



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:23 PM UTC

PDB ID : 6XUL / pdb_00006xul
Title : Apo Ab 5b1
Authors : Diskin, R.; Borenstein-Katz, A.
Deposited on : 2020-01-20
Resolution : 2.41 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

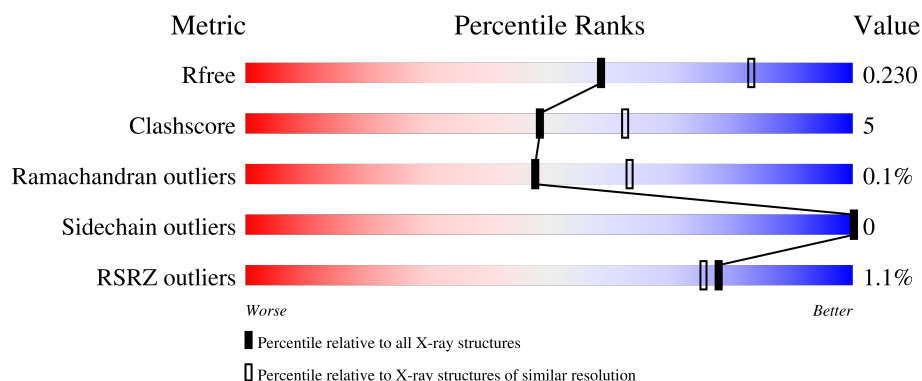
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

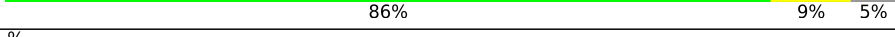
The reported resolution of this entry is 2.41 Å.

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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	230	
1	C	230	
1	E	230	
1	G	230	
1	H	230	

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Mol	Chain	Length	Quality of chain
1	J	230	% 83%11%5%
2	B	218	89%11%
2	D	218	87%12%
2	F	218	% 89%11%
2	I	218	87%13%
2	K	218	84%16%
2	L	218	% 87%12%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20926 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	1	0
			1665	1051	288	319	7			
1	C	218	Total	C	N	O	S	0	1	0
			1665	1051	288	319	7			
1	E	218	Total	C	N	O	S	0	1	0
			1665	1051	288	319	7			
1	G	219	Total	C	N	O	S	0	0	0
			1668	1052	289	321	6			
1	J	218	Total	C	N	O	S	0	1	0
			1665	1051	288	319	7			
1	H	218	Total	C	N	O	S	0	1	0
			1665	1051	288	319	7			

- Molecule 2 is a protein called Light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	217	Total	C	N	O	S	0	1	0
			1651	1026	284	336	5			
2	D	217	Total	C	N	O	S	0	1	0
			1651	1026	284	336	5			
2	F	217	Total	C	N	O	S	0	1	0
			1651	1026	284	336	5			
2	I	217	Total	C	N	O	S	0	2	0
			1659	1031	287	336	5			
2	K	217	Total	C	N	O	S	0	0	0
			1648	1024	284	336	4			
2	L	217	Total	C	N	O	S	0	1	0
			1651	1026	284	336	5			

- Molecule 3 is water.

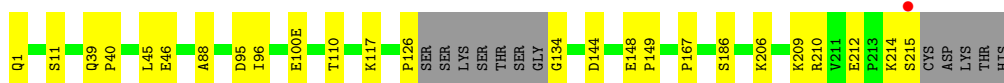
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total 138	O 138	0	0
3	B	130	Total 130	O 130	0	0
3	C	103	Total 103	O 103	0	0
3	D	54	Total 54	O 54	0	0
3	E	98	Total 98	O 98	0	0
3	F	62	Total 62	O 62	0	0
3	G	125	Total 125	O 125	0	0
3	I	89	Total 89	O 89	0	0
3	J	85	Total 85	O 85	0	0
3	K	35	Total 35	O 35	0	0
3	H	62	Total 62	O 62	0	0
3	L	41	Total 41	O 41	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.

