



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:24 PM UTC

PDB ID : 2C1Y / pdb_00002c1y
Title : Structure of PDI-related Chaperone, Wind mutant-Y55K
Authors : Sevvana, M.; Ma, Q.; Barnewitz, K.; Guo, C.; Soling, H.-D.; Ferrari, D.M.;
Sheldrick, G.M.
Deposited on : 2005-09-22
Resolution : 2.25 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

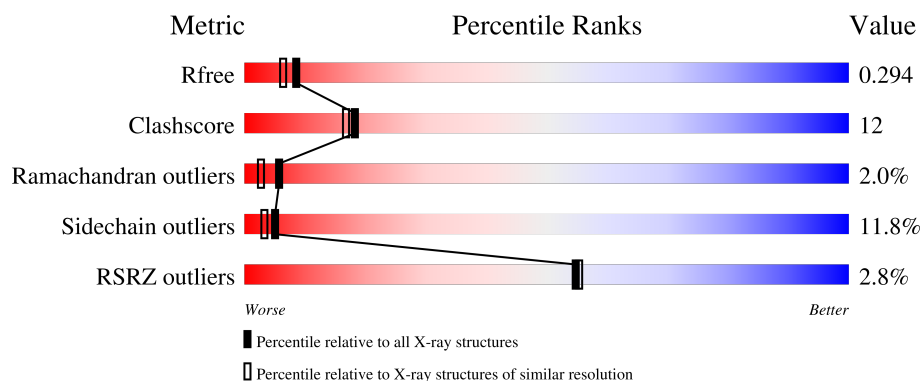
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	248	
1	B	248	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2704 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 WINDBEUTEL PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	0	0
			1720	1108	282	326	4			
1	B	128	Total	C	N	O	S	0	0	0
			929	596	153	178	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	55	LYS	TYR	engineered mutation	UNP O44342
B	55	LYS	TYR	engineered mutation	UNP O44342

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	35	Total	O	0	0
			35	35		
2	B	20	Total	O	0	0
			20	20		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	35.42Å 119.09Å 64.03Å 90.00° 100.53° 90.00°	Depositor
Resolution (Å)	20.00 – 2.25 20.00 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-2.25) 97.5 (20.00-2.25)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.25Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.223 , 0.292 0.225 , 0.294	Depositor DCC
R_{free} test set	1220 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	45.6	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.9	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	0.94	EDS
Total number of atoms	2704	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% 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	1.89	32/1751 (1.8%)	1.71	38/2377 (1.6%)
1	B	1.96	19/950 (2.0%)	1.68	18/1293 (1.4%)
All	All	1.92	51/2701 (1.9%)	1.70	56/3670 (1.5%)

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	A	0	2

All (51) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	144	ILE	CA-C	10.65	1.66	1.52
1	A	246	LYS	C-O	10.53	1.35	1.24
1	A	118	TYR	C-O	8.90	1.34	1.23
1	A	140	THR	CA-CB	8.66	1.65	1.53
1	B	136	VAL	CA-CB	8.47	1.65	1.54
1	B	53	TYR	N-CA	7.82	1.57	1.46
1	A	241	VAL	CA-CB	7.80	1.65	1.54
1	A	37	LYS	C-O	-7.32	1.15	1.24
1	B	134	ALA	CA-CB	7.02	1.64	1.53
1	B	47	VAL	C-O	-6.97	1.17	1.24
1	B	108	ILE	C-O	-6.92	1.16	1.24
1	B	51	ILE	CA-CB	6.70	1.63	1.54
1	A	52	ALA	C-O	6.64	1.31	1.23
1	A	91	ASN	N-CA	-6.43	1.37	1.46
1	A	114	ASN	N-CA	6.39	1.53	1.46
1	A	39	VAL	C-O	-6.22	1.17	1.24
1	A	247	VAL	CA-C	6.12	1.59	1.52
1	A	105	PHE	C-O	-6.09	1.16	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	97	ARG	NE-CZ	6.07	1.39	1.33
1	B	115	ALA	CA-CB	-5.91	1.43	1.53
1	A	208	PHE	CA-C	5.87	1.60	1.52
1	A	51	ILE	CA-CB	5.80	1.59	1.54
1	B	82	GLY	CA-C	-5.77	1.48	1.52
1	A	246	LYS	C-N	5.77	1.40	1.33
1	A	184	ASP	CB-CG	5.74	1.66	1.52
1	A	215	ARG	CA-C	5.72	1.60	1.52
1	B	47	VAL	CA-C	-5.70	1.45	1.52
1	B	132	LEU	C-O	-5.69	1.17	1.24
1	B	53	TYR	C-N	-5.64	1.26	1.33
1	A	38	THR	CA-C	5.62	1.60	1.52
1	A	158	LYS	CA-C	5.61	1.60	1.52
1	A	130	ASP	N-CA	-5.55	1.39	1.46
1	B	145	GLY	N-CA	5.51	1.53	1.45
1	B	81	VAL	CA-CB	5.44	1.61	1.54
1	A	54	PRO	N-CA	-5.40	1.40	1.47
1	A	114	ASN	CA-C	5.39	1.59	1.52
1	A	71	LYS	CA-C	5.39	1.59	1.52
1	A	233	LEU	C-O	-5.29	1.18	1.24
1	A	79	ALA	CA-CB	5.26	1.65	1.54
1	A	235	LYS	C-O	-5.25	1.17	1.24
1	B	90	GLU	N-CA	5.23	1.52	1.46
1	A	173	GLU	CG-CD	5.21	1.65	1.52
1	B	85	ASP	N-CA	5.20	1.52	1.46
1	B	37	LYS	CA-C	5.14	1.59	1.52
1	A	190	ASN	C-O	-5.14	1.18	1.24
1	A	156	VAL	N-CA	5.14	1.52	1.46
1	A	235	LYS	CA-C	-5.13	1.46	1.52
1	A	181	GLN	CA-C	5.12	1.59	1.52
1	B	140	THR	N-CA	5.11	1.51	1.46
1	B	140	THR	CA-CB	5.05	1.61	1.54
1	A	188	GLN	N-CA	5.04	1.52	1.46

