



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:48 AM UTC

PDB ID : 1CNC / pdb_00001cnc
Title : COMPENSATORY PLASTIC EFFECTS IN THE REDESIGN OF
PROTEIN-ZINC BINDING SITES
Authors : Ippolito, J.A.; Christianson, D.W.
Deposited on : 1994-06-13
Resolution : 2.20 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

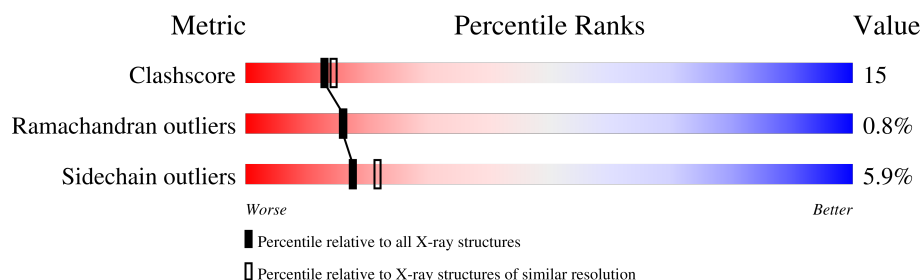
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	259	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2131 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	255	Total	C	N	O	S	0	0	0
			2025	1300	345	377	3			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	CYS	HIS	conflict	UNP P00918

- 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 water.

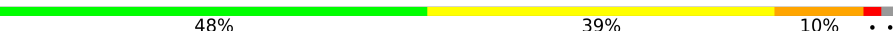
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	105	Total	O	0	0
			105	105		

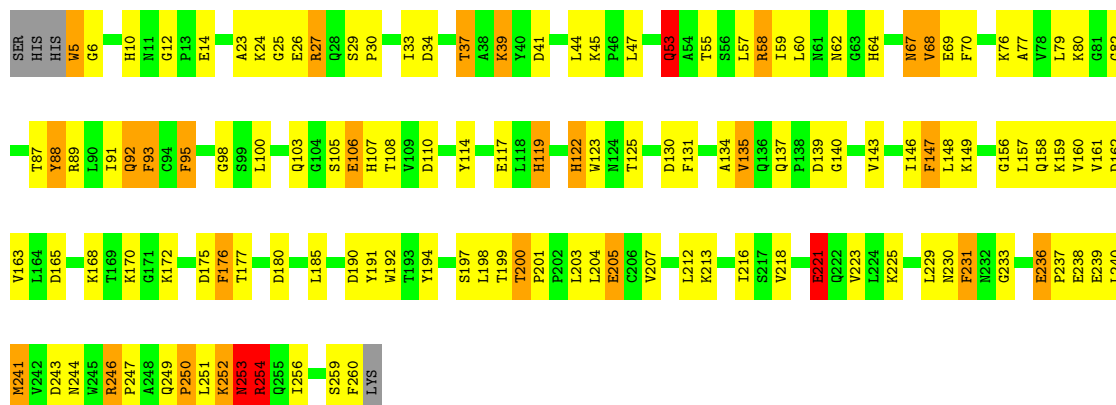
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

• Molecule 1: CARBONIC ANHYDRASE II

Chain A: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

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)	7.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.179 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2131	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1.81	28/2084 (1.3%)	2.18	81/2829 (2.9%)

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	180	ASP	N-CA	7.74	1.55	1.45
1	A	98	GLY	N-CA	6.66	1.50	1.44
1	A	241	MET	N-CA	6.59	1.54	1.46
1	A	246	ARG	NE-CZ	6.12	1.39	1.33
1	A	251	LEU	N-CA	5.97	1.53	1.46
1	A	204	LEU	C-N	-5.97	1.26	1.33
1	A	177	THR	N-CA	5.94	1.52	1.45
1	A	57	LEU	CA-C	5.93	1.58	1.52
1	A	87	THR	CA-C	-5.92	1.45	1.52
1	A	93	PHE	C-O	5.91	1.31	1.23
1	A	159	LYS	C-O	5.74	1.30	1.24
1	A	149	LYS	CA-C	5.73	1.59	1.52
1	A	114	TYR	CA-C	5.68	1.60	1.53
1	A	177	THR	C-N	-5.59	1.25	1.33
1	A	119	HIS	CE1-NE2	-5.57	1.26	1.32
1	A	77	ALA	CA-CB	-5.55	1.45	1.53
1	A	253	ASN	C-O	5.51	1.30	1.24
1	A	190	ASP	N-CA	5.50	1.52	1.46
1	A	10	HIS	CA-CB	5.49	1.62	1.53
1	A	137	GLN	C-O	5.33	1.30	1.24
1	A	175	ASP	C-N	-5.32	1.24	1.34
1	A	39	LYS	C-N	-5.32	1.25	1.33
1	A	147	PHE	CA-C	5.18	1.59	1.52
1	A	254	ARG	CZ-NH1	5.14	1.40	1.32
1	A	156	GLY	C-O	5.10	1.30	1.23
1	A	239	GLU	CA-C	5.06	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	10	HIS	CE1-NE2	-5.02	1.27	1.32
1	A	88	TYR	N-CA	5.02	1.52	1.46

