

# Integrative Structure Validation Report ?

February 18, 2025 - 08:33 AM PST

*The following software was used in the production of this report:*

*Integrative Modeling Validation* Version 2.0

*Python-IHM* Version 1.8

*MolProbity* Version 4.5.2

PDB ID	9A23
PDB-Dev ID	PDBDEV_00000140
Structure Title	Photoinduced intermediate J of bacteriorhodopsin from 1 to 30 picosecond with a contracted retinal binding pocket
Structure Authors	Ren, Z.
Deposited on	2022-07-15

*This is a PDB-IHM IM Structure Validation Report for a publicly released PDB-IHM entry.*

*We welcome your comments at [helpdesk@pdb-ihm.org](mailto:helpdesk@pdb-ihm.org)*

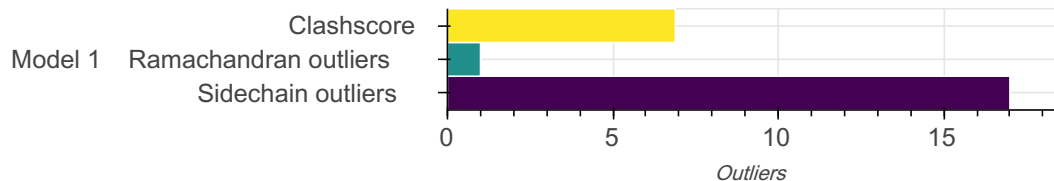
*A user guide is available at [https://pdb-ihm.org/validation\\_help.html](https://pdb-ihm.org/validation_help.html) with specific help available everywhere you see the ? symbol.*

*List of references used to build this report is available [here](#).*

## Overall quality ?

*This validation report contains model quality assessments for all structures, data quality and fit to model assessments for SAS and crosslinking-MS datasets. Data quality and fit to model assessments for other datasets and model uncertainty are under development. Number of plots is limited to 256.*

Model Quality: MolProbity Analysis



### Ensemble information ?

*This entry consists of 0 distinct ensemble(s).*

### Summary ?

*This entry consists of 1 model(s). A total of 21 datasets were used to build this entry.*

### Representation ?

*This entry has 1 representation(s).*

ID	Model(s)	Entity ID	Molecule name	Chain(s) [auth]	Total residues	Rigid segments	Flexible segments	Model coverage/ Starting model coverage (%)	Scale
1	1	1	BACTERIORHODOPSIN	A	248	-	1-248	100.00 / 100.00	Atomic
		2	RETINAL	B [A]	Non-polymeric	-	-	Not available / Not available	Atomic
		3	water	C [A]	Non-polymeric	-	-	Not available / Not available	Atomic

### Datasets used for modeling ?

*There are 21 unique datasets used to build the models in this entry.*

ID	Dataset type	Database name	Data access code
1	Experimental model	PDB	<a href="#">6g7h</a>
2	X-ray diffraction data	PDB	<a href="#">6g7h</a>

ID	Dataset type	Database name	Data access code
3	X-ray diffraction data	PDB	<a href="#">6g7i</a>
4	X-ray diffraction data	PDB	<a href="#">6g7j</a>
5	X-ray diffraction data	PDB	<a href="#">6g7k</a>
6	X-ray diffraction data	PDB	<a href="#">6ga2</a>
7	X-ray diffraction data	PDB	<a href="#">6ga4</a>
8	X-ray diffraction data	PDB	<a href="#">6ga5</a>
9	X-ray diffraction data	PDB	<a href="#">6ga6</a>
10	X-ray diffraction data	PDB	<a href="#">6ga7</a>
11	X-ray diffraction data	PDB	<a href="#">6ga8</a>
12	X-ray diffraction data	PDB	<a href="#">6ga9</a>
13	X-ray diffraction data	PDB	<a href="#">6gaa</a>
14	X-ray diffraction data	PDB	<a href="#">6gab</a>
15	X-ray diffraction data	PDB	<a href="#">6gac</a>
16	X-ray diffraction data	PDB	<a href="#">6gad</a>
17	X-ray diffraction data	PDB	<a href="#">6gae</a>
18	X-ray diffraction data	PDB	<a href="#">6gaf</a>
19	X-ray diffraction data	PDB	<a href="#">6gag</a>
20	X-ray diffraction data	PDB	<a href="#">6gah</a>
21	X-ray diffraction data	PDB	<a href="#">6gai</a>

## Methodology and software ?

*This entry is a result of 1 distinct protocol(s).*

Step number	Protocol ID	Method name	Method type	Method description	Number of computed models	Multi state modeling	Multi scale modeling
1	1	Singular value decomposition analysis of difference Fourier maps	Singular value decomposition	None	1	False	False

*There are 2 software packages reported in this entry.*

ID	Software name	Software version	Software classification	Software location
1	<a href="#">PHENIX</a>	(1.13_2998: ???)	refinement	<a href="https://phenix-online.org/">https://phenix-online.org/</a>
2	dynamiX	Not available	Data reduction	Not available

## Data quality ?

### X-ray diffraction

Validation for this section is under development.

## Model quality ?

For models with atomic structures, MolProbity analysis is performed. For models with coarse-grained or multi-scale structures, excluded volume analysis is performed.

