



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:41 PM UTC

PDB ID : 9G5G / pdb_00009g5g
Title : Glycoside Hydrolase Family 157 from Labilicabulum antarcticum (LaGH157)
in complex with Laminaribiose
Authors : Caseiro, C.; Alves, V.D.; Carvalho, A.L.; Bule, P.
Deposited on : 2024-07-16
Resolution : 2.71 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

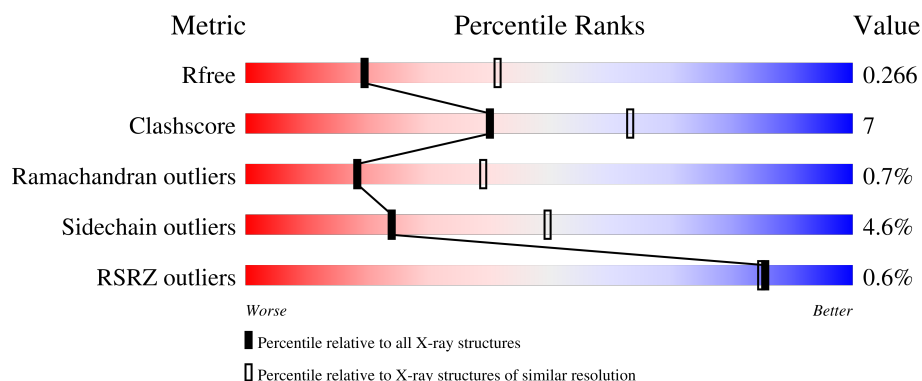
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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	537	80% 17% ..
1	B	537	% 75% 20% ...
1	C	537	% 80% 17% ..
1	D	537	80% 17% ..
2	E	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	F	2	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 17320 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 Glycoside hydrolase family 2 catalytic domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	528	Total	C	N	O	S	0	0	0
			4249	2719	685	830	15			
1	B	528	Total	C	N	O	S	0	0	0
			4249	2719	685	830	15			
1	C	528	Total	C	N	O	S	0	0	0
			4249	2719	685	830	15			
1	D	528	Total	C	N	O	S	0	0	0
			4249	2719	685	830	15			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A1Y1CQ89
A	530	LEU	-	expression tag	UNP A0A1Y1CQ89
A	531	GLU	-	expression tag	UNP A0A1Y1CQ89
A	532	HIS	-	expression tag	UNP A0A1Y1CQ89
A	533	HIS	-	expression tag	UNP A0A1Y1CQ89
A	534	HIS	-	expression tag	UNP A0A1Y1CQ89
A	535	HIS	-	expression tag	UNP A0A1Y1CQ89
A	536	HIS	-	expression tag	UNP A0A1Y1CQ89
A	537	HIS	-	expression tag	UNP A0A1Y1CQ89
B	1	MET	-	initiating methionine	UNP A0A1Y1CQ89
B	530	LEU	-	expression tag	UNP A0A1Y1CQ89
B	531	GLU	-	expression tag	UNP A0A1Y1CQ89
B	532	HIS	-	expression tag	UNP A0A1Y1CQ89
B	533	HIS	-	expression tag	UNP A0A1Y1CQ89
B	534	HIS	-	expression tag	UNP A0A1Y1CQ89
B	535	HIS	-	expression tag	UNP A0A1Y1CQ89
B	536	HIS	-	expression tag	UNP A0A1Y1CQ89
B	537	HIS	-	expression tag	UNP A0A1Y1CQ89
C	1	MET	-	initiating methionine	UNP A0A1Y1CQ89
C	530	LEU	-	expression tag	UNP A0A1Y1CQ89

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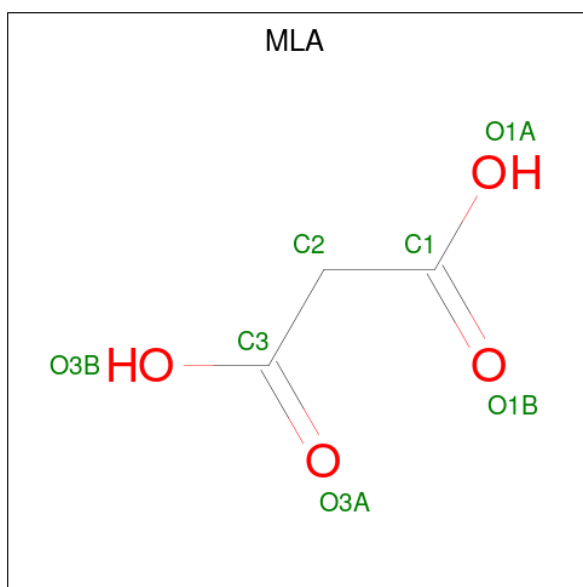
Chain	Residue	Modelled	Actual	Comment	Reference
C	531	GLU	-	expression tag	UNP A0A1Y1CQ89
C	532	HIS	-	expression tag	UNP A0A1Y1CQ89
C	533	HIS	-	expression tag	UNP A0A1Y1CQ89
C	534	HIS	-	expression tag	UNP A0A1Y1CQ89
C	535	HIS	-	expression tag	UNP A0A1Y1CQ89
C	536	HIS	-	expression tag	UNP A0A1Y1CQ89
C	537	HIS	-	expression tag	UNP A0A1Y1CQ89
D	1	MET	-	initiating methionine	UNP A0A1Y1CQ89
D	530	LEU	-	expression tag	UNP A0A1Y1CQ89
D	531	GLU	-	expression tag	UNP A0A1Y1CQ89
D	532	HIS	-	expression tag	UNP A0A1Y1CQ89
D	533	HIS	-	expression tag	UNP A0A1Y1CQ89
D	534	HIS	-	expression tag	UNP A0A1Y1CQ89
D	535	HIS	-	expression tag	UNP A0A1Y1CQ89
D	536	HIS	-	expression tag	UNP A0A1Y1CQ89
D	537	HIS	-	expression tag	UNP A0A1Y1CQ89

- Molecule 2 is an oligosaccharide called beta-D-glucopyranose-(1-3)-beta-D-glucopyranose.



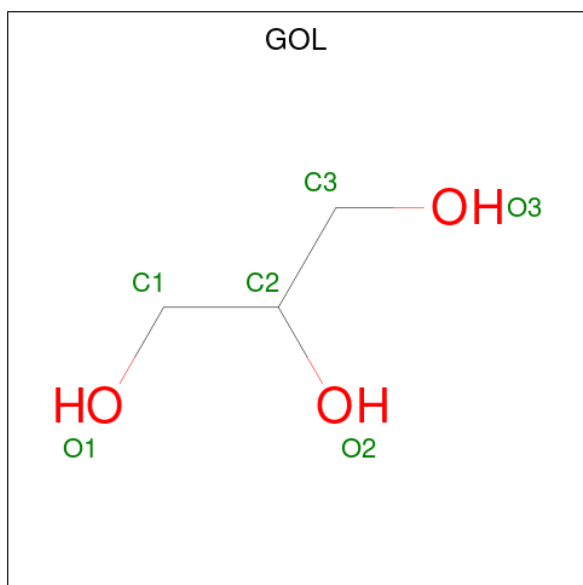
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	E	2	Total	C	O	0	0	0
			23	12	11			
2	F	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is MALONIC ACID (CCD ID: MLA) (formula: C₃H₄O₄).



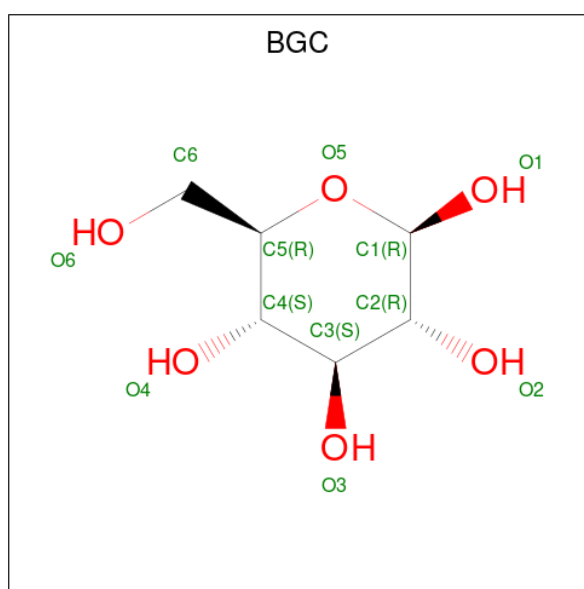
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	3	4		
3	A	1	Total	C	O	0	0
			7	3	4		
3	C	1	Total	C	O	0	0
			7	3	4		
3	D	1	Total	C	O	0	0
			7	3	4		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



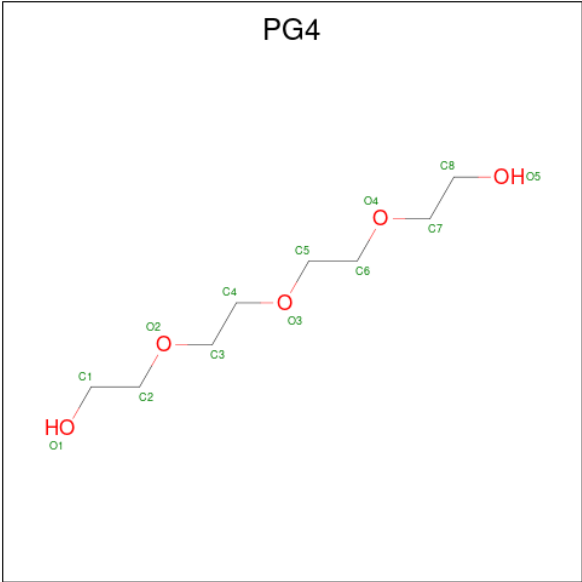
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is beta-D-glucopyranose (CCD ID: BGC) (formula: C₆H₁₂O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			12	6	6		
5	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 6 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C₈H₁₈O₅).



