



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 7, 2026 – 11:32 PM JST

PDB ID : 9WIU / pdb_00009wiu
Title : SbSOMT in apo state
Authors : Pow, K.C.; Hao, Q.
Deposited on : 2025-08-29
Resolution : 2.04 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

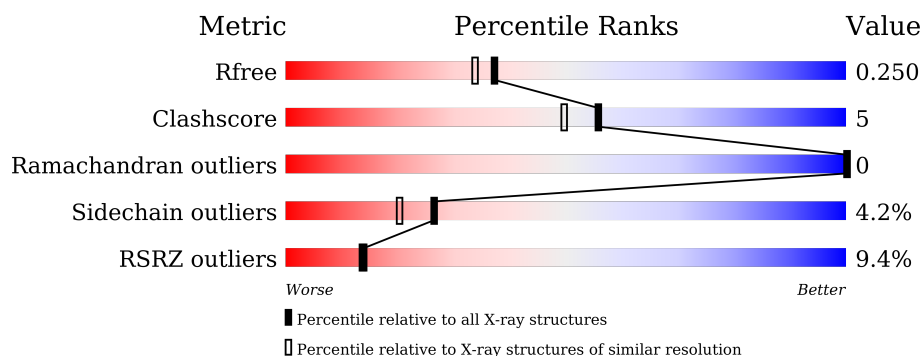
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	2260 (2.04-2.04)
Clashscore	190562	2333 (2.04-2.04)
Ramachandran outliers	187476	2318 (2.04-2.04)
Sidechain outliers	187428	2318 (2.04-2.04)
RSRZ outliers	180081	2260 (2.04-2.04)

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	366	2% 86% 10% ..
1	B	366	3% 87% 9% ..
1	C	366	5% 82% 13% ..
1	D	366	5% 86% 11% ..
1	E	366	22% 87% 7% ..
1	F	366	17% 85% 9% 5%

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	PEG	A	402	-	-	X	-

2 Entry composition [i](#)

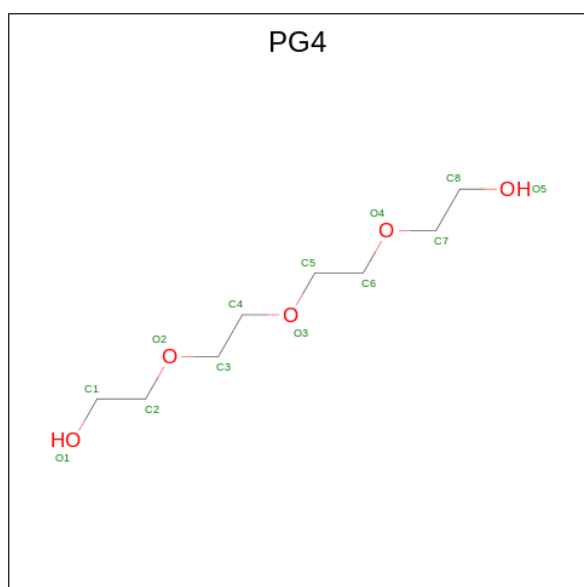
There are 8 unique types of molecules in this entry. The entry contains 17300 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 O-methyltransferase domain-containing protein.

