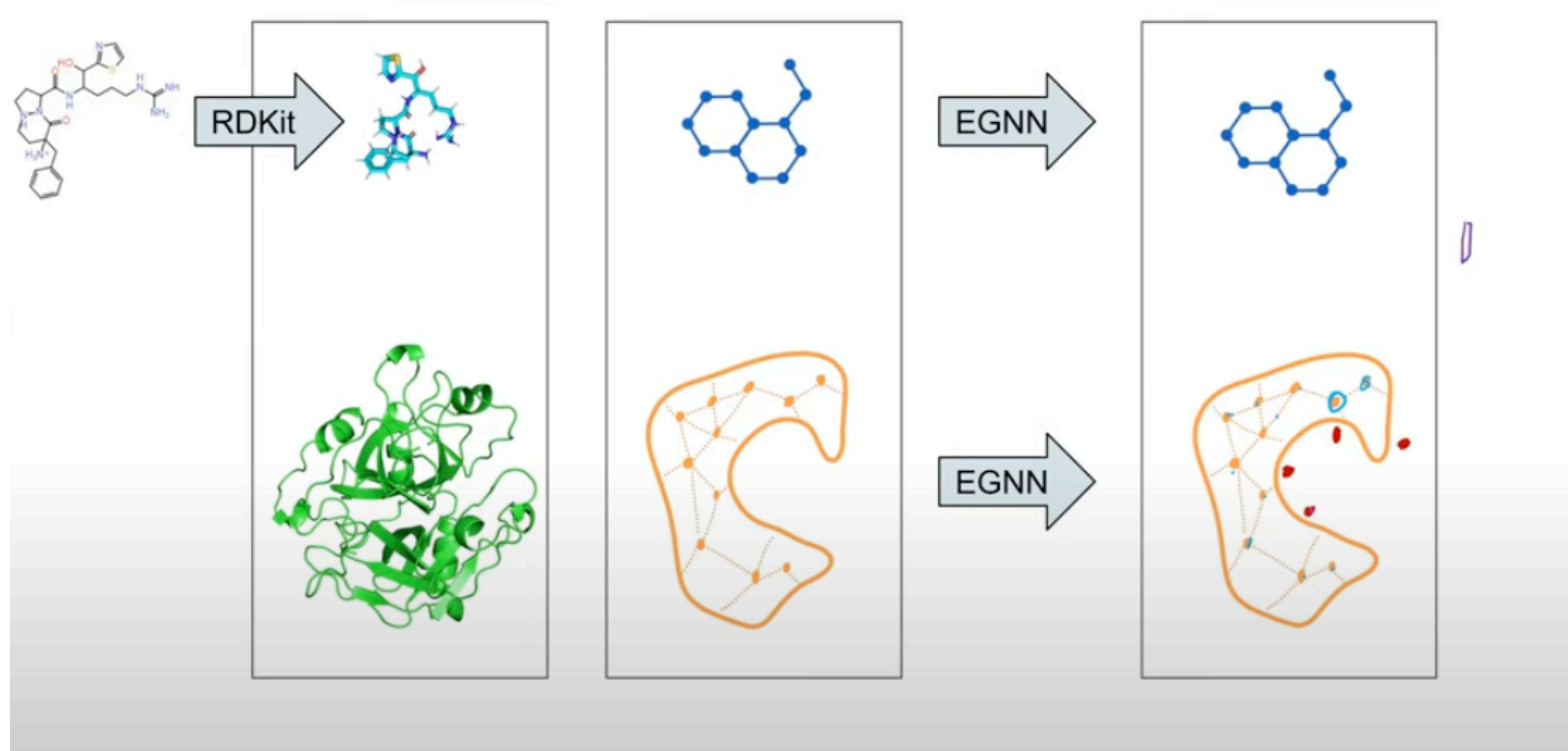


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Equibind: Flexible Drug Prediction