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

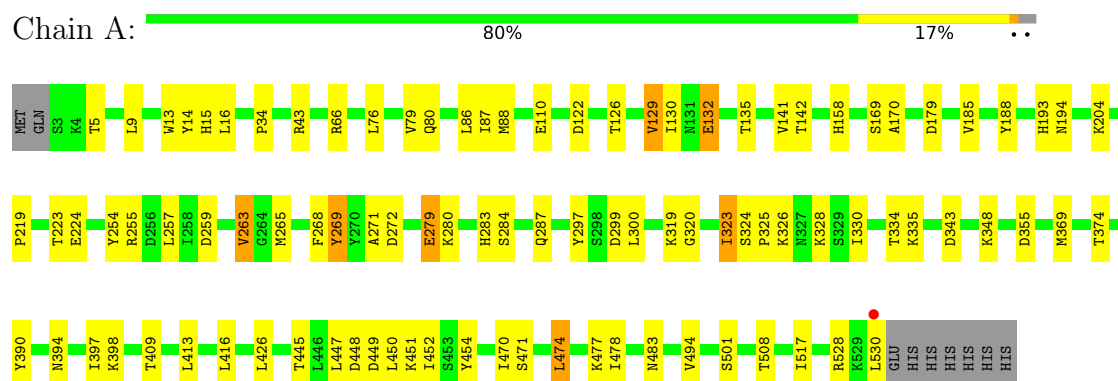
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	70	Total	O	0	0
			70	70		
7	B	35	Total	O	0	0
			35	35		
7	C	29	Total	O	0	0
			29	29		
7	D	55	Total	O	0	0
			55	55		

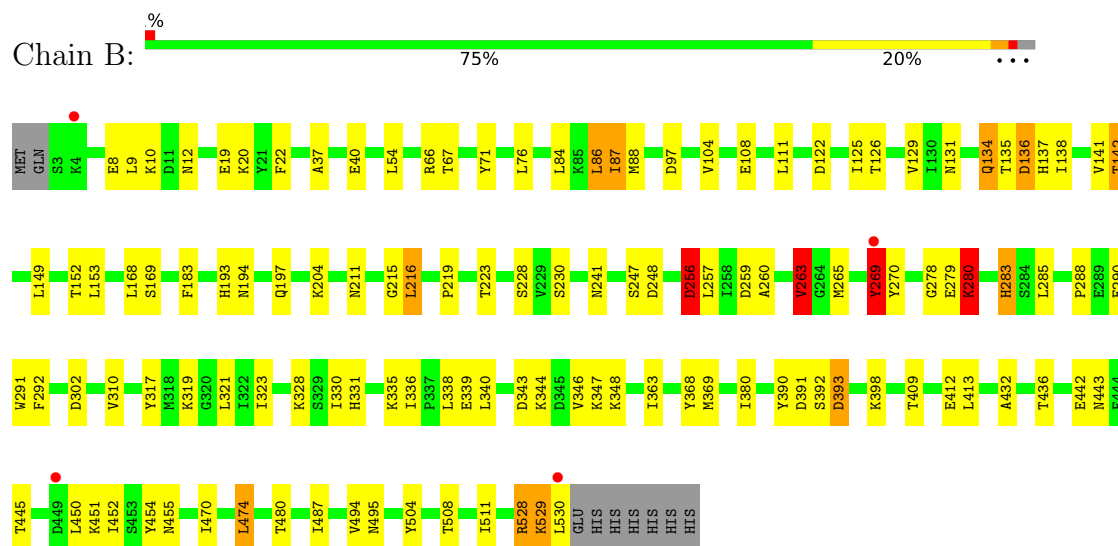
3 Residue-property plots

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.

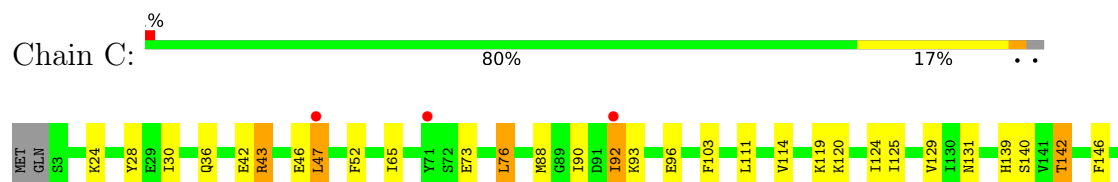
- Molecule 1: Glycoside hydrolase family 2 catalytic domain-containing protein

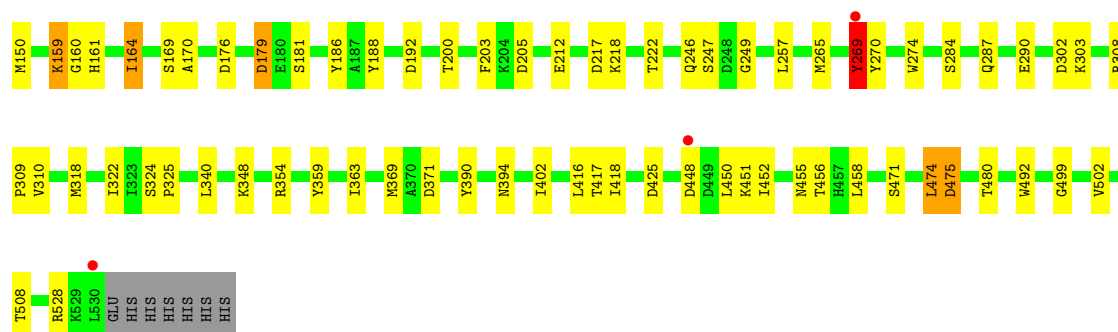


- Molecule 1: Glycoside hydrolase family 2 catalytic domain-containing protein



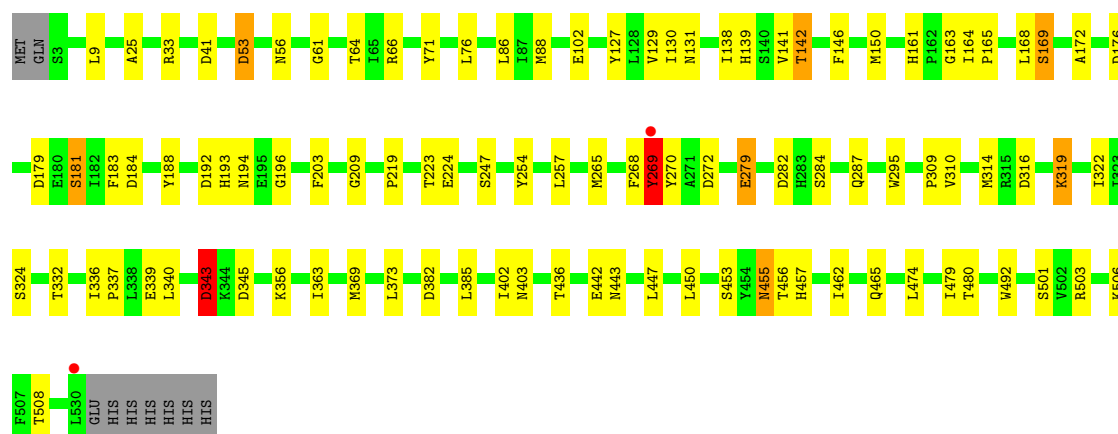
- Molecule 1: Glycoside hydrolase family 2 catalytic domain-containing protein





- Molecule 1: Glycoside hydrolase family 2 catalytic domain-containing protein

Chain D: 80% 17% ..



- Molecule 2: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain E: 50% 50%



- Molecule 2: beta-D-glucopyranose-(1-3)-beta-D-glucopyranose

Chain F: 50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	208.63Å 208.63Å 165.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	121.95 – 2.71 121.95 – 2.71	Depositor EDS
% Data completeness (in resolution range)	98.5 (121.95-2.71) 98.6 (121.95-2.71)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.211 , 0.272 0.202 , 0.266	Depositor DCC
R_{free} test set	3618 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	53.9	Xtriage
Anisotropy	1.411	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 74.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17320	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.48% 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: BGC, PG4, MLA, GOL

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	0.64	0/4348	1.23	13/5879 (0.2%)
1	B	0.57	0/4348	1.12	17/5879 (0.3%)
1	C	0.57	0/4348	1.09	7/5879 (0.1%)
1	D	0.61	0/4348	1.18	13/5879 (0.2%)
All	All	0.60	0/17392	1.16	50/23516 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	2
1	C	0	2
All	All	0	7

There are no bond length outliers.

