



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:04 AM UTC

PDB ID : 5E9A / pdb_00005e9a
Title : Crystal structure analysis of the cold-adapted beta-galactosidase from *Rahnella* sp. R3
Authors : Zhang, Y.Z.; Fan, Y.T.
Deposited on : 2015-10-14
Resolution : 2.56 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

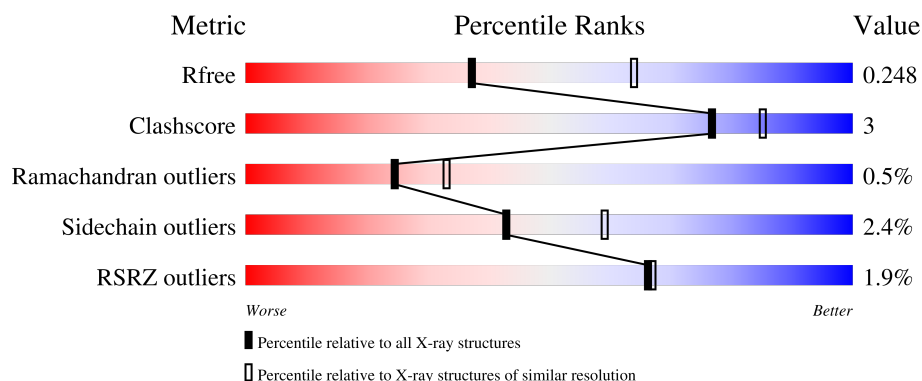
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.56 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	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

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	712	2% 84% 10% 5%
1	B	712	2% 86% 9% . .
1	C	712	2% 88% 7% .
1	D	712	2% 86% 9% .
1	E	712	2% 85% 10% . .

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Mol	Chain	Length	Quality of chain
1	F	712	 2% 88% 8% . .

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
3	ACT	F	702	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 32981 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	679	Total	C	N	O	S	0	0	0
			5387	3420	945	993	29			
1	B	684	Total	C	N	O	S	0	0	0
			5424	3443	952	1000	29			
1	C	684	Total	C	N	O	S	0	0	0
			5424	3443	952	1000	29			
1	D	684	Total	C	N	O	S	0	0	0
			5424	3443	952	1000	29			
1	E	684	Total	C	N	O	S	0	1	0
			5432	3448	955	1000	29			
1	F	684	Total	C	N	O	S	0	1	0
			5432	3448	955	1000	29			