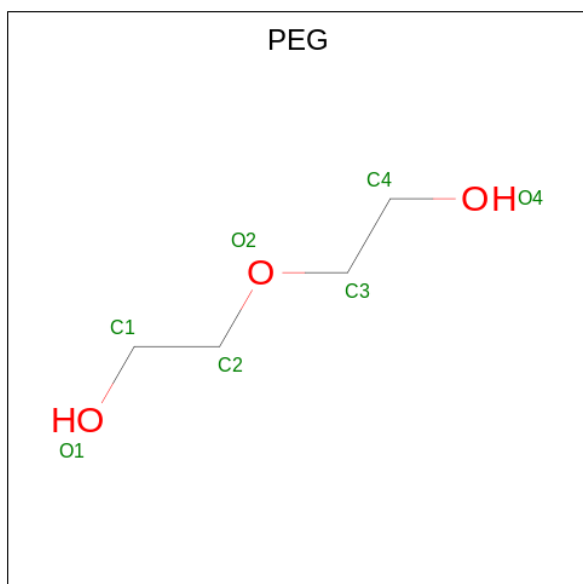
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	11	0
			2812	1803	470	514	25			
1	B	355	Total	C	N	O	S	0	9	0
			2826	1808	477	518	23			
1	C	353	Total	C	N	O	S	0	13	0
			2848	1820	479	524	25			
1	D	359	Total	C	N	O	S	0	6	0
			2834	1812	479	520	23			
1	E	352	Total	C	N	O	S	0	0	0
			2737	1752	461	502	22			
1	F	349	Total	C	N	O	S	0	4	0
			2756	1765	466	504	21			

- Molecule 2 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



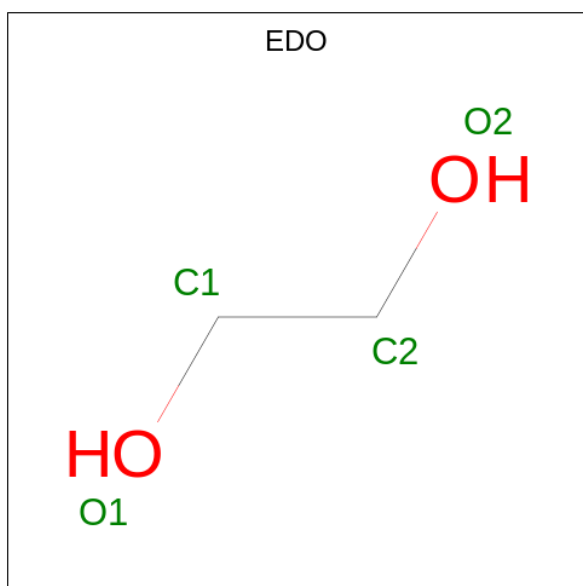
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



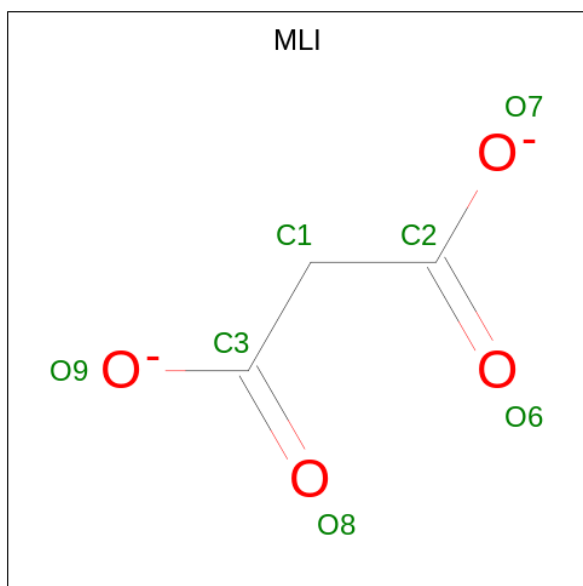
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0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

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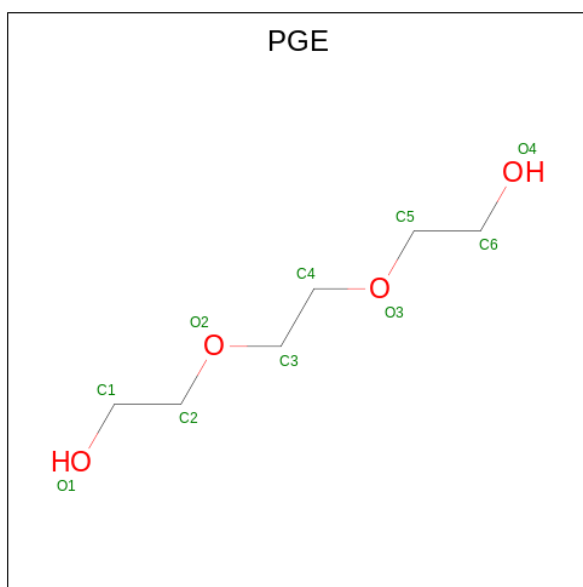
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is MALONATE ION (CCD ID: MLI) (formula: $C_3H_2O_4$).



