



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:55 PM UTC

PDB ID : 1ECZ / pdb_00001ecz
Title : PROTEASE INHIBITOR ECOTIN
Authors : Shin, D.H.; Suh, S.W.
Deposited on : 1996-08-06
Resolution : 2.68 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

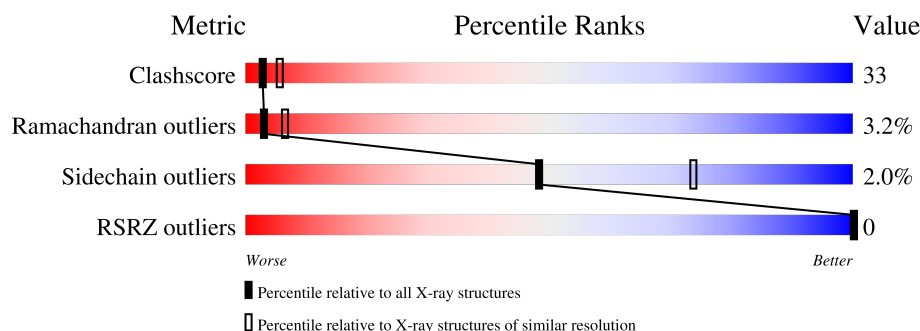
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.68 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))
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	142	
1	B	142	

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	BOG	A	1001	X	-	-	-
2	BOG	A	1009	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	BOG	A	1011	X	-	-	-
2	BOG	A	1015	X	-	-	-
2	BOG	A	1019	X	-	-	-
2	BOG	A	1021	X	-	-	-
2	BOG	A	1025	X	-	-	-
2	BOG	A	1029	X	-	-	-
2	BOG	A	1033	X	-	-	-
2	BOG	A	1041	X	-	-	-
2	BOG	B	1005	X	-	-	-
2	BOG	B	1007	X	-	-	-
2	BOG	B	1013	X	-	-	-
2	BOG	B	1017	X	-	-	-
2	BOG	B	1023	X	-	-	-
2	BOG	B	1027	X	-	-	-
2	BOG	B	1031	X	-	-	-
2	BOG	B	1035	X	-	X	-
2	BOG	B	1037	X	-	-	-
2	BOG	B	1039	X	-	-	-

2 Entry composition [i](#)

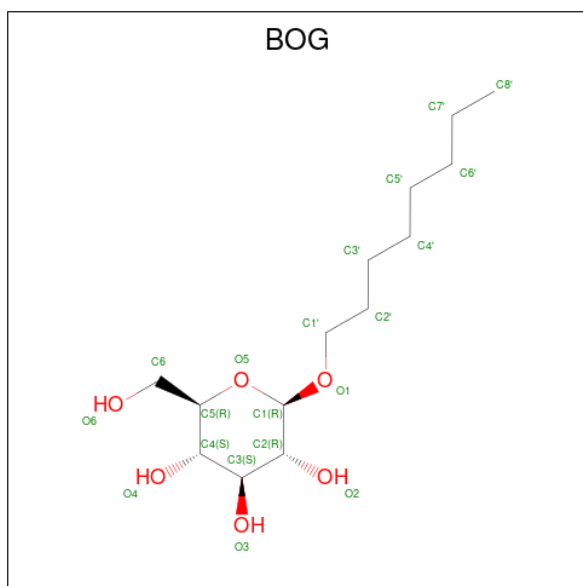
There are 3 unique types of molecules in this entry. The entry contains 2767 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ECOTIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	142	Total	C	N	O	S	0	0	0
			1130	721	187	216	6			
1	B	142	Total	C	N	O	S	0	0	0
			1130	721	187	216	6			

- Molecule 2 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: $C_{14}H_{28}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			20	14	6		
2	A	1	Total	C	O	0	0
			20	14	6		
2	A	1	Total	C	O	0	0
			20	14	6		
2	A	1	Total	C	O	0	0
			20	14	6		

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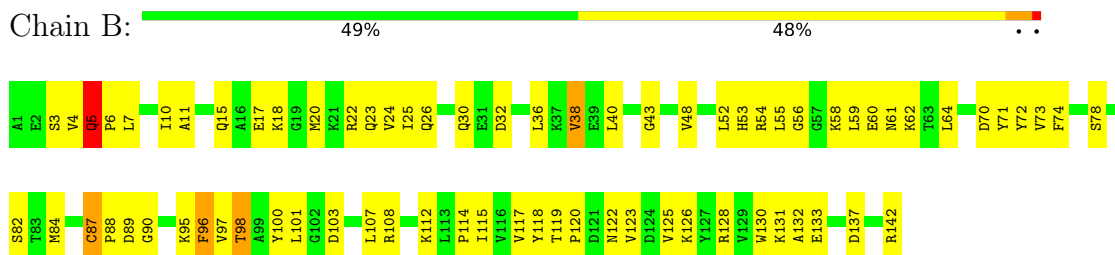
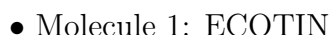
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 20 14 6	0	0
2	A	1	Total C O 20 14 6	0	0
2	A	1	Total C O 20 14 6	0	0
2	A	1	Total C O 20 14 6	0	0
2	A	1	Total C O 20 14 6	0	0
2	A	1	Total C O 20 14 6	0	0
2	A	1	Total C O 12 6 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0
2	B	1	Total C O 20 14 6	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	49	Total O 49 49	0	0
3	B	46	Total O 46 46	0	0

- Molecule 1: ECOTIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	39.22Å 84.86Å 98.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.68 6.00 – 2.69	Depositor EDS
% Data completeness (in resolution range)	78.1 (6.00-2.68) 70.8 (6.00-2.69)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.68Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.195 , 0.309 0.229 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 234.8	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	2767	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.90 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6568e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BOG

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	0.47	0/1152	0.95	5/1558 (0.3%)
1	B	0.44	0/1152	0.96	5/1558 (0.3%)
All	All	0.45	0/2304	0.96	10/3116 (0.3%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	5	GLN	N-CA-C	7.26	125.86	109.81
1	B	98	THR	N-CA-C	7.14	119.74	110.53
1	B	24	VAL	N-CA-C	6.49	117.61	107.28
1	A	122	ASN	N-CA-C	6.34	119.00	111.71
1	B	122	ASN	N-CA-C	6.19	118.03	111.28
1	A	70	ASP	N-CA-C	6.14	119.25	109.24
1	A	5	GLN	N-CA-C	6.02	123.12	109.81
1	A	24	VAL	N-CA-C	5.88	116.63	107.28
1	A	98	THR	N-CA-C	5.52	118.00	110.55
1	B	101	LEU	N-CA-C	-5.01	107.02	113.23

There are no chirality outliers.

There are no planarity outliers.

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	1130	0	1144	74	0
1	B	1130	0	1146	80	0
2	A	212	0	291	38	0
2	B	200	0	280	30	0
3	A	49	0	0	3	0
3	B	46	0	0	3	0
All	All	2767	0	2861	180	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 33.