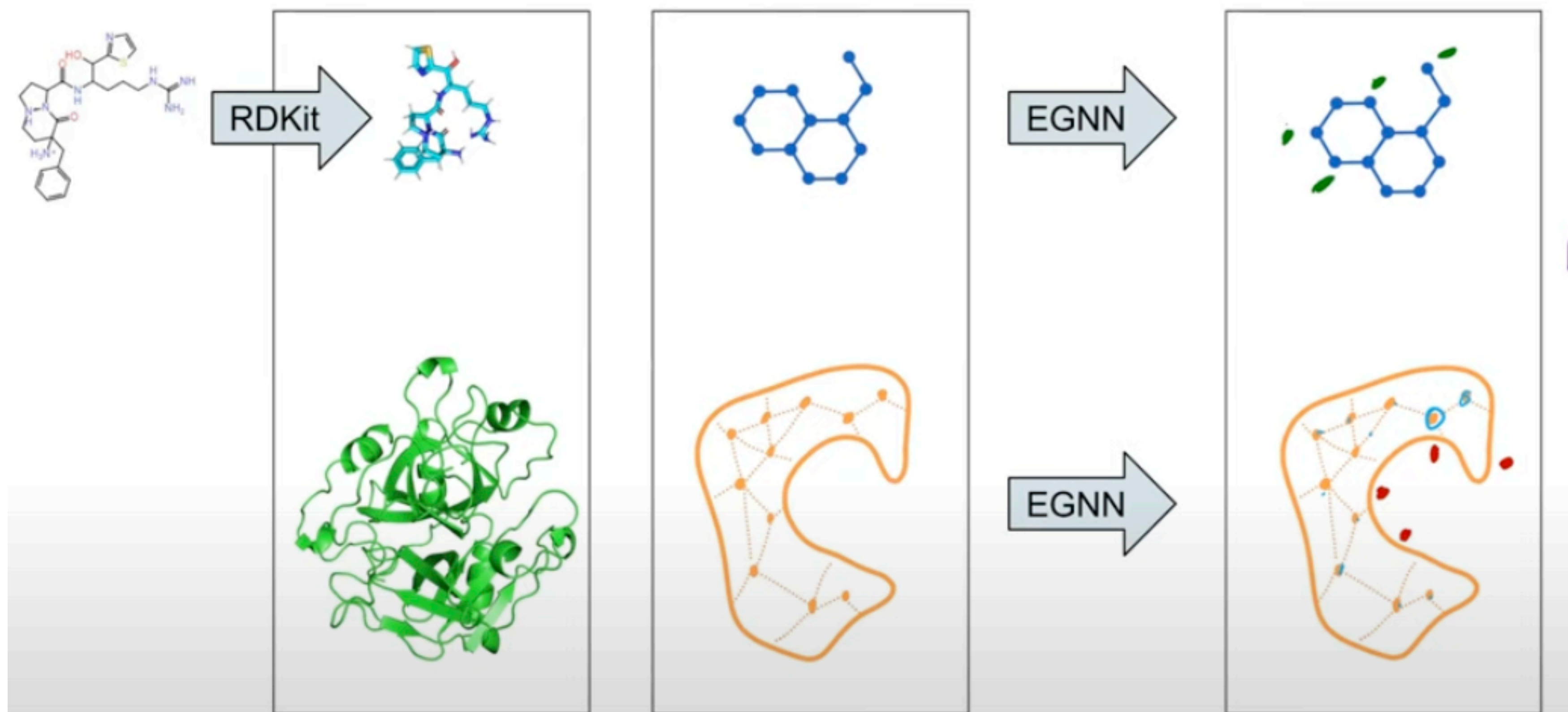


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Equibind: Flexible Drug Prediction