There are 150 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP A0A0B4U8I5
A	-23	ASN	-	expression tag	UNP A0A0B4U8I5
A	-22	HIS	-	expression tag	UNP A0A0B4U8I5
A	-21	LYS	-	expression tag	UNP A0A0B4U8I5
A	-20	VAL	-	expression tag	UNP A0A0B4U8I5
A	-19	HIS	-	expression tag	UNP A0A0B4U8I5
A	-18	HIS	-	expression tag	UNP A0A0B4U8I5
A	-17	HIS	-	expression tag	UNP A0A0B4U8I5
A	-16	HIS	-	expression tag	UNP A0A0B4U8I5
A	-15	HIS	-	expression tag	UNP A0A0B4U8I5
A	-14	HIS	-	expression tag	UNP A0A0B4U8I5
A	-13	ILE	-	expression tag	UNP A0A0B4U8I5
A	-12	GLU	-	expression tag	UNP A0A0B4U8I5
A	-11	GLY	-	expression tag	UNP A0A0B4U8I5
A	-10	ARG	-	expression tag	UNP A0A0B4U8I5
A	-9	HIS	-	expression tag	UNP A0A0B4U8I5
A	-8	MET	-	expression tag	UNP A0A0B4U8I5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLU	-	expression tag	UNP A0A0B4U8I5
A	-6	LEU	-	expression tag	UNP A0A0B4U8I5
A	-5	GLY	-	expression tag	UNP A0A0B4U8I5
A	-4	THR	-	expression tag	UNP A0A0B4U8I5
A	-3	LEU	-	expression tag	UNP A0A0B4U8I5
A	-2	GLU	-	expression tag	UNP A0A0B4U8I5
A	-1	GLY	-	expression tag	UNP A0A0B4U8I5
A	0	SER	-	expression tag	UNP A0A0B4U8I5
B	-24	MET	-	initiating methionine	UNP A0A0B4U8I5
B	-23	ASN	-	expression tag	UNP A0A0B4U8I5
B	-22	HIS	-	expression tag	UNP A0A0B4U8I5
B	-21	LYS	-	expression tag	UNP A0A0B4U8I5
B	-20	VAL	-	expression tag	UNP A0A0B4U8I5
B	-19	HIS	-	expression tag	UNP A0A0B4U8I5
B	-18	HIS	-	expression tag	UNP A0A0B4U8I5
B	-17	HIS	-	expression tag	UNP A0A0B4U8I5
B	-16	HIS	-	expression tag	UNP A0A0B4U8I5
B	-15	HIS	-	expression tag	UNP A0A0B4U8I5
B	-14	HIS	-	expression tag	UNP A0A0B4U8I5
B	-13	ILE	-	expression tag	UNP A0A0B4U8I5
B	-12	GLU	-	expression tag	UNP A0A0B4U8I5
B	-11	GLY	-	expression tag	UNP A0A0B4U8I5
B	-10	ARG	-	expression tag	UNP A0A0B4U8I5
B	-9	HIS	-	expression tag	UNP A0A0B4U8I5
B	-8	MET	-	expression tag	UNP A0A0B4U8I5
B	-7	GLU	-	expression tag	UNP A0A0B4U8I5
B	-6	LEU	-	expression tag	UNP A0A0B4U8I5
B	-5	GLY	-	expression tag	UNP A0A0B4U8I5
B	-4	THR	-	expression tag	UNP A0A0B4U8I5
B	-3	LEU	-	expression tag	UNP A0A0B4U8I5
B	-2	GLU	-	expression tag	UNP A0A0B4U8I5
B	-1	GLY	-	expression tag	UNP A0A0B4U8I5
B	0	SER	-	expression tag	UNP A0A0B4U8I5
C	-24	MET	-	initiating methionine	UNP A0A0B4U8I5
C	-23	ASN	-	expression tag	UNP A0A0B4U8I5
C	-22	HIS	-	expression tag	UNP A0A0B4U8I5
C	-21	LYS	-	expression tag	UNP A0A0B4U8I5
C	-20	VAL	-	expression tag	UNP A0A0B4U8I5
C	-19	HIS	-	expression tag	UNP A0A0B4U8I5
C	-18	HIS	-	expression tag	UNP A0A0B4U8I5
C	-17	HIS	-	expression tag	UNP A0A0B4U8I5
C	-16	HIS	-	expression tag	UNP A0A0B4U8I5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-15	HIS	-	expression tag	UNP A0A0B4U8I5
C	-14	HIS	-	expression tag	UNP A0A0B4U8I5
C	-13	ILE	-	expression tag	UNP A0A0B4U8I5
C	-12	GLU	-	expression tag	UNP A0A0B4U8I5
C	-11	GLY	-	expression tag	UNP A0A0B4U8I5
C	-10	ARG	-	expression tag	UNP A0A0B4U8I5
C	-9	HIS	-	expression tag	UNP A0A0B4U8I5
C	-8	MET	-	expression tag	UNP A0A0B4U8I5
C	-7	GLU	-	expression tag	UNP A0A0B4U8I5
C	-6	LEU	-	expression tag	UNP A0A0B4U8I5
C	-5	GLY	-	expression tag	UNP A0A0B4U8I5
C	-4	THR	-	expression tag	UNP A0A0B4U8I5
C	-3	LEU	-	expression tag	UNP A0A0B4U8I5
C	-2	GLU	-	expression tag	UNP A0A0B4U8I5
C	-1	GLY	-	expression tag	UNP A0A0B4U8I5
C	0	SER	-	expression tag	UNP A0A0B4U8I5
D	-24	MET	-	initiating methionine	UNP A0A0B4U8I5
D	-23	ASN	-	expression tag	UNP A0A0B4U8I5
D	-22	HIS	-	expression tag	UNP A0A0B4U8I5
D	-21	LYS	-	expression tag	UNP A0A0B4U8I5
D	-20	VAL	-	expression tag	UNP A0A0B4U8I5
D	-19	HIS	-	expression tag	UNP A0A0B4U8I5
D	-18	HIS	-	expression tag	UNP A0A0B4U8I5
D	-17	HIS	-	expression tag	UNP A0A0B4U8I5
D	-16	HIS	-	expression tag	UNP A0A0B4U8I5
D	-15	HIS	-	expression tag	UNP A0A0B4U8I5
D	-14	HIS	-	expression tag	UNP A0A0B4U8I5
D	-13	ILE	-	expression tag	UNP A0A0B4U8I5
D	-12	GLU	-	expression tag	UNP A0A0B4U8I5
D	-11	GLY	-	expression tag	UNP A0A0B4U8I5
D	-10	ARG	-	expression tag	UNP A0A0B4U8I5
D	-9	HIS	-	expression tag	UNP A0A0B4U8I5
D	-8	MET	-	expression tag	UNP A0A0B4U8I5
D	-7	GLU	-	expression tag	UNP A0A0B4U8I5
D	-6	LEU	-	expression tag	UNP A0A0B4U8I5
D	-5	GLY	-	expression tag	UNP A0A0B4U8I5
D	-4	THR	-	expression tag	UNP A0A0B4U8I5
D	-3	LEU	-	expression tag	UNP A0A0B4U8I5
D	-2	GLU	-	expression tag	UNP A0A0B4U8I5
D	-1	GLY	-	expression tag	UNP A0A0B4U8I5
D	0	SER	-	expression tag	UNP A0A0B4U8I5
E	-24	MET	-	initiating methionine	UNP A0A0B4U8I5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-23	ASN	-	expression tag	UNP A0A0B4U8I5
E	-22	HIS	-	expression tag	UNP A0A0B4U8I5
E	-21	LYS	-	expression tag	UNP A0A0B4U8I5
E	-20	VAL	-	expression tag	UNP A0A0B4U8I5
E	-19	HIS	-	expression tag	UNP A0A0B4U8I5
E	-18	HIS	-	expression tag	UNP A0A0B4U8I5
E	-17	HIS	-	expression tag	UNP A0A0B4U8I5
E	-16	HIS	-	expression tag	UNP A0A0B4U8I5
E	-15	HIS	-	expression tag	UNP A0A0B4U8I5
E	-14	HIS	-	expression tag	UNP A0A0B4U8I5
E	-13	ILE	-	expression tag	UNP A0A0B4U8I5
E	-12	GLU	-	expression tag	UNP A0A0B4U8I5
E	-11	GLY	-	expression tag	UNP A0A0B4U8I5
E	-10	ARG	-	expression tag	UNP A0A0B4U8I5
E	-9	HIS	-	expression tag	UNP A0A0B4U8I5
E	-8	MET	-	expression tag	UNP A0A0B4U8I5
E	-7	GLU	-	expression tag	UNP A0A0B4U8I5
E	-6	LEU	-	expression tag	UNP A0A0B4U8I5
E	-5	GLY	-	expression tag	UNP A0A0B4U8I5
E	-4	THR	-	expression tag	UNP A0A0B4U8I5
E	-3	LEU	-	expression tag	UNP A0A0B4U8I5
E	-2	GLU	-	expression tag	UNP A0A0B4U8I5
E	-1	GLY	-	expression tag	UNP A0A0B4U8I5
E	0	SER	-	expression tag	UNP A0A0B4U8I5
F	-24	MET	-	initiating methionine	UNP A0A0B4U8I5
F	-23	ASN	-	expression tag	UNP A0A0B4U8I5
F	-22	HIS	-	expression tag	UNP A0A0B4U8I5
F	-21	LYS	-	expression tag	UNP A0A0B4U8I5
F	-20	VAL	-	expression tag	UNP A0A0B4U8I5
F	-19	HIS	-	expression tag	UNP A0A0B4U8I5
F	-18	HIS	-	expression tag	UNP A0A0B4U8I5
F	-17	HIS	-	expression tag	UNP A0A0B4U8I5
F	-16	HIS	-	expression tag	UNP A0A0B4U8I5
F	-15	HIS	-	expression tag	UNP A0A0B4U8I5
F	-14	HIS	-	expression tag	UNP A0A0B4U8I5
F	-13	ILE	-	expression tag	UNP A0A0B4U8I5
F	-12	GLU	-	expression tag	UNP A0A0B4U8I5
F	-11	GLY	-	expression tag	UNP A0A0B4U8I5
F	-10	ARG	-	expression tag	UNP A0A0B4U8I5
F	-9	HIS	-	expression tag	UNP A0A0B4U8I5
F	-8	MET	-	expression tag	UNP A0A0B4U8I5
F	-7	GLU	-	expression tag	UNP A0A0B4U8I5

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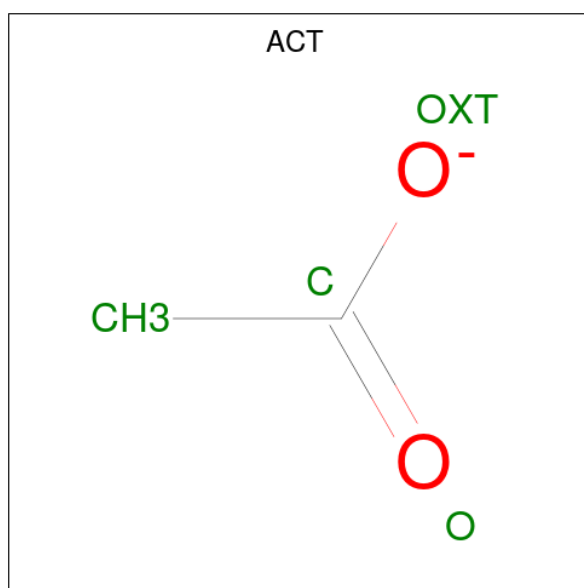
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Chain	Residue	Modelled	Actual	Comment	Reference
F	-6	LEU	-	expression tag	UNP A0A0B4U8I5
F	-5	GLY	-	expression tag	UNP A0A0B4U8I5
F	-4	THR	-	expression tag	UNP A0A0B4U8I5
F	-3	LEU	-	expression tag	UNP A0A0B4U8I5
F	-2	GLU	-	expression tag	UNP A0A0B4U8I5
F	-1	GLY	-	expression tag	UNP A0A0B4U8I5
F	0	SER	-	expression tag	UNP A0A0B4U8I5

