



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2021 – 10:53 AM EDT

PDB ID : 3IAP
Title : E. coli (lacZ) beta-galactosidase (E416Q)
Authors : Lo, S.; Dugdale, M.L.; Jeerh, N.; Ku, T.; Roth, N.J.; Huber, R.E.
Deposited on : 2009-07-14
Resolution : 2.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

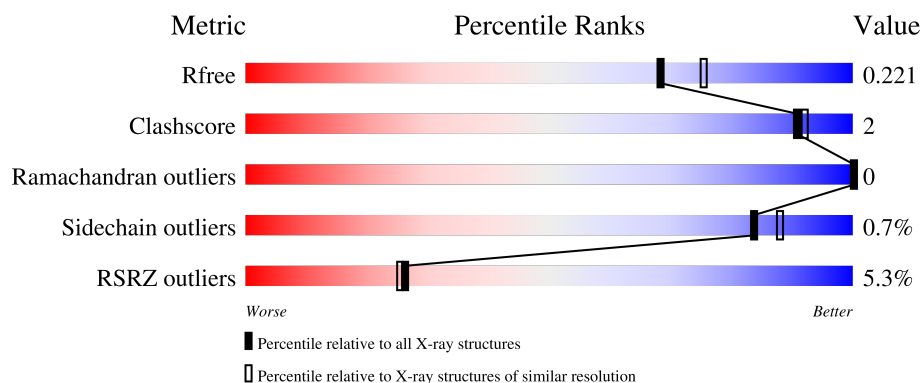
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	1023	<div> <div>5%</div> <div>94%</div> <div>5%</div> </div>
1	B	1023	<div> <div>6%</div> <div>94%</div> <div>• •</div> </div>
1	C	1023	<div> <div>5%</div> <div>94%</div> <div>• •</div> </div>
1	D	1023	<div> <div>6%</div> <div>94%</div> <div>5%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NA	B	3104	-	-	-	X
3	NA	D	3103	-	-	-	X
4	BTB	B	6001	-	-	-	X
4	BTB	C	6001	-	-	X	-
4	BTB	D	6001	-	-	-	X
5	DMS	A	7006	-	-	-	X
5	DMS	B	7030	-	-	-	X
5	DMS	C	7008	-	-	-	X
5	DMS	C	7020	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 36912 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 Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1011	Total	C	N	O	S	0	0	0
			8125	5138	1441	1508	38			
1	B	1011	Total	C	N	O	S	0	0	0
			8125	5138	1441	1508	38			
1	C	1011	Total	C	N	O	S	0	0	0
			8125	5138	1441	1508	38			
1	D	1011	Total	C	N	O	S	0	0	0
			8125	5138	1441	1508	38			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP B8LFD6
A	2	SER	-	expression tag	UNP B8LFD6
A	3	HIS	-	expression tag	UNP B8LFD6
A	4	MET	-	expression tag	UNP B8LFD6
A	5	LEU	-	expression tag	UNP B8LFD6
A	6	GLU	-	expression tag	UNP B8LFD6
A	7	ASP	-	expression tag	UNP B8LFD6
A	8	PRO	-	expression tag	UNP B8LFD6
A	416	GLN	GLU	engineered mutation	UNP B8LFD6
B	1	GLY	-	expression tag	UNP B8LFD6
B	2	SER	-	expression tag	UNP B8LFD6
B	3	HIS	-	expression tag	UNP B8LFD6
B	4	MET	-	expression tag	UNP B8LFD6
B	5	LEU	-	expression tag	UNP B8LFD6
B	6	GLU	-	expression tag	UNP B8LFD6
B	7	ASP	-	expression tag	UNP B8LFD6
B	8	PRO	-	expression tag	UNP B8LFD6
B	416	GLN	GLU	engineered mutation	UNP B8LFD6
C	1	GLY	-	expression tag	UNP B8LFD6
C	2	SER	-	expression tag	UNP B8LFD6
C	3	HIS	-	expression tag	UNP B8LFD6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4	MET	-	expression tag	UNP B8LFD6
C	5	LEU	-	expression tag	UNP B8LFD6
C	6	GLU	-	expression tag	UNP B8LFD6
C	7	ASP	-	expression tag	UNP B8LFD6
C	8	PRO	-	expression tag	UNP B8LFD6
C	416	GLN	GLU	engineered mutation	UNP B8LFD6
D	1	GLY	-	expression tag	UNP B8LFD6
D	2	SER	-	expression tag	UNP B8LFD6
D	3	HIS	-	expression tag	UNP B8LFD6
D	4	MET	-	expression tag	UNP B8LFD6
D	5	LEU	-	expression tag	UNP B8LFD6
D	6	GLU	-	expression tag	UNP B8LFD6
D	7	ASP	-	expression tag	UNP B8LFD6
D	8	PRO	-	expression tag	UNP B8LFD6
D	416	GLN	GLU	engineered mutation	UNP B8LFD6

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0
2	B	2	Total Mg 2 2	0	0
2	C	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

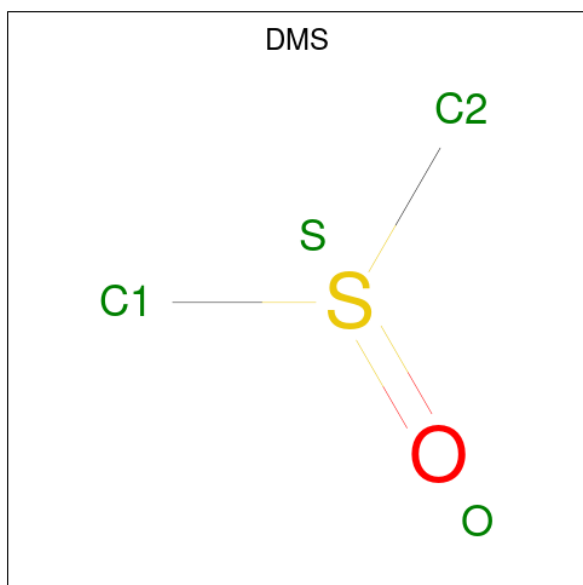
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	4	Total Na 4 4	0	0
3	B	4	Total Na 4 4	0	0
3	C	4	Total Na 4 4	0	0
3	D	4	Total Na 4 4	0	0

- Molecule 4 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (three-letter code: BTB) (formula: C₈H₁₉NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



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

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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0
5	D	1	Total 4	C 2	O 1	S 1	0	0

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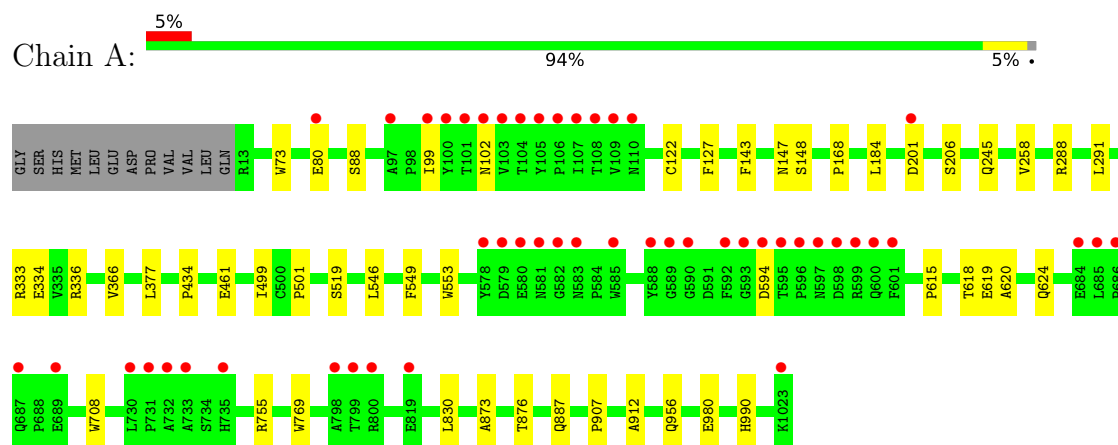
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1038	Total 1038	O 1038	0	0
6	B	974	Total 974	O 974	0	0
6	C	889	Total 889	O 889	0	0
6	D	931	Total 931	O 931	0	0

