



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 11:59 PM UTC

PDB ID : 7KB8 / pdb_00007kb8
Title : Co-crystal structure of alpha glucosidase with compound 8
Authors : Karade, S.S.; Mariuzza, R.A.
Deposited on : 2020-10-01
Resolution : 2.38 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

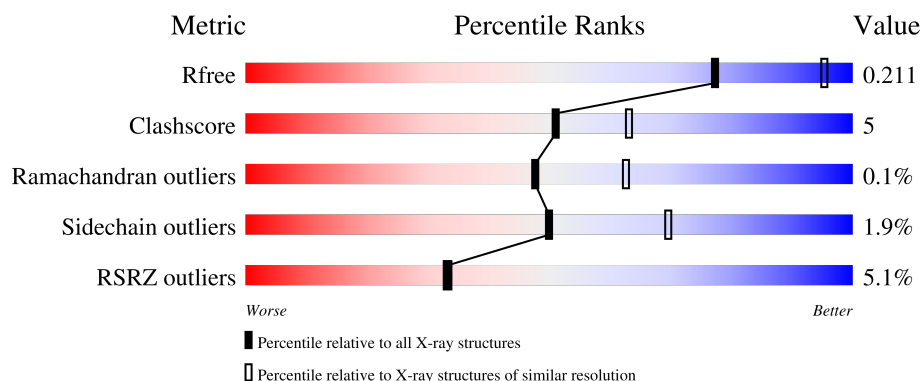
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	977	2% 78% 10% 13%
1	C	977	5% 78% 9% 12%
2	B	554	2% 13% 84%
2	D	554	3% 12% 84%

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
6	PEG	C	1512	-	-	X	-

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 15963 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 Isoform 2 of Neutral alpha-glucosidase AB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	854	Total	C	N	O	S	0	4	0
			6898	4419	1192	1259	28			
1	C	857	Total	C	N	O	S	0	8	0
			6894	4420	1184	1260	30			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP Q8BHN3-2
A	3	GLY	-	expression tag	UNP Q8BHN3-2
A	4	ILE	-	expression tag	UNP Q8BHN3-2
A	5	LEU	-	expression tag	UNP Q8BHN3-2
A	6	PRO	-	expression tag	UNP Q8BHN3-2
A	7	SER	-	expression tag	UNP Q8BHN3-2
A	8	PRO	-	expression tag	UNP Q8BHN3-2
A	9	GLY	-	expression tag	UNP Q8BHN3-2
A	10	MET	-	expression tag	UNP Q8BHN3-2
A	11	PRO	-	expression tag	UNP Q8BHN3-2
A	12	ALA	-	expression tag	UNP Q8BHN3-2
A	13	LEU	-	expression tag	UNP Q8BHN3-2
A	14	LEU	-	expression tag	UNP Q8BHN3-2
A	15	SER	-	expression tag	UNP Q8BHN3-2
A	16	LEU	-	expression tag	UNP Q8BHN3-2
A	17	VAL	-	expression tag	UNP Q8BHN3-2
A	18	SER	-	expression tag	UNP Q8BHN3-2
A	19	LEU	-	expression tag	UNP Q8BHN3-2
A	20	LEU	-	expression tag	UNP Q8BHN3-2
A	21	SER	-	expression tag	UNP Q8BHN3-2
A	22	VAL	-	expression tag	UNP Q8BHN3-2
A	23	LEU	-	expression tag	UNP Q8BHN3-2
A	24	LEU	-	expression tag	UNP Q8BHN3-2
A	25	MET	-	expression tag	UNP Q8BHN3-2
A	26	GLY	-	expression tag	UNP Q8BHN3-2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	27	CYS	-	expression tag	UNP Q8BHN3-2
A	28	VAL	-	expression tag	UNP Q8BHN3-2
A	29	ALA	-	expression tag	UNP Q8BHN3-2
A	30	GLU	-	expression tag	UNP Q8BHN3-2
A	31	THR	-	expression tag	UNP Q8BHN3-2
A	32	GLY	-	expression tag	UNP Q8BHN3-2
A	97	ASP	ASN	engineered mutation	UNP Q8BHN3-2
A	967	SER	-	expression tag	UNP Q8BHN3-2
A	968	ALA	-	expression tag	UNP Q8BHN3-2
A	969	TRP	-	expression tag	UNP Q8BHN3-2
A	970	SER	-	expression tag	UNP Q8BHN3-2
A	971	HIS	-	expression tag	UNP Q8BHN3-2
A	972	PRO	-	expression tag	UNP Q8BHN3-2
A	973	GLN	-	expression tag	UNP Q8BHN3-2
A	974	PHE	-	expression tag	UNP Q8BHN3-2
A	975	GLU	-	expression tag	UNP Q8BHN3-2
A	976	LYS	-	expression tag	UNP Q8BHN3-2
A	977	LEU	-	expression tag	UNP Q8BHN3-2
A	978	GLU	-	expression tag	UNP Q8BHN3-2
C	2	MET	-	initiating methionine	UNP Q8BHN3-2
C	3	GLY	-	expression tag	UNP Q8BHN3-2
C	4	ILE	-	expression tag	UNP Q8BHN3-2
C	5	LEU	-	expression tag	UNP Q8BHN3-2
C	6	PRO	-	expression tag	UNP Q8BHN3-2
C	7	SER	-	expression tag	UNP Q8BHN3-2
C	8	PRO	-	expression tag	UNP Q8BHN3-2
C	9	GLY	-	expression tag	UNP Q8BHN3-2
C	10	MET	-	expression tag	UNP Q8BHN3-2
C	11	PRO	-	expression tag	UNP Q8BHN3-2
C	12	ALA	-	expression tag	UNP Q8BHN3-2
C	13	LEU	-	expression tag	UNP Q8BHN3-2
C	14	LEU	-	expression tag	UNP Q8BHN3-2
C	15	SER	-	expression tag	UNP Q8BHN3-2
C	16	LEU	-	expression tag	UNP Q8BHN3-2
C	17	VAL	-	expression tag	UNP Q8BHN3-2
C	18	SER	-	expression tag	UNP Q8BHN3-2
C	19	LEU	-	expression tag	UNP Q8BHN3-2
C	20	LEU	-	expression tag	UNP Q8BHN3-2
C	21	SER	-	expression tag	UNP Q8BHN3-2
C	22	VAL	-	expression tag	UNP Q8BHN3-2
C	23	LEU	-	expression tag	UNP Q8BHN3-2
C	24	LEU	-	expression tag	UNP Q8BHN3-2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	25	MET	-	expression tag	UNP Q8BHN3-2
C	26	GLY	-	expression tag	UNP Q8BHN3-2
C	27	CYS	-	expression tag	UNP Q8BHN3-2
C	28	VAL	-	expression tag	UNP Q8BHN3-2
C	29	ALA	-	expression tag	UNP Q8BHN3-2
C	30	GLU	-	expression tag	UNP Q8BHN3-2
C	31	THR	-	expression tag	UNP Q8BHN3-2
C	32	GLY	-	expression tag	UNP Q8BHN3-2
C	97	ASP	ASN	engineered mutation	UNP Q8BHN3-2
C	967	SER	-	expression tag	UNP Q8BHN3-2
C	968	ALA	-	expression tag	UNP Q8BHN3-2
C	969	TRP	-	expression tag	UNP Q8BHN3-2
C	970	SER	-	expression tag	UNP Q8BHN3-2
C	971	HIS	-	expression tag	UNP Q8BHN3-2
C	972	PRO	-	expression tag	UNP Q8BHN3-2
C	973	GLN	-	expression tag	UNP Q8BHN3-2
C	974	PHE	-	expression tag	UNP Q8BHN3-2
C	975	GLU	-	expression tag	UNP Q8BHN3-2
C	976	LYS	-	expression tag	UNP Q8BHN3-2
C	977	LEU	-	expression tag	UNP Q8BHN3-2
C	978	GLU	-	expression tag	UNP Q8BHN3-2