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	C	1	Total C O 4 2 2	0	0
3	D	1	Total C O 4 2 2	0	0
3	E	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

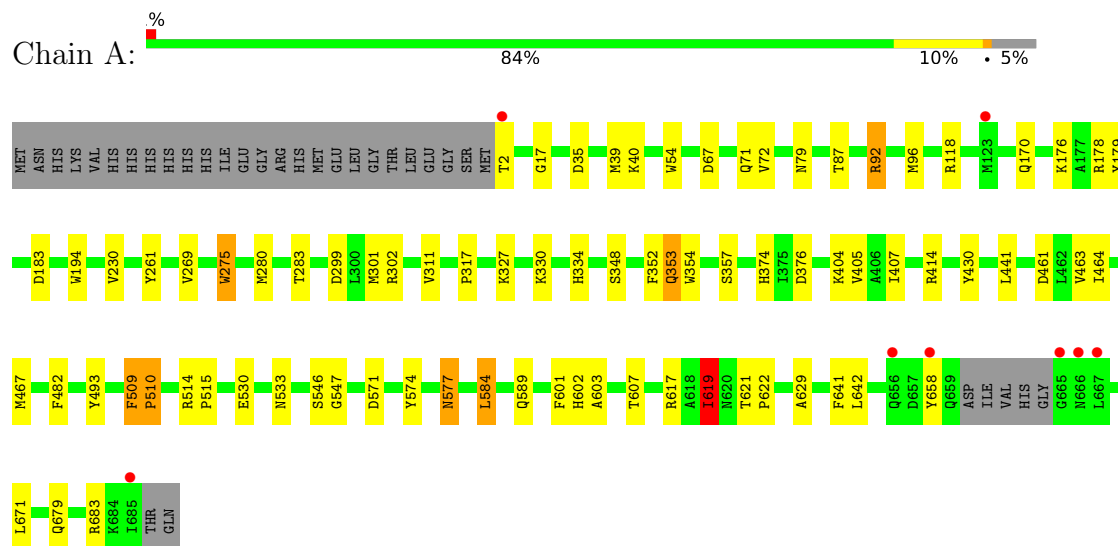
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	105	Total O 105 105	0	0
4	B	56	Total O 56 56	0	0
4	C	66	Total O 66 66	0	0
4	D	99	Total O 99 99	0	0
4	E	48	Total O 48 48	0	0
4	F	54	Total O 54 54	0	0

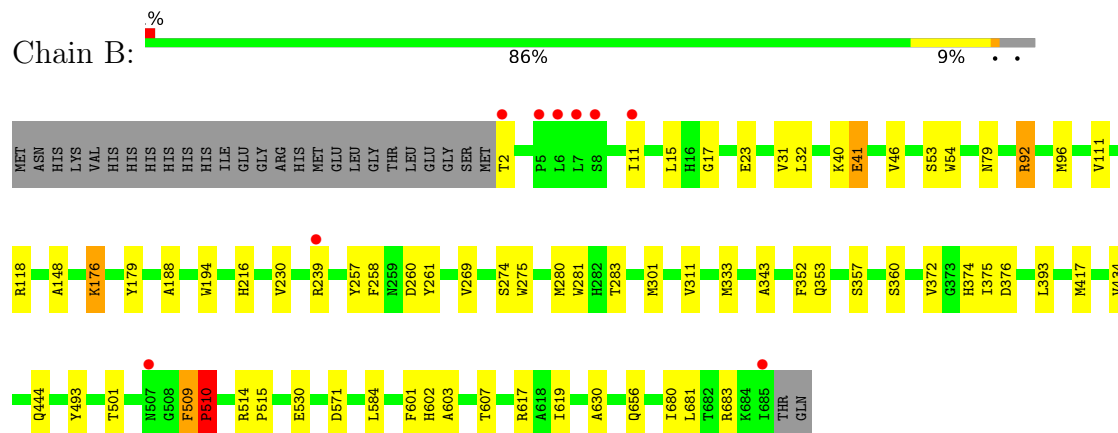
3 Residue-property plots [i](#)

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

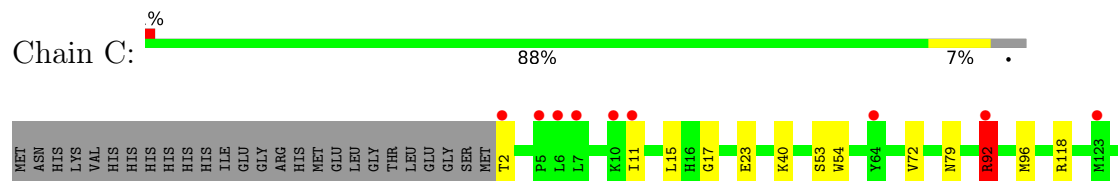
• Molecule 1: Beta-galactosidase

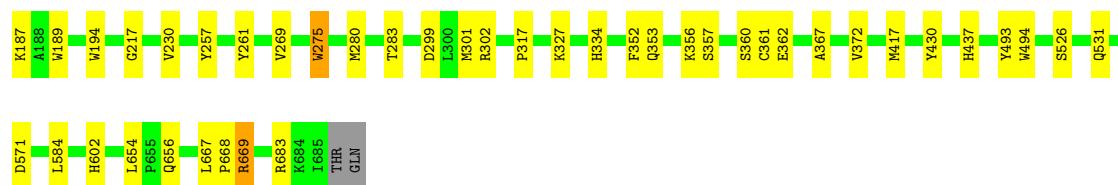


• Molecule 1: Beta-galactosidase

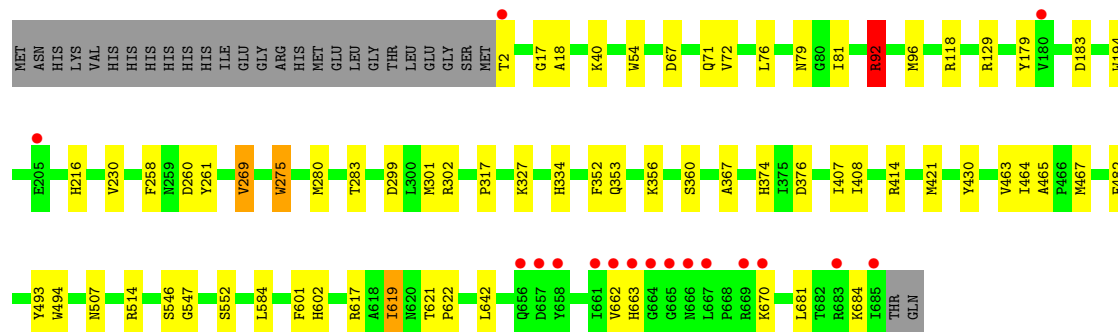
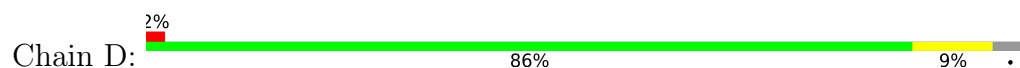