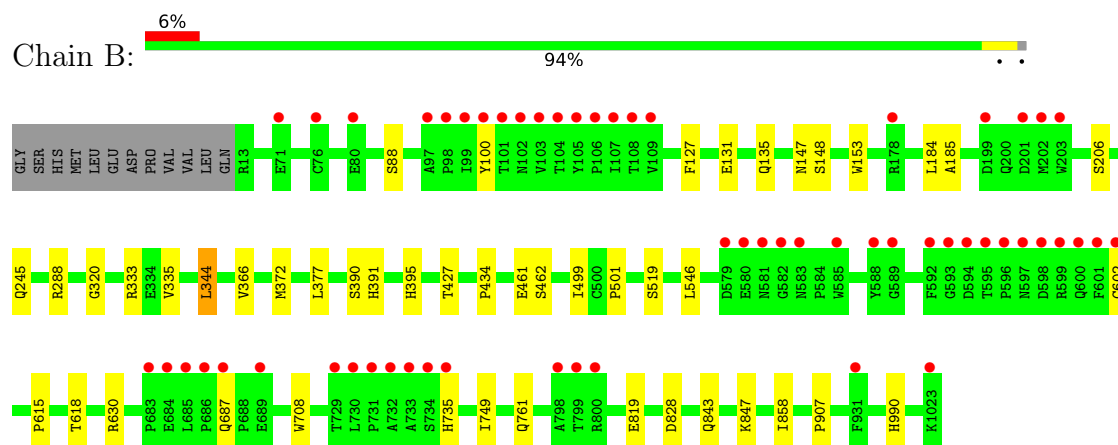
3 Residue-property plots [i](#)

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.

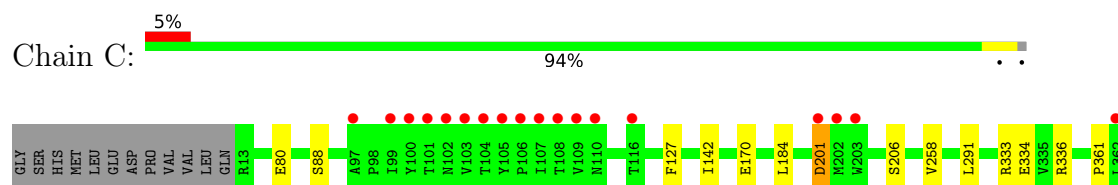
- Molecule 1: Beta-galactosidase

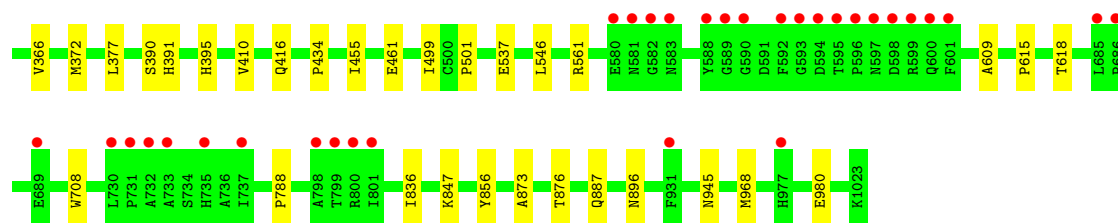


- Molecule 1: Beta-galactosidase

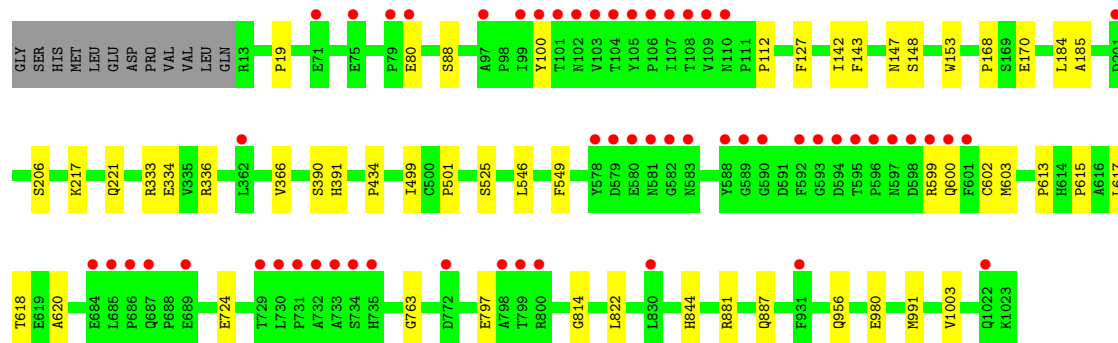
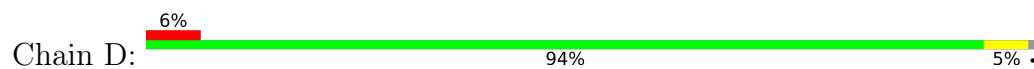


- Molecule 1: Beta-galactosidase





• Molecule 1: Beta-galactosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	151.23Å 162.34Å 202.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.38 – 2.00 53.36 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (53.38-2.00) 87.6 (53.36-2.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.20	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.2.0019, CNS	Depositor
R, R_{free}	0.181 , 0.220 0.181 , 0.221	Depositor DCC
R_{free} test set	4186 reflections (1.43%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtrriage
Anisotropy	0.083	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	36912	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.0401e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DMS, MG, NA, BTB

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	0.34	0/8367	0.50	0/11415
1	B	0.34	0/8367	0.50	0/11415
1	C	0.34	0/8367	0.50	0/11415
1	D	0.34	0/8367	0.50	0/11415
All	All	0.34	0/33468	0.50	0/45660

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	8125	0	7718	26	0
1	B	8125	0	7718	25	0
1	C	8125	0	7718	27	0
1	D	8125	0	7717	25	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	0	0	0
3	C	4	0	0	0	0
3	D	4	0	0	0	0
4	A	14	0	19	3	0
4	B	14	0	19	4	0
4	C	14	0	19	9	0
4	D	14	0	18	2	0
5	A	128	0	192	0	0
5	B	132	0	198	2	0
5	C	128	0	192	0	0
5	D	112	0	168	0	0
6	A	1038	0	0	0	0
6	B	974	0	0	0	0
6	C	889	0	0	0	0
6	D	931	0	0	0	0
All	All	36912	0	31696	107	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 2.

