



Full wwPDB X-ray Structure Validation Report ⓘ

May 20, 2026 – 08:07 PM EDT

PDB ID : 9YAV / pdb_00009yav
Title : Rana catesbeiana saxiphilin mutant - F561A
Authors : Chen, Z.; Zakrzewska, S.; Minor, D.L.
Deposited on : 2025-09-16
Resolution : 2.23 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

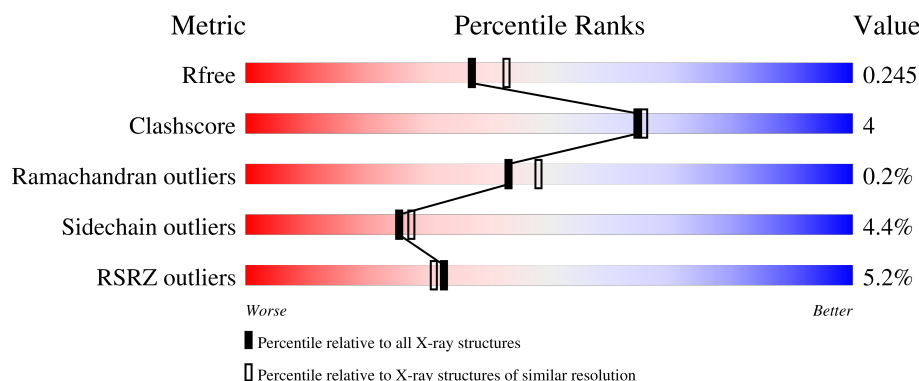
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	853	<div> <div>5%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>..</div> </div> </div>
1	B	853	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>11%</div> <div>..</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13107 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 Saxiphilin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	829	Total	C	N	O	S	0	0	0
			6389	3988	1106	1236	59			
1	B	823	Total	C	N	O	S	0	0	0
			6348	3965	1098	1226	59			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	561	ALA	PHE	engineered mutation	UNP P31226
A	826	SER	-	expression tag	UNP P31226
A	827	ASN	-	expression tag	UNP P31226
A	828	SER	-	expression tag	UNP P31226
A	829	LEU	-	expression tag	UNP P31226
A	830	GLU	-	expression tag	UNP P31226
A	831	VAL	-	expression tag	UNP P31226
A	832	LEU	-	expression tag	UNP P31226
A	833	PHE	-	expression tag	UNP P31226
A	834	GLN	-	expression tag	UNP P31226
B	561	ALA	PHE	engineered mutation	UNP P31226
B	826	SER	-	expression tag	UNP P31226
B	827	ASN	-	expression tag	UNP P31226
B	828	SER	-	expression tag	UNP P31226
B	829	LEU	-	expression tag	UNP P31226
B	830	GLU	-	expression tag	UNP P31226
B	831	VAL	-	expression tag	UNP P31226
B	832	LEU	-	expression tag	UNP P31226
B	833	PHE	-	expression tag	UNP P31226
B	834	GLN	-	expression tag	UNP P31226

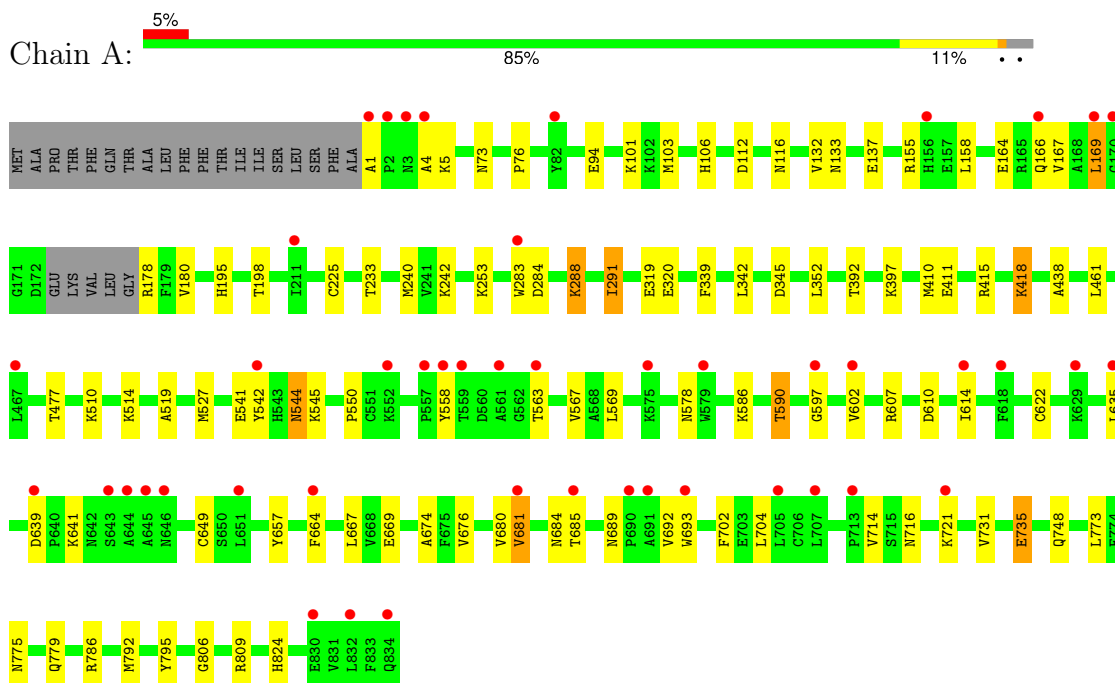
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	207	Total 207	O 207	0	0
2	B	163	Total 163	O 163	0	0