• Molecule 1: Beta-galactosidase

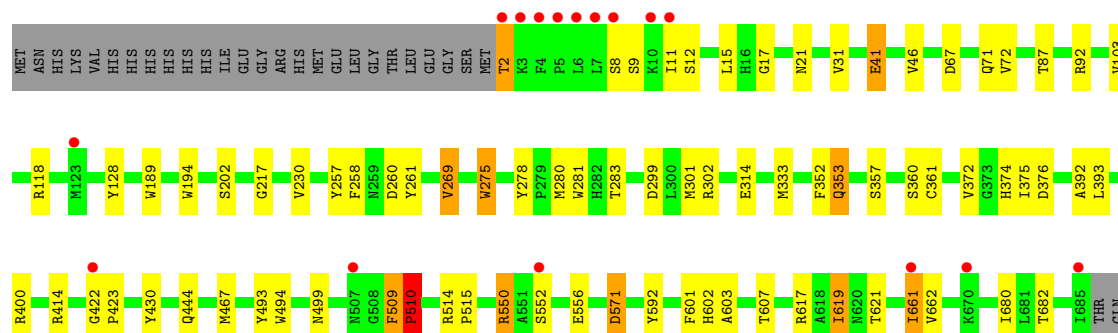
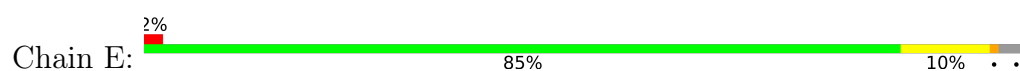




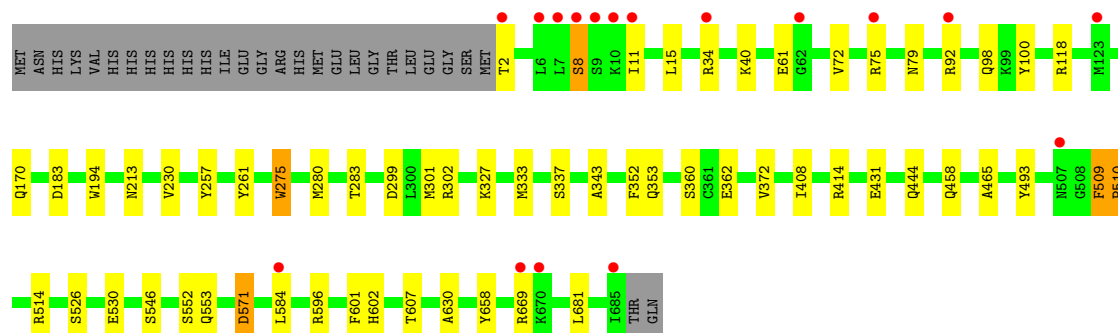
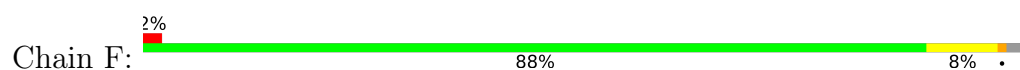
• Molecule 1: Beta-galactosidase



• Molecule 1: Beta-galactosidase



• 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	146.43Å 106.83Å 164.24Å 90.00° 109.00° 90.00°	Depositor
Resolution (Å)	138.45 – 2.56 138.45 – 2.56	Depositor EDS
% Data completeness (in resolution range)	98.5 (138.45-2.56) 98.5 (138.45-2.56)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.55Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.199 , 0.247 0.204 , 0.248	Depositor DCC
R_{free} test set	2020 reflections (1.33%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	32981	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.29% of the height of the origin peak. No significant pseudotranslation is detected.*

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: ZN, ACT

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	0.93	1/5540 (0.0%)	1.05	12/7537 (0.2%)
1	B	0.88	0/5579	1.00	12/7592 (0.2%)
1	C	0.86	0/5579	0.97	6/7592 (0.1%)
1	D	0.92	1/5579 (0.0%)	1.00	8/7592 (0.1%)
1	E	0.84	0/5590	1.01	16/7607 (0.2%)
1	F	0.84	0/5590	1.01	8/7606 (0.1%)
All	All	0.88	2/33457 (0.0%)	1.01	62/45526 (0.1%)

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	A	0	1
1	B	0	1
1	D	0	1
1	E	0	2
1	F	0	1
All	All	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	662	VAL	CA-CB	5.54	1.61	1.54
1	A	178	ARG	C-O	-5.20	1.18	1.24

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	509	PHE	CA-C-N	18.55	143.03	119.84
1	A	509	PHE	C-N-CA	18.55	143.03	119.84
1	F	509	PHE	CA-C-N	16.77	140.81	119.84
1	F	509	PHE	C-N-CA	16.77	140.81	119.84
1	E	509	PHE	CA-C-N	13.53	136.76	119.84
1	E	509	PHE	C-N-CA	13.53	136.76	119.84
1	B	509	PHE	CA-C-N	11.52	134.24	119.84
1	B	509	PHE	C-N-CA	11.52	134.24	119.84
1	E	661	ILE	CB-CA-C	-9.31	99.56	112.14
1	E	275	TRP	N-CA-C	7.10	119.72	109.14
1	B	352	PHE	CA-C-N	7.01	134.93	121.54
1	B	352	PHE	C-N-CA	7.01	134.93	121.54
1	B	352	PHE	N-CA-CB	6.90	121.11	109.87
1	A	509	PHE	C-N-CD	-6.82	97.03	125.00
1	B	352	PHE	O-C-N	6.65	131.20	123.02
1	E	352	PHE	CA-C-N	6.57	134.08	121.54
1	E	352	PHE	C-N-CA	6.57	134.08	121.54
1	D	275	TRP	N-CA-C	6.34	118.41	108.96
1	A	179	TYR	N-CA-C	-6.33	99.38	109.76
1	E	352	PHE	O-C-N	6.24	130.31	123.13
1	F	509	PHE	C-N-CD	-6.21	99.52	125.00
1	B	619	ILE	CB-CA-C	-6.18	100.99	110.50
1	E	552	SER	N-CA-C	6.15	123.90	110.80
1	E	352	PHE	N-CA-CB	6.14	120.48	110.17
1	B	510	PRO	N-CA-C	-6.07	99.97	112.47
1	E	550	ARG	NE-CZ-NH2	6.02	124.61	119.20
1	A	619	ILE	CB-CA-C	-6.01	101.24	110.50
1	C	352	PHE	N-CA-CB	5.92	118.83	109.71
1	F	669	ARG	CG-CD-NE	-5.89	99.03	112.00
1	A	275	TRP	N-CA-C	5.88	116.85	108.74
1	E	619	ILE	CB-CA-C	-5.82	100.64	110.71
1	D	17	GLY	N-CA-C	5.73	120.37	111.08
1	E	509	PHE	C-N-CD	-5.64	101.88	125.00
1	A	87	THR	N-CA-C	-5.49	103.15	110.07
1	E	510	PRO	N-CA-C	-5.46	101.22	112.47
1	A	352	PHE	N-CA-CB	5.44	118.74	109.87
1	C	92	ARG	NE-CZ-NH1	5.43	126.94	121.50
1	B	148	ALA	N-CA-C	5.42	117.88	111.33
1	F	571	ASP	N-CA-C	5.40	117.19	109.14
1	B	434	VAL	N-CA-C	-5.40	105.24	110.42
1	D	352	PHE	CA-C-N	5.39	131.83	121.54
1	D	352	PHE	C-N-CA	5.39	131.83	121.54
1	A	17	GLY	N-CA-C	5.34	120.29	111.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	509	PHE	C-N-CD	-5.32	103.18	125.00
1	A	533	ASN	N-CA-C	-5.32	101.36	108.86
1	A	352	PHE	CA-C-N	5.30	131.67	121.54
1	A	352	PHE	C-N-CA	5.30	131.67	121.54
1	F	75	ARG	CB-CA-C	-5.30	101.84	110.85
1	D	269	VAL	N-CA-CB	-5.26	106.43	112.21
1	F	275	TRP	N-CA-C	5.22	116.75	108.96
1	E	571	ASP	N-CA-C	5.22	116.22	108.86
1	D	92	ARG	NE-CZ-NH1	5.19	126.69	121.50
1	C	275	TRP	N-CA-C	5.18	116.69	108.96
1	B	111	VAL	N-CA-C	-5.18	104.17	108.63
1	E	87	THR	N-CA-C	-5.18	103.51	109.93
1	C	667	LEU	CA-C-N	-5.16	115.41	120.52
1	C	667	LEU	C-N-CA	-5.16	115.41	120.52
1	C	17	GLY	N-CA-C	5.14	119.97	111.59
1	F	352	PHE	N-CA-CB	5.06	118.04	109.94
1	D	179	TYR	N-CA-C	-5.05	102.29	110.32
1	D	18	ALA	N-CA-C	5.03	116.16	108.42
1	E	269	VAL	N-CA-CB	-5.02	105.78	112.26