All (180) 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)
2:B:1035:BOG:C3	2:B:1035:BOG:H1'2	1.70	1.19
2:A:1015:BOG:H2'1	2:A:1015:BOG:H5	1.20	1.18
2:A:1021:BOG:H1'1	2:A:1021:BOG:H5	1.09	1.08
1:B:112:LYS:HD3	2:B:1013:BOG:H8'3	1.40	1.02
2:B:1035:BOG:H3	2:B:1035:BOG:C1'	1.89	1.02
2:A:1021:BOG:H1'1	2:A:1021:BOG:C5	1.91	1.00
1:B:74:PHE:HB3	1:B:119:THR:HG22	1.44	0.99
1:A:104:ALA:HB2	2:A:1033:BOG:H1'2	1.48	0.93
2:A:1015:BOG:H5	2:A:1015:BOG:C2'	1.99	0.92
2:B:1035:BOG:H1'2	2:B:1035:BOG:H3	0.94	0.92
2:A:1021:BOG:H5	2:A:1021:BOG:C1'	2.00	0.92
1:B:54:ARG:HB2	2:B:1035:BOG:H62	1.52	0.89
2:A:1011:BOG:H1	2:A:1011:BOG:H3'2	1.52	0.89
1:A:74:PHE:HB3	1:A:119:THR:HG22	1.55	0.88
2:A:1021:BOG:H1'2	2:A:1021:BOG:H3	1.56	0.86
2:A:1025:BOG:H3'1	2:A:1025:BOG:H1	1.59	0.85
1:B:133:GLU:OE2	2:B:1023:BOG:H2	1.78	0.83
1:B:5:GLN:HG2	2:B:1005:BOG:H61	1.59	0.83
1:B:133:GLU:CD	2:B:1023:BOG:H2	2.05	0.81
2:B:1023:BOG:H5'2	2:B:1023:BOG:H1'1	1.61	0.81
1:B:17:GLU:HG2	1:B:18:LYS:H	1.50	0.77
2:A:1021:BOG:C1'	2:A:1021:BOG:H3	2.16	0.76
1:A:24:VAL:HG22	1:A:116:VAL:HG22	1.69	0.74
2:B:1035:BOG:C3	2:B:1035:BOG:C1'	2.58	0.73
1:B:87:CYS:HB3	1:B:88:PRO:HD2	1.71	0.72
1:A:87:CYS:HB3	1:A:88:PRO:HD2	1.73	0.71
1:B:15:GLN:HA	1:B:22:ARG:NH2	2.06	0.70
2:A:1015:BOG:H2'1	2:A:1015:BOG:C5	2.12	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1011:BOG:H1	2:A:1011:BOG:C3'	2.16	0.69
1:B:112:LYS:CD	2:B:1013:BOG:H8'3	2.22	0.69
1:B:74:PHE:CB	1:B:119:THR:HG22	2.23	0.67
1:A:56:GLY:O	1:A:77:VAL:HA	1.95	0.67
1:B:53:HIS:HA	1:B:82:SER:HB3	1.77	0.66
1:A:87:CYS:C	1:A:89:ASP:H	2.03	0.66
1:B:54:ARG:HB2	2:B:1035:BOG:C6	2.23	0.66
2:A:1021:BOG:C5	2:A:1021:BOG:C1'	2.69	0.64
1:B:5:GLN:HB2	1:B:6:PRO:HD3	1.78	0.64
1:B:5:GLN:CG	2:B:1005:BOG:H61	2.28	0.64
1:A:133:GLU:O	1:B:128:ARG:HD3	1.98	0.63
1:A:5:GLN:HB2	1:A:6:PRO:HD3	1.81	0.62
1:A:140:VAL:HG23	1:A:142:ARG:HG2	1.80	0.62
1:A:54:ARG:HG3	2:A:1011:BOG:H3	1.81	0.62
1:B:73:VAL:HG22	1:B:118:TYR:HB2	1.81	0.62
1:A:104:ALA:HB2	2:A:1033:BOG:C1'	2.26	0.61
2:A:1021:BOG:C1'	2:A:1021:BOG:C3	2.78	0.61
2:A:1029:BOG:H1'2	2:A:1029:BOG:O2	1.99	0.60
1:A:59:LEU:HD12	1:A:73:VAL:O	2.01	0.60
2:A:1015:BOG:H5	2:A:1015:BOG:C1'	2.32	0.58
1:B:43:GLY:HA3	1:B:98:THR:HA	1.85	0.58
1:A:134:GLU:HB2	2:A:1001:BOG:H61	1.85	0.58
1:A:107:LEU:HD12	1:A:115:ILE:HD13	1.86	0.58
1:B:74:PHE:HE2	1:B:123:VAL:HG21	1.69	0.58
1:A:103:ASP:HB2	1:B:103:ASP:HB2	1.86	0.58
2:A:1015:BOG:H3'1	1:B:142:ARG:HD2	1.86	0.57
1:B:84:MET:HB2	2:B:1007:BOG:O3	2.05	0.57
2:B:1031:BOG:H5	2:B:1031:BOG:O2	2.03	0.56
1:A:54:ARG:NH2	2:A:1011:BOG:H1'2	2.19	0.56
1:B:72:TYR:HE1	1:B:115:ILE:HG23	1.71	0.56
1:A:43:GLY:HA3	1:A:98:THR:HA	1.86	0.56
2:A:1015:BOG:C5	2:A:1015:BOG:C1'	2.84	0.56
1:A:58:LYS:NZ	1:A:60:GLU:HB3	2.21	0.56
1:A:6:PRO:HA	2:A:1015:BOG:H3'2	1.87	0.55
1:B:87:CYS:C	1:B:89:ASP:H	2.13	0.55
1:A:56:GLY:HA3	1:A:78:SER:OG	2.06	0.55
1:A:74:PHE:CB	1:A:119:THR:HG22	2.33	0.55
1:B:62:LYS:HE2	1:B:73:VAL:HG21	1.89	0.55
1:B:15:GLN:HA	1:B:22:ARG:HH21	1.72	0.54
1:A:20:MET:HB3	1:A:120:PRO:HA	1.89	0.54
1:A:48:VAL:HB	1:A:53:HIS:CE1	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:ASP:HA	2:B:1039:BOG:H5'2	1.88	0.54
1:A:130:TRP:CD2	1:B:132:ALA:HB2	2.43	0.54
1:B:133:GLU:OE1	2:B:1023:BOG:H2	2.08	0.53
1:A:5:GLN:CB	1:A:6:PRO:HD3	2.38	0.53
1:A:58:LYS:HZ1	1:A:60:GLU:HB3	1.74	0.52
1:B:5:GLN:CB	1:B:6:PRO:HD3	2.39	0.52
2:A:1025:BOG:H1	2:A:1025:BOG:C3'	2.23	0.52
1:B:17:GLU:HG2	1:B:18:LYS:N	2.23	0.52
1:B:48:VAL:HB	1:B:53:HIS:CE1	2.45	0.52
1:A:95:LYS:HD3	3:A:760:HOH:O	2.09	0.52
1:A:141:VAL:HG12	1:A:141:VAL:O	2.10	0.51
1:A:88:PRO:C	1:A:90:GLY:H	2.18	0.51
2:A:1015:BOG:H2'2	1:B:142:ARG:HD3	1.93	0.51
1:A:54:ARG:CG	2:A:1011:BOG:H3	2.40	0.51
1:A:100:TYR:CG	2:A:1011:BOG:H1'1	2.45	0.51
1:A:13:TYR:OH	1:A:69:TYR:HD2	1.94	0.51
1:B:5:GLN:N	1:B:5:GLN:OE1	2.43	0.51
1:A:18:LYS:HG3	3:A:775:HOH:O	2.11	0.51
1:A:87:CYS:O	1:A:89:ASP:N	2.44	0.51
1:B:11:ALA:HB1	1:B:64:LEU:HD23	1.92	0.51
1:B:25:ILE:HB	1:B:115:ILE:HB	1.93	0.50
1:A:37:LYS:HB2	1:B:130:TRP:CZ3	2.47	0.50
1:A:134:GLU:HB2	2:A:1001:BOG:C6	2.42	0.50
1:A:44:GLN:O	1:A:46:LEU:HG	2.12	0.50
1:A:54:ARG:CZ	2:A:1011:BOG:H1'2	2.42	0.50
1:B:23:GLN:HG3	1:B:125:VAL:HG21	1.94	0.49
1:A:87:CYS:C	1:A:89:ASP:N	2.69	0.49
2:A:1009:BOG:O2	2:A:1009:BOG:H1'2	2.12	0.49
1:A:7:LEU:HD22	1:A:24:VAL:HG21	1.93	0.49
2:A:1029:BOG:C3'	2:A:1029:BOG:H1	2.42	0.49
1:A:26:GLN:OE1	1:A:114:PRO:HB3	2.12	0.49
2:B:1035:BOG:O3	2:B:1035:BOG:H8'3	2.13	0.49
1:B:58:LYS:NZ	1:B:60:GLU:HB3	2.28	0.49
1:B:30:GLN:HG3	1:B:36:LEU:HD11	1.95	0.48
1:A:123:VAL:HG12	1:A:124:ASP:N	2.28	0.48
1:A:15:GLN:HA	1:A:22:ARG:NH2	2.28	0.48
1:A:54:ARG:O	1:A:80:PRO:HA	2.13	0.48
1:A:11:ALA:HB1	1:A:64:LEU:HD23	1.95	0.48
1:A:38:VAL:HG12	1:A:107:LEU:HB2	1.94	0.48
1:A:39:GLU:HB2	1:A:106:MET:HE2	1.94	0.48
2:B:1035:BOG:H3	2:B:1035:BOG:H3'2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:GLY:HA3	1:B:78:SER:OG	2.14	0.47
1:B:20:MET:CB	1:B:120:PRO:HA	2.45	0.47
1:B:108:ARG:CZ	2:B:1039:BOG:H1'1	2.45	0.47
1:A:87:CYS:HA	2:A:1041:BOG:O4	2.15	0.47
2:A:1033:BOG:H2'2	2:A:1033:BOG:H1	1.69	0.47
1:A:11:ALA:HB1	1:A:64:LEU:CD2	2.44	0.47
1:A:22:ARG:HG3	1:A:118:TYR:CE1	2.50	0.46
1:B:52:LEU:HD12	2:B:1035:BOG:C1	2.45	0.46
2:B:1035:BOG:C1'	2:B:1035:BOG:H5	2.45	0.46
1:B:26:GLN:OE1	1:B:114:PRO:HB3	2.16	0.46
1:B:23:GLN:HG3	1:B:125:VAL:CG2	2.45	0.46
1:A:130:TRP:CE2	1:B:132:ALA:HB2	2.51	0.45
1:B:112:LYS:HB3	2:B:1013:BOG:H7'1	1.99	0.45
1:B:17:GLU:H	1:B:20:MET:HE2	1.80	0.45
1:B:59:LEU:HD12	1:B:73:VAL:O	2.17	0.45
1:A:130:TRP:CE3	1:B:132:ALA:HB2	2.52	0.45
1:A:6:PRO:HB2	1:A:9:LYS:HB2	1.98	0.45
1:A:77:VAL:O	1:A:77:VAL:HG13	2.17	0.45
1:A:87:CYS:HA	2:A:1041:BOG:O3	2.16	0.45
1:A:72:TYR:N	1:A:72:TYR:CD1	2.85	0.44
1:B:87:CYS:O	1:B:89:ASP:N	2.50	0.44
1:A:4:VAL:HG13	1:A:10:ILE:HD11	1.99	0.44
1:B:5:GLN:HG2	2:B:1005:BOG:O4	2.17	0.44
2:B:1039:BOG:H1	2:B:1039:BOG:H2'2	1.67	0.44
1:B:96:PHE:CE2	1:B:126:LYS:HD2	2.52	0.44
1:A:140:VAL:CG2	1:A:142:ARG:HG2	2.47	0.44
1:B:7:LEU:HD23	1:B:22:ARG:NH1	2.33	0.43
1:B:40:LEU:HD11	1:B:107:LEU:HD11	2.00	0.43
1:B:88:PRO:C	1:B:90:GLY:H	2.25	0.43
1:B:87:CYS:C	1:B:89:ASP:N	2.76	0.43
2:B:1037:BOG:H6'2	2:B:1037:BOG:H2'1	2.01	0.43
1:B:38:VAL:HG12	1:B:107:LEU:HB2	2.01	0.43
1:B:54:ARG:HH11	1:B:100:TYR:HB2	1.83	0.43
1:B:95:LYS:O	1:B:97:VAL:HG23	2.19	0.43
1:A:42:ILE:HD12	1:A:101:LEU:HD21	2.01	0.43
1:B:43:GLY:CA	1:B:98:THR:HA	2.48	0.43
1:B:137:ASP:HB3	3:B:786:HOH:O	2.17	0.43
1:B:72:TYR:CD1	1:B:72:TYR:N	2.85	0.43
1:B:61:ASN:ND2	1:B:72:TYR:CE2	2.86	0.42
1:B:61:ASN:HB3	2:B:1037:BOG:H7'2	2.00	0.42
2:A:1025:BOG:H4'1	2:A:1025:BOG:H1'2	1.91	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:LYS:HE3	1:A:9:LYS:HB3	1.93	0.42
1:B:48:VAL:CG2	1:B:95:LYS:HD2	2.49	0.42
1:A:47:GLU:HG2	1:A:92:LYS:HB3	2.01	0.42
1:A:127:TYR:CZ	1:B:137:ASP:HB2	2.54	0.42
2:A:1019:BOG:H1	2:A:1019:BOG:H2'1	1.83	0.42
2:B:1031:BOG:H4'1	2:B:1031:BOG:H1'1	1.82	0.42
1:A:30:GLN:HE21	1:A:30:GLN:HA	1.85	0.42
2:A:1029:BOG:H1	2:A:1029:BOG:H3'2	2.01	0.42
1:B:4:VAL:O	1:B:4:VAL:HG13	2.20	0.42
1:B:20:MET:HB3	1:B:120:PRO:HA	2.00	0.41
1:B:88:PRO:HD3	3:B:792:HOH:O	2.20	0.41
1:A:5:GLN:O	1:B:142:ARG:NH1	2.53	0.41
1:B:58:LYS:HZ1	1:B:60:GLU:HB3	1.84	0.41
3:A:704:HOH:O	1:B:131:LYS:HB3	2.20	0.41
1:A:25:ILE:HB	1:A:115:ILE:HB	2.03	0.41
1:A:138:ASN:OD1	1:B:126:LYS:HE3	2.20	0.41
1:B:62:LYS:HB2	1:B:71:TYR:CE1	2.56	0.41
1:A:30:GLN:HG3	1:A:36:LEU:HD11	2.02	0.41
1:A:100:TYR:HB2	2:A:1011:BOG:H1'1	2.03	0.41
1:B:43:GLY:HA2	1:B:55:LEU:HD23	2.03	0.41
1:B:52:LEU:HD12	2:B:1035:BOG:O5	2.20	0.41
1:A:26:GLN:CD	1:A:114:PRO:HB3	2.46	0.41
1:A:40:LEU:HD11	1:A:107:LEU:HD11	2.02	0.41
1:B:52:LEU:HD22	3:B:727:HOH:O	2.20	0.41
1:A:46:LEU:O	1:A:94:LYS:HA	2.20	0.40
1:B:108:ARG:NH2	2:B:1039:BOG:H1'1	2.36	0.40
1:A:123:VAL:CG1	1:A:124:ASP:N	2.85	0.40
1:A:62:LYS:HB2	1:A:71:TYR:CE1	2.57	0.40
1:A:74:PHE:HE2	1:A:123:VAL:HG21	1.86	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	140/142 (99%)	113 (81%)	23 (16%)	4 (3%)	3	8
1	B	140/142 (99%)	114 (81%)	21 (15%)	5 (4%)	2	5
All	All	280/284 (99%)	227 (81%)	44 (16%)	9 (3%)	3	6

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	B	5	GLN
1	A	3	SER
1	B	3	SER
1	B	96	PHE
1	B	87	CYS
1	A	88	PRO
1	A	10	ILE
1	B	10	ILE

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	125/125 (100%)	123 (98%)	2 (2%)	55	78
1	B	125/125 (100%)	122 (98%)	3 (2%)	43	70
All	All	250/250 (100%)	245 (98%)	5 (2%)	48	74

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

Mol	Chain	Res	Type
1	A	54	ARG
1	A	117	VAL
1	B	38	VAL
1	B	70	ASP
1	B	117	VAL

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	30	GLN
1	A	44	GLN
1	A	53	HIS
1	B	30	GLN
1	B	44	GLN
1	B	53	HIS

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 ⓘ

21 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	$\# Z > 2$
2	BOG	A	1009	-	20,20,20	0.44	0	25,25,25	0.56	0
2	BOG	A	1011	-	20,20,20	0.52	0	25,25,25	0.61	0
2	BOG	A	1003	-	20,20,20	0.46	0	25,25,25	0.79	2 (8%)
2	BOG	A	1021	-	20,20,20	0.46	0	25,25,25	0.82	2 (8%)
2	BOG	A	1029	-	20,20,20	0.42	0	25,25,25	0.56	0
2	BOG	A	1001	-	20,20,20	0.50	0	25,25,25	0.64	0
2	BOG	B	1031	-	20,20,20	0.50	0	25,25,25	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BOG	B	1027	-	20,20,20	0.49	0	25,25,25	0.62	0
2	BOG	B	1007	-	20,20,20	0.43	0	25,25,25	0.60	0
2	BOG	A	1019	-	20,20,20	0.43	0	25,25,25	0.66	0
2	BOG	B	1037	-	20,20,20	0.45	0	25,25,25	0.62	1 (4%)
2	BOG	A	1041	-	12,12,20	0.30	0	17,17,25	0.56	0
2	BOG	B	1039	-	20,20,20	0.50	0	25,25,25	0.80	0
2	BOG	B	1017	-	20,20,20	0.48	0	25,25,25	0.62	0
2	BOG	B	1023	-	20,20,20	0.48	0	25,25,25	0.66	1 (4%)
2	BOG	A	1015	-	20,20,20	0.48	0	25,25,25	0.80	1 (4%)
2	BOG	A	1033	-	20,20,20	0.49	0	25,25,25	0.68	0
2	BOG	A	1025	-	20,20,20	0.46	0	25,25,25	0.66	0
2	BOG	B	1005	-	20,20,20	0.50	0	25,25,25	0.59	0
2	BOG	B	1035	-	20,20,20	0.45	0	25,25,25	0.90	2 (8%)
2	BOG	B	1013	-	20,20,20	0.46	0	25,25,25	0.61	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	BOG	A	1009	-	1/1/5/5	5/11/31/31	0/1/1/1
2	BOG	A	1011	-	1/1/5/5	6/11/31/31	0/1/1/1
2	BOG	A	1003	-	-	6/11/31/31	0/1/1/1
2	BOG	A	1021	-	1/1/5/5	4/11/31/31	0/1/1/1
2	BOG	A	1029	-	1/1/5/5	5/11/31/31	0/1/1/1
2	BOG	A	1001	-	1/1/5/5	8/11/31/31	0/1/1/1
2	BOG	B	1031	-	1/1/5/5	4/11/31/31	0/1/1/1
2	BOG	B	1027	-	1/1/5/5	8/11/31/31	0/1/1/1
2	BOG	B	1007	-	1/1/5/5	8/11/31/31	0/1/1/1
2	BOG	A	1019	-	1/1/5/5	6/11/31/31	0/1/1/1
2	BOG	B	1037	-	1/1/5/5	7/11/31/31	0/1/1/1
2	BOG	A	1041	-	1/1/5/5	0/2/22/31	0/1/1/1
2	BOG	B	1039	-	1/1/5/5	9/11/31/31	0/1/1/1
2	BOG	B	1017	-	1/1/5/5	5/11/31/31	0/1/1/1
2	BOG	B	1023	-	1/1/5/5	6/11/31/31	0/1/1/1
2	BOG	A	1015	-	1/1/5/5	5/11/31/31	0/1/1/1
2	BOG	A	1033	-	1/1/5/5	8/11/31/31	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BOG	A	1025	-	1/1/5/5	8/11/31/31	0/1/1/1
2	BOG	B	1005	-	1/1/5/5	7/11/31/31	0/1/1/1
2	BOG	B	1035	-	1/1/5/5	5/11/31/31	0/1/1/1
2	BOG	B	1013	-	1/1/5/5	4/11/31/31	0/1/1/1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1035	BOG	C1'-O1-C1	2.98	118.76	113.68
2	A	1003	BOG	C1'-O1-C1	2.66	118.22	113.68
2	A	1021	BOG	C1'-O1-C1	2.64	118.20	113.68
2	B	1035	BOG	O1-C1-C2	2.64	112.28	108.27
2	A	1021	BOG	O1-C1-C2	2.25	111.69	108.27
2	A	1015	BOG	C3'-C2'-C1'	2.18	122.96	113.47
2	A	1003	BOG	O1-C1-C2	2.15	111.53	108.27
2	B	1023	BOG	O1-C1-C2	2.07	111.41	108.27
2	B	1037	BOG	O1-C1-C2	2.06	111.40	108.27

All (20) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1001	BOG	C1
2	A	1009	BOG	C1
2	A	1011	BOG	C1
2	A	1015	BOG	C1
2	A	1019	BOG	C1
2	A	1021	BOG	C1
2	A	1025	BOG	C1
2	A	1029	BOG	C1
2	A	1033	BOG	C1
2	A	1041	BOG	C1
2	B	1005	BOG	C1
2	B	1007	BOG	C1
2	B	1013	BOG	C1
2	B	1017	BOG	C1
2	B	1023	BOG	C1
2	B	1027	BOG	C1
2	B	1031	BOG	C1
2	B	1035	BOG	C1
2	B	1037	BOG	C1

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Mol	Chain	Res	Type	Atom
2	B	1039	BOG	C1