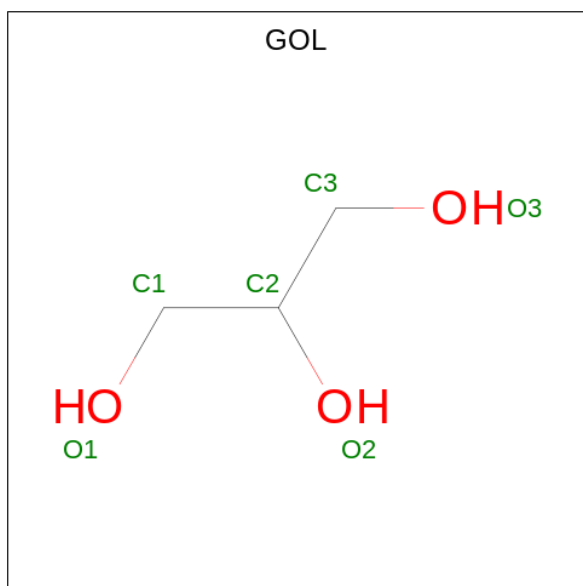
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	3	4		
5	C	1	Total	C	O	0	0
			7	3	4		

- Molecule 6 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			6	3	3		

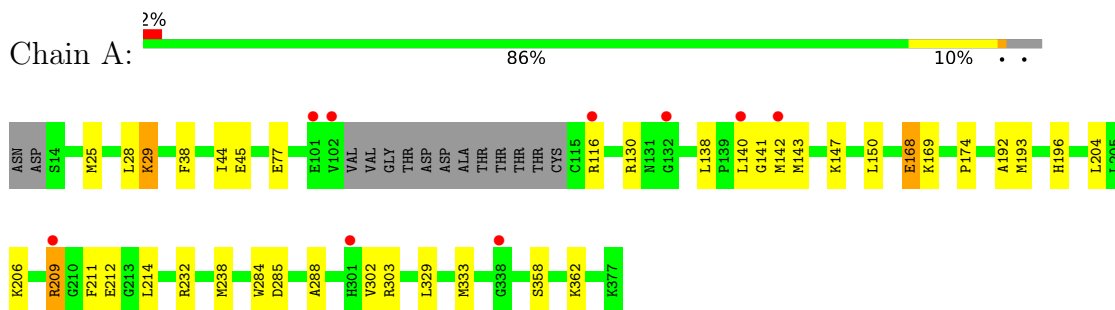
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	101	Total 101	O 101	0	0
8	B	90	Total 90	O 90	0	0
8	C	63	Total 63	O 63	0	0
8	D	54	Total 54	O 54	0	0
8	E	24	Total 24	O 24	0	0
8	F	13	Total 13	O 13	0	0

