



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:08 PM GMT

PDB ID : 3T08
Title : E. coli (LacZ) beta-galactosidase (S796A) IPTG complex
Authors : Jancewicz, L.J.; Wheatley, R.W.; Sutendra, G.; Lee, M.; Fraser, M.; Huber, R.E.
Deposited on : 2011-07-19
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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

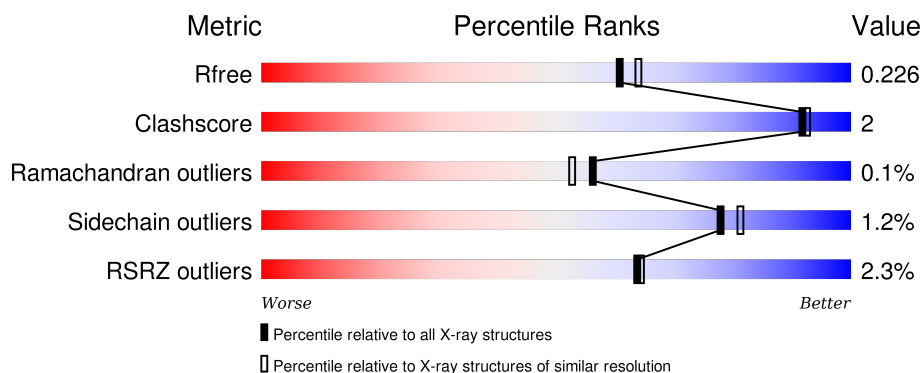
1 Overall quality at a glance

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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1052	<div> <div>2%</div> <div>90%</div> <div>7%</div> <div>.</div> </div>
1	B	1052	<div> <div>2%</div> <div>91%</div> <div>6%</div> <div>.</div> </div>
1	C	1052	<div> <div>2%</div> <div>90%</div> <div>6%</div> <div>.</div> </div>
1	D	1052	<div> <div>3%</div> <div>90%</div> <div>7%</div> <div>.</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
2	MG	B	3002	-	-	-	X
3	NA	A	3103	-	-	-	X
3	NA	C	3103	-	-	-	X
5	DMS	A	8002	-	-	-	X
5	DMS	A	8003	-	-	-	X
5	DMS	A	8004	-	-	-	X
5	DMS	A	8006	-	-	-	X
5	DMS	A	8007	-	-	-	X
5	DMS	A	8010	-	-	-	X
5	DMS	A	8011	-	-	-	X
5	DMS	A	8013	-	-	-	X
5	DMS	A	8015	-	-	-	X
5	DMS	A	8016	-	-	-	X
5	DMS	A	8018	-	-	-	X
5	DMS	A	8020	-	-	-	X
5	DMS	B	8002	-	-	-	X
5	DMS	B	8003	-	-	-	X
5	DMS	B	8004	-	-	-	X
5	DMS	B	8005	-	-	-	X
5	DMS	B	8006	-	-	-	X
5	DMS	B	8007	-	-	-	X
5	DMS	B	8009	-	-	-	X
5	DMS	B	8011	-	-	-	X
5	DMS	B	8015	-	-	-	X
5	DMS	B	8016	-	-	-	X
5	DMS	B	8017	-	-	-	X
5	DMS	C	8002	-	-	-	X
5	DMS	C	8003	-	-	-	X
5	DMS	C	8004	-	-	-	X
5	DMS	C	8006	-	-	-	X
5	DMS	C	8007	-	-	-	X
5	DMS	C	8009	-	-	-	X
5	DMS	C	8013	-	-	-	X
5	DMS	C	8014	-	-	-	X
5	DMS	C	8015	-	-	-	X
5	DMS	D	8002	-	-	-	X
5	DMS	D	8003	-	-	-	X
5	DMS	D	8004	-	-	-	X
5	DMS	D	8005	-	-	-	X
5	DMS	D	8006	-	-	-	X
5	DMS	D	8009	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	DMS	D	8012	-	-	-	X
5	DMS	D	8013	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 36085 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	1015	Total	C	N	O	S	21	0	0
			8156	5159	1445	1514	38			
1	B	1015	Total	C	N	O	S	12	0	0
			8156	5159	1445	1514	38			
1	C	1015	Total	C	N	O	S	12	0	0
			8156	5159	1445	1514	38			
1	D	1015	Total	C	N	O	S	23	0	0
			8156	5159	1445	1514	38			