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	509	PHE	Peptide
1	B	509	PHE	Peptide
1	D	670	LYS	Peptide
1	E	422	GLY	Peptide
1	E	509	PHE	Peptide
1	F	509	PHE	Peptide

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	5387	0	5151	41	0
1	B	5424	0	5186	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	5424	0	5186	26	0
1	D	5424	0	5186	32	0
1	E	5432	0	5199	38	0
1	F	5432	0	5199	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0
3	C	4	0	3	1	0
3	D	4	0	3	0	0
3	E	4	0	3	1	0
3	F	4	0	3	2	0
4	A	105	0	0	5	0
4	B	56	0	0	1	0
4	C	66	0	0	2	0
4	D	99	0	0	2	0
4	E	48	0	0	2	0
4	F	54	0	0	3	0
All	All	32981	0	31125	185	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 3.

All (185) 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)
3:E:702:ACT:H2	4:E:825:HOH:O	1.81	0.80
1:E:661:ILE:HD11	1:E:682:THR:HB	1.66	0.78
1:F:414:ARG:HD2	4:F:808:HOH:O	1.90	0.71
1:D:92:ARG:HG2	1:D:92:ARG:HH11	1.57	0.69
1:E:230:VAL:HG21	1:E:261:TYR:CZ	2.28	0.69
1:C:362:GLU:OE2	3:C:702:ACT:H2	1.93	0.68
1:F:230:VAL:HG21	1:F:261:TYR:CZ	2.28	0.67
1:B:656:GLN:OE1	1:B:683:ARG:NH1	2.28	0.66
1:C:230:VAL:HG21	1:C:261:TYR:CZ	2.31	0.65
1:E:661:ILE:HD11	1:E:682:THR:CB	2.26	0.65
1:B:230:VAL:HG21	1:B:261:TYR:CZ	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:299:ASP:OD1	1:D:302:ARG:NH2	2.31	0.63
1:A:230:VAL:HG21	1:A:261:TYR:CZ	2.35	0.61
1:F:275:TRP:CD1	1:F:301:MET:HG3	2.36	0.61
1:F:327:LYS:NZ	4:F:801:HOH:O	2.33	0.60
1:D:275:TRP:CD1	1:D:301:MET:HG3	2.36	0.60
1:A:619:ILE:HD11	1:A:642:LEU:HD21	1.81	0.60
1:C:275:TRP:CD1	1:C:301:MET:HG3	2.38	0.59
1:D:230:VAL:HG21	1:D:261:TYR:CZ	2.38	0.59
1:E:353:GLN:NE2	4:E:801:HOH:O	2.36	0.59
1:A:353:GLN:NE2	4:A:801:HOH:O	2.35	0.59
1:C:92:ARG:HG2	1:C:92:ARG:HH11	1.68	0.58
3:F:702:ACT:H1	4:F:842:HOH:O	2.02	0.58
1:F:362:GLU:OE2	3:F:702:ACT:H2	2.03	0.57
1:D:507:ASN:O	1:D:514:ARG:NH1	2.37	0.57
1:B:281:TRP:CD2	1:B:333:MET:HE2	2.39	0.57
1:F:280:MET:HE2	1:F:283:THR:HG21	1.87	0.57
1:E:11:ILE:HG21	1:E:15:LEU:HD21	1.86	0.56
1:A:92:ARG:HH11	1:A:92:ARG:N	2.05	0.55
1:C:437:HIS:HA	1:C:602:HIS:HD2	1.72	0.55
1:D:414:ARG:HD2	4:D:818:HOH:O	2.06	0.55
1:E:499:ASN:OD1	1:E:499:ASN:C	2.51	0.54
1:A:601:PHE:HD2	1:A:602:HIS:HD2	1.55	0.54
1:C:40:LYS:HD2	1:C:79:ASN:HB3	1.90	0.54
1:A:275:TRP:CD1	1:A:301:MET:HG3	2.43	0.53
1:A:299:ASP:OD1	1:A:302:ARG:NH2	2.42	0.53
1:E:275:TRP:CD1	1:E:301:MET:HG3	2.44	0.52
1:F:510:PRO:HD2	1:F:514:ARG:HB2	1.90	0.52
1:A:619:ILE:CD1	1:A:642:LEU:HD21	2.40	0.52
1:A:374:HIS:HD2	1:A:376:ASP:H	1.58	0.52
1:D:601:PHE:HD2	1:D:602:HIS:HD2	1.58	0.52
1:A:54:TRP:CZ2	1:A:96:MET:HE1	2.45	0.52
1:E:194:TRP:CE2	1:F:118:ARG:HD3	2.44	0.51
1:E:202:SER:OG	1:F:98:GLN:NE2	2.43	0.51
1:C:654:LEU:O	1:C:669:ARG:HG3	2.09	0.51
1:B:11:ILE:HG21	1:B:15:LEU:HD21	1.92	0.51
1:B:601:PHE:HD2	1:B:602:HIS:HD2	1.59	0.51
1:B:603:ALA:O	1:B:607:THR:HG23	2.11	0.51
1:E:601:PHE:HD2	1:E:602:HIS:HD2	1.58	0.51
1:A:67:ASP:O	1:A:71:GLN:HG2	2.11	0.50
1:B:374:HIS:HD2	1:B:376:ASP:H	1.58	0.50
1:F:658:TYR:CD2	1:F:681:LEU:HD23	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:SER:OG	1:A:547:GLY:N	2.45	0.49
1:A:330:LYS:NZ	4:A:802:HOH:O	2.43	0.49
1:C:654:LEU:HD12	1:C:668:PRO:O	2.12	0.49
1:B:92:ARG:O	1:B:92:ARG:HD2	2.12	0.49
1:A:510:PRO:HD2	1:A:514:ARG:HB2	1.94	0.49
1:E:17:GLY:HA3	1:E:46:VAL:O	2.12	0.49
1:B:681:LEU:HD12	1:B:681:LEU:N	2.28	0.48
1:D:619:ILE:HD11	1:D:642:LEU:HD21	1.95	0.48
1:C:656:GLN:OE1	1:C:683:ARG:CZ	2.62	0.48
1:D:430:TYR:HD1	1:D:467:MET:HE3	1.79	0.48
1:D:327:LYS:HG2	1:F:526:SER:O	2.14	0.48
1:E:392:ALA:HB3	1:E:662:VAL:HG12	1.95	0.47
1:B:393:LEU:HD11	1:B:680:ILE:HD13	1.95	0.47
1:B:194:TRP:CE2	1:C:118:ARG:HD3	2.50	0.47
1:F:40:LYS:HD2	1:F:79:ASN:HB3	1.96	0.47
1:A:280:MET:HE2	1:A:283:THR:HG21	1.97	0.47
1:A:603:ALA:O	1:A:607:THR:HG23	2.14	0.47
1:D:546:SER:OG	1:D:547:GLY:N	2.48	0.47
1:E:280:MET:HE2	1:E:283:THR:HG21	1.97	0.47
1:A:414:ARG:HD2	4:A:820:HOH:O	2.14	0.47
1:D:356:LYS:HG3	1:D:367:ALA:HB3	1.97	0.47
1:A:35:ASP:O	1:A:39:MET:HG3	2.15	0.47
1:B:374:HIS:HD2	1:B:376:ASP:N	2.13	0.47
1:B:17:GLY:HA3	1:B:46:VAL:O	2.14	0.46
1:B:275:TRP:CD1	1:B:301:MET:HG3	2.49	0.46
1:B:514:ARG:HB3	1:B:515:PRO:HD3	1.96	0.46
1:D:408:ILE:HD12	1:D:465:ALA:HB2	1.96	0.46
1:A:327:LYS:HG2	1:C:526:SER:O	2.16	0.46
1:A:629:ALA:HA	1:A:641:PHE:O	2.15	0.46
1:C:327:LYS:NZ	4:C:804:HOH:O	2.47	0.46
1:D:194:TRP:CE2	1:E:118:ARG:HD3	2.51	0.46
1:A:430:TYR:HD1	1:A:467:MET:HE3	1.80	0.46
1:A:40:LYS:HD2	1:A:79:ASN:HB3	1.98	0.46
1:D:40:LYS:HD3	1:D:79:ASN:HB3	1.97	0.46
1:F:333:MET:HE3	1:F:337:SER:HB3	1.98	0.46
1:E:510:PRO:HD2	1:E:514:ARG:HB2	1.98	0.46
1:D:280:MET:HE2	1:D:283:THR:HG21	1.98	0.46
