



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:57 PM UTC

PDB ID : 1RAZ / pdb_00001raz
Title : THE STRUCTURE OF HUMAN CARBONIC ANHYDRASE II IN COM-
PLEX WITH BROMIDE AND AZIDE
Authors : Jonsson, B.M.; Hakansson, K.; Liljas, A.
Deposited on : 1993-04-02
Resolution : 1.90 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

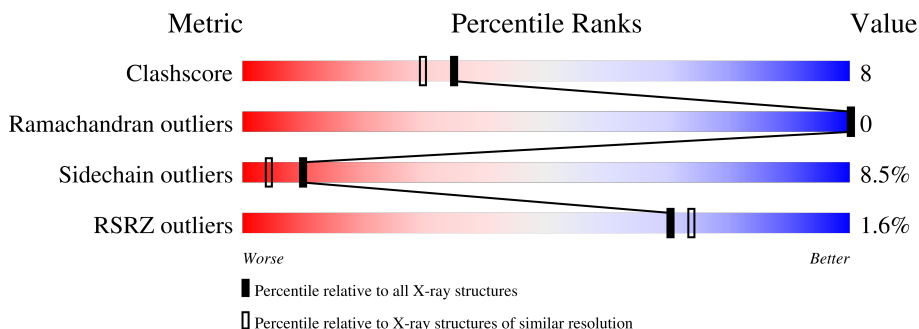
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	259	2% 57% 34% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2299 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 CARBONIC ANHYDRASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	4	0
			2079	1333	360	384	2			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Br	0	0
			1	1		

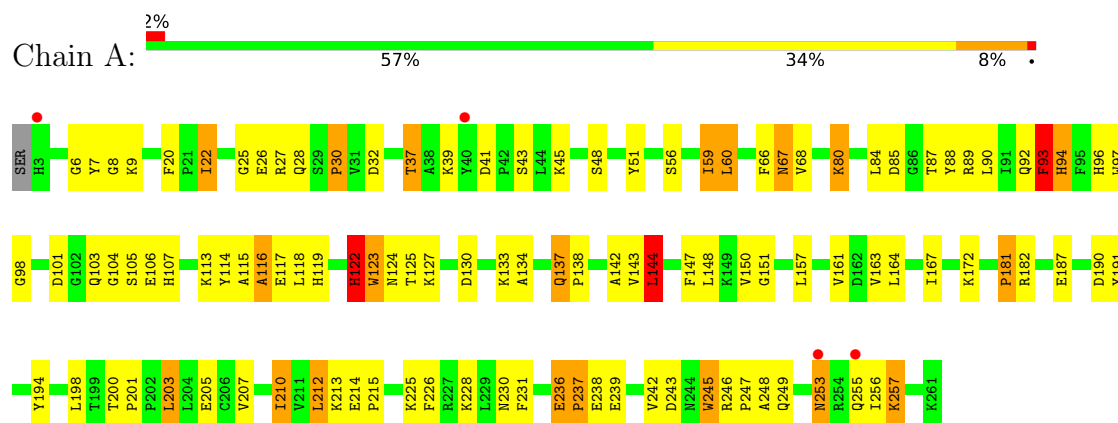
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	218	Total	O	0	0
			218	218		

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: CARBONIC ANHYDRASE II



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.70Å 41.70Å 73.00Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90 70.64 – 1.92	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90) 54.2 (70.64-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.37 (at 1.92Å)	Xtriage
Refinement program	PROFFT	Depositor
R, R_{free}	0.183 , (Not available) 0.185 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	7.3	Xtriage
Anisotropy	1.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 70.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.047 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2299	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.54% 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

Bond lengths and bond angles in the following residue types are not validated in this section: BR, ZN

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	1.48	8/2161 (0.4%)	2.26	119/2931 (4.1%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	144	LEU	N-CA	6.77	1.54	1.46
1	A	130	ASP	N-CA	5.99	1.53	1.45
1	A	59	ILE	C-O	5.92	1.30	1.24
1	A	117	GLU	N-CA	5.65	1.53	1.46
1	A	125	THR	N-CA	-5.47	1.39	1.46
1	A	150	VAL	N-CA	5.42	1.52	1.46
1	A	191	TYR	CA-CB	5.33	1.63	1.53
1	A	133	LYS	CA-C	5.03	1.59	1.52

