



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:59 PM UTC

PDB ID : 4RG7 / pdb_00004rg7
Title : Crystal structure of APC3
Authors : Yamaguchi, M.; Yu, S.; Miller, D.J.; Schulman, B.A.
Deposited on : 2014-09-29
Resolution : 4.25 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
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

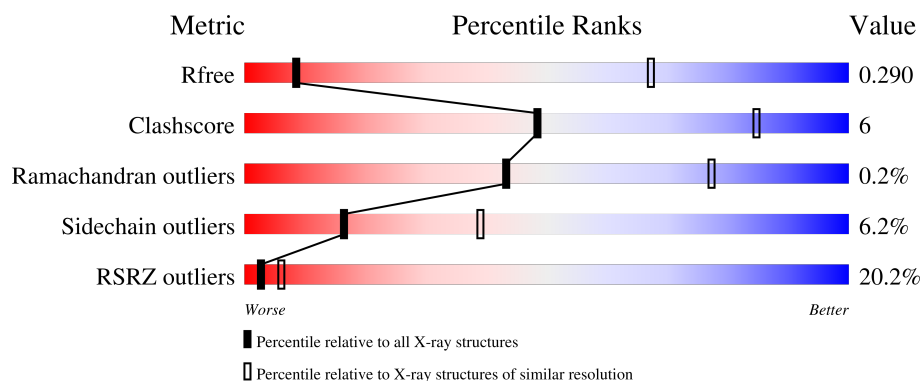
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.25 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	1029 (4.62-3.90)
Clashscore	190562	1074 (4.62-3.90)
Ramachandran outliers	187476	1001 (4.62-3.88)
Sidechain outliers	187428	1021 (4.66-3.86)
RSRZ outliers	180081	1026 (4.62-3.90)

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	560	16% 71% 12% • 16%
1	B	560	18% 74% 8% • 17%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6066 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 Cell division cycle protein 27 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	472	Total	C	N	O	S	0	0	0
			3127	1968	543	599	17			
1	B	467	Total	C	N	O	S	0	0	0
			2939	1831	514	578	16			

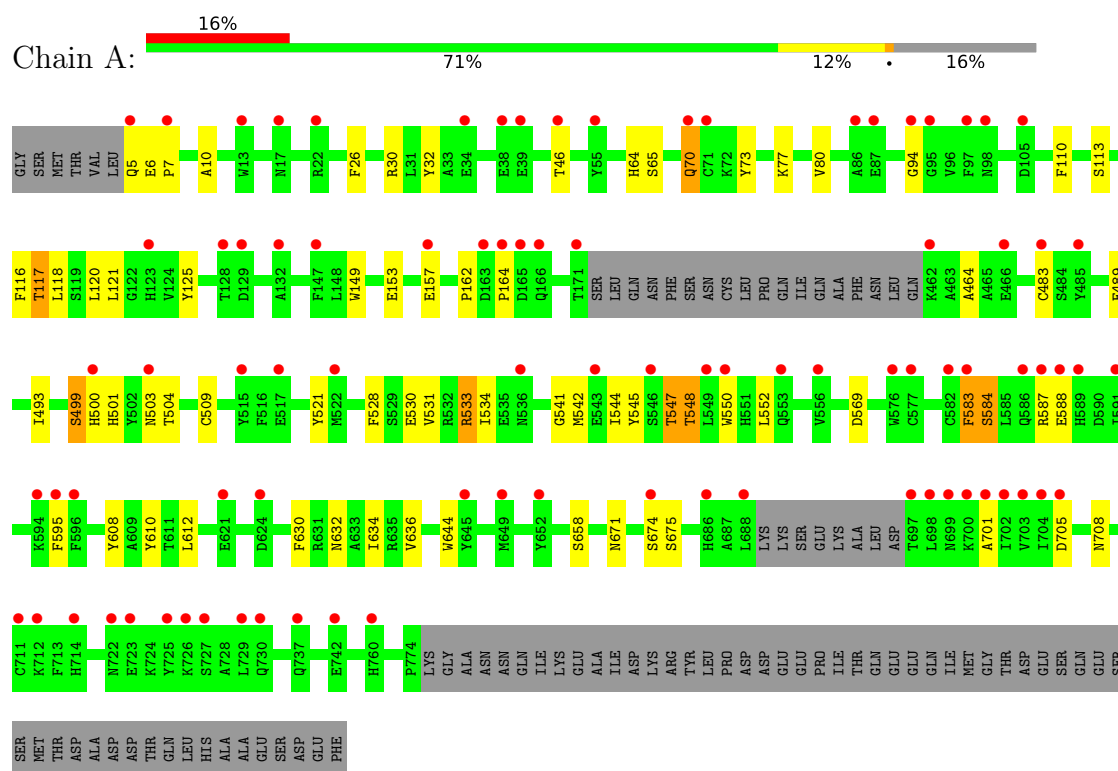
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P30260
A	0	SER	-	expression tag	UNP P30260
B	-1	GLY	-	expression tag	UNP P30260
B	0	SER	-	expression tag	UNP P30260

