



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:34 PM UTC

PDB ID : 6T0E / pdb_00006t0e
Title : The glucuronoyl esterase OtCE15A S267A variant from *Opitutus terrae* in complex with benzyl D-glucuronoate and D-glucuronate
Authors : Mazurkewich, S.; Navarro Poulsen, J.C.; Larsbrink, J.; Lo Leggio, L.
Deposited on : 2019-10-03
Resolution : 1.89 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

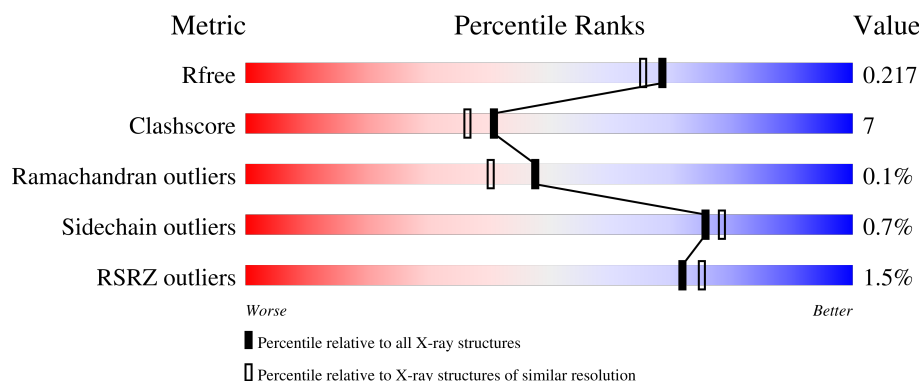
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.89 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	421	
1	B	421	

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
2	GCU	B	501	-	-	X	-
7	PEG	B	517	-	-	X	-
8	PGE	A	531	-	-	X	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 13299 atoms, of which 6366 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 glucuronoyl esterase OtCE15A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	392	Total	C	H	N	O	S	0	5	0
			6027	1946	2947	568	559	7			
1	B	394	Total	C	H	N	O	S	0	5	0
			6036	1954	2940	573	561	8			

There are 44 discrepancies between the modelled and reference sequences:

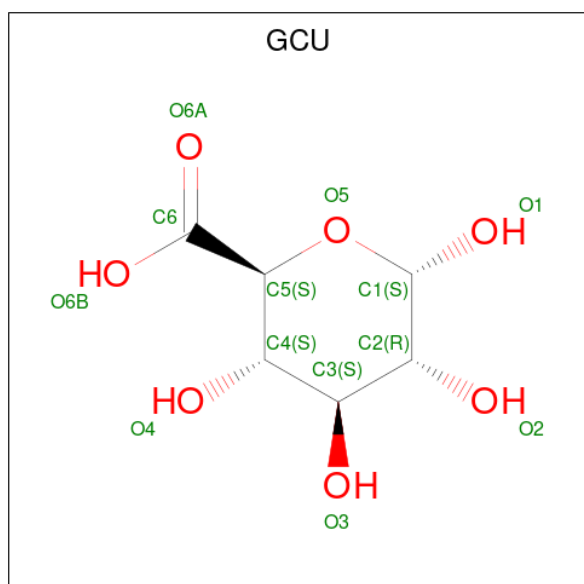
Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MET	-	initiating methionine	UNP B1ZMF4
A	13	GLY	-	expression tag	UNP B1ZMF4
A	14	SER	-	expression tag	UNP B1ZMF4
A	15	SER	-	expression tag	UNP B1ZMF4
A	16	HIS	-	expression tag	UNP B1ZMF4
A	17	HIS	-	expression tag	UNP B1ZMF4
A	18	HIS	-	expression tag	UNP B1ZMF4
A	19	HIS	-	expression tag	UNP B1ZMF4
A	20	HIS	-	expression tag	UNP B1ZMF4
A	21	HIS	-	expression tag	UNP B1ZMF4
A	22	SER	-	expression tag	UNP B1ZMF4
A	23	SER	-	expression tag	UNP B1ZMF4
A	24	GLU	-	expression tag	UNP B1ZMF4
A	25	ASN	-	expression tag	UNP B1ZMF4
A	26	LEU	-	expression tag	UNP B1ZMF4
A	27	TYR	-	expression tag	UNP B1ZMF4
A	28	PHE	-	expression tag	UNP B1ZMF4
A	29	GLN	-	expression tag	UNP B1ZMF4
A	30	GLY	-	expression tag	UNP B1ZMF4
A	31	HIS	-	expression tag	UNP B1ZMF4
A	32	SER	-	expression tag	UNP B1ZMF4
A	267	ALA	SER	engineered mutation	UNP B1ZMF4
B	12	MET	-	initiating methionine	UNP B1ZMF4
B	13	GLY	-	expression tag	UNP B1ZMF4
B	14	SER	-	expression tag	UNP B1ZMF4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	15	SER	-	expression tag	UNP B1ZMF4
B	16	HIS	-	expression tag	UNP B1ZMF4
B	17	HIS	-	expression tag	UNP B1ZMF4
B	18	HIS	-	expression tag	UNP B1ZMF4
B	19	HIS	-	expression tag	UNP B1ZMF4
B	20	HIS	-	expression tag	UNP B1ZMF4
B	21	HIS	-	expression tag	UNP B1ZMF4
B	22	SER	-	expression tag	UNP B1ZMF4
B	23	SER	-	expression tag	UNP B1ZMF4
B	24	GLU	-	expression tag	UNP B1ZMF4
B	25	ASN	-	expression tag	UNP B1ZMF4
B	26	LEU	-	expression tag	UNP B1ZMF4
B	27	TYR	-	expression tag	UNP B1ZMF4
B	28	PHE	-	expression tag	UNP B1ZMF4
B	29	GLN	-	expression tag	UNP B1ZMF4
B	30	GLY	-	expression tag	UNP B1ZMF4
B	31	HIS	-	expression tag	UNP B1ZMF4
B	32	SER	-	expression tag	UNP B1ZMF4
B	267	ALA	SER	engineered mutation	UNP B1ZMF4

- Molecule 2 is alpha-D-glucopyranuronic acid (CCD ID: GCU) (formula: C₆H₁₀O₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			22	6	9	7		

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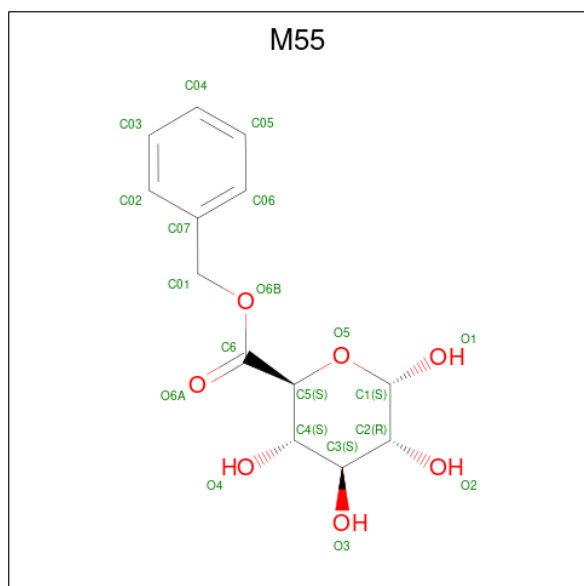
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	H	O	0	0
			22	6	9	7		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

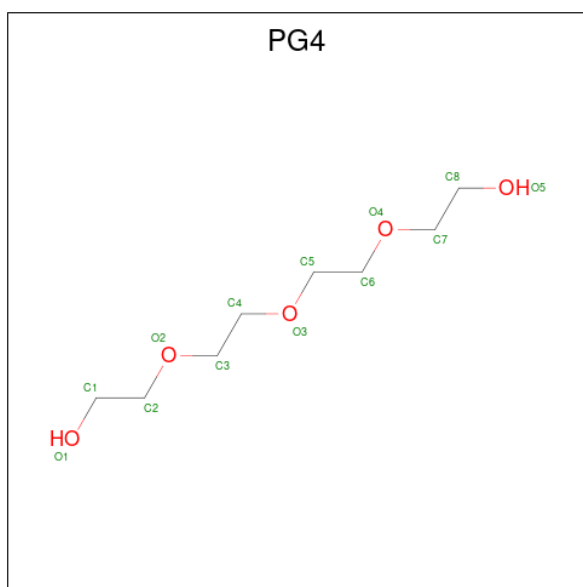
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is benzyl alpha-D-glucopyranuronate (CCD ID: M55) (formula: C₁₃H₁₆O₇) (labeled as "Ligand of Interest" by depositor).