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	231	PHE	CA-CB-CG	13.26	127.06	113.80
1	A	92	GLN	OE1-CD-NE2	-10.61	111.99	122.60
1	A	93	PHE	CA-CB-CG	10.55	124.35	113.80
1	A	10	HIS	CA-CB-CG	-10.32	103.48	113.80
1	A	67	ASN	CA-CB-CG	9.66	122.26	112.60
1	A	177	THR	CA-C-N	9.61	136.00	122.36
1	A	177	THR	C-N-CA	9.61	136.00	122.36
1	A	80	LYS	CA-C-O	-9.48	111.33	121.38
1	A	95	PHE	CA-CB-CG	8.79	122.59	113.80
1	A	165	ASP	CA-CB-CG	8.66	121.26	112.60
1	A	207	VAL	N-CA-C	8.23	120.46	108.53
1	A	139	ASP	CA-C-N	7.98	128.84	119.98
1	A	139	ASP	C-N-CA	7.98	128.84	119.98
1	A	198	LEU	N-CA-C	-7.69	100.17	110.55
1	A	80	LYS	O-C-N	7.53	131.17	123.26
1	A	158	GLN	OE1-CD-NE2	-7.40	115.20	122.60
1	A	191	TYR	N-CA-C	7.36	119.92	108.96
1	A	158	GLN	CA-C-O	-7.28	112.84	120.55
1	A	119	HIS	CA-CB-CG	7.08	120.88	113.80
1	A	238	GLU	CA-C-O	7.05	128.67	120.49
1	A	114	TYR	O-C-N	6.98	130.93	122.84
1	A	53	GLN	N-CA-CB	-6.97	99.77	110.92
1	A	250	PRO	CA-C-O	-6.84	113.91	121.23
1	A	200	THR	O-C-N	6.77	127.62	121.80
1	A	14	GLU	CA-CB-CG	6.76	127.62	114.10
1	A	107	HIS	CA-C-O	-6.63	113.85	121.47
1	A	92	GLN	CB-CG-CD	6.57	123.76	112.60
1	A	175	ASP	CA-CB-CG	6.56	119.16	112.60
1	A	250	PRO	O-C-N	6.47	130.45	123.01
1	A	68	VAL	O-C-N	6.28	130.45	123.10
1	A	26	GLU	N-CA-C	6.28	120.78	113.18
1	A	27	ARG	NE-CZ-NH2	6.25	124.82	119.20
1	A	176	PHE	CB-CA-C	6.14	121.04	111.70
1	A	221	GLU	CB-CG-CD	6.10	122.98	112.60
1	A	5	TRP	CA-CB-CG	6.07	125.14	113.60
1	A	158	GLN	O-C-N	6.06	128.55	122.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ASP	CB-CA-C	6.04	116.15	110.17
1	A	230	ASN	CA-CB-CG	6.02	118.62	112.60
1	A	168	LYS	N-CA-C	5.92	118.21	111.11
1	A	259	SER	N-CA-C	-5.90	105.84	113.16
1	A	147	PHE	O-C-N	5.86	129.62	123.06
1	A	205	GLU	CA-C-N	5.80	131.31	122.37
1	A	205	GLU	C-N-CA	5.80	131.31	122.37
1	A	254	ARG	NE-CZ-NH2	5.70	124.33	119.20
1	A	233	GLY	N-CA-C	-5.68	104.98	112.82
1	A	23	ALA	O-C-N	5.64	128.63	122.20
1	A	192	TRP	CA-C-O	-5.64	114.61	120.70
1	A	197	SER	N-CA-C	5.63	115.72	108.34
1	A	252	LYS	N-CA-C	5.58	118.93	111.24
1	A	122	HIS	CA-C-O	-5.51	114.33	120.66
1	A	194	TYR	CA-C-N	5.45	126.66	119.84
1	A	194	TYR	C-N-CA	5.45	126.66	119.84
1	A	110	ASP	CA-CB-CG	5.42	118.02	112.60
1	A	252	LYS	CB-CA-C	-5.41	103.75	112.09
1	A	34	ASP	N-CA-C	-5.41	99.71	108.41
1	A	130	ASP	O-C-N	5.38	129.29	123.10
1	A	137	GLN	CA-C-N	5.38	125.20	119.28
1	A	137	GLN	C-N-CA	5.38	125.20	119.28
1	A	236	GLU	CG-CD-OE2	-5.36	106.07	118.40
1	A	137	GLN	CB-CG-CD	5.34	121.67	112.60
1	A	37	THR	CA-CB-CG2	5.31	119.53	110.50
1	A	12	GLY	O-C-N	5.28	127.17	122.42
1	A	191	TYR	CA-C-O	5.27	127.08	121.45
1	A	221	GLU	CA-CB-CG	5.26	124.63	114.10
1	A	239	GLU	CA-C-O	-5.26	114.87	120.40
1	A	106	GLU	N-CA-C	-5.26	105.69	112.68
1	A	70	PHE	CA-CB-CG	5.24	119.04	113.80
1	A	6	GLY	O-C-N	5.24	129.51	122.70
1	A	236	GLU	CG-CD-OE1	5.22	130.41	118.40
1	A	244	ASN	OD1-CG-ND2	-5.22	117.38	122.60
1	A	108	THR	CA-CB-CG2	5.21	119.35	110.50
1	A	199	THR	CA-CB-OG1	-5.15	101.87	109.60
1	A	47	LEU	CA-C-O	-5.15	115.95	121.56
1	A	172	LYS	N-CA-CB	5.14	117.58	110.17
1	A	53	GLN	CA-CB-CG	5.13	124.36	114.10
1	A	149	LYS	N-CA-CB	5.13	118.75	110.85
1	A	25	GLY	CA-C-N	5.12	131.56	121.58
1	A	25	GLY	C-N-CA	5.12	131.56	121.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	GLN	OE1-CD-NE2	-5.11	117.50	122.60
1	A	185	LEU	CB-CA-C	5.08	116.04	108.87
1	A	37	THR	CA-CB-OG1	-5.05	102.02	109.60