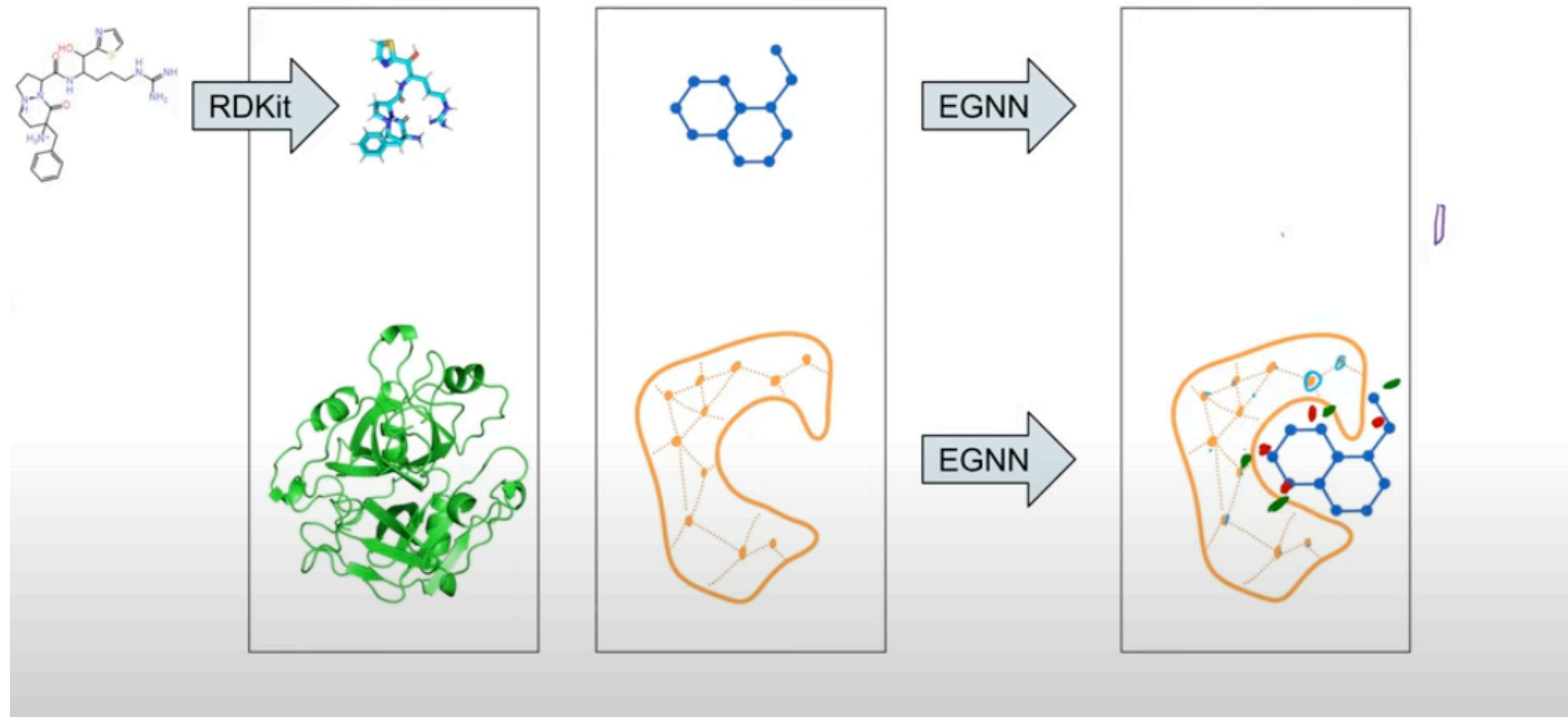
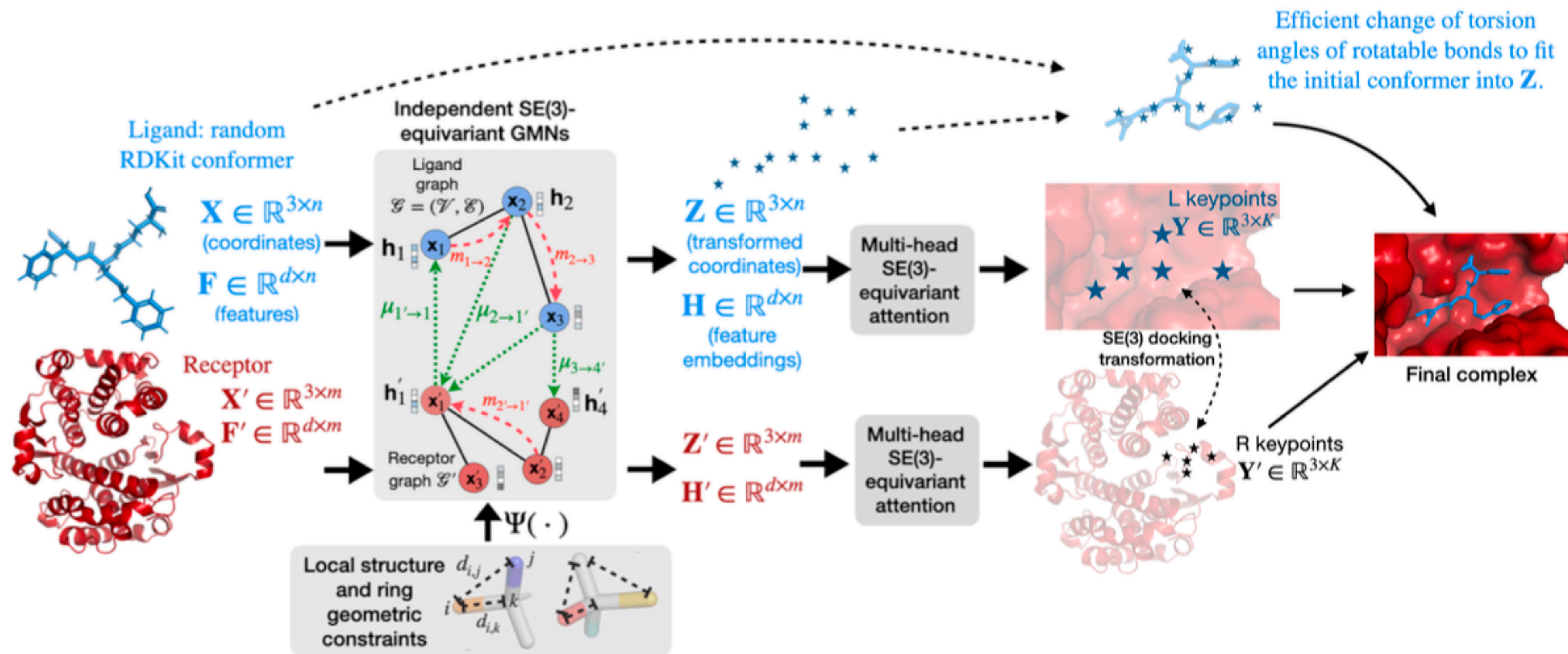


Figure : Equibind Architecture overview. Screenshot from 'Absci Invites: Seminar Series YouTube: <https://www.youtube.com/watch?v=JAvh9e6XEGM&t=2360s>.

