



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 11:08 AM UTC

PDB ID : 1JZ2 / pdb_00001jz2
Title : E. COLI (lacZ) BETA-GALACTOSIDASE-TRAPPED 2-F-GALACTOSYL-
ENZYME INTERMEDIATE (ORTHORHOMBIC)
Authors : Juers, D.H.; McCarter, J.D.; Mackenzie, L.; Withers, S.G.; Matthews, B.W.
Deposited on : 2001-09-13
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

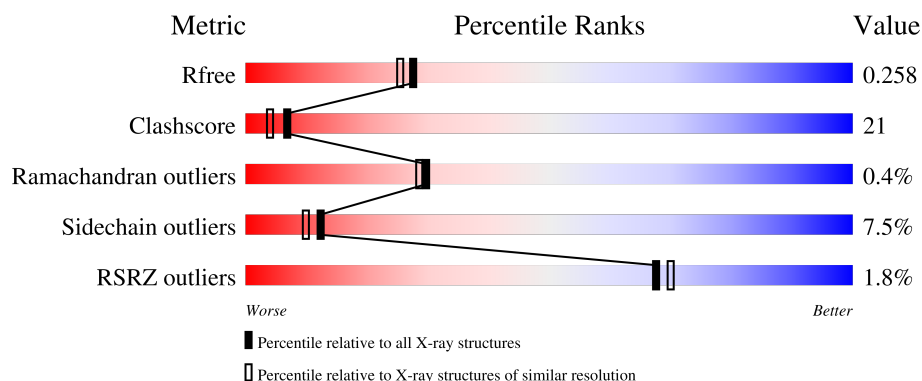
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

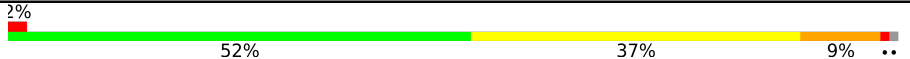
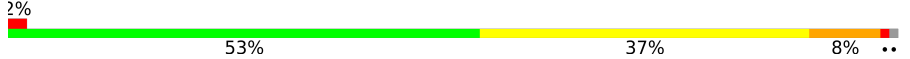
The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1023	
1	B	1023	
1	C	1023	
1	D	1023	

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	2FG	A	2001	X	-	-	-
2	2FG	B	2001	X	-	-	-
2	2FG	C	2001	X	-	-	-
2	2FG	D	2001	X	-	-	-
5	DMS	A	8406	-	-	X	-
5	DMS	A	8412	-	-	X	-
5	DMS	A	8414	-	-	X	-
5	DMS	A	8417	-	X	-	-
5	DMS	A	8419	-	-	X	-
5	DMS	B	8504	-	-	X	-
5	DMS	B	8506	-	-	X	-
5	DMS	C	8421	-	-	X	-
5	DMS	D	8427	-	-	X	-
6	BTB	B	2002	-	-	X	-

2 Entry composition [i](#)

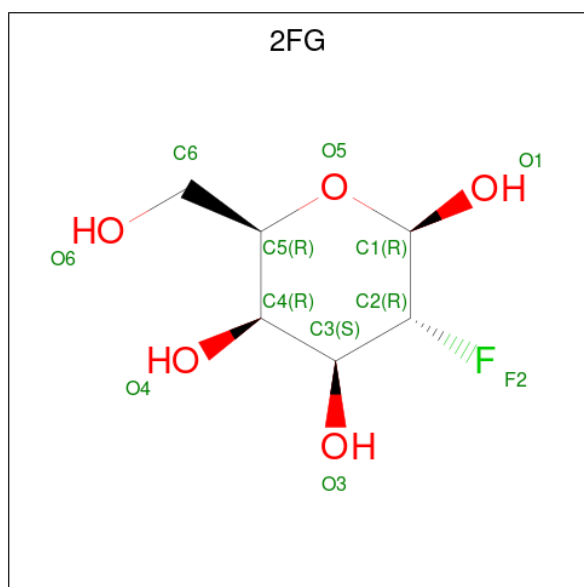
There are 7 unique types of molecules in this entry. The entry contains 35825 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Beta-Galactosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1011	Total	C	N	O	S	0	0	0
			8125	5138	1440	1509	38			
1	B	1011	Total	C	N	O	S	0	0	0
			8125	5138	1440	1509	38			
1	C	1011	Total	C	N	O	S	0	0	0
			8125	5138	1440	1509	38			
1	D	1011	Total	C	N	O	S	0	0	0
			8125	5138	1440	1509	38			

- Molecule 2 is 2-deoxy-2-fluoro-beta-D-galactopyranose (CCD ID: 2FG) (formula: $C_6H_{11}FO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	F	O	0	0
			11	6	1	4		
2	B	1	Total	C	F	O	0	0
			11	6	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	F	O	0	0
			11	6	1	4		
2	D	1	Total	C	F	O	0	0
			11	6	1	4		

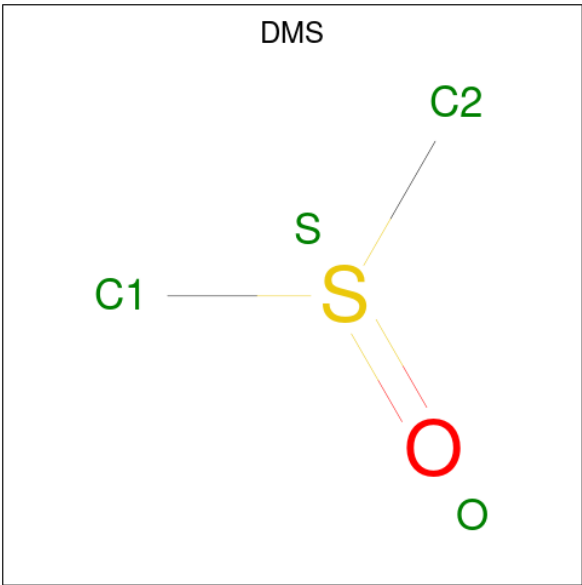
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: 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		
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		
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		
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	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

