

## Summary of integrative structure determination of Deep learning enables the atomic structure determination of the Fanconi Anemia core complex from cryoEM (PDB ID: 9A0J, PDB-Dev ID: PDBDEV\_00000055)



<u>Resolution</u>	Atomic
<u>Number of rigid bodies, flexible units</u>	76, 4
<i>Rigid bodies</i>	<ul style="list-style-type: none"> <li>- B: 378-434, 1-370, 441-780, 231-365, 441-660, 651-770, 1-235, 466-626</li> <li>- b: 378-434, 1-370, 441-780, 231-365, 441-660, 651-770, 1-235, 466-626</li> <li>- C: 331-570, 176-335, 1-335, 1-175</li> <li>- E: 266-520, 1-150, 261-520</li> <li>- F: 140-341</li> <li>- G: 44-645, 1-320, 181-320, 201-435, 204-315, 1-175, 321-648</li> <li>- g: 44-645, 1-320, 181-320, 201-435, 204-315, 1-175, 321-648</li> <li>- L: 191-300, 301-373, 104-373, 101-300, 2-91, 101-205, 1-100</li> <li>- l: 191-300, 301-373, 104-373, 101-300, 2-91, 101-205, 1-100</li> <li>- P: 28-442, 1-300, 711-820, 1-200, 186-480, 301-480, 510-609, 491-615, 714-803, 804-888, 453-507, 491-820</li> <li>- p: 28-442, 1-300, 711-820, 1-200, 186-480, 301-480, 510-609, 491-615, 714-803, 804-888, 453-507, 491-820</li> </ul>
<i>Flexible units</i>	<ul style="list-style-type: none"> <li>- B: 435-440</li> <li>- b: 435-440</li> <li>- C: -</li> <li>- E: 151-170</li> <li>- F: 342-350</li> <li>- G: -</li> <li>- g: -</li> <li>- L: -</li> <li>- l: -</li> <li>- P: -</li> <li>- p: -</li> </ul>
<u>Structural coverage (rigid bodies)</u>	100%
<b>3. Restraints</b>	
<u>Physical principles</u>	Information about physical principles was not provided
<u>Experimental data</u>	<ul style="list-style-type: none"> <li>- 1 unique CrossLinkRestraint: BS3, 451 cross-links</li> <li>- 1 unique EM3DRestraint: None</li> </ul>
<b>4. Validation</b>	
<u>Number of ensembles</u>	0
<u>Number of models in ensembles</u>	Not applicable
<u>Number of deposited models</u>	1
<u>Model precision (uncertainty of models)</u>	Model precision can not be calculated with one structure

<u>Data quality</u>	Data quality has not been assessed
<u>Model quality: assessment of atomic segments</u>	Model-1: Clashscore = 0.0, Number of Ramachandran outliers = 36, Number of sidechain outliers = 9
<u>Model quality: assessment of excluded volume</u>	Not applicable
<u>Fit to data used for modeling</u>	Fit of model to information used to compute it has not been determined
<u>Fit to data used for validation</u>	Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
1. <u>Method</u>	Production sampling
<u>Name</u>	Monte Carlo
2. <u>Method</u>	Rosetta Hybridize
<u>Name</u>	Rosetta Hybridize
<u>Software</u>	<ul style="list-style-type: none"> <li>- <a href="#">Rosetta</a> (version Rosetta version unknown:ff8ee24ee5f65423d5064cba818ede41d012fa8; 2020-08-10 10:39:53 -0700 from git@github.com:RosettaCommons/main.git)</li> <li>- <a href="#">trRosetta</a> (version 1.0.0)</li> <li>- <a href="#">HHpred</a> (version website)</li> </ul>