



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 08:05 AM UTC

PDB ID : 7K9T / pdb_00007k9t
Title : Co-crystal structure of alpha glucosidase with compound 5
Authors : Karade, S.S.; Mariuzza, R.A.
Deposited on : 2020-09-29
Resolution : 2.10 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

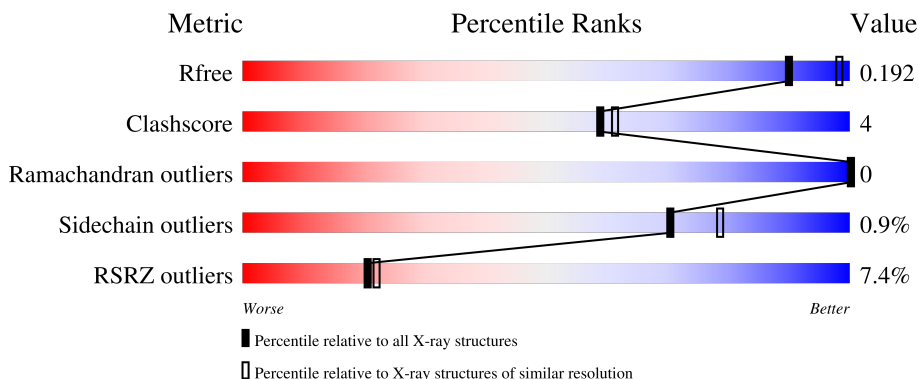
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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% 79% 8% 13%
1	C	977	8% 80% 8% 12%
2	B	547	3% 14% 85%
2	D	547	5% 15% 84%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 16450 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 glucosidase 2 alpha neutral subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	850	Total	C	N	O	S	0	5	0
			6862	4397	1179	1256	30			
1	C	857	Total	C	N	O	S	0	8	0
			6947	4451	1201	1265	30			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	MET	-	initiating methionine	UNP A1A4T2
A	3	GLY	-	expression tag	UNP A1A4T2
A	4	ILE	-	expression tag	UNP A1A4T2
A	5	LEU	-	expression tag	UNP A1A4T2
A	6	PRO	-	expression tag	UNP A1A4T2
A	7	SER	-	expression tag	UNP A1A4T2
A	8	PRO	-	expression tag	UNP A1A4T2
A	9	GLY	-	expression tag	UNP A1A4T2
A	10	MET	-	expression tag	UNP A1A4T2
A	11	PRO	-	expression tag	UNP A1A4T2
A	12	ALA	-	expression tag	UNP A1A4T2
A	13	LEU	-	expression tag	UNP A1A4T2
A	14	LEU	-	expression tag	UNP A1A4T2
A	15	SER	-	expression tag	UNP A1A4T2
A	16	LEU	-	expression tag	UNP A1A4T2
A	17	VAL	-	expression tag	UNP A1A4T2
A	18	SER	-	expression tag	UNP A1A4T2
A	19	LEU	-	expression tag	UNP A1A4T2
A	20	LEU	-	expression tag	UNP A1A4T2
A	21	SER	-	expression tag	UNP A1A4T2
A	22	VAL	-	expression tag	UNP A1A4T2
A	23	LEU	-	expression tag	UNP A1A4T2
A	24	LEU	-	expression tag	UNP A1A4T2
A	25	MET	-	expression tag	UNP A1A4T2
A	26	GLY	-	expression tag	UNP A1A4T2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	CYS	-	expression tag	UNP A1A4T2
A	28	VAL	-	expression tag	UNP A1A4T2
A	29	ALA	-	expression tag	UNP A1A4T2
A	30	GLU	-	expression tag	UNP A1A4T2
A	31	THR	-	expression tag	UNP A1A4T2
A	32	GLY	-	expression tag	UNP A1A4T2
A	97	ASP	ASN	engineered mutation	UNP A1A4T2
A	967	SER	-	expression tag	UNP A1A4T2
A	968	ALA	-	expression tag	UNP A1A4T2
A	969	TRP	-	expression tag	UNP A1A4T2
A	970	SER	-	expression tag	UNP A1A4T2
A	971	HIS	-	expression tag	UNP A1A4T2
A	972	PRO	-	expression tag	UNP A1A4T2
A	973	GLN	-	expression tag	UNP A1A4T2
A	974	PHE	-	expression tag	UNP A1A4T2
A	975	GLU	-	expression tag	UNP A1A4T2
A	976	LYS	-	expression tag	UNP A1A4T2
A	977	LEU	-	expression tag	UNP A1A4T2
A	978	GLU	-	expression tag	UNP A1A4T2
C	2	MET	-	initiating methionine	UNP A1A4T2
C	3	GLY	-	expression tag	UNP A1A4T2
C	4	ILE	-	expression tag	UNP A1A4T2
C	5	LEU	-	expression tag	UNP A1A4T2
C	6	PRO	-	expression tag	UNP A1A4T2
C	7	SER	-	expression tag	UNP A1A4T2
C	8	PRO	-	expression tag	UNP A1A4T2
C	9	GLY	-	expression tag	UNP A1A4T2
C	10	MET	-	expression tag	UNP A1A4T2
C	11	PRO	-	expression tag	UNP A1A4T2
C	12	ALA	-	expression tag	UNP A1A4T2
C	13	LEU	-	expression tag	UNP A1A4T2
C	14	LEU	-	expression tag	UNP A1A4T2
C	15	SER	-	expression tag	UNP A1A4T2
C	16	LEU	-	expression tag	UNP A1A4T2
C	17	VAL	-	expression tag	UNP A1A4T2
C	18	SER	-	expression tag	UNP A1A4T2
C	19	LEU	-	expression tag	UNP A1A4T2
C	20	LEU	-	expression tag	UNP A1A4T2
C	21	SER	-	expression tag	UNP A1A4T2
C	22	VAL	-	expression tag	UNP A1A4T2
C	23	LEU	-	expression tag	UNP A1A4T2
C	24	LEU	-	expression tag	UNP A1A4T2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	25	MET	-	expression tag	UNP A1A4T2
C	26	GLY	-	expression tag	UNP A1A4T2
C	27	CYS	-	expression tag	UNP A1A4T2
C	28	VAL	-	expression tag	UNP A1A4T2
C	29	ALA	-	expression tag	UNP A1A4T2
C	30	GLU	-	expression tag	UNP A1A4T2
C	31	THR	-	expression tag	UNP A1A4T2
C	32	GLY	-	expression tag	UNP A1A4T2
C	97	ASP	ASN	engineered mutation	UNP A1A4T2
C	967	SER	-	expression tag	UNP A1A4T2
C	968	ALA	-	expression tag	UNP A1A4T2
C	969	TRP	-	expression tag	UNP A1A4T2
C	970	SER	-	expression tag	UNP A1A4T2
C	971	HIS	-	expression tag	UNP A1A4T2
C	972	PRO	-	expression tag	UNP A1A4T2
C	973	GLN	-	expression tag	UNP A1A4T2
C	974	PHE	-	expression tag	UNP A1A4T2
C	975	GLU	-	expression tag	UNP A1A4T2
C	976	LYS	-	expression tag	UNP A1A4T2
C	977	LEU	-	expression tag	UNP A1A4T2
C	978	GLU	-	expression tag	UNP A1A4T2

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	83	Total	C	N	O	S	0	0	0
			600	356	99	135	10			
2	D	87	Total	C	N	O	S	0	0	0
			639	382	103	144	10			

There are 88 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

Continued on next page...

