



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 02:11 am BST

PDB ID : 1DP0
Title : E. COLI BETA-GALACTOSIDASE AT 1.7 ANGSTROM
Authors : Juers, D.H.; Jacobson, R.H.; Wigley, D.; Zhang, X.J.; Huber, R.E.; Tronrud, D.E.; Matthews, B.W.
Deposited on : 1999-12-22
Resolution : 1.70 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 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	:	2.11
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)	:	2.11

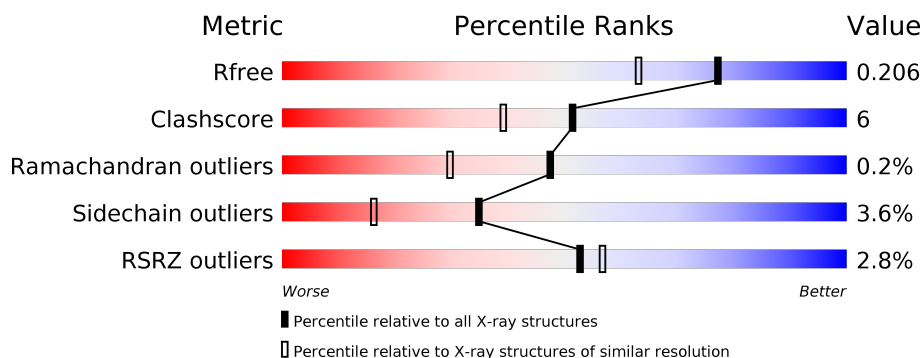
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	1023	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>..</div> </div> </div>
1	B	1023	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>21%</div> <div>..</div> </div> </div>
1	C	1023	<div> <div>3%</div> <div> <div></div> <div>75%</div> <div>20%</div> <div>...</div> </div> </div>
1	D	1023	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>19%</div> <div>..</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	DMS	A	8413	-	X	-	-
4	DMS	A	8502	-	X	-	-
4	DMS	B	8407	-	X	-	-
4	DMS	B	8413	-	X	-	-
4	DMS	B	8415	-	X	-	-
4	DMS	D	8407	-	X	-	-
4	DMS	D	8701	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 37408 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			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP P00722
A	2	SER	-	CLONING ARTIFACT	UNP P00722
A	3	HIS	-	CLONING ARTIFACT	UNP P00722
A	4	MET	-	CLONING ARTIFACT	UNP P00722
A	5	LEU	-	CLONING ARTIFACT	UNP P00722
A	6	GLU	-	CLONING ARTIFACT	UNP P00722
A	7	ASP	-	CLONING ARTIFACT	UNP P00722
A	8	PRO	-	CLONING ARTIFACT	UNP P00722
B	1	GLY	-	CLONING ARTIFACT	UNP P00722
B	2	SER	-	CLONING ARTIFACT	UNP P00722
B	3	HIS	-	CLONING ARTIFACT	UNP P00722
B	4	MET	-	CLONING ARTIFACT	UNP P00722
B	5	LEU	-	CLONING ARTIFACT	UNP P00722
B	6	GLU	-	CLONING ARTIFACT	UNP P00722
B	7	ASP	-	CLONING ARTIFACT	UNP P00722
B	8	PRO	-	CLONING ARTIFACT	UNP P00722
C	1	GLY	-	CLONING ARTIFACT	UNP P00722
C	2	SER	-	CLONING ARTIFACT	UNP P00722
C	3	HIS	-	CLONING ARTIFACT	UNP P00722
C	4	MET	-	CLONING ARTIFACT	UNP P00722
C	5	LEU	-	CLONING ARTIFACT	UNP P00722

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Chain	Residue	Modelled	Actual	Comment	Reference
C	6	GLU	-	CLONING ARTIFACT	UNP P00722
C	7	ASP	-	CLONING ARTIFACT	UNP P00722
C	8	PRO	-	CLONING ARTIFACT	UNP P00722
D	1	GLY	-	CLONING ARTIFACT	UNP P00722
D	2	SER	-	CLONING ARTIFACT	UNP P00722
D	3	HIS	-	CLONING ARTIFACT	UNP P00722
D	4	MET	-	CLONING ARTIFACT	UNP P00722
D	5	LEU	-	CLONING ARTIFACT	UNP P00722
D	6	GLU	-	CLONING ARTIFACT	UNP P00722
D	7	ASP	-	CLONING ARTIFACT	UNP P00722
D	8	PRO	-	CLONING ARTIFACT	UNP P00722

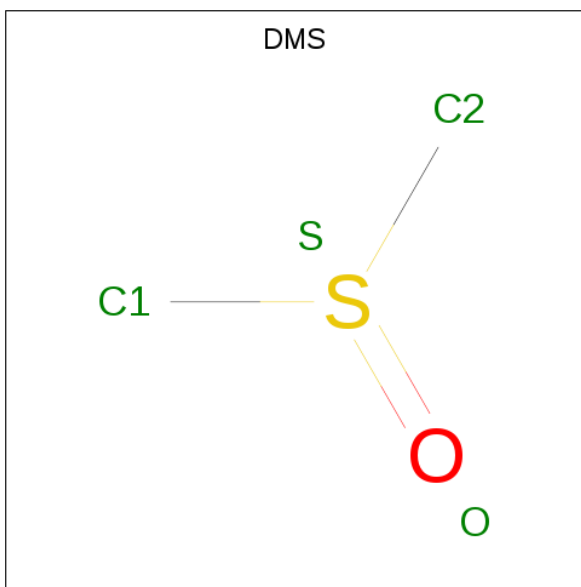
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Mg 3 3	0	0
2	A	4	Total Mg 4 4	0	0
2	D	4	Total Mg 4 4	0	0
2	C	5	Total Mg 5 5	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	5	Total Na 5 5	0	0
3	A	5	Total Na 5 5	0	0
3	D	5	Total Na 5 5	0	0
3	C	5	Total Na 5 5	0	0

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C₂H₆OS).



