

**Summary of integrative structure determination of Integrative structure determination of the A3G-CRL5-Vif complex (flexible) (PDB ID: 9A1J, PDB-Dev ID: PDBDEV\_0000091)**

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- CFBF: chain(s) A (182 residues)</li> <li>- Vif: chain(s) B (175 residues)</li> <li>- EloB: chain(s) C (161 residues)</li> <li>- EloC: chain(s) D (112 residues)</li> <li>- CUL5: chain(s) E (780 residues)</li> <li>- Rbx2: chain(s) F (113 residues)</li> <li>- A3G: chain(s) G (384 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- Experimental model, PDB: <a href="#">4N9F</a></li> <li>- Experimental model, PDB: <a href="#">1LDJ</a></li> <li>- Experimental model, PDB: <a href="#">2ECL</a></li> <li>- Experimental model, PDB: <a href="#">2MA9</a></li> <li>- Comparative model, Zenodo: <a href="#">10.5281/zenodo.5176959</a></li> <li>- Experimental model, PDB: <a href="#">5K81</a></li> <li>- Comparative model, Zenodo: <a href="#">10.5281/zenodo.5176959</a></li> <li>- Experimental model, PDB: <a href="#">3V4K</a></li> <li>- Comparative model, Zenodo: <a href="#">10.5281/zenodo.5176959</a></li> <li>- Mass Spectrometry data, PRIDE: <a href="#">PXD025391</a></li> <li>- Crosslinking-MS data, Zenodo: <a href="#">10.5281/zenodo.5176959</a></li> <li>- Crosslinking-MS data, Zenodo: <a href="#">10.5281/zenodo.5176959</a></li> </ul>
<b>2. Representation</b>	
<a href="#">Number of representations</a>	1
<a href="#">Scale</a>	Multiscale: Coarse-grained: 1 - 5 residue(s) per bead
<a href="#">Number of <i>rigid</i> and <i>flexible</i> segments</a>	15, 16
<b>3. Restraints</b>	
<a href="#">Physical principles</a>	Information about physical principles was not provided
<a href="#">Experimental data</a>	<ul style="list-style-type: none"> <li>- 1 unique CrossLinkRestraint: DSSO, 100 crosslinks</li> <li>- 1 unique CrossLinkRestraint: DSSO, 32 crosslinks</li> </ul>
<b>4. Validation</b>	
<a href="#">Number of ensembles</a>	1
<a href="#">Number of models in ensembles</a>	198632
<a href="#">Number of deposited models</a>	1

<a href="#"><i>Model precision (uncertainty of models)</i></a>	19.85, Å
<a href="#"><i>Data quality</i></a>	Data quality has not been assessed
<a href="#"><i>Model quality: assessment of excluded volume</i></a>	Satisfaction: 99.72%
<a href="#"><i>Fit to data used for modeling</i></a>	Satisfaction of crosslinks: 81.91%
<a href="#"><i>Fit to data used for validation</i></a>	Fit of model to information not used to compute it has not been determined
<b>5. Methodology and Software</b>	
<a href="#"><i>1. Name</i></a>	Sampling
<a href="#"><i>Method</i></a>	Replica exchange monte carlo
<a href="#"><i>Number of computed models</i></a>	203100
<a href="#"><i>Software</i></a>	<ul style="list-style-type: none"> <li>- <a href="#">IMP PMI module</a> (version develop-548de65454)</li> <li>- <a href="#">Integrative Modeling Platform (IMP)</a> (version develop-548de65454)</li> <li>- <a href="#">MODELLER</a> (version 9.20)</li> <li>- <a href="#">MODELLER</a> (version 9.19)</li> </ul>