



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 05:50 pm BST

PDB ID : 4WXG
Title : Crystal structure of L-Serine Hydroxymethyltransferase in complex with a mixture of L-Threonine and Glycine
Authors : Hernandez, K.; Zelen, I.; Petrillo, G.; Uson, I.; Wandtke, C.; Bujons, J.; Joglar, J.; Parella, T.; Clapes, P.
Deposited on : 2014-11-13
Resolution : 2.00 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 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 : 2.11
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) : 2.11

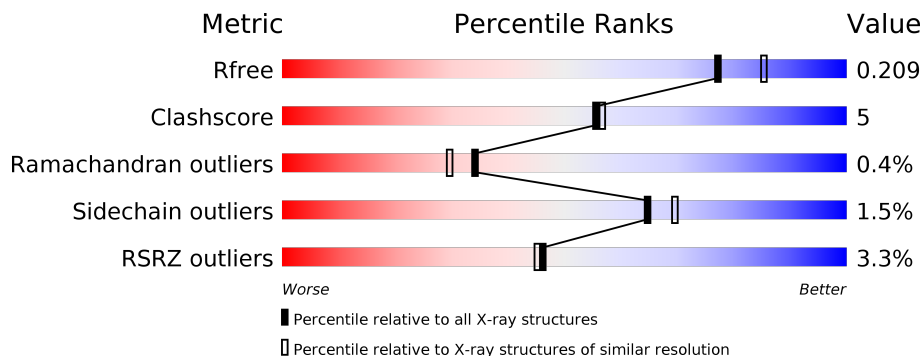
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	428	
1	C	428	

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
4	GOL	A	503	-	X	-	-

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 6742 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.

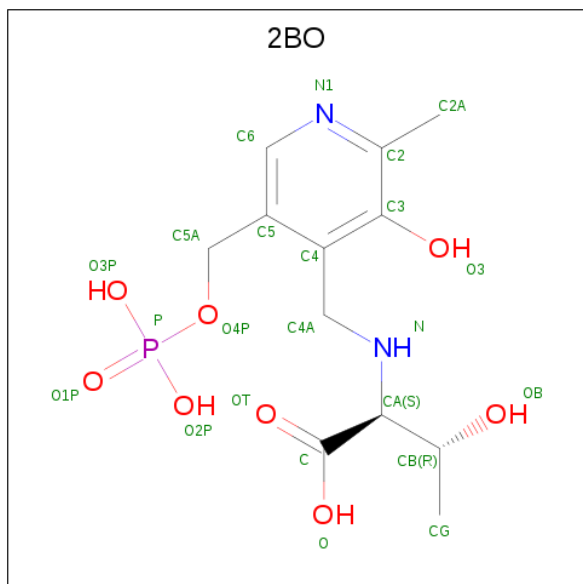
- Molecule 1 is a protein called Serine hydroxymethyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	410	3143	1991	538	605	9	0	4	0
1	C	410	3143	1991	538	605	9	0	4	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP Q5M0B4
A	-10	ARG	-	expression tag	UNP Q5M0B4
A	-9	GLY	-	expression tag	UNP Q5M0B4
A	-8	SER	-	expression tag	UNP Q5M0B4
A	-7	HIS	-	expression tag	UNP Q5M0B4
A	-6	HIS	-	expression tag	UNP Q5M0B4
A	-5	HIS	-	expression tag	UNP Q5M0B4
A	-4	HIS	-	expression tag	UNP Q5M0B4
A	-3	HIS	-	expression tag	UNP Q5M0B4
A	-2	HIS	-	expression tag	UNP Q5M0B4
A	-1	GLY	-	expression tag	UNP Q5M0B4
A	0	SER	-	expression tag	UNP Q5M0B4
C	-11	MET	-	initiating methionine	UNP Q5M0B4
C	-10	ARG	-	expression tag	UNP Q5M0B4
C	-9	GLY	-	expression tag	UNP Q5M0B4
C	-8	SER	-	expression tag	UNP Q5M0B4
C	-7	HIS	-	expression tag	UNP Q5M0B4
C	-6	HIS	-	expression tag	UNP Q5M0B4
C	-5	HIS	-	expression tag	UNP Q5M0B4
C	-4	HIS	-	expression tag	UNP Q5M0B4
C	-3	HIS	-	expression tag	UNP Q5M0B4
C	-2	HIS	-	expression tag	UNP Q5M0B4
C	-1	GLY	-	expression tag	UNP Q5M0B4
C	0	SER	-	expression tag	UNP Q5M0B4

- Molecule 2 is N-({3-hydroxy-2-methyl-5-[(phosphonoxy)methyl]pyridin-4-yl}methyl)-L-threonine (three-letter code: 2BO) (formula: C₁₂H₁₉N₂O₈P) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total	C	N	O	P	0	1
			27	14	2	10	1		
2	C	1	Total	C	N	O	P	0	1
			27	14	2	10	1		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
3	A	1	Total	Na	0	0
			1	1		
3	C	1	Total	Na	0	0
			1	1		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃) (labeled as "Ligand of Interest" by author).



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

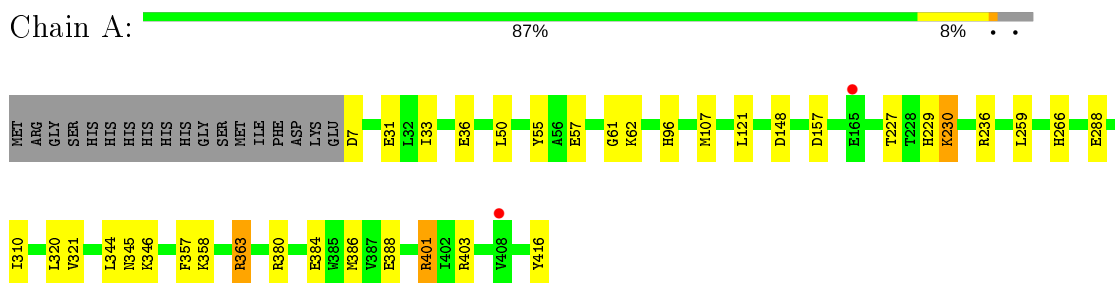
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	229	Total	O	0	1
			230	230		
5	C	163	Total	O	0	1
			164	164		

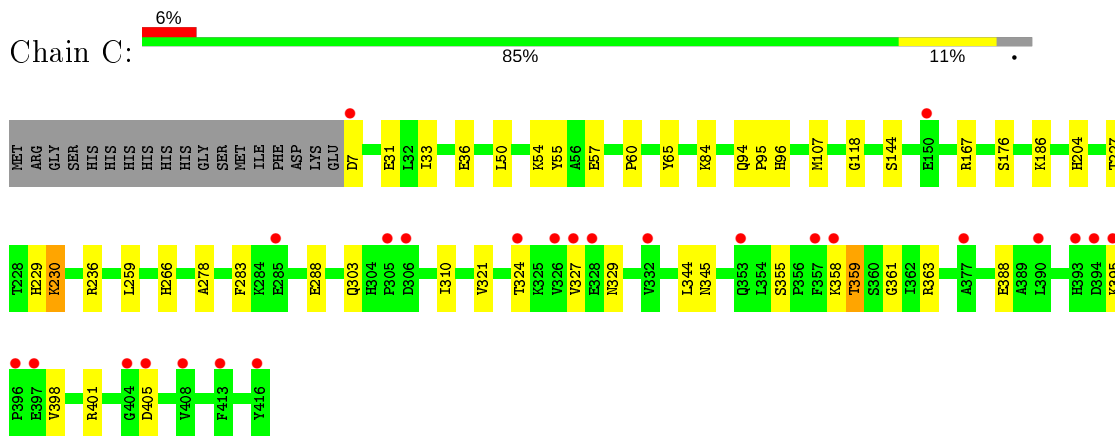
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Serine hydroxymethyltransferase



