



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 07:19 AM GMT

PDB ID : 3VD7
Title : E. coli (lacZ) beta-galactosidase (N460S) in complex with galactotetrazole
Authors : Wheatley, R.W.; Kappelhoff, J.C.; Hahn, J.N.; Dugdale, M.L.; Dutkoski, M.J.;
Tamman, S.D.; Fraser, M.E.; Huber, R.E.
Deposited on : 2012-01-04
Resolution : 2.87 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

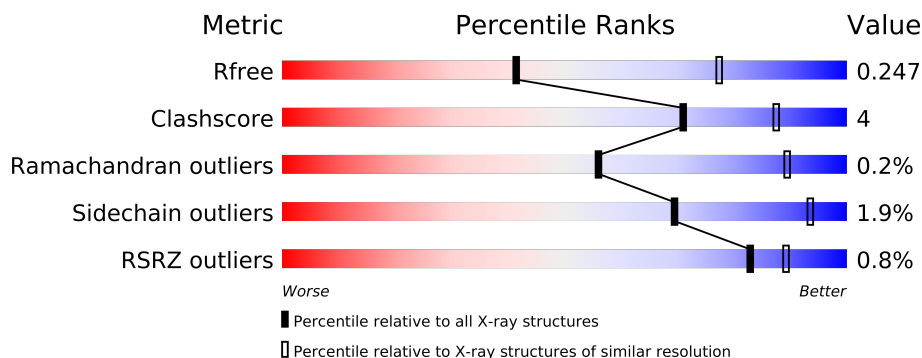
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.87 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}	66092	1360 (2.90-2.86)
Clashscore	79885	1696 (2.90-2.86)
Ramachandran outliers	78287	1647 (2.90-2.86)
Sidechain outliers	78261	1650 (2.90-2.86)
RSRZ outliers	66119	1362 (2.90-2.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1052	
1	B	1052	
1	C	1052	
1	D	1052	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	GTZ	A	2001	-	X
2	GTZ	B	2001	-	X
2	GTZ	D	2001	-	X
5	DMS	A	8002	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Geometry	Electron density
5	DMS	A	8003	-	X
5	DMS	A	8004	-	X
5	DMS	A	8005	-	X
5	DMS	A	8006	-	X
5	DMS	B	8001	-	X
5	DMS	B	8003	-	X
5	DMS	B	8005	-	X
5	DMS	B	8008	-	X
5	DMS	C	8002	-	X
5	DMS	C	8006	-	X
5	DMS	D	8002	-	X
5	DMS	D	8006	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 33041 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Beta-galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1011	Total	C	N	O	S	0	0	0
			8124	5137	1439	1510	38			
1	B	1011	Total	C	N	O	S	0	0	0
			8124	5137	1439	1510	38			
1	C	1011	Total	C	N	O	S	0	0	0
			8124	5137	1439	1510	38			
1	D	1011	Total	C	N	O	S	0	0	0
			8124	5137	1439	1510	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

Continued on next page...

Continued from previous page...

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	-	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

Continued on next page...

Continued from previous page...

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	-	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

Continued on next page...

Continued from previous page...

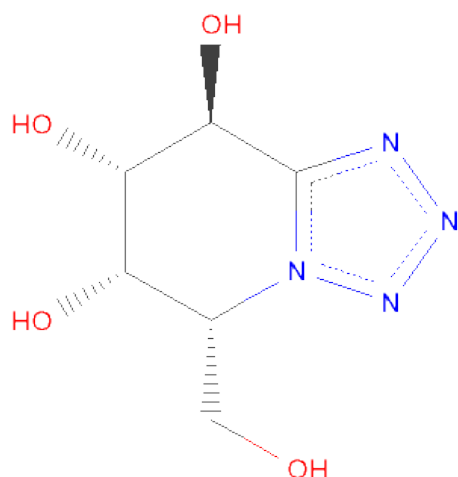
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ASP	-	EXPRESSION TAG	UNP P00722
C	2	LYS	-	EXPRESSION TAG	UNP P00722
C	3	ASP	-	EXPRESSION TAG	UNP P00722
C	4	PRO	-	EXPRESSION TAG	UNP P00722
C	5	MET	-	EXPRESSION TAG	UNP P00722
C	6	ILE	-	EXPRESSION TAG	UNP P00722
C	7	ASP	-	EXPRESSION TAG	UNP P00722
C	8	PRO	-	EXPRESSION TAG	UNP P00722
C	460	SER	ASN	ENGINEERED MUTATION	UNP P00722
D	-28	MET	-	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

Continued on next page...

Continued from previous page...

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 (5R, 6S, 7S, 8S)-5-HYDROXYMETHYL-6,7,8-TRIHYDROXY-TETRAZOL O[1,5-A]PIPERIDINE (three-letter code: GTZ) (formula: C₆H₁₀N₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	6	4	4		
2	B	1	Total	C	N	O	0	0
			14	6	4	4		
2	C	1	Total	C	N	O	0	0
			14	6	4	4		
2	D	1	Total	C	N	O	0	0
			14	6	4	4		

- 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	1	Total	Mg	0	0
			1	1		

Continued on next page...

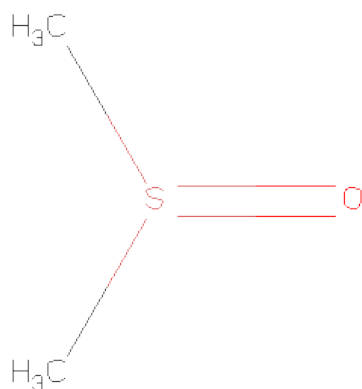
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	Mg	0	0
			1	1		
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	2	Total	Na	0	0
			2	2		
4	A	2	Total	Na	0	0
			2	2		
4	D	2	Total	Na	0	0
			2	2		
4	C	2	Total	Na	0	0
			2	2		

- 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		
5	A	1	Total	C	O	S	0	0
			4	2	1	1		
5	A	1	Total	C	O	S	0	0
			4	2	1	1		

Continued on next page...

Continued from previous page...

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	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	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

Continued on next page...

Continued from previous page...

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

- Molecule 6 is water.