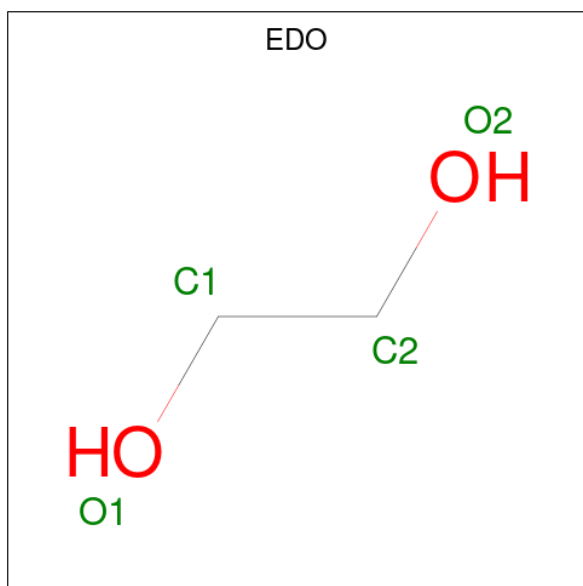
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			36	13	16	7		

- Molecule 5 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			31	8	18	5		

- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		

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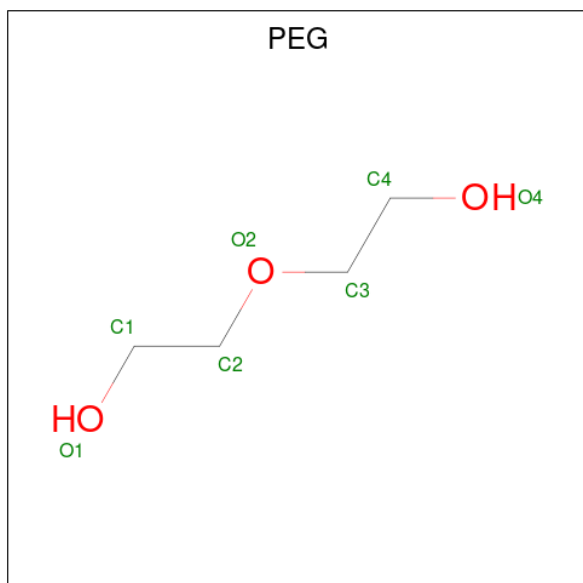
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



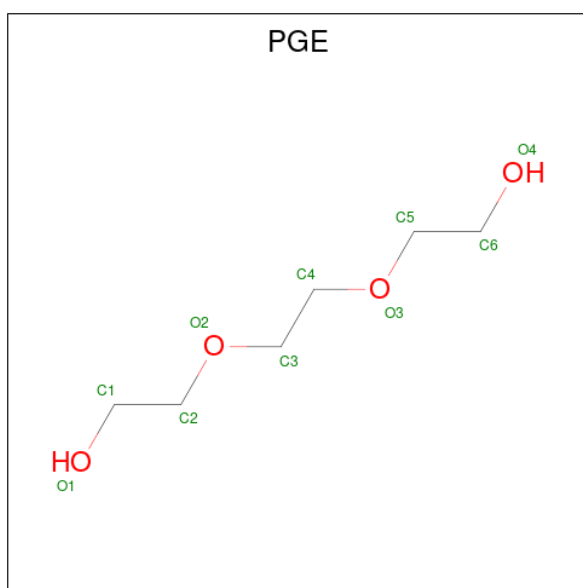
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			17	4	10	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	H	O	0	0
			17	4	10	3		
7	A	1	Total	C	H	O	0	0
			17	4	10	3		
7	A	1	Total	C	H	O	0	0
			17	4	10	3		
7	B	1	Total	C	H	O	0	0
			17	4	10	3		
7	B	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 8 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).

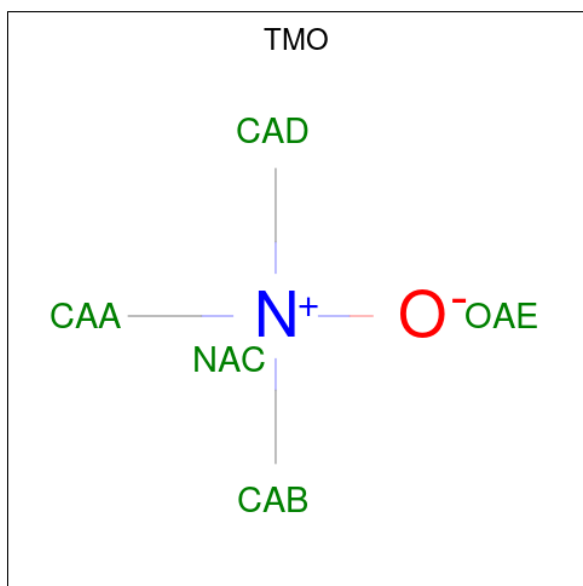


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	H	O	0	0
			24	6	14	4		
8	A	1	Total	C	H	O	0	0
			24	6	14	4		
8	A	1	Total	C	H	O	0	0
			24	6	14	4		
8	A	1	Total	C	H	O	0	0
			24	6	14	4		
8	B	1	Total	C	H	O	0	0
			24	6	14	4		

- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

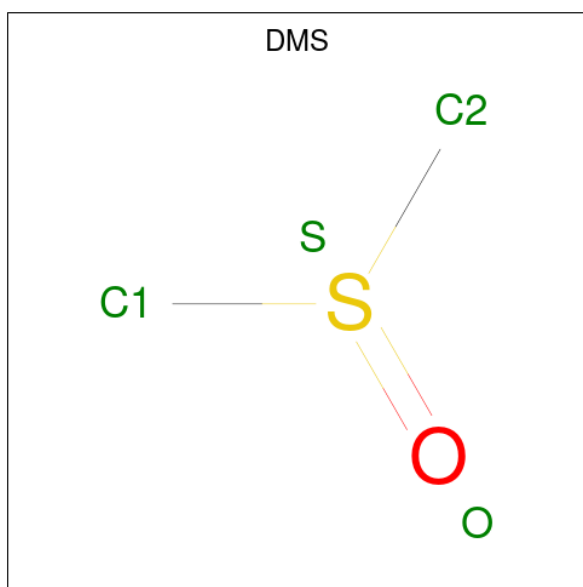
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Mg	0	0
			1	1		

- Molecule 10 is trimethylamine oxide (CCD ID: TMO) (formula: C_3H_9NO).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	A	1	Total	C	H	N	O	0	0
			14	3	9	1	1		
10	A	1	Total	C	H	N	O	0	0
			14	3	9	1	1		
10	A	1	Total	C	H	N	O	0	0
			14	3	9	1	1		
10	B	1	Total	C	H	N	O	0	0
			14	3	9	1	1		
10	B	1	Total	C	H	N	O	0	0
			14	3	9	1	1		
10	B	1	Total	C	H	N	O	0	0
			14	3	9	1	1		

- Molecule 11 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	A	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
11	A	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
11	B	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
11	B	1	Total	C	H	O	S	0	0
			10	2	6	1	1		
11	B	1	Total	C	H	O	S	0	0
			10	2	6	1	1		

- Molecule 12 is water.

