



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 07:57 PM UTC

PDB ID : 7KQY / pdb_00007kqy
Title : Crystal Structure and Characterization of Human Heavy-Chain only Antibodies reveals a novel, stable dimeric structure similar to Monoclonal Antibodies
Authors : Bahmanjah, S.; Mieczkowski, C.; Yu, Y.; Baker, J.; Raghunathan, G.; Tomazela, D.; Hsieh, M.; McCoy, M.; Strickland, C.; Fayadat-Dilman, L.
Deposited on : 2020-11-18
Resolution : 2.91 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

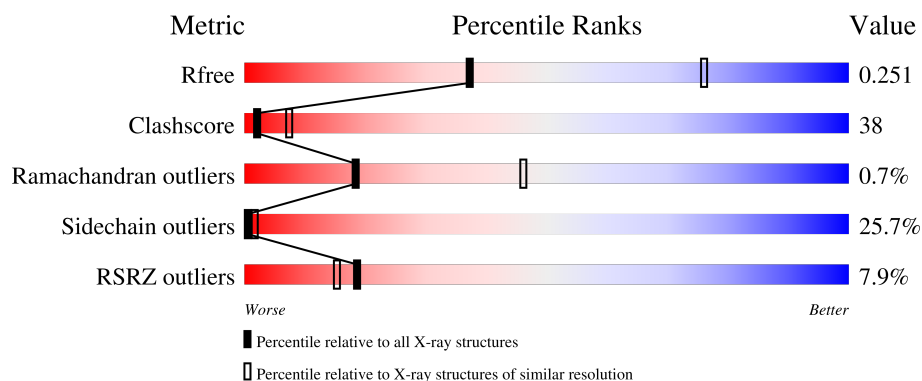
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.91 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	2995 (2.94-2.90)
Clashscore	190562	3213 (2.94-2.90)
Ramachandran outliers	187476	3128 (2.94-2.90)
Sidechain outliers	187428	3130 (2.94-2.90)
RSRZ outliers	180081	2995 (2.94-2.90)

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	448	
1	B	448	
1	C	448	
1	D	448	
1	E	448	

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Mol	Chain	Length	Quality of chain
1	F	448	4%14%19%11%54%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9265 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.

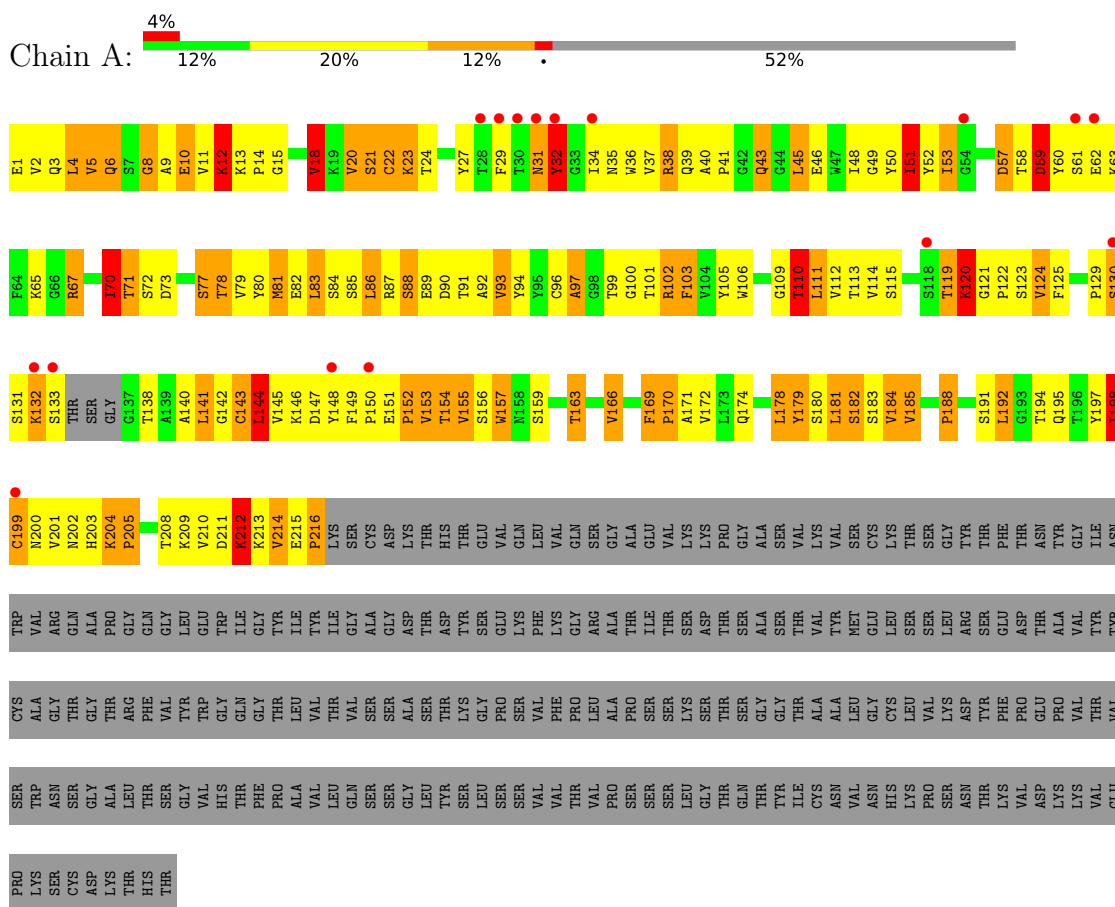
- Molecule 1 is a protein called Heavy-Chain only Human Antibodies.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	0	0
			1588	1006	259	318	5			
1	B	203	Total	C	N	O	S	0	0	0
			1504	953	244	302	5			
1	C	202	Total	C	N	O	S	0	0	0
			1508	959	246	298	5			
1	D	207	Total	C	N	O	S	0	0	0
			1542	981	249	307	5			
1	E	216	Total	C	N	O	S	0	0	0
			1605	1015	262	323	5			
1	F	204	Total	C	N	O	S	0	0	0
			1518	962	248	303	5			