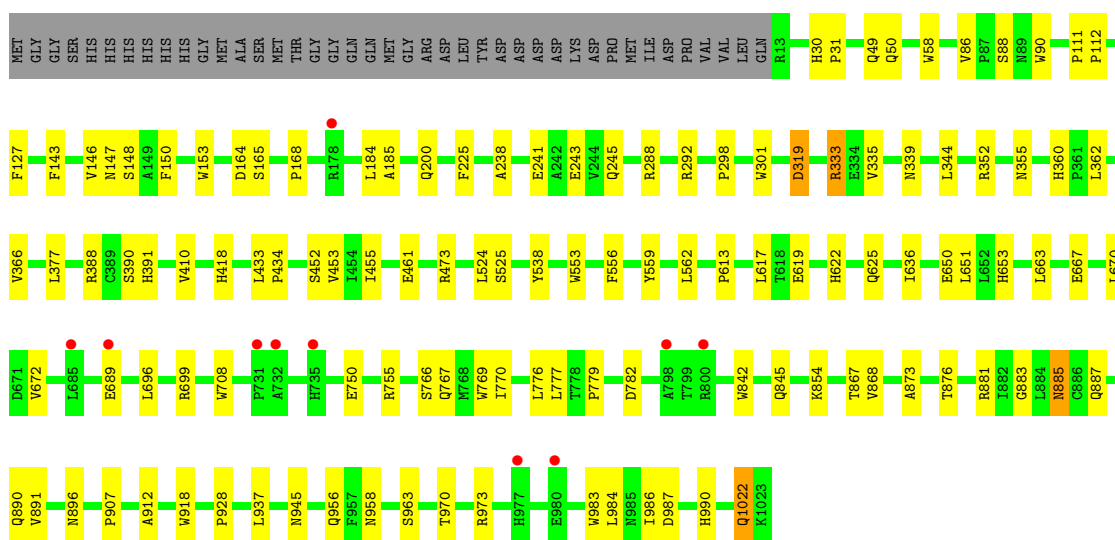
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	64	Total 64	O 64	0	0
6	B	93	Total 93	O 93	0	0
6	C	79	Total 79	O 79	0	0
6	D	123	Total 123	O 123	0	0

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.

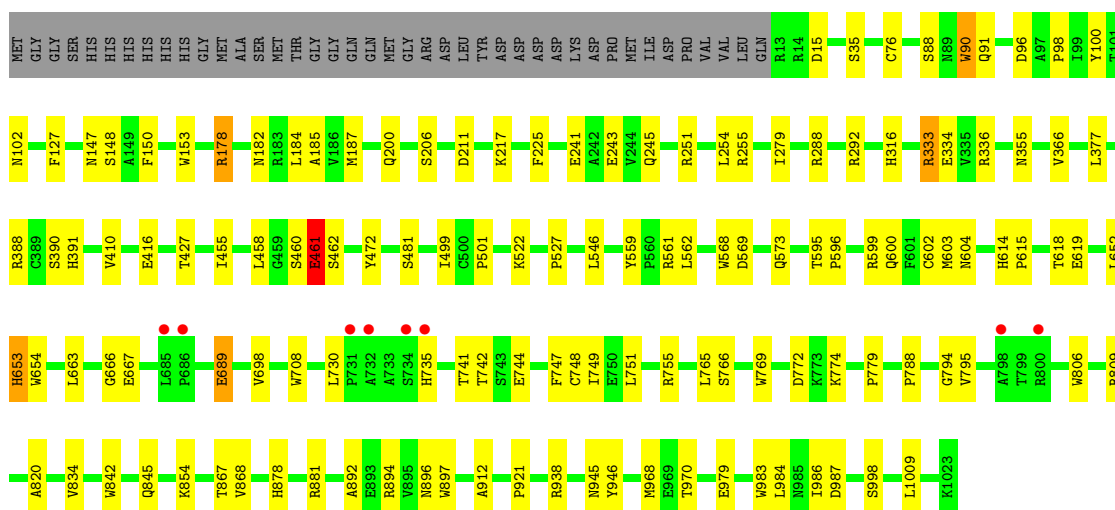
- Molecule 1: Beta-galactosidase

Chain A: 

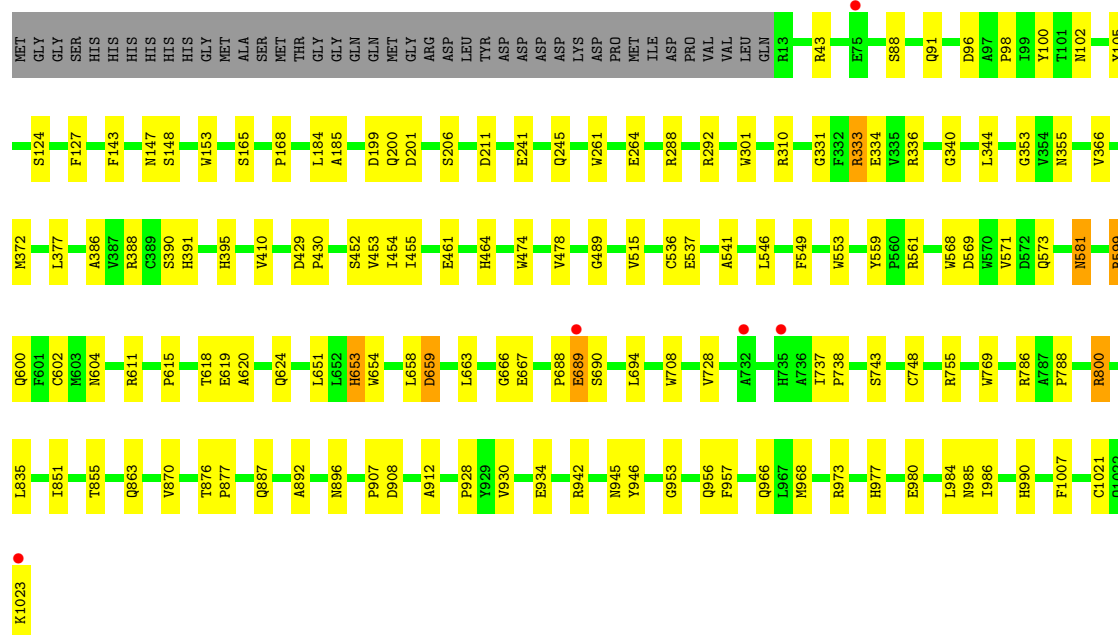


- Molecule 1: Beta-galactosidase

Chain B: 



- Molecule 1: Beta-galactosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	128.46Å 152.37Å 135.11Å 90.00° 104.25° 90.00°	Depositor
Resolution (Å)	44.78 – 2.87 44.78 – 2.87	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.78-2.87) 93.2 (44.78-2.87)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.188 , 0.250 0.188 , 0.247	Depositor DCC
R_{free} test set	4895 reflections (4.78%)	DCC
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 1.4	EDS
Estimated twinning fraction	0.008 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 107299 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	33041	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.49% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.42	0/8366	0.56	0/11412
1	B	0.44	0/8366	0.57	0/11412
1	C	0.44	0/8366	0.58	0/11412
1	D	0.44	0/8366	0.56	0/11412
All	All	0.43	0/33464	0.57	0/45648

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8124	0	7715	70	0
1	B	8124	0	7715	70	0
1	C	8124	0	7715	72	0
1	D	8124	0	7715	77	0
2	A	14	0	9	0	0
2	B	14	0	9	0	0
2	C	14	0	9	0	0
2	D	14	0	9	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
4	C	2	0	0	0	0
4	D	2	0	0	0	0
5	A	24	0	36	0	0
5	B	32	0	48	0	0
5	C	32	0	48	0	0
5	D	28	0	42	2	0
6	A	64	0	0	1	0
6	B	93	0	0	1	0
6	C	79	0	0	2	0
6	D	123	0	0	0	0
All	All	33041	0	31070	284	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 4.