- Molecule 2 is a protein called Glucosidase 2 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	87	Total	C	N	O	S	0	0	0
			624	371	102	141	10			
2	D	87	Total	C	N	O	S	0	0	0
			632	377	104	141	10			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	MET	-	initiating methionine	UNP O08795
B	-15	GLY	-	expression tag	UNP O08795
B	-14	ILE	-	expression tag	UNP O08795
B	-13	LEU	-	expression tag	UNP O08795
B	-12	PRO	-	expression tag	UNP O08795
B	-11	SER	-	expression tag	UNP O08795
B	-10	PRO	-	expression tag	UNP O08795
B	-9	GLY	-	expression tag	UNP O08795
B	-8	MET	-	expression tag	UNP O08795

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	PRO	-	expression tag	UNP O08795
B	-6	ALA	-	expression tag	UNP O08795
B	-5	LEU	-	expression tag	UNP O08795
B	-4	LEU	-	expression tag	UNP O08795
B	-3	SER	-	expression tag	UNP O08795
B	-2	LEU	-	expression tag	UNP O08795
B	-1	VAL	-	expression tag	UNP O08795
B	0	SER	-	expression tag	UNP O08795
B	1	LEU	-	expression tag	UNP O08795
B	2	LEU	-	expression tag	UNP O08795
B	3	SER	-	expression tag	UNP O08795
B	4	VAL	-	expression tag	UNP O08795
B	5	LEU	-	expression tag	UNP O08795
B	6	LEU	-	expression tag	UNP O08795
B	7	MET	-	expression tag	UNP O08795
B	8	GLY	-	expression tag	UNP O08795
B	9	CYS	-	expression tag	UNP O08795
B	10	VAL	-	expression tag	UNP O08795
B	11	ALA	-	expression tag	UNP O08795
B	12	GLU	-	expression tag	UNP O08795
B	13	THR	-	expression tag	UNP O08795
B	14	GLY	-	expression tag	UNP O08795
B	518	SER	-	expression tag	UNP O08795
B	519	ALA	-	expression tag	UNP O08795
B	520	TRP	-	expression tag	UNP O08795
B	521	SER	-	expression tag	UNP O08795
B	522	HIS	-	expression tag	UNP O08795
B	523	PRO	-	expression tag	UNP O08795
B	524	GLN	-	expression tag	UNP O08795
B	525	PHE	-	expression tag	UNP O08795
B	526	GLU	-	expression tag	UNP O08795
B	527	LYS	-	expression tag	UNP O08795
B	528	LEU	-	expression tag	UNP O08795
B	529	GLU	-	expression tag	UNP O08795
B	530	THR	-	expression tag	UNP O08795
B	531	LYS	-	expression tag	UNP O08795
B	532	HIS	-	expression tag	UNP O08795
B	533	HIS	-	expression tag	UNP O08795
B	534	HIS	-	expression tag	UNP O08795
B	535	HIS	-	expression tag	UNP O08795
B	536	HIS	-	expression tag	UNP O08795
B	537	HIS	-	expression tag	UNP O08795

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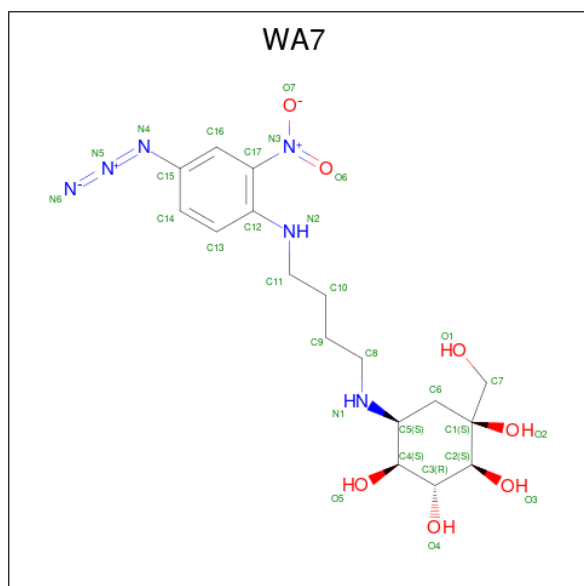
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	MET	-	initiating methionine	UNP O08795
D	-15	GLY	-	expression tag	UNP O08795
D	-14	ILE	-	expression tag	UNP O08795
D	-13	LEU	-	expression tag	UNP O08795
D	-12	PRO	-	expression tag	UNP O08795
D	-11	SER	-	expression tag	UNP O08795
D	-10	PRO	-	expression tag	UNP O08795
D	-9	GLY	-	expression tag	UNP O08795
D	-8	MET	-	expression tag	UNP O08795
D	-7	PRO	-	expression tag	UNP O08795
D	-6	ALA	-	expression tag	UNP O08795
D	-5	LEU	-	expression tag	UNP O08795
D	-4	LEU	-	expression tag	UNP O08795
D	-3	SER	-	expression tag	UNP O08795
D	-2	LEU	-	expression tag	UNP O08795
D	-1	VAL	-	expression tag	UNP O08795
D	0	SER	-	expression tag	UNP O08795
D	1	LEU	-	expression tag	UNP O08795
D	2	LEU	-	expression tag	UNP O08795
D	3	SER	-	expression tag	UNP O08795
D	4	VAL	-	expression tag	UNP O08795
D	5	LEU	-	expression tag	UNP O08795
D	6	LEU	-	expression tag	UNP O08795
D	7	MET	-	expression tag	UNP O08795
D	8	GLY	-	expression tag	UNP O08795
D	9	CYS	-	expression tag	UNP O08795
D	10	VAL	-	expression tag	UNP O08795
D	11	ALA	-	expression tag	UNP O08795
D	12	GLU	-	expression tag	UNP O08795
D	13	THR	-	expression tag	UNP O08795
D	14	GLY	-	expression tag	UNP O08795
D	518	SER	-	expression tag	UNP O08795
D	519	ALA	-	expression tag	UNP O08795
D	520	TRP	-	expression tag	UNP O08795
D	521	SER	-	expression tag	UNP O08795
D	522	HIS	-	expression tag	UNP O08795
D	523	PRO	-	expression tag	UNP O08795
D	524	GLN	-	expression tag	UNP O08795
D	525	PHE	-	expression tag	UNP O08795
D	526	GLU	-	expression tag	UNP O08795
D	527	LYS	-	expression tag	UNP O08795
D	528	LEU	-	expression tag	UNP O08795

