



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 27, 2021 – 02:13 PM EDT

PDB ID : 7KAD
Title : Co-crystal structure of alpha glucosidase with compound 6
Authors : Karade, S.S.; Mariuzza, R.A.
Deposited on : 2020-09-30
Resolution : 2.51 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
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) : 2.23.2

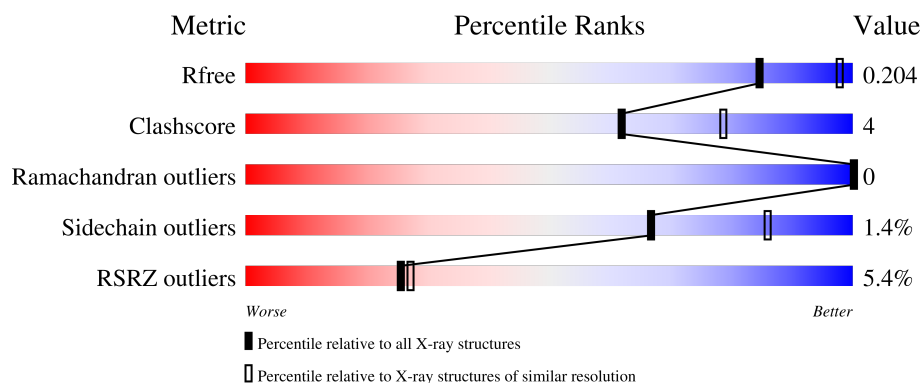
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	
1	C	977	
2	B	554	
2	D	554	

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
4	EDO	A	1020	-	-	-	X
5	PGE	A	1016	-	-	-	X
7	SO4	A	1034	-	-	X	-
7	SO4	A	1037	-	-	X	-
7	SO4	C	1028	-	-	-	X

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 15939 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	7	0
			6903	4426	1189	1258	30			
1	C	857	Total	C	N	O	S	0	8	0
			6903	4425	1198	1250	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
			623	371	102	140	10			
2	D	87	Total	C	N	O	S	0	0	0
			624	374	103	137	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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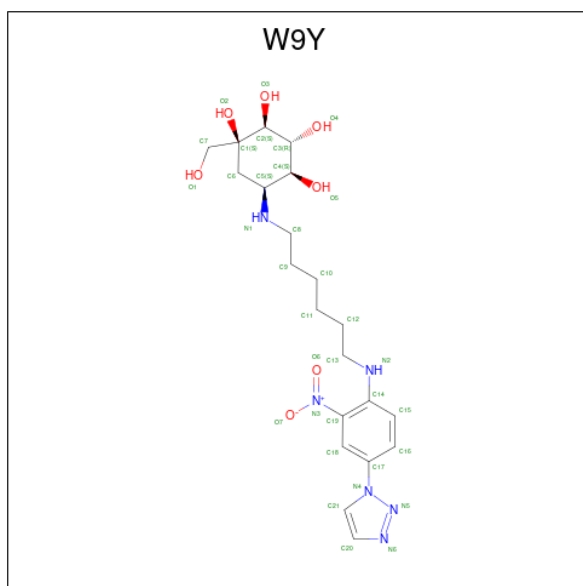
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	MET	-	initiating methionine	UNP O08795
D	-15	GLY	-	expression tag	UNP O08795
D	-14	ILE	-	expression tag	UNP O08795
D	-13	LEU	-	expression tag	UNP O08795
D	-12	PRO	-	expression tag	UNP O08795
D	-11	SER	-	expression tag	UNP O08795
D	-10	PRO	-	expression 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-[(6-{[2-nitro-4-(1H-1,2,3-triazol-1-yl)phenyl]amino}hexyl)amino]cyclohexane-1,2,3,4-tetrol (three-letter code: W9Y) (formula: C₂₁H₃₂N₆O₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			34	21	6	7		
3	C	1	Total	C	N	O	0	0
			34	21	6	7		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

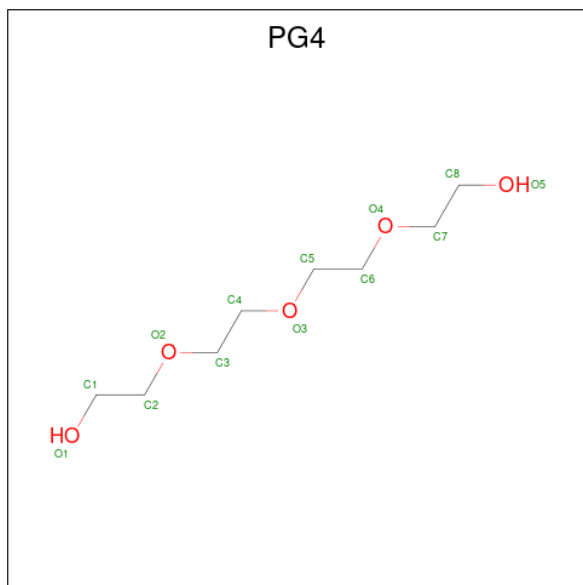


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total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

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 9 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