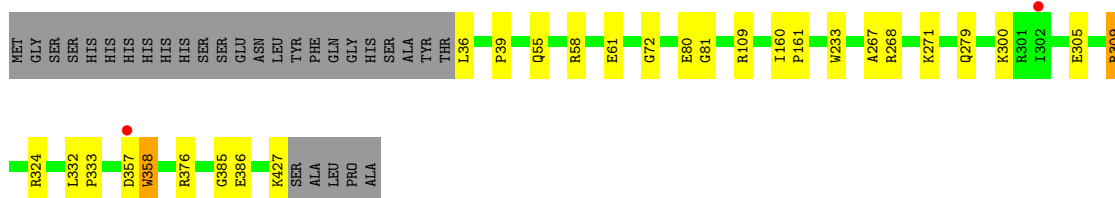
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	219	Total	O	0	1
			220	220		
12	B	193	Total	O	0	0
			193	193		

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.

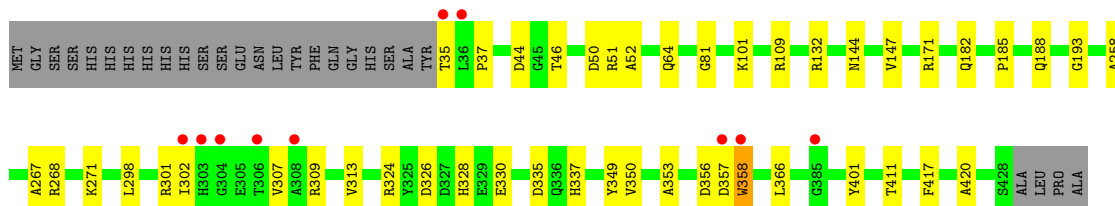
- Molecule 1: glucuronoyl esterase OtCE15A

Chain A: 



- Molecule 1: glucuronoyl esterase OtCE15A

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.72Å 87.61Å 173.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.45 – 1.89 44.45 – 1.89	Depositor EDS
% Data completeness (in resolution range)	98.6 (44.45-1.89) 90.6 (44.45-1.89)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.35 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.162 , 0.215 0.165 , 0.217	Depositor DCC
R_{free} test set	1988 reflections (3.09%)	wwPDB-VP
Wilson B-factor (Å ²)	28.5	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13299	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 4.32% 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, EDO, MG, GCU, M55, CL, PGE, TMO, DMS

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	0.54	1/3171 (0.0%)	0.65	1/4333 (0.0%)
1	B	0.48	0/3187	0.61	0/4352
All	All	0.51	1/6358 (0.0%)	0.63	1/8685 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	GLN	C-O	-5.26	1.18	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	55	GLN	N-CA-C	5.33	117.09	111.28

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	3080	2947	2953	27	0
1	B	3096	2940	2971	50	0
2	A	13	9	9	2	0
2	B	13	9	9	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
4	A	20	16	0	0	0
5	A	13	18	18	1	0
6	A	76	114	114	4	0
6	B	60	90	90	11	0
7	A	28	40	40	1	0
7	B	14	20	20	5	0
8	A	40	56	56	9	0
8	B	10	14	14	0	0
9	A	1	0	0	0	0
10	A	15	27	27	2	0
10	B	20	36	36	5	0
11	A	8	12	12	0	0
11	B	12	18	18	0	0
12	A	220	0	0	3	0
12	B	193	0	0	6	0
All	All	6933	6366	6387	84	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 7.

All (84) 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:B:328:HIS:HD2	1:B:330:GLU:OE2	1.65	0.78
1:B:35:THR:HG23	1:B:37:PRO:HD2	1.68	0.74
1:B:35:THR:HG22	1:B:337:HIS:CE1	2.25	0.72
1:B:358[B]:TRP:HE1	2:B:501:GCU:HO2	1.39	0.70
1:B:171:ARG:NH1	12:B:601:HOH:O	2.24	0.70
1:B:51:ARG:NH2	10:B:521:TMO:HAA	2.07	0.70
1:B:171:ARG:HG2	10:B:520:TMO:HAD	1.78	0.65
1:A:357[B]:ASP:N	1:A:357[B]:ASP:OD1	2.26	0.64
1:A:39:PRO:CD	8:A:531:PGE:H12	2.27	0.64
1:B:358[A]:TRP:CD1	2:B:501:GCU:HO2	2.19	0.61
1:A:58:ARG:NH1	1:A:61:GLU:OE1	2.34	0.60
1:B:267:ALA:HB1	2:B:501:GCU:C6	2.31	0.60
1:B:258:ALA:H	6:B:507:EDO:H11	1.66	0.60
1:B:358[A]:TRP:CD1	2:B:501:GCU:O2	2.55	0.60
10:B:523:TMO:HABB	12:B:745:HOH:O	2.01	0.60
1:A:385:GLY:HA2	1:A:386:GLU:OE1	2.02	0.59
1:B:411:THR:HA	7:B:517:PEG:H32	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:THR:HG21	1:B:335:ASP:CB	2.32	0.59
1:A:39:PRO:HD2	8:A:531:PGE:H12	1.86	0.57
1:A:267:ALA:HB1	2:A:501:GCU:C6	2.36	0.55
1:A:36:LEU:N	12:A:605:HOH:O	2.38	0.55
1:B:309:ARG:O	1:B:313:VAL:HG23	2.07	0.54
1:B:50:ASP:OD2	1:B:52:ALA:N	2.41	0.54
1:B:420:ALA:HB3	6:B:504:EDO:O1	2.08	0.54
