



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 11:17 AM UTC

PDB ID : 7XSG / pdb_00007xsg
Title : Crystal structure of ClAgl29B
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Deposited on : 2022-05-14
Resolution : 1.61 Å(reported)

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

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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

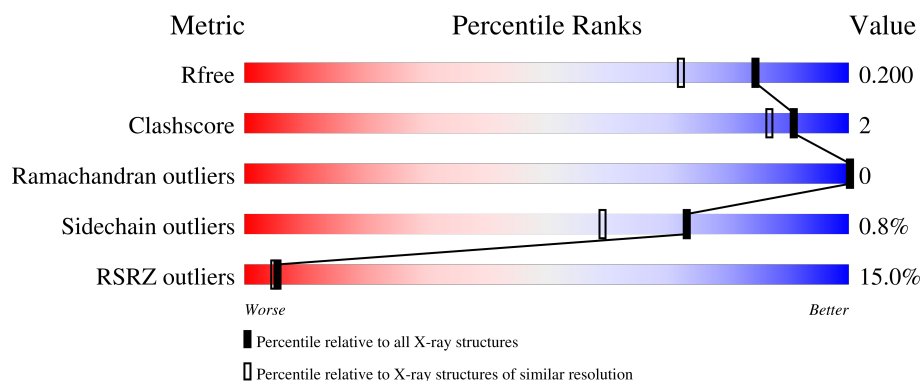
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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.

Mol	Chain	Length	Quality of chain
1	A	587	22% 87% • • 7%
1	B	587	6% 89% • 7%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10033 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 Alpha-L-fucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	8	0
			4481	2882	727	855	17			
1	B	545	Total	C	N	O	S	0	12	0
			4504	2893	731	863	17			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP K1KV82
A	1	GLY	-	expression tag	UNP K1KV82
A	2	SER	-	expression tag	UNP K1KV82
A	3	SER	-	expression tag	UNP K1KV82
A	4	HIS	-	expression tag	UNP K1KV82
A	5	HIS	-	expression tag	UNP K1KV82
A	6	HIS	-	expression tag	UNP K1KV82
A	7	HIS	-	expression tag	UNP K1KV82
A	8	HIS	-	expression tag	UNP K1KV82
A	9	HIS	-	expression tag	UNP K1KV82
A	10	SER	-	expression tag	UNP K1KV82
A	11	SER	-	expression tag	UNP K1KV82
A	12	GLY	-	expression tag	UNP K1KV82
A	13	LEU	-	expression tag	UNP K1KV82
A	14	VAL	-	expression tag	UNP K1KV82
A	15	PRO	-	expression tag	UNP K1KV82
A	16	ARG	-	expression tag	UNP K1KV82
A	17	GLY	-	expression tag	UNP K1KV82
A	18	SER	-	expression tag	UNP K1KV82
A	19	HIS	-	expression tag	UNP K1KV82
A	20	MET	-	expression tag	UNP K1KV82
B	0	MET	-	initiating methionine	UNP K1KV82
B	1	GLY	-	expression tag	UNP K1KV82
B	2	SER	-	expression tag	UNP K1KV82
B	3	SER	-	expression tag	UNP K1KV82

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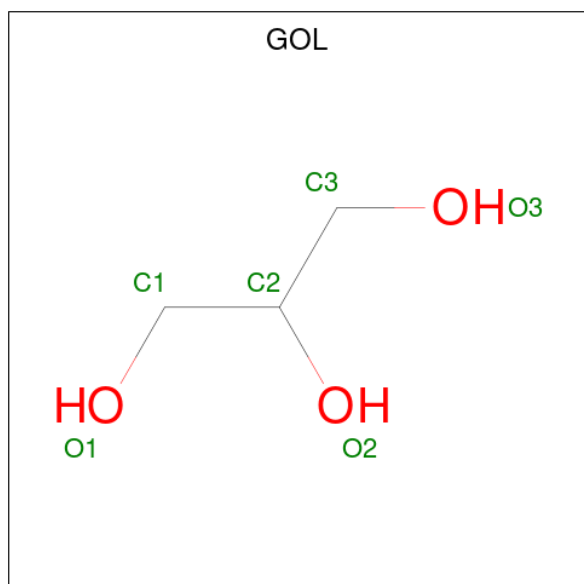
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Chain	Residue	Modelled	Actual	Comment	Reference
B	4	HIS	-	expression tag	UNP K1KV82
B	5	HIS	-	expression tag	UNP K1KV82
B	6	HIS	-	expression tag	UNP K1KV82
B	7	HIS	-	expression tag	UNP K1KV82
B	8	HIS	-	expression tag	UNP K1KV82
B	9	HIS	-	expression tag	UNP K1KV82
B	10	SER	-	expression tag	UNP K1KV82
B	11	SER	-	expression tag	UNP K1KV82
B	12	GLY	-	expression tag	UNP K1KV82
B	13	LEU	-	expression tag	UNP K1KV82
B	14	VAL	-	expression tag	UNP K1KV82
B	15	PRO	-	expression tag	UNP K1KV82
B	16	ARG	-	expression tag	UNP K1KV82
B	17	GLY	-	expression tag	UNP K1KV82
B	18	SER	-	expression tag	UNP K1KV82
B	19	HIS	-	expression tag	UNP K1KV82
B	20	MET	-	expression tag	UNP K1KV82