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	2025	0	1979	60	1
2	A	1	0	0	0	0
3	A	105	0	0	4	1
All	All	2131	0	1979	60	1

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 15.

All (60) 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:58:ARG:HD2	1:A:69:GLU:OE1	1.73	0.87
1:A:161:VAL:HG13	1:A:225:LYS:HD3	1.56	0.87
1:A:60:LEU:HB2	3:A:362:HOH:O	1.78	0.83
1:A:236:GLU:HB3	1:A:237:PRO:HD2	1.60	0.82
1:A:253:ASN:HD22	1:A:254:ARG:N	1.80	0.80
1:A:64:HIS:NE2	3:A:355:HOH:O	2.18	0.77
1:A:253:ASN:ND2	1:A:254:ARG:N	2.38	0.71
1:A:161:VAL:CG1	1:A:225:LYS:HD3	2.22	0.69
1:A:64:HIS:ND1	3:A:330:HOH:O	2.19	0.67
1:A:91:ILE:HG23	1:A:92:GLN:HG2	1.77	0.65
1:A:213:LYS:HD3	1:A:260:PHE:CZ	2.32	0.64
1:A:252:LYS:O	1:A:253:ASN:CG	2.42	0.63
1:A:45:LYS:O	1:A:82:GLY:HA2	2.00	0.62
1:A:253:ASN:HD22	1:A:253:ASN:C	2.07	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:ALA:O	1:A:140:GLY:HA3	2.00	0.61
1:A:131:PHE:O	1:A:135:VAL:HG13	2.00	0.61
1:A:62:ASN:O	1:A:170:LYS:NZ	2.34	0.60
1:A:93:PHE:HE1	1:A:95:PHE:HE1	1.50	0.59
1:A:58:ARG:HD2	1:A:69:GLU:CD	2.32	0.54
1:A:201:PRO:HA	1:A:203:LEU:HG	1.89	0.54
1:A:58:ARG:HA	1:A:176:PHE:HB3	1.89	0.54
1:A:231:PHE:CE1	1:A:241:MET:HG3	2.45	0.52
1:A:249:GLN:HB3	1:A:250:PRO:HD2	1.90	0.52
1:A:106:GLU:OE1	1:A:119:HIS:HE1	1.92	0.51
1:A:60:LEU:HD23	1:A:60:LEU:N	2.26	0.50
1:A:88:TYR:HA	1:A:123:TRP:O	2.12	0.50
1:A:253:ASN:ND2	1:A:253:ASN:C	2.69	0.49
1:A:240:LEU:HG	3:A:335:HOH:O	2.13	0.49
1:A:250:PRO:HG2	1:A:252:LYS:HE3	1.95	0.48
1:A:93:PHE:CE1	1:A:95:PHE:HE1	2.31	0.48
1:A:119:HIS:HB3	1:A:143:VAL:CG1	2.43	0.48
1:A:213:LYS:HD3	1:A:260:PHE:CE2	2.48	0.48
1:A:147:PHE:C	1:A:148:LEU:HD12	2.39	0.47
1:A:157:LEU:HD22	1:A:218:VAL:HG11	1.96	0.47
1:A:27:ARG:CG	1:A:205:GLU:HB3	2.45	0.46
1:A:41:ASP:CG	1:A:44:LEU:HD13	2.40	0.46
1:A:93:PHE:HA	1:A:119:HIS:O	2.17	0.46