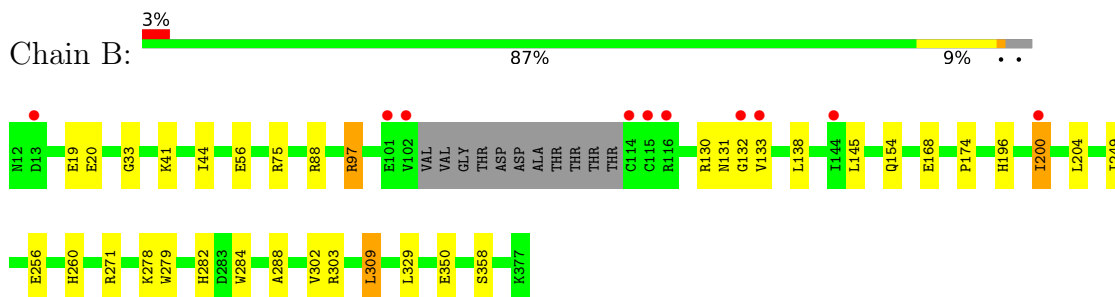
3 Residue-property plots [i](#)

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.

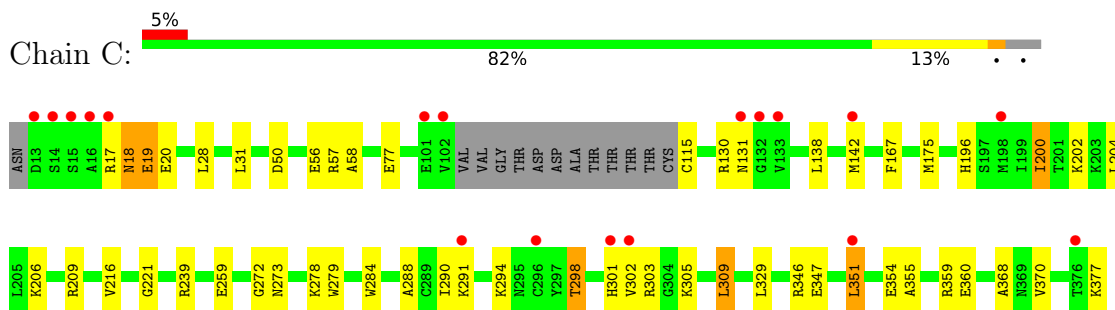
- Molecule 1: O-methyltransferase domain-containing protein



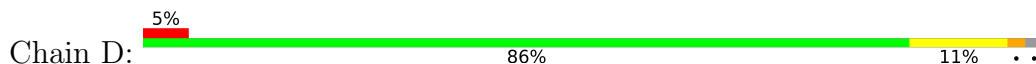
- Molecule 1: O-methyltransferase domain-containing protein

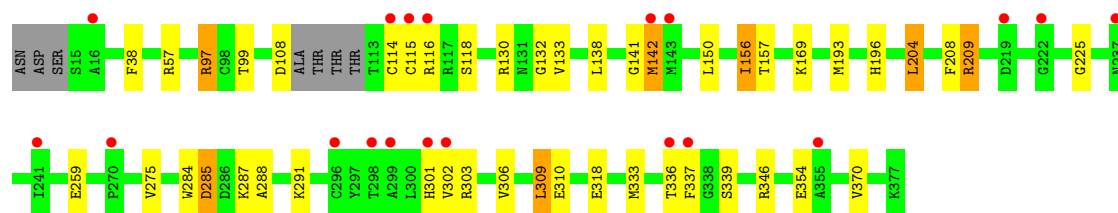


- Molecule 1: O-methyltransferase domain-containing protein

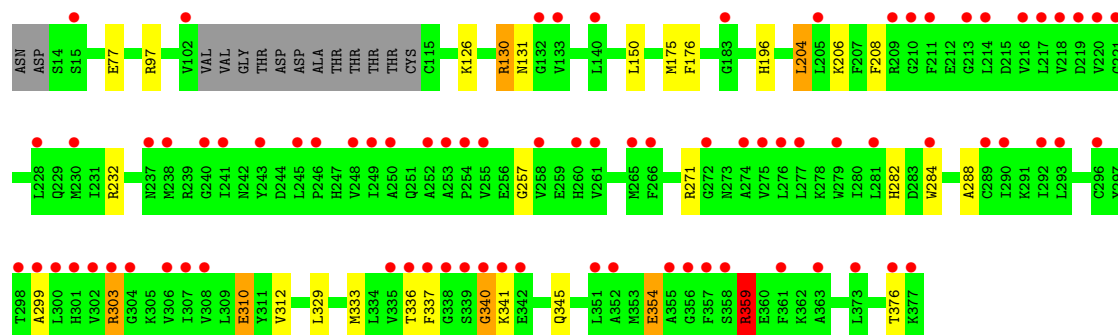
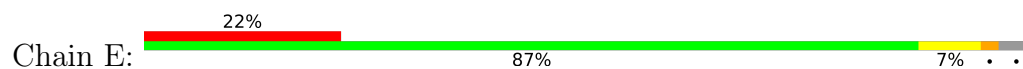