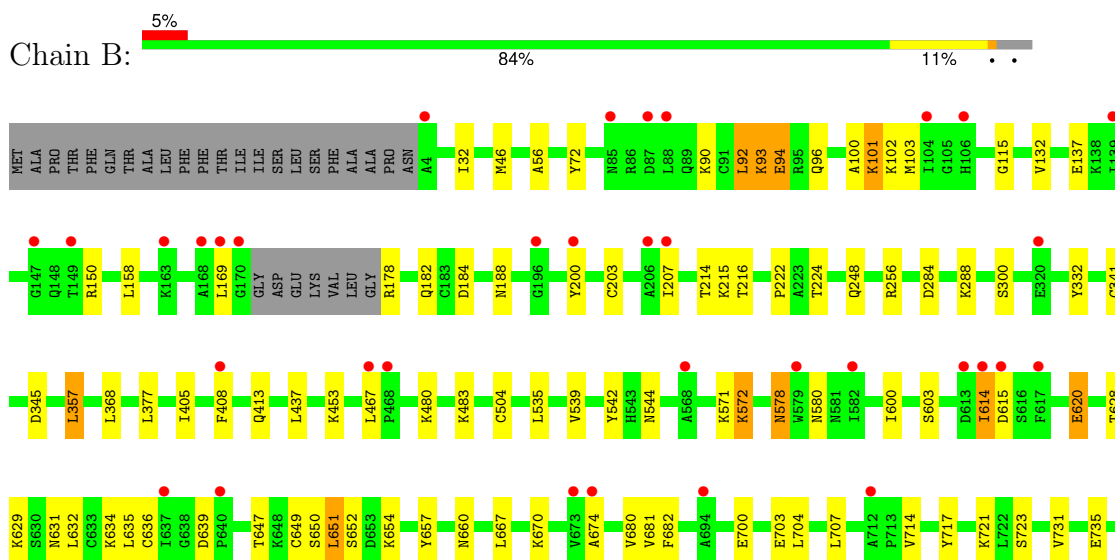
3 Residue-property plots [i](#)

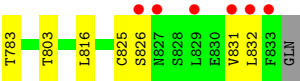
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: Saxiphilin





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.34Å 110.24Å 254.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.17 – 2.23 48.17 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.17-2.23) 99.9 (48.17-2.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.22Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.210 , 0.244 0.212 , 0.245	Depositor DCC
R_{free} test set	6711 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	55.7	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 54.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13107	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.65% 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	0.22	0/6516	0.40	0/8795
1	B	0.22	0/6474	0.41	0/8737
All	All	0.22	0/12990	0.40	0/17532

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	6389	0	6254	50	0
1	B	6348	0	6218	47	0
2	A	207	0	0	1	0
2	B	163	0	0	3	0
All	All	13107	0	12472	97	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 4.

