



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:17 AM UTC

PDB ID : 4POP / pdb_00004pop
Title : ThiT with LMG139 bound
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Deposited on : 2014-02-26
Resolution : 2.20 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

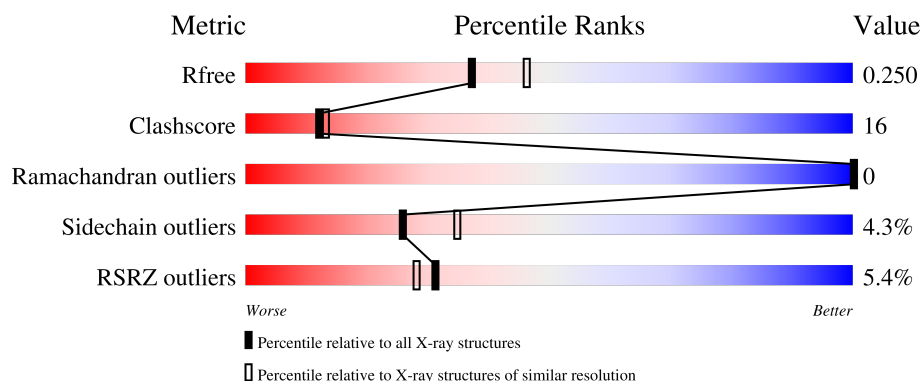
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	192	3% 77% 14% 8%
1	B	192	7% 81% 10% 8%

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
5	PEG	A	215	-	-	X	-
5	PEG	B	215	-	-	X	-
6	PG4	A	220	-	-	X	-
6	PG4	B	218	-	-	X	-
7	1PE	A	222	-	-	X	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 3367 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.

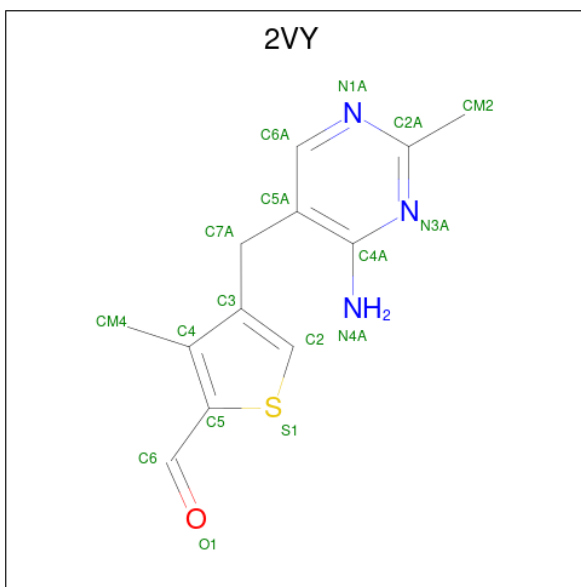
- Molecule 1 is a protein called Thiamine transporter ThiT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1377	945	214	215	3			
1	B	176	Total	C	N	O	S	0	1	0
			1375	941	215	216	3			

There are 20 discrepancies between the modelled and reference sequences:

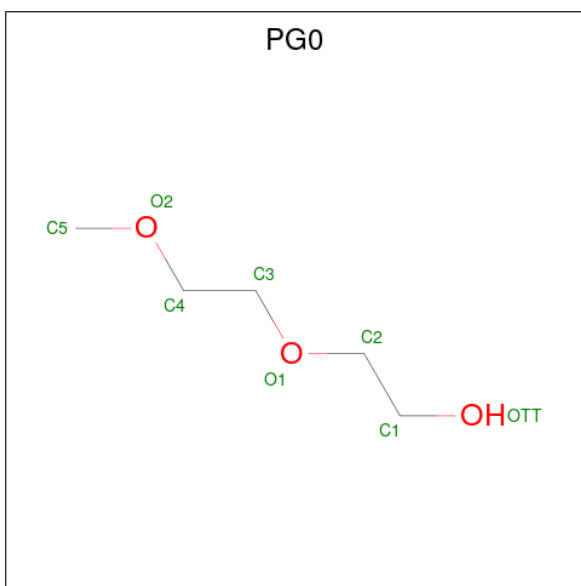
Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	MET	-	initiating methionine	UNP A2RI47
A	-8	HIS	-	expression tag	UNP A2RI47
A	-7	HIS	-	expression tag	UNP A2RI47
A	-6	HIS	-	expression tag	UNP A2RI47
A	-5	HIS	-	expression tag	UNP A2RI47
A	-4	HIS	-	expression tag	UNP A2RI47
A	-3	HIS	-	expression tag	UNP A2RI47
A	-2	HIS	-	expression tag	UNP A2RI47
A	-1	HIS	-	expression tag	UNP A2RI47
A	0	ALA	-	expression tag	UNP A2RI47
B	-9	MET	-	initiating methionine	UNP A2RI47
B	-8	HIS	-	expression tag	UNP A2RI47
B	-7	HIS	-	expression tag	UNP A2RI47
B	-6	HIS	-	expression tag	UNP A2RI47
B	-5	HIS	-	expression tag	UNP A2RI47
B	-4	HIS	-	expression tag	UNP A2RI47
B	-3	HIS	-	expression tag	UNP A2RI47
B	-2	HIS	-	expression tag	UNP A2RI47
B	-1	HIS	-	expression tag	UNP A2RI47
B	0	ALA	-	expression tag	UNP A2RI47

- Molecule 2 is 4-[(4-amino-2-methylpyrimidin-5-yl)methyl]-3-methylthiophene-2-carbaldehyde (CCD ID: 2VY) (formula: C₁₂H₁₃N₃OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			17	12	3	1	1		
2	B	1	Total	C	N	O	S	0	0
			17	12	3	1	1		

- Molecule 3 is 2-(2-METHOXYETHOXY)ETHANOL (CCD ID: PG0) (formula: C₅H₁₂O₃).



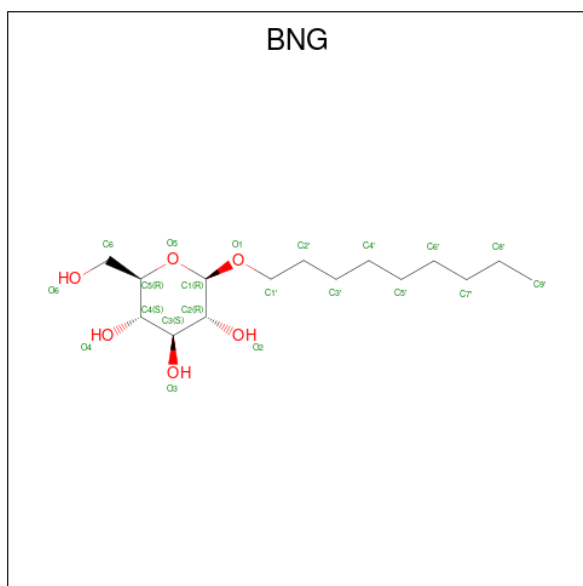
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	5	3		
3	A	1	Total	C	O	0	0
			8	5	3		