All (284) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:88:SER:HA	1:A:366:VAL:HG21	1.49	0.95
1:D:800:ARG:HG3	1:D:800:ARG:O	1.71	0.91
1:D:653:HIS:CD2	1:D:667:GLU:HG3	2.07	0.90
1:C:372:MET:HE1	1:C:395:HIS:HB3	1.58	0.85
1:C:750:GLU:HG2	1:C:755:ARG:HG2	1.57	0.84
1:B:200:GLN:HG2	1:B:391:HIS:HB2	1.61	0.81
1:D:654:TRP:NE1	1:D:666:GLY:HA3	1.97	0.80
1:C:38:ASN:HB3	1:C:41:GLU:HG3	1.63	0.78
1:A:890:GLN:HG3	1:A:891:VAL:N	2.00	0.75
1:C:142:ILE:HG12	1:C:170:GLU:HG2	1.67	0.74
1:D:653:HIS:NE2	1:D:667:GLU:HG3	2.03	0.72
1:D:619:GLU:HA	1:D:912:ALA:HB2	1.71	0.72
1:D:755:ARG:HB2	1:D:769:TRP:HB2	1.73	0.70
1:A:770:ILE:HD11	1:A:1022:GLN:HG2	1.72	0.70
1:C:88:SER:HA	1:C:366:VAL:HG21	1.74	0.69
1:B:91:GLN:HG3	1:B:96:ASP:OD1	1.95	0.67
1:B:410:VAL:HG22	1:B:455:ILE:HB	1.77	0.66
1:D:689:GLU:CD	1:D:689:GLU:H	1.99	0.66
1:D:245:GLN:HG2	1:D:288:ARG:HG2	1.78	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:541:ALA:HB3	1:D:604:ASN:O	1.97	0.65
1:A:928:PRO:HB2	1:A:973:ARG:HH11	1.63	0.64
1:B:390:SER:HB2	1:B:391:HIS:CE1	2.33	0.64
1:B:806:TRP:HA	1:B:809:ARG:HD2	1.80	0.64
1:D:887:GLN:NE2	1:D:980:GLU:O	2.30	0.63
1:A:153:TRP:HB2	1:A:185:ALA:HB3	1.82	0.62
1:D:153:TRP:HB2	1:D:185:ALA:HB3	1.82	0.62
1:A:524:LEU:HD11	1:A:562:LEU:HG	1.83	0.61
1:B:245:GLN:HG2	1:B:288:ARG:HG2	1.81	0.61
1:D:91:GLN:HB3	1:D:98:PRO:HD3	1.83	0.61
1:B:766:SER:HA	1:B:779:PRO:HB3	1.83	0.61
1:A:963:SER:HB3	1:A:983:TRP:CE2	2.35	0.61
1:D:91:GLN:HG3	1:D:96:ASP:OD1	2.00	0.60
1:C:147:ASN:HA	1:C:165:SER:HB3	1.83	0.60
1:C:144:ASP:HA	1:C:168:PRO:HB3	1.84	0.60
1:B:788:PRO:HD2	1:B:968:MET:HG3	1.83	0.60
1:C:613:PRO:HB3	1:C:617:LEU:HD23	1.84	0.59
1:A:49:GLN:HB2	1:A:50:GLN:OE1	2.02	0.59
1:A:755:ARG:HB2	1:A:769:TRP:HB2	1.85	0.59
1:C:794:GLY:HA2	1:C:998:SER:O	2.02	0.59
1:D:88:SER:HA	1:D:366:VAL:HG21	1.84	0.58
1:C:200:GLN:HG2	1:C:391:HIS:HB2	1.84	0.58
1:B:854:LYS:HG2	1:B:868:VAL:HG22	1.86	0.58
1:A:766:SER:HA	1:A:779:PRO:HB3	1.86	0.57
1:C:377:LEU:HD22	1:C:708:TRP:HA	1.84	0.57
1:B:355:ASN:OD1	1:B:388:ARG:HD3	2.05	0.57
1:C:806:TRP:HA	1:C:809:ARG:HD2	1.87	0.57
1:B:689:GLU:CD	1:B:689:GLU:H	2.08	0.57
1:D:573:GLN:HB2	1:D:602:CYS:O	2.04	0.56
1:C:622:HIS:O	1:C:625:GLN:HG3	2.04	0.56
1:D:896:ASN:HB3	1:D:945:ASN:HB2	1.88	0.56
1:A:984:LEU:HD21	1:A:986:ILE:HD11	1.87	0.56
1:D:800:ARG:CG	1:D:800:ARG:O	2.49	0.56
1:B:127:PHE:HE2	1:B:184:LEU:HG	1.70	0.55
1:B:599:ARG:HB2	1:B:600:GLN:OE1	2.07	0.55
1:A:377:LEU:HD22	1:A:708:TRP:HA	1.87	0.55
1:A:147:ASN:HA	1:A:165:SER:HB3	1.88	0.55
1:A:245:GLN:HG2	1:A:288:ARG:HG2	1.88	0.55
1:A:854:LYS:HG2	1:A:868:VAL:HG22	1.88	0.54
1:B:600:GLN:HB2	1:B:603:MET:HE2	1.89	0.54
1:B:127:PHE:CE2	1:B:184:LEU:HG	2.42	0.54
1:D:200:GLN:HG2	1:D:391:HIS:HB2	1.89	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:896:ASN:HB3	1:A:945:ASN:HB2	1.90	0.54
1:A:885:ASN:C	1:A:885:ASN:OD1	2.45	0.54
1:A:319:ASP:N	1:A:319:ASP:OD1	2.39	0.54
1:C:696:LEU:HB2	1:C:722:LEU:HD11	1.89	0.54
1:C:1011:ALA:HB3	1:C:1014:TYR:CZ	2.43	0.54
1:D:377:LEU:HD22	1:D:708:TRP:HA	1.89	0.54
1:A:767:GLN:HA	1:A:776:LEU:HD12	1.90	0.53
1:C:984:LEU:HD21	1:C:986:ILE:HD11	1.90	0.53
1:C:369:GLU:O	1:C:373:VAL:HG23	2.09	0.53
1:C:334:GLU:OE1	1:C:336:ARG:NH1	2.41	0.53
1:C:241:GLU:HG2	1:C:292:ARG:HG2	1.91	0.53
1:C:153:TRP:HB2	1:C:185:ALA:HB3	1.91	0.53
1:C:433:LEU:HB3	1:C:434:PRO:HD3	1.90	0.52
1:D:930:VAL:HA	1:D:973:ARG:HD3	1.90	0.52
1:C:522:LYS:HA	1:D:559:TYR:CE2	2.44	0.52
1:C:788:PRO:HD2	1:C:968:MET:HG3	1.91	0.52
1:B:377:LEU:CD2	1:B:708:TRP:HA	2.39	0.52
1:B:147:ASN:HB3	1:B:206:SER:HA	1.91	0.52
1:B:499:ILE:HG22	1:B:501:PRO:HD3	1.92	0.52
1:D:863:GLN:HG2	1:D:1021:CYS:HB3	1.91	0.52
1:A:352:ARG:HG2	1:A:553:TRP:CH2	2.44	0.52
1:B:88:SER:HA	1:B:366:VAL:HG21	1.92	0.52
1:D:331:GLY:O	5:D:8001:DMS:H11	2.10	0.51
1:B:854:LYS:HA	1:B:867:THR:O	2.10	0.51
1:C:355:ASN:OD1	1:C:388:ARG:HD3	2.10	0.51
1:C:610:ASP:O	1:C:611:ARG:HB2	2.11	0.51
1:D:907:PRO:HG2	1:D:990:HIS:O	2.10	0.51
1:C:382:ASN:ND2	1:C:617:LEU:HD21	2.25	0.51
1:A:245:GLN:HG2	1:A:288:ARG:CG	2.41	0.51
1:B:153:TRP:HB2	1:B:185:ALA:HB3	1.92	0.51
1:A:782:ASP:HB2	1:A:842:TRP:CZ2	2.45	0.51
1:D:355:ASN:OD1	1:D:388:ARG:HD3	2.11	0.51
1:B:100:TYR:CZ	1:B:602:CYS:HB3	2.46	0.50
1:D:942:ARG:HA	1:D:953:GLY:O	2.11	0.50
1:D:654:TRP:HE1	1:D:666:GLY:HA3	1.76	0.50
1:B:573:GLN:HB2	1:B:602:CYS:O	2.10	0.50
1:B:652:LEU:HD11	1:B:698:VAL:HB	1.93	0.50
1:C:766:SER:HA	1:C:779:PRO:HB3	1.92	0.50
1:A:143:PHE:O	1:A:168:PRO:HA	2.12	0.50
1:C:353:GLY:HA2	1:C:386:ALA:O	2.11	0.50
1:D:581:ASN:OD1	1:D:581:ASN:N	2.43	0.50
1:C:49:GLN:HB2	1:C:50:GLN:OE1	2.12	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:873:ALA:O	1:A:876:THR:HG22	2.12	0.50
1:C:896:ASN:HB3	1:C:945:ASN:HB2	1.94	0.50
1:D:454:ILE:HG13	1:D:455:ILE:HG13	1.94	0.49
1:C:60:PHE:HA	1:C:122:CYS:O	2.13	0.49
1:A:88:SER:HA	1:A:366:VAL:CG2	2.32	0.49
1:A:883:GLY:HA3	1:A:987:ASP:HA	1.93	0.49
1:D:331:GLY:O	5:D:8001:DMS:C1	2.60	0.49
1:D:147:ASN:HA	1:D:165:SER:HB3	1.95	0.49
1:A:360:HIS:HE1	1:A:362:LEU:HD12	1.77	0.49
1:D:147:ASN:HA	1:D:148:SER:HA	1.62	0.48
1:D:536:CYS:O	1:D:537:GLU:HG3	2.13	0.48
1:B:892:ALA:HB3	1:B:946:TYR:CE1	2.48	0.48
1:D:372:MET:HE1	1:D:395:HIS:HB3	1.96	0.48
1:D:908:ASP:HB3	1:D:1007:PHE:CD1	2.48	0.48
1:A:525:SER:O	1:B:561:ARG:HD3	2.13	0.48
1:B:897:TRP:CZ2	1:B:938:ARG:HG2	2.49	0.48
1:C:887:GLN:NE2	1:C:980:GLU:O	2.46	0.48
1:C:619:GLU:HA	1:C:912:ALA:HB2	1.95	0.48
1:D:474:TRP:CZ2	1:D:478:VAL:HG21	2.48	0.48
1:B:794:GLY:HA2	1:B:998:SER:O	2.14	0.48
1:D:143:PHE:O	1:D:168:PRO:HA	2.13	0.48
1:C:780:LEU:HA	1:C:886:CYS:HB3	1.95	0.48
1:B:427:THR:HG21	1:B:462:SER:HB3	1.95	0.48
1:A:127:PHE:CE2	1:A:184:LEU:HG	2.48	0.47
1:A:241:GLU:HG2	1:A:292:ARG:HG2	1.95	0.47
1:C:854:LYS:HA	1:C:867:THR:O	2.13	0.47
1:D:892:ALA:HB3	1:D:946:TYR:CE1	2.49	0.47
1:D:654:TRP:CE2	1:D:666:GLY:HA3	2.49	0.47
1:B:878:HIS:HB3	1:B:1009:LEU:O	2.14	0.47
1:C:100:TYR:CE1	1:C:602:CYS:HB3	2.49	0.47
1:B:894:ARG:NH1	1:B:921:PRO:HD3	2.30	0.47
1:D:334:GLU:OE1	1:D:336:ARG:NH1	2.45	0.47
1:C:746:ASP:OD2	1:C:757:GLN:NE2	2.48	0.47
1:D:615:PRO:O	1:D:618:THR:HG22	2.13	0.47
1:D:549:PHE:CE2	1:D:620:ALA:HA	2.50	0.47
1:C:143:PHE:O	1:C:168:PRO:HA	2.14	0.47
1:C:571:VAL:HG21	1:C:611:ARG:NH1	2.30	0.47
1:C:146:VAL:HG11	1:C:150:PHE:CD2	2.50	0.47
1:C:789:LEU:HG	1:C:792:ASP:OD2	2.15	0.46
1:A:619:GLU:HA	1:A:912:ALA:HB2	1.98	0.46
1:C:965:GLN:HA	1:C:968:MET:HE3	1.96	0.46