There are 152 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	EXPRESSION TAG	UNP P00722
A	-27	GLY	-	EXPRESSION TAG	UNP P00722
A	-26	GLY	-	EXPRESSION TAG	UNP P00722
A	-25	SER	-	EXPRESSION TAG	UNP P00722
A	-24	HIS	-	EXPRESSION TAG	UNP P00722
A	-23	HIS	-	EXPRESSION TAG	UNP P00722
A	-22	HIS	-	EXPRESSION TAG	UNP P00722
A	-21	HIS	-	EXPRESSION TAG	UNP P00722
A	-20	HIS	-	EXPRESSION TAG	UNP P00722
A	-19	HIS	-	EXPRESSION TAG	UNP P00722
A	-18	GLY	-	EXPRESSION TAG	UNP P00722
A	-17	MET	-	EXPRESSION TAG	UNP P00722
A	-16	ALA	-	EXPRESSION TAG	UNP P00722
A	-15	SER	-	EXPRESSION TAG	UNP P00722
A	-14	MET	-	EXPRESSION TAG	UNP P00722
A	-13	THR	-	EXPRESSION TAG	UNP P00722
A	-12	GLY	-	EXPRESSION TAG	UNP P00722
A	-11	GLY	-	EXPRESSION TAG	UNP P00722
A	-10	GLN	-	EXPRESSION TAG	UNP P00722
A	-9	GLN	-	EXPRESSION TAG	UNP P00722
A	-8	MET	-	EXPRESSION TAG	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	EXPRESSION TAG	UNP P00722
A	-6	ARG	-	EXPRESSION TAG	UNP P00722
A	-5	ASP	-	EXPRESSION TAG	UNP P00722
A	-4	LEU	-	EXPRESSION TAG	UNP P00722
A	-3	TYR	-	EXPRESSION TAG	UNP P00722
A	-2	ASP	-	EXPRESSION TAG	UNP P00722
A	-1	ASP	-	EXPRESSION TAG	UNP P00722
A	0	ASP	-	EXPRESSION TAG	UNP P00722
A	1	ASP	-	EXPRESSION TAG	UNP P00722
A	2	LYS	-	EXPRESSION TAG	UNP P00722
A	3	ASP	-	EXPRESSION TAG	UNP P00722
A	4	PRO	-	EXPRESSION TAG	UNP P00722
A	5	MET	-	EXPRESSION TAG	UNP P00722
A	6	ILE	-	EXPRESSION TAG	UNP P00722
A	7	ASP	-	EXPRESSION TAG	UNP P00722
A	8	PRO	-	EXPRESSION TAG	UNP P00722
A	796	ALA	SER	ENGINEERED MUTATION	UNP P00722
B	-28	MET	-	EXPRESSION TAG	UNP P00722
B	-27	GLY	-	EXPRESSION TAG	UNP P00722
B	-26	GLY	-	EXPRESSION TAG	UNP P00722
B	-25	SER	-	EXPRESSION TAG	UNP P00722
B	-24	HIS	-	EXPRESSION TAG	UNP P00722
B	-23	HIS	-	EXPRESSION TAG	UNP P00722
B	-22	HIS	-	EXPRESSION TAG	UNP P00722
B	-21	HIS	-	EXPRESSION TAG	UNP P00722
B	-20	HIS	-	EXPRESSION TAG	UNP P00722
B	-19	HIS	-	EXPRESSION TAG	UNP P00722
B	-18	GLY	-	EXPRESSION TAG	UNP P00722
B	-17	MET	-	EXPRESSION TAG	UNP P00722
B	-16	ALA	-	EXPRESSION TAG	UNP P00722
B	-15	SER	-	EXPRESSION TAG	UNP P00722
B	-14	MET	-	EXPRESSION TAG	UNP P00722
B	-13	THR	-	EXPRESSION TAG	UNP P00722
B	-12	GLY	-	EXPRESSION TAG	UNP P00722
B	-11	GLY	-	EXPRESSION TAG	UNP P00722
B	-10	GLN	-	EXPRESSION TAG	UNP P00722
B	-9	GLN	-	EXPRESSION TAG	UNP P00722
B	-8	MET	-	EXPRESSION TAG	UNP P00722
B	-7	GLY	-	EXPRESSION TAG	UNP P00722
B	-6	ARG	-	EXPRESSION TAG	UNP P00722
B	-5	ASP	-	EXPRESSION TAG	UNP P00722
B	-4	LEU	-	EXPRESSION TAG	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	TYR	-	EXPRESSION TAG	UNP P00722
B	-2	ASP	-	EXPRESSION TAG	UNP P00722
B	-1	ASP	-	EXPRESSION TAG	UNP P00722
B	0	ASP	-	EXPRESSION TAG	UNP P00722
B	1	ASP	-	EXPRESSION TAG	UNP P00722
B	2	LYS	-	EXPRESSION TAG	UNP P00722
B	3	ASP	-	EXPRESSION TAG	UNP P00722
B	4	PRO	-	EXPRESSION TAG	UNP P00722
B	5	MET	-	EXPRESSION TAG	UNP P00722
B	6	ILE	-	EXPRESSION TAG	UNP P00722
B	7	ASP	-	EXPRESSION TAG	UNP P00722
B	8	PRO	-	EXPRESSION TAG	UNP P00722
B	796	ALA	SER	ENGINEERED MUTATION	UNP P00722
C	-28	MET	-	EXPRESSION TAG	UNP P00722
C	-27	GLY	-	EXPRESSION TAG	UNP P00722
C	-26	GLY	-	EXPRESSION TAG	UNP P00722
C	-25	SER	-	EXPRESSION TAG	UNP P00722
C	-24	HIS	-	EXPRESSION TAG	UNP P00722
C	-23	HIS	-	EXPRESSION TAG	UNP P00722
C	-22	HIS	-	EXPRESSION TAG	UNP P00722
C	-21	HIS	-	EXPRESSION TAG	UNP P00722
C	-20	HIS	-	EXPRESSION TAG	UNP P00722
C	-19	HIS	-	EXPRESSION TAG	UNP P00722
C	-18	GLY	-	EXPRESSION TAG	UNP P00722
C	-17	MET	-	EXPRESSION TAG	UNP P00722
C	-16	ALA	-	EXPRESSION TAG	UNP P00722
C	-15	SER	-	EXPRESSION TAG	UNP P00722
C	-14	MET	-	EXPRESSION TAG	UNP P00722
C	-13	THR	-	EXPRESSION TAG	UNP P00722
C	-12	GLY	-	EXPRESSION TAG	UNP P00722
C	-11	GLY	-	EXPRESSION TAG	UNP P00722
C	-10	GLN	-	EXPRESSION TAG	UNP P00722
C	-9	GLN	-	EXPRESSION TAG	UNP P00722
C	-8	MET	-	EXPRESSION TAG	UNP P00722
C	-7	GLY	-	EXPRESSION TAG	UNP P00722
C	-6	ARG	-	EXPRESSION TAG	UNP P00722
C	-5	ASP	-	EXPRESSION TAG	UNP P00722
C	-4	LEU	-	EXPRESSION TAG	UNP P00722
C	-3	TYR	-	EXPRESSION TAG	UNP P00722
C	-2	ASP	-	EXPRESSION TAG	UNP P00722
C	-1	ASP	-	EXPRESSION TAG	UNP P00722
C	0	ASP	-	EXPRESSION TAG	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ASP	-	EXPRESSION TAG	UNP P00722
C	2	LYS	-	EXPRESSION TAG	UNP P00722
C	3	ASP	-	EXPRESSION TAG	UNP P00722
C	4	PRO	-	EXPRESSION TAG	UNP P00722
C	5	MET	-	EXPRESSION TAG	UNP P00722
C	6	ILE	-	EXPRESSION TAG	UNP P00722
C	7	ASP	-	EXPRESSION TAG	UNP P00722
C	8	PRO	-	EXPRESSION TAG	UNP P00722
C	796	ALA	SER	ENGINEERED MUTATION	UNP P00722
D	-28	MET	-	EXPRESSION TAG	UNP P00722
D	-27	GLY	-	EXPRESSION TAG	UNP P00722
D	-26	GLY	-	EXPRESSION TAG	UNP P00722
D	-25	SER	-	EXPRESSION TAG	UNP P00722
D	-24	HIS	-	EXPRESSION TAG	UNP P00722
D	-23	HIS	-	EXPRESSION TAG	UNP P00722
D	-22	HIS	-	EXPRESSION TAG	UNP P00722
D	-21	HIS	-	EXPRESSION TAG	UNP P00722
D	-20	HIS	-	EXPRESSION TAG	UNP P00722
D	-19	HIS	-	EXPRESSION TAG	UNP P00722
D	-18	GLY	-	EXPRESSION TAG	UNP P00722
D	-17	MET	-	EXPRESSION TAG	UNP P00722
D	-16	ALA	-	EXPRESSION TAG	UNP P00722
D	-15	SER	-	EXPRESSION TAG	UNP P00722
D	-14	MET	-	EXPRESSION TAG	UNP P00722
D	-13	THR	-	EXPRESSION TAG	UNP P00722
D	-12	GLY	-	EXPRESSION TAG	UNP P00722
D	-11	GLY	-	EXPRESSION TAG	UNP P00722
D	-10	GLN	-	EXPRESSION TAG	UNP P00722
D	-9	GLN	-	EXPRESSION TAG	UNP P00722
D	-8	MET	-	EXPRESSION TAG	UNP P00722
D	-7	GLY	-	EXPRESSION TAG	UNP P00722
D	-6	ARG	-	EXPRESSION TAG	UNP P00722
D	-5	ASP	-	EXPRESSION TAG	UNP P00722
D	-4	LEU	-	EXPRESSION TAG	UNP P00722
D	-3	TYR	-	EXPRESSION TAG	UNP P00722
D	-2	ASP	-	EXPRESSION TAG	UNP P00722
D	-1	ASP	-	EXPRESSION TAG	UNP P00722
D	0	ASP	-	EXPRESSION TAG	UNP P00722
D	1	ASP	-	EXPRESSION TAG	UNP P00722
D	2	LYS	-	EXPRESSION TAG	UNP P00722
D	3	ASP	-	EXPRESSION TAG	UNP P00722
D	4	PRO	-	EXPRESSION TAG	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
D	5	MET	-	EXPRESSION TAG	UNP P00722
D	6	ILE	-	EXPRESSION TAG	UNP P00722
D	7	ASP	-	EXPRESSION TAG	UNP P00722
D	8	PRO	-	EXPRESSION TAG	UNP P00722
D	796	ALA	SER	ENGINEERED MUTATION	UNP P00722

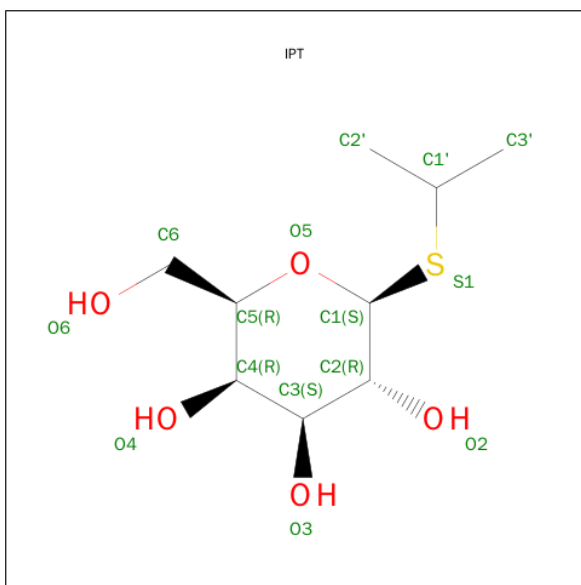
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Mg 3 3	0	0
2	A	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0
2	C	2	Total Mg 2 2	0	0

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

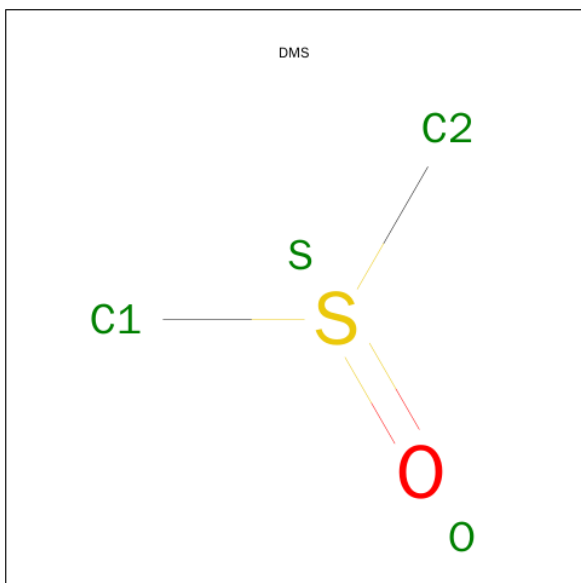
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total Na 3 3	0	0
3	A	3	Total Na 3 3	0	0
3	D	3	Total Na 3 3	0	0
3	C	4	Total Na 4 4	0	0

