



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 07:04 PM BST

PDB ID : 4DUX
Title : E. coli (lacZ) beta-galactosidase (N460S) in complex with L-ribose
Authors : Wheatley, R.W.; Lo, S.; Janzcewicz, L.J.; Dugdale, M.L.; Huber, R.E.
Deposited on : 2012-02-22
Resolution : 2.30 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 : 2.13.1
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) : 2.13.1

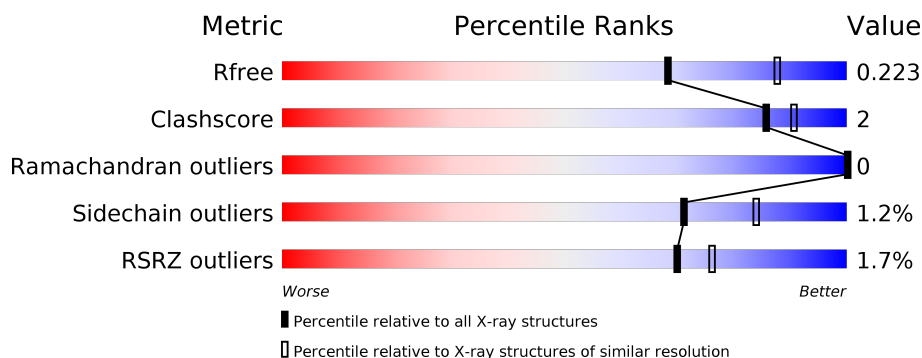
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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	1052	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div></div> </div> <div></div> </div>
1	B	1052	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div></div> </div> <div></div> </div>
1	C	1052	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>7%</div> <div></div> </div> <div></div> </div>
1	D	1052	<div> <div>2%</div> <div> <div></div> <div>91%</div> <div>5%</div> <div></div> </div> <div></div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 35621 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	0	0	0
			8155	5158	1444	1515	38			
1	B	1015	Total	C	N	O	S	0	0	0
			8155	5158	1444	1515	38			
1	C	1015	Total	C	N	O	S	0	0	0
			8155	5158	1444	1515	38			
1	D	1015	Total	C	N	O	S	0	0	0
			8155	5158	1444	1515	38			

There are 152 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-28	MET	-	initiating methionine	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	460	SER	ASN	engineered mutation	UNP P00722
B	-28	MET	-	initiating methionine	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	460	SER	ASN	engineered mutation	UNP P00722
C	-28	MET	-	initiating methionine	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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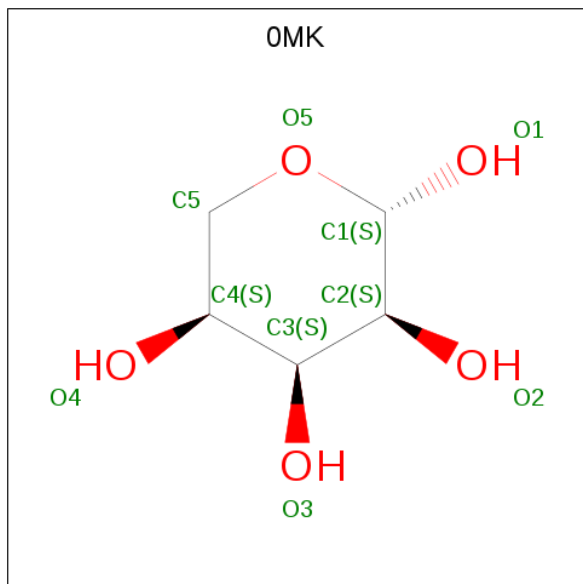
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ASP	-	expression tag	UNP P00722
C	2	LYS	-	expression tag	UNP P00722
C	3	ASP	-	expression tag	UNP P00722
C	4	PRO	-	expression tag	UNP P00722
C	5	MET	-	expression tag	UNP P00722
C	6	ILE	-	expression tag	UNP P00722
C	7	ASP	-	expression tag	UNP P00722
C	8	PRO	-	expression tag	UNP P00722
C	460	SER	ASN	engineered mutation	UNP P00722
D	-28	MET	-	initiating methionine	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	460	SER	ASN	engineered mutation	UNP P00722

- Molecule 2 is beta-L-ribofuranose (three-letter code: 0MK) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		

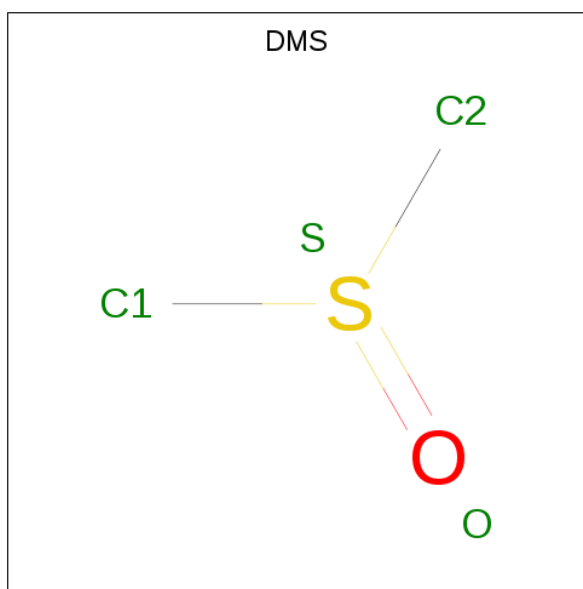
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

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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	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

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

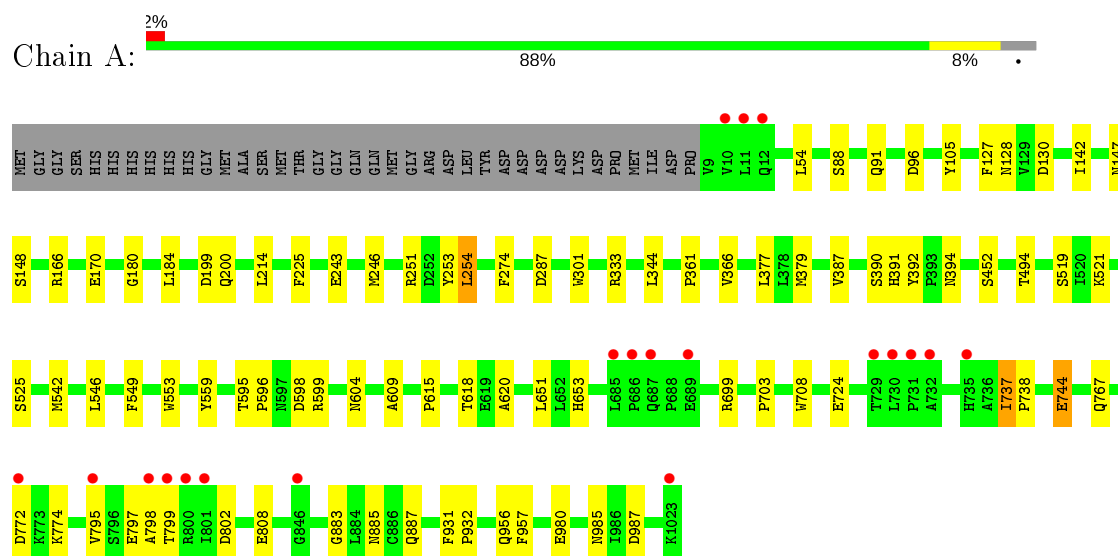
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	689	Total	O	0	0
			689	689		
6	B	593	Total	O	0	0
			593	593		
6	C	661	Total	O	0	0
			661	661		
6	D	686	Total	O	0	0
			686	686		

