



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 09:11 AM UTC

PDB ID : 6IGE / pdb_00006ige
Title : Crystal structure of Human Papillomavirus type 33 pentamer
Authors : Li, Z.H.; Song, S.; He, M.Z.; Gu, Y.; Li, S.W.
Deposited on : 2018-09-25
Resolution : 2.90 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

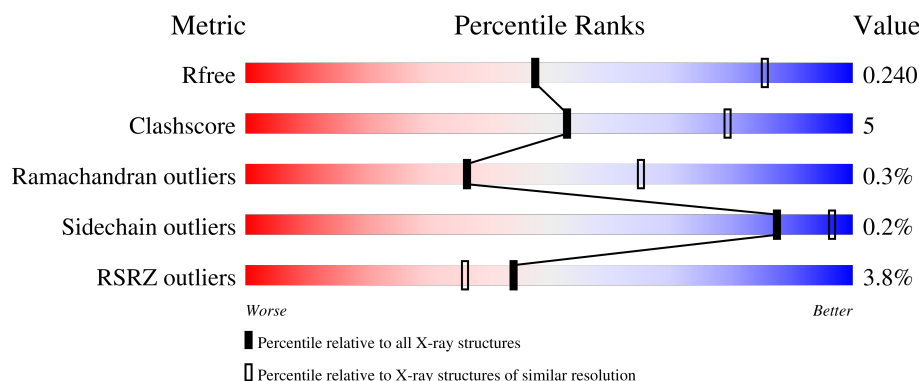
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	499	% 73% 11% 16%
1	B	499	% 71% 11% 17%
1	C	499	72% 10% 17%
1	D	499	% 72% 11% 17%
1	E	499	% 74% 11% 15%

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Mol	Chain	Length	Quality of chain
1	F	499	 14% 72% 11% 17%
1	G	499	 5% 74% 10% 16%
1	H	499	 4% 73% 11% 17%
1	I	499	 3% 72% 11% 16%
1	J	499	 2% 72% 10% 17%

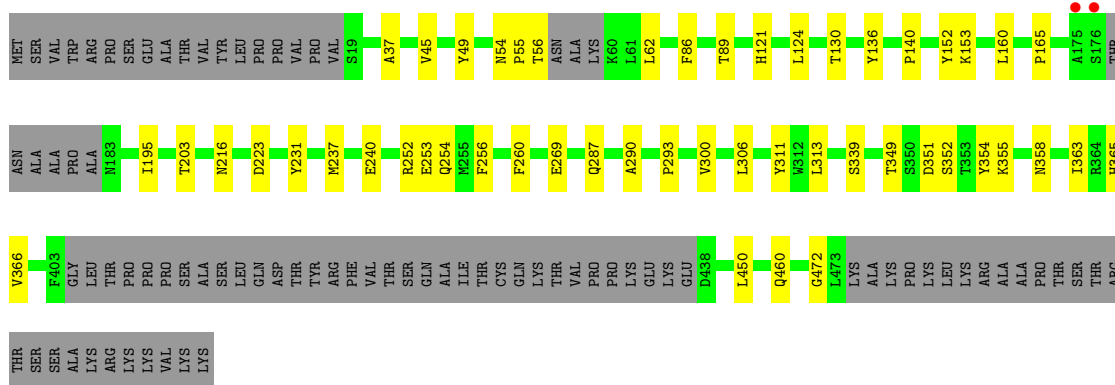
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 33023 atoms, of which 0 are hydrogens and 0 are deuteriums.

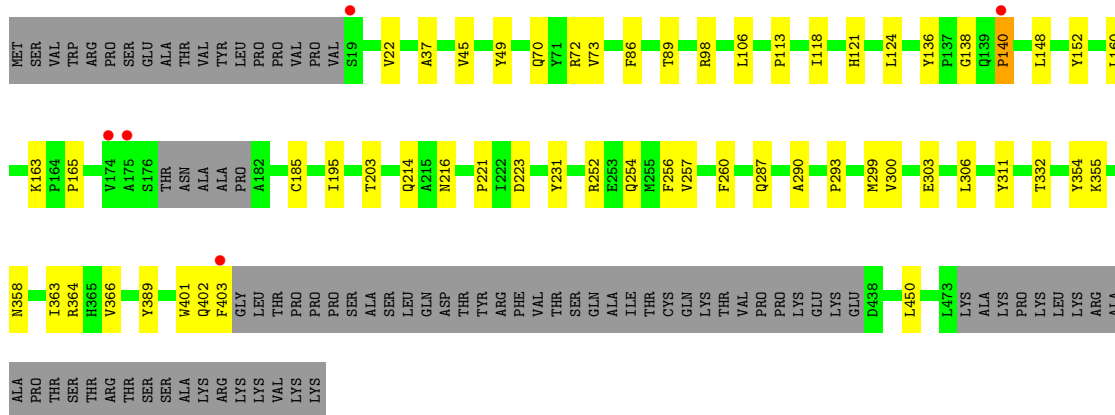
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Major capsid protein L1.

