



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:36 PM UTC

PDB ID : 5C56 / pdb_00005c56
Title : Crystal structure of USP7/HAUSP in complex with ICP0
Authors : Cheng, J.; Li, Z.; Gong, R.; Fang, J.; Yang, Y.; Sun, C.; Yang, H.; Xu, Y.
Deposited on : 2015-06-19
Resolution : 2.69 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

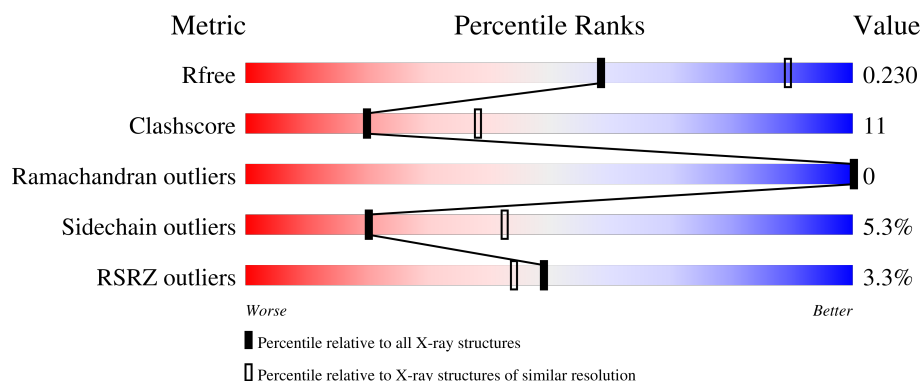
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	B	21	
2	A	548	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4446 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 Ubiquitin E3 ligase ICP0.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	13	Total	C	N	O	S	0	0	0
			104	61	26	16	1			

- Molecule 2 is a protein called Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	528	Total	C	N	O	S	0	0	0
			4336	2760	732	817	27			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	555	GLY	-	expression tag	UNP Q93009
A	556	PRO	-	expression tag	UNP Q93009
A	557	LEU	-	expression tag	UNP Q93009
A	558	GLY	-	expression tag	UNP Q93009
A	559	SER	-	expression tag	UNP Q93009

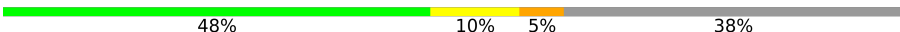
- Molecule 3 is water.

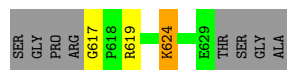
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	O	0	0
			1	1		
3	A	5	Total	O	0	0
			5	5		

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.

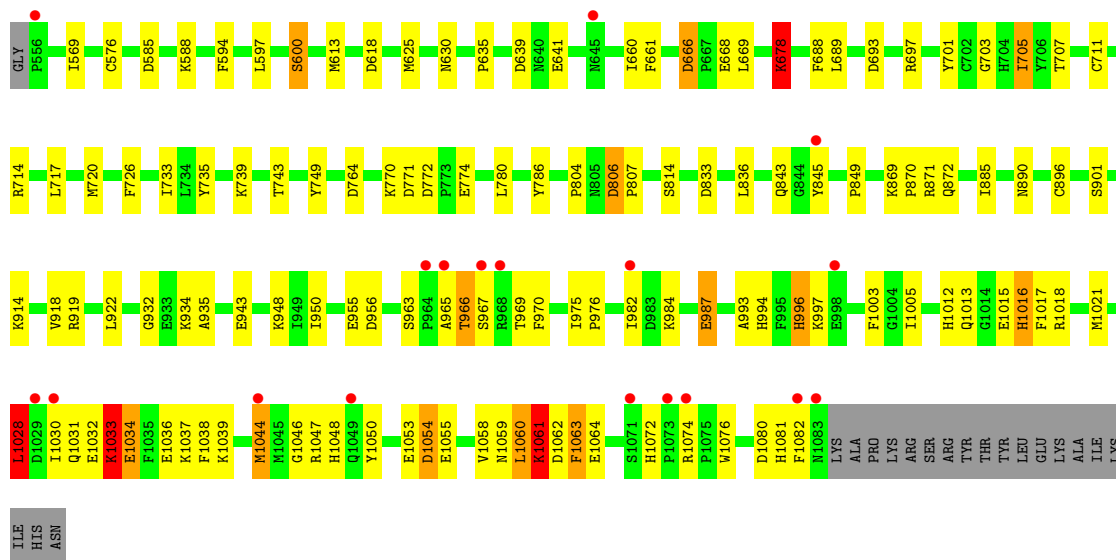
- Molecule 1: Ubiquitin E3 ligase ICP0

Chain B: 