- Molecule 1: O-methyltransferase domain-containing protein

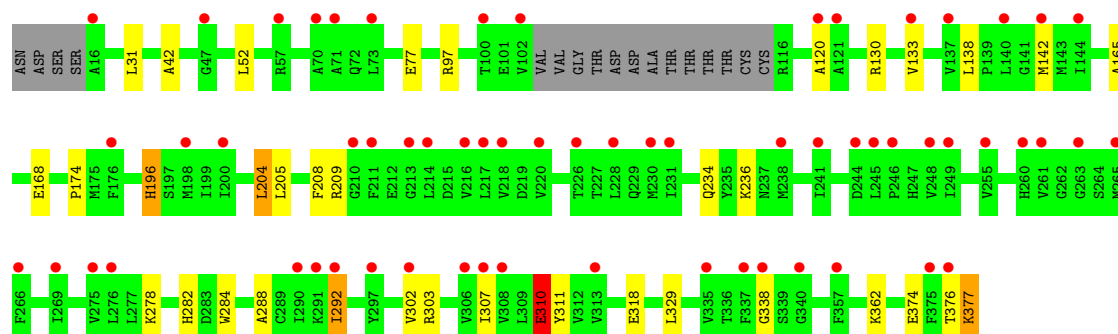
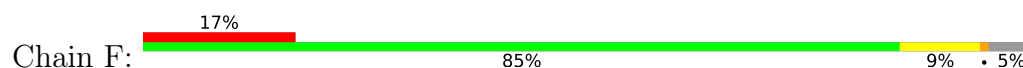




● Molecule 1: O-methyltransferase domain-containing protein



● Molecule 1: O-methyltransferase domain-containing protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.39Å 160.07Å 200.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.16 – 2.04 80.16 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.3 (80.16-2.04) 99.3 (80.16-2.04)	Depositor EDS
R_{merge}	0.25	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.126)	Depositor
R, R_{free}	0.227 , 0.247 0.231 , 0.250	Depositor DCC
R_{free} test set	8845 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.9	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	0.95	EDS
Total number of atoms	17300	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.29% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PEG, PGE, PG4, GOL, EDO, MLI

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	0.62	0/2887	0.95	3/3901 (0.1%)
1	B	0.62	0/2891	0.96	0/3910
1	C	0.61	0/2909	0.96	4/3934 (0.1%)
1	D	0.58	0/2894	0.95	4/3919 (0.1%)
1	E	0.56	0/2794	0.95	3/3782 (0.1%)
1	F	0.55	0/2813	0.98	5/3807 (0.1%)
All	All	0.59	0/17188	0.96	19/23253 (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	2
1	C	0	1
1	D	0	1
1	E	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	196	HIS	CA-CB-CG	10.21	124.01	113.80
1	F	310	GLU	CB-CG-CD	8.66	127.33	112.60
1	D	142	MET	CG-SD-CE	7.64	117.70	100.90
1	D	302	VAL	CA-C-O	-6.46	114.33	121.17
1	D	310	GLU	CB-CG-CD	6.41	123.50	112.60

