



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:44 am BST

PDB ID : 4NBM
Title : Crystal structure of UVB photoreceptor UVR8 and light-induced structural changes at 180K
Authors : Yang, X.; Zeng, X.; Zhao, K.-H.; Ren, Z.
Deposited on : 2013-10-23
Resolution : 1.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

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:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

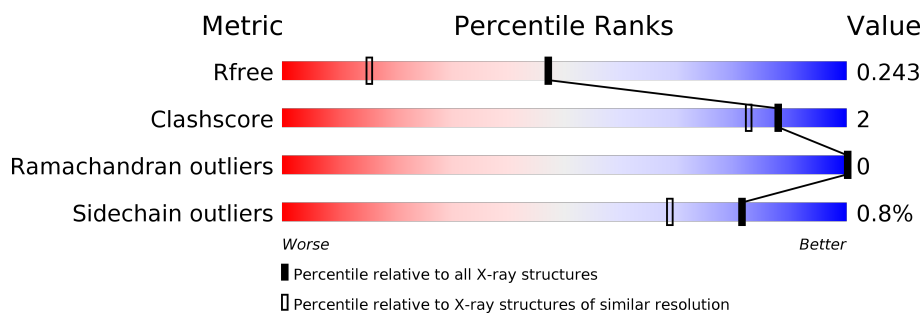
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	377	94% . .
1	B	377	92% 6% .
1	C	377	92% 6% .
1	D	377	92% 5% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13218 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ultraviolet-B receptor UVR8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	369	Total	C	N	O	S	0	12	0
			2888	1797	522	553	16			
1	B	369	Total	C	N	O	S	0	10	0
			2868	1783	518	551	16			
1	C	369	Total	C	N	O	S	0	11	0
			2881	1794	523	549	15			
1	D	369	Total	C	N	O	S	0	13	0
			2892	1798	526	553	15			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	382	LEU	-	EXPRESSION TAG	UNP Q9FN03
A	383	GLU	-	EXPRESSION TAG	UNP Q9FN03
A	384	HIS	-	EXPRESSION TAG	UNP Q9FN03
A	385	HIS	-	EXPRESSION TAG	UNP Q9FN03
A	386	HIS	-	EXPRESSION TAG	UNP Q9FN03
A	387	HIS	-	EXPRESSION TAG	UNP Q9FN03
A	388	HIS	-	EXPRESSION TAG	UNP Q9FN03
A	389	HIS	-	EXPRESSION TAG	UNP Q9FN03
B	382	LEU	-	EXPRESSION TAG	UNP Q9FN03
B	383	GLU	-	EXPRESSION TAG	UNP Q9FN03
B	384	HIS	-	EXPRESSION TAG	UNP Q9FN03
B	385	HIS	-	EXPRESSION TAG	UNP Q9FN03
B	386	HIS	-	EXPRESSION TAG	UNP Q9FN03
B	387	HIS	-	EXPRESSION TAG	UNP Q9FN03
B	388	HIS	-	EXPRESSION TAG	UNP Q9FN03
B	389	HIS	-	EXPRESSION TAG	UNP Q9FN03
C	382	LEU	-	EXPRESSION TAG	UNP Q9FN03
C	383	GLU	-	EXPRESSION TAG	UNP Q9FN03
C	384	HIS	-	EXPRESSION TAG	UNP Q9FN03
C	385	HIS	-	EXPRESSION TAG	UNP Q9FN03
C	386	HIS	-	EXPRESSION TAG	UNP Q9FN03

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Chain	Residue	Modelled	Actual	Comment	Reference
C	387	HIS	-	EXPRESSION TAG	UNP Q9FN03
C	388	HIS	-	EXPRESSION TAG	UNP Q9FN03
C	389	HIS	-	EXPRESSION TAG	UNP Q9FN03
D	382	LEU	-	EXPRESSION TAG	UNP Q9FN03
D	383	GLU	-	EXPRESSION TAG	UNP Q9FN03
D	384	HIS	-	EXPRESSION TAG	UNP Q9FN03
D	385	HIS	-	EXPRESSION TAG	UNP Q9FN03
D	386	HIS	-	EXPRESSION TAG	UNP Q9FN03
D	387	HIS	-	EXPRESSION TAG	UNP Q9FN03
D	388	HIS	-	EXPRESSION TAG	UNP Q9FN03
D	389	HIS	-	EXPRESSION TAG	UNP Q9FN03

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Mg 3 3	0	0
2	A	7	Total Mg 7 7	0	0
2	D	5	Total Mg 5 5	0	0
2	C	8	Total Mg 8 8	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	440	Total O 440 440	0	0
3	B	399	Total O 399 399	0	0
3	C	418	Total O 418 418	0	0
3	D	409	Total O 409 409	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-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 outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Ultraviolet-B receptor UVR8

Chain A:  94%



• Molecule 1: Ultraviolet-B receptor UVR8

Chain B:  92%



• Molecule 1: Ultraviolet-B receptor UVR8

Chain C:  92%



• Molecule 1: Ultraviolet-B receptor UVR8

Chain D:  92%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	113.31Å 76.83Å 191.25Å 90.00° 96.75° 90.00°	Depositor
Resolution (Å)	29.86 – 1.61 29.11 – 1.79	Depositor EDS
% Data completeness (in resolution range)	78.5 (29.86-1.61) 72.3 (29.11-1.79)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.150 , 0.182 0.227 , 0.243	Depositor DCC
R_{free} test set	5473 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	14.1	Xtriage
Anisotropy	0.195	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13218	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.15 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.0344e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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 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	0.35	0/2962	0.53	0/4014
1	B	0.33	0/2939	0.53	0/3985
1	C	0.34	0/2955	0.53	0/4006
1	D	0.32	0/2966	0.51	0/4020
All	All	0.33	0/11822	0.52	0/16025

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2888	0	2760	10	0
1	B	2868	0	2736	13	0
1	C	2881	0	2760	11	0
1	D	2892	0	2766	13	0
2	A	7	0	0	0	0
2	B	3	0	0	0	0
2	C	8	0	0	0	0
2	D	5	0	0	0	0
3	A	440	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	399	0	0	1	0
3	C	418	0	0	2	0
3	D	409	0	0	1	0
All	All	13218	0	11022	46	0

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 2.