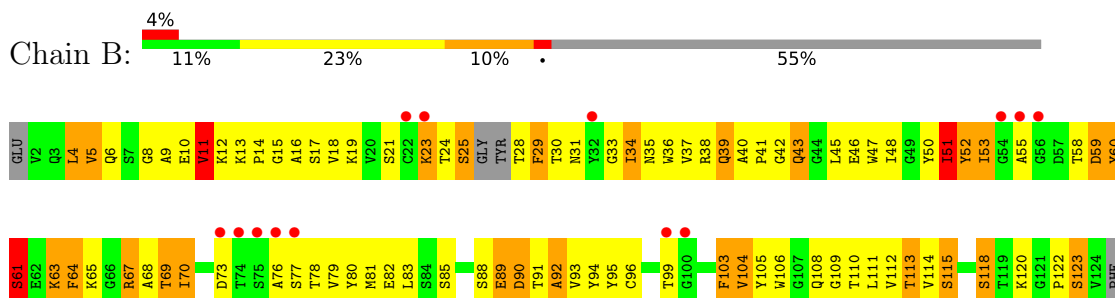
3 Residue-property plots [i](#)

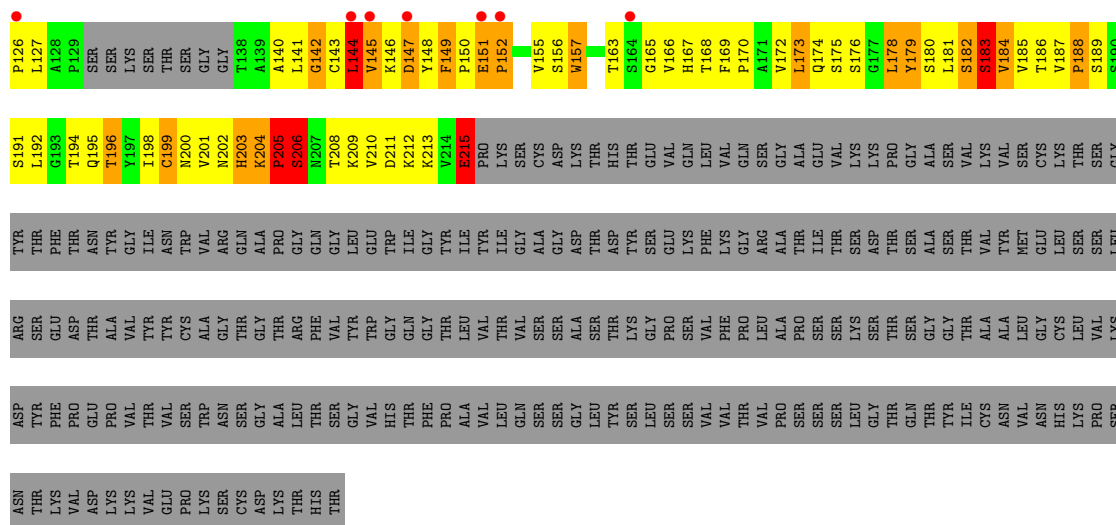
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Heavy-Chain only Human Antibodies