1:B:101:LYS:NZ	12:B:606:HOH:O	2.41	0.54
1:B:182:GLN:HB3	7:B:517:PEG:H22	1.91	0.53
1:A:80:GLU:H	6:A:521:EDO:HO1	1.58	0.52
1:A:81:GLY:O	1:A:109:ARG:HD2	2.09	0.52
1:A:279:GLN:OE1	10:A:534:TMO:HAB	2.09	0.52
1:A:309:ARG:HG3	1:A:309:ARG:HH11	1.74	0.52
1:B:81:GLY:O	1:B:109[B]:ARG:HD2	2.10	0.52
10:A:534:TMO:HAAA	12:A:789:HOH:O	2.10	0.52
1:B:358[A]:TRP:HD1	2:B:501:GCU:HO2	1.56	0.51
1:A:268:ARG:HA	1:A:271:LYS:HE2	1.93	0.51
1:B:417:PHE:O	6:B:504:EDO:O1	2.24	0.51
1:B:328:HIS:CD2	1:B:330:GLU:OE2	2.56	0.50
1:B:51:ARG:HH21	10:B:521:TMO:HAA	1.74	0.50
1:B:301:ARG:HD2	1:B:366:LEU:HD12	1.94	0.50
1:B:44:ASP:OD1	1:B:44:ASP:N	2.41	0.50
1:B:64:GLN:HG2	12:B:639:HOH:O	2.13	0.49
1:B:268:ARG:HA	1:B:271:LYS:HE2	1.95	0.48
1:B:358[A]:TRP:HD1	2:B:501:GCU:O2	1.93	0.48
1:B:258:ALA:H	6:B:507:EDO:C1	2.27	0.47
1:B:350:VAL:O	1:B:401:TYR:HA	2.14	0.47
1:A:358[B]:TRP:NE1	2:A:501:GCU:O2	2.47	0.47
1:A:72:GLY:HA3	1:A:233:TRP:HA	1.95	0.47
1:B:182:GLN:CB	7:B:517:PEG:H22	2.44	0.47
1:B:171:ARG:HG2	10:B:520:TMO:CAD	2.45	0.47
1:B:324:ARG:HH11	6:B:510:EDO:H21	1.80	0.46
1:B:301:ARG:C	1:B:302:ILE:HG13	2.40	0.46
1:B:356[A]:ASP:OD1	1:B:357[A]:ASP:O	2.34	0.46
7:A:525:PEG:O1	7:A:525:PEG:H42	2.16	0.45
1:B:35:THR:HB	1:B:298:LEU:HD22	1.98	0.45
1:B:328:HIS:CE1	6:B:510:EDO:HO1	2.30	0.45
1:A:36:LEU:HB2	8:A:531:PGE:H32	1.99	0.45
1:B:188:GLN:H	6:B:516:EDO:H22	1.82	0.45
1:A:39:PRO:HD3	8:A:531:PGE:H12	1.96	0.45
1:A:309:ARG:HG3	1:A:309:ARG:NH1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:ASN:O	1:B:147:VAL:HG22	2.17	0.45
1:A:160[B]:ILE:HG23	1:A:161:PRO:HD2	1.98	0.45
1:A:300:LYS:HE2	1:A:332:LEU:HB2	1.98	0.44
1:B:182:GLN:H	1:B:182:GLN:CD	2.25	0.44
1:A:305:GLU:HB2	1:A:358[A]:TRP:CE2	2.53	0.44
1:B:193:GLY:HA3	7:B:518:PEG:H42	2.00	0.43
1:A:333:PRO:O	6:A:506:EDO:H12	2.19	0.43
1:B:324:ARG:HD3	6:B:510:EDO:O2	2.19	0.43
1:A:376:ARG:CB	8:A:528:PGE:H22	2.49	0.43
1:A:39:PRO:HD2	8:A:531:PGE:C1	2.48	0.43
1:B:307:VAL:HG12	1:B:326:ASP:OD1	2.19	0.43
1:A:36:LEU:HD12	8:A:531:PGE:H4	2.01	0.42
1:A:324:ARG:O	1:A:324:ARG:HG2	2.20	0.42
1:B:353:ALA:HB3	1:B:356[B]:ASP:HB2	2.02	0.42
1:A:80:GLU:N	6:A:521:EDO:O1	2.42	0.41
1:B:349:TYR:CE2	6:B:504:EDO:H21	2.55	0.41
1:B:132:ARG:NH1	12:B:616:HOH:O	2.53	0.41
5:A:504:PG4:H72	12:B:675:HOH:O	2.19	0.41
8:A:528:PGE:H2	8:A:528:PGE:C5	2.50	0.41
1:B:302:ILE:HD12	1:B:302:ILE:O	2.21	0.41
6:A:510:EDO:H11	12:A:794:HOH:O	2.20	0.41
1:B:185:PRO:HB2	6:B:516:EDO:H21	2.02	0.41
1:B:188:GLN:H	6:B:516:EDO:C2	2.34	0.41
8:A:528:PGE:H2	8:A:528:PGE:O3	2.21	0.40
1:A:305:GLU:HG3	1:A:358[A]:TRP:CZ2	2.56	0.40
1:B:182:GLN:HB3	7:B:517:PEG:H31	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	395/421 (94%)	381 (96%)	12 (3%)	2 (0%)	24	16
1	B	397/421 (94%)	381 (96%)	16 (4%)	0	100	100
All	All	792/842 (94%)	762 (96%)	28 (4%)	2 (0%)	48	29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358[A]	TRP
1	A	358[B]	TRP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	302/321 (94%)	300 (99%)	2 (1%)	76	78
1	B	304/321 (95%)	301 (99%)	3 (1%)	68	70
All	All	606/642 (94%)	601 (99%)	5 (1%)	76	75