Continued from previous page...

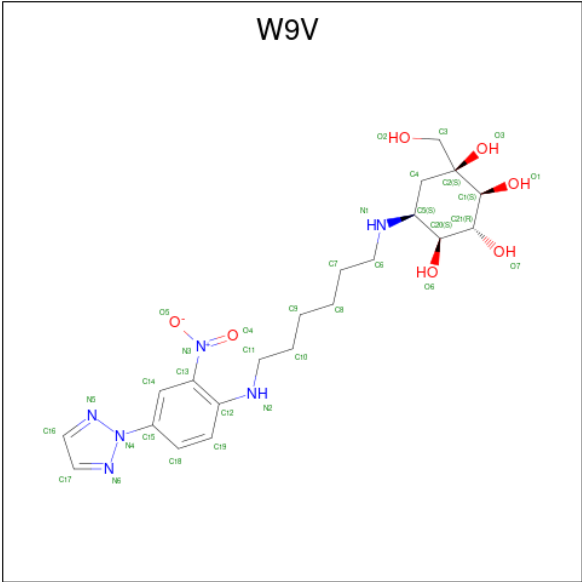
Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	PRO	-	expression tag	UNP O08795
B	-6	ALA	-	expression tag	UNP O08795
B	-5	LEU	-	expression tag	UNP O08795
B	-4	LEU	-	expression tag	UNP O08795
B	-3	SER	-	expression tag	UNP O08795
B	-2	LEU	-	expression tag	UNP O08795
B	-1	VAL	-	expression tag	UNP O08795
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	LEU	-	expression tag	UNP O08795
B	522	GLU	-	expression tag	UNP O08795
B	523	THR	-	expression tag	UNP O08795
B	524	LYS	-	expression tag	UNP O08795
B	525	HIS	-	expression tag	UNP O08795
B	526	HIS	-	expression tag	UNP O08795
B	527	HIS	-	expression tag	UNP O08795
B	528	HIS	-	expression tag	UNP O08795
B	529	HIS	-	expression tag	UNP O08795
B	530	HIS	-	expression tag	UNP O08795
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

Continued on next page...

Continued from previous page...

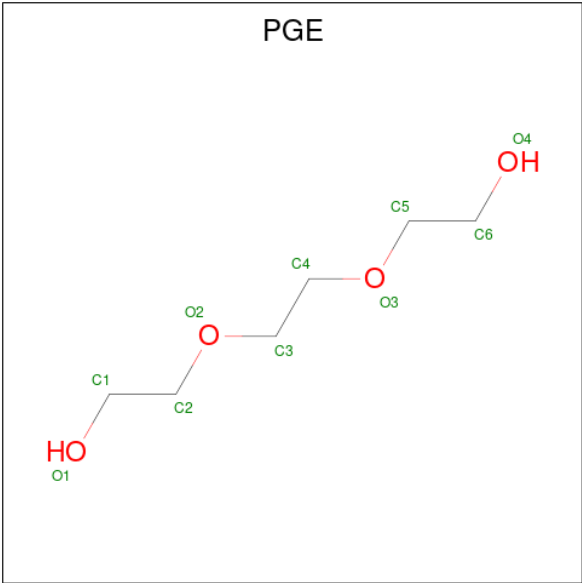
Chain	Residue	Modelled	Actual	Comment	Reference
D	-9	GLY	-	expression tag	UNP O08795
D	-8	MET	-	expression tag	UNP O08795
D	-7	PRO	-	expression tag	UNP O08795
D	-6	ALA	-	expression tag	UNP O08795
D	-5	LEU	-	expression tag	UNP O08795
D	-4	LEU	-	expression tag	UNP O08795
D	-3	SER	-	expression tag	UNP O08795
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	LEU	-	expression tag	UNP O08795
D	522	GLU	-	expression tag	UNP O08795
D	523	THR	-	expression tag	UNP O08795
D	524	LYS	-	expression tag	UNP O08795
D	525	HIS	-	expression tag	UNP O08795
D	526	HIS	-	expression tag	UNP O08795
D	527	HIS	-	expression tag	UNP O08795
D	528	HIS	-	expression tag	UNP O08795
D	529	HIS	-	expression tag	UNP O08795
D	530	HIS	-	expression tag	UNP O08795

- Molecule 3 is (1S,2S,3R,4S,5S)-1-(hydroxymethyl)-5-[[[(5Z)-6-[[2-nitro-4-(2H-1,2,3-triazol-2-yl)phenyl]amino}hex-5-en-1-yl]amino}cyclohexane-1,2,3,4-tetrol (CCD ID: W9V) (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 TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: C₆H₁₄O₄).



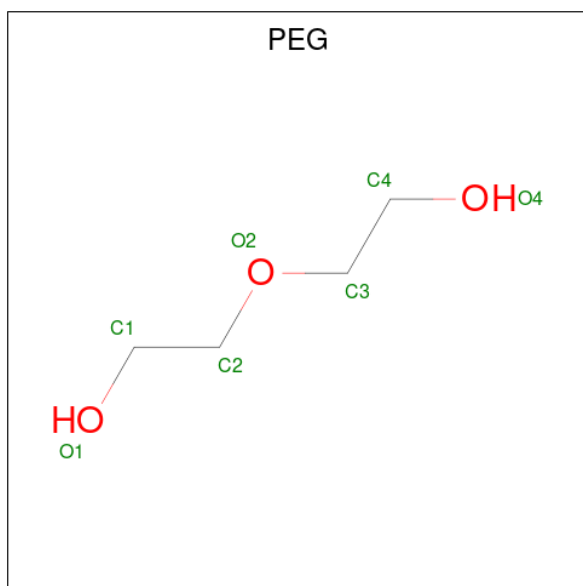
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		

Continued on next page...

Continued from previous page...

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	B	1	Total	C	O	0	0
			10	6	4		
4	C	1	Total	C	O	0	0
			10	6	4		
4	C	1	Total	C	O	0	0
			10	6	4		

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



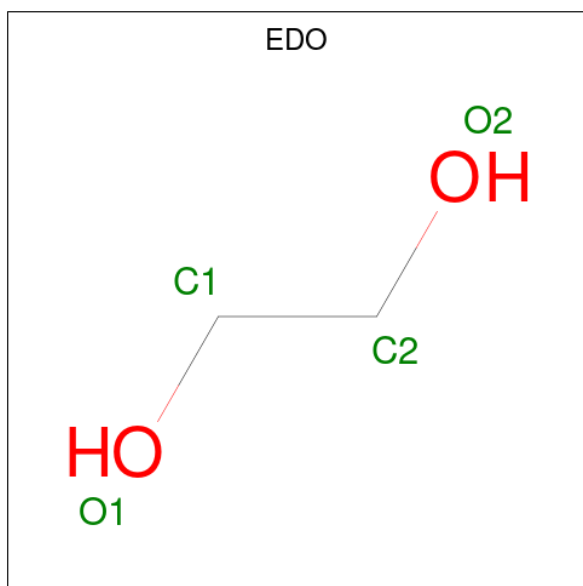
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		

Continued on next page...

Continued from previous page...

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

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

Continued on next page...

Continued from previous page...