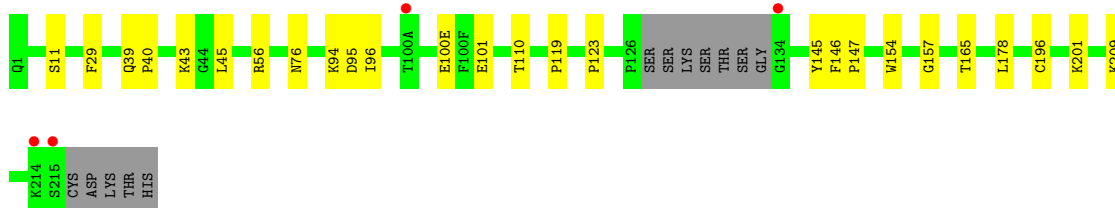
- Molecule 1: Heavy chain

Chain A: 



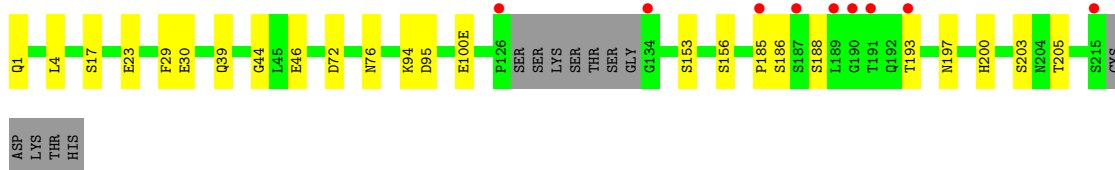
- Molecule 1: Heavy chain

Chain C: 



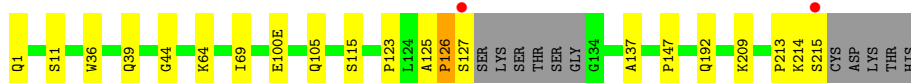
- Molecule 1: Heavy chain

Chain E: 

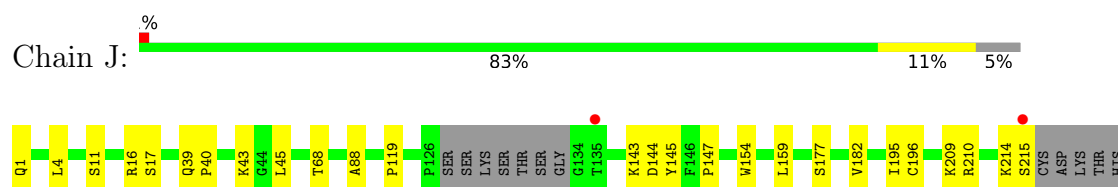


- Molecule 1: Heavy chain

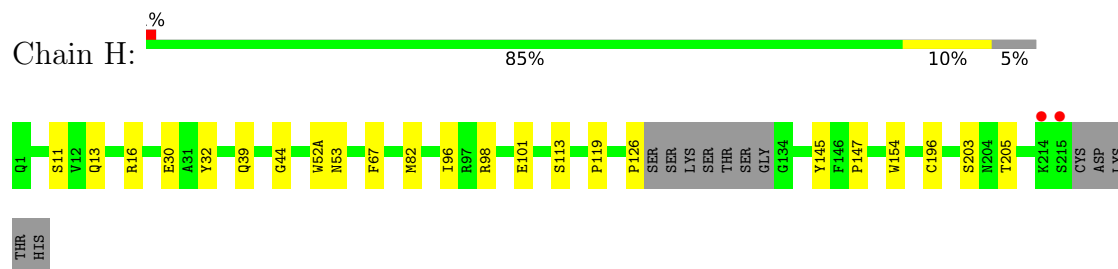
Chain G: 