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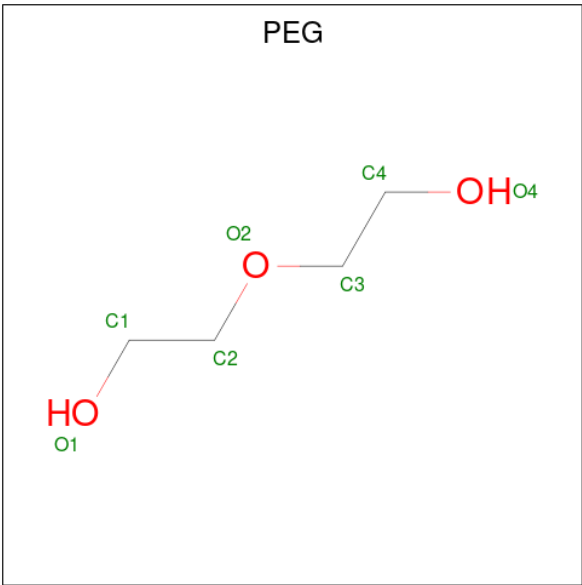
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			8	5	3		

- Molecule 4 is nonyl beta-D-glucopyranoside (CCD ID: BNG) (formula: $C_{15}H_{30}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			21	15	6		
4	A	1	Total	C	O	0	0
			21	15	6		
4	A	1	Total	C	O	0	0
			21	15	6		
4	B	1	Total	C	O	0	0
			21	15	6		
4	B	1	Total	C	O	0	0
			21	15	6		

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



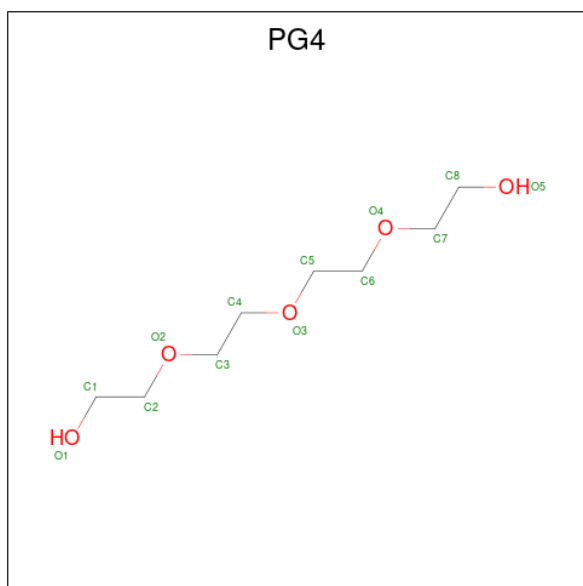
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total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

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

- Molecule 6 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



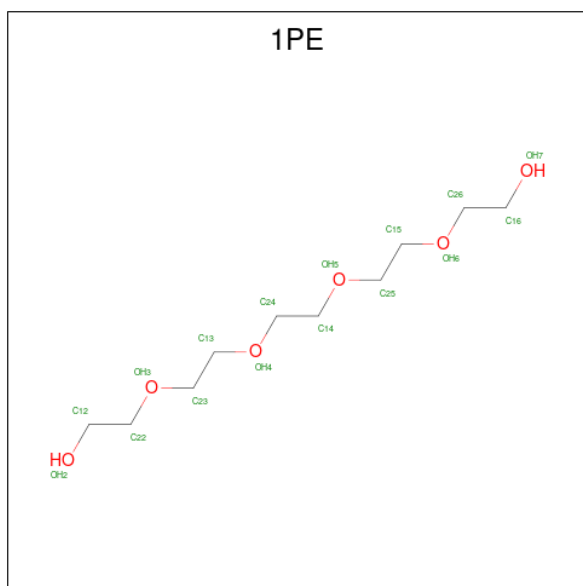
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	8	5		
6	A	1	Total	C	O	0	0
			13	8	5		
6	A	1	Total	C	O	0	0
			13	8	5		
6	A	1	Total	C	O	0	0
			13	8	5		

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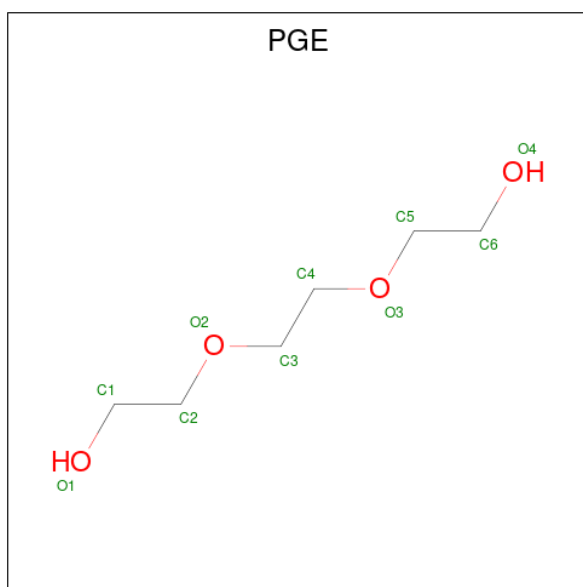
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			13	8	5		
6	B	1	Total	C	O	0	0
			13	8	5		
6	B	1	Total	C	O	0	0
			13	8	5		
6	B	1	Total	C	O	0	0
			13	8	5		
6	B	1	Total	C	O	0	0
			13	8	5		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



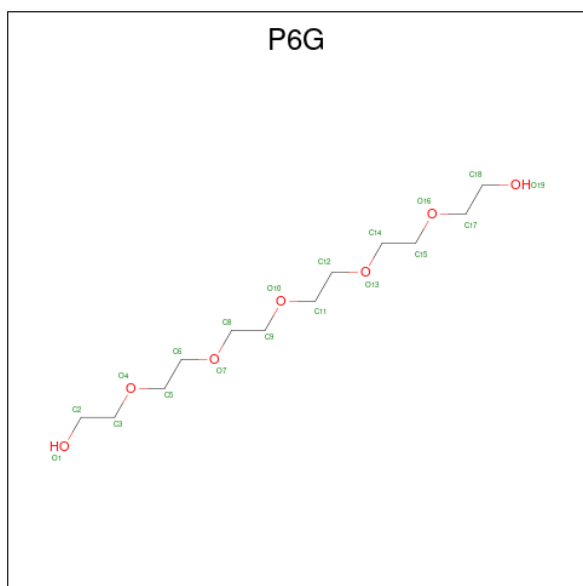
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			16	10	6		
7	A	1	Total	C	O	0	0
			16	10	6		
7	B	1	Total	C	O	0	0
			16	10	6		

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



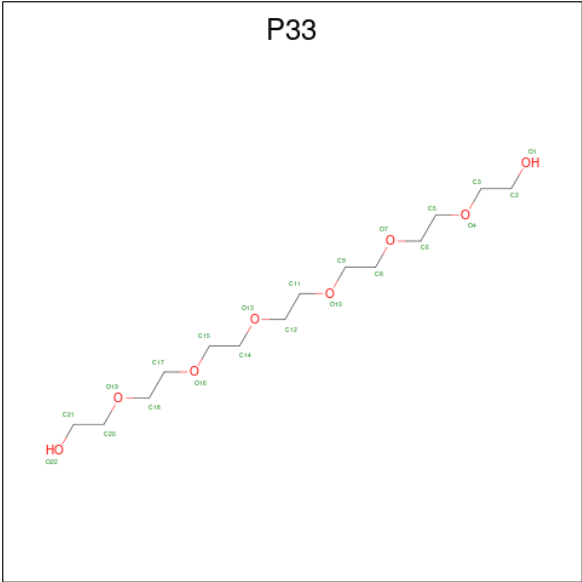
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



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

- Molecule 10 is 3,6,9,12,15,18-HEXA OXAICOSANE-1,20-DIOL (CCD ID: P33) (formula: $C_{14}H_{30}O_8$).



