



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:12 PM UTC

PDB ID : 5IJT / pdb_00005ijt
Title : Human Peroxiredoxin 2 Oxidized (SS)
Authors : Haynes, A.C.; Bolduc, J.A.; Lowther, W.T.
Deposited on : 2016-03-02
Resolution : 2.15 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

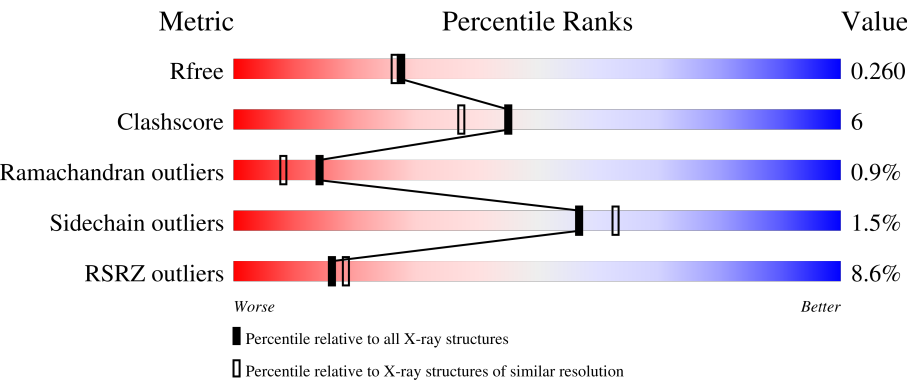
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	198	9% 69% 13% 18%
1	B	198	6% 72% 12% • 14%
1	C	198	13% 65% 13% • 21%
1	D	198	7% 69% 11% • 20%
1	E	198	7% 81% 9% 10%

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Mol	Chain	Length	Quality of chain
1	F	198	4% 79% 10% • 11%
1	G	198	4% 72% 9% • 17%
1	H	198	4% 72% 11% • 16%
1	I	198	14% 68% 20% 13%
1	J	198	7% 74% 14% • 11%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 26406 atoms, of which 13166 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 Peroxiredoxin-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	162	Total	C	H	N	O	S	0	0	0
			2549	820	1281	214	232	2			
1	B	171	Total	C	H	N	O	S	0	0	0
			2674	862	1343	225	241	3			
1	C	157	Total	C	H	N	O	S	0	0	0
			2466	795	1236	206	227	2			
1	D	158	Total	C	H	N	O	S	0	0	0
			2489	803	1250	207	227	2			
1	E	178	Total	C	H	N	O	S	0	0	0
			2762	891	1377	234	257	3			
1	F	177	Total	C	H	N	O	S	0	0	0
			2750	887	1373	233	254	3			
1	G	164	Total	C	H	N	O	S	0	0	0
			2576	829	1291	216	238	2			
1	H	167	Total	C	H	N	O	S	0	0	0
			2610	842	1304	218	243	3			
1	I	173	Total	C	H	N	O	S	0	0	0
			2692	871	1343	226	249	3			
1	J	176	Total	C	H	N	O	S	0	0	0
			2739	884	1368	232	252	3			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	F	2	Total	Zn	0	0
			2	2		
2	H	1	Total	Zn	0	0
			1	1		

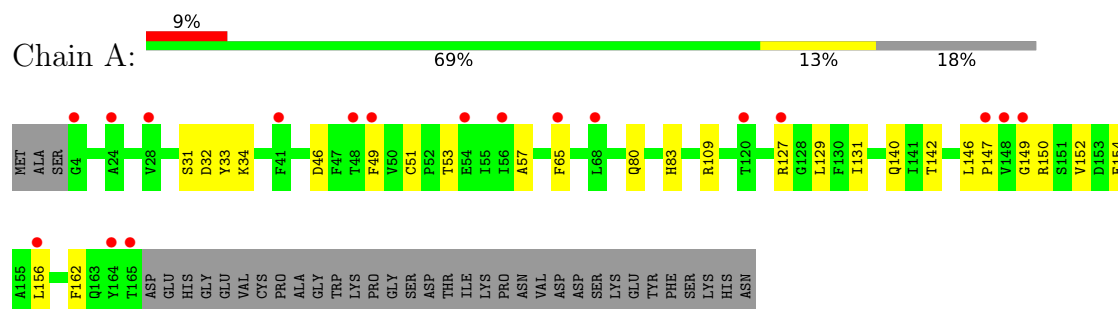
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	O 1	0	0
3	B	16	Total 16	O 16	0	0
3	D	5	Total 5	O 5	0	0
3	E	17	Total 17	O 17	0	0
3	F	15	Total 15	O 15	0	0
3	G	5	Total 5	O 5	0	0
3	H	16	Total 16	O 16	0	0
3	I	9	Total 9	O 9	0	0
3	J	11	Total 11	O 11	0	0