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

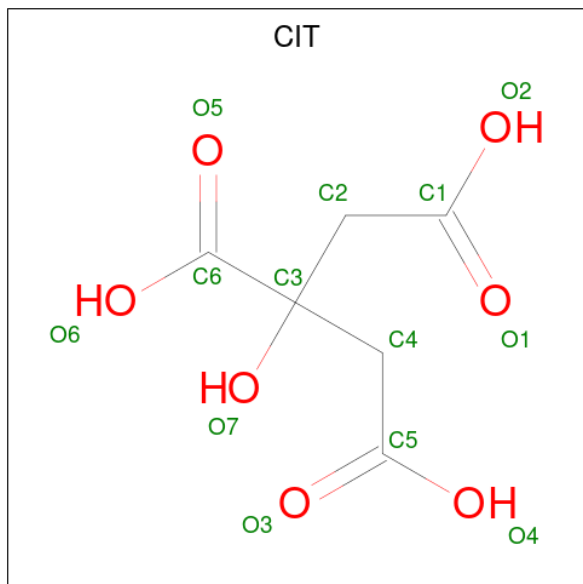
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Na 1 1	0	0
2	B	1	Total Na 1 1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

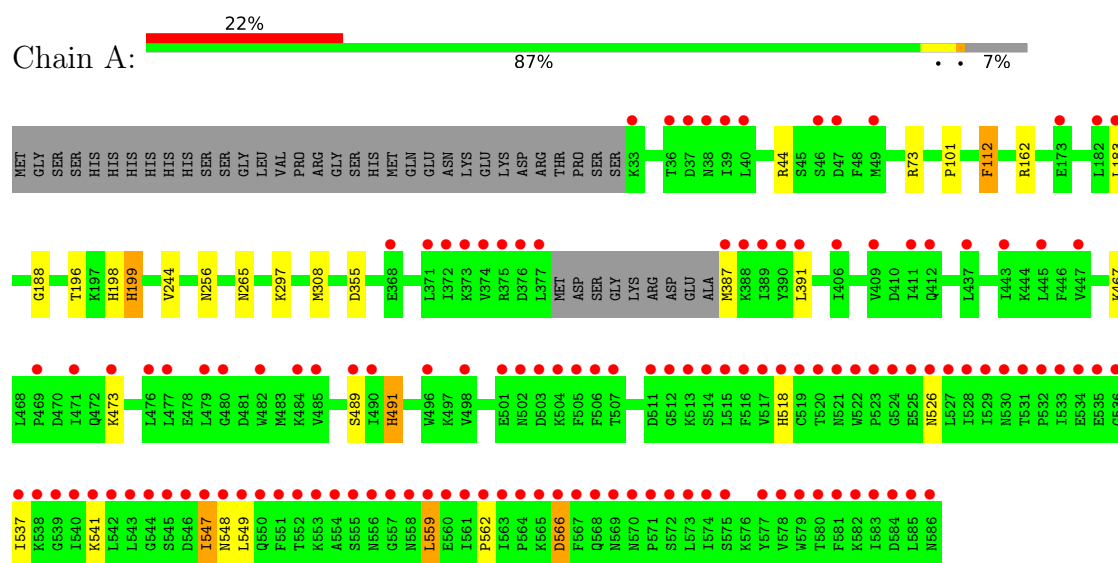
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	393	Total	O	0	0
			393	393		
6	B	615	Total	O	0	0
			615	615		