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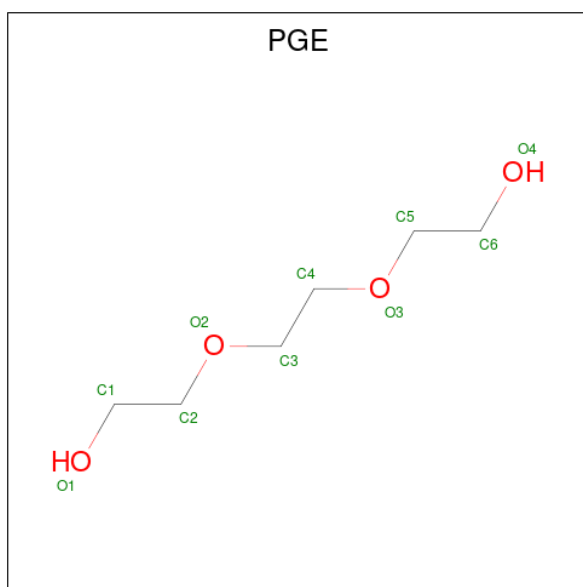
Chain	Residue	Modelled	Actual	Comment	Reference
D	529	GLU	-	expression tag	UNP O08795
D	530	THR	-	expression tag	UNP O08795
D	531	LYS	-	expression tag	UNP O08795
D	532	HIS	-	expression tag	UNP O08795
D	533	HIS	-	expression tag	UNP O08795
D	534	HIS	-	expression tag	UNP O08795
D	535	HIS	-	expression tag	UNP O08795
D	536	HIS	-	expression tag	UNP O08795
D	537	HIS	-	expression tag	UNP O08795

- Molecule 3 is (1S,2S,3R,4S,5S)-1-(hydroxymethyl)-5-[(4-{[2-nitro-4-(triazan-1-yl)phenyl]amino}butyl)amino]cyclohexane-1,2,3,4-tetrol (CCD ID: WA7) (formula: C₁₇H₂₆N₆O₇) (labeled as "Ligand of Interest" by depositor).



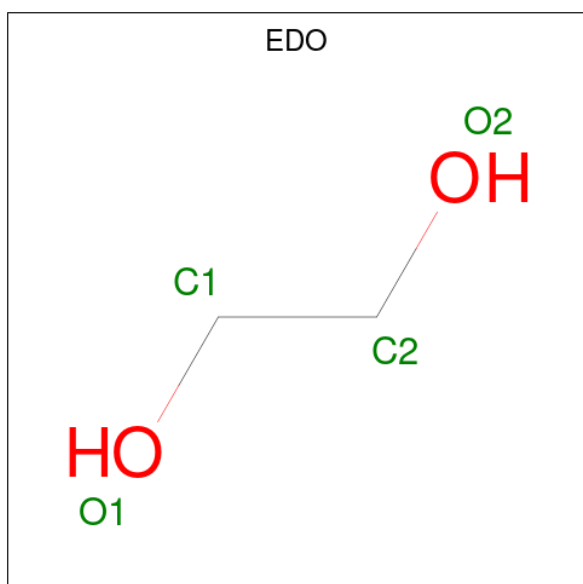
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			30	17	6	7		
3	C	1	Total	C	N	O	0	0
			30	17	6	7		

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



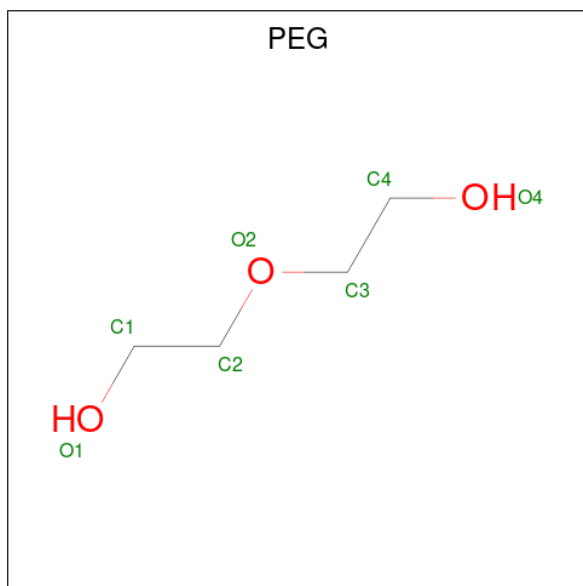
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0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

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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

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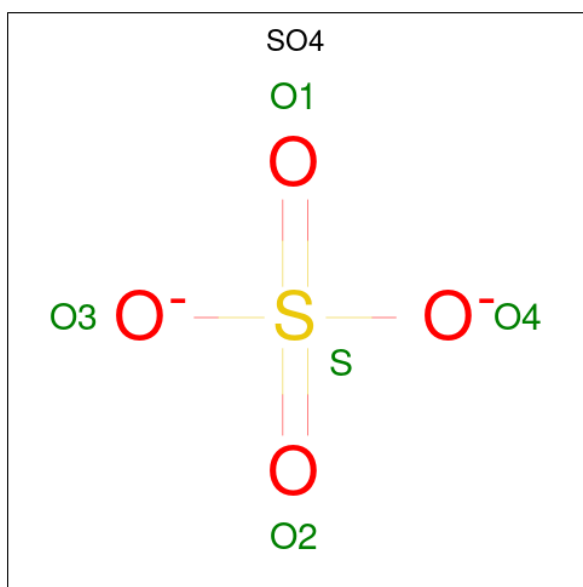
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 7 4 3	0	0
6	A	1	Total C O 7 4 3	0	0
6	A	1	Total C O 7 4 3	0	0
6	A	1	Total C O 7 4 3	0	0
6	B	1	Total C O 7 4 3	0	0
6	C	1	Total C O 7 4 3	0	0
6	C	1	Total C O 7 4 3	0	0
6	C	1	Total C O 7 4 3	0	0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

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	2	Total Ca 2 2	0	0
7	D	2	Total Ca 2 2	0	0

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		

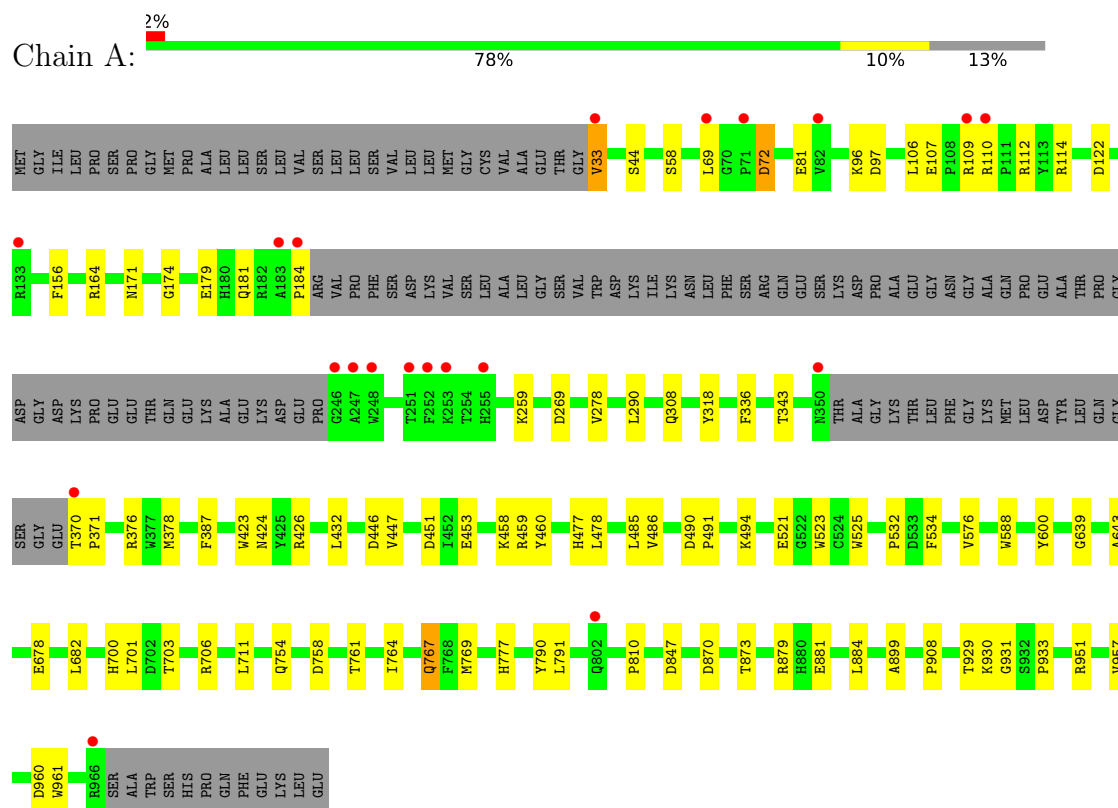
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	315	Total	O	0	0
			315	315		
9	B	13	Total	O	0	0
			13	13		
9	C	247	Total	O	0	0
			247	247		
9	D	15	Total	O	0	0
			15	15		