- Molecule 4 is ISOPROPYL-1-BETA-D-THIOGALACTOSIDE (three-letter code: IPT) (formula: C₉H₁₈O₅S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			15	9	5	1		
4	B	1	Total	C	O	S	0	0
			15	9	5	1		
4	C	1	Total	C	O	S	0	0
			15	9	5	1		
4	D	1	Total	C	O	S	0	0
			15	9	5	1		

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



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	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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
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
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	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	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

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
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

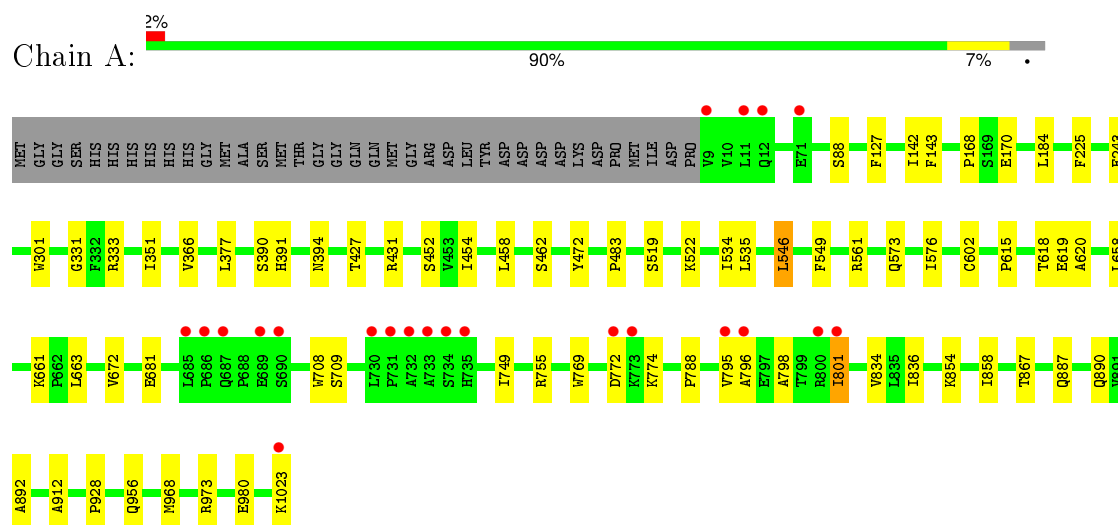
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	754	Total 754	O 754	0	0
6	B	816	Total 816	O 816	0	0
6	C	814	Total 814	O 814	0	0
6	D	711	Total 711	O 711	0	0

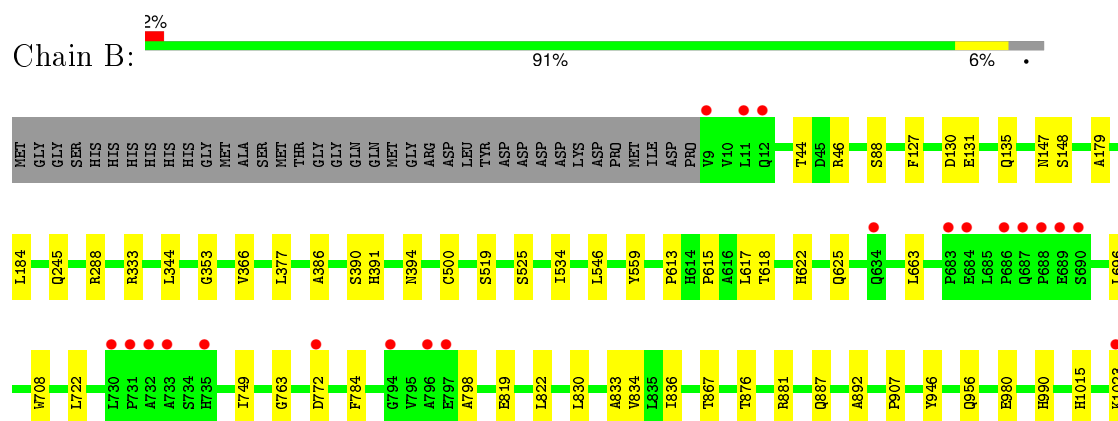
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

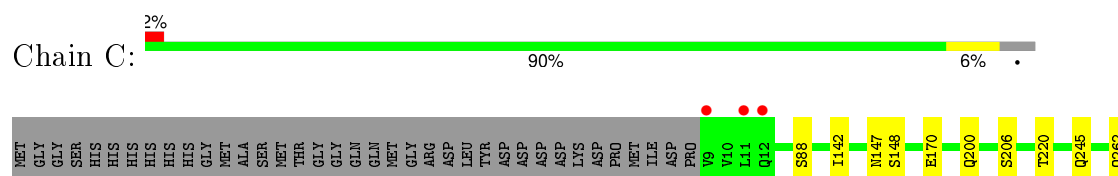
• Molecule 1: Beta-galactosidase

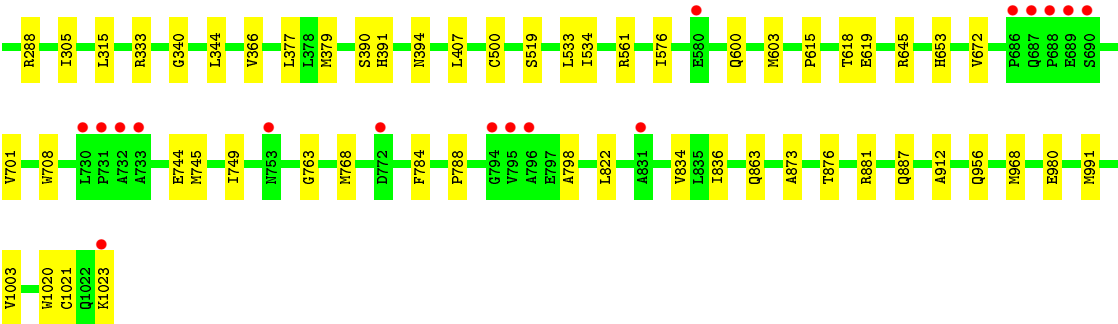


• Molecule 1: Beta-galactosidase

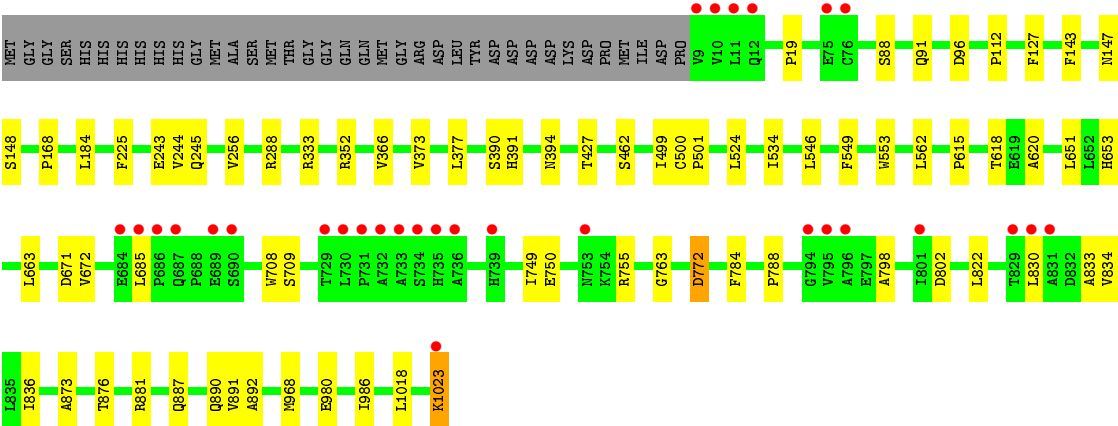
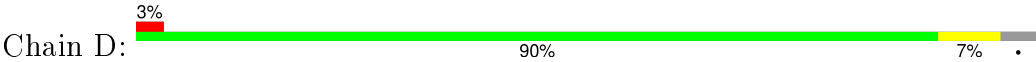