All (107) 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)
4:B:6001:BTB:H11	4:B:6001:BTB:H61	1.18	1.11
4:B:6001:BTB:H61	4:B:6001:BTB:C1	1.89	1.03
4:B:6001:BTB:H11	4:B:6001:BTB:C6	1.91	1.00
4:D:6001:BTB:H41	4:D:6001:BTB:H62	1.46	0.98
1:C:416:GLN:HE22	4:C:6001:BTB:H81	1.35	0.91
1:B:461:GLU:OE1	4:B:6001:BTB:H72	1.85	0.76
1:A:102:ASN:HA	1:A:201:ASP:HB2	1.72	0.72
1:C:372:MET:HE1	1:C:395:HIS:HB3	1.74	0.69
1:C:416:GLN:HE22	4:C:6001:BTB:C8	2.06	0.68
4:D:6001:BTB:H41	4:D:6001:BTB:C6	2.22	0.66
1:C:416:GLN:NE2	4:C:6001:BTB:H81	2.11	0.63
1:A:830:LEU:HD22	1:B:828:ASP:HB3	1.82	0.62
1:C:377:LEU:HD22	1:C:708:TRP:HA	1.83	0.61
1:A:461:GLU:OE1	4:A:6001:BTB:H11	2.01	0.60
1:D:600:GLN:HB2	1:D:603:MET:HE2	1.86	0.58
1:D:599:ARG:HE	1:D:797:GLU:HG2	1.70	0.57
1:B:372:MET:HE1	1:B:395:HIS:HB3	1.88	0.56
1:A:127:PHE:CE2	1:A:184:LEU:HG	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:6001:BTB:H71	4:C:6001:BTB:O4	2.05	0.55
1:C:887:GLN:NE2	1:C:980:GLU:O	2.37	0.54
1:C:127:PHE:CE2	1:C:184:LEU:HG	2.42	0.54
1:C:461:GLU:OE1	4:C:6001:BTB:H31	2.09	0.52
1:A:377:LEU:HD22	1:A:708:TRP:HA	1.91	0.51
1:D:127:PHE:CE2	1:D:184:LEU:HG	2.46	0.50
1:D:88:SER:HA	1:D:366:VAL:HG21	1.91	0.50
1:B:147:ASN:HB3	1:B:206:SER:HA	1.94	0.50
1:C:142:ILE:HG12	1:C:170:GLU:HG2	1.94	0.50
1:D:334:GLU:OE1	1:D:336:ARG:NH1	2.40	0.49
1:B:127:PHE:HE2	1:B:184:LEU:HG	1.77	0.49
1:D:147:ASN:HB3	1:D:206:SER:HA	1.93	0.49
1:B:88:SER:HA	1:B:366:VAL:HG21	1.94	0.49
1:A:88:SER:HA	1:A:366:VAL:HG21	1.95	0.49
1:A:147:ASN:HB3	1:A:206:SER:HA	1.93	0.49
1:A:873:ALA:O	1:A:876:THR:HG22	2.12	0.49
1:D:147:ASN:HA	1:D:148:SER:HA	1.67	0.48
1:C:361:PRO:HB3	1:C:609:ALA:HB1	1.95	0.48
1:B:377:LEU:HD22	1:B:708:TRP:HA	1.94	0.48
1:A:245:GLN:HG2	1:A:288:ARG:HG2	1.95	0.48
1:C:88:SER:HA	1:C:366:VAL:HG21	1.96	0.48
1:A:334:GLU:OE1	1:A:336:ARG:NH1	2.45	0.48
1:B:615:PRO:O	1:B:618:THR:HG22	2.14	0.47
1:A:127:PHE:HE2	1:A:184:LEU:HG	1.80	0.47
1:C:201:ASP:OD1	4:C:6001:BTB:H71	2.14	0.47
1:C:615:PRO:O	1:C:618:THR:HG22	2.14	0.47
1:B:100:TYR:CZ	1:B:602:CYS:HB3	2.50	0.47
1:B:153:TRP:HB2	1:B:185:ALA:HB3	1.97	0.46
1:B:127:PHE:CE2	1:B:184:LEU:HG	2.51	0.46
1:B:335:VAL:HG22	1:B:344:LEU:HD12	1.98	0.46
1:D:499:ILE:HG22	1:D:501:PRO:HD3	1.97	0.46
1:B:427:THR:HG21	1:B:462:SER:HB3	1.98	0.45
1:C:873:ALA:O	1:C:876:THR:HG22	2.16	0.45
1:B:245:GLN:HG2	1:B:288:ARG:HG2	1.98	0.45
1:C:561:ARG:HD3	1:D:525:SER:O	2.16	0.45
1:D:887:GLN:NE2	1:D:980:GLU:O	2.47	0.45
4:A:6001:BTB:H11	4:A:6001:BTB:H52	1.60	0.45
1:C:390:SER:HA	1:C:391:HIS:HA	1.75	0.45
1:D:100:TYR:CE1	1:D:602:CYS:HB3	2.52	0.45
1:A:99:ILE:HG23	1:A:594:ASP:HB2	1.99	0.45
1:A:147:ASN:HA	1:A:148:SER:HA	1.68	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:537:GLU:OE1	4:C:6001:BTB:H32	2.17	0.45
1:A:499:ILE:HG22	1:A:501:PRO:HD3	2.00	0.44
1:B:390:SER:HA	1:B:391:HIS:HA	1.79	0.44
4:A:6001:BTB:H71	4:A:6001:BTB:H42	1.58	0.44
1:C:836:ILE:HB	1:C:856:TYR:HB2	1.99	0.44
1:D:549:PHE:CE2	1:D:620:ALA:HA	2.53	0.44
1:D:153:TRP:HB2	1:D:185:ALA:HB3	1.99	0.43
1:D:217:LYS:HE3	1:D:221:GLN:HB2	2.00	0.43
1:D:763:GLY:HA3	1:D:822:LEU:HD13	2.00	0.43
1:A:434:PRO:HB3	1:D:434:PRO:HB3	2.01	0.43
1:B:147:ASN:HA	1:B:148:SER:HA	1.66	0.43
1:C:201:ASP:HB3	4:C:6001:BTB:H72	1.99	0.43
1:A:258:VAL:HG23	1:A:291:LEU:HD13	2.00	0.43
1:A:553:TRP:CZ2	1:A:624:GLN:HG2	2.54	0.43
1:B:100:TYR:CE1	1:B:602:CYS:HB3	2.53	0.43
1:B:907:PRO:HG2	1:B:990:HIS:O	2.19	0.43
1:B:499:ILE:HG22	1:B:501:PRO:HD3	2.01	0.42
1:D:143:PHE:O	1:D:168:PRO:HA	2.19	0.42
1:A:143:PHE:O	1:A:168:PRO:HA	2.19	0.42
1:A:619:GLU:HA	1:A:912:ALA:HB2	2.01	0.42
1:B:320:GLY:HA2	5:B:7006:DMS:O	2.20	0.42
1:D:613:PRO:HB3	1:D:617:LEU:HD23	2.00	0.42
1:B:434:PRO:HB3	1:C:434:PRO:HB3	2.01	0.42
1:D:390:SER:HA	1:D:391:HIS:HA	1.79	0.42
1:B:630:ARG:HH21	5:B:7023:DMS:H23	1.85	0.42
1:A:907:PRO:HG2	1:A:990:HIS:O	2.20	0.42
1:C:258:VAL:HG23	1:C:291:LEU:HD13	2.02	0.42
1:D:142:ILE:HG23	1:D:170:GLU:HG2	2.02	0.42
1:B:749:ILE:HD13	1:B:858:ILE:HD12	2.02	0.41
1:C:896:ASN:HB3	1:C:945:ASN:HB2	2.02	0.41
1:A:615:PRO:O	1:A:618:THR:HG22	2.20	0.41
1:A:549:PHE:CE2	1:A:620:ALA:HA	2.55	0.41
1:A:755:ARG:HB2	1:A:769:TRP:HB2	2.02	0.41
1:B:843:GLN:HA	1:B:847:LYS:O	2.20	0.41
1:A:73:TRP:CE2	1:A:122:CYS:HB3	2.55	0.41
1:C:847:LYS:NZ	1:D:724:GLU:O	2.53	0.41
1:B:131:GLU:HG3	1:B:135:GLN:HG3	2.01	0.41
1:C:788:PRO:HD2	1:C:968:MET:HG3	2.03	0.41
4:C:6001:BTB:H51	4:C:6001:BTB:H12	1.59	0.41
1:A:887:GLN:NE2	1:A:980:GLU:O	2.50	0.41
1:C:410:VAL:HG22	1:C:455:ILE:HB	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:19:PRO:HD3	1:D:112:PRO:CB	2.51	0.41
1:D:991:MET:HE2	1:D:1003:VAL:HG21	2.03	0.41
1:C:499:ILE:HG22	1:C:501:PRO:HD3	2.03	0.40
1:D:615:PRO:O	1:D:618:THR:HG22	2.21	0.40
1:D:814:GLY:HA3	1:D:844:HIS:CG	2.56	0.40
1:A:102:ASN:HA	1:A:201:ASP:CB	2.47	0.40
1:C:334:GLU:OE1	1:C:336:ARG:NH1	2.47	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	1009/1023 (99%)	972 (96%)	37 (4%)	0	100	100
1	B	1009/1023 (99%)	977 (97%)	32 (3%)	0	100	100
1	C	1009/1023 (99%)	977 (97%)	32 (3%)	0	100	100
1	D	1009/1023 (99%)	973 (96%)	36 (4%)	0	100	100
All	All	4036/4092 (99%)	3899 (97%)	137 (3%)	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	864/875 (99%)	859 (99%)	5 (1%)	86	90
1	B	864/875 (99%)	856 (99%)	8 (1%)	78	83
1	C	864/875 (99%)	859 (99%)	5 (1%)	86	90
1	D	864/875 (99%)	859 (99%)	5 (1%)	86	90
All	All	3456/3500 (99%)	3433 (99%)	23 (1%)	84	88

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	GLU
1	A	333	ARG
1	A	519	SER
1	A	546	LEU
1	A	956	GLN
1	B	333	ARG
1	B	344	LEU
1	B	519	SER
1	B	546	LEU
1	B	687	GLN
1	B	735	HIS
1	B	761	GLN
1	B	819	GLU
1	C	80	GLU
1	C	201	ASP
1	C	206	SER
1	C	333	ARG
1	C	546	LEU
1	D	80	GLU
1	D	333	ARG
1	D	546	LEU
1	D	881	ARG
1	D	956	GLN

