



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:05 AM UTC

PDB ID : 4ZF5 / pdb_00004zf5
Title : Crystal structure of Green Fluorescent Protein (GFP); S65T, Y66(C12Y), H148D; circular permutant (50-51)
Authors : Oltrogge, L.M.; Boxer, S.G.
Deposited on : 2015-04-21
Resolution : 1.70 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

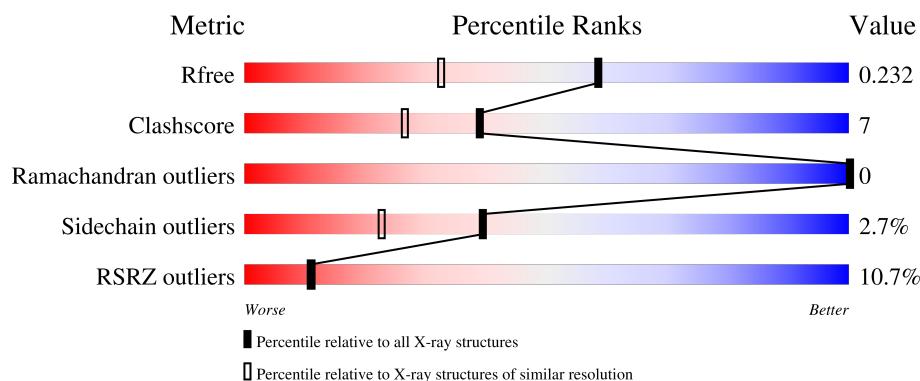
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	252	4% 78% 10% 11%
1	B	252	15% 71% 14% 14%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3564 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 Green fluorescent protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	225	Total	C	Cl	N	O	S	0	1	0
			1798	1136	2	307	349	4			
1	B	217	Total	C	Cl	N	O	S	0	0	0
			1708	1083	2	290	329	4			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	expression tag	UNP P42212
A	-9	GLY	-	expression tag	UNP P42212
A	-8	HIS	-	expression tag	UNP P42212
A	-7	HIS	-	expression tag	UNP P42212
A	-6	HIS	-	expression tag	UNP P42212
A	-5	HIS	-	expression tag	UNP P42212
A	-4	HIS	-	expression tag	UNP P42212
A	-3	HIS	-	expression tag	UNP P42212
A	-2	SER	-	expression tag	UNP P42212
A	-1	SER	-	expression tag	UNP P42212
A	0	GLY	-	expression tag	UNP P42212
A	14	LEU	PHE	engineered mutation	UNP P42212
A	15	4NU	SER	chromophore	UNP P42212
A	?	4NU	TYR	chromophore	UNP P42212
A	?	4NU	GLY	chromophore	UNP P42212
A	30	ARG	GLN	engineered mutation	UNP P42212
A	49	SER	PHE	engineered mutation	UNP P42212
A	55	LYS	ASN	engineered mutation	UNP P42212
A	61	VAL	GLU	engineered mutation	UNP P42212
A	78	THR	ILE	engineered mutation	UNP P42212
A	95	PHE	TYR	engineered mutation	UNP P42212
A	98	ASP	HIS	engineered mutation	UNP P42212
A	103	THR	MET	engineered mutation	UNP P42212
A	113	ALA	VAL	engineered mutation	UNP P42212
A	116	THR	LYS	engineered mutation	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
A	117	VAL	ILE	engineered mutation	UNP P42212
A	121	VAL	ILE	engineered mutation	UNP P42212
A	155	THR	SER	engineered mutation	UNP P42212
A	156	VAL	ALA	engineered mutation	UNP P42212