1:D:129:ARG:HG3	4:D:832:HOH:O	2.15	0.46
1:A:407:ILE:HG12	1:A:464:ILE:HB	1.98	0.45
1:D:407:ILE:HG12	1:D:464:ILE:HB	1.98	0.45
1:F:601:PHE:HD2	1:F:602:HIS:HD2	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:LEU:HD11	1:B:680:ILE:CD1	2.47	0.45
1:A:317:PRO:HA	1:A:334:HIS:CE1	2.51	0.45
1:D:317:PRO:HA	1:D:334:HIS:CE1	2.51	0.45
1:E:603:ALA:O	1:E:607:THR:HG23	2.17	0.45
1:A:194:TRP:CE2	1:B:118:ARG:HD3	2.51	0.45
1:E:67:ASP:O	1:E:71:GLN:HG2	2.17	0.45
1:D:118:ARG:HD3	1:F:194:TRP:CE2	2.51	0.45
1:F:408:ILE:HD12	1:F:465:ALA:HB2	1.99	0.45
1:E:556:GLU:OE1	1:E:592:TYR:OH	2.22	0.45
1:E:41:GLU:HG2	1:E:375:ILE:HD11	1.99	0.45
1:F:61:GLU:OE2	1:F:100:TYR:OH	2.35	0.45
1:B:32:LEU:HB3	4:B:850:HOH:O	2.17	0.44
1:B:176:LYS:O	1:B:179:TYR:O	2.35	0.44
1:D:463:VAL:HG23	1:D:482:PHE:CZ	2.52	0.44
1:E:430:TYR:HD1	1:E:467:MET:HE3	1.82	0.44
1:B:54:TRP:CZ2	1:B:96:MET:HE1	2.52	0.44
1:B:258:PHE:CE2	1:B:260:ASP:HB2	2.52	0.44
1:B:274:SER:HA	1:B:311:VAL:O	2.17	0.44
1:B:280:MET:HE2	1:B:283:THR:HG21	1.99	0.44
1:E:444:GLN:CD	1:E:607:THR:HG22	2.42	0.44
1:A:577:ASN:HB3	4:A:862:HOH:O	2.16	0.44
1:E:661:ILE:CD1	1:E:682:THR:HG21	2.47	0.44
1:C:92:ARG:HH11	1:C:92:ARG:CG	2.30	0.44
1:D:67:ASP:O	1:D:71:GLN:HG2	2.17	0.44
1:E:281:TRP:CD2	1:E:333:MET:HE2	2.52	0.44
1:B:23:GLU:OE1	1:B:53:SER:OG	2.30	0.44
1:A:39:MET:HA	1:A:354:TRP:CH2	2.53	0.43
1:D:374:HIS:HD2	1:D:376:ASP:H	1.66	0.43
1:D:258:PHE:CE2	1:D:260:ASP:HB2	2.53	0.43
1:A:353:GLN:HG2	4:A:892:HOH:O	2.18	0.43
1:C:417:MET:HE1	1:C:430:TYR:CD1	2.53	0.43
1:D:54:TRP:CZ2	1:D:96:MET:HE1	2.53	0.43
1:A:327:LYS:NZ	4:C:805:HOH:O	2.51	0.43
1:F:213:ASN:OD1	1:F:213:ASN:N	2.51	0.43
1:A:514:ARG:HB3	1:A:515:PRO:HD3	2.00	0.43
1:A:584:LEU:HD12	1:A:589:GLN:HG2	2.00	0.43
1:A:311:VAL:HG13	1:A:348:SER:HB3	2.00	0.43
1:C:356:LYS:HG3	1:C:367:ALA:HB3	2.01	0.43
1:B:216:HIS:NE2	1:C:361:CYS:HA	2.34	0.43
1:A:658:TYR:HD1	1:A:683:ARG:HB2	1.83	0.43
1:E:278:TYR:OH	1:E:314:GLU:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:103:VAL:HG12	1:E:128:TYR:HB2	2.01	0.43
1:E:550:ARG:HH21	1:E:550:ARG:HG2	1.84	0.43
1:A:327:LYS:HE2	1:C:531:GLN:OE1	2.19	0.42
1:C:280:MET:HE2	1:C:283:THR:HG21	2.01	0.42
1:B:92:ARG:HD2	1:B:92:ARG:C	2.43	0.42
1:F:11:ILE:HG21	1:F:15:LEU:HD21	2.00	0.42
1:E:299:ASP:OD1	1:E:302:ARG:NH2	2.52	0.42
1:F:444:GLN:CD	1:F:607:THR:HG22	2.44	0.42
1:F:414:ARG:NH1	1:F:431:GLU:OE2	2.53	0.42
1:B:510:PRO:HD2	1:B:514:ARG:HB2	2.01	0.42
1:F:553:GLN:OE1	1:F:596:ARG:NH1	2.44	0.42
1:E:374:HIS:HD2	1:E:376:ASP:N	2.17	0.42
1:A:118:ARG:HD3	1:C:194:TRP:CE2	2.55	0.42
1:B:188:ALA:HB1	1:B:501:THR:HG21	2.02	0.42
1:B:417:MET:HE2	1:B:417:MET:HB3	1.90	0.42
1:E:189:TRP:CD1	1:E:217:GLY:HA3	2.55	0.42
1:A:404:LYS:HD3	1:A:461:ASP:OD2	2.19	0.41
1:A:621:THR:OG1	1:A:622:PRO:HD2	2.20	0.41
1:A:671:LEU:HD11	1:A:679:GLN:OE1	2.20	0.41
1:E:374:HIS:HD2	1:E:376:ASP:H	1.68	0.41
1:E:510:PRO:HD2	1:E:514:ARG:CB	2.50	0.41
1:C:189:TRP:CD1	1:C:217:GLY:HA3	2.55	0.41
1:A:405:VAL:HG11	1:A:441:LEU:HD13	2.01	0.41
1:B:41:GLU:HG2	1:B:375:ILE:HD11	2.02	0.41
1:E:514:ARG:HB3	1:E:515:PRO:HD3	2.02	0.41
1:D:621:THR:OG1	1:D:622:PRO:HD2	2.20	0.41
1:E:258:PHE:CE2	1:E:260:ASP:HB2	2.56	0.41
1:E:619:ILE:CG2	1:E:621:THR:HG22	2.51	0.41
1:A:463:VAL:HG23	1:A:482:PHE:CZ	2.56	0.41
1:C:54:TRP:CZ2	1:C:96:MET:HE1	2.55	0.41
1:B:40:LYS:HD2	1:B:79:ASN:HB3	2.03	0.41
1:C:11:ILE:HG21	1:C:15:LEU:HD21	2.02	0.41
1:C:317:PRO:HA	1:C:334:HIS:CE1	2.56	0.41
1:D:76:LEU:HD22	1:D:81:ILE:HG21	2.02	0.41
1:D:216:HIS:NE2	1:E:361:CYS:HA	2.36	0.41
1:D:619:ILE:CD1	1:D:642:LEU:HD21	2.50	0.41
1:D:681:LEU:N	1:D:681:LEU:HD12	2.36	0.41
1:F:299:ASP:OD1	1:F:302:ARG:NH2	2.54	0.41
1:D:421:MET:HE2	1:D:421:MET:HB3	1.96	0.41
1:B:444:GLN:CD	1:B:607:THR:HG22	2.46	0.40
1:C:299:ASP:OD1	1:C:302:ARG:NH2	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:574:TYR:O	1:A:577:ASN:HB2	2.21	0.40
1:B:343:ALA:HB1	1:B:630:ALA:HB3	2.02	0.40
1:D:642:LEU:HD23	1:D:642:LEU:HA	1.92	0.40
1:E:2:THR:C	1:E:400:ARG:HE	2.30	0.40
1:F:343:ALA:HB1	1:F:630:ALA:HB3	2.02	0.40
1:F:8:SER:HB3	1:F:11:ILE:HG12	2.03	0.40
1:C:23:GLU:OE1	1:C:53:SER:OG	2.37	0.40
1:E:393:LEU:HD11	1:E:680:ILE:HD13	2.03	0.40
1:E:414:ARG:HD3	1:E:430:TYR:HD2	1.85	0.40
1:C:92:ARG:HG2	1:C:92:ARG:NH1	2.34	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	675/712 (95%)	650 (96%)	22 (3%)	3 (0%)	30	39
1	B	682/712 (96%)	652 (96%)	26 (4%)	4 (1%)	21	28
1	C	682/712 (96%)	654 (96%)	25 (4%)	3 (0%)	30	39
1	D	682/712 (96%)	654 (96%)	25 (4%)	3 (0%)	30	39
1	E	683/712 (96%)	649 (95%)	29 (4%)	5 (1%)	18	25
1	F	683/712 (96%)	651 (95%)	28 (4%)	4 (1%)	21	28
All	All	4087/4272 (96%)	3910 (96%)	155 (4%)	22 (0%)	24	33