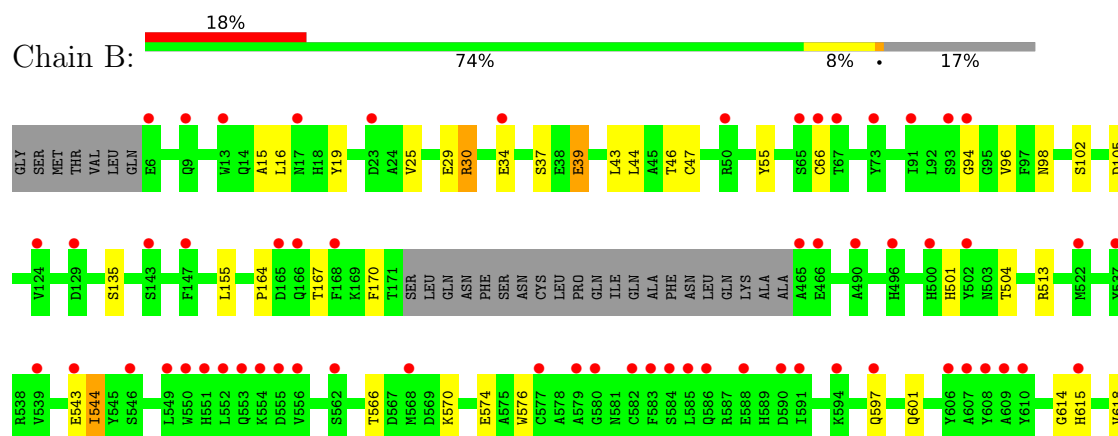
3 Residue-property plots [i](#)

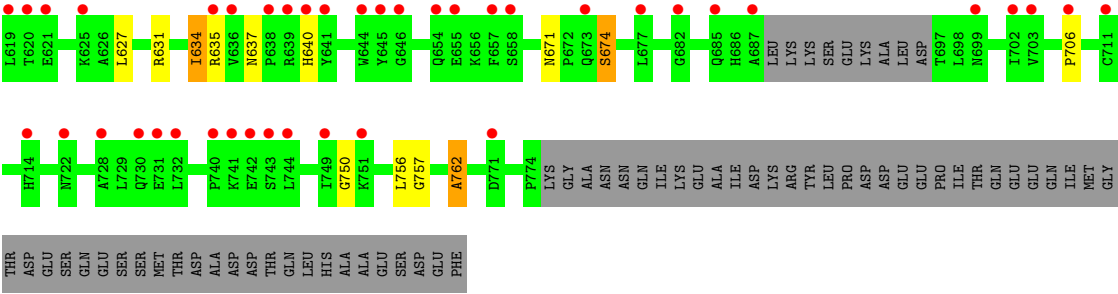
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Cell division cycle protein 27 homolog



