



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 21, 2020 – 09:33 AM BST

PDB ID : 4P99
Title : Ca²⁺-stabilized adhesin helps an Antarctic bacterium reach out and bind ice
Authors : Guo, S.; Vance, D.R.T.; Campbell, R.L.; Davies, P.L.
Deposited on : 2014-04-02
Resolution : 1.80 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

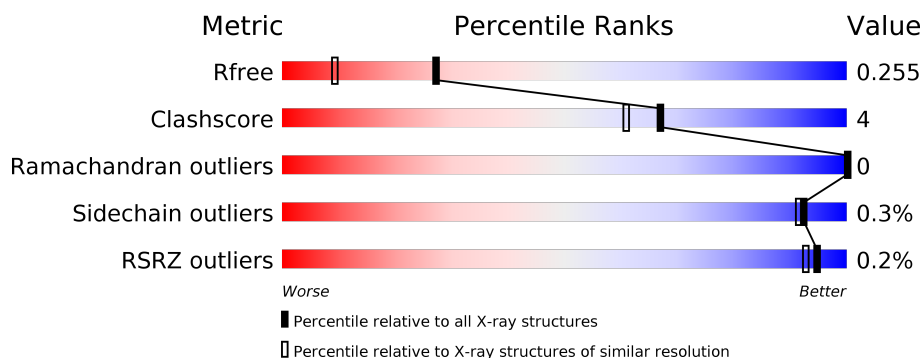
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 on 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	437	
1	B	437	
1	C	437	
1	D	437	

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BOG	D	535	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13555 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 MpAFP_RII tetra-tandemer.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	415	Total	C	N	O	0	1	0
			2827	1673	448	706			
1	B	415	Total	C	N	O	0	2	0
			2830	1675	448	707			
1	C	415	Total	C	N	O	0	0	0
			2818	1668	447	703			
1	D	415	Total	C	N	O	0	2	0
			2826	1674	447	705			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	25	Total	Ca	0	0
			25	25		
2	A	25	Total	Ca	0	0
			25	25		
2	D	24	Total	Ca	0	0
			24	24		
2	C	30	Total	Ca	0	1
			31	31		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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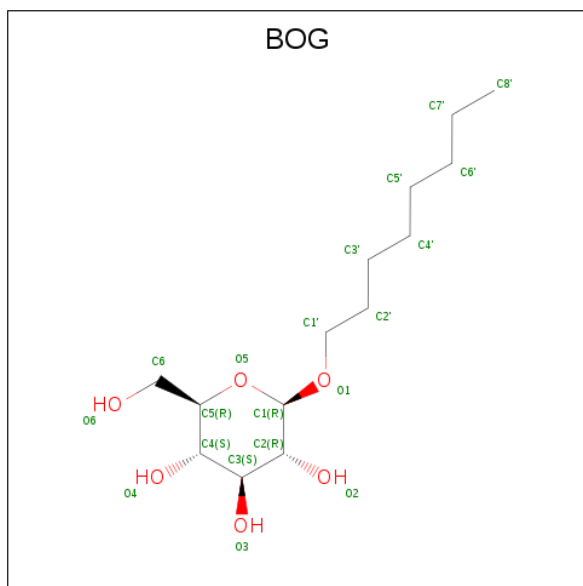
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0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

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

- Molecule 4 is octyl beta-D-glucopyranoside (three-letter code: BOG) (formula: C₁₄H₂₈O₆).



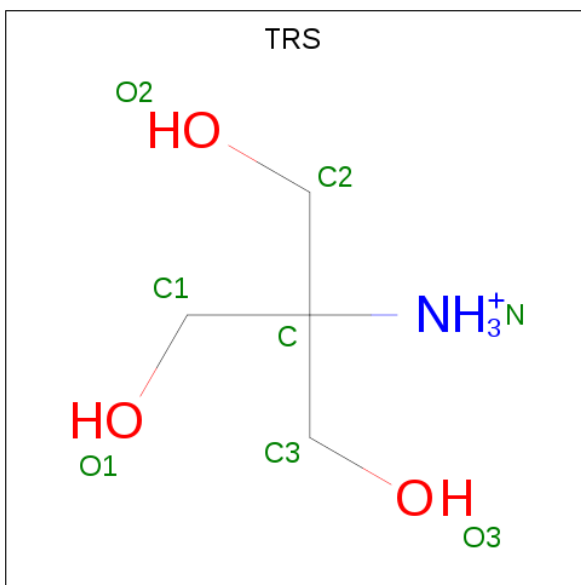
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			20	14	6		
4	C	1	Total	C	O	0	0
			20	14	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			20	14	6		

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			8	4	1	3		

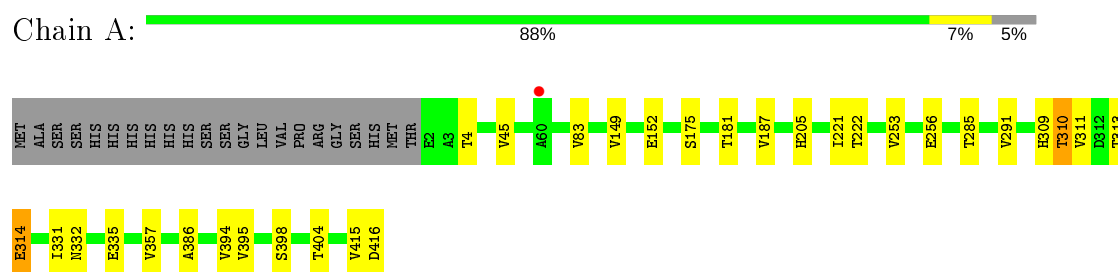
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	429	Total	O	0	17
			445	445		
6	B	419	Total	O	0	22
			441	441		
6	C	493	Total	O	0	34
			529	529		
6	D	463	Total	O	0	27
			490	490		