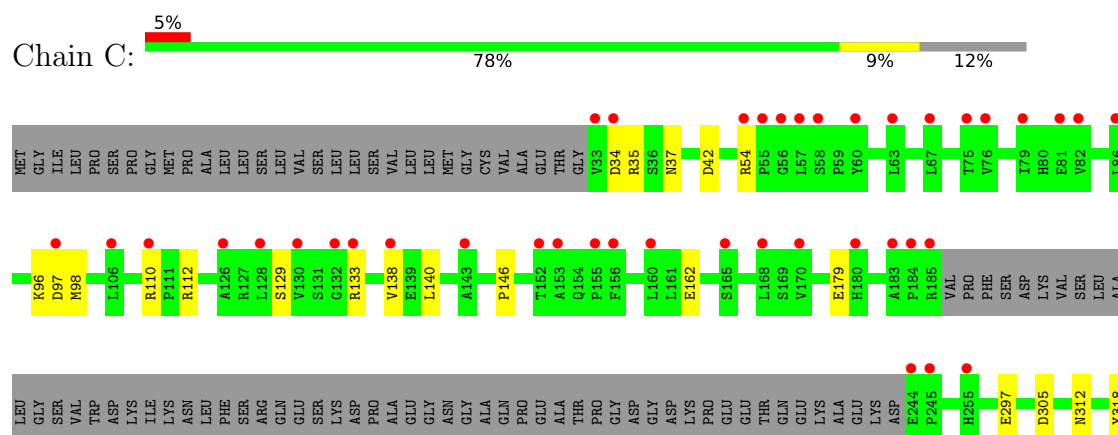
3 Residue-property plots [i](#)

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.

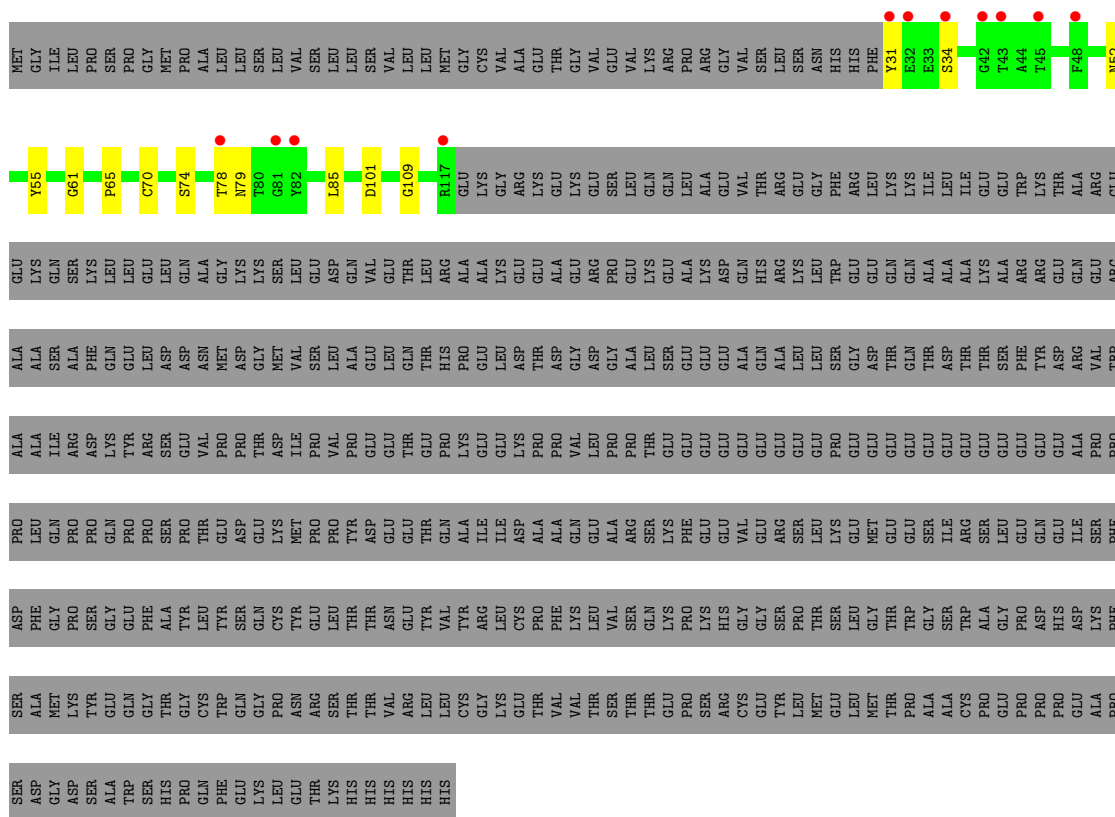
• Molecule 1: Isoform 2 of Neutral alpha-glucosidase AB



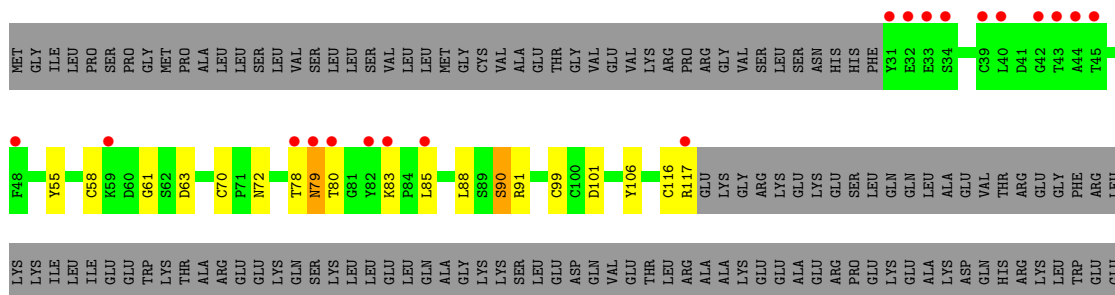
• Molecule 1: Isoform 2 of Neutral alpha-glucosidase AB



- Molecule 2: Glucosidase 2 subunit beta



- Molecule 2: Glucosidase 2 subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	102.78Å 102.78Å 240.12Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.02 – 2.38 40.02 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.7 (40.02-2.38) 93.5 (40.02-2.38)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.75 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.14_3228	Depositor
R, R_{free}	0.174 , 0.210 0.175 , 0.211	Depositor DCC
R_{free} test set	1979 reflections (1.76%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.008 for -h,-k,l 0.038 for h,-h-k,-l 0.020 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15963	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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: SO4, PEG, PGE, CA, EDO, WA7

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	0.31	0/7120	0.53	0/9694
1	C	0.31	0/7130	0.52	0/9714
2	B	0.28	0/636	0.53	0/870
2	D	0.28	0/644	0.52	0/880
All	All	0.31	0/15530	0.53	0/21158

There are no bond length outliers.