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	1017	GLN
1	C	416	GLN
1	C	418	HIS
1	C	604	ASN

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Mol	Chain	Res	Type
1	C	624	GLN
1	D	418	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 153 ligands modelled in this entry, 24 are monoatomic - leaving 129 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
4	BTB	A	6001	3	13,13,13	0.45	0	7,16,16	0.21	0
5	DMS	D	7004	-	3,3,3	2.65	1 (33%)	3,3,3	0.53	0
5	DMS	A	7008	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	D	7002	-	3,3,3	2.65	1 (33%)	3,3,3	0.50	0
5	DMS	B	7026	-	3,3,3	2.65	1 (33%)	3,3,3	0.46	0
5	DMS	A	7030	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	D	7012	-	3,3,3	2.65	1 (33%)	3,3,3	0.46	0
5	DMS	C	7006	-	3,3,3	2.67	1 (33%)	3,3,3	0.46	0
5	DMS	B	7009	-	3,3,3	2.64	1 (33%)	3,3,3	0.51	0
5	DMS	C	7025	-	3,3,3	2.65	1 (33%)	3,3,3	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	D	7026	-	3,3,3	2.67	1 (33%)	3,3,3	0.48	0
5	DMS	C	7010	-	3,3,3	2.65	1 (33%)	3,3,3	0.51	0
5	DMS	D	7014	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
5	DMS	C	7002	-	3,3,3	2.60	1 (33%)	3,3,3	0.53	0
4	BTB	C	6001	-	13,13,13	0.56	0	7,16,16	0.64	0
5	DMS	B	7028	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	B	7030	-	3,3,3	2.67	1 (33%)	3,3,3	0.55	0
5	DMS	C	7003	-	3,3,3	2.64	1 (33%)	3,3,3	0.50	0
5	DMS	C	7012	-	3,3,3	2.69	1 (33%)	3,3,3	0.52	0
5	DMS	D	7023	-	3,3,3	2.64	1 (33%)	3,3,3	0.46	0
5	DMS	D	7009	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	A	7032	-	3,3,3	2.68	1 (33%)	3,3,3	0.51	0
5	DMS	C	7004	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	A	7023	-	3,3,3	2.70	1 (33%)	3,3,3	0.50	0
5	DMS	B	7024	-	3,3,3	2.66	1 (33%)	3,3,3	0.52	0
5	DMS	A	7024	-	3,3,3	2.68	1 (33%)	3,3,3	0.50	0
5	DMS	A	7022	-	3,3,3	2.64	1 (33%)	3,3,3	0.53	0
5	DMS	A	7026	-	3,3,3	2.67	1 (33%)	3,3,3	0.56	0
5	DMS	B	7002	-	3,3,3	2.61	1 (33%)	3,3,3	0.55	0
5	DMS	A	7029	-	3,3,3	2.66	1 (33%)	3,3,3	0.44	0
5	DMS	A	7009	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	A	7027	-	3,3,3	2.66	1 (33%)	3,3,3	0.56	0
5	DMS	D	7015	-	3,3,3	2.68	1 (33%)	3,3,3	0.54	0
5	DMS	A	7013	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
5	DMS	A	7011	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	C	7015	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	D	7028	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	C	7026	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	B	7023	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
5	DMS	B	7031	-	3,3,3	2.67	1 (33%)	3,3,3	0.57	0
5	DMS	B	7021	-	3,3,3	2.64	1 (33%)	3,3,3	0.48	0
5	DMS	C	7024	-	3,3,3	2.63	1 (33%)	3,3,3	0.49	0
5	DMS	D	7029	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
4	BTB	B	6001	-	13,13,13	0.76	0	7,16,16	0.84	0
5	DMS	B	7020	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	D	7005	-	3,3,3	2.58	1 (33%)	3,3,3	0.40	0
5	DMS	D	7019	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	B	7017	-	3,3,3	2.65	1 (33%)	3,3,3	0.46	0
5	DMS	D	7025	-	3,3,3	2.63	1 (33%)	3,3,3	0.54	0
5	DMS	C	7009	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	D	7016	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
4	BTB	D	6001	3	13,13,13	0.87	0	7,16,16	0.82	0
5	DMS	B	7006	-	3,3,3	2.64	1 (33%)	3,3,3	0.46	0
5	DMS	A	7014	-	3,3,3	2.64	1 (33%)	3,3,3	0.36	0
5	DMS	C	7030	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	A	7002	-	3,3,3	2.66	1 (33%)	3,3,3	0.44	0
5	DMS	B	7014	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
5	DMS	C	7034	-	3,3,3	2.66	1 (33%)	3,3,3	0.55	0
5	DMS	B	7029	-	3,3,3	2.64	1 (33%)	3,3,3	0.48	0
5	DMS	C	7018	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	C	7016	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
5	DMS	C	7027	-	3,3,3	2.66	1 (33%)	3,3,3	0.53	0
5	DMS	D	7027	-	3,3,3	2.66	1 (33%)	3,3,3	0.52	0
5	DMS	C	7007	-	3,3,3	2.68	1 (33%)	3,3,3	0.48	0
5	DMS	D	7003	-	3,3,3	2.64	1 (33%)	3,3,3	0.52	0
5	DMS	C	7011	-	3,3,3	2.68	1 (33%)	3,3,3	0.51	0
5	DMS	A	7004	-	3,3,3	2.68	1 (33%)	3,3,3	0.50	0
5	DMS	A	7031	-	3,3,3	2.67	1 (33%)	3,3,3	0.50	0
5	DMS	A	7021	-	3,3,3	2.60	1 (33%)	3,3,3	0.54	0
5	DMS	D	7010	-	3,3,3	2.66	1 (33%)	3,3,3	0.53	0
5	DMS	A	7005	-	3,3,3	2.66	1 (33%)	3,3,3	0.59	0
5	DMS	A	7020	-	3,3,3	2.65	1 (33%)	3,3,3	0.45	0
5	DMS	A	7010	-	3,3,3	2.65	1 (33%)	3,3,3	0.44	0
5	DMS	D	7007	-	3,3,3	2.68	1 (33%)	3,3,3	0.50	0
5	DMS	D	7020	-	3,3,3	2.64	1 (33%)	3,3,3	0.46	0
5	DMS	A	7015	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	C	7028	-	3,3,3	2.67	1 (33%)	3,3,3	0.58	0
5	DMS	B	7032	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	A	7012	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	C	7031	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	A	7028	-	3,3,3	2.65	1 (33%)	3,3,3	0.50	0
5	DMS	B	7018	-	3,3,3	2.67	1 (33%)	3,3,3	0.54	0
5	DMS	A	7006	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	B	7013	-	3,3,3	2.65	1 (33%)	3,3,3	0.54	0
5	DMS	A	7001	-	3,3,3	2.62	1 (33%)	3,3,3	0.46	0
5	DMS	C	7020	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	C	7014	-	3,3,3	2.66	1 (33%)	3,3,3	0.49	0
5	DMS	A	7007	-	3,3,3	2.66	1 (33%)	3,3,3	0.43	0
5	DMS	B	7001	-	3,3,3	2.63	1 (33%)	3,3,3	0.51	0
5	DMS	D	7022	-	3,3,3	2.66	1 (33%)	3,3,3	0.49	0
5	DMS	A	7016	-	3,3,3	2.68	1 (33%)	3,3,3	0.49	0
5	DMS	C	7029	-	3,3,3	2.68	1 (33%)	3,3,3	0.57	0
5	DMS	D	7013	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	D	7017	-	3,3,3	2.66	1 (33%)	3,3,3	0.53	0
5	DMS	B	7033	-	3,3,3	2.66	1 (33%)	3,3,3	0.52	0
5	DMS	D	7006	-	3,3,3	2.64	1 (33%)	3,3,3	0.49	0
5	DMS	C	7013	-	3,3,3	2.68	1 (33%)	3,3,3	0.51	0
5	DMS	C	7023	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	B	7011	-	3,3,3	2.65	1 (33%)	3,3,3	0.50	0
5	DMS	C	7005	-	3,3,3	2.64	1 (33%)	3,3,3	0.41	0
5	DMS	D	7024	-	3,3,3	2.65	1 (33%)	3,3,3	0.47	0
5	DMS	A	7019	-	3,3,3	2.72	1 (33%)	3,3,3	0.64	0
5	DMS	B	7003	-	3,3,3	2.65	1 (33%)	3,3,3	0.55	0
5	DMS	B	7007	-	3,3,3	2.69	1 (33%)	3,3,3	0.50	0
5	DMS	B	7025	-	3,3,3	2.67	1 (33%)	3,3,3	0.53	0
5	DMS	B	7010	-	3,3,3	2.68	1 (33%)	3,3,3	0.50	0
5	DMS	D	7018	-	3,3,3	2.66	1 (33%)	3,3,3	0.48	0
5	DMS	C	7021	-	3,3,3	2.67	1 (33%)	3,3,3	0.52	0
5	DMS	B	7015	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	A	7003	-	3,3,3	2.66	1 (33%)	3,3,3	0.50	0
5	DMS	D	7001	-	3,3,3	2.64	1 (33%)	3,3,3	0.52	0
5	DMS	B	7004	-	3,3,3	2.67	1 (33%)	3,3,3	0.55	0
5	DMS	D	7021	-	3,3,3	2.66	1 (33%)	3,3,3	0.54	0
5	DMS	C	7017	3	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	C	7001	-	3,3,3	2.63	1 (33%)	3,3,3	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	C	7008	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	C	7019	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	B	7022	-	3,3,3	2.64	1 (33%)	3,3,3	0.46	0
5	DMS	B	7005	-	3,3,3	2.64	1 (33%)	3,3,3	0.41	0
5	DMS	C	7022	-	3,3,3	2.65	1 (33%)	3,3,3	0.53	0
5	DMS	D	7011	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	B	7019	-	3,3,3	2.68	1 (33%)	3,3,3	0.57	0
5	DMS	A	7017	-	3,3,3	2.66	1 (33%)	3,3,3	0.47	0
5	DMS	A	7025	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	B	7008	-	3,3,3	2.65	1 (33%)	3,3,3	0.50	0
5	DMS	A	7018	-	3,3,3	2.64	1 (33%)	3,3,3	0.50	0
5	DMS	B	7027	-	3,3,3	2.65	1 (33%)	3,3,3	0.57	0
5	DMS	B	7012	-	3,3,3	2.68	1 (33%)	3,3,3	0.56	0
5	DMS	B	7016	3	3,3,3	2.66	1 (33%)	3,3,3	0.52	0