- Molecule 1: Cell division cycle protein 27 homolog





4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	118.41Å 118.41Å 273.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.67 – 4.25 49.67 – 4.25	Depositor EDS
% Data completeness (in resolution range)	99.6 (49.67-4.25) 91.9 (49.67-4.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 4.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.255 , 0.282 0.262 , 0.290	Depositor DCC
R_{free} test set	765 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	154.3	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.44 , 718.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.088 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6066	wwPDB-VP
Average B, all atoms (Å ²)	170.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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	0.44	0/3199	1.07	14/4402 (0.3%)
1	B	0.42	0/2993	1.10	13/4127 (0.3%)
All	All	0.43	0/6192	1.09	27/8529 (0.3%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	96	VAL	N-CA-C	-15.21	95.36	110.72
1	A	708	ASN	CA-C-N	9.51	128.86	118.97
1	A	708	ASN	C-N-CA	9.51	128.86	118.97
1	A	94	GLY	N-CA-C	-9.11	99.27	114.76
1	A	6	GLU	CA-C-N	-8.34	111.22	119.64
1	A	6	GLU	C-N-CA	-8.34	111.22	119.64
1	B	94	GLY	N-CA-C	8.14	127.19	111.31
1	B	635	ARG	CA-C-N	6.62	129.03	120.56
1	B	635	ARG	C-N-CA	6.62	129.03	120.56
1	B	637	ASN	CA-C-N	6.53	125.76	118.97
1	B	637	ASN	C-N-CA	6.53	125.76	118.97
1	A	588	GLU	N-CA-C	-6.35	98.55	108.90
1	B	640	HIS	N-CA-C	6.12	119.44	107.57
1	A	118	LEU	N-CA-C	-5.90	104.93	111.36
1	B	170	PHE	N-CA-C	5.83	117.71	108.67
1	B	757	GLY	CA-C-N	5.74	132.51	121.54
1	B	757	GLY	C-N-CA	5.74	132.51	121.54
1	A	583	PHE	CB-CA-C	-5.42	101.03	110.09
1	B	762	ALA	N-CA-C	5.40	116.85	110.97
1	A	464	ALA	N-CA-C	5.38	117.23	111.36
1	A	10	ALA	CA-C-N	5.21	127.79	120.28
1	A	10	ALA	C-N-CA	5.21	127.79	120.28
1	A	584	SER	N-CA-C	-5.19	105.24	112.45
1	B	756	LEU	CA-C-N	-5.07	111.47	121.41
1	B	756	LEU	C-N-CA	-5.07	111.47	121.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	542	MET	N-CA-C	-5.04	106.39	112.54
1	A	499	SER	N-CA-C	5.01	117.48	111.71

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	3127	0	2378	40	0
1	B	2939	0	2102	25	0
All	All	6066	0	4480	58	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 6.