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

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

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

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

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

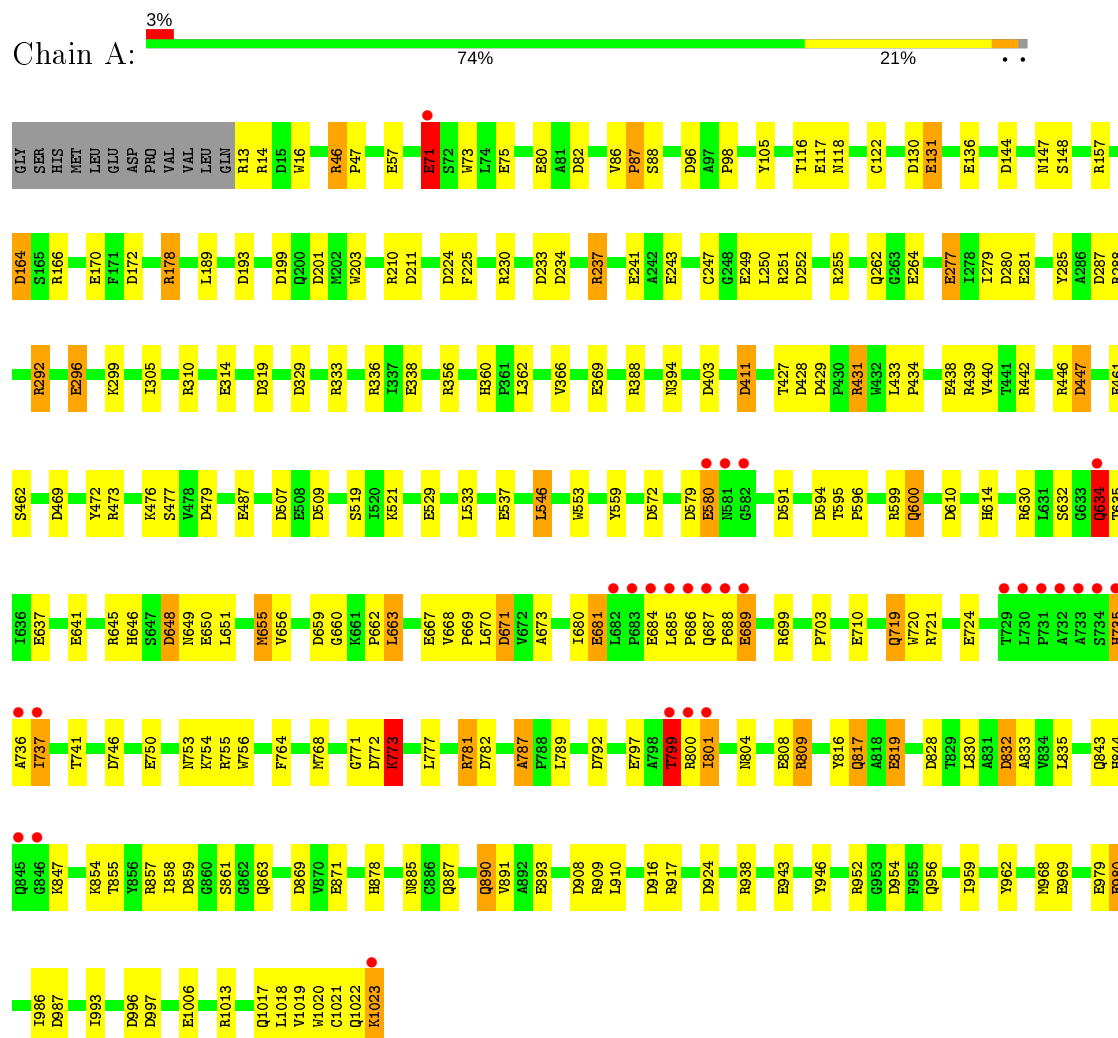
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1134	Total 1134	O 1134	0	0
5	B	1104	Total 1104	O 1104	0	0
5	C	1072	Total 1072	O 1072	0	0
5	D	1114	Total 1114	O 1114	0	0

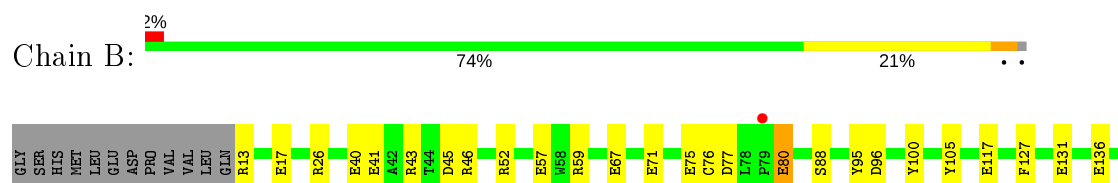
3 Residue-property plots

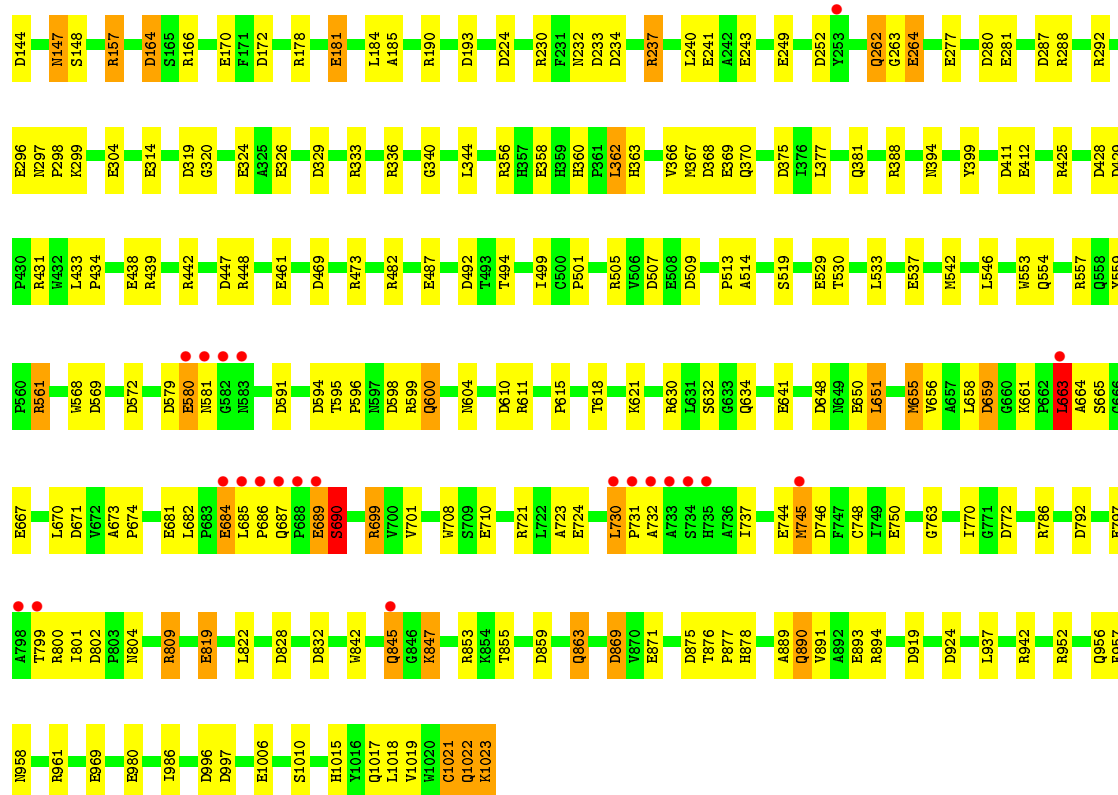
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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