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

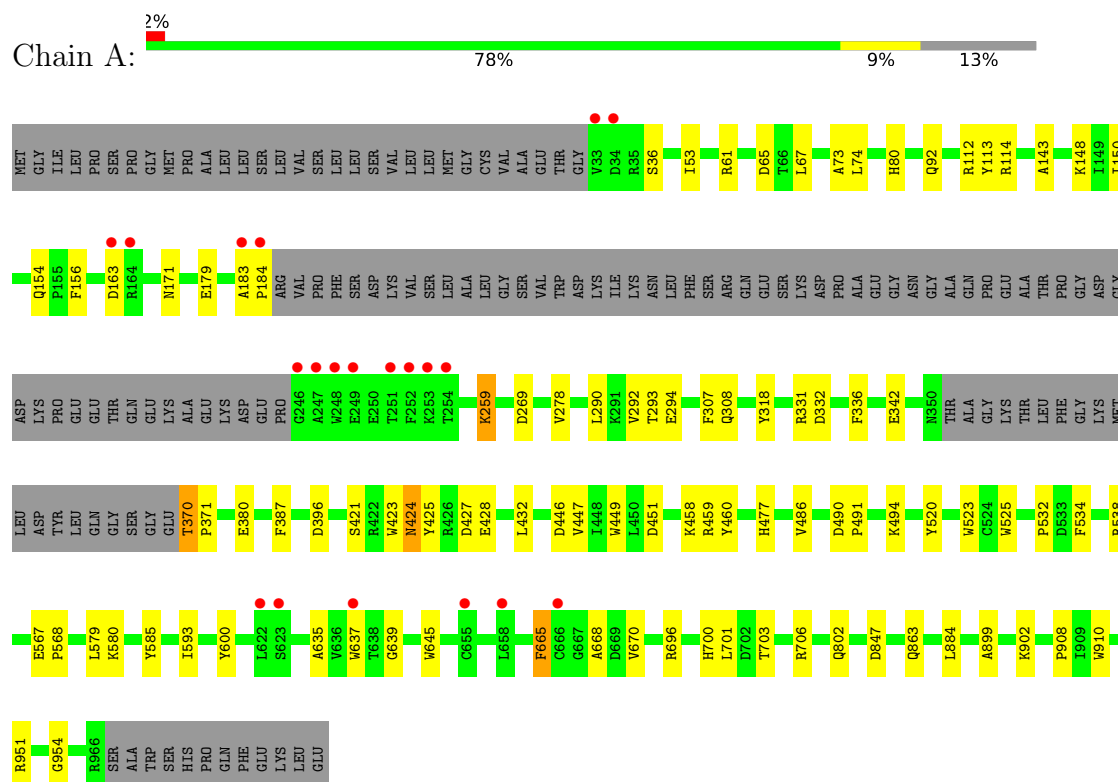
- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	228	Total O 228 228	0	0
10	B	15	Total O 15 15	0	0
10	C	195	Total O 195 195	0	0
10	D	15	Total O 15 15	0	0

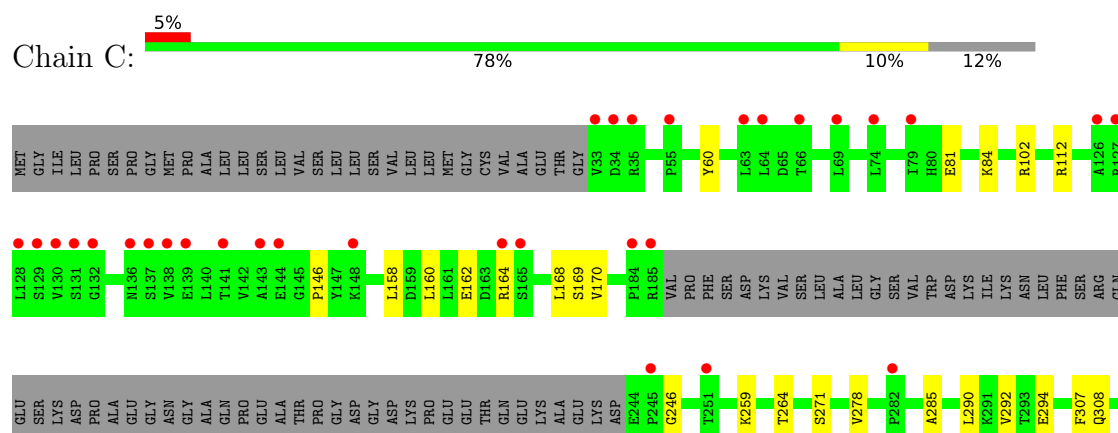
3 Residue-property plots

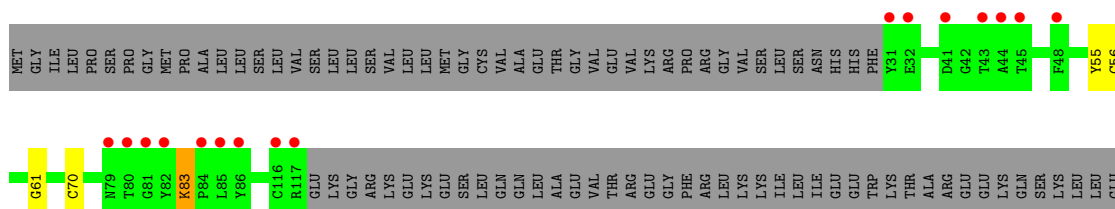
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Isoform 2 of Neutral alpha-glucosidase AB