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	GLU	CB-CA-C	-9.35	104.56	111.20
1	A	272	ASP	CA-CB-CG	7.97	120.57	112.60
1	B	122	ASP	CA-CB-CG	7.72	120.32	112.60
1	B	280	LYS	CB-CA-C	-7.02	95.63	110.31
1	A	122	ASP	CA-CB-CG	6.98	119.58	112.60
1	B	135	THR	CA-CB-OG1	-6.92	99.22	109.60
1	D	279	GLU	CB-CA-C	6.80	119.96	110.16
1	B	248	ASP	CA-CB-CG	6.75	119.36	112.60
1	A	135	THR	CA-CB-OG1	-6.64	99.64	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	508	THR	CA-CB-OG1	-6.54	99.80	109.60
1	C	205	ASP	CA-CB-CG	6.45	119.05	112.60
1	A	5	THR	CA-CB-OG1	-6.09	100.47	109.60
1	B	391	ASP	CA-CB-CG	6.03	118.63	112.60
1	B	270	TYR	N-CA-C	-5.95	105.69	113.12
1	C	212	GLU	CB-CG-CD	5.82	122.49	112.60
1	A	450	LEU	N-CA-CB	-5.81	100.45	109.69
1	A	297	TYR	CB-CA-C	5.78	119.40	109.51
1	B	263	VAL	N-CA-C	-5.76	107.13	112.43
1	A	279	GLU	CB-CG-CD	5.75	122.38	112.60
1	D	316	ASP	CA-CB-CG	5.74	118.34	112.60
1	D	332	THR	CA-CB-OG1	-5.74	101.00	109.60
1	B	292	PHE	CA-CB-CG	5.72	119.52	113.80
1	B	256	ASP	CA-CB-CG	5.62	118.22	112.60
1	D	268	PHE	N-CA-C	5.62	117.37	108.67
1	C	142	THR	CA-CB-OG1	-5.61	101.18	109.60
1	A	449	ASP	CA-CB-CG	5.61	118.21	112.60
1	B	278	GLY	CA-C-O	-5.58	117.39	122.24
1	B	134	GLN	CA-C-N	5.53	127.63	120.44
1	B	134	GLN	C-N-CA	5.53	127.63	120.44
1	B	409	THR	CA-CB-OG1	-5.51	101.33	109.60
1	A	397	ILE	N-CA-C	-5.45	108.53	113.71
1	D	41	ASP	CA-CB-CG	5.43	118.03	112.60
1	B	302	ASP	CA-CB-CG	5.41	118.01	112.60
1	C	425	ASP	CA-CB-CG	5.40	118.00	112.60
1	D	270	TYR	N-CA-CB	-5.28	102.39	110.26
1	B	152	THR	CA-CB-OG1	-5.26	101.70	109.60
1	D	53	ASP	CA-CB-CG	5.26	117.86	112.60
1	D	282	ASP	CA-CB-CG	5.24	117.84	112.60
1	D	343	ASP	CA-CB-CG	5.23	117.83	112.60
1	C	114	VAL	N-CA-CB	5.22	117.65	110.54
1	D	163	GLY	CA-C-N	-5.20	117.61	123.02
1	D	163	GLY	C-N-CA	-5.20	117.61	123.02
1	B	40	GLU	CB-CA-C	-5.19	101.94	110.08
1	B	97	ASP	CA-CB-CG	5.15	117.75	112.60
1	A	268	PHE	N-CA-CB	5.14	118.39	110.21
1	C	52	PHE	CA-CB-CG	5.10	118.90	113.80
1	C	475	ASP	CA-CB-CG	5.08	117.68	112.60
1	A	448	ASP	CA-CB-CG	5.07	117.67	112.60
1	A	355	ASP	CA-CB-CG	-5.05	107.55	112.60
1	D	272	ASP	CA-CB-CG	5.05	117.65	112.60