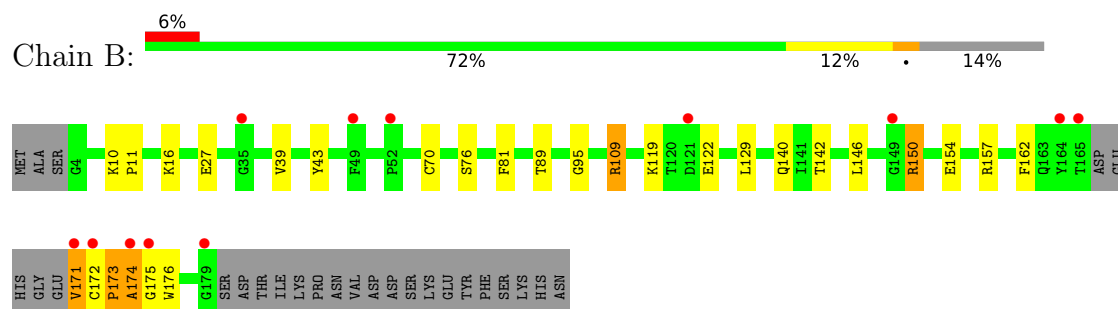
3 Residue-property plots [i](#)

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.

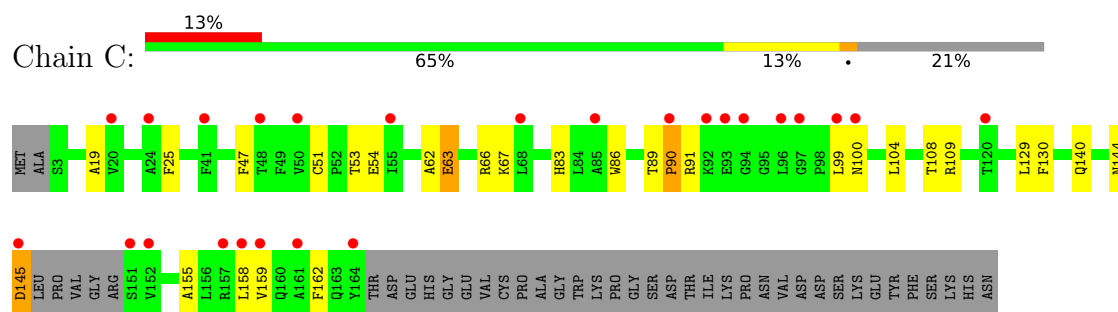
• Molecule 1: Peroxiredoxin-2



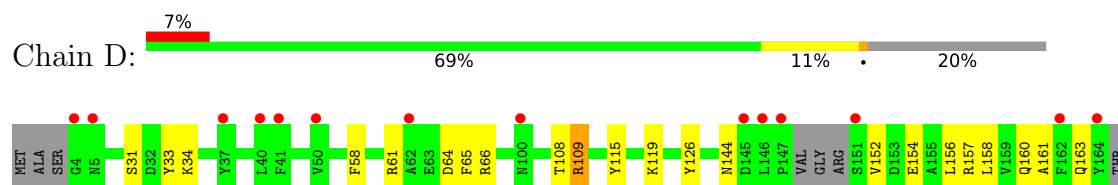
• Molecule 1: Peroxiredoxin-2



• Molecule 1: Peroxiredoxin-2

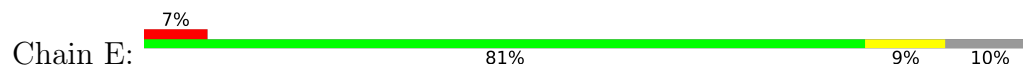


• Molecule 1: Peroxiredoxin-2



ASP GLU HIS GLY VAL CYS PRO GLY TRP LYS PRO GLY SER ASP THR ILE LYS PRO ASN VAL ASP ASP SER LYS GLU TYR PHE SER LYS HIS ASN

• Molecule 1: Peroxiredoxin-2



MET ALA SER G4 G23 L30 K36 Y43 T48 C51 A57 Y72 S76 T108 R109 T120 Y126 L129 G134 D145 R150 S151 V152 A155 V159 E167 H168 V171 C172 P173 A174 G175 W176 G179 S180 D181 THR ILE LYS

PRO ASN VAL ASP SER LYS TYR PHE SER LYS HIS ASN

• Molecule 1: Peroxiredoxin-2



MET ALA SER G4 V21 D22 G23 A24 V39 P44 C51 P52 I56 A57 C70 R91 R109 D133 L146 P147 V148 G149 R150 S151 V152 T165 D166 E167 V171 P173 S180 ASP THR ILE LYS PRO ASN VAL ASP SER LYS GLU TYR PHE SER

