# Summary of integrative structure determination of Integrative structure of cGMP-GAFab complex (PDB ID: 9A0M, PDB-Dev ID: PDBDEV_00000058)

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| ***1. Model Composition*** | |
| *Entry composition* | - GAFab: chain(s) A, B (399 residues)<br>- GUANOSINE-3',5'-MONOPHOSPHATE: chain(s) C [A], D [B] |
| *Datasets used for modeling* | - Crosslinking-MS data, PRIDE: PXD020817<br>- Experimental model, PDB: 6X88<br>- Experimental model, PDB: 6MZB |
| ***2. Representation*** | |
| *Number of representations* | 1 |
| *Scale* | Atomic |
| *Number of rigid and flexible segments* | 0, 2 |
| ***3. Restraints*** | |
| *Physical principles* | Information about physical principles was not provided |
| *Experimental data* | - 1 unique CrossLinkRestraint: sulfo-SDA, 40 crosslinks<br>- 1 unique CrossLinkRestraint: BS3, 24 crosslinks<br>- 1 unique CrossLinkRestraint: EDC, 5 crosslinks |
| ***4. Validation*** | |
| *Number of ensembles* | 0 |
| *Number of models in ensembles* | Not applicable |
| *Number of deposited models* | 1 |
| *Model precision (uncertainty of models)* | Not available |
| *Data quality* | Data quality has not been assessed |
| *Model quality: assessment of atomic segments* | - Clashscore: 104.67<br>- Ramachandran outliers: 36<br>- Sidechain outliers: 32 |
| *Fit to data used for modeling* | Satisfaction of crosslinks: 100.00% |
| *Fit to data used for validation* | Fit of model to information not used to compute it has not been determined |
| ***5. Methodology and Software*** | |

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| *1. Name* | None |
| *Software* | - Integrative Modeling Platform (IMP) (version Not available)<br>- Modeller (version Not available) |