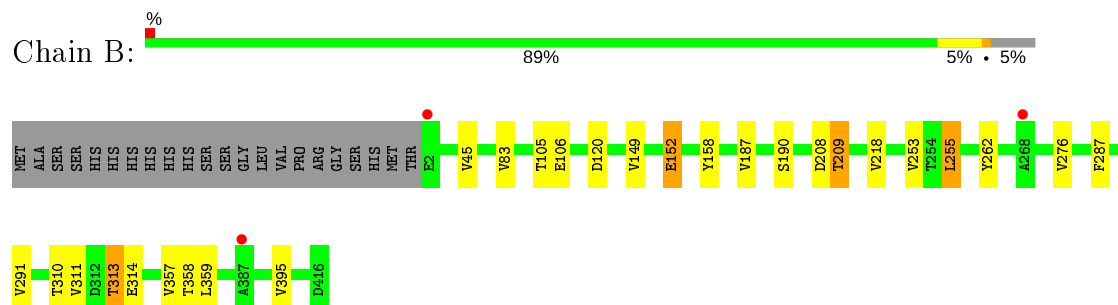
3 Residue-property plots [i](#)

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

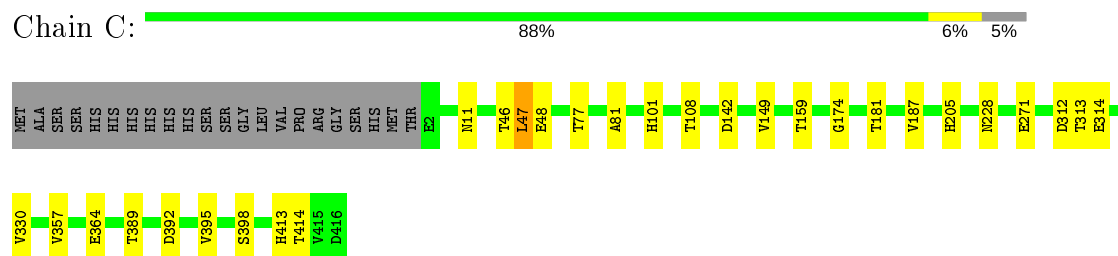
• Molecule 1: MpAFP_RII tetra-tandemer



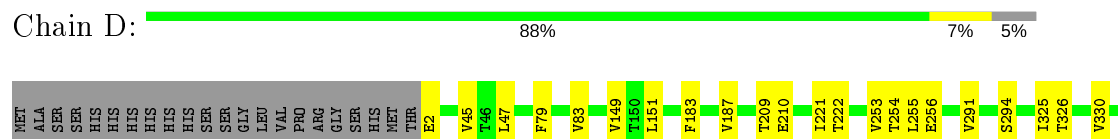
• Molecule 1: MpAFP_RII tetra-tandemer



• Molecule 1: MpAFP_RII tetra-tandemer



• Molecule 1: MpAFP_RII tetra-tandemer



V357	T358	L359	N362	G363	E364	T365	N373	V395	S398	T414	V415	D416
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	47.46 Å 47.47 Å 191.16 Å 90.04° 90.01° 90.02°	Depositor
Resolution (Å)	47.47 – 1.80 47.47 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.3 (47.47-1.80) 96.1 (47.47-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 1.79 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.221 , 0.257 0.220 , 0.255	Depositor DCC
R_{free} test set	7470 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	16.4	Xtriage
Anisotropy	0.977	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 76.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.468 for k,-h,l 0.468 for -k,h,l 0.316 for h,-k,-l 0.315 for -h,k,-l 0.477 for -h,-k,l 0.315 for k,h,-l 0.310 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13555	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: TRS, CA, EDO, 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	0.87	5/2846 (0.2%)	0.74	0/3931
1	B	0.89	5/2852 (0.2%)	0.75	1/3939 (0.0%)
1	C	0.88	5/2837 (0.2%)	0.74	0/3919
1	D	0.84	3/2851 (0.1%)	0.70	0/3939
All	All	0.87	18/11386 (0.2%)	0.74	1/15728 (0.0%)

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	B	0	2

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	256	GLU	CD-OE2	-6.17	1.18	1.25
1	B	313	THR	CB-CG2	-6.17	1.31	1.52
1	C	174	GLY	C-O	-6.12	1.13	1.23
1	C	271	GLU	CD-OE1	-6.02	1.19	1.25
1	A	335	GLU	CD-OE1	-5.82	1.19	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	208	ASP	C-N-CA	-5.05	109.07	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	106[A]	GLU	Mainchain
1	B	209	THR	Mainchain

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	2827	0	2559	20	1
1	B	2830	0	2564	15	0
1	C	2818	0	2554	24	0
1	D	2826	0	2569	21	0
2	A	25	0	0	0	0
2	B	25	0	0	0	0
2	C	31	0	0	0	0
2	D	24	0	0	0	0
3	A	40	0	55	0	0
3	B	60	0	89	0	0
3	C	36	0	54	2	0
3	D	40	0	60	0	0
4	C	40	0	55	3	1
4	D	20	0	28	9	0
5	C	8	0	12	1	0
6	A	445	0	0	5	0
6	B	441	0	0	3	0
6	C	529	0	0	3	0
6	D	490	0	0	1	0
All	All	13555	0	10599	86	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 86 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)
4:C:542:BOG:O1	4:C:542:BOG:O6	1.87	0.92
1:A:310:THR:OG1	6:A:899:HOH:O	1.57	0.82
4:C:542:BOG:H61	4:C:542:BOG:O3	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:VAL:HG22	1:B:83:VAL:HG22	1.73	0.71
1:C:149:VAL:HG22	1:C:187:VAL:HG22	1.73	0.71

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:394:VAL:CG2	4:C:542:BOG:O4[1_554]	2.07	0.13

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	414/437 (95%)	403 (97%)	11 (3%)	0	100	100
1	B	415/437 (95%)	411 (99%)	4 (1%)	0	100	100
1	C	413/437 (94%)	406 (98%)	7 (2%)	0	100	100
1	D	415/437 (95%)	404 (97%)	11 (3%)	0	100	100
All	All	1657/1748 (95%)	1624 (98%)	33 (2%)	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	304/322 (94%)	304 (100%)	0	100	100
1	B	305/322 (95%)	303 (99%)	2 (1%)	84	81
1	C	303/322 (94%)	302 (100%)	1 (0%)	92	91
1	D	305/322 (95%)	304 (100%)	1 (0%)	92	91
All	All	1217/1288 (94%)	1213 (100%)	4 (0%)	92	91