All (124) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1003	BOG	C2-C1-O1-C1'
2	A	1009	BOG	O5-C1-O1-C1'
2	A	1011	BOG	C2'-C1'-O1-C1
2	A	1015	BOG	C2'-C1'-O1-C1
2	A	1019	BOG	C2'-C1'-O1-C1
2	A	1025	BOG	C2-C1-O1-C1'
2	A	1025	BOG	O5-C1-O1-C1'
2	A	1025	BOG	C2'-C1'-O1-C1
2	A	1029	BOG	O5-C1-O1-C1'
2	A	1033	BOG	C2'-C1'-O1-C1
2	B	1005	BOG	C2-C1-O1-C1'
2	B	1005	BOG	O5-C1-O1-C1'
2	B	1007	BOG	C2-C1-O1-C1'
2	B	1013	BOG	C2'-C1'-O1-C1
2	B	1017	BOG	C2'-C1'-O1-C1
2	B	1023	BOG	C2'-C1'-O1-C1
2	B	1027	BOG	C2'-C1'-O1-C1
2	B	1031	BOG	O5-C1-O1-C1'
2	B	1035	BOG	C2-C1-O1-C1'
2	B	1035	BOG	C2'-C1'-O1-C1
2	B	1039	BOG	O5-C1-O1-C1'
2	B	1039	BOG	C2'-C1'-O1-C1
2	A	1011	BOG	O5-C1-O1-C1'
2	A	1015	BOG	O5-C1-O1-C1'
2	A	1033	BOG	O5-C1-O1-C1'
2	B	1007	BOG	O5-C1-O1-C1'
2	A	1009	BOG	C2-C1-O1-C1'
2	A	1011	BOG	C2-C1-O1-C1'
2	A	1033	BOG	C2-C1-O1-C1'
2	A	1001	BOG	C2'-C3'-C4'-C5'
2	A	1003	BOG	C3'-C4'-C5'-C6'
2	A	1001	BOG	O1-C1'-C2'-C3'
2	B	1027	BOG	O1-C1'-C2'-C3'
2	B	1039	BOG	O1-C1'-C2'-C3'
2	B	1007	BOG	O1-C1'-C2'-C3'
2	B	1035	BOG	O1-C1'-C2'-C3'
2	A	1001	BOG	C2-C1-O1-C1'

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Mol	Chain	Res	Type	Atoms
2	B	1023	BOG	C2-C1-O1-C1'
2	B	1039	BOG	C2-C1-O1-C1'
2	A	1001	BOG	C1'-C2'-C3'-C4'
2	A	1001	BOG	O5-C1-O1-C1'
2	A	1029	BOG	C3'-C4'-C5'-C6'
2	B	1023	BOG	C4'-C5'-C6'-C7'
2	A	1011	BOG	C3'-C4'-C5'-C6'
2	A	1029	BOG	C2'-C3'-C4'-C5'
2	B	1027	BOG	C2'-C3'-C4'-C5'
2	B	1005	BOG	C1'-C2'-C3'-C4'
2	A	1003	BOG	C1'-C2'-C3'-C4'
2	B	1027	BOG	C1'-C2'-C3'-C4'
2	B	1037	BOG	C4'-C5'-C6'-C7'
2	A	1015	BOG	C4'-C5'-C6'-C7'
2	B	1023	BOG	C3'-C4'-C5'-C6'
2	B	1035	BOG	C1'-C2'-C3'-C4'
2	A	1019	BOG	C3'-C4'-C5'-C6'
2	B	1013	BOG	C2'-C3'-C4'-C5'
2	B	1023	BOG	O5-C1-O1-C1'
2	A	1033	BOG	C1'-C2'-C3'-C4'
2	A	1029	BOG	C2-C1-O1-C1'
2	A	1019	BOG	C1'-C2'-C3'-C4'
2	B	1039	BOG	C1'-C2'-C3'-C4'
2	A	1033	BOG	C3'-C4'-C5'-C6'
2	B	1037	BOG	C2'-C3'-C4'-C5'
2	B	1017	BOG	C2'-C3'-C4'-C5'
2	B	1007	BOG	O5-C5-C6-O6
2	B	1037	BOG	O5-C5-C6-O6
2	B	1039	BOG	C2'-C3'-C4'-C5'
2	A	1025	BOG	O5-C5-C6-O6
2	B	1027	BOG	C4'-C5'-C6'-C7'
2	B	1027	BOG	C3'-C4'-C5'-C6'
2	A	1021	BOG	C4'-C5'-C6'-C7'
2	B	1005	BOG	C3'-C4'-C5'-C6'
2	B	1007	BOG	C4'-C5'-C6'-C7'
2	B	1035	BOG	C4'-C5'-C6'-C7'
2	B	1031	BOG	C2-C1-O1-C1'
2	A	1019	BOG	O5-C5-C6-O6
2	B	1027	BOG	O5-C5-C6-O6
2	B	1031	BOG	C1'-C2'-C3'-C4'
2	A	1019	BOG	C2'-C3'-C4'-C5'
2	B	1007	BOG	C3'-C4'-C5'-C6'

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Mol	Chain	Res	Type	Atoms
2	B	1039	BOG	C3'-C4'-C5'-C6'
2	B	1037	BOG	C5'-C6'-C7'-C8'
2	B	1039	BOG	C5'-C6'-C7'-C8'
2	A	1001	BOG	C5'-C6'-C7'-C8'
2	A	1015	BOG	C5'-C6'-C7'-C8'
2	B	1017	BOG	C5'-C6'-C7'-C8'
2	B	1039	BOG	C4'-C5'-C6'-C7'
2	A	1025	BOG	C5'-C6'-C7'-C8'
2	B	1013	BOG	C5'-C6'-C7'-C8'
2	A	1009	BOG	C2'-C1'-O1-C1
2	B	1005	BOG	C2'-C1'-O1-C1
2	A	1021	BOG	C2-C1-O1-C1'
2	A	1033	BOG	C2'-C3'-C4'-C5'
2	A	1033	BOG	C5'-C6'-C7'-C8'
2	A	1025	BOG	C2'-C3'-C4'-C5'
2	B	1007	BOG	C1'-C2'-C3'-C4'
2	A	1009	BOG	C3'-C4'-C5'-C6'
2	A	1021	BOG	C3'-C4'-C5'-C6'
2	A	1003	BOG	C5'-C6'-C7'-C8'
2	B	1017	BOG	C4'-C5'-C6'-C7'
2	A	1009	BOG	C4'-C5'-C6'-C7'
2	A	1011	BOG	C5'-C6'-C7'-C8'
2	B	1023	BOG	C5'-C6'-C7'-C8'
2	A	1001	BOG	C4'-C5'-C6'-C7'
2	A	1015	BOG	C2'-C3'-C4'-C5'
2	B	1031	BOG	O1-C1'-C2'-C3'
2	B	1037	BOG	C2-C1-O1-C1'
2	A	1001	BOG	C4-C5-C6-O6
2	A	1025	BOG	O1-C1'-C2'-C3'
2	A	1033	BOG	C4'-C5'-C6'-C7'
2	B	1005	BOG	C5'-C6'-C7'-C8'
2	B	1037	BOG	O1-C1'-C2'-C3'
2	A	1029	BOG	C2'-C1'-O1-C1
2	B	1027	BOG	C5'-C6'-C7'-C8'
2	A	1003	BOG	C2'-C3'-C4'-C5'
2	B	1013	BOG	C3'-C4'-C5'-C6'
2	A	1019	BOG	C4'-C5'-C6'-C7'
2	A	1021	BOG	C1'-C2'-C3'-C4'
2	B	1037	BOG	O5-C1-O1-C1'
2	A	1011	BOG	O1-C1'-C2'-C3'
2	A	1025	BOG	C4-C5-C6-O6
2	B	1007	BOG	C2'-C3'-C4'-C5'

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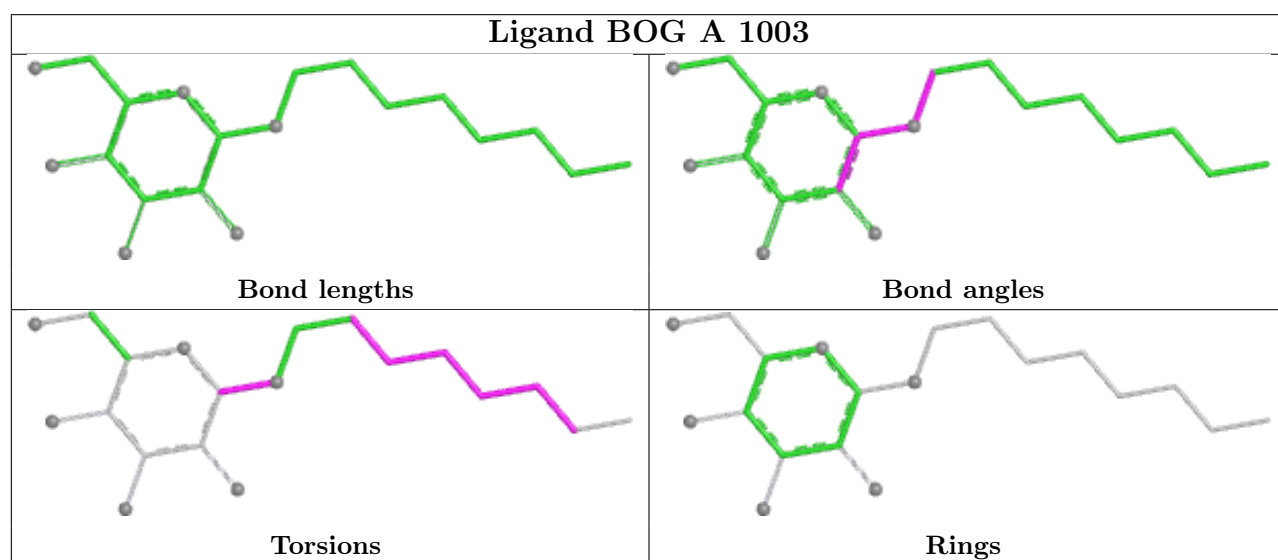
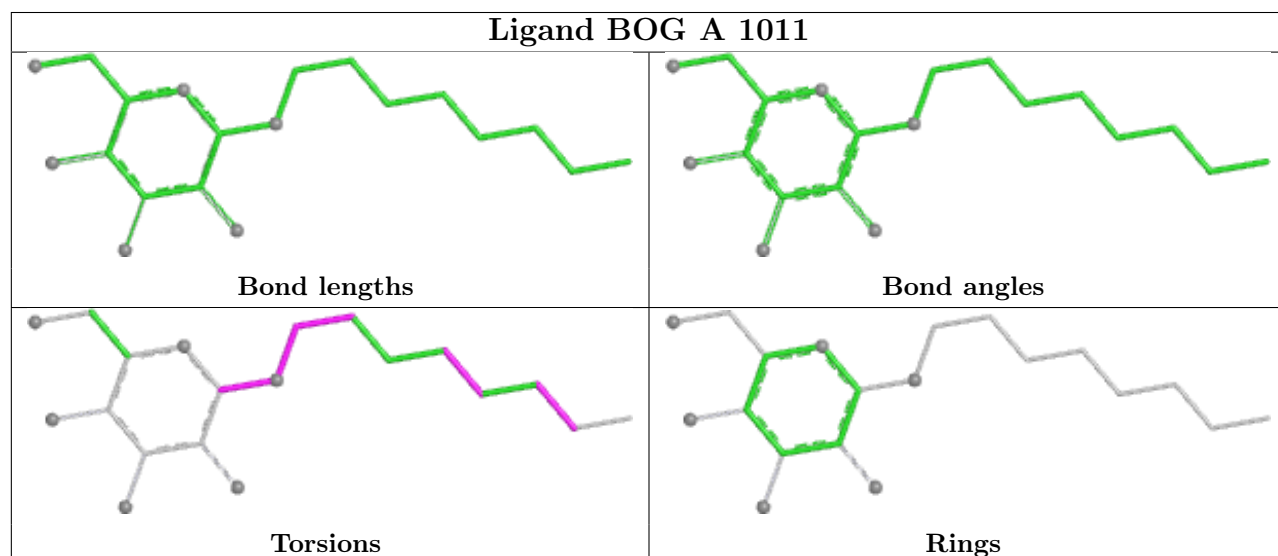
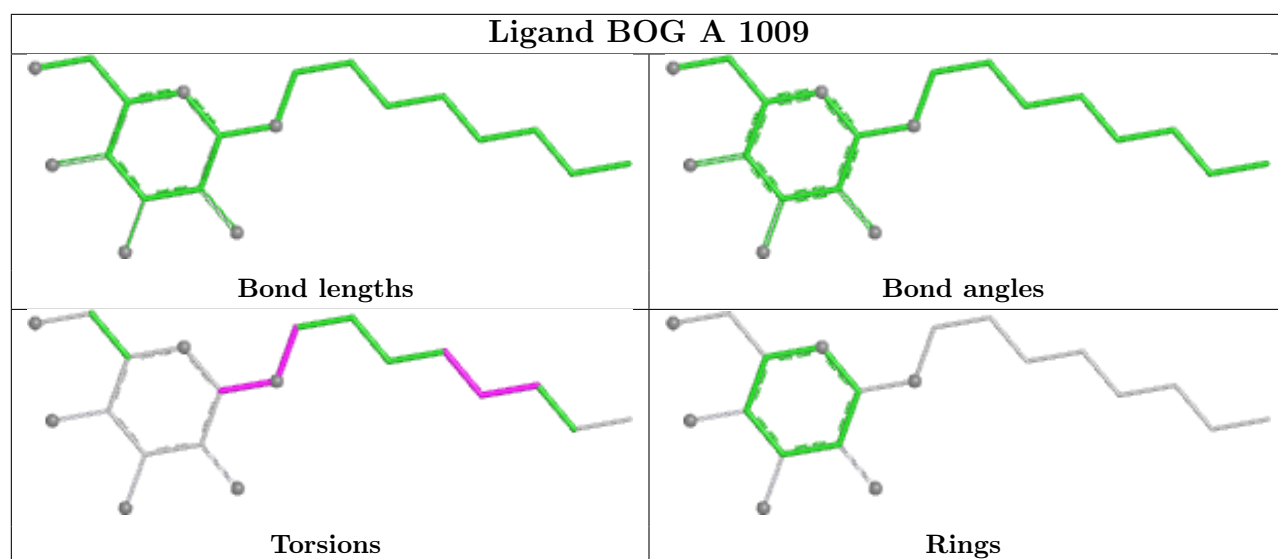
Mol	Chain	Res	Type	Atoms
2	A	1003	BOG	C4'-C5'-C6'-C7'
2	B	1005	BOG	C2'-C3'-C4'-C5'
2	B	1017	BOG	C1'-C2'-C3'-C4'