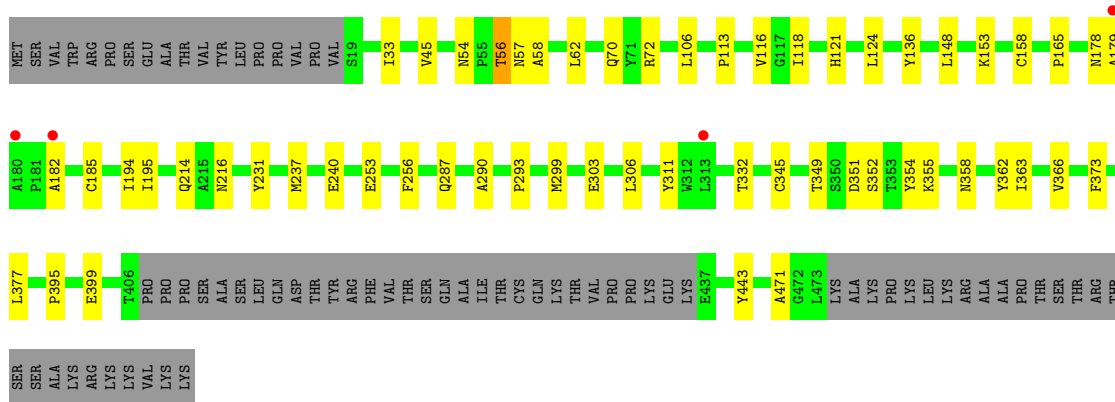
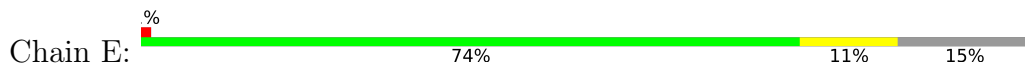
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3309	2113	548	628	20			
1	B	413	Total	C	N	O	S	0	0	0
			3280	2096	542	622	20			
1	C	412	Total	C	N	O	S	0	0	0
			3273	2092	541	620	20			
1	D	416	Total	C	N	O	S	0	0	0
			3300	2108	547	625	20			
1	E	425	Total	C	N	O	S	0	0	0
			3360	2144	557	639	20			
1	F	415	Total	C	N	O	S	0	0	0
			3296	2106	545	625	20			
1	G	417	Total	C	N	O	S	0	0	0
			3310	2115	548	627	20			
1	H	416	Total	C	N	O	S	0	0	0
			3304	2110	547	627	20			
1	I	419	Total	C	N	O	S	0	0	0
			3315	2117	549	629	20			
1	J	412	Total	C	N	O	S	0	0	0
			3276	2095	542	619	20			



