



wwPDB X-ray Structure Validation Summary Report i

Feb 5, 2024 – 12:21 PM JST

PDB ID : 8WY1
Title : The structure of cyclization domain in cyclic beta-1,2-glucan synthase from Thermoanaerobacter italicus
Authors : Tanaka, N.; Saito, R.; Kobayashi, K.; Nakai, H.; Kamo, S.; Kuramochi, K.; Taguchi, H.; Nakajima, M.; Masaike, T.
Deposited on : 2023-10-30
Resolution : 3.90 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 i 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](#) ①) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

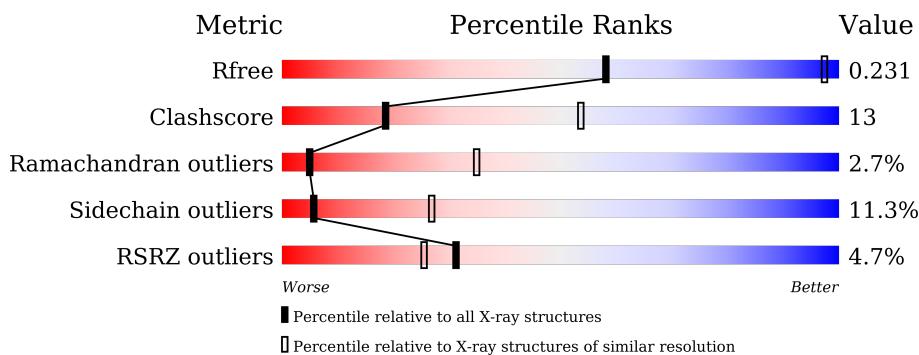
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

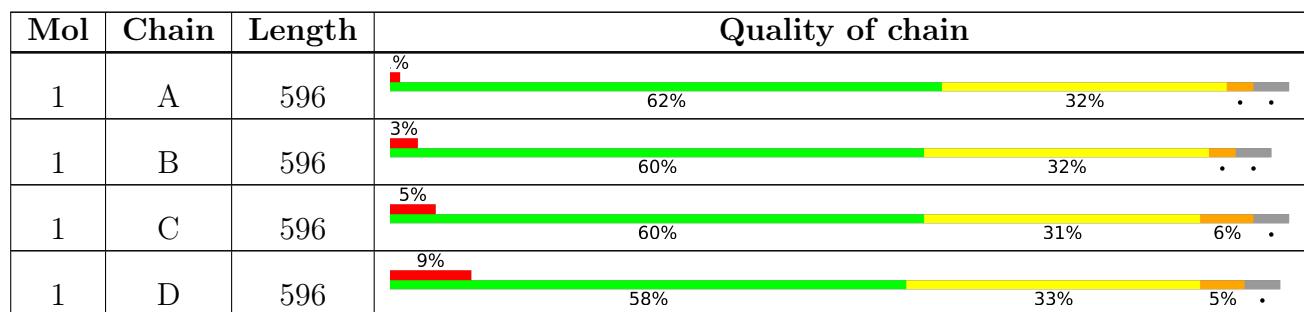
The reported resolution of this entry is 3.90 Å.

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	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)

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.