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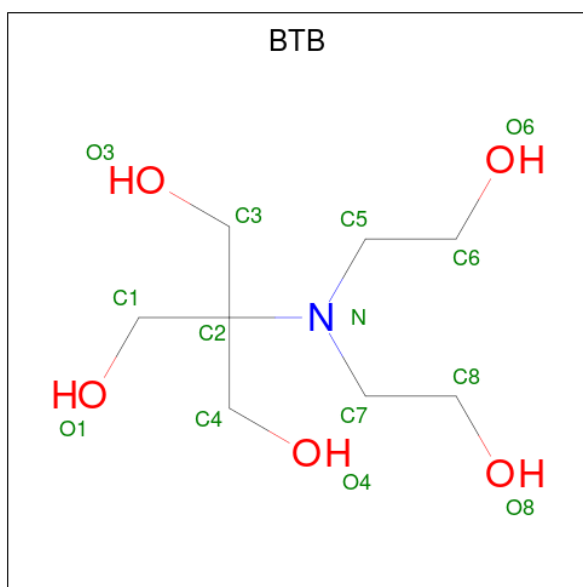
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total 4	C 2	O 1	S 1	0	0
5	B	1	Total 4	C 2	O 1	S 1	0	0
5	B	1	Total 4	C 2	O 1	S 1	0	0
5	B	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	C	1	Total 4	C 2	O 1	S 1	0	0
5	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
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 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: C₈H₁₉NO₅).



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

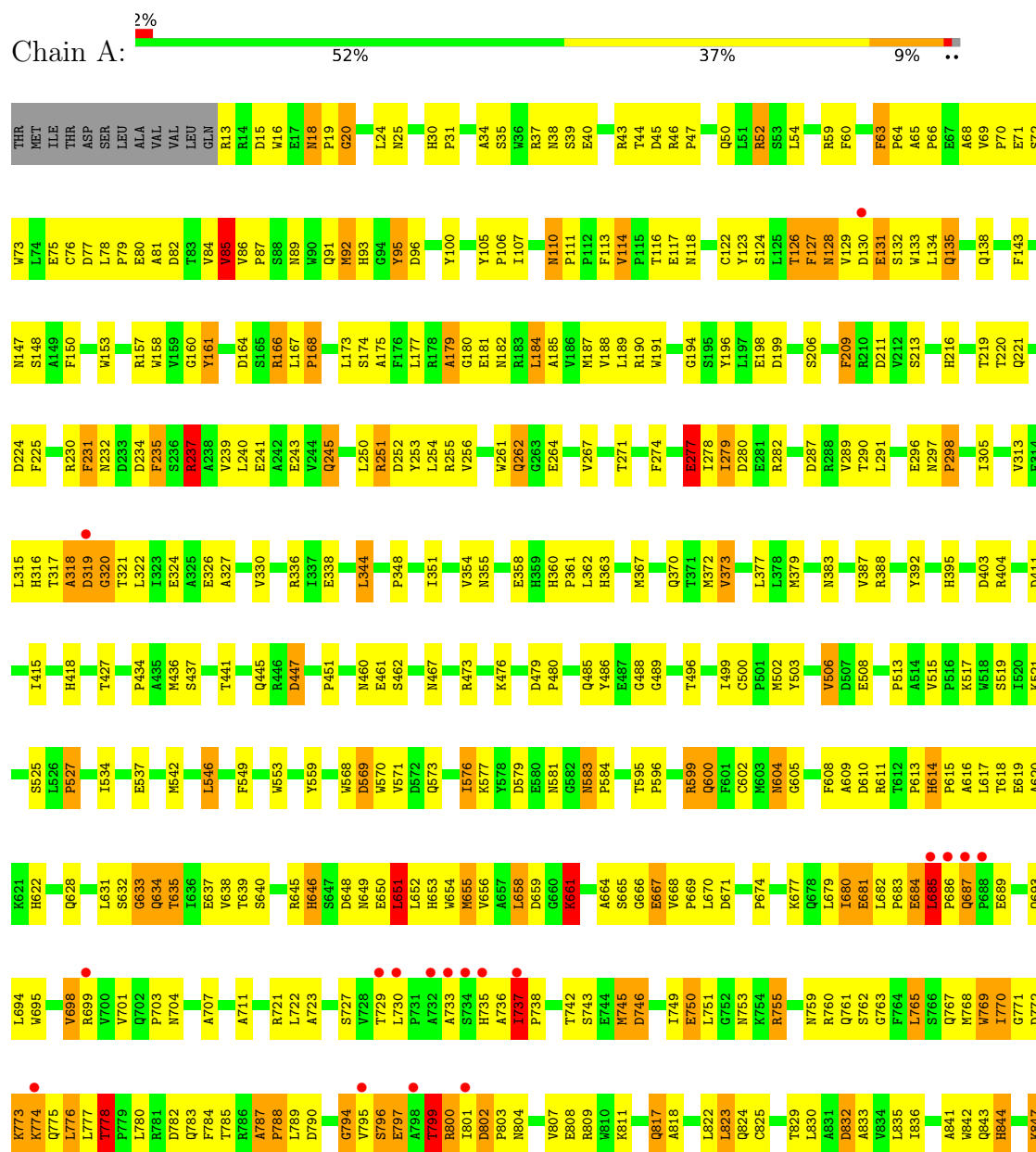
- Molecule 7 is water.