• Molecule 1: Beta-galactosidase





● 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	151.16Å 161.59Å 202.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.52 – 2.00 68.46 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (74.52-2.00) 87.0 (68.46-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.175 , 0.223 0.179 , 0.226	Depositor DCC
R_{free} test set	4165 reflections (1.46%)	DCC
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 288504 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	36085	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.95 % 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 5.3883e-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, 0.375 respectively for untwinned datasets, and 0.333, 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: NA, MG, DMS, IPT

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	0.38	0/8398	0.54	0/11457
1	B	0.39	0/8398	0.54	0/11457
1	C	0.39	0/8398	0.54	0/11457
1	D	0.38	0/8398	0.53	0/11457
All	All	0.39	0/33592	0.54	0/45828

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	8156	0	7753	39	0
1	B	8156	0	7753	28	0
1	C	8156	0	7753	31	0
1	D	8156	0	7753	35	0
2	A	2	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	0	0	0
3	C	4	0	0	0	0
3	D	3	0	0	0	0
4	A	15	0	17	0	0
4	B	15	0	17	0	0
4	C	15	0	17	0	0
4	D	15	0	17	0	0
5	A	80	0	120	2	0
5	B	72	0	108	0	0
5	C	76	0	114	2	0
5	D	56	0	84	1	0
6	A	754	0	0	4	0
6	B	816	0	0	0	0
6	C	814	0	0	0	0
6	D	711	0	0	1	0
All	All	36085	0	31506	132	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 (132) 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:749:ILE:HD12	1:A:834:VAL:HG11	1.73	0.71
1:B:749:ILE:HD12	1:B:834:VAL:HG11	1.72	0.70
1:B:245:GLN:HG2	1:B:288:ARG:HG2	1.73	0.70
1:A:377:LEU:HD22	1:A:708:TRP:HA	1.76	0.68
1:D:1023:LYS:HG3	1:D:1023:LYS:O	1.94	0.67
1:D:887:GLN:NE2	1:D:980:GLU:O	2.32	0.62
1:C:615:PRO:O	1:C:618:THR:HG22	1.99	0.62
1:D:427:THR:HG21	1:D:462:SER:HB3	1.82	0.61
1:C:377:LEU:HD22	1:C:708:TRP:HA	1.83	0.60
1:C:576:ILE:HG12	5:C:8009:DMS:C2	2.32	0.60
1:D:88:SER:HA	1:D:366:VAL:HG21	1.84	0.59
1:A:351:ILE:HD13	1:A:534:ILE:HD13	1.85	0.57
1:A:887:GLN:NE2	1:A:980:GLU:O	2.36	0.57
1:C:887:GLN:NE2	1:C:980:GLU:O	2.38	0.57
1:B:127:PHE:HE2	1:B:184:LEU:HG	1.70	0.56
1:D:377:LEU:HD22	1:D:708:TRP:HA	1.86	0.56
1:B:127:PHE:CE2	1:B:184:LEU:HG	2.42	0.55
1:A:331:GLY:H	5:A:8001:DMS:H13	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:755:ARG:HB3	1:A:769:TRP:HE3	1.72	0.53
1:C:142:ILE:HG12	1:C:170:GLU:HG2	1.88	0.53
1:A:88:SER:HA	1:A:366:VAL:HG21	1.91	0.53
1:D:499:ILE:HG22	1:D:501:PRO:HD3	1.91	0.52
1:A:795:VAL:O	1:A:801:ILE:HD12	2.10	0.51
1:D:873:ALA:O	1:D:876:THR:HG22	2.11	0.51
1:A:331:GLY:H	5:A:8001:DMS:C1	2.23	0.51
1:D:749:ILE:HD11	1:D:836:ILE:HD11	1.92	0.51
1:C:245:GLN:HG2	1:C:288:ARG:HG2	1.92	0.51
1:B:131:GLU:OE2	1:B:179:ALA:HB2	2.11	0.51
1:C:749:ILE:HD12	1:C:834:VAL:HG11	1.94	0.50
1:B:763:GLY:HA3	1:B:822:LEU:HD13	1.93	0.50
1:A:142:ILE:HG12	1:A:170:GLU:HG2	1.94	0.49
1:A:576:ILE:HD11	6:A:4547:HOH:O	2.10	0.49
1:A:749:ILE:HG13	1:A:858:ILE:HD12	1.94	0.49
1:C:863:GLN:HG2	1:C:1021:CYS:HB3	1.94	0.49
1:A:225:PHE:HA	1:A:243:GLU:O	2.13	0.49
1:D:651:LEU:HD11	1:D:653:HIS:CE1	2.48	0.48
1:B:88:SER:HA	1:B:366:VAL:HG21	1.95	0.48
1:C:619:GLU:HA	1:C:912:ALA:HB2	1.94	0.48
1:A:127:PHE:HE2	1:A:184:LEU:HG	1.79	0.48
1:D:763:GLY:HA3	1:D:822:LEU:HD13	1.95	0.48
1:A:755:ARG:HB3	1:A:769:TRP:CE3	2.48	0.47
1:B:784:PHE:HA	1:B:881:ARG:O	2.14	0.47
1:D:772:ASP:OD1	1:D:772:ASP:N	2.48	0.47
1:B:390:SER:HB2	1:B:391:HIS:CE1	2.50	0.47
1:C:763:GLY:HA3	1:C:822:LEU:HD13	1.97	0.47
1:D:91:GLN:HG3	1:D:96:ASP:OD1	2.14	0.47
1:D:500:CYS:HA	1:D:534:ILE:O	2.15	0.47
1:D:245:GLN:HG2	1:D:288:ARG:HG2	1.97	0.47
1:D:749:ILE:HD12	1:D:834:VAL:HG11	1.97	0.47
1:B:887:GLN:NE2	1:B:980:GLU:O	2.48	0.47
1:C:873:ALA:O	1:C:876:THR:HG22	2.15	0.47