Equibind: Flexible Drug Prediction

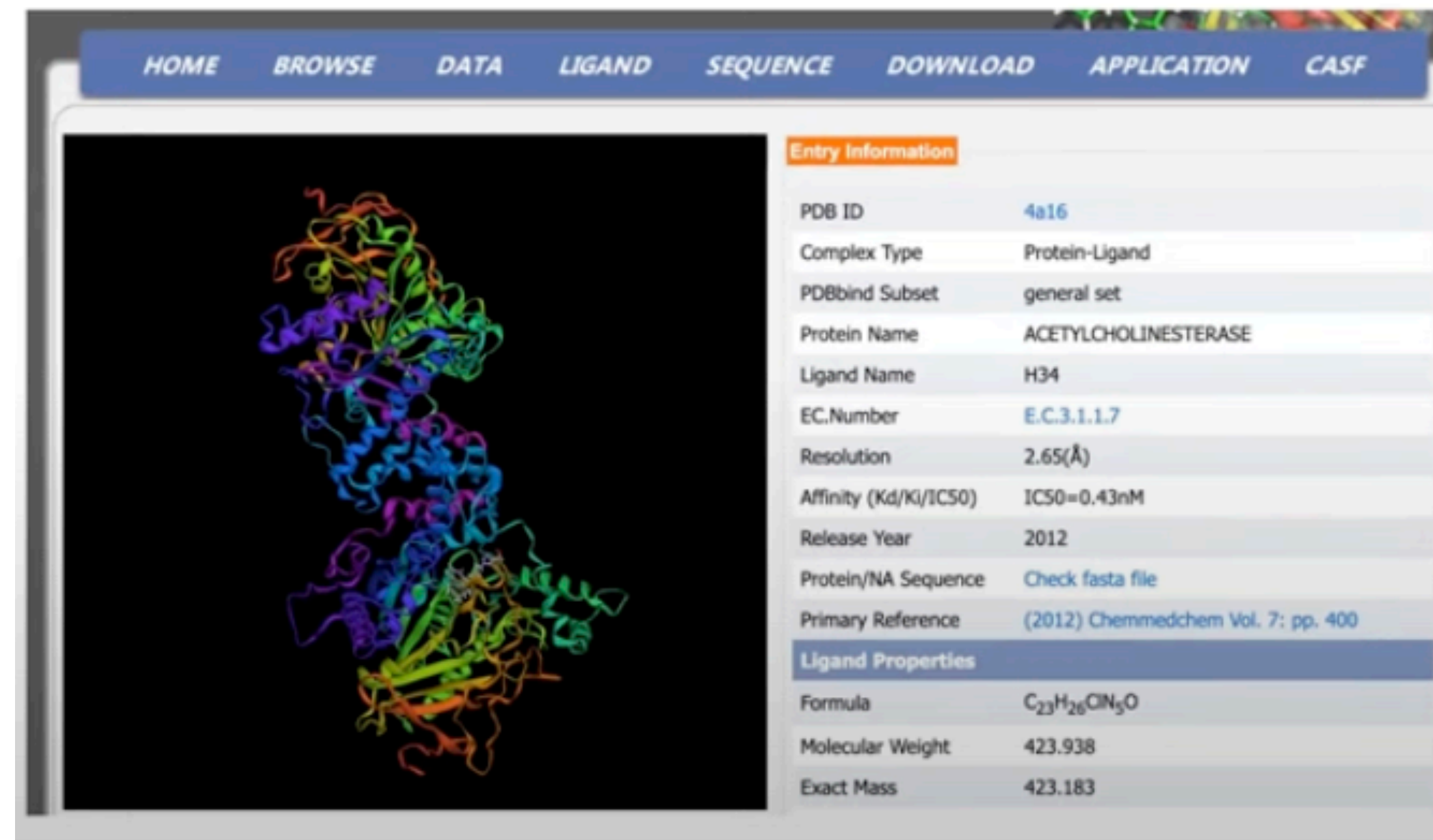


Efficient Point Cloud Intersection Loss



Datasets

- PDDBind experimental data- expensive X-ray crystallography techniques.
- Size:~ 19k complexes
- Test set:2020 released structures, Train set: <=2019 structures, no shared ligands