1:D:651:LEU:HD12	1:D:651:LEU:O	2.14	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:1022:GLN:HB2	6:C:4018:HOH:O	2.15	0.46
1:C:55:ASN:ND2	1:C:87:PRO:HD3	2.29	0.46
1:B:241:GLU:HG2	1:B:292:ARG:HG2	1.96	0.46
1:A:30:HIS:ND1	1:A:31:PRO:O	2.32	0.46
1:D:788:PRO:HD2	1:D:968:MET:HG3	1.98	0.46
1:D:43:ARG:HH12	1:D:264:GLU:HG2	1.81	0.46
1:D:261:TRP:HB2	1:D:310:ARG:HB3	1.97	0.46
1:A:937:LEU:HD11	1:A:956:GLN:HB2	1.98	0.46
1:C:127:PHE:CE2	1:C:184:LEU:HG	2.51	0.46
1:B:91:GLN:HB3	1:B:98:PRO:HD3	1.97	0.46
1:A:928:PRO:HB2	1:A:973:ARG:NH1	2.29	0.46
1:C:730:LEU:H	1:C:730:LEU:HD12	1.81	0.46
1:D:241:GLU:HG2	1:D:292:ARG:HG2	1.97	0.46
1:B:654:TRP:CE2	1:B:666:GLY:HA3	2.51	0.46
1:A:127:PHE:HE2	1:A:184:LEU:HG	1.81	0.45
1:D:957:PHE:HA	1:D:985:ASN:O	2.16	0.45
1:B:416:GLU:HG3	1:B:460:SER:O	2.16	0.45
1:A:750:GLU:HG3	1:A:755:ARG:HG2	1.98	0.45
1:C:652:LEU:HD11	1:C:698:VAL:HB	1.98	0.45
1:D:301:TRP:CH2	1:D:452:SER:HA	2.52	0.45
1:A:390:SER:HA	1:A:391:HIS:HA	1.75	0.45
1:A:146:VAL:HG11	1:A:150:PHE:CD2	2.51	0.45
1:A:651:LEU:HD13	1:A:667:GLU:HG2	1.99	0.45
1:B:979:GLU:OE1	1:B:983:TRP:NE1	2.44	0.45
1:B:147:ASN:O	1:B:206:SER:HB2	2.17	0.44
1:B:615:PRO:O	1:B:618:THR:HG22	2.17	0.44
1:A:355:ASN:OD1	1:A:388:ARG:HD3	2.16	0.44
1:B:984:LEU:HD21	1:B:986:ILE:HD11	1.99	0.44
1:D:127:PHE:CE2	1:D:184:LEU:HG	2.52	0.44
1:A:301:TRP:CH2	1:A:452:SER:HA	2.53	0.44
1:B:742:THR:HG23	1:B:747:PHE:HE2	1.82	0.44
1:A:559:TYR:CE2	1:B:522:LYS:HA	2.53	0.44
1:D:390:SER:HA	1:D:391:HIS:HA	1.70	0.44
1:A:770:ILE:CD1	1:A:1022:GLN:HG2	2.46	0.44
1:D:928:PRO:HB2	1:D:973:ARG:HH11	1.83	0.44
1:C:718:GLN:HG3	1:C:719:GLN:N	2.32	0.44
1:C:1004:SER:OG	1:C:1006:GLU:OE2	2.34	0.44
1:A:148:SER:HA	1:A:165:SER:HB3	1.99	0.44
1:D:464:HIS:HB2	1:D:489:GLY:HA3	1.99	0.44
1:A:650:GLU:HB3	1:A:670:LEU:HD12	2.00	0.44
1:B:559:TYR:HB2	1:B:562:LEU:HD12	2.00	0.44
1:A:335:VAL:HG22	1:A:344:LEU:HD12	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:613:PRO:HB3	1:C:617:LEU:CD2	2.48	0.43
1:A:238:ALA:HB2	1:A:298:PRO:HG3	1.99	0.43
1:C:583:ASN:HA	1:C:584:PRO:HD3	1.77	0.43
1:B:741:THR:HB	1:B:748:CYS:HB3	1.99	0.43
1:C:907:PRO:HA	1:C:910:LEU:HD23	2.00	0.43
1:C:651:LEU:HD13	1:C:667:GLU:HG2	2.00	0.43
1:B:896:ASN:HB3	1:B:945:ASN:HB2	2.01	0.43
1:C:568:TRP:HA	1:C:569:ASP:HA	1.76	0.43
1:A:653:HIS:HB3	1:A:699:ARG:HG3	2.00	0.43
1:C:245:GLN:HG2	1:C:288:ARG:HG2	2.00	0.43
1:C:142:ILE:HG12	1:C:170:GLU:CG	2.43	0.43
1:B:769:TRP:HE1	1:B:774:LYS:HG2	1.83	0.43
1:A:622:HIS:ND1	1:A:625:GLN:OE1	2.51	0.43
1:C:147:ASN:HA	1:C:148:SER:HA	1.63	0.43
1:B:755:ARG:HB2	1:B:769:TRP:HB2	2.01	0.43
1:C:200:GLN:CG	1:C:391:HIS:HB2	2.49	0.43
1:A:854:LYS:HA	1:A:867:THR:O	2.19	0.43
1:B:416:GLU:OE1	1:B:460:SER:HB3	2.19	0.43
1:C:257:THR:HA	1:C:270:GLY:O	2.19	0.43
1:A:410:VAL:HG22	1:A:455:ILE:HB	2.00	0.43
1:A:339:ASN:O	1:B:527:PRO:HB3	2.18	0.43
1:D:688:PRO:HG3	1:D:694:LEU:HD21	2.01	0.43
1:D:553:TRP:CZ2	1:D:624:GLN:HG2	2.54	0.43
1:D:124:SER:HA	1:D:184:LEU:O	2.19	0.43
1:A:907:PRO:HG2	1:A:990:HIS:O	2.19	0.43
1:C:427:THR:HG21	1:C:462:SER:HB3	1.99	0.43
1:D:353:GLY:HA2	1:D:386:ALA:O	2.18	0.43
1:D:658:LEU:O	1:D:659:ASP:C	2.57	0.43
1:A:636:ILE:HD11	1:A:696:LEU:HD21	2.00	0.42
1:D:966:GLN:OE1	1:D:977:HIS:HD2	2.02	0.42
1:D:102:ASN:HA	1:D:201:ASP:OD1	2.19	0.42
1:A:559:TYR:HB2	1:A:562:LEU:HD12	2.00	0.42
1:C:302:SER:HB3	6:C:4026:HOH:O	2.18	0.42
1:B:460:SER:O	1:B:461:GLU:C	2.58	0.42
1:D:571:VAL:HG21	1:D:611:ARG:NH1	2.34	0.42
1:C:308:LEU:HD22	1:C:329:ASP:HB3	2.01	0.42
1:B:653:HIS:CD2	1:B:667:GLU:HG3	2.55	0.42
1:C:395:HIS:HA	1:C:396:PRO:HD2	1.82	0.42
1:A:881:ARG:HE	1:A:987:ASP:CG	2.23	0.42
1:C:258:VAL:HG22	1:C:313:VAL:HG22	2.02	0.42
1:B:619:GLU:HA	1:B:912:ALA:HB2	2.00	0.42
1:B:820:ALA:HB2	1:B:842:TRP:CE2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:255:ARG:HB2	1:B:316:HIS:CE1	2.54	0.42
1:D:410:VAL:HG22	1:D:455:ILE:HB	2.02	0.42
1:B:35:SER:HB2	1:B:217:LYS:HD2	2.02	0.42
1:B:595:THR:HA	1:B:596:PRO:C	2.39	0.42
1:C:576:ILE:HA	1:C:576:ILE:HD13	1.94	0.42
1:D:737:ILE:HA	1:D:738:PRO:HD3	1.90	0.42
1:B:150:PHE:HA	1:B:187:MET:O	2.20	0.42
1:C:333:ARG:NH2	1:C:453:VAL:O	2.53	0.41
1:B:90:TRP:CD1	1:B:90:TRP:C	2.93	0.41
1:A:433:LEU:HB3	1:A:434:PRO:HD3	2.02	0.41
1:C:372:MET:CE	1:C:395:HIS:HB3	2.38	0.41
1:B:334:GLU:OE1	1:B:336:ARG:NH1	2.53	0.41
1:B:15:ASP:OD2	1:C:13:ARG:NH2	2.50	0.41
1:D:333:ARG:NH2	1:D:453:VAL:O	2.53	0.41
1:B:749:ILE:HG12	1:B:834:VAL:HG11	2.02	0.41
1:D:340:GLY:O	1:D:561:ARG:HG2	2.19	0.41
1:D:100:TYR:CE1	1:D:602:CYS:HB3	2.55	0.41
1:D:147:ASN:HB3	1:D:206:SER:HA	2.01	0.41
1:B:568:TRP:HA	1:B:569:ASP:HA	1.88	0.41
1:B:225:PHE:HA	1:B:243:GLU:O	2.20	0.41
1:A:333:ARG:NH2	1:A:453:VAL:O	2.53	0.41
1:A:225:PHE:HA	1:A:243:GLU:O	2.20	0.41
1:D:786:ARG:HD2	1:D:934:GLU:HG2	2.02	0.41
1:B:653:HIS:HD2	1:B:667:GLU:HG3	1.85	0.41
1:C:661:LYS:HA	1:C:662:PRO:HD3	1.95	0.41
1:B:333:ARG:NH2	6:B:4010:HOH:O	2.50	0.41
1:D:429:ASP:HA	1:D:430:PRO:HD2	1.93	0.41
1:A:111:PRO:HA	1:A:112:PRO:HA	1.88	0.41
1:D:984:LEU:HD21	1:D:986:ILE:HD11	2.02	0.41
1:A:58:TRP:CD1	1:A:86:VAL:HB	2.56	0.41
1:C:689:GLU:CD	1:C:689:GLU:H	2.24	0.41
1:D:100:TYR:CZ	1:D:602:CYS:HB3	2.56	0.41
1:C:585:TRP:CE3	1:C:974:HIS:CE1	3.09	0.41
1:B:881:ARG:HE	1:B:987:ASP:CG	2.23	0.41
1:A:613:PRO:HB3	1:A:617:LEU:HD23	2.03	0.41
1:A:50:GLN:N	1:A:50:GLN:CD	2.74	0.41
1:D:851:ILE:O	1:D:870:VAL:HA	2.21	0.41
1:A:777:LEU:HD12	1:A:887:GLN:HG2	2.02	0.41
1:B:147:ASN:HA	1:B:148:SER:HA	1.66	0.41
1:A:670:LEU:HD23	1:A:670:LEU:HA	1.93	0.41
1:B:251:ARG:HB2	1:B:254:LEU:HG	2.03	0.41
1:A:473:ARG:NH1	6:A:4040:HOH:O	2.53	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:458:LEU:HD11	1:B:472:TYR:HB2	2.03	0.41
1:A:553:TRP:CD2	1:A:556:PHE:HD1	2.38	0.40
1:A:418:HIS:ND1	1:A:461:GLU:OE1	2.54	0.40
1:C:173:LEU:O	1:C:174:SER:C	2.59	0.40
1:A:200:GLN:HG2	1:A:391:HIS:HB2	2.03	0.40
1:B:178:ARG:HG3	1:B:182:ASN:OD1	2.21	0.40
1:D:835:LEU:HD11	1:D:855:THR:HB	2.03	0.40
1:D:876:THR:OG1	1:D:877:PRO:HD2	2.21	0.40
1:D:105:TYR:CE2	1:D:199:ASP:HB2	2.56	0.40
1:D:599:ARG:HH11	1:D:600:GLN:NE2	2.20	0.40
1:A:896:ASN:HA	1:A:918:TRP:O	2.22	0.40
1:B:730:LEU:HD12	1:B:730:LEU:H	1.85	0.40
1:D:568:TRP:CD2	1:D:569:ASP:HB3	2.57	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	1009/1052 (96%)	955 (95%)	53 (5%)	1 (0%)	59	92
1	B	1009/1052 (96%)	949 (94%)	56 (6%)	4 (0%)	43	82
1	C	1009/1052 (96%)	951 (94%)	58 (6%)	0	100	100
1	D	1009/1052 (96%)	958 (95%)	47 (5%)	4 (0%)	43	82
All	All	4036/4208 (96%)	3813 (94%)	214 (5%)	9 (0%)	56	89