- Molecule 1: Serine hydroxymethyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	115.43Å 115.43Å 191.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.43 – 2.00 45.44 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.6 (49.43-2.00) 98.6 (45.44-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.171 , 0.203 0.181 , 0.209	Depositor DCC
R_{free} test set	4344 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtrriage
Anisotropy	0.010	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6742	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2BO, GOL, NA

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	0.96	2/3225 (0.1%)	1.02	14/4377 (0.3%)
1	C	0.92	2/3225 (0.1%)	0.98	7/4377 (0.2%)
All	All	0.94	4/6450 (0.1%)	1.00	21/8754 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	288	GLU	CD-OE1	-6.42	1.18	1.25
1	A	416	TYR	CE1-CZ	6.04	1.46	1.38
1	C	65	TYR	CE1-CZ	5.30	1.45	1.38
1	C	65	TYR	CG-CD2	5.06	1.45	1.39

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	236	ARG	NE-CZ-NH2	-10.78	114.91	120.30
1	A	401	ARG	NE-CZ-NH1	-9.57	115.51	120.30
1	A	236	ARG	NE-CZ-NH2	-9.22	115.69	120.30
1	A	229[A]	HIS	N-CA-C	8.18	133.09	111.00
1	A	229[B]	HIS	N-CA-C	8.18	133.09	111.00
1	A	236	ARG	CG-CD-NE	-8.05	94.89	111.80
1	A	401	ARG	NE-CZ-NH2	7.59	124.10	120.30
1	A	157	ASP	CB-CG-OD1	7.13	124.72	118.30
1	C	229[A]	HIS	N-CA-C	6.99	129.86	111.00
1	C	229[B]	HIS	N-CA-C	6.99	129.86	111.00
1	C	236	ARG	CG-CD-NE	-6.41	98.34	111.80
1	C	167	ARG	NE-CZ-NH2	-6.20	117.20	120.30
1	A	363	ARG	NE-CZ-NH1	6.15	123.37	120.30
1	A	148	ASP	CB-CG-OD1	-5.90	112.99	118.30
1	A	229[A]	HIS	CB-CA-C	-5.71	98.98	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229[B]	HIS	CB-CA-C	-5.71	98.98	110.40
1	A	386	MET	CG-SD-CE	-5.66	91.15	100.20
1	C	236	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	A	148	ASP	CB-CG-OD2	5.28	123.06	118.30
1	A	403	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	C	186	LYS	CD-CE-NZ	-5.16	99.83	111.70

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	3143	0	3114	31	0
1	C	3143	0	3114	32	0
2	A	27	0	8	0	0
2	C	27	0	8	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	6	0	8	0	0
5	A	230	0	0	8	1
5	C	164	0	0	7	0
All	All	6742	0	6252	64	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 5.

All (64) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:355:SER:HB3	1:C:358:LYS:HD3	1.35	1.07
1:C:388:GLU:OE2	1:C:401:ARG:NH1	2.02	0.93
1:C:310:ILE:HG12	5:C:651:HOH:O	1.79	0.82
1:A:31[A]:GLU:HG3	5:A:604:HOH:O	1.79	0.80
1:C:7:ASP:OD1	5:C:601:HOH:O	2.05	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:310:ILE:HD13	5:A:602:HOH:O	1.94	0.67
1:A:345:ASN:HD21	1:A:363:ARG:HH21	1.42	0.67
1:C:355:SER:HB3	1:C:358:LYS:CD	2.19	0.65
1:C:401:ARG:NH2	1:C:405:ASP:OD2	2.30	0.64
1:C:96:HIS:HD2	5:C:674:HOH:O	1.82	0.63
1:C:107:MET:HE1	1:C:259:LEU:HD21	1.82	0.61
1:C:57:GLU:OE2	5:C:602[A]:HOH:O	2.17	0.60
1:A:107:MET:HE1	1:A:259:LEU:HG	1.84	0.60
1:C:266:HIS:H	1:C:266:HIS:CD2	2.21	0.58
1:A:266:HIS:CD2	1:A:266:HIS:H	2.22	0.58
1:A:7:ASP:HB3	5:A:797:HOH:O	2.03	0.58
1:A:57:GLU:OE2	5:A:601[A]:HOH:O	2.18	0.57
1:A:346:LYS:HE3	1:A:357:PHE:O	2.06	0.55
1:A:345:ASN:ND2	1:A:363:ARG:HH21	2.05	0.54
1:A:310:ILE:HG12	1:A:320:LEU:HB2	1.90	0.53
5:A:608:HOH:O	1:C:54:LYS:HE3	2.09	0.51
1:A:227:THR:HG21	1:A:230[A]:LYS:NZ	2.26	0.51
1:C:310:ILE:CD1	5:C:651:HOH:O	2.59	0.50
1:C:31[B]:GLU:HG3	5:C:719:HOH:O	2.11	0.50
1:C:345:ASN:HD21	1:C:363:ARG:HH21	1.60	0.49
1:C:395:LYS:HB3	1:C:398:VAL:HG23	1.95	0.48
1:A:107:MET:HE1	1:A:259:LEU:CG	2.44	0.47
1:A:31[B]:GLU:OE1	1:A:36[B]:GLU:OE1	2.33	0.46
1:A:96:HIS:HD2	5:A:686:HOH:O	1.98	0.46
1:C:324:THR:HA	1:C:327:VAL:O	2.16	0.46
1:A:380:ARG:O	1:A:384:GLU:HG2	2.16	0.46
1:A:321:VAL:HA	5:A:602:HOH:O	2.15	0.45
1:A:310:ILE:CD1	5:A:602:HOH:O	2.61	0.45
1:A:121:LEU:H	1:A:121:LEU:HG	1.47	0.45
1:C:94:GLN:N	1:C:95:PRO:CD	2.80	0.45
1:C:176:SER:HA	1:C:204:HIS:CD2	2.52	0.45
1:A:33:ILE:HG13	1:A:344:LEU:HA	1.99	0.45
1:C:107:MET:HB2	1:C:107:MET:HE2	1.86	0.44
1:A:388:GLU:OE2	1:A:401:ARG:NH1	2.46	0.44
1:A:107:MET:HB2	1:A:107:MET:HE2	1.75	0.43
1:C:227:THR:HG21	1:C:230[A]:LYS:NZ	2.34	0.43
1:C:107:MET:HE3	1:C:259:LEU:HD11	2.00	0.42
1:C:107:MET:CE	1:C:259:LEU:HD21	2.49	0.42
1:A:61:GLY:O	1:A:62:LYS:HG3	2.19	0.42
1:C:355:SER:CB	1:C:358:LYS:HD3	2.24	0.42
1:A:266:HIS:CD2	1:A:266:HIS:N	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:ILE:HB	1:C:36[A]:GLU:CG	2.50	0.41
1:C:118:GLY:O	1:C:144:SER:HA	2.20	0.41
1:C:107:MET:HE1	1:C:259:LEU:CD2	2.49	0.41
1:C:329:ASN:HB2	1:C:359:THR:O	2.21	0.41
1:A:266:HIS:H	1:A:266:HIS:HD2	1.66	0.40
1:C:321:VAL:O	1:C:361:GLY:HA2	2.21	0.40
1:C:278:ALA:HA	1:C:283:PHE:CG	2.56	0.40
1:C:266:HIS:H	1:C:266:HIS:HD2	1.67	0.40