1:B:377:LEU:HD22	1:B:708:TRP:HA	1.97	0.47
1:D:890:GLN:HE21	1:D:892:ALA:HB2	1.79	0.47
1:D:788:PRO:HD2	1:D:968:MET:HG3	1.97	0.46
1:C:744:GLU:HG3	1:C:745:MET:HG2	1.97	0.46
1:A:658:LEU:O	1:A:661:LYS:HE3	2.15	0.46
1:C:305:ILE:HD11	1:C:645:ARG:HB3	1.96	0.46
1:A:615:PRO:O	1:A:618:THR:HG22	2.15	0.46
1:A:431:ARG:HG3	6:A:4592:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:VAL:O	1:D:377:LEU:HG	2.16	0.46
1:C:788:PRO:HD2	1:C:968:MET:HG3	1.98	0.46
1:B:615:PRO:O	1:B:618:THR:HG22	2.14	0.46
1:A:796:ALA:HA	1:A:801:ILE:HA	1.98	0.46
1:C:147:ASN:HA	1:C:148:SER:HA	1.60	0.45
1:A:890:GLN:HE21	1:A:892:ALA:HB2	1.81	0.45
1:B:749:ILE:HD11	1:B:836:ILE:HD11	1.99	0.45
1:A:427:THR:HG21	1:A:462:SER:HB3	1.98	0.45
1:B:622:HIS:ND1	1:B:625:GLN:OE1	2.47	0.45
1:A:708:TRP:CE3	1:A:709:SER:HB3	2.52	0.45
1:D:19:PRO:HD3	1:D:112:PRO:HB3	1.98	0.45
1:A:143:PHE:O	1:A:168:PRO:HA	2.17	0.45
1:A:561:ARG:HD3	1:B:525:SER:O	2.16	0.45
1:B:749:ILE:CD1	1:B:834:VAL:HG11	2.46	0.44
1:C:340:GLY:O	1:C:561:ARG:HG2	2.18	0.44
1:C:784:PHE:HA	1:C:881:ARG:O	2.18	0.44
1:C:200:GLN:HG2	1:C:391:HIS:HB2	1.98	0.44
1:D:750:GLU:HG3	1:D:755:ARG:HG2	1.99	0.44
1:D:147:ASN:HA	1:D:148:SER:HA	1.62	0.44
1:D:244:VAL:HG21	1:D:256:VAL:HG11	2.00	0.44
1:B:907:PRO:HG2	1:B:990:HIS:O	2.18	0.44
1:D:615:PRO:O	1:D:618:THR:HG22	2.18	0.44
1:D:708:TRP:CE3	1:D:709:SER:HB3	2.53	0.43
1:A:127:PHE:CE2	1:A:184:LEU:HG	2.53	0.43
1:B:44:THR:OG1	1:B:46:ARG:HG3	2.18	0.43
1:D:986:ILE:HG21	1:D:1018:LEU:HD21	2.00	0.43
1:B:147:ASN:HA	1:B:148:SER:HA	1.65	0.43
1:A:301:TRP:CH2	1:A:452:SER:HA	2.54	0.43
1:C:768:MET:HE1	1:C:1020:TRP:CH2	2.54	0.43
1:C:379:MET:HE1	1:C:407:LEU:HD13	2.00	0.43
1:C:576:ILE:HG12	5:C:8009:DMS:H21	2.00	0.43
1:A:774:LYS:HE3	6:A:4536:HOH:O	2.18	0.43
1:A:458:LEU:HD11	1:A:472:TYR:HB2	2.00	0.43
1:C:749:ILE:HD11	1:C:836:ILE:HD11	2.01	0.43
1:C:88:SER:HA	1:C:366:VAL:HG21	2.01	0.43
1:D:352:ARG:HG2	1:D:553:TRP:CH2	2.54	0.43
1:A:522:LYS:HA	1:B:559:TYR:CE2	2.54	0.42
1:A:549:PHE:CE2	1:A:620:ALA:HA	2.54	0.42
1:D:225:PHE:HA	1:D:243:GLU:O	2.20	0.42
1:B:696:LEU:HB2	1:B:722:LEU:HD11	2.00	0.42
1:D:127:PHE:CE2	1:D:184:LEU:HG	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:788:PRO:HD2	1:A:968:MET:HG3	2.01	0.42
1:D:830:LEU:HD12	1:D:833:ALA:HB3	2.00	0.42
1:A:854:LYS:HA	1:A:867:THR:O	2.20	0.42
1:B:867:THR:HG23	1:B:1015:HIS:HE1	1.85	0.42
1:B:500:CYS:HA	1:B:534:ILE:O	2.20	0.42
1:C:220:THR:HG22	1:C:315:LEU:HD21	2.02	0.42
1:C:600:GLN:HB2	1:C:603:MET:HE2	2.02	0.42
1:D:143:PHE:O	1:D:168:PRO:HA	2.19	0.41
1:A:573:GLN:HB2	1:A:602:CYS:O	2.20	0.41
1:D:890:GLN:HG3	1:D:891:VAL:N	2.35	0.41
1:C:147:ASN:O	1:C:206:SER:HB2	2.19	0.41
1:A:928:PRO:HB2	1:A:973:ARG:HH11	1.85	0.41
1:D:524:LEU:HD11	1:D:562:LEU:HG	2.03	0.41
1:D:784:PHE:HA	1:D:881:ARG:O	2.20	0.41
1:A:390:SER:HA	1:A:391:HIS:HA	1.82	0.41
1:A:546:LEU:HA	6:A:4112:HOH:O	2.20	0.41
1:B:353:GLY:HA2	1:B:386:ALA:O	2.20	0.41
1:D:549:PHE:CE2	1:D:620:ALA:HA	2.56	0.41
1:A:749:ILE:HD11	1:A:836:ILE:HD11	2.02	0.41
1:A:619:GLU:HA	1:A:912:ALA:HB2	2.03	0.41
1:C:533:LEU:HD23	1:C:533:LEU:C	2.42	0.41
1:C:991:MET:HE2	1:C:1003:VAL:HG21	2.03	0.41
1:B:892:ALA:HB3	1:B:946:TYR:CE1	2.56	0.41
1:B:830:LEU:HD12	1:B:833:ALA:HB3	2.03	0.40
1:C:500:CYS:HA	1:C:534:ILE:O	2.21	0.40
1:C:390:SER:HA	1:C:391:HIS:HA	1.81	0.40
1:A:454:ILE:O	1:A:483:PRO:HD2	2.20	0.40
1:B:390:SER:HA	1:B:391:HIS:HA	1.81	0.40
5:D:8004:DMS:H21	6:D:4438:HOH:O	2.20	0.40
1:D:390:SER:HA	1:D:391:HIS:HA	1.87	0.40
1:B:613:PRO:HB3	1:B:617:LEU:HD23	2.03	0.40
1:C:653:HIS:CD2	1:C:701:VAL:HG21	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1013/1052 (96%)	983 (97%)	29 (3%)	1 (0%)	56	53
1	B	1013/1052 (96%)	979 (97%)	33 (3%)	1 (0%)	56	53
1	C	1013/1052 (96%)	978 (96%)	34 (3%)	1 (0%)	56	53
1	D	1013/1052 (96%)	979 (97%)	32 (3%)	2 (0%)	52	48
All	All	4052/4208 (96%)	3919 (97%)	128 (3%)	5 (0%)	56	53