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	211	ASP
1	B	461	GLU
1	B	765	LEU
1	B	102	ASN
1	D	211	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	599	ARG
1	D	659	ASP
1	D	461	GLU
1	A	164	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	864/898 (96%)	852 (99%)	12 (1%)	78	95
1	B	864/898 (96%)	844 (98%)	20 (2%)	63	91
1	C	864/898 (96%)	845 (98%)	19 (2%)	64	92
1	D	864/898 (96%)	849 (98%)	15 (2%)	73	94
All	All	3456/3592 (96%)	3390 (98%)	66 (2%)	69	93

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	TRP
1	A	319	ASP
1	A	333	ARG
1	A	538	TYR
1	A	663	LEU
1	A	672	VAL
1	A	689	GLU
1	A	845	GLN
1	A	885	ASN
1	A	958	ASN
1	A	970	THR
1	A	1022	GLN
1	B	76	CYS
1	B	90	TRP
1	B	178	ARG
1	B	279	ILE
1	B	333	ARG
1	B	461	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	481	SER
1	B	546	LEU
1	B	604	ASN
1	B	614	HIS
1	B	653	HIS
1	B	663	LEU
1	B	689	GLU
1	B	735	HIS
1	B	744	GLU
1	B	751	LEU
1	B	772	ASP
1	B	795	VAL
1	B	845	GLN
1	B	970	THR
1	C	90	TRP
1	C	178	ARG
1	C	259	SER
1	C	277	GLU
1	C	333	ARG
1	C	338	GLU
1	C	519	SER
1	C	546	LEU
1	C	689	GLU
1	C	728	VAL
1	C	744	GLU
1	C	748	CYS
1	C	751	LEU
1	C	761	GLN
1	C	774	LYS
1	C	845	GLN
1	C	885	ASN
1	C	916	ASP
1	C	970	THR
1	D	333	ARG
1	D	344	LEU
1	D	515	VAL
1	D	546	LEU
1	D	581	ASN
1	D	653	HIS
1	D	663	LEU
1	D	689	GLU
1	D	690	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	728	VAL
1	D	743	SER
1	D	748	CYS
1	D	800	ARG
1	D	956	GLN
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	C	757	GLN
1	D	221	GLN
1	D	510	GLN
1	D	843	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 47 ligands modelled in this entry, 14 are monoatomic - leaving 33 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
2	GTZ	A	2001	4	15,15,15	2.19	4 (26%)	18,22,22	1.93	6 (33%)
5	DMS	A	8001	-	3,3,3	2.68	1 (33%)	3,3,3	0.55	0
5	DMS	A	8002	-	3,3,3	2.68	1 (33%)	3,3,3	0.57	0
5	DMS	A	8003	-	3,3,3	2.63	1 (33%)	3,3,3	0.40	0
5	DMS	A	8004	-	3,3,3	2.64	1 (33%)	3,3,3	0.30	0
5	DMS	A	8005	-	3,3,3	2.63	1 (33%)	3,3,3	0.57	0
5	DMS	A	8006	-	3,3,3	2.65	1 (33%)	3,3,3	0.58	0
2	GTZ	B	2001	4	15,15,15	2.20	4 (26%)	18,22,22	1.82	4 (22%)
5	DMS	B	8001	-	3,3,3	2.54	1 (33%)	3,3,3	0.53	0
5	DMS	B	8002	-	3,3,3	2.72	1 (33%)	3,3,3	0.53	0
5	DMS	B	8003	-	3,3,3	2.73	1 (33%)	3,3,3	0.59	0
5	DMS	B	8004	-	3,3,3	2.62	1 (33%)	3,3,3	0.54	0
5	DMS	B	8005	-	3,3,3	2.64	1 (33%)	3,3,3	0.50	0
5	DMS	B	8006	-	3,3,3	2.69	1 (33%)	3,3,3	0.63	0
5	DMS	B	8007	-	3,3,3	2.67	1 (33%)	3,3,3	0.53	0
5	DMS	B	8008	-	3,3,3	2.57	1 (33%)	3,3,3	0.39	0
2	GTZ	C	2001	4	15,15,15	2.21	4 (26%)	18,22,22	1.96	6 (33%)
5	DMS	C	8001	-	3,3,3	2.66	1 (33%)	3,3,3	0.63	0
5	DMS	C	8002	-	3,3,3	2.66	1 (33%)	3,3,3	0.58	0
5	DMS	C	8003	-	3,3,3	2.64	1 (33%)	3,3,3	0.52	0
5	DMS	C	8004	-	3,3,3	2.65	1 (33%)	3,3,3	0.52	0
5	DMS	C	8005	-	3,3,3	2.71	1 (33%)	3,3,3	0.73	0
5	DMS	C	8006	-	3,3,3	2.66	1 (33%)	3,3,3	0.51	0
5	DMS	C	8007	-	3,3,3	2.62	1 (33%)	3,3,3	0.39	0
5	DMS	C	8008	-	3,3,3	2.63	1 (33%)	3,3,3	0.50	0
2	GTZ	D	2001	4	15,15,15	2.20	5 (33%)	18,22,22	2.41	6 (33%)
5	DMS	D	8001	-	3,3,3	2.66	1 (33%)	3,3,3	0.66	0
5	DMS	D	8002	-	3,3,3	2.70	1 (33%)	3,3,3	0.61	0
5	DMS	D	8003	-	3,3,3	2.61	1 (33%)	3,3,3	0.67	0
5	DMS	D	8004	-	3,3,3	2.69	1 (33%)	3,3,3	0.61	0
5	DMS	D	8005	-	3,3,3	2.68	1 (33%)	3,3,3	0.65	0
5	DMS	D	8006	-	3,3,3	2.62	1 (33%)	3,3,3	0.52	0
5	DMS	D	8007	-	3,3,3	2.65	1 (33%)	3,3,3	0.53	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	GTZ	A	2001	4	-	0/2/22/22	0/0/2/2
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
2	GTZ	B	2001	4	-	0/2/22/22	0/0/2/2
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
2	GTZ	C	2001	4	-	0/2/22/22	0/0/2/2
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
2	GTZ	D	2001	4	-	0/2/22/22	0/0/2/2
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