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	ARG	Sidechain
1	B	75	ARG	Sidechain
1	B	97	ARG	Sidechain
1	C	239	ARG	Sidechain
1	D	97[A]	ARG	Sidechain

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	2812	0	2825	29	0
1	B	2826	0	2834	25	0
1	C	2848	0	2837	33	1
1	D	2834	0	2837	39	1
1	E	2737	0	2735	23	0
1	F	2756	0	2754	28	0
2	A	13	0	18	1	0
3	A	7	0	10	4	0
4	A	36	0	54	3	0
4	B	20	0	30	3	0
4	C	20	0	30	7	0
4	D	8	0	12	1	0
4	E	8	0	12	2	0
5	A	7	0	2	0	0
5	C	7	0	2	0	0
6	B	10	0	14	1	0
7	D	6	0	8	1	0
8	A	101	0	0	1	0
8	B	90	0	0	1	0
8	C	63	0	0	1	0
8	D	54	0	0	2	0
8	E	24	0	0	0	0
8	F	13	0	0	0	0
All	All	17300	0	17014	159	1

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 5.

The worst 5 of 159 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:377:LYS:NZ	8:C:501:HOH:O	1.98	0.96
1:A:329:LEU:HD21	3:A:402:PEG:H31	1.60	0.82
1:D:114:CYS:HG	1:D:115:CYS:HG	1.20	0.81
1:F:302:VAL:HA	1:F:377:LYS:HE3	1.65	0.78
1:A:140:LEU:HD21	3:A:402:PEG:H21	1.66	0.77

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:259:GLU:OE1	1:D:301:HIS:ND1[3_454]	2.07	0.13

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	358/366 (98%)	355 (99%)	3 (1%)	0	100	100
1	B	359/366 (98%)	354 (99%)	5 (1%)	0	100	100
1	C	362/366 (99%)	359 (99%)	3 (1%)	0	100	100
1	D	361/366 (99%)	355 (98%)	6 (2%)	0	100	100
1	E	348/366 (95%)	342 (98%)	6 (2%)	0	100	100
1	F	349/366 (95%)	343 (98%)	6 (2%)	0	100	100
All	All	2137/2196 (97%)	2108 (99%)	29 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	302/303 (100%)	291 (96%)	11 (4%)	31	26
1	B	303/303 (100%)	291 (96%)	12 (4%)	28	22
1	C	305/303 (101%)	288 (94%)	17 (6%)	19	12
1	D	303/303 (100%)	287 (95%)	16 (5%)	20	13
1	E	291/303 (96%)	280 (96%)	11 (4%)	29	24
1	F	292/303 (96%)	280 (96%)	12 (4%)	27	21
All	All	1796/1818 (99%)	1717 (96%)	79 (4%)	26	19

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	97	ARG
1	F	236	LYS
1	E	204	LEU
1	E	359	ARG
1	F	307	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	93	HIS
1	F	345	GLN
1	F	301	HIS
1	D	18	ASN
1	E	345	GLN

5.3.3 RNA ⓘ

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](#)

29 ligands are modelled in this entry.

