



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:55 PM UTC

PDB ID : 7ZK1 / pdb_00007zk1
Title : Crystal structure of cystinosin from Arabidopsis thaliana bound to sybody and nanobody
Authors : Loebel, M.; Newstead, S.; Omari, K.E.
Deposited on : 2022-04-12
Resolution : 2.65 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

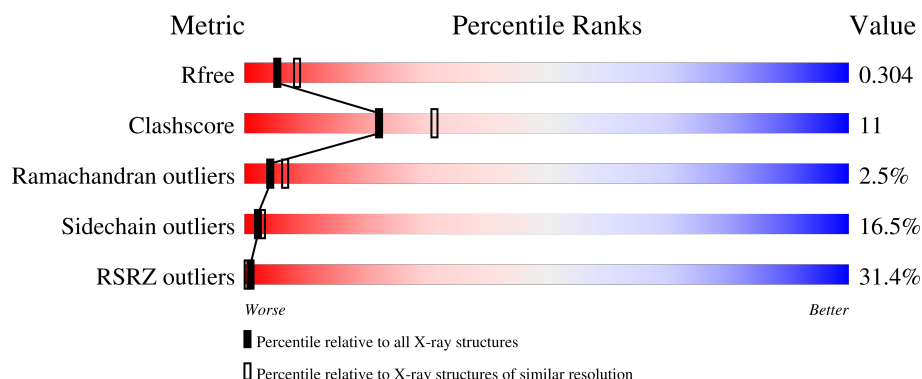
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	277	35% 60% 22% 6% 12%
2	B	128	27% 69% 25% • • •
3	C	121	18% 67% 26% 6% •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3957 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 Cystinosin homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1987	1330	310	335	12			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	271	GLY	-	expression tag	UNP P57758
A	272	GLU	-	expression tag	UNP P57758
A	273	ASN	-	expression tag	UNP P57758
A	274	LEU	-	expression tag	UNP P57758
A	275	TYR	-	expression tag	UNP P57758
A	276	PHE	-	expression tag	UNP P57758
A	277	GLN	-	expression tag	UNP P57758

- Molecule 2 is a protein called Llama derived nanobody.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	127	Total	C	N	O	S	0	1	0
			976	609	175	188	4			

- Molecule 3 is a protein called Synthetic nanobody (Sybody).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	121	Total	C	N	O	S	0	0	0
			962	604	170	184	4			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	14	Total O 14 14	0	0

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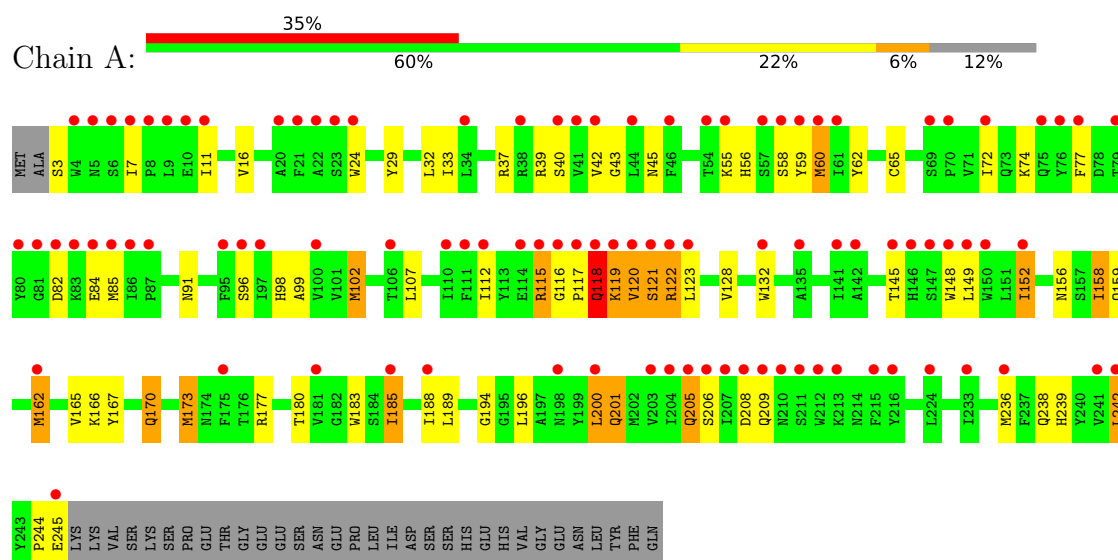
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	11	Total	O	0	0
			11	11		
4	C	7	Total	O	0	0
			7	7		