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)
5:A:802:HOH:O	5:A:802:HOH:O[7_555]	2.05	0.15

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	412/428 (96%)	400 (97%)	10 (2%)	2 (0%)	29	23
1	C	412/428 (96%)	398 (97%)	11 (3%)	3 (1%)	22	16
All	All	824/856 (96%)	798 (97%)	21 (2%)	5 (1%)	34	19

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230[A]	LYS
1	A	230[B]	LYS
1	C	230[A]	LYS
1	C	230[B]	LYS
1	C	359	THR

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	331/343 (96%)	328 (99%)	3 (1%)	78	83
1	C	331/343 (96%)	324 (98%)	7 (2%)	53	57
All	All	662/686 (96%)	652 (98%)	10 (2%)	65	69

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LEU
1	A	55	TYR
1	A	358	LYS
1	C	50	LEU
1	C	55	TYR
1	C	60	PRO
1	C	84	LYS
1	C	288	GLU
1	C	303	GLN
1	C	344	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	96	HIS
1	A	266	HIS
1	A	303	GLN
1	A	341	ASN
1	A	345	ASN
1	A	347	ASN
1	A	353	GLN
1	C	17	ASN
1	C	94	GLN
1	C	96	HIS
1	C	266	HIS

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Mol	Chain	Res	Type
1	C	335	ASN
1	C	345	ASN
1	C	347	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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
2	2BO	A	501[B]	-	20,20,23	5.19	4 (20%)	26,28,33	3.76	10 (38%)
4	GOL	A	503	-	5,5,5	1.79	2 (40%)	5,5,5	1.68	1 (20%)
2	2BO	A	501[A]	-	20,23,23	1.83	4 (20%)	26,33,33	4.18	11 (42%)
2	2BO	C	501[A]	-	20,23,23	1.68	4 (20%)	26,33,33	3.56	11 (42%)
2	2BO	C	501[B]	-	20,20,23	4.18	4 (20%)	26,28,33	2.93	10 (38%)

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	2BO	A	501[B]	-	-	10/15/12/19	0/1/1/1
4	GOL	A	503	-	-	4/4/4/4	-
2	2BO	A	501[A]	-	-	10/15/19/19	0/1/1/1
2	2BO	C	501[A]	-	-	6/15/19/19	0/1/1/1
2	2BO	C	501[B]	-	-	6/15/12/19	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501[B]	2BO	CB-CA	21.96	2.18	1.53
2	C	501[B]	2BO	CB-CA	17.29	2.05	1.53
2	A	501[B]	2BO	C4A-N	-5.28	1.31	1.46
2	A	501[A]	2BO	C4A-N	-5.28	1.31	1.46
2	C	501[A]	2BO	C4A-N	-5.20	1.31	1.46
2	C	501[B]	2BO	C4A-N	-5.20	1.31	1.46
2	A	501[A]	2BO	CB-CA	3.29	1.63	1.53
2	A	501[B]	2BO	O4P-C5A	-3.20	1.33	1.45
2	A	501[A]	2BO	O4P-C5A	-3.20	1.33	1.45
4	A	503	GOL	O1-C1	2.80	1.54	1.42
2	C	501[A]	2BO	C3-C2	-2.78	1.38	1.40
2	C	501[B]	2BO	C3-C2	-2.78	1.38	1.40
4	A	503	GOL	O2-C2	2.36	1.50	1.43
2	C	501[A]	2BO	CB-CA	2.32	1.60	1.53
2	A	501[B]	2BO	C3-C4	2.24	1.43	1.40
2	A	501[A]	2BO	C3-C4	2.24	1.43	1.40
2	C	501[A]	2BO	C3-C4	2.01	1.43	1.40
2	C	501[B]	2BO	C3-C4	2.01	1.43	1.40

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501[A]	2BO	C4A-N-CA	16.86	137.13	113.78
2	C	501[A]	2BO	C4A-N-CA	14.99	134.54	113.78
2	A	501[B]	2BO	CB-CA-N	-13.96	76.48	111.73
2	C	501[B]	2BO	CB-CA-N	-10.41	85.43	111.73
2	A	501[B]	2BO	CG-CB-CA	7.04	126.55	112.30
2	A	501[A]	2BO	CB-CA-N	-5.86	96.92	111.73
2	C	501[A]	2BO	O4P-C5A-C5	5.23	119.33	109.35
2	C	501[B]	2BO	O4P-C5A-C5	5.23	119.33	109.35
2	C	501[B]	2BO	C4A-N-CA	4.83	120.48	113.78
2	A	501[B]	2BO	C5A-C5-C6	-4.30	112.30	119.37
2	A	501[A]	2BO	C5A-C5-C6	-4.30	112.30	119.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501[B]	2BO	C4A-N-CA	4.21	119.61	113.78
2	A	501[B]	2BO	O2P-P-O4P	-4.11	95.81	106.73
2	A	501[A]	2BO	O2P-P-O4P	-4.11	95.81	106.73
2	C	501[A]	2BO	O2P-P-O4P	-4.09	95.85	106.73
2	C	501[B]	2BO	O2P-P-O4P	-4.09	95.85	106.73
2	A	501[A]	2BO	CG-CB-CA	4.06	120.51	112.30
2	A	501[B]	2BO	C3-C4-C5	-3.87	115.00	118.72
2	A	501[A]	2BO	C3-C4-C5	-3.87	115.00	118.72
2	C	501[B]	2BO	CG-CB-CA	3.71	119.80	112.30
2	A	501[A]	2BO	OB-CB-CA	3.61	116.36	109.14
2	C	501[A]	2BO	CB-CA-N	-3.41	103.12	111.73
2	A	501[B]	2BO	O4P-C5A-C5	3.28	115.60	109.35
2	A	501[A]	2BO	O4P-C5A-C5	3.28	115.60	109.35
2	A	501[B]	2BO	C4A-C4-C5	3.20	123.27	119.71
2	A	501[A]	2BO	C4A-C4-C5	3.20	123.27	119.71
4	A	503	GOL	O2-C2-C1	2.99	122.28	109.12
2	C	501[A]	2BO	CG-CB-CA	2.92	118.21	112.30
2	A	501[B]	2BO	O4P-P-O1P	2.65	113.90	106.47
2	A	501[A]	2BO	O4P-P-O1P	2.65	113.90	106.47
2	C	501[A]	2BO	OB-CB-CA	2.57	114.28	109.14
2	C	501[A]	2BO	O2P-P-O1P	2.23	119.42	110.68
2	C	501[B]	2BO	O2P-P-O1P	2.23	119.42	110.68
2	C	501[A]	2BO	OB-CB-CG	-2.15	103.39	109.74
2	C	501[B]	2BO	OB-CB-CG	-2.15	103.39	109.74
2	C	501[A]	2BO	O3P-P-O2P	2.09	115.62	107.64
2	C	501[B]	2BO	O3P-P-O2P	2.09	115.62	107.64
2	A	501[B]	2BO	OB-CB-CG	-2.09	103.56	109.74
2	A	501[A]	2BO	OB-CB-CG	-2.09	103.56	109.74
2	C	501[A]	2BO	C4-C4A-N	2.08	117.52	111.78
2	C	501[B]	2BO	C4-C4A-N	2.08	117.52	111.78
2	C	501[A]	2BO	C2A-C2-C3	2.07	123.45	120.89
2	C	501[B]	2BO	C2A-C2-C3	2.07	123.45	120.89