All (58) 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:32:TYR:OH	1:A:64:HIS:NE2	2.06	0.87
1:A:550:TRP:NE1	1:A:584:SER:OG	2.09	0.86
1:A:501:HIS:NE2	1:B:34:GLU:OE1	2.16	0.78
1:B:102:SER:OG	1:B:105:ASP:N	2.24	0.67
1:A:149:TRP:NE1	1:A:153:GLU:OE1	2.30	0.65
1:B:164:PRO:HA	1:B:167:THR:HG22	1.79	0.63
1:A:113:SER:O	1:A:117:THR:HG23	2.01	0.60
1:A:509:CYS:SG	1:A:541:GLY:HA3	2.43	0.59
1:B:750:GLY:HA2	1:B:762:ALA:HA	1.85	0.57
1:A:110:PHE:CD2	1:A:117:THR:HG21	2.39	0.57
1:A:489:GLU:O	1:A:493:ILE:HG12	2.07	0.53
1:A:630:PHE:O	1:A:634:ILE:HG12	2.09	0.53
1:B:671:ASN:O	1:B:674:SER:OG	2.27	0.53
1:A:545:TYR:HA	1:A:548:THR:HG23	1.90	0.52
1:A:610:TYR:HD2	1:A:632:ASN:HB3	1.75	0.52
1:A:610:TYR:CD2	1:A:632:ASN:HB3	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:513:ARG:HA	1:B:544:ILE:HD11	1.91	0.51
1:A:528:PHE:HA	1:A:531:VAL:HG12	1.92	0.51
1:A:73:TYR:CD1	1:A:117:THR:HG22	2.46	0.50
1:A:530:GLU:OE1	1:A:533:ARG:NH1	2.45	0.50
1:A:116:PHE:CE1	1:B:15:ALA:HA	2.46	0.50
1:A:671:ASN:O	1:A:674:SER:OG	2.30	0.50
1:B:615:HIS:O	1:B:618:VAL:HG22	2.11	0.50
1:A:110:PHE:HB3	1:A:113:SER:HB2	1.94	0.49
1:A:162:PRO:O	1:A:164:PRO:HD3	2.14	0.48
1:A:701:ALA:O	1:A:705:ASP:N	2.42	0.47
1:B:37:SER:OG	1:B:39:GLU:HG2	2.15	0.47
1:B:570:LYS:O	1:B:576:TRP:NE1	2.42	0.47
1:A:80:VAL:HG21	1:A:120:LEU:HD11	1.96	0.46
1:A:116:PHE:HE1	1:B:15:ALA:HA	1.81	0.46
1:B:501:HIS:O	1:B:504:THR:HG22	2.16	0.46
1:A:70:GLN:H	1:A:70:GLN:HG3	1.46	0.45
1:A:583:PHE:CE2	1:A:595:PHE:HE2	2.34	0.45
1:B:543:GLU:HG2	1:B:544:ILE:HG23	1.98	0.45
1:A:547:THR:O	1:A:550:TRP:HB3	2.17	0.44
1:A:521:TYR:HB2	1:A:552:LEU:HD21	2.00	0.44
1:A:608:TYR:CE2	1:A:612:LEU:HD11	2.53	0.44
1:A:504:THR:HG21	1:B:30:ARG:HH22	1.81	0.44
1:B:597:GLN:O	1:B:601:GLN:N	2.48	0.44
1:B:43:LEU:HD23	1:B:43:LEU:HA	1.67	0.43
1:A:26:PHE:O	1:A:30:ARG:HG2	2.18	0.43
1:A:569:ASP:OD1	1:B:55:TYR:HE2	2.01	0.43
1:A:499:SER:O	1:A:503:ASN:ND2	2.52	0.43
1:B:29:GLU:HG3	1:B:44:LEU:HD11	2.00	0.43
1:A:531:VAL:HA	1:A:534:ILE:HG22	2.01	0.42
1:A:121:LEU:HD22	1:A:125:TYR:CE2	2.54	0.42
1:A:504:THR:CB	1:B:30:ARG:HH22	2.32	0.42
1:A:5:GLN:N	1:A:7:PRO:HD2	2.35	0.41
1:B:30:ARG:NE	1:B:30:ARG:HA	2.35	0.41
1:A:584:SER:C	1:A:587:ARG:H	2.28	0.41
1:B:614:GLY:O	1:B:618:VAL:HG13	2.21	0.41
1:B:634:ILE:H	1:B:634:ILE:HG13	1.73	0.41
1:B:631:ARG:O	1:B:634:ILE:HG13	2.21	0.41
1:A:157:GLU:HA	1:A:483:CYS:SG	2.61	0.41
1:A:634:ILE:HD12	1:A:644:TRP:CE2	2.56	0.40
1:A:46:THR:HG23	1:B:19:TYR:OH	2.20	0.40
1:A:117:THR:HG23	1:A:117:THR:H	1.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:VAL:HG12	1:B:47:CYS:HB3	2.04	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	466/560 (83%)	439 (94%)	27 (6%)	0	100	100
1	B	461/560 (82%)	434 (94%)	25 (5%)	2 (0%)	30	66
All	All	927/1120 (83%)	873 (94%)	52 (6%)	2 (0%)	43	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	98	ASN
1	B	706	PRO