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	510	PRO
1	B	510	PRO

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Mol	Chain	Res	Type
1	D	663	HIS
1	E	493	TYR
1	E	510	PRO
1	F	510	PRO
1	C	493	TYR
1	D	493	TYR
1	A	493	TYR
1	B	353	GLN
1	D	353	GLN
1	E	257	TYR
1	E	353	GLN
1	F	257	TYR
1	F	493	TYR
1	A	353	GLN
1	B	493	TYR
1	C	353	GLN
1	C	257	TYR
1	E	423	PRO
1	F	353	GLN
1	B	257	TYR

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	563/592 (95%)	549 (98%)	14 (2%)	42	58
1	B	567/592 (96%)	553 (98%)	14 (2%)	42	58
1	C	567/592 (96%)	555 (98%)	12 (2%)	47	63
1	D	567/592 (96%)	555 (98%)	12 (2%)	47	63
1	E	568/592 (96%)	552 (97%)	16 (3%)	38	54
1	F	568/592 (96%)	553 (97%)	15 (3%)	40	57
All	All	3400/3552 (96%)	3317 (98%)	83 (2%)	43	59

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	72	VAL
1	A	92	ARG
1	A	170	GLN
1	A	176	LYS
1	A	183	ASP
1	A	269	VAL
1	A	357	SER
1	A	530	GLU
1	A	571	ASP
1	A	577	ASN
1	A	584	LEU
1	A	617	ARG
1	A	619	ILE
1	B	2	THR
1	B	31	VAL
1	B	41	GLU
1	B	92	ARG
1	B	176	LYS
1	B	239	ARG
1	B	269	VAL
1	B	357	SER
1	B	360	SER
1	B	372	VAL
1	B	530	GLU
1	B	571	ASP
1	B	584	LEU
1	B	617	ARG
1	C	2	THR
1	C	72	VAL
1	C	92	ARG
1	C	187	LYS
1	C	269	VAL
1	C	357	SER
1	C	360	SER
1	C	372	VAL
1	C	494	TRP
1	C	571	ASP
1	C	584	LEU
1	C	669	ARG
1	D	2	THR
1	D	72	VAL
1	D	92	ARG