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
4	BTB	A	6001	3	-	3/21/21/21	-
4	BTB	C	6001	-	-	11/21/21/21	-
4	BTB	B	6001	-	-	11/21/21/21	-
4	BTB	D	6001	3	-	4/21/21/21	-

All (125) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	7019	DMS	O-S	4.57	1.81	1.50
5	A	7023	DMS	O-S	4.53	1.80	1.50
5	C	7012	DMS	O-S	4.51	1.80	1.50
5	B	7007	DMS	O-S	4.51	1.80	1.50
5	A	7032	DMS	O-S	4.50	1.80	1.50
5	A	7004	DMS	O-S	4.50	1.80	1.50
5	A	7016	DMS	O-S	4.50	1.80	1.50
5	D	7015	DMS	O-S	4.50	1.80	1.50
5	B	7012	DMS	O-S	4.50	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	7011	DMS	O-S	4.50	1.80	1.50
5	C	7013	DMS	O-S	4.49	1.80	1.50
5	A	7013	DMS	O-S	4.49	1.80	1.50
5	D	7007	DMS	O-S	4.49	1.80	1.50
5	B	7030	DMS	O-S	4.49	1.80	1.50
5	C	7029	DMS	O-S	4.49	1.80	1.50
5	C	7007	DMS	O-S	4.49	1.80	1.50
5	C	7028	DMS	O-S	4.49	1.80	1.50
5	A	7009	DMS	O-S	4.49	1.80	1.50
5	D	7011	DMS	O-S	4.49	1.80	1.50
5	B	7019	DMS	O-S	4.49	1.80	1.50
5	A	7024	DMS	O-S	4.49	1.80	1.50
5	C	7015	DMS	O-S	4.49	1.80	1.50
5	A	7026	DMS	O-S	4.49	1.80	1.50
5	B	7010	DMS	O-S	4.49	1.80	1.50
5	D	7014	DMS	O-S	4.49	1.80	1.50
5	C	7016	DMS	O-S	4.49	1.80	1.50
5	D	7026	DMS	O-S	4.48	1.80	1.50
5	D	7027	DMS	O-S	4.48	1.80	1.50
5	A	7031	DMS	O-S	4.48	1.80	1.50
5	C	7020	DMS	O-S	4.48	1.80	1.50
5	B	7018	DMS	O-S	4.48	1.80	1.50
5	B	7004	DMS	O-S	4.48	1.80	1.50
5	B	7023	DMS	O-S	4.48	1.80	1.50
5	C	7006	DMS	O-S	4.48	1.80	1.50
5	C	7030	DMS	O-S	4.48	1.80	1.50
5	C	7021	DMS	O-S	4.48	1.80	1.50
5	B	7031	DMS	O-S	4.48	1.80	1.50
5	D	7013	DMS	O-S	4.48	1.80	1.50
5	D	7016	DMS	O-S	4.48	1.80	1.50
5	C	7023	DMS	O-S	4.48	1.80	1.50
5	D	7029	DMS	O-S	4.47	1.80	1.50
5	B	7024	DMS	O-S	4.47	1.80	1.50
5	A	7005	DMS	O-S	4.47	1.80	1.50
5	C	7026	DMS	O-S	4.47	1.80	1.50
5	C	7014	DMS	O-S	4.47	1.80	1.50
5	A	7025	DMS	O-S	4.47	1.80	1.50
5	B	7025	DMS	O-S	4.47	1.80	1.50
5	C	7034	DMS	O-S	4.47	1.80	1.50
5	C	7004	DMS	O-S	4.47	1.80	1.50
5	B	7015	DMS	O-S	4.47	1.80	1.50
5	A	7007	DMS	O-S	4.47	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	7032	DMS	O-S	4.47	1.80	1.50
5	A	7029	DMS	O-S	4.47	1.80	1.50
5	D	7017	DMS	O-S	4.47	1.80	1.50
5	B	7014	DMS	O-S	4.47	1.80	1.50
5	C	7008	DMS	O-S	4.47	1.80	1.50
5	A	7030	DMS	O-S	4.47	1.80	1.50
5	D	7002	DMS	O-S	4.47	1.80	1.50
5	D	7028	DMS	O-S	4.47	1.80	1.50
5	A	7006	DMS	O-S	4.47	1.80	1.50
5	A	7012	DMS	O-S	4.47	1.80	1.50
5	D	7021	DMS	O-S	4.47	1.80	1.50
5	B	7020	DMS	O-S	4.47	1.80	1.50
5	A	7015	DMS	O-S	4.47	1.80	1.50
5	C	7018	DMS	O-S	4.47	1.80	1.50
5	A	7027	DMS	O-S	4.47	1.80	1.50
5	A	7017	DMS	O-S	4.47	1.80	1.50
5	D	7018	DMS	O-S	4.47	1.80	1.50
5	D	7019	DMS	O-S	4.47	1.80	1.50
5	B	7033	DMS	O-S	4.47	1.80	1.50
5	B	7028	DMS	O-S	4.47	1.80	1.50
5	A	7008	DMS	O-S	4.47	1.80	1.50
5	A	7011	DMS	O-S	4.46	1.80	1.50
5	C	7031	DMS	O-S	4.46	1.80	1.50
5	C	7017	DMS	O-S	4.46	1.80	1.50
5	C	7027	DMS	O-S	4.46	1.80	1.50
5	B	7013	DMS	O-S	4.46	1.80	1.50
5	D	7022	DMS	O-S	4.46	1.80	1.50
5	A	7002	DMS	O-S	4.46	1.80	1.50
5	A	7020	DMS	O-S	4.46	1.80	1.50
5	B	7008	DMS	O-S	4.46	1.80	1.50
5	C	7009	DMS	O-S	4.46	1.80	1.50
5	C	7019	DMS	O-S	4.46	1.80	1.50
5	D	7010	DMS	O-S	4.46	1.80	1.50
5	B	7016	DMS	O-S	4.46	1.80	1.50
5	B	7027	DMS	O-S	4.45	1.80	1.50
5	A	7003	DMS	O-S	4.45	1.80	1.50
5	D	7009	DMS	O-S	4.45	1.80	1.50
5	B	7026	DMS	O-S	4.45	1.80	1.50
5	B	7017	DMS	O-S	4.45	1.80	1.50
5	C	7022	DMS	O-S	4.45	1.80	1.50
5	A	7010	DMS	O-S	4.45	1.80	1.50
5	C	7010	DMS	O-S	4.45	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	7028	DMS	O-S	4.45	1.80	1.50
5	B	7011	DMS	O-S	4.45	1.80	1.50
5	D	7024	DMS	O-S	4.45	1.80	1.50
5	C	7025	DMS	O-S	4.44	1.80	1.50
5	B	7003	DMS	O-S	4.44	1.80	1.50
5	D	7004	DMS	O-S	4.44	1.80	1.50
5	A	7014	DMS	O-S	4.44	1.80	1.50
5	C	7005	DMS	O-S	4.44	1.80	1.50
5	D	7006	DMS	O-S	4.44	1.80	1.50
5	B	7022	DMS	O-S	4.44	1.80	1.50
5	D	7003	DMS	O-S	4.44	1.80	1.50
5	B	7006	DMS	O-S	4.44	1.80	1.50
5	D	7012	DMS	O-S	4.44	1.80	1.50
5	D	7001	DMS	O-S	4.44	1.80	1.50
5	B	7029	DMS	O-S	4.43	1.80	1.50
5	B	7009	DMS	O-S	4.43	1.80	1.50
5	A	7022	DMS	O-S	4.43	1.80	1.50
5	C	7003	DMS	O-S	4.42	1.80	1.50
5	D	7020	DMS	O-S	4.42	1.80	1.50
5	B	7021	DMS	O-S	4.42	1.80	1.50
5	D	7023	DMS	O-S	4.42	1.80	1.50
5	B	7005	DMS	O-S	4.42	1.80	1.50
5	A	7018	DMS	O-S	4.42	1.80	1.50
5	D	7025	DMS	O-S	4.42	1.80	1.50
5	C	7024	DMS	O-S	4.41	1.80	1.50
5	B	7001	DMS	O-S	4.41	1.80	1.50
5	C	7001	DMS	O-S	4.41	1.80	1.50
5	A	7001	DMS	O-S	4.40	1.79	1.50
5	B	7002	DMS	O-S	4.39	1.79	1.50
5	C	7002	DMS	O-S	4.38	1.79	1.50
5	A	7021	DMS	O-S	4.37	1.79	1.50
5	D	7005	DMS	O-S	4.32	1.79	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	6001	BTB	N-C2-C3-O3
4	B	6001	BTB	N-C2-C4-O4
4	B	6001	BTB	C6-C5-N-C2