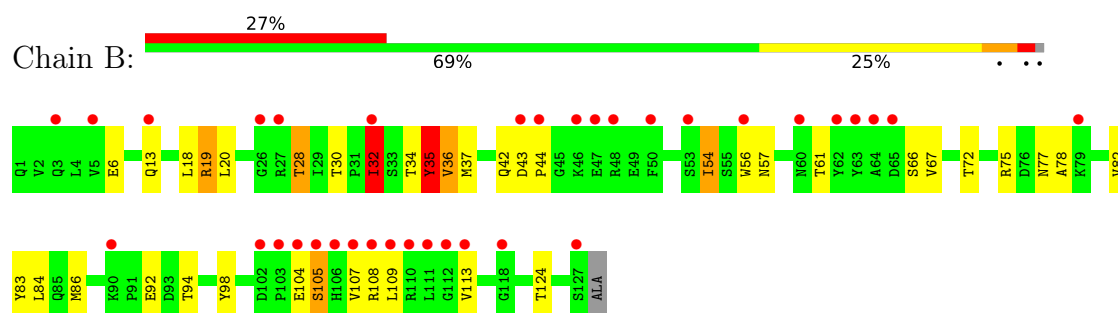
3 Residue-property plots [i](#)

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.

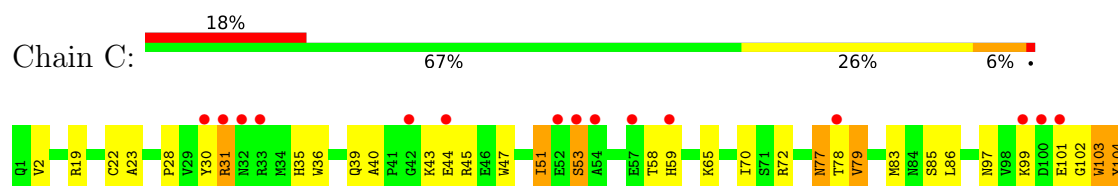
• Molecule 1: Cystinosin homolog

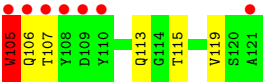


• Molecule 2: Llama derived nanobody



• Molecule 3: Synthetic nanobody (Sybody)





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	62.79Å 319.96Å 45.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	79.99 – 2.65 79.99 – 2.65	Depositor EDS
% Data completeness (in resolution range)	93.4 (79.99-2.65) 93.7 (79.99-2.65)	Depositor EDS
R_{merge}	0.54	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.65Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.230 , 0.270 0.257 , 0.304	Depositor DCC
R_{free} test set	1331 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	66.3	Xtriage
Anisotropy	0.564	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	3957	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% 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 [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	0.80	0/2049	1.21	1/2789 (0.0%)
2	B	0.82	1/996 (0.1%)	1.16	3/1351 (0.2%)
3	C	0.71	0/987	1.10	4/1340 (0.3%)
All	All	0.78	1/4032 (0.0%)	1.17	8/5480 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	32	ILE	CG1-CD1	5.20	1.72	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	35	TYR	N-CA-C	7.41	121.91	113.02
3	C	106	GLN	N-CA-C	6.23	119.86	110.64
2	B	105	SER	N-CA-C	5.76	118.12	108.96
1	A	167	TYR	N-CA-C	5.30	117.87	111.40
2	B	57	ASN	CA-CB-CG	5.15	117.75	112.60
3	C	105	TRP	CA-C-N	5.10	130.80	121.97
3	C	105	TRP	C-N-CA	5.10	130.80	121.97
3	C	104	TYR	N-CA-C	-5.06	101.85	109.85

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	1987	0	1986	46	0
2	B	976	0	949	21	0
3	C	962	0	904	22	0
4	A	14	0	0	1	0
4	B	11	0	0	1	0
4	C	7	0	0	0	0
All	All	3957	0	3839	82	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 11.