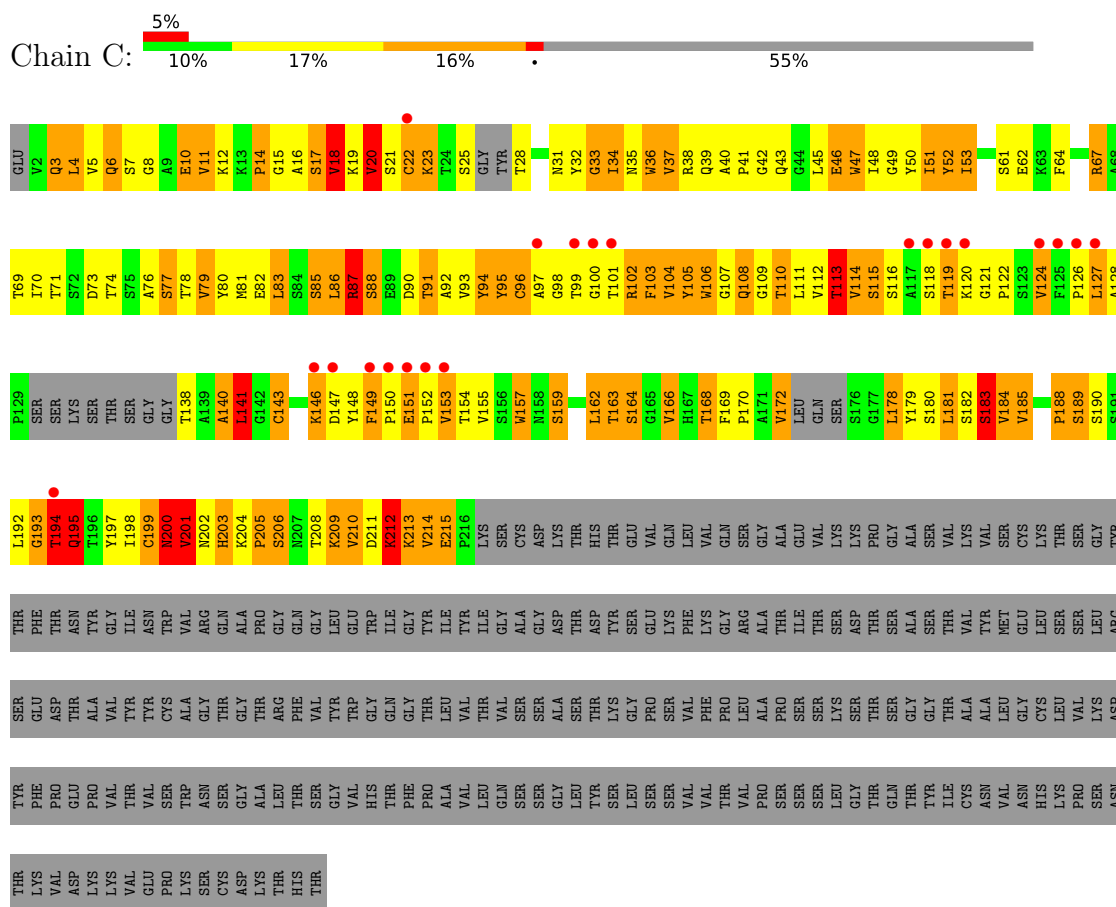


• Molecule 1: Heavy-Chain only Human Antibodies

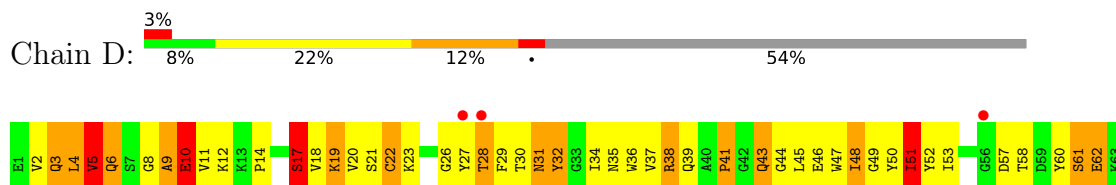




● Molecule 1: Heavy-Chain only Human Antibodies



● Molecule 1: Heavy-Chain only Human Antibodies





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.62Å 73.42Å 140.41Å 90.00° 125.71° 90.00°	Depositor
Resolution (Å)	114.01 – 2.91 114.01 – 2.91	Depositor EDS
% Data completeness (in resolution range)	73.4 (114.01-2.91) 73.5 (114.01-2.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, R_{free}	0.207 , 0.260 (Not available) , 0.251	Depositor DCC
R_{free} test set	1082 reflections (3.49%)	wwPDB-VP
Wilson B-factor (Å ²)	54.5	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 58.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.009 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	9265	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.71% 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

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	2.19	103/1625 (6.3%)	1.63	19/2215 (0.9%)
1	B	2.27	109/1536 (7.1%)	1.70	21/2094 (1.0%)
1	C	2.09	81/1542 (5.3%)	1.66	12/2102 (0.6%)
1	D	2.36	111/1578 (7.0%)	1.83	24/2152 (1.1%)
1	E	2.10	83/1643 (5.1%)	1.71	24/2241 (1.1%)
1	F	1.95	63/1552 (4.1%)	1.59	12/2115 (0.6%)
All	All	2.16	550/9476 (5.8%)	1.69	112/12919 (0.9%)