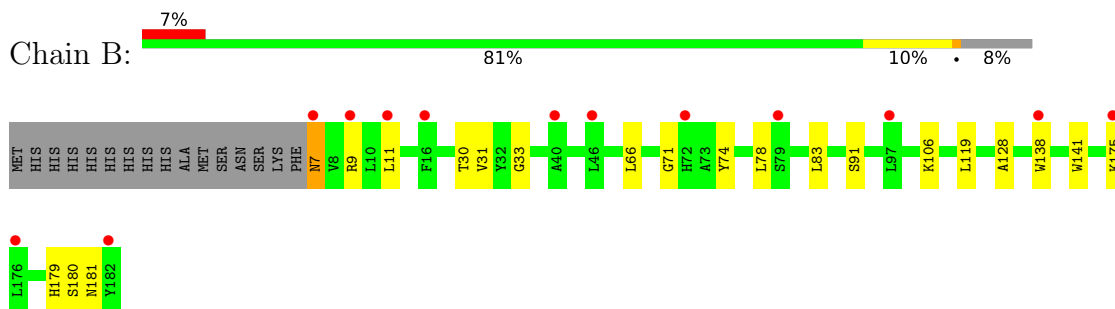
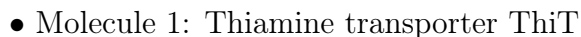
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	1	Total	C O	0	0
			22	14 8		

- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	43	Total	O	0	1
			44	44		
11	B	45	Total	O	0	0
			45	45		

i

- Molecule 1: Thiamine transporter ThiT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	62.61Å 84.12Å 127.15Å 90.00° 95.13° 90.00°	Depositor
Resolution (Å)	47.77 – 2.20 47.77 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (47.77-2.20) 99.1 (47.77-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.199 , 0.248 0.207 , 0.250	Depositor DCC
R_{free} test set	1660 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 73.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3367	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.26% 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, BNG, PEG, 1PE, 2VY, PGE, PG0, P33, PG4

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	0.83	1/1416 (0.1%)	0.94	0/1930
1	B	0.78	0/1413	0.90	0/1926
All	All	0.81	1/2829 (0.0%)	0.92	0/3856

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	ALA	CA-CB	-6.01	1.44	1.53

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	1377	0	1471	39	0
1	B	1375	0	1469	23	0
2	A	17	0	13	0	0
2	B	17	0	13	0	0
3	A	16	0	24	2	0
3	B	8	0	12	0	0
4	A	63	0	90	9	0
4	B	42	0	60	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	70	0	90	26	0
5	B	77	0	100	25	0
6	A	52	0	72	20	0
6	B	65	0	90	21	0
7	A	32	0	44	7	0
7	B	16	0	22	2	0
8	A	10	0	14	1	0
9	A	19	0	26	7	0
10	B	22	0	30	2	0
11	A	44	0	0	3	0
11	B	45	0	0	3	0
All	All	3367	0	3640	108	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 16.

The worst 5 of 108 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)
5:A:215:PEG:H31	9:A:224:P6G:H121	1.43	0.98
4:A:206:BNG:O3	6:A:220:PG4:H21	1.73	0.87
6:B:218:PG4:H32	6:B:218:PG4:H61	1.54	0.87
5:B:215:PEG:O4	6:B:218:PG4:H52	1.77	0.85
7:A:222:1PE:H141	6:B:216:PG4:H32	1.56	0.85

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	175/192 (91%)	174 (99%)	1 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	175/192 (91%)	172 (98%)	3 (2%)	0	100	100
All	All	350/384 (91%)	346 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	141/155 (91%)	135 (96%)	6 (4%)	26	35
1	B	141/155 (91%)	135 (96%)	6 (4%)	26	35
All	All	282/310 (91%)	270 (96%)	12 (4%)	26	35

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	9	ARG
1	B	11	LEU
1	B	175	LYS
1	B	66	LEU
1	A	66	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	HIS
1	B	72	HIS

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](#)