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	798	ALA
1	D	798	ALA
1	A	798	ALA
1	B	798	ALA
1	D	802	ASP

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	867/897 (97%)	855 (99%)	12 (1%)	74	77
1	B	867/897 (97%)	854 (98%)	13 (2%)	72	75
1	C	867/897 (97%)	859 (99%)	8 (1%)	84	88
1	D	867/897 (97%)	858 (99%)	9 (1%)	82	85
All	All	3468/3588 (97%)	3426 (99%)	42 (1%)	78	81

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	333	ARG

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Mol	Chain	Res	Type
1	A	394	ASN
1	A	519	SER
1	A	535	LEU
1	A	546	LEU
1	A	663	LEU
1	A	672	VAL
1	A	681	GLU
1	A	772	ASP
1	A	801	ILE
1	A	956	GLN
1	A	1023	LYS
1	B	130	ASP
1	B	135	GLN
1	B	333	ARG
1	B	344	LEU
1	B	394	ASN
1	B	519	SER
1	B	546	LEU
1	B	663	LEU
1	B	772	ASP
1	B	819	GLU
1	B	876	THR
1	B	956	GLN
1	B	1023	LYS
1	C	262	GLN
1	C	333	ARG
1	C	344	LEU
1	C	394	ASN
1	C	519	SER
1	C	672	VAL
1	C	956	GLN
1	C	1023	LYS
1	D	333	ARG
1	D	394	ASN
1	D	546	LEU
1	D	663	LEU
1	D	671	ASP
1	D	672	VAL
1	D	685	LEU
1	D	772	ASP
1	D	1023	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	702	GLN
1	C	757	GLN
1	C	1017	GLN
1	D	702	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 97 ligands modelled in this entry, 22 are monoatomic - leaving 75 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	IPT	A	2001	3	15,15,15	0.87	1 (6%)	19,21,21	0.60	0
5	DMS	A	8001	-	3,3,3	2.60	1 (33%)	3,3,3	0.37	0
5	DMS	A	8002	-	3,3,3	2.56	1 (33%)	3,3,3	0.43	0
5	DMS	A	8003	-	3,3,3	2.58	1 (33%)	3,3,3	0.44	0
5	DMS	A	8004	-	3,3,3	2.63	1 (33%)	3,3,3	0.45	0
5	DMS	A	8005	-	3,3,3	2.58	1 (33%)	3,3,3	0.46	0
5	DMS	A	8006	-	3,3,3	2.62	1 (33%)	3,3,3	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	A	8007	-	3,3,3	2.61	1 (33%)	3,3,3	0.51	0
5	DMS	A	8008	-	3,3,3	2.63	1 (33%)	3,3,3	0.47	0
5	DMS	A	8009	-	3,3,3	2.58	1 (33%)	3,3,3	0.48	0
5	DMS	A	8010	-	3,3,3	2.57	1 (33%)	3,3,3	0.41	0
5	DMS	A	8011	-	3,3,3	2.61	1 (33%)	3,3,3	0.45	0
5	DMS	A	8012	-	3,3,3	2.65	1 (33%)	3,3,3	0.46	0
5	DMS	A	8013	-	3,3,3	2.63	1 (33%)	3,3,3	0.53	0
5	DMS	A	8014	-	3,3,3	2.61	1 (33%)	3,3,3	0.45	0
5	DMS	A	8015	-	3,3,3	2.59	1 (33%)	3,3,3	0.39	0
5	DMS	A	8016	-	3,3,3	2.60	1 (33%)	3,3,3	0.50	0
5	DMS	A	8017	-	3,3,3	2.61	1 (33%)	3,3,3	0.45	0
5	DMS	A	8018	-	3,3,3	2.60	1 (33%)	3,3,3	0.45	0
5	DMS	A	8019	-	3,3,3	2.60	1 (33%)	3,3,3	0.43	0
5	DMS	A	8020	-	3,3,3	2.61	1 (33%)	3,3,3	0.53	0
4	IPT	B	2001	3	15,15,15	0.75	1 (6%)	19,21,21	0.87	0
5	DMS	B	8001	-	3,3,3	2.48	1 (33%)	3,3,3	0.42	0
5	DMS	B	8002	-	3,3,3	2.45	1 (33%)	3,3,3	0.67	0
5	DMS	B	8003	-	3,3,3	2.59	1 (33%)	3,3,3	0.43	0
5	DMS	B	8004	-	3,3,3	2.60	1 (33%)	3,3,3	0.41	0
5	DMS	B	8005	-	3,3,3	2.57	1 (33%)	3,3,3	0.31	0
5	DMS	B	8006	-	3,3,3	2.65	1 (33%)	3,3,3	0.50	0
5	DMS	B	8007	-	3,3,3	2.59	1 (33%)	3,3,3	0.51	0
5	DMS	B	8008	-	3,3,3	2.65	1 (33%)	3,3,3	0.46	0
5	DMS	B	8009	-	3,3,3	2.61	1 (33%)	3,3,3	0.50	0
5	DMS	B	8010	-	3,3,3	2.57	1 (33%)	3,3,3	0.35	0
5	DMS	B	8011	-	3,3,3	2.60	1 (33%)	3,3,3	0.49	0
5	DMS	B	8012	-	3,3,3	2.63	1 (33%)	3,3,3	0.49	0
5	DMS	B	8014	-	3,3,3	2.62	1 (33%)	3,3,3	0.44	0
5	DMS	B	8015	-	3,3,3	2.61	1 (33%)	3,3,3	0.47	0
5	DMS	B	8016	-	3,3,3	2.58	1 (33%)	3,3,3	0.51	0
5	DMS	B	8017	-	3,3,3	2.60	1 (33%)	3,3,3	0.51	0
5	DMS	B	8018	-	3,3,3	2.61	1 (33%)	3,3,3	0.41	0
5	DMS	B	8019	-	3,3,3	2.62	1 (33%)	3,3,3	0.47	0
5	DMS	C	1024	-	3,3,3	2.63	1 (33%)	3,3,3	0.51	0
4	IPT	C	2001	3	15,15,15	0.84	1 (6%)	19,21,21	0.81	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	C	8001	-	3,3,3	2.52	1 (33%)	3,3,3	0.43	0
5	DMS	C	8002	-	3,3,3	2.58	1 (33%)	3,3,3	0.45	0
5	DMS	C	8003	-	3,3,3	2.61	1 (33%)	3,3,3	0.43	0
5	DMS	C	8004	-	3,3,3	2.63	1 (33%)	3,3,3	0.47	0
5	DMS	C	8005	-	3,3,3	2.57	1 (33%)	3,3,3	0.36	0
5	DMS	C	8006	-	3,3,3	2.59	1 (33%)	3,3,3	0.43	0
5	DMS	C	8007	-	3,3,3	2.61	1 (33%)	3,3,3	0.55	0
5	DMS	C	8008	-	3,3,3	2.60	1 (33%)	3,3,3	0.41	0
5	DMS	C	8009	-	3,3,3	2.59	1 (33%)	3,3,3	0.42	0
5	DMS	C	8010	-	3,3,3	2.57	1 (33%)	3,3,3	0.40	0
5	DMS	C	8011	-	3,3,3	2.56	1 (33%)	3,3,3	0.36	0
5	DMS	C	8012	-	3,3,3	2.63	1 (33%)	3,3,3	0.48	0
5	DMS	C	8013	-	3,3,3	2.61	1 (33%)	3,3,3	0.45	0
5	DMS	C	8014	3	3,3,3	2.64	1 (33%)	3,3,3	0.50	0
5	DMS	C	8015	-	3,3,3	2.60	1 (33%)	3,3,3	0.40	0
5	DMS	C	8016	-	3,3,3	2.59	1 (33%)	3,3,3	0.43	0
5	DMS	C	8017	-	3,3,3	2.63	1 (33%)	3,3,3	0.48	0
5	DMS	C	8018	-	3,3,3	2.62	1 (33%)	3,3,3	0.35	0
4	IPT	D	2001	3	15,15,15	0.83	1 (6%)	19,21,21	0.80	0
5	DMS	D	8001	-	3,3,3	2.58	1 (33%)	3,3,3	0.46	0
5	DMS	D	8002	-	3,3,3	2.58	1 (33%)	3,3,3	0.58	0
5	DMS	D	8003	-	3,3,3	2.57	1 (33%)	3,3,3	0.37	0
5	DMS	D	8004	-	3,3,3	2.59	1 (33%)	3,3,3	0.53	0
5	DMS	D	8005	-	3,3,3	2.51	1 (33%)	3,3,3	0.35	0
5	DMS	D	8006	-	3,3,3	2.63	1 (33%)	3,3,3	0.48	0
5	DMS	D	8007	-	3,3,3	2.61	1 (33%)	3,3,3	0.42	0
5	DMS	D	8008	-	3,3,3	2.63	1 (33%)	3,3,3	0.44	0
5	DMS	D	8009	-	3,3,3	2.56	1 (33%)	3,3,3	0.47	0
5	DMS	D	8010	-	3,3,3	2.61	1 (33%)	3,3,3	0.51	0
5	DMS	D	8011	-	3,3,3	2.62	1 (33%)	3,3,3	0.46	0
5	DMS	D	8012	-	3,3,3	2.60	1 (33%)	3,3,3	0.41	0
5	DMS	D	8013	-	3,3,3	2.62	1 (33%)	3,3,3	0.51	0
5	DMS	D	8014	-	3,3,3	2.60	1 (33%)	3,3,3	0.46	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	IPT	A	2001	3	-	0/6/26/26	0/1/1/1
5	DMS	A	8001	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8002	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8003	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8004	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8005	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8006	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8007	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8008	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8009	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8010	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8011	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8012	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8013	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8014	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8015	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8016	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8017	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8018	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8019	-	-	0/0/0/0	0/0/0/0
5	DMS	A	8020	-	-	0/0/0/0	0/0/0/0
4	IPT	B	2001	3	-	0/6/26/26	0/1/1/1
5	DMS	B	8001	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8002	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8003	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8004	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8005	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8006	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8007	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8008	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8009	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8010	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8011	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8012	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8014	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8015	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8016	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8017	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8018	-	-	0/0/0/0	0/0/0/0
5	DMS	B	8019	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	DMS	C	1024	-	-	0/0/0/0	0/0/0/0
4	IPT	C	2001	3	-	0/6/26/26	0/1/1/1
5	DMS	C	8001	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8002	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8003	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8004	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8005	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8006	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8007	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8008	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8009	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8010	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8011	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8012	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8013	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8014	3	-	0/0/0/0	0/0/0/0
5	DMS	C	8015	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8016	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8017	-	-	0/0/0/0	0/0/0/0
5	DMS	C	8018	-	-	0/0/0/0	0/0/0/0
4	IPT	D	2001	3	-	0/6/26/26	0/1/1/1
5	DMS	D	8001	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8002	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8003	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8004	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8005	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8006	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8007	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8008	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8009	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8010	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8011	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8012	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8013	-	-	0/0/0/0	0/0/0/0
5	DMS	D	8014	-	-	0/0/0/0	0/0/0/0