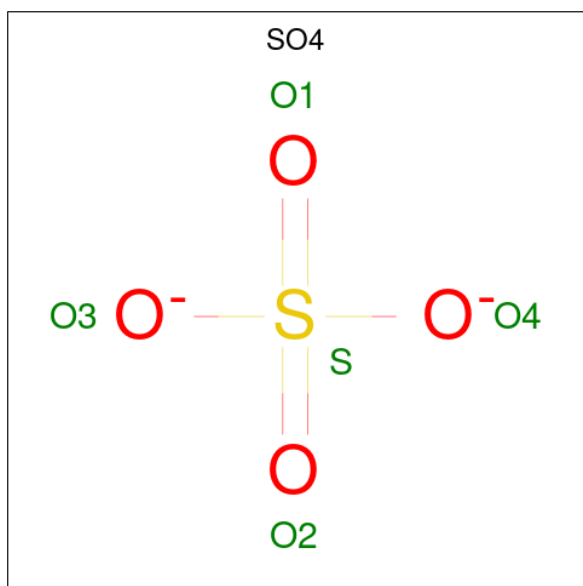
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	A	1	Total 4	C 2	O 2	0	0
6	C	1	Total 4	C 2	O 2	0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

Continued on next page...

Continued from previous page...

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

- Molecule 7 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

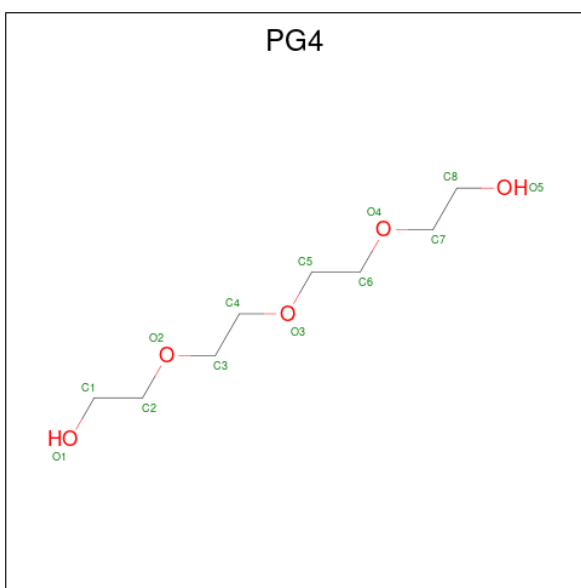


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	A	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		
7	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is CALCIUM ION (CCD ID: CA) (formula: Ca).

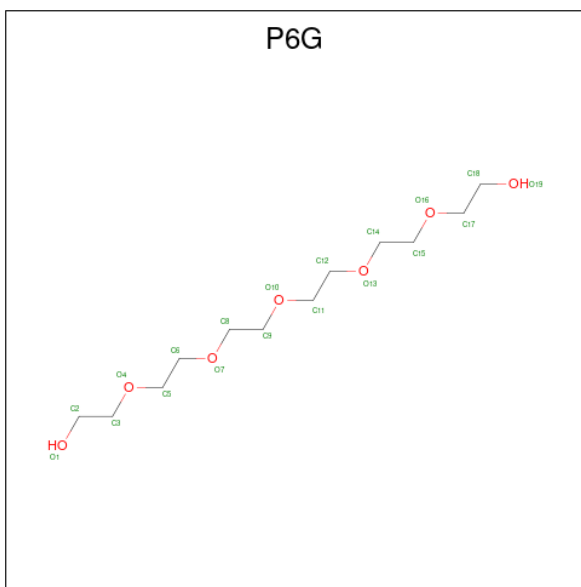
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	2	Total	Ca	0	0
			2	2		
8	D	2	Total	Ca	0	0
			2	2		

- Molecule 9 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



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

- Molecule 10 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	C	1	Total	C	O	0	0
			19	12	7		

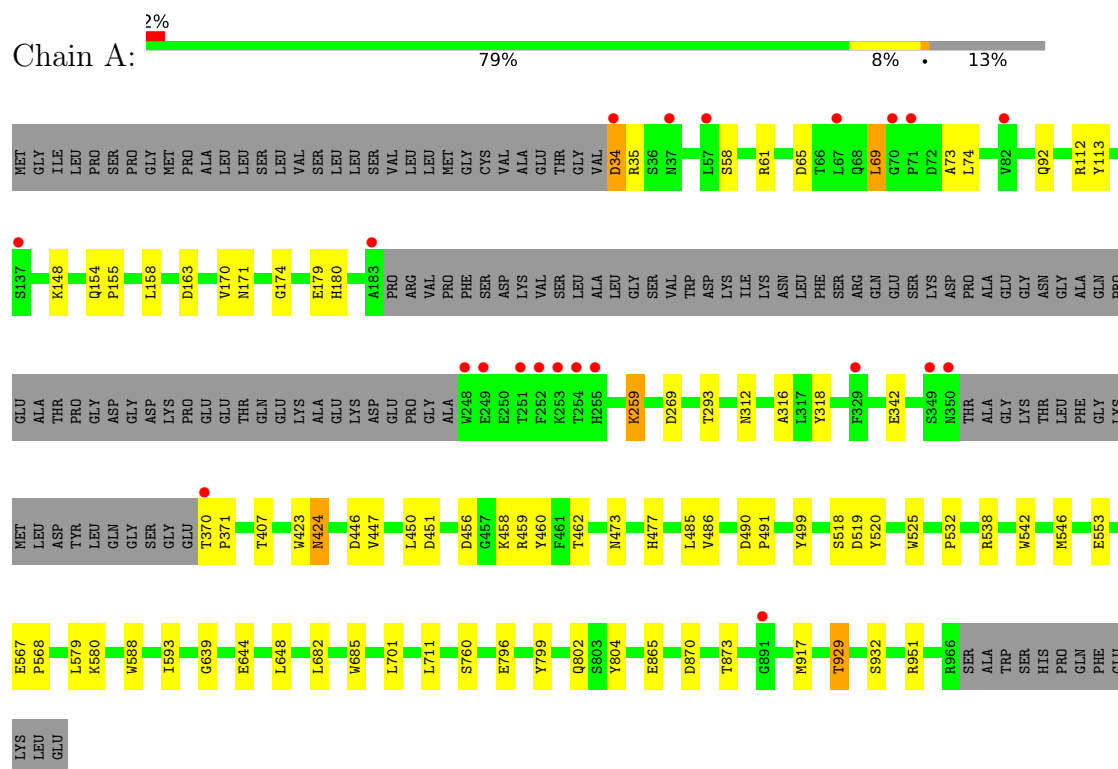
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	504	Total 504	O 504	0	0
11	B	34	Total 34	O 34	0	0
11	C	411	Total 411	O 411	0	0
11	D	32	Total 32	O 32	0	0