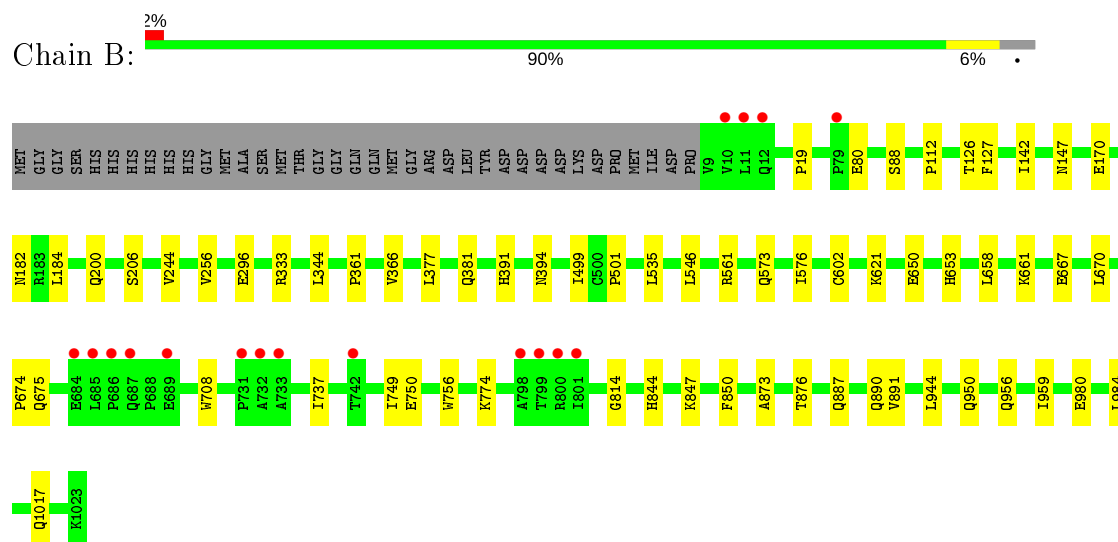
3 Residue-property plots [i](#)

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

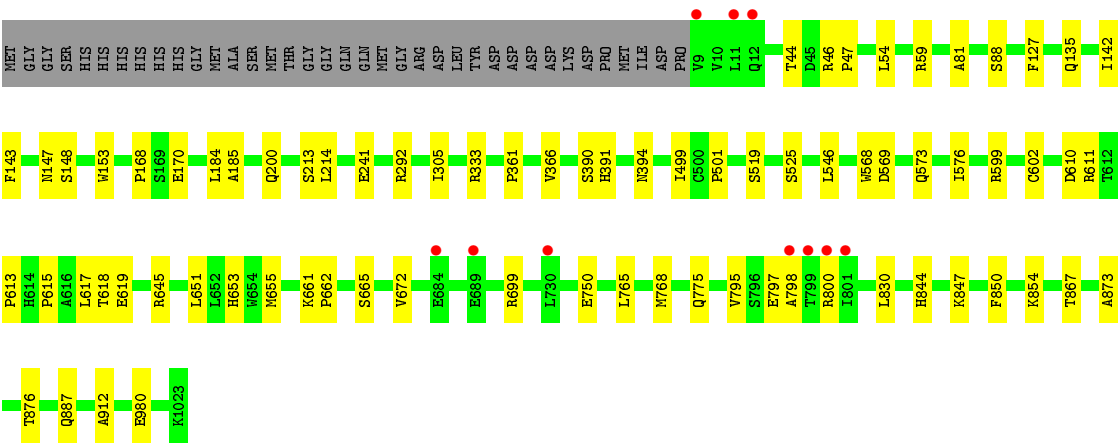


• Molecule 1: Beta-galactosidase

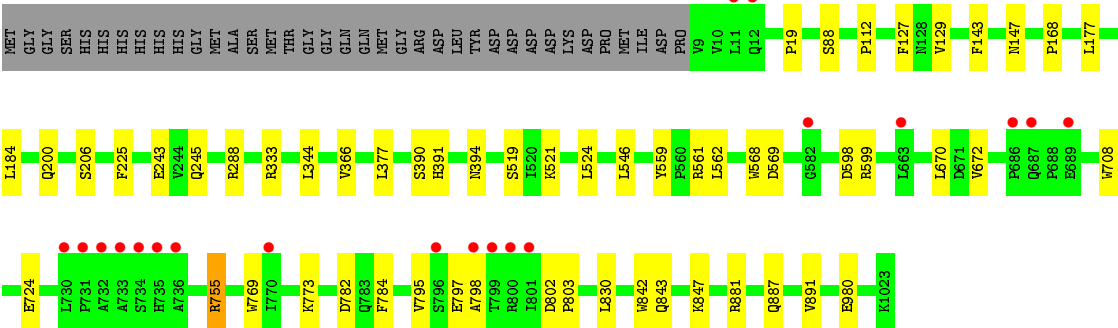
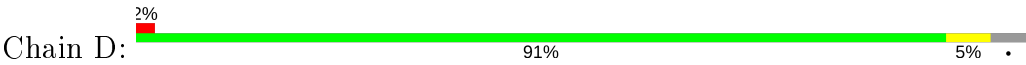


• Molecule 1: Beta-galactosidase





• 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	150.65Å 168.10Å 201.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.54 – 2.30 86.54 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (86.54-2.30) 98.8 (86.54-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.5.0109, CNS	Depositor
R, R_{free}	0.170 , 0.221 0.173 , 0.223	Depositor DCC
R_{free} test set	3223 reflections (1.44%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtrriage
Anisotropy	0.041	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.8	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	0.96	EDS
Total number of atoms	35621	wwPDB-VP
Average B, all atoms (Å ²)	37.0	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 39.35 % 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 3.2169e-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: NA, MG, DMS, 0MK