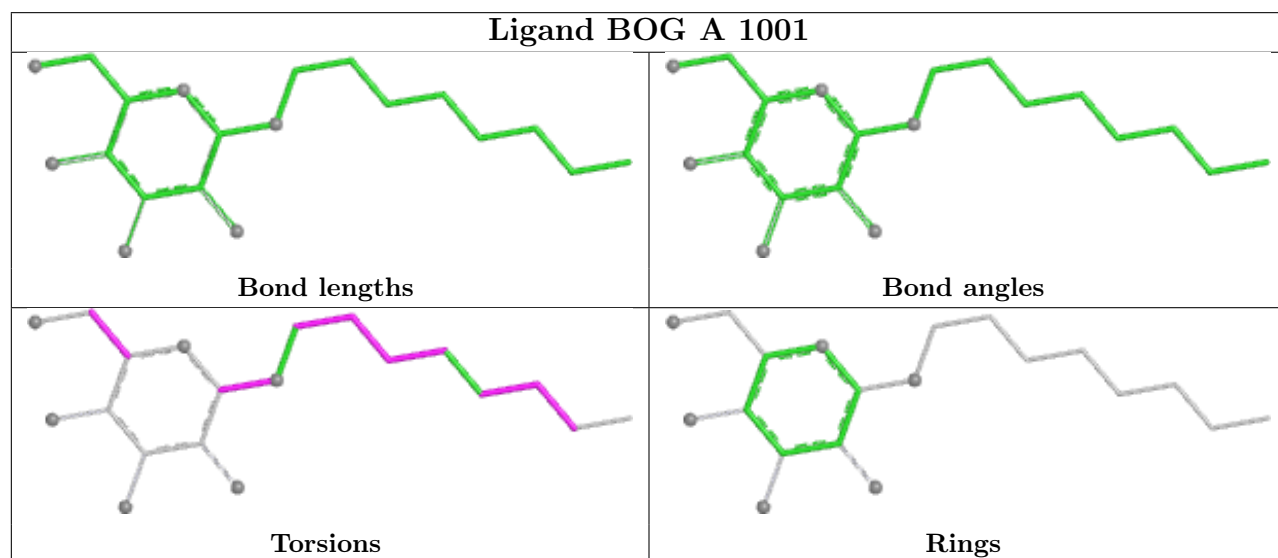
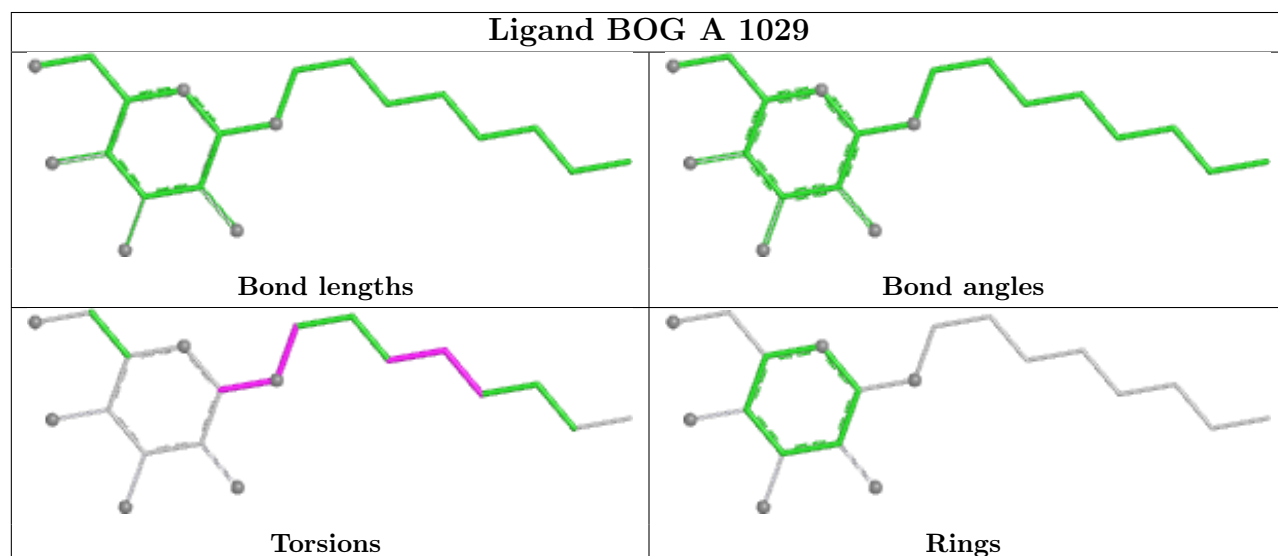
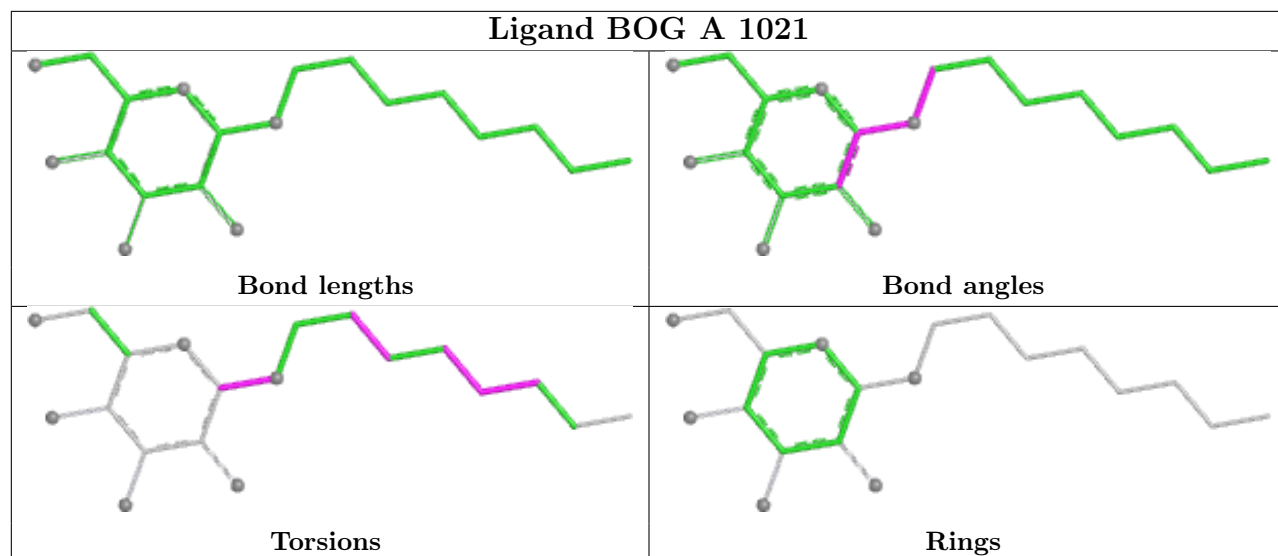
There are no ring outliers.

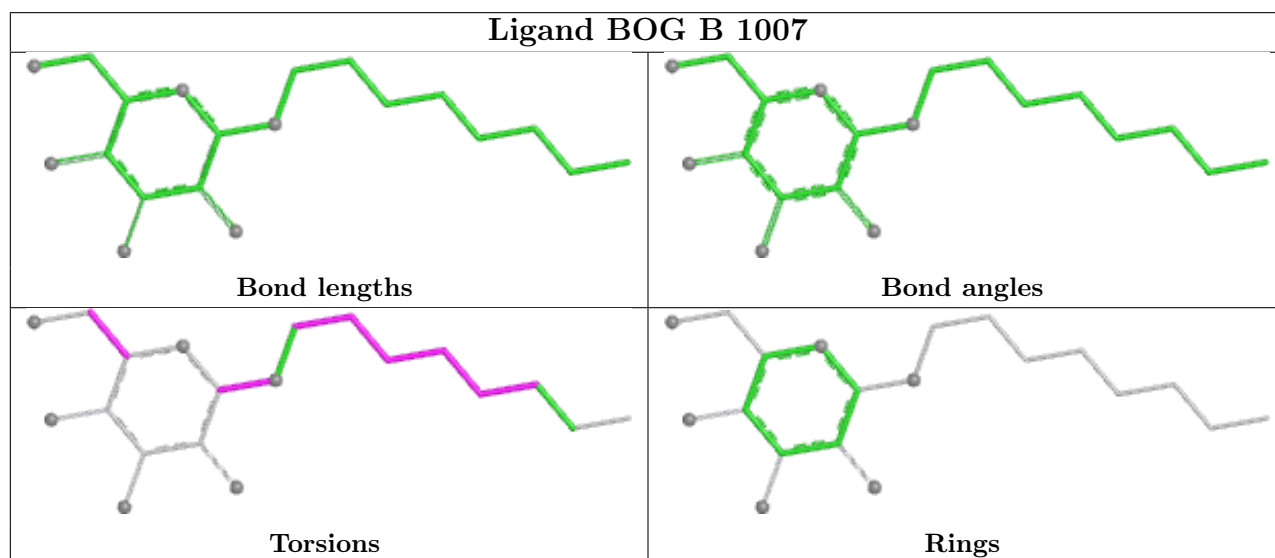
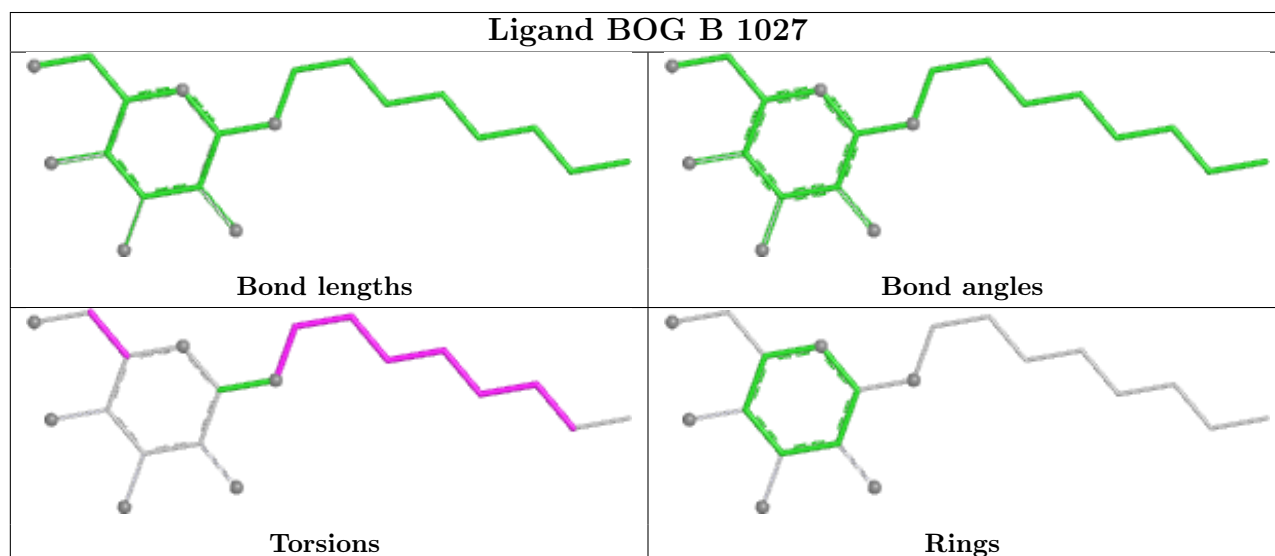
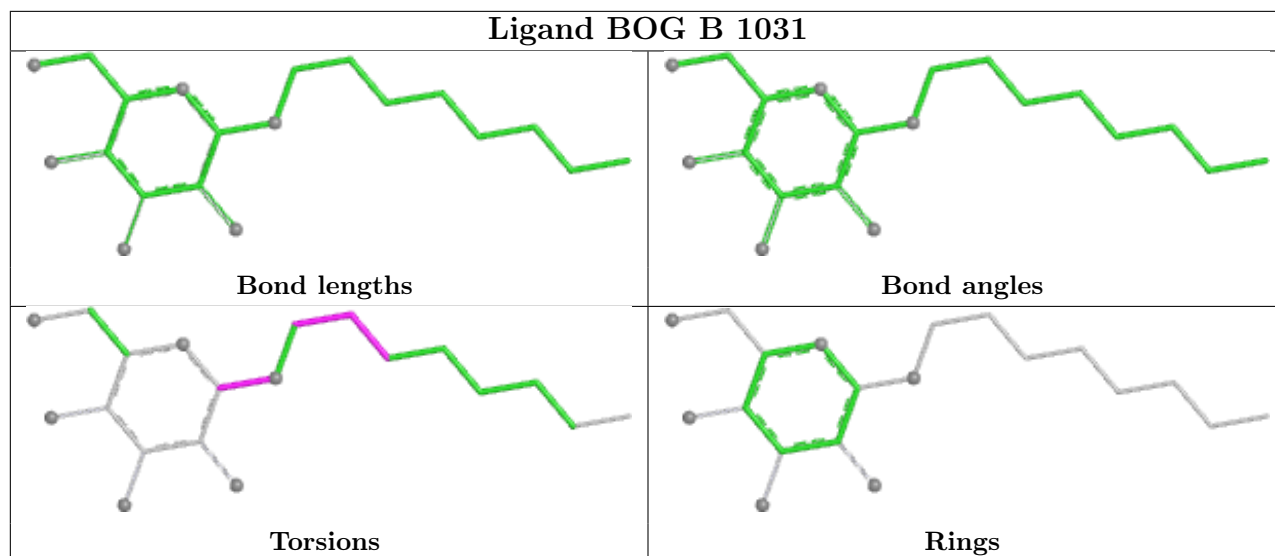
18 monomers are involved in 68 short contacts:

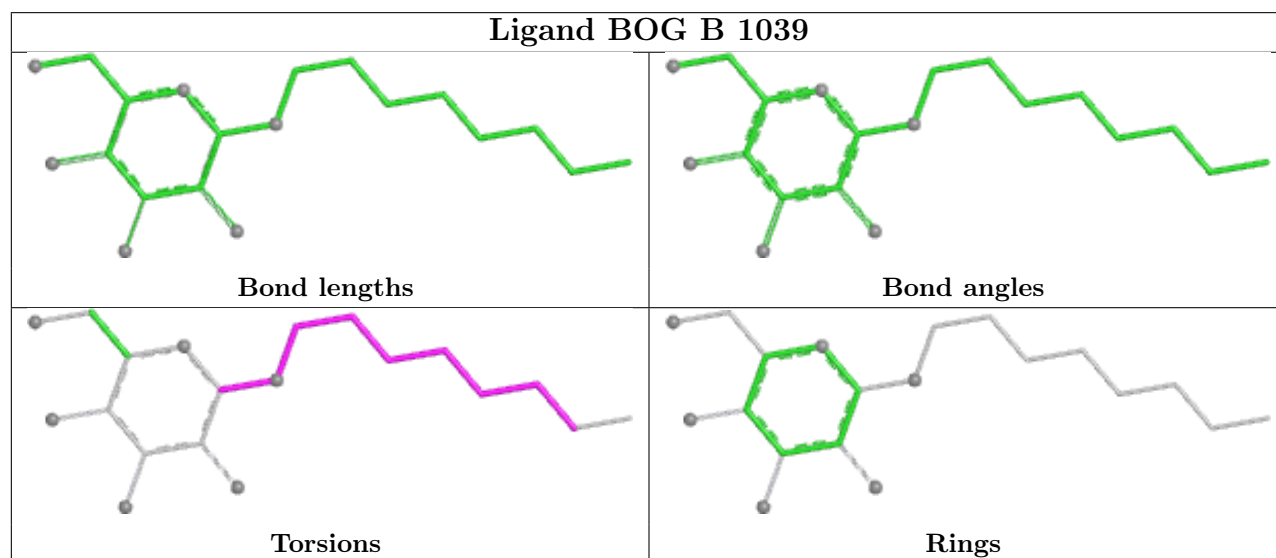
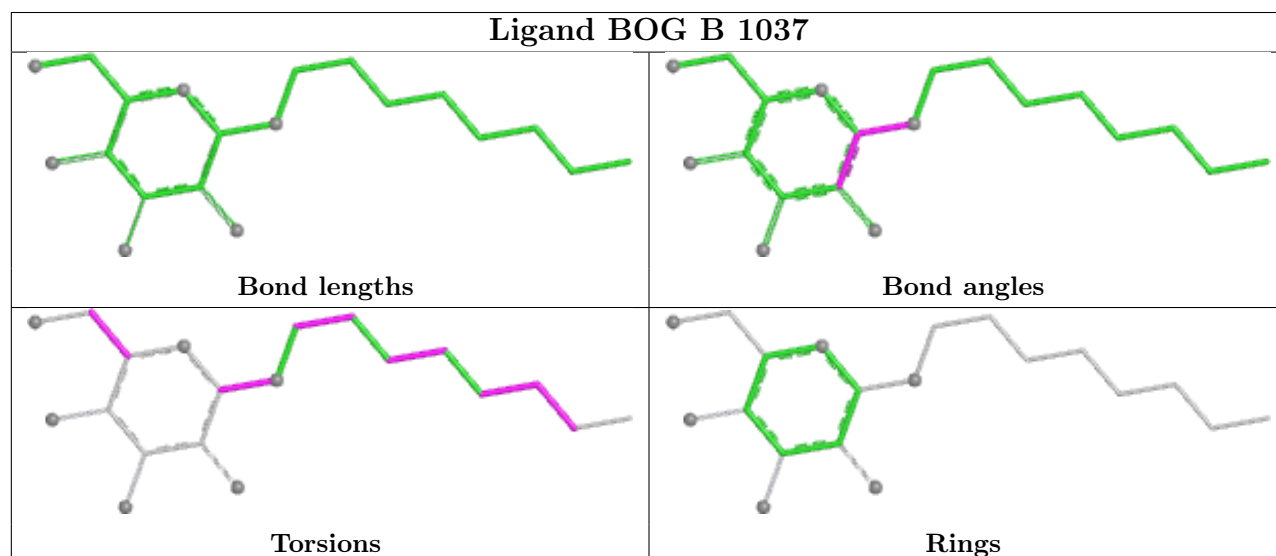
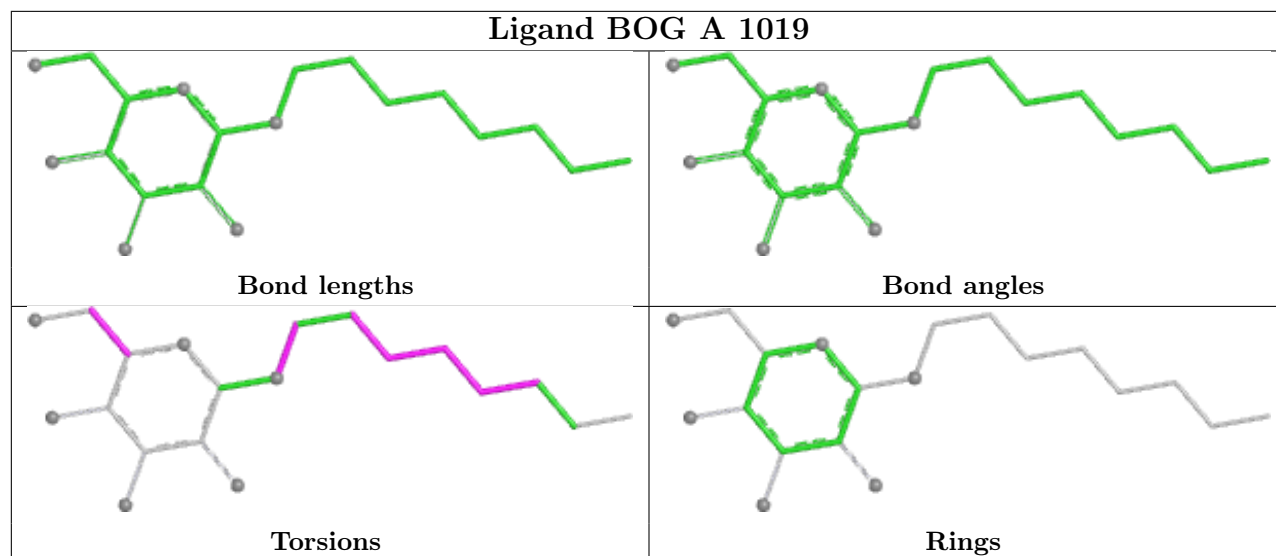
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1009	BOG	1	0
2	A	1011	BOG	8	0
2	A	1021	BOG	7	0
2	A	1029	BOG	3	0
2	A	1001	BOG	2	0
2	B	1031	BOG	2	0
2	B	1007	BOG	1	0
2	A	1019	BOG	1	0
2	B	1037	BOG	2	0
2	A	1041	BOG	2	0
2	B	1039	BOG	4	0
2	B	1023	BOG	4	0
2	A	1015	BOG	8	0
2	A	1033	BOG	3	0
2	A	1025	BOG	3	0
2	B	1005	BOG	3	0
2	B	1035	BOG	11	0
2	B	1013	BOG	3	0

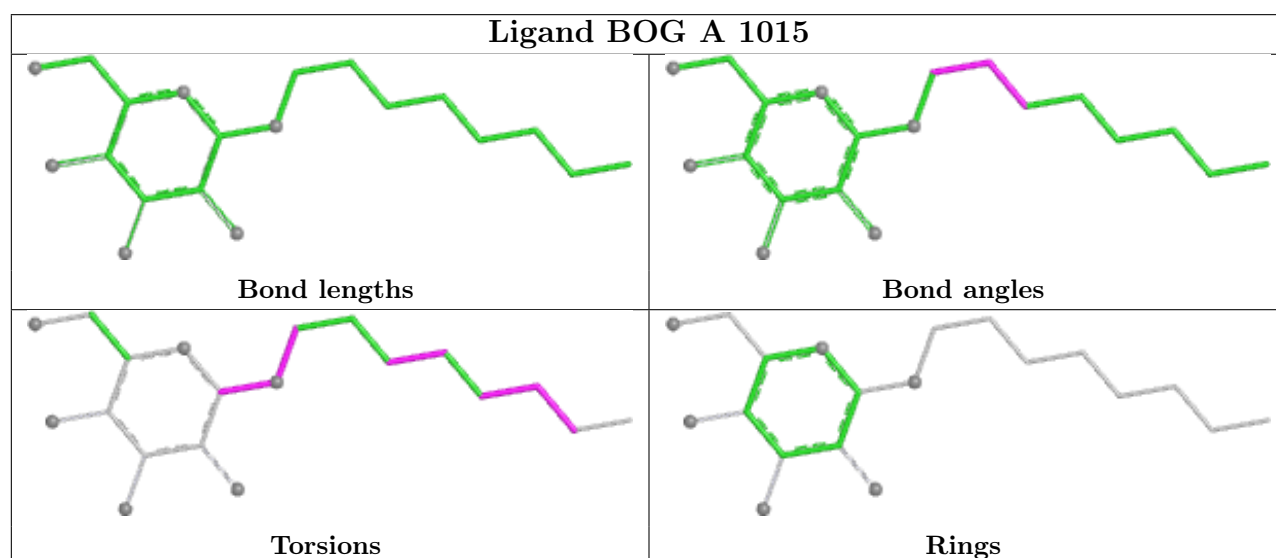
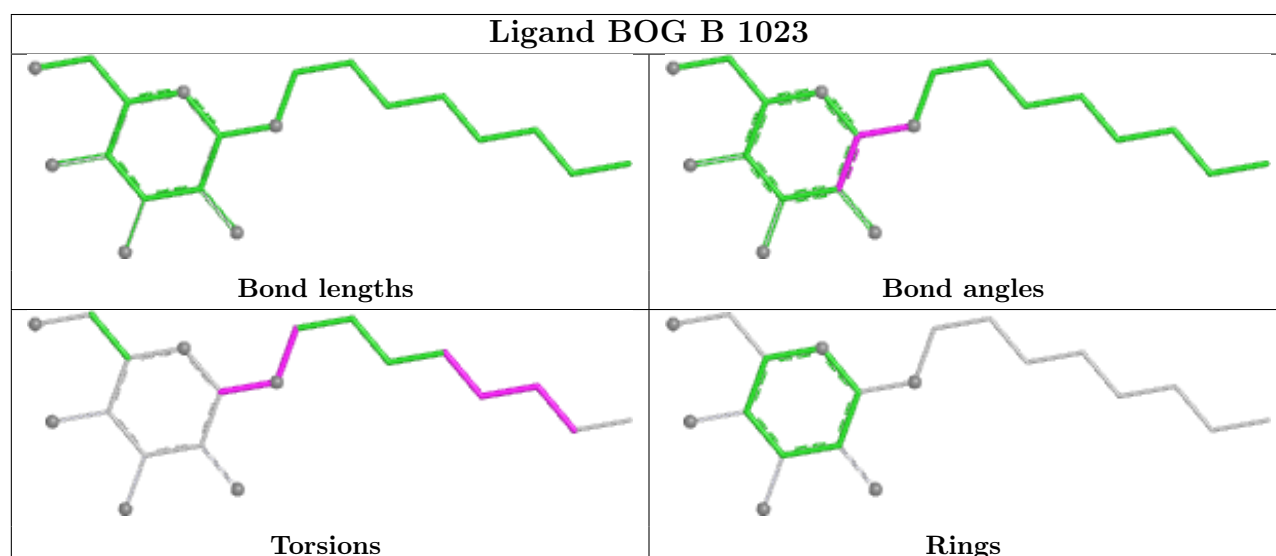
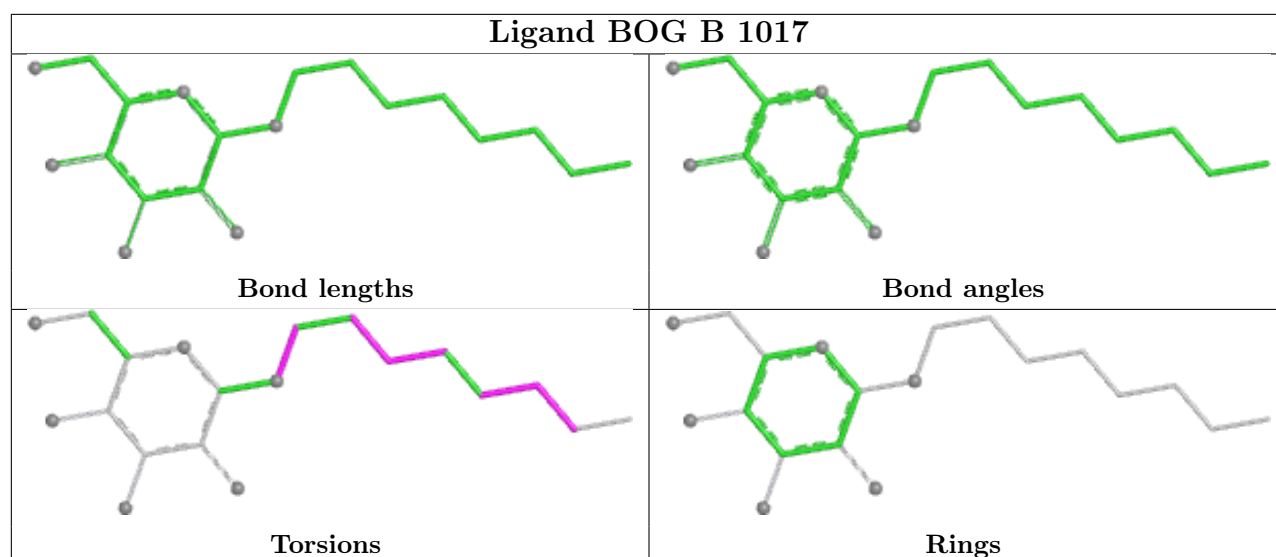
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