All (82) 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:62:TYR:HA	1:A:152:ILE:HG12	1.59	0.84
1:A:65:CYS:HB2	1:A:152:ILE:HD11	1.63	0.79
3:C:36:TRP:HD1	3:C:70:ILE:HD12	1.48	0.79
1:A:183:TRP:NE1	1:A:185:ILE:HG13	1.99	0.77
2:B:54:ILE:HG23	2:B:61:THR:HG22	1.68	0.75
1:A:173:MET:HE1	3:C:102:GLY:HA2	1.72	0.71
1:A:180:THR:HG21	1:A:239:HIS:ND1	2.06	0.69
1:A:118:GLN:HG2	1:A:120:VAL:HG22	1.74	0.68
1:A:85:MET:HE3	1:A:205:GLN:HG2	1.75	0.68
1:A:183:TRP:HE1	1:A:185:ILE:HG13	1.59	0.67
3:C:22:CYS:HB3	3:C:79:VAL:HG12	1.77	0.67
1:A:208:ASP:OD2	1:A:209:GLN:NE2	2.28	0.66
3:C:36:TRP:HD1	3:C:70:ILE:CD1	2.09	0.65
1:A:32:LEU:HD11	1:A:102:MET:HG3	1.79	0.64
3:C:102:GLY:H	3:C:107:THR:HG22	1.62	0.64
2:B:28:THR:HG21	2:B:35:TYR:OH	1.97	0.63
2:B:32:ILE:O	2:B:35:TYR:HB2	1.98	0.63
1:A:65:CYS:HB2	1:A:152:ILE:CD1	2.29	0.63
2:B:37:MET:HB2	2:B:82:VAL:HG11	1.80	0.63
1:A:149:LEU:O	1:A:152:ILE:HG22	2.01	0.61
1:A:59:TYR:HB2	1:A:159:GLN:HG3	1.83	0.61
1:A:115:ARG:HA	1:A:115:ARG:HE	1.66	0.60
1:A:238:GLN:HA	1:A:242:LEU:HB2	1.86	0.58
1:A:7:ILE:HG23	2:B:107:VAL:HG22	1.87	0.57
1:A:183:TRP:HE1	1:A:185:ILE:CG1	2.18	0.56
1:A:117:PRO:HG2	3:C:47:TRP:CH2	2.40	0.56
2:B:18:LEU:HB3	2:B:86:MET:HE3	1.88	0.56
2:B:19:ARG:NH1	2:B:83:TYR:CD2	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:GLY:O	3:C:107:THR:HG21	2.06	0.55
2:B:75:ARG:NH2	4:B:202:HOH:O	2.40	0.55
1:A:173:MET:O	1:A:177:ARG:HB2	2.07	0.54
4:A:314:HOH:O	3:C:105:TRP:HB2	2.07	0.54
2:B:105:SER:HB3	2:B:108:ARG:HB2	1.90	0.54
2:B:32:ILE:HA	2:B:35:TYR:CD1	2.44	0.53
1:A:55:LYS:HB2	1:A:162:MET:HB3	1.91	0.53
1:A:29:TYR:O	1:A:33:ILE:HG12	2.10	0.52
1:A:60:MET:HA	1:A:96:SER:HB3	1.92	0.52
3:C:23:ALA:HA	3:C:78:THR:HG22	1.92	0.51
1:A:206:SER:O	1:A:209:GLN:O	2.29	0.51
2:B:75:ARG:HD3	2:B:77:ASN:OD1	2.11	0.51
1:A:40:SER:HB2	1:A:115:ARG:HB3	1.93	0.51
2:B:94:THR:HG23	2:B:124:THR:HA	1.93	0.51
3:C:105:TRP:C	3:C:105:TRP:CD1	2.89	0.51