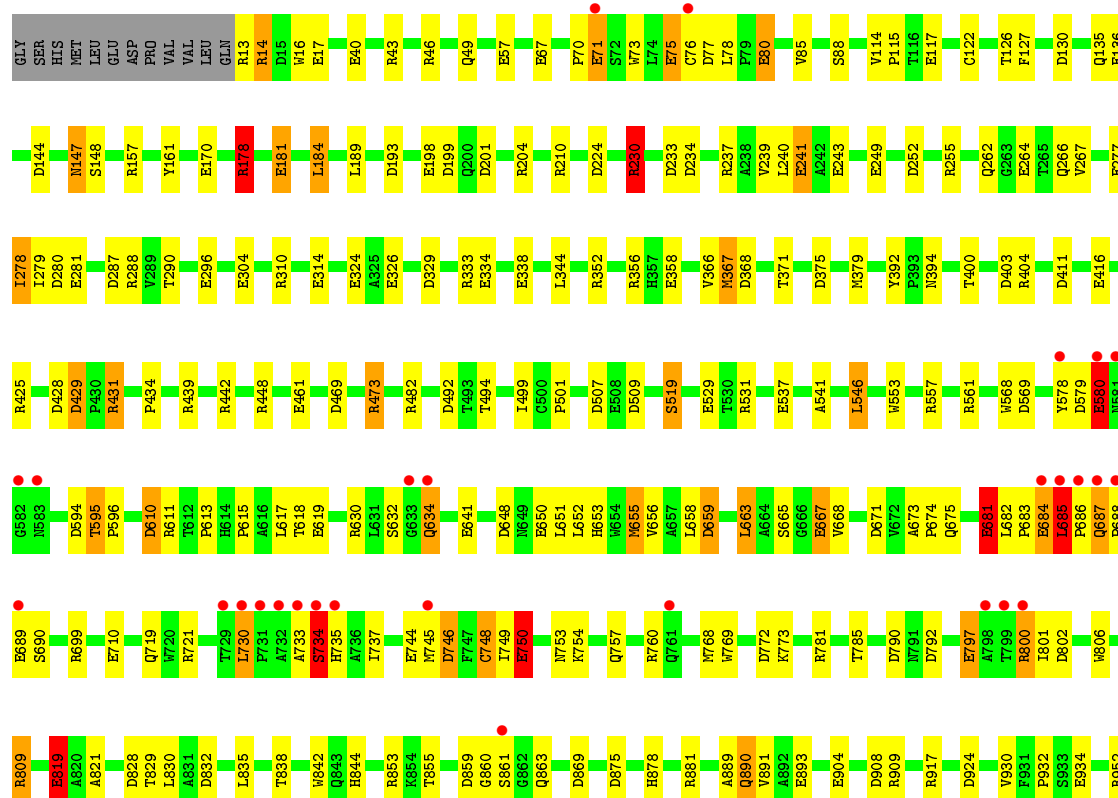
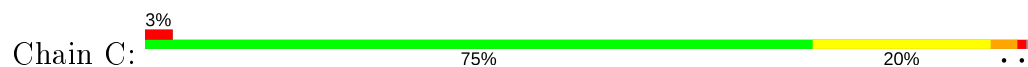