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	GOL	C1-C2-C3-O3
2	A	501[B]	2BO	C5-C4-C4A-N
2	A	501[B]	2BO	C5A-O4P-P-O2P
2	A	501[B]	2BO	C5A-O4P-P-O3P
2	A	501[B]	2BO	N-CA-CB-OB

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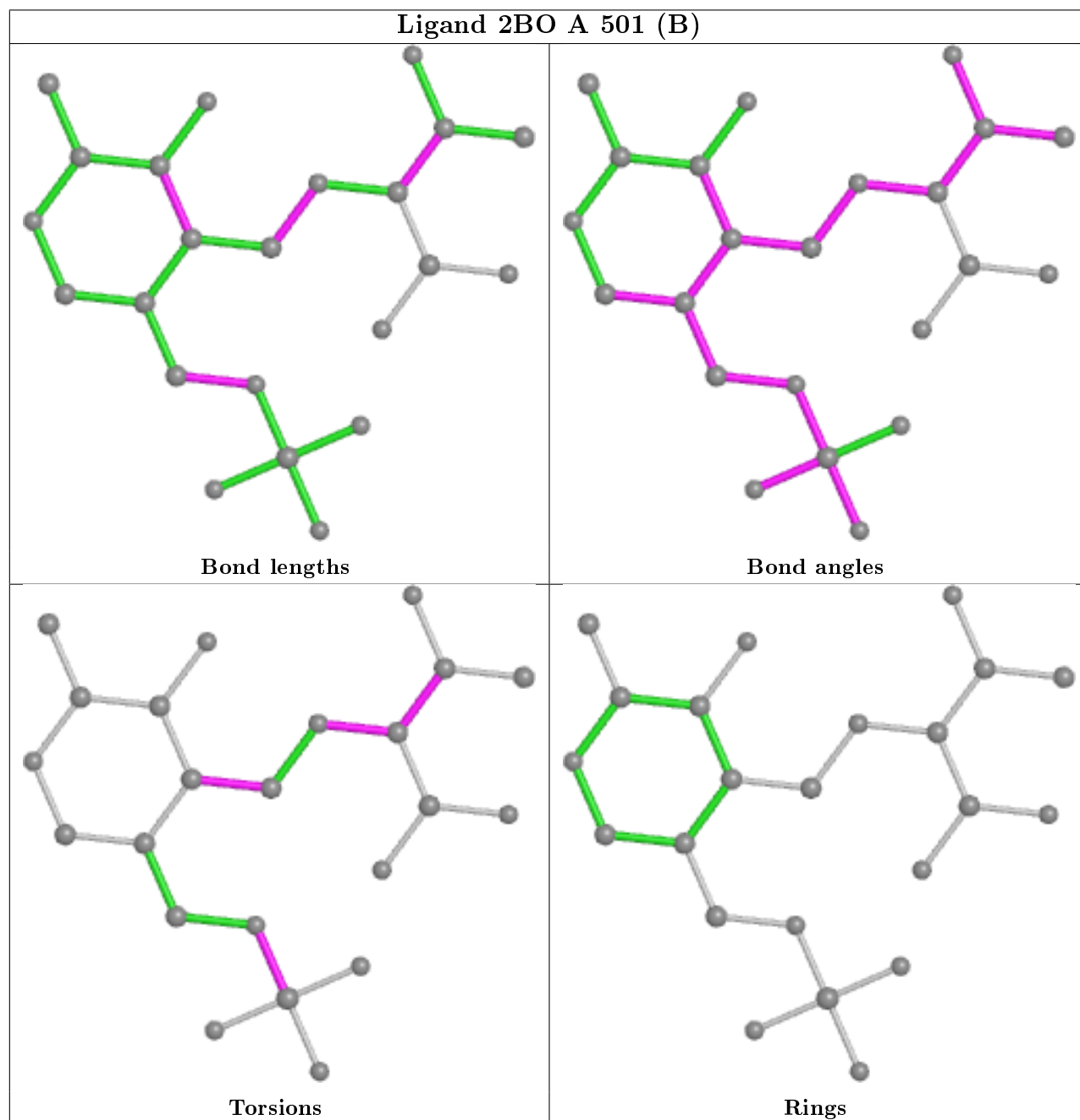
Mol	Chain	Res	Type	Atoms
2	A	501[B]	2BO	N-CA-CB-CG
2	A	501[B]	2BO	C-CA-CB-OB
2	A	501[B]	2BO	C-CA-CB-CG
2	A	501[A]	2BO	C5-C4-C4A-N
2	A	501[A]	2BO	C5A-O4P-P-O2P
2	A	501[A]	2BO	C5A-O4P-P-O3P
2	A	501[A]	2BO	C-CA-N-C4A
2	A	501[A]	2BO	N-CA-CB-CG
2	A	501[A]	2BO	C-CA-CB-OB
2	A	501[A]	2BO	C-CA-CB-CG
2	C	501[A]	2BO	C5-C4-C4A-N
2	C	501[A]	2BO	C-CA-N-C4A
2	C	501[B]	2BO	C5-C4-C4A-N
4	A	503	GOL	O1-C1-C2-O2
2	A	501[A]	2BO	N-CA-CB-OB
4	A	503	GOL	O1-C1-C2-C3
4	A	503	GOL	O2-C2-C3-O3
2	C	501[A]	2BO	C-CA-CB-OB
2	C	501[B]	2BO	C-CA-CB-OB
2	C	501[B]	2BO	N-CA-CB-CG
2	A	501[B]	2BO	C-CA-N-C4A
2	C	501[B]	2BO	C-CA-N-C4A
2	A	501[B]	2BO	C3-C4-C4A-N
2	A	501[A]	2BO	C3-C4-C4A-N
2	C	501[A]	2BO	C3-C4-C4A-N
2	C	501[B]	2BO	C3-C4-C4A-N
2	A	501[B]	2BO	CB-CA-N-C4A
2	C	501[B]	2BO	CB-CA-N-C4A
2	C	501[A]	2BO	N-CA-CB-CG
2	A	501[A]	2BO	CB-CA-N-C4A
2	C	501[A]	2BO	CB-CA-N-C4A