1:A:77:PHE:HE1	1:A:84:GLU:O	1.94	0.51
1:A:119:LYS:C	1:A:121:SER:H	2.19	0.50
1:A:183:TRP:HH2	1:A:236:MET:HG2	1.77	0.50
2:B:113:VAL:HG12	2:B:113:VAL:O	2.11	0.50
1:A:29:TYR:OH	1:A:98:HIS:HE1	1.96	0.49
2:B:35:TYR:O	2:B:36:VAL:O	2.29	0.49
3:C:35:HIS:HB2	3:C:97:ASN:HB3	1.95	0.49
1:A:91:ASN:HD21	1:A:201:GLN:HE22	1.61	0.48
1:A:183:TRP:CD1	1:A:239:HIS:CE1	3.00	0.48
3:C:30:TYR:O	3:C:53:SER:O	2.31	0.48
1:A:128:VAL:HG13	1:A:132:TRP:CD1	2.49	0.48
3:C:51:ILE:HD12	3:C:58:THR:HG22	1.95	0.48
2:B:37:MET:CB	2:B:82:VAL:HG11	2.43	0.47
3:C:40:ALA:HB3	3:C:43:LYS:HD3	1.96	0.47
2:B:34:THR:HA	2:B:56:TRP:HB2	1.96	0.47
1:A:148:TRP:O	1:A:152:ILE:HB	2.16	0.46
3:C:28:PRO:HA	3:C:77:ASN:HD21	1.79	0.46
1:A:58:SER:OG	1:A:158:ILE:HD11	2.16	0.45
3:C:105:TRP:C	3:C:105:TRP:HD1	2.25	0.45
1:A:116:GLY:O	1:A:117:PRO:C	2.60	0.45
1:A:16:VAL:HG11	1:A:200:LEU:HB3	1.99	0.44
2:B:84:LEU:HG	2:B:86:MET:HG2	1.99	0.44
1:A:56:HIS:CE1	1:A:99:ALA:HB1	2.53	0.44
1:A:128:VAL:HG13	1:A:132:TRP:HD1	1.82	0.44
1:A:180:THR:CG2	1:A:239:HIS:ND1	2.79	0.44
1:A:117:PRO:HB3	3:C:59:HIS:CG	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:PRO:O	1:A:119:LYS:N	2.51	0.43
2:B:42:GLN:HB2	2:B:98:TYR:HE1	1.83	0.43
1:A:72:ILE:HG12	1:A:148:TRP:HB2	2.01	0.43
3:C:83:MET:HB2	3:C:86:LEU:HD21	1.99	0.43
3:C:28:PRO:HG2	3:C:31:ARG:HB2	1.99	0.43
1:A:24:TRP:CD1	1:A:194:GLY:HA3	2.54	0.42
2:B:37:MET:HE2	2:B:82:VAL:HG22	2.00	0.42
1:A:170:GLN:OE1	3:C:105:TRP:CD2	2.73	0.42
1:A:40:SER:HA	1:A:115:ARG:HB2	2.03	0.41
2:B:20:LEU:HD12	2:B:84:LEU:HD23	2.01	0.41
3:C:36:TRP:CD1	3:C:70:ILE:CD1	2.98	0.41
2:B:18:LEU:HB3	2:B:86:MET:CE	2.50	0.40
1:A:170:GLN:HG2	3:C:103:TRP:HB3	2.03	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	241/277 (87%)	224 (93%)	12 (5%)	5 (2%)	5	9
2	B	126/128 (98%)	111 (88%)	10 (8%)	5 (4%)	2	3
3	C	119/121 (98%)	111 (93%)	6 (5%)	2 (2%)	7	12
All	All	486/526 (92%)	446 (92%)	28 (6%)	12 (2%)	4	7