2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 18842 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 Glycosyltransferase 36.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	574	Total	C 4715	N 3047	O 772	S 881	15	0	0
1	B	573	Total	C 4706	N 3042	O 771	S 878	15	0	0
1	C	573	Total	C 4706	N 3042	O 771	S 878	15	0	0
1	D	574	Total	C 4715	N 3047	O 772	S 881	15	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1004	MET	-	initiating methionine	UNP D3T4C1
A	1592	LEU	-	expression tag	UNP D3T4C1
A	1593	GLU	-	expression tag	UNP D3T4C1
A	1594	HIS	-	expression tag	UNP D3T4C1
A	1595	HIS	-	expression tag	UNP D3T4C1
A	1596	HIS	-	expression tag	UNP D3T4C1
A	1597	HIS	-	expression tag	UNP D3T4C1
A	1598	HIS	-	expression tag	UNP D3T4C1
A	1599	HIS	-	expression tag	UNP D3T4C1
B	1004	MET	-	initiating methionine	UNP D3T4C1
B	1592	LEU	-	expression tag	UNP D3T4C1
B	1593	GLU	-	expression tag	UNP D3T4C1
B	1594	HIS	-	expression tag	UNP D3T4C1
B	1595	HIS	-	expression tag	UNP D3T4C1
B	1596	HIS	-	expression tag	UNP D3T4C1
B	1597	HIS	-	expression tag	UNP D3T4C1
B	1598	HIS	-	expression tag	UNP D3T4C1
B	1599	HIS	-	expression tag	UNP D3T4C1
C	1004	MET	-	initiating methionine	UNP D3T4C1
C	1592	LEU	-	expression tag	UNP D3T4C1
C	1593	GLU	-	expression tag	UNP D3T4C1

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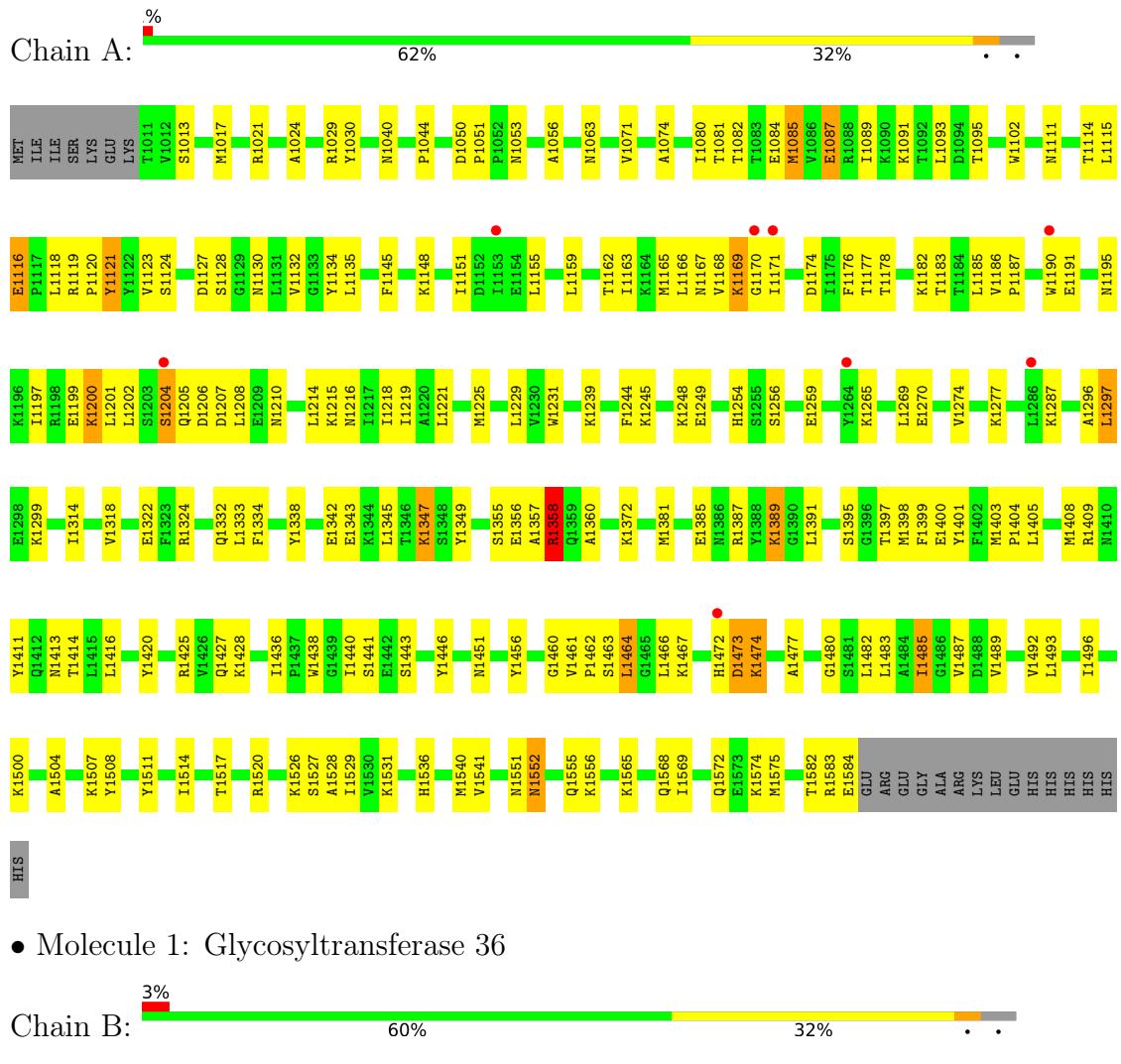
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Chain	Residue	Modelled	Actual	Comment	Reference
C	1594	HIS	-	expression tag	UNP D3T4C1
C	1595	HIS	-	expression tag	UNP D3T4C1
C	1596	HIS	-	expression tag	UNP D3T4C1
C	1597	HIS	-	expression tag	UNP D3T4C1
C	1598	HIS	-	expression tag	UNP D3T4C1
C	1599	HIS	-	expression tag	UNP D3T4C1
D	1004	MET	-	initiating methionine	UNP D3T4C1
D	1592	LEU	-	expression tag	UNP D3T4C1
D	1593	GLU	-	expression tag	UNP D3T4C1
D	1594	HIS	-	expression tag	UNP D3T4C1
D	1595	HIS	-	expression tag	UNP D3T4C1
D	1596	HIS	-	expression tag	UNP D3T4C1
D	1597	HIS	-	expression tag	UNP D3T4C1
D	1598	HIS	-	expression tag	UNP D3T4C1
D	1599	HIS	-	expression tag	UNP D3T4C1