46 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	$\# Z > 2$
5	PEG	A	215	-	6,6,6	0.60	0	5,5,5	1.60	1 (20%)
3	PG0	A	203	-	7,7,7	0.30	0	6,6,6	0.29	0
5	PEG	A	213	-	6,6,6	0.57	0	5,5,5	0.40	0
5	PEG	B	210	-	6,6,6	0.58	0	5,5,5	0.69	0
5	PEG	A	212	-	6,6,6	0.58	0	5,5,5	0.64	0
5	PEG	A	214	-	6,6,6	0.59	0	5,5,5	0.38	0
8	PGE	A	223	-	9,9,9	0.40	0	8,8,8	0.31	0
2	2VY	A	201	-	17,18,18	2.97	5 (29%)	23,25,25	3.94	13 (56%)
5	PEG	A	211	-	6,6,6	0.58	0	5,5,5	0.42	0
5	PEG	B	215	-	6,6,6	0.60	0	5,5,5	0.65	0
6	PG4	A	217	-	12,12,12	0.68	0	11,11,11	0.47	0
5	PEG	A	207	-	6,6,6	0.61	0	5,5,5	0.48	0
5	PEG	B	214	-	6,6,6	0.57	0	5,5,5	0.33	0
5	PEG	A	208	-	6,6,6	0.58	0	5,5,5	0.46	0
7	1PE	A	222	-	15,15,15	0.74	0	14,14,14	0.50	0
4	BNG	B	203	-	21,21,21	0.80	0	26,26,26	1.02	2 (7%)
5	PEG	B	205	-	6,6,6	0.62	0	5,5,5	0.26	0
4	BNG	A	204	-	21,21,21	0.80	0	26,26,26	1.00	1 (3%)
7	1PE	B	221	-	15,15,15	0.69	0	14,14,14	0.42	0
6	PG4	B	218	-	12,12,12	0.77	0	11,11,11	0.64	0
5	PEG	B	207	-	6,6,6	0.57	0	5,5,5	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	PG4	A	219	-	12,12,12	0.72	0	11,11,11	0.27	0
5	PEG	A	210	-	6,6,6	0.57	0	5,5,5	0.56	0
6	PG4	B	220	-	12,12,12	0.73	0	11,11,11	0.25	0
6	PG4	B	219	-	12,12,12	0.77	0	11,11,11	0.36	0
5	PEG	B	212	-	6,6,6	0.60	0	5,5,5	0.27	0
2	2VY	B	201	-	17,18,18	3.29	6 (35%)	23,25,25	3.41	13 (56%)
3	PG0	B	202	-	7,7,7	0.27	0	6,6,6	0.18	0
3	PG0	A	202	-	7,7,7	0.31	0	6,6,6	0.26	0
6	PG4	A	218	-	12,12,12	0.74	0	11,11,11	0.19	0
5	PEG	B	213	-	6,6,6	0.59	0	5,5,5	0.36	0
4	BNG	A	206	-	21,21,21	0.96	1 (4%)	26,26,26	1.05	3 (11%)
7	1PE	A	221	-	15,15,15	0.76	0	14,14,14	0.26	0
5	PEG	B	209	-	6,6,6	0.64	0	5,5,5	0.31	0
4	BNG	B	204	-	21,21,21	0.87	0	26,26,26	1.21	1 (3%)
5	PEG	B	211	-	6,6,6	0.61	0	5,5,5	0.24	0
6	PG4	A	220	-	12,12,12	0.72	0	11,11,11	0.65	0
9	P6G	A	224	-	18,18,18	0.77	0	17,17,17	0.43	0
5	PEG	A	209	-	6,6,6	0.60	0	5,5,5	0.33	0
6	PG4	B	217	-	12,12,12	0.75	0	11,11,11	0.37	0
5	PEG	B	208	-	6,6,6	0.58	0	5,5,5	0.27	0
4	BNG	A	205	-	21,21,21	0.78	0	26,26,26	1.21	4 (15%)
5	PEG	A	216	-	6,6,6	0.59	0	5,5,5	0.27	0
6	PG4	B	216	-	12,12,12	0.77	0	11,11,11	0.30	0
5	PEG	B	206	-	6,6,6	0.59	0	5,5,5	0.45	0
10	P33	B	222	-	21,21,21	0.92	0	20,20,20	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
5	PEG	A	215	-	-	2/4/4/4	-
3	PG0	A	203	-	-	3/5/5/5	-
5	PEG	A	213	-	-	2/4/4/4	-
5	PEG	B	210	-	-	2/4/4/4	-
5	PEG	A	212	-	-	4/4/4/4	-
5	PEG	A	214	-	-	2/4/4/4	-
8	PGE	A	223	-	-	4/7/7/7	-
2	2VY	A	201	-	-	2/6/6/6	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PEG	A	211	-	-	2/4/4/4	-
5	PEG	B	215	-	-	2/4/4/4	-
6	PG4	A	217	-	-	6/10/10/10	-
5	PEG	A	207	-	-	0/4/4/4	-
5	PEG	B	214	-	-	2/4/4/4	-
5	PEG	A	208	-	-	1/4/4/4	-
7	1PE	A	222	-	-	9/13/13/13	-
4	BNG	B	203	-	-	3/12/32/32	0/1/1/1
5	PEG	B	205	-	-	3/4/4/4	-
4	BNG	A	204	-	-	9/12/32/32	0/1/1/1
7	1PE	B	221	-	-	6/13/13/13	-
6	PG4	B	218	-	-	6/10/10/10	-
5	PEG	B	207	-	-	0/4/4/4	-
6	PG4	A	219	-	-	4/10/10/10	-
5	PEG	A	210	-	-	2/4/4/4	-
6	PG4	B	220	-	-	5/10/10/10	-
6	PG4	B	219	-	-	4/10/10/10	-
5	PEG	B	212	-	-	1/4/4/4	-
2	2VY	B	201	-	-	0/6/6/6	0/2/2/2
3	PG0	B	202	-	-	2/5/5/5	-
3	PG0	A	202	-	-	3/5/5/5	-
6	PG4	A	218	-	-	8/10/10/10	-
5	PEG	B	213	-	-	3/4/4/4	-
4	BNG	A	206	-	-	8/12/32/32	0/1/1/1
7	1PE	A	221	-	-	5/13/13/13	-
5	PEG	B	209	-	-	2/4/4/4	-
4	BNG	B	204	-	-	4/12/32/32	0/1/1/1
5	PEG	B	211	-	-	2/4/4/4	-
6	PG4	A	220	-	-	6/10/10/10	-
9	P6G	A	224	-	-	7/16/16/16	-
5	PEG	A	209	-	-	3/4/4/4	-
6	PG4	B	217	-	-	8/10/10/10	-
5	PEG	B	208	-	-	3/4/4/4	-
4	BNG	A	205	-	-	5/12/32/32	0/1/1/1
5	PEG	A	216	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	PG4	B	216	-	-	4/10/10/10	-
5	PEG	B	206	-	-	2/4/4/4	-
10	P33	B	222	-	-	9/19/19/19	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	201	2VY	O1-C6	8.65	1.41	1.22
2	A	201	2VY	O1-C6	8.11	1.39	1.22
2	B	201	2VY	C2-C3	7.11	1.43	1.36
2	A	201	2VY	C2-C3	6.77	1.42	1.36
2	B	201	2VY	C6-C5	5.02	1.53	1.45

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	201	2VY	C2-S1-C5	10.18	100.58	91.65
2	A	201	2VY	O1-C6-C5	-9.82	111.92	123.51
2	B	201	2VY	O1-C6-C5	-9.57	112.21	123.51
2	B	201	2VY	C2-S1-C5	7.61	98.33	91.65
2	A	201	2VY	C3-C2-S1	-7.45	105.07	113.46

There are no chirality outliers.

5 of 172 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	201	2VY	S1-C5-C6-O1
2	A	201	2VY	C4-C5-C6-O1
4	A	204	BNG	C2'-C1'-O1-C1
4	A	206	BNG	O5-C1-O1-C1'
7	A	222	1PE	C16-C26-OH6-C15

There are no ring outliers.

32 monomers are involved in 98 short contacts:

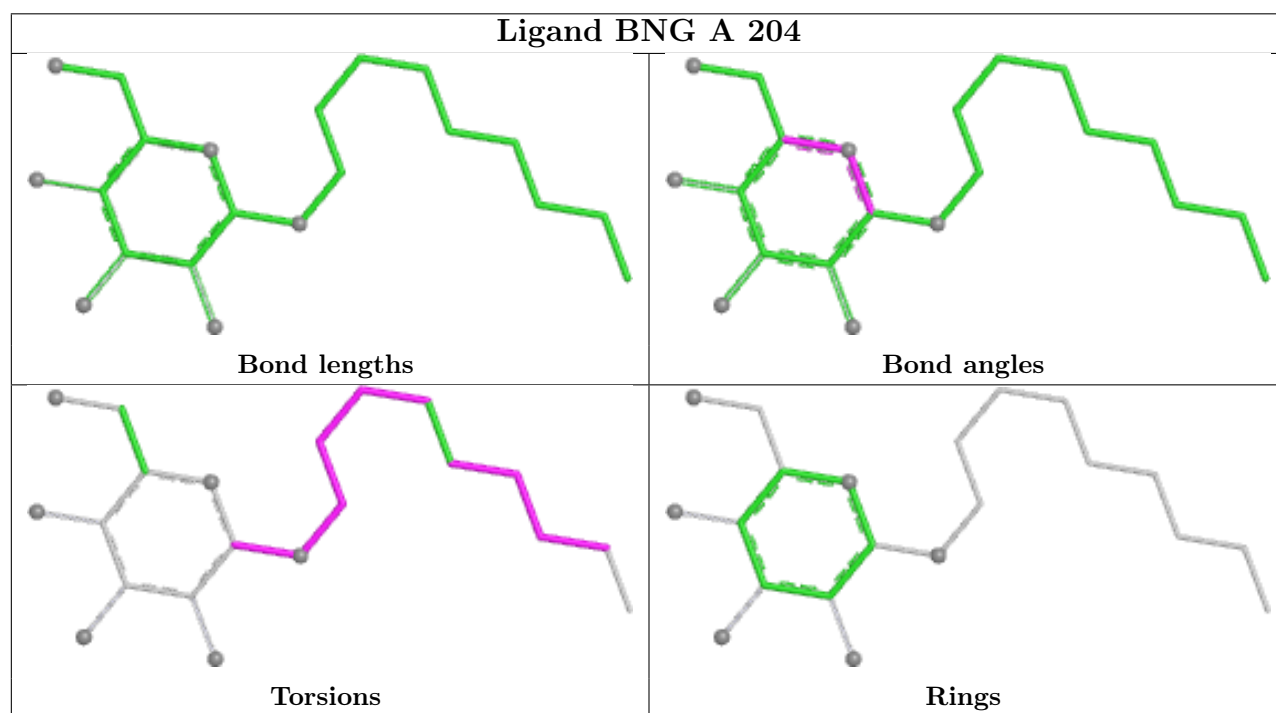
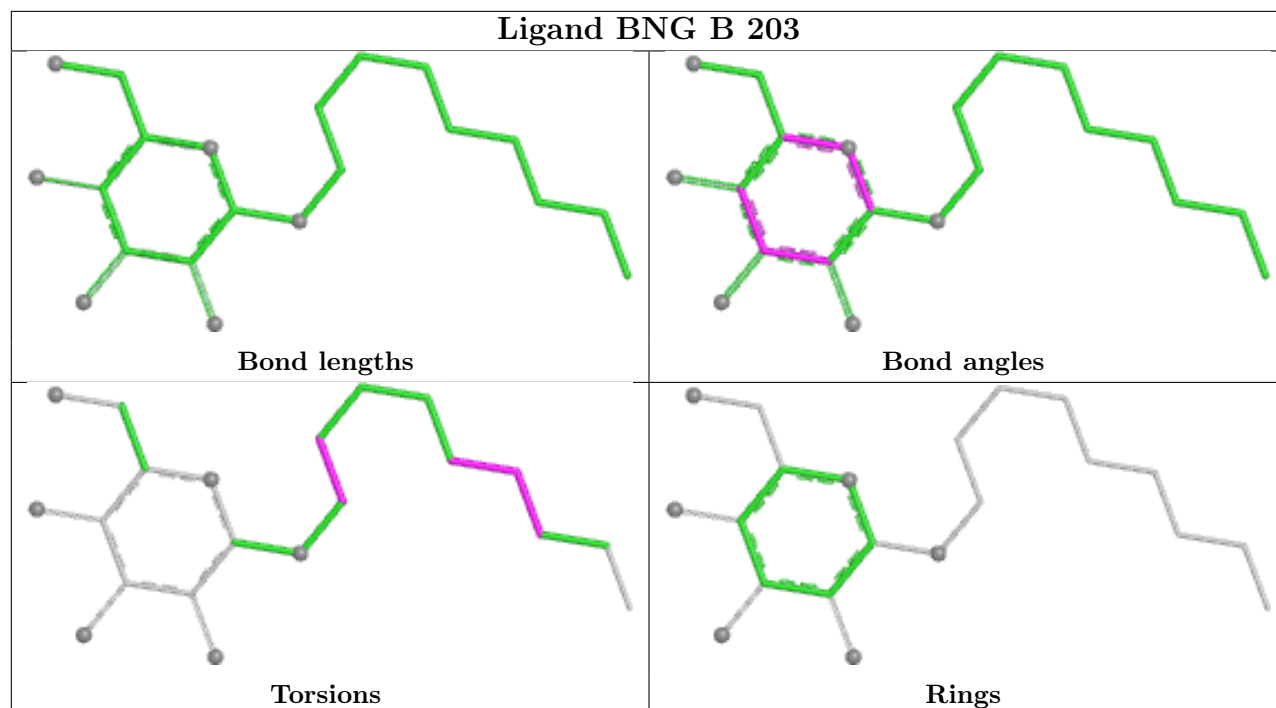
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	215	PEG	12	0
3	A	203	PG0	1	0
5	A	213	PEG	2	0
5	B	210	PEG	2	0