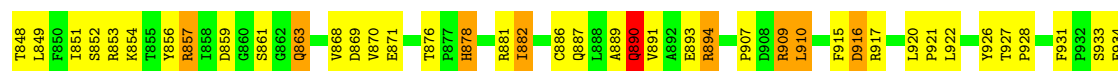
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	753	Total	O	0	0
			753	753		
7	B	734	Total	O	0	0
			734	734		
7	C	716	Total	O	0	0
			716	716		
7	D	754	Total	O	0	0
			754	754		

3 Residue-property plots

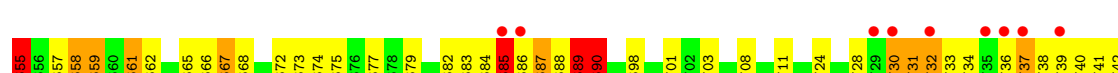
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Beta-Galactosidase

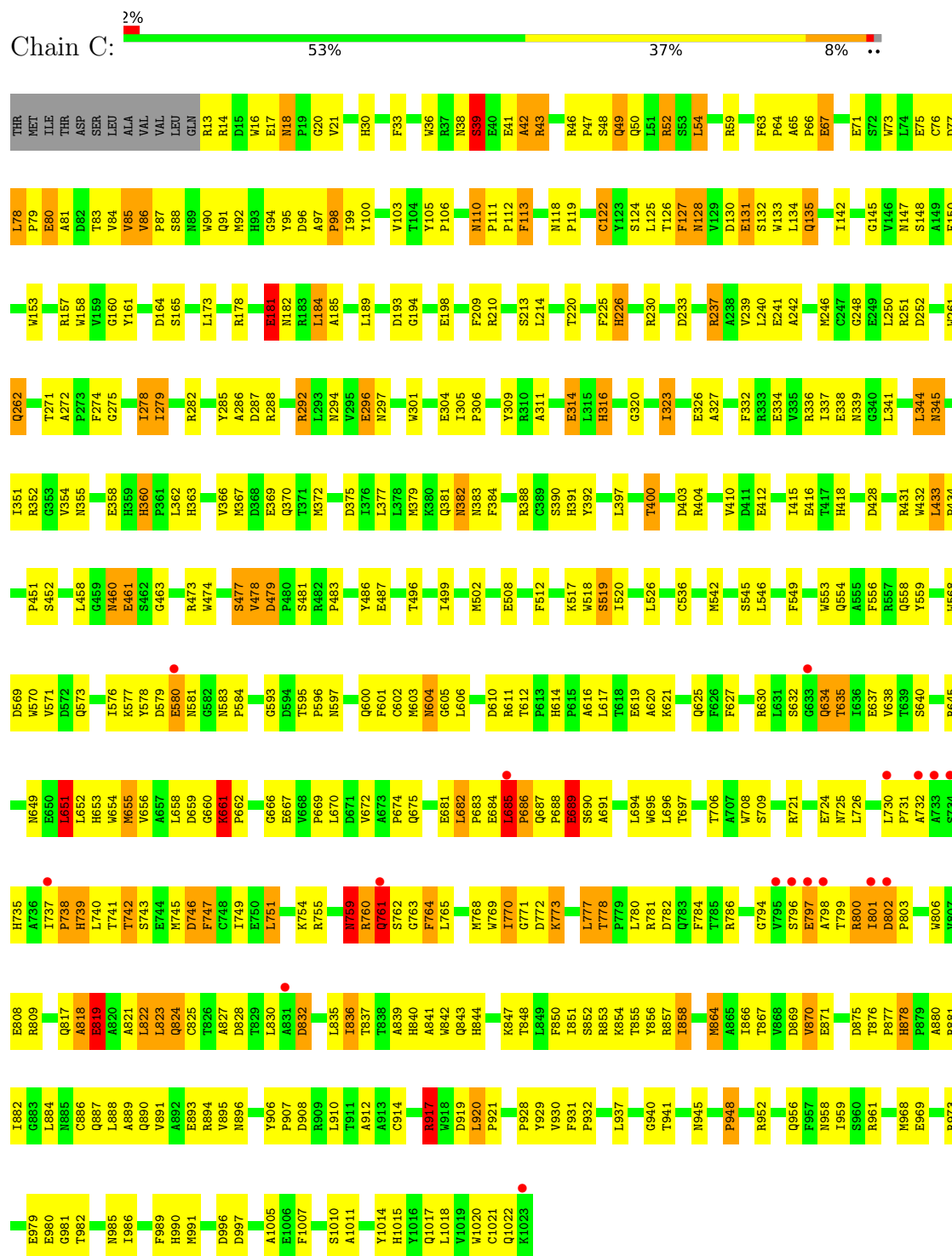




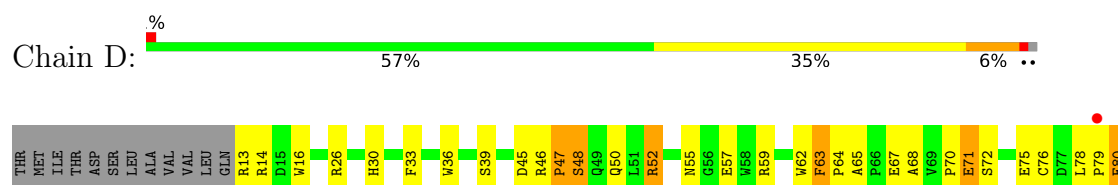
● Molecule 1: Beta-Galactosidase

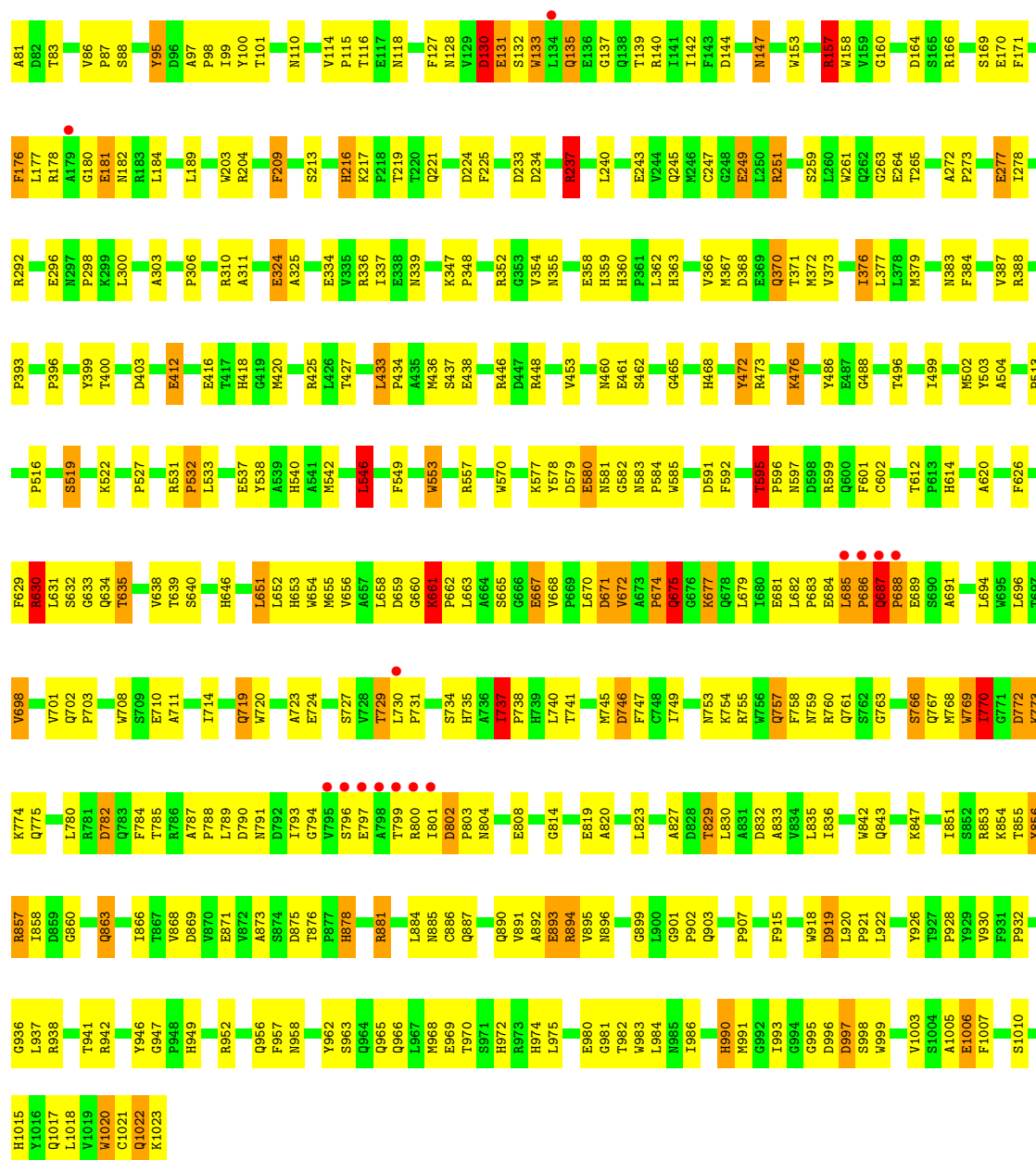


● Molecule 1: Beta-Galactosidase



● 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	151.50Å 167.70Å 201.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.60 – 2.10 27.60 – 2.10	Depositor EDS
% Data completeness (in resolution range)	92.0 (27.60-2.10) 92.0 (27.60-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.10Å)	Xtriage
Refinement program	TNT	Depositor
R, R_{free}	0.167 , 0.270 0.165 , 0.258	Depositor DCC
R_{free} test set	3979 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 124.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	35825	wwPDB-VP
Average B, all atoms (Å ²)	33.0	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 44.88 % 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 1.4330e-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, 2FG, MG, DMS, BTB

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.20	6/8367 (0.1%)	1.90	183/11415 (1.6%)
1	B	1.19	6/8367 (0.1%)	1.87	173/11415 (1.5%)
1	C	1.14	3/8367 (0.0%)	1.87	168/11415 (1.5%)
1	D	1.18	5/8367 (0.1%)	1.85	171/11415 (1.5%)
All	All	1.18	20/33468 (0.1%)	1.87	695/45660 (1.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	1	0
1	D	1	0
All	All	2	0

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	479	ASP	C-N	-6.05	1.26	1.33
1	B	920	LEU	CA-C	-5.84	1.46	1.52
1	D	731	PRO	N-CD	5.81	1.55	1.47
1	C	685	LEU	C-O	5.79	1.31	1.24
1	B	804	ASN	N-CA	-5.71	1.38	1.46