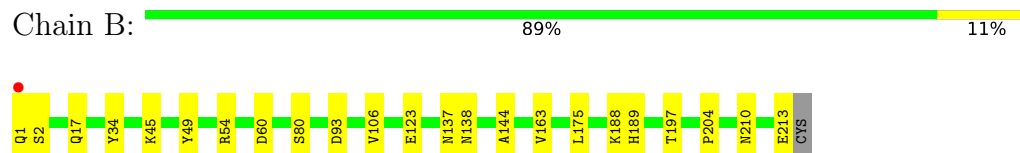
- Molecule 1: Heavy chain



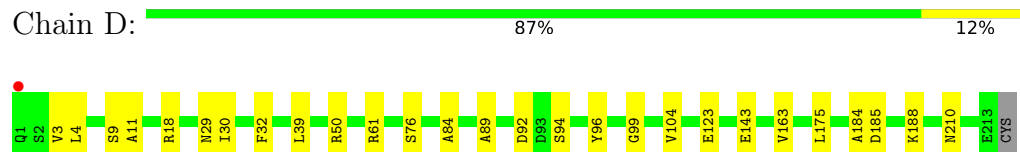
- Molecule 1: Heavy chain



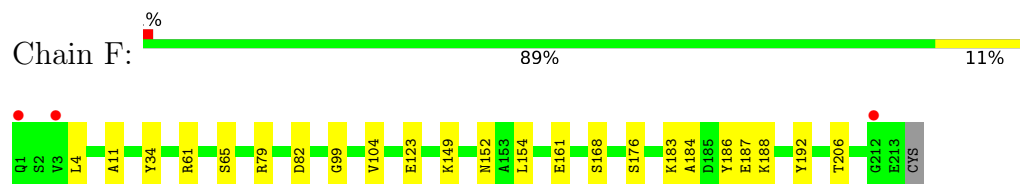
- Molecule 2: Light chain



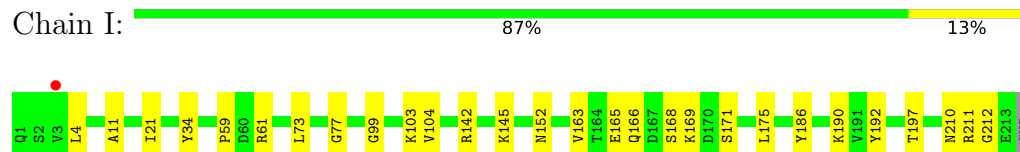
- Molecule 2: Light chain



- Molecule 2: Light chain

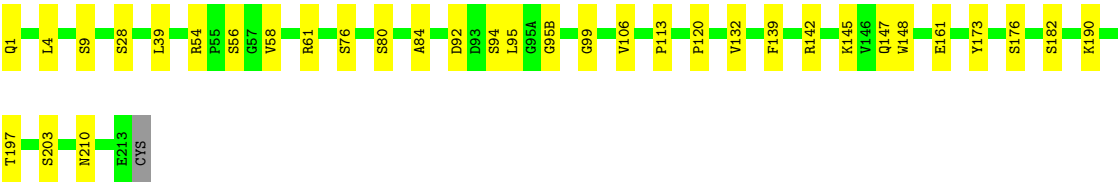


- Molecule 2: Light chain

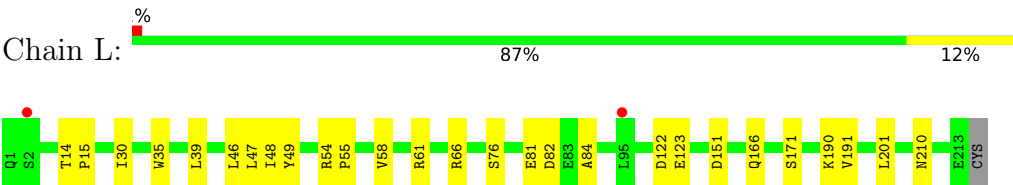


- Molecule 2: Light chain





• Molecule 2: Light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	155.02Å 155.02Å 121.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.88 – 2.41 47.88 – 2.41	Depositor EDS
% Data completeness (in resolution range)	99.7 (47.88-2.41) 99.7 (47.88-2.41)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.36 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.168 , 0.230 0.168 , 0.230	Depositor DCC
R_{free} test set	1976 reflections (1.56%)	wwPDB-VP
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l 0.032 for h,-h-k,-l 0.017 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20926	wwPDB-VP
Average B, all atoms (Å ²)	49.0	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 51.67 % 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 5.4292e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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	0.39	0/1709	0.57	0/2323
1	C	0.35	0/1709	0.54	0/2323
1	E	0.35	0/1709	0.56	0/2323
1	G	0.36	0/1709	0.58	0/2323
1	H	0.33	0/1709	0.54	0/2323
1	J	0.33	0/1709	0.52	0/2323
2	B	0.34	0/1691	0.56	0/2300
2	D	0.31	0/1691	0.49	0/2300
2	F	0.32	0/1691	0.53	0/2300
2	I	0.33	0/1702	0.53	0/2314
2	K	0.30	0/1685	0.48	0/2292
2	L	0.28	0/1691	0.51	0/2300
All	All	0.33	0/20405	0.54	0/27744

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	1665	0	1624	22	0
1	C	1665	0	1624	20	0
1	E	1665	0	1624	18	0
1	G	1668	0	1625	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	1665	0	1624	19	0
1	J	1665	0	1624	18	0
2	B	1651	0	1588	17	0
2	D	1651	0	1588	18	0
2	F	1651	0	1588	16	0
2	I	1659	0	1601	16	0
2	K	1648	0	1584	21	0
2	L	1651	0	1588	19	0
3	A	138	0	0	7	0
3	B	130	0	0	6	0
3	C	103	0	0	5	0
3	D	54	0	0	4	0
3	E	98	0	0	7	1
3	F	62	0	0	4	0
3	G	125	0	0	9	1
3	H	62	0	0	3	0
3	I	89	0	0	2	0
3	J	85	0	0	4	0
3	K	35	0	0	6	0
3	L	41	0	0	6	0
All	All	20926	0	19282	215	1

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 5.