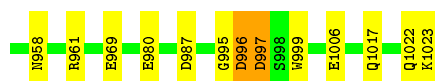
• Molecule 1: BETA-GALACTOSIDASE



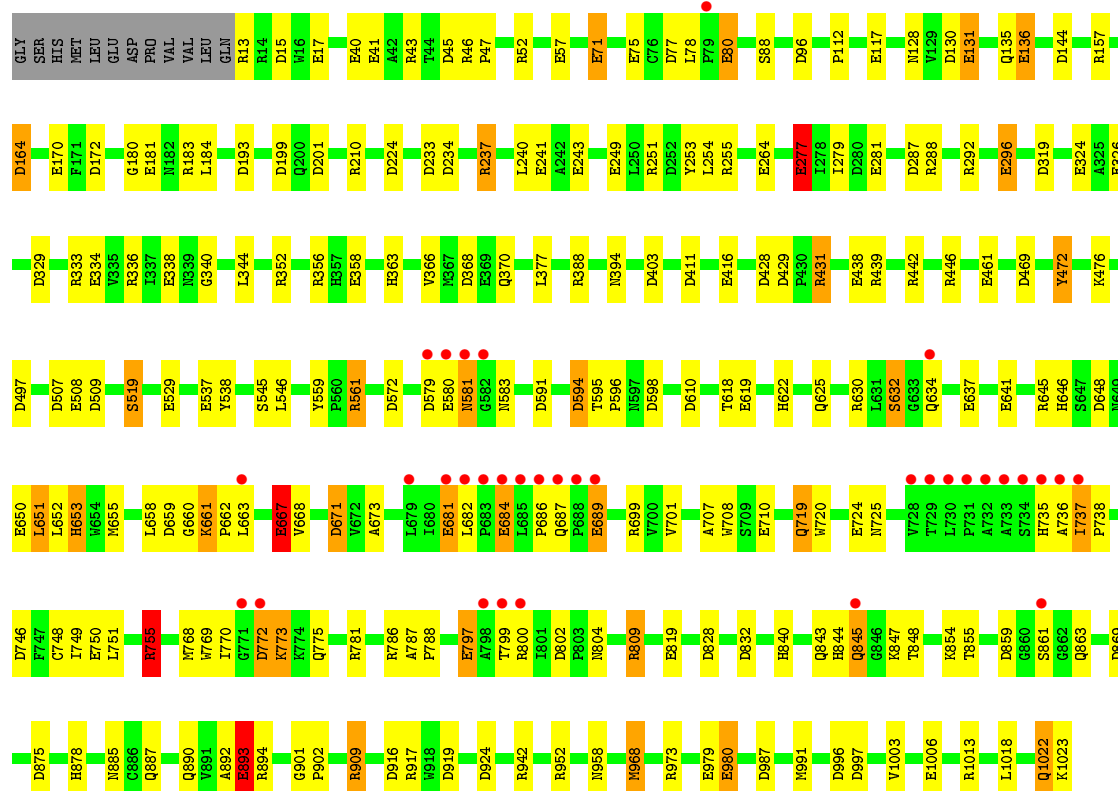
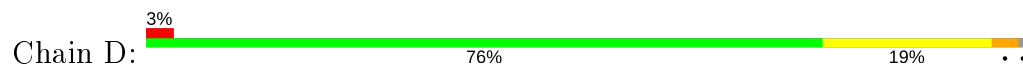


• Molecule 1: BETA-GALACTOSIDASE





● 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	149.60 Å 168.38 Å 200.69 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.70 27.49 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.6 (15.00-1.70) 98.6 (27.49-1.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 1.70 Å)	Xtrriage
Refinement program	TNT	Depositor
R, R_{free}	0.157 , 0.211 0.159 , 0.206	Depositor DCC
R_{free} test set	7913 reflections (1.46%)	wwPDB-VP
Wilson B-factor (Å ²)	13.2	Xtrriage
Anisotropy	0.235	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 90.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	37408	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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 35.66 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.6394e-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

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	1.13	39/8367 (0.5%)	1.63	166/11415 (1.5%)
1	B	1.15	50/8367 (0.6%)	1.64	163/11415 (1.4%)
1	C	1.14	51/8367 (0.6%)	1.63	150/11415 (1.3%)
1	D	1.17	47/8367 (0.6%)	1.62	163/11415 (1.4%)
All	All	1.15	187/33468 (0.6%)	1.63	642/45660 (1.4%)

The worst 5 of 187 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	71	GLU	CD-OE2	11.39	1.38	1.25
1	D	893	GLU	CD-OE2	10.72	1.37	1.25
1	D	277	GLU	CD-OE2	10.36	1.37	1.25
1	C	80	GLU	CD-OE2	9.44	1.36	1.25
1	D	650	GLU	CD-OE2	9.05	1.35	1.25

The worst 5 of 642 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	809	ARG	NE-CZ-NH1	28.53	134.56	120.30
1	B	699	ARG	NE-CZ-NH1	17.58	129.09	120.30
1	D	781	ARG	NE-CZ-NH1	16.66	128.63	120.30
1	B	699	ARG	NE-CZ-NH2	-16.65	111.97	120.30
1	C	442	ARG	NE-CZ-NH2	-16.61	112.00	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	97	0
1	B	8125	0	7716	81	0
1	C	8125	0	7716	89	0
1	D	8125	0	7716	78	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	5	0	0	0	0
2	D	4	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	112	0	168	10	0
4	B	108	0	162	5	0
4	C	112	0	168	4	0
4	D	116	0	174	7	0
5	A	1134	0	0	20	0
5	B	1104	0	0	9	0
5	C	1072	0	0	12	0
5	D	1114	0	0	13	0
All	All	37408	0	31536	358	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 6.

The worst 5 of 358 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:8407:DMS:S	4:D:8407:DMS:C1	2.02	1.47
4:A:8413:DMS:S	4:A:8413:DMS:C2	2.01	1.46
4:B:8415:DMS:C1	4:B:8415:DMS:S	2.03	1.45
4:B:8407:DMS:S	4:B:8407:DMS:C1	2.06	1.44
4:B:8508:DMS:C2	4:B:8508:DMS:S	2.10	1.40

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	1009/1023 (99%)	974 (96%)	34 (3%)	1 (0%)	51	33
1	B	1009/1023 (99%)	971 (96%)	34 (3%)	4 (0%)	34	18
1	C	1009/1023 (99%)	973 (96%)	35 (4%)	1 (0%)	51	33
1	D	1009/1023 (99%)	977 (97%)	31 (3%)	1 (0%)	51	33
All	All	4036/4092 (99%)	3895 (96%)	134 (3%)	7 (0%)	47	30

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	732	ALA
1	B	690	SER
1	B	731	PRO
1	C	734	SER
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	864/875 (99%)	835 (97%)	29 (3%)	37	18
1	B	864/875 (99%)	834 (96%)	30 (4%)	36	17
1	C	864/875 (99%)	833 (96%)	31 (4%)	35	16
1	D	864/875 (99%)	830 (96%)	34 (4%)	32	13
All	All	3456/3500 (99%)	3332 (96%)	124 (4%)	35	16