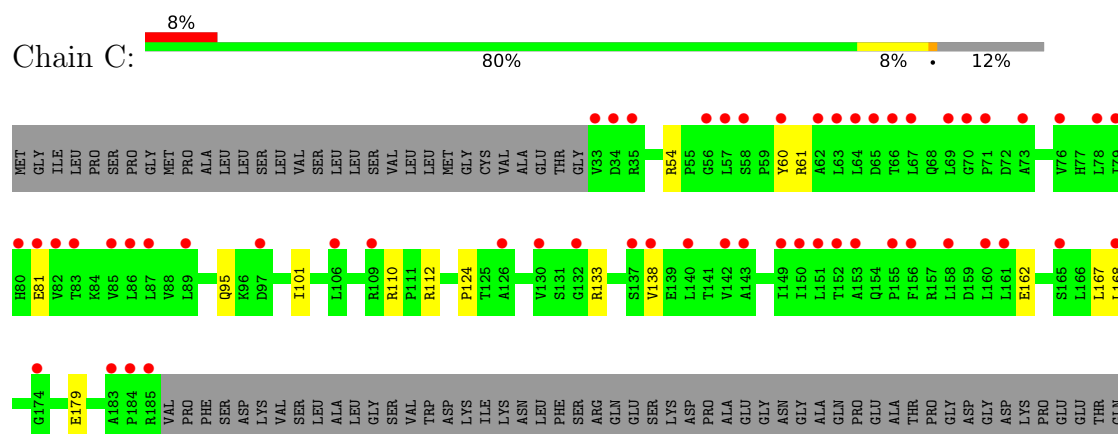
3 Residue-property plots [i](#)

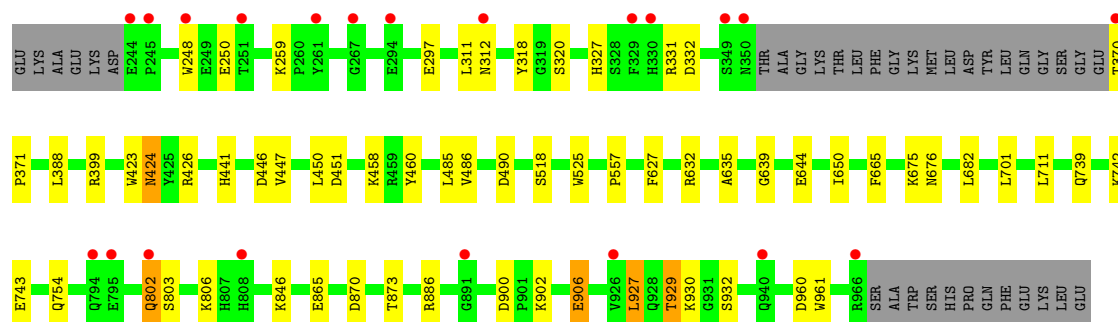
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Alpha glucosidase 2 alpha neutral subunit

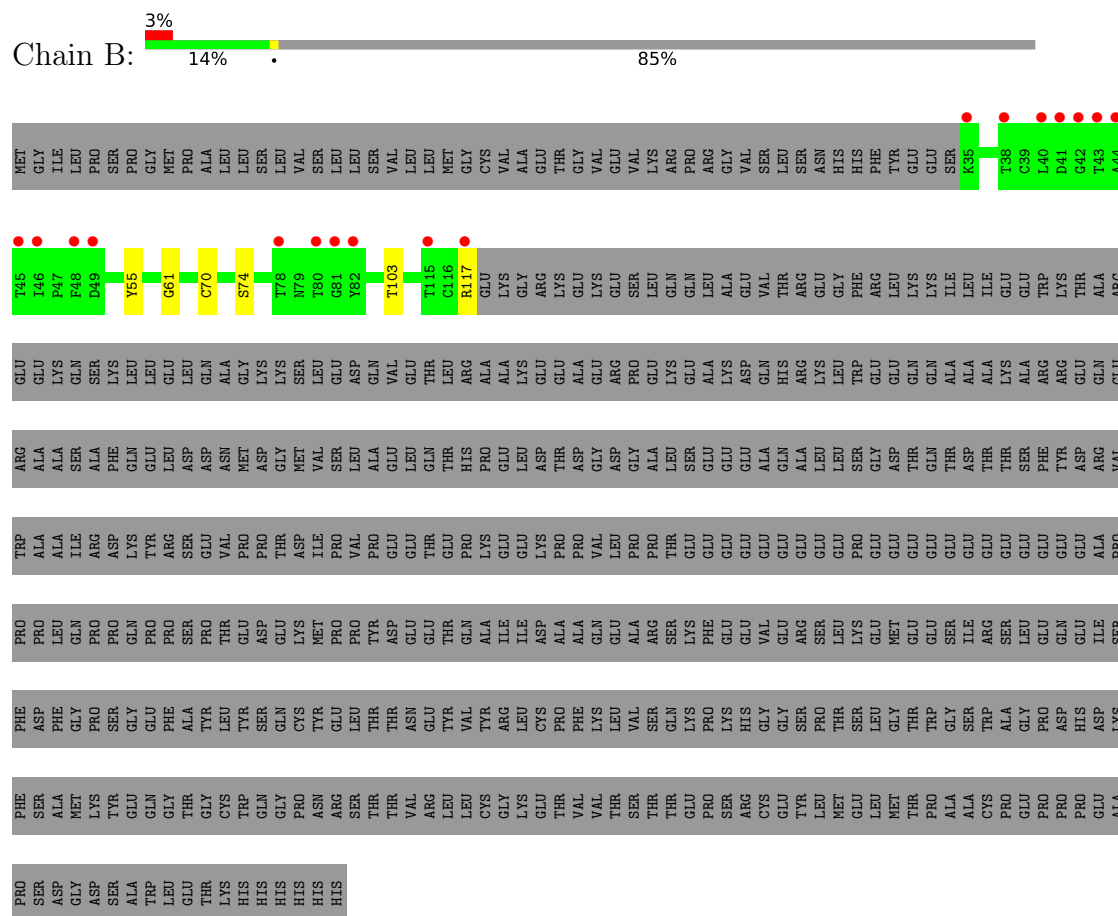


- Molecule 1: Alpha glucosidase 2 alpha neutral subunit

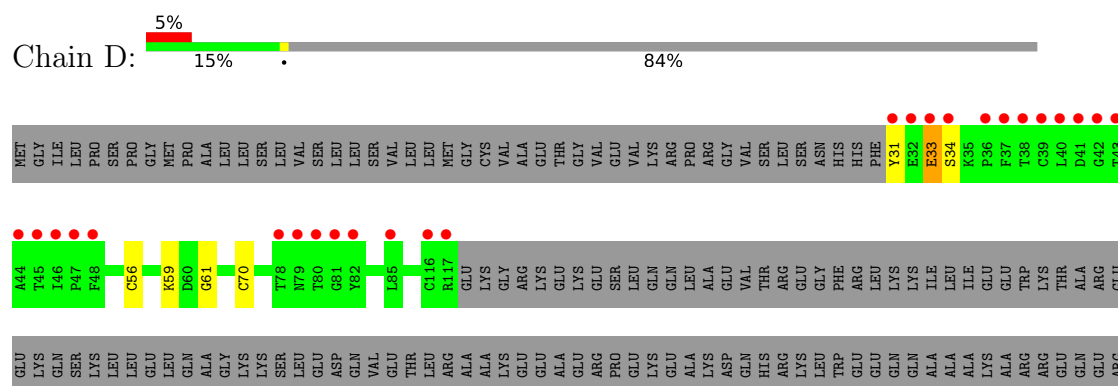




• Molecule 2: Glucosidase 2 subunit beta



• Molecule 2: Glucosidase 2 subunit beta



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

4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	102.87Å 102.87Å 240.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.35 – 2.10 42.35 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.35-2.10) 94.2 (42.35-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.87 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.171 , 0.192 0.171 , 0.192	Depositor DCC
R_{free} test set	2002 reflections (1.21%)	wwPDB-VP
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.7	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 0.034 for h,-h-k,-l 0.020 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16450	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.57% 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: P6G, W9V, SO4, PEG, CA, EDO, PG4, PGE