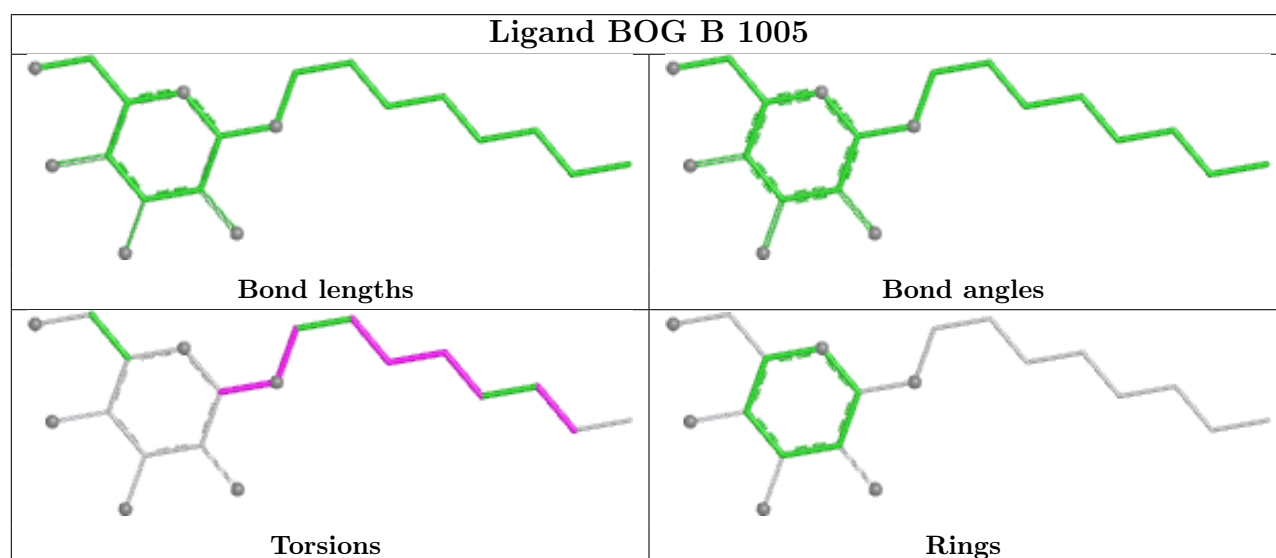
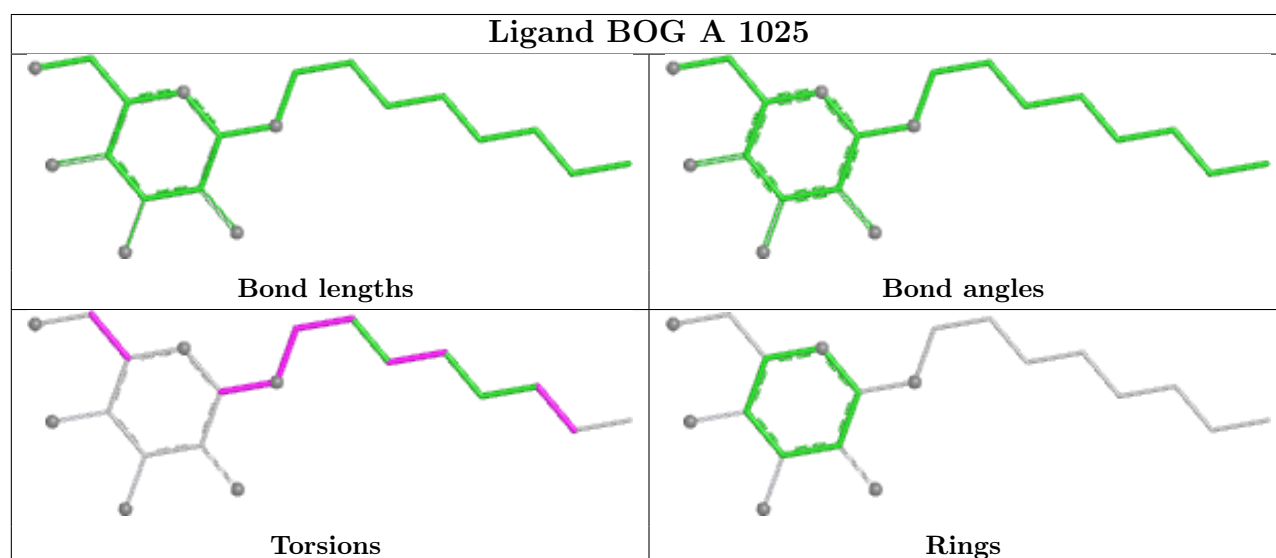
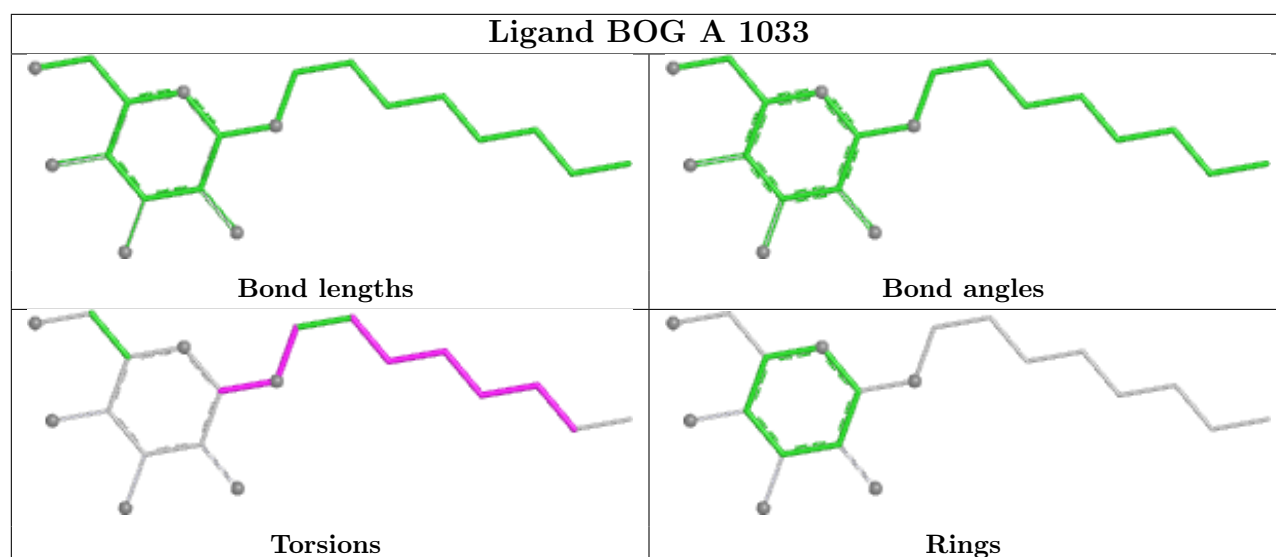


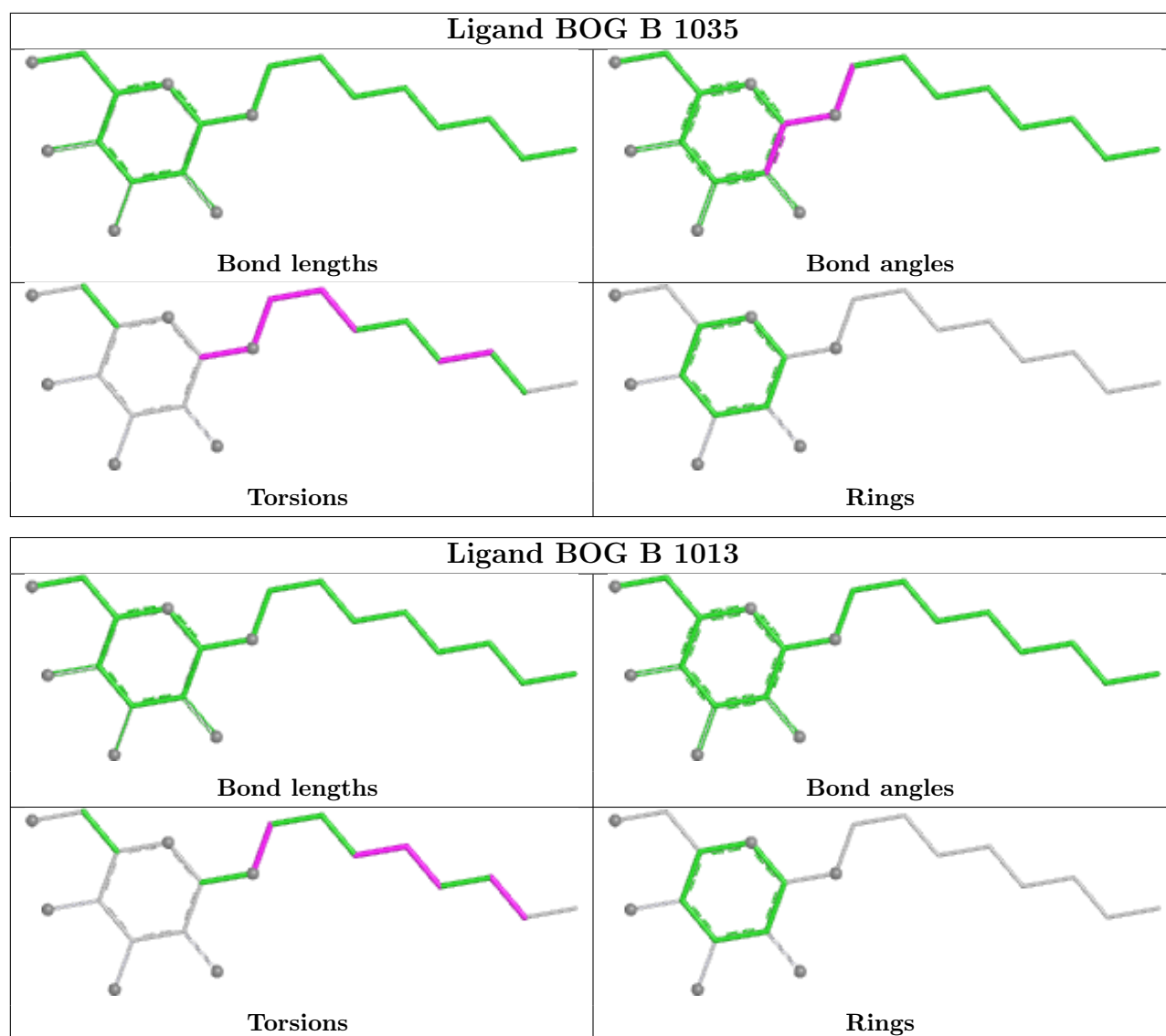












5.7 Other polymers [i](#)

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	142/142 (100%)	-0.75	0 100 100	7, 35, 70, 81	0
1	B	142/142 (100%)	-0.74	0 100 100	11, 36, 68, 90	0
All	All	284/284 (100%)	-0.74	0 100 100	7, 35, 70, 90	0

There are no RSRZ outliers to report.

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.

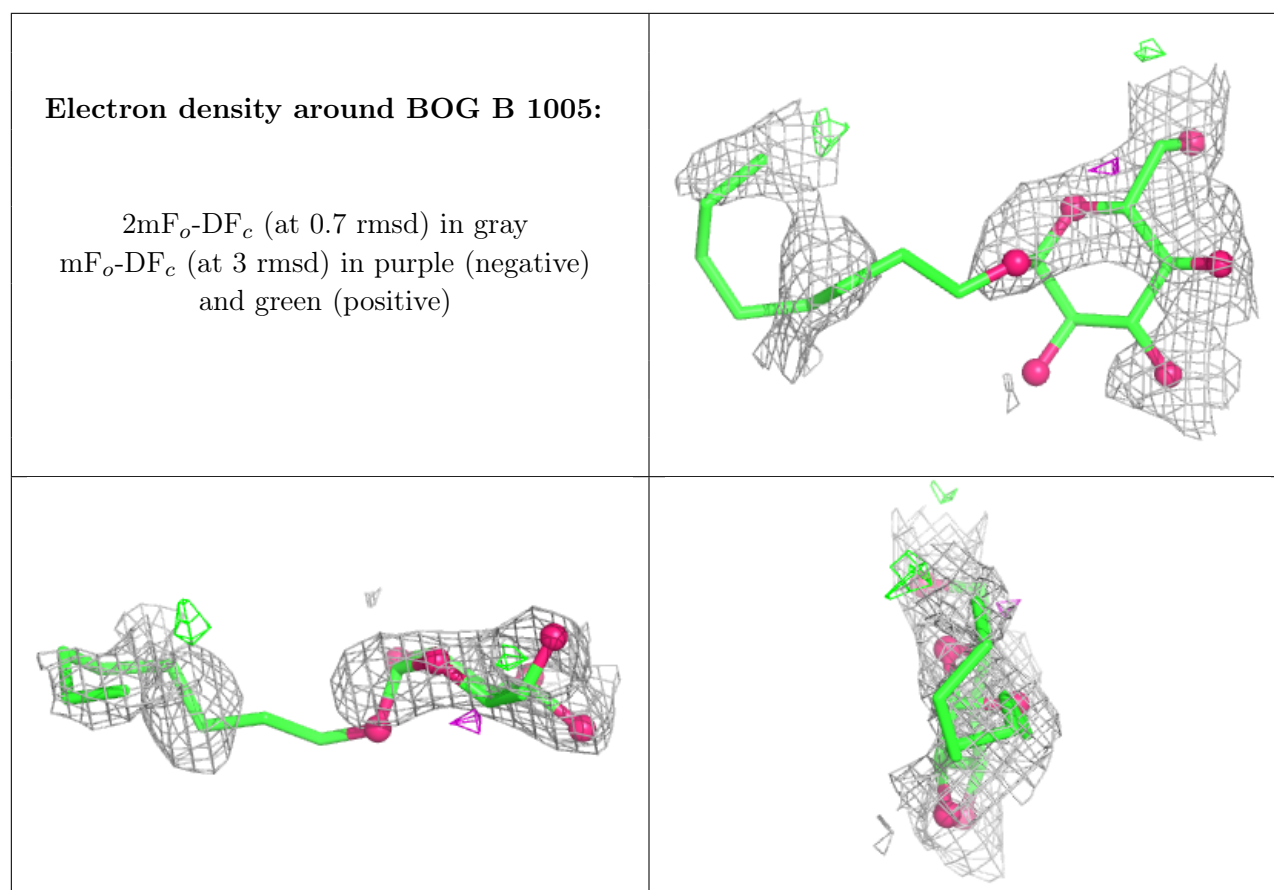
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	BOG	B	1005	20/20	0.73	0.11	31,69,89,95	0
2	BOG	B	1023	20/20	0.80	0.11	9,44,80,90	0
2	BOG	A	1041	12/20	0.82	0.07	13,58,66,72	0
2	BOG	B	1007	20/20	0.83	0.07	25,55,63,64	0
2	BOG	A	1003	20/20	0.83	0.08	15,50,66,75	0
2	BOG	B	1027	20/20	0.83	0.08	30,47,65,73	0
2	BOG	B	1037	20/20	0.83	0.09	26,55,78,85	0

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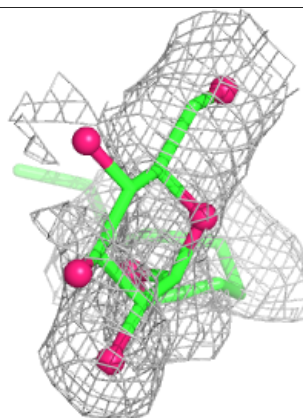
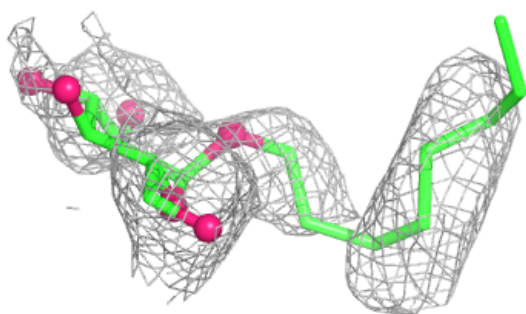
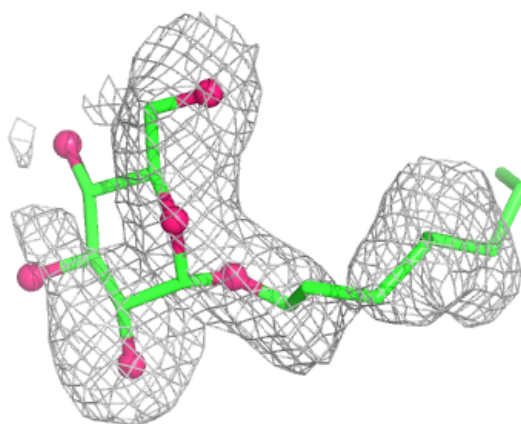
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	BOG	A	1009	20/20	0.84	0.08	16,51,69,74	0
2	BOG	B	1017	20/20	0.85	0.09	21,56,66,70	0
2	BOG	A	1001	20/20	0.85	0.08	10,60,74,82	0
2	BOG	B	1013	20/20	0.86	0.07	35,50,87,91	0
2	BOG	A	1021	20/20	0.87	0.09	17,71,89,97	0
2	BOG	A	1019	20/20	0.88	0.07	2,41,59,65	0
2	BOG	A	1011	20/20	0.88	0.08	13,51,64,78	0
2	BOG	A	1025	20/20	0.89	0.10	5,51,77,98	0
2	BOG	A	1033	20/20	0.89	0.07	28,68,81,83	0
2	BOG	B	1039	20/20	0.89	0.07	18,42,69,70	0
2	BOG	B	1035	20/20	0.90	0.08	10,56,72,84	0
2	BOG	A	1029	20/20	0.90	0.09	2,78,97,99	0
2	BOG	B	1031	20/20	0.90	0.09	9,65,83,86	0
2	BOG	A	1015	20/20	0.92	0.08	11,47,79,84	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.