A	188	GLY	-	linker	UNP P42212
A	189	GLY	-	linker	UNP P42212
A	190	THR	-	linker	UNP P42212
A	191	GLY	-	linker	UNP P42212
A	192	GLY	-	linker	UNP P42212
A	193	SER	-	linker	UNP P42212
A	194	ALA	-	linker	UNP P42212
A	195	SER	-	linker	UNP P42212
A	196	GLN	-	linker	UNP P42212
A	223	ARG	SER	engineered mutation	UNP P42212
A	232	ILE	TYR	engineered mutation	UNP P42212
A	241	SER	CYS	engineered mutation	UNP P42212
B	-10	MET	-	expression tag	UNP P42212
B	-9	GLY	-	expression tag	UNP P42212
B	-8	HIS	-	expression tag	UNP P42212
B	-7	HIS	-	expression tag	UNP P42212
B	-6	HIS	-	expression tag	UNP P42212
B	-5	HIS	-	expression tag	UNP P42212
B	-4	HIS	-	expression tag	UNP P42212
B	-3	HIS	-	expression tag	UNP P42212
B	-2	SER	-	expression tag	UNP P42212
B	-1	SER	-	expression tag	UNP P42212
B	0	GLY	-	expression tag	UNP P42212
B	14	LEU	PHE	engineered mutation	UNP P42212
B	15	4NU	SER	chromophore	UNP P42212
B	?	4NU	TYR	chromophore	UNP P42212
B	?	4NU	GLY	chromophore	UNP P42212
B	30	ARG	GLN	engineered mutation	UNP P42212
B	49	SER	PHE	engineered mutation	UNP P42212
B	55	LYS	ASN	engineered mutation	UNP P42212
B	61	VAL	GLU	engineered mutation	UNP P42212
B	78	THR	ILE	engineered mutation	UNP P42212
B	95	PHE	TYR	engineered mutation	UNP P42212
B	98	ASP	HIS	engineered mutation	UNP P42212
B	103	THR	MET	engineered mutation	UNP P42212
B	113	ALA	VAL	engineered mutation	UNP P42212
B	116	THR	LYS	engineered mutation	UNP P42212
B	117	VAL	ILE	engineered mutation	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	121	VAL	ILE	engineered mutation	UNP P42212
B	155	THR	SER	engineered mutation	UNP P42212
B	156	VAL	ALA	engineered mutation	UNP P42212
B	188	GLY	-	linker	UNP P42212
B	189	GLY	-	linker	UNP P42212
B	190	THR	-	linker	UNP P42212
B	191	GLY	-	linker	UNP P42212
B	192	GLY	-	linker	UNP P42212
B	193	SER	-	linker	UNP P42212
B	194	ALA	-	linker	UNP P42212
B	195	SER	-	linker	UNP P42212
B	196	GLN	-	linker	UNP P42212
B	223	ARG	SER	engineered mutation	UNP P42212
B	232	ILE	TYR	engineered mutation	UNP P42212
B	241	SER	CYS	engineered mutation	UNP P42212