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Mol	Chain	Res	Type	Atoms
4	C	6001	BTB	O1-C1-C2-C3
4	C	6001	BTB	O1-C1-C2-C4
4	C	6001	BTB	N-C2-C3-O3
4	C	6001	BTB	C6-C5-N-C7
4	C	6001	BTB	N-C7-C8-O8
4	D	6001	BTB	C6-C5-N-C2
4	B	6001	BTB	N-C5-C6-O6
4	C	6001	BTB	N-C5-C6-O6
4	B	6001	BTB	N-C7-C8-O8
4	A	6001	BTB	N-C5-C6-O6
4	D	6001	BTB	N-C7-C8-O8
4	B	6001	BTB	C1-C2-C3-O3
4	B	6001	BTB	C4-C2-C3-O3
4	B	6001	BTB	C3-C2-C4-O4
4	C	6001	BTB	C1-C2-C3-O3
4	B	6001	BTB	C8-C7-N-C2
4	D	6001	BTB	C8-C7-N-C2
4	A	6001	BTB	N-C2-C4-O4
4	B	6001	BTB	C1-C2-N-C7
4	C	6001	BTB	O1-C1-C2-N
4	C	6001	BTB	C1-C2-N-C5
4	C	6001	BTB	C3-C2-N-C5
4	D	6001	BTB	N-C2-C4-O4
4	A	6001	BTB	C1-C2-C4-O4
4	B	6001	BTB	C1-C2-C4-O4
4	C	6001	BTB	C4-C2-C3-O3

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	6001	BTB	3	0
4	C	6001	BTB	9	0
5	B	7023	DMS	1	0
4	B	6001	BTB	4	0
4	D	6001	BTB	2	0
5	B	7006	DMS	1	0

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

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	1011/1023 (98%)	-0.06	50 (4%) 29 28	6, 18, 50, 88	0
1	B	1011/1023 (98%)	-0.03	58 (5%) 23 23	6, 19, 50, 97	0
1	C	1011/1023 (98%)	0.03	50 (4%) 29 28	8, 21, 51, 89	0
1	D	1011/1023 (98%)	0.03	57 (5%) 24 23	7, 19, 54, 92	0
All	All	4044/4092 (98%)	-0.01	215 (5%) 26 25	6, 19, 51, 97	0

All (215) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	105	TYR	13.3
1	B	104	THR	11.7
1	D	106	PRO	11.0
1	B	103	VAL	10.8
1	A	108	THR	10.5
1	A	105	TYR	10.3
1	B	108	THR	10.0
1	D	108	THR	10.0
1	D	594	ASP	9.7
1	D	105	TYR	9.4
1	D	593	GLY	9.2
1	A	107	ILE	9.2
1	C	104	THR	9.1
1	B	593	GLY	9.1
1	C	105	TYR	8.7
1	A	103	VAL	8.4
1	D	103	VAL	8.4
1	B	107	ILE	7.8
1	B	100	TYR	7.8
1	B	595	THR	7.8
1	A	102	ASN	7.7

