Summary of integrative structure determination of structure of the human myeloid-derived growth factor (hmydgf) engaging the chicken kdel receptor 2 (ckdelr2) (PDBDEV00000036)

1. Model Composition	
Entry composition	- ER lumen protein-retaining receptor 2: Chain A (207 residues) - Myeloid-derived growth factor: Chain B (142 residues)
Datasets used for modeling	- Experimental model, PDB ID: 6O6W - Experimental model, PDB ID: 6I6H
2. Representation	
Atomic structural coverage	100%
Number of rigid bodies, flexible units	2, 0
Rigid bodies	- B: 1-142:Experimental model/6O6W. - A: 1-207:Experimental model/6I6H.
Flexible units	- B: - - A: -
Resolution	- Rigid bodies: 1 residue per bead. - Flexible regions: N/A
3. Restraints	
Physical principles	Information about physical principles was not provided
Experimental data	- 36 unique DerivedDistanceRestraint: Upper Bound Distance: 3.0
4. Validation	
Sampling validation	- Information related to sampling validation has not been provided
Clustering algorithm ,clustering feature	Distance threshold-based clustering used if ensembles are deposited, Not applicable
Number of ensembles	0
Number of models in ensembles	Not applicable
Model precision (uncertainty of models)	Model precision can not be calculated with one structure
Quality of data	- Quality of input data has not be assessed
Model quality: assessment of atomic segments	Clashscore: 5.16, Ramachandran outliers: 0.29% , Sidechain outliers: 6.95%
Model quality: assessment of excluded volume	- Not applicable

Fit of the model to information used to compute it	- Fit of model to information used to compute it has not been determined
Fit of the model to information not used to compute it	- Fit of model to information not used to compute it has not been determined
5. Methodology and Software	
Method	?
Name	?
Details	- Method details unspecified
Software	- HADDOCK (version None) - No location specified