



# Full wwPDB Integrative Structure Validation Report

July 06, 2020 -- 10:16 PM

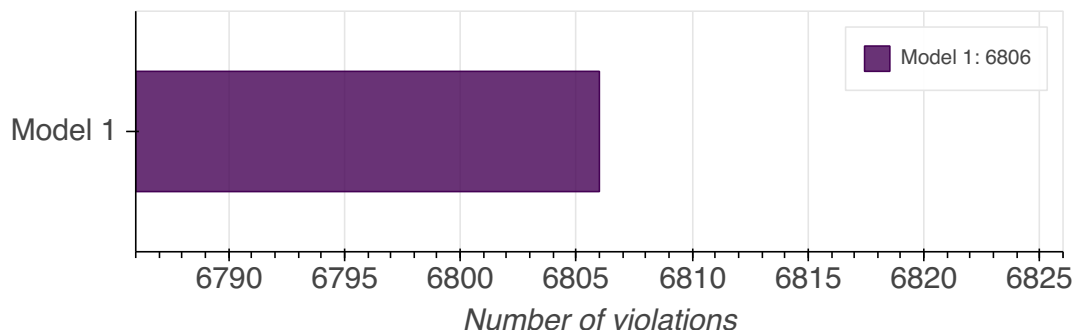
The following software were used in the production of this report:

*Integrative Modeling Validation Package : Version 1.0*

<b>PDB ID</b>	<b>PDBDEV_00000038</b>
Molecule Name	Integrative structure of the non-canonical human COP9 Signalosome
Title	Structural dynamics of the human COP9 signalosome revealed by cross-linking mass spectrometry and integrative modeling.
Authors	Gutierrez C;Chemmmama IE;Mao H;Yu C;Echeverria I;Block SA;Rychnovsky SD;Zheng N;Sali A;Huang L

## Overall quality

### Model quality: Excluded Volume Analysis



### Ensemble information

*This entry consists of 1 distinct ensemble.*

### Entry composition

*There is 1 unique type of model in this entry. This model is titled Cluster 0BMSO+DHSO+DSSO in state State\_0/None respectively.*

Model ID	Subunit number	Subunit ID	Subunit name	Chain ID	Total residues
1	1	1	CSN1	A	491
1	2	2	CSN2	B	443
1	3	3	CSN3	C	423
1	4	4	CSN4	D	406
1	5	5	CSN5	E	334
1	6	6	CSN6	F	327
1	7	7	CSN7	G	264
1	8	8	CSN8	H	209
1	9	9	CSN9	I	57

### Methodology and software

Step number	Protocol ID	Method name	Method type	Number of computed models	Multi state modeling	Multi scale modeling
1	1	Replica exchange monte carlo	Sampling	7500000	False	True

## Data quality

### Model quality

#### Excluded volume satisfaction

*Excluded volume satisfaction for the models in the entry are listed below.*

Models	Excluded Volume Satisfaction	Number of violations
1	99.79	6806.0

### Fit of model to data used for modeling

### Fit of model to data not used for modeling

### Uncertainty of data and model