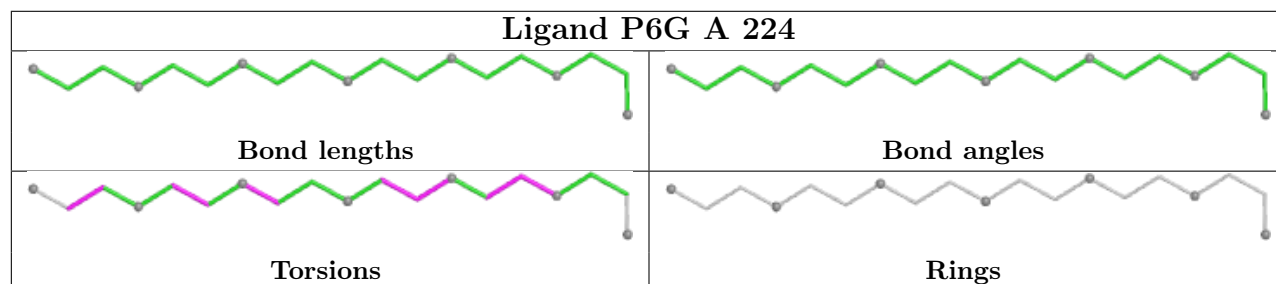
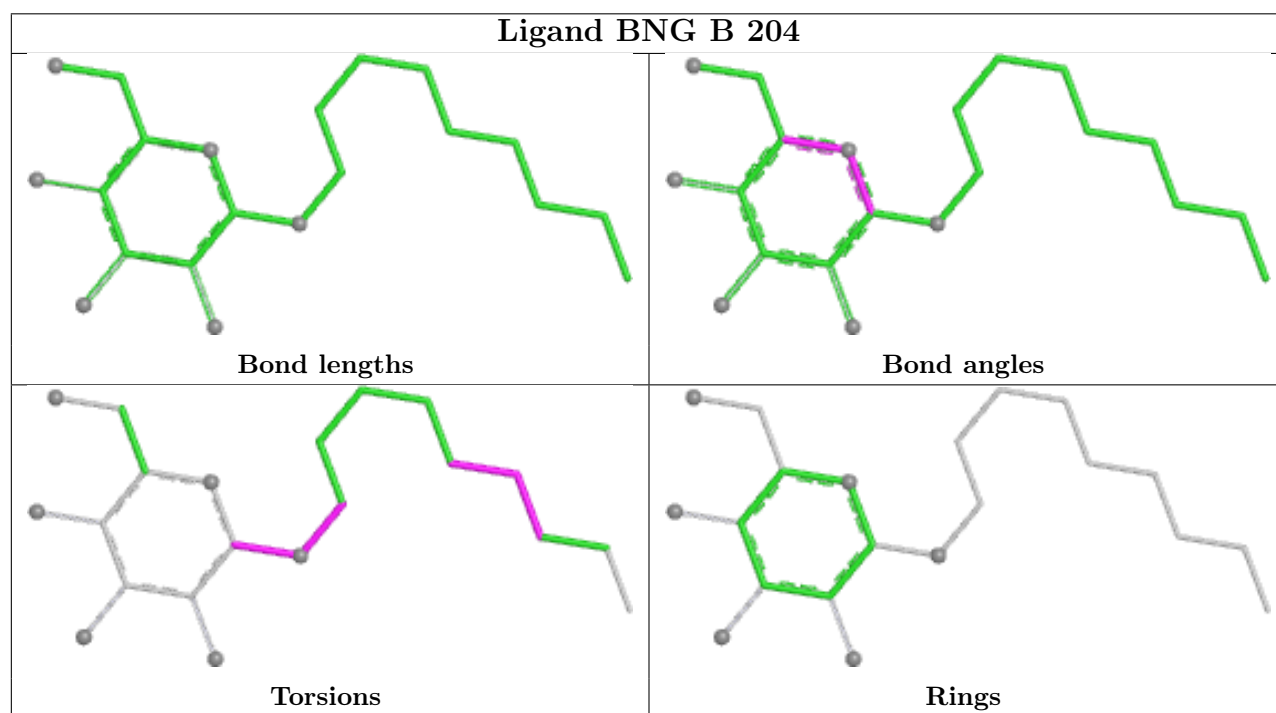
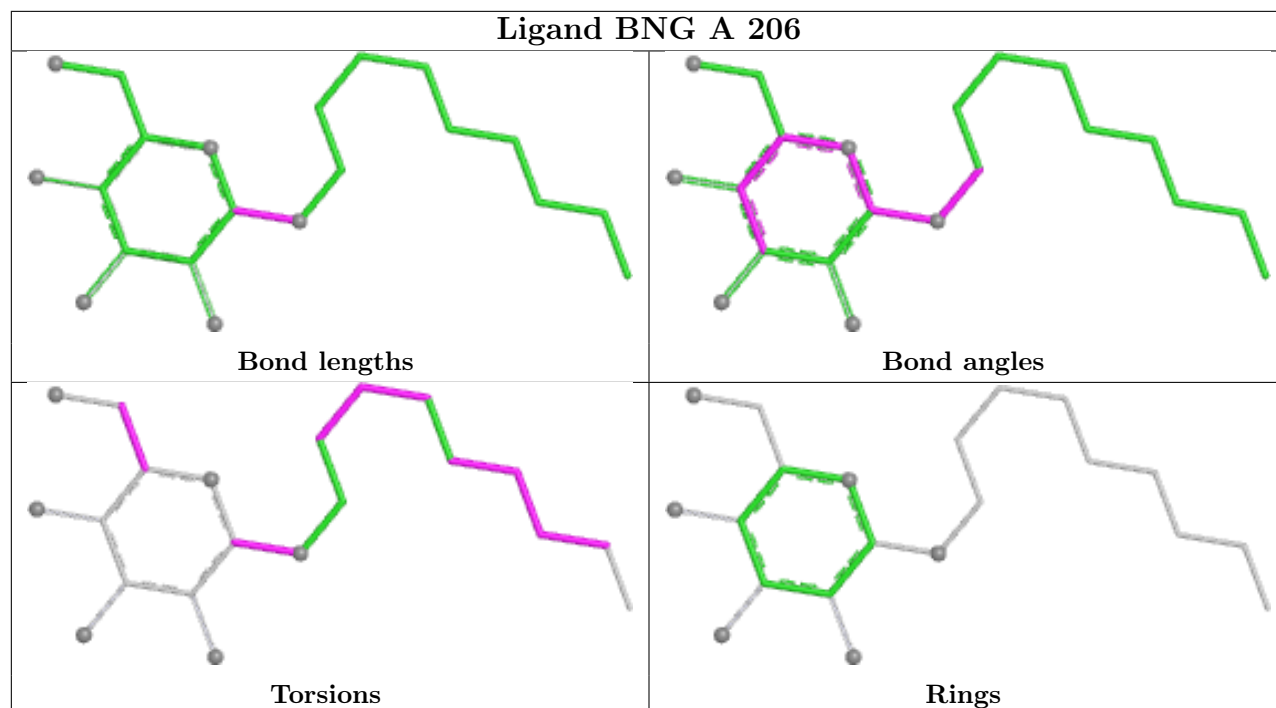
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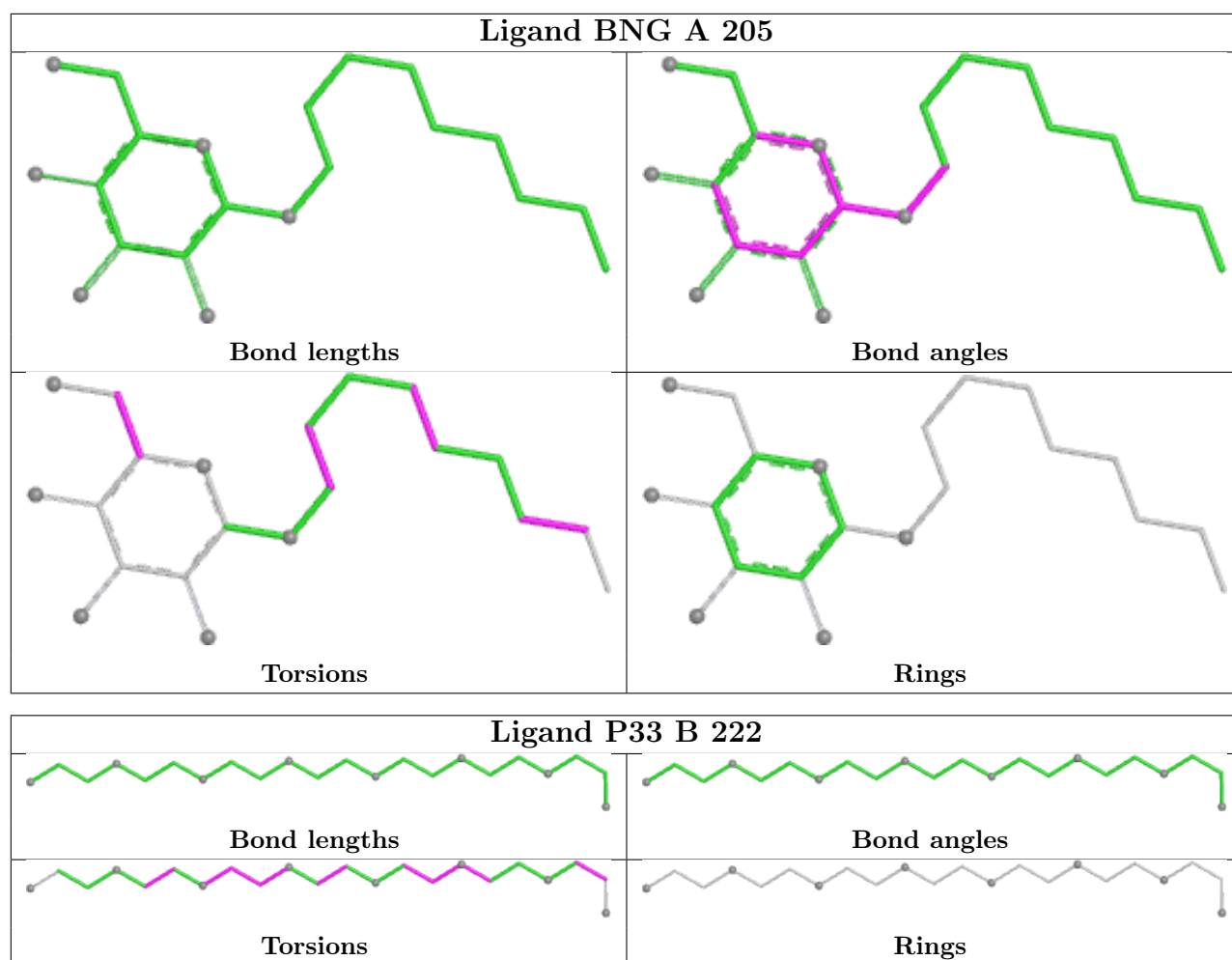
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	223	PGE	1	0
5	A	211	PEG	2	0
5	B	215	PEG	15	0
6	A	217	PG4	2	0
5	A	207	PEG	2	0
5	B	214	PEG	3	0
5	A	208	PEG	1	0
7	A	222	1PE	7	0
4	B	203	BNG	4	0
5	B	205	PEG	3	0
7	B	221	1PE	2	0
6	B	218	PG4	15	0
5	B	207	PEG	2	0
5	A	210	PEG	1	0
6	B	220	PG4	2	0
3	A	202	PG0	1	0
6	A	218	PG4	1	0
4	A	206	BNG	8	0
5	B	209	PEG	2	0
4	B	204	BNG	2	0
6	A	220	PG4	17	0
9	A	224	P6G	7	0
5	A	209	PEG	3	0
6	B	217	PG4	1	0
4	A	205	BNG	1	0
5	A	216	PEG	3	0
6	B	216	PG4	3	0
10	B	222	P33	2	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	177/192 (92%)	0.49	6 (3%)	48	45	31, 48, 75, 104	0
1	B	176/192 (91%)	0.71	13 (7%)	20	18	29, 50, 86, 115	1 (0%)
All	All	353/384 (91%)	0.60	19 (5%)	31	28	29, 49, 80, 115	1 (0%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	182	TYR	4.5
1	B	79	SER	4.0
1	B	16	PHE	3.6
1	B	176	LEU	3.4
1	A	27	ILE	3.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PEG	B	209	7/7	0.58	0.23	85,88,91,92	0
5	PEG	A	216	7/7	0.61	0.19	104,111,143,145	0
5	PEG	A	210	7/7	0.67	0.27	107,110,163,179	0
3	PG0	A	202	8/8	0.72	0.26	85,103,127,162	0
5	PEG	B	212	7/7	0.72	0.27	74,81,105,107	0
6	PG4	B	220	13/13	0.73	0.20	83,90,120,120	0
5	PEG	B	207	7/7	0.74	0.27	66,68,76,78	0
6	PG4	A	219	13/13	0.74	0.23	95,105,118,120	13
5	PEG	A	212	7/7	0.74	0.30	82,87,95,113	0
8	PGE	A	223	10/10	0.75	0.33	80,98,121,162	0
9	P6G	A	224	19/19	0.75	0.23	44,87,137,195	0
6	PG4	B	219	13/13	0.76	0.26	73,99,111,111	0
5	PEG	B	214	7/7	0.76	0.22	63,87,103,134	0
5	PEG	A	214	7/7	0.77	0.23	110,124,162,210	0
4	BNG	A	206	21/21	0.78	0.20	46,88,105,109	0
4	BNG	A	204	21/21	0.79	0.20	49,95,118,123	0
6	PG4	A	220	13/13	0.79	0.23	46,92,136,167	0
5	PEG	A	213	7/7	0.79	0.18	79,83,99,101	0
5	PEG	A	208	7/7	0.80	0.35	92,108,132,193	0
5	PEG	B	211	7/7	0.81	0.24	103,107,111,113	0
10	P33	B	222	22/22	0.81	0.26	42,58,92,108	22
5	PEG	A	211	7/7	0.82	0.17	76,88,95,98	0
7	1PE	A	221	16/16	0.82	0.21	67,96,107,111	0
7	1PE	B	221	16/16	0.82	0.21	73,96,111,117	0
5	PEG	B	213	7/7	0.83	0.19	72,79,95,97	0
7	1PE	A	222	16/16	0.83	0.17	57,73,107,110	0
5	PEG	B	215	7/7	0.84	0.15	49,63,79,84	0
6	PG4	B	218	13/13	0.84	0.18	58,72,82,91	0
5	PEG	B	208	7/7	0.85	0.18	90,95,111,119	0
5	PEG	A	207	7/7	0.85	0.14	74,78,85,86	0
4	BNG	A	205	21/21	0.85	0.15	50,78,92,100	0
6	PG4	A	217	13/13	0.85	0.18	73,77,96,97	0
3	PG0	B	202	8/8	0.85	0.23	78,82,96,107	0
5	PEG	A	209	7/7	0.86	0.16	49,61,90,95	0
6	PG4	B	216	13/13	0.87	0.17	60,73,91,97	0
5	PEG	B	210	7/7	0.87	0.19	70,89,90,91	0
3	PG0	A	203	8/8	0.88	0.24	74,93,111,113	0
4	BNG	B	203	21/21	0.89	0.13	53,68,81,88	0
5	PEG	B	206	7/7	0.89	0.15	65,77,82,85	0
5	PEG	A	215	7/7	0.89	0.13	46,53,70,80	0
6	PG4	A	218	13/13	0.89	0.18	62,69,78,80	13
5	PEG	B	205	7/7	0.91	0.14	57,66,76,84	0
6	PG4	B	217	13/13	0.93	0.17	44,73,102,103	0