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Mol	Chain	Res	Type	RSRZ
1	C	106	PRO	7.5
1	D	600	GLN	7.3
1	B	732	ALA	7.3
1	D	595	THR	7.3
1	B	598	ASP	7.2
1	B	596	PRO	7.2
1	A	595	THR	7.2
1	C	595	THR	7.1
1	D	107	ILE	7.0
1	D	596	PRO	7.0
1	D	102	ASN	6.9
1	C	102	ASN	6.6
1	A	596	PRO	6.5
1	D	733	ALA	6.4
1	B	106	PRO	6.4
1	B	102	ASN	6.4
1	C	597	ASN	6.3
1	A	106	PRO	6.3
1	C	732	ALA	6.2
1	B	594	ASP	6.2
1	C	109	VAL	6.1
1	C	596	PRO	6.1
1	A	104	THR	6.1
1	B	689	GLU	6.0
1	D	109	VAL	6.0
1	C	799	THR	6.0
1	B	600	GLN	5.9
1	B	109	VAL	5.7
1	D	581	ASN	5.7
1	C	108	THR	5.6
1	B	101	THR	5.6
1	D	588	TYR	5.6
1	B	731	PRO	5.5
1	A	598	ASP	5.5
1	D	735	HIS	5.4
1	C	103	VAL	5.4
1	C	107	ILE	5.3
1	D	104	THR	5.3
1	B	597	ASN	5.2
1	A	101	THR	5.1
1	A	732	ALA	5.1
1	D	101	THR	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	594	ASP	5.0
1	C	689	GLU	5.0
1	D	592	PHE	5.0
1	B	686	PRO	5.0
1	C	600	GLN	4.9
1	D	732	ALA	4.9
1	A	580	GLU	4.9
1	C	580	GLU	4.9
1	B	798	ALA	4.9
1	C	599	ARG	4.9
1	C	594	ASP	4.8
1	A	689	GLU	4.8
1	C	800	ARG	4.7
1	D	598	ASP	4.7
1	B	97	ALA	4.6
1	D	597	ASN	4.6
1	A	686	PRO	4.6
1	D	580	GLU	4.6
1	B	581	ASN	4.6
1	C	101	THR	4.5
1	D	800	ARG	4.5
1	C	201	ASP	4.5
1	A	733	ALA	4.4
1	A	588	TYR	4.4
1	B	601	PHE	4.4
1	A	600	GLN	4.3
1	C	100	TYR	4.3
1	C	731	PRO	4.3
1	B	730	LEU	4.3
1	A	593	GLY	4.3
1	C	593	GLY	4.3
1	B	201	ASP	4.3
1	A	599	ARG	4.2
1	B	733	ALA	4.2
1	A	592	PHE	4.1
1	A	109	VAL	4.1
1	C	733	ALA	4.0
1	A	735	HIS	3.9
1	D	99	ILE	3.9
1	D	599	ARG	3.9
1	D	730	LEU	3.9
1	C	601	PHE	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	731	PRO	3.9
1	B	599	ARG	3.9
1	B	588	TYR	3.9
1	B	592	PHE	3.8
1	D	100	TYR	3.8
1	A	597	ASN	3.8
1	D	583	ASN	3.8
1	B	800	ARG	3.7
1	D	687	GLN	3.7
1	B	931	PHE	3.6
1	B	580	GLU	3.6
1	D	582	GLY	3.5
1	B	203	TRP	3.5
1	D	686	PRO	3.5
1	D	97	ALA	3.5
1	A	687	GLN	3.5
1	D	601	PHE	3.5
1	A	582	GLY	3.5
1	A	585	TRP	3.5
1	C	798	ALA	3.4
1	C	931	PHE	3.4
1	A	583	ASN	3.4
1	D	689	GLU	3.4
1	A	798	ALA	3.4
1	D	685	LEU	3.3
1	B	199	ASP	3.2
1	B	602	CYS	3.2
1	C	588	TYR	3.2
1	B	583	ASN	3.2
1	A	685	LEU	3.2
1	C	735	HIS	3.2
1	A	601	PHE	3.2
1	B	579	ASP	3.2
1	A	799	THR	3.2
1	C	686	PRO	3.1
1	A	684	GLU	3.1
1	A	99	ILE	3.1
1	B	80	GLU	3.1
1	A	100	TYR	3.0
1	A	819	GLU	3.0
1	D	684	GLU	3.0
1	D	80	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	800	ARG	3.0
1	C	97	ALA	3.0
1	B	582	GLY	3.0
1	D	589	GLY	3.0
1	A	581	ASN	2.9
1	C	730	LEU	2.9
1	B	799	THR	2.9
1	C	685	LEU	2.9
1	D	362	LEU	2.9
1	B	98	PRO	2.9
1	A	110	ASN	2.8
1	C	583	ASN	2.8
1	D	590	GLY	2.8
1	B	684	GLU	2.8
1	A	579	ASP	2.8
1	C	592	PHE	2.8
1	A	578	TYR	2.8
1	D	799	THR	2.8
1	C	598	ASP	2.7
1	B	735	HIS	2.7
1	B	99	ILE	2.7
1	B	76	CYS	2.7
1	A	97	ALA	2.7
1	B	585	TRP	2.6
1	A	589	GLY	2.6
1	A	590	GLY	2.6
1	D	798	ALA	2.6
1	C	977	HIS	2.6
1	B	687	GLN	2.6
1	C	589	GLY	2.6
1	C	590	GLY	2.5
1	C	801	ILE	2.5
1	D	830	LEU	2.5
1	B	589	GLY	2.5
1	D	579	ASP	2.5
1	D	201	ASP	2.5
1	C	581	ASN	2.4
1	C	582	GLY	2.4
1	D	110	ASN	2.4
1	B	734	SER	2.4
1	B	729	THR	2.4
1	B	71	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	110	ASN	2.3
1	D	772	ASP	2.3
1	B	178	ARG	2.3
1	B	685	LEU	2.3
1	B	202	MET	2.3
1	A	201	ASP	2.3
1	C	99	ILE	2.3
1	C	202	MET	2.2
1	B	1023	LYS	2.2
1	D	578	TYR	2.2
1	D	71	GLU	2.2
1	A	731	PRO	2.2
1	C	362	LEU	2.2
1	D	729	THR	2.2
1	D	75	GLU	2.1
1	B	683	PRO	2.1
1	D	1022	GLN	2.1
1	C	116	THR	2.1
1	D	931	PHE	2.1
1	C	203	TRP	2.1
1	D	734	SER	2.0
1	A	1023	LYS	2.0
1	D	79	PRO	2.0
1	A	80	GLU	2.0
1	A	730	LEU	2.0
1	C	737	ILE	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 monosaccharides 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(\AA^2)	Q<0.9
5	DMS	C	7020	4/4	-0.06	0.61	141,141,141,142	0
3	NA	B	3104	1/1	0.12	0.53	87,87,87,87	0
4	BTB	D	6001	14/14	0.30	0.59	77,83,85,85	0
5	DMS	C	7015	4/4	0.51	0.33	100,100,100,101	0
4	BTB	B	6001	14/14	0.53	0.59	107,108,108,108	0
5	DMS	B	7030	4/4	0.56	0.49	91,91,91,91	0
5	DMS	C	7021	4/4	0.56	0.27	93,93,93,93	0
5	DMS	B	7019	4/4	0.60	0.38	64,65,65,66	0
5	DMS	B	7025	4/4	0.60	0.36	131,131,131,131	0
5	DMS	C	7008	4/4	0.61	0.55	134,134,134,134	0
5	DMS	A	7019	4/4	0.62	0.38	55,55,56,57	0
5	DMS	A	7012	4/4	0.65	0.30	89,89,89,89	0
5	DMS	D	7017	4/4	0.65	0.26	93,93,93,93	0
5	DMS	B	7012	4/4	0.68	0.26	76,76,76,77	0
5	DMS	D	7019	4/4	0.69	0.30	114,114,115,115	0
5	DMS	A	7026	4/4	0.70	0.31	84,85,85,85	0
5	DMS	C	7026	4/4	0.71	0.38	92,92,92,92	0
5	DMS	B	7018	4/4	0.71	0.37	75,75,75,76	0
5	DMS	B	7031	4/4	0.71	0.33	77,77,78,78	0
5	DMS	D	7016	4/4	0.72	0.33	93,94,94,94	0
3	NA	D	3103	1/1	0.73	0.61	83,83,83,83	0
5	DMS	A	7032	4/4	0.73	0.21	69,69,69,70	0
5	DMS	A	7006	4/4	0.73	0.43	100,101,101,101	0
5	DMS	A	7025	4/4	0.73	0.24	65,66,66,67	0
4	BTB	A	6001	14/14	0.74	0.32	31,48,54,55	0
5	DMS	B	7015	4/4	0.75	0.20	75,75,75,76	0
5	DMS	C	7024	4/4	0.75	0.33	83,83,83,83	0
5	DMS	A	7003	4/4	0.76	0.28	84,84,85,85	0
5	DMS	B	7016	4/4	0.76	0.36	85,85,85,85	0
5	DMS	D	7027	4/4	0.76	0.22	55,56,57,58	0
5	DMS	D	7021	4/4	0.77	0.26	80,80,80,80	0
5	DMS	B	7032	4/4	0.77	0.24	55,56,56,57	0
5	DMS	D	7009	4/4	0.78	0.28	75,75,75,75	0
4	BTB	C	6001	14/14	0.78	0.31	43,45,47,52	0
3	NA	C	3104	1/1	0.79	0.21	59,59,59,59	0
5	DMS	B	7021	4/4	0.79	0.29	68,68,68,68	0