1:A:157:LEU:O	1:A:157:LEU:HG	2.16	0.45
1:A:246:ARG:HA	1:A:247:PRO:HD3	1.82	0.45
1:A:29:SER:HB3	1:A:30:PRO:HA	2.00	0.43
1:A:123:TRP:CZ3	1:A:125:THR:HA	2.53	0.43
1:A:59:ILE:HA	1:A:67:ASN:O	2.19	0.43
1:A:148:LEU:HG	1:A:216:ILE:HG13	2.00	0.43
1:A:146:ILE:HG12	1:A:212:LEU:HD12	2.01	0.42
1:A:53:GLN:O	1:A:76:LYS:HB3	2.19	0.42
1:A:89:ARG:O	1:A:122:HIS:HA	2.20	0.42
1:A:105:SER:HA	1:A:117:GLU:HB2	2.01	0.42
1:A:41:ASP:OD2	1:A:44:LEU:HD13	2.19	0.42
1:A:27:ARG:HG3	1:A:205:GLU:HB3	2.02	0.42
1:A:103:GLN:NE2	1:A:243:ASP:OD1	2.46	0.42
1:A:93:PHE:CE1	1:A:95:PHE:CE1	3.07	0.41
1:A:253:ASN:C	1:A:254:ARG:O	2.63	0.41
1:A:68:VAL:HG21	1:A:93:PHE:CZ	2.55	0.41
1:A:58:ARG:CD	1:A:69:GLU:OE1	2.57	0.41
1:A:5:TRP:CH2	1:A:200:THR:HB	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ILE:HG12	1:A:256:ILE:HD13	2.02	0.41
1:A:236:GLU:HB3	1:A:237:PRO:CD	2.41	0.40
1:A:221:GLU:CD	1:A:221:GLU:H	2.29	0.40
1:A:41:ASP:OD2	1:A:44:LEU:CD1	2.70	0.40
1:A:160:VAL:O	1:A:163:VAL:HG12	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:ASP:OD2	3:A:329:HOH:O[2_445]	1.72	0.48

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	253/259 (98%)	238 (94%)	13 (5%)	2 (1%)	16 16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	ASN
1	A	254	ARG

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	220/224 (98%)	207 (94%)	13 (6%)	18	22

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LYS
1	A	37	THR
1	A	39	LYS
1	A	53	GLN
1	A	55	THR
1	A	58	ARG
1	A	79	LEU
1	A	100	LEU
1	A	135	VAL
1	A	221	GLU
1	A	223	VAL
1	A	229	LEU
1	A	253	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	17	HIS
1	A	74	GLN
1	A	136	GLN
1	A	158	GLN
1	A	253	ASN

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

Of 1 ligands modelled in this entry, 1 is 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.