LYS HIS ASN

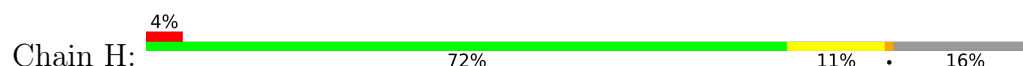
• Molecule 1: Peroxiredoxin-2



MET ALA SER G4 A19 K36 V39 Y43 F49 Y50 I55 S59 F65 C70 S76 R92 N100 L104 R110 D114 G134 Q140 T141 T142 V148 G149 R150 S151 E154 A155 L156 V159 E167 HIS GLY GLU VAL CYS PRO

ALA GLY TRP LYS PRO GLY SER THR ILE LYS PRO ASN VAL ASP ASP SER LYS TYR PHE SER LYS HIS ASN

• Molecule 1: Peroxiredoxin-2



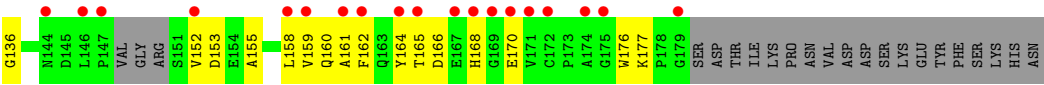
MET ALA SER G4 P44 T48 F49 A57 E63 R66 E71 Y88 E93 L104 R109 K119 T120 D121 Y126 D133 R139 N144 P147 V148 ARG S151 V152 A161 T165 H168 G169 E170 V171 C172 PRO ALA GLY TRP LYS PRO

GLY SER THR ASP ILE LYS PRO ASN VAL ASP ASP SER LYS GLU TYR PHE SER LYS HIS ASN

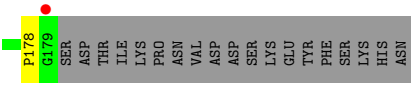
• Molecule 1: Peroxiredoxin-2



MET ALA SER G4 P11 F15 D22 K29 I30 S31 D32 Y33 Y37 P44 L45 D46 F47 Y50 T53 E54 T55 T56 A57 R61 D64 L68 D78 H83 W86 E93 L104 E113 L118 D121 R127 G128 L129 D133



● Molecule 1: Peroxiredoxin-2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.01Å 198.78Å 116.52Å 90.00° 96.28° 90.00°	Depositor
Resolution (Å)	44.46 – 2.15 44.46 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.46-2.15) 94.0 (44.46-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.207 , 0.257 0.212 , 0.260	Depositor DCC
R_{free} test set	3612 reflections (2.94%)	wwPDB-VP
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.627	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	26406	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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

5.1 Standard geometry

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

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	0.53	0/1295	0.64	0/1755
1	B	0.79	0/1361	0.81	0/1845
1	C	0.54	0/1255	0.67	0/1698
1	D	0.67	1/1265 (0.1%)	0.79	1/1713 (0.1%)
1	E	0.77	0/1417	0.82	0/1922
1	F	0.88	0/1409	0.89	1/1911 (0.1%)
1	G	0.69	0/1312	0.78	0/1778
1	H	0.85	0/1333	0.88	0/1806
1	I	0.65	0/1380	0.70	0/1871
1	J	0.72	0/1403	0.79	0/1903
All	All	0.72	1/13430 (0.0%)	0.78	2/18202 (0.0%)

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 outliers	#Planarity outliers
1	H	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	109	ARG	CB-CG	5.02	1.67	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	109	ARG	NE-CZ-NH1	5.09	126.59	121.50
1	D	115	TYR	CA-CB-CG	-5.03	104.84	113.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	H	151	SER	Peptide

5.2 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 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	1268	1281	1280	21	0
1	B	1331	1343	1341	24	0
1	C	1230	1236	1235	19	0
1	D	1239	1250	1248	16	0
1	E	1385	1377	1376	16	0
1	F	1377	1373	1372	15	0
1	G	1285	1291	1290	14	0
1	H	1306	1304	1303	11	1
1	I	1349	1343	1341	20	1
1	J	1371	1368	1367	20	0
2	B	1	0	0	0	1
2	F	2	0	0	0	1
2	H	1	0	0	0	0
3	A	1	0	0	0	0
3	B	16	0	0	0	0
3	D	5	0	0	1	0
3	E	17	0	0	0	0
3	F	15	0	0	0	0
3	G	5	0	0	0	0
3	H	16	0	0	1	0
3	I	9	0	0	1	0
3	J	11	0	0	0	0
All	All	13240	13166	13153	155	2

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 6.