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	0.18	0/7086	0.43	0/9649
1	C	0.19	0/7182	0.43	0/9775
2	B	0.16	0/611	0.42	0/835
2	D	0.18	0/652	0.42	0/891
All	All	0.18	0/15531	0.43	0/21150

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	6862	0	6590	60	0
1	C	6947	0	6714	61	0
2	B	600	0	504	5	0
2	D	639	0	533	5	0
3	A	34	0	0	0	0
3	C	34	0	0	0	0
4	A	60	0	84	7	0
4	B	10	0	14	1	0
4	C	20	0	28	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	42	0	60	3	2
5	C	42	0	60	2	2
6	A	48	0	71	5	0
6	C	44	0	60	10	0
6	D	8	0	12	0	0
7	A	20	0	0	0	0
7	C	10	0	0	0	0
8	B	2	0	0	0	0
8	D	2	0	0	0	0
9	B	13	0	18	1	0
9	D	13	0	18	2	0
10	C	19	0	26	0	0
11	A	504	0	0	16	0
11	B	34	0	0	2	0
11	C	411	0	0	19	0
11	D	32	0	0	1	0
All	All	16450	0	14792	134	2

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)
1:A:553:GLU:OE2	11:A:1101:HOH:O	1.89	0.89
1:C:886:ARG:NH2	11:C:1102:HOH:O	2.08	0.87
1:A:644:GLU:OE1	11:A:1102:HOH:O	1.95	0.81
1:A:180:HIS:O	11:A:1103:HOH:O	2.01	0.79
1:A:588:TRP:HE1	4:A:1013:PGE:H22	1.49	0.75

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1008:PEG:C3	5:C:1019:PEG:C2[3_665]	1.50	0.70
5:A:1008:PEG:O2	5:C:1019:PEG:C2[3_665]	1.70	0.50

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	849/977 (87%)	824 (97%)	25 (3%)	0	100	100
1	C	859/977 (88%)	831 (97%)	28 (3%)	0	100	100
2	B	81/547 (15%)	79 (98%)	2 (2%)	0	100	100
2	D	85/547 (16%)	79 (93%)	6 (7%)	0	100	100
All	All	1874/3048 (62%)	1813 (97%)	61 (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	743/846 (88%)	736 (99%)	7 (1%)	70	78
1	C	755/846 (89%)	748 (99%)	7 (1%)	70	78
2	B	69/478 (14%)	69 (100%)	0	100	100
2	D	73/478 (15%)	72 (99%)	1 (1%)	59	67
All	All	1640/2648 (62%)	1625 (99%)	15 (1%)	70	78