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: Alpha-L-fucosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.13Å 123.41Å 166.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.42 – 1.61 45.42 – 1.61	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.42-1.61) 99.5 (45.42-1.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 1.61Å)	Xtriage
Refinement program	REFMAC 5.8.0349	Depositor
R, R_{free}	0.172 , 0.188 0.185 , 0.200	Depositor DCC
R_{free} test set	9719 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	14.5	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10033	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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, NA, GOL, CIT

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	0.58	2/4604 (0.0%)	0.87	2/6237 (0.0%)
1	B	0.59	3/4627 (0.1%)	0.85	1/6268 (0.0%)
All	All	0.58	5/9231 (0.1%)	0.86	3/12505 (0.0%)

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	2
1	B	0	2
All	All	0	4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	199	HIS	CE1-NE2	7.42	1.40	1.32
1	B	98	HIS	C-N	6.89	1.42	1.33
1	B	290	HIS	CE1-NE2	5.90	1.38	1.32
1	A	199	HIS	CE1-NE2	5.80	1.38	1.32
1	A	491	HIS	CE1-NE2	5.37	1.38	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	112	PHE	CA-CB-CG	5.66	119.46	113.80
1	A	566	ASP	CA-CB-CG	5.53	118.13	112.60
1	A	112	PHE	CA-CB-CG	5.38	119.18	113.80

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	162[A]	ARG	Sidechain
1	A	44	ARG	Sidechain
1	B	162[A]	ARG	Sidechain
1	B	44	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	4481	0	4316	18	0
1	B	4504	0	4330	12	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	12	0	16	1	0
3	B	6	0	8	0	0
4	A	13	0	5	0	0
5	B	7	0	10	0	0
6	A	393	0	0	2	0
6	B	615	0	0	3	0
All	All	10033	0	8685	30	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 2.

All (30) 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:A:256:ASN:HD21	1:A:265:ASN:H	1.19	0.86
1:A:387:MET:HE3	1:A:391:LEU:HD11	1.80	0.64
1:A:541:LYS:HA	1:A:549:LEU:HD13	1.83	0.61
1:A:547:ILE:HD12	1:A:548:ASN:O	2.02	0.59
1:A:73:ARG:HG3	6:A:701:HOH:O	2.05	0.56
1:B:55:TYR:HE1	1:B:63:GLU:OE1	1.89	0.56
1:B:62:ARG:HD2	6:B:702:HOH:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:GLY:O	1:B:491:HIS:HE1	1.88	0.55
1:A:183:LEU:HD21	1:A:473[A]:LYS:HE3	1.94	0.50
1:B:372:ILE:HG23	1:B:375:ARG:HH21	1.78	0.48
1:A:387:MET:HE3	1:A:391:LEU:CD1	2.43	0.47
1:B:244:VAL:HG13	1:B:308[B]:MET:SD	2.55	0.47
1:A:244:VAL:HG13	1:A:308[B]:MET:SD	2.54	0.47
1:A:526:ASN:HD22	1:A:562:PRO:HA	1.80	0.46
1:B:489:SER:OG	1:B:518:HIS:HE1	1.98	0.46
1:B:491:HIS:HD2	6:B:1201:HOH:O	1.97	0.46
1:A:537:ILE:HD13	1:A:559:LEU:HD21	1.98	0.45
1:A:467:LYS:HA	3:A:604:GOL:H12	1.98	0.45
1:B:55:TYR:CE1	1:B:63:GLU:OE1	2.70	0.45
1:A:549:LEU:HD12	1:A:549:LEU:N	2.33	0.44
1:A:549:LEU:N	1:A:549:LEU:CD1	2.81	0.43
1:B:468:LEU:O	1:B:473:LYS:HE3	2.18	0.43
1:A:489:SER:OG	1:A:518:HIS:HE1	2.02	0.42
1:A:188:GLY:O	1:A:491:HIS:HE1	2.02	0.42
1:A:101:PRO:HB3	1:A:355:ASP:HB3	2.01	0.42
1:B:477[B]:LEU:HD23	1:B:477[B]:LEU:C	2.46	0.41
1:B:62:ARG:NH1	6:B:702:HOH:O	2.46	0.41
1:A:198:HIS:CG	1:A:199:HIS:H	2.38	0.41
1:A:297:LYS:HE3	6:A:775:HOH:O	2.21	0.40
1:B:113:LEU:HB3	1:B:194:PRO:HA	2.04	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	549/587 (94%)	534 (97%)	15 (3%)	0	100	100
1	B	553/587 (94%)	538 (97%)	15 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1102/1174 (94%)	1072 (97%)	30 (3%)	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	488/517 (94%)	483 (99%)	5 (1%)	68	50
1	B	492/517 (95%)	489 (99%)	3 (1%)	78	66
All	All	980/1034 (95%)	972 (99%)	8 (1%)	73	59

