

Summary of integrative structure determination of Bovine adenylyl cyclase 8 in complex with the G protein heterodimer G beta gamma (PDB ID: 9A3T, PDB-Dev ID: PDBDEV_0000214)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - Adenylate cyclase type 8: Chain A (890 residues) - Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2: Chain C (46 residues) - Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1: Chain B (339 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Crosslinking-MS data, Linker name and number of cross-links: PDH, 2 cross-links - Experimental model, PDB ID: 1XHM - Experimental model, PDB ID: 8BUZ
2. Representation	
Resolution	Atomic
Number of rigid bodies, flexible units	0, 3
Flexible units	<ul style="list-style-type: none"> - A: 1-890 - B: 1-339 - C: 1-46
Structural coverage (rigid bodies)	100%
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	<ul style="list-style-type: none"> - 1 unique CrossLinkRestraint: PDH, 2 cross-links - 1 unique CrossLinkRestraint: DMTMM, 1 cross-links
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	1
Model precision (uncertainty of models)	Model precision can not be calculated with one structure
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	Model-1: Clashscore = 11.51, Number of Ramachandran outliers = 11, Number of sidechain outliers = 125

<i>Model quality: assessment of excluded volume</i>	Not applicable
<i>Fit to data used for modeling</i>	Fit of model to information used to compute it has not been determined
<i>Fit to data used for validation</i>	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
1. <i>Method</i>	Identification of crosslinked residues
<i>Name</i>	Crosslinked residues were identified from the acquired mass spectrometry data based on the presence of heavy/light pairs of linked peptides.
2. <i>Method</i>	Docking
<i>Name</i>	Accessible interaction space was assessed with DisVis, solvent accessible residues were determined with GetArea. The information from these steps was used for docking with HADDOCK.
<i>Number of computed models</i>	1
<i>Software</i>	<ul style="list-style-type: none"> - xQuest (version 2.1.5) - HADDOCK (version 2.4) - DisVis (version Not available) - GetArea (version Not available)