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





HIS	THR	ALA	SER	ASP	LEU
PRO	GLY	TYR	PRO	ASP	GLN
GLN	CYS	LEU	THR	ASN	ALA
PHE	TRP	TYR	VAL	MET	GLY
GLY	GLN	SER	ASP	PRO	LYS
LYS	GLY	GLN	THR	GLY	LYS
LEU	PRO	CYS	ASP	MET	SER
LEU	ASN	TYR	LYS	SER	LEU
GLU	THR	TYR	ILE	VAL	GLU
THR	ARG	GLU	PRO	SER	GLU
LYS	ARG	LEU	VAL	LEU	ASN
HIS	THR	THR	THR	ALA	GLN
HIS	THR	THR	THR	GLY	THR
HIS	VAL	ASN	GLU	LEU	GLU
HIS	ARG	GLU	GLU	GLU	THR
HIS	LEU	TYR	THR	GLU	LEU
HIS	LEU	VAL	GLN	HIS	ARG
	CYS	TYR	ALA	PRO	ALA
	GLY	ARG	ILE	GLY	ALA
	LYS	LEU	ILE	LEU	LYS
	GLU	CYS	ASP	ASP	GLU
	THR	PRO	ALA	THR	GLU
	VAL	PHE	ALA	ASP	ALA
	THR	LYS	GLN	GLY	GLY
	SER	VAL	ALA	GLY	ARG
	THR	SER	ARG	ALA	PRO
	THR	GLN	SER	LEU	GLU
	GLU	LYS	LYS	LEU	LYS
	GLU	PRO	THR	GLU	ALA
	VAL	PHE	LYS	GLU	ALA
	VAL	LYS	PHE	GLU	ALA
	THR	THR	GLY	GLY	GLY
	SER	VAL	LYS	THR	ASP
	THR	SER	ALA	GLY	ARG
	THR	SER	ARG	GLY	PRO
	GLU	CYS	GLY	GLU	GLU
	GLY	GLY	VAL	GLU	GLU
	TYR	SER	ARG	GLU	GLU
	LEU	PRO	SER	LEU	GLN
	MET	THR	LEU	LEU	GLN
	GLU	SER	LYS	SER	THR
	LEU	LEU	GLU	GLY	ALA
	MET	GLY	MET	ASP	ALA
	THR	THR	GLU	THR	LYS
	PRO	ALA	GLY	GLN	ALA
	ALA	SER	THR	THR	ALA
	CYS	TRP	ILE	ASP	ALA
	PRO	ALA	ARG	THR	LYS
	GLU	GLY	SER	THR	ALA
	PRO	PRO	LEU	SER	ALA
	PRO	PRO	GLU	PHE	ARG
	PRO	ASP	GLN	TYR	ARG
	GLU	HIS	GLU	ASP	GLY
	ALA	ASP	ILE	ARG	GLN
	ALA	LYS	SER	VAL	GLU
	PRO	PHE	PHE	TRP	GLU
	SER	SER	ALA	ALA	ALA
	ASP	ALA	LEU	ALA	ALA
	GLY	MET	GLY	ILE	SER
	ASP	LYS	PRO	ARG	ALA
	SER	TYR	SER	ASP	PHE
	ALA	GLU	GLY	LYS	GLN
	TRP	GLN	THR	TYR	GLY
	SER	GLY	PHE	ARG	LEU

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	102.69Å 102.69Å 240.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.28 – 2.51 42.28 – 2.51	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.28-2.51) 94.9 (42.28-2.51)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.93 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.14_3228	Depositor
R, R_{free}	0.172 , 0.203 0.174 , 0.204	Depositor DCC
R_{free} test set	2037 reflections (2.09%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l 0.042 for h,-h-k,-l 0.026 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15939	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 2.49% 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: PEG, PG4, W9Y, CA, SO4, PGE, EDO

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	0.26	0/7132	0.47	0/9711
1	C	0.26	0/7136	0.46	0/9718
2	B	0.25	0/635	0.51	0/870
2	D	0.26	0/636	0.49	0/868
All	All	0.26	0/15539	0.47	0/21167

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	6903	0	6645	63	0
1	C	6903	0	6632	56	0
2	B	623	0	508	7	0
2	D	624	0	516	4	0
3	A	34	0	0	2	0
3	C	34	0	0	0	0
4	A	72	0	108	12	0
4	B	12	0	18	2	0
4	C	48	0	70	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	50	0	68	4	0
5	C	10	0	14	1	0
6	A	56	0	80	4	0
6	C	35	0	50	1	0
7	A	25	0	0	5	0
7	C	40	0	0	0	0
8	B	2	0	0	0	0
8	D	2	0	0	0	0
9	C	13	0	18	0	0
10	A	228	0	0	6	0
10	B	15	0	0	2	0
10	C	195	0	0	9	0
10	D	15	0	0	1	0
All	All	15939	0	14727	134	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 4.

The worst 5 of 134 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1001:W9Y:C20	4:A:1002:EDO:O1	2.00	1.09
1:A:150:ILE:O	10:A:1101:HOH:O	1.83	0.95
2:D:56:CYS:O	10:D:701:HOH:O	1.98	0.82
1:A:293:THR:HA	4:A:1011:EDO:H22	1.65	0.79
2:B:48:PHE:O	10:B:701:HOH:O	2.03	0.77

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	855/977 (88%)	826 (97%)	29 (3%)	0	100	100
1	C	859/977 (88%)	829 (96%)	30 (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	1884/3062 (62%)	1819 (96%)	65 (4%)	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	747/846 (88%)	737 (99%)	10 (1%)	69	87
1	C	742/846 (88%)	731 (98%)	11 (2%)	65	85
2	B	69/485 (14%)	69 (100%)	0	100	100
2	D	68/485 (14%)	67 (98%)	1 (2%)	65	85
All	All	1626/2662 (61%)	1604 (99%)	22 (1%)	67	86