The worst 5 of 155 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:154:GLU:OE2	1:B:150:ARG:NH2	2.02	0.94
1:G:19:ALA:HB2	1:G:104:LEU:HD23	1.63	0.79
1:B:109:ARG:NH1	1:E:109:ARG:HD3	1.99	0.77
1:B:154:GLU:OE2	1:B:157:ARG:NH2	2.23	0.70
1:B:119:LYS:NZ	1:B:122:GLU:OE2	2.19	0.66

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:93:GLU:OE2	2:F:202:ZN:ZN[2_455]	1.56	0.64
1:H:168:HIS:HE2	2:B:201:ZN:ZN[2_555]	1.17	0.43

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	160/198 (81%)	149 (93%)	10 (6%)	1 (1%)	21	15
1	B	167/198 (84%)	158 (95%)	6 (4%)	3 (2%)	6	2
1	C	153/198 (77%)	141 (92%)	11 (7%)	1 (1%)	18	13
1	D	154/198 (78%)	140 (91%)	14 (9%)	0	100	100
1	E	176/198 (89%)	170 (97%)	6 (3%)	0	100	100
1	F	175/198 (88%)	168 (96%)	6 (3%)	1 (1%)	21	15
1	G	162/198 (82%)	154 (95%)	6 (4%)	2 (1%)	10	5
1	H	163/198 (82%)	156 (96%)	5 (3%)	2 (1%)	10	5
1	I	169/198 (85%)	159 (94%)	7 (4%)	3 (2%)	6	2
1	J	174/198 (88%)	163 (94%)	9 (5%)	2 (1%)	11	6
All	All	1653/1980 (84%)	1558 (94%)	80 (5%)	15 (1%)	14	8

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	174	ALA
1	C	90	PRO
1	G	150	ARG
1	J	168	HIS
1	B	175	GLY

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	135/166 (81%)	133 (98%)	2 (2%)	57	63
1	B	141/166 (85%)	138 (98%)	3 (2%)	47	51
1	C	131/166 (79%)	127 (97%)	4 (3%)	35	35
1	D	132/166 (80%)	131 (99%)	1 (1%)	73	79
1	E	147/166 (89%)	147 (100%)	0	100	100
1	F	146/166 (88%)	144 (99%)	2 (1%)	59	65
1	G	137/166 (82%)	135 (98%)	2 (2%)	57	63
1	H	140/166 (84%)	136 (97%)	4 (3%)	37	38
1	I	143/166 (86%)	142 (99%)	1 (1%)	76	81
1	J	145/166 (87%)	143 (99%)	2 (1%)	59	65
All	All	1397/1660 (84%)	1376 (98%)	21 (2%)	57	63

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	63	GLU
1	H	144	ASN
1	J	151	SER
1	I	121	ASP
1	H	104	LEU

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

Mol	Chain	Res	Type
1	C	5	ASN
1	C	163	GLN
1	D	163	GLN
1	E	140	GLN
1	F	144	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 4 ligands modelled in this entry, 4 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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	162/198 (81%)	1.03	18 (11%)	10 12	60, 89, 119, 133	0
1	B	171/198 (86%)	0.48	12 (7%)	22 26	42, 63, 108, 142	0
1	C	157/198 (79%)	1.23	25 (15%)	5 6	59, 90, 128, 151	0
1	D	158/198 (79%)	0.77	14 (8%)	15 17	47, 76, 113, 144	0
1	E	178/198 (89%)	0.88	13 (7%)	21 24	45, 71, 117, 157	0
1	F	177/198 (89%)	0.40	8 (4%)	38 43	41, 65, 100, 125	0
1	G	164/198 (82%)	0.61	7 (4%)	40 45	46, 70, 109, 163	0
1	H	167/198 (84%)	0.45	7 (4%)	40 46	42, 62, 101, 126	0
1	I	173/198 (87%)	1.05	28 (16%)	4 6	49, 88, 138, 229	0
1	J	176/198 (88%)	0.58	13 (7%)	20 24	47, 69, 120, 145	0
All	All	1683/1980 (85%)	0.74	145 (8%)	16 18	41, 74, 118, 229	0

The worst 5 of 145 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	171	VAL	7.0
1	G	50	VAL	5.8
1	H	148	VAL	5.4
1	C	164	TYR	5.4
1	I	164	TYR	5.4

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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($\text{\AA}^2$)	Q<0.9
2	ZN	F	202	1/1	0.93	0.18	120,120,120,120	0
2	ZN	F	201	1/1	0.95	0.07	102,102,102,102	0
2	ZN	H	201	1/1	0.96	0.14	147,147,147,147	0
2	ZN	B	201	1/1	0.98	0.04	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.