



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:49 AM UTC

PDB ID : 1NAR / pdb_00001nar
Title : CRYSTAL STRUCTURE OF NARBONIN REFINED AT 1.8 ANGSTROMS RESOLUTION
Authors : Hennig, M.; Schlesier, B.; Wilson, K.S.
Deposited on : 1993-09-10
Resolution : 1.80 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

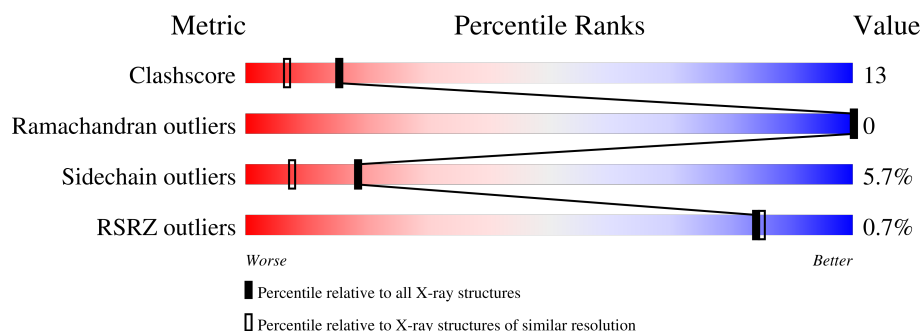
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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))
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	290	62% 28% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2846 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 NARBONIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2333	1498	384	449	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	ALA	LYS	conflict	UNP Q08884

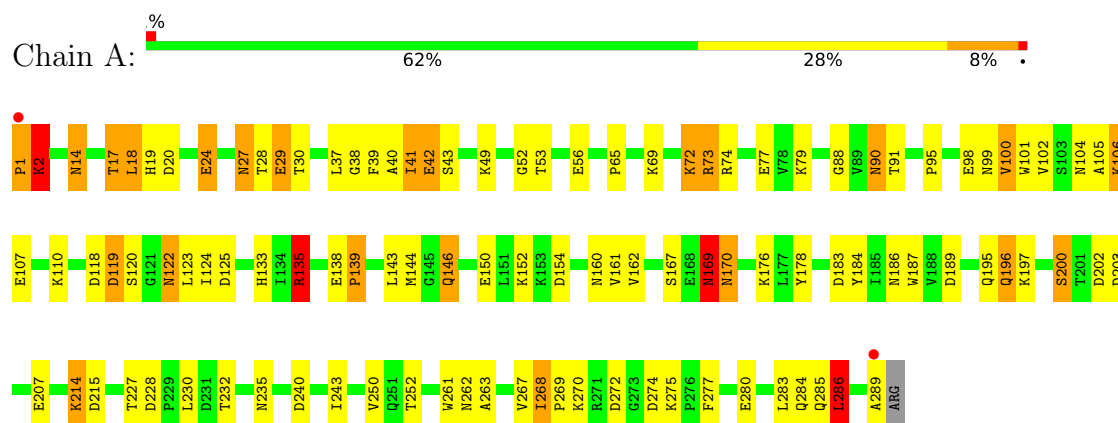
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	513	Total	O	0	0
			513	513		

3 Residue-property plots

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: NARBONIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.90Å 75.50Å 50.90Å 90.00° 120.50° 90.00°	Depositor
Resolution (Å)	10.00 – 1.80 10.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-1.80) 95.6 (10.00-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	14.03 (at 1.79Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.159 , (Not available) 0.189 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	15.1	Xtriage
Anisotropy	0.177	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 94.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.020 for -h-l,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2846	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.32% 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	1.16	5/2394 (0.2%)	2.26	107/3250 (3.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2	LYS	N-CA	-9.95	1.32	1.46
1	A	91	THR	CA-CB	6.59	1.60	1.53
1	A	38	GLY	C-O	5.78	1.29	1.23
1	A	139	PRO	N-CD	-5.02	1.40	1.47
1	A	38	GLY	N-CA	-5.02	1.40	1.45