The worst 5 of 695 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	363	HIS	CA-CB-CG	-15.86	97.94	113.80
1	B	802	ASP	CA-C-N	13.97	135.68	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	802	ASP	C-N-CA	13.97	135.68	119.47
1	B	252	ASP	CA-CB-CG	-13.31	99.29	112.60
1	A	318	ALA	CA-C-O	12.72	134.37	120.63

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	690	SER	CA
1	D	157	ARG	CA

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8125	0	7716	385	0
1	B	8125	0	7716	346	0
1	C	8125	0	7716	350	0
1	D	8125	0	7716	277	0
2	A	11	0	8	1	0
2	B	11	0	8	0	0
2	C	11	0	8	0	0
2	D	11	0	9	0	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	3	0	0	0	0
4	C	3	0	0	0	0
4	D	3	0	0	0	0
5	A	76	0	114	36	0
5	B	80	0	120	35	0
5	C	60	0	90	18	0
5	D	60	0	90	17	0
6	B	14	0	19	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	D	14	0	19	6	0
7	A	753	0	0	25	0
7	B	734	0	0	13	0
7	C	716	0	0	18	0
7	D	754	0	0	20	0
All	All	35825	0	31349	1367	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 21.

The worst 5 of 1367 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:C:634:GLN:HE21	1:C:634:GLN:N	1.45	1.13
1:B:687:GLN:HG3	1:B:688:PRO:HD2	1.21	1.12
1:C:778:THR:HG23	1:C:887:GLN:HB3	1.33	1.11
1:A:655:MET:HB3	1:A:699:ARG:HH12	0.95	1.09
1:C:634:GLN:H	1:C:634:GLN:NE2	1.49	1.09

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1009/1023 (99%)	957 (95%)	50 (5%)	2 (0%)	43	44
1	B	1009/1023 (99%)	945 (94%)	58 (6%)	6 (1%)	21	18
1	C	1009/1023 (99%)	948 (94%)	54 (5%)	7 (1%)	18	15
1	D	1009/1023 (99%)	957 (95%)	49 (5%)	3 (0%)	36	36
All	All	4036/4092 (99%)	3807 (94%)	211 (5%)	18 (0%)	30	28

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	690	SER
1	B	732	ALA
1	B	796	SER
1	B	801	ILE
1	B	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	864/875 (99%)	793 (92%)	71 (8%)	10	8
1	B	864/875 (99%)	802 (93%)	62 (7%)	13	11
1	C	864/875 (99%)	798 (92%)	66 (8%)	12	9
1	D	864/875 (99%)	803 (93%)	61 (7%)	13	11
All	All	3456/3500 (99%)	3196 (92%)	260 (8%)	12	10