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	105	THR
1	B	209	THR
1	C	159	THR
1	D	2	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	269	ASN
1	C	11	ASN
1	C	91	ASN
1	D	373	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 153 ligands modelled in this entry, 105 are monoatomic - leaving 48 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	C	536	-	3,3,3	0.44	0	2,2,2	0.41	0
4	BOG	C	542	2	20,20,20	0.81	1 (5%)	25,25,25	2.60	9 (36%)
3	EDO	B	536	-	3,3,3	0.71	0	2,2,2	0.44	0
3	EDO	D	526	-	3,3,3	0.53	0	2,2,2	0.27	0
4	BOG	D	535	-	20,20,20	0.89	1 (5%)	25,25,25	2.44	10 (40%)
3	EDO	D	531	-	3,3,3	0.43	0	2,2,2	0.15	0
3	EDO	C	537	-	3,3,3	0.46	0	2,2,2	0.41	0
3	EDO	D	527	-	3,3,3	0.55	0	2,2,2	0.19	0
3	EDO	A	527	-	3,3,3	0.51	0	2,2,2	0.37	0
3	EDO	B	533	-	3,3,3	0.53	0	2,2,2	0.11	0
3	EDO	C	538	-	3,3,3	0.46	0	2,2,2	0.39	0
3	EDO	A	531	-	3,3,3	0.38	0	2,2,2	0.49	0
3	EDO	B	537	-	3,3,3	0.14	0	2,2,2	0.69	0
3	EDO	D	533	-	3,3,3	0.42	0	2,2,2	0.25	0
3	EDO	A	535	-	3,3,3	0.47	0	2,2,2	0.28	0
3	EDO	B	538	-	3,3,3	0.26	0	2,2,2	1.05	0
3	EDO	B	531	-	3,3,3	0.32	0	2,2,2	0.26	0
3	EDO	B	530	-	3,3,3	0.62	0	2,2,2	0.06	0
3	EDO	B	535	-	3,3,3	0.32	0	2,2,2	0.30	0
3	EDO	A	530	-	3,3,3	0.12	0	2,2,2	0.17	0
3	EDO	B	534	-	3,3,3	0.41	0	2,2,2	0.47	0
4	BOG	C	503	2	20,20,20	0.71	0	25,25,25	1.46	5 (20%)
3	EDO	C	535	-	3,3,3	0.31	0	2,2,2	0.92	0
3	EDO	D	528	-	3,3,3	0.51	0	2,2,2	0.29	0
3	EDO	A	532	-	3,3,3	0.27	0	2,2,2	0.30	0
3	EDO	A	525	-	3,3,3	0.77	0	2,2,2	0.41	0
3	EDO	B	525	-	3,3,3	0.51	0	2,2,2	0.29	0
3	EDO	C	533	-	3,3,3	0.54	0	2,2,2	0.47	0
3	EDO	D	529	-	3,3,3	0.50	0	2,2,2	0.26	0
3	EDO	D	501	-	3,3,3	0.65	0	2,2,2	0.91	0
3	EDO	D	534	-	3,3,3	0.22	0	2,2,2	0.54	0
3	EDO	A	534	-	3,3,3	0.48	0	2,2,2	0.37	0
3	EDO	B	529	-	3,3,3	0.36	0	2,2,2	0.65	0
3	EDO	B	524	-	3,3,3	0.51	0	2,2,2	0.40	0
3	EDO	C	539	-	3,3,3	0.47	0	2,2,2	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	526	2	3,3,3	0.53	0	2,2,2	0.59	0
3	EDO	C	532	-	3,3,3	0.39	0	2,2,2	1.17	0
3	EDO	D	532	-	3,3,3	0.36	0	2,2,2	0.29	0
3	EDO	B	532	-	3,3,3	0.51	0	2,2,2	0.45	0
3	EDO	A	529	2	3,3,3	0.51	0	2,2,2	0.85	0
3	EDO	A	528	2	3,3,3	0.51	0	2,2,2	0.25	0
3	EDO	B	526	-	3,3,3	0.43	0	2,2,2	0.42	0
3	EDO	B	528	2	3,3,3	0.48	0	2,2,2	0.13	0
3	EDO	B	527	-	3,3,3	0.46	0	2,2,2	0.27	0
5	TRS	C	541	-	7,7,7	0.67	0	9,9,9	0.97	1 (11%)
3	EDO	C	534	-	3,3,3	0.46	0	2,2,2	0.56	0
3	EDO	D	530	-	3,3,3	0.43	0	2,2,2	0.76	0
3	EDO	C	540	-	3,3,3	0.23	0	2,2,2	0.33	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	EDO	C	536	-	-	1/1/1/1	-
4	BOG	C	542	2	-	5/11/31/31	0/1/1/1
3	EDO	B	536	-	-	1/1/1/1	-
3	EDO	D	526	-	-	1/1/1/1	-
4	BOG	D	535	-	-	5/11/31/31	0/1/1/1
3	EDO	D	531	-	-	1/1/1/1	-
3	EDO	C	537	-	-	0/1/1/1	-
3	EDO	D	527	-	-	0/1/1/1	-
3	EDO	A	527	-	-	0/1/1/1	-
3	EDO	B	533	-	-	0/1/1/1	-
3	EDO	C	538	-	-	1/1/1/1	-
3	EDO	A	531	-	-	1/1/1/1	-
3	EDO	B	537	-	-	0/1/1/1	-
3	EDO	D	533	-	-	1/1/1/1	-
3	EDO	A	535	-	-	0/1/1/1	-
3	EDO	B	538	-	-	0/1/1/1	-
3	EDO	B	531	-	-	1/1/1/1	-
3	EDO	B	530	-	-	1/1/1/1	-
3	EDO	B	535	-	-	1/1/1/1	-
3	EDO	A	530	-	-	1/1/1/1	-
3	EDO	B	534	-	-	1/1/1/1	-
4	BOG	C	503	2	-	6/11/31/31	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	535	-	-	1/1/1/1	-
3	EDO	D	528	-	-	0/1/1/1	-
3	EDO	A	532	-	-	1/1/1/1	-
3	EDO	A	525	-	-	1/1/1/1	-
3	EDO	B	525	-	-	0/1/1/1	-
3	EDO	C	533	-	-	0/1/1/1	-
3	EDO	D	529	-	-	0/1/1/1	-
3	EDO	D	501	-	-	1/1/1/1	-
3	EDO	D	534	-	-	0/1/1/1	-
3	EDO	A	534	-	-	0/1/1/1	-
3	EDO	B	529	-	-	0/1/1/1	-
3	EDO	B	524	-	-	1/1/1/1	-
3	EDO	C	539	-	-	0/1/1/1	-
3	EDO	A	526	2	-	0/1/1/1	-
3	EDO	C	532	-	-	0/1/1/1	-
3	EDO	D	532	-	-	1/1/1/1	-
3	EDO	B	532	-	-	1/1/1/1	-
3	EDO	A	529	2	-	1/1/1/1	-
3	EDO	A	528	2	-	0/1/1/1	-
3	EDO	B	526	-	-	0/1/1/1	-
3	EDO	B	528	2	-	0/1/1/1	-
3	EDO	B	527	-	-	0/1/1/1	-
5	TRS	C	541	-	-	6/9/9/9	-
3	EDO	C	534	-	-	1/1/1/1	-
3	EDO	D	530	-	-	1/1/1/1	-
3	EDO	C	540	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	535	BOG	O5-C5	-2.40	1.38	1.44
4	C	542	BOG	C4-C5	-2.05	1.48	1.53