The worst 5 of 550 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	126	PRO	C-O	-10.80	1.13	1.23
1	E	210	VAL	C-O	-10.08	1.12	1.24
1	D	113	THR	C-O	-10.08	1.12	1.24
1	C	18	VAL	C-O	-10.02	1.14	1.24
1	B	41	PRO	C-O	-9.99	1.16	1.24

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	152	PRO	N-CD-CG	-11.01	90.59	103.80
1	D	148	TYR	CA-C-O	-10.61	110.12	121.36
1	D	104	VAL	CA-C-N	10.09	139.44	121.89
1	D	104	VAL	C-N-CA	10.09	139.44	121.89
1	A	110	THR	CB-CA-C	10.07	127.15	109.72

There are no chirality outliers.

There are no planarity outliers.

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	1588	0	1558	93	0
1	B	1504	0	1468	83	22
1	C	1508	0	1478	188	22
1	D	1542	0	1511	127	0
1	E	1605	0	1570	123	0
1	F	1518	0	1494	141	0
All	All	9265	0	9079	683	22

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 38.

The worst 5 of 683 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:F:4:LEU:CD1	1:F:107:GLY:HA3	1.19	1.57
1:F:4:LEU:HD12	1:F:107:GLY:CA	1.10	1.56
1:F:5:VAL:CG1	1:F:23:LYS:CB	1.89	1.50
1:D:200:ASN:ND2	1:D:211:ASP:CB	1.72	1.50
1:F:5:VAL:CG1	1:F:23:LYS:HB2	1.43	1.47

The worst 5 of 22 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:B:23:LYS:CE	1:C:194:THR:CB[2_546]	0.36	1.84
1:B:25:SER:C	1:C:195:GLN:OE1[2_546]	0.50	1.70
1:B:23:LYS:NZ	1:C:194:THR:CA[2_546]	0.62	1.58
1:B:23:LYS:CD	1:C:194:THR:CG2[2_546]	0.73	1.47
1:B:23:LYS:NZ	1:C:194:THR:N[2_546]	0.99	1.21

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	209/448 (47%)	198 (95%)	10 (5%)	1 (0%)	24	53
1	B	195/448 (44%)	187 (96%)	8 (4%)	0	100	100
1	C	194/448 (43%)	180 (93%)	12 (6%)	2 (1%)	12	37
1	D	201/448 (45%)	183 (91%)	16 (8%)	2 (1%)	12	37
1	E	214/448 (48%)	198 (92%)	13 (6%)	3 (1%)	9	29
1	F	198/448 (44%)	182 (92%)	15 (8%)	1 (0%)	24	53
All	All	1211/2688 (45%)	1128 (93%)	74 (6%)	9 (1%)	18	46

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	147	ASP
1	D	30	THR
1	E	135	SER
1	A	131	SER
1	E	136	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	178/376 (47%)	129 (72%)	49 (28%)	0	1
1	B	168/376 (45%)	137 (82%)	31 (18%)	1	5
1	C	168/376 (45%)	107 (64%)	61 (36%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	172/376 (46%)	132 (77%)	40 (23%)	1	2
1	E	180/376 (48%)	140 (78%)	40 (22%)	1	3
1	F	170/376 (45%)	125 (74%)	45 (26%)	0	1
All	All	1036/2256 (46%)	770 (74%)	266 (26%)	0	2

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	32	TYR
1	F	61	SER
1	F	196	THR
1	C	88	SER
1	C	74	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	31	ASN
1	E	108	GLN
1	F	202	ASN
1	F	167	HIS
1	F	200	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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 [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	213/448 (47%)	0.39	16 (7%)	20 16	10, 32, 61, 76	0
1	B	203/448 (45%)	0.36	20 (9%)	13 11	14, 31, 57, 72	0
1	C	202/448 (45%)	0.67	21 (10%)	11 10	18, 45, 71, 100	0
1	D	207/448 (46%)	0.38	13 (6%)	26 20	14, 35, 79, 110	0
1	E	216/448 (48%)	0.46	9 (4%)	40 32	26, 43, 71, 90	0
1	F	204/448 (45%)	0.61	19 (9%)	14 12	25, 47, 75, 86	0
All	All	1245/2688 (46%)	0.48	98 (7%)	18 15	10, 39, 71, 110	0

The worst 5 of 98 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	152	PRO	6.0
1	A	28	THR	5.7
1	D	200	ASN	5.4
1	C	147	ASP	5.2
1	D	150	PRO	5.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.