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	TYR	N-CA-C	-8.64	96.31	109.96
1	A	97	ARG	N-CA-C	-8.20	102.28	111.71
1	B	81	VAL	N-CA-C	-8.00	96.49	108.17
1	B	130	ASP	N-CA-C	7.68	120.73	111.82
1	A	42	PHE	CA-C-N	-7.67	111.06	119.19

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	42	PHE	C-N-CA	-7.67	111.06	119.19
1	A	121	LEU	CA-C-N	-7.67	111.88	119.78
1	A	121	LEU	C-N-CA	-7.67	111.88	119.78
1	A	136	VAL	N-CA-C	7.60	117.72	110.42
1	A	252	PRO	N-CA-C	7.56	128.05	112.47
1	B	52	ALA	N-CA-C	-7.11	100.48	110.50
1	A	163	ILE	CA-C-N	-6.89	112.68	119.78
1	A	163	ILE	C-N-CA	-6.89	112.68	119.78
1	B	73	THR	N-CA-C	6.79	120.59	109.24
1	B	144	ILE	CB-CA-C	6.74	122.35	111.29
1	A	41	ARG	CG-CD-NE	-6.65	97.38	112.00
1	B	144	ILE	N-CA-C	6.64	123.15	109.34
1	A	183	THR	N-CA-C	6.59	121.61	112.45
1	B	139	ASN	N-CA-C	6.46	121.95	113.30
1	A	189	GLN	N-CA-C	6.17	118.08	111.36
1	A	41	ARG	NE-CZ-NH2	-5.88	113.91	119.20
1	A	151	LYS	N-CA-C	5.88	118.16	111.11
1	A	234	ARG	N-CA-C	5.83	117.63	111.28
1	A	232	LEU	N-CA-C	5.78	117.26	111.07
1	A	115	ALA	N-CA-C	-5.76	106.20	113.18
1	A	134	ALA	N-CA-C	5.75	117.54	111.28
1	B	22	VAL	N-CA-C	5.71	126.99	111.00
1	A	211	GLU	N-CA-C	5.68	117.17	110.97
1	A	24	CYS	N-CA-C	5.59	122.70	110.80
1	A	100	VAL	CB-CA-C	-5.54	103.47	111.34
1	A	215	ARG	N-CA-C	5.52	116.97	111.07
1	A	176	GLN	N-CA-C	-5.50	105.19	111.14
1	A	182	LEU	N-CA-C	5.50	118.21	109.96
1	B	144	ILE	O-C-N	-5.48	115.72	122.57
1	B	67	LYS	CB-CG-CD	-5.46	98.74	111.30
1	A	101	ASP	CA-C-N	5.45	127.85	120.38
1	A	101	ASP	C-N-CA	5.45	127.85	120.38
1	A	251	ALA	CA-C-N	5.43	126.63	119.84
1	A	251	ALA	C-N-CA	5.43	126.63	119.84
1	B	53	TYR	N-CA-C	5.38	121.69	109.81
1	B	53	TYR	CA-C-N	-5.37	114.72	120.03
1	B	53	TYR	C-N-CA	-5.37	114.72	120.03
1	B	91	ASN	N-CA-C	5.34	119.75	113.23
1	B	68	SER	CA-C-N	5.34	127.44	120.28
1	B	68	SER	C-N-CA	5.34	127.44	120.28
1	A	196	ILE	N-CA-C	-5.32	104.56	110.62
1	B	67	LYS	CB-CA-C	-5.31	100.48	110.67