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	535	BOG	O1-C1-C2	6.68	118.73	108.30
4	C	542	BOG	C4-C3-C2	5.67	120.73	110.82
4	C	542	BOG	O3-C3-C2	-4.83	99.18	110.35
4	C	542	BOG	O5-C1-O1	-4.66	98.93	109.97
4	C	542	BOG	O3-C3-C4	-4.57	99.78	110.35

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

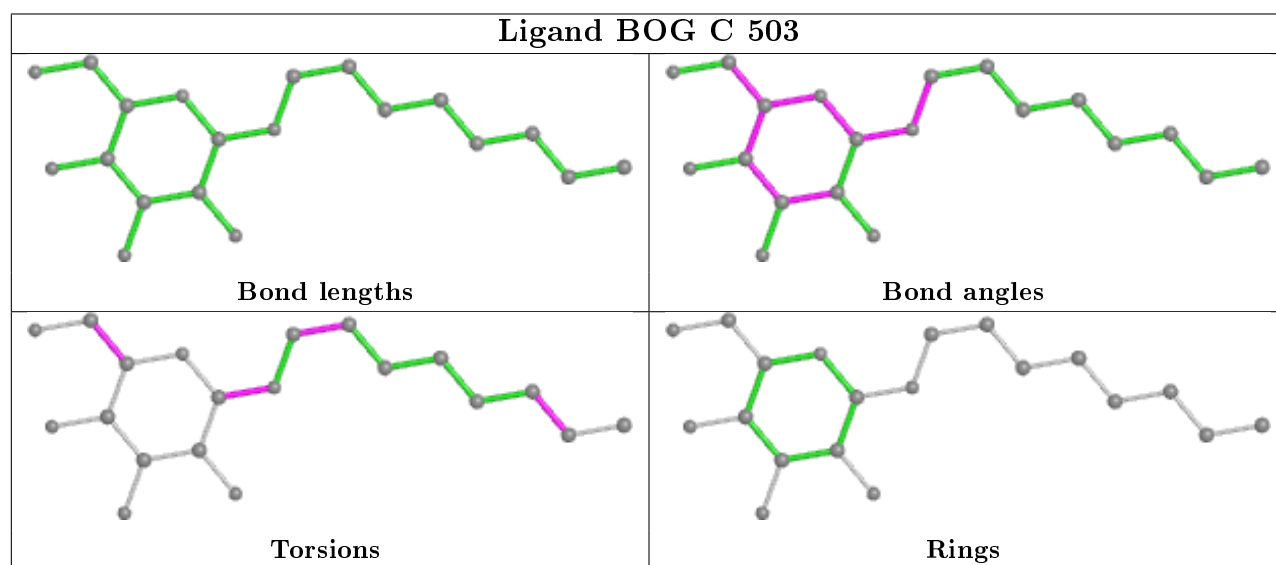
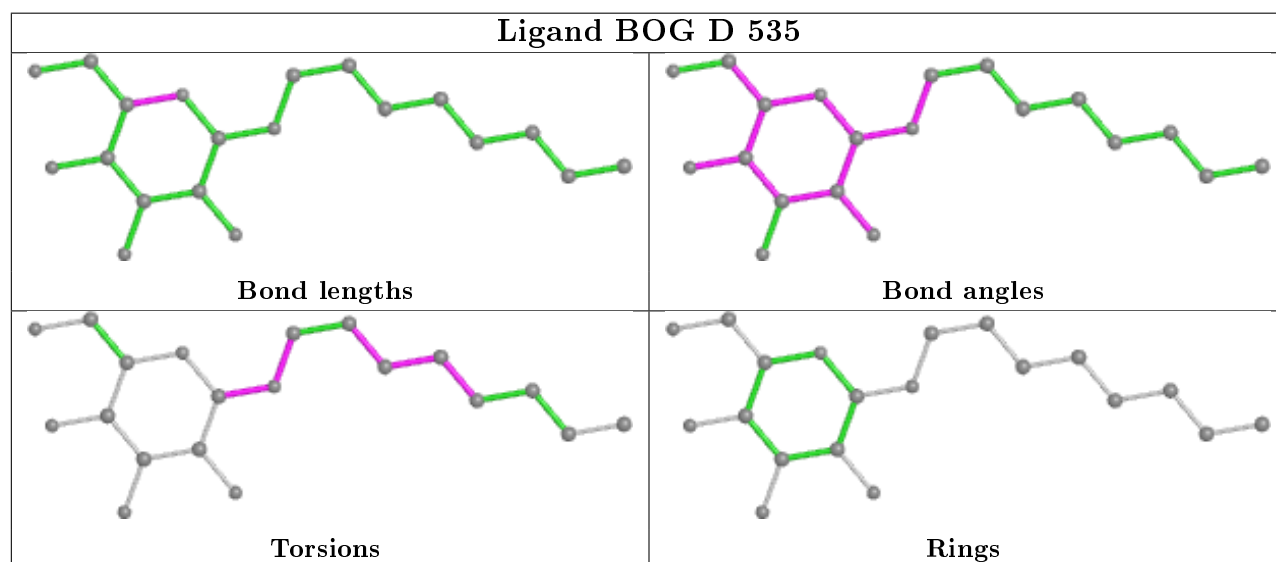
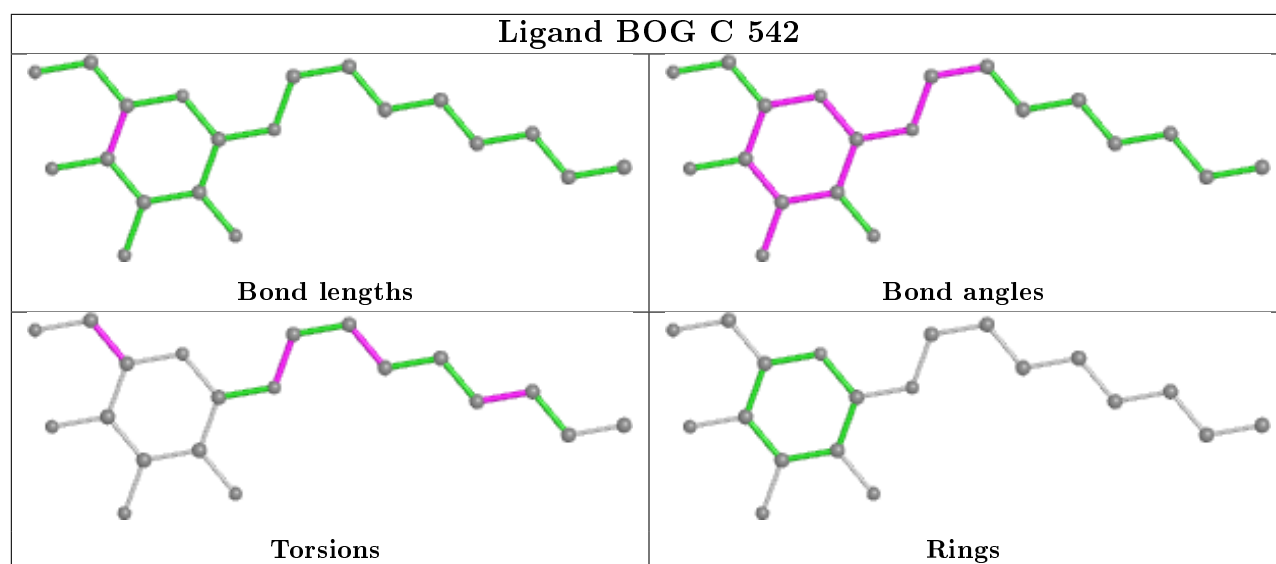
Mol	Chain	Res	Type	Atoms
4	D	535	BOG	C2'-C1'-O1-C1
4	C	503	BOG	O5-C1-O1-C1'
5	C	541	TRS	N-C-C3-O3
4	D	535	BOG	C2'-C3'-C4'-C5'
4	C	542	BOG	O5-C5-C6-O6

There are no ring outliers.

