

**Summary of integrative structure determination of INTEGRATIVE STRUCTURE OF
BTG2 IN COMPLEX WITH RRM1-2 OF PABPC1 (PDB ID: 9A1R, PDB-Dev ID:
PDBDEV_00000099)**

1. Model Composition	
Entry composition	<ul style="list-style-type: none"> - POLY(A) BINDING PROTEIN CYTOPLASMIC 1: chain(s) A (175 residues) - PROTEIN BTG2: chain(s) B (121 residues)
Datasets used for modeling	<ul style="list-style-type: none"> - Experimental model, PDB: 4F02 - Experimental model, PDB: 3DJU - NMR data, BMRB: 50526
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	- 1066 unique DerivedDistanceRestraint: Upper Bound Distance: 2.0
4. Validation	
Number of ensembles	0
Number of models in ensembles	Not applicable
Number of deposited models	4
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: 10.66-13.43 - Ramachandran outliers: 1-1 - Sidechain outliers: 19-21
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>	Rigid-body minimization
<i>Method</i>	Rigid-body minimization in HADDOCK (it0)
<i>Number of computed models</i>	1000
2. <i>Name</i>	Simulated annealing
<i>Method</i>	Semi-flexible SA in HADDOCK (it1)
<i>Number of computed models</i>	200
3. <i>Name</i>	Refinement
<i>Method</i>	Water refinement in HADDOCK (itw)
<i>Number of computed models</i>	200
<i>Software</i>	HADDOCK (version 2.4)