- Molecule 2: Ubiquitin carboxyl-terminal hydrolase 7

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.88Å 80.38Å 151.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.46 – 2.69 42.46 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.3 (42.46-2.69) 99.3 (42.46-2.69)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.215 , 0.263 0.226 , 0.230	Depositor DCC
R_{free} test set	1435 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å ²)	69.0	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4446	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 4.61% 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	B	0.63	0/105	1.10	0/137
2	A	0.62	0/4436	1.07	22/5989 (0.4%)
All	All	0.62	0/4541	1.07	22/6126 (0.4%)

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
2	A	0	7

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1062	ASP	N-CA-C	-10.52	100.19	113.23
2	A	1060	LEU	CA-C-N	-8.07	111.97	122.79
2	A	1060	LEU	C-N-CA	-8.07	111.97	122.79
2	A	871	ARG	N-CA-C	7.34	123.13	113.30
2	A	1005	ILE	N-CA-C	6.77	113.72	107.56
2	A	717	LEU	CA-C-N	-6.07	112.76	119.19
2	A	717	LEU	C-N-CA	-6.07	112.76	119.19
2	A	1063	PHE	N-CA-C	6.03	120.80	113.38
2	A	1033	LYS	CA-C-N	-5.83	113.35	122.73
2	A	1033	LYS	C-N-CA	-5.83	113.35	122.73
2	A	666	ASP	N-CA-C	5.67	122.35	109.81
2	A	678	LYS	CA-C-N	-5.67	114.81	122.86
2	A	678	LYS	C-N-CA	-5.67	114.81	122.86
2	A	935	ALA	N-CA-C	5.61	118.19	109.60
2	A	1046	GLY	CA-C-N	-5.46	113.73	122.53
2	A	1046	GLY	C-N-CA	-5.46	113.73	122.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	806	ASP	CA-C-N	5.33	124.66	118.85
2	A	806	ASP	C-N-CA	5.33	124.66	118.85
2	A	707	THR	CA-C-N	-5.30	114.49	119.85
2	A	707	THR	C-N-CA	-5.30	114.49	119.85
2	A	693	ASP	CA-C-N	5.17	124.96	119.28
2	A	693	ASP	C-N-CA	5.17	124.96	119.28

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	1028	LEU	Peptide
2	A	1031	GLN	Peptide
2	A	1034	GLU	Peptide
2	A	1053	GLU	Peptide
2	A	1061	LYS	Peptide
2	A	932	GLY	Peptide
2	A	934	LYS	Peptide