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	GLU	CA-CB-CG	5.27	124.64	114.10
1	B	52	ALA	O-C-N	-5.21	116.72	122.86
1	A	149	CYS	N-CA-C	5.13	117.16	110.43
1	A	252	PRO	N-CA-CB	5.12	108.62	103.25
1	A	116	ASP	CA-C-N	-5.12	115.56	122.77
1	A	116	ASP	C-N-CA	-5.12	115.56	122.77
1	A	52	ALA	N-CA-C	-5.05	102.38	109.96
1	A	150	ILE	CA-C-N	5.02	127.31	120.54
1	A	150	ILE	C-N-CA	5.02	127.31	120.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	251	ALA	Peptide
1	A	85	ASP	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	A	1720	0	1611	44	0
1	B	929	0	847	19	0
2	A	35	0	0	7	0
2	B	20	0	0	2	0
All	All	2704	0	2458	62	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 12.

All (62) 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:252:PRO:CB	2:A:2034:HOH:O	1.64	1.32
1:A:210:GLU:O	1:A:214:LYS:HG3	1.69	0.92

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:ARG:CG	2:A:2014:HOH:O	2.18	0.90
1:B:129:LEU:HD22	1:B:133:LYS:HE3	1.54	0.89
1:A:252:PRO:N	2:A:2033:HOH:O	2.12	0.81
1:A:97:ARG:NE	2:A:2014:HOH:O	2.12	0.79
1:A:97:ARG:CD	2:A:2014:HOH:O	2.35	0.75
1:A:163:ILE:HG12	1:A:168:GLN:HG3	1.70	0.73
1:A:159:ASN:O	1:A:163:ILE:HG23	1.89	0.72
1:B:133:LYS:NZ	1:B:145:GLY:O	2.23	0.70
1:A:97:ARG:HG2	2:A:2014:HOH:O	1.88	0.69
1:A:234:ARG:O	1:A:238:ILE:HG13	1.94	0.68
1:B:129:LEU:CD2	1:B:133:LYS:HE3	2.24	0.68
1:B:149:CYS:C	2:B:2020:HOH:O	2.39	0.66
1:A:23:THR:O	1:A:24:CYS:O	2.14	0.64
1:A:112:LYS:HE3	1:A:139:ASN:O	1.97	0.64
1:A:53:TYR:N	1:A:54:PRO:HD3	2.12	0.64
1:A:36:GLU:O	1:A:40:GLU:HG3	1.97	0.64
1:A:110:LEU:HB3	1:A:119:VAL:HG12	1.82	0.60
1:B:69:ALA:O	1:B:73:THR:HG22	2.01	0.60
1:A:204:VAL:O	1:A:204:VAL:HG12	2.02	0.59
1:B:44:TYR:CD2	1:B:142:LEU:HD11	2.37	0.58
1:B:63:THR:O	1:B:67:LYS:HG3	2.04	0.58
1:A:100:VAL:HG23	1:A:100:VAL:O	2.05	0.57
1:A:179:GLN:HG3	1:A:191:ALA:HB1	1.87	0.56
1:B:48:LYS:HG3	1:B:106:PRO:HB2	1.87	0.56
1:B:110:LEU:C	1:B:110:LEU:HD23	2.31	0.56
1:A:53:TYR:H	1:A:54:PRO:HD3	1.70	0.55
1:B:97:ARG:HD3	1:B:98:TYR:CE2	2.43	0.53
1:A:207:ASP:OD1	1:A:207:ASP:N	2.38	0.53
1:A:100:VAL:O	1:A:100:VAL:CG2	2.58	0.52
1:B:46:VAL:HG23	1:B:76:LEU:HD11	1.92	0.51
1:A:69:ALA:O	1:A:73:THR:HG22	2.12	0.50
1:A:169:LEU:HG	1:A:202:HIS:CE1	2.46	0.50
1:A:27:CYS:HB3	1:A:80:THR:HG23	1.94	0.50
1:A:46:VAL:HG23	1:A:76:LEU:HD11	1.95	0.49
1:B:102:ASP:HB3	1:B:105:PHE:CE2	2.48	0.48
1:A:129:LEU:HD22	1:A:133:LYS:HE3	1.95	0.48
1:B:44:TYR:HD2	1:B:142:LEU:HD11	1.79	0.48
1:B:73:THR:HG23	2:B:2009:HOH:O	2.14	0.48
1:A:121:LEU:O	1:A:122:PRO:C	2.55	0.47
1:A:179:GLN:HG3	1:A:191:ALA:CB	2.44	0.47
1:A:248:THR:HG23	1:A:248:THR:O	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ASP:HA	1:A:105:PHE:CE2	2.49	0.47
1:A:187:GLN:HE21	1:A:190:ASN:HD22	1.61	0.47
1:A:97:ARG:NH2	1:A:116:ASP:OD1	2.49	0.45
1:A:163:ILE:HG12	1:A:168:GLN:CG	2.45	0.45
1:B:71:LYS:HE3	1:B:71:LYS:HB2	1.29	0.45
1:A:212:GLU:HA	1:A:212:GLU:OE1	2.16	0.45
1:A:204:VAL:O	1:A:204:VAL:CG1	2.66	0.44
1:A:23:THR:O	1:A:23:THR:OG1	2.34	0.44
1:A:88:GLU:O	1:A:89:LEU:C	2.61	0.43
1:A:184:ASP:OD2	1:A:186:GLU:HB3	2.18	0.43
1:A:97:ARG:NH1	2:A:2015:HOH:O	2.52	0.43
1:A:102:ASP:OD2	1:A:102:ASP:N	2.43	0.43
1:A:134:ALA:HA	1:A:137:SER:OG	2.19	0.42
1:B:49:PHE:O	1:B:106:PRO:HA	2.20	0.42
1:A:85:ASP:HB3	1:A:89:LEU:HD23	2.02	0.42
1:B:64:ALA:O	1:B:68:SER:HB3	2.20	0.41
1:B:102:ASP:C	1:B:104:ASN:H	2.27	0.41
1:A:41:ARG:HD2	1:B:41:ARG:O	2.21	0.40
1:A:187:GLN:NE2	1:A:190:ASN:HD22	2.18	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	229/248 (92%)	211 (92%)	13 (6%)	5 (2%)	5	2
1	B	126/248 (51%)	116 (92%)	8 (6%)	2 (2%)	7	4
All	All	355/496 (72%)	327 (92%)	21 (6%)	7 (2%)	6	3