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	890	GLN
1	C	394	ASN
1	D	755	ARG
1	B	956	GLN
1	C	135	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	624	GLN
1	B	817	GLN
1	D	804	ASN
1	B	646	HIS
1	B	878	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 148 ligands modelled in this entry, 36 are monoatomic - leaving 112 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	DMS	A	8408	-	3,3,3	0.46	0	3,3,3	0.60	0
4	DMS	C	8408	-	3,3,3	0.42	0	3,3,3	0.79	0
4	DMS	B	8420	-	3,3,3	1.37	1 (33%)	3,3,3	0.37	0
4	DMS	D	8401	-	3,3,3	1.15	0	3,3,3	0.35	0
4	DMS	C	8401	-	3,3,3	0.82	0	3,3,3	0.28	0
4	DMS	C	8601	-	3,3,3	1.34	1 (33%)	3,3,3	1.03	0
4	DMS	C	8425	3	3,3,3	1.89	1 (33%)	3,3,3	0.42	0
4	DMS	B	8601	-	3,3,3	2.09	1 (33%)	3,3,3	0.66	0
4	DMS	A	8419	-	3,3,3	0.80	0	3,3,3	0.33	0
4	DMS	A	8407	-	3,3,3	2.43	2 (66%)	3,3,3	0.55	0
4	DMS	C	8410	-	3,3,3	1.18	0	3,3,3	0.03	0
4	DMS	A	8425	3	3,3,3	1.82	1 (33%)	3,3,3	0.44	0
4	DMS	B	8411	-	3,3,3	0.82	0	3,3,3	0.62	0
4	DMS	C	8423	-	3,3,3	0.91	0	3,3,3	0.21	0
4	DMS	C	8420	-	3,3,3	1.33	1 (33%)	3,3,3	0.60	0
4	DMS	D	8703	-	3,3,3	1.75	1 (33%)	3,3,3	0.32	0
4	DMS	D	8404	-	3,3,3	1.46	1 (33%)	3,3,3	0.23	0
4	DMS	D	8407	-	3,3,3	2.61	2 (66%)	3,3,3	1.39	1 (33%)
4	DMS	C	8413	-	3,3,3	1.64	1 (33%)	3,3,3	0.10	0
4	DMS	D	8425	3	3,3,3	0.63	0	3,3,3	0.74	0
4	DMS	A	8410	-	3,3,3	1.52	1 (33%)	3,3,3	1.01	0
4	DMS	D	8408	-	3,3,3	1.20	0	3,3,3	0.13	0
4	DMS	A	8404	-	3,3,3	1.33	0	3,3,3	0.05	0
4	DMS	B	8423	-	3,3,3	0.48	0	3,3,3	0.66	0
4	DMS	C	8403	-	3,3,3	0.83	0	3,3,3	0.36	0
4	DMS	A	8413	-	3,3,3	2.90	3 (100%)	3,3,3	0.62	0
4	DMS	B	8416	-	3,3,3	1.34	1 (33%)	3,3,3	0.69	0
4	DMS	A	8416	-	3,3,3	0.90	0	3,3,3	0.56	0
4	DMS	A	8602	-	3,3,3	0.92	0	3,3,3	0.42	0
4	DMS	B	8410	-	3,3,3	1.28	0	3,3,3	0.51	0
4	DMS	C	8404	-	3,3,3	0.79	0	3,3,3	1.36	1 (33%)
4	DMS	C	8506	-	3,3,3	1.50	1 (33%)	3,3,3	0.85	0
4	DMS	B	8404	-	3,3,3	0.43	0	3,3,3	0.38	0
4	DMS	D	8421	-	3,3,3	0.61	0	3,3,3	0.34	0
4	DMS	A	8504	-	3,3,3	0.25	0	3,3,3	0.54	0
4	DMS	A	8420	-	3,3,3	0.71	0	3,3,3	1.08	0
4	DMS	A	8403	-	3,3,3	1.60	1 (33%)	3,3,3	0.43	0
4	DMS	D	8411	-	3,3,3	1.06	0	3,3,3	0.27	0
4	DMS	D	8412	-	3,3,3	0.47	0	3,3,3	0.48	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	DMS	C	8405	-	3,3,3	1.52	0	3,3,3	0.55	0
4	DMS	B	8405	-	3,3,3	1.35	0	3,3,3	0.61	0
4	DMS	B	8401	-	3,3,3	0.43	0	3,3,3	0.33	0
4	DMS	C	8415	-	3,3,3	1.88	1 (33%)	3,3,3	0.85	0
4	DMS	C	8411	-	3,3,3	1.06	0	3,3,3	0.19	0
4	DMS	A	8402	-	3,3,3	1.09	0	3,3,3	0.38	0
4	DMS	D	8413	-	3,3,3	1.49	1 (33%)	3,3,3	0.93	0
4	DMS	D	8410	-	3,3,3	1.20	0	3,3,3	0.50	0
4	DMS	B	8508	-	3,3,3	2.96	1 (33%)	3,3,3	0.87	0
4	DMS	D	8415	-	3,3,3	2.21	1 (33%)	3,3,3	0.48	0
4	DMS	D	8419	-	3,3,3	0.30	0	3,3,3	0.38	0
4	DMS	D	8416	-	3,3,3	0.37	0	3,3,3	0.33	0
4	DMS	D	8705	-	3,3,3	1.99	1 (33%)	3,3,3	1.04	0
4	DMS	B	8421	-	3,3,3	0.31	0	3,3,3	0.53	0
4	DMS	B	8502	-	3,3,3	0.88	0	3,3,3	1.51	1 (33%)
4	DMS	C	8427	-	3,3,3	0.94	0	3,3,3	0.28	0
4	DMS	B	8414	-	3,3,3	1.14	0	3,3,3	0.87	0
4	DMS	A	8414	-	3,3,3	1.25	0	3,3,3	0.29	0
4	DMS	D	8402	-	3,3,3	1.20	0	3,3,3	0.29	0
4	DMS	B	8406	-	3,3,3	1.42	0	3,3,3	0.36	0
4	DMS	C	8419	-	3,3,3	0.57	0	3,3,3	0.36	0
4	DMS	A	8406	-	3,3,3	1.34	0	3,3,3	0.74	0
4	DMS	C	8402	-	3,3,3	1.65	1 (33%)	3,3,3	0.25	0
4	DMS	D	8403	-	3,3,3	1.53	1 (33%)	3,3,3	0.46	0
4	DMS	D	8417	-	3,3,3	1.25	0	3,3,3	0.38	0
4	DMS	D	8414	-	3,3,3	0.50	0	3,3,3	0.37	0
4	DMS	C	8602	-	3,3,3	1.61	1 (33%)	3,3,3	0.53	0
4	DMS	D	8423	-	3,3,3	1.38	0	3,3,3	0.26	0
4	DMS	D	8406	-	3,3,3	0.99	0	3,3,3	0.78	0
4	DMS	D	8405	-	3,3,3	0.89	0	3,3,3	0.84	0
4	DMS	B	8409	-	3,3,3	1.87	1 (33%)	3,3,3	0.65	0
4	DMS	B	8407	-	3,3,3	3.01	3 (100%)	3,3,3	0.34	0
4	DMS	A	8417	-	3,3,3	1.09	0	3,3,3	0.18	0
4	DMS	A	8502	-	3,3,3	2.39	2 (66%)	3,3,3	1.50	1 (33%)
4	DMS	C	8504	-	3,3,3	0.53	0	3,3,3	0.37	0
4	DMS	D	8701	-	3,3,3	2.31	3 (100%)	3,3,3	0.80	0
4	DMS	C	8414	-	3,3,3	1.92	1 (33%)	3,3,3	0.91	0
4	DMS	D	8427	-	3,3,3	0.84	0	3,3,3	0.11	0
4	DMS	C	8417	-	3,3,3	0.74	0	3,3,3	0.73	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	DMS	D	8409	-	3,3,3	2.10	1 (33%)	3,3,3	0.75	0
4	DMS	B	8417	-	3,3,3	0.69	0	3,3,3	0.57	0
4	DMS	A	8412	-	3,3,3	0.83	0	3,3,3	0.29	0
4	DMS	A	8427	-	3,3,3	0.65	0	3,3,3	0.68	0
4	DMS	C	8503	-	3,3,3	0.92	0	3,3,3	0.33	0
4	DMS	A	8503	-	3,3,3	1.25	0	3,3,3	0.32	0
4	DMS	B	8504	-	3,3,3	0.76	0	3,3,3	0.31	0
4	DMS	B	8427	-	3,3,3	1.15	0	3,3,3	0.09	0
4	DMS	C	8416	-	3,3,3	1.15	0	3,3,3	0.64	0
4	DMS	B	8402	-	3,3,3	1.42	0	3,3,3	0.21	0
4	DMS	B	8412	-	3,3,3	0.66	0	3,3,3	0.43	0
4	DMS	B	8413	-	3,3,3	2.74	3 (100%)	3,3,3	0.72	0
4	DMS	A	8411	-	3,3,3	1.13	0	3,3,3	0.27	0
4	DMS	D	8503	-	3,3,3	1.03	0	3,3,3	0.60	0
4	DMS	B	8408	-	3,3,3	0.19	0	3,3,3	0.70	0
4	DMS	C	8407	-	3,3,3	1.74	1 (33%)	3,3,3	0.41	0
4	DMS	A	8421	-	3,3,3	1.03	0	3,3,3	1.09	0
4	DMS	C	8421	-	3,3,3	0.64	0	3,3,3	1.63	1 (33%)
4	DMS	A	8409	-	3,3,3	2.26	1 (33%)	3,3,3	0.66	0
4	DMS	D	8501	-	3,3,3	0.46	0	3,3,3	0.20	0
4	DMS	A	8401	-	3,3,3	0.65	0	3,3,3	0.52	0
4	DMS	D	8506	-	3,3,3	1.79	1 (33%)	3,3,3	0.30	0
4	DMS	A	8423	-	3,3,3	1.58	0	3,3,3	0.53	0
4	DMS	D	8508	-	3,3,3	1.69	1 (33%)	3,3,3	0.53	0
4	DMS	C	8409	-	3,3,3	2.08	1 (33%)	3,3,3	1.03	0
4	DMS	B	8415	-	3,3,3	2.64	2 (66%)	3,3,3	1.57	1 (33%)
4	DMS	A	8501	-	3,3,3	1.57	1 (33%)	3,3,3	0.33	0
4	DMS	C	8412	-	3,3,3	1.21	0	3,3,3	0.54	0
4	DMS	A	8405	-	3,3,3	0.79	0	3,3,3	0.66	0
4	DMS	A	8415	-	3,3,3	2.10	2 (66%)	3,3,3	0.58	0
4	DMS	B	8403	-	3,3,3	1.22	0	3,3,3	0.78	0
4	DMS	C	8501	-	3,3,3	0.99	0	3,3,3	0.96	0
4	DMS	B	8506	-	3,3,3	1.69	1 (33%)	3,3,3	0.44	0
4	DMS	B	8425	3	3,3,3	3.18	2 (66%)	3,3,3	0.46	0