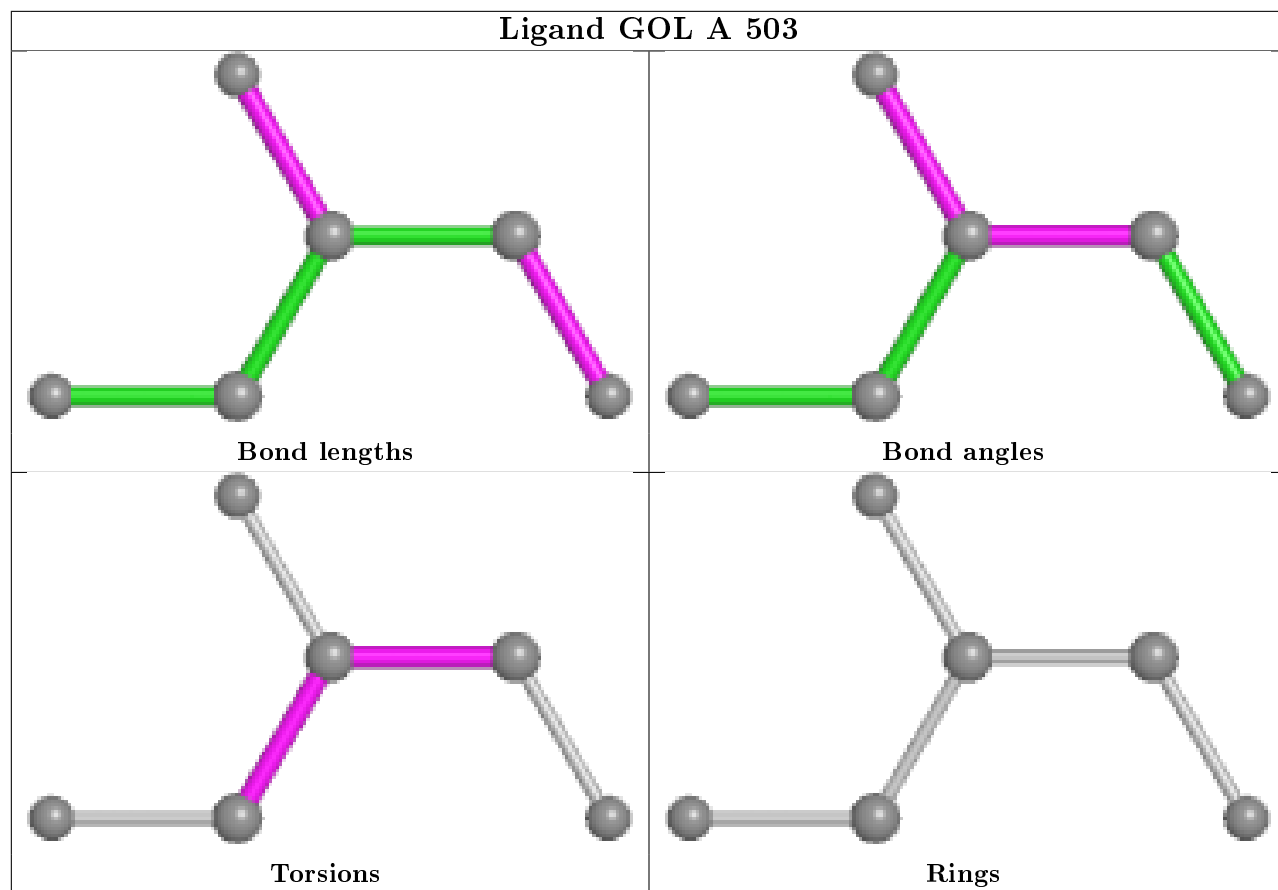
There are no ring outliers.

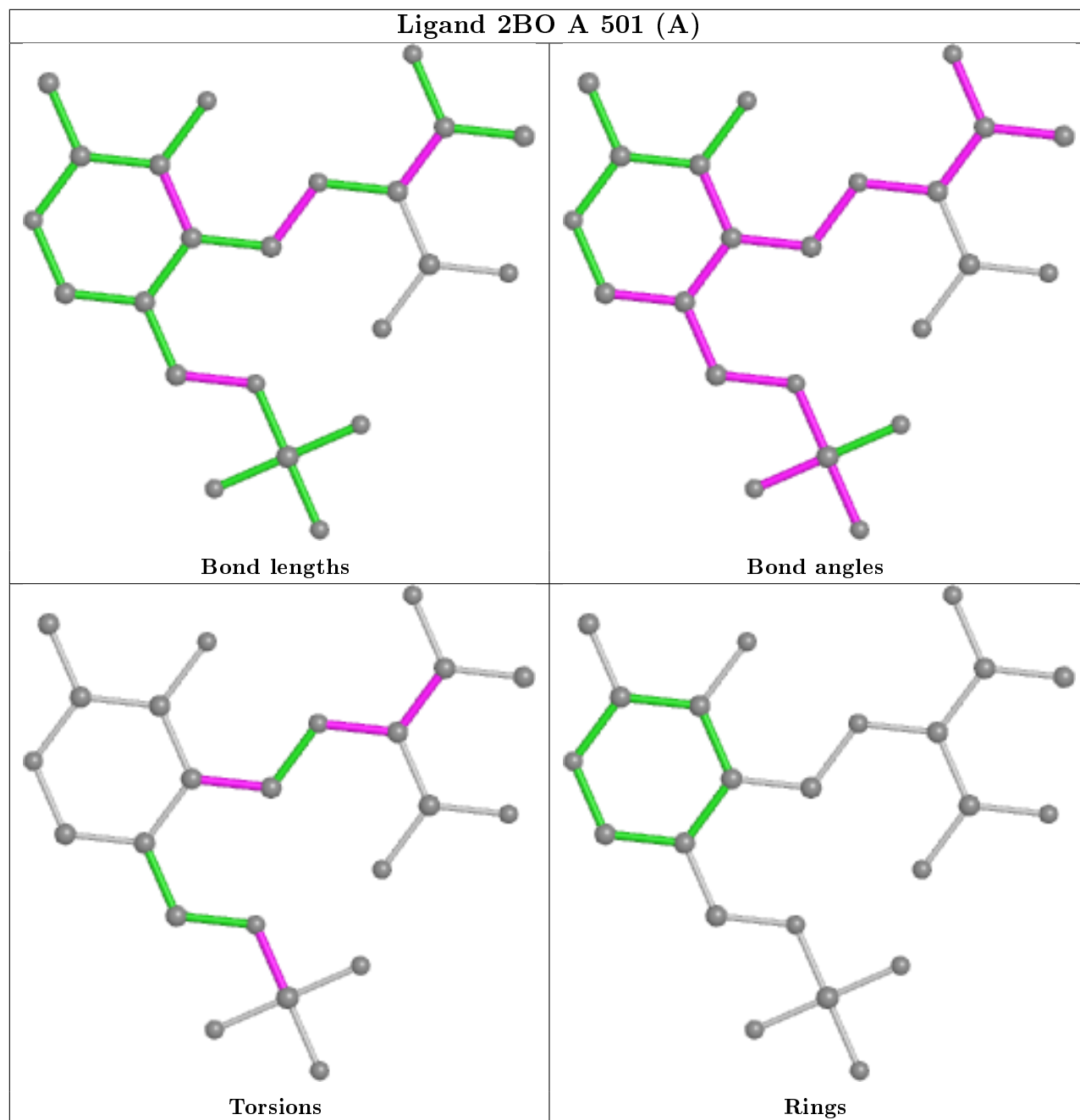
No monomer is involved in short contacts.