Baselines

SMINA

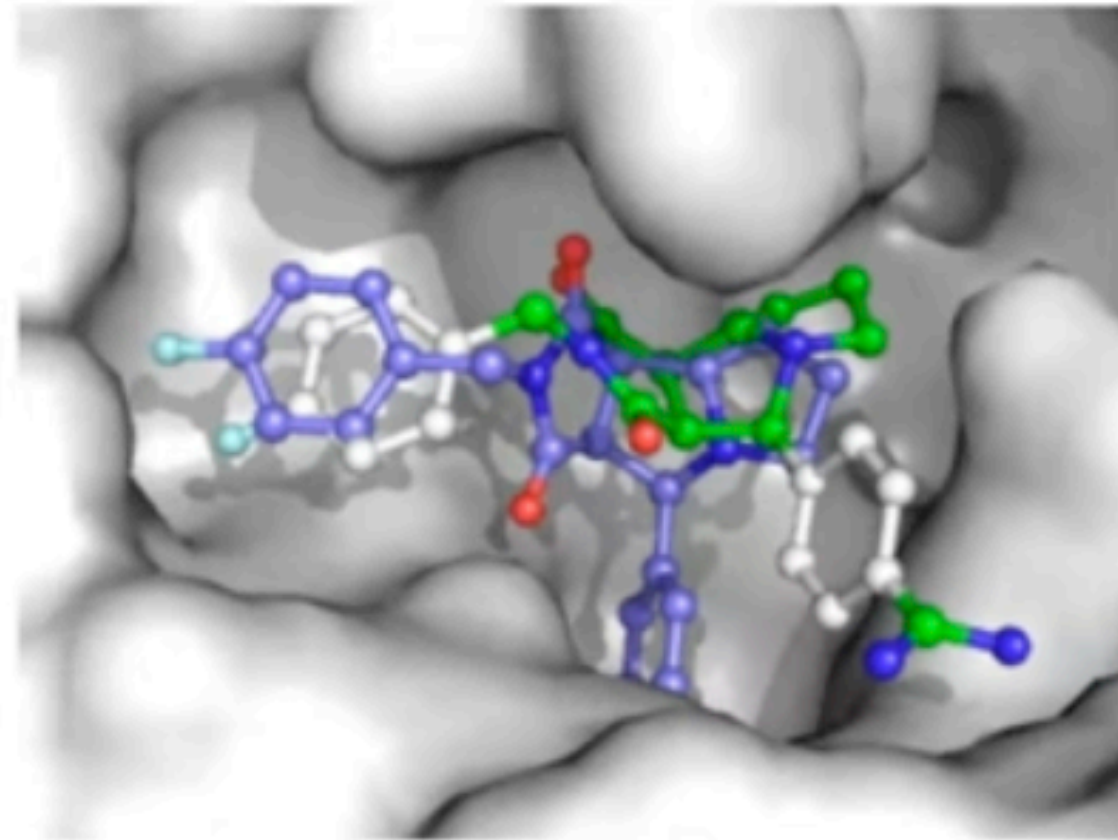
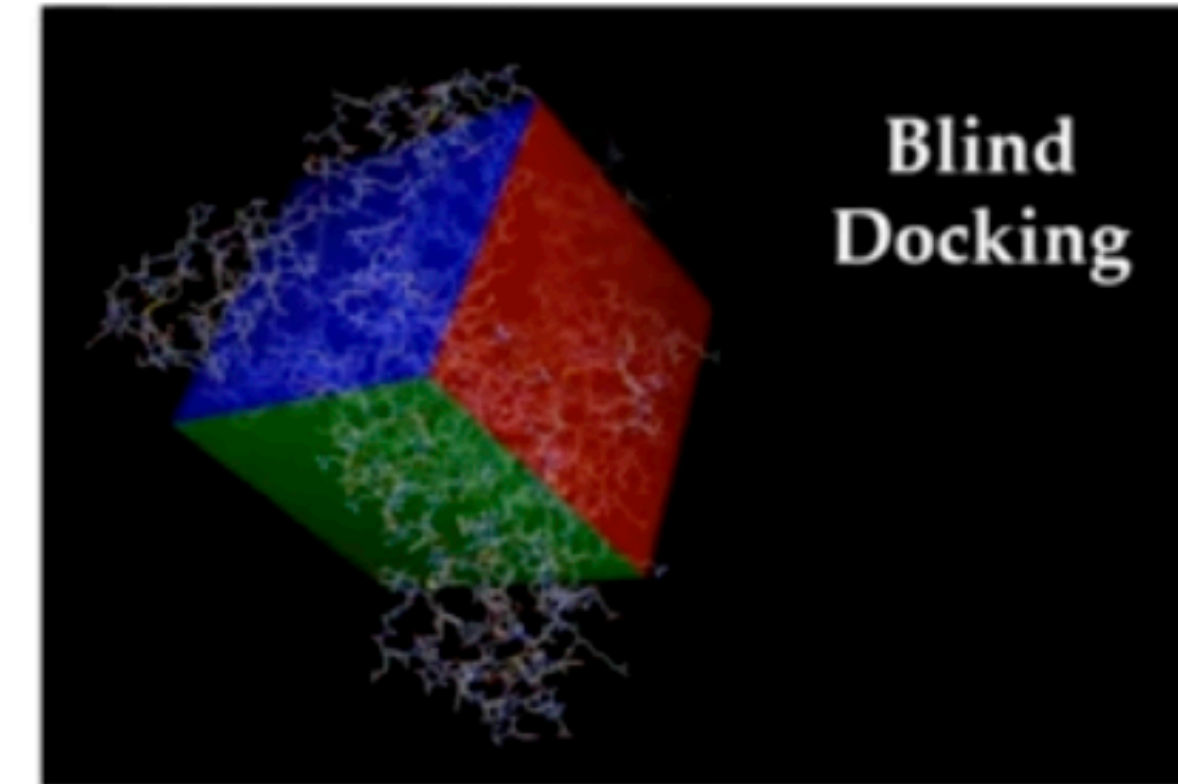