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	242	LEU
2	B	78	ALA
3	C	103	TRP
1	A	118	GLN

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Mol	Chain	Res	Type
1	A	244	PRO
2	B	36	VAL
1	A	121	SER
3	C	105	TRP
1	A	122	ARG
2	B	32	ILE
2	B	43	ASP
2	B	44	PRO

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	218/249 (88%)	183 (84%)	35 (16%)	2	3
2	B	102/102 (100%)	88 (86%)	14 (14%)	3	5
3	C	98/98 (100%)	78 (80%)	20 (20%)	1	1
All	All	418/449 (93%)	349 (84%)	69 (16%)	2	3

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	SER
1	A	11	ILE
1	A	37	ARG
1	A	39	ARG
1	A	42	VAL
1	A	45	ASN
1	A	60	MET
1	A	74	LYS
1	A	82	ASP
1	A	102	MET
1	A	107	LEU
1	A	112	ILE
1	A	115	ARG
1	A	118	GLN

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Mol	Chain	Res	Type
1	A	119	LYS
1	A	120	VAL
1	A	122	ARG
1	A	123	LEU
1	A	145	THR
1	A	152	ILE
1	A	156	ASN
1	A	158	ILE
1	A	162	MET
1	A	165	VAL
1	A	166	LYS
1	A	170	GLN
1	A	173	MET
1	A	185	ILE
1	A	188	ILE
1	A	189	LEU
1	A	196	LEU
1	A	200	LEU
1	A	201	GLN
1	A	205	GLN
1	A	245	GLU
2	B	6	GLU
2	B	13	GLN
2	B	19	ARG
2	B	28	THR
2	B	30	THR
2	B	32	ILE
2	B	35	TYR
2	B	54	ILE
2	B	66	SER
2	B	67	VAL
2	B	72	THR
2	B	92	GLU
2	B	104	GLU
2	B	109	LEU
3	C	2	VAL
3	C	19	ARG
3	C	31	ARG
3	C	39	GLN
3	C	44	GLU
3	C	45	ARG
3	C	51	ILE

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Mol	Chain	Res	Type
3	C	53	SER
3	C	65	LYS
3	C	72	ARG
3	C	77	ASN
3	C	79	VAL
3	C	85	SER
3	C	99	LYS
3	C	101	GLU
3	C	104	TYR
3	C	105	TRP
3	C	113	GLN
3	C	115	THR
3	C	119	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	75	GLN
1	A	91	ASN
1	A	98	HIS
1	A	156	ASN
1	A	159	GLN
1	A	170	GLN
1	A	174	ASN
1	A	198	ASN
1	A	218	ASN
3	C	74	ASN
3	C	77	ASN
3	C	82	GLN
3	C	84	ASN
3	C	97	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 ⓘ

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	243/277 (87%)	2.09	97 (39%)	1 0	65, 80, 106, 122	0
2	B	127/128 (99%)	1.62	35 (27%)	1 1	41, 88, 111, 116	1 (0%)
3	C	121/121 (100%)	1.31	22 (18%)	3 2	67, 86, 97, 104	0
All	All	491/526 (93%)	1.78	154 (31%)	1 0	41, 83, 108, 122	1 (0%)

All (154) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	111	LEU	9.8
1	A	84	GLU	9.7
1	A	7	ILE	9.4
2	B	107	VAL	9.1
3	C	108	TYR	8.7
2	B	110	ARG	8.5
1	A	118	GLN	8.5
1	A	117	PRO	8.2
1	A	212	TRP	7.6
1	A	120	VAL	7.5
1	A	119	LYS	7.3
1	A	80	TYR	6.8
1	A	207	ILE	6.7
2	B	62	TYR	6.6
1	A	145	THR	6.5
2	B	65	ASP	6.1
3	C	57	GLU	6.1
2	B	106	HIS	6.1
1	A	150	TRP	6.0
1	A	116	GLY	5.9
1	A	216	TYR	5.8
3	C	54	ALA	5.8
3	C	42	GLY	5.7