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	ILE	O-C-N	12.00	134.67	123.03
1	A	67	ASN	CA-CB-CG	10.94	123.54	112.60
1	A	210	ILE	CA-C-O	-10.88	109.65	120.31
1	A	90	LEU	CA-C-N	-9.59	113.35	122.66
1	A	90	LEU	C-N-CA	-9.59	113.35	122.66
1	A	116	ALA	O-C-N	9.32	133.04	123.26
1	A	133	LYS	O-C-N	9.12	135.69	122.28
1	A	230	ASN	CA-CB-CG	8.35	120.95	112.60
1	A	96	HIS	CA-CB-CG	-8.30	105.50	113.80
1	A	97	TRP	CA-C-N	-8.30	113.54	122.67
1	A	97	TRP	C-N-CA	-8.30	113.54	122.67
1	A	94	HIS	O-C-N	8.30	132.30	123.42
1	A	194	TYR	O-C-N	8.14	129.12	121.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	VAL	CA-C-N	-8.03	110.87	122.19
1	A	143	VAL	C-N-CA	-8.03	110.87	122.19
1	A	230	ASN	CA-C-N	7.94	134.16	120.58
1	A	230	ASN	C-N-CA	7.94	134.16	120.58
1	A	187	GLU	CA-C-N	7.65	134.05	122.65
1	A	187	GLU	C-N-CA	7.65	134.05	122.65
1	A	226	PHE	CA-CB-CG	7.55	121.35	113.80
1	A	212	LEU	CA-C-O	7.54	129.49	120.81
1	A	93	PHE	CA-CB-CG	7.46	121.26	113.80
1	A	182	ARG	NE-CZ-NH1	7.44	128.94	121.50
1	A	157	LEU	CA-C-N	7.37	130.16	120.28
1	A	157	LEU	C-N-CA	7.37	130.16	120.28
1	A	182	ARG	CD-NE-CZ	7.17	134.44	124.40
1	A	236	GLU	CA-CB-CG	7.06	128.23	114.10
1	A	142	ALA	CA-C-N	-7.03	113.75	123.10
1	A	142	ALA	C-N-CA	-7.03	113.75	123.10
1	A	239	GLU	CA-CB-CG	7.01	128.13	114.10
1	A	80	LYS	CA-C-O	-6.98	113.98	121.45
1	A	181	PRO	CB-CA-C	6.90	119.90	110.52
1	A	231	PHE	CA-CB-CG	6.89	120.69	113.80
1	A	107	HIS	N-CA-CB	6.85	120.16	110.36
1	A	20	PHE	O-C-N	6.82	127.53	121.32
1	A	101	ASP	CA-CB-CG	6.81	119.41	112.60
1	A	191	TYR	O-C-N	6.75	130.86	123.10
1	A	68	VAL	N-CA-CB	6.70	119.04	111.21
1	A	137	GLN	O-C-N	6.58	127.46	121.80
1	A	6	GLY	O-C-N	6.56	131.23	122.70
1	A	133	LYS	CA-C-O	-6.52	112.04	120.00
1	A	236	GLU	CB-CG-CD	6.49	123.64	112.60
1	A	51	TYR	CA-CB-CG	6.47	125.55	113.90
1	A	123	TRP	CA-C-O	-6.47	113.85	121.16
1	A	87	THR	CA-C-N	6.43	132.25	123.11
1	A	87	THR	C-N-CA	6.43	132.25	123.11
1	A	118	LEU	CA-C-O	6.41	128.00	120.69
1	A	253	ASN	CA-CB-CG	-6.32	106.28	112.60
1	A	212	LEU	N-CA-CB	6.24	119.15	109.85
1	A	242	VAL	CA-C-N	-6.15	113.52	122.19
1	A	242	VAL	C-N-CA	-6.15	113.52	122.19
1	A	124	ASN	CA-C-N	6.14	129.12	120.28
1	A	124	ASN	C-N-CA	6.14	129.12	120.28
1	A	94	HIS	CA-C-O	-6.11	114.69	121.23
1	A	237	PRO	CB-CA-C	6.11	119.34	111.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	LYS	N-CA-C	-6.09	103.98	112.45
1	A	87	THR	CA-CB-OG1	-6.08	100.48	109.60
1	A	124	ASN	O-C-N	6.04	130.67	122.82