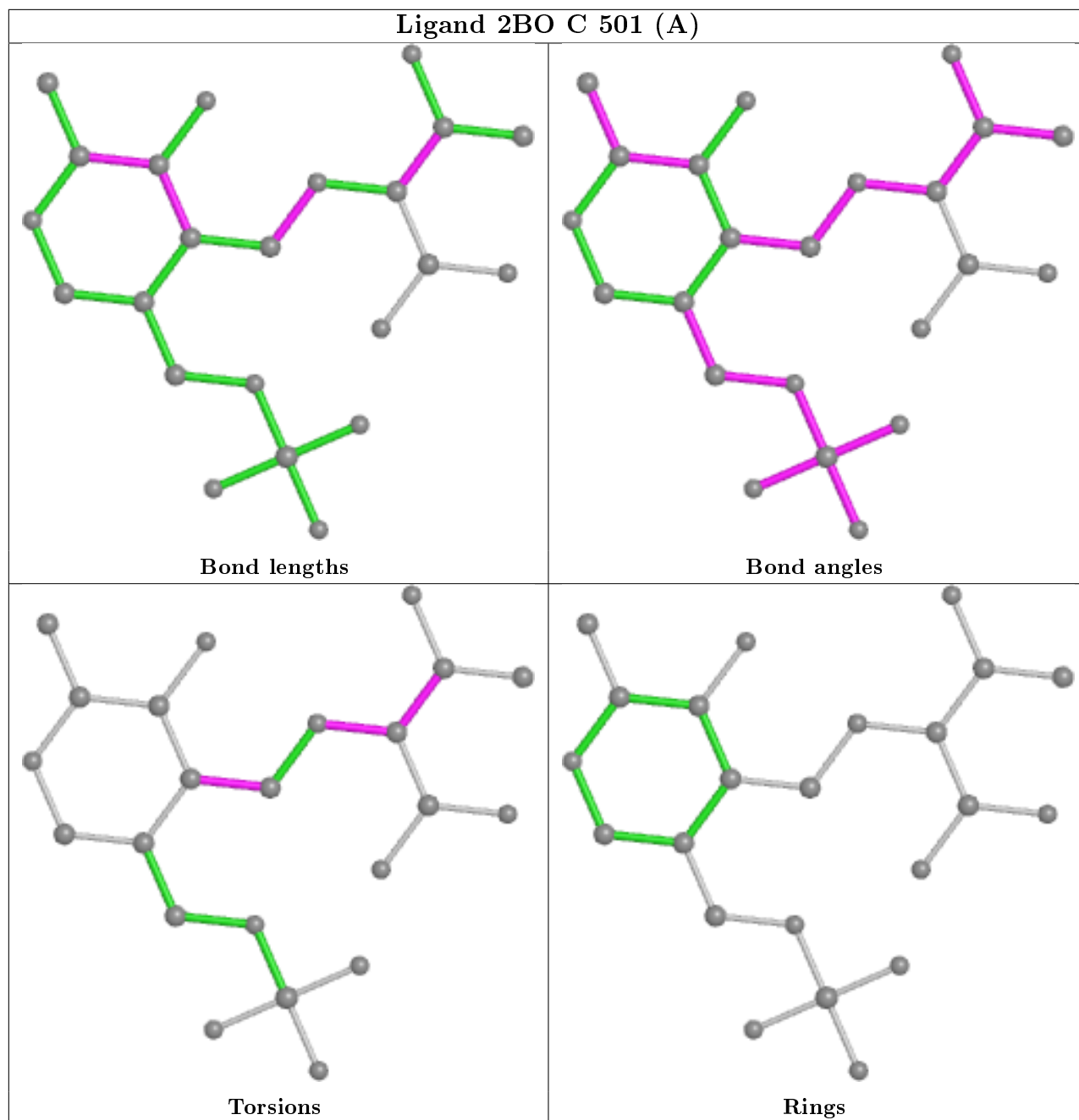
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

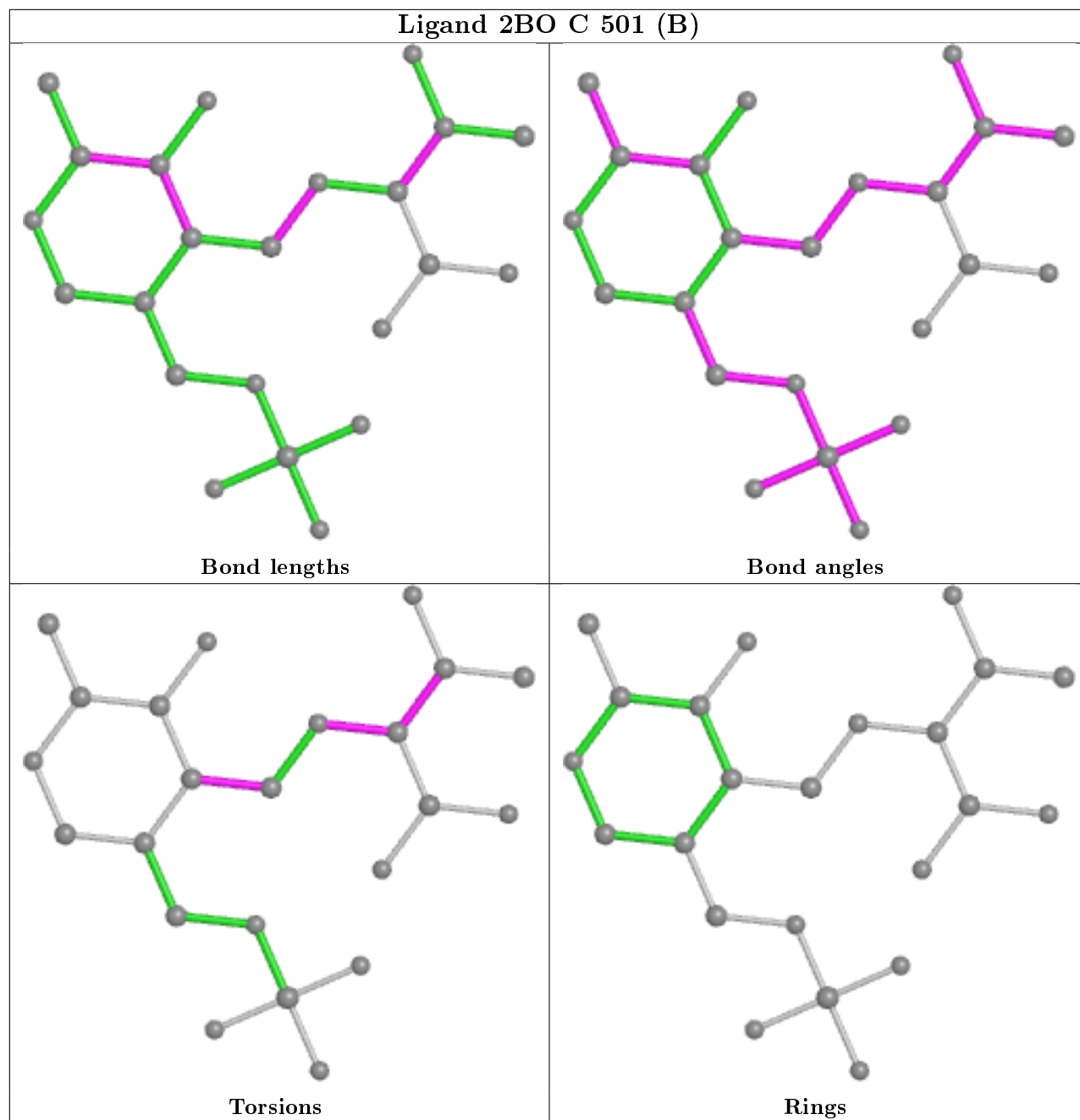
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents 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