- Molecule 1: Major capsid protein L1

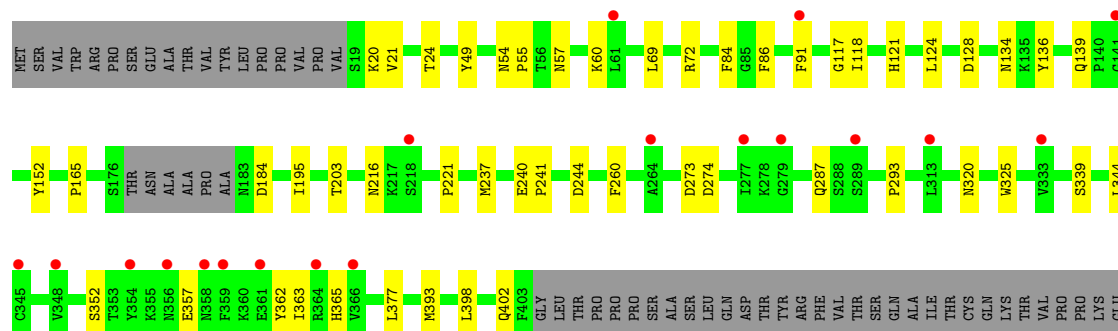


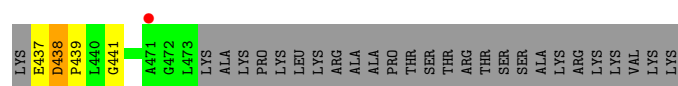
- Molecule 1: Major capsid protein L1



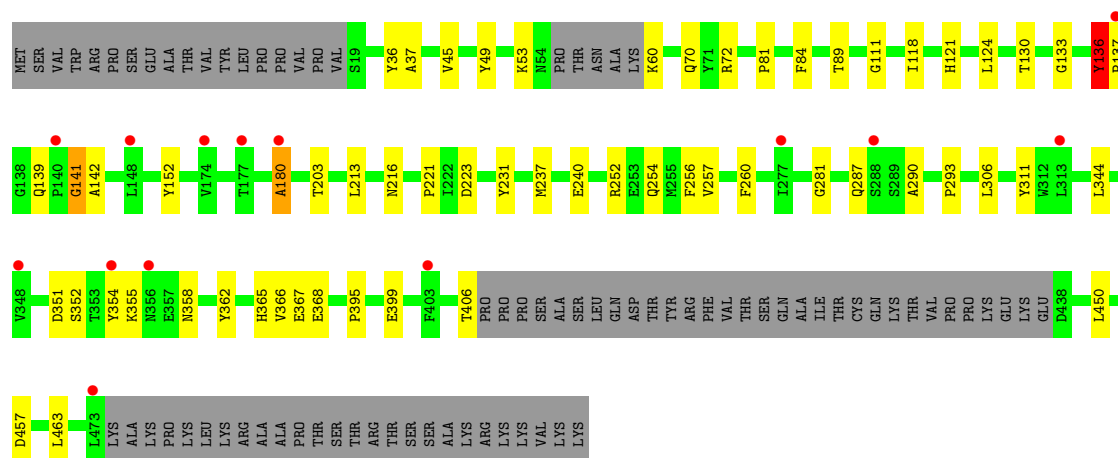
- Molecule 1: Major capsid protein L1



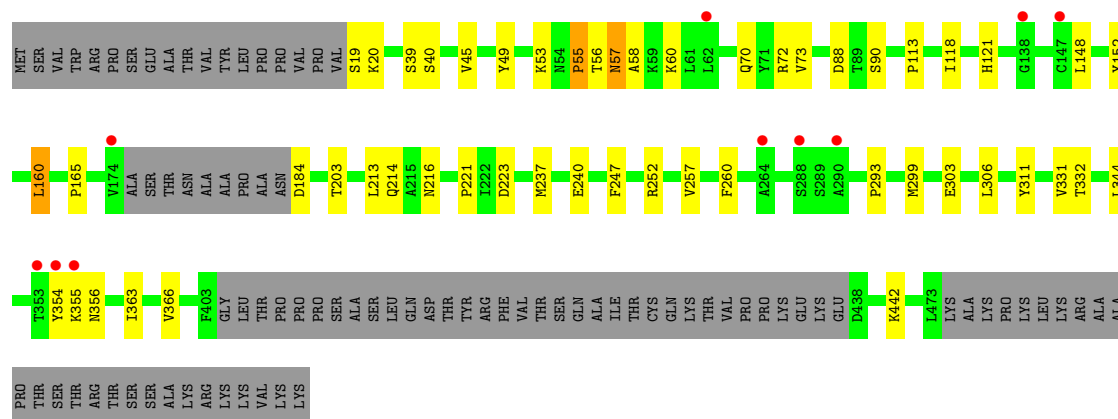




• Molecule 1: Major capsid protein L1



• Molecule 1: Major capsid protein L1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.83Å 171.94Å 145.69Å 90.00° 97.04° 90.00°	Depositor
Resolution (Å)	48.20 – 2.90 48.20 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.5 (48.20-2.90) 98.4 (48.20-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.210 , 0.240 0.211 , 0.240	Depositor DCC
R_{free} test set	5330 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	61.6	Xtriage
Anisotropy	0.490	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	33023	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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	0.14	0/3395	0.37	0/4604
1	B	0.12	0/3365	0.37	0/4562
1	C	0.12	0/3358	0.33	0/4553
1	D	0.13	0/3386	0.36	0/4592
1	E	0.14	0/3448	0.39	0/4680
1	F	0.12	0/3381	0.35	0/4583
1	G	0.15	0/3396	0.35	0/4605
1	H	0.13	0/3390	0.35	0/4597
1	I	0.15	0/3401	0.41	1/4614 (0.0%)
1	J	0.13	0/3362	0.37	0/4559
All	All	0.13	0/33882	0.37	1/45949 (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	I	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	136	TYR	N-CA-C	5.35	121.63	109.81

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	136	TYR	Peptide
1	I	180	ALA	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	3309	0	3202	38	0
1	B	3280	0	3170	44	1
1	C	3273	0	3166	39	0
1	D	3300	0	3196	45	0
1	E	3360	0	3254	45	0
1	F	3296	0	3190	43	1
1	G	3310	0	3206	38	0
1	H	3304	0	3197	40	0
1	I	3315	0	3209	45	1
1	J	3276	0	3175	45	1
All	All	33023	0	31965	324	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 5.