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2001	GTZ	NA-NB	5.23	1.41	1.30
2	A	2001	GTZ	NA-NB	5.09	1.41	1.30
2	D	2001	GTZ	NA-NB	5.08	1.41	1.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	GTZ	NA-NB	5.05	1.41	1.30
2	B	2001	GTZ	N1-NB	4.73	1.41	1.34
2	D	2001	GTZ	N1-NB	4.70	1.41	1.34
2	A	2001	GTZ	N1-NB	4.66	1.41	1.34
2	C	2001	GTZ	N1-NB	4.63	1.41	1.34
5	B	8003	DMS	O-S	4.58	1.81	1.50
5	B	8002	DMS	O-S	4.57	1.81	1.50
5	D	8002	DMS	O-S	4.54	1.80	1.50
5	C	8005	DMS	O-S	4.53	1.80	1.50
5	D	8004	DMS	O-S	4.51	1.80	1.50
5	A	8001	DMS	O-S	4.51	1.80	1.50
5	A	8002	DMS	O-S	4.49	1.80	1.50
5	D	8005	DMS	O-S	4.49	1.80	1.50
5	B	8006	DMS	O-S	4.49	1.80	1.50
5	C	8002	DMS	O-S	4.48	1.80	1.50
5	D	8001	DMS	O-S	4.47	1.80	1.50
5	B	8007	DMS	O-S	4.47	1.80	1.50
5	C	8001	DMS	O-S	4.46	1.80	1.50
5	D	8007	DMS	O-S	4.46	1.80	1.50
5	A	8004	DMS	O-S	4.45	1.80	1.50
5	C	8003	DMS	O-S	4.45	1.80	1.50
5	C	8006	DMS	O-S	4.44	1.80	1.50
5	C	8004	DMS	O-S	4.44	1.80	1.50
5	A	8006	DMS	O-S	4.43	1.80	1.50
5	B	8005	DMS	O-S	4.41	1.80	1.50
5	C	8007	DMS	O-S	4.41	1.80	1.50
5	A	8005	DMS	O-S	4.40	1.79	1.50
5	C	8008	DMS	O-S	4.40	1.79	1.50
5	A	8003	DMS	O-S	4.39	1.79	1.50
5	B	8004	DMS	O-S	4.38	1.79	1.50
5	D	8006	DMS	O-S	4.37	1.79	1.50
5	D	8003	DMS	O-S	4.37	1.79	1.50
5	B	8008	DMS	O-S	4.29	1.79	1.50
5	B	8001	DMS	O-S	4.26	1.78	1.50
2	B	2001	GTZ	NA-N5	3.33	1.41	1.34
2	D	2001	GTZ	NA-N5	3.20	1.41	1.34
2	A	2001	GTZ	NA-N5	3.14	1.41	1.34
2	B	2001	GTZ	C1-N1	3.11	1.36	1.31
2	C	2001	GTZ	NA-N5	3.06	1.40	1.34
2	A	2001	GTZ	C1-N1	3.02	1.36	1.31
2	C	2001	GTZ	C1-N1	2.95	1.36	1.31
2	D	2001	GTZ	C1-N1	2.93	1.36	1.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2001	GTZ	C1-C2	-2.00	1.48	1.51