All (97) 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:B:504:CYS:SG	2:B:901:HOH:O	2.44	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:602:VAL:HG23	1:A:614:ILE:HG13	1.67	0.75
1:A:240:MET:HE1	1:A:339:PHE:HD1	1.53	0.74
1:A:410:MET:HE1	1:A:438:ALA:HA	1.68	0.74
1:B:92:LEU:HD23	1:B:115:GLY:HA2	1.71	0.72
1:B:572:LYS:NZ	1:B:700:GLU:O	2.21	0.69
1:A:590:THR:HG22	1:A:597:GLY:HA3	1.78	0.64
1:B:92:LEU:HD12	1:B:96:GLN:HE21	1.61	0.64
1:A:667:LEU:HB2	1:A:674:ALA:HB2	1.82	0.62
1:A:607:ARG:HH21	1:A:806:GLY:HA2	1.66	0.61
1:B:620:GLU:HG3	1:B:634:LYS:HB2	1.83	0.61
1:B:284:ASP:HB3	1:B:288:LYS:HD2	1.83	0.61
1:B:101:LYS:HB3	1:B:103:MET:HG3	1.83	0.60
1:A:133:ASN:HD21	1:A:137:GLU:HB2	1.66	0.60
1:A:411:GLU:OE1	1:A:415:ARG:NH1	2.34	0.60
1:B:600:ILE:HD13	1:B:723:SER:HB3	1.83	0.60
1:A:657:TYR:OH	1:A:669:GLU:OE1	2.18	0.59
1:A:242:LYS:NZ	1:A:345:ASP:OD1	2.31	0.59
1:A:225:CYS:HB2	1:A:809:ARG:HH12	1.67	0.58
1:B:615:ASP:HA	1:B:631:ASN:HB2	1.86	0.57
1:B:357:LEU:HG	1:B:377:LEU:HG	1.86	0.57
1:A:569:LEU:HD22	1:A:681:VAL:HG22	1.88	0.55
1:A:133:ASN:ND2	1:A:137:GLU:HB2	2.21	0.54
1:B:216:THR:HG21	1:B:222:PRO:HA	1.88	0.54
1:B:681:VAL:HG11	1:B:714:VAL:HG21	1.90	0.54
1:B:647:THR:HB	1:B:654:LYS:HB3	1.91	0.53
1:B:603:SER:OG	1:B:803:THR:O	2.27	0.52
1:A:1:ALA:HB1	1:A:4:ALA:HB2	1.90	0.52
1:B:332:TYR:CG	1:B:341:CYS:HB2	2.46	0.51
1:A:567:VAL:HG12	1:A:721:LYS:HA	1.93	0.51
1:A:319:GLU:HG2	1:A:320:GLU:H	1.74	0.51
1:A:569:LEU:HD11	1:A:702:PHE:HB3	1.92	0.51
1:B:650:SER:O	1:B:652:SER:N	2.45	0.50
1:A:542:TYR:CZ	1:A:544:ASN:HB3	2.46	0.50
1:A:283:TRP:CZ2	1:A:291:ILE:HD13	2.47	0.49
1:A:510:LYS:O	1:A:514:LYS:HG3	2.12	0.49
1:B:628:THR:HG23	1:B:629:LYS:HG3	1.95	0.49
1:B:572:LYS:HD3	1:B:703:GLU:HG3	1.95	0.49
1:A:112:ASP:OD1	1:A:116:ASN:N	2.46	0.48
1:B:56:ALA:HB2	1:B:405:ILE:HD13	1.95	0.48
1:B:614:ILE:HA	1:B:632:LEU:HD11	1.95	0.48
1:A:76:PRO:HB3	1:A:392:THR:HG21	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:783:THR:HG22	2:B:951:HOH:O	2.15	0.47
1:A:284:ASP:HB3	1:A:288:LYS:HE3	1.96	0.47
1:B:256:ARG:NH2	1:B:345:ASP:O	2.40	0.46
1:B:667:LEU:HB2	1:B:674:ALA:HB2	1.98	0.46
1:B:90:LYS:O	1:B:93:LYS:HG2	2.15	0.46
1:A:684:ASN:C	1:A:689:ASN:HB3	2.41	0.46
1:B:248:GLN:HA	1:B:368:LEU:HD11	1.96	0.46
1:A:101:LYS:NZ	2:A:907:HOH:O	2.45	0.46