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	168	LEU
1	C	929	THR
1	C	424	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	33	GLU
1	C	906	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	788	GLN
1	C	802	GLN
1	C	880	HIS
1	C	77	HIS
1	C	181	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 61 ligands modelled in this entry, 4 are monoatomic - leaving 57 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	EDO	A	1006	-	3,3,3	0.42	0	2,2,2	0.45	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PEG	A	1008	-	6,6,6	0.66	0	5,5,5	1.51	1 (20%)
6	EDO	C	1012	-	3,3,3	0.48	0	2,2,2	0.39	0
4	PGE	C	1018	-	9,9,9	0.36	0	8,8,8	0.24	0
5	PEG	C	1008	-	6,6,6	0.52	0	5,5,5	0.69	0
6	EDO	A	1023	-	3,3,3	0.45	0	2,2,2	0.42	0
4	PGE	B	604	-	9,9,9	0.32	0	8,8,8	0.33	0
6	EDO	C	1002	-	3,3,3	0.39	0	2,2,2	0.40	0
6	EDO	A	1012	-	3,3,3	0.42	0	2,2,2	0.48	0
6	EDO	C	1010	-	3,3,3	0.45	0	2,2,2	0.32	0
7	SO4	A	1029	-	4,4,4	0.23	0	6,6,6	0.15	0
6	EDO	C	1013	-	3,3,3	0.44	0	2,2,2	0.40	0
5	PEG	C	1009	-	6,6,6	0.50	0	5,5,5	0.29	0
6	EDO	C	1015	-	3,3,3	0.46	0	2,2,2	0.34	0
4	PGE	A	1025	-	9,9,9	0.31	0	8,8,8	0.36	0
5	PEG	A	1007	-	6,6,6	0.53	0	5,5,5	0.39	0
9	PG4	B	603	-	12,12,12	0.54	0	11,11,11	0.34	0
7	SO4	C	1022	-	4,4,4	0.23	0	6,6,6	0.10	0
5	PEG	A	1016	-	6,6,6	0.49	0	5,5,5	0.24	0
7	SO4	A	1028	-	4,4,4	0.24	0	6,6,6	0.05	0
6	EDO	D	2005	-	3,3,3	0.41	0	2,2,2	0.53	0
5	PEG	C	1011	-	6,6,6	0.49	0	5,5,5	0.29	0
6	EDO	A	1017	-	3,3,3	0.44	0	2,2,2	0.44	0
6	EDO	C	1021	-	3,3,3	0.45	0	2,2,2	0.29	0
5	PEG	A	1015	-	6,6,6	0.50	0	5,5,5	0.29	0
4	PGE	A	1020	-	9,9,9	0.32	0	8,8,8	0.32	0
5	PEG	C	1014	-	6,6,6	0.51	0	5,5,5	0.33	0
6	EDO	A	1011	-	3,3,3	0.41	0	2,2,2	0.47	0
6	EDO	A	1005	-	3,3,3	0.48	0	2,2,2	0.41	0
3	W9V	C	1001	-	36,36,36	2.09	4 (11%)	42,50,50	3.95	17 (40%)
6	EDO	A	1009	-	3,3,3	0.38	0	2,2,2	0.64	0
5	PEG	A	1003	-	6,6,6	0.50	0	5,5,5	0.26	0
6	EDO	D	2001	-	3,3,3	0.54	0	2,2,2	0.63	0
4	PGE	A	1013	-	9,9,9	0.31	0	8,8,8	0.31	0
7	SO4	A	1027	-	4,4,4	0.25	0	6,6,6	0.07	0
5	PEG	A	1014	-	6,6,6	0.50	0	5,5,5	0.35	0
9	PG4	D	2004	-	12,12,12	0.53	0	11,11,11	0.69	0
4	PGE	A	1021	-	9,9,9	0.33	0	8,8,8	0.25	0
10	P6G	C	1020	-	18,18,18	0.55	0	17,17,17	0.33	0
3	W9V	A	1001	-	36,36,36	2.04	2 (5%)	42,50,50	3.95	17 (40%)
5	PEG	C	1019	-	6,6,6	0.56	0	5,5,5	0.58	0
6	EDO	A	1010	-	3,3,3	0.48	0	2,2,2	0.21	0
6	EDO	A	1022	-	3,3,3	0.40	0	2,2,2	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	C	1017	-	3,3,3	0.41	0	2,2,2	0.40	0
6	EDO	A	1019	-	3,3,3	0.42	0	2,2,2	0.48	0
6	EDO	C	1003	-	3,3,3	0.41	0	2,2,2	0.41	0
6	EDO	C	1016	-	3,3,3	0.43	0	2,2,2	0.46	0
7	SO4	C	1023	-	4,4,4	0.22	0	6,6,6	0.11	0
6	EDO	A	1018	-	3,3,3	0.48	0	2,2,2	0.29	0
6	EDO	C	1006	-	3,3,3	0.39	0	2,2,2	0.41	0
6	EDO	C	1007	-	3,3,3	0.45	0	2,2,2	0.33	0
6	EDO	A	1004	-	3,3,3	0.39	0	2,2,2	0.50	0
4	PGE	A	1002	-	9,9,9	0.30	0	8,8,8	0.37	0
4	PGE	C	1005	-	9,9,9	0.34	0	8,8,8	0.31	0
5	PEG	C	1004	-	6,6,6	0.50	0	5,5,5	0.27	0
7	SO4	A	1026	-	4,4,4	0.23	0	6,6,6	0.13	0
4	PGE	A	1024	-	9,9,9	0.32	0	8,8,8	0.38	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	EDO	A	1006	-	-	1/1/1/1	-
5	PEG	A	1008	-	-	0/4/4/4	-
6	EDO	C	1012	-	-	0/1/1/1	-
4	PGE	C	1018	-	-	4/7/7/7	-
5	PEG	C	1008	-	-	1/4/4/4	-
6	EDO	A	1023	-	-	0/1/1/1	-
4	PGE	B	604	-	-	4/7/7/7	-
6	EDO	C	1002	-	-	0/1/1/1	-
6	EDO	A	1012	-	-	0/1/1/1	-
6	EDO	C	1010	-	-	1/1/1/1	-
6	EDO	C	1013	-	-	1/1/1/1	-
5	PEG	C	1009	-	-	2/4/4/4	-
6	EDO	C	1015	-	-	1/1/1/1	-
4	PGE	A	1025	-	-	4/7/7/7	-
5	PEG	A	1007	-	-	2/4/4/4	-
9	PG4	B	603	-	-	6/10/10/10	-
5	PEG	A	1016	-	-	2/4/4/4	-
6	EDO	D	2005	-	-	0/1/1/1	-
5	PEG	C	1011	-	-	2/4/4/4	-
6	EDO	A	1017	-	-	1/1/1/1	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	C	1021	-	-	1/1/1/1	-
5	PEG	A	1015	-	-	1/4/4/4	-
4	PGE	A	1020	-	-	3/7/7/7	-
5	PEG	C	1014	-	-	0/4/4/4	-
6	EDO	A	1011	-	-	1/1/1/1	-
6	EDO	A	1005	-	-	0/1/1/1	-
3	W9V	C	1001	-	-	6/20/45/45	0/3/3/3
6	EDO	A	1009	-	-	0/1/1/1	-
5	PEG	A	1003	-	-	3/4/4/4	-
6	EDO	D	2001	-	-	0/1/1/1	-
4	PGE	A	1013	-	-	3/7/7/7	-
5	PEG	A	1014	-	-	2/4/4/4	-
9	PG4	D	2004	-	-	7/10/10/10	-
4	PGE	A	1021	-	-	3/7/7/7	-
10	P6G	C	1020	-	-	9/16/16/16	-
3	W9V	A	1001	-	-	11/20/45/45	0/3/3/3
5	PEG	C	1019	-	-	4/4/4/4	-
6	EDO	A	1010	-	-	1/1/1/1	-
6	EDO	A	1022	-	-	1/1/1/1	-
6	EDO	C	1017	-	-	1/1/1/1	-
6	EDO	A	1019	-	-	1/1/1/1	-
6	EDO	C	1003	-	-	1/1/1/1	-
6	EDO	C	1016	-	-	0/1/1/1	-
6	EDO	A	1018	-	-	1/1/1/1	-
6	EDO	C	1006	-	-	1/1/1/1	-
6	EDO	C	1007	-	-	0/1/1/1	-
6	EDO	A	1004	-	-	0/1/1/1	-
4	PGE	A	1002	-	-	6/7/7/7	-
4	PGE	C	1005	-	-	2/7/7/7	-
5	PEG	C	1004	-	-	3/4/4/4	-
4	PGE	A	1024	-	-	5/7/7/7	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1001	W9V	O4-N3	10.63	1.41	1.22
3	A	1001	W9V	O4-N3	10.49	1.40	1.22
3	A	1001	W9V	C12-N2	3.87	1.47	1.37
3	C	1001	W9V	C12-N2	3.86	1.47	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1001	W9V	C15-N4	2.10	1.46	1.43

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1001	W9V	O3-C2-C3	-15.54	87.62	108.25
3	A	1001	W9V	O3-C2-C3	-14.65	88.79	108.25
3	C	1001	W9V	O3-C2-C4	-11.59	84.09	108.40
3	A	1001	W9V	O3-C2-C1	-10.90	84.48	108.40
3	A	1001	W9V	O3-C2-C4	-10.51	86.35	108.40

There are no chirality outliers.

5 of 109 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	W9V	C4-C2-C3-O2
3	A	1001	W9V	C1-C2-C3-O2
3	C	1001	W9V	C4-C2-C3-O2
3	C	1001	W9V	C1-C2-C3-O2
9	D	2004	PG4	C5-C6-O4-C7

There are no ring outliers.

24 monomers are involved in 35 short contacts:

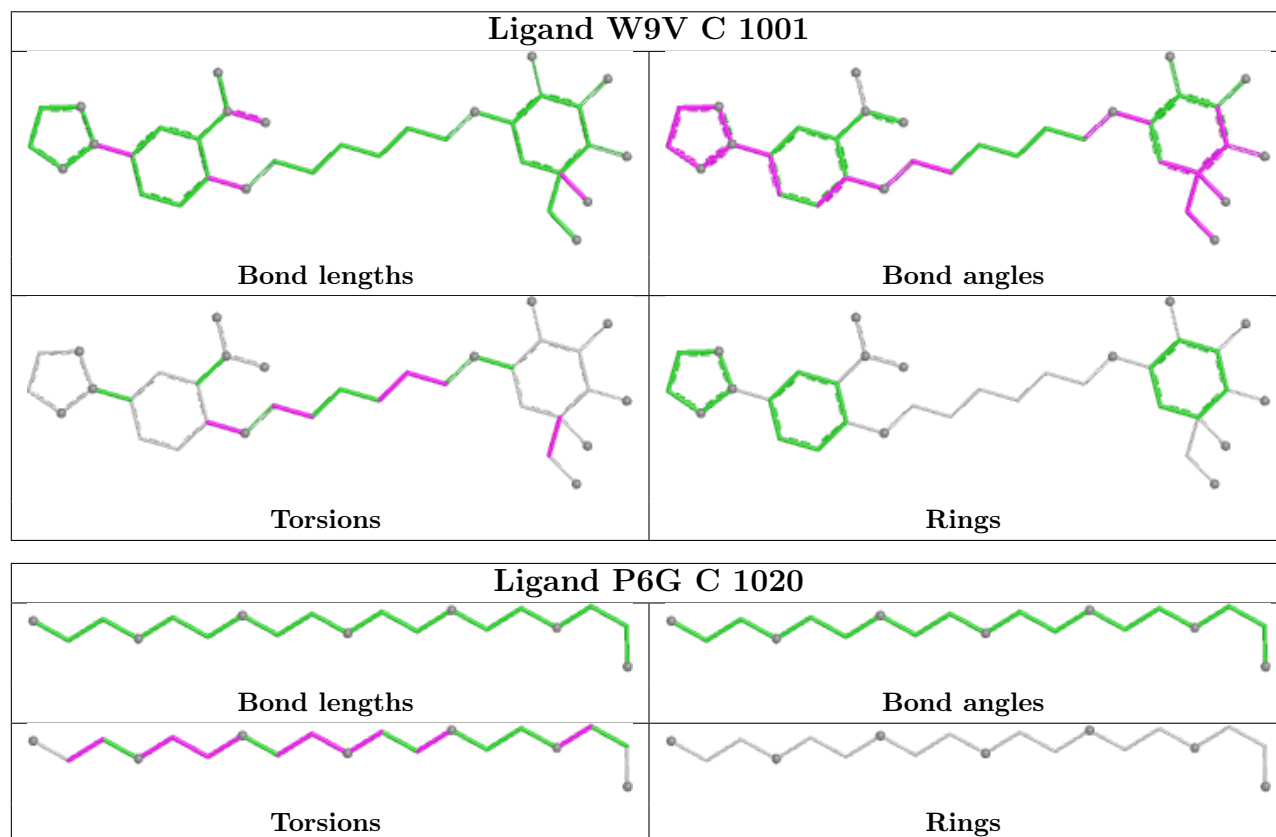
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1008	PEG	0	2
4	C	1018	PGE	2	0
5	C	1008	PEG	2	0
6	A	1023	EDO	1	0
4	B	604	PGE	1	0
6	C	1002	EDO	3	0
4	A	1025	PGE	1	0
9	B	603	PG4	1	0
5	A	1016	PEG	2	0
6	C	1021	EDO	3	0
6	A	1011	EDO	1	0
6	A	1005	EDO	1	0
4	A	1013	PGE	1	0
5	A	1014	PEG	1	0
9	D	2004	PG4	2	0
4	A	1021	PGE	1	0

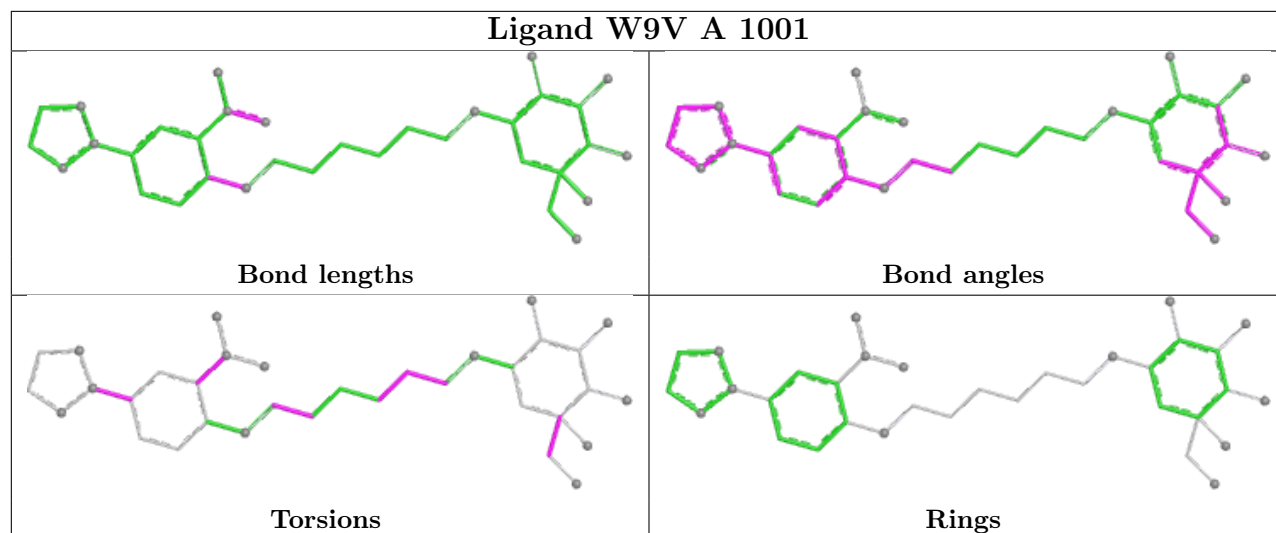
Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1019	PEG	0	2
6	C	1017	EDO	1	0
6	A	1019	EDO	1	0
6	C	1003	EDO	1	0
6	C	1016	EDO	1	0
6	C	1007	EDO	1	0
6	A	1004	EDO	1	0
4	A	1024	PGE	4	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	850/977 (87%)	-0.04	21 (2%) 58 61	20, 35, 61, 102	5 (0%)
1	C	857/977 (87%)	0.32	76 (8%) 15 16	17, 39, 78, 104	8 (0%)
2	B	83/547 (15%)	0.87	17 (20%) 2 3	31, 49, 88, 102	0
2	D	87/547 (15%)	1.18	25 (28%) 1 1	31, 53, 100, 119	0
All	All	1877/3048 (61%)	0.22	139 (7%) 20 22	17, 38, 78, 119	13 (0%)

The worst 5 of 139 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	183	ALA	6.1
2	D	48	PHE	5.7
1	A	248	TRP	5.7
2	D	44	ALA	5.5
2	D	43	THR	5.0