5	DMS	C	7034	4/4	0.79	0.27	74,75,75,75	0
5	DMS	C	7012	4/4	0.80	0.24	59,59,59,60	0
5	DMS	D	7024	4/4	0.80	0.24	67,68,68,68	0
5	DMS	C	7009	4/4	0.80	0.23	86,86,86,86	0
5	DMS	A	7008	4/4	0.81	0.21	60,61,62,62	0
5	DMS	B	7010	4/4	0.81	0.25	67,67,67,68	0
3	NA	C	3103	1/1	0.81	0.33	42,42,42,42	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	DMS	A	7015	4/4	0.81	0.24	57,58,58,59	0
5	DMS	C	7011	4/4	0.82	0.27	49,50,50,50	0
5	DMS	A	7004	4/4	0.82	0.22	59,59,60,60	0
5	DMS	D	7013	4/4	0.82	0.26	87,87,87,87	0
5	DMS	C	7019	4/4	0.83	0.32	112,112,113,113	0
5	DMS	C	7030	4/4	0.83	0.26	68,68,68,68	0
5	DMS	A	7018	4/4	0.84	0.32	57,57,58,59	0
2	MG	D	3002	1/1	0.84	0.14	51,51,51,51	0
5	DMS	A	7009	4/4	0.84	0.27	61,61,62,62	0
5	DMS	D	7011	4/4	0.85	0.36	63,63,63,63	0
5	DMS	C	7029	4/4	0.85	0.20	76,76,76,77	0
5	DMS	A	7024	4/4	0.85	0.43	86,86,86,87	0
5	DMS	B	7020	4/4	0.85	0.33	96,96,96,96	0
5	DMS	C	7017	4/4	0.86	0.34	69,70,70,70	0
5	DMS	C	7016	4/4	0.87	0.20	70,71,71,71	0
5	DMS	D	7015	4/4	0.87	0.20	46,47,48,48	0
5	DMS	B	7026	4/4	0.88	0.30	82,83,83,83	0
5	DMS	A	7014	4/4	0.88	0.40	41,44,44,44	0
5	DMS	A	7007	4/4	0.88	0.23	49,49,49,50	0
5	DMS	B	7006	4/4	0.88	0.24	58,58,58,59	0
5	DMS	B	7033	4/4	0.88	0.13	54,54,55,56	0
5	DMS	A	7013	4/4	0.88	0.20	59,59,60,60	0
5	DMS	C	7004	4/4	0.89	0.21	44,45,45,46	0
5	DMS	A	7020	4/4	0.89	0.18	48,48,48,49	0
3	NA	B	3103	1/1	0.89	0.17	34,34,34,34	0
5	DMS	B	7014	4/4	0.89	0.18	84,84,84,85	0
5	DMS	A	7011	4/4	0.89	0.22	58,58,58,58	0
5	DMS	D	7028	4/4	0.89	0.29	76,77,77,77	0
5	DMS	C	7023	4/4	0.90	0.21	66,66,67,67	0
5	DMS	A	7002	4/4	0.90	0.18	41,42,43,43	0
5	DMS	B	7004	4/4	0.90	0.17	46,46,47,47	0
5	DMS	B	7024	4/4	0.90	0.25	59,59,60,60	0
5	DMS	B	7013	4/4	0.90	0.21	70,70,70,70	0
5	DMS	D	7004	4/4	0.90	0.21	43,43,44,44	0
3	NA	C	3102	1/1	0.90	0.15	44,44,44,44	0
5	DMS	D	7010	4/4	0.90	0.25	48,49,49,49	0
5	DMS	C	7014	4/4	0.90	0.18	67,67,67,67	0
5	DMS	B	7027	4/4	0.91	0.22	57,57,57,57	0
2	MG	C	3002	1/1	0.91	0.12	55,55,55,55	0
5	DMS	C	7018	4/4	0.91	0.20	62,62,62,63	0
5	DMS	D	7023	4/4	0.91	0.19	42,42,42,42	0
5	DMS	A	7005	4/4	0.91	0.23	43,44,44,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	DMS	C	7006	4/4	0.91	0.17	45,46,46,46	0
3	NA	B	3102	1/1	0.91	0.22	47,47,47,47	0
5	DMS	D	7029	4/4	0.91	0.23	78,78,78,78	0
5	DMS	D	7002	4/4	0.92	0.23	37,37,39,40	0
5	DMS	D	7018	4/4	0.92	0.23	62,63,63,63	0
5	DMS	A	7030	4/4	0.92	0.13	59,60,60,61	0
5	DMS	D	7020	4/4	0.92	0.18	57,57,58,58	0
5	DMS	C	7022	4/4	0.92	0.23	68,69,69,69	0
5	DMS	B	7008	4/4	0.92	0.28	75,75,75,75	0
3	NA	D	3102	1/1	0.92	0.23	44,44,44,44	0
5	DMS	A	7017	4/4	0.92	0.32	66,66,66,66	0
5	DMS	B	7028	4/4	0.92	0.27	63,63,63,63	0
5	DMS	B	7029	4/4	0.92	0.22	63,63,63,63	0
3	NA	A	3103	1/1	0.93	0.09	31,31,31,31	0
3	NA	A	3102	1/1	0.93	0.12	41,41,41,41	0
5	DMS	A	7021	4/4	0.93	0.24	36,37,37,38	0
5	DMS	A	7027	4/4	0.93	0.17	51,51,51,52	0
5	DMS	B	7009	4/4	0.93	0.16	37,38,38,39	0
5	DMS	A	7028	4/4	0.93	0.17	57,58,58,58	0
5	DMS	D	7022	4/4	0.93	0.16	46,47,47,48	0
5	DMS	B	7011	4/4	0.93	0.31	69,69,69,69	0
5	DMS	A	7023	4/4	0.93	0.14	32,32,33,35	0
5	DMS	D	7025	4/4	0.93	0.20	55,56,56,56	0
5	DMS	D	7026	4/4	0.93	0.23	73,74,74,74	0
5	DMS	C	7013	4/4	0.93	0.18	58,58,59,59	0
5	DMS	D	7014	4/4	0.93	0.23	67,67,67,67	0
5	DMS	B	7022	4/4	0.93	0.16	60,60,60,61	0
3	NA	D	3104	1/1	0.94	0.14	32,32,32,32	0
5	DMS	C	7027	4/4	0.94	0.13	54,55,55,55	0
5	DMS	B	7002	4/4	0.94	0.18	33,34,35,35	0
5	DMS	C	7002	4/4	0.94	0.14	27,30,30,31	0
2	MG	A	3002	1/1	0.94	0.12	42,42,42,42	0
5	DMS	B	7017	4/4	0.94	0.12	50,50,50,50	0
5	DMS	D	7006	4/4	0.94	0.19	52,52,52,53	0
5	DMS	A	7016	4/4	0.94	0.20	53,54,54,54	0
5	DMS	A	7031	4/4	0.94	0.18	73,73,73,73	0
5	DMS	C	7028	4/4	0.95	0.15	40,41,41,42	0
5	DMS	A	7029	4/4	0.95	0.17	41,42,42,42	0
5	DMS	D	7012	4/4	0.95	0.21	45,46,46,46	0
5	DMS	C	7010	4/4	0.95	0.14	43,43,43,43	0
5	DMS	C	7031	4/4	0.95	0.12	52,53,53,53	0
5	DMS	B	7007	4/4	0.95	0.14	32,32,33,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NA	C	3101	1/1	0.95	0.11	17,17,17,17	0
5	DMS	C	7007	4/4	0.95	0.15	35,35,35,37	0
5	DMS	D	7007	4/4	0.95	0.15	32,32,33,33	0
3	NA	A	3104	1/1	0.95	0.11	50,50,50,50	0
5	DMS	B	7023	4/4	0.96	0.12	66,66,67,67	0
5	DMS	C	7025	4/4	0.96	0.14	51,51,51,51	0
5	DMS	B	7005	4/4	0.96	0.16	38,38,39,39	0
5	DMS	D	7001	4/4	0.97	0.11	20,20,22,23	0
3	NA	D	3101	1/1	0.97	0.09	15,15,15,15	0
5	DMS	C	7005	4/4	0.97	0.17	38,38,38,38	0
5	DMS	D	7005	4/4	0.97	0.18	31,31,32,32	0
2	MG	C	3001	1/1	0.97	0.06	19,19,19,19	0
5	DMS	B	7003	4/4	0.97	0.10	36,36,36,36	0
5	DMS	A	7022	4/4	0.97	0.09	27,28,28,29	0
5	DMS	A	7010	4/4	0.97	0.14	48,49,49,49	0
5	DMS	C	7003	4/4	0.97	0.10	30,30,30,31	0
3	NA	A	3101	1/1	0.98	0.08	11,11,11,11	0
5	DMS	C	7001	4/4	0.98	0.08	19,19,20,21	0
5	DMS	A	7001	4/4	0.98	0.07	17,17,17,20	0
3	NA	B	3101	1/1	0.98	0.09	13,13,13,13	0
5	DMS	B	7001	4/4	0.98	0.08	20,20,20,21	0
2	MG	D	3001	1/1	0.98	0.07	18,18,18,18	0
5	DMS	D	7003	4/4	0.98	0.08	27,28,28,29	0
2	MG	B	3002	1/1	0.98	0.07	44,44,44,44	0
2	MG	A	3001	1/1	0.99	0.04	18,18,18,18	0
2	MG	B	3001	1/1	0.99	0.05	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.