1:B:542:TYR:CZ	1:B:544:ASN:HB3	2.51	0.46
1:A:1:ALA:HB1	1:A:4:ALA:CB	2.46	0.46
1:A:169:LEU:HD12	1:A:169:LEU:HA	1.81	0.45
1:A:704:LEU:HG	1:A:714:VAL:HA	1.98	0.45
1:B:620:GLU:HG2	1:B:635:LEU:HG	1.99	0.45
1:B:32:ILE:HG21	1:B:408:PHE:HB2	1.99	0.45
1:A:103:MET:HE3	1:A:106:HIS:CG	2.52	0.45
1:B:682:PHE:CZ	1:B:714:VAL:HG13	2.52	0.45
1:B:483:LYS:NZ	2:B:904:HOH:O	2.49	0.44
1:B:651:LEU:HD23	1:B:651:LEU:HA	1.84	0.44
1:A:418:LYS:HE2	1:A:418:LYS:HB3	1.81	0.44
1:A:477:THR:HG22	1:A:773:LEU:HD21	2.00	0.44
1:B:90:LYS:NZ	1:B:94:GLU:OE1	2.41	0.44
1:B:660:ASN:HB3	1:B:680:VAL:HG22	2.00	0.44
1:A:542:TYR:O	1:A:779:GLN:N	2.51	0.43
1:B:46:MET:HE2	1:B:72:TYR:CG	2.53	0.43
1:B:681:VAL:HG11	1:B:714:VAL:CG2	2.47	0.43
1:A:681:VAL:O	1:A:685:THR:OG1	2.25	0.43
1:A:541:GLU:OE1	1:A:775:ASN:ND2	2.37	0.43
1:A:735:GLU:H	1:A:735:GLU:HG3	1.34	0.43
1:A:622:CYS:HB2	1:A:635:LEU:HD12	2.00	0.43
1:B:578:ASN:HD21	1:B:580:ASN:CG	2.26	0.43
1:B:631:ASN:HA	1:B:634:LYS:HE3	2.01	0.43
1:B:184:ASP:OD1	1:B:188:ASN:N	2.52	0.42
1:B:203:CYS:HB2	1:B:214:THR:HG21	2.01	0.42
1:A:639:ASP:N	1:A:639:ASP:OD1	2.51	0.42
1:B:413:GLN:OE1	1:B:437:LEU:N	2.46	0.42
1:B:636:CYS:HA	1:B:657:TYR:HD2	1.84	0.42
1:A:225:CYS:HB2	1:A:809:ARG:NH1	2.34	0.42
1:A:792:MET:HE2	1:A:792:MET:HB2	1.90	0.42
1:B:535:LEU:HB3	1:B:731:VAL:HG22	2.01	0.42
1:A:550:PRO:CG	1:A:558:TYR:HB3	2.49	0.42
1:A:240:MET:HE3	1:A:342:LEU:HD23	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ALA:O	1:B:102:LYS:HG3	2.20	0.42
1:B:137:GLU:HB3	1:B:831:VAL:HG21	2.02	0.42
1:B:200:TYR:HD2	1:B:215:LYS:HG2	1.84	0.42
1:A:527:MET:HG3	1:A:795:TYR:CZ	2.54	0.41
1:B:178:ARG:CZ	1:B:178:ARG:HA	2.50	0.41
1:A:664:PHE:HD2	1:A:693:TRP:HH2	1.67	0.41
1:B:717:TYR:O	1:B:721:LYS:HB3	2.21	0.41
1:A:319:GLU:HG2	1:A:320:GLU:N	2.35	0.41
1:A:676:VAL:HB	1:A:680:VAL:HG21	2.01	0.41
1:A:519:ALA:HA	1:A:731:VAL:O	2.21	0.40
1:A:716:ASN:OD1	1:A:716:ASN:N	2.54	0.40
1:A:291:ILE:H	1:A:291:ILE:HG12	1.43	0.40
1:A:73:ASN:HB3	1:A:397:LYS:HE2	2.03	0.40
1:A:195:HIS:HB3	1:A:198:THR:HG22	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	825/853 (97%)	792 (96%)	32 (4%)	1 (0%)	48	54
1	B	819/853 (96%)	785 (96%)	31 (4%)	3 (0%)	30	30
All	All	1644/1706 (96%)	1577 (96%)	63 (4%)	4 (0%)	43	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	651	LEU
1	A	544	ASN
1	B	300	SER
1	B	620	GLU