1	A	249	GLN	O-C-N	6.02	128.50	121.39
1	A	41	ASP	CA-CB-CG	6.01	118.61	112.60
1	A	144	LEU	O-C-N	-5.99	116.39	123.22
1	A	214	GLU	CB-CG-CD	5.92	122.66	112.60
1	A	85	ASP	CA-CB-CG	5.89	118.49	112.60
1	A	60	LEU	O-C-N	5.83	130.23	123.41
1	A	122	HIS	CA-C-N	-5.80	113.53	122.87
1	A	122	HIS	C-N-CA	-5.80	113.53	122.87
1	A	144	LEU	CB-CA-C	5.79	119.30	109.80
1	A	93	PHE	N-CA-C	-5.76	100.54	109.24
1	A	245	TRP	CA-C-O	5.76	126.92	120.70
1	A	150	VAL	CB-CA-C	5.68	117.72	111.08
1	A	101	ASP	N-CA-C	5.66	118.39	111.82
1	A	56	SER	N-CA-C	-5.64	102.17	110.52
1	A	198	LEU	N-CA-C	-5.63	102.56	110.50
1	A	25	GLY	CA-C-N	5.63	131.57	121.66
1	A	25	GLY	C-N-CA	5.63	131.57	121.66
1	A	68	VAL	N-CA-C	-5.61	99.79	107.99
1	A	143	VAL	CA-CB-CG2	5.60	119.91	110.40
1	A	98	GLY	O-C-N	5.57	128.44	123.59
1	A	37	THR	CA-CB-CG2	5.57	119.97	110.50
1	A	107	HIS	CA-CB-CG	-5.52	108.28	113.80
1	A	28	GLN	CA-C-O	5.48	127.54	121.56
1	A	105	SER	CA-C-O	5.44	128.18	121.87
1	A	123	TRP	O-C-N	5.44	130.02	123.16
1	A	214	GLU	N-CA-C	5.44	116.50	109.65
1	A	118	LEU	CA-C-N	-5.43	115.34	123.00
1	A	118	LEU	C-N-CA	-5.43	115.34	123.00
1	A	191	TYR	CA-C-O	-5.39	115.68	121.45
1	A	22	ILE	O-C-N	5.34	128.15	122.06
1	A	248	ALA	CA-C-O	5.34	127.06	121.19
1	A	194	TYR	CA-C-N	5.34	126.51	119.84
1	A	194	TYR	C-N-CA	5.34	126.51	119.84
1	A	125	THR	O-C-N	5.33	128.45	122.22
1	A	114	TYR	O-C-N	5.31	129.95	123.10
1	A	84	LEU	N-CA-C	5.30	118.37	110.52
1	A	203	LEU	N-CA-CB	-5.30	103.94	111.84
1	A	32	ASP	CB-CA-C	5.30	118.50	109.80
1	A	106	GLU	N-CA-C	-5.28	105.66	112.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	GLU	CB-CG-CD	5.25	121.53	112.60
1	A	207	VAL	N-CA-C	5.23	116.12	108.53
1	A	236	GLU	CG-CD-OE1	5.22	130.42	118.40
1	A	226	PHE	N-CA-C	-5.21	105.68	111.36
1	A	134	ALA	CB-CA-C	5.20	119.05	110.88
1	A	133	LYS	CA-CB-CG	5.18	124.45	114.10
1	A	105	SER	O-C-N	-5.17	116.90	122.79
1	A	207	VAL	CA-CB-CG2	5.15	119.16	110.40
1	A	92	GLN	CA-CB-CG	5.13	124.35	114.10
1	A	256	ILE	N-CA-CB	5.11	117.12	110.99
1	A	87	THR	N-CA-CB	-5.09	102.49	110.69
1	A	41	ASP	CB-CA-C	5.06	116.91	110.13
1	A	96	HIS	CA-C-N	-5.05	114.08	122.11
1	A	96	HIS	C-N-CA	-5.05	114.08	122.11
1	A	97	TRP	CB-CG-CD2	-5.04	119.74	126.80
1	A	84	LEU	CA-C-O	-5.04	115.78	121.72
1	A	116	ALA	CA-C-N	-5.04	115.13	122.44
1	A	116	ALA	C-N-CA	-5.04	115.13	122.44
1	A	151	GLY	O-C-N	5.04	129.25	122.70
1	A	26	GLU	N-CA-C	5.02	119.46	113.23
1	A	8	GLY	CA-C-N	5.01	126.95	120.44
1	A	8	GLY	C-N-CA	5.01	126.95	120.44