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	8425	DMS	O-S	5.10	1.84	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	8508	DMS	C2-S	4.62	2.10	1.75
4	B	8407	DMS	C1-S	4.11	2.06	1.75
4	B	8413	DMS	O-S	3.73	1.75	1.50
4	A	8409	DMS	O-S	3.69	1.75	1.50

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	8421	DMS	C2-S-C1	-2.81	83.96	98.44
4	A	8502	DMS	C2-S-C1	2.59	111.79	98.44
4	B	8502	DMS	C2-S-C1	2.58	111.71	98.44
4	B	8415	DMS	C2-S-C1	2.46	111.09	98.44
4	D	8407	DMS	C2-S-C1	2.41	110.84	98.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	8425	DMS	2	0
4	C	8420	DMS	1	0
4	D	8703	DMS	1	0
4	D	8407	DMS	1	0
4	A	8413	DMS	1	0
4	A	8420	DMS	1	0
4	D	8412	DMS	2	0
4	B	8508	DMS	1	0
4	B	8406	DMS	1	0
4	C	8602	DMS	2	0
4	B	8407	DMS	2	0
4	A	8502	DMS	1	0
4	D	8427	DMS	3	0
4	A	8427	DMS	3	0
4	C	8407	DMS	1	0
4	A	8409	DMS	1	0
4	B	8415	DMS	1	0
4	A	8405	DMS	1	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%)	-0.17	28 (2%) 53 57	9, 15, 43, 100	0
1	B	1011/1023 (98%)	-0.18	23 (2%) 60 65	8, 15, 43, 95	0
1	C	1011/1023 (98%)	-0.15	28 (2%) 53 57	9, 16, 45, 96	0
1	D	1011/1023 (98%)	-0.16	34 (3%) 45 50	9, 16, 46, 95	0
All	All	4044/4092 (98%)	-0.16	113 (2%) 53 57	8, 16, 45, 100	0