There are no bond angle outliers.

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	6898	0	6646	65	0
1	C	6894	0	6599	64	0
2	B	624	0	504	9	0
2	D	632	0	530	19	0
3	A	30	0	0	0	0
3	C	30	0	0	0	0
4	A	40	0	56	7	0
4	C	10	0	14	1	0
5	A	32	0	46	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	16	0	23	4	0
5	C	68	0	100	9	0
5	D	8	0	12	1	0
6	A	42	0	60	3	0
6	B	7	0	10	0	0
6	C	21	0	30	13	0
6	D	7	0	10	2	0
7	B	2	0	0	0	0
7	D	2	0	0	0	0
8	C	10	0	0	1	0
9	A	315	0	0	10	0
9	B	13	0	0	2	0
9	C	247	0	0	14	0
9	D	15	0	0	1	0
All	All	15963	0	14640	156	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 5.

The worst 5 of 156 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:37:ASN:OD1	9:C:1601:HOH:O	1.82	0.97
1:C:840:ARG:HB3	6:C:1512:PEG:H32	1.61	0.81
1:C:619:PRO:O	9:C:1602:HOH:O	1.99	0.80
1:A:521:GLU:H	5:A:1019:EDO:H11	1.47	0.80
1:C:54:ARG:O	9:C:1603:HOH:O	2.00	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	852/977 (87%)	820 (96%)	31 (4%)	1 (0%)	48	62
1	C	859/977 (88%)	825 (96%)	34 (4%)	0	100	100
2	B	85/554 (15%)	82 (96%)	3 (4%)	0	100	100
2	D	85/554 (15%)	82 (96%)	3 (4%)	0	100	100
All	All	1881/3062 (61%)	1809 (96%)	71 (4%)	1 (0%)	48	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	643	ALA

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	747/846 (88%)	736 (98%)	11 (2%)	57	75
1	C	742/846 (88%)	732 (99%)	10 (1%)	61	78
2	B	69/485 (14%)	66 (96%)	3 (4%)	26	41
2	D	71/485 (15%)	65 (92%)	6 (8%)	10	15
All	All	1629/2662 (61%)	1599 (98%)	30 (2%)	50	71

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	97	ASP
2	D	83	LYS
1	C	446	ASP
2	D	90	SER
2	D	78	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	807	HIS
2	D	50	GLN
1	C	330	HIS
1	C	470	GLN
1	C	545	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 55 ligands modelled in this entry, 4 are monoatomic - leaving 51 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	$\# Z > 2$
6	PEG	C	1508	-	6,6,6	0.50	0	5,5,5	0.31	0
4	PGE	A	1002	-	9,9,9	0.40	0	8,8,8	0.55	0
5	EDO	A	1013	-	3,3,3	0.44	0	2,2,2	0.46	0
5	EDO	C	1507	-	3,3,3	0.58	0	2,2,2	0.21	0
5	EDO	C	1513	-	3,3,3	0.53	0	2,2,2	0.31	0
5	EDO	D	603	-	3,3,3	0.43	0	2,2,2	0.44	0
5	EDO	C	1515	-	3,3,3	0.73	0	2,2,2	0.41	0
5	EDO	C	1517	-	3,3,3	0.47	0	2,2,2	0.34	0
6	PEG	D	602	-	6,6,6	0.13	0	5,5,5	0.18	0
5	EDO	C	1509	-	3,3,3	0.44	0	2,2,2	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	C	1518	-	3,3,3	0.42	0	2,2,2	0.67	0
6	PEG	A	1004	-	6,6,6	0.53	0	5,5,5	0.39	0
5	EDO	B	602	-	3,3,3	0.55	0	2,2,2	0.20	0
3	WA7	A	1001	-	31,31,31	3.80	12 (38%)	35,43,43	1.57	6 (17%)
5	EDO	A	1014	-	3,3,3	0.66	0	2,2,2	0.16	0
5	EDO	A	1019	-	3,3,3	0.52	0	2,2,2	0.27	0
5	EDO	C	1511	-	3,3,3	0.44	0	2,2,2	0.48	0
5	EDO	C	1514	-	3,3,3	0.51	0	2,2,2	0.21	0
5	EDO	C	1503	-	3,3,3	0.60	0	2,2,2	0.19	0
5	EDO	C	1522	-	3,3,3	0.56	0	2,2,2	0.31	0
4	PGE	A	1007	-	9,9,9	0.43	0	8,8,8	0.38	0
5	EDO	C	1516	-	3,3,3	0.37	0	2,2,2	0.82	0
5	EDO	C	1520	-	3,3,3	0.34	0	2,2,2	0.74	0
6	PEG	C	1504	-	6,6,6	0.51	0	5,5,5	0.40	0
5	EDO	B	603	-	3,3,3	0.46	0	2,2,2	0.34	0
5	EDO	C	1519	-	3,3,3	0.45	0	2,2,2	0.27	0
6	PEG	C	1512	-	6,6,6	0.47	0	5,5,5	0.91	0
6	PEG	B	601	-	6,6,6	0.53	0	5,5,5	0.42	0
5	EDO	A	1016	-	3,3,3	0.50	0	2,2,2	0.44	0
5	EDO	B	604	-	3,3,3	0.41	0	2,2,2	0.44	0
5	EDO	C	1501	-	3,3,3	0.47	0	2,2,2	0.43	0
5	EDO	A	1018	-	3,3,3	0.44	0	2,2,2	0.49	0
5	EDO	A	1015	-	3,3,3	0.47	0	2,2,2	0.64	0
6	PEG	A	1009	-	6,6,6	0.35	0	5,5,5	0.16	0
5	EDO	B	605	-	3,3,3	0.56	0	2,2,2	0.37	0
5	EDO	D	601	-	3,3,3	0.53	0	2,2,2	0.21	0
5	EDO	C	1510	-	3,3,3	0.44	0	2,2,2	0.20	0
6	PEG	A	1005	-	6,6,6	0.54	0	5,5,5	0.61	0
6	PEG	A	1010	-	6,6,6	0.51	0	5,5,5	0.30	0
5	EDO	A	1003	-	3,3,3	0.53	0	2,2,2	0.31	0
6	PEG	A	1017	-	6,6,6	0.48	0	5,5,5	0.30	0
4	PGE	A	1006	-	9,9,9	0.35	0	8,8,8	0.48	0
8	SO4	C	1524	-	4,4,4	0.29	0	6,6,6	0.19	0
5	EDO	A	1012	-	3,3,3	0.63	0	2,2,2	0.36	0
4	PGE	A	1008	-	9,9,9	0.21	0	8,8,8	0.15	0
4	PGE	C	1505	-	9,9,9	0.39	0	8,8,8	0.32	0
3	WA7	C	1502	-	31,31,31	3.60	11 (35%)	35,43,43	1.27	3 (8%)
5	EDO	C	1506	-	3,3,3	0.49	0	2,2,2	0.43	0
6	PEG	A	1011	-	6,6,6	0.51	0	5,5,5	0.26	0
5	EDO	C	1521	-	3,3,3	0.23	0	2,2,2	0.06	0
8	SO4	C	1523	-	4,4,4	0.29	0	6,6,6	0.41	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
6	PEG	C	1508	-	-	2/4/4/4	-
4	PGE	A	1002	-	-	3/7/7/7	-
5	EDO	A	1013	-	-	1/1/1/1	-
5	EDO	C	1507	-	-	0/1/1/1	-
5	EDO	C	1513	-	-	0/1/1/1	-
5	EDO	D	603	-	-	1/1/1/1	-
5	EDO	C	1515	-	-	1/1/1/1	-
5	EDO	C	1517	-	-	0/1/1/1	-
6	PEG	D	602	-	-	3/4/4/4	-
5	EDO	C	1509	-	-	0/1/1/1	-
5	EDO	C	1518	-	-	1/1/1/1	-
6	PEG	A	1004	-	-	2/4/4/4	-
5	EDO	B	602	-	-	1/1/1/1	-
3	WA7	A	1001	-	-	7/17/42/42	0/2/2/2
5	EDO	A	1014	-	-	1/1/1/1	-
5	EDO	A	1019	-	-	0/1/1/1	-
5	EDO	C	1511	-	-	0/1/1/1	-
5	EDO	C	1514	-	-	1/1/1/1	-
5	EDO	C	1503	-	-	1/1/1/1	-
5	EDO	C	1522	-	-	1/1/1/1	-
4	PGE	A	1007	-	-	3/7/7/7	-
5	EDO	C	1516	-	-	1/1/1/1	-
5	EDO	C	1520	-	-	1/1/1/1	-
6	PEG	C	1504	-	-	3/4/4/4	-
5	EDO	B	603	-	-	1/1/1/1	-
5	EDO	C	1519	-	-	1/1/1/1	-
6	PEG	C	1512	-	-	2/4/4/4	-
6	PEG	B	601	-	-	2/4/4/4	-
5	EDO	A	1016	-	-	0/1/1/1	-
5	EDO	B	604	-	-	1/1/1/1	-
5	EDO	C	1501	-	-	0/1/1/1	-
5	EDO	A	1018	-	-	1/1/1/1	-
5	EDO	A	1015	-	-	1/1/1/1	-
6	PEG	A	1009	-	-	1/4/4/4	-
5	EDO	B	605	-	-	1/1/1/1	-
5	EDO	D	601	-	-	1/1/1/1	-
5	EDO	C	1510	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	PEG	A	1005	-	-	0/4/4/4	-
6	PEG	A	1010	-	-	1/4/4/4	-
5	EDO	A	1003	-	-	0/1/1/1	-
6	PEG	A	1017	-	-	1/4/4/4	-
4	PGE	A	1006	-	-	3/7/7/7	-
5	EDO	A	1012	-	-	0/1/1/1	-
4	PGE	A	1008	-	-	5/7/7/7	-
4	PGE	C	1505	-	-	4/7/7/7	-
3	WA7	C	1502	-	-	8/17/42/42	0/2/2/2
5	EDO	C	1506	-	-	1/1/1/1	-
6	PEG	A	1011	-	-	0/4/4/4	-
5	EDO	C	1521	-	-	0/1/1/1	-