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	0.43	0/8397	0.56	1/11455 (0.0%)
1	B	0.41	0/8397	0.55	0/11455
1	C	0.41	0/8397	0.55	0/11455
1	D	0.42	0/8397	0.56	0/11455
All	All	0.42	0/33588	0.55	1/45820 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	553	TRP	CA-CB-CG	-5.13	103.96	113.70

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	8155	0	7752	46	0
1	B	8155	0	7752	28	0
1	C	8155	0	7752	39	0
1	D	8155	0	7752	30	0
2	A	20	0	20	1	0
2	B	30	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	20	0	19	1	0
2	D	20	0	20	2	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	3	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	0	0
4	D	3	0	0	0	0
5	A	72	0	108	1	0
5	B	56	0	84	0	0
5	C	60	0	90	2	0
5	D	72	0	108	1	0
6	A	689	0	0	2	0
6	B	593	0	0	1	0
6	C	661	0	0	3	0
6	D	686	0	0	1	0
All	All	35621	0	31487	143	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 (143) 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:142:ILE:HG12	1:A:170:GLU:HG2	1.70	0.72
1:A:246:MET:HE2	1:A:274:PHE:CE2	2.29	0.67
1:B:887:GLN:NE2	1:B:980:GLU:O	2.31	0.64
1:A:887:GLN:NE2	1:A:980:GLU:O	2.30	0.63
1:C:241:GLU:HG3	1:C:292:ARG:HG2	1.79	0.63
1:D:599:ARG:NH2	1:D:798:ALA:HA	2.14	0.62
1:B:127:PHE:CE1	1:B:184:LEU:HG	2.36	0.61
1:B:381:GLN:O	1:B:621:LYS:HE3	2.01	0.61
2:A:2001:0MK:H5	2:A:2002:0MK:H6	1.83	0.60
1:D:599:ARG:HH21	1:D:798:ALA:HA	1.67	0.59
1:D:245:GLN:HG2	1:D:288:ARG:HG2	1.85	0.59
1:D:887:GLN:NE2	1:D:980:GLU:O	2.32	0.59
1:B:142:ILE:HG12	1:B:170:GLU:HG2	1.85	0.58
1:A:251:ARG:HB2	1:A:254:LEU:HD22	1.85	0.58
1:B:653:HIS:CD2	1:B:667:GLU:HG2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:651:LEU:HD11	1:C:653:HIS:CE1	2.40	0.56
1:A:377:LEU:HD22	1:A:708:TRP:HA	1.86	0.56
2:C:2001:0MK:H5	2:C:2002:0MK:H6	1.87	0.56
1:C:765:LEU:HD21	1:C:768:MET:HE2	1.87	0.56
1:A:724:GLU:O	1:B:847:LYS:NZ	2.38	0.56
1:C:142:ILE:HG12	1:C:170:GLU:HG2	1.88	0.55
1:C:613:PRO:HB3	1:C:617:LEU:HD23	1.89	0.55
1:A:599:ARG:HH11	1:A:798:ALA:HA	1.73	0.54
1:C:873:ALA:O	1:C:876:THR:HG22	2.08	0.54
1:A:127:PHE:CE1	1:A:184:LEU:HG	2.42	0.54
1:C:88:SER:HA	1:C:366:VAL:HG21	1.90	0.53
1:D:755:ARG:HB3	1:D:769:TRP:HB2	1.91	0.53
1:A:91:GLN:HG3	1:A:96:ASP:OD1	2.09	0.53
1:A:767:GLN:NE2	1:A:774:LYS:HE2	2.24	0.52
1:D:88:SER:HA	1:D:366:VAL:HG21	1.92	0.52
1:D:127:PHE:CE1	1:D:184:LEU:HG	2.45	0.51
1:C:847:LYS:NZ	1:D:724:GLU:O	2.43	0.51
1:A:54:LEU:HD11	1:A:214:LEU:HG	1.92	0.51
1:A:802:ASP:O	1:A:808:GLU:HG3	2.10	0.51
1:B:873:ALA:O	1:B:876:THR:HG22	2.10	0.51
1:A:253:TYR:CE1	1:A:254:LEU:HD13	2.45	0.51
1:C:59:ARG:NH2	1:C:81:ALA:O	2.44	0.51
1:C:200:GLN:HG2	1:C:391:HIS:HB2	1.93	0.50
1:C:44:THR:OG1	1:C:46:ARG:HG3	2.11	0.50
1:C:47:PRO:HA	5:C:8012:DMS:O	2.11	0.50
1:A:651:LEU:HD23	1:A:703:PRO:HG3	1.93	0.50
2:D:2001:0MK:H5	2:D:2002:0MK:H6	1.92	0.50
1:C:887:GLN:NE2	1:C:980:GLU:O	2.40	0.49
1:B:377:LEU:HD22	1:B:708:TRP:HA	1.94	0.49
1:A:521:LYS:HG2	1:A:559:TYR:CZ	2.47	0.49
1:B:1017:GLN:HB2	6:B:4520:HOH:O	2.13	0.49
1:D:784:PHE:HA	1:D:881:ARG:O	2.12	0.49
1:D:200:GLN:HG2	1:D:391:HIS:HB2	1.94	0.49
1:C:797:GLU:HB2	1:C:800:ARG:HD2	1.95	0.49
1:B:88:SER:HA	1:B:366:VAL:HG21	1.94	0.49
1:B:127:PHE:HE1	1:B:184:LEU:HG	1.75	0.48
1:D:598:ASP:OD1	1:D:797:GLU:HA	2.12	0.48
1:A:127:PHE:HE1	1:A:184:LEU:HG	1.78	0.48
1:A:200:GLN:HG2	1:A:391:HIS:HB2	1.94	0.48
1:C:699:ARG:NH2	6:C:4618:HOH:O	2.36	0.48
1:D:599:ARG:HH22	1:D:795:VAL:HG21	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:615:PRO:O	1:C:618:THR:HG22	2.14	0.48
5:C:8012:DMS:H13	6:C:4479:HOH:O	2.12	0.47
1:C:655:MET:HG2	1:C:665:SER:HB3	1.96	0.47
1:C:768:MET:HB3	1:C:775:GLN:HB2	1.96	0.47
1:D:225:PHE:HA	1:D:243:GLU:O	2.15	0.47
1:A:615:PRO:O	1:A:618:THR:HG22	2.14	0.47
1:A:494:THR:HA	5:A:8017:DMS:C2	2.45	0.47
1:B:959:ILE:HD12	1:B:984:LEU:HD13	1.96	0.47
1:A:88:SER:HA	1:A:366:VAL:HG21	1.96	0.47
1:C:619:GLU:HA	1:C:912:ALA:HB2	1.96	0.46
1:C:153:TRP:HB2	1:C:185:ALA:HB3	1.97	0.46