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	255	ARG	Sidechain
1	A	43	ARG	Sidechain
1	A	66	ARG	Sidechain
1	B	528	ARG	Sidechain
1	B	66	ARG	Sidechain
1	C	308	ARG	Sidechain
1	C	43	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4249	0	4139	40	0
1	B	4249	0	4139	64	0
1	C	4249	0	4139	64	0
1	D	4249	0	4139	56	0
2	E	23	0	21	2	0
2	F	23	0	21	1	0
3	A	14	0	4	0	0
3	C	7	0	2	1	0
3	D	7	0	2	0	0
4	A	12	0	16	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0
5	B	12	0	12	0	0
5	D	12	0	12	0	0
6	C	13	0	18	0	0
7	A	70	0	0	2	0
7	B	35	0	0	4	0
7	C	29	0	0	1	0
7	D	55	0	0	4	0
All	All	17320	0	16680	222	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 (222) 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:D:447:LEU:HD11	1:D:501:SER:HB2	1.61	0.83
1:A:328:LYS:HE2	1:A:508:THR:O	1.77	0.83
1:A:76:LEU:HD21	1:A:88:MET:HE1	1.66	0.77
1:D:455:ASN:C	1:D:455:ASN:HD22	1.98	0.71
1:A:158:HIS:ND1	7:A:703:HOH:O	2.25	0.68
1:D:86:LEU:HD21	1:D:88:MET:HE3	1.76	0.68
1:D:336:ILE:HB	1:D:373:LEU:HB2	1.76	0.67
1:D:442:GLU:O	1:D:443:ASN:HB2	1.93	0.66
1:C:28:TYR:CD2	1:C:65:ILE:HD11	2.31	0.65
1:D:131:ASN:OD1	1:D:169:SER:HB2	1.97	0.64
1:A:323:ILE:N	1:A:323:ILE:HD12	2.13	0.64
1:B:412:GLU:HB3	7:B:725:HOH:O	1.98	0.63
1:D:71:TYR:HB2	1:D:88:MET:HE2	1.80	0.63
1:A:335:LYS:HE2	1:A:374:THR:HG22	1.80	0.63
1:B:363:ILE:CD1	1:B:369:MET:HE2	2.29	0.62
1:D:9:LEU:HG	1:D:219:PRO:HG2	1.82	0.62
1:B:228:SER:O	1:B:241:ASN:HB2	2.00	0.62
1:B:141:VAL:O	1:B:142:THR:OG1	2.16	0.61
1:C:179:ASP:HB2	1:C:528:ARG:HA	1.81	0.60
1:D:224:GLU:OE1	2:F:1:BGC:H1	2.02	0.59
1:B:259:ASP:O	1:B:260:ALA:HB3	2.02	0.59
1:D:161:HIS:CD2	1:D:164:ILE:HD13	2.38	0.59
1:B:347:LYS:HA	1:B:347:LYS:HE2	1.85	0.59
1:B:432:ALA:HB2	1:B:487:ILE:HD11	1.85	0.58
1:D:319:LYS:NZ	1:D:345:ASP:OD2	2.36	0.58
1:A:320:GLY:O	1:A:398:LYS:NZ	2.35	0.58
1:A:530:LEU:HB2	7:A:734:HOH:O	2.04	0.58
1:C:28:TYR:HD2	1:C:65:ILE:HD11	1.65	0.58
1:B:317:TYR:O	1:B:398:LYS:HE3	2.04	0.57
1:B:511:ILE:HA	7:B:718:HOH:O	2.05	0.57
1:D:340:LEU:HD12	1:D:369:MET:HE1	1.87	0.57
1:C:222:THR:HG21	1:C:257:LEU:HD13	1.88	0.56
1:A:451:LYS:C	1:A:452:ILE:HD12	2.30	0.56
1:B:215:GLY:C	1:B:216:LEU:HD12	2.29	0.56
1:C:274:TRP:O	1:C:290:GLU:OE2	2.24	0.55
1:C:159:LYS:HD2	1:C:160:GLY:N	2.22	0.55
1:C:340:LEU:HD12	1:C:369:MET:HE1	1.86	0.55
1:D:25:ALA:HA	1:D:64:THR:O	2.06	0.55
1:D:131:ASN:OD1	1:D:169:SER:CB	2.53	0.55
1:D:322:ILE:HA	1:D:340:LEU:HD23	1.89	0.55
1:B:12:ASN:O	1:B:263:VAL:HG11	2.06	0.55
1:A:193:HIS:O	1:A:194:ASN:C	2.51	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:249:GLY:HA2	3:C:602:MLA:O1B	2.07	0.54
1:C:181:SER:O	1:C:218:LYS:NZ	2.40	0.54
1:B:363:ILE:HD12	1:B:369:MET:HE2	1.89	0.54
1:D:506:LYS:NZ	7:D:705:HOH:O	2.40	0.54
1:A:269:TYR:CE2	1:A:271:ALA:O	2.60	0.53
1:B:280:LYS:HG3	7:B:708:HOH:O	2.07	0.53
1:C:111:LEU:HD23	1:C:111:LEU:C	2.34	0.53
1:A:15:HIS:O	1:A:16:LEU:HD12	2.08	0.53
1:C:131:ASN:HA	1:C:169:SER:HB2	1.90	0.53
1:C:200:THR:O	1:C:499:GLY:HA3	2.09	0.52
1:D:130:ILE:HG21	1:D:150:MET:HE1	1.91	0.52
1:B:125:ILE:O	1:B:126:THR:OG1	2.22	0.52
1:C:324:SER:HA	1:C:325:PRO:C	2.33	0.52
1:A:426:LEU:HD13	1:A:517:ILE:HG22	1.90	0.52
1:A:284:SER:OG	1:A:287:GLN:HG2	2.09	0.52
1:C:131:ASN:HD22	1:C:169:SER:CB	2.22	0.52
1:B:256:ASP:O	1:B:259:ASP:O	2.28	0.52
1:A:224:GLU:OE2	2:E:1:BGC:H1	2.10	0.52
1:A:86:LEU:HD22	1:A:88:MET:HB2	1.92	0.51
1:A:34:PRO:HB2	1:A:300:LEU:HD12	1.92	0.51
1:C:90:ILE:HG22	1:C:92:ILE:HD12	1.92	0.51
1:B:104:VAL:O	1:B:108:GLU:HG3	2.11	0.51
1:B:442:GLU:O	1:B:443:ASN:CG	2.53	0.51
1:C:284:SER:HB3	1:C:287:GLN:HB2	1.93	0.51
1:D:179:ASP:OD1	1:D:181:SER:OG	2.28	0.51
1:D:447:LEU:CD1	1:D:501:SER:HB2	2.38	0.51
1:D:141:VAL:O	1:D:142:THR:OG1	2.28	0.50
1:C:359:TYR:HE1	1:C:371:ASP:OD2	1.93	0.50
1:B:339:GLU:C	1:B:340:LEU:HD12	2.37	0.50
1:D:254:TYR:CD2	1:D:314:MET:HE1	2.47	0.50
1:A:348:LYS:HB3	1:A:390:TYR:HB2	1.94	0.50
1:C:246:GLN:CD	1:C:310:VAL:HG21	2.36	0.50
1:C:179:ASP:OD1	1:C:179:ASP:C	2.54	0.50
1:B:76:LEU:HD11	1:B:88:MET:HE1	1.94	0.49
1:D:247:SER:HA	1:D:310:VAL:HG23	1.94	0.49
1:B:19:GLU:O	1:B:20:LYS:C	2.52	0.49
1:C:24:LYS:HB3	1:C:318:MET:HE3	1.94	0.49
1:C:247:SER:HA	1:C:310:VAL:HG22	1.94	0.49
1:C:146:PHE:O	1:C:150:MET:HG2	2.12	0.49
1:D:456:THR:O	1:D:457:HIS:HB2	2.12	0.49
1:A:110:GLU:OE1	1:A:110:GLU:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:495:ASN:C	1:B:495:ASN:OD1	2.56	0.49
1:B:9:LEU:HD22	1:B:219:PRO:HG2	1.94	0.49
1:B:230:SER:HB3	1:B:291:TRP:CD1	2.47	0.49
1:B:131:ASN:OD1	1:B:169:SER:HB2	2.13	0.48
1:B:168:LEU:HD22	1:B:183:PHE:CE2	2.48	0.48
1:D:363:ILE:HD12	1:D:369:MET:HE2	1.95	0.48
1:D:455:ASN:C	1:D:455:ASN:ND2	2.70	0.48
1:B:149:LEU:O	1:B:153:LEU:HD22	2.13	0.48
1:C:164:ILE:N	1:C:164:ILE:HD12	2.29	0.48
1:B:257:LEU:HB2	1:B:265:MET:HE1	1.95	0.48
1:D:139:HIS:CD2	1:D:492:TRP:CE2	3.02	0.48
1:C:247:SER:N	1:C:310:VAL:HG22	2.29	0.47
1:D:168:LEU:HD22	1:D:183:PHE:CE2	2.49	0.47
1:D:503:ARG:NH1	1:D:503:ARG:HG3	2.29	0.47
1:A:324:SER:HA	1:A:325:PRO:C	2.40	0.47
1:C:176:ASP:N	1:C:176:ASP:OD1	2.45	0.47
1:B:86:LEU:HD23	1:B:87:ILE:N	2.30	0.47
1:B:247:SER:HA	1:B:310:VAL:HG23	1.96	0.47
1:C:257:LEU:HB2	1:C:265:MET:HE1	1.97	0.47
1:B:138:ILE:O	1:B:142:THR:N	2.45	0.47
1:C:203:PHE:CZ	1:C:257:LEU:HD21	2.50	0.47
1:C:475:ASP:HB3	7:C:728:HOH:O	2.13	0.47
1:B:197:GLN:OE1	1:B:455:ASN:ND2	2.48	0.47
1:A:132:GLU:OE2	2:E:1:BGC:O1	2.34	0.46
1:A:335:LYS:CE	1:A:374:THR:HG22	2.44	0.46
1:C:450:LEU:HG	1:C:452:ILE:CD1	2.45	0.46
1:B:323:ILE:HD12	1:B:323:ILE:N	2.30	0.46
1:A:470:ILE:O	1:A:474:LEU:HD22	2.16	0.46
1:D:363:ILE:CD1	1:D:369:MET:HE2	2.46	0.46
1:C:131:ASN:HD22	1:C:169:SER:HB2	1.80	0.46
1:D:385:LEU:HB2	1:D:402:ILE:O	2.16	0.46
1:A:257:LEU:HB2	1:A:265:MET:HE1	1.96	0.46
1:B:204:LYS:NZ	1:B:328:LYS:O	2.49	0.46
1:D:192:ASP:HB2	1:D:203:PHE:CD1	2.51	0.46
1:D:254:TYR:CE2	1:D:314:MET:HE1	2.51	0.46
1:D:192:ASP:HB2	1:D:203:PHE:CG	2.51	0.46
1:A:330:ILE:HD13	1:A:413:LEU:HD11	1.99	0.45
1:B:111:LEU:HD23	1:B:153:LEU:HD12	1.98	0.45
1:B:451:LYS:C	1:B:452:ILE:HD12	2.40	0.45
1:B:330:ILE:HD13	1:B:413:LEU:HD11	1.98	0.45
1:C:471:SER:HA	1:C:474:LEU:CD2	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:ILE:N	1:A:323:ILE:CD1	2.78	0.45
1:C:76:LEU:HD21	1:C:88:MET:HE3	1.97	0.45
1:C:247:SER:CA	1:C:310:VAL:HG22	2.46	0.45
1:D:138:ILE:O	1:D:142:THR:N	2.49	0.45
1:A:13:TRP:HA	1:A:263:VAL:HG21	1.99	0.45
1:B:436:THR:HG21	1:B:450:LEU:HD11	1.99	0.45
1:B:454:TYR:CE1	1:B:494:VAL:HG21	2.51	0.45
1:A:129:VAL:HG12	1:A:130:ILE:HG22	1.99	0.45
1:A:170:ALA:O	1:A:188:TYR:HA	2.17	0.45
1:B:22:PHE:CE2	1:B:263:VAL:HA	2.52	0.45
1:B:285:LEU:HD22	1:C:354:ARG:NH1	2.31	0.45
1:C:309:PRO:O	1:C:310:VAL:C	2.60	0.45
1:D:176:ASP:OD1	1:D:176:ASP:N	2.50	0.45
1:C:28:TYR:OH	1:C:30:ILE:HD13	2.17	0.44
1:A:141:VAL:O	1:A:142:THR:OG1	2.32	0.44
1:B:37:ALA:HB2	1:B:280:LYS:HG2	1.98	0.44
1:B:134:GLN:O	1:B:137:HIS:HB3	2.17	0.44
1:B:319:LYS:HE3	1:B:319:LYS:HB3	1.74	0.44
1:C:416:LEU:HD23	1:C:417:THR:N	2.32	0.44
1:C:502:VAL:O	1:C:508:THR:HA	2.18	0.44
1:C:363:ILE:CD1	1:C:369:MET:HE2	2.47	0.44
1:B:193:HIS:O	1:B:194:ASN:C	2.60	0.44
1:D:146:PHE:CE1	1:D:150:MET:HE3	2.52	0.44
1:D:165:PRO:HA	1:D:184:ASP:OD2	2.17	0.44
1:A:179:ASP:HB2	1:A:528:ARG:HA	2.00	0.44
1:B:392:SER:O	1:B:393:ASP:CB	2.66	0.44
1:C:159:LYS:HD2	1:C:160:GLY:CA	2.48	0.43
1:C:322:ILE:HD13	1:C:402:ILE:CD1	2.48	0.43
1:D:193:HIS:O	1:D:194:ASN:C	2.59	0.43
1:A:14:TYR:OH	1:A:185:VAL:HG21	2.18	0.43
1:B:380:ILE:O	1:B:504:TYR:OH	2.27	0.43
1:A:87:ILE:HG12	1:A:126:THR:HB	2.00	0.43
1:D:61:GLY:C	7:D:702:HOH:O	2.62	0.43
1:D:209:GLY:HA3	7:D:733:HOH:O	2.19	0.43
1:B:331:HIS:CE1	1:B:336:ILE:HG23	2.54	0.43
1:B:346:VAL:O	1:B:347:LYS:HE2	2.18	0.43
1:C:348:LYS:HB3	1:C:390:TYR:HB2	2.01	0.43
1:A:447:LEU:HD11	1:A:501:SER:HB2	2.00	0.43
1:C:92:ILE:HG23	1:C:103:PHE:CZ	2.54	0.43
1:B:280:LYS:HB2	1:B:280:LYS:HE2	1.66	0.43
1:C:192:ASP:HB2	1:C:203:PHE:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:192:ASP:HB2	1:C:203:PHE:CG	2.54	0.43
1:D:337:PRO:HG2	7:D:755:HOH:O	2.17	0.43
1:D:33:ARG:HH22	1:D:53:ASP:CG	2.27	0.42
1:D:56:ASN:ND2	1:D:295:TRP:CH2	2.87	0.42
1:D:130:ILE:CG2	1:D:150:MET:HE1	2.49	0.42
1:D:319:LYS:HA	1:D:343:ASP:OD2	2.20	0.42
1:D:436:THR:HG21	1:D:450:LEU:HD11	2.01	0.42
1:A:369:MET:HE3	1:A:369:MET:HB3	1.80	0.42
1:B:285:LEU:CD2	1:C:354:ARG:NH1	2.82	0.42
1:C:455:ASN:C	1:C:455:ASN:HD22	2.27	0.42
1:D:33:ARG:NH2	1:D:53:ASP:OD1	2.52	0.42
1:A:454:TYR:CE2	1:A:494:VAL:HG21	2.54	0.42
1:B:269:TYR:HD1	1:B:269:TYR:HA	1.74	0.42
1:B:529:LYS:HD2	1:B:529:LYS:HA	1.46	0.42
1:C:269:TYR:HD1	1:C:269:TYR:HA	1.68	0.42
1:C:471:SER:HA	1:C:474:LEU:HD23	2.01	0.42
1:C:451:LYS:C	1:C:452:ILE:HD12	2.45	0.42
1:B:136:ASP:HB2	7:B:726:HOH:O	2.20	0.42
1:C:159:LYS:HD2	1:C:159:LYS:C	2.45	0.42
1:B:338:LEU:CD2	1:B:340:LEU:HD13	2.50	0.42
1:D:127:TYR:CD1	1:D:164:ILE:HG21	2.55	0.42
1:D:455:ASN:HA	1:D:462:ILE:O	2.18	0.42
1:B:454:TYR:CZ	1:B:494:VAL:HG21	2.55	0.41
1:B:470:ILE:O	1:B:474:LEU:HD22	2.20	0.41
1:C:186:TYR:CE2	1:C:218:LYS:HB2	2.55	0.41
1:D:76:LEU:HD23	1:D:76:LEU:HA	1.86	0.41
1:D:257:LEU:HB2	1:D:265:MET:HE1	2.01	0.41
1:B:20:LYS:HE3	1:B:368:TYR:CZ	2.55	0.41
1:C:217:ASP:OD1	1:C:217:ASP:N	2.52	0.41
1:D:172:ALA:HB2	1:D:188:TYR:HB3	2.02	0.41
1:D:284:SER:OG	1:D:287:GLN:HG2	2.21	0.41
1:C:139:HIS:CG	1:C:492:TRP:NE1	2.89	0.41
1:B:283:HIS:HE1	1:B:290:GLU:O	2.04	0.41
1:C:416:LEU:HD23	1:C:416:LEU:C	2.45	0.41
1:B:340:LEU:HD22	1:B:369:MET:HE1	2.02	0.41
1:C:170:ALA:O	1:C:188:TYR:HA	2.21	0.41
1:C:369:MET:HE3	1:C:369:MET:HB3	1.97	0.41
1:D:196:GLY:H	1:D:465:GLN:CD	2.28	0.41
1:B:71:TYR:CB	1:B:76:LEU:HD12	2.50	0.41
1:C:47:LEU:HD22	1:C:47:LEU:H	1.86	0.41
1:C:93:LYS:HB2	1:C:96:GLU:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:LYS:HA	1:C:161:HIS:CD2	2.56	0.41
1:A:9:LEU:HB3	1:A:219:PRO:HG2	2.03	0.40
1:A:79:VAL:O	1:A:80:GLN:C	2.64	0.40
1:B:54:LEU:HD12	1:B:84:LEU:HD12	2.03	0.40
1:B:328:LYS:HE2	1:B:508:THR:O	2.22	0.40
1:C:36:GLN:NE2	1:C:46:GLU:OE2	2.54	0.40
1:C:474:LEU:HD13	1:C:474:LEU:HA	1.99	0.40
1:A:76:LEU:HD21	1:A:88:MET:CE	2.43	0.40
1:B:71:TYR:HB2	1:B:76:LEU:CD1	2.51	0.40
1:D:269:TYR:HD1	1:D:269:TYR:HA	1.74	0.40
1:B:348:LYS:HB3	1:B:390:TYR:HB2	2.03	0.40
1:C:146:PHE:CZ	1:C:150:MET:HE3	2.57	0.40
1:D:324:SER:HB2	1:D:339:GLU:HG3	2.04	0.40
1:A:259:ASP:O	1:A:326:LYS:HD3	2.21	0.40
1:A:416:LEU:HD23	1:A:416:LEU:C	2.47	0.40
1:C:418:ILE:O	1:C:418:ILE:HG13	2.20	0.40