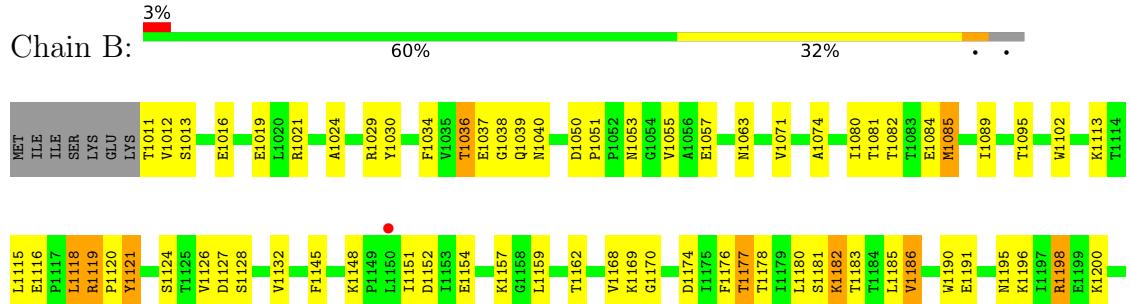
3 Residue-property plots

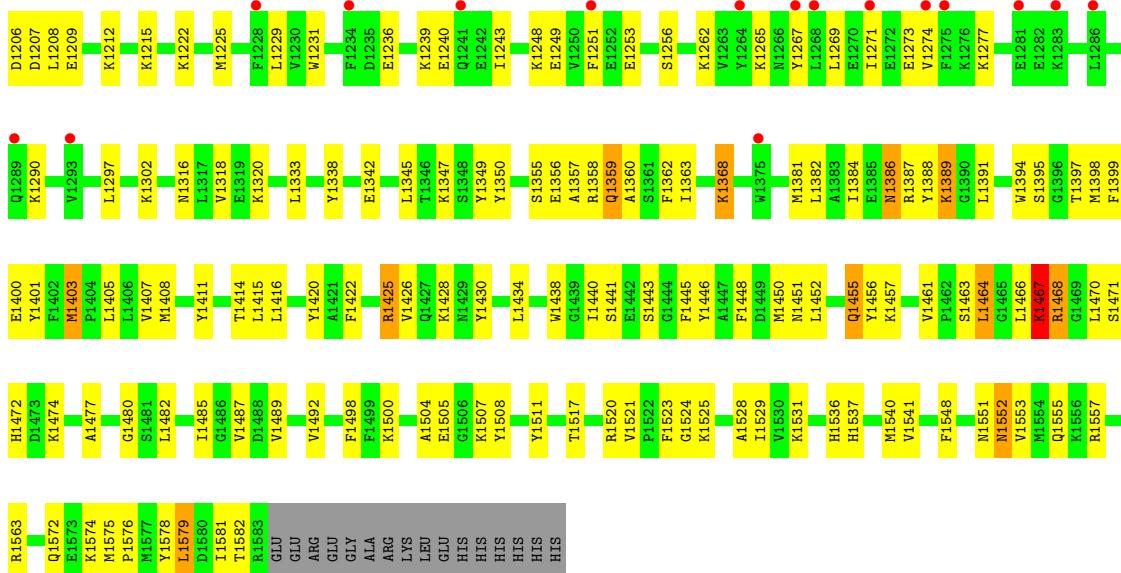
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Glycosyltransferase 36