1:B:674:PRO:O	1:B:675:GLN:HB2	2.16	0.46
1:C:147:ASN:HA	1:C:148:SER:HA	1.69	0.46
5:D:8003:DMS:H13	6:D:4676:HOH:O	2.16	0.46
1:C:830:LEU:HD21	1:D:830:LEU:HD21	1.97	0.46
1:C:573:GLN:HB2	1:C:602:CYS:O	2.15	0.46
1:A:379:MET:HE1	1:A:387:VAL:HB	1.97	0.46
1:A:599:ARG:HH12	1:A:795:VAL:HG21	1.81	0.45
1:A:883:GLY:HA3	1:A:987:ASP:HA	1.99	0.45
1:B:499:ILE:HG22	1:B:501:PRO:HD3	1.98	0.45
1:A:598:ASP:OD1	1:A:797:GLU:HA	2.16	0.45
1:B:19:PRO:HD3	1:B:112:PRO:HB3	1.98	0.45
1:A:744:GLU:HG3	1:A:744:GLU:O	2.16	0.45
1:C:54:LEU:HD11	1:C:214:LEU:HG	1.99	0.45
1:C:844:HIS:HE1	6:C:4183:HOH:O	2.00	0.45
1:D:129:VAL:HG21	1:D:177:LEU:HD13	1.98	0.44
1:A:301:TRP:CH2	1:A:452:SER:HA	2.52	0.44
1:D:377:LEU:HD22	1:D:708:TRP:HA	1.99	0.44
1:B:126:THR:HA	1:B:182:ASN:O	2.17	0.44
1:B:890:GLN:HG3	1:B:891:VAL:N	2.31	0.44
1:D:568:TRP:CD2	1:D:569:ASP:HB3	2.52	0.44
1:B:147:ASN:HB3	1:B:206:SER:HA	1.98	0.44
1:B:573:GLN:HB2	1:B:602:CYS:O	2.17	0.44
1:C:854:LYS:HA	1:C:867:THR:O	2.18	0.44
1:D:143:PHE:O	1:D:168:PRO:HA	2.18	0.43
1:D:390:SER:HA	1:D:391:HIS:HA	1.77	0.43
1:B:361:PRO:HB2	1:B:576:ILE:HG12	1.99	0.43
1:C:390:SER:HA	1:C:391:HIS:HA	1.74	0.43
1:C:599:ARG:HH12	1:C:795:VAL:HG21	1.83	0.43
1:A:166:ARG:HG3	1:A:392:TYR:HB2	2.01	0.43
1:A:128:ASN:HA	1:A:180:GLY:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:SER:HA	1:A:391:HIS:HA	1.85	0.43
1:B:749:ILE:HB	1:B:756:TRP:HB2	2.00	0.43
1:B:944:LEU:O	1:B:950:GLN:HA	2.19	0.43
1:D:843:GLN:HA	1:D:847:LYS:O	2.18	0.43
1:D:521:LYS:HG2	1:D:559:TYR:CZ	2.54	0.43
1:D:782:ASP:OD1	1:D:842:TRP:HH2	2.02	0.43
1:A:361:PRO:HB3	1:A:609:ALA:HB1	2.02	0.42
1:C:127:PHE:CE1	1:C:184:LEU:HG	2.55	0.42
1:C:599:ARG:NH1	1:C:798:ALA:HA	2.35	0.42
1:D:19:PRO:HD3	1:D:112:PRO:HB3	2.01	0.42
1:A:931:PHE:HA	1:A:932:PRO:HD3	1.86	0.42
1:C:610:ASP:O	1:C:611:ARG:HB2	2.20	0.42
1:B:244:VAL:HG21	1:B:256:VAL:HG11	2.01	0.42
1:C:568:TRP:CD2	1:C:569:ASP:HB3	2.54	0.42
1:A:525:SER:O	1:B:561:ARG:HD3	2.20	0.42
1:C:525:SER:O	1:D:561:ARG:HD3	2.20	0.42
1:A:699:ARG:NH2	6:A:4595:HOH:O	2.53	0.42
1:A:147:ASN:HA	1:A:148:SER:HA	1.66	0.42
1:D:147:ASN:HB3	1:D:206:SER:HA	2.02	0.42
1:D:670:LEU:HA	1:D:670:LEU:HD23	1.86	0.42
1:B:650:GLU:HB3	1:B:670:LEU:HD12	2.01	0.41
1:C:361:PRO:HB2	1:C:576:ILE:HG12	2.02	0.41
1:C:305:ILE:HD11	1:C:645:ARG:HB3	2.01	0.41
1:A:595:THR:HA	1:A:596:PRO:C	2.40	0.41
1:B:658:LEU:O	1:B:661:LYS:HE3	2.20	0.41
1:A:105:TYR:CE1	1:A:199:ASP:HB2	2.55	0.41
1:A:225:PHE:HA	1:A:243:GLU:O	2.21	0.41
1:A:549:PHE:CE2	1:A:620:ALA:HA	2.55	0.41
1:A:542:MET:HA	1:A:604:ASN:HA	2.02	0.41
1:C:661:LYS:HA	1:C:662:PRO:HD3	1.93	0.41
1:A:737:ILE:HA	1:A:738:PRO:HD3	1.90	0.41
1:D:802:ASP:HA	1:D:803:PRO:HD2	1.97	0.41
1:C:143:PHE:O	1:C:168:PRO:HA	2.21	0.41
1:C:765:LEU:HD21	1:C:768:MET:CE	2.49	0.41
1:A:287:ASP:N	1:A:287:ASP:OD1	2.52	0.41
1:A:599:ARG:HH12	1:A:795:VAL:CG2	2.34	0.41
1:A:957:PHE:HA	1:A:985:ASN:O	2.21	0.41
1:B:814:GLY:HA3	1:B:844:HIS:CG	2.56	0.41
1:A:246:MET:CE	1:A:274:PHE:CE2	3.02	0.41
1:C:499:ILE:HG22	1:C:501:PRO:HD3	2.03	0.41
1:D:524:LEU:HD11	1:D:562:LEU:HG	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:653:HIS:HB2	6:A:4467:HOH:O	2.21	0.40
1:D:568:TRP:CZ2	2:D:2001:0MK:H3	2.56	0.40
1:D:127:PHE:HE1	1:D:184:LEU:HG	1.86	0.40
1:A:246:MET:HE2	1:A:274:PHE:CZ	2.56	0.40
1:B:200:GLN:HG2	1:B:391:HIS:HB2	2.04	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	1013/1052 (96%)	985 (97%)	28 (3%)	0	100	100
1	B	1013/1052 (96%)	974 (96%)	39 (4%)	0	100	100
1	C	1013/1052 (96%)	977 (96%)	36 (4%)	0	100	100
1	D	1013/1052 (96%)	976 (96%)	37 (4%)	0	100	100
All	All	4052/4208 (96%)	3912 (96%)	140 (4%)	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	868/898 (97%)	855 (98%)	13 (2%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	868/898 (97%)	856 (99%)	12 (1%)	67	81
1	C	868/898 (97%)	859 (99%)	9 (1%)	76	87
1	D	868/898 (97%)	859 (99%)	9 (1%)	76	87
All	All	3472/3592 (97%)	3429 (99%)	43 (1%)	71	84