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	EDO	C	402	-	3,3,3	0.28	0	2,2,2	0.31	0
4	EDO	C	405	-	3,3,3	0.16	0	2,2,2	0.05	0
4	EDO	E	402	-	3,3,3	0.55	0	2,2,2	0.79	0
4	EDO	A	408	-	3,3,3	0.35	0	2,2,2	0.57	0
3	PEG	A	402	-	6,6,6	0.49	0	5,5,5	0.44	0
6	PGE	B	402	-	9,9,9	0.46	0	8,8,8	0.32	0
7	GOL	D	401	-	5,5,5	0.10	0	5,5,5	0.35	0
4	EDO	B	401	-	3,3,3	0.58	0	2,2,2	0.57	0
4	EDO	C	403	-	3,3,3	0.73	0	2,2,2	0.88	0
4	EDO	B	406	-	3,3,3	0.19	0	2,2,2	0.31	0
4	EDO	A	407	-	3,3,3	0.16	0	2,2,2	0.34	0
4	EDO	E	401	-	3,3,3	0.66	0	2,2,2	0.98	0
5	MLI	C	401	-	6,6,6	1.41	1 (16%)	7,7,7	1.15	0
4	EDO	A	403	-	3,3,3	0.14	0	2,2,2	0.24	0
4	EDO	A	406	-	3,3,3	0.20	0	2,2,2	0.35	0
4	EDO	A	404	-	3,3,3	0.29	0	2,2,2	0.22	0
4	EDO	B	403	-	3,3,3	0.08	0	2,2,2	0.16	0
2	PG4	A	401	-	12,12,12	0.36	0	11,11,11	0.25	0
4	EDO	A	409	-	3,3,3	0.33	0	2,2,2	0.03	0
4	EDO	A	411	-	3,3,3	0.13	0	2,2,2	0.30	0
4	EDO	D	402	-	3,3,3	0.25	0	2,2,2	0.33	0
4	EDO	B	405	-	3,3,3	0.74	0	2,2,2	1.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	405	-	3,3,3	0.18	0	2,2,2	0.34	0
4	EDO	A	412	-	3,3,3	0.20	0	2,2,2	0.38	0
4	EDO	C	406	-	3,3,3	0.15	0	2,2,2	0.40	0
4	EDO	B	404	-	3,3,3	0.10	0	2,2,2	0.38	0
5	MLI	A	410	-	6,6,6	1.90	2 (33%)	7,7,7	1.10	0
4	EDO	C	404	-	3,3,3	0.18	0	2,2,2	0.37	0
4	EDO	D	403	-	3,3,3	0.20	0	2,2,2	0.24	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
4	EDO	C	402	-	-	1/1/1/1	-
4	EDO	C	405	-	-	0/1/1/1	-
4	EDO	E	402	-	-	1/1/1/1	-
4	EDO	A	408	-	-	1/1/1/1	-
3	PEG	A	402	-	-	2/4/4/4	-
6	PGE	B	402	-	-	7/7/7/7	-
7	GOL	D	401	-	-	0/4/4/4	-
4	EDO	B	401	-	-	1/1/1/1	-
4	EDO	C	403	-	-	1/1/1/1	-
4	EDO	B	406	-	-	0/1/1/1	-
4	EDO	A	407	-	-	1/1/1/1	-
4	EDO	E	401	-	-	1/1/1/1	-
5	MLI	C	401	-	-	2/4/4/4	-
4	EDO	A	403	-	-	0/1/1/1	-
4	EDO	A	406	-	-	1/1/1/1	-
4	EDO	A	404	-	-	1/1/1/1	-
4	EDO	B	403	-	-	0/1/1/1	-
2	PG4	A	401	-	-	5/10/10/10	-
4	EDO	A	409	-	-	1/1/1/1	-
4	EDO	A	411	-	-	1/1/1/1	-
4	EDO	D	402	-	-	1/1/1/1	-
4	EDO	B	405	-	-	1/1/1/1	-
4	EDO	A	405	-	-	1/1/1/1	-
4	EDO	A	412	-	-	1/1/1/1	-
4	EDO	C	406	-	-	1/1/1/1	-
4	EDO	B	404	-	-	1/1/1/1	-
5	MLI	A	410	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	C	404	-	-	0/1/1/1	-
4	EDO	D	403	-	-	0/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	410	MLI	O8-C3	2.88	1.31	1.22
5	A	410	MLI	C1-C2	2.66	1.55	1.51
5	C	401	MLI	O6-C2	2.16	1.29	1.22

There are no bond angle outliers.