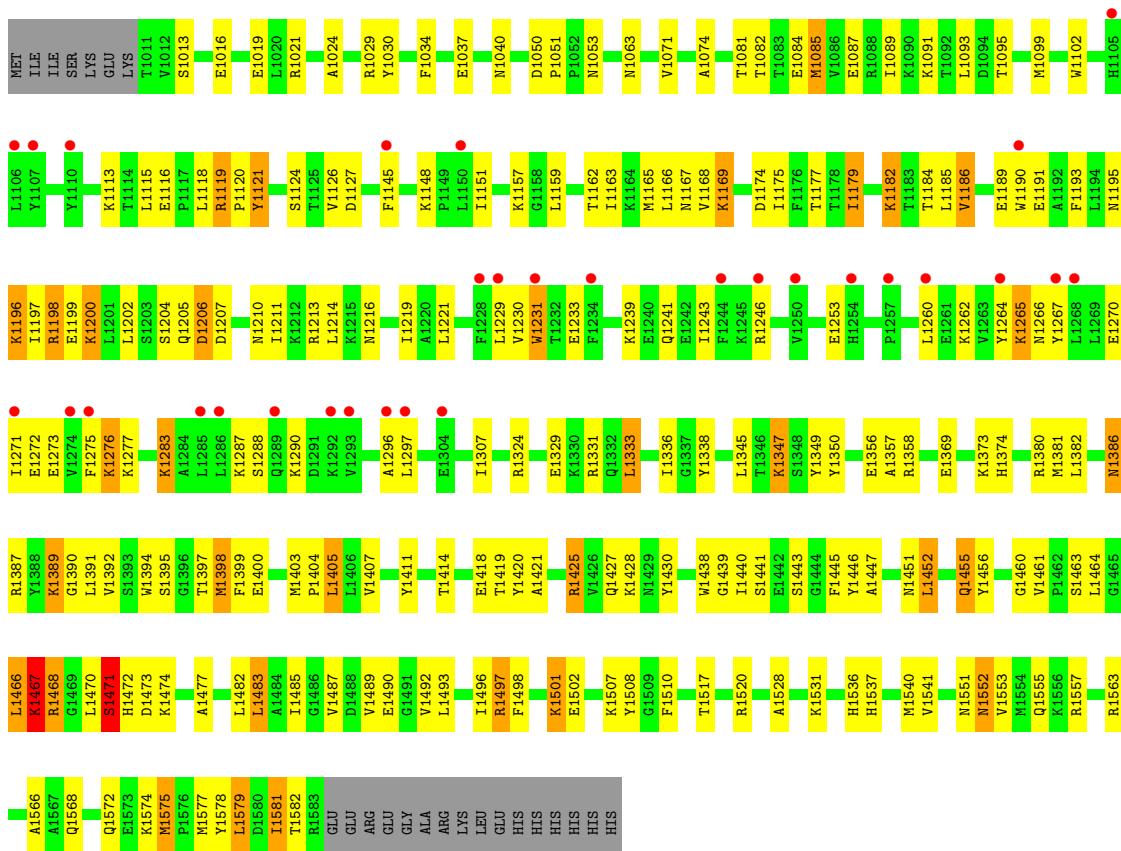


- Molecule 1: Glycosyltransferase 36



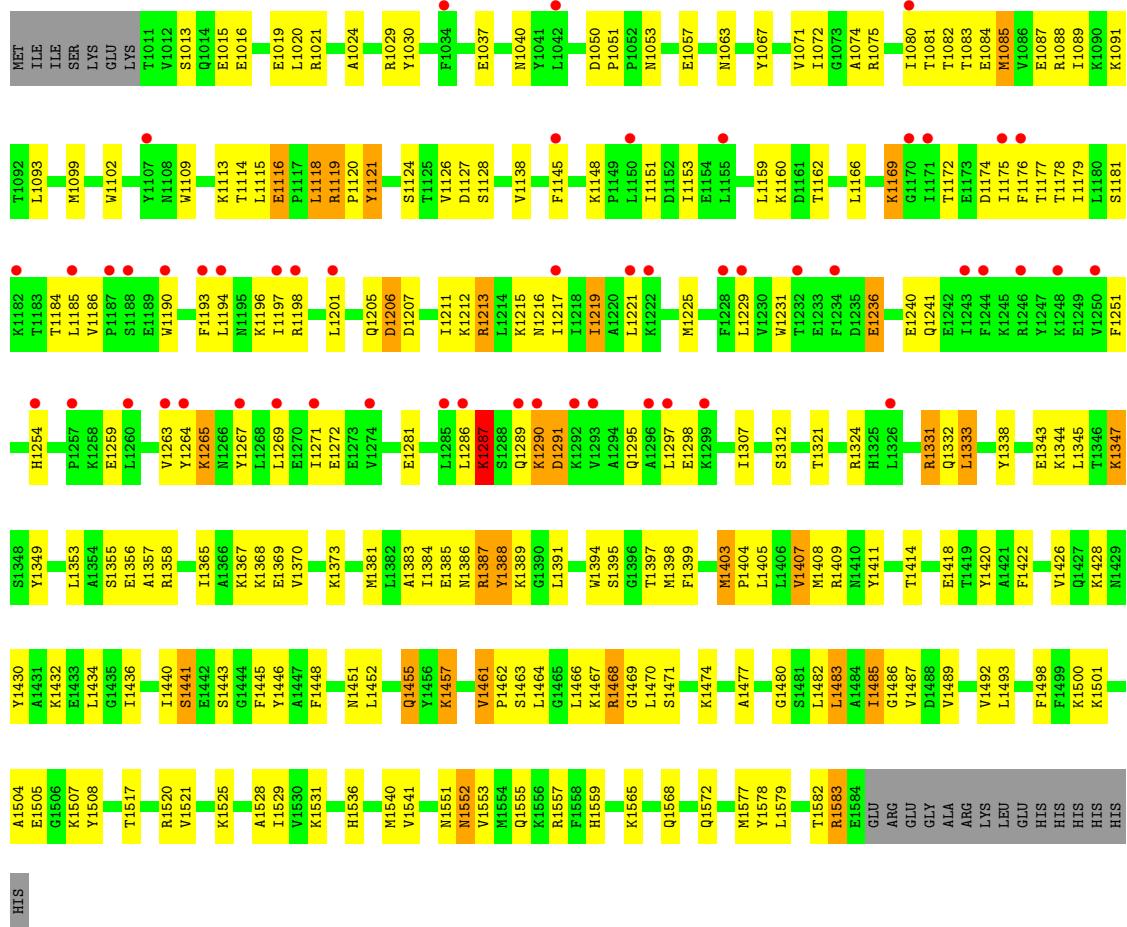


- Molecule 1: Glycosyltransferase 36



- Molecule 1: Glycosyltransferase 36





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4 Data and refinement statistics i

