



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:15 AM UTC

PDB ID : 5CWF / pdb_00005cwf
Title : Crystal structure of de novo designed helical repeat protein DHR8
Authors : Bhabha, G.; Ekiert, D.C.
Deposited on : 2015-07-28
Resolution : 1.80 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

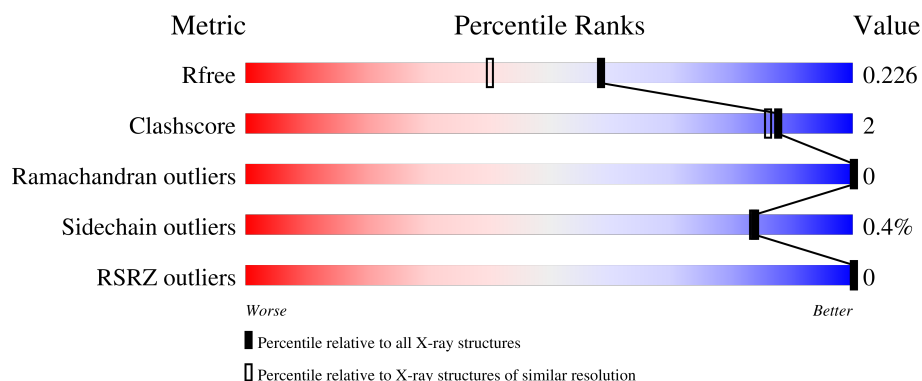
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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 of 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	191	 86% 6% 7%
1	B	191	 88% 8%
1	C	191	 84% 7% 8%
1	D	191	 89% 8%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11528 atoms, of which 5605 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 Designed helical repeat protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	177	Total	C	H	N	O	S	0	20	0
			2942	876	1492	266	299	9			
1	B	176	Total	C	H	N	O	S	0	4	0
			2689	812	1347	248	274	8			
1	C	175	Total	C	H	N	O	S	0	10	0
			2728	825	1360	251	284	8			
1	D	176	Total	C	H	N	O	S	0	4	0
			2771	828	1406	248	280	9			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	8	Total	Ca	0	0
			8	8		
2	B	11	Total	Ca	0	7
			11	11		
2	C	8	Total	Ca	0	3
			8	8		
2	D	5	Total	Ca	0	0
			5	5		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	2
			118	118		
3	B	78	Total	O	0	0
			78	78		
3	C	66	Total	O	0	1
			66	66		
3	D	104	Total	O	0	1
			104	104		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	75.69Å 76.36Å 133.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.38 – 1.80 44.38 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.38-1.80) 89.6 (44.38-1.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.63 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.194 , 0.220 0.199 , 0.226	Depositor DCC
R_{free} test set	3591 reflections (4.58%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.138 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	11528	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: CA

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	0.56	0/1528	0.69	0/2042
1	B	0.52	0/1354	0.73	1/1816 (0.1%)
1	C	0.51	0/1395	0.70	0/1873
1	D	0.57	0/1380	0.71	0/1846
All	All	0.54	0/5657	0.71	1/7577 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	6	LYS	N-CA-C	5.50	118.04	111.71

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	1450	1492	1401	6	0
1	B	1342	1347	1334	4	0
1	C	1368	1360	1330	9	0
1	D	1365	1406	1389	5	0
2	A	8	0	0	0	0
2	B	11	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	8	0	0	0	0
2	D	5	0	0	0	0
3	A	118	0	0	1	0
3	B	78	0	0	0	0
3	C	66	0	0	0	0
3	D	104	0	0	1	0
All	All	5923	5605	5454	22	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 (22) 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:D:5:MET:HE1	1:D:55:LEU:HA	1.85	0.58
1:A:5:MET:HE1	1:A:55:LEU:HA	1.86	0.58
1:C:48:ASP:OD1	1:C:49:GLU:N	2.38	0.57
1:A:87:LEU:HG	1:A:99:MET:HG3	1.88	0.55
1:D:112:ASN:ND2	3:D:301:HOH:O	2.31	0.54
1:B:11:ALA:O	1:B:15:ALA:N	2.39	0.53
1:C:132:LEU:HG	1:C:144:MET:HG3	1.90	0.52
1:C:87:LEU:HG	1:C:99:MET:HG3	1.90	0.52
1:B:48:ASP:OD1	1:B:49:GLU:N	2.42	0.51
1:C:75:GLU:OE2	1:C:119[B]:ARG:NH2	2.47	0.48
1:D:5:MET:HE1	1:D:55:LEU:CA	2.43	0.48
1:A:29[B]:ARG:NH2	3:A:310:HOH:O	2.47	0.47
1:A:164:ARG:HD2	1:B:119:ARG:NH2	2.30	0.46
1:C:11:ALA:O	1:C:15:ALA:N	2.47	0.43
1:D:87:LEU:HG	1:D:99:MET:HG3	2.00	0.42
1:A:76[A]:ILE:HD11	1:A:118:ALA:HB1	2.01	0.41
1:A:37[A]:GLU:HG3	1:A:84:VAL:CG1	2.51	0.41
1:C:120[A]:GLU:HG2	1:C:160:ASP:HB2	2.03	0.41
1:C:132:LEU:HD21	1:C:141:ALA:HA	2.02	0.41
1:B:112:ASN:ND2	1:B:158:ASN:OD1	2.55	0.40
1:C:119[B]:ARG:NH2	1:D:164:ARG:HD2	2.36	0.40
1:C:15:ALA:HB2	1:C:62:LEU:CD1	2.51	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	195/191 (102%)	193 (99%)	2 (1%)	0	100	100
1	B	176/191 (92%)	175 (99%)	1 (1%)	0	100	100
1	C	181/191 (95%)	181 (100%)	0	0	100	100
1	D	178/191 (93%)	177 (99%)	1 (1%)	0	100	100
All	All	730/764 (96%)	726 (100%)	4 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 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 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	155/151 (103%)	152 (98%)	3 (2%)	50	41
1	B	131/151 (87%)	131 (100%)	0	100	100
1	C	136/151 (90%)	136 (100%)	0	100	100
1	D	140/151 (93%)	140 (100%)	0	100	100
All	All	562/604 (93%)	559 (100%)	3 (0%)	84	80