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	ASP
1	A	254	LEU
1	A	333	ARG
1	A	344	LEU
1	A	394	ASN
1	A	519	SER
1	A	546	LEU
1	A	737	ILE
1	A	744	GLU
1	A	772	ASP
1	A	799	THR
1	A	885	ASN
1	A	956	GLN
1	B	80	GLU
1	B	296	GLU
1	B	333	ARG
1	B	344	LEU
1	B	394	ASN
1	B	535	LEU
1	B	546	LEU
1	B	737	ILE
1	B	750	GLU
1	B	774	LYS
1	B	850	PHE
1	B	956	GLN
1	C	135	GLN
1	C	213	SER
1	C	333	ARG
1	C	394	ASN
1	C	519	SER
1	C	546	LEU
1	C	672	VAL
1	C	750	GLU

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Mol	Chain	Res	Type
1	C	850	PHE
1	D	333	ARG
1	D	344	LEU
1	D	394	ASN
1	D	519	SER
1	D	546	LEU
1	D	672	VAL
1	D	755	ARG
1	D	773	LYS
1	D	891	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 96 ligands modelled in this entry, 22 are monoatomic - leaving 74 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	DMS	C	8008	-	3,3,3	2.63	1 (33%)	3,3,3	0.58	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	2.74	1 (33%)	3,3,3	0.58	0
5	DMS	A	8013	-	3,3,3	2.68	1 (33%)	3,3,3	0.82	0
5	DMS	D	8015	-	3,3,3	2.67	1 (33%)	3,3,3	0.58	0
5	DMS	C	8014	-	3,3,3	2.65	1 (33%)	3,3,3	0.54	0
5	DMS	A	8004	-	3,3,3	2.60	1 (33%)	3,3,3	0.47	0
2	0MK	D	2002	-	10,10,10	0.82	0	14,14,14	2.02	2 (14%)
5	DMS	D	8018	-	3,3,3	2.64	1 (33%)	3,3,3	0.50	0
5	DMS	B	8011	-	3,3,3	2.67	1 (33%)	3,3,3	0.66	0
5	DMS	D	8016	-	3,3,3	2.65	1 (33%)	3,3,3	0.36	0
5	DMS	C	8001	-	3,3,3	2.60	1 (33%)	3,3,3	0.90	0
5	DMS	B	8001	-	3,3,3	2.55	1 (33%)	3,3,3	0.70	0
5	DMS	B	8005	-	3,3,3	2.60	1 (33%)	3,3,3	0.47	0
5	DMS	A	8001	-	3,3,3	2.60	1 (33%)	3,3,3	1.08	0
5	DMS	C	8011	-	3,3,3	2.63	1 (33%)	3,3,3	0.60	0
2	0MK	B	2002	-	10,10,10	0.73	0	14,14,14	1.88	2 (14%)
5	DMS	A	8011	-	3,3,3	2.63	1 (33%)	3,3,3	0.57	0
5	DMS	C	8015	-	3,3,3	2.69	1 (33%)	3,3,3	0.68	0
5	DMS	B	8004	-	3,3,3	2.62	1 (33%)	3,3,3	0.52	0
5	DMS	A	8006	-	3,3,3	2.70	1 (33%)	3,3,3	0.71	0
5	DMS	D	8017	-	3,3,3	2.71	1 (33%)	3,3,3	0.74	0
2	0MK	B	2001	4	10,10,10	0.44	0	14,14,14	1.11	0
5	DMS	D	8014	-	3,3,3	2.64	1 (33%)	3,3,3	0.65	0
5	DMS	B	8007	-	3,3,3	2.58	1 (33%)	3,3,3	0.51	0
5	DMS	D	8003	-	3,3,3	2.66	1 (33%)	3,3,3	0.60	0
5	DMS	C	8010	-	3,3,3	2.54	1 (33%)	3,3,3	0.51	0
2	0MK	A	2002	-	10,10,10	0.76	0	14,14,14	2.00	3 (21%)
5	DMS	C	8013	-	3,3,3	2.68	1 (33%)	3,3,3	0.57	0
5	DMS	D	8008	-	3,3,3	2.70	1 (33%)	3,3,3	0.50	0
5	DMS	D	8011	-	3,3,3	2.66	1 (33%)	3,3,3	0.46	0
5	DMS	D	8004	-	3,3,3	2.51	1 (33%)	3,3,3	0.72	0
2	0MK	B	2003	-	10,10,10	0.80	0	14,14,14	1.47	2 (14%)
5	DMS	D	8012	-	3,3,3	2.69	1 (33%)	3,3,3	0.52	0
5	DMS	A	8008	-	3,3,3	2.65	1 (33%)	3,3,3	0.68	0
5	DMS	B	8013	-	3,3,3	2.66	1 (33%)	3,3,3	0.59	0
5	DMS	B	8009	-	3,3,3	2.69	1 (33%)	3,3,3	0.55	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	A	8016	-	3,3,3	2.62	1 (33%)	3,3,3	0.58	0
5	DMS	D	8009	-	3,3,3	2.62	1 (33%)	3,3,3	0.79	0
5	DMS	B	8008	-	3,3,3	2.63	1 (33%)	3,3,3	0.57	0
5	DMS	B	8010	-	3,3,3	2.65	1 (33%)	3,3,3	0.52	0
5	DMS	A	8010	-	3,3,3	2.65	1 (33%)	3,3,3	0.58	0
5	DMS	A	8014	-	3,3,3	2.64	1 (33%)	3,3,3	0.50	0
2	0MK	D	2001	4	10,10,10	0.52	0	14,14,14	0.95	1 (7%)
5	DMS	D	8006	-	3,3,3	2.52	1 (33%)	3,3,3	0.51	0
2	0MK	C	2002	-	10,10,10	0.75	0	14,14,14	1.89	2 (14%)
5	DMS	C	8007	-	3,3,3	2.62	1 (33%)	3,3,3	0.76	0
5	DMS	A	8017	-	3,3,3	2.54	1 (33%)	3,3,3	0.43	0
5	DMS	B	8002	-	3,3,3	2.57	1 (33%)	3,3,3	0.74	0
5	DMS	D	8005	-	3,3,3	2.54	1 (33%)	3,3,3	0.47	0
5	DMS	C	8012	-	3,3,3	2.45	1 (33%)	3,3,3	0.25	0
5	DMS	B	8012	-	3,3,3	2.65	1 (33%)	3,3,3	0.56	0
5	DMS	B	8006	-	3,3,3	2.61	1 (33%)	3,3,3	0.49	0
5	DMS	C	8005	-	3,3,3	2.37	1 (33%)	3,3,3	0.42	0
5	DMS	A	8012	-	3,3,3	2.67	1 (33%)	3,3,3	0.51	0
5	DMS	C	8002	-	3,3,3	2.57	1 (33%)	3,3,3	0.77	0
5	DMS	A	8018	-	3,3,3	2.62	1 (33%)	3,3,3	0.69	0
5	DMS	A	8002	-	3,3,3	2.57	1 (33%)	3,3,3	0.45	0
5	DMS	C	8006	-	3,3,3	2.72	1 (33%)	3,3,3	0.63	0
5	DMS	A	8015	-	3,3,3	2.63	1 (33%)	3,3,3	0.65	0
2	0MK	C	2001	4	10,10,10	0.60	0	14,14,14	0.98	1 (7%)
2	0MK	A	2001	4	10,10,10	0.44	0	14,14,14	1.03	0
5	DMS	D	8007	-	3,3,3	2.66	1 (33%)	3,3,3	0.76	0
5	DMS	D	8013	-	3,3,3	2.66	1 (33%)	3,3,3	0.67	0
5	DMS	B	8014	-	3,3,3	2.66	1 (33%)	3,3,3	0.58	0
5	DMS	D	8010	-	3,3,3	2.66	1 (33%)	3,3,3	0.56	0
5	DMS	C	8003	-	3,3,3	2.37	1 (33%)	3,3,3	0.42	0
5	DMS	C	8009	-	3,3,3	2.52	1 (33%)	3,3,3	0.45	0
5	DMS	D	8002	-	3,3,3	2.56	1 (33%)	3,3,3	0.71	0
5	DMS	C	8004	-	3,3,3	2.68	1 (33%)	3,3,3	0.57	0
5	DMS	A	8009	-	3,3,3	2.54	1 (33%)	3,3,3	0.27	0
5	DMS	D	8001	-	3,3,3	2.58	1 (33%)	3,3,3	1.00	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	A	8005	-	3,3,3	2.53	1 (33%)	3,3,3	0.61	0
5	DMS	B	8003	-	3,3,3	2.62	1 (33%)	3,3,3	0.59	0
5	DMS	A	8003	-	3,3,3	2.61	1 (33%)	3,3,3	0.44	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
2	0MK	D	2001	4	-	-	0/1/1/1
2	0MK	A	2002	-	-	-	0/1/1/1
2	0MK	C	2002	-	-	-	0/1/1/1
2	0MK	B	2003	-	-	-	0/1/1/1
2	0MK	B	2002	-	-	-	0/1/1/1
2	0MK	D	2002	-	-	-	0/1/1/1
2	0MK	C	2001	4	-	-	0/1/1/1
2	0MK	B	2001	4	-	-	0/1/1/1
2	0MK	A	2001	4	-	-	0/1/1/1