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	WA7	O6-N3	13.40	1.45	1.22
3	C	1502	WA7	N6-N5	12.75	1.49	1.23
3	A	1001	WA7	N6-N5	12.43	1.48	1.23
3	C	1502	WA7	O6-N3	10.65	1.41	1.22
3	A	1001	WA7	N5-N4	4.52	1.39	1.24

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	WA7	C11-N2-C12	-3.96	113.75	123.35
3	C	1502	WA7	C17-C12-N2	-3.94	116.62	123.38
3	A	1001	WA7	C15-N4-N5	3.89	123.51	115.95
3	C	1502	WA7	O6-N3-C17	-3.63	112.83	119.03
3	A	1001	WA7	O6-N3-C17	3.62	125.22	119.03

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

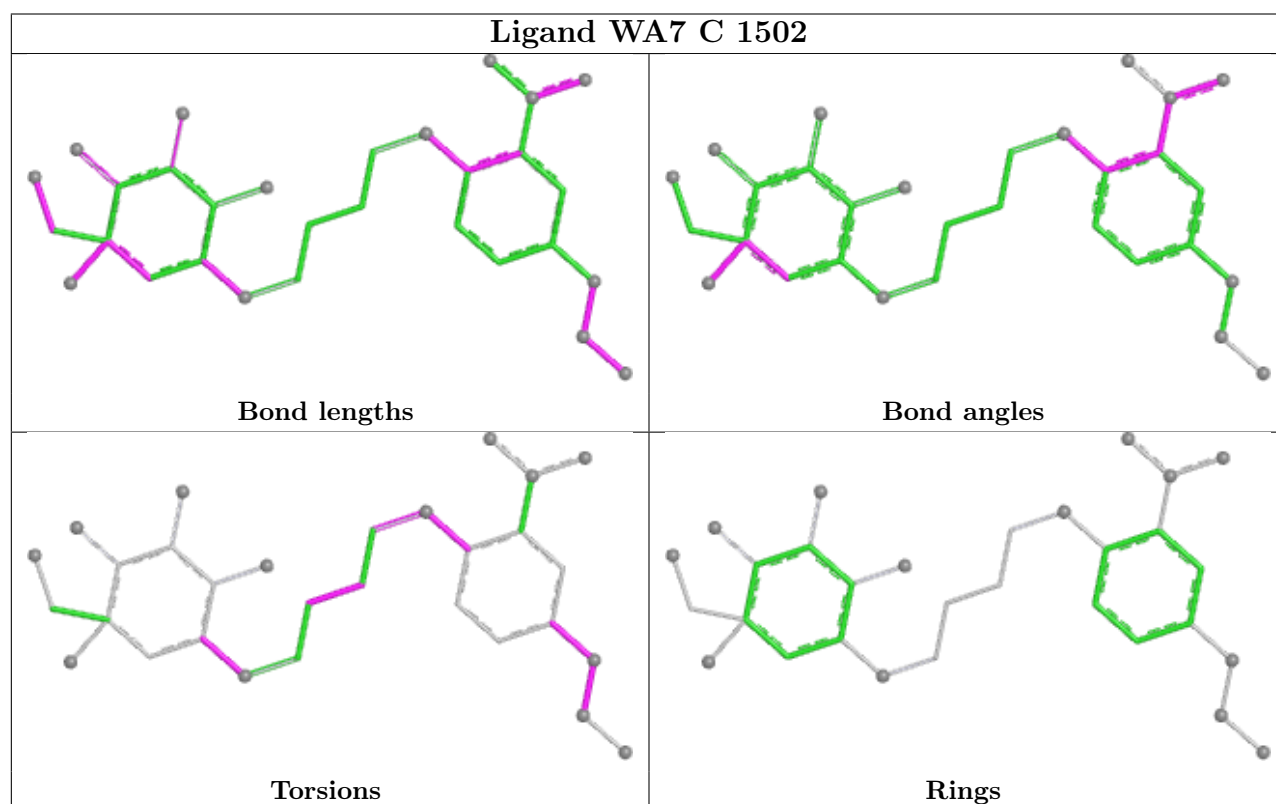
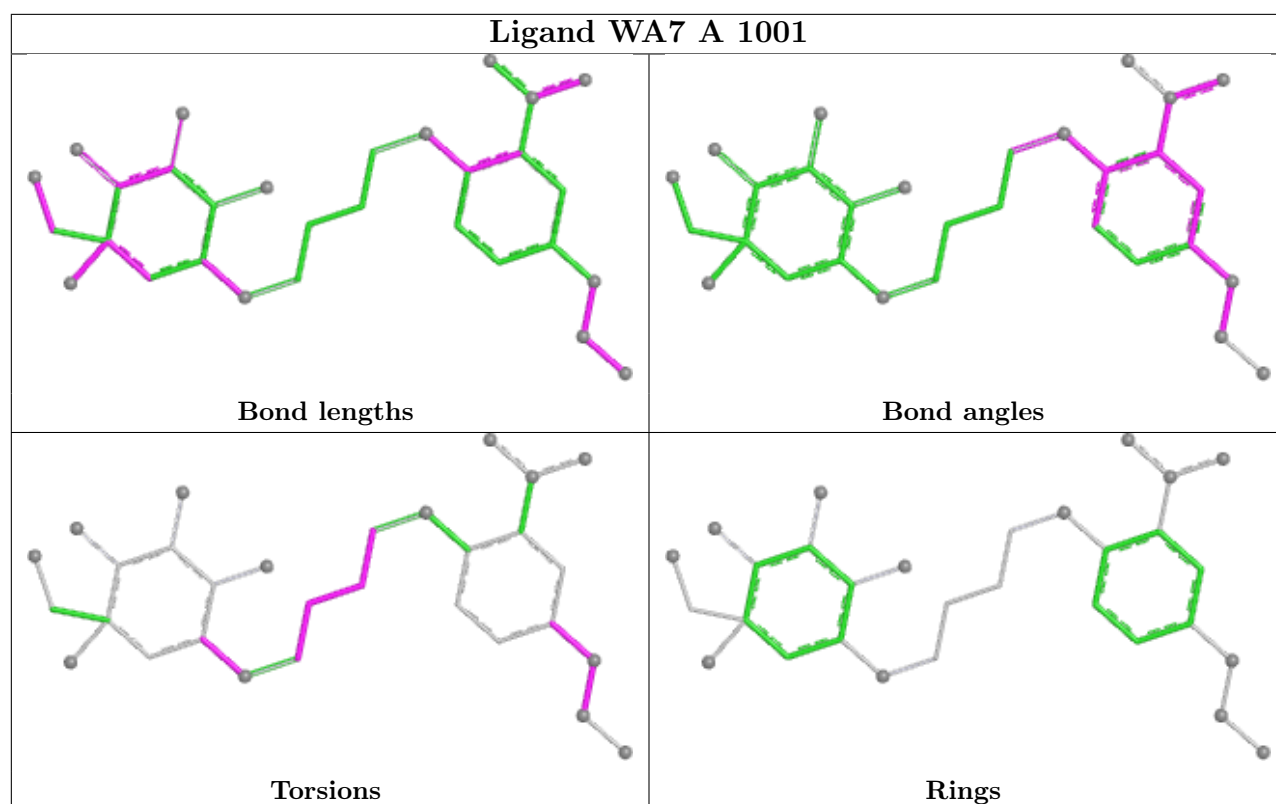
Mol	Chain	Res	Type	Atoms
3	A	1001	WA7	C6-C5-N1-C8
3	A	1001	WA7	C14-C15-N4-N5
3	A	1001	WA7	C16-C15-N4-N5
3	C	1502	WA7	C14-C15-N4-N5
3	C	1502	WA7	C16-C15-N4-N5