The worst 5 of 215 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:E:193:THR:OG1	3:E:301:HOH:O	1.85	0.92
2:F:168:SER:OG	3:F:301:HOH:O	1.88	0.91
2:L:201:LEU:O	3:L:301:HOH:O	1.88	0.90
1:C:43:LYS:O	3:C:301:HOH:O	1.93	0.86
2:B:144:ALA:O	3:B:301:HOH:O	1.95	0.85

All (1) 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)
3:E:348:HOH:O	3:G:421:HOH:O[2_545]	2.08	0.12

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	215/230 (94%)	211 (98%)	4 (2%)	0	100	100
1	C	215/230 (94%)	207 (96%)	8 (4%)	0	100	100
1	E	215/230 (94%)	205 (95%)	10 (5%)	0	100	100
1	G	215/230 (94%)	209 (97%)	5 (2%)	1 (0%)	24	35
1	H	215/230 (94%)	209 (97%)	6 (3%)	0	100	100
1	J	215/230 (94%)	209 (97%)	6 (3%)	0	100	100
2	B	216/218 (99%)	211 (98%)	5 (2%)	0	100	100
2	D	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
2	F	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
2	I	217/218 (100%)	209 (96%)	6 (3%)	2 (1%)	14	20
2	K	215/218 (99%)	207 (96%)	8 (4%)	0	100	100
2	L	216/218 (99%)	205 (95%)	11 (5%)	0	100	100
All	All	2586/2688 (96%)	2497 (97%)	86 (3%)	3 (0%)	48	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	126	PRO
2	I	77	GLY
2	I	212	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	184/194 (95%)	184 (100%)	0	100	100
1	C	184/194 (95%)	184 (100%)	0	100	100
1	E	184/194 (95%)	184 (100%)	0	100	100
1	G	184/194 (95%)	184 (100%)	0	100	100
1	H	184/194 (95%)	184 (100%)	0	100	100
1	J	184/194 (95%)	184 (100%)	0	100	100
2	B	187/187 (100%)	187 (100%)	0	100	100
2	D	187/187 (100%)	187 (100%)	0	100	100
2	F	187/187 (100%)	187 (100%)	0	100	100
2	I	188/187 (100%)	188 (100%)	0	100	100
2	K	186/187 (100%)	186 (100%)	0	100	100
2	L	187/187 (100%)	187 (100%)	0	100	100
All	All	2226/2286 (97%)	2226 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	31	ASN
1	G	192	GLN
1	G	164	HIS
2	I	137	ASN
2	B	38	GLN

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	218/230 (94%)	-0.71	1 (0%) 87 86	21, 34, 58, 94	1 (0%)
1	C	218/230 (94%)	-0.46	4 (1%) 67 64	26, 40, 84, 111	1 (0%)
1	E	218/230 (94%)	-0.28	9 (4%) 41 37	23, 43, 97, 121	1 (0%)
1	G	219/230 (95%)	-0.67	2 (0%) 81 79	24, 36, 64, 91	0
1	H	218/230 (94%)	-0.33	2 (0%) 81 79	32, 49, 82, 106	1 (0%)
1	J	218/230 (94%)	-0.31	2 (0%) 81 79	31, 48, 84, 109	1 (0%)
2	B	217/218 (99%)	-0.68	1 (0%) 87 86	26, 38, 58, 91	1 (0%)
2	D	217/218 (99%)	-0.21	1 (0%) 87 86	33, 53, 85, 100	1 (0%)
2	F	217/218 (99%)	-0.24	3 (1%) 73 70	31, 50, 81, 118	1 (0%)
2	I	217/218 (99%)	-0.58	1 (0%) 87 86	25, 41, 58, 96	2 (0%)
2	K	217/218 (99%)	0.15	0 100 100	37, 63, 83, 102	0
2	L	217/218 (99%)	-0.03	2 (0%) 81 79	35, 62, 81, 117	1 (0%)
All	All	2611/2688 (97%)	-0.36	28 (1%) 78 75	21, 46, 81, 121	11 (0%)

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	215	SER	3.0
1	E	134	GLY	2.9
2	B	1	GLN	2.9
2	L	2	SER	2.9
1	E	190	GLY	2.8

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.