5 of 260 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	677	LYS
1	D	734	SER
1	B	661	LYS
1	B	635	THR
1	D	761	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	216	HIS
1	D	845	GLN
1	D	266	GLN
1	D	718	GLN
1	D	949	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 95 ligands modelled in this entry, 20 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$
5	DMS	D	8405	-	3,3,3	1.26	0	3,3,3	0.07	0
5	DMS	B	8425	-	3,3,3	1.18	0	3,3,3	0.22	0
5	DMS	A	8411	-	3,3,3	0.43	0	3,3,3	0.86	0
2	2FG	C	2001	4,1	11,11,12	1.04	1 (9%)	12,15,17	1.81	3 (25%)
5	DMS	B	8408	-	3,3,3	0.74	0	3,3,3	0.64	0
5	DMS	C	8401	-	3,3,3	1.41	1 (33%)	3,3,3	1.10	0
5	DMS	D	8409	-	3,3,3	1.57	1 (33%)	3,3,3	0.14	0
5	DMS	B	8502	-	3,3,3	1.48	1 (33%)	3,3,3	0.82	0
5	DMS	D	8411	-	3,3,3	0.90	0	3,3,3	0.21	0
5	DMS	A	8423	-	3,3,3	1.15	0	3,3,3	0.11	0
5	DMS	C	8421	-	3,3,3	1.33	1 (33%)	3,3,3	0.70	0
5	DMS	B	8504	-	3,3,3	0.69	0	3,3,3	0.34	0
5	DMS	B	8506	-	3,3,3	1.26	0	3,3,3	0.59	0
5	DMS	D	8408	-	3,3,3	0.48	0	3,3,3	0.63	0
5	DMS	A	8406	-	3,3,3	0.88	0	3,3,3	0.46	0
5	DMS	C	8414	-	3,3,3	0.36	0	3,3,3	0.15	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	B	8414	-	3,3,3	1.75	1 (33%)	3,3,3	0.62	0
5	DMS	A	8401	-	3,3,3	1.37	0	3,3,3	0.34	0
5	DMS	C	8405	-	3,3,3	0.90	0	3,3,3	0.16	0
5	DMS	C	8419	-	3,3,3	0.85	0	3,3,3	0.14	0
5	DMS	C	8402	-	3,3,3	0.87	0	3,3,3	0.33	0
6	BTB	B	2002	-	13,13,13	1.43	2 (15%)	7,16,16	1.20	1 (14%)
5	DMS	A	8412	-	3,3,3	0.47	0	3,3,3	0.35	0
5	DMS	B	8421	-	3,3,3	0.81	0	3,3,3	0.24	0
5	DMS	A	8404	-	3,3,3	0.77	0	3,3,3	0.38	0
5	DMS	A	8405	-	3,3,3	1.14	0	3,3,3	0.24	0
5	DMS	A	8419	-	3,3,3	0.80	0	3,3,3	0.19	0
5	DMS	D	8501	-	3,3,3	0.33	0	3,3,3	0.32	0
5	DMS	A	8409	-	3,3,3	1.79	2 (66%)	3,3,3	0.37	0
5	DMS	C	8403	-	3,3,3	0.99	0	3,3,3	0.93	0
5	DMS	D	8401	-	3,3,3	1.18	0	3,3,3	0.60	0
5	DMS	B	8403	-	3,3,3	1.30	0	3,3,3	0.44	0
2	2FG	B	2001	4,1	11,11,12	1.18	1 (9%)	12,15,17	1.71	2 (16%)
5	DMS	B	8406	-	3,3,3	0.85	0	3,3,3	0.27	0
6	BTB	D	2002	-	13,13,13	1.33	2 (15%)	7,16,16	0.90	0
5	DMS	C	8412	-	3,3,3	0.90	0	3,3,3	0.15	0
5	DMS	D	8421	-	3,3,3	0.69	0	3,3,3	0.10	0
5	DMS	B	8405	-	3,3,3	1.00	0	3,3,3	0.12	0
5	DMS	B	8508	-	3,3,3	1.94	1 (33%)	3,3,3	0.77	0
5	DMS	A	8410	-	3,3,3	0.71	0	3,3,3	0.09	0
5	DMS	B	8412	-	3,3,3	1.08	0	3,3,3	0.09	0
5	DMS	D	8416	-	3,3,3	0.66	0	3,3,3	0.63	0
5	DMS	A	8402	-	3,3,3	2.36	2 (66%)	3,3,3	0.53	0
5	DMS	C	8423	-	3,3,3	1.30	0	3,3,3	0.23	0
5	DMS	B	8407	-	3,3,3	1.25	0	3,3,3	1.09	0
5	DMS	B	8423	-	3,3,3	1.01	0	3,3,3	0.09	0
5	DMS	D	8403	-	3,3,3	1.73	1 (33%)	3,3,3	0.64	0
5	DMS	A	8501	-	3,3,3	0.35	0	3,3,3	0.26	0
5	DMS	B	8409	-	3,3,3	1.48	0	3,3,3	0.12	0
5	DMS	A	8502	-	3,3,3	1.03	0	3,3,3	0.12	0
5	DMS	B	8401	-	3,3,3	1.96	1 (33%)	3,3,3	0.32	0
5	DMS	D	8412	-	3,3,3	1.73	1 (33%)	3,3,3	0.29	0
5	DMS	C	8404	-	3,3,3	1.32	0	3,3,3	0.45	0
5	DMS	A	8403	-	3,3,3	0.79	0	3,3,3	0.38	0
5	DMS	C	8504	-	3,3,3	0.59	0	3,3,3	0.31	0
5	DMS	A	8414	-	3,3,3	1.12	0	3,3,3	0.31	0
5	DMS	C	8417	-	3,3,3	0.63	0	3,3,3	0.27	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	DMS	A	8504	-	3,3,3	1.04	0	3,3,3	0.08	0
5	DMS	B	8402	-	3,3,3	0.81	0	3,3,3	0.41	0
2	2FG	D	2001	4,1	11,11,12	1.24	2 (18%)	12,15,17	1.36	2 (16%)
5	DMS	C	8409	-	3,3,3	1.36	0	3,3,3	0.22	0
5	DMS	D	8406	-	3,3,3	0.65	0	3,3,3	0.60	0
5	DMS	C	8408	-	3,3,3	1.05	0	3,3,3	0.59	0
5	DMS	B	8404	-	3,3,3	0.55	0	3,3,3	0.42	0
5	DMS	D	8423	-	3,3,3	1.00	0	3,3,3	0.19	0
5	DMS	D	8402	-	3,3,3	1.92	2 (66%)	3,3,3	0.11	0
5	DMS	B	8417	-	3,3,3	0.59	0	3,3,3	0.14	0
2	2FG	A	2001	4,1	11,11,12	0.78	0	12,15,17	1.45	2 (16%)
5	DMS	A	8407	-	3,3,3	1.25	0	3,3,3	0.81	0
5	DMS	A	8417	-	3,3,3	2.20	2 (66%)	3,3,3	1.19	1 (33%)
5	DMS	D	8414	-	3,3,3	0.32	0	3,3,3	0.40	0
5	DMS	A	8408	-	3,3,3	0.51	0	3,3,3	0.30	0
5	DMS	C	8411	-	3,3,3	1.11	0	3,3,3	0.43	0
5	DMS	D	8427	-	3,3,3	1.21	0	3,3,3	0.79	0
5	DMS	B	8411	-	3,3,3	1.06	0	3,3,3	0.40	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	2FG	D	2001	4,1	1/1/4/5	1/2/19/22	0/1/1/1
2	2FG	C	2001	4,1	1/1/4/5	1/2/19/22	0/1/1/1
2	2FG	B	2001	4,1	1/1/4/5	1/2/19/22	0/1/1/1
6	BTB	D	2002	-	-	12/21/21/21	-
2	2FG	A	2001	4,1	1/1/4/5	1/2/19/22	0/1/1/1
6	BTB	B	2002	-	-	4/21/21/21	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	8402	DMS	C2-S	3.43	2.00	1.76
5	B	8508	DMS	C1-S	2.98	1.97	1.76
5	D	8412	DMS	C1-S	2.97	1.97	1.76
5	B	8414	DMS	C2-S	2.95	1.97	1.76
5	A	8417	DMS	C2-S	2.92	1.96	1.76