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	446	ASP
1	C	685	TRP
1	C	665	PHE
1	C	806	LYS
1	A	637	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	545	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 72 ligands modelled in this entry, 4 are monoatomic - leaving 68 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$
5	PGE	A	1007	-	9,9,9	0.32	0	8,8,8	0.27	0
6	PEG	C	1010	-	6,6,6	0.49	0	5,5,5	0.33	0
6	PEG	A	1017	-	6,6,6	0.50	0	5,5,5	0.23	0
4	EDO	C	1009	-	3,3,3	0.43	0	2,2,2	0.40	0
6	PEG	A	1023	-	6,6,6	0.18	0	5,5,5	0.09	0
6	PEG	C	1017	-	6,6,6	0.11	0	5,5,5	0.11	0
3	W9Y	C	1001	-	34,36,36	2.46	11 (32%)	41,50,50	1.85	7 (17%)
4	EDO	A	1031	-	3,3,3	0.45	0	2,2,2	0.36	0
7	SO4	A	1036	-	4,4,4	0.14	0	6,6,6	0.06	0
7	SO4	C	1024	-	4,4,4	0.14	0	6,6,6	0.14	0
9	PG4	C	1020	-	12,12,12	0.52	0	11,11,11	0.17	0
4	EDO	A	1018	-	3,3,3	0.46	0	2,2,2	0.25	0
4	EDO	A	1002	-	3,3,3	0.25	0	2,2,2	0.17	0
4	EDO	A	1012	-	3,3,3	0.49	0	2,2,2	0.20	0
4	EDO	C	1011	-	3,3,3	0.45	0	2,2,2	0.33	0
7	SO4	C	1026	-	4,4,4	0.13	0	6,6,6	0.10	0
7	SO4	A	1034	-	4,4,4	0.15	0	6,6,6	0.13	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PEG	A	1019	-	6,6,6	0.48	0	5,5,5	0.28	0
6	PEG	A	1025	-	6,6,6	0.47	0	5,5,5	0.30	0
7	SO4	C	1028	-	4,4,4	0.12	0	6,6,6	0.11	0
4	EDO	A	1003	-	3,3,3	0.46	0	2,2,2	0.32	0
4	EDO	A	1015	-	3,3,3	0.23	0	2,2,2	0.28	0
4	EDO	C	1004	-	3,3,3	0.49	0	2,2,2	0.24	0
6	PEG	A	1024	-	6,6,6	0.48	0	5,5,5	0.28	0
4	EDO	A	1020	-	3,3,3	0.45	0	2,2,2	0.41	0
6	PEG	A	1014	-	6,6,6	0.48	0	5,5,5	0.25	0
4	EDO	A	1022	-	3,3,3	0.46	0	2,2,2	0.39	0
6	PEG	A	1009	-	6,6,6	0.49	0	5,5,5	0.29	0
4	EDO	C	1012	-	3,3,3	0.46	0	2,2,2	0.36	0
7	SO4	A	1037	-	4,4,4	0.24	0	6,6,6	0.39	0
4	EDO	A	1008	-	3,3,3	0.43	0	2,2,2	0.46	0
4	EDO	A	1021	-	3,3,3	0.47	0	2,2,2	0.28	0
4	EDO	C	1003	-	3,3,3	0.44	0	2,2,2	0.46	0
4	EDO	A	1027	-	3,3,3	0.46	0	2,2,2	0.33	0
4	EDO	B	602	-	3,3,3	0.41	0	2,2,2	0.47	0
4	EDO	B	603	-	3,3,3	0.47	0	2,2,2	0.31	0
4	EDO	C	1005	-	3,3,3	0.49	0	2,2,2	0.25	0
7	SO4	A	1033	-	4,4,4	0.14	0	6,6,6	0.05	0
4	EDO	C	1018	-	3,3,3	0.49	0	2,2,2	0.51	0
7	SO4	C	1027	-	4,4,4	0.14	0	6,6,6	0.10	0
4	EDO	C	1014	-	3,3,3	0.34	0	2,2,2	0.27	0
5	PGE	C	1006	-	9,9,9	0.33	0	8,8,8	0.27	0
3	W9Y	A	1001	-	34,36,36	2.48	10 (29%)	41,50,50	1.82	10 (24%)
6	PEG	C	1019	-	6,6,6	0.49	0	5,5,5	0.31	0
4	EDO	C	1008	-	3,3,3	0.44	0	2,2,2	0.37	0
7	SO4	C	1025	-	4,4,4	0.12	0	6,6,6	0.19	0
6	PEG	C	1007	-	6,6,6	0.48	0	5,5,5	0.26	0
7	SO4	C	1022	-	4,4,4	0.13	0	6,6,6	0.10	0
4	EDO	A	1006	-	3,3,3	0.51	0	2,2,2	0.20	0