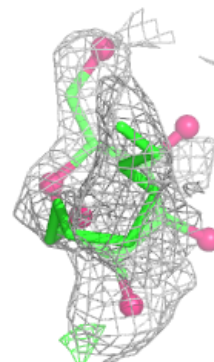
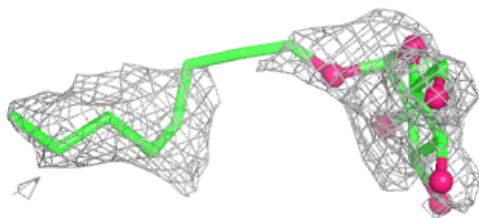
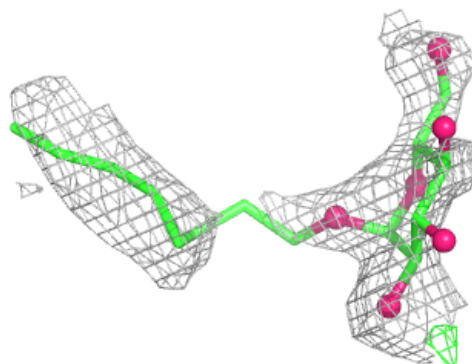


Electron density around BOG B 1023:

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

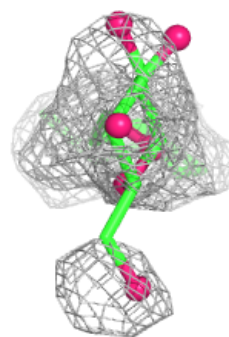
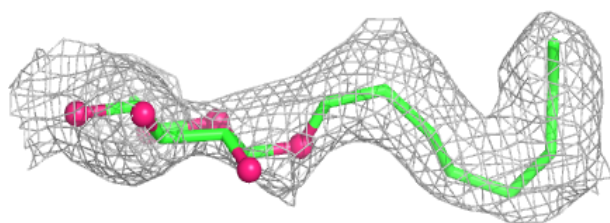
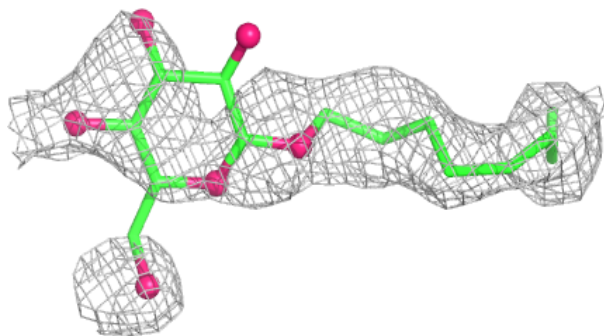
**Electron density around BOG B 1007:**

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

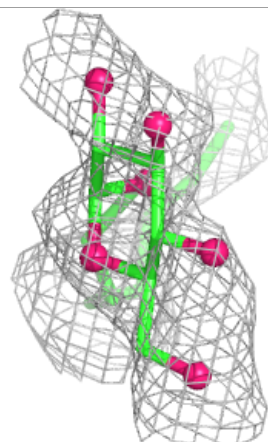
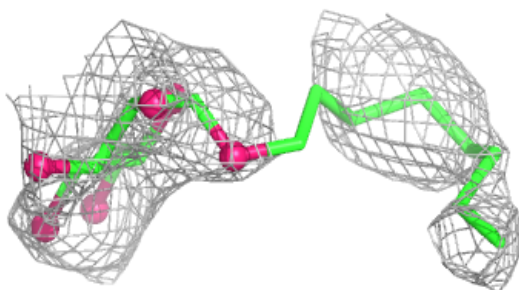
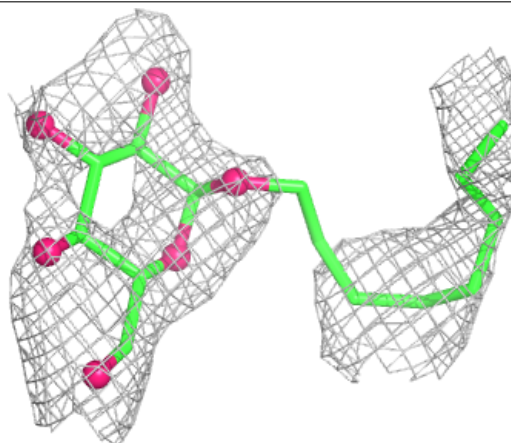


Electron density around BOG A 1003:

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

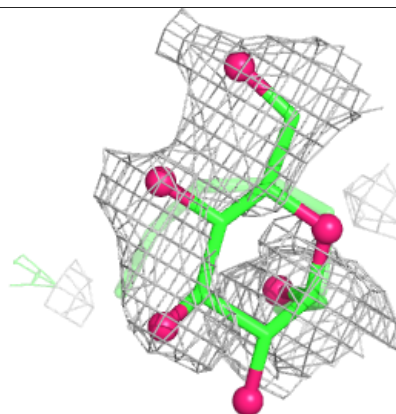
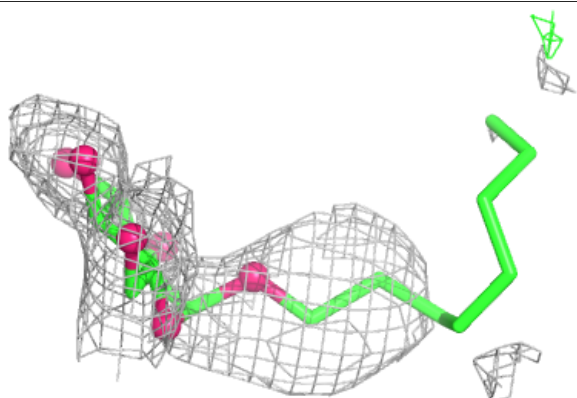
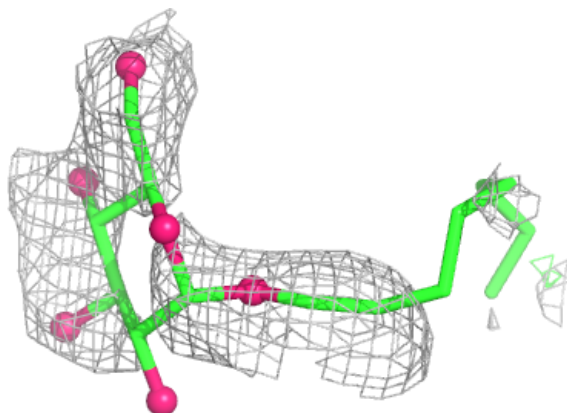
**Electron density around BOG B 1027:**

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and green (positive)

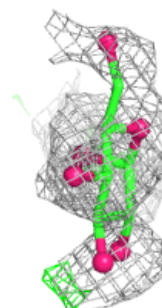
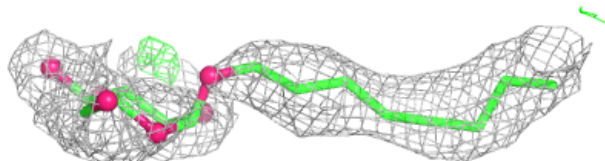
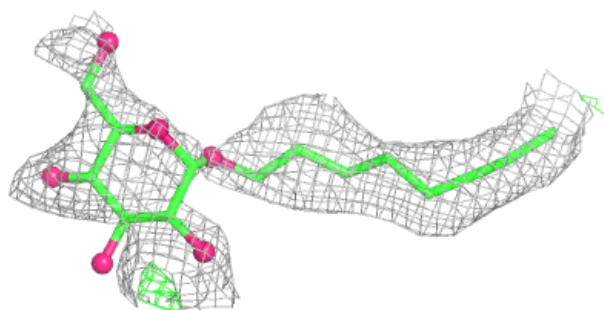


Electron density around BOG B 1037:

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

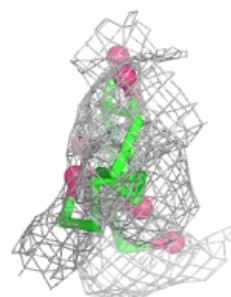
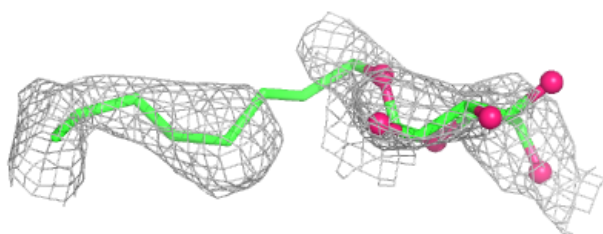
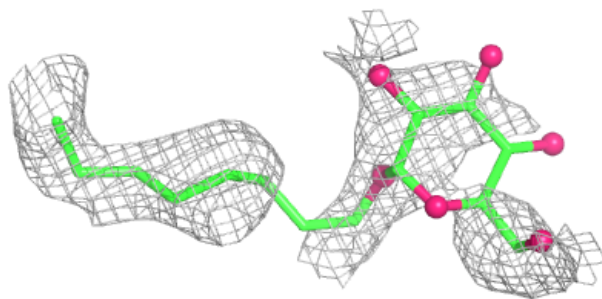
**Electron density around BOG A 1009:**

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



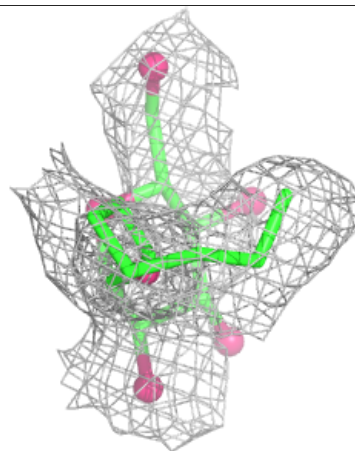
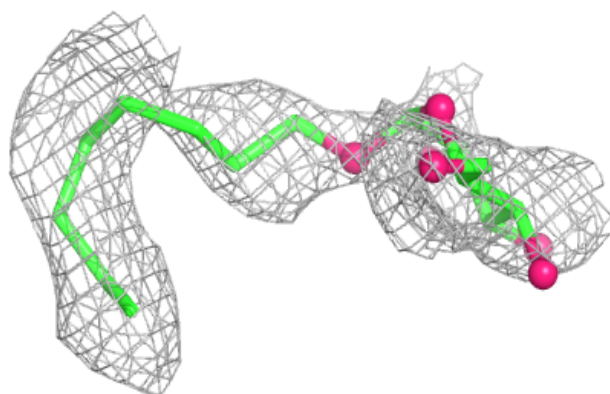
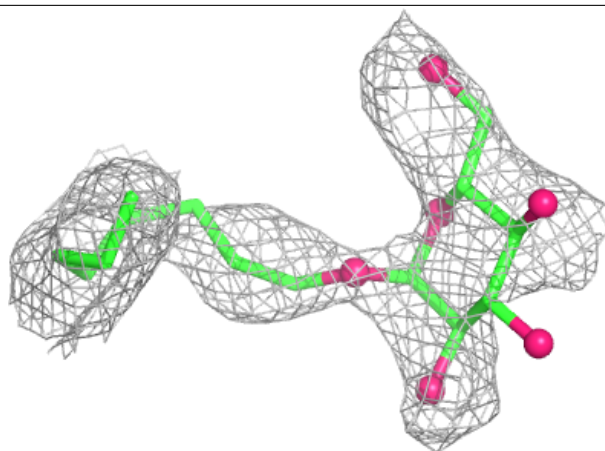
Electron density around BOG B 1017:

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



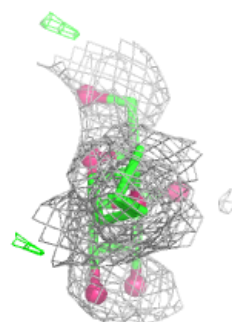
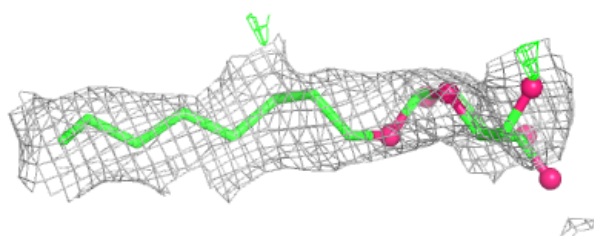
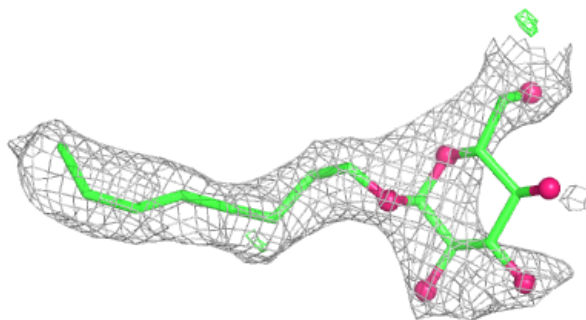
Electron density around BOG A 1001:

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

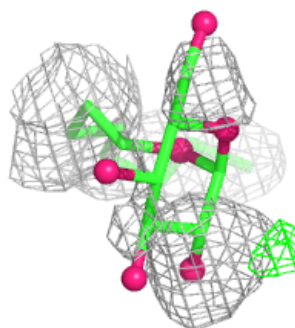
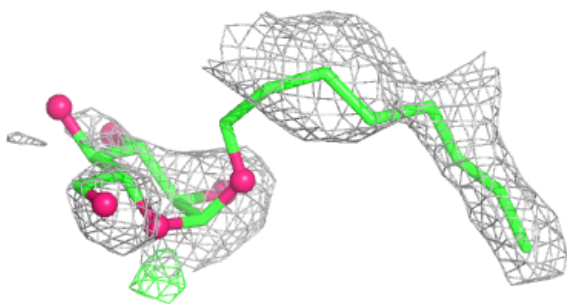
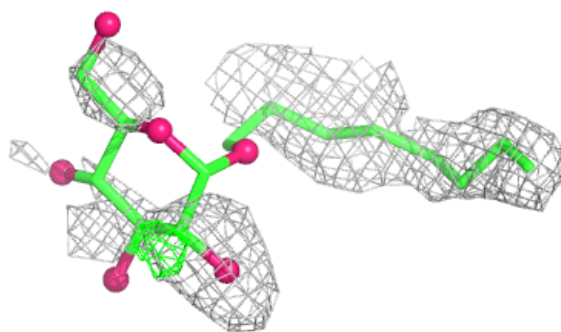


Electron density around BOG B 1013:

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

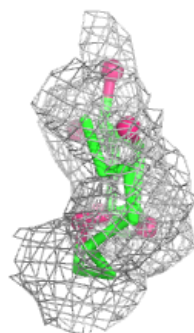
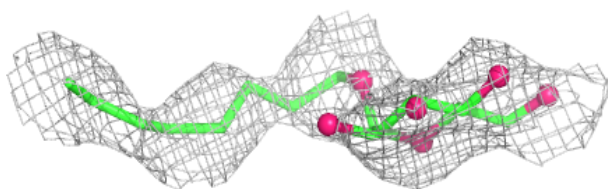
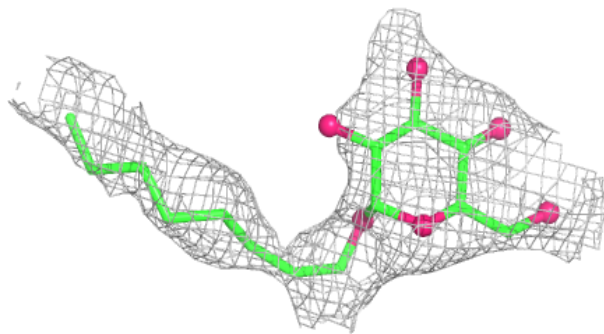
**Electron density around BOG A 1021:**

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

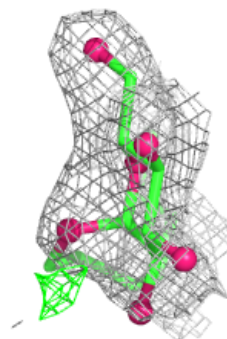
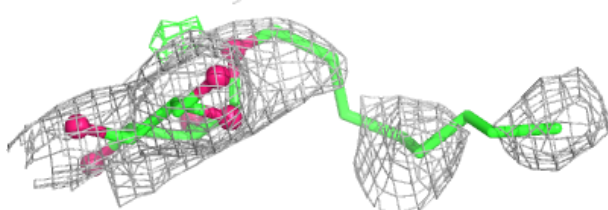
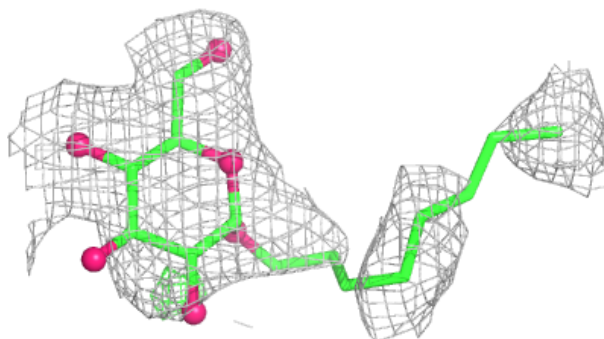


Electron density around BOG A 1019:

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

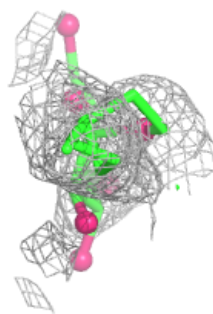
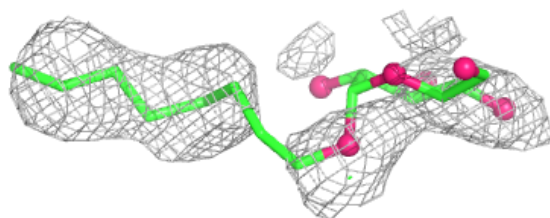
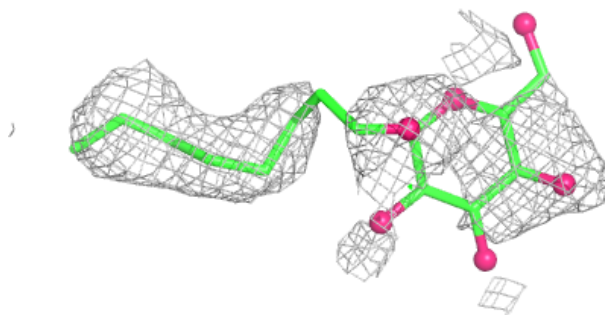
**Electron density around BOG A 1011:**

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

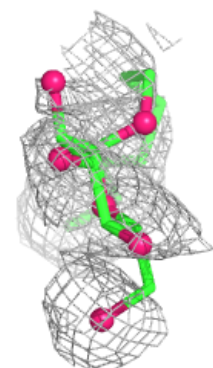
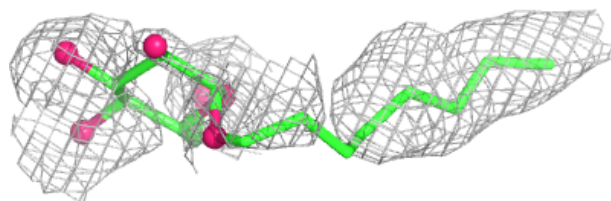
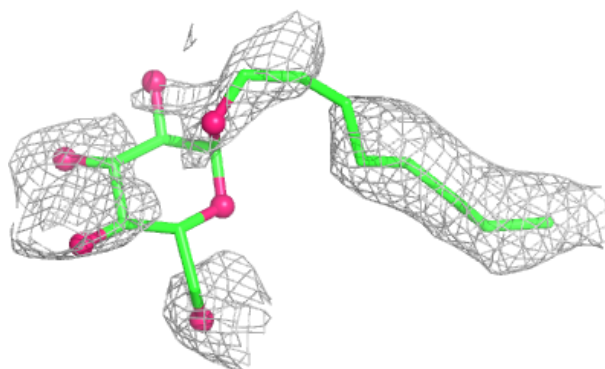


Electron density around BOG A 1025:

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

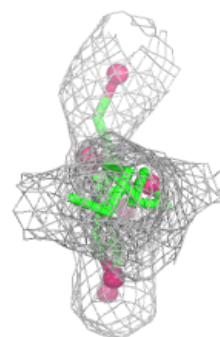
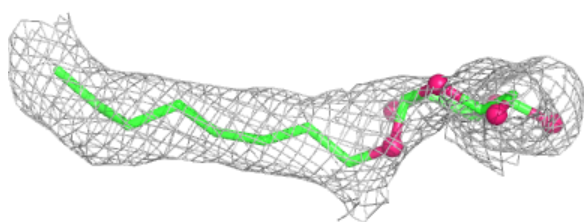
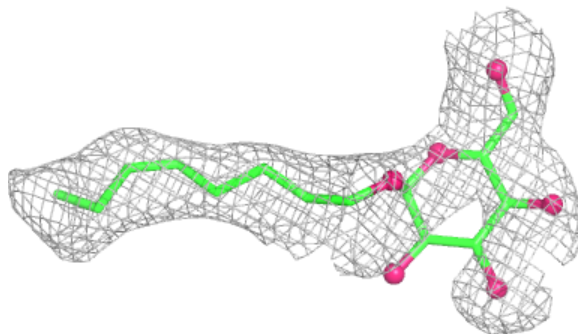
**Electron density around BOG A 1033:**

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

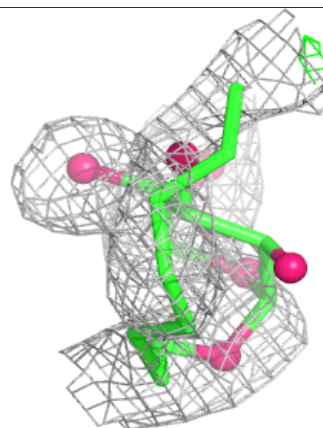
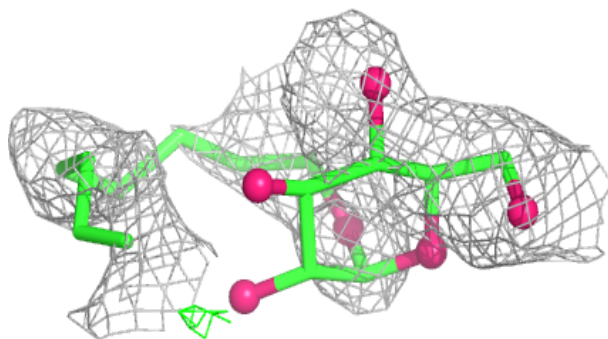
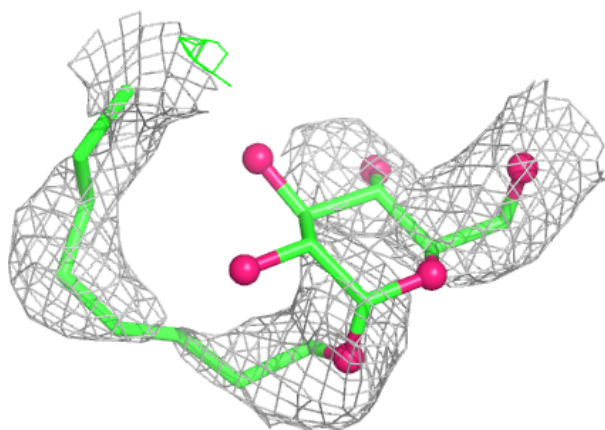


Electron density around BOG B 1039:

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

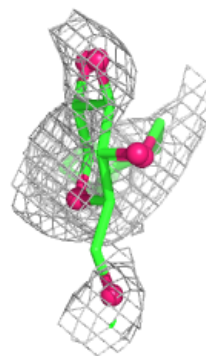
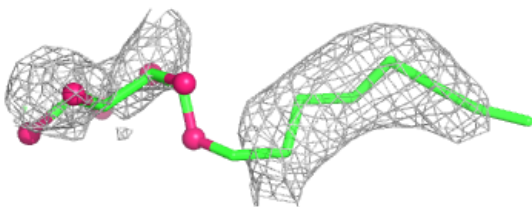
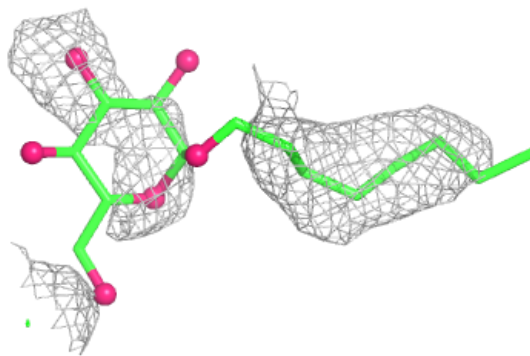
**Electron density around BOG B 1035:**

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



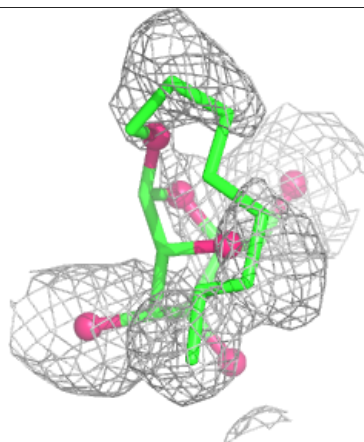
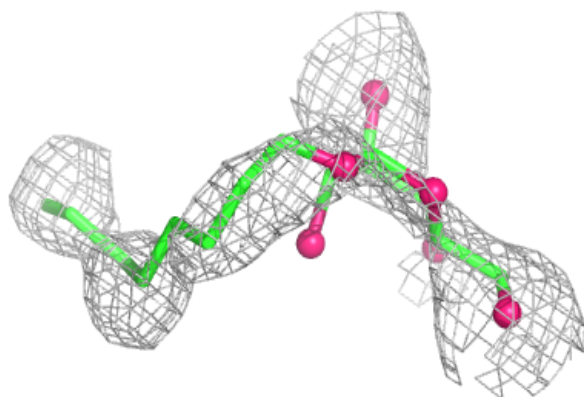
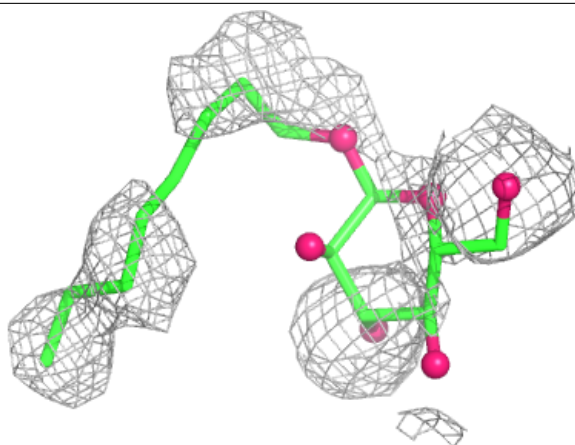
Electron density around BOG A 1029:

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



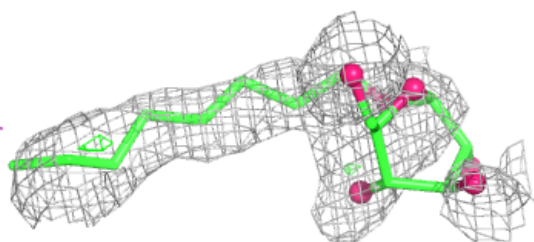
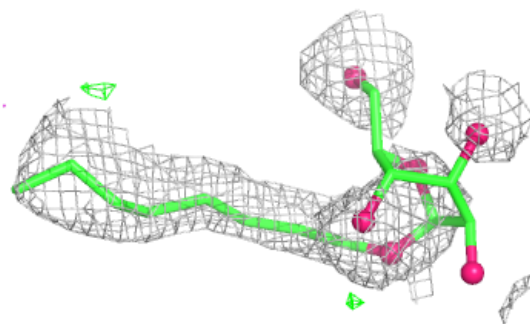
Electron density around BOG B 1031:

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



Electron density around BOG A 1015:

$2mF_o-DF_c$ (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.