All (65) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	8007	DMS	O-S	4.57	1.81	1.50
5	C	8006	DMS	O-S	4.57	1.81	1.50
5	D	8017	DMS	O-S	4.54	1.80	1.50
5	B	8009	DMS	O-S	4.54	1.80	1.50
5	D	8008	DMS	O-S	4.53	1.80	1.50
5	A	8006	DMS	O-S	4.53	1.80	1.50
5	D	8012	DMS	O-S	4.52	1.80	1.50
5	C	8004	DMS	O-S	4.51	1.80	1.50
5	A	8012	DMS	O-S	4.49	1.80	1.50
5	C	8015	DMS	O-S	4.49	1.80	1.50
5	C	8013	DMS	O-S	4.48	1.80	1.50
5	B	8014	DMS	O-S	4.48	1.80	1.50
5	A	8013	DMS	O-S	4.48	1.80	1.50
5	D	8003	DMS	O-S	4.48	1.80	1.50
5	D	8015	DMS	O-S	4.47	1.80	1.50
5	D	8007	DMS	O-S	4.47	1.80	1.50
5	C	8014	DMS	O-S	4.47	1.80	1.50
5	B	8011	DMS	O-S	4.46	1.80	1.50
5	B	8013	DMS	O-S	4.46	1.80	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	8013	DMS	O-S	4.46	1.80	1.50
5	B	8010	DMS	O-S	4.46	1.80	1.50
5	D	8010	DMS	O-S	4.46	1.80	1.50
5	D	8011	DMS	O-S	4.45	1.80	1.50
5	D	8016	DMS	O-S	4.45	1.80	1.50
5	B	8012	DMS	O-S	4.43	1.80	1.50
5	A	8010	DMS	O-S	4.43	1.80	1.50
5	A	8008	DMS	O-S	4.43	1.80	1.50
5	D	8018	DMS	O-S	4.42	1.80	1.50
5	A	8014	DMS	O-S	4.41	1.80	1.50
5	D	8014	DMS	O-S	4.41	1.80	1.50
5	B	8003	DMS	O-S	4.41	1.80	1.50
5	B	8008	DMS	O-S	4.41	1.80	1.50
5	B	8004	DMS	O-S	4.40	1.80	1.50
5	C	8008	DMS	O-S	4.40	1.80	1.50
5	A	8011	DMS	O-S	4.40	1.80	1.50
5	A	8003	DMS	O-S	4.40	1.79	1.50
5	C	8011	DMS	O-S	4.40	1.79	1.50
5	A	8015	DMS	O-S	4.39	1.79	1.50
5	A	8016	DMS	O-S	4.39	1.79	1.50
5	A	8018	DMS	O-S	4.39	1.79	1.50
5	C	8007	DMS	O-S	4.39	1.79	1.50
5	D	8009	DMS	O-S	4.39	1.79	1.50
5	A	8004	DMS	O-S	4.38	1.79	1.50
5	A	8001	DMS	O-S	4.36	1.79	1.50
5	B	8006	DMS	O-S	4.35	1.79	1.50
5	B	8005	DMS	O-S	4.35	1.79	1.50
5	C	8001	DMS	O-S	4.35	1.79	1.50
5	D	8001	DMS	O-S	4.31	1.79	1.50
5	C	8002	DMS	O-S	4.31	1.79	1.50
5	B	8007	DMS	O-S	4.30	1.79	1.50
5	D	8002	DMS	O-S	4.29	1.79	1.50
5	B	8002	DMS	O-S	4.29	1.79	1.50
5	B	8001	DMS	O-S	4.28	1.79	1.50
5	A	8002	DMS	O-S	4.28	1.79	1.50
5	C	8010	DMS	O-S	4.26	1.79	1.50
5	A	8009	DMS	O-S	4.25	1.79	1.50
5	D	8006	DMS	O-S	4.24	1.78	1.50
5	D	8005	DMS	O-S	4.24	1.78	1.50
5	A	8017	DMS	O-S	4.23	1.78	1.50
5	A	8005	DMS	O-S	4.22	1.78	1.50
5	C	8009	DMS	O-S	4.22	1.78	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	8004	DMS	O-S	4.22	1.78	1.50
5	C	8012	DMS	O-S	4.14	1.78	1.50
5	C	8003	DMS	O-S	4.00	1.77	1.50
5	C	8005	DMS	O-S	4.00	1.77	1.50