6	PEG	C	1015	-	6,6,6	0.47	0	5,5,5	0.25	0
7	SO4	C	1021	-	4,4,4	0.14	0	6,6,6	0.11	0
5	PGE	A	1026	-	9,9,9	0.31	0	8,8,8	0.36	0
5	PGE	A	1004	-	9,9,9	0.32	0	8,8,8	0.26	0
4	EDO	C	1016	-	3,3,3	0.15	0	2,2,2	0.18	0
6	PEG	A	1028	-	6,6,6	0.48	0	5,5,5	0.29	0
4	EDO	A	1013	-	3,3,3	0.43	0	2,2,2	0.40	0
7	SO4	C	1023	-	4,4,4	0.13	0	6,6,6	0.11	0
4	EDO	A	1029	-	3,3,3	0.47	0	2,2,2	0.27	0
4	EDO	A	1010	-	3,3,3	0.51	0	2,2,2	0.16	0
4	EDO	C	1002	-	3,3,3	0.46	0	2,2,2	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PGE	A	1005	-	9,9,9	0.31	0	8,8,8	0.31	0
4	EDO	A	1011	-	3,3,3	0.42	0	2,2,2	0.49	0
5	PGE	A	1016	-	9,9,9	0.32	0	8,8,8	0.31	0
7	SO4	A	1035	-	4,4,4	0.13	0	6,6,6	0.08	0
4	EDO	C	1013	-	3,3,3	0.52	0	2,2,2	0.22	0
4	EDO	B	601	-	3,3,3	0.45	0	2,2,2	0.36	0
4	EDO	A	1030	-	3,3,3	0.45	0	2,2,2	0.38	0
4	EDO	A	1032	-	3,3,3	0.45	0	2,2,2	0.34	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
5	PGE	A	1007	-	-	4/7/7/7	-
6	PEG	C	1010	-	-	3/4/4/4	-
6	PEG	A	1017	-	-	1/4/4/4	-
4	EDO	C	1009	-	-	1/1/1/1	-
6	PEG	A	1023	-	-	3/4/4/4	-
6	PEG	C	1017	-	-	3/4/4/4	-
3	W9Y	C	1001	-	-	9/20/45/45	0/3/3/3
4	EDO	A	1031	-	-	0/1/1/1	-
9	PG4	C	1020	-	-	7/10/10/10	-
4	EDO	A	1018	-	-	0/1/1/1	-
4	EDO	A	1002	-	-	0/1/1/1	-
4	EDO	A	1012	-	-	1/1/1/1	-
4	EDO	C	1011	-	-	1/1/1/1	-
6	PEG	A	1019	-	-	0/4/4/4	-
6	PEG	A	1025	-	-	2/4/4/4	-
4	EDO	A	1003	-	-	0/1/1/1	-
4	EDO	A	1015	-	-	1/1/1/1	-
4	EDO	C	1004	-	-	0/1/1/1	-
6	PEG	A	1024	-	-	2/4/4/4	-
4	EDO	A	1020	-	-	1/1/1/1	-
6	PEG	A	1014	-	-	1/4/4/4	-
4	EDO	A	1022	-	-	0/1/1/1	-
6	PEG	A	1009	-	-	4/4/4/4	-
4	EDO	C	1012	-	-	0/1/1/1	-
4	EDO	A	1008	-	-	0/1/1/1	-
4	EDO	A	1021	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	C	1003	-	-	0/1/1/1	-
4	EDO	A	1027	-	-	1/1/1/1	-
4	EDO	B	602	-	-	1/1/1/1	-
4	EDO	B	603	-	-	1/1/1/1	-
4	EDO	C	1005	-	-	1/1/1/1	-
4	EDO	C	1018	-	-	1/1/1/1	-
4	EDO	C	1014	-	-	0/1/1/1	-
5	PGE	C	1006	-	-	3/7/7/7	-
3	W9Y	A	1001	-	-	15/20/45/45	0/3/3/3
6	PEG	C	1019	-	-	3/4/4/4	-
4	EDO	C	1008	-	-	1/1/1/1	-
6	PEG	C	1007	-	-	1/4/4/4	-
4	EDO	A	1006	-	-	0/1/1/1	-
6	PEG	C	1015	-	-	3/4/4/4	-
5	PGE	A	1026	-	-	4/7/7/7	-
5	PGE	A	1004	-	-	6/7/7/7	-
4	EDO	C	1016	-	-	1/1/1/1	-
6	PEG	A	1028	-	-	3/4/4/4	-
4	EDO	A	1013	-	-	0/1/1/1	-
4	EDO	A	1029	-	-	1/1/1/1	-
4	EDO	A	1010	-	-	0/1/1/1	-
4	EDO	C	1002	-	-	0/1/1/1	-
5	PGE	A	1005	-	-	2/7/7/7	-
4	EDO	A	1011	-	-	0/1/1/1	-
5	PGE	A	1016	-	-	5/7/7/7	-
4	EDO	C	1013	-	-	1/1/1/1	-
4	EDO	B	601	-	-	1/1/1/1	-
4	EDO	A	1030	-	-	0/1/1/1	-
4	EDO	A	1032	-	-	0/1/1/1	-