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2001	2FG	F2-C2-C1	4.02	111.43	108.26
2	B	2001	2FG	F2-C2-C1	3.78	111.24	108.26
2	A	2001	2FG	O5-C5-C6	-3.04	101.74	107.66
2	C	2001	2FG	C1-O5-C5	2.90	116.07	112.19
2	B	2001	2FG	O3-C3-C2	2.89	114.72	109.55

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	2001	2FG	C1
2	B	2001	2FG	C1
2	C	2001	2FG	C1
2	D	2001	2FG	C1

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	2002	BTB	O1-C1-C2-N
6	B	2002	BTB	C1-C2-C3-O3
6	B	2002	BTB	C4-C2-C3-O3
6	B	2002	BTB	N-C2-C3-O3
6	D	2002	BTB	C1-C2-C3-O3

There are no ring outliers.

41 monomers are involved in 120 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	8405	DMS	1	0
5	B	8425	DMS	2	0
5	B	8408	DMS	1	0
5	D	8409	DMS	2	0
5	B	8502	DMS	1	0
5	D	8411	DMS	2	0
5	C	8421	DMS	6	0
5	B	8504	DMS	11	0
5	B	8506	DMS	6	0
5	D	8408	DMS	1	0
5	A	8406	DMS	8	0
5	C	8419	DMS	2	0
6	B	2002	BTB	7	0
5	A	8412	DMS	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	8404	DMS	2	0
5	A	8419	DMS	5	0
5	D	8501	DMS	1	0
5	A	8409	DMS	1	0
6	D	2002	BTB	6	0
5	C	8412	DMS	3	0
5	B	8508	DMS	1	0
5	A	8410	DMS	2	0
5	B	8412	DMS	3	0
5	A	8402	DMS	3	0
5	B	8423	DMS	1	0
5	D	8403	DMS	1	0
5	A	8501	DMS	2	0
5	B	8409	DMS	2	0
5	C	8404	DMS	3	0
5	C	8504	DMS	2	0
5	A	8414	DMS	4	0
5	C	8417	DMS	1	0
5	A	8504	DMS	2	0
5	C	8409	DMS	1	0
5	B	8404	DMS	2	0
5	D	8423	DMS	3	0
5	B	8417	DMS	3	0
2	A	2001	2FG	1	0
5	A	8407	DMS	2	0
5	D	8427	DMS	6	0
5	B	8411	DMS	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1011/1023 (98%)	-0.33	18 (1%) 67 70	14, 27, 61, 100	0
1	B	1011/1023 (98%)	-0.31	23 (2%) 61 64	15, 28, 64, 100	0
1	C	1011/1023 (98%)	-0.32	17 (1%) 69 71	14, 28, 62, 100	0
1	D	1011/1023 (98%)	-0.36	15 (1%) 72 74	12, 27, 62, 98	0
All	All	4044/4092 (98%)	-0.33	73 (1%) 67 70	12, 28, 63, 100	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	796	SER	5.8
1	B	795	VAL	5.0
1	C	795	VAL	4.9
1	D	798	ALA	4.0
1	B	801	ILE	3.9