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Mol	Chain	Res	Type	RSRZ
1	A	8	PRO	5.7
1	A	6	SER	5.5
3	C	109	ASP	5.4
1	A	213	LYS	5.4
2	B	112	GLY	5.4
1	A	211	SER	5.4
2	B	105	SER	5.4
3	C	52	GLU	5.3
1	A	141	ILE	5.2
1	A	205	GLN	5.2
1	A	208	ASP	5.1
3	C	101	GLU	4.9
1	A	83	LYS	4.9
3	C	106	GLN	4.8
1	A	4	TRP	4.7
1	A	5	ASN	4.7
3	C	100	ASP	4.5
2	B	104	GLU	4.4
3	C	44	GLU	4.4
3	C	53	SER	4.3
1	A	42	VAL	4.2
1	A	72	ILE	4.2
1	A	11	ILE	4.1
2	B	113	VAL	4.0
1	A	148	TRP	4.0
1	A	57	SER	4.0
1	A	123	LEU	4.0
2	B	102	ASP	4.0
1	A	215	PHE	4.0
1	A	206	SER	3.9
2	B	103	PRO	3.9
1	A	85	MET	3.9
2	B	108	ARG	3.8
1	A	9	LEU	3.8
3	C	110	TYR	3.7
1	A	38	ARG	3.7
2	B	13	GLN	3.7
1	A	242	LEU	3.7
1	A	97	ILE	3.7
1	A	149	LEU	3.6
1	A	46	PHE	3.6
1	A	147	SER	3.6

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Mol	Chain	Res	Type	RSRZ
3	C	33	ARG	3.5
1	A	20	ALA	3.5
1	A	210	ASN	3.5
1	A	76	TYR	3.4
1	A	111	PHE	3.4
1	A	41	VAL	3.4
1	A	209	GLN	3.4
1	A	204	ILE	3.3
2	B	32	ILE	3.3
1	A	185	ILE	3.3
1	A	142	ALA	3.2
1	A	87	PRO	3.1
3	C	105	TRP	3.1
1	A	44	LEU	3.1
1	A	236	MET	3.1
1	A	60	MET	3.1
3	C	121	ALA	3.1
1	A	132	TRP	3.1
1	A	114	GLU	3.0
1	A	24	TRP	3.0
1	A	79	THR	3.0
1	A	121	SER	3.0
1	A	82	ASP	3.0
1	A	75	GLN	2.9
1	A	34	LEU	2.9
1	A	115	ARG	2.9
2	B	50	PHE	2.9
1	A	58	SER	2.9
1	A	55	LYS	2.9
2	B	64	ALA	2.9
1	A	245	GLU	2.8
1	A	188	ILE	2.8
2	B	109	LEU	2.8
3	C	30	TYR	2.8
1	A	69	SER	2.7
3	C	59	HIS	2.7
1	A	21	PHE	2.6
1	A	23	SER	2.6
1	A	59	TYR	2.6
3	C	31	ARG	2.5
3	C	32	ASN	2.5
1	A	241	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	60	ASN	2.4
2	B	118	GLY	2.4
1	A	122	ARG	2.4
2	B	63	TYR	2.4
1	A	146	HIS	2.4
1	A	96	SER	2.4
1	A	110	ILE	2.4
2	B	53	SER	2.4
2	B	127	SER	2.4
1	A	162	MET	2.3
2	B	47	GLU	2.3
1	A	81	GLY	2.3
1	A	22	ALA	2.3
1	A	54	THR	2.3
3	C	78	THR	2.3
1	A	77	PHE	2.3
1	A	70	PRO	2.3
1	A	100	VAL	2.3
1	A	10	GLU	2.2
2	B	26	GLY	2.2
2	B	90	LYS	2.2
1	A	95	PHE	2.2
1	A	112	ILE	2.2
1	A	106	THR	2.2
1	A	224	LEU	2.2
1	A	175	PHE	2.2
3	C	107	THR	2.1
3	C	99	LYS	2.1
1	A	200	LEU	2.1
2	B	46	LYS	2.1
2	B	5	VAL	2.1
2	B	56	TRP	2.1
2	B	79	LYS	2.1
2	B	27	ARG	2.1
2	B	44	PRO	2.1
1	A	198	ASN	2.1
1	A	86	ILE	2.1
1	A	181	VAL	2.1
1	A	203	VAL	2.1
2	B	43	ASP	2.0
1	A	40	SER	2.0
1	A	233	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	135	ALA	2.0
2	B	3	GLN	2.0
1	A	61	ILE	2.0
1	A	152	ILE	2.0
2	B	48	ARG	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.