All (107) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	GLU	CA-CB-CG	23.24	160.58	114.10
1	A	74	ARG	CG-CD-NE	16.55	148.40	112.00
1	A	261	TRP	O-C-N	-14.59	104.04	123.01
1	A	29	GLU	CB-CG-CD	14.55	137.33	112.60
1	A	138	GLU	O-C-N	14.15	133.97	121.80
1	A	38	GLY	CA-C-N	12.82	144.77	121.70
1	A	38	GLY	C-N-CA	12.82	144.77	121.70
1	A	19	HIS	CA-CB-CG	-12.27	101.53	113.80
1	A	1	PRO	CA-C-N	10.82	148.20	121.80
1	A	1	PRO	C-N-CA	10.82	148.20	121.80
1	A	41	ILE	N-CA-CB	-9.62	92.00	111.91
1	A	119	ASP	CA-CB-CG	9.59	122.19	112.60
1	A	262	ASN	OD1-CG-ND2	9.54	132.14	122.60
1	A	228	ASP	CA-CB-CG	8.86	121.46	112.60
1	A	73	ARG	CB-CG-CD	8.60	131.09	111.30
1	A	215	ASP	CA-CB-CG	8.47	121.07	112.60
1	A	138	GLU	CA-C-N	8.46	147.30	127.00
1	A	138	GLU	C-N-CA	8.46	147.30	127.00
1	A	285	GLN	OE1-CD-NE2	-8.40	114.20	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	261	TRP	N-CA-CB	8.00	123.98	110.46
1	A	2	LYS	CA-C-O	-7.91	109.32	120.16
1	A	280	GLU	CB-CG-CD	7.86	125.96	112.60
1	A	261	TRP	CA-C-O	-7.75	111.87	120.70
1	A	39	PHE	N-CA-CB	7.70	123.59	110.50
1	A	19	HIS	N-CA-CB	7.64	123.58	110.98
1	A	40	ALA	N-CA-C	-7.52	97.00	108.96
1	A	99	ASN	CA-C-O	-7.43	110.29	119.28
1	A	200	SER	N-CA-C	7.34	122.33	113.23
1	A	100	VAL	N-CA-C	-7.18	106.50	113.53
1	A	274	ASP	CA-CB-CG	7.18	119.78	112.60
1	A	285	GLN	CB-CG-CD	7.17	124.78	112.60
1	A	98	GLU	CA-C-O	-7.03	112.16	120.10
1	A	14	ASN	CA-CB-CG	-7.02	105.58	112.60
1	A	74	ARG	CD-NE-CZ	7.00	134.20	124.40
1	A	200	SER	CA-CB-OG	-6.92	97.25	111.10
1	A	19	HIS	O-C-N	6.88	130.51	122.19
1	A	120	SER	CA-C-O	-6.86	111.61	119.78
1	A	268	ILE	N-CA-C	6.71	114.19	107.55
1	A	27	ASN	CB-CG-ND2	-6.66	106.41	116.40
1	A	139	PRO	N-CD-CG	6.62	111.75	103.80
1	A	24	GLU	CB-CA-C	-6.61	98.40	110.63
1	A	100	VAL	N-CA-CB	6.56	120.97	112.12
1	A	18	LEU	CA-C-N	-6.52	112.33	122.37
1	A	18	LEU	C-N-CA	-6.52	112.33	122.37
1	A	169	ASN	CA-CB-CG	6.50	119.09	112.60
1	A	104	ASN	OD1-CG-ND2	-6.46	116.14	122.60
1	A	105	ALA	CA-C-O	-6.45	114.06	120.70
1	A	72	LYS	CA-C-O	-6.42	112.59	119.97
1	A	102	VAL	CA-C-O	-6.36	114.33	120.95
1	A	106	LYS	CG-CD-CE	6.29	125.77	111.30
1	A	77	GLU	CB-CG-CD	6.26	123.24	112.60
1	A	160	ASN	CA-CB-CG	6.25	118.85	112.60
1	A	214	LYS	CA-CB-CG	6.18	126.46	114.10
1	A	243	ILE	CA-C-N	6.18	126.97	119.99