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	DMS	A	8407	4/4	0.72	0.20	41,44,100,100	0
5	DMS	A	8417	4/4	0.77	0.18	44,45,60,100	0
5	DMS	B	8425	4/4	0.81	0.20	65,81,100,100	0
5	DMS	B	8508	4/4	0.81	0.15	41,70,84,100	0
5	DMS	D	8427	4/4	0.82	0.16	63,100,100,100	0
5	DMS	B	8407	4/4	0.84	0.16	26,40,100,100	0
5	DMS	C	8421	4/4	0.86	0.15	44,48,73,100	0
5	DMS	C	8423	4/4	0.86	0.15	38,49,66,90	0
5	DMS	D	8423	4/4	0.86	0.19	40,91,100,100	0
5	DMS	B	8502	4/4	0.86	0.17	38,65,97,100	0
5	DMS	D	8421	4/4	0.87	0.17	47,80,81,100	0
5	DMS	B	8417	4/4	0.87	0.18	37,100,100,100	0
5	DMS	D	8416	4/4	0.87	0.14	47,57,62,100	0
5	DMS	B	8409	4/4	0.88	0.19	34,48,100,100	0
5	DMS	C	8404	4/4	0.88	0.14	22,47,56,100	0
5	DMS	A	8423	4/4	0.89	0.17	65,80,99,100	0
5	DMS	A	8502	4/4	0.89	0.20	35,83,93,100	0
5	DMS	B	8506	4/4	0.89	0.12	20,33,57,90	0
5	DMS	B	8406	4/4	0.89	0.18	67,84,100,100	0
5	DMS	B	8421	4/4	0.89	0.13	39,46,73,100	0
5	DMS	C	8409	4/4	0.89	0.12	46,57,75,75	0
6	BTB	D	2002	14/14	0.89	0.16	23,49,100,100	0
5	DMS	B	8423	4/4	0.90	0.17	59,81,83,100	0
5	DMS	C	8417	4/4	0.90	0.16	43,51,92,100	0
5	DMS	D	8409	4/4	0.90	0.14	38,41,72,100	0
5	DMS	C	8419	4/4	0.90	0.15	43,81,100,100	0
5	DMS	A	8414	4/4	0.91	0.14	26,74,75,100	0
5	DMS	D	8501	4/4	0.91	0.10	32,52,88,100	0
5	DMS	A	8410	4/4	0.91	0.15	44,82,100,100	0
5	DMS	D	8406	4/4	0.92	0.16	29,61,81,100	0
5	DMS	A	8501	4/4	0.92	0.10	46,49,91,100	0
5	DMS	A	8404	4/4	0.92	0.10	24,30,52,100	0
5	DMS	C	8414	4/4	0.92	0.14	31,48,89,100	0
5	DMS	B	8408	4/4	0.92	0.15	30,62,100,100	0
5	DMS	B	8402	4/4	0.92	0.12	35,39,52,74	0
5	DMS	B	8414	4/4	0.92	0.12	34,37,53,100	0
6	BTB	B	2002	14/14	0.92	0.14	12,53,100,100	0
5	DMS	B	8404	4/4	0.92	0.11	23,45,47,96	0
3	MG	A	3001	1/1	0.93	0.04	26,26,26,26	0
5	DMS	C	8504	4/4	0.93	0.12	42,65,81,81	0
4	NA	A	3103	1/1	0.93	0.08	42,42,42,42	0
5	DMS	A	8409	4/4	0.93	0.11	33,36,40,75	0
5	DMS	D	8414	4/4	0.93	0.12	30,60,62,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	DMS	B	8504	4/4	0.93	0.17	43,79,90,100	0
4	NA	D	3103	1/1	0.94	0.06	39,39,39,39	0
5	DMS	C	8411	4/4	0.94	0.11	42,47,52,56	0
3	MG	C	3002	1/1	0.94	0.06	26,26,26,26	0
5	DMS	A	8419	4/4	0.94	0.12	54,61,62,77	0
5	DMS	B	8405	4/4	0.94	0.14	29,48,83,100	0
5	DMS	A	8406	4/4	0.94	0.16	41,54,65,100	0
5	DMS	A	8412	4/4	0.94	0.13	31,40,69,100	0
5	DMS	C	8405	4/4	0.94	0.14	39,42,52,97	0
5	DMS	C	8408	4/4	0.94	0.13	21,53,78,100	0
4	NA	C	3103	1/1	0.95	0.13	48,48,48,48	0
5	DMS	D	8411	4/4	0.95	0.12	44,53,66,100	0
5	DMS	A	8402	4/4	0.95	0.13	24,49,63,100	0
5	DMS	A	8504	4/4	0.95	0.14	55,69,100,100	0
5	DMS	A	8408	4/4	0.95	0.11	40,50,100,100	0
4	NA	D	3102	1/1	0.95	0.06	30,30,30,30	0
5	DMS	A	8405	4/4	0.95	0.12	35,37,65,100	0
5	DMS	D	8402	4/4	0.95	0.14	24,44,46,100	0
5	DMS	D	8405	4/4	0.95	0.09	25,38,56,79	0
5	DMS	C	8412	4/4	0.95	0.10	29,31,58,80	0
5	DMS	D	8403	4/4	0.96	0.09	30,33,36,37	0
4	NA	B	3103	1/1	0.96	0.06	40,40,40,40	0
5	DMS	C	8402	4/4	0.96	0.07	19,27,40,49	0
5	DMS	D	8408	4/4	0.96	0.10	28,52,55,88	0
2	2FG	A	2001	11/12	0.96	0.06	14,22,28,29	0
3	MG	B	3002	1/1	0.96	0.07	27,27,27,27	0
5	DMS	B	8412	4/4	0.96	0.14	34,50,86,100	0
4	NA	C	3102	1/1	0.97	0.06	23,23,23,23	0
5	DMS	A	8403	4/4	0.97	0.11	21,37,52,98	0
3	MG	C	3001	1/1	0.97	0.03	23,23,23,23	0
2	2FG	D	2001	11/12	0.97	0.05	18,23,24,26	0
5	DMS	B	8411	4/4	0.97	0.11	35,40,41,50	0
5	DMS	D	8412	4/4	0.97	0.11	26,44,50,100	0
4	NA	C	3101	1/1	0.97	0.04	19,19,19,19	0
5	DMS	B	8401	4/4	0.98	0.06	21,26,29,38	0
3	MG	D	3001	1/1	0.98	0.03	19,19,19,19	0
4	NA	A	3102	1/1	0.98	0.04	31,31,31,31	0
2	2FG	B	2001	11/12	0.98	0.05	17,24,29,29	0
5	DMS	A	8411	4/4	0.98	0.07	40,42,43,51	0
5	DMS	C	8401	4/4	0.98	0.05	18,25,29,36	0
2	2FG	C	2001	11/12	0.98	0.05	19,23,26,26	0
5	DMS	C	8403	4/4	0.98	0.07	33,35,40,41	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	B	3001	1/1	0.98	0.03	21,21,21,21	0
3	MG	D	3002	1/1	0.99	0.07	26,26,26,26	0
4	NA	B	3101	1/1	0.99	0.02	19,19,19,19	0
5	DMS	B	8403	4/4	0.99	0.07	21,32,32,53	0
4	NA	D	3101	1/1	0.99	0.04	21,21,21,21	0
4	NA	A	3101	1/1	0.99	0.03	21,21,21,21	0
3	MG	A	3002	1/1	0.99	0.03	27,27,27,27	0
5	DMS	A	8401	4/4	0.99	0.05	23,24,26,27	0
5	DMS	D	8401	4/4	0.99	0.05	21,23,30,34	0
4	NA	B	3102	1/1	1.00	0.02	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.