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40[A]	GLU
1	A	40[B]	GLU
1	A	91	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	91	ASN
1	B	169	GLN
1	D	23	ASN
1	D	91	ASN
1	D	158	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 32 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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	177/191 (92%)	-1.18	0 100 100	14, 37, 76, 97	10 (5%)
1	B	176/191 (92%)	-0.97	0 100 100	18, 41, 121, 147	2 (1%)
1	C	175/191 (91%)	-0.96	0 100 100	12, 43, 115, 194	6 (3%)
1	D	176/191 (92%)	-1.17	0 100 100	20, 38, 74, 99	2 (1%)
All	All	704/764 (92%)	-1.07	0 100 100	12, 40, 93, 194	20 (2%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	A	207	1/1	0.96	0.06	88,88,88,88	1
2	CA	B	206	1/1	0.97	0.06	54,54,54,54	1
2	CA	B	209[A]	1/1	0.97	0.08	52,52,52,52	1
2	CA	C	204	1/1	0.97	0.05	53,53,53,53	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	B	207[B]	1/1	0.98	0.09	50,50,50,50	1
2	CA	B	208[A]	1/1	0.98	0.06	40,40,40,40	1
2	CA	C	206[A]	1/1	0.98	0.11	50,50,50,50	1
2	CA	C	207	1/1	0.98	0.04	40,40,40,40	1
2	CA	B	204[B]	1/1	0.99	0.03	23,23,23,23	1
2	CA	B	211[B]	1/1	0.99	0.03	24,24,24,24	1
2	CA	A	206	1/1	0.99	0.04	31,31,31,31	1
2	CA	A	205	1/1	0.99	0.03	39,39,39,39	1
2	CA	A	208	1/1	0.99	0.03	31,31,31,31	1
2	CA	D	202	1/1	0.99	0.02	35,35,35,35	1
2	CA	D	203	1/1	0.99	0.03	45,45,45,45	1
2	CA	D	205	1/1	0.99	0.09	43,43,43,43	0
2	CA	B	201	1/1	1.00	0.03	16,16,16,16	1
2	CA	B	210[B]	1/1	1.00	0.07	33,33,33,33	1
2	CA	B	202	1/1	1.00	0.01	23,23,23,23	0
2	CA	C	201	1/1	1.00	0.01	23,23,23,23	0
2	CA	C	202	1/1	1.00	0.01	25,25,25,25	1
2	CA	C	203	1/1	1.00	0.02	42,42,42,42	1
2	CA	B	203	1/1	1.00	0.02	37,37,37,37	0
2	CA	C	205[A]	1/1	1.00	0.06	33,33,33,33	1
2	CA	A	201	1/1	1.00	0.01	25,25,25,25	0
2	CA	B	205[A]	1/1	1.00	0.02	25,25,25,25	1
2	CA	C	208[B]	1/1	1.00	0.02	40,40,40,40	1
2	CA	D	201	1/1	1.00	0.01	21,21,21,21	0
2	CA	A	202	1/1	1.00	0.02	25,25,25,25	1
2	CA	A	203	1/1	1.00	0.02	29,29,29,29	1
2	CA	D	204	1/1	1.00	0.01	26,26,26,26	1
2	CA	A	204	1/1	1.00	0.01	21,21,21,21	1

6.5 Other polymers

There are no such residues in this entry.