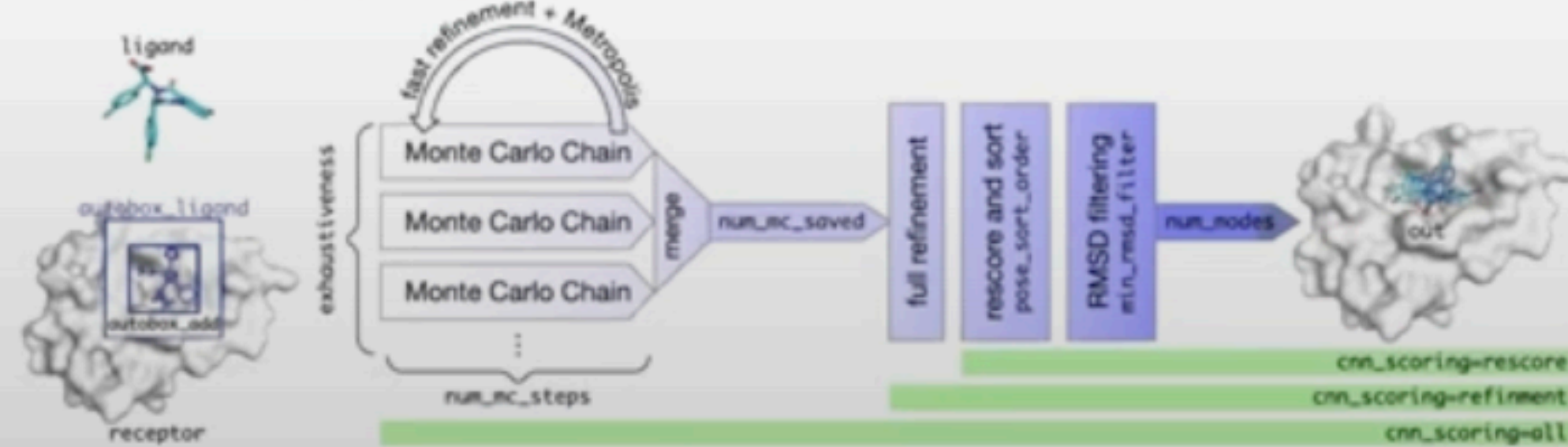
Image is © Esben Jannik Bjerrum/Cheminformania.com. Reprinted with permission.

QuickVina-W



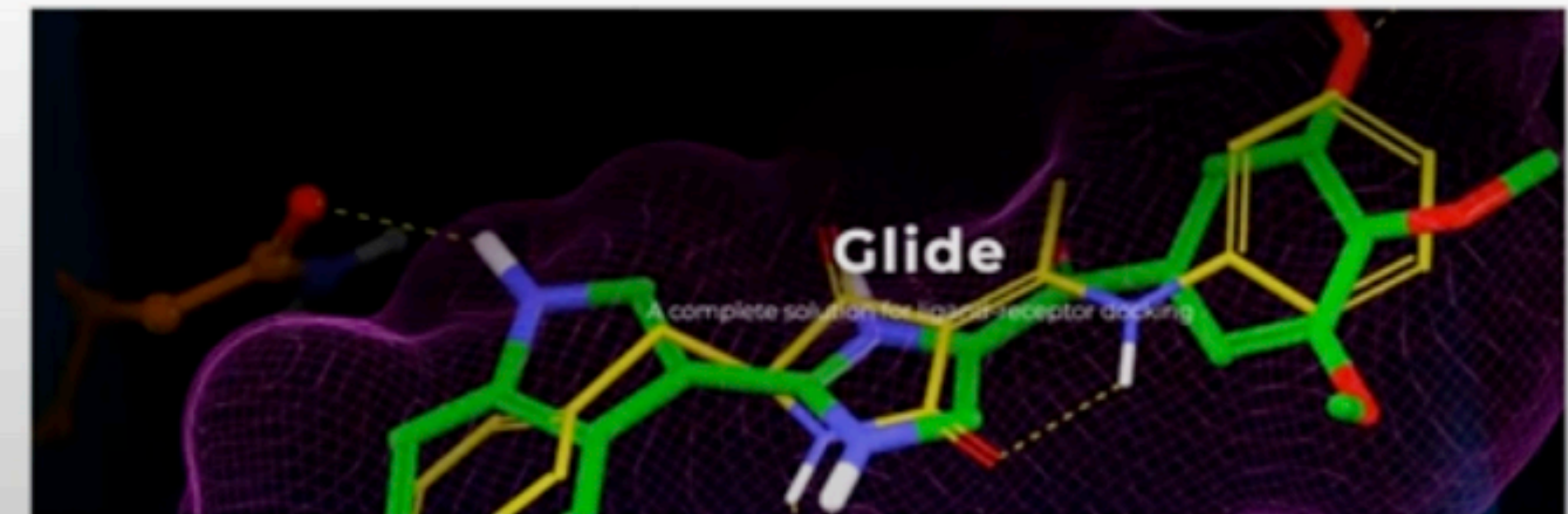
GNINA (2021) - deep learning based scoring

