



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 12:30 AM UTC

PDB ID : 1D0Q / pdb_00001d0q
Title : STRUCTURE OF THE ZINC-BINDING DOMAIN OF BACILLUS
STEARTHERMOPHILUS DNA PRIMASE
Authors : Pan, H.; Wigley, D.B.
Deposited on : 1999-09-14
Resolution : 1.71 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

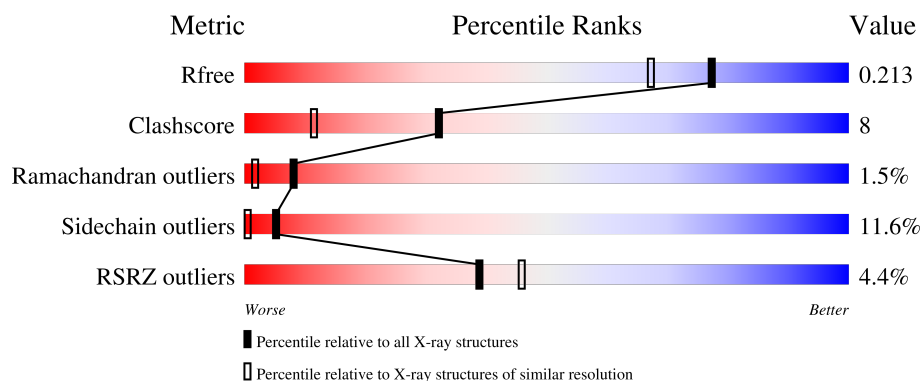
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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	103	5% 55% 30% 10% ..
1	B	103	4% 59% 27% 11% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1746 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 DNA PRIMASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	102	Total	C	N	O	S	0	0	0
			791	506	136	145	4			
1	B	102	Total	C	N	O	S	0	0	0
			791	506	136	145	4			

- 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		
2	B	1	Total	Zn	0	0
			1	1		

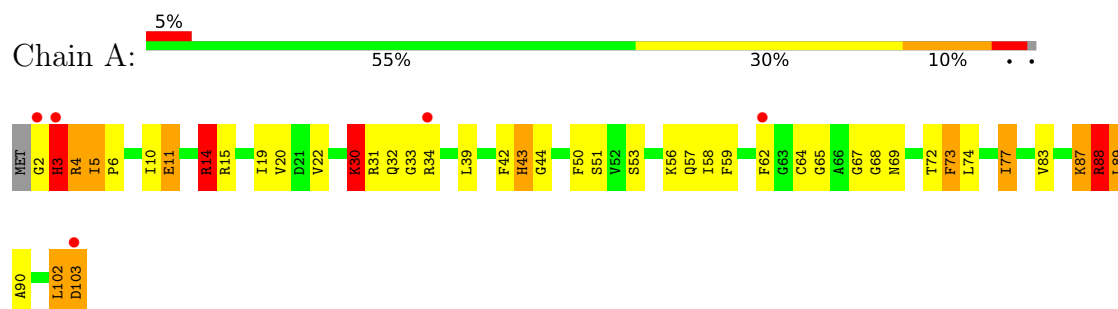
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	87	Total	O	0	0
			87	87		
3	B	75	Total	O	0	0
			75	75		

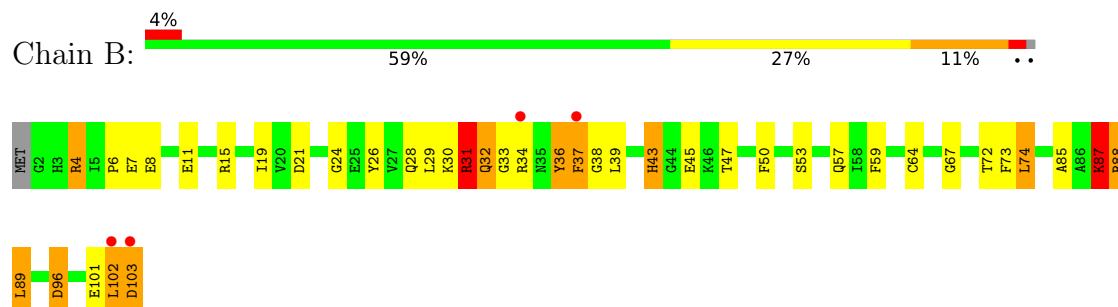
3 Residue-property plots [i](#)

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: DNA PRIMASE



• Molecule 1: DNA PRIMASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	36.17Å 58.74Å 45.75Å 90.00° 91.73° 90.00°	Depositor
Resolution (Å)	15.00 – 1.71 15.00 – 1.71	Depositor EDS
% Data completeness (in resolution range)	(Not available) (15.00-1.71) 96.0 (15.00-1.71)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 1.65Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.204 , 0.225 0.194 , 0.213	Depositor DCC
R_{free} test set	1132 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	14.0	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 47.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.064 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1746	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.63% 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: 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	0.69	0/809	2.82	63/1090 (5.8%)
1	B	0.63	0/809	2.68	55/1090 (5.0%)
All	All	0.66	0/1618	2.76	118/2180 (5.4%)

There are no bond length outliers.

All (118) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	88	ARG	CD-NE-CZ	29.20	165.28	124.40
1	B	102	LEU	CA-C-N	26.47	169.35	121.70
1	B	102	LEU	C-N-CA	26.47	169.35	121.70
1	A	102	LEU	CA-C-N	16.98	152.26	121.70
1	A	102	LEU	C-N-CA	16.98	152.26	121.70
1	A	102	LEU	O-C-N	-14.69	103.05	122.59
1	A	43	HIS	ND1-CE1-NE2	-12.89	95.50	108.40
1	A	43	HIS	ND1-CG-CD2	-12.31	93.79	106.10
1	B	102	LEU	O-C-N	-11.90	106.76	122.59
1	A	3	HIS	CA-C-N	11.89	144.25	121.54
1	A	3	HIS	C-N-CA	11.89	144.25	121.54
1	B	102	LEU	CA-C-O	11.27	136.63	120.51
1	B	103	ASP	CA-CB-CG	-11.23	101.37	112.60
1	A	43	HIS	CB-CG-CD2	11.11	145.65	131.20
1	A	43	HIS	CG-ND1-CE1	10.35	126.89	109.30
1	A	14	ARG	NH1-CZ-NH2	-9.47	106.98	119.30
1	A	102	LEU	CA-C-O	9.38	133.92	120.51
1	A	3	HIS	CA-CB-CG	9.32	123.12	113.80
1	A	88	ARG	CB-CG-CD	9.09	132.21	111.30
1	A	88	ARG	NH1-CZ-NH2	8.99	130.99	119.30
1	B	32	GLN	CA-C-O	8.66	131.00	120.27
1	A	103	ASP	CA-CB-CG	8.48	121.08	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	4	ARG	CA-C-O	8.38	130.09	119.12
1	A	33	GLY	CA-C-O	-8.29	110.03	121.46
1	A	30	LYS	CA-CB-CG	8.18	130.46	114.10
1	A	3	HIS	CA-C-O	8.16	132.18	120.51
1	A	3	HIS	O-C-N	-8.01	111.94	122.59
1	B	24	GLY	O-C-N	-7.70	114.07	122.54
1	A	14	ARG	NE-CZ-NH1	7.66	129.16	121.50
1	B	32	GLN	CA-CB-CG	7.65	129.41	114.10
1	B	28	GLN	OE1-CD-NE2	7.62	130.22	122.60
1	B	11	GLU	CB-CG-CD	7.58	125.48	112.60
1	B	43	HIS	O-C-N	7.42	131.88	123.27
1	A	33	GLY	O-C-N	7.36	134.22	122.36
1	A	62	PHE	CA-CB-CG	7.28	121.08	113.80
1	A	90	ALA	CA-C-O	-7.15	112.84	120.42
1	B	39	LEU	CA-C-O	6.95	128.97	121.05
1	A	33	GLY	CA-C-N	-6.91	111.60	122.65
1	A	33	GLY	C-N-CA	-6.91	111.60	122.65
1	B	32	GLN	O-C-N	-6.87	115.64	123.40
1	B	85	ALA	O-C-N	-6.86	114.33	122.15
1	A	5	ILE	CA-C-O	6.85	124.04	119.38
1	B	74	LEU	N-CA-CB	6.79	120.21	110.16
1	A	10	ILE	CA-C-O	-6.78	113.67	120.85
1	B	36	TYR	O-C-N	-6.77	114.43	123.23
1	B	96	ASP	CB-CG-OD1	6.70	133.82	118.40
1	B	24	GLY	CA-C-O	6.68	127.53	119.65
1	A	3	HIS	N-CA-CB	-6.48	99.53	110.49
1	B	53	SER	CA-C-O	6.47	125.54	119.59
1	A	88	ARG	NE-CZ-NH2	-6.46	113.38	119.20
1	A	39	LEU	CA-C-O	6.45	128.40	121.05
1	B	15	ARG	NE-CZ-NH1	-6.43	115.07	121.50
1	A	64	CYS	CA-C-O	6.37	125.53	118.52
1	A	22	VAL	O-C-N	-6.30	115.74	121.91
1	A	89	LEU	N-CA-CB	-6.29	100.53	110.28
1	A	77	ILE	O-C-N	6.27	128.29	121.83
1	B	67	GLY	CA-C-O	-6.26	115.68	121.63
1	B	72	THR	CA-C-O	-6.20	114.31	120.82
1	B	37	PHE	CA-CB-CG	-6.08	107.72	113.80
1	B	87	LYS	CA-CB-CG	6.08	126.26	114.10
1	B	32	GLN	OE1-CD-NE2	-6.04	116.56	122.60
1	B	50	PHE	CA-CB-CG	6.04	119.83	113.80
1	B	53	SER	CA-C-N	6.01	125.72	119.05
1	B	53	SER	C-N-CA	6.01	125.72	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	31	ARG	CA-C-N	6.01	130.97	121.72
1	B	31	ARG	C-N-CA	6.01	130.97	121.72
1	A	73	PHE	CA-C-O	-6.00	114.52	120.82
1	A	58	ILE	CA-C-O	-5.94	115.81	121.64
1	A	44	GLY	O-C-N	5.87	130.33	122.70
1	A	88	ARG	NE-CZ-NH1	-5.87	115.63	121.50
1	B	88	ARG	CA-C-O	-5.86	114.21	120.42
1	B	37	PHE	N-CA-C	5.85	118.74	109.50
1	A	42	PHE	CA-CB-CG	-5.74	108.06	113.80
1	A	72	THR	N-CA-C	-5.72	104.95	111.07
1	B	6	PRO	N-CA-CB	5.72	108.32	103.35
1	A	87	LYS	CA-C-O	-5.71	114.50	120.55
1	A	53	SER	CB-CA-C	-5.71	103.35	109.85
1	A	22	VAL	CA-C-O	5.66	127.17	121.17
1	B	36	TYR	CA-C-O	5.65	126.81	120.70
1	B	96	ASP	CA-CB-CG	-5.64	106.96	112.60
1	A	3	HIS	CG-CD2-NE2	5.63	112.83	107.20
1	A	22	VAL	N-CA-C	5.63	115.83	110.42
1	A	20	VAL	N-CA-C	-5.62	105.25	110.53
1	A	64	CYS	O-C-N	-5.60	116.08	121.85
1	B	26	TYR	CA-C-N	5.60	130.87	122.75
1	B	26	TYR	C-N-CA	5.60	130.87	122.75
1	B	21	ASP	CA-C-O	5.60	126.48	120.55
1	B	47	THR	CA-C-O	5.58	124.88	120.19
1	B	15	ARG	CD-NE-CZ	5.56	132.19	124.40
1	A	6	PRO	N-CA-CB	5.54	108.17	103.35
1	B	72	THR	O-C-N	5.52	127.76	122.07
1	A	51	SER	N-CA-CB	-5.51	101.34	111.37
1	A	50	PHE	CA-CB-CG	5.45	119.25	113.80
1	A	65	GLY	CA-C-O	-5.43	113.29	119.04
1	B	88	ARG	NH1-CZ-NH2	5.39	126.31	119.30
1	B	7	GLU	CA-C-O	5.37	126.64	120.90
1	B	36	TYR	N-CA-CB	5.31	120.08	110.83
1	B	8	GLU	CG-CD-OE2	-5.31	106.19	118.40
1	A	88	ARG	CA-CB-CG	-5.30	103.50	114.10
1	A	68	GLY	O-C-N	5.24	130.94	123.56
1	B	34	ARG	CA-C-O	-5.23	112.96	119.18
1	B	38	GLY	CA-C-O	-5.21	115.91	121.38
1	A	90	ALA	O-C-N	5.21	128.08	122.15
1	A	56	LYS	CA-C-O	5.18	125.35	119.18
1	B	96	ASP	OD1-CG-OD2	-5.18	110.47	122.90
1	A	14	ARG	NE-CZ-NH2	5.17	123.85	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	47	THR	CA-C-N	5.17	125.08	119.76
1	B	47	THR	C-N-CA	5.17	125.08	119.76
1	B	26	TYR	O-C-N	-5.17	116.62	122.10
1	A	83	VAL	CA-C-O	-5.15	115.59	120.95
1	B	96	ASP	CA-C-O	-5.14	115.19	121.05
1	B	73	PHE	CA-CB-CG	-5.13	108.67	113.80
1	A	43	HIS	CG-CD2-NE2	5.09	112.30	107.20
1	A	69	ASN	OD1-CG-ND2	5.05	127.65	122.60
1	A	77	ILE	CA-CB-CG2	5.05	119.08	110.50
1	A	72	THR	CA-CB-OG1	-5.02	102.06	109.60
1	A	31	ARG	N-CA-C	5.00	117.48	110.23
1	B	59	PHE	O-C-N	-5.00	116.41	123.11

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	791	0	771	16	0
1	B	791	0	770	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	87	0	0	4	0
3	B	75	0	0	0	0
All	All	1746	0	1541	25	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 (25) 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:B:19:ILE:H	1:B:57:GLN:HE22	1.17	0.89
1:A:19:ILE:H	1:A:57:GLN:HE22	1.31	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:HIS:NE2	1:A:5:ILE:HG13	2.11	0.64
1:B:19:ILE:H	1:B:57:GLN:NE2	1.93	0.59
1:A:19:ILE:H	1:A:57:GLN:NE2	2.00	0.57
1:B:19:ILE:N	1:B:57:GLN:HE22	1.97	0.56
1:B:32:GLN:HB3	1:B:37:PHE:CD1	2.40	0.56
1:B:87:LYS:HE2	1:B:88:ARG:HG2	1.88	0.56
1:A:3:HIS:CE1	1:A:4:ARG:HB2	2.44	0.53
1:A:2:GLY:N	1:B:96:ASP:OD2	2.44	0.50
1:B:43:HIS:CG	1:B:64:CYS:HB3	2.47	0.49
1:B:29:LEU:HB3	1:B:36:TYR:HB3	1.95	0.49
1:A:3:HIS:CG	1:A:4:ARG:N	2.81	0.48
1:A:88:ARG:HD2	3:A:331:HOH:O	2.14	0.48
1:A:3:HIS:CG	1:A:4:ARG:H	2.32	0.47
1:A:59:PHE:CE2	1:A:73:PHE:HB2	2.50	0.47
1:A:74:LEU:HA	1:A:77:ILE:HG22	1.96	0.46
1:A:30:LYS:HG3	3:A:249:HOH:O	2.16	0.46
1:A:30:LYS:HG2	3:A:208:HOH:O	2.15	0.46
1:A:67:GLY:O	1:B:4:ARG:HA	2.18	0.44
1:A:19:ILE:N	1:A:57:GLN:HE22	2.06	0.44
1:A:11:GLU:HG2	3:A:218:HOH:O	2.18	0.43
1:A:14:ARG:NH2	1:B:101:GLU:OE2	2.51	0.42
1:B:31:ARG:HD3	1:B:33:GLY:O	2.21	0.41
1:B:74:LEU:HD11	1:B:89:LEU:HD13	2.03	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	100/103 (97%)	95 (95%)	2 (2%)	3 (3%)	3	0
1	B	100/103 (97%)	97 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	200/206 (97%)	192 (96%)	5 (2%)	3 (2%)	8 2

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	LEU
1	A	3	HIS
1	A	4	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	82/83 (99%)	70 (85%)	12 (15%)	3 0
1	B	82/83 (99%)	75 (92%)	7 (8%)	10 1
All	All	164/166 (99%)	145 (88%)	19 (12%)	5 0

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

Mol	Chain	Res	Type
1	A	3	HIS
1	A	11	GLU
1	A	14	ARG
1	A	15	ARG
1	A	30	LYS
1	A	32	GLN
1	A	34	ARG
1	A	43	HIS
1	A	87	LYS
1	A	88	ARG
1	A	89	LEU
1	A	103	ASP
1	B	30	LYS
1	B	31	ARG
1	B	45	GLU

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Mol	Chain	Res	Type
1	B	87	LYS
1	B	89	LEU
1	B	102	LEU
1	B	103	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	B	3	HIS
1	B	35	ASN
1	B	57	GLN
1	B	60	HIS

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

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 [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	102/103 (99%)	0.21	5 (4%) 35 41	15, 23, 39, 69	0
1	B	102/103 (99%)	0.16	4 (3%) 43 51	17, 22, 39, 75	0
All	All	204/206 (99%)	0.19	9 (4%) 39 46	15, 23, 39, 75	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	HIS	3.9
1	A	2	GLY	3.7
1	B	102	LEU	3.5
1	B	103	ASP	3.1
1	B	34	ARG	2.5
1	A	103	ASP	2.2
1	A	34	ARG	2.2
1	A	62	PHE	2.1
1	B	37	PHE	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](#)

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($\text{\AA}^2$)	Q<0.9
2	ZN	B	151	1/1	0.97	0.12	15,15,15,15	0
2	ZN	A	151	1/1	0.98	0.12	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.