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	402	PGE	O2-C3-C4-O3
2	A	401	PG4	O3-C5-C6-O4
4	A	406	EDO	O1-C1-C2-O2
4	A	407	EDO	O1-C1-C2-O2
4	B	405	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	405	EDO	1	0
4	A	408	EDO	2	0
3	A	402	PEG	4	0
6	B	402	PGE	1	0
7	D	401	GOL	1	0
4	C	403	EDO	3	0
4	B	406	EDO	1	0
4	E	401	EDO	2	0
2	A	401	PG4	1	0
4	D	402	EDO	1	0
4	B	405	EDO	2	0
4	A	405	EDO	1	0
4	C	406	EDO	3	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	352/366 (96%)	0.25	9 (2%) 57 59	22, 43, 66, 111	11 (3%)
1	B	355/366 (96%)	0.28	10 (2%) 55 57	21, 45, 74, 109	9 (2%)
1	C	353/366 (96%)	0.60	18 (5%) 33 33	22, 52, 82, 106	13 (3%)
1	D	359/366 (98%)	0.73	19 (5%) 32 32	23, 57, 91, 130	6 (1%)
1	E	352/366 (96%)	1.22	81 (23%) 2 1	37, 77, 150, 177	0
1	F	349/366 (95%)	1.24	62 (17%) 4 3	27, 89, 121, 132	4 (1%)
All	All	2120/2196 (96%)	0.72	199 (9%) 14 14	21, 55, 117, 177	43 (2%)

The worst 5 of 199 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	102	VAL	6.3
1	C	16	ALA	5.8
1	E	102	VAL	5.1
1	E	302	VAL	4.7
1	C	14	SER	4.5

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 oligosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
5	MLI	A	410	7/7	0.49	0.27	73,75,83,86	0
4	EDO	A	404	4/4	0.61	0.25	60,66,77,81	0
4	EDO	D	403	4/4	0.68	0.22	75,87,88,89	0
4	EDO	C	405	4/4	0.69	0.22	65,80,86,88	0
4	EDO	C	406	4/4	0.72	0.15	78,81,82,83	0
4	EDO	E	402	4/4	0.73	0.25	64,68,71,74	0
4	EDO	B	404	4/4	0.73	0.20	70,75,76,76	0
4	EDO	A	408	4/4	0.75	0.23	61,66,68,81	0
4	EDO	A	406	4/4	0.76	0.22	68,76,79,80	0
4	EDO	B	406	4/4	0.78	0.19	69,70,71,72	0
4	EDO	A	405	4/4	0.78	0.13	69,76,76,82	0
3	PEG	A	402	7/7	0.81	0.25	77,85,95,96	0
4	EDO	E	401	4/4	0.81	0.24	66,75,76,77	0
5	MLI	C	401	7/7	0.82	0.16	56,66,83,89	0
6	PGE	B	402	10/10	0.82	0.20	67,73,75,80	0
4	EDO	A	403	4/4	0.83	0.16	57,65,66,67	0
4	EDO	B	403	4/4	0.83	0.22	79,86,86,86	0
4	EDO	D	402	4/4	0.84	0.25	77,82,84,85	0
4	EDO	B	401	4/4	0.85	0.25	57,57,58,64	0
4	EDO	C	402	4/4	0.85	0.18	63,66,71,72	0
4	EDO	C	404	4/4	0.85	0.15	64,65,66,68	0
4	EDO	B	405	4/4	0.86	0.29	40,42,46,52	0
4	EDO	A	412	4/4	0.87	0.14	58,60,60,64	0
4	EDO	C	403	4/4	0.87	0.17	59,60,64,66	0
4	EDO	A	411	4/4	0.87	0.14	54,62,64,66	0
7	GOL	D	401	6/6	0.87	0.14	67,76,81,82	0
4	EDO	A	407	4/4	0.88	0.33	51,52,54,55	0
2	PG4	A	401	13/13	0.89	0.17	71,73,81,81	0
4	EDO	A	409	4/4	0.91	0.12	65,65,66,68	0

6.5 Other polymers

There are no such residues in this entry.