From: GNINA 1.0: molecular docking with deep learning



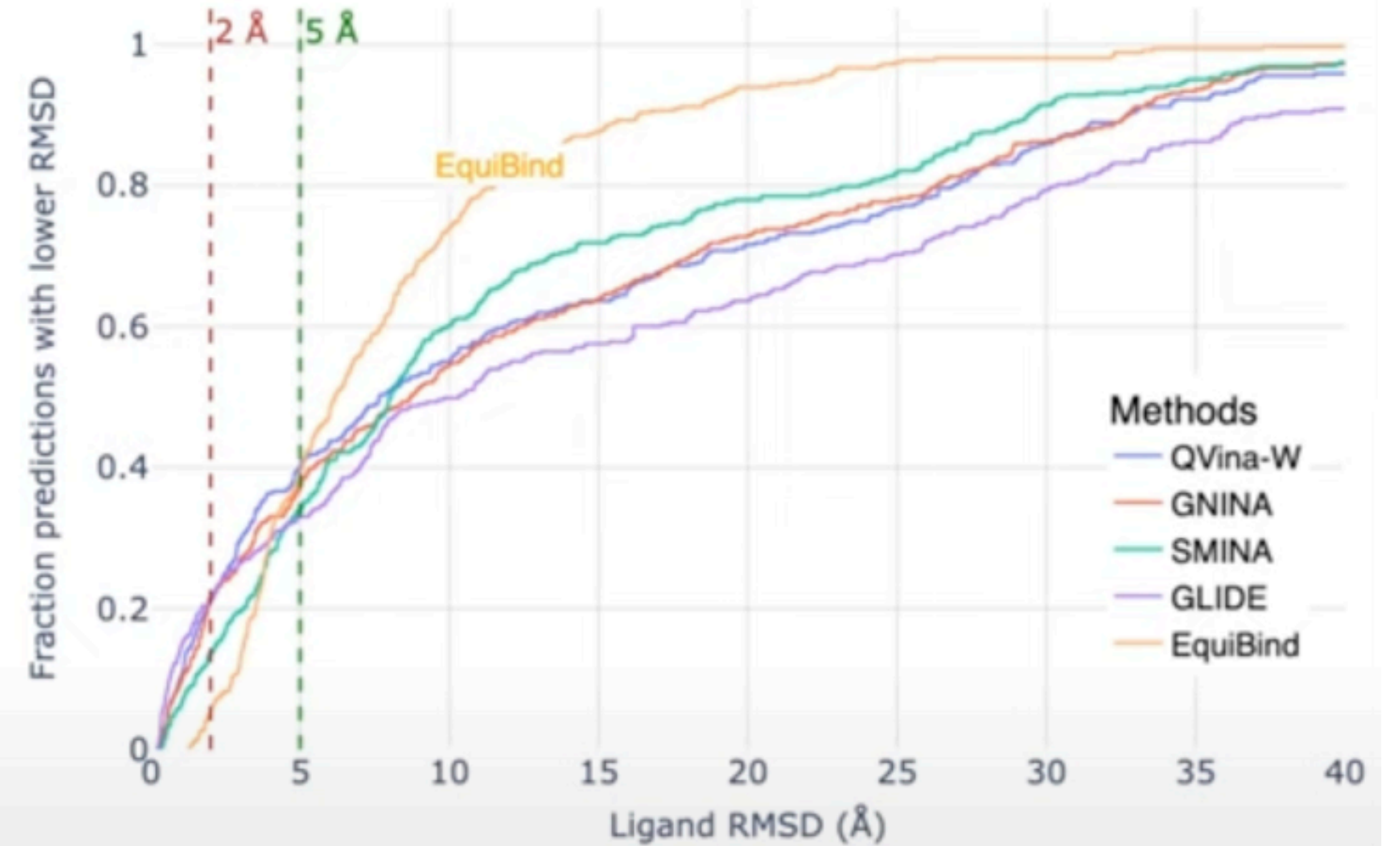
Schrödinger

Glide (commercial)



