

**Summary of integrative structure determination of structure of complement c3(h2o) revealed by quantitative cross-linking/mass spectrometry and modeling (PDBDEV00000021)**

<b>1. Model Composition</b>	
<a href="#">Entry composition</a>	<ul style="list-style-type: none"> <li>- alpha: Chain B (992 residues)</li> <li>- beta: Chain A (645 residues)</li> </ul>
<a href="#">Datasets used for modeling</a>	<ul style="list-style-type: none"> <li>- Experimental model, PDB ID: 2A73</li> <li>- Experimental model, PDB ID: 2I07</li> <li>- Mass Spectrometry data, PXD003486</li> <li>- CX-MS data, Linker name and number of cross-links: BS3, 115 cross-links</li> </ul>
<b>2. Representation</b>	
<a href="#">Atomic structural coverage</a>	98%
<a href="#">Number of rigid bodies, flexible units</a>	13, 12
<i>Rigid bodies</i>	<ul style="list-style-type: none"> <li>- A: 1-73:Experimental model/2A73, 80-289:Experimental model/2A73, 292-643:Experimental model/2A73.</li> <li>- B: 2-70:Experimental model/2A73, 80-96:Experimental model/2A73, 97-155:Experimental model/2A73, 158-261:Experimental model/2A73, 264-312:Experimental model/2A73, 315-457:Experimental model/2A73, 464-618:Experimental model/2A73, 621-680:Experimental model/2A73, 683-824:Experimental model/2A73, 827-992:Experimental model/2A73.</li> </ul>
<i>Flexible units</i>	<ul style="list-style-type: none"> <li>- A: 74-79, 290-291, 644-645.</li> <li>- B: 1-1, 71-79, 156-157, 262-263, 313-314, 458-463, 619-620, 681-682, 825-826.</li> </ul>
<a href="#">Resolution</a>	<ul style="list-style-type: none"> <li>- Rigid bodies: 1 residue per bead.</li> <li>- Flexible regions: N/A</li> </ul>
<b>3. Restraints</b>	
<a href="#">Physical principles</a>	Information about physical principles was not provided
<a href="#">Experimental data</a>	- 1 unique CrossLinkRestraint: BS3, 115 cross-links
<b>4. Validation</b>	
<a href="#">Sampling validation</a>	- Information related to sampling validation has not been provided
<a href="#">Clustering algorithm ,clustering feature</a>	Distance threshold-based clustering used if ensembles are deposited, RMSD
<a href="#">Number of ensembles</a>	4
<a href="#">Number of models in ensembles</a>	200, 200, 89, 111
<a href="#">Model precision (uncertainty of models)</a>	18.709Å, 10.436Å, 16.24Å, 14.615Å

<a href="#"><i>Quality of data</i></a>	- Quality of input data has not be assessed
<a href="#"><i>Model quality: assessment of atomic segments</i></a>	Not applicable
<a href="#"><i>Model quality: assessment of excluded volume</i></a>	<ul style="list-style-type: none"> <li>- Model-1: Number of violations-3677.0</li> <li>- Model-2: Number of violations-3514.0</li> <li>- Model-3: Number of violations-3754.0</li> <li>- Model-4: Number of violations-3684.0</li> </ul>
<a href="#"><i>Fit of the model to information used to compute it</i></a>	<ul style="list-style-type: none"> <li>- CX-MS Fit of mediod: model # 1, percentage satisfied 80.87%</li> <li>- CX-MS Fit of mediod: model # 2, percentage satisfied 89.66%</li> <li>- CX-MS Fit of mediod: model # 3, percentage satisfied 83.48%</li> <li>- CX-MS Fit of mediod: model # 4, percentage satisfied 84.35%</li> </ul>
<a href="#"><i>Fit of the model to information not used to compute it</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>Method</i></a>	Sampling
<a href="#"><i>Name</i></a>	Replica exchange Monte Carlo
<a href="#"><i>Details</i></a>	- Method details unspecified
<a href="#"><i>Software</i></a>	<ul style="list-style-type: none"> <li>- Integrative Modeling Platform (IMP) (version develop-0a5706e202)</li> <li>- IMP PMI module (version 67456c0)</li> <li>- No location specified</li> </ul>