### Standard geometry: bond outliers ?

There are no bond length outliers.

### Standard geometry: angle outliers ?

There are no bond angle outliers.

### Too-close contacts ?

The following all-atom clashscore is based on a MolProbity analysis. All-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The table below contains clashscores for all atomic models in this entry.

Model ID	Clash score	Number of clashes
1	6.89	25

There are 25 clashes. The table below contains the detailed list of all clashes based on a MolProbity analysis. Bad clashes are  $\geq 0.4$  Angstrom.

Atom 1	Atom 2	Clash(Å)	Model ID (Worst)	Models (Total)
A:7:ARG:NH2	A:61:LEU:O	0.57	1	1
A:185:TYR:CE1	B:1:RET:H203	0.56	1	1
A:48:LEU:O	A:52:ILE:HG13	0.56	1	1
A:156:PHE:HB3	A:171:PHE:CZ	0.56	1	1
A:160:ALA:HA	A:163:MET:HG3	0.55	1	1
A:145:MET:HE1	A:182:TRP:HB3	0.54	1	1
A:38:ASP:OD1	A:41:LYS:NZ	0.54	1	1
A:56:MET:HG3	A:81:ALA:HB1	0.54	1	1
A:174:LEU:HD11	A:223:LEU:HB2	0.52	1	1
A:221:LEU:O	A:225:ARG:HG3	0.52	1	1
A:5:THR:OG1	A:6:GLY:N	0.52	1	1
A:153:PHE:CE2	A:179:VAL:HG21	0.52	1	1
A:66:LEU:HD11	A:77:PRO:HB2	0.52	1	1
A:149:LEU:HD13	A:179:VAL:HG13	0.47	1	1
A:184:ALA:O	A:187:VAL:HG13	0.47	1	1

Atom 1	Atom 2	Clash(Å)	Model ID (Worst)	Models (Total)
A:121:THR:HG23	A:137:TRP:HE3	0.47	1	1
A:25:LEU:O	A:29:VAL:HG13	0.45	1	1
A:142:THR:O	A:145:MET:HB3	0.45	1	1
A:147:TYR:O	A:151:VAL:HG23	0.45	1	1
A:66:LEU:HD13	A:79:TYR:CZ	0.44	1	1
A:85:ASP:C	A:85:ASP:OD1	0.43	1	1
A:90:THR:N	A:91:PRO:HD2	0.42	1	1
B:1:RET:C8	B:1:RET:H171	0.41	1	1
A:190:LEU:HA	A:190:LEU:HD12	0.40	1	1
A:60:MET:HE1	C:1:HOH:O	0.40	1	1

### Torsion angles: Protein backbone ?

In the following table, Ramachandran outliers are listed. The Analysed column shows the number of residues for which the backbone conformation was analysed.

Model ID	Analysed	Favored	Allowed	Outliers
1	228	220	7	1

There are 1 unique backbone outliers. Detailed list of outliers are tabulated below.

Chain	Res	Type	Models (Total)
A	73	GLY	1

### Torsion angles : Protein sidechains ?

In the following table, sidechain rotameric outliers are listed. The Analysed column shows the number of residues for which the sidechain conformation was analysed.

Model ID	Analysed	Favored	Allowed	Outliers
1	181	149	15	17

There are 17 unique sidechain outliers. Detailed list of outliers are tabulated below.

Chain	Res	Type	Models (Total)
A	15	LEU	1
A	30	LYS	1
A	56	MET	1
A	61	LEU	1
A	75	GLN	1
A	93	LEU	1
A	95	LEU	1
A	108	ILE	1

Chain	Res	Type	Models (Total)
A	123	LEU	1
A	145	MET	1
A	163	MET	1
A	164	ARG	1
A	169	SER	1
A	187	VAL	1
A	193	SER	1
A	207	LEU	1
A	229	ILE	1

### Fit of model to data used for modeling ?

#### X-ray diffraction

Validation for this section is under development.

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Validation for this section is under development.

### Acknowledgments

*The development of integrative model validation metrics, implementation of a model validation pipeline, and creation of a validation report for integrative structures are funded by NSF awards to the [PDB-IHM team](#) (DBI-1756248, DBI-2112966, DBI-2112967, DBI-2112968, and DBI-1756250) and awards from NSF, NIH, and DOE to the [RCSB PDB](#) (DBI-2321666, R01GM157729, and DE-SC0019749). The PDB-IHM team and members of the [Sali lab](#) contributed model validation metrics and software packages.*

*Dr. Jill Trehwella, Dr. Dina Schneidman, and members of the [SASBDB](#) repository are acknowledged for their advice and support in implementing SAS validation methods. Team members from the labs of Dr. Juri Rappsilber, Dr. Alexander Leitner, Dr. Andrea Graziadei, and members of [PRIDE](#) database are acknowledged for their advice and support in implementing crosslinking-MS validation methods. We are grateful to Dr. Shruthi Viswanath for discussions about uncertainty assessment of integrative structural models.*

*Members of the [wwPDB Integrative/Hybrid Methods Task Force](#) provided recommendations and community support for the project.*