5 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	542	BOG	3	1
4	D	535	BOG	9	0
3	C	539	EDO	1	0
3	C	532	EDO	1	0
5	C	541	TRS	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	415/437 (94%)	-0.22	1 (0%) 95 93	11, 20, 33, 48	0
1	B	415/437 (94%)	-0.16	3 (0%) 87 86	12, 21, 32, 57	0
1	C	415/437 (94%)	-0.31	0 100 100	11, 17, 24, 40	0
1	D	415/437 (94%)	-0.29	0 100 100	11, 18, 27, 38	0
All	All	1660/1748 (94%)	-0.24	4 (0%) 95 93	11, 19, 30, 57	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	ALA	2.6
1	B	268	ALA	2.5
1	B	2	GLU	2.1
1	B	387	ALA	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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(\AA^2)	Q<0.9
3	EDO	D	528	4/4	0.73	0.16	34,42,43,44	0
3	EDO	D	526	4/4	0.73	0.16	41,42,44,46	0
3	EDO	C	535	4/4	0.76	0.16	33,36,40,48	0
4	BOG	D	535	20/20	0.77	0.21	44,55,60,63	0
3	EDO	B	531	4/4	0.77	0.14	37,40,41,42	0
3	EDO	D	533	4/4	0.78	0.14	51,51,51,51	0
3	EDO	B	536	4/4	0.79	0.27	43,43,43,43	0
4	BOG	C	542	20/20	0.79	0.18	35,53,63,63	0
3	EDO	D	531	4/4	0.81	0.15	48,48,52,54	0
3	EDO	D	532	4/4	0.81	0.15	52,52,52,52	0
3	EDO	A	534	4/4	0.81	0.15	40,40,40,40	0
3	EDO	D	534	4/4	0.82	0.14	49,49,49,49	0
3	EDO	C	534	4/4	0.83	0.15	40,40,41,44	0
3	EDO	D	530	4/4	0.84	0.13	42,44,45,47	0
3	EDO	B	525	4/4	0.85	0.12	44,45,46,49	0
3	EDO	A	535	4/4	0.85	0.23	52,52,52,52	0
3	EDO	B	524	4/4	0.85	0.11	23,25,28,42	0
3	EDO	A	530	4/4	0.85	0.15	42,42,44,44	0
3	EDO	A	527	4/4	0.86	0.17	34,43,45,48	0
3	EDO	C	537	4/4	0.86	0.16	35,40,44,48	0
3	EDO	B	537	4/4	0.87	0.13	20,20,20,20	0
3	EDO	B	534	4/4	0.87	0.10	40,44,46,46	0
3	EDO	C	540	4/4	0.88	0.20	36,36,36,36	0
3	EDO	B	533	4/4	0.88	0.13	27,30,37,42	0
4	BOG	C	503	20/20	0.89	0.13	32,41,46,54	0
3	EDO	C	533	4/4	0.89	0.13	28,33,37,39	0
3	EDO	B	529	4/4	0.89	0.14	29,37,38,45	0
3	EDO	B	527	4/4	0.90	0.11	34,37,38,48	0
2	CA	C	502[A]	1/1	0.91	0.11	11,11,11,11	1
2	CA	A	522	1/1	0.91	0.21	57,57,57,57	0
2	CA	C	502[B]	1/1	0.91	0.11	18,18,18,18	1
3	EDO	D	527	4/4	0.91	0.10	45,46,47,47	0
3	EDO	A	532	4/4	0.92	0.19	39,39,39,39	0
3	EDO	B	528	4/4	0.93	0.11	16,17,17,20	0
5	TRS	C	541	8/8	0.93	0.17	29,34,39,41	0
3	EDO	A	525	4/4	0.93	0.09	24,25,29,35	0
3	EDO	B	532	4/4	0.94	0.13	25,30,41,48	0
3	EDO	D	501	4/4	0.94	0.17	41,41,41,41	0
3	EDO	B	530	4/4	0.94	0.13	28,33,35,37	0
2	CA	C	524	1/1	0.94	0.05	44,44,44,44	0
2	CA	B	519	1/1	0.94	0.06	41,41,41,41	0
3	EDO	B	535	4/4	0.94	0.08	32,32,32,32	0
3	EDO	C	532	4/4	0.94	0.10	21,27,27,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	A	526	4/4	0.94	0.07	20,20,20,20	0
2	CA	A	510	1/1	0.94	0.09	38,38,38,38	0
3	EDO	C	538	4/4	0.94	0.08	18,23,25,28	0
2	CA	C	519	1/1	0.94	0.07	42,42,42,42	0
2	CA	D	523	1/1	0.95	0.07	44,44,44,44	0
3	EDO	A	529	4/4	0.95	0.09	21,29,30,36	0
3	EDO	C	539	4/4	0.95	0.12	20,25,32,33	0
3	EDO	B	538	4/4	0.95	0.10	20,20,20,20	0
2	CA	D	522	1/1	0.96	0.09	42,42,42,42	0
3	EDO	A	531	4/4	0.96	0.11	19,29,35,42	0
2	CA	A	520	1/1	0.96	0.05	35,35,35,35	0