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2002	0MK	C5-C4-C3	6.13	117.20	109.67
2	A	2002	0MK	C5-C4-C3	5.73	116.71	109.67
2	B	2002	0MK	C5-C4-C3	5.65	116.61	109.67
2	C	2002	0MK	C5-C4-C3	5.65	116.61	109.67
2	B	2003	0MK	C5-C4-C3	4.21	114.83	109.67
2	A	2002	0MK	C4-C3-C2	3.68	117.27	110.89
2	D	2002	0MK	C4-C3-C2	3.68	117.27	110.89
2	B	2002	0MK	C4-C3-C2	3.41	116.80	110.89
2	C	2002	0MK	C4-C3-C2	3.30	116.60	110.89
2	C	2001	0MK	C5-O5-C1	2.30	116.58	112.71
2	A	2002	0MK	C5-O5-C1	-2.15	109.09	112.71
2	D	2001	0MK	O5-C5-C4	-2.07	107.58	110.77
2	B	2003	0MK	C4-C3-C2	2.03	114.40	110.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2002	0MK	1	0
5	D	8003	DMS	1	0
2	A	2002	0MK	1	0
2	D	2001	0MK	2	0
2	C	2002	0MK	1	0
5	A	8017	DMS	1	0
5	C	8012	DMS	2	0
2	C	2001	0MK	1	0
2	A	2001	0MK	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	1015/1052 (96%)	-0.30	20 (1%) 65 71	18, 32, 60, 98	0
1	B	1015/1052 (96%)	-0.26	17 (1%) 70 76	19, 36, 64, 94	0
1	C	1015/1052 (96%)	-0.33	10 (0%) 82 86	16, 34, 60, 96	0
1	D	1015/1052 (96%)	-0.26	20 (1%) 65 71	17, 33, 61, 96	0
All	All	4060/4208 (96%)	-0.29	67 (1%) 70 76	16, 34, 61, 98	0