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2001	GTZ	C2-C1-N1	-5.48	128.29	129.12
2	D	2001	GTZ	C4-C3-C2	5.29	117.18	110.64
2	C	2001	GTZ	C2-C1-N1	-4.58	128.42	129.12
2	A	2001	GTZ	C1-N1-NB	4.22	109.04	105.36
2	D	2001	GTZ	C1-N1-NB	4.18	109.00	105.36
2	B	2001	GTZ	C1-N1-NB	4.13	108.96	105.36
2	A	2001	GTZ	C4-C3-C2	4.09	115.70	110.64
2	B	2001	GTZ	C4-C3-C2	3.99	115.57	110.64
2	C	2001	GTZ	C4-C3-C2	3.90	115.47	110.64
2	C	2001	GTZ	C1-N1-NB	3.33	108.26	105.36
2	D	2001	GTZ	C3-C4-C5	2.89	116.23	111.62
2	A	2001	GTZ	N1-NB-NA	-2.87	106.79	110.11
2	D	2001	GTZ	N1-NB-NA	-2.81	106.86	110.11
2	B	2001	GTZ	N1-NB-NA	-2.71	106.97	110.11
2	A	2001	GTZ	C2-C1-N1	-2.71	128.71	129.12
2	C	2001	GTZ	NB-NA-N5	-2.37	104.11	106.06
2	B	2001	GTZ	C1-N5-NA	2.26	111.89	108.75
2	C	2001	GTZ	N1-NB-NA	-2.22	107.54	110.11
2	C	2001	GTZ	C1-N5-NA	2.20	111.80	108.75
2	D	2001	GTZ	C1-N5-NA	2.15	111.73	108.75
2	A	2001	GTZ	C1-N5-NA	2.15	111.73	108.75
2	A	2001	GTZ	C3-C4-C5	2.07	114.91	111.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1011/1052 (96%)	-0.29	10 (0%) 79 86	14, 41, 78, 121	0
1	B	1011/1052 (96%)	-0.40	8 (0%) 83 89	11, 34, 68, 116	0
1	C	1011/1052 (96%)	-0.42	8 (0%) 83 89	12, 35, 63, 99	0
1	D	1011/1052 (96%)	-0.49	5 (0%) 88 93	13, 33, 63, 101	0
All	All	4044/4208 (96%)	-0.40	31 (0%) 83 89	11, 35, 69, 121	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	732	ALA	5.3
1	B	732	ALA	4.1
1	C	1023	LYS	3.4
1	A	731	PRO	3.4
1	C	732	ALA	3.3
1	B	798	ALA	3.2
1	D	732	ALA	3.2
1	B	731	PRO	3.2
1	C	689	GLU	3.1
1	A	689	GLU	2.9
1	C	800	ARG	2.8
1	C	731	PRO	2.8
1	B	734	SER	2.7
1	A	980	GLU	2.7
1	B	686	PRO	2.7
1	A	798	ALA	2.7
1	B	685	LEU	2.6
1	C	580	GLU	2.6
1	A	685	LEU	2.5
1	B	735	HIS	2.4
1	D	735	HIS	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	1023	LYS	2.4
1	D	75	GLU	2.4
1	A	800	ARG	2.3
1	A	977	HIS	2.2
1	D	689	GLU	2.2
1	A	178	ARG	2.2
1	C	799	THR	2.2
1	A	735	HIS	2.2
1	C	583	ASN	2.1
1	B	800	ARG	2.1