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	309	ARG
1	A	427	LYS
1	B	46	THR
1	B	358[A]	TRP
1	B	358[B]	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	HIS
1	A	55	GLN
1	A	289	ASN
1	B	55	GLN

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Mol	Chain	Res	Type
1	B	303	HIS
1	B	413	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 63 ligands modelled in this entry, 2 are monoatomic - leaving 61 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	PG4	A	504	-	12,12,12	0.31	0	11,11,11	0.19	0
6	EDO	B	503	-	3,3,3	0.22	0	2,2,2	0.40	0
6	EDO	A	512	-	3,3,3	0.18	0	2,2,2	0.15	0
6	EDO	B	507	-	3,3,3	0.14	0	2,2,2	0.13	0
6	EDO	A	510	-	3,3,3	0.10	0	2,2,2	0.09	0
10	TMO	B	523	-	4,4,4	7.73	1 (25%)	6,6,6	0.43	0
6	EDO	B	502	-	3,3,3	0.11	0	2,2,2	0.31	0
6	EDO	A	520	-	3,3,3	0.10	0	2,2,2	0.11	0
7	PEG	A	527	-	6,6,6	0.30	0	5,5,5	0.25	0
10	TMO	A	533	-	4,4,4	6.49	1 (25%)	6,6,6	0.28	0
6	EDO	A	521	-	3,3,3	0.07	0	2,2,2	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	PGE	A	529	-	9,9,9	0.16	0	8,8,8	0.14	0
8	PGE	A	531	-	9,9,9	0.28	0	8,8,8	0.19	0
2	GCU	B	501	-	13,13,13	0.98	1 (7%)	18,19,19	1.11	3 (16%)
6	EDO	A	505	-	3,3,3	0.34	0	2,2,2	0.44	0
6	EDO	B	506	-	3,3,3	0.12	0	2,2,2	0.21	0
4	M55	A	503	-	21,21,21	1.09	2 (9%)	29,29,29	1.32	2 (6%)
7	PEG	A	526	-	6,6,6	0.29	0	5,5,5	0.18	0
6	EDO	A	516	-	3,3,3	0.10	0	2,2,2	0.22	0
6	EDO	A	517	-	3,3,3	0.07	0	2,2,2	0.15	0
6	EDO	B	509	-	3,3,3	0.07	0	2,2,2	0.11	0
7	PEG	A	525	-	6,6,6	0.25	0	5,5,5	0.27	0
6	EDO	A	508	-	3,3,3	0.09	0	2,2,2	0.15	0
6	EDO	A	509	-	3,3,3	0.11	0	2,2,2	0.21	0
6	EDO	A	522	-	3,3,3	0.12	0	2,2,2	0.24	0
8	PGE	B	519	-	9,9,9	0.32	0	8,8,8	0.17	0
6	EDO	B	515	-	3,3,3	0.14	0	2,2,2	0.08	0
6	EDO	A	513	-	3,3,3	0.29	0	2,2,2	0.37	0
11	DMS	B	524	-	3,3,3	0.72	0	3,3,3	1.07	0
11	DMS	B	526	-	3,3,3	0.72	0	3,3,3	0.91	0
8	PGE	A	530	-	9,9,9	0.27	0	8,8,8	0.31	0
6	EDO	B	514	-	3,3,3	0.09	0	2,2,2	0.13	0
6	EDO	A	514	-	3,3,3	0.07	0	2,2,2	0.27	0
11	DMS	A	537	-	3,3,3	0.75	0	3,3,3	0.79	0
8	PGE	A	528	-	9,9,9	0.28	0	8,8,8	0.15	0
11	DMS	A	536	-	3,3,3	0.69	0	3,3,3	0.56	0
6	EDO	A	518	-	3,3,3	0.11	0	2,2,2	0.20	0
6	EDO	A	507	-	3,3,3	0.04	0	2,2,2	0.13	0
6	EDO	A	515	-	3,3,3	0.12	0	2,2,2	0.01	0
2	GCU	A	501	-	13,13,13	1.04	1 (7%)	18,19,19	1.08	1 (5%)
11	DMS	B	525	-	3,3,3	0.63	0	3,3,3	0.77	0
10	TMO	B	522	-	4,4,4	6.09	1 (25%)	6,6,6	0.39	0
6	EDO	B	504	-	3,3,3	0.27	0	2,2,2	0.19	0
10	TMO	A	535	-	4,4,4	6.11	1 (25%)	6,6,6	0.39	0
7	PEG	B	517	-	6,6,6	0.31	0	5,5,5	0.29	0
6	EDO	A	511	-	3,3,3	0.15	0	2,2,2	0.05	0
6	EDO	B	510	-	3,3,3	0.07	0	2,2,2	0.04	0
6	EDO	B	505	-	3,3,3	0.07	0	2,2,2	0.14	0
6	EDO	B	508	-	3,3,3	0.13	0	2,2,2	0.06	0
6	EDO	B	513	-	3,3,3	0.04	0	2,2,2	0.04	0
7	PEG	A	524	-	6,6,6	0.21	0	5,5,5	0.17	0
10	TMO	A	534	-	4,4,4	6.46	1 (25%)	6,6,6	0.37	0
6	EDO	A	519	-	3,3,3	0.08	0	2,2,2	0.29	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	B	512	-	3,3,3	0.07	0	2,2,2	0.12	0
6	EDO	B	516	-	3,3,3	0.11	0	2,2,2	0.23	0
10	TMO	B	520	-	4,4,4	6.99	1 (25%)	6,6,6	0.72	0
7	PEG	B	518	-	6,6,6	0.13	0	5,5,5	0.23	0
10	TMO	B	521	-	4,4,4	6.21	1 (25%)	6,6,6	0.47	0
6	EDO	A	523	-	3,3,3	0.12	0	2,2,2	0.03	0
6	EDO	A	506	-	3,3,3	0.03	0	2,2,2	0.13	0
6	EDO	B	511	-	3,3,3	0.14	0	2,2,2	0.10	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	PG4	A	504	-	-	2/10/10/10	-
6	EDO	B	503	-	-	0/1/1/1	-
6	EDO	A	512	-	-	1/1/1/1	-
6	EDO	B	507	-	-	1/1/1/1	-
6	EDO	A	510	-	-	0/1/1/1	-
6	EDO	B	502	-	-	0/1/1/1	-
6	EDO	A	520	-	-	1/1/1/1	-
7	PEG	A	527	-	-	0/4/4/4	-
6	EDO	A	521	-	-	0/1/1/1	-
8	PGE	A	529	-	-	3/7/7/7	-
8	PGE	A	531	-	-	2/7/7/7	-
2	GCU	B	501	-	-	2/4/24/24	0/1/1/1
6	EDO	A	505	-	-	0/1/1/1	-
6	EDO	B	506	-	-	1/1/1/1	-
4	M55	A	503	-	-	0/9/29/29	0/2/2/2
7	PEG	A	526	-	-	0/4/4/4	-
6	EDO	A	516	-	-	0/1/1/1	-
6	EDO	A	517	-	-	0/1/1/1	-
6	EDO	B	509	-	-	0/1/1/1	-
7	PEG	A	525	-	-	2/4/4/4	-
6	EDO	A	508	-	-	0/1/1/1	-
6	EDO	A	509	-	-	0/1/1/1	-
6	EDO	A	522	-	-	0/1/1/1	-
8	PGE	B	519	-	-	2/7/7/7	-
6	EDO	B	515	-	-	1/1/1/1	-
6	EDO	A	513	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	PGE	A	530	-	-	1/7/7/7	-
6	EDO	B	514	-	-	1/1/1/1	-
6	EDO	A	514	-	-	1/1/1/1	-
8	PGE	A	528	-	-	2/7/7/7	-
6	EDO	A	518	-	-	0/1/1/1	-
6	EDO	A	507	-	-	0/1/1/1	-
6	EDO	A	515	-	-	1/1/1/1	-
2	GCU	A	501	-	-	4/4/24/24	0/1/1/1
6	EDO	B	504	-	-	0/1/1/1	-
7	PEG	B	517	-	-	1/4/4/4	-
6	EDO	A	511	-	-	0/1/1/1	-
6	EDO	B	510	-	-	0/1/1/1	-
6	EDO	B	505	-	-	0/1/1/1	-
6	EDO	B	508	-	-	0/1/1/1	-
6	EDO	B	513	-	-	0/1/1/1	-
7	PEG	A	524	-	-	0/4/4/4	-
6	EDO	A	519	-	-	1/1/1/1	-
6	EDO	B	512	-	-	0/1/1/1	-
6	EDO	B	516	-	-	1/1/1/1	-
7	PEG	B	518	-	-	1/4/4/4	-
6	EDO	A	523	-	-	0/1/1/1	-
6	EDO	A	506	-	-	0/1/1/1	-
6	EDO	B	511	-	-	0/1/1/1	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	523	TMO	OAE-NAC	-15.34	1.21	1.42
10	B	520	TMO	OAE-NAC	-13.93	1.23	1.42
10	A	533	TMO	OAE-NAC	-12.90	1.25	1.42
10	A	534	TMO	OAE-NAC	-12.86	1.25	1.42
10	B	521	TMO	OAE-NAC	-12.27	1.25	1.42
10	A	535	TMO	OAE-NAC	-12.17	1.26	1.42
10	B	522	TMO	OAE-NAC	-12.14	1.26	1.42
4	A	503	M55	O6B-C6	3.34	1.40	1.33
2	A	501	GCU	O6B-C6	-2.43	1.22	1.30
4	A	503	M55	O6B-C01	-2.23	1.41	1.45
2	B	501	GCU	C5-C6	-2.13	1.48	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	M55	O6B-C6-C5	4.45	119.53	110.57
2	A	501	GCU	O4-C4-C5	3.21	117.09	109.76
4	A	503	M55	C4-C5-C6	-3.08	104.97	111.49
2	B	501	GCU	O4-C4-C5	2.23	114.86	109.76
2	B	501	GCU	C4-C3-C2	-2.07	107.19	110.83
2	B	501	GCU	O6B-C6-C5	2.06	121.09	113.64

There are no chirality outliers.

All (32) torsion outliers are listed below:

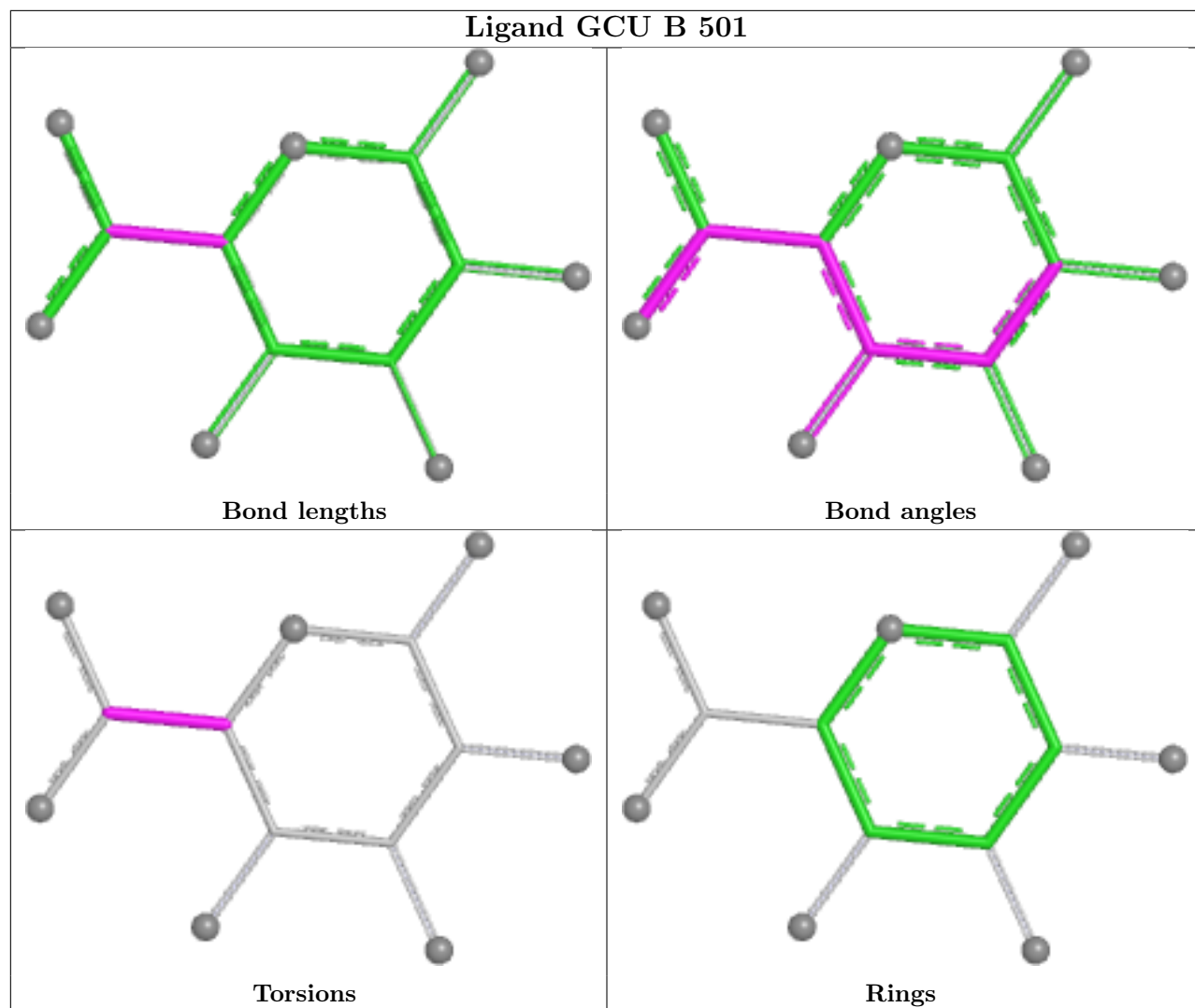
Mol	Chain	Res	Type	Atoms
5	A	504	PG4	O4-C7-C8-O5
6	B	514	EDO	O1-C1-C2-O2
8	A	529	PGE	O1-C1-C2-O2
6	A	520	EDO	O1-C1-C2-O2
8	A	531	PGE	O1-C1-C2-O2
6	A	515	EDO	O1-C1-C2-O2
8	A	528	PGE	O3-C5-C6-O4
7	B	518	PEG	C4-C3-O2-C2
8	A	530	PGE	C1-C2-O2-C3
2	A	501	GCU	C4-C5-C6-O6A
2	A	501	GCU	C4-C5-C6-O6B
7	A	525	PEG	O2-C3-C4-O4
8	A	531	PGE	C4-C3-O2-C2
8	A	529	PGE	C4-C3-O2-C2
6	B	515	EDO	O1-C1-C2-O2
7	B	517	PEG	O1-C1-C2-O2
7	A	525	PEG	C4-C3-O2-C2
6	A	512	EDO	O1-C1-C2-O2
6	B	506	EDO	O1-C1-C2-O2
6	B	507	EDO	O1-C1-C2-O2
6	B	516	EDO	O1-C1-C2-O2
5	A	504	PG4	O2-C3-C4-O3
8	B	519	PGE	O2-C3-C4-O3
6	A	514	EDO	O1-C1-C2-O2
6	A	519	EDO	O1-C1-C2-O2
8	A	529	PGE	O3-C5-C6-O4
8	A	528	PGE	C3-C4-O3-C5
2	A	501	GCU	O5-C5-C6-O6A
2	A	501	GCU	O5-C5-C6-O6B
2	B	501	GCU	O5-C5-C6-O6A
2	B	501	GCU	O5-C5-C6-O6B
8	B	519	PGE	C1-C2-O2-C3

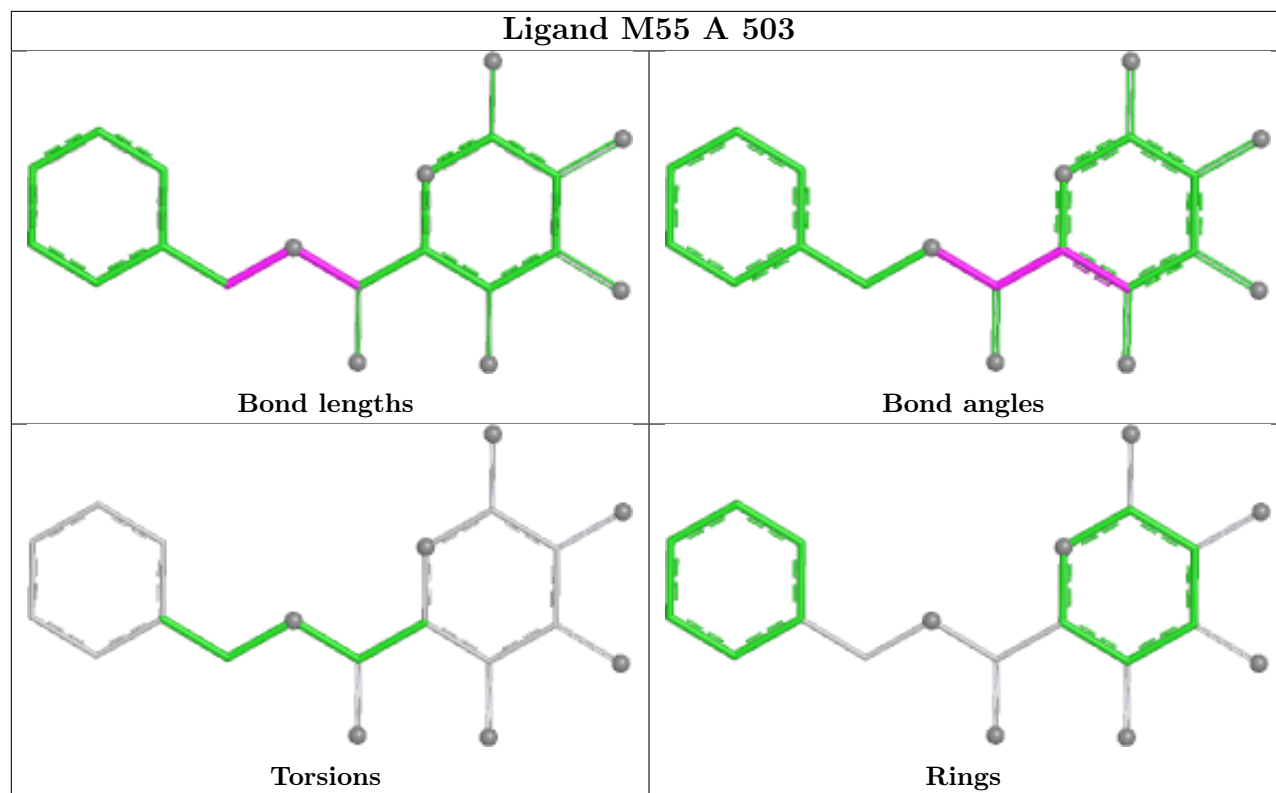
There are no ring outliers.