The worst 5 of 113 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	735	HIS	11.5
1	A	686	PRO	11.3
1	D	735	HIS	10.1
1	C	732	ALA	9.2
1	D	734	SER	8.5

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 carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NA	A	3105	1/1	0.69	0.30	35,35,35,35	1
4	DMS	B	8406	4/4	0.83	0.19	33,40,56,80	0
4	DMS	D	8506	4/4	0.86	0.14	35,45,47,55	0
4	DMS	C	8419	4/4	0.87	0.18	40,44,52,66	0
4	DMS	D	8407	4/4	0.88	0.15	30,32,39,45	0
4	DMS	D	8425	4/4	0.88	0.22	19,20,30,32	4
2	MG	A	3003	1/1	0.89	0.23	45,45,45,45	0
4	DMS	D	8415	4/4	0.89	0.14	24,41,60,70	0
4	DMS	D	8417	4/4	0.89	0.17	27,30,32,100	0
4	DMS	C	8417	4/4	0.89	0.16	31,33,56,69	0
4	DMS	D	8703	4/4	0.89	0.17	32,49,51,100	0
4	DMS	B	8415	4/4	0.89	0.12	26,29,34,47	0
4	DMS	A	8406	4/4	0.90	0.19	15,43,66,76	0
3	NA	C	3105	1/1	0.90	0.13	28,28,28,28	1
4	DMS	A	8417	4/4	0.90	0.22	28,29,56,92	0
4	DMS	C	8602	4/4	0.91	0.13	33,53,55,72	0
4	DMS	C	8423	4/4	0.91	0.12	32,41,45,57	0
3	NA	B	3105	1/1	0.91	0.12	31,31,31,31	1
4	DMS	A	8427	4/4	0.91	0.22	42,70,92,100	0
2	MG	B	3003	1/1	0.91	0.12	34,34,34,34	0
4	DMS	A	8423	4/4	0.91	0.15	34,53,63,100	0
4	DMS	A	8416	4/4	0.91	0.20	23,34,99,100	0
4	DMS	B	8407	4/4	0.92	0.19	28,30,40,44	0
4	DMS	B	8420	4/4	0.92	0.18	50,62,76,100	0
4	DMS	B	8417	4/4	0.92	0.15	26,32,64,100	0
4	DMS	B	8413	4/4	0.92	0.17	34,35,45,47	0
4	DMS	B	8427	4/4	0.92	0.10	34,34,63,64	0
4	DMS	A	8421	4/4	0.92	0.17	49,54,57,60	0
4	DMS	D	8705	4/4	0.92	0.15	22,30,36,36	0
2	MG	C	3003	1/1	0.92	0.11	22,22,22,22	1
4	DMS	D	8423	4/4	0.92	0.17	35,52,61,69	0
4	DMS	C	8503	4/4	0.93	0.14	28,49,51,55	0
4	DMS	C	8427	4/4	0.93	0.14	45,60,64,73	0
4	DMS	A	8503	4/4	0.93	0.12	32,40,42,44	0
4	DMS	D	8427	4/4	0.93	0.16	53,58,61,100	0
4	DMS	D	8416	4/4	0.93	0.17	27,41,49,100	0
4	DMS	C	8415	4/4	0.93	0.11	22,33,34,42	0
4	DMS	A	8415	4/4	0.93	0.14	21,32,59,100	0
4	DMS	B	8508	4/4	0.94	0.11	21,30,45,49	0
3	NA	D	3105	1/1	0.94	0.13	29,29,29,29	1
4	DMS	C	8420	4/4	0.94	0.14	42,45,67,100	0
4	DMS	A	8413	4/4	0.94	0.14	31,40,40,44	0
4	DMS	B	8504	4/4	0.94	0.09	23,36,42,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	DMS	B	8421	4/4	0.94	0.13	28,50,52,58	0
4	DMS	C	8416	4/4	0.94	0.20	40,48,58,61	0
2	MG	A	3005	1/1	0.94	0.10	30,30,30,30	0
4	DMS	D	8503	4/4	0.94	0.10	26,52,54,54	0
4	DMS	C	8506	4/4	0.94	0.12	34,34,45,48	0
4	DMS	D	8501	4/4	0.94	0.08	27,29,33,46	0
2	MG	D	3003	1/1	0.94	0.19	47,47,47,47	0
4	DMS	B	8416	4/4	0.94	0.17	30,40,50,52	0
4	DMS	D	8404	4/4	0.94	0.11	22,23,40,100	0
4	DMS	A	8502	4/4	0.94	0.12	24,25,48,56	0
3	NA	D	3104	1/1	0.94	0.08	34,34,34,34	0
4	DMS	B	8425	4/4	0.94	0.15	24,31,35,42	0
4	DMS	C	8421	4/4	0.95	0.14	28,43,46,72	0
4	DMS	A	8407	4/4	0.95	0.15	23,24,33,36	0
2	MG	C	3004	1/1	0.95	0.19	36,36,36,36	0
4	DMS	A	8420	4/4	0.95	0.11	35,38,40,58	0
4	DMS	C	8504	4/4	0.95	0.12	31,35,50,66	0
4	DMS	D	8508	4/4	0.95	0.09	30,34,36,45	0
4	DMS	B	8423	4/4	0.95	0.10	33,34,57,82	0
4	DMS	A	8501	4/4	0.95	0.09	17,22,33,34	0
4	DMS	B	8414	4/4	0.95	0.13	29,46,48,100	0
4	DMS	A	8602	4/4	0.95	0.21	35,49,100,100	0
4	DMS	D	8409	4/4	0.96	0.12	27,29,37,40	0
4	DMS	A	8412	4/4	0.96	0.15	30,33,36,100	0
4	DMS	A	8404	4/4	0.96	0.08	19,24,28,31	0
4	DMS	B	8502	4/4	0.96	0.14	25,26,36,36	0
4	DMS	C	8601	4/4	0.96	0.12	29,42,47,56	0
4	DMS	C	8425	4/4	0.96	0.17	29,34,40,62	0
4	DMS	A	8414	4/4	0.96	0.14	29,30,52,100	0