All (46) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317[A]:CYS:SG	3:A:744:HOH:O	2.55	0.64
1:A:317[B]:CYS:SG	3:A:744:HOH:O	2.56	0.61
1:A:285:TRP:HB2	1:A:337:TRP:HA	1.85	0.58
1:C:80[B]:VAL:HG11	1:C:125:ILE:HG21	1.86	0.57
1:C:285:TRP:HB2	1:C:337:TRP:HA	1.86	0.57
1:C:14:PRO:HB2	1:C:16:LYS:HE3	1.86	0.57
1:D:181:ALA:HB2	1:D:233:TRP:CD1	2.40	0.56
1:B:19:ILE:HD12	1:B:71:SER:HA	1.87	0.56
1:C:17:VAL:HG21	1:C:349:VAL:HG21	1.87	0.56
1:B:285:TRP:HB2	1:B:337:TRP:HA	1.88	0.55
1:D:285:TRP:HB2	1:D:337:TRP:HA	1.87	0.55
1:A:15:ARG:NE	3:A:777:HOH:O	2.38	0.55
1:A:17:VAL:HG21	1:A:349:VAL:HG21	1.90	0.54
1:D:80[B]:VAL:HG11	1:D:125:ILE:HG21	1.90	0.53
1:C:15:ARG:NE	3:C:754:HOH:O	2.29	0.51
1:B:115:LYS:NZ	3:B:767:HOH:O	2.23	0.51
1:C:372:LYS:HG2	3:C:747:HOH:O	2.09	0.51
1:B:20:ILE:HD13	1:B:343:VAL:HG23	1.92	0.51
1:D:20:ILE:HD13	1:D:343:VAL:HG23	1.94	0.50
1:D:19:ILE:HD12	1:D:71:SER:HA	1.93	0.50
1:C:132:CYS:HB2	1:C:144:TRP:CE2	2.49	0.48
1:B:16:LYS:HA	1:B:347:ASN:HD21	1.78	0.47
1:A:304:LYS:HE2	1:B:109:PHE:CZ	2.50	0.47
1:B:331:VAL:HG23	1:B:332:GLN:HG3	1.97	0.46
1:D:346[A]:ARG:NE	3:D:800:HOH:O	2.47	0.45
1:D:13:PRO:HA	1:D:14:PRO:HD3	1.87	0.45
1:C:19:ILE:HD12	1:C:71:SER:HA	1.98	0.45
1:D:31:LEU:HD12	1:D:35:ILE:HD11	1.98	0.45
1:B:181:ALA:HB2	1:B:233:TRP:CD1	2.52	0.44
1:B:228:MET:HE3	1:B:239:VAL:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:THR:HB	1:C:80[B]:VAL:HG12	2.00	0.44
1:C:181:ALA:HB2	1:C:233:TRP:CD1	2.53	0.43
1:D:372:LYS:HB3	1:D:372:LYS:HE3	1.83	0.43
1:A:181:ALA:HB2	1:A:233:TRP:CD1	2.54	0.43
1:D:176:MET:HG2	1:D:187:VAL:HG22	2.00	0.43
1:A:232:GLY:HA3	1:A:235:HIS:CE1	2.54	0.42
1:D:73:THR:HB	1:D:80[B]:VAL:HG12	1.99	0.42
1:D:24:ALA:HA	1:D:337:TRP:CD1	2.55	0.42
1:B:31:LEU:HD12	1:B:35:ILE:HD11	2.02	0.41
1:B:24:ALA:HA	1:B:337:TRP:CD1	2.55	0.41
1:D:16:LYS:HE2	1:D:16:LYS:HB3	1.89	0.41
1:A:121[B]:ARG:HD2	3:A:715:HOH:O	2.21	0.41
1:C:176:MET:HG2	1:C:187:VAL:HG22	2.03	0.41
1:B:132:CYS:HB2	1:B:144:TRP:CE2	2.56	0.40
1:A:132:CYS:HB2	1:A:144:TRP:CE2	2.57	0.40
1:B:16:LYS:HA	1:B:347:ASN:ND2	2.36	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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	379/377 (100%)	377 (100%)	2 (0%)	0	100	100
1	B	377/377 (100%)	376 (100%)	1 (0%)	0	100	100
1	C	378/377 (100%)	376 (100%)	2 (0%)	0	100	100
1	D	380/377 (101%)	377 (99%)	3 (1%)	0	100	100
All	All	1514/1508 (100%)	1506 (100%)	8 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	304/300 (101%)	303 (100%)	1 (0%)	92	86
1	B	302/300 (101%)	300 (99%)	2 (1%)	84	72
1	C	303/300 (101%)	301 (99%)	2 (1%)	84	72
1	D	305/300 (102%)	301 (99%)	4 (1%)	69	49
All	All	1214/1200 (101%)	1205 (99%)	9 (1%)	81	72

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	372	LYS
1	B	35	ILE
1	B	251	SER
1	C	228	MET
1	C	251	SER
1	D	35	ILE
1	D	233	TRP
1	D	251	SER
1	D	372	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 23 ligands modelled in this entry, 23 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.