- Molecule 2 is water.

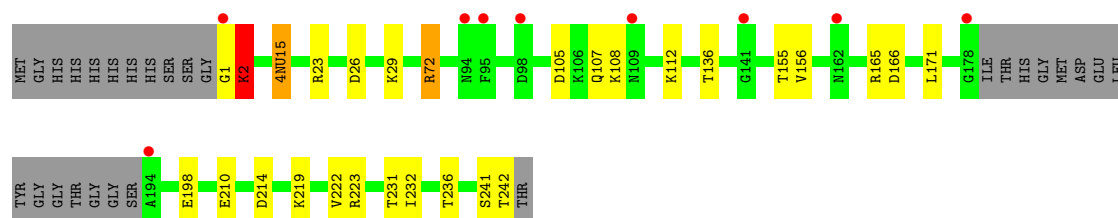
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	40	Total O 40 40	0	0
2	B	18	Total O 18 18	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

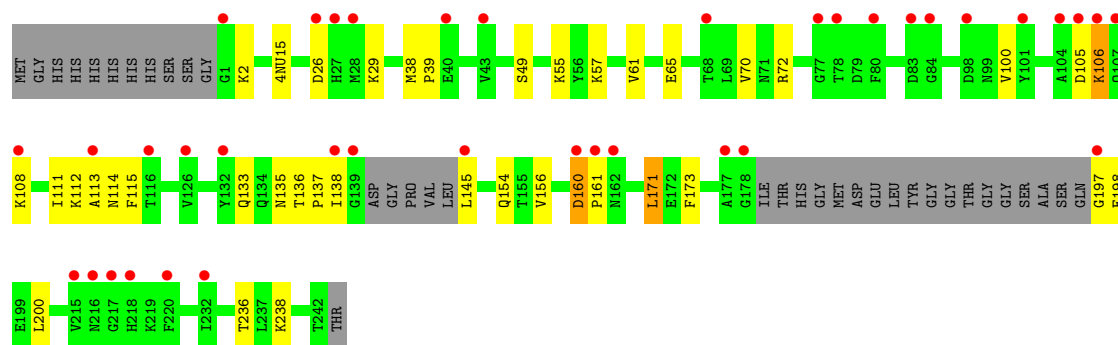
• Molecule 1: Green fluorescent protein

Chain A: 



• Molecule 1: Green fluorescent protein

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.14Å 68.13Å 58.00Å 90.00° 102.33° 90.00°	Depositor
Resolution (Å)	56.66 – 1.70 56.66 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (56.66-1.70) 99.3 (56.66-1.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.198 , 0.232 0.199 , 0.232	Depositor DCC
R_{free} test set	1926 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 52.2	EDS
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3564	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical 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: 4NU

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	0/1810	0.82	2/2446 (0.1%)
1	B	0.47	0/1718	0.81	2/2324 (0.1%)
All	All	0.52	0/3528	0.81	4/4770 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	160	ASP	CA-C-N	5.47	125.30	119.28
1	B	160	ASP	C-N-CA	5.47	125.30	119.28
1	A	2	LYS	CB-CA-C	-5.26	105.09	111.82
1	A	2	LYS	N-CA-C	5.13	118.89	111.56

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	1798	0	1745	29	0
1	B	1708	0	1635	23	0
2	A	40	0	0	0	0
2	B	18	0	0	0	0
All	All	3564	0	3380	47	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 7.