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	526/537 (98%)	493 (94%)	31 (6%)	2 (0%)	30	52
1	B	526/537 (98%)	491 (93%)	30 (6%)	5 (1%)	12	30
1	C	526/537 (98%)	490 (93%)	30 (6%)	6 (1%)	11	27
1	D	526/537 (98%)	496 (94%)	28 (5%)	2 (0%)	30	52
All	All	2104/2148 (98%)	1970 (94%)	119 (6%)	15 (1%)	18	39

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	393	ASP
1	C	448	ASP
1	B	142	THR
1	A	254	TYR
1	B	279	GLU
1	C	394	ASN
1	D	142	THR
1	A	394	ASN
1	B	269	TYR
1	C	142	THR
1	C	269	TYR
1	C	302	ASP
1	C	458	LEU
1	D	269	TYR
1	B	288	PRO

5.3.2 Protein sidechains [i](#)

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	465/474 (98%)	444 (96%)	21 (4%)	24	50
1	B	465/474 (98%)	440 (95%)	25 (5%)	20	43
1	C	465/474 (98%)	445 (96%)	20 (4%)	26	52
1	D	465/474 (98%)	446 (96%)	19 (4%)	27	54
All	All	1860/1896 (98%)	1775 (95%)	85 (5%)	24	50

All (85) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	129	VAL
1	A	169	SER
1	A	204	LYS
1	A	223	THR
1	A	263	VAL
1	A	269	TYR
1	A	279	GLU

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Mol	Chain	Res	Type
1	A	280	LYS
1	A	283	HIS
1	A	299	ASP
1	A	319	LYS
1	A	323	ILE
1	A	334	THR
1	A	343	ASP
1	A	409	THR
1	A	445	THR
1	A	471	SER
1	A	474	LEU
1	A	477	LYS
1	A	478	ILE
1	A	483	ASN
1	B	8	GLU
1	B	10	LYS
1	B	67	THR
1	B	86	LEU
1	B	87	ILE
1	B	129	VAL
1	B	136	ASP
1	B	211	ASN
1	B	216	LEU
1	B	223	THR
1	B	256	ASP
1	B	263	VAL
1	B	269	TYR
1	B	280	LYS
1	B	283	HIS
1	B	321	LEU
1	B	335	LYS
1	B	343	ASP
1	B	344	LYS
1	B	445	THR
1	B	474	LEU
1	B	480	THR
1	B	528	ARG
1	B	529	LYS
1	B	530	LEU
1	C	42	GLU
1	C	43	ARG
1	C	47	LEU

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Mol	Chain	Res	Type
1	C	73	GLU
1	C	76	LEU
1	C	92	ILE
1	C	120	LYS
1	C	124	ILE
1	C	125	ILE
1	C	129	VAL
1	C	140	SER
1	C	159	LYS
1	C	164	ILE
1	C	179	ASP
1	C	269	TYR
1	C	270	TYR
1	C	303	LYS
1	C	456	THR
1	C	474	LEU
1	C	480	THR
1	D	66	ARG
1	D	102	GLU
1	D	129	VAL
1	D	169	SER
1	D	181	SER
1	D	223	THR
1	D	269	TYR
1	D	279	GLU
1	D	309	PRO
1	D	319	LYS
1	D	343	ASP
1	D	356	LYS
1	D	382	ASP
1	D	403	ASN
1	D	453	SER
1	D	455	ASN
1	D	474	LEU
1	D	479	ILE
1	D	480	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	A	139	HIS

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Mol	Chain	Res	Type
1	A	151	ASN
1	A	194	ASN
1	A	283	HIS
1	A	465	GLN
1	B	139	HIS
1	B	193	HIS
1	B	211	ASN
1	B	283	HIS
1	B	342	ASN
1	B	362	ASN
1	B	399	ASN
1	B	443	ASN
1	B	483	ASN
1	C	74	ASN
1	C	131	ASN
1	C	139	HIS
1	C	287	GLN
1	C	403	ASN
1	C	427	ASN
1	C	455	ASN
1	D	12	ASN
1	D	139	HIS
1	D	151	ASN
1	D	193	HIS
1	D	194	ASN
1	D	241	ASN
1	D	253	ASN
1	D	399	ASN
1	D	403	ASN
1	D	455	ASN
1	D	473	GLN
1	D	483	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

4 monosaccharides are modelled in this entry.

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$
2	BGC	E	1	2	12,12,12	0.30	0	17,17,17	0.61	0
2	BGC	E	2	2	11,11,12	0.37	0	15,15,17	0.49	0
2	BGC	F	1	2	12,12,12	0.54	0	17,17,17	1.00	1 (5%)
2	BGC	F	2	2	11,11,12	0.38	0	15,15,17	0.47	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
2	BGC	E	1	2	-	2/2/22/22	0/1/1/1
2	BGC	E	2	2	-	0/2/19/22	0/1/1/1
2	BGC	F	1	2	-	2/2/22/22	0/1/1/1
2	BGC	F	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	F	1	BGC	O1-C1-O5	-2.07	104.26	110.41

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	1	BGC	O5-C5-C6-O6
2	E	1	BGC	O5-C5-C6-O6
2	F	1	BGC	C4-C5-C6-O6

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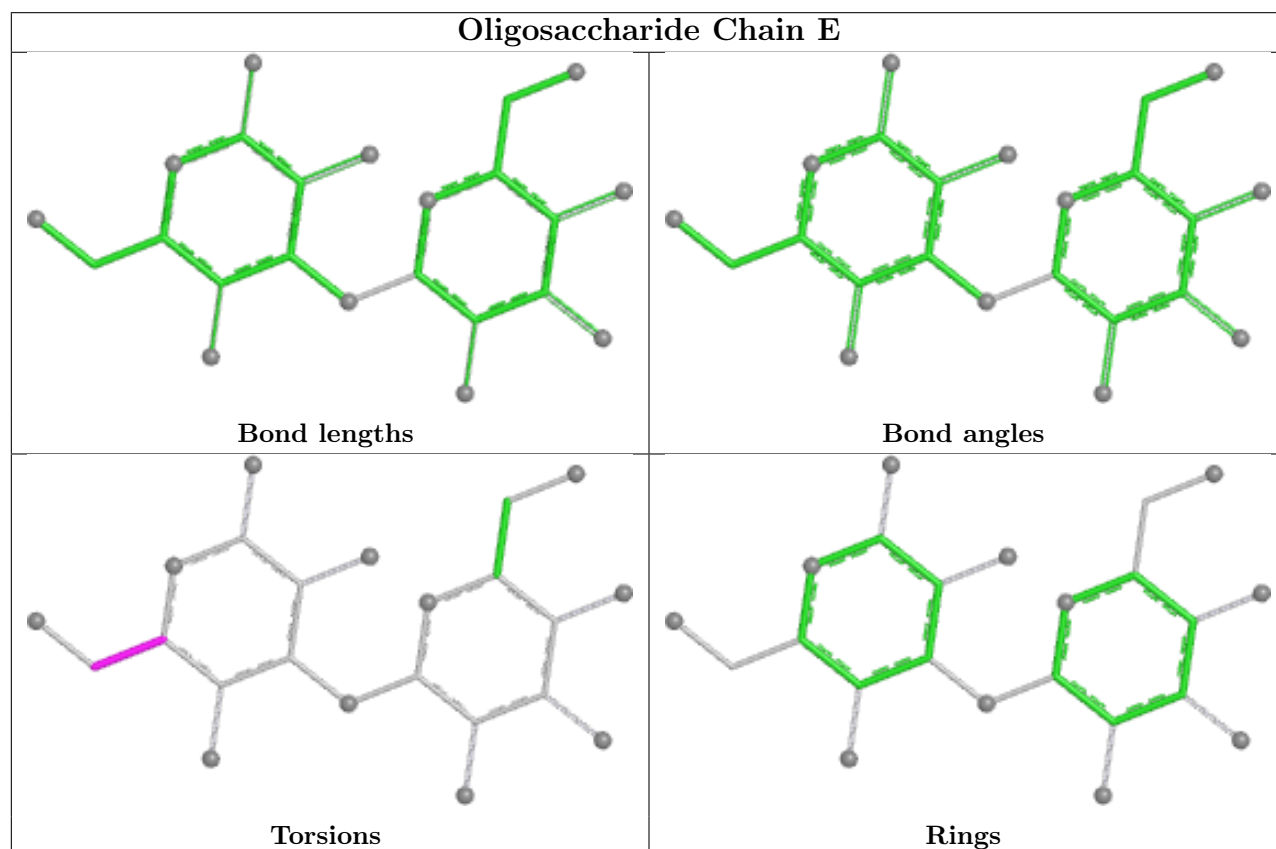
Mol	Chain	Res	Type	Atoms
2	E	1	BGC	C4-C5-C6-O6