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	2079	0	2021	31	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	218	0	0	3	0
All	All	2299	0	2021	31	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 8.

All (31) 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:161:VAL:HG13	1:A:225:LYS:HD2	1.72	0.72
1:A:27:ARG:HG3	1:A:205:GLU:HB3	1.73	0.70
1:A:147:PHE:HB2	1:A:215:PRO:HB3	1.74	0.67
1:A:201:PRO:HA	1:A:203:LEU:HG	1.79	0.64
1:A:67:ASN:HD22	1:A:94:HIS:HB3	1.63	0.63
1:A:190:ASP:HB2	1:A:213:LYS:HE3	1.81	0.63
1:A:88:TYR:HB3	1:A:122:HIS:HB2	1.81	0.62
1:A:236:GLU:HB3	1:A:237:PRO:HD2	1.87	0.57
1:A:59:ILE:HG12	1:A:167:ILE:HD13	1.86	0.56
1:A:255:GLN:HG2	1:A:257:LYS:HE2	1.89	0.55
1:A:246:ARG:HG2	1:A:247:PRO:HD2	1.90	0.54
1:A:190:ASP:CB	1:A:213:LYS:HE3	2.37	0.53
1:A:161:VAL:CG1	1:A:225:LYS:HD2	2.38	0.52
1:A:89:ARG:HG2	4:A:480:HOH:O	2.11	0.51
1:A:243:ASP:HA	1:A:245:TRP:CD1	2.47	0.48
1:A:144:LEU:HA	1:A:210:ILE:O	2.13	0.48
1:A:137:GLN:HE21	1:A:138:PRO:HD2	1.79	0.48
1:A:27:ARG:CG	1:A:205:GLU:HB3	2.43	0.47
1:A:104:GLY:HA3	1:A:115:ALA:O	2.14	0.47
1:A:60:LEU:HD12	1:A:172:LYS:O	2.16	0.46
1:A:67:ASN:ND2	1:A:94:HIS:HB3	2.32	0.44
1:A:88:TYR:HA	1:A:123:TRP:O	2.19	0.43
1:A:7:TYR:OH	1:A:200:THR:HG22	2.18	0.43
1:A:93:PHE:HA	1:A:119:HIS:O	2.18	0.42
1:A:163:VAL:O	1:A:164:LEU:C	2.60	0.42
1:A:30:PRO:HD2	1:A:246:ARG:HD3	2.01	0.42
1:A:59:ILE:HD11	1:A:66:PHE:CD1	2.54	0.42
1:A:228:LYS:HE2	4:A:402:HOH:O	2.19	0.41
1:A:243:ASP:HA	1:A:245:TRP:NE1	2.35	0.41
1:A:228:LYS:HG2	4:A:465:HOH:O	2.20	0.40
1:A:116:ALA:HB3	1:A:148:LEU:HB2	2.02	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	A	260/259 (100%)	248 (95%)	12 (5%)	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	A	227/224 (101%)	208 (92%)	19 (8%)	10	4

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LYS
1	A	22	ILE
1	A	30	PRO
1	A	37	THR
1	A	39	LYS
1	A	43	SER
1	A	45	LYS
1	A	48	SER
1	A	80	LYS
1	A	93	PHE
1	A	103	GLN
1	A	113	LYS
1	A	122	HIS

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Mol	Chain	Res	Type
1	A	127	LYS
1	A	144	LEU
1	A	181	PRO
1	A	212	LEU
1	A	253	ASN
1	A	257	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	137	GLN

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	258/259 (99%)	0.48	4 (1%) 70 74	2, 9, 23, 28	5 (1%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	253	ASN	4.5
1	A	3	HIS	3.7
1	A	40	TYR	2.1
1	A	255	GLN	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	A	262	1/1	0.98	0.08	6,6,6,6	0
3	BR	A	500	1/1	0.98	0.07	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.