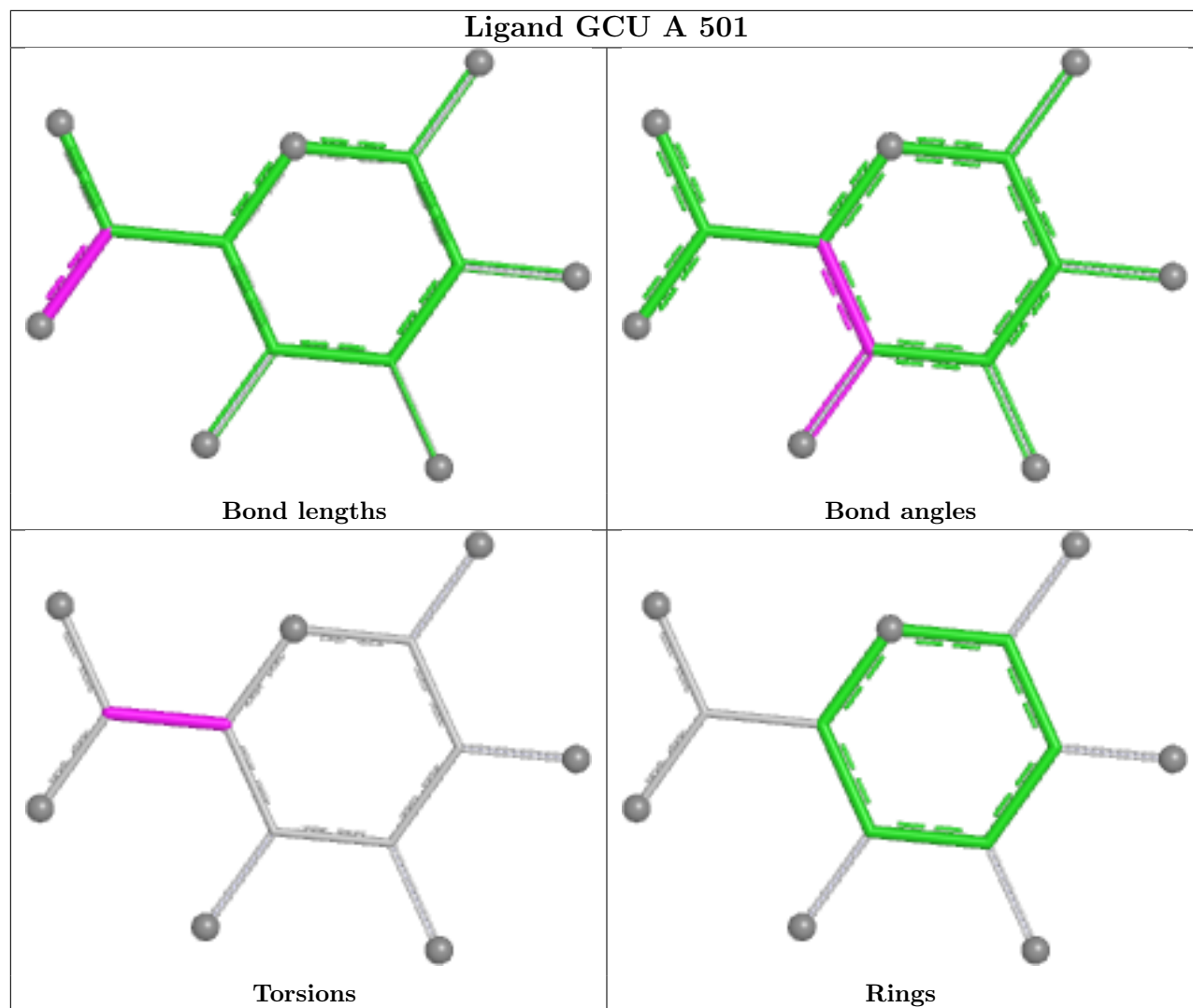
19 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	PG4	1	0
6	B	507	EDO	2	0
6	A	510	EDO	1	0
10	B	523	TMO	1	0
6	A	521	EDO	2	0
8	A	531	PGE	6	0
2	B	501	GCU	6	0
7	A	525	PEG	1	0
8	A	528	PGE	3	0
2	A	501	GCU	2	0
6	B	504	EDO	3	0
7	B	517	PEG	4	0
6	B	510	EDO	3	0
10	A	534	TMO	2	0
6	B	516	EDO	3	0
10	B	520	TMO	2	0
7	B	518	PEG	1	0
10	B	521	TMO	2	0
6	A	506	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	392/421 (93%)	-0.33	2 (0%) 87 89	17, 34, 61, 87	5 (1%)
1	B	394/421 (93%)	-0.02	10 (2%) 58 62	17, 40, 80, 102	5 (1%)
All	All	786/842 (93%)	-0.17	12 (1%) 72 75	17, 37, 71, 102	10 (1%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	357[A]	ASP	7.5
1	B	358[A]	TRP	5.5
1	B	35	THR	4.2
1	B	302	ILE	3.7
1	B	36	LEU	2.9
1	B	303	HIS	2.8
1	B	385	GLY	2.3
1	B	304	GLY	2.2
1	B	306	THR	2.2
1	A	302	ILE	2.1
1	B	308	ALA	2.1
1	A	357[A]	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	EDO	A	523	4/4	0.60	0.16	63,75,90,90	0
8	PGE	A	529	10/10	0.64	0.18	53,76,88,95	0
6	EDO	B	515	4/4	0.65	0.26	67,92,149,149	0
8	PGE	B	519	10/10	0.68	0.20	52,74,83,90	0
6	EDO	B	513	4/4	0.70	0.12	68,82,89,96	0
6	EDO	A	512	4/4	0.70	0.17	53,71,87,90	0
7	PEG	A	527	7/7	0.71	0.18	51,64,82,82	0
7	PEG	A	526	7/7	0.72	0.16	59,85,105,105	0
6	EDO	A	508	4/4	0.76	0.17	66,79,91,91	0
8	PGE	A	531	10/10	0.76	0.15	41,66,72,75	0
7	PEG	A	524	7/7	0.76	0.13	51,74,82,88	0
11	DMS	A	537	4/4	0.77	0.16	51,70,84,93	0
6	EDO	B	511	4/4	0.78	0.14	61,73,87,87	0
6	EDO	B	508	4/4	0.78	0.17	50,74,89,89	0
6	EDO	A	518	4/4	0.79	0.14	62,77,94,94	0
10	TMO	B	521	5/5	0.80	0.16	63,75,86,86	0
6	EDO	A	513	4/4	0.80	0.13	55,70,84,84	0
11	DMS	B	525	4/4	0.80	0.14	49,59,73,90	0
6	EDO	B	512	4/4	0.81	0.14	64,77,88,88	0
6	EDO	B	505	4/4	0.81	0.12	65,78,86,87	0
6	EDO	A	511	4/4	0.82	0.16	57,68,73,73	0
7	PEG	B	517	7/7	0.82	0.14	40,59,71,71	0
6	EDO	A	515	4/4	0.83	0.11	48,58,70,82	0
5	PG4	A	504	13/13	0.83	0.14	39,60,73,73	0
10	TMO	A	533	5/5	0.83	0.14	54,65,78,81	0
6	EDO	B	506	4/4	0.84	0.12	53,65,82,84	0
7	PEG	A	525	7/7	0.84	0.12	56,68,81,81	0
6	EDO	A	506	4/4	0.84	0.13	51,63,65,76	0
6	EDO	B	509	4/4	0.84	0.12	52,62,68,75	0
6	EDO	B	510	4/4	0.84	0.12	72,86,91,96	0
7	PEG	B	518	7/7	0.84	0.14	47,61,77,77	0
8	PGE	A	528	10/10	0.84	0.13	48,66,93,100	0
8	PGE	A	530	10/10	0.85	0.13	39,61,79,84	0
6	EDO	A	510	4/4	0.86	0.12	50,60,67,69	0
6	EDO	A	522	4/4	0.86	0.17	48,63,103,103	0
10	TMO	A	535	5/5	0.86	0.14	49,63,90,90	0
6	EDO	B	514	4/4	0.87	0.12	54,68,83,86	0