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	710/730 (97%)	678 (96%)	32 (4%)	24	26
1	B	706/730 (97%)	676 (96%)	30 (4%)	26	29
All	All	1416/1460 (97%)	1354 (96%)	62 (4%)	25	27

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	94	GLU
1	A	132	VAL
1	A	155	ARG
1	A	158	LEU
1	A	164	GLU
1	A	166	GLN
1	A	167	VAL
1	A	169	LEU
1	A	178	ARG
1	A	180	VAL
1	A	233	THR
1	A	253	LYS
1	A	288	LYS
1	A	291	ILE
1	A	352	LEU
1	A	418	LYS
1	A	461	LEU
1	A	545	LYS
1	A	563	THR
1	A	578	ASN
1	A	586	LYS
1	A	590	THR
1	A	610	ASP
1	A	641	LYS
1	A	649	CYS
1	A	681	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	692	VAL
1	A	735	GLU
1	A	748	GLN
1	A	786	ARG
1	A	824	HIS
1	B	92	LEU
1	B	93	LYS
1	B	94	GLU
1	B	101	LYS
1	B	132	VAL
1	B	150	ARG
1	B	158	LEU
1	B	169	LEU
1	B	182	GLN
1	B	207	ILE
1	B	224	THR
1	B	357	LEU
1	B	453	LYS
1	B	467	LEU
1	B	480	LYS
1	B	539	VAL
1	B	571	LYS
1	B	572	LYS
1	B	578	ASN
1	B	614	ILE
1	B	639	ASP
1	B	649	CYS
1	B	670	LYS
1	B	704	LEU
1	B	707	LEU
1	B	735	GLU
1	B	816	LEU
1	B	825	CYS
1	B	826	SER
1	B	832	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	315	GLN
1	A	323	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	378	ASN
1	A	436	GLN
1	A	609	ASN
1	A	660	ASN
1	A	787	GLN
1	B	6	GLN
1	B	73	ASN
1	B	89	GLN
1	B	96	GLN
1	B	120	GLN
1	B	228	HIS
1	B	248	GLN
1	B	315	GLN
1	B	827	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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	829/853 (97%)	0.40	46 (5%)	30 29	46, 79, 171, 207	0
1	B	823/853 (96%)	0.47	40 (4%)	35 33	51, 86, 151, 214	0
All	All	1652/1706 (96%)	0.44	86 (5%)	33 31	46, 84, 165, 214	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	ALA	6.8
1	B	169	LEU	5.4
1	B	170	GLY	5.3
1	B	833	PHE	5.1
1	B	88	LEU	5.1
1	B	614	ILE	5.0
1	B	829	LEU	4.9
1	B	207	ILE	4.6
1	B	4	ALA	4.0
1	A	834	GLN	3.9
1	B	826	SER	3.8
1	A	558	TYR	3.7
1	B	831	VAL	3.4
1	B	640	PRO	3.3
1	A	644	ALA	3.2
1	B	613	ASP	3.2
1	A	830	GLU	3.2
1	A	2	PRO	3.2
1	B	168	ALA	3.1
1	A	557	PRO	3.1
1	B	579	TRP	3.1
1	A	664	PHE	3.0
1	A	467	LEU	3.0
1	A	618	PHE	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	468	PRO	2.9
1	B	467	LEU	2.9
1	B	827	ASN	2.9
1	A	639	ASP	2.8
1	A	170	GLY	2.8
1	A	614	ILE	2.8
1	B	617	PHE	2.8
1	B	615	ASP	2.7
1	A	561	ALA	2.7
1	A	563	THR	2.7
1	A	579	TRP	2.7
1	B	832	LEU	2.7
1	B	106	HIS	2.6
1	A	166	GLN	2.6
1	A	691	ALA	2.6
1	B	87	ASP	2.6
1	A	643	SER	2.6
1	A	559	THR	2.6
1	A	156	HIS	2.6
1	A	693	TRP	2.5
1	A	552	LYS	2.5
1	A	602	VAL	2.5
1	A	832	LEU	2.5
1	A	713	PRO	2.5
1	B	582	ILE	2.4
1	A	283	TRP	2.4
1	B	147	GLY	2.4
1	A	651	LEU	2.4
1	B	673	VAL	2.4
1	A	3	ASN	2.3
1	A	597	GLY	2.3
1	B	85	ASN	2.3
1	B	196	GLY	2.3
1	A	575	LYS	2.2
1	B	104	ILE	2.2
1	B	637	ILE	2.2
1	A	629	LYS	2.2
1	B	149	THR	2.2
1	A	705	LEU	2.2
1	B	320	GLU	2.2
1	A	721	LYS	2.2
1	B	206	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	82	TYR	2.1
1	A	542	TYR	2.1
1	A	646	ASN	2.1
1	B	408	PHE	2.1
1	B	712	ALA	2.1
1	A	707	LEU	2.1
1	B	568	ALA	2.1
1	A	211	ILE	2.1
1	A	690	PRO	2.1
1	B	200	TYR	2.1
1	A	685	THR	2.0
1	A	4	ALA	2.0
1	A	645	ALA	2.0
1	B	694	ALA	2.0
1	A	635	LEU	2.0
1	A	681	VAL	2.0
1	B	674	ALA	2.0
1	A	169	LEU	2.0
1	B	139	ILE	2.0
1	B	163	LYS	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.