6.1 Protein, DNA and RNA chains

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	410/428 (95%)	-0.19	2 (0%) 91 90	22, 30, 50, 74	0
1	C	410/428 (95%)	0.07	25 (6%) 21 20	22, 36, 65, 86	0
All	All	820/856 (95%)	-0.06	27 (3%) 46 45	22, 33, 59, 86	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	324	THR	3.7
1	C	394	ASP	3.7
1	C	357	PHE	3.2
1	C	328	GLU	3.2
1	C	396	PRO	3.1
1	C	306	ASP	2.9
1	A	408	VAL	2.8
1	C	413	PHE	2.8
1	C	390	LEU	2.8
1	C	327	VAL	2.7
1	C	397	GLU	2.6
1	C	305	PRO	2.6
1	C	353	GLN	2.6
1	C	395	LYS	2.6
1	C	408	VAL	2.6
1	C	150	GLU	2.6
1	C	393	HIS	2.4
1	C	358	LYS	2.4
1	C	332	VAL	2.3
1	A	165	GLU	2.2
1	C	285	GLU	2.1
1	C	404	GLY	2.1
1	C	377	ALA	2.1
1	C	416	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	326	VAL	2.1
1	C	405	ASP	2.0
1	C	7	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

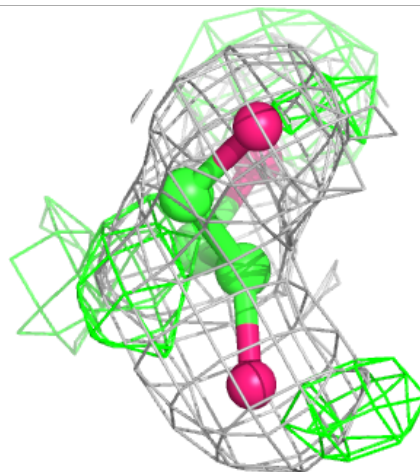
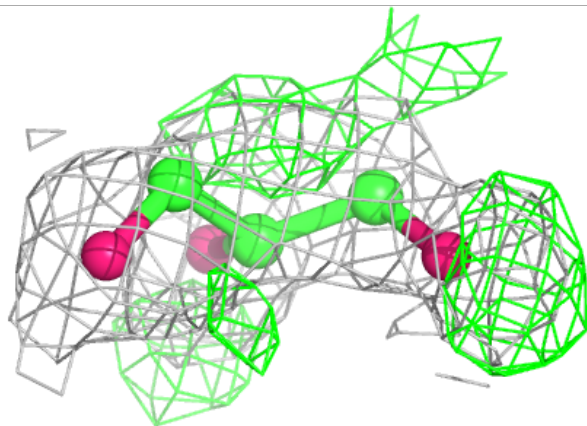
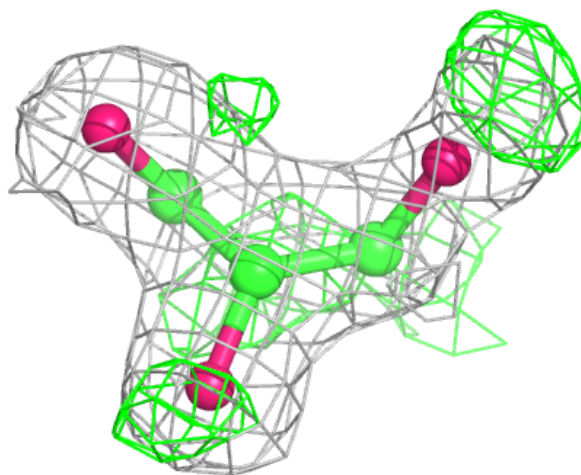
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	503	6/6	0.83	0.24	36,42,49,54	0
3	NA	C	502	1/1	0.91	0.23	60,60,60,60	0
2	2BO	A	501[B]	20/23	0.97	0.17	25,32,41,45	4
2	2BO	A	501[A]	23/23	0.97	0.17	25,32,38,45	7
2	2BO	C	501[A]	23/23	0.97	0.14	26,36,43,49	7
2	2BO	C	501[B]	20/23	0.97	0.14	26,35,40,43	4
3	NA	A	502	1/1	0.97	0.11	40,40,40,40	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.

