



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1L0M
Title : Solution structure of Bacteriorhodopsin
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This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

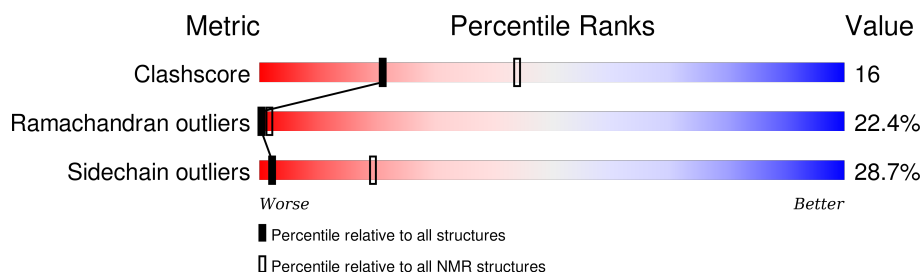
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	212	<div> <div></div> <div>45%</div> <div>31%</div> <div>13%</div> <div>11%</div> </div>

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3333 atoms, of which 1691 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Bacteriorhodopsin.

Mol	Chain	Residues	Atoms						Trace
1	A	212	Total	C	H	N	O	S	0
			3333	1104	1691	247	282	9	

4 Residue-property plots [i](#)

These plots are provided for all protein, RNA and DNA chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: Bacteriorhodopsin



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *refined using molecular dynamics*.

Of the ? calculated structures, 1 were deposited, based on the following criterion: ?.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
Sybyl	structure solution	6.6
Sybyl	refinement	6.6

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	2.00	6/1688 (0.4%)	1.76	28/2309 (1.2%)
All	All	2.00	6/1688 (0.4%)	1.76	28/2309 (1.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0	58
All	All	0	58

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	TRP	NE1-CE2	43.76	1.94	1.37
1	A	182	TRP	CD2-CE2	37.36	1.86	1.41
1	A	182	TRP	CD1-NE1	30.93	1.90	1.38
1	A	182	TRP	CG-CD2	30.78	1.96	1.43
1	A	182	TRP	CG-CD1	26.14	1.73	1.36
1	A	185	TYR	CG-CD2	6.18	1.47	1.39

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	185	TYR	CG-CD2-CE2	-24.60	101.62	121.30
1	A	185	TYR	CB-CG-CD1	-13.71	112.78	121.00
1	A	156	PHE	CB-CG-CD2	-10.27	113.61	120.80
1	A	208	PHE	CB-CG-CD2	-9.38	114.23	120.80
1	A	185	TYR	CA-CB-CG	8.84	130.19	113.40
1	A	185	TYR	CB-CG-CD2	8.48	126.09	121.00
1	A	39	ALA	CB-CA-C	8.17	122.36	110.10
1	A	134	ARG	C-N-CA	8.16	142.09	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	TYR	CA-CB-CG	7.78	128.17	113.40
1	A	132	SER	CB-CA-C	7.70	124.72	110.10
1	A	124	VAL	CA-CB-CG1	7.49	122.13	110.90
1	A	95	LEU	C-N-CA	7.44	140.31	121.70
1	A	131	TYR	CB-CG-CD2	-7.32	116.61	121.00
1	A	28	LEU	CB-CG-CD1	7.24	123.30	111.00
1	A	133	TYR	CB-CA-C	7.14	124.67	110.40
1	A	182	TRP	NE1-CE2-CZ2	6.72	137.80	130.40
1	A	87	LEU	C-N-CA	6.46	137.84	121.70
1	A	82	ARG	NE-CZ-NH2	-6.31	117.14	120.30
1	A	182	TRP	CD2-CE2-CZ2	-6.30	114.74	122.30
1	A	52	ILE	CA-CB-CG2	6.28	123.47	110.90
1	A	185	TYR	CE1-CZ-CE2	-5.96	110.26	119.80
1	A	156	PHE	CB-CA-C	5.55	121.49	110.40
1	A	185	TYR	CD1-CE1-CZ	-5.49	114.86	119.80
1	A	208	PHE	CA-CB-CG	5.33	126.69	113.90
1	A	26	TYR	CA-CB-CG	5.29	123.45	113.40
1	A	87	LEU	CA-C-N	5.25	128.75	117.20
1	A	131	TYR	C-N-CA	5.17	134.61	121.70
1	A	41	LYS	N-CA-C	5.01	124.52	111.00