All (75) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2001	IPT	C1-S1	-2.85	1.75	1.80
4	C	2001	IPT	C1-S1	-2.67	1.76	1.80
4	D	2001	IPT	C1-S1	-2.63	1.76	1.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2001	IPT	C1-S1	-2.04	1.77	1.80
5	B	8002	DMS	O-S	4.14	1.78	1.50
5	B	8001	DMS	O-S	4.16	1.78	1.50
5	D	8005	DMS	O-S	4.19	1.79	1.50
5	C	8001	DMS	O-S	4.22	1.79	1.50
5	C	8011	DMS	O-S	4.29	1.79	1.50
5	A	8002	DMS	O-S	4.29	1.79	1.50
5	D	8009	DMS	O-S	4.29	1.79	1.50
5	A	8010	DMS	O-S	4.30	1.79	1.50
5	C	8005	DMS	O-S	4.30	1.79	1.50
5	B	8005	DMS	O-S	4.30	1.79	1.50
5	A	8009	DMS	O-S	4.31	1.79	1.50
5	D	8001	DMS	O-S	4.31	1.79	1.50
5	B	8010	DMS	O-S	4.31	1.79	1.50
5	C	8010	DMS	O-S	4.32	1.79	1.50
5	A	8005	DMS	O-S	4.32	1.79	1.50
5	D	8003	DMS	O-S	4.33	1.80	1.50
5	A	8003	DMS	O-S	4.33	1.80	1.50
5	C	8006	DMS	O-S	4.33	1.80	1.50
5	B	8017	DMS	O-S	4.34	1.80	1.50
5	D	8002	DMS	O-S	4.34	1.80	1.50
5	A	8016	DMS	O-S	4.34	1.80	1.50
5	B	8016	DMS	O-S	4.34	1.80	1.50
5	B	8011	DMS	O-S	4.35	1.80	1.50
5	C	8002	DMS	O-S	4.35	1.80	1.50
5	C	8016	DMS	O-S	4.35	1.80	1.50
5	D	8014	DMS	O-S	4.35	1.80	1.50
5	D	8004	DMS	O-S	4.35	1.80	1.50
5	B	8009	DMS	O-S	4.36	1.80	1.50
5	B	8003	DMS	O-S	4.36	1.80	1.50
5	C	8009	DMS	O-S	4.36	1.80	1.50
5	B	8007	DMS	O-S	4.36	1.80	1.50
5	A	8017	DMS	O-S	4.36	1.80	1.50
5	A	8018	DMS	O-S	4.37	1.80	1.50
5	A	8015	DMS	O-S	4.37	1.80	1.50
5	C	8008	DMS	O-S	4.37	1.80	1.50
5	C	8007	DMS	O-S	4.37	1.80	1.50
5	A	8011	DMS	O-S	4.37	1.80	1.50
5	D	8012	DMS	O-S	4.37	1.80	1.50
5	C	8013	DMS	O-S	4.37	1.80	1.50
5	C	8015	DMS	O-S	4.37	1.80	1.50
5	A	8019	DMS	O-S	4.38	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	8007	DMS	O-S	4.38	1.80	1.50
5	A	8014	DMS	O-S	4.38	1.80	1.50
5	A	8007	DMS	O-S	4.38	1.80	1.50
5	B	8015	DMS	O-S	4.38	1.80	1.50
5	B	8014	DMS	O-S	4.38	1.80	1.50
5	C	8018	DMS	O-S	4.38	1.80	1.50
5	B	8018	DMS	O-S	4.38	1.80	1.50
5	B	8004	DMS	O-S	4.38	1.80	1.50
5	D	8010	DMS	O-S	4.38	1.80	1.50
5	D	8013	DMS	O-S	4.39	1.80	1.50
5	C	8003	DMS	O-S	4.39	1.80	1.50
5	A	8020	DMS	O-S	4.39	1.80	1.50
5	B	8019	DMS	O-S	4.39	1.80	1.50
5	D	8011	DMS	O-S	4.39	1.80	1.50
5	A	8001	DMS	O-S	4.40	1.80	1.50
5	C	8017	DMS	O-S	4.40	1.80	1.50
5	C	8012	DMS	O-S	4.40	1.80	1.50
5	A	8013	DMS	O-S	4.40	1.80	1.50
5	A	8006	DMS	O-S	4.40	1.80	1.50
5	C	8004	DMS	O-S	4.40	1.80	1.50
5	D	8006	DMS	O-S	4.41	1.80	1.50
5	C	1024	DMS	O-S	4.41	1.80	1.50
5	B	8012	DMS	O-S	4.41	1.80	1.50
5	A	8008	DMS	O-S	4.41	1.80	1.50
5	D	8008	DMS	O-S	4.42	1.80	1.50
5	A	8004	DMS	O-S	4.42	1.80	1.50
5	C	8014	DMS	O-S	4.43	1.80	1.50
5	B	8006	DMS	O-S	4.45	1.80	1.50
5	A	8012	DMS	O-S	4.45	1.80	1.50
5	B	8008	DMS	O-S	4.45	1.80	1.50