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	DMS	B	8008	4/4	0.25	8.23	74,76,77,78	0
5	DMS	A	8005	4/4	0.37	7.81	74,75,75,78	0
2	GTZ	D	2001	14/14	0.30	6.88	63,80,90,90	0
2	GTZ	B	2001	14/14	0.27	6.03	53,71,77,79	0
5	DMS	A	8004	4/4	0.28	5.53	57,59,60,60	0
5	DMS	B	8003	4/4	0.21	5.15	59,60,60,62	0
5	DMS	A	8002	4/4	0.23	4.63	70,72,72,75	0
5	DMS	C	8002	4/4	0.19	4.12	63,63,64,64	0
5	DMS	A	8006	4/4	0.26	3.78	69,70,71,73	0
5	DMS	B	8005	4/4	0.26	3.29	64,66,66,70	0
5	DMS	C	8006	4/4	0.26	3.16	74,75,76,78	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GTZ	A	2001	14/14	0.22	3.03	56,76,80,81	0
5	DMS	D	8006	4/4	0.23	2.97	58,60,60,61	0
5	DMS	A	8003	4/4	0.24	2.90	50,52,53,53	0
5	DMS	D	8002	4/4	0.19	2.84	44,46,47,47	0
5	DMS	B	8001	4/4	0.16	2.11	44,45,46,47	0
5	DMS	D	8004	4/4	0.33	1.97	62,65,66,67	0
5	DMS	D	8001	4/4	0.16	1.88	45,45,46,47	0
5	DMS	D	8005	4/4	0.23	1.63	61,65,65,68	0
4	NA	A	3101	1/1	0.17	1.47	46,46,46,46	0
2	GTZ	C	2001	14/14	0.17	1.46	51,61,64,65	0
5	DMS	C	8008	4/4	0.21	1.33	62,62,63,63	0
5	DMS	B	8007	4/4	0.17	1.24	68,72,72,74	0
5	DMS	B	8006	4/4	0.22	1.18	52,52,54,54	0
5	DMS	D	8007	4/4	0.16	1.13	47,48,51,52	0
5	DMS	C	8007	4/4	0.19	1.09	65,66,66,67	0
5	DMS	C	8003	4/4	0.16	1.02	59,59,60,61	0
5	DMS	C	8005	4/4	0.26	0.80	55,55,56,58	0
5	DMS	C	8004	4/4	0.18	0.56	48,49,51,51	0
5	DMS	C	8001	4/4	0.14	0.52	44,45,45,51	0
5	DMS	B	8004	4/4	0.14	0.46	44,45,45,46	0
5	DMS	B	8002	4/4	0.14	0.15	51,52,52,53	0
5	DMS	A	8001	4/4	0.13	0.01	52,53,53,55	0
4	NA	C	3102	1/1	0.10	-0.79	29,29,29,29	0
4	NA	A	2102	1/1	0.12	-0.82	25,25,25,25	0
4	NA	C	3101	1/1	0.11	-0.83	49,49,49,49	0
5	DMS	D	8003	4/4	0.15	-0.87	38,39,41,42	0
4	NA	D	3101	1/1	0.10	-1.08	46,46,46,46	0
3	MG	D	3001	1/1	0.10	-1.50	37,37,37,37	0
3	MG	C	3002	1/1	0.09	-1.94	31,31,31,31	0
4	NA	B	3101	1/1	0.07	-1.95	44,44,44,44	0
3	MG	B	3002	1/1	0.07	-2.50	36,36,36,36	0
3	MG	C	3001	1/1	0.06	-3.41	35,35,35,35	0
3	MG	A	3001	1/1	0.06	-4.13	44,44,44,44	0
4	NA	B	3102	1/1	0.07	-4.35	19,19,19,19	0
3	MG	B	3001	1/1	0.06	-4.84	30,30,30,30	0
4	NA	D	3102	1/1	0.06	-4.87	21,21,21,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.