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	222/485 (46%)	210 (95%)	12 (5%)	20	43
1	B	182/485 (38%)	169 (93%)	13 (7%)	13	36
All	All	404/970 (42%)	379 (94%)	25 (6%)	16	39

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	SER
1	A	70	GLN
1	A	77	LYS
1	A	117	THR
1	A	500	HIS
1	A	533	ARG
1	A	544	ILE
1	A	547	THR
1	A	548	THR
1	A	636	VAL
1	A	658	SER
1	A	675	SER
1	B	16	LEU
1	B	30	ARG
1	B	39	GLU
1	B	46	THR
1	B	66	CYS
1	B	135	SER
1	B	155	LEU
1	B	544	ILE
1	B	566	THR
1	B	574	GLU
1	B	627	LEU
1	B	634	ILE
1	B	674	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	510	GLN
1	A	640	HIS

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

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	472/560 (84%)	1.18	88 (18%) 3 7	109, 147, 238, 310	0
1	B	467/560 (83%)	1.25	102 (21%) 2 5	90, 192, 271, 345	0
All	All	939/1120 (83%)	1.22	190 (20%) 3 6	90, 164, 263, 345	0

All (190) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	537	TYR	6.7
1	A	97	PHE	6.2
1	A	595	PHE	5.9
1	B	636	VAL	5.5
1	A	7	PRO	5.3
1	B	610	TYR	5.2
1	B	165	ASP	5.2
1	B	685	GLN	5.1
1	A	726	LYS	5.0
1	B	579	ALA	5.0
1	B	94	GLY	5.0
1	B	594	LYS	4.9
1	A	760	HIS	4.9
1	A	164	PRO	4.8
1	A	583	PHE	4.8
1	A	700	LYS	4.7
1	A	705	ASP	4.7
1	B	550	TRP	4.7
1	B	714	HIS	4.6
1	A	165	ASP	4.4
1	A	702	ILE	4.4
1	A	500	HIS	4.4
1	B	703	VAL	4.4
1	B	586	GLN	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	645	TYR	4.3
1	A	536	ASN	4.3
1	A	586	GLN	4.3
1	B	608	TYR	4.2
1	B	673	GLN	4.2
1	B	615	HIS	4.2
1	B	553	GLN	4.2
1	A	697	THR	4.0
1	A	722	ASN	4.0
1	B	625	LYS	4.0
1	B	655	GLU	4.0
1	A	652	TYR	4.0
1	B	638	PRO	3.9
1	B	751	LYS	3.8
1	B	644	TRP	3.8
1	A	587	ARG	3.8
1	B	609	ALA	3.8
1	B	591	ILE	3.8
1	A	5	GLN	3.8
1	B	658	SER	3.7
1	A	699	ASN	3.7
1	B	490	ALA	3.7
1	B	590	ASP	3.7
1	B	699	ASN	3.7
1	A	87	GLU	3.6
1	B	702	ILE	3.6
1	A	714	HIS	3.6
1	A	588	GLU	3.6
1	B	13	TRP	3.5
1	B	620	THR	3.5
1	A	725	TYR	3.4
1	B	500	HIS	3.4
1	A	688	LEU	3.3
1	B	744	LEU	3.3
1	B	65	SER	3.3
1	B	728	ALA	3.3
1	B	91	ILE	3.3
1	B	687	ALA	3.3
1	A	624	ASP	3.3
1	A	38	GLU	3.2
1	B	554	LYS	3.2
1	B	67	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	86	ALA	3.2