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	112	PHE
1	A	196	THR
1	A	547	ILE
1	A	559	LEU
1	A	566	ASP
1	B	49	MET
1	B	112	PHE
1	B	196	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	GLN
1	A	255	GLN
1	A	256	ASN
1	A	518	HIS
1	A	526	ASN
1	A	550	GLN
1	B	186	ASN

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Mol	Chain	Res	Type
1	B	255	GLN
1	B	259	GLN
1	B	270	GLN
1	B	275	GLN
1	B	491	HIS
1	B	518	HIS
1	B	526	ASN
1	B	548	ASN
1	B	586	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 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	GOL	A	602	-	5,5,5	0.10	0	5,5,5	0.16	0
3	GOL	A	604	-	5,5,5	0.03	0	5,5,5	0.25	0
3	GOL	B	602	-	5,5,5	0.18	0	5,5,5	0.47	0
4	CIT	A	603	-	12,12,12	1.38	1 (8%)	17,17,17	1.23	2 (11%)
5	PEG	B	603	-	6,6,6	0.34	0	5,5,5	0.28	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
3	GOL	A	602	-	-	0/4/4/4	-
3	GOL	A	604	-	-	3/4/4/4	-
3	GOL	B	602	-	-	0/4/4/4	-
4	CIT	A	603	-	-	0/16/16/16	-
5	PEG	B	603	-	-	1/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	603	CIT	C3-C6	2.36	1.55	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	603	CIT	O5-C6-C3	-2.68	116.91	122.09
4	A	603	CIT	O6-C6-C3	2.32	117.59	113.14

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	604	GOL	O1-C1-C2-C3
3	A	604	GOL	O1-C1-C2-O2
3	A	604	GOL	O2-C2-C3-O3
5	B	603	PEG	O2-C3-C4-O4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	604	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	545/587 (92%)	1.00	129 (23%) 2 1	5, 19, 51, 100	8 (1%)
1	B	545/587 (92%)	-0.20	34 (6%) 26 27	5, 12, 34, 67	12 (2%)
All	All	1090/1174 (92%)	0.40	163 (14%) 5 5	5, 15, 47, 100	20 (1%)