1	A	243	ILE	C-N-CA	6.18	126.97	119.99
1	A	17	THR	CA-C-O	-6.17	111.78	119.38
1	A	235	ASN	N-CA-CB	-6.16	102.59	111.70
1	A	286	LEU	CA-CB-CG	6.10	137.66	116.30
1	A	187	TRP	CA-C-O	-6.08	113.57	120.32
1	A	189	ASP	CA-C-O	-6.04	114.64	120.92
1	A	203	ASP	N-CA-CB	6.02	119.07	110.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	18	LEU	CA-C-O	-5.99	114.10	121.11
1	A	183	ASP	CA-C-O	-5.96	112.05	119.38
1	A	133	HIS	CA-CB-CG	-5.92	107.88	113.80
1	A	203	ASP	CA-C-O	-5.90	114.17	120.42
1	A	144	MET	CA-C-N	5.81	126.39	119.94
1	A	144	MET	C-N-CA	5.81	126.39	119.94
1	A	29	GLU	N-CA-CB	5.79	118.70	110.13
1	A	27	ASN	CA-C-N	-5.77	113.55	122.49
1	A	27	ASN	C-N-CA	-5.77	113.55	122.49
1	A	144	MET	CG-SD-CE	5.71	113.46	100.90
1	A	52	GLY	N-CA-C	-5.70	107.46	115.32
1	A	122	ASN	OD1-CG-ND2	-5.65	116.95	122.60
1	A	196	GLN	CB-CG-CD	-5.59	103.10	112.60
1	A	135	ARG	CD-NE-CZ	5.56	132.19	124.40
1	A	262	ASN	O-C-N	5.49	131.78	123.00
1	A	195	GLN	OE1-CD-NE2	-5.45	117.15	122.60
1	A	138	GLU	C-N-CD	-5.45	108.61	120.60
1	A	19	HIS	CB-CG-CD2	-5.44	124.13	131.20
1	A	240	ASP	CA-C-O	-5.41	114.82	120.55
1	A	2	LYS	CA-C-N	5.37	125.31	119.78
1	A	2	LYS	C-N-CA	5.37	125.31	119.78
1	A	146	GLN	OE1-CD-NE2	-5.34	117.26	122.60
1	A	138	GLU	CA-C-O	-5.33	114.44	120.46
1	A	232	THR	CA-C-N	5.30	127.91	120.28
1	A	232	THR	C-N-CA	5.30	127.91	120.28
1	A	139	PRO	CA-N-CD	-5.30	104.08	111.50
1	A	161	VAL	CA-C-O	-5.29	114.89	120.39
1	A	107	GLU	N-CA-C	5.27	117.03	111.28
1	A	42	GLU	CA-CB-CG	5.25	124.60	114.10
1	A	286	LEU	CB-CA-C	5.25	120.75	110.67
1	A	252	THR	CA-CB-OG1	-5.24	101.75	109.60
1	A	262	ASN	CA-C-O	-5.23	111.91	120.80
1	A	178	TYR	CA-C-O	-5.20	115.04	120.55
1	A	272	ASP	CA-CB-CG	-5.18	107.42	112.60
1	A	41	ILE	CB-CA-C	5.17	118.78	110.82
1	A	284	GLN	CG-CD-NE2	5.16	124.14	116.40
1	A	20	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	43	SER	N-CA-C	-5.15	102.14	110.32
1	A	104	ASN	CA-C-N	5.14	127.43	120.44
1	A	104	ASN	C-N-CA	5.14	127.43	120.44
1	A	56	GLU	CG-CD-OE2	-5.13	106.59	118.40
1	A	53	THR	CA-CB-OG1	-5.13	101.91	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	187	TRP	N-CA-C	5.09	117.36	108.76
1	A	139	PRO	N-CA-CB	5.02	108.13	102.60
1	A	28	THR	O-C-N	5.02	128.32	122.24
1	A	37	LEU	O-C-N	5.01	128.89	123.13