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	799	THR	6.5
1	A	732	ALA	6.2
1	A	735	HIS	5.7
1	B	11	LEU	5.7
1	A	800	ARG	5.3
1	A	685	LEU	5.2
1	D	735	HIS	5.2
1	D	799	THR	4.7
1	B	12	GLN	4.6
1	D	731	PRO	4.5
1	C	11	LEU	4.5
1	D	689	GLU	4.4
1	D	686	PRO	4.4
1	C	801	ILE	4.1
1	A	686	PRO	3.9
1	A	731	PRO	3.9
1	B	689	GLU	3.9
1	B	799	THR	3.8
1	C	799	THR	3.8
1	D	732	ALA	3.7
1	B	686	PRO	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	800	ARG	3.5
1	D	801	ILE	3.4
1	B	800	ARG	3.4
1	B	798	ALA	3.4
1	A	12	GLN	3.3
1	C	800	ARG	3.3
1	A	798	ALA	3.2
1	B	684	GLU	3.2
1	B	732	ALA	3.1
1	C	12	GLN	3.0
1	D	11	LEU	3.0
1	D	12	GLN	3.0
1	A	689	GLU	2.9
1	D	730	LEU	2.9
1	C	798	ALA	2.8
1	B	10	VAL	2.8
1	B	801	ILE	2.8
1	A	1023	LYS	2.8
1	A	11	LEU	2.7
1	B	733	ALA	2.7
1	A	795	VAL	2.7
1	B	79	PRO	2.7
1	B	731	PRO	2.7
1	C	730	LEU	2.7
1	D	796	SER	2.7
1	A	801	ILE	2.6
1	A	730	LEU	2.4
1	C	689	GLU	2.4
1	A	687	GLN	2.4
1	B	685	LEU	2.3
1	A	772	ASP	2.3
1	D	733	ALA	2.3
1	B	742	THR	2.2
1	C	684	GLU	2.1
1	D	736	ALA	2.1
1	D	687	GLN	2.1
1	A	729	THR	2.1
1	D	798	ALA	2.1
1	A	10	VAL	2.1
1	C	9	VAL	2.1
1	D	734	SER	2.1
1	B	687	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	663	LEU	2.0
1	A	846	GLY	2.0
1	D	582	GLY	2.0
1	D	770	ILE	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 monosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	0MK	A	2002	10/10	0.77	0.21	65,73,79,81	0
2	0MK	B	2002	10/10	0.80	0.26	80,86,90,90	0
5	DMS	C	8006	4/4	0.81	0.21	61,64,66,73	0
2	0MK	C	2002	10/10	0.81	0.28	64,71,77,79	0
2	0MK	D	2002	10/10	0.82	0.23	65,74,79,79	0
5	DMS	B	8009	4/4	0.83	0.25	78,80,80,82	0
5	DMS	A	8002	4/4	0.86	0.26	50,52,58,61	0
5	DMS	B	8006	4/4	0.86	0.37	71,74,75,78	0
5	DMS	A	8013	4/4	0.87	0.27	74,75,75,77	0
5	DMS	D	8012	4/4	0.87	0.18	53,60,64,64	0
5	DMS	D	8006	4/4	0.87	0.16	74,76,77,80	0
2	0MK	B	2003	10/10	0.87	0.15	67,70,74,77	0
5	DMS	C	8015	4/4	0.88	0.29	71,73,75,77	0
5	DMS	B	8004	4/4	0.88	0.22	59,61,64,65	0
5	DMS	D	8014	4/4	0.89	0.23	72,73,74,76	0
5	DMS	C	8007	4/4	0.89	0.22	69,71,72,74	0
5	DMS	C	8002	4/4	0.89	0.20	49,52,55,57	0
5	DMS	B	8014	4/4	0.89	0.23	65,66,69,70	0
5	DMS	A	8010	4/4	0.90	0.26	72,72,75,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	DMS	A	8015	4/4	0.90	0.21	67,67,70,70	0
5	DMS	B	8011	4/4	0.91	0.29	76,77,78,81	0
5	DMS	B	8010	4/4	0.91	0.25	66,69,69,70	0
5	DMS	C	8008	4/4	0.91	0.27	69,72,73,74	0
5	DMS	A	8018	4/4	0.92	0.25	63,67,67,68	0
5	DMS	C	8014	4/4	0.92	0.24	74,75,75,75	0
5	DMS	D	8002	4/4	0.92	0.25	56,58,59,60	0
5	DMS	B	8013	4/4	0.92	0.20	66,66,68,70	0
5	DMS	D	8009	4/4	0.92	0.22	59,60,60,63	0
5	DMS	A	8011	4/4	0.92	0.15	73,74,75,75	0
5	DMS	D	8017	4/4	0.92	0.27	65,66,68,69	0
5	DMS	A	8012	4/4	0.92	0.22	68,70,70,71	0
5	DMS	D	8004	4/4	0.93	0.22	63,64,65,67	0
5	DMS	A	8004	4/4	0.93	0.14	62,65,66,66	0
5	DMS	A	8008	4/4	0.93	0.35	70,70,70,71	0
4	NA	B	3104	1/1	0.93	0.18	50,50,50,50	0
5	DMS	D	8013	4/4	0.93	0.14	65,65,66,69	0
5	DMS	B	8012	4/4	0.93	0.22	73,74,75,76	0
5	DMS	C	8009	4/4	0.93	0.20	57,58,60,61	0
5	DMS	C	8004	4/4	0.93	0.19	74,74,75,75	0
5	DMS	A	8016	4/4	0.94	0.23	74,74,74,75	0
5	DMS	A	8014	4/4	0.94	0.16	71,72,72,73	0
5	DMS	B	8007	4/4	0.94	0.15	53,56,57,59	0
5	DMS	C	8012	4/4	0.94	0.22	73,74,74,76	0
5	DMS	C	8011	4/4	0.94	0.20	64,66,66,68	0
5	DMS	C	8013	4/4	0.94	0.15	78,78,78,80	0
4	NA	C	3104	1/1	0.94	0.15	51,51,51,51	0
5	DMS	A	8007	4/4	0.94	0.19	44,46,49,51	0
5	DMS	B	8002	4/4	0.95	0.20	47,49,53,55	0
3	MG	B	3002	1/1	0.95	0.11	34,34,34,34	0
4	NA	B	3101	1/1	0.95	0.09	32,32,32,32	0
5	DMS	C	8001	4/4	0.95	0.25	50,53,53,54	0
5	DMS	A	8017	4/4	0.95	0.23	67,67,67,70	0
5	DMS	D	8001	4/4	0.95	0.21	40,40,42,43	0
5	DMS	D	8005	4/4	0.95	0.19	53,53,58,59	0
4	NA	C	3101	1/1	0.95	0.11	30,30,30,30	0
4	NA	C	3103	1/1	0.95	0.35	42,42,42,42	0
5	DMS	D	8007	4/4	0.95	0.18	50,53,54,58	0
4	NA	D	3103	1/1	0.95	0.12	46,46,46,46	0
3	MG	D	3002	1/1	0.96	0.15	34,34,34,34	0
5	DMS	A	8009	4/4	0.96	0.24	48,54,57,58	0
3	MG	A	3002	1/1	0.96	0.06	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	C	3002	1/1	0.96	0.12	39,39,39,39	0
4	NA	A	3101	1/1	0.96	0.06	28,28,28,28	0
5	DMS	D	8015	4/4	0.96	0.24	59,61,62,62	0
5	DMS	D	8003	4/4	0.96	0.20	52,53,56,58	0
5	DMS	B	8003	4/4	0.96	0.19	50,51,54,55	0
4	NA	A	3102	1/1	0.96	0.10	26,26,26,26	0
5	DMS	A	8005	4/4	0.96	0.21	53,55,56,59	0
5	DMS	D	8011	4/4	0.96	0.27	66,68,70,72	0
5	DMS	A	8006	4/4	0.97	0.13	51,51,52,54	0
5	DMS	D	8016	4/4	0.97	0.20	60,63,64,64	0
5	DMS	B	8008	4/4	0.97	0.16	56,58,59,63	0
4	NA	A	3103	1/1	0.97	0.11	45,45,45,45	0
5	DMS	D	8008	4/4	0.97	0.22	56,56,58,60	0
5	DMS	C	8010	4/4	0.97	0.18	41,49,50,51	0
5	DMS	D	8010	4/4	0.97	0.15	60,60,62,62	0
4	NA	D	3102	1/1	0.97	0.09	30,30,30,30	0
4	NA	C	3102	1/1	0.97	0.12	27,27,27,27	0
3	MG	B	3001	1/1	0.97	0.09	29,29,29,29	0
2	0MK	C	2001	10/10	0.98	0.10	24,25,28,31	0
2	0MK	D	2001	10/10	0.98	0.10	22,25,28,29	0
4	NA	B	3103	1/1	0.98	0.10	49,49,49,49	0
5	DMS	A	8003	4/4	0.98	0.14	51,54,55,55	0
5	DMS	D	8018	4/4	0.98	0.12	52,52,53,54	0
5	DMS	B	8005	4/4	0.98	0.18	59,61,62,63	0
3	MG	D	3001	1/1	0.98	0.06	29,29,29,29	0
5	DMS	A	8001	4/4	0.98	0.18	37,38,38,39	0
2	0MK	B	2001	10/10	0.98	0.11	20,24,28,29	0
5	DMS	C	8005	4/4	0.98	0.17	47,49,51,52	0
5	DMS	C	8003	4/4	0.98	0.14	52,55,56,56	0
5	DMS	B	8001	4/4	0.98	0.22	45,47,48,49	0
4	NA	B	3102	1/1	0.98	0.10	27,27,27,27	0
2	0MK	A	2001	10/10	0.99	0.10	19,20,26,28	0
3	MG	C	3001	1/1	0.99	0.09	29,29,29,29	0
4	NA	D	3101	1/1	0.99	0.10	26,26,26,26	0
3	MG	A	3001	1/1	0.99	0.10	27,27,27,27	0

6.5 Other polymers

There are no such residues in this entry.