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	W9Y	O6-N3	9.99	1.39	1.22
3	C	1001	W9Y	O6-N3	9.11	1.38	1.22
3	C	1001	W9Y	O2-C1	-4.66	1.36	1.44
3	A	1001	W9Y	O2-C1	-4.64	1.36	1.44
3	A	1001	W9Y	N5-N4	-4.56	1.30	1.37

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	W9Y	C16-C17-N4	7.39	125.61	119.15
3	A	1001	W9Y	C17-N4-N5	4.80	126.94	117.19
3	A	1001	W9Y	C21-N4-N5	-4.72	107.91	112.72
3	C	1001	W9Y	C18-C17-N4	-4.22	113.69	119.07
3	A	1001	W9Y	C18-C19-C14	-3.96	117.94	121.53

There are no chirality outliers.

5 of 100 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	W9Y	C9-C8-N1-C5
6	C	1017	PEG	C1-C2-O2-C3
5	C	1006	PGE	O2-C3-C4-O3
9	C	1020	PG4	O3-C5-C6-O4
5	A	1016	PGE	O2-C3-C4-O3

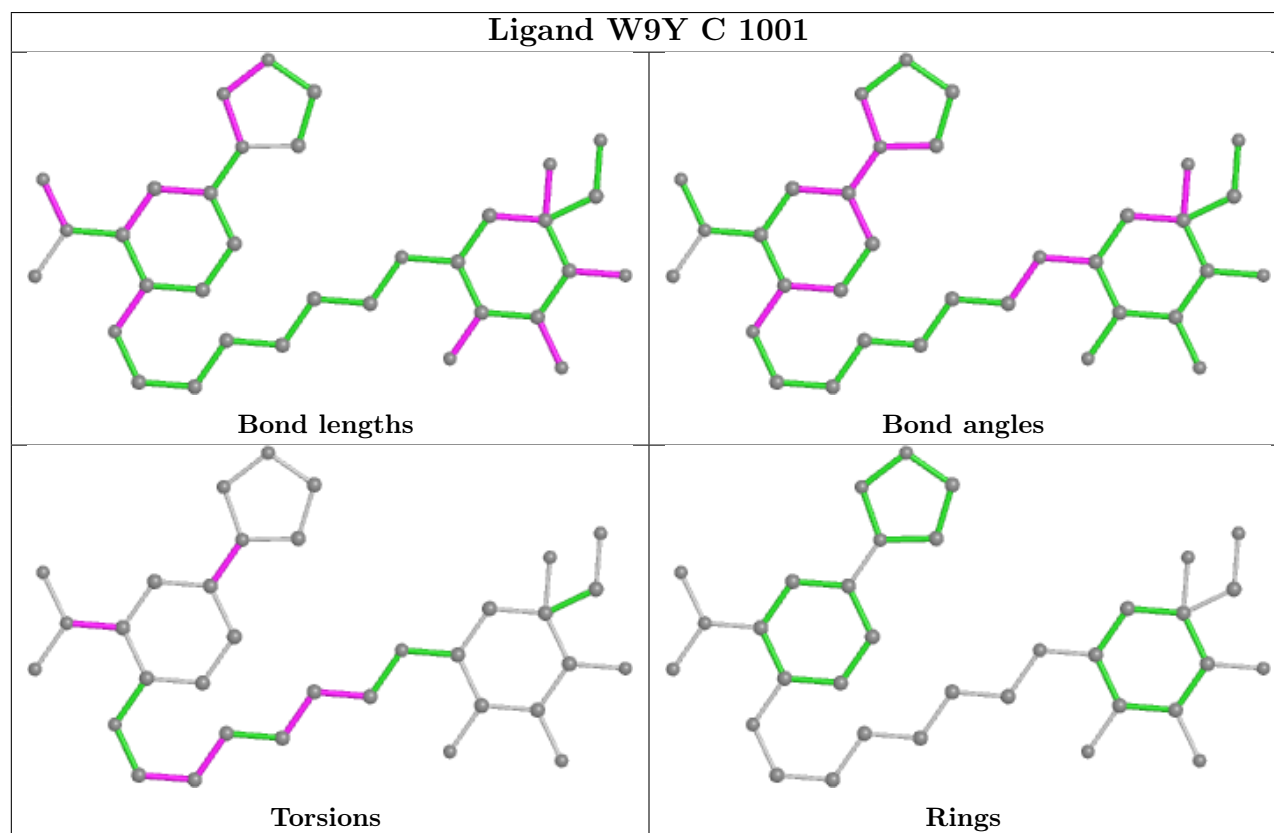
There are no ring outliers.

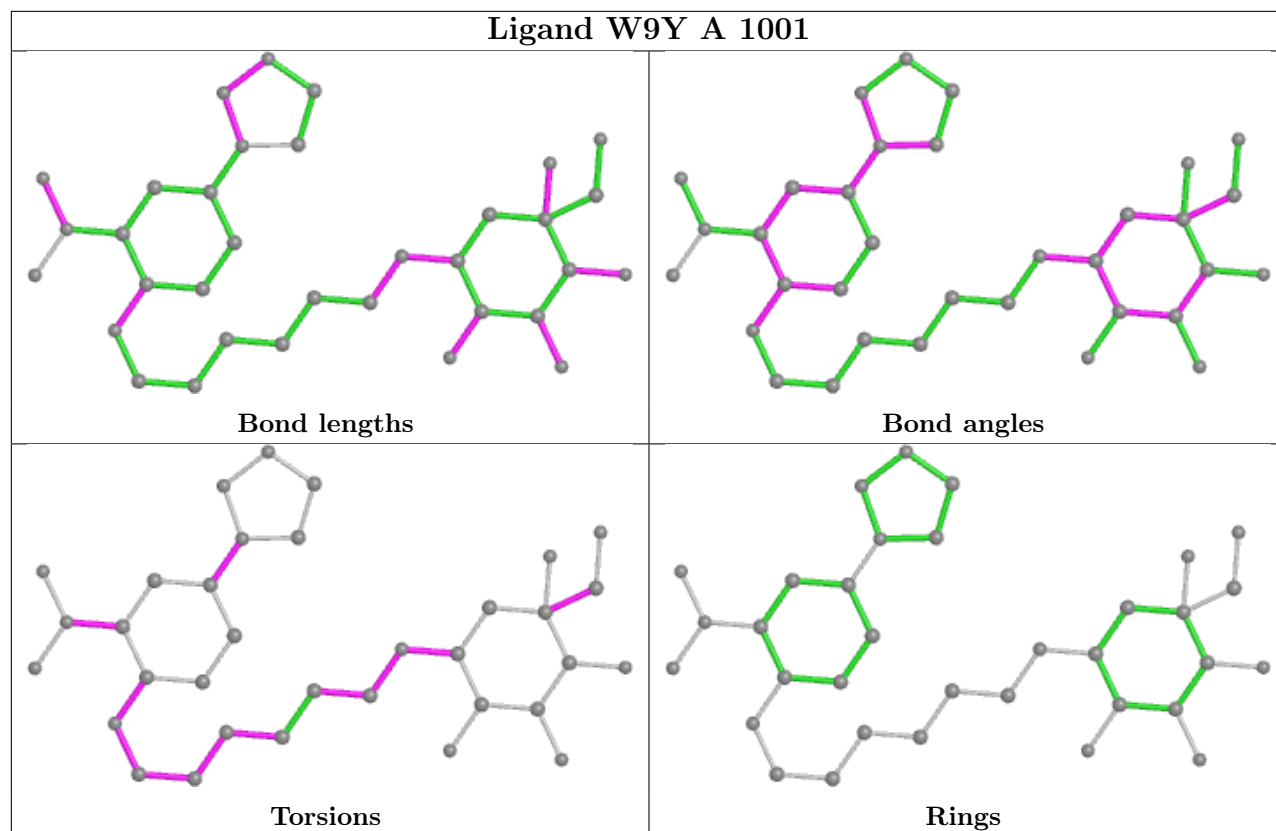
21 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1007	PGE	1	0
6	A	1017	PEG	2	0
4	C	1009	EDO	1	0
4	A	1031	EDO	2	0
4	A	1018	EDO	1	0
4	A	1002	EDO	3	0
4	A	1012	EDO	2	0
4	C	1011	EDO	1	0
7	A	1034	SO4	2	0
6	A	1025	PEG	2	0
7	A	1037	SO4	3	0
4	A	1008	EDO	1	0
4	B	602	EDO	2	0
4	C	1014	EDO	1	0
5	C	1006	PGE	1	0
3	A	1001	W9Y	2	0
6	C	1007	PEG	1	0
5	A	1004	PGE	3	0
4	A	1029	EDO	2	0
4	C	1002	EDO	1	0
4	A	1011	EDO	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 [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	854/977 (87%)	-0.22	20 (2%) 60 63	31, 42, 67, 125	0
1	C	857/977 (87%)	-0.01	47 (5%) 25 26	32, 48, 86, 107	0
2	B	87/554 (15%)	0.55	19 (21%) 0 0	40, 59, 99, 121	0
2	D	87/554 (15%)	0.58	16 (18%) 1 1	37, 59, 105, 116	0
All	All	1885/3062 (61%)	-0.05	102 (5%) 25 27	31, 46, 84, 125	0