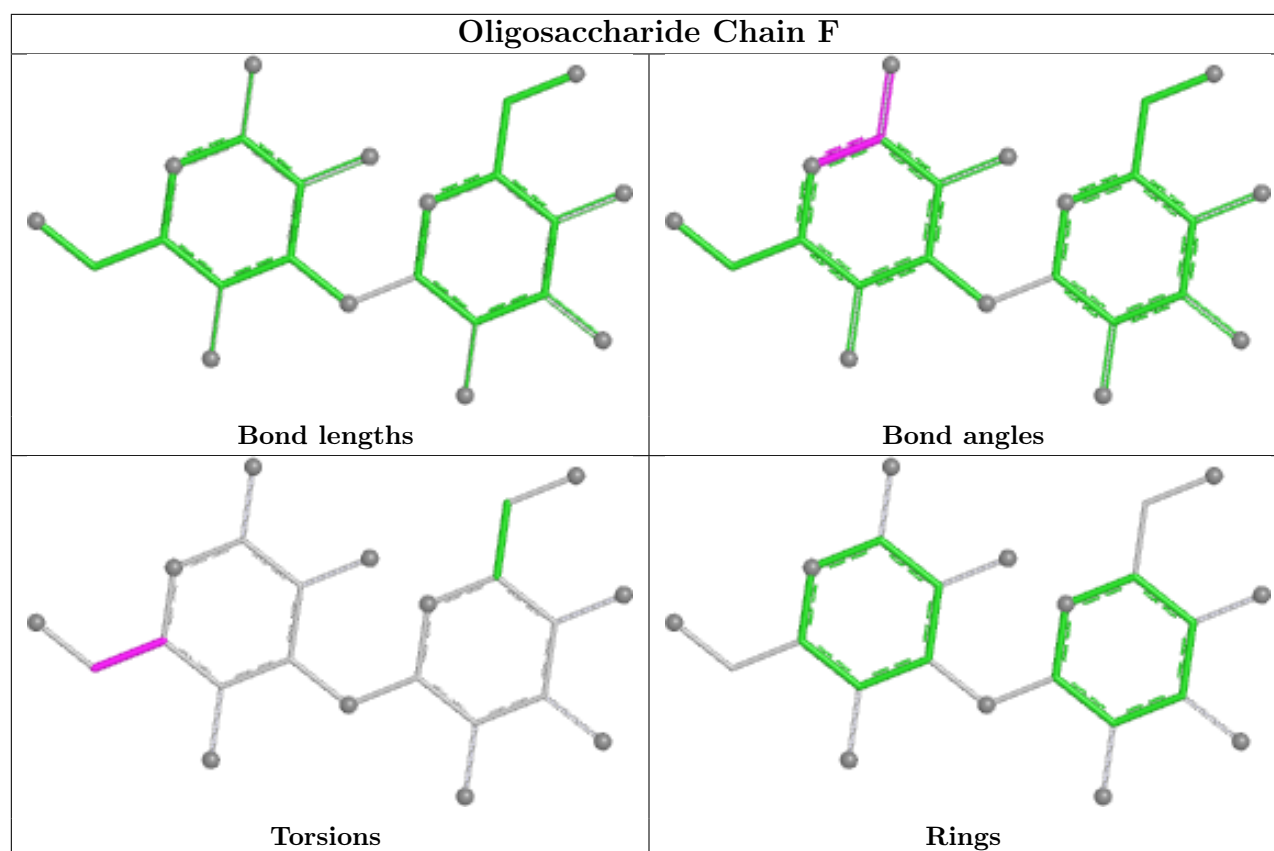
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	1	BGC	2	0
2	F	1	BGC	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 oligosaccharide.





5.6 Ligand geometry [i](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	MLA	D	602	-	6,6,6	1.34	0	7,7,7	1.01	0
5	BGC	D	601	-	12,12,12	1.44	2 (16%)	17,17,17	1.07	1 (5%)
4	GOL	C	601	-	5,5,5	0.20	0	5,5,5	0.51	0
3	MLA	C	602	-	6,6,6	1.12	0	7,7,7	1.06	0
3	MLA	A	602	-	6,6,6	1.41	0	7,7,7	1.02	0
3	MLA	A	601	-	6,6,6	1.49	1 (16%)	7,7,7	0.86	0
4	GOL	B	601	-	5,5,5	0.20	0	5,5,5	0.43	0
4	GOL	A	603	-	5,5,5	0.20	0	5,5,5	0.51	0
4	GOL	A	604	-	5,5,5	0.10	0	5,5,5	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	BGC	B	602	-	12,12,12	0.74	0	17,17,17	1.27	2 (11%)
6	PG4	C	603	-	12,12,12	0.34	0	11,11,11	0.35	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MLA	D	602	-	-	0/4/4/4	-
5	BGC	D	601	-	-	2/2/22/22	0/1/1/1
4	GOL	C	601	-	-	0/4/4/4	-
3	MLA	C	602	-	-	2/4/4/4	-
3	MLA	A	602	-	-	4/4/4/4	-
3	MLA	A	601	-	-	3/4/4/4	-
4	GOL	B	601	-	-	1/4/4/4	-
4	GOL	A	603	-	-	2/4/4/4	-
4	GOL	A	604	-	-	2/4/4/4	-
5	BGC	B	602	-	-	0/2/22/22	0/1/1/1
6	PG4	C	603	-	-	6/10/10/10	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	601	BGC	O5-C5	3.05	1.51	1.44
3	A	601	MLA	O1A-C1	-2.44	1.22	1.30
5	D	601	BGC	O5-C1	2.31	1.48	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	602	BGC	O5-C1-C2	-2.84	105.31	110.30
5	D	601	BGC	O1-C1-O5	2.70	118.44	110.41
5	B	602	BGC	O2-C2-C3	2.01	115.12	110.38

There are no chirality outliers.

All (22) torsion outliers are listed below:

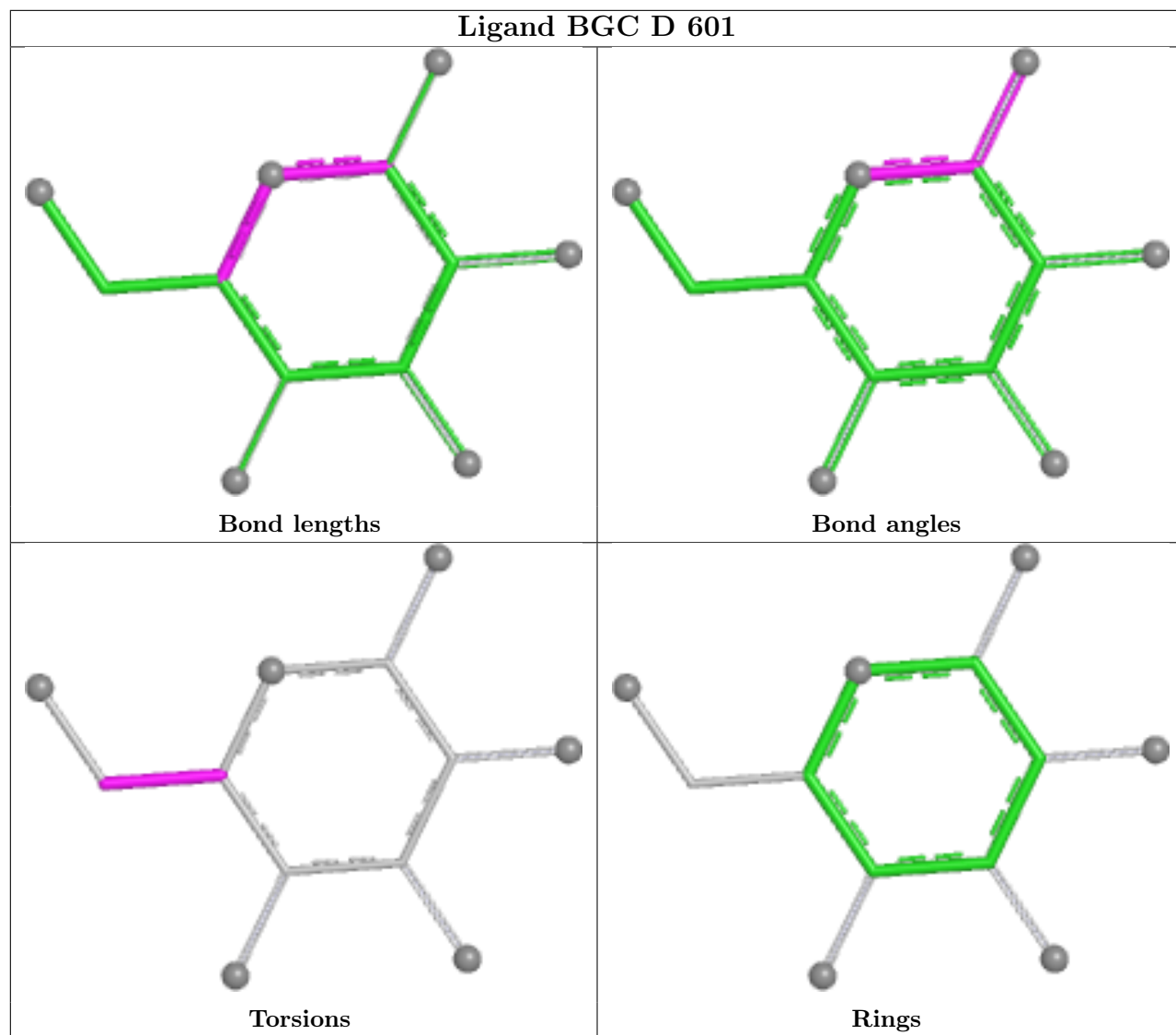
Mol	Chain	Res	Type	Atoms
4	A	603	GOL	O1-C1-C2-C3
4	A	604	GOL	O1-C1-C2-C3
6	C	603	PG4	O1-C1-C2-O2
5	D	601	BGC	C4-C5-C6-O6
6	C	603	PG4	O2-C3-C4-O3
4	A	603	GOL	O1-C1-C2-O2
6	C	603	PG4	O4-C7-C8-O5
3	A	602	MLA	O1B-C1-C2-C3
5	D	601	BGC	O5-C5-C6-O6
6	C	603	PG4	C8-C7-O4-C6
3	A	601	MLA	O1A-C1-C2-C3
3	A	602	MLA	O1A-C1-C2-C3
4	A	604	GOL	O1-C1-C2-O2
3	A	601	MLA	O1B-C1-C2-C3
6	C	603	PG4	O3-C5-C6-O4
3	A	602	MLA	C1-C2-C3-O3B
3	A	602	MLA	C1-C2-C3-O3A
4	B	601	GOL	O2-C2-C3-O3
3	C	602	MLA	C1-C2-C3-O3B
6	C	603	PG4	C4-C3-O2-C2
3	C	602	MLA	C1-C2-C3-O3A
3	A	601	MLA	C1-C2-C3-O3A