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	24	CYS
1	A	104	ASN
1	A	252	PRO
1	B	144	ILE
1	A	185	PRO
1	B	146	ARG
1	A	53	TYR

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	164/218 (75%)	144 (88%)	20 (12%)	5	3
1	B	90/218 (41%)	80 (89%)	10 (11%)	6	4
All	All	254/436 (58%)	224 (88%)	30 (12%)	5	3

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	THR
1	A	28	VAL
1	A	55	LYS
1	A	84	LYS
1	A	85	ASP
1	A	89	LEU
1	A	102	ASP
1	A	126	ASP
1	A	129	LEU
1	A	130	ASP
1	A	132	LEU
1	A	159	ASN
1	A	163	ILE
1	A	180	GLU
1	A	184	ASP
1	A	185	PRO
1	A	187	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	207	ASP
1	A	248	THR
1	A	250	THR
1	B	24	CYS
1	B	28	VAL
1	B	71	LYS
1	B	77	LEU
1	B	102	ASP
1	B	104	ASN
1	B	112	LYS
1	B	129	LEU
1	B	130	ASP
1	B	132	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	HIS
1	A	139	ASN
1	A	187	GLN
1	A	202	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	231/248 (93%)	0.09	7 (3%) 52 53	30, 47, 75, 96	0
1	B	128/248 (51%)	-0.02	3 (2%) 61 61	29, 46, 69, 75	0
All	All	359/496 (72%)	0.05	10 (2%) 55 55	29, 47, 73, 96	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	251	ALA	3.1
1	B	145	GLY	2.5
1	A	209	LEU	2.4
1	A	249	LYS	2.4
1	A	247	VAL	2.4
1	A	202	HIS	2.3
1	A	253	GLU	2.3
1	A	23	THR	2.2
1	B	144	ILE	2.2
1	B	146	ARG	2.1

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.