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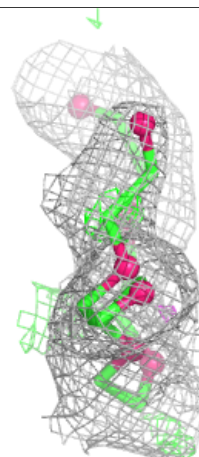
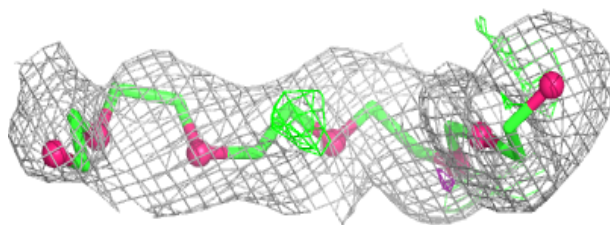
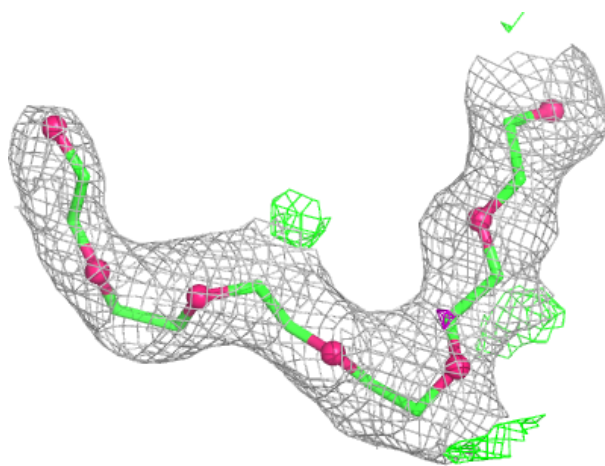
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BNG	B	204	21/21	0.94	0.10	45,69,86,88	0
2	2VY	A	201	17/17	0.96	0.08	27,37,51,57	0
2	2VY	B	201	17/17	0.97	0.08	27,41,53,63	0

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.