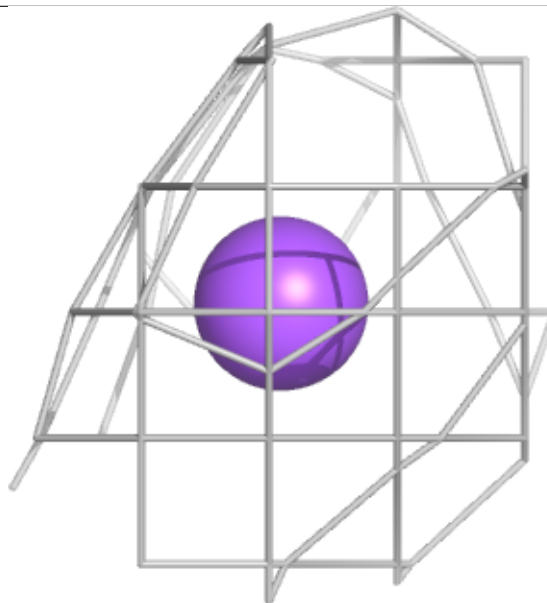
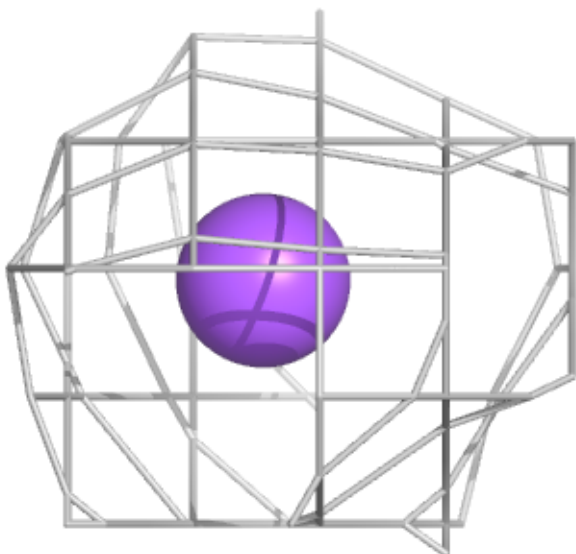
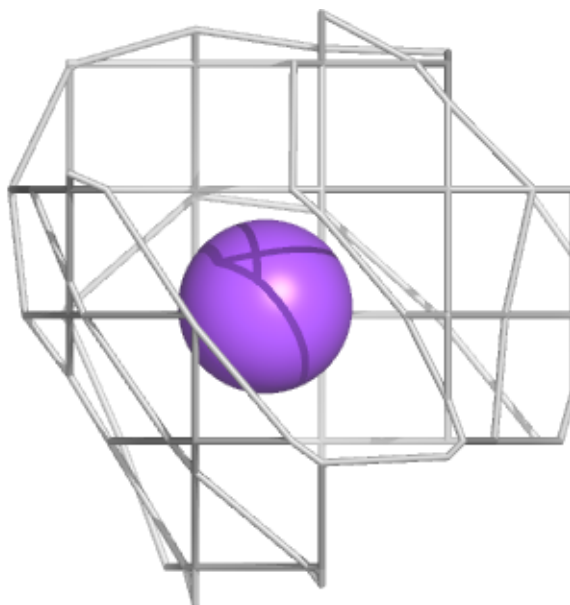
Electron density around GOL A 503:

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



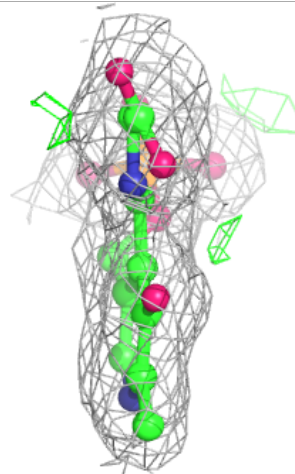
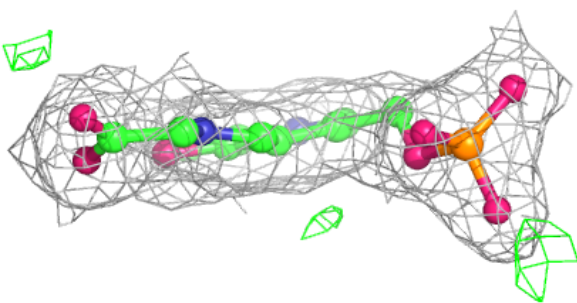
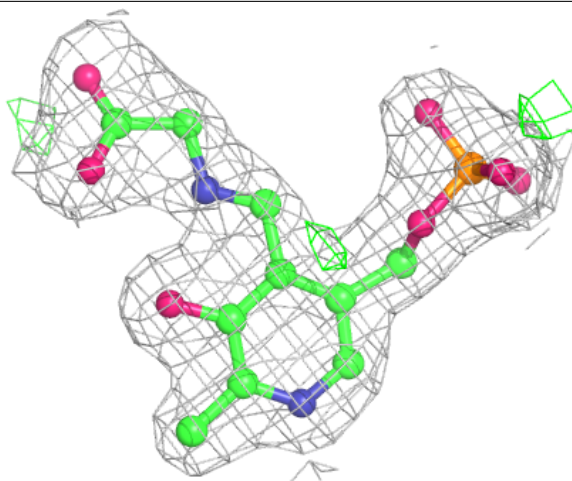
Electron density around NA C 502:

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



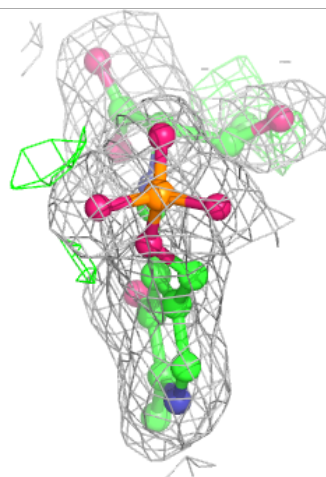
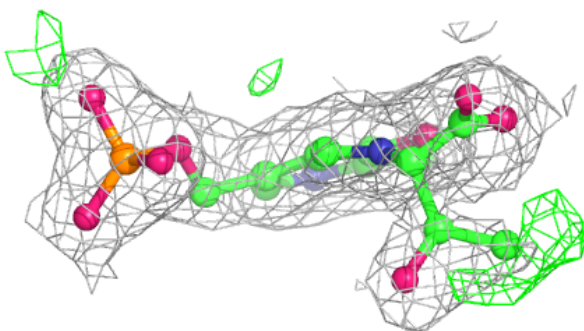
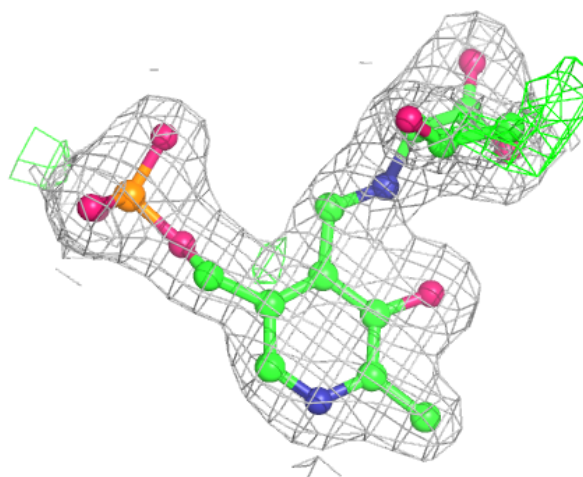
Electron density around 2BO A 501 (B):

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



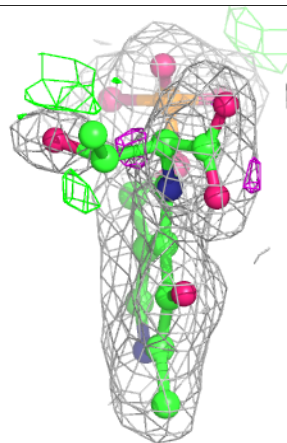
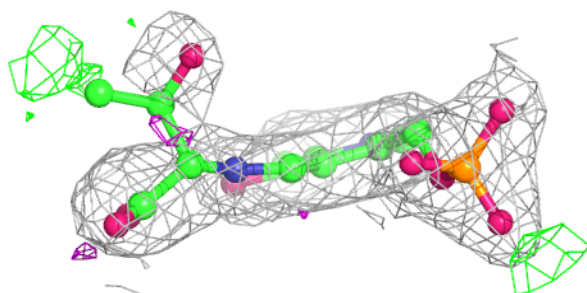