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	166	GLU	Peptide
1	A	153	PHE	Peptide
1	A	56	MET	Peptide
1	A	28	LEU	Peptide
1	A	43	TYR	Sidechain,Peptide
1	A	45	ILE	Peptide
1	A	131	TYR	Sidechain
1	A	62	LEU	Peptide
1	A	198	ILE	Peptide
1	A	164	ARG	Sidechain,Peptide
1	A	156	PHE	Sidechain,Peptide
1	A	40	LYS	Peptide
1	A	104	ASP	Peptide
1	A	88	PHE	Sidechain
1	A	203	ILE	Peptide
1	A	29	VAL	Peptide
1	A	46	THR	Peptide

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Mol	Chain	Res	Type	Group
1	A	98	ALA	Peptide
1	A	132	SER	Peptide
1	A	89	THR	Peptide
1	A	24	THR	Peptide
1	A	155	GLY	Peptide
1	A	100	LEU	Peptide
1	A	154	PHE	Peptide
1	A	30	LYS	Peptide
1	A	142	THR	Peptide
1	A	91	PRO	Peptide
1	A	77	PRO	Peptide
1	A	150	TYR	Sidechain,Peptide
1	A	64	TYR	Sidechain
1	A	42	PHE	Sidechain
1	A	79	TYR	Sidechain,Peptide
1	A	106	GLY	Peptide
1	A	20	MET	Peptide
1	A	37	PRO	Peptide
1	A	189	TRP	Peptide
1	A	26	TYR	Sidechain
1	A	185	TYR	Sidechain
1	A	15	LEU	Peptide
1	A	81	ALA	Peptide
1	A	60	MET	Peptide
1	A	133	TYR	Sidechain
1	A	107	THR	Peptide
1	A	82	ARG	Sidechain
1	A	96	ASP	Peptide
1	A	124	VAL	Peptide
1	A	27	PHE	Sidechain,Peptide
1	A	208	PHE	Sidechain
1	A	130	VAL	Peptide
1	A	136	VAL	Peptide
1	A	182	TRP	Peptide
1	A	22	LEU	Peptide

6.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1642	1691	1690	52
All	All	1642	1691	1690	52

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:182:TRP:CD2	1:A:182:TRP:CE2	1.59	1.86
1:A:182:TRP:CG	1:A:182:TRP:CD2	1.53	1.96
1:A:182:TRP:CD1	1:A:182:TRP:NE1	1.37	1.90
1:A:182:TRP:NE1	1:A:182:TRP:CE2	1.34	1.94
1:A:182:TRP:CD2	1:A:185:TYR:CD2	1.24	2.26
1:A:182:TRP:CE2	1:A:185:TYR:CD2	1.21	2.28
1:A:182:TRP:CD1	1:A:185:TYR:CD2	1.20	2.27
1:A:182:TRP:CG	1:A:185:TYR:CD2	1.18	2.30
1:A:182:TRP:NE1	1:A:185:TYR:CD2	1.10	2.19
1:A:182:TRP:CG	1:A:185:TYR:HD2	1.05	1.66
1:A:182:TRP:CD2	1:A:185:TYR:HD2	1.02	1.62
1:A:182:TRP:CE2	1:A:185:TYR:CE2	0.94	2.55
1:A:182:TRP:CE2	1:A:185:TYR:HD2	0.89	1.80
1:A:182:TRP:CG	1:A:185:TYR:CB	0.77	2.68
1:A:182:TRP:CD1	1:A:185:TYR:HD2	0.75	1.80
1:A:182:TRP:NE1	1:A:185:TYR:CE2	0.74	2.56
1:A:39:ALA:HB3	1:A:40:LYS:HB3	0.72	1.60
1:A:182:TRP:CG	1:A:185:TYR:CG	0.72	2.76
1:A:182:TRP:NE1	1:A:185:TYR:HD2	0.72	1.82
1:A:182:TRP:HA	1:A:185:TYR:HB2	0.66	1.66
1:A:28:LEU:O	1:A:28:LEU:HD13	0.63	1.92
1:A:156:PHE:CD1	1:A:159:LYS:HG2	0.63	2.29
1:A:182:TRP:CG	1:A:185:TYR:HB2	0.60	2.30
1:A:129:LYS:CE	1:A:129:LYS:HA	0.58	2.29
1:A:52:ILE:HG23	1:A:88:PHE:CZ	0.56	2.35
1:A:56:MET:HG3	1:A:88:PHE:CZ	0.56	2.34
1:A:182:TRP:CD1	1:A:185:TYR:CG	0.54	2.93
1:A:156:PHE:HD2	1:A:171:PHE:CB	0.54	2.16
1:A:185:TYR:H	1:A:186:PRO:CD	0.52	2.17
1:A:102:ASP:HB3	1:A:107:THR:HG21	0.51	1.81
1:A:182:TRP:CZ2	1:A:185:TYR:CE2	0.50	2.99
1:A:156:PHE:O	1:A:156:PHE:CD1	0.50	2.64
1:A:156:PHE:CD2	1:A:171:PHE:CB	0.49	2.96
1:A:156:PHE:CE2	1:A:167:VAL:HA	0.47	2.45
1:A:106:GLY:C	1:A:107:THR:HG22	0.47	2.30