3	EDO	D	529	4/4	0.96	0.10	26,28,29,43	0
2	CA	A	518	1/1	0.96	0.06	29,29,29,29	0
3	EDO	B	526	4/4	0.96	0.14	23,26,27,31	0
2	CA	C	521	1/1	0.97	0.04	25,25,25,25	0
3	EDO	C	536	4/4	0.97	0.11	19,25,31,42	0
2	CA	A	504	1/1	0.97	0.07	28,28,28,28	0
2	CA	D	525	1/1	0.97	0.04	49,49,49,49	0
2	CA	A	533	1/1	0.97	0.04	45,45,45,45	0
2	CA	B	516	1/1	0.97	0.04	33,33,33,33	0
3	EDO	A	528	4/4	0.97	0.05	19,20,24,25	0
2	CA	A	505	1/1	0.98	0.07	29,29,29,29	0
2	CA	C	518	1/1	0.98	0.06	46,46,46,46	0
2	CA	D	505	1/1	0.98	0.05	24,24,24,24	0
2	CA	C	507	1/1	0.98	0.06	16,16,16,16	0
2	CA	D	521	1/1	0.98	0.04	21,21,21,21	0
2	CA	B	518	1/1	0.98	0.04	35,35,35,35	0
2	CA	A	521	1/1	0.98	0.05	26,26,26,26	0
2	CA	A	519	1/1	0.98	0.05	26,26,26,26	0
2	CA	C	529	1/1	0.98	0.05	37,37,37,37	0
2	CA	D	511	1/1	0.98	0.04	18,18,18,18	0
2	CA	D	503	1/1	0.98	0.07	18,18,18,18	0
2	CA	D	524	1/1	0.98	0.07	47,47,47,47	0
2	CA	B	523	1/1	0.98	0.14	23,23,23,23	0
2	CA	C	530	1/1	0.98	0.06	40,40,40,40	0
2	CA	C	514	1/1	0.99	0.04	15,15,15,15	0
2	CA	B	508	1/1	0.99	0.03	20,20,20,20	0
2	CA	D	502	1/1	0.99	0.05	19,19,19,19	0
2	CA	C	522	1/1	0.99	0.06	37,37,37,37	0
2	CA	D	504	1/1	0.99	0.03	18,18,18,18	0
2	CA	B	507	1/1	0.99	0.03	17,17,17,17	0
2	CA	D	514	1/1	0.99	0.03	15,15,15,15	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	B	521	1/1	0.99	0.06	27,27,27,27	0
2	CA	D	506	1/1	0.99	0.03	22,22,22,22	0
2	CA	C	527	1/1	0.99	0.04	26,26,26,26	0
2	CA	B	517	1/1	0.99	0.03	16,16,16,16	0
2	CA	C	501	1/1	0.99	0.05	7,7,7,7	1
2	CA	D	509	1/1	0.99	0.03	20,20,20,20	0
2	CA	C	515	1/1	0.99	0.03	15,15,15,15	0
2	CA	A	517	1/1	0.99	0.04	19,19,19,19	0
2	CA	D	515	1/1	0.99	0.03	23,23,23,23	0
2	CA	A	514	1/1	0.99	0.03	18,18,18,18	0
2	CA	B	515	1/1	0.99	0.05	17,17,17,17	0
2	CA	C	513	1/1	0.99	0.04	19,19,19,19	0
2	CA	D	517	1/1	0.99	0.05	18,18,18,18	0
2	CA	A	516	1/1	0.99	0.04	18,18,18,18	0
2	CA	C	531	1/1	0.99	0.02	35,35,35,35	0
2	CA	C	526	1/1	0.99	0.06	15,15,15,15	0
2	CA	B	520	1/1	0.99	0.05	18,18,18,18	0
2	CA	B	540	1/1	0.99	0.03	38,38,38,38	0
2	CA	B	511	1/1	0.99	0.06	16,16,16,16	0
2	CA	C	523	1/1	0.99	0.05	16,16,16,16	0
2	CA	A	511	1/1	0.99	0.09	9,9,9,9	1
2	CA	B	512	1/1	0.99	0.05	24,24,24,24	0
2	CA	C	508	1/1	0.99	0.03	15,15,15,15	0
2	CA	D	513	1/1	0.99	0.03	16,16,16,16	0
2	CA	A	513	1/1	0.99	0.06	18,18,18,18	0
2	CA	B	501	1/1	0.99	0.05	20,20,20,20	0
2	CA	A	501	1/1	0.99	0.06	21,21,21,21	0
2	CA	D	519	1/1	0.99	0.04	16,16,16,16	0
2	CA	B	513	1/1	0.99	0.06	18,18,18,18	0
2	CA	B	505	1/1	0.99	0.04	22,22,22,22	0
2	CA	B	510	1/1	0.99	0.05	20,20,20,20	0
2	CA	C	517	1/1	0.99	0.02	25,25,25,25	0
2	CA	C	510	1/1	0.99	0.03	25,25,25,25	0
2	CA	B	509	1/1	0.99	0.04	31,31,31,31	0
2	CA	C	512	1/1	0.99	0.05	16,16,16,16	0
2	CA	B	522	1/1	0.99	0.05	25,25,25,25	0
2	CA	A	524	1/1	0.99	0.05	19,19,19,19	0
2	CA	C	511	1/1	0.99	0.07	16,16,16,16	0
2	CA	D	507	1/1	0.99	0.04	16,16,16,16	0
2	CA	D	520	1/1	0.99	0.04	23,23,23,23	0
2	CA	B	514	1/1	0.99	0.04	24,24,24,24	0
2	CA	A	508	1/1	0.99	0.03	18,18,18,18	0