All (163) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	559	LEU	9.5
1	A	567	PHE	8.0
1	A	554	ALA	7.4
1	A	547	ILE	7.4
1	A	561	ILE	7.1
1	A	377	LEU	6.9
1	A	527	LEU	6.9
1	A	549	LEU	6.9
1	B	377	LEU	6.6
1	A	522	TRP	6.5
1	A	529	ILE	6.4
1	A	552	THR	6.3
1	A	528	ILE	6.0
1	A	563	ILE	5.6
1	A	579	TRP	5.6
1	A	551	PHE	5.5
1	A	556	ASN	5.5
1	A	540	ILE	5.3
1	A	573	LEU	5.3
1	A	574	ILE	5.1
1	A	550	GLN	5.1
1	A	557	GLY	5.1
1	A	564	PRO	5.0
1	A	558	ASN	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	524	GLY	4.9
1	A	374	VAL	4.8
1	A	581	PHE	4.8
1	A	526	ASN	4.7
1	B	374	VAL	4.7
1	A	537	ILE	4.6
1	A	531	THR	4.6
1	A	566	ASP	4.6
1	A	532	PRO	4.6
1	A	548	ASN	4.6
1	A	568	GLN	4.5
1	B	33	LYS	4.5
1	A	562	PRO	4.5
1	A	40	LEU	4.4
1	A	39	ILE	4.4
1	A	372	ILE	4.4
1	A	571	PRO	4.3
1	A	553	LYS	4.3
1	A	560	GLU	4.3
1	A	543	LEU	4.3
1	A	565	LYS	4.3
1	A	578	VAL	4.2
1	A	533	ILE	4.2
1	B	372	ILE	4.2
1	B	387	MET	4.2
1	A	569	ASN	4.2
1	A	517	VAL	4.2
1	A	545	SER	4.1
1	A	555	SER	4.1
1	A	583	ILE	4.1
1	A	546	ASP	4.0
1	A	523	PRO	4.0
1	A	542	LEU	4.0
1	A	572	SER	4.0
1	A	580	THR	3.8
1	A	391	LEU	3.8
1	A	512	GLY	3.8
1	A	515	LEU	3.7
1	A	530	ASN	3.7
1	A	33	LYS	3.7
1	A	538	LYS	3.7
1	A	485	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	388	LYS	3.7
1	A	520	THR	3.7
1	A	539	GLY	3.7
1	B	555	SER	3.7
1	B	554	ALA	3.6
1	B	586	ASN	3.6
1	A	536	GLY	3.6
1	A	388	LYS	3.6
1	A	387	MET	3.6
1	A	498	VAL	3.6
1	A	585	LEU	3.5
1	A	389	ILE	3.5
1	A	525	GLU	3.5
1	A	586	ASN	3.4
1	B	534	GLU	3.4
1	A	373	LYS	3.4
1	A	503	ASP	3.4
1	A	577	TYR	3.3
1	A	575	SER	3.3
1	A	375	ARG	3.3
1	A	506	PHE	3.2
1	A	519	CYS	3.2
1	A	570	ASN	3.2
1	B	548	ASN	3.2
1	B	557	GLY	3.2
1	B	556	ASN	3.2
1	A	409	VAL	3.0
1	B	409	VAL	3.0
1	B	536	GLY	3.0
1	B	389	ILE	3.0
1	B	375	ARG	3.0
1	A	183	LEU	3.0
1	A	584	ASP	2.9
1	A	496	TRP	2.9
1	A	482	TRP	2.9
1	A	473[A]	LYS	2.9
1	A	390	TYR	2.9
1	A	504	LYS	2.9
1	A	501	GLU	2.8
1	A	505	PHE	2.8
1	A	544	GLY	2.8
1	A	371	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	535	GLU	2.7
1	B	408	ASP	2.7
1	B	585	LEU	2.7
1	A	534	GLU	2.7
1	A	514	SER	2.6
1	B	553	LYS	2.6
1	A	376	ASP	2.6
1	A	411	ILE	2.6
1	B	411	ILE	2.6
1	B	412	GLN	2.6
1	A	582	LYS	2.6
1	A	521	ASN	2.6
1	B	373	LYS	2.6
1	B	511	ASP	2.5
1	A	516	PHE	2.5
1	A	476	LEU	2.5
1	A	477	LEU	2.5
1	A	513	LYS	2.5
1	A	406	ILE	2.5
1	A	541	LYS	2.5
1	B	99	GLU	2.5
1	A	182	LEU	2.5
1	B	391	LEU	2.5
1	A	368	GLU	2.5
1	A	46	SER	2.5
1	B	512	GLY	2.4
1	A	412	GLN	2.4
1	A	36	THR	2.4
1	B	537	ILE	2.4
1	A	502	ASN	2.4
1	A	445	LEU	2.4
1	B	376	ASP	2.4
1	B	550	GLN	2.3
1	A	37	ASP	2.3
1	A	443	ILE	2.3
1	A	535	GLU	2.3
1	B	390	TYR	2.3
1	A	490	ILE	2.3
1	A	47	ASP	2.2
1	A	49[A]	MET	2.2
1	A	38	ASN	2.2
1	A	484	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	480	GLY	2.2
1	A	507	THR	2.2
1	A	173	GLU	2.2
1	A	511	ASP	2.1
1	A	489	SER	2.1
1	A	469	PRO	2.1
1	A	447	VAL	2.1
1	A	479	LEU	2.1
1	A	471	ILE	2.1
1	B	39	ILE	2.1
1	A	437	LEU	2.0
1	A	518	HIS	2.0
1	B	513	LYS	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
5	PEG	B	603	7/7	0.72	0.24	36,41,47,48	0
3	GOL	A	604	6/6	0.76	0.21	37,43,46,48	0
4	CIT	A	603	13/13	0.90	0.10	22,25,28,29	0
2	NA	A	601	1/1	0.90	0.26	33,33,33,33	0
3	GOL	B	602	6/6	0.91	0.12	19,21,25,27	0
3	GOL	A	602	6/6	0.96	0.07	19,21,22,23	0
2	NA	B	601	1/1	0.98	0.08	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.