1	B	742	GLU	3.1
1	A	594	LYS	3.1
1	B	597	GLN	3.1
1	A	517	GLU	3.1
1	B	606	TYR	3.0
1	A	95	GLY	3.0
1	A	645	TYR	3.0
1	B	166	GLN	3.0
1	A	591	ILE	3.0
1	B	577	CYS	3.0
1	B	546	SER	3.0
1	A	727	SER	3.0
1	A	742	GLU	3.0
1	B	607	ALA	3.0
1	B	66	CYS	3.0
1	B	740	PRO	2.9
1	A	701	ALA	2.9
1	A	171	THR	2.9
1	B	584	SER	2.9
1	B	465	ALA	2.9
1	B	711	CYS	2.9
1	B	466	GLU	2.9
1	B	539	VAL	2.8
1	A	686	HIS	2.8
1	A	556	VAL	2.8
1	A	649	MET	2.8
1	B	143	SER	2.8
1	A	723	GLU	2.8
1	A	698	LEU	2.8
1	B	635	ARG	2.8
1	A	485	TYR	2.7
1	B	93	SER	2.7
1	B	682	GLY	2.7
1	B	732	LEU	2.7
1	B	502	TYR	2.7
1	B	129	ASP	2.7
1	B	706	PRO	2.7
1	A	674	SER	2.7
1	B	552	LEU	2.7
1	A	703	VAL	2.7
1	A	577	CYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	582	CYS	2.6
1	B	168	PHE	2.6
1	B	582	CYS	2.6
1	B	23	ASP	2.6
1	A	94	GLY	2.6
1	B	580	GLY	2.6
1	A	711	CYS	2.6
1	B	585	LEU	2.6
1	B	639	ARG	2.6
1	B	556	VAL	2.5
1	A	483	CYS	2.5
1	A	17	ASN	2.5
1	A	550	TRP	2.5
1	A	621	GLU	2.5
1	B	730	GLN	2.5
1	A	105	ASP	2.5
1	B	124	VAL	2.5
1	A	132	ALA	2.5
1	B	147	PHE	2.4
1	B	677	LEU	2.4
1	A	123	HIS	2.4
1	A	543	GLU	2.4
1	A	515	TYR	2.4
1	B	771	ASP	2.4
1	B	543	GLU	2.4
1	B	549	LEU	2.4
1	B	621	GLU	2.4
1	A	596	PHE	2.4
1	A	39	GLU	2.3
1	A	730	GLN	2.3
1	B	657	PHE	2.3
1	A	166	GLN	2.3
1	B	583	PHE	2.3
1	B	722	ASN	2.3
1	B	619	LEU	2.3
1	A	546	SER	2.3
1	B	641	TYR	2.3
1	B	555	ASP	2.3
1	B	9	GLN	2.3
1	A	737	GLN	2.3
1	A	503	ASN	2.3
1	A	13	TRP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	646	GLY	2.3
1	A	128	THR	2.2
1	A	589	HIS	2.2
1	A	70	GLN	2.2
1	A	712	LYS	2.2
1	A	22	ARG	2.2
1	B	743	SER	2.2
1	A	704	ILE	2.2
1	B	731	GLU	2.2
1	A	98	ASN	2.2
1	B	654	GLN	2.2
1	B	551	HIS	2.2
1	A	462	LYS	2.2
1	B	568	MET	2.2
1	B	741	LYS	2.2
1	B	6	GLU	2.2
1	A	549	LEU	2.1
1	A	46	THR	2.1
1	B	73	TYR	2.1
1	A	34	GLU	2.1
1	B	588	GLU	2.1
1	A	147	PHE	2.1
1	A	129	ASP	2.1
1	B	640	HIS	2.1
1	A	576	TRP	2.1
1	A	466	GLU	2.1
1	B	562	SER	2.1
1	B	50	ARG	2.1
1	B	522	MET	2.1
1	B	496	HIS	2.1
1	A	522	MET	2.0
1	A	55	TYR	2.0
1	A	71	CYS	2.0
1	A	729	LEU	2.0
1	B	749	ILE	2.0
1	A	163	ASP	2.0
1	B	17	ASN	2.0
1	B	34	GLU	2.0
1	A	553	GLN	2.0
1	A	157	GLU	2.0

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.