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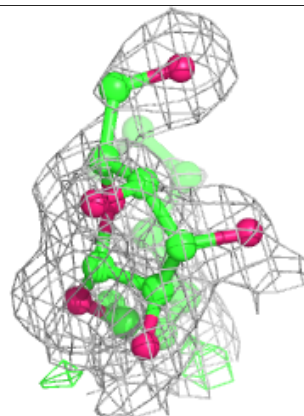
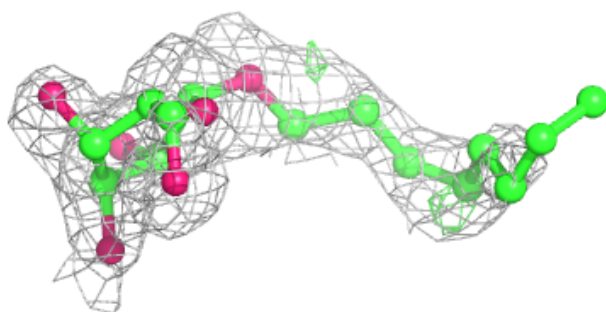
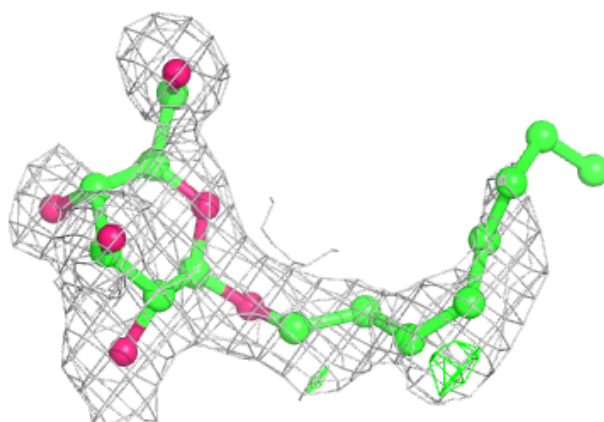
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CA	A	509	1/1	0.99	0.02	17,17,17,17	0
2	CA	B	502	1/1	0.99	0.02	28,28,28,28	0
2	CA	D	510	1/1	0.99	0.05	18,18,18,18	0
2	CA	C	516	1/1	0.99	0.04	16,16,16,16	0
2	CA	D	516	1/1	0.99	0.10	19,19,19,19	0
2	CA	C	520	1/1	0.99	0.03	35,35,35,35	0
2	CA	C	528	1/1	1.00	0.04	15,15,15,15	0
2	CA	C	505	1/1	1.00	0.05	15,15,15,15	0
2	CA	A	506	1/1	1.00	0.02	18,18,18,18	0
2	CA	B	503	1/1	1.00	0.02	19,19,19,19	0
2	CA	C	509	1/1	1.00	0.03	19,19,19,19	0
2	CA	B	506	1/1	1.00	0.03	18,18,18,18	0
2	CA	B	504	1/1	1.00	0.02	19,19,19,19	0
2	CA	A	515	1/1	1.00	0.05	20,20,20,20	0
2	CA	B	539	1/1	1.00	0.06	4,4,4,4	1
2	CA	A	523	1/1	1.00	0.07	18,18,18,18	0
2	CA	A	503	1/1	1.00	0.05	17,17,17,17	0
2	CA	A	502	1/1	1.00	0.03	17,17,17,17	0
2	CA	D	508	1/1	1.00	0.06	19,19,19,19	0
2	CA	D	518	1/1	1.00	0.02	19,19,19,19	0
2	CA	C	504	1/1	1.00	0.03	19,19,19,19	0
2	CA	A	512	1/1	1.00	0.04	17,17,17,17	0
2	CA	A	507	1/1	1.00	0.02	16,16,16,16	0
2	CA	D	512	1/1	1.00	0.04	16,16,16,16	0
2	CA	C	506	1/1	1.00	0.03	19,19,19,19	0
2	CA	C	525	1/1	1.00	0.02	15,15,15,15	0