The worst 5 of 324 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:I:142:ALA:HB1	1:J:355:LYS:HD2	1.46	0.95
1:J:53:LYS:HG3	1:J:55:PRO:HD3	1.70	0.73
1:J:70:GLN:OE1	1:J:72:ARG:NH2	2.24	0.71
1:F:121:HIS:HB2	1:F:221:PRO:HA	1.74	0.68
1:B:306:LEU:O	1:B:311:TYR:OH	2.07	0.68

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:B:357:GLU:OE1	1:I:89:THR:OG1[1_554]	2.14	0.06
1:F:399:GLU:OE2	1:J:442:LYS:NZ[2_546]	2.16	0.04

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	411/499 (82%)	395 (96%)	15 (4%)	1 (0%)	43	72
1	B	405/499 (81%)	392 (97%)	12 (3%)	1 (0%)	43	72
1	C	404/499 (81%)	392 (97%)	11 (3%)	1 (0%)	43	72
1	D	410/499 (82%)	399 (97%)	10 (2%)	1 (0%)	43	72
1	E	421/499 (84%)	404 (96%)	17 (4%)	0	100	100
1	F	407/499 (82%)	394 (97%)	13 (3%)	0	100	100
1	G	411/499 (82%)	395 (96%)	15 (4%)	1 (0%)	43	72
1	H	410/499 (82%)	396 (97%)	12 (3%)	2 (0%)	24	54
1	I	413/499 (83%)	392 (95%)	17 (4%)	4 (1%)	12	39
1	J	406/499 (81%)	390 (96%)	14 (3%)	2 (0%)	24	54
All	All	4098/4990 (82%)	3949 (96%)	136 (3%)	13 (0%)	36	65

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	136	TYR
1	I	137	PRO
1	I	180	ALA
1	J	57	ASN
1	I	141	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	367/439 (84%)	366 (100%)	1 (0%)	86	96
1	B	364/439 (83%)	363 (100%)	1 (0%)	86	96
1	C	364/439 (83%)	364 (100%)	0	100	100
1	D	366/439 (83%)	365 (100%)	1 (0%)	86	96
1	E	372/439 (85%)	370 (100%)	2 (0%)	81	93
1	F	366/439 (83%)	366 (100%)	0	100	100
1	G	367/439 (84%)	367 (100%)	0	100	100
1	H	367/439 (84%)	366 (100%)	1 (0%)	86	96
1	I	367/439 (84%)	366 (100%)	1 (0%)	86	96
1	J	364/439 (83%)	363 (100%)	1 (0%)	86	96
All	All	3664/4390 (84%)	3656 (100%)	8 (0%)	87	96

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	160	LEU
1	I	406	THR
1	E	148	LEU
1	E	56	THR
1	H	398	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	134	ASN
1	J	192	ASN
1	F	259	HIS
1	I	372	GLN
1	F	134	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 [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 [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	417/499 (83%)	-0.02	3 (0%) 84 79	35, 59, 101, 151	0
1	B	413/499 (82%)	-0.19	7 (1%) 69 61	31, 49, 88, 121	0
1	C	412/499 (82%)	0.03	2 (0%) 87 83	43, 68, 99, 164	0
1	D	416/499 (83%)	0.01	5 (1%) 76 69	39, 61, 105, 140	0
1	E	425/499 (85%)	-0.19	4 (0%) 81 75	31, 47, 95, 178	0
1	F	415/499 (83%)	1.13	68 (16%) 4 3	64, 116, 147, 183	0
1	G	417/499 (83%)	0.55	25 (5%) 27 21	48, 82, 139, 163	0
1	H	416/499 (83%)	0.67	20 (4%) 35 28	64, 97, 141, 170	0
1	I	419/499 (83%)	0.25	14 (3%) 49 40	38, 65, 115, 182	0
1	J	412/499 (82%)	0.24	10 (2%) 59 50	42, 71, 120, 149	0
All	All	4162/4990 (83%)	0.25	158 (3%) 44 36	31, 70, 133, 183	0

The worst 5 of 158 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	140	PRO	4.4
1	B	473	LEU	4.1
1	F	293	PRO	3.7
1	G	275	LEU	3.7
1	E	179	ALA	3.7

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.