There are no ring outliers.

23 monomers are involved in 45 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1013	EDO	1	0
5	C	1513	EDO	1	0
5	D	603	EDO	1	0
6	D	602	PEG	2	0
5	C	1518	EDO	2	0
5	B	602	EDO	1	0
5	A	1019	EDO	1	0
5	C	1503	EDO	1	0
4	A	1007	PGE	1	0
5	C	1516	EDO	3	0
5	C	1520	EDO	1	0
6	C	1504	PEG	1	0
5	C	1519	EDO	1	0
6	C	1512	PEG	12	0
5	B	604	EDO	2	0
5	A	1015	EDO	2	0
6	A	1009	PEG	1	0
5	B	605	EDO	1	0
6	A	1005	PEG	2	0
4	A	1006	PGE	3	0
8	C	1524	SO4	1	0
4	A	1008	PGE	3	0
4	C	1505	PGE	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 [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	854/977 (87%)	-0.13	20 (2%) 61 60	21, 43, 69, 106	4 (0%)
1	C	857/977 (87%)	0.16	46 (5%) 31 31	20, 48, 82, 102	8 (0%)
2	B	87/554 (15%)	0.65	11 (12%) 8 7	38, 59, 92, 101	0
2	D	87/554 (15%)	0.86	19 (21%) 2 2	41, 60, 94, 104	0
All	All	1885/3062 (61%)	0.08	96 (5%) 33 33	20, 46, 82, 106	12 (0%)

The worst 5 of 96 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	183	ALA	5.2
2	B	48	PHE	5.1
2	D	48	PHE	5.0
2	B	43	THR	4.6
1	A	248	TRP	4.3

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($\text{\AA}^2$)	Q<0.9
6	PEG	B	601	7/7	0.68	0.20	58,67,74,76	0
8	SO4	C	1524	5/5	0.76	0.16	73,79,90,97	0
5	EDO	C	1510	4/4	0.77	0.17	70,78,78,79	0
6	PEG	A	1010	7/7	0.78	0.19	53,59,66,68	0
5	EDO	C	1517	4/4	0.79	0.20	61,67,68,73	0
5	EDO	C	1515	4/4	0.80	0.19	36,49,58,64	0
5	EDO	C	1522	4/4	0.81	0.19	62,63,64,83	0
6	PEG	C	1508	7/7	0.82	0.17	58,67,75,80	0
5	EDO	D	601	4/4	0.82	0.21	58,63,66,71	0
4	PGE	C	1505	10/10	0.83	0.16	54,65,71,77	0
5	EDO	C	1521	4/4	0.83	0.27	86,92,100,104	0
6	PEG	A	1017	7/7	0.84	0.13	54,64,69,72	0
4	PGE	A	1002	10/10	0.84	0.18	50,66,73,79	0
6	PEG	C	1504	7/7	0.84	0.14	53,66,70,73	0
5	EDO	B	605	4/4	0.84	0.20	53,61,62,75	0
4	PGE	A	1007	10/10	0.84	0.14	50,65,74,79	0
5	EDO	B	603	4/4	0.85	0.16	58,62,64,81	0
4	PGE	A	1008	10/10	0.85	0.18	79,84,92,102	0
5	EDO	C	1503	4/4	0.86	0.17	59,59,61,62	0
5	EDO	C	1507	4/4	0.86	0.15	63,66,66,73	0
5	EDO	A	1013	4/4	0.86	0.16	64,66,67,67	0
5	EDO	A	1015	4/4	0.86	0.13	54,57,61,85	0
6	PEG	A	1004	7/7	0.86	0.16	51,62,68,73	0
6	PEG	C	1512	7/7	0.86	0.27	50,52,61,63	0
6	PEG	D	602	7/7	0.86	0.16	62,69,74,75	0
6	PEG	A	1009	7/7	0.86	0.15	60,62,71,72	0
5	EDO	C	1519	4/4	0.87	0.15	63,67,73,74	0
4	PGE	A	1006	10/10	0.87	0.14	49,62,74,75	0
6	PEG	A	1005	7/7	0.87	0.14	43,54,64,65	0
5	EDO	C	1513	4/4	0.87	0.16	51,54,54,62	0
3	WA7	C	1502	30/30	0.88	0.14	35,59,81,85	0
5	EDO	C	1518	4/4	0.88	0.13	49,55,61,66	0
6	PEG	A	1011	7/7	0.88	0.14	60,62,66,69	0
5	EDO	C	1506	4/4	0.88	0.14	46,57,60,63	0
5	EDO	A	1012	4/4	0.88	0.19	53,55,60,76	0
5	EDO	A	1014	4/4	0.89	0.16	42,52,59,70	0
3	WA7	A	1001	30/30	0.89	0.13	36,60,82,94	0
5	EDO	C	1501	4/4	0.90	0.14	54,58,63,70	0
5	EDO	C	1514	4/4	0.90	0.13	53,63,65,65	0
8	SO4	C	1523	5/5	0.90	0.17	61,67,82,104	0
5	EDO	C	1520	4/4	0.90	0.12	58,60,65,70	0
5	EDO	B	602	4/4	0.91	0.12	54,61,68,70	0
5	EDO	C	1516	4/4	0.91	0.12	49,51,54,56	0