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Mol	Chain	Res	Type
1	D	183	ASP
1	D	269	VAL
1	D	360	SER
1	D	494	TRP
1	D	552	SER
1	D	584	LEU
1	D	617	ARG
1	D	619	ILE
1	D	684	LYS
1	E	2	THR
1	E	8	SER
1	E	9	SER
1	E	12	SER
1	E	21	ASN
1	E	31	VAL
1	E	41	GLU
1	E	72	VAL
1	E	92	ARG
1	E	269	VAL
1	E	357	SER
1	E	360	SER
1	E	372	VAL
1	E	494	TRP
1	E	571	ASP
1	E	617	ARG
1	F	2	THR
1	F	8	SER
1	F	34	ARG
1	F	72	VAL
1	F	92	ARG
1	F	170	GLN
1	F	183	ASP
1	F	360	SER
1	F	372	VAL
1	F	458	GLN
1	F	530	GLU
1	F	546	SER
1	F	552	SER
1	F	571	ASP
1	F	584	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	HIS
1	A	229	GLN
1	A	374	HIS
1	A	589	GLN
1	A	650	GLN
1	B	340	GLN
1	B	353	GLN
1	B	374	HIS
1	B	429	HIS
1	B	650	GLN
1	C	121	HIS
1	C	229	GLN
1	C	259	ASN
1	C	340	GLN
1	C	350	GLN
1	C	374	HIS
1	C	429	HIS
1	C	583	ASN
1	C	602	HIS
1	C	646	ASN
1	D	121	HIS
1	D	229	GLN
1	D	374	HIS
1	D	643	GLN
1	D	650	GLN
1	D	666	ASN
1	E	259	ASN
1	E	350	GLN
1	E	353	GLN
1	E	374	HIS
1	E	429	HIS
1	E	597	ASN
1	E	650	GLN
1	F	21	ASN
1	F	219	ASN
1	F	353	GLN
1	F	374	HIS
1	F	458	GLN
1	F	583	ASN
1	F	646	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	$\# Z > 2$
3	ACT	B	702	-	3,3,3	0.84	0	3,3,3	0.92	0
3	ACT	E	702	-	3,3,3	0.67	0	3,3,3	1.38	0
3	ACT	F	702	-	3,3,3	0.86	0	3,3,3	0.42	0
3	ACT	C	702	-	3,3,3	0.85	0	3,3,3	0.24	0
3	ACT	A	702	-	3,3,3	0.88	0	3,3,3	0.59	0
3	ACT	D	702	-	3,3,3	0.44	0	3,3,3	1.88	2 (66%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	D	702	ACT	OXT-C-CH3	2.43	125.24	115.05
3	D	702	ACT	O-C-CH3	-2.15	113.72	122.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	702	ACT	1	0
3	F	702	ACT	2	0
3	C	702	ACT	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

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	679/712 (95%)	-0.18	8 (1%) 76 78	15, 25, 44, 81	0
1	B	684/712 (96%)	-0.01	9 (1%) 75 76	19, 30, 49, 82	0
1	C	684/712 (96%)	0.09	9 (1%) 75 76	19, 32, 52, 80	0
1	D	684/712 (96%)	-0.14	17 (2%) 58 59	16, 25, 45, 84	0
1	E	684/712 (96%)	0.12	16 (2%) 61 62	21, 34, 52, 87	1 (0%)
1	F	684/712 (96%)	0.18	17 (2%) 58 59	21, 34, 56, 81	1 (0%)
All	All	4099/4272 (95%)	0.01	76 (1%) 66 67	15, 30, 51, 87	2 (0%)

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	663	HIS	4.7
1	E	11	ILE	4.6
1	B	2	THR	4.2
1	E	670	LYS	4.0
1	E	7	LEU	4.0
1	C	2	THR	4.0
1	D	658	TYR	3.8
1	B	7	LEU	3.8
1	F	2	THR	3.7
1	D	661	ILE	3.4
1	B	507	ASN	3.4
1	A	666	ASN	3.4
1	E	2	THR	3.4
1	A	2	THR	3.4
1	C	6	LEU	3.2
1	F	8	SER	3.1
1	F	507	ASN	3.1
1	E	6	LEU	3.0
1	C	5	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	667	LEU	3.0
1	D	665	GLY	3.0
1	F	11	ILE	2.9
1	D	662	VAL	2.8
1	C	92	ARG	2.8
1	F	62	GLY	2.7
1	E	10	LYS	2.7
1	B	6	LEU	2.7
1	C	7	LEU	2.7
1	F	123	MET	2.7
1	A	667	LEU	2.6
1	E	507	ASN	2.6
1	E	5	PRO	2.6
1	F	669	ARG	2.6
1	D	2	THR	2.6
1	A	665	GLY	2.6
1	A	685	ILE	2.6
1	D	685	ILE	2.6
1	E	661	ILE	2.6
1	F	7	LEU	2.6
1	B	8	SER	2.5
1	F	670	LYS	2.5
1	B	11	ILE	2.5
1	A	658	TYR	2.4
1	B	685	ILE	2.4
1	C	10	LYS	2.4
1	B	5	PRO	2.3
1	F	34	ARG	2.3
1	C	64	TYR	2.3
1	D	656	GLN	2.3
1	D	666	ASN	2.3
1	D	664	GLY	2.3
1	D	683	ARG	2.2
1	F	92	ARG	2.2
1	F	6	LEU	2.2
1	D	205	GLU	2.2
1	D	669	ARG	2.2
1	D	180	VAL	2.2
1	E	4	PHE	2.2
1	C	123	MET	2.1
1	C	11	ILE	2.1
1	F	75	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	657	ASP	2.1
1	A	656	GLN	2.1
1	E	422	GLY	2.1
1	D	670	LYS	2.1
1	A	123	MET	2.1
1	B	239	ARG	2.1
1	E	8	SER	2.1
1	F	584	LEU	2.1
1	E	685	ILE	2.1
1	F	685	ILE	2.1
1	F	10	LYS	2.1
1	E	552	SER	2.1
1	E	123	MET	2.1
1	E	3	LYS	2.0
1	F	9	SER	2.0

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(Å ²)	Q<0.9
3	ACT	B	702	4/4	0.66	0.20	35,38,40,43	0
3	ACT	D	702	4/4	0.66	0.22	34,37,40,45	0
3	ACT	A	702	4/4	0.75	0.19	35,37,39,43	0
3	ACT	F	702	4/4	0.78	0.17	41,43,44,45	0
3	ACT	C	702	4/4	0.80	0.17	41,42,44,49	0
3	ACT	E	702	4/4	0.88	0.15	30,32,32,34	0
2	ZN	D	701	1/1	0.99	0.02	27,27,27,27	0
2	ZN	E	701	1/1	0.99	0.02	37,37,37,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	F	701	1/1	0.99	0.02	36,36,36,36	0
2	ZN	A	701	1/1	1.00	0.01	24,24,24,24	0
2	ZN	B	701	1/1	1.00	0.02	32,32,32,32	0
2	ZN	C	701	1/1	1.00	0.02	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.