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	2333	0	2278	62	0
2	A	513	0	0	23	0
All	All	2846	0	2278	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 13.

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:119:ASP:HB3	2:A:699:HOH:O	1.23	1.37
1:A:135:ARG:HD2	1:A:135:ARG:H	1.14	1.13
1:A:1:PRO:O	2:A:575:HOH:O	1.66	1.12
1:A:169:ASN:HB3	2:A:637:HOH:O	1.62	0.98
1:A:135:ARG:HD2	1:A:135:ARG:N	1.86	0.89
1:A:162:VAL:H	1:A:186:ASN:HD22	1.21	0.88
1:A:202:ASP:HB3	2:A:741:HOH:O	1.78	0.84
1:A:18:LEU:HD21	1:A:267:VAL:HG11	1.70	0.74
1:A:135:ARG:HH11	1:A:135:ARG:HG3	1.53	0.73
1:A:90:ASN:H	1:A:90:ASN:HD22	1.38	0.71
1:A:250:VAL:HG21	1:A:286:LEU:HD12	1.75	0.69
1:A:27:ASN:HD21	1:A:30:THR:CG2	2.07	0.68
1:A:152:LYS:HD3	1:A:184:TYR:HD2	1.58	0.68
1:A:122:ASN:CB	2:A:591:HOH:O	2.42	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:VAL:HG12	1:A:277:PHE:CZ	2.29	0.67
1:A:263:ALA:O	1:A:267:VAL:HG13	1.95	0.67
1:A:135:ARG:H	1:A:135:ARG:CD	1.94	0.66
1:A:170:ASN:HD22	1:A:170:ASN:C	2.03	0.66
1:A:122:ASN:HB2	2:A:591:HOH:O	1.98	0.64
1:A:230:LEU:O	2:A:502:HOH:O	2.15	0.64
1:A:267:VAL:HG23	1:A:268:ILE:HD13	1.79	0.63
1:A:27:ASN:HD21	1:A:30:THR:HG22	1.65	0.61
1:A:162:VAL:H	1:A:186:ASN:ND2	1.96	0.60
1:A:167:SER:H	1:A:170:ASN:HD21	1.48	0.60
1:A:72:LYS:HE2	2:A:686:HOH:O	2.02	0.59
1:A:122:ASN:HB3	2:A:591:HOH:O	2.04	0.58
1:A:125:ASP:OD2	2:A:686:HOH:O	2.17	0.57
1:A:250:VAL:HG21	1:A:286:LEU:CD1	2.35	0.56
1:A:79:LYS:HE2	2:A:555:HOH:O	2.05	0.56
1:A:122:ASN:HD22	1:A:124:ILE:H	1.55	0.55
1:A:167:SER:H	1:A:170:ASN:ND2	2.07	0.53
1:A:49:LYS:HE3	2:A:417:HOH:O	2.11	0.51
1:A:275:LYS:NZ	2:A:595:HOH:O	2.37	0.49
1:A:152:LYS:HD3	1:A:184:TYR:CD2	2.45	0.49
1:A:27:ASN:ND2	1:A:30:THR:HG22	2.27	0.48
1:A:27:ASN:ND2	1:A:30:THR:CG2	2.76	0.47
1:A:123:LEU:O	2:A:686:HOH:O	2.20	0.47
1:A:135:ARG:HD3	2:A:374:HOH:O	2.14	0.47
1:A:88:GLY:HA3	1:A:90:ASN:ND2	2.30	0.47
1:A:1:PRO:CD	2:A:584:HOH:O	2.63	0.47
1:A:122:ASN:ND2	1:A:124:ILE:H	2.12	0.46
1:A:135:ARG:NH1	2:A:731:HOH:O	2.42	0.46
1:A:73:ARG:HD2	1:A:118:ASP:OD2	2.16	0.46
1:A:110:LYS:NZ	1:A:154:ASP:OD2	2.41	0.46
1:A:90:ASN:H	1:A:90:ASN:ND2	2.09	0.46
1:A:146:GLN:O	1:A:150:GLU:HG2	2.17	0.45
1:A:176:LYS:NZ	2:A:780:HOH:O	2.47	0.45
1:A:18:LEU:CD2	1:A:267:VAL:HG11	2.45	0.45
1:A:196:GLN:HA	1:A:196:GLN:OE1	2.16	0.45
1:A:227:THR:O	1:A:270:LYS:NZ	2.46	0.45
1:A:1:PRO:HB2	1:A:2:LYS:H	1.33	0.43
1:A:1:PRO:N	2:A:584:HOH:O	2.52	0.43
1:A:139:PRO:HB2	1:A:143:LEU:HG	2.01	0.43
1:A:269:PRO:HA	2:A:391:HOH:O	2.18	0.43
1:A:2:LYS:CE	1:A:29:GLU:O	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:PRO:O	1:A:69:LYS:HG3	2.17	0.43
1:A:30:THR:HG21	2:A:546:HOH:O	2.18	0.42
1:A:95:PRO:HB3	1:A:101:TRP:CD1	2.55	0.42
1:A:289:ALA:HB3	2:A:658:HOH:O	2.20	0.41
1:A:14:ASN:HD22	1:A:14:ASN:HA	1.66	0.41
1:A:17:THR:HB	1:A:267:VAL:HG21	2.02	0.40
1:A:196:GLN:NE2	2:A:637:HOH:O	2.53	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	287/290 (99%)	280 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	262/263 (100%)	247 (94%)	15 (6%)	18	8

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	24	GLU
1	A	41	ILE
1	A	42	GLU
1	A	90	ASN
1	A	100	VAL
1	A	106	LYS
1	A	135	ARG
1	A	169	ASN
1	A	170	ASN
1	A	197	LYS
1	A	200	SER
1	A	214	LYS
1	A	283	LEU
1	A	286	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	14	ASN
1	A	19	HIS
1	A	75	HIS
1	A	90	ASN
1	A	104	ASN
1	A	122	ASN
1	A	133	HIS
1	A	170	ASN
1	A	179	ASN
1	A	186	ASN
1	A	194	ASN
1	A	195	GLN
1	A	217	HIS
1	A	234	HIS
1	A	235	ASN
1	A	251	GLN
1	A	284	GLN

5.3.3 RNA ⓘ

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	A	289/290 (99%)	0.00	2 (0%) 84 85	4, 13, 27, 39	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	PRO	3.7
1	A	289	ALA	2.2

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.