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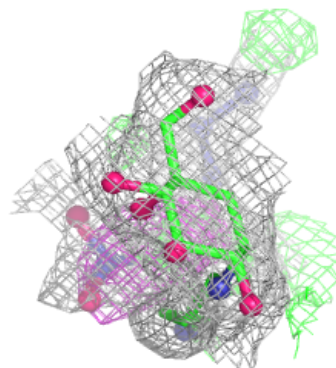
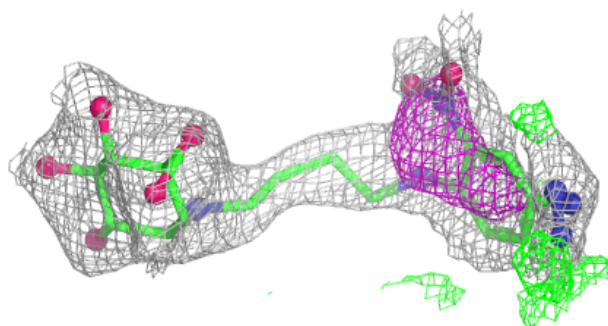
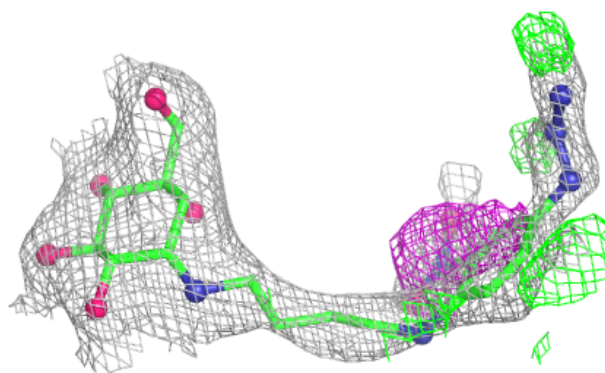
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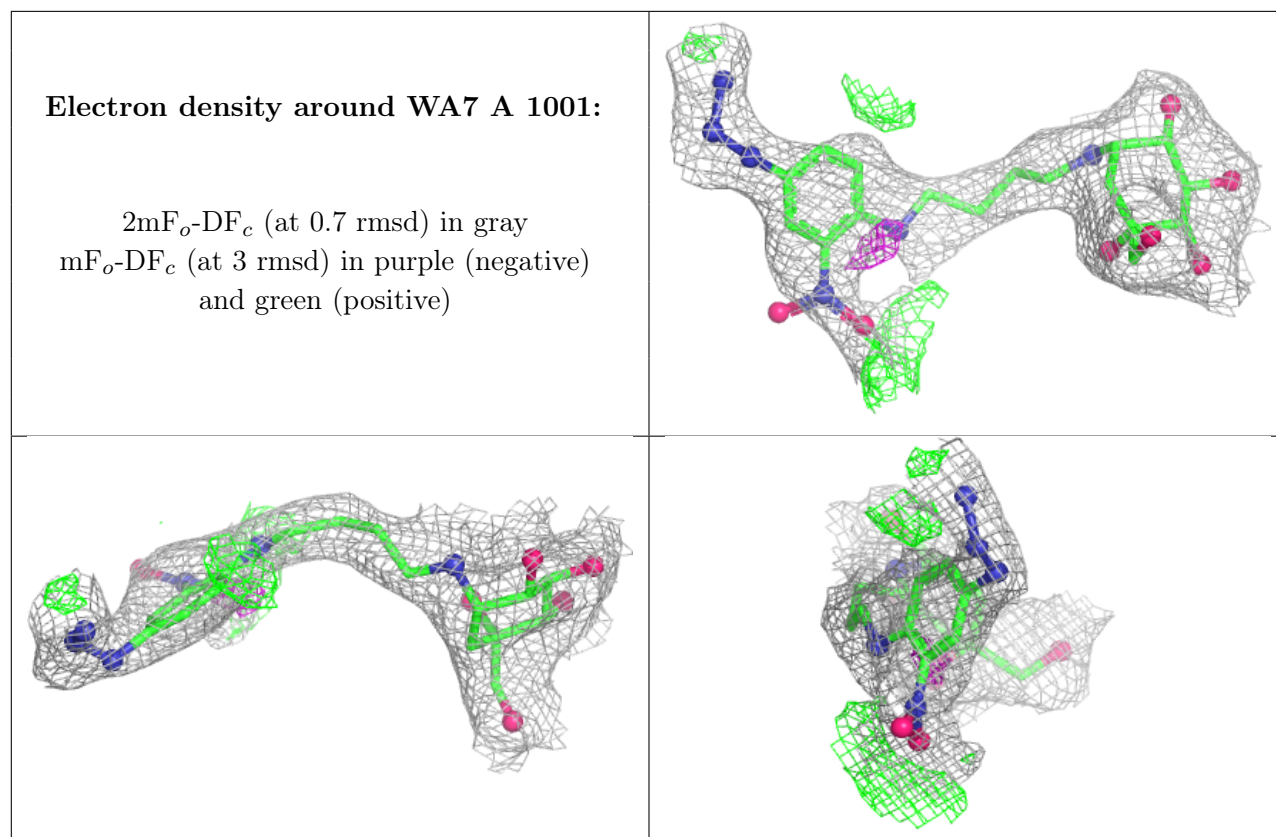
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	C	1509	4/4	0.92	0.11	56,56,64,70	0
5	EDO	A	1019	4/4	0.92	0.12	55,60,63,66	0
5	EDO	D	603	4/4	0.92	0.12	54,63,64,65	0
5	EDO	C	1511	4/4	0.92	0.11	44,47,49,71	0
5	EDO	A	1016	4/4	0.93	0.09	47,53,54,56	0
5	EDO	A	1018	4/4	0.93	0.19	54,55,58,61	0
5	EDO	B	604	4/4	0.94	0.09	54,54,62,64	0
5	EDO	A	1003	4/4	0.97	0.12	46,52,52,53	0
7	CA	D	605	1/1	0.99	0.02	45,45,45,45	0
7	CA	B	607	1/1	0.99	0.02	51,51,51,51	0
7	CA	D	604	1/1	0.99	0.04	51,51,51,51	0
7	CA	B	606	1/1	1.00	0.02	45,45,45,45	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around WA7 C 1502:

2mF_o-DF_c (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
 and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.