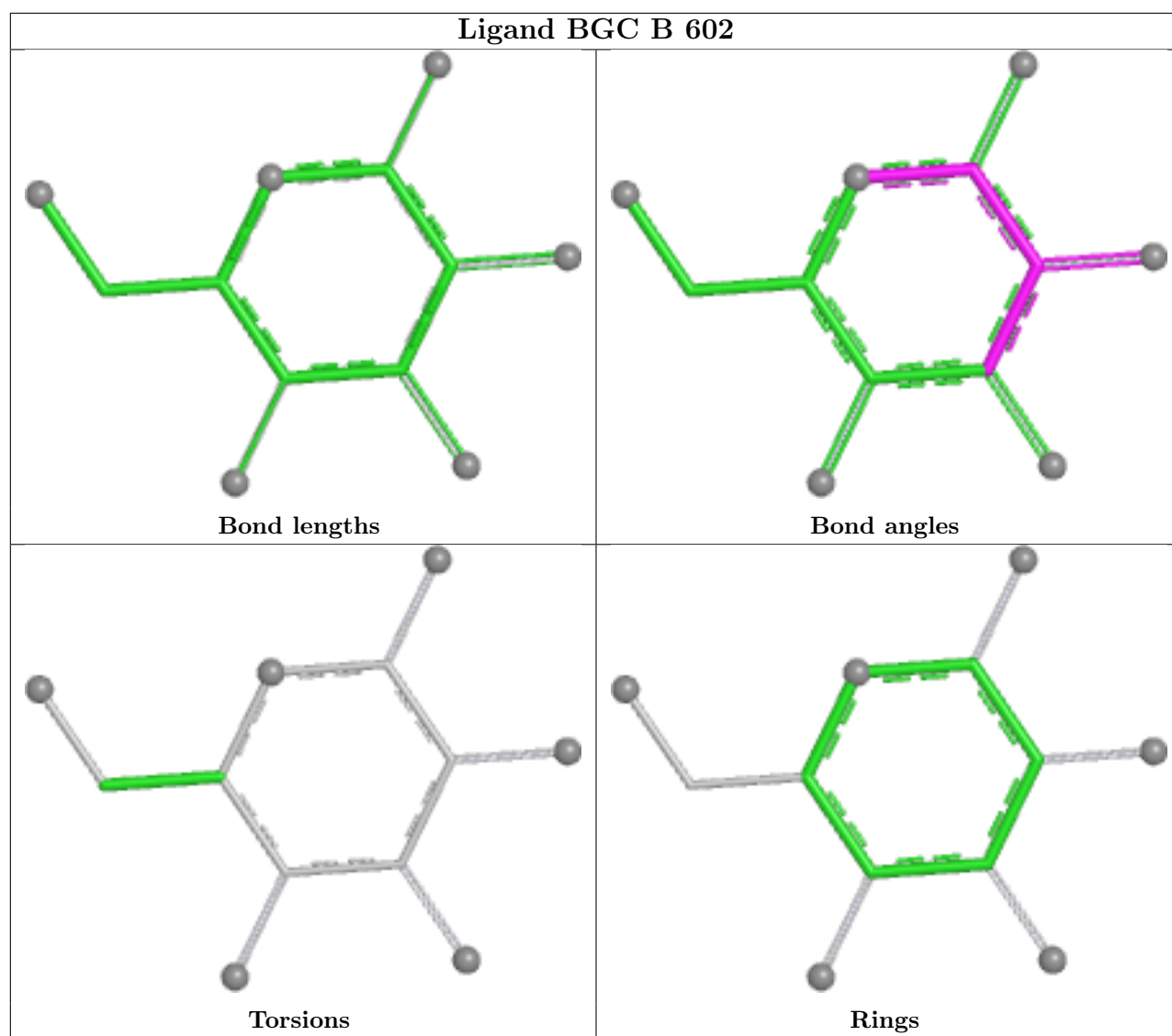
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	602	MLA	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	528/537 (98%)	-0.41	1 (0%) 91 90	57, 70, 91, 114	0
1	B	528/537 (98%)	0.03	4 (0%) 82 81	68, 94, 123, 147	0
1	C	528/537 (98%)	0.08	6 (1%) 78 76	66, 94, 142, 160	0
1	D	528/537 (98%)	-0.32	2 (0%) 88 88	54, 72, 92, 114	0
All	All	2112/2148 (98%)	-0.16	13 (0%) 85 85	54, 81, 126, 160	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	530	LEU	3.9
1	B	269	TYR	3.6
1	A	530	LEU	3.3
1	C	448	ASP	3.2
1	D	530	LEU	2.7
1	C	269	TYR	2.4
1	C	47	LEU	2.4
1	D	269	TYR	2.4
1	B	449	ASP	2.3
1	C	530	LEU	2.2
1	C	71	TYR	2.1
1	B	4	LYS	2.1
1	C	92	ILE	2.1

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

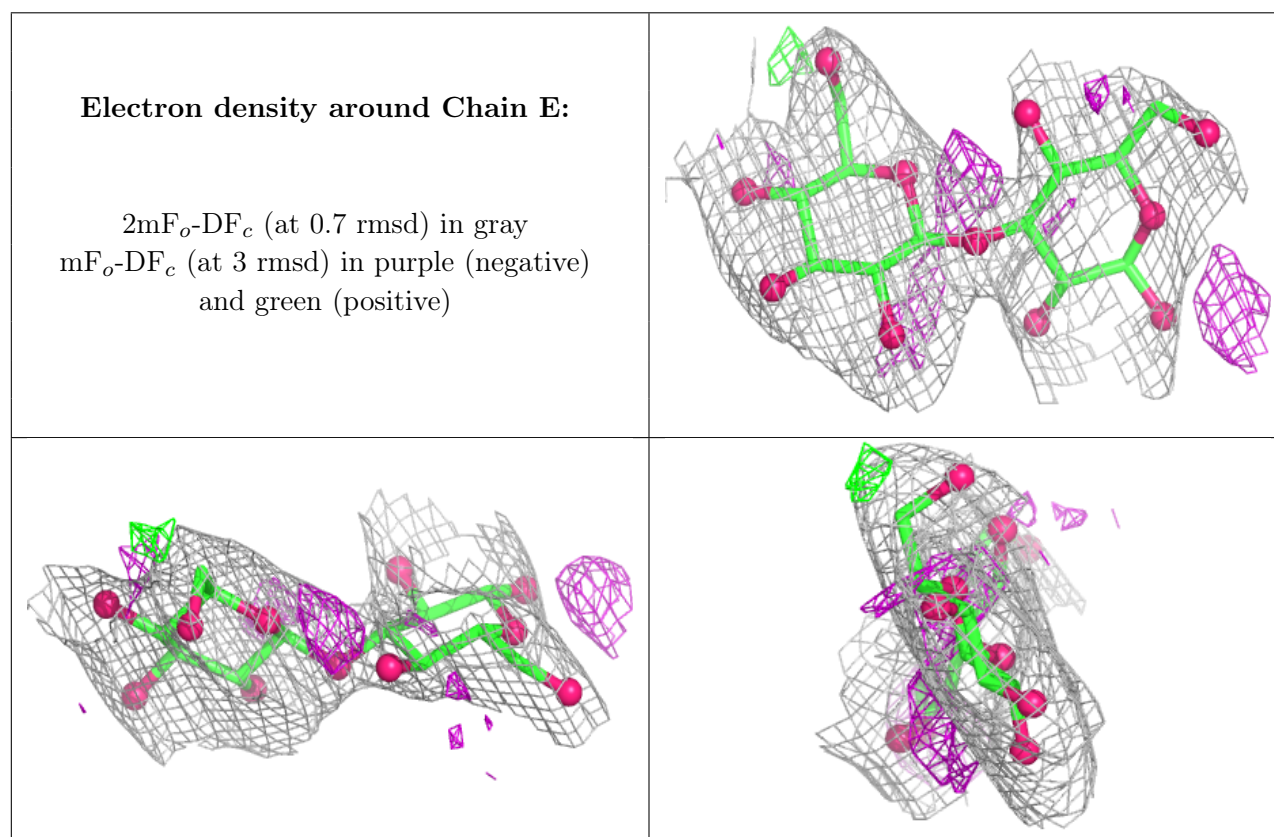
There are no non-standard protein/DNA/RNA residues in this entry.