All (47) 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:171:LEU:HD23	1:B:171:LEU:HD22	1.41	1.02
1:A:165:ARG:HG2	1:A:165:ARG:HH11	1.35	0.89
1:B:160:ASP:OD2	1:B:238:LYS:NZ	2.04	0.89
1:A:107:GLN:OE1	1:A:108:LYS:NZ	2.07	0.86
1:A:165:ARG:HH21	1:A:242:THR:HG22	1.45	0.81
1:A:1:GLY:HA2	1:A:166:ASP:HB3	1.64	0.79
1:A:214:ASP:OD2	1:A:219:LYS:NZ	2.14	0.78
1:A:72:ARG:NH1	1:A:210:GLU:OE1	2.19	0.74
1:B:105:ASP:OD1	1:B:108:LYS:NZ	2.20	0.74
1:A:108:LYS:HB3	1:A:136:THR:HG22	1.74	0.69
1:A:171:LEU:HD13	1:A:236:THR:HG22	1.75	0.68
1:A:198:GLU:CD	1:A:198:GLU:H	2.04	0.66
1:B:38:MET:O	1:B:197:GLY:N	2.29	0.64
1:A:156:VAL:HG23	1:B:156:VAL:HG13	1.80	0.62
1:A:222:VAL:O	1:A:223:ARG:HD3	2.01	0.61
1:B:26:ASP:HA	1:B:29:LYS:HE3	1.82	0.60
1:A:15:4NU:CL1	1:A:155:THR:OG1	2.53	0.60
1:A:165:ARG:HH11	1:A:165:ARG:CG	2.13	0.60
1:A:1:GLY:N	1:A:241:SER:O	2.36	0.59
1:B:55:LYS:HE3	1:B:57:LYS:HE3	1.83	0.59
1:A:105:ASP:HB2	1:A:112:LYS:HG3	1.85	0.58
1:A:105:ASP:OD2	1:A:112:LYS:HE3	2.04	0.58
1:A:156:VAL:HG11	1:B:173:PHE:CD1	2.39	0.58
1:A:210:GLU:HG2	1:A:223:ARG:HD2	1.86	0.58
1:A:165:ARG:HG2	1:A:165:ARG:NH1	2.11	0.56
1:B:105:ASP:CG	1:B:108:LYS:NZ	2.64	0.54
1:A:1:GLY:C	1:A:2:LYS:HG3	2.33	0.54
1:A:165:ARG:NH2	1:A:242:THR:HG22	2.20	0.54
1:A:105:ASP:OD2	1:A:108:LYS:HE2	2.09	0.53
1:B:105:ASP:OD2	1:B:112:LYS:HD2	2.09	0.52
1:A:171:LEU:HD13	1:A:236:THR:CG2	2.40	0.51
1:B:105:ASP:CG	1:B:108:LYS:HZ3	2.17	0.51
1:A:232:ILE:HG21	1:B:161:PRO:HD3	1.96	0.48
1:B:105:ASP:OD2	1:B:112:LYS:HB3	2.14	0.47
1:B:61:VAL:HG13	1:B:138:ILE:HD11	1.98	0.46
1:A:165:ARG:CG	1:A:165:ARG:NH1	2.75	0.45
1:B:100:VAL:HG13	1:B:115:PHE:CD1	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:ALA:HB3	1:B:133:GLN:HB3	1.98	0.45
1:A:26:ASP:HA	1:A:29:LYS:HG3	1.98	0.45
1:B:39:PRO:HB3	1:B:200:LEU:HD11	1.98	0.45
1:A:156:VAL:HG22	1:B:154:GLN:HB3	1.99	0.44
1:B:65:GLU:OE2	1:B:72:ARG:NH2	2.51	0.43
1:B:106:LYS:HB2	1:B:106:LYS:HE2	1.75	0.43
1:B:136:THR:HA	1:B:137:PRO:HD3	1.92	0.42
1:B:70:VAL:HG11	1:B:72:ARG:NH1	2.35	0.41
1:A:23:ARG:HD2	1:A:231:THR:O	2.21	0.40
1:B:111:ILE:HG12	1:B:135:ASN:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	219/252 (87%)	216 (99%)	3 (1%)	0	100	100
1	B	208/252 (82%)	202 (97%)	6 (3%)	0	100	100
All	All	427/504 (85%)	418 (98%)	9 (2%)	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	196/215 (91%)	194 (99%)	2 (1%)	68	58
1	B	182/215 (85%)	174 (96%)	8 (4%)	25	10
All	All	378/430 (88%)	368 (97%)	10 (3%)	39	23

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	72	ARG
1	B	2	LYS
1	B	49	SER
1	B	106	LYS
1	B	114	ASN
1	B	145	LEU
1	B	171	LEU
1	B	198	GLU
1	B	236	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	27	HIS
1	B	71	ASN
1	B	85	ASN
1	B	162	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4NU	A	15	1	21,25,26	2.32	3 (14%)	26,36,38	2.37	13 (50%)
1	4NU	B	15	1	21,25,26	2.29	2 (9%)	26,36,38	2.27	10 (38%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4NU	A	15	1	-	2/11/47/48	0/2/2/2
1	4NU	B	15	1	-	4/11/47/48	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	15	4NU	CG2-CB2	-8.95	1.41	1.51
1	B	15	4NU	CG2-CB2	-8.90	1.41	1.51
1	B	15	4NU	C1-N3	4.19	1.44	1.37
1	A	15	4NU	C1-N3	3.83	1.43	1.37
1	A	15	4NU	CA3-N3	-2.35	1.42	1.47