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($\text{\AA}^2$)	Q<0.9
6	EDO	C	1012	4/4	0.45	0.23	89,94,101,104	0
7	SO4	A	1027	5/5	0.61	0.19	80,89,94,119	0
5	PEG	C	1019	7/7	0.65	0.27	74,83,103,109	0
6	EDO	A	1017	4/4	0.71	0.20	61,67,77,87	0
7	SO4	A	1028	5/5	0.72	0.11	77,95,101,132	0
6	EDO	A	1010	4/4	0.73	0.19	53,59,66,66	0
5	PEG	A	1008	7/7	0.76	0.38	59,62,80,83	7
6	EDO	A	1011	4/4	0.77	0.20	59,70,70,84	0
6	EDO	C	1003	4/4	0.79	0.19	55,61,65,71	0
10	P6G	C	1020	19/19	0.79	0.18	48,76,89,89	0
5	PEG	A	1007	7/7	0.80	0.16	59,69,82,92	0
5	PEG	C	1014	7/7	0.80	0.19	53,67,79,83	0
6	EDO	C	1021	4/4	0.80	0.19	62,73,80,82	0
7	SO4	A	1026	5/5	0.81	0.19	59,67,79,103	0
5	PEG	C	1009	7/7	0.81	0.17	49,61,72,85	0
4	PGE	A	1020	10/10	0.81	0.18	55,65,83,92	0
6	EDO	A	1019	4/4	0.81	0.17	44,56,56,69	0
6	EDO	C	1017	4/4	0.82	0.17	59,60,66,76	0
7	SO4	C	1022	5/5	0.82	0.11	72,77,86,93	0
5	PEG	A	1014	7/7	0.82	0.17	58,62,76,80	0
6	EDO	C	1015	4/4	0.83	0.16	46,62,63,70	0
4	PGE	A	1021	10/10	0.83	0.18	51,64,72,80	0
4	PGE	B	604	10/10	0.84	0.15	56,68,82,88	0
5	PEG	A	1015	7/7	0.85	0.16	49,64,75,83	0
9	PG4	B	603	13/13	0.85	0.17	54,69,70,74	0
9	PG4	D	2004	13/13	0.85	0.18	54,68,79,82	0
6	EDO	C	1013	4/4	0.85	0.18	51,51,56,68	0
6	EDO	A	1018	4/4	0.86	0.14	58,59,60,61	0
5	PEG	A	1003	7/7	0.86	0.15	43,62,69,83	0
5	PEG	C	1004	7/7	0.86	0.15	51,63,75,80	0
6	EDO	C	1010	4/4	0.86	0.16	49,51,52,53	0
4	PGE	A	1002	10/10	0.87	0.15	51,62,75,75	0
4	PGE	C	1018	10/10	0.87	0.15	37,53,73,79	0
6	EDO	D	2001	4/4	0.87	0.14	42,54,55,64	0
5	PEG	C	1008	7/7	0.87	0.15	53,56,76,77	0
4	PGE	A	1025	10/10	0.87	0.14	55,61,70,80	0
4	PGE	A	1013	10/10	0.88	0.14	57,65,71,71	0
7	SO4	C	1023	5/5	0.88	0.15	61,65,87,95	0
6	EDO	A	1009	4/4	0.88	0.21	55,57,64,68	0
4	PGE	A	1024	10/10	0.88	0.17	38,57,70,73	0
7	SO4	A	1029	5/5	0.88	0.12	70,81,106,126	0
6	EDO	C	1002	4/4	0.89	0.15	49,52,55,75	0
5	PEG	A	1016	7/7	0.89	0.13	49,57,72,74	0

Continued on next page...

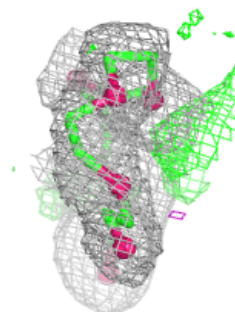
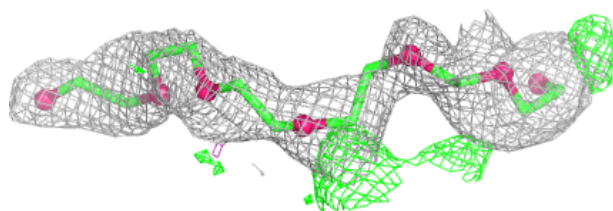
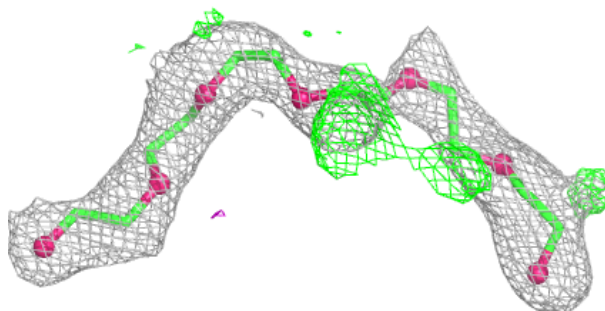
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	C	1016	4/4	0.89	0.12	38,41,47,51	0
6	EDO	C	1007	4/4	0.90	0.14	52,52,66,72	0
6	EDO	C	1006	4/4	0.90	0.14	47,51,60,66	0
6	EDO	A	1006	4/4	0.91	0.15	50,50,55,66	0
5	PEG	C	1011	7/7	0.91	0.13	45,56,67,90	0
6	EDO	A	1022	4/4	0.91	0.18	46,56,60,63	0
3	W9V	A	1001	34/34	0.91	0.16	23,62,102,113	0
4	PGE	C	1005	10/10	0.91	0.13	40,57,66,73	0
6	EDO	A	1004	4/4	0.91	0.14	54,55,55,60	0
3	W9V	C	1001	34/34	0.92	0.15	24,51,97,107	0
6	EDO	A	1005	4/4	0.92	0.12	38,38,39,50	0
6	EDO	D	2005	4/4	0.92	0.12	46,52,54,58	0
6	EDO	A	1023	4/4	0.94	0.10	42,46,46,57	0
6	EDO	A	1012	4/4	0.96	0.09	35,36,39,43	0
8	CA	B	601	1/1	0.99	0.03	39,39,39,39	0
8	CA	B	602	1/1	0.99	0.02	34,34,34,34	0
8	CA	D	2002	1/1	0.99	0.03	40,40,40,40	0
8	CA	D	2003	1/1	1.00	0.02	33,33,33,33	0

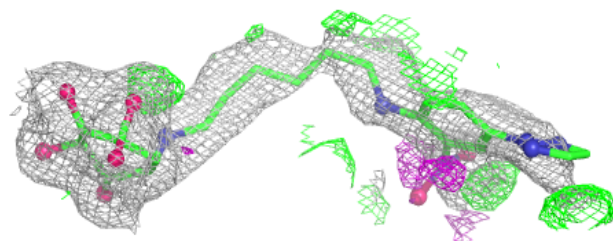
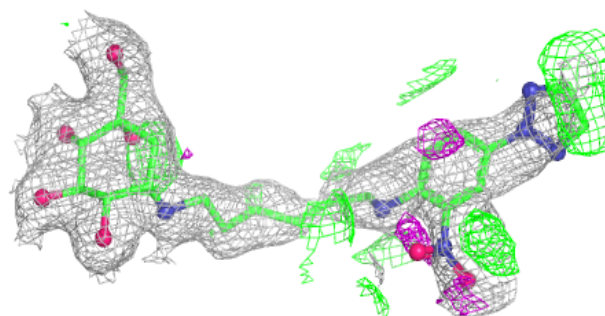
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around P6G C 1020:

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

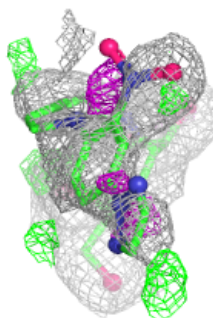
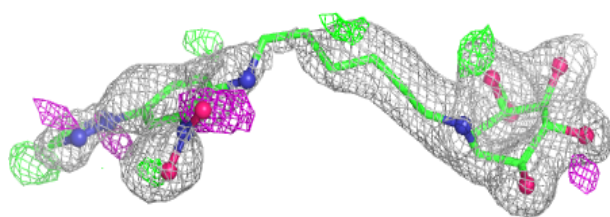
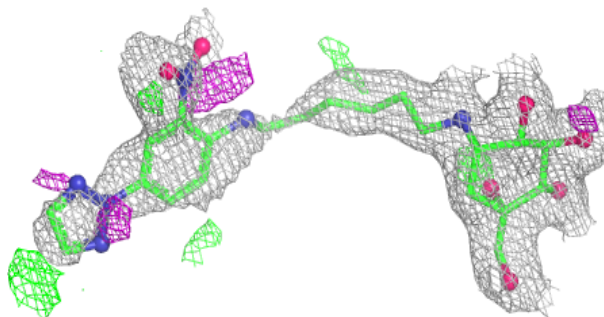
**Electron density around W9V A 1001:**

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



Electron density around W9V 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.