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	172.72Å 172.72Å 395.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.60 – 3.90 89.60 – 3.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (89.60-3.90) 100.0 (89.60-3.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	3.32 (at 3.89Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R , R_{free}	0.198 , 0.232 0.204 , 0.231	Depositor DCC
R_{free} test set	2738 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	104.0	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 104.1	EDS
L-test for twinning ²	$< L > = 0.45$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18842	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $< |L| >$, $< L^2 >$ 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 [\(i\)](#)

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	0.69	0/4814	0.90	1/6485 (0.0%)
1	B	0.70	0/4805	0.91	0/6473
1	C	0.70	0/4805	0.90	1/6473 (0.0%)
1	D	0.69	0/4814	0.90	0/6485
All	All	0.70	0/19238	0.90	2/25916 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	1398	MET	CA-CB-CG	-6.50	102.25	113.30
1	A	1358	ARG	NE-CZ-NH1	-6.21	117.19	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [\(i\)](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4715	0	4756	104	0
1	B	4706	0	4750	143	0
1	C	4706	0	4750	153	0
1	D	4715	0	4756	119	0
All	All	18842	0	19012	499	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 13.

The worst 5 of 499 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:B:1036:THR:HG23	1:B:1039:GLN:HG2	1.40	1.00
1:C:1050:ASP:HB3	1:C:1051:PRO:HD3	1.51	0.93
1:B:1387:ARG:HB3	1:C:1387:ARG:HB3	1.52	0.89
1:A:1050:ASP:HB3	1:A:1051:PRO:HD3	1.59	0.83
1:B:1395:SER:OG	1:B:1400:GLU:OE2	1.99	0.78

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	572/596 (96%)	478 (84%)	79 (14%)	15 (3%)	5 35
1	B	571/596 (96%)	483 (85%)	74 (13%)	14 (2%)	5 36
1	C	571/596 (96%)	468 (82%)	88 (15%)	15 (3%)	5 35
1	D	572/596 (96%)	463 (81%)	91 (16%)	18 (3%)	4 32
All	All	2286/2384 (96%)	1892 (83%)	332 (14%)	62 (3%)	5 35

5 of 62 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1356	GLU
1	A	1473	ASP
1	B	1356	GLU
1	B	1471	SER
1	C	1356	GLU

5.3.2 Protein sidechains [\(i\)](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	512/532 (96%)	460 (90%)	52 (10%)	7 30
1	B	511/532 (96%)	460 (90%)	51 (10%)	7 30
1	C	511/532 (96%)	449 (88%)	62 (12%)	5 24
1	D	512/532 (96%)	445 (87%)	67 (13%)	4 22
All	All	2046/2128 (96%)	1814 (89%)	232 (11%)	6 27

5 of 232 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1184	THR
1	D	1466	LEU
1	C	1405	LEU
1	D	1461	VAL
1	D	1331	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1039	GLN
1	B	1332	GLN
1	B	1453	ASN
1	C	1552	ASN
1	D	1039	GLN

5.3.3 RNA [\(i\)](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [\(i\)](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [\(i\)](#)

There are no ligands in this entry.

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	574/596 (96%)	0.42	8 (1%) 75 66	60, 104, 157, 203	0
1	B	573/596 (96%)	0.44	17 (2%) 50 38	65, 105, 187, 230	0
1	C	573/596 (96%)	0.55	31 (5%) 25 21	60, 113, 212, 269	0
1	D	574/596 (96%)	0.66	52 (9%) 9 7	68, 119, 215, 279	0
All	All	2294/2384 (96%)	0.52	108 (4%) 31 25	60, 109, 199, 279	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1264	TYR	4.9
1	C	1286	LEU	4.8
1	B	1271	ILE	4.3
1	D	1201	LEU	4.1
1	B	1275	PHE	4.1

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 monosaccharides in this entry.

6.4 Ligands [\(i\)](#)

There are no ligands in this entry.

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.