

Summary of integrative structure determination of Structure of the human myeloid-derived growth factor (hMYDGF) engaging the chicken KDEL receptor 2 (cKDELR2) (PDB ID: 9A00, PDB-Dev ID: PDBDEV_00000036)

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - ER lumen protein-retaining receptor 2: chain(s) A (207 residues) - Myeloid-derived growth factor: chain(s) B (142 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB: 6O6W - Experimental model, PDB: 6I6H
2. Representation	
Number of representations	1
Scale	Atomic
Number of rigid and flexible segments	2, 0
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 36 unique DerivedDistanceRestraint: Upper Bound Distance: 3.0
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	2
Model precision (uncertainty of models)	Not available
Data quality	Data quality has not been assessed
Model quality: assessment of atomic segments	<ul style="list-style-type: none"> - Clashscore: 4.09-4.80 - Ramachandran outliers: 1-1 - Sidechain outliers: 19-23
Fit to data used for modeling	Fit of model to information used to compute it has not been determined
Fit to data used for validation	Fit of model to information not used to compute it has not been determined
5. Methodology and Software	

1. <i>Name</i>	?
<i>Method</i>	?
<i>Number of computed models</i>	?
<i>Software</i>	HADDOCK (version Not available)