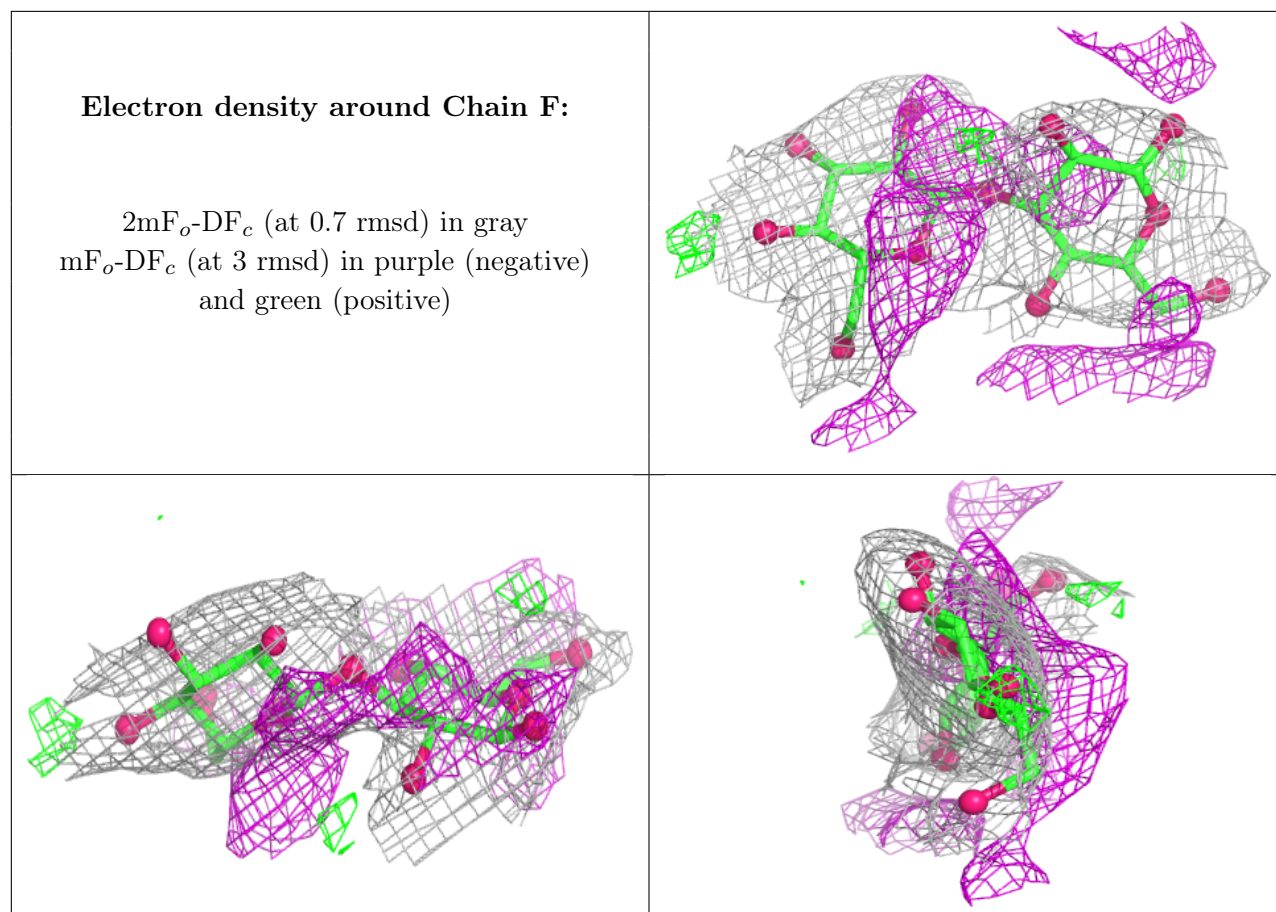
6.3 Carbohydrates [i](#)

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
2	BGC	F	1	12/12	0.86	0.15	73,79,89,89	0
2	BGC	E	1	12/12	0.90	0.12	80,93,105,105	0
2	BGC	F	2	11/12	0.91	0.11	48,52,74,80	0
2	BGC	E	2	11/12	0.92	0.11	39,43,58,67	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





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.

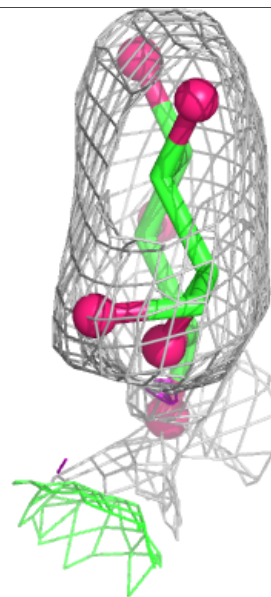
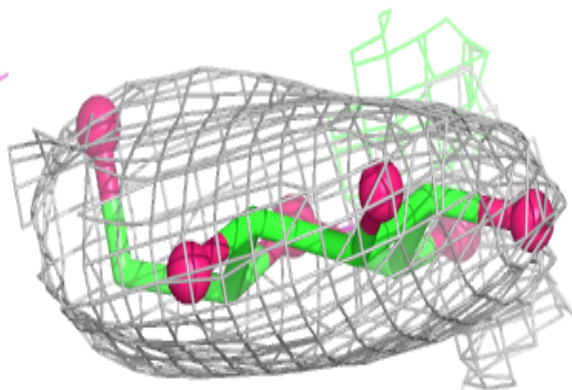
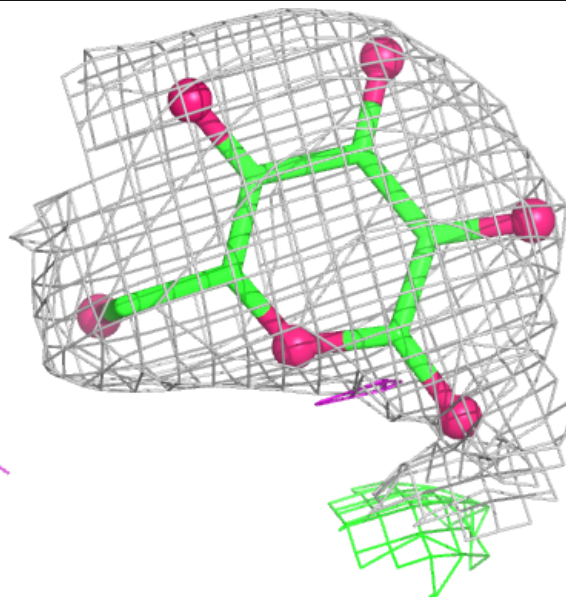
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MLA	D	602	7/7	0.56	0.10	94,102,107,110	0
3	MLA	A	601	7/7	0.80	0.17	89,95,106,114	0
4	GOL	B	601	6/6	0.81	0.13	75,88,94,95	0
3	MLA	C	602	7/7	0.83	0.13	75,82,90,93	0
4	GOL	A	603	6/6	0.85	0.15	74,84,85,86	0
4	GOL	C	601	6/6	0.85	0.15	62,70,75,91	0
5	BGC	B	602	12/12	0.88	0.12	57,64,73,84	0
5	BGC	D	601	12/12	0.88	0.14	49,66,85,88	0
6	PG4	C	603	13/13	0.88	0.18	59,78,88,89	0
4	GOL	A	604	6/6	0.89	0.15	61,64,66,72	0
3	MLA	A	602	7/7	0.89	0.11	66,83,95,98	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.

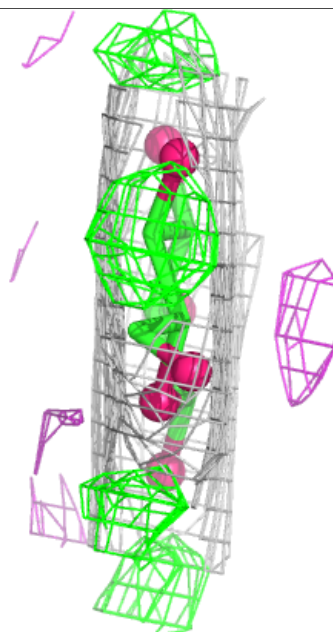
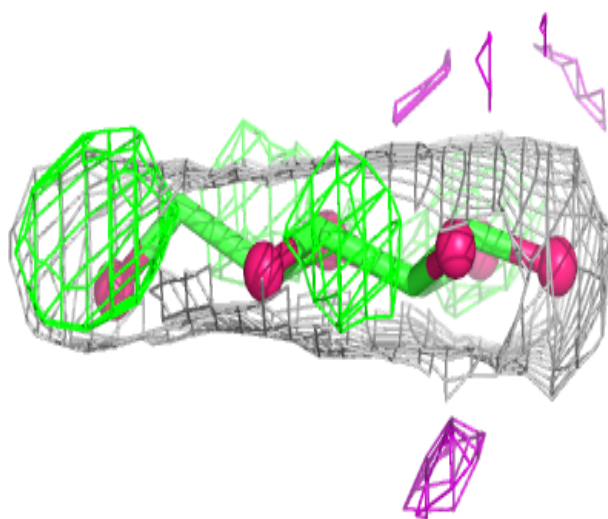
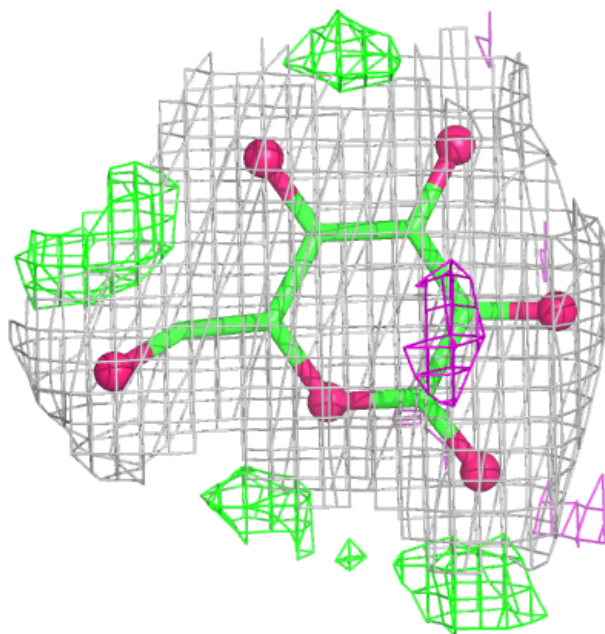
Electron density around BGC B 602:

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



Electron density around BGC D 601:

$2mF_o-DF_c$ (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.