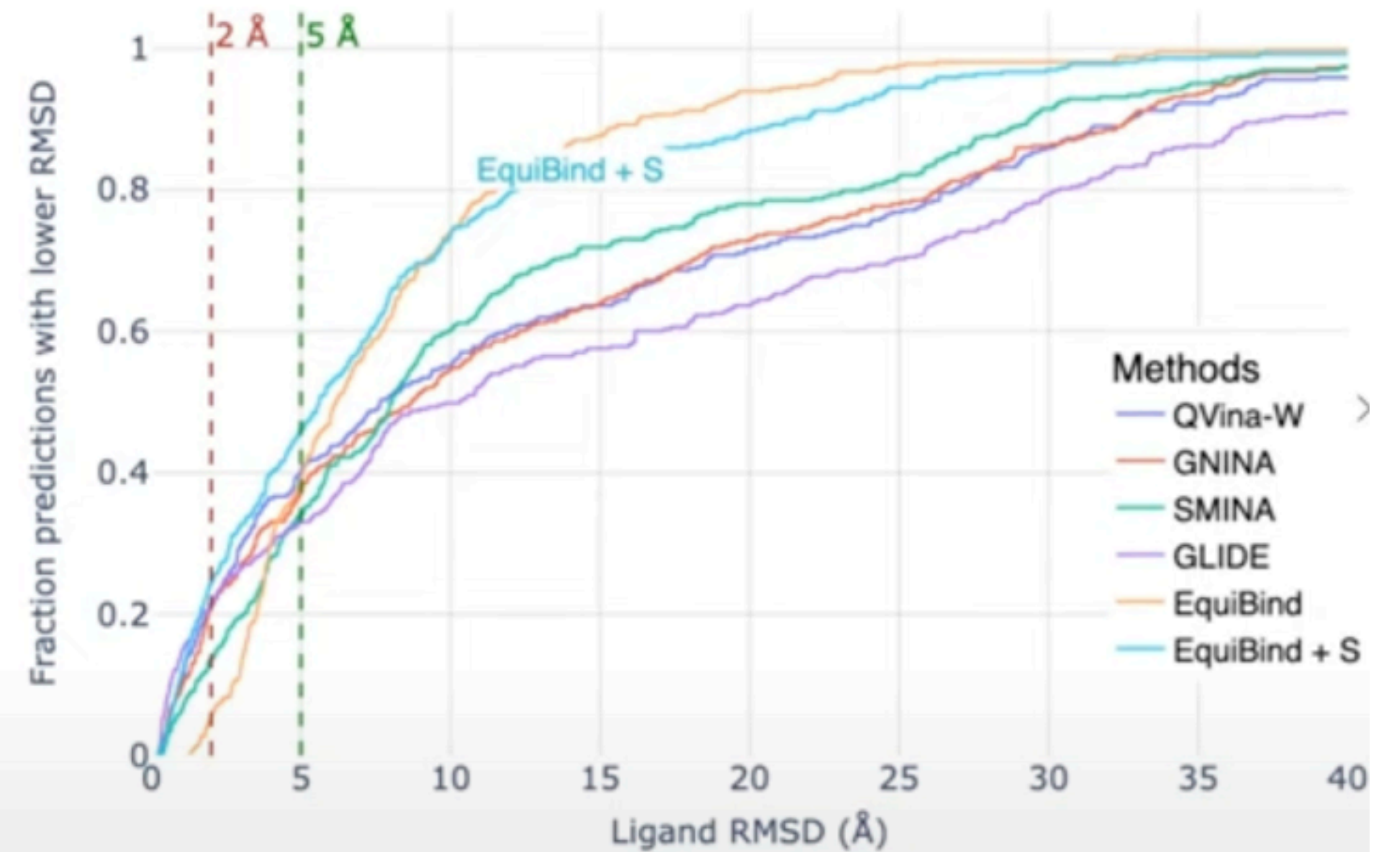
Equibind:Results

METHODS	AVG. SEC. 16-CPU	AVG. SEC. GPU	LIGAND RMSD ↓					
			PERCENTILES ↓				% BELOW THRESHOLD ↑	
			MEAN	25TH	50TH	75TH	5 Å	2 Å
QVINA-W	49	-	13.6	2.5	7.7	23.7	40.2	20.9
GNINA	247	146	13.3	2.8	8.7	22.1	37.1	21.2
SMINA	146	-	12.1	3.8	8.1	17.9	33.9	13.5
GLIDE (C.)	1405*	-	16.2	2.6	9.3	28.1	33.6	21.8
EQUIBIND	0.16	0.04	8.2	3.8	6.2	10.3	39.1	5.5



Equibind:Results

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EQUIBIND	0.16	0.04	8.2	3.8	6.2	10.3	39.1	5.5
EQUIBIND+Q	8	8	8.4	2.6	6.6	11.1	38.0	18.7
EQUIBIND+Q2	15	15	8.7	2.6	6.8	11.1	40.7	21.6
EQUIBIND+S	146	146	8.3	2.1	5.6	10.5	46.4	24.6



Limitations and Future Work

Current Limitation

- Only implicitly models side chain atom positions
- Uses local frame encoding features
- Applied to α -carbon graph of receptor

Thank You!