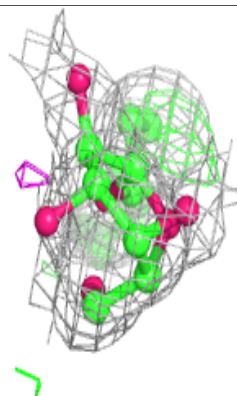
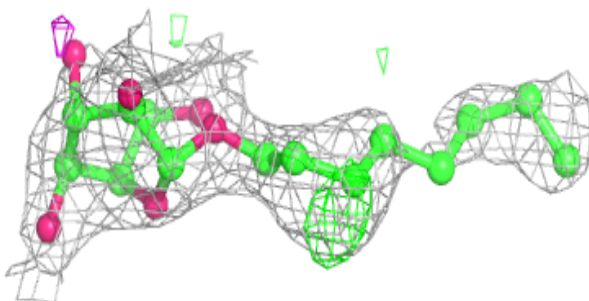
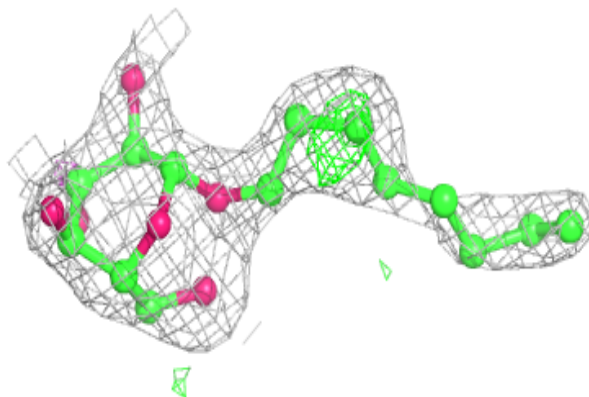
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

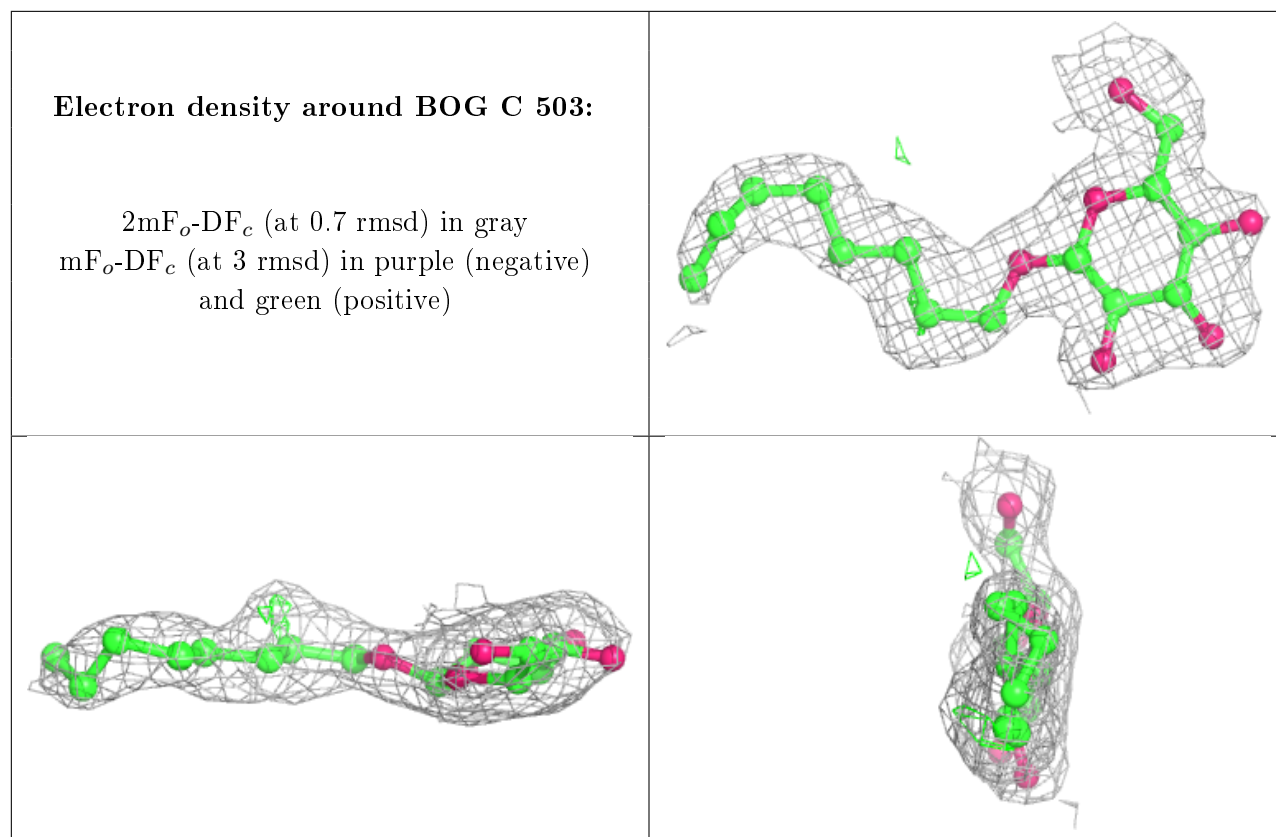
Electron density around BOG D 535:

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

**Electron density around BOG C 542:**

$2mF_o-DF_c$ (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.