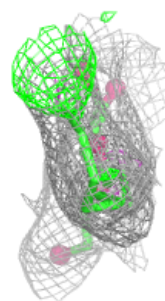
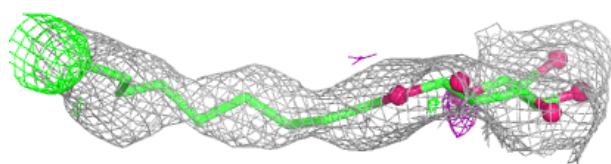
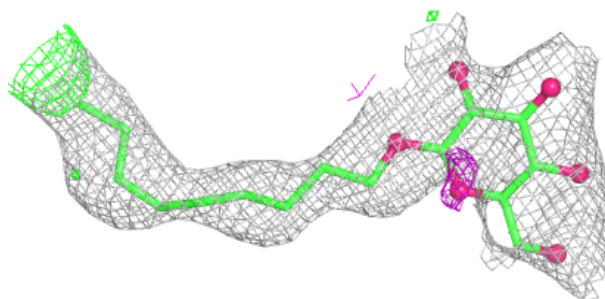
Electron density around P6G A 224:

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

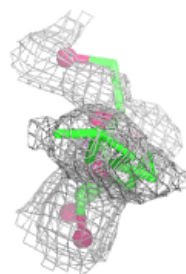
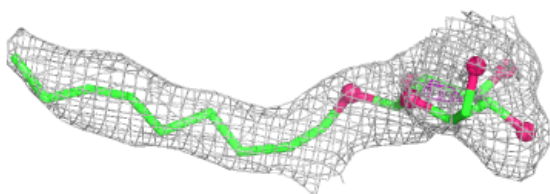
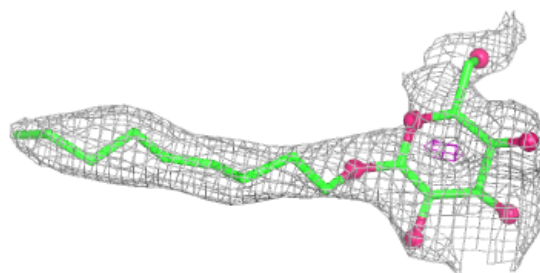


Electron density around BNG A 206:

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

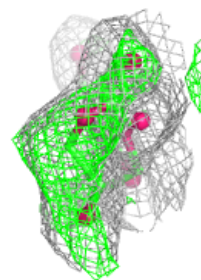
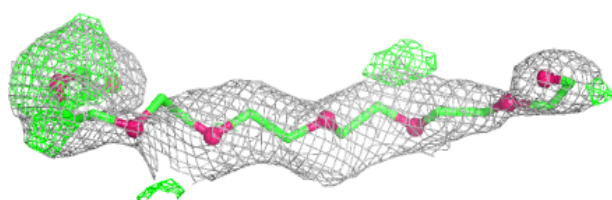
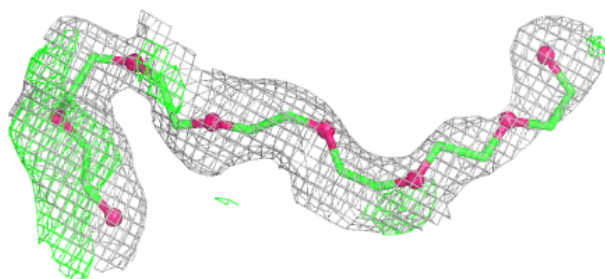
**Electron density around BNG A 204:**

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

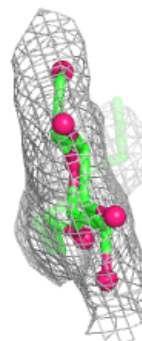
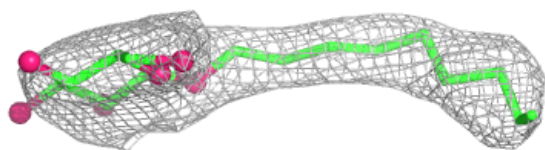


Electron density around P33 B 222:

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

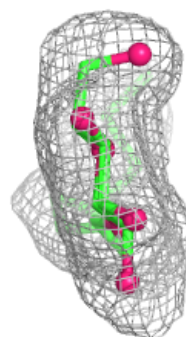
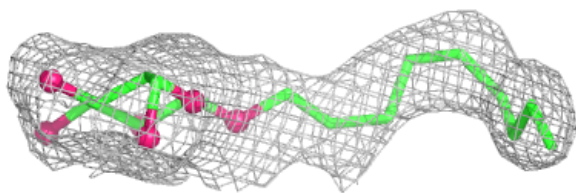
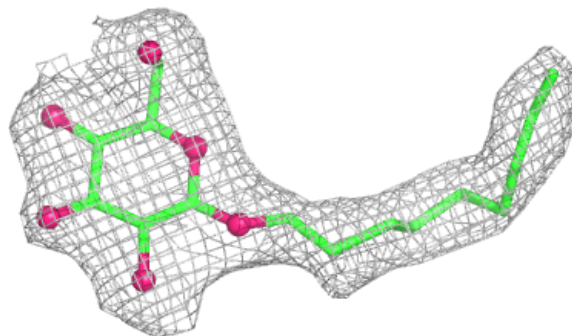
**Electron density around BNG A 205:**

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and green (positive)

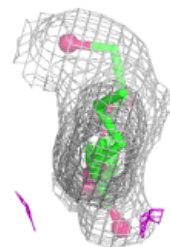
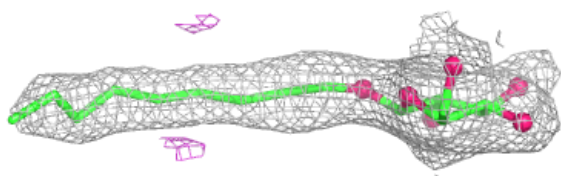
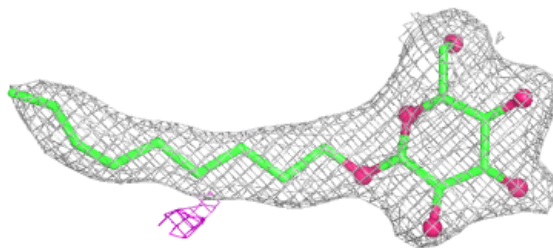


Electron density around BNG B 203:

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

**Electron density around BNG B 204:**

$2mF_o-DF_c$ (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.