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:135:PHE:CG	1:A:136:VAL:N	0.46	2.84
1:A:204:GLU:HG3	1:A:205:THR:N	0.45	2.26
1:A:25:LEU:N	1:A:26:TYR:HA	0.44	2.28
1:A:182:TRP:CA	1:A:185:TYR:HB2	0.43	2.39
1:A:45:ILE:HG12	1:A:48:LEU:CB	0.43	2.43
1:A:107:THR:HG23	1:A:108:ILE:N	0.43	2.28
1:A:75:GLN:O	1:A:76:ASN:CB	0.42	2.67
1:A:182:TRP:CG	1:A:185:TYR:HB3	0.41	2.46
1:A:128:THR:N	1:A:133:TYR:CD2	0.41	2.89
1:A:127:LEU:O	1:A:133:TYR:CG	0.41	2.74
1:A:156:PHE:CE2	1:A:166:GLU:CB	0.41	3.04
1:A:95:LEU:N	1:A:96:ASP:O	0.41	2.54
1:A:45:ILE:HG12	1:A:48:LEU:HB3	0.41	1.93
1:A:52:ILE:HG23	1:A:88:PHE:CE2	0.40	2.51
1:A:189:TRP:N	1:A:189:TRP:CD2	0.40	2.89
1:A:149:LEU:O	1:A:153:PHE:N	0.40	2.54
1:A:156:PHE:CE1	1:A:159:LYS:HB2	0.40	2.50

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	210/212 (99%)	102 (49%)	61 (29%)	47 (22%)	0	2
All	All	210/212 (99%)	102 (49%)	61 (29%)	47 (22%)	0	2

All 47 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	14	ALA
1	A	40	LYS
1	A	17	THR
1	A	180	VAL
1	A	208	PHE
1	A	22	LEU

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Mol	Chain	Res	Type
1	A	185	TYR
1	A	199	VAL
1	A	39	ALA
1	A	158	SER
1	A	108	ILE
1	A	179	VAL
1	A	146	LEU
1	A	204	GLU
1	A	166	GLU
1	A	91	PRO
1	A	135	PHE
1	A	203	ILE
1	A	156	PHE
1	A	115	ASP
1	A	136	VAL
1	A	41	LYS
1	A	76	ASN
1	A	53	ALA
1	A	191	ILE
1	A	124	VAL
1	A	197	GLY
1	A	167	VAL
1	A	84	ALA
1	A	107	THR
1	A	198	ILE
1	A	95	LEU
1	A	194	GLU
1	A	52	ILE
1	A	73	GLY
1	A	186	PRO
1	A	117	ILE
1	A	188	VAL
1	A	101	VAL
1	A	32	MET
1	A	157	THR
1	A	173	VAL
1	A	105	GLN
1	A	90	THR
1	A	96	ASP
1	A	161	GLU
1	A	66	LEU

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	171/171 (100%)	122 (71%)	49 (29%)	2	19
All	All	171/171 (100%)	122 (71%)	49 (29%)	2	19

All 49 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	40	LYS
1	A	129	LYS
1	A	17	THR
1	A	208	PHE
1	A	127	LEU
1	A	128	THR
1	A	133	TYR
1	A	207	LEU
1	A	57	TYR
1	A	69	VAL
1	A	89	THR
1	A	30	LYS
1	A	93	LEU
1	A	108	ILE
1	A	28	LEU
1	A	29	VAL
1	A	15	LEU
1	A	135	PHE
1	A	99	LEU
1	A	185	TYR
1	A	109	LEU
1	A	166	GLU
1	A	146	LEU
1	A	189	TRP
1	A	137	TRP
1	A	112	VAL
1	A	203	ILE
1	A	140	ILE
1	A	175	ARG

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Mol	Chain	Res	Type
1	A	88	PHE
1	A	95	LEU
1	A	194	GLU
1	A	154	PHE
1	A	82	ARG
1	A	182	TRP
1	A	60	MET
1	A	131	TYR
1	A	167	VAL
1	A	212	ASP
1	A	138	TRP
1	A	7	ARG
1	A	169	SER
1	A	171	PHE
1	A	26	TYR
1	A	13	LEU
1	A	35	SER
1	A	118	MET
1	A	46	THR
1	A	161	GLU

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry ⓘ

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided