



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 08:34 AM UTC

PDB ID : 3BOL / pdb_00003bol
Title : Cobalamin-dependent methionine synthase (1-566) from *Thermotoga maritima* complexed with Zn²⁺
Authors : Koutmos, M.; Smith, J.L.; Ludwig, M.L.
Deposited on : 2007-12-17
Resolution : 1.85 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

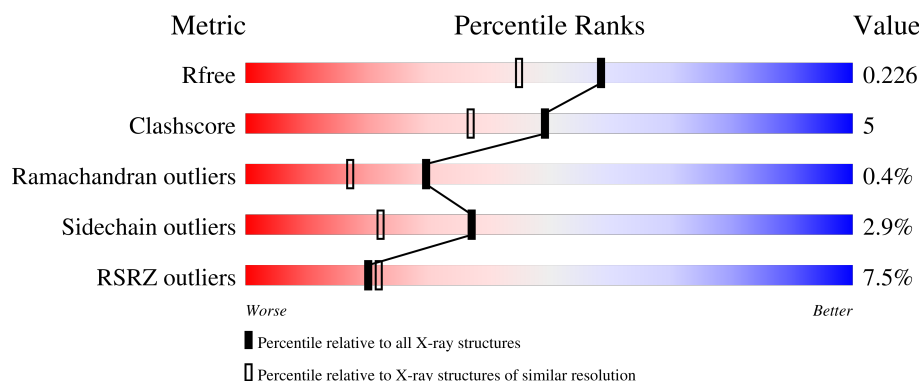
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	566	4% 87% 11% ...
1	B	566	10% 82% 13% ..

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 9055 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 5-methyltetrahydrofolate S-homocysteine methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	557	Total	C	N	O	S	0	0	0
			4375	2807	731	824	13			
1	B	549	Total	C	N	O	S	0	0	0
			4312	2768	720	811	13			

- 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	2	Total	Zn	0	0
			2	2		

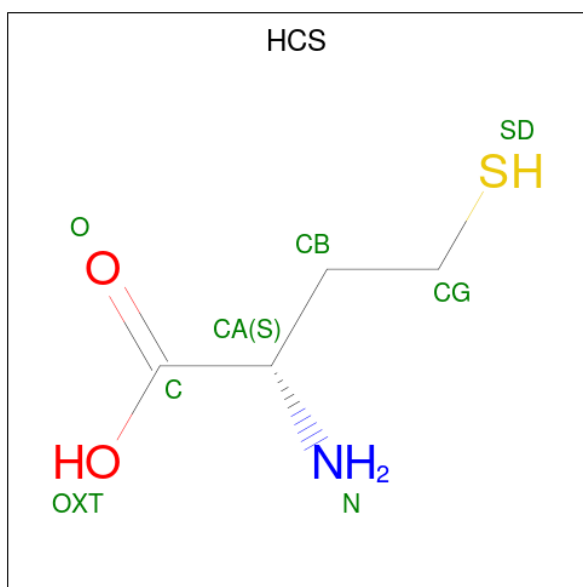
- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	K	0	0
			1	1		
3	B	1	Total	K	0	0
			1	1		

- Molecule 4 is YTTRIUM (III) ION (CCD ID: YT3) (formula: Y).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Y	0	0
			1	1		

- Molecule 5 is 2-AMINO-4-MERCAPTO-BUTYRIC ACID (CCD ID: HCS) (formula: C₄H₉NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			8	4	1	2	1		

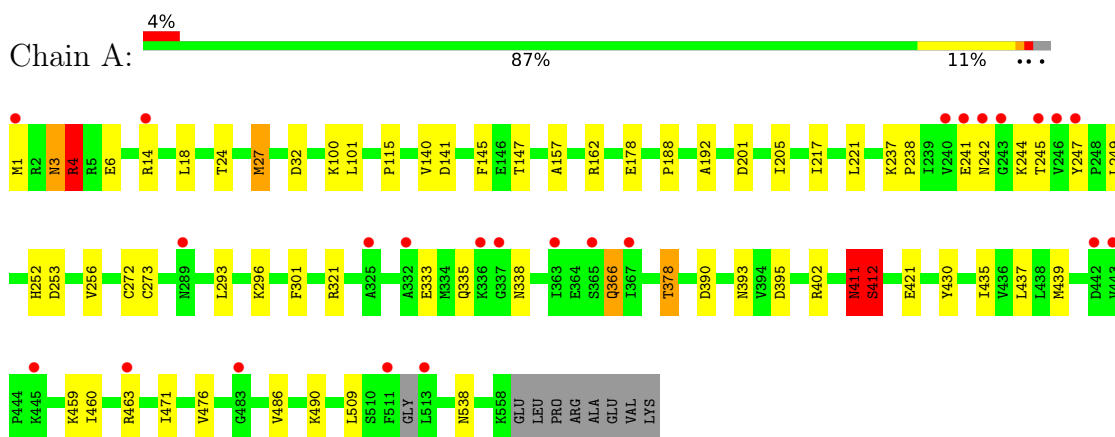
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	239	Total	O	0	0
			239	239		
6	B	115	Total	O	0	0
			115	115		

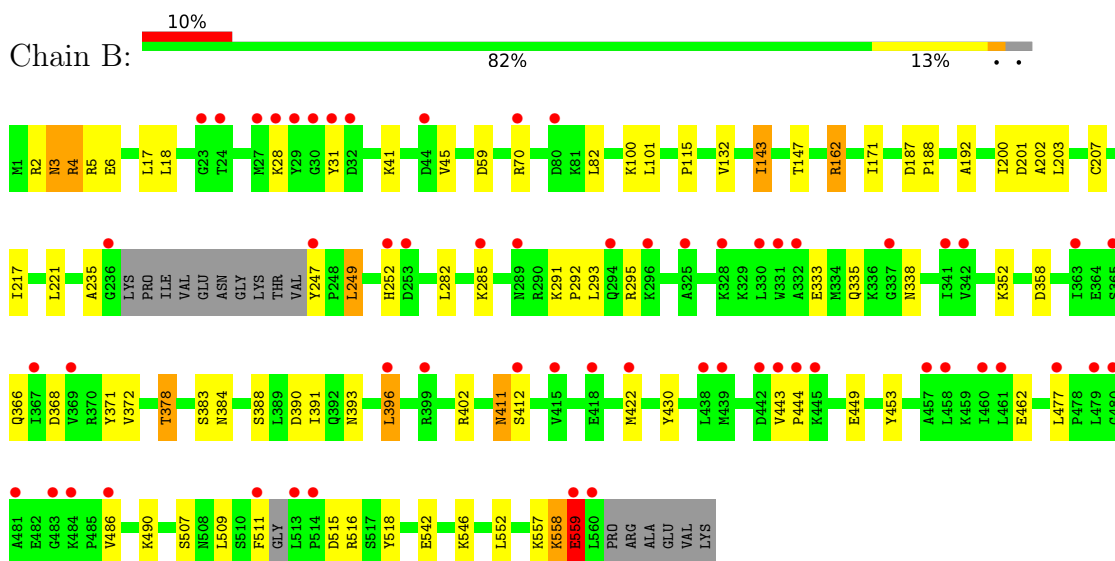
3 Residue-property plots

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: 5-methyltetrahydrofolate S-homocysteine methyltransferase



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.63Å 85.84Å 125.59Å 90.00° 100.67° 90.00°	Depositor
Resolution (Å)	47.62 – 1.85 47.62 – 1.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.62-1.85) 100.0 (47.62-1.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.50 (at 1.86Å)	Xtriage
Refinement program	REFMAC, CNS 1.2 / REFMAC 5.2.0019	Depositor
R, R_{free}	0.193 , 0.228 0.192 , 0.226	Depositor DCC
R_{free} test set	5351 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	24.1	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9055	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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: K, ZN, HCS, YT3

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	0.94	1/4455 (0.0%)	0.98	5/6020 (0.1%)
1	B	0.78	0/4390	0.95	5/5930 (0.1%)
All	All	0.86	1/8845 (0.0%)	0.97	10/11950 (0.1%)

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	1
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	412	SER	N-CA	-5.80	1.38	1.46

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	247	TYR	CA-C-N	8.37	129.42	120.47
1	B	247	TYR	C-N-CA	8.37	129.42	120.47
1	A	4	ARG	NE-CZ-NH1	-7.90	113.60	121.50
1	A	4	ARG	NE-CZ-NH2	7.00	125.50	119.20
1	A	411	ASN	CA-C-N	5.62	132.27	121.54
1	A	411	ASN	C-N-CA	5.62	132.27	121.54
1	A	378	THR	N-CA-C	5.40	118.33	111.69
1	B	4	ARG	NE-CZ-NH1	-5.25	116.25	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	559	GLU	N-CA-C	5.19	121.85	110.80
1	B	378	THR	N-CA-C	5.06	116.61	111.14

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	411	ASN	Peptide
1	B	411	ASN	Peptide

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	4375	0	4435	39	1
1	B	4312	0	4363	56	0
2	A	1	0	0	0	0
2	B	2	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	1
5	B	8	0	7	0	0
6	A	239	0	0	4	0
6	B	115	0	0	2	0
All	All	9055	0	8805	95	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 5.

All (95) 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:335:GLN:NE2	1:B:366:GLN:HG2	1.61	1.15
1:B:335:GLN:HE21	1:B:366:GLN:CG	1.71	1.02
1:B:335:GLN:HE21	1:B:366:GLN:HG2	0.90	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:ILE:HD11	1:B:203:LEU:HD21	1.55	0.88
1:B:207:CYS:SG	2:B:703:ZN:ZN	1.66	0.84
1:B:200:ILE:CD1	1:B:203:LEU:HD21	2.09	0.83
1:A:3:ASN:C	1:A:3:ASN:HD22	1.91	0.79
1:B:291:LYS:HG2	1:B:292:PRO:HD2	1.70	0.74
1:A:4:ARG:HD3	1:A:201:ASP:OD2	1.92	0.69
1:B:200:ILE:CD1	1:B:203:LEU:CD2	2.72	0.68
1:B:31:TYR:CE1	1:B:45:VAL:HG21	2.30	0.67
1:A:241:GLU:O	1:A:244:LYS:HG2	1.97	0.65
1:B:3:ASN:C	1:B:3:ASN:HD22	2.05	0.64
1:B:333:GLU:HB3	1:B:338:ASN:HB3	1.81	0.62
1:B:507:SER:O	1:B:511:PHE:HD2	1.82	0.62
1:A:412:SER:HA	1:A:435:ILE:O	2.00	0.61
1:A:27:MET:HE3	1:A:32:ASP:HB3	1.85	0.59
1:A:335:GLN:HE21	1:A:366:GLN:HG2	1.69	0.57
1:B:3:ASN:ND2	1:B:6:GLU:H	2.02	0.57
1:B:200:ILE:HD12	1:B:203:LEU:HD23	1.87	0.57
1:B:188:PRO:HG3	1:B:217:ILE:HG23	1.88	0.56
1:A:321:ARG:HD3	1:A:538:ASN:OD1	2.05	0.56
1:A:459:LYS:O	1:A:463:ARG:HG2	2.05	0.56
1:A:101:LEU:HD13	6:A:917:HOH:O	2.06	0.56
1:B:4:ARG:HD3	1:B:201:ASP:OD2	2.06	0.56
1:A:252:HIS:O	1:A:256:VAL:HG13	2.06	0.56
1:A:3:ASN:ND2	1:A:6:GLU:H	2.04	0.56
1:B:252:HIS:HD2	6:B:903:HOH:O	1.90	0.55
1:B:200:ILE:HD12	1:B:203:LEU:CD2	2.36	0.55
1:B:372:VAL:HG11	1:B:396:LEU:HD22	1.88	0.55
1:A:3:ASN:C	1:A:3:ASN:ND2	2.65	0.54
1:B:192:ALA:HB2	1:B:221:LEU:HD12	1.91	0.52
1:B:115:PRO:HG3	1:B:378:THR:HG23	1.92	0.52
1:B:515:ASP:HB3	1:B:518:TYR:HD1	1.74	0.52
1:A:238:PRO:HB3	1:A:247:TYR:CE1	2.45	0.52
1:A:4:ARG:CD	1:A:201:ASP:OD2	2.58	0.51
1:A:192:ALA:HB2	1:A:221:LEU:HD12	1.93	0.51
1:B:558:LYS:HD3	1:B:559:GLU:CB	2.41	0.51
1:B:390:ASP:HA	1:B:411:ASN:HB3	1.91	0.51
1:B:486:VAL:O	1:B:490:LYS:HG3	2.11	0.51
1:A:301:PHE:CZ	1:A:471:ILE:HG13	2.46	0.51
1:B:402:ARG:HG3	1:B:430:TYR:CE1	2.46	0.50
1:B:2:ARG:HD2	1:B:101:LEU:CD2	2.41	0.50
1:B:171:ILE:HG12	1:B:202:ALA:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:ARG:HG2	1:A:430:TYR:CE1	2.48	0.49
1:B:3:ASN:ND2	1:B:5:ARG:HB3	2.28	0.48
1:A:393:ASN:OD1	1:A:395:ASP:HB3	2.13	0.48
1:A:486:VAL:HG12	1:A:490:LYS:HE3	1.95	0.48
1:B:3:ASN:HD21	1:B:5:ARG:HB3	1.79	0.47
1:B:41:LYS:O	1:B:41:LYS:HG2	2.14	0.47
1:A:1:MET:HG3	1:A:140:VAL:O	2.13	0.47
1:B:235:ALA:C	1:B:249:LEU:HB2	2.40	0.47
1:B:542:GLU:HG2	1:B:546:LYS:HE2	1.96	0.47
1:B:507:SER:O	1:B:511:PHE:CD2	2.64	0.47
1:B:358:ASP:HA	1:B:388:SER:HB3	1.97	0.47
1:A:476:VAL:HG11	1:A:509:LEU:HB2	1.95	0.46
1:B:70:ARG:HG2	1:B:82:LEU:HD22	1.97	0.46
1:A:27:MET:HE1	6:A:828:HOH:O	2.16	0.46
1:B:383:SER:O	1:B:384:ASN:HB2	2.17	0.45
1:B:552:LEU:HB3	1:B:558:LYS:HG3	1.98	0.45
1:B:59:ASP:HA	1:B:100:LYS:HD2	1.99	0.45
1:A:272:CYS:O	1:A:273:CYS:C	2.60	0.44
1:A:100:LYS:HE2	6:A:1050:HOH:O	2.16	0.44
1:B:282:LEU:HD12	1:B:282:LEU:HA	1.86	0.44
1:A:162:ARG:HA	1:A:162:ARG:HD3	1.81	0.43
1:A:4:ARG:HD3	1:A:201:ASP:CG	2.43	0.43
1:A:437:LEU:HG	1:A:439:MET:HG2	2.01	0.43
1:A:188:PRO:HG3	1:A:217:ILE:HG23	2.00	0.43
1:B:200:ILE:HD11	1:B:203:LEU:CD2	2.34	0.43
1:B:4:ARG:CD	1:B:201:ASP:OD2	2.67	0.43
1:A:145:PHE:CE2	1:A:157:ALA:HB1	2.54	0.43
1:B:162:ARG:HD3	1:B:162:ARG:HA	1.67	0.43
1:A:390:ASP:HA	1:A:411:ASN:HB3	2.01	0.43
1:B:557:LYS:O	1:B:558:LYS:HB3	2.19	0.43
1:B:391:ILE:HG21	1:B:396:LEU:HB3	1.99	0.42
1:B:443:VAL:HG11	1:B:477:LEU:HD21	2.00	0.42
1:B:187:ASP:HB2	1:B:188:PRO:CD	2.49	0.42
1:B:3:ASN:C	1:B:3:ASN:ND2	2.74	0.42
1:B:511:PHE:CZ	1:B:516:ARG:HD3	2.55	0.42
1:A:205:ILE:HD13	1:A:217:ILE:HG22	2.02	0.41
1:A:238:PRO:HB2	1:A:245:THR:HG23	2.02	0.41
1:A:460:ILE:HA	1:A:463:ARG:HE	1.85	0.41
1:A:249:LEU:HD11	1:A:253:ASP:HB3	2.02	0.41
1:A:333:GLU:HB3	1:A:338:ASN:HB3	2.03	0.41
1:B:188:PRO:CG	1:B:217:ILE:HG23	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:ASP:O	1:B:371:TYR:HB3	2.21	0.41
1:A:115:PRO:HG3	1:A:378:THR:HG23	2.01	0.41
1:A:237:LYS:HG3	1:A:238:PRO:HD2	2.03	0.41
1:A:1:MET:HA	1:A:141:ASP:OD1	2.21	0.41
1:A:14:ARG:HD2	6:A:1062:HOH:O	2.21	0.41
1:B:252:HIS:CD2	6:B:903:HOH:O	2.70	0.41
1:B:393:ASN:HB3	1:B:396:LEU:HB2	2.03	0.41
1:B:444:PRO:HG3	1:B:453:TYR:CE1	2.56	0.41
1:B:444:PRO:HB3	1:B:449:GLU:HB3	2.03	0.41
1:B:132:VAL:HG13	1:B:143:ILE:HD12	2.02	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:421:GLU:OE2	4:A:705:YT3:Y[1_455]	2.19	0.01

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	553/566 (98%)	536 (97%)	16 (3%)	1 (0%)	43	31
1	B	543/566 (96%)	525 (97%)	15 (3%)	3 (1%)	21	10
All	All	1096/1132 (97%)	1061 (97%)	31 (3%)	4 (0%)	30	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	412	SER
1	B	559	GLU
1	A	412	SER

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Mol	Chain	Res	Type
1	B	28	LYS

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	479/494 (97%)	467 (98%)	12 (2%)	42	27
1	B	471/494 (95%)	455 (97%)	16 (3%)	32	17
All	All	950/988 (96%)	922 (97%)	28 (3%)	37	22

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	4	ARG
1	A	18	LEU
1	A	24	THR
1	A	27	MET
1	A	147	THR
1	A	178	GLU
1	A	242	ASN
1	A	293	LEU
1	A	296	LYS
1	A	366	GLN
1	A	412	SER
1	B	3	ASN
1	B	17	LEU
1	B	18	LEU
1	B	143	ILE
1	B	147	THR
1	B	162	ARG
1	B	249	LEU
1	B	285	LYS
1	B	293	LEU
1	B	295	ARG

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Mol	Chain	Res	Type
1	B	352	LYS
1	B	396	LEU
1	B	422	MET
1	B	462	GLU
1	B	509	LEU
1	B	558	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	335	GLN
1	B	3	ASN
1	B	252	HIS
1	B	257	HIS
1	B	335	GLN
1	B	384	ASN
1	B	549	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 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	HCS	B	710	2	6,7,7	1.14	0	5,8,8	1.69	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	HCS	B	710	2	-	1/7/7/7	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	710	HCS	CB-CG-SD	-3.16	110.45	113.74

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	710	HCS	OXT-C-CA-N

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

6.1 Protein, DNA and RNA chains

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	557/566 (98%)	0.02	24 (4%)	40 43	12, 23, 44, 56	0
1	B	549/566 (96%)	0.55	59 (10%)	11 10	16, 31, 55, 64	0
All	All	1106/1132 (97%)	0.29	83 (7%)	20 22	12, 27, 52, 64	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	560	LEU	6.7
1	B	511	PHE	5.9
1	B	29	TYR	5.5
1	B	247	TYR	4.2
1	B	363	ILE	4.1
1	B	31	TYR	3.9
1	A	483	GLY	3.8
1	A	511	PHE	3.7
1	B	331	TRP	3.6
1	B	236	GLY	3.5
1	B	443	VAL	3.5
1	A	246	VAL	3.3
1	B	28	LYS	3.3
1	B	289	ASN	3.1
1	B	330	LEU	2.9
1	B	445	LYS	2.9
1	B	27	MET	2.9
1	B	559	GLU	2.9
1	B	296	LYS	2.9
1	B	369	VAL	2.9
1	B	412	SER	2.9
1	A	513	LEU	2.9
1	A	367	ILE	2.8
1	A	243	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	30	GLY	2.8
1	B	480	GLY	2.8
1	A	365	SER	2.7
1	B	439	MET	2.7
1	B	253	ASP	2.6
1	A	1	MET	2.6
1	B	457	ALA	2.6
1	A	245	THR	2.6
1	B	418	GLU	2.6
1	B	422	MET	2.6
1	B	342	VAL	2.5
1	A	337	GLY	2.5
1	B	325	ALA	2.5
1	B	332	ALA	2.5
1	A	363	ILE	2.5
1	B	399	ARG	2.4
1	B	479	LEU	2.4
1	B	367	ILE	2.4
1	A	443	VAL	2.4
1	A	442	ASP	2.3
1	B	396	LEU	2.3
1	B	477	LEU	2.3
1	A	241	GLU	2.3
1	B	486	VAL	2.3
1	B	80	ASP	2.3
1	B	415	VAL	2.3
1	B	442	ASP	2.3
1	A	242	ASN	2.3
1	A	332	ALA	2.3
1	A	247	TYR	2.2
1	A	325	ALA	2.2
1	B	24	THR	2.2
1	B	458	LEU	2.2
1	B	23	GLY	2.2
1	B	32	ASP	2.2
1	B	44	ASP	2.2
1	B	444	PRO	2.2
1	B	513	LEU	2.2
1	B	484	LYS	2.2
1	B	483	GLY	2.2
1	B	365	SER	2.1
1	A	14	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	463	ARG	2.1
1	B	70	ARG	2.1
1	B	461	LEU	2.1
1	B	328	LYS	2.1
1	A	289	ASN	2.1
1	B	481	ALA	2.1
1	A	445	LYS	2.1
1	B	341	ILE	2.1
1	B	438	LEU	2.1
1	A	336	LYS	2.0
1	B	460	ILE	2.0
1	B	337	GLY	2.0
1	B	294	GLN	2.0
1	B	285	LYS	2.0
1	B	252	HIS	2.0
1	B	514	PRO	2.0
1	A	240	VAL	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
5	HCS	B	710	8/8	0.90	0.15	21,22,26,27	8
2	ZN	B	703	1/1	0.98	0.06	12,12,12,12	1
4	YT3	A	705	1/1	0.98	0.08	34,34,34,34	0
2	ZN	B	702	1/1	0.98	0.05	29,29,29,29	1
2	ZN	A	701	1/1	0.99	0.04	21,21,21,21	0
3	K	A	703	1/1	0.99	0.04	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	K	B	704	1/1	1.00	0.04	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.