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	8001	DMS	2	0
5	C	8009	DMS	2	0
5	D	8004	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	1012/1052 (96%)	-0.15	22 (2%) 65 66	24, 36, 58, 94	0
1	B	1013/1052 (96%)	-0.15	21 (2%) 67 67	23, 35, 59, 96	0
1	C	1013/1052 (96%)	-0.13	20 (1%) 68 69	24, 35, 61, 93	0
1	D	1012/1052 (96%)	-0.03	30 (2%) 54 55	24, 38, 63, 95	0
All	All	4050/4208 (96%)	-0.11	93 (2%) 64 64	23, 36, 60, 96	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	731	PRO	6.7
1	B	730	LEU	5.7
1	A	689	GLU	5.1
1	B	689	GLU	4.9
1	D	801	ILE	4.9
1	D	689	GLU	4.8
1	D	687	GLN	4.8
1	B	732	ALA	4.7
1	D	11	LEU	4.7
1	C	731	PRO	4.7
1	C	730	LEU	4.6
1	D	735	HIS	4.6
1	A	735	HIS	4.5
1	D	730	LEU	4.3
1	A	801	ILE	4.3
1	A	11	LEU	4.3
1	D	795	VAL	4.2
1	C	686	PRO	4.1
1	A	730	LEU	4.0
1	B	1023	LYS	3.9
1	A	686	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	11	LEU	3.7
1	D	686	PRO	3.6
1	B	686	PRO	3.6
1	C	1023	LYS	3.6
1	A	687	GLN	3.5
1	C	689	GLU	3.5
1	A	772	ASP	3.4
1	D	732	ALA	3.4
1	B	11	LEU	3.4
1	B	733	ALA	3.3
1	C	733	ALA	3.3
1	B	690	SER	3.3
1	A	795	VAL	3.3
1	B	687	GLN	3.2
1	A	800	ARG	3.2
1	C	688	PRO	3.2
1	D	76	CYS	3.2
1	C	795	VAL	3.2
1	A	1023	LYS	3.2
1	C	580	GLU	3.1
1	B	797	GLU	3.1
1	D	12	GLN	3.0
1	D	1023	LYS	3.0
1	A	685	LEU	3.0
1	D	685	LEU	2.9
1	D	731	PRO	2.9
1	C	796	ALA	2.9
1	A	733	ALA	2.9
1	B	12	GLN	2.9
1	D	796	ALA	2.8
1	A	12	GLN	2.8
1	C	12	GLN	2.8
1	D	684	GLU	2.8
1	D	794	GLY	2.8
1	C	9	VAL	2.8
1	B	683	PRO	2.7
1	C	753	ASN	2.7
1	A	732	ALA	2.7
1	D	10	VAL	2.6
1	D	734	SER	2.6
1	C	772	ASP	2.6
1	D	830	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	734	SER	2.5
1	B	796	ALA	2.5
1	C	732	ALA	2.5
1	A	731	PRO	2.5
1	D	753	ASN	2.4
1	D	829	THR	2.4
1	D	75	GLU	2.4
1	B	684	GLU	2.4
1	B	794	GLY	2.4
1	D	729	THR	2.4
1	C	831	ALA	2.3
1	B	9	VAL	2.3
1	A	773	LYS	2.3
1	B	772	ASP	2.3
1	C	687	GLN	2.3
1	C	794	GLY	2.3
1	B	735	HIS	2.3
1	D	690	SER	2.2
1	A	71	GLU	2.2
1	D	736	ALA	2.2
1	B	634	GLN	2.1
1	A	9	VAL	2.1
1	C	690	SER	2.1
1	B	688	PRO	2.1
1	D	733	ALA	2.1
1	D	9	VAL	2.1
1	D	831	ALA	2.1
1	A	796	ALA	2.1
1	A	690	SER	2.0
1	D	739	HIS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
5	DMS	A	8006	4/4	0.55	0.31	16.78	107,107,107,108	0
5	DMS	A	8011	4/4	0.80	0.26	12.76	84,84,85,85	0
5	DMS	A	8003	4/4	0.96	0.18	11.84	54,57,57,61	0
5	DMS	C	8006	4/4	0.94	0.32	10.55	84,86,86,86	0
5	DMS	C	8003	4/4	0.98	0.16	10.45	59,60,62,64	0
5	DMS	C	8004	4/4	0.89	0.23	10.17	68,68,69,73	0
5	DMS	B	8015	4/4	0.88	0.26	10.13	82,83,84,86	0
5	DMS	A	8015	4/4	0.94	0.17	9.74	57,62,63,64	0
5	DMS	D	8004	4/4	0.96	0.17	9.17	60,63,63,64	0
5	DMS	B	8003	4/4	0.98	0.20	8.67	59,60,62,62	0
5	DMS	D	8012	4/4	0.95	0.16	7.48	66,69,69,70	0
5	DMS	D	8006	4/4	0.74	0.25	7.34	81,81,83,86	0
5	DMS	C	8014	4/4	0.97	0.29	7.30	59,63,65,67	0
5	DMS	C	8007	4/4	0.99	0.17	6.11	55,56,58,60	0
5	DMS	B	8005	4/4	0.97	0.17	6.04	51,52,53,53	0
5	DMS	B	8004	4/4	0.96	0.15	5.72	56,58,60,60	0
5	DMS	B	8002	4/4	0.97	0.17	5.29	41,41,42,43	0
5	DMS	D	8013	4/4	0.91	0.20	5.25	75,75,76,77	0
5	DMS	C	8013	4/4	0.97	0.17	5.15	75,76,76,77	0
5	DMS	B	8017	4/4	0.91	0.17	4.86	60,61,63,68	0
5	DMS	C	8002	4/4	0.97	0.14	4.67	41,44,45,46	0
5	DMS	D	8009	4/4	0.97	0.15	4.66	50,53,54,56	0
5	DMS	C	8015	4/4	0.91	0.19	4.64	69,69,69,72	0
5	DMS	A	8018	4/4	0.91	0.20	4.58	84,86,86,86	0
5	DMS	D	8003	4/4	0.98	0.16	4.55	58,59,59,59	0
5	DMS	A	8016	4/4	0.96	0.23	4.28	56,57,58,60	0
5	DMS	D	8002	4/4	0.95	0.17	4.21	42,46,48,48	0
5	DMS	A	8002	4/4	0.98	0.14	3.99	43,46,48,50	0
5	DMS	A	8007	4/4	0.96	0.22	3.94	63,63,64,64	0
5	DMS	B	8016	4/4	0.94	0.14	3.91	46,48,48,50	0
3	NA	C	3103	1/1	0.93	0.16	3.70	48,48,48,48	0
5	DMS	A	8004	4/4	0.95	0.13	3.61	63,66,68,68	0
5	DMS	B	8009	4/4	0.81	0.22	3.49	70,72,73,76	0
5	DMS	A	8013	4/4	0.95	0.14	3.27	69,69,70,71	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	DMS	D	8005	4/4	0.97	0.15	3.13	45,47,49,50	0
2	MG	B	3002	1/1	0.95	0.14	3.12	33,33,33,33	0
5	DMS	B	8007	4/4	0.94	0.15	2.92	60,60,60,62	0
5	DMS	A	8020	4/4	0.92	0.18	2.87	77,78,78,79	0
5	DMS	B	8006	4/4	0.86	0.17	2.78	80,82,83,85	0
5	DMS	B	8011	4/4	0.95	0.16	2.74	58,59,59,59	0
5	DMS	A	8010	4/4	0.96	0.20	2.73	58,58,60,61	0
5	DMS	C	8009	4/4	0.96	0.15	2.55	51,52,52,54	0
3	NA	A	3103	1/1	0.96	0.13	2.39	46,46,46,46	0
5	DMS	A	8019	4/4	0.95	0.17	1.99	90,90,90,90	0
5	DMS	A	8005	4/4	0.98	0.14	1.98	52,54,55,57	0
5	DMS	D	8001	4/4	0.98	0.14	1.97	41,45,47,50	0
5	DMS	A	8001	4/4	0.97	0.14	1.90	34,46,46,49	0
3	NA	B	3102	1/1	0.97	0.12	1.43	31,31,31,31	0
5	DMS	B	8018	4/4	0.86	0.17	1.38	82,82,84,84	0
5	DMS	B	8010	4/4	0.96	0.15	1.34	57,57,59,60	0
5	DMS	A	8009	4/4	0.99	0.13	1.22	42,45,45,47	0
2	MG	C	3002	1/1	0.98	0.10	1.10	29,29,29,29	0
3	NA	B	3103	1/1	0.93	0.13	1.06	59,59,59,59	0
5	DMS	D	8010	4/4	0.96	0.14	0.94	51,53,55,55	0
5	DMS	B	8001	4/4	0.98	0.12	0.83	35,38,40,43	0
5	DMS	C	8010	4/4	0.97	0.12	0.72	53,54,54,56	0
5	DMS	C	8001	4/4	0.98	0.13	0.56	40,41,42,48	0
5	DMS	D	8007	4/4	0.97	0.14	0.42	59,61,61,62	0
3	NA	C	3104	1/1	0.94	0.15	0.37	48,48,48,48	0
4	IPT	D	2001	15/15	0.92	0.13	0.32	39,47,51,52	0
5	DMS	C	8005	4/4	0.99	0.11	0.25	52,52,53,55	0
2	MG	A	3001	1/1	0.92	0.10	0.14	32,32,32,32	0
4	IPT	C	2001	15/15	0.90	0.12	0.13	36,45,47,52	0
5	DMS	C	8016	4/4	0.98	0.12	0.08	63,63,64,67	0
3	NA	A	3102	1/1	0.97	0.12	0.05	31,31,31,31	0
3	NA	D	3103	1/1	0.85	0.10	-0.09	59,59,59,59	0
4	IPT	A	2001	15/15	0.93	0.10	-0.14	38,45,53,53	0
2	MG	A	3002	1/1	0.93	0.10	-0.22	36,36,36,36	0
5	DMS	C	8017	4/4	0.93	0.11	-0.59	73,73,74,77	0
2	MG	D	3002	1/1	0.98	0.10	-0.72	36,36,36,36	0
4	IPT	B	2001	15/15	0.96	0.09	-0.86	32,42,45,47	0
2	MG	B	3001	1/1	0.91	0.10	-1.12	31,31,31,31	0
3	NA	C	3102	1/1	0.99	0.11	-1.17	32,32,32,32	0
2	MG	C	3001	1/1	0.94	0.09	-1.37	33,33,33,33	0
3	NA	D	3102	1/1	0.98	0.10	-1.59	33,33,33,33	0
3	NA	C	3101	1/1	0.99	0.07	-2.41	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NA	A	3101	1/1	0.98	0.05	-2.68	33,33,33,33	0
3	NA	B	3101	1/1	0.99	0.06	-3.38	28,28,28,28	0
3	NA	D	3101	1/1	0.96	0.07	-3.73	37,37,37,37	0
2	MG	D	3001	1/1	0.96	0.07	-3.95	35,35,35,35	0
5	DMS	B	8012	4/4	0.70	0.36	-	112,113,113,114	0
5	DMS	B	8019	4/4	0.79	0.22	-	87,88,88,91	0
5	DMS	A	8012	4/4	0.88	0.26	-	71,73,73,76	0
5	DMS	B	8008	4/4	0.96	0.11	-	56,56,56,57	0
5	DMS	A	8014	4/4	0.90	0.22	-	85,85,86,86	0
5	DMS	D	8008	4/4	0.96	0.15	-	67,67,69,69	0
5	DMS	C	1024	4/4	0.86	0.18	-	85,85,87,88	0
5	DMS	B	8014	4/4	0.90	0.19	-	78,79,79,82	0
5	DMS	C	8018	4/4	0.95	0.25	-	71,74,76,76	0
5	DMS	D	8014	4/4	0.90	0.24	-	79,79,80,80	0
5	DMS	C	8008	4/4	0.96	0.15	-	60,62,62,62	0
2	MG	B	3007	1/1	0.88	0.06	-	56,56,56,56	0
5	DMS	C	8012	4/4	0.85	0.27	-	81,82,83,84	0
5	DMS	A	8008	4/4	0.93	0.16	-	65,66,68,68	0
5	DMS	D	8011	4/4	0.95	0.14	-	74,74,75,77	0
5	DMS	C	8011	4/4	0.93	0.24	-	55,60,61,61	0
5	DMS	A	8017	4/4	0.94	0.15	-	70,70,71,72	0

6.5 Other polymers

There are no such residues in this entry.