The worst 5 of 102 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	184	PRO	9.3
2	D	81	GLY	6.7
2	D	43	THR	6.7
2	B	82	TYR	4.7
2	B	48	PHE	4.6

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](#)

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(\AA^2)	Q<0.9
4	EDO	C	1013	4/4	0.52	0.27	70,73,83,95	0
6	PEG	A	1023	7/7	0.60	0.30	68,81,98,102	0
4	EDO	A	1015	4/4	0.71	0.28	79,84,95,102	0
4	EDO	A	1020	4/4	0.74	0.53	78,80,84,95	0
5	PGE	A	1016	10/10	0.77	0.41	58,73,80,84	0
4	EDO	C	1016	4/4	0.77	0.28	79,82,85,86	0
7	SO4	C	1028	5/5	0.77	0.44	92,93,103,129	0
6	PEG	A	1025	7/7	0.78	0.32	56,63,78,85	0
4	EDO	A	1010	4/4	0.80	0.21	48,57,58,62	0
6	PEG	A	1019	7/7	0.82	0.21	62,66,73,90	0
4	EDO	C	1012	4/4	0.82	0.33	72,74,77,78	0
5	PGE	A	1007	10/10	0.82	0.25	66,71,80,80	0
4	EDO	A	1003	4/4	0.82	0.27	66,67,68,71	0
4	EDO	A	1012	4/4	0.83	0.28	58,59,68,73	0
4	EDO	C	1018	4/4	0.83	0.22	62,83,84,92	0
5	PGE	A	1005	10/10	0.83	0.21	57,65,77,79	0
4	EDO	C	1005	4/4	0.84	0.27	57,59,64,64	0
9	PG4	C	1020	13/13	0.84	0.20	58,65,83,84	0
4	EDO	C	1004	4/4	0.85	0.17	56,61,63,73	0
6	PEG	A	1009	7/7	0.85	0.16	57,63,67,72	0
6	PEG	C	1017	7/7	0.85	0.27	72,73,80,83	0
6	PEG	A	1017	7/7	0.85	0.27	61,73,79,84	0
4	EDO	A	1006	4/4	0.85	0.23	50,54,55,56	0
4	EDO	B	603	4/4	0.86	0.22	61,64,66,67	0
6	PEG	A	1014	7/7	0.86	0.25	55,61,79,87	0
6	PEG	A	1028	7/7	0.86	0.22	63,68,72,78	0
7	SO4	A	1034	5/5	0.87	0.34	83,97,114,135	0
7	SO4	C	1027	5/5	0.87	0.52	77,82,87,111	0
4	EDO	C	1014	4/4	0.87	0.13	62,65,73,85	0
5	PGE	C	1006	10/10	0.87	0.21	57,69,77,88	0
7	SO4	A	1037	5/5	0.88	0.47	62,70,79,103	0
3	W9Y	A	1001	34/34	0.88	0.19	30,59,97,106	0
6	PEG	C	1019	7/7	0.88	0.22	56,65,71,73	0
5	PGE	A	1026	10/10	0.88	0.36	57,70,78,82	0
7	SO4	C	1024	5/5	0.89	0.40	79,89,110,130	0
3	W9Y	C	1001	34/34	0.89	0.20	36,64,99,107	0
7	SO4	A	1036	5/5	0.89	0.40	83,84,113,129	0
6	PEG	C	1010	7/7	0.89	0.28	54,67,73,73	0
5	PGE	A	1004	10/10	0.90	0.24	58,67,71,73	0
7	SO4	C	1026	5/5	0.90	0.44	76,84,103,113	0
4	EDO	A	1030	4/4	0.90	0.46	62,64,76,83	0
7	SO4	A	1033	5/5	0.90	0.35	94,109,115,128	0
7	SO4	C	1022	5/5	0.90	0.22	61,69,77,109	0