4	DMS	B	8410	4/4	0.96	0.14	25,34,35,42	0
4	DMS	A	8419	4/4	0.96	0.09	37,41,49,51	0
4	DMS	C	8407	4/4	0.96	0.14	27,33,35,41	0
4	DMS	C	8501	4/4	0.96	0.09	24,28,37,39	0
4	DMS	B	8409	4/4	0.96	0.10	26,28,37,38	0
4	DMS	A	8410	4/4	0.97	0.12	22,33,34,34	0
4	DMS	B	8408	4/4	0.97	0.11	28,30,37,48	0
4	DMS	D	8421	4/4	0.97	0.09	42,48,75,100	0
4	DMS	A	8504	4/4	0.97	0.08	22,36,38,65	0
4	DMS	A	8409	4/4	0.97	0.17	24,32,43,100	0
4	DMS	A	8408	4/4	0.97	0.07	15,33,34,49	0
4	DMS	C	8410	4/4	0.97	0.15	24,33,35,36	0
4	DMS	C	8413	4/4	0.97	0.15	30,33,36,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NA	D	3103	1/1	0.97	0.12	33,33,33,33	0
4	DMS	A	8425	4/4	0.97	0.10	32,36,39,39	0
4	DMS	C	8409	4/4	0.97	0.13	30,32,35,38	0
4	DMS	D	8413	4/4	0.97	0.14	26,34,34,44	0
4	DMS	D	8406	4/4	0.97	0.09	23,24,25,32	0
4	DMS	B	8601	4/4	0.97	0.09	38,38,41,42	0
4	DMS	B	8404	4/4	0.97	0.06	21,24,32,33	0
3	NA	B	3104	1/1	0.97	0.12	29,29,29,29	0
4	DMS	B	8506	4/4	0.97	0.10	42,43,45,47	0
4	DMS	D	8419	4/4	0.97	0.09	27,36,41,47	0
4	DMS	B	8402	4/4	0.98	0.07	13,16,19,21	0
4	DMS	B	8412	4/4	0.98	0.09	25,30,31,32	0
4	DMS	D	8402	4/4	0.98	0.07	15,20,20,23	0
3	NA	A	3104	1/1	0.98	0.08	25,25,25,25	0
4	DMS	A	8411	4/4	0.98	0.07	27,27,27,37	0
3	NA	A	3103	1/1	0.98	0.07	26,26,26,26	0
4	DMS	D	8411	4/4	0.98	0.09	22,23,27,62	0
4	DMS	C	8408	4/4	0.98	0.08	21,34,35,36	0
2	MG	C	3006	1/1	0.98	0.16	27,27,27,27	0
4	DMS	D	8412	4/4	0.98	0.12	23,25,29,41	0
4	DMS	D	8701	4/4	0.98	0.10	14,14,19,32	0
4	DMS	C	8405	4/4	0.98	0.07	23,23,24,27	0
4	DMS	C	8414	4/4	0.98	0.09	21,30,46,50	0
4	DMS	B	8405	4/4	0.98	0.08	25,27,28,29	0
4	DMS	D	8403	4/4	0.98	0.08	16,22,27,34	0
4	DMS	D	8408	4/4	0.98	0.11	18,28,29,34	0
4	DMS	C	8402	4/4	0.98	0.07	14,19,24,26	0
4	DMS	D	8414	4/4	0.98	0.14	22,39,95,100	0
3	NA	C	3104	1/1	0.98	0.10	28,28,28,28	0
4	DMS	C	8412	4/4	0.98	0.11	29,33,33,100	0
4	DMS	A	8402	4/4	0.98	0.07	14,16,20,26	0
3	NA	C	3103	1/1	0.98	0.06	23,23,23,23	0
4	DMS	C	8404	4/4	0.98	0.07	18,18,24,27	0
4	DMS	C	8403	4/4	0.98	0.09	18,20,22,23	0
4	DMS	D	8410	4/4	0.98	0.12	27,29,32,37	0
2	MG	D	3002	1/1	0.99	0.06	15,15,15,15	0
2	MG	A	3002	1/1	0.99	0.05	15,15,15,15	0
4	DMS	A	8403	4/4	0.99	0.06	20,21,21,25	0
4	DMS	A	8401	4/4	0.99	0.09	12,13,14,16	0
4	DMS	B	8401	4/4	0.99	0.08	14,17,18,19	0
4	DMS	C	8401	4/4	0.99	0.07	15,15,19,19	0
4	DMS	C	8411	4/4	0.99	0.11	21,26,27,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MG	D	3005	1/1	0.99	0.08	21,21,21,21	0
2	MG	D	3001	1/1	0.99	0.06	13,13,13,13	0
3	NA	A	3101	1/1	0.99	0.06	16,16,16,16	0
4	DMS	D	8405	4/4	0.99	0.09	22,23,33,39	0
4	DMS	A	8405	4/4	0.99	0.07	20,24,25,33	0
3	NA	B	3103	1/1	0.99	0.07	23,23,23,23	0
4	DMS	B	8411	4/4	0.99	0.06	23,26,29,80	0
4	DMS	B	8403	4/4	0.99	0.09	15,19,24,26	0
3	NA	B	3101	1/1	0.99	0.06	14,14,14,14	0
4	DMS	D	8401	4/4	0.99	0.06	12,13,16,17	0
3	NA	C	3101	1/1	0.99	0.06	13,13,13,13	0
3	NA	C	3102	1/1	0.99	0.06	14,14,14,14	0
2	MG	B	3002	1/1	0.99	0.06	15,15,15,15	0
2	MG	B	3001	1/1	1.00	0.06	12,12,12,12	0
3	NA	A	3102	1/1	1.00	0.08	12,12,12,12	0
2	MG	C	3002	1/1	1.00	0.07	13,13,13,13	0
3	NA	D	3101	1/1	1.00	0.05	16,16,16,16	0
3	NA	D	3102	1/1	1.00	0.06	12,12,12,12	0
3	NA	B	3102	1/1	1.00	0.05	13,13,13,13	0
2	MG	C	3001	1/1	1.00	0.04	13,13,13,13	0
2	MG	A	3001	1/1	1.00	0.06	16,16,16,16	0

6.5 Other polymers

There are no such residues in this entry.