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	B	104	0	109	2	0
2	A	4336	0	4250	99	0
3	A	5	0	0	0	0
3	B	1	0	0	0	0
All	All	4446	0	4359	100	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 (100) 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)
2:A:1061:LYS:HE2	2:A:1064:GLU:HG3	1.41	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:869:LYS:HD3	2:A:872:GLN:HE22	1.41	0.85
2:A:1016:HIS:NE2	2:A:1054:ASP:OD1	2.16	0.77
2:A:996:HIS:ND1	2:A:1080:ASP:OD1	2.14	0.76
2:A:1013:GLN:HE22	2:A:1059:ASN:HA	1.52	0.75
2:A:1037:LYS:HZ3	2:A:1082:PHE:H	1.35	0.75
2:A:984:LYS:H	2:A:984:LYS:HD2	1.57	0.70
2:A:1039:LYS:HE3	2:A:1050:TYR:HB3	1.71	0.69
2:A:1032:GLU:H	2:A:1032:GLU:CD	2.00	0.69
2:A:1033:LYS:O	2:A:1036:GLU:HB3	1.93	0.68
2:A:966:THR:OG1	2:A:969:THR:OG1	2.13	0.65
2:A:996:HIS:HA	2:A:1080:ASP:OD1	1.98	0.64
2:A:1047:ARG:HG3	2:A:1048:HIS:H	1.62	0.63
2:A:1016:HIS:HE1	2:A:1018:ARG:CZ	2.12	0.62
2:A:1016:HIS:HE2	2:A:1054:ASP:CG	2.07	0.61
2:A:955:GLU:N	2:A:955:GLU:OE2	2.34	0.61
2:A:1061:LYS:HE2	2:A:1064:GLU:CG	2.24	0.60
2:A:697:ARG:HG2	2:A:780:LEU:HD12	1.82	0.60
2:A:843:GLN:NE2	2:A:849:PRO:O	2.34	0.59
2:A:996:HIS:HB3	2:A:1082:PHE:CE1	2.38	0.59
2:A:1018:ARG:HA	2:A:1021:MET:HE2	1.85	0.58
2:A:1044:MET:HE2	2:A:1072:HIS:HE1	1.68	0.58
2:A:1037:LYS:NZ	2:A:1082:PHE:H	2.02	0.58
2:A:1061:LYS:CB	2:A:1064:GLU:HB2	2.34	0.57
2:A:869:LYS:HB3	2:A:870:PRO:HD2	1.86	0.57
1:B:624:LYS:NZ	2:A:764:ASP:OD1	2.37	0.57
2:A:1039:LYS:HG3	2:A:1050:TYR:CD2	2.39	0.57
2:A:1050:TYR:HE2	2:A:1080:ASP:OD2	1.88	0.56
2:A:994:HIS:HE1	2:A:1028:LEU:HD11	1.71	0.56
2:A:1061:LYS:HA	2:A:1063:PHE:H	1.72	0.55
2:A:1037:LYS:HZ2	2:A:1082:PHE:HB2	1.70	0.54
2:A:833:ASP:HB3	2:A:836:LEU:HD13	1.89	0.54
2:A:635:PRO:HG2	2:A:688:PHE:CE2	2.43	0.54
2:A:1038:PHE:HA	2:A:1080:ASP:O	2.08	0.54
2:A:1061:LYS:HB2	2:A:1064:GLU:HB2	1.89	0.54
2:A:1034:GLU:HA	2:A:1034:GLU:OE1	2.07	0.53
2:A:1016:HIS:CE1	2:A:1018:ARG:CZ	2.91	0.53
2:A:1044:MET:HE2	2:A:1072:HIS:CE1	2.44	0.53
2:A:1047:ARG:HG3	2:A:1048:HIS:N	2.25	0.52
2:A:689:LEU:HD11	2:A:705:ILE:HD13	1.93	0.51
2:A:1037:LYS:HZ3	2:A:1082:PHE:N	2.04	0.50
2:A:869:LYS:N	2:A:872:GLN:OE1	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:919:ARG:HB2	2:A:955:GLU:HB3	1.93	0.50
2:A:625:MET:HE1	2:A:661:PHE:HB2	1.93	0.49
2:A:1012:HIS:O	2:A:1015:GLU:HB3	2.11	0.49
2:A:1016:HIS:CD2	2:A:1017:PHE:N	2.80	0.49
2:A:982:ILE:HD11	2:A:987:GLU:HB2	1.94	0.49
2:A:804:PRO:O	2:A:806:ASP:N	2.45	0.49
2:A:1015:GLU:O	2:A:1058:VAL:N	2.45	0.49
2:A:594:PHE:HZ	2:A:613:MET:HE2	1.78	0.49
2:A:772:ASP:OD1	2:A:774:GLU:HG3	2.13	0.49
2:A:1034:GLU:HA	2:A:1037:LYS:H	1.78	0.48
2:A:963:SER:O	2:A:965:ALA:N	2.47	0.48
2:A:919:ARG:CZ	2:A:955:GLU:HG2	2.44	0.48
2:A:701:TYR:CZ	2:A:703:GLY:HA2	2.49	0.48
2:A:1061:LYS:H	2:A:1061:LYS:HG2	1.53	0.47
2:A:597:LEU:O	2:A:600:SER:HB3	2.15	0.47
2:A:869:LYS:HD3	2:A:872:GLN:NE2	2.20	0.47
2:A:1050:TYR:CE2	2:A:1080:ASP:OD2	2.67	0.47
2:A:714:ARG:NH2	2:A:749:TYR:HB2	2.30	0.47
2:A:918:VAL:HB	2:A:955:GLU:HA	1.97	0.46
2:A:1028:LEU:O	2:A:1030:ILE:N	2.49	0.46
2:A:1060:LEU:HA	2:A:1060:LEU:HD23	1.62	0.46
2:A:996:HIS:HD2	2:A:1082:PHE:CG	2.33	0.46
2:A:993:ALA:HB3	2:A:1076:TRP:CZ3	2.50	0.46
2:A:1039:LYS:HG3	2:A:1050:TYR:HD2	1.80	0.46
2:A:585:ASP:OD2	2:A:588:LYS:NZ	2.49	0.45
2:A:896:CYS:HB2	2:A:970:PHE:O	2.16	0.45
2:A:1061:LYS:HB3	2:A:1064:GLU:HB2	1.98	0.45
2:A:735:TYR:HB3	2:A:743:THR:HG22	1.98	0.45
2:A:1032:GLU:CD	2:A:1032:GLU:N	2.71	0.44
2:A:1039:LYS:O	2:A:1080:ASP:HB2	2.17	0.44
2:A:689:LEU:HD22	2:A:720:MET:HE2	2.00	0.44
2:A:678:LYS:O	2:A:678:LYS:HG2	2.16	0.44
2:A:1012:HIS:HB3	2:A:1015:GLU:CB	2.47	0.43
2:A:996:HIS:HB3	2:A:1082:PHE:CD1	2.53	0.43
2:A:1016:HIS:CD2	2:A:1017:PHE:H	2.36	0.43
2:A:666:ASP:HB3	2:A:669:LEU:H	1.83	0.43
2:A:943:GLU:CD	2:A:950:ILE:HD11	2.43	0.43
2:A:1054:ASP:HA	2:A:1055:GLU:HA	1.42	0.43
1:B:617:GLY:N	1:B:619:ARG:HH12	2.16	0.43
2:A:726:PHE:CZ	2:A:770:LYS:HG3	2.55	0.42
2:A:804:PRO:C	2:A:806:ASP:H	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:845:TYR:HA	2:A:869:LYS:NZ	2.34	0.42
2:A:1013:GLN:C	2:A:1015:GLU:H	2.28	0.41
2:A:1013:GLN:HB2	2:A:1060:LEU:HG	2.03	0.41
2:A:733:ILE:HG13	2:A:771:ASP:HB2	2.02	0.41
2:A:569:ILE:HD13	2:A:660:ILE:HB	2.01	0.41
2:A:786:TYR:CD1	2:A:786:TYR:C	2.98	0.41
2:A:890:ASN:O	2:A:914:LYS:HG2	2.21	0.41
2:A:922:LEU:HD23	2:A:922:LEU:HA	1.86	0.41
2:A:997:LYS:HB3	2:A:997:LYS:HE3	1.78	0.41
2:A:1003:PHE:HZ	2:A:1081:HIS:O	2.03	0.41
2:A:1061:LYS:HA	2:A:1063:PHE:N	2.36	0.41
2:A:806:ASP:HA	2:A:807:PRO:HD3	1.81	0.40
2:A:630:ASN:O	2:A:739:LYS:HE3	2.21	0.40
2:A:975:ILE:HA	2:A:976:PRO:HD3	1.98	0.40
2:A:1013:GLN:NE2	2:A:1059:ASN:HA	2.29	0.40
2:A:1061:LYS:HD3	2:A:1064:GLU:CD	2.46	0.40
2:A:701:TYR:CE2	2:A:703:GLY:HA2	2.56	0.40