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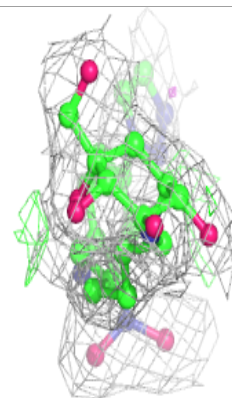
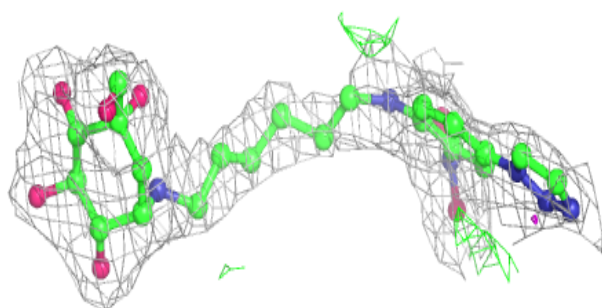
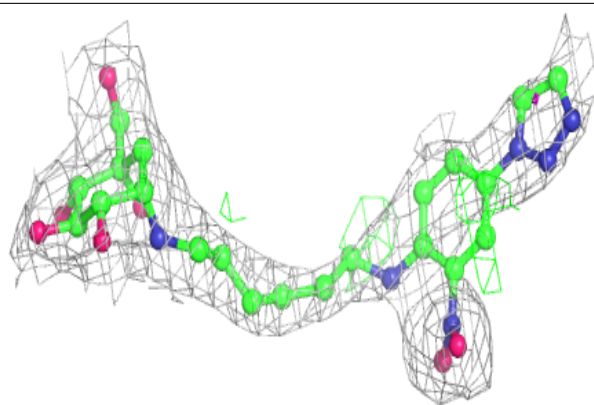
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	C	1003	4/4	0.91	0.13	47,54,55,65	0
4	EDO	A	1027	4/4	0.91	0.31	41,59,60,61	0
4	EDO	A	1002	4/4	0.91	0.26	67,68,68,84	0
7	SO4	C	1025	5/5	0.91	0.43	72,77,98,113	0
4	EDO	C	1008	4/4	0.91	0.26	44,66,71,74	0
4	EDO	A	1031	4/4	0.91	0.18	52,64,64,65	0
4	EDO	A	1008	4/4	0.91	0.23	40,56,65,72	0
4	EDO	C	1002	4/4	0.91	0.28	50,56,65,68	0
7	SO4	C	1021	5/5	0.92	0.27	81,88,95,107	0
7	SO4	A	1035	5/5	0.92	0.43	76,77,104,111	0
6	PEG	A	1024	7/7	0.92	0.38	58,69,73,77	0
4	EDO	A	1013	4/4	0.92	0.36	46,49,64,67	0
4	EDO	A	1011	4/4	0.93	0.20	48,51,53,53	0
4	EDO	A	1029	4/4	0.93	0.17	53,55,56,57	0
4	EDO	B	601	4/4	0.93	0.10	50,55,65,66	0
6	PEG	C	1007	7/7	0.93	0.31	48,66,71,87	0
4	EDO	C	1009	4/4	0.93	0.23	58,59,60,68	0
6	PEG	C	1015	7/7	0.94	0.28	52,59,73,76	0
4	EDO	A	1018	4/4	0.94	0.22	58,59,62,66	0
4	EDO	A	1032	4/4	0.94	0.48	55,58,59,67	0
4	EDO	C	1011	4/4	0.94	0.24	55,56,58,58	0
4	EDO	A	1021	4/4	0.95	0.14	49,50,51,59	0
8	CA	D	601	1/1	0.95	0.08	56,56,56,56	0
7	SO4	C	1023	5/5	0.95	0.24	56,76,79,94	0
4	EDO	B	602	4/4	0.97	0.16	41,52,65,65	0
4	EDO	A	1022	4/4	0.97	0.09	46,49,52,53	0
8	CA	B	604	1/1	0.98	0.08	46,46,46,46	0
8	CA	D	602	1/1	0.99	0.09	44,44,44,44	0
8	CA	B	605	1/1	0.99	0.05	53,53,53,53	0

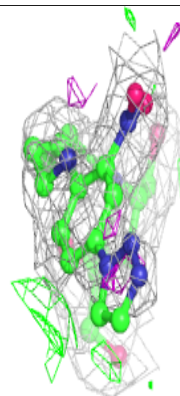
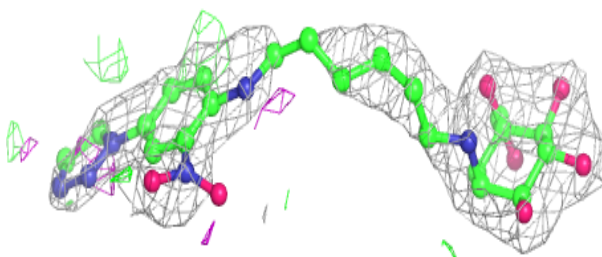
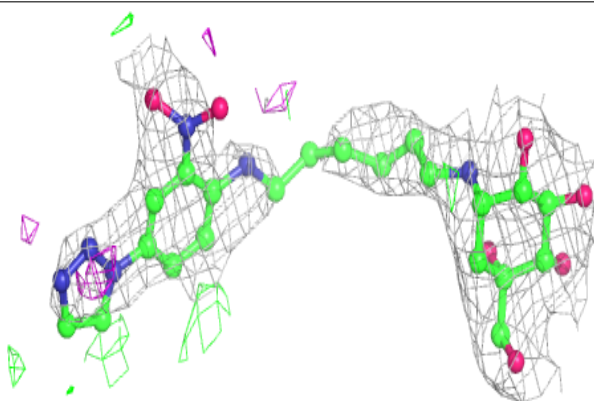
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around W9Y A 1001:

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

**Electron density around W9Y C 1001:**

$2mF_o-DF_c$ (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.