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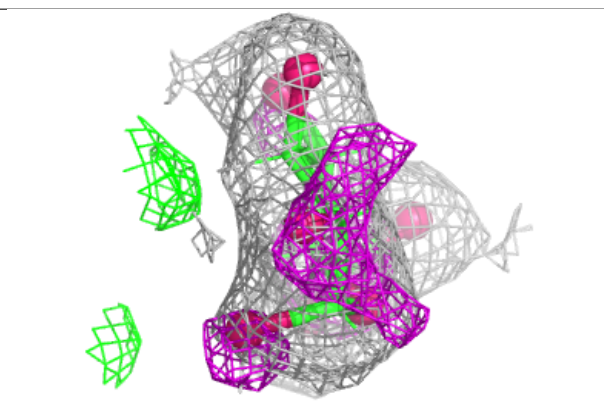
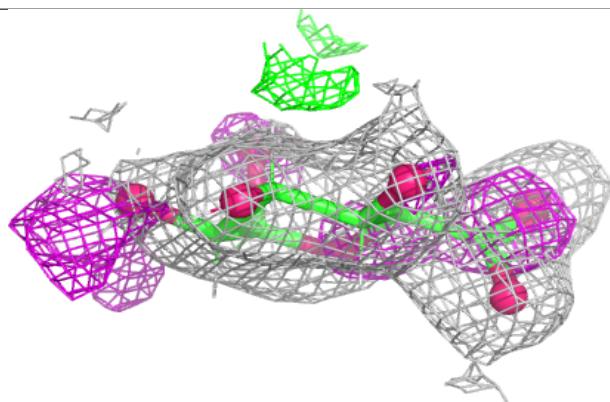
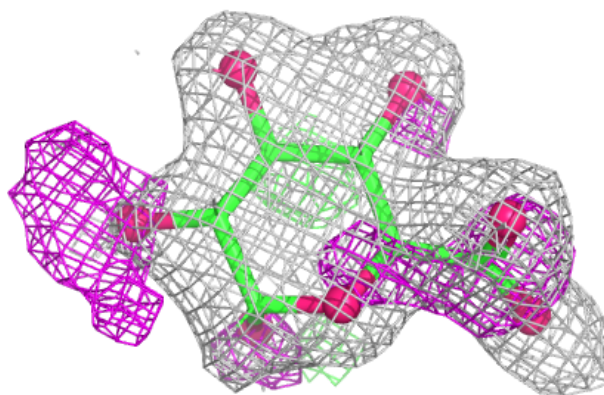
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	EDO	A	516	4/4	0.87	0.12	53,74,79,89	0
6	EDO	A	519	4/4	0.87	0.12	46,68,82,82	0
11	DMS	B	526	4/4	0.87	0.12	59,71,87,97	0
6	EDO	B	507	4/4	0.88	0.21	48,58,67,67	0
11	DMS	A	536	4/4	0.88	0.16	55,79,89,89	0
6	EDO	B	516	4/4	0.88	0.14	38,56,68,73	0
11	DMS	B	524	4/4	0.88	0.15	44,65,78,78	0
10	TMO	A	534	5/5	0.88	0.14	43,61,74,74	0
2	GCU	A	501	13/13	0.88	0.09	28,41,50,55	0
6	EDO	A	509	4/4	0.89	0.14	42,55,68,76	0
6	EDO	A	514	4/4	0.89	0.12	44,59,74,74	0
10	TMO	B	520	5/5	0.89	0.13	43,54,70,70	0
6	EDO	B	502	4/4	0.89	0.10	59,75,90,90	0
10	TMO	B	522	5/5	0.89	0.12	55,66,79,79	0
6	EDO	A	520	4/4	0.90	0.10	49,65,72,79	0
6	EDO	B	504	4/4	0.90	0.29	42,50,57,62	0
2	GCU	B	501	13/13	0.90	0.08	42,52,63,69	0
6	EDO	A	517	4/4	0.90	0.09	46,57,73,88	0
3	CL	A	502	1/1	0.91	0.11	54,54,54,54	0
10	TMO	B	523	5/5	0.92	0.12	41,58,71,71	0
6	EDO	A	521	4/4	0.92	0.09	52,62,69,69	0
6	EDO	A	507	4/4	0.93	0.10	50,60,71,77	0
6	EDO	A	505	4/4	0.93	0.13	25,40,48,58	0
4	M55	A	503	20/20	0.93	0.08	40,54,69,70	0
6	EDO	B	503	4/4	0.94	0.10	26,48,57,60	0
9	MG	A	532	1/1	0.97	0.12	48,48,48,48	0

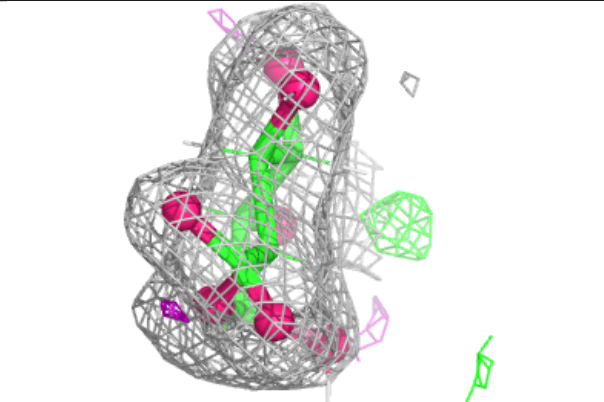
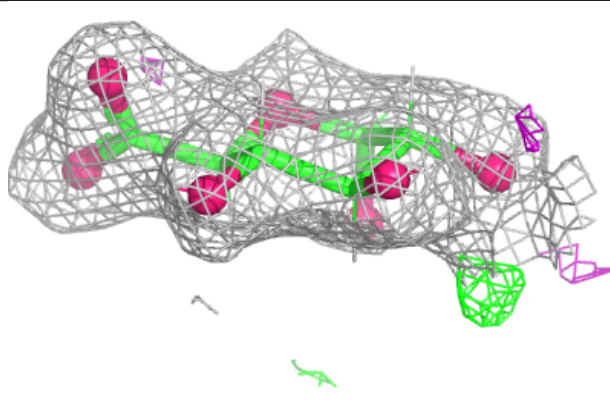
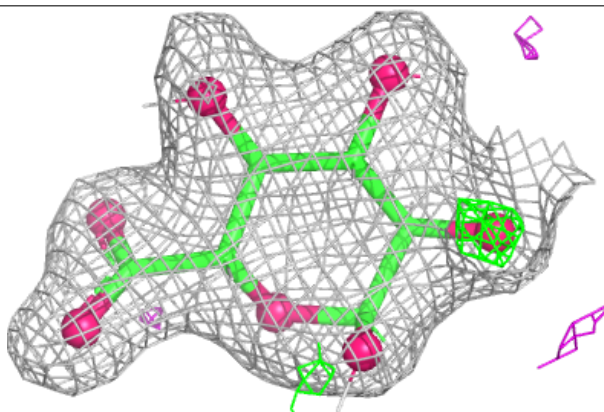
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GCU A 501:

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

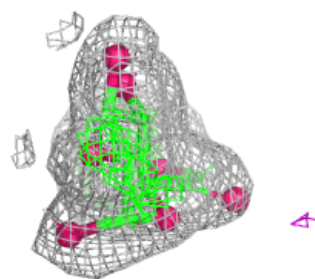
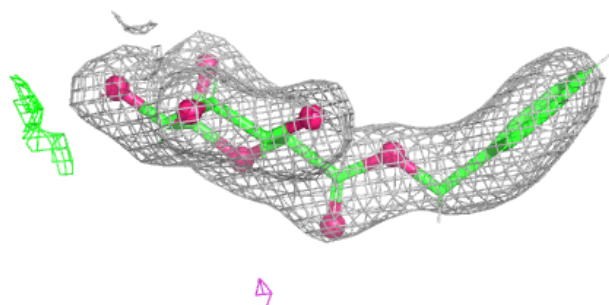
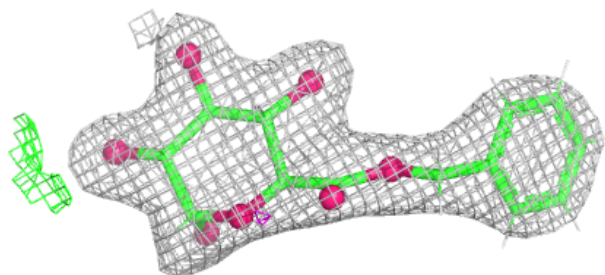
**Electron density around GCU B 501:**

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



Electron density around M55 A 503:

$2mF_o-DF_c$ (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.