There are no symmetry-related clashes.

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	B	11/21 (52%)	10 (91%)	1 (9%)	0	100	100
2	A	526/548 (96%)	504 (96%)	22 (4%)	0	100	100
All	All	537/569 (94%)	514 (96%)	23 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	B	10/15 (67%)	9 (90%)	1 (10%)	7	16
2	A	484/501 (97%)	459 (95%)	25 (5%)	21	43
All	All	494/516 (96%)	468 (95%)	26 (5%)	20	43

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	624	LYS
2	A	576	CYS
2	A	600	SER
2	A	618	ASP
2	A	639	ASP
2	A	641	GLU
2	A	668	GLU
2	A	678	LYS
2	A	705	ILE
2	A	711	CYS
2	A	814	SER
2	A	885	ILE
2	A	901	SER
2	A	948	LYS
2	A	956	ASP
2	A	966	THR
2	A	967	SER
2	A	987	GLU
2	A	996	HIS
2	A	1016	HIS
2	A	1028	LEU
2	A	1033	LYS
2	A	1044	MET
2	A	1054	ASP
2	A	1061	LYS
2	A	1074	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	627	HIS
2	A	581	ASN
2	A	747	GLN
2	A	1013	GLN
2	A	1025	GLN
2	A	1031	GLN
2	A	1059	ASN
2	A	1072	HIS
2	A	1083	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 [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	B	13/21 (61%)	0.27	0 100 100	59, 70, 90, 91	0
2	A	528/548 (96%)	0.25	18 (3%) 48 43	42, 74, 113, 134	0
All	All	541/569 (95%)	0.25	18 (3%) 49 44	42, 74, 113, 134	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	845	TYR	4.5
2	A	1030	ILE	4.1
2	A	1083	ASN	3.4
2	A	556	PRO	3.3
2	A	1073	PRO	3.2
2	A	1082	PHE	2.9
2	A	968	ARG	2.7
2	A	1049	GLN	2.7
2	A	965	ALA	2.6
2	A	1071	SER	2.4
2	A	967	SER	2.4
2	A	964	PRO	2.2
2	A	1029	ASP	2.2
2	A	1044	MET	2.1
2	A	645	ASN	2.1
2	A	998	GLU	2.1
2	A	1074	ARG	2.1
2	A	982	ILE	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.