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	4NU	C2-N3-C1	-6.07	105.26	108.07
1	B	15	4NU	CB2-CG2-CD2	4.69	123.58	111.69
1	A	15	4NU	O2-C2-CA2	4.35	133.80	131.02
1	A	15	4NU	CB2-CG2-CD1	3.93	121.66	111.69
1	B	15	4NU	C3-CA3-N3	3.81	121.10	112.43
1	A	15	4NU	C2-N3-C1	-3.77	106.32	108.07
1	A	15	4NU	CZ-CE2-CL2	3.63	118.75	115.82
1	A	15	4NU	C2-CA2-N2	3.43	111.41	108.95
1	A	15	4NU	CB2-CG2-CD2	3.33	120.14	111.69
1	B	15	4NU	CB2-CG2-CD1	3.32	120.13	111.69
1	A	15	4NU	C3-CA3-N3	3.19	119.68	112.43
1	A	15	4NU	C1-CA1-N1	-3.15	104.14	109.78
1	A	15	4NU	O3-C3-CA3	-2.68	113.40	125.47
1	A	15	4NU	N3-C1-N2	2.57	113.51	111.48
1	B	15	4NU	N3-C1-N2	2.56	113.50	111.48
1	B	15	4NU	O2-C2-CA2	-2.53	129.40	131.02
1	B	15	4NU	CA3-N3-C2	2.34	128.82	123.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	4NU	C1-CA1-N1	-2.34	105.59	109.78
1	A	15	4NU	CB2-CA2-C2	-2.17	119.57	122.48
1	B	15	4NU	CA1-C1-N3	-2.16	122.13	124.69
1	B	15	4NU	CB2-CA2-C2	-2.13	119.63	122.48
1	A	15	4NU	CA1-C1-N3	-2.08	122.23	124.69
1	A	15	4NU	O4-CZ-CE2	2.02	124.79	122.70

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	15	4NU	CA2-CB2-CG2-CD1
1	B	15	4NU	CA2-CB2-CG2-CD1
1	A	15	4NU	CA2-CB2-CG2-CD2
1	B	15	4NU	CA2-CB2-CG2-CD2
1	B	15	4NU	N2-C1-CA1-CB1
1	B	15	4NU	N3-C1-CA1-CB1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	15	4NU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	224/252 (88%)	0.35	9 (4%) 42 46	12, 21, 36, 46	1 (0%)
1	B	216/252 (85%)	1.19	38 (17%) 4 3	18, 34, 51, 62	0
All	All	440/504 (87%)	0.76	47 (10%) 11 11	12, 27, 49, 62	1 (0%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	GLY	8.3
1	B	197	GLY	4.7
1	A	194	ALA	4.0
1	B	101	TYR	4.0
1	B	162	ASN	3.9
1	B	138	ILE	3.6
1	B	161	PRO	3.5
1	B	145	LEU	3.5
1	B	84	GLY	3.4
1	B	80	PHE	3.3
1	B	105	ASP	3.3
1	B	106	LYS	2.9
1	A	95	PHE	2.8
1	B	83	ASP	2.8
1	B	232	ILE	2.8
1	B	113	ALA	2.8
1	A	94	ASN	2.7
1	B	107	GLN	2.6
1	A	162	ASN	2.6
1	B	40	GLU	2.6
1	B	132	TYR	2.6
1	A	109	ASN	2.6
1	A	141	GLY	2.5
1	B	139	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	178	GLY	2.5
1	B	116	THR	2.5
1	A	98	ASP	2.4
1	B	215	VAL	2.4
1	B	27	HIS	2.4
1	B	178	GLY	2.3
1	B	68	THR	2.3
1	B	160	ASP	2.3
1	B	177	ALA	2.3
1	B	217	GLY	2.3
1	B	26	ASP	2.3
1	B	216	ASN	2.3
1	B	126	VAL	2.3
1	B	104	ALA	2.2
1	B	1	GLY	2.2
1	B	220	PHE	2.2
1	B	78	THR	2.2
1	B	98	ASP	2.1
1	B	43	VAL	2.1
1	B	28	MET	2.1
1	B	218	HIS	2.1
1	B	108	LYS	2.1
1	B	77	GLY	2.0

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

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
1	4NU	B	15	24/25	0.91	0.09	16,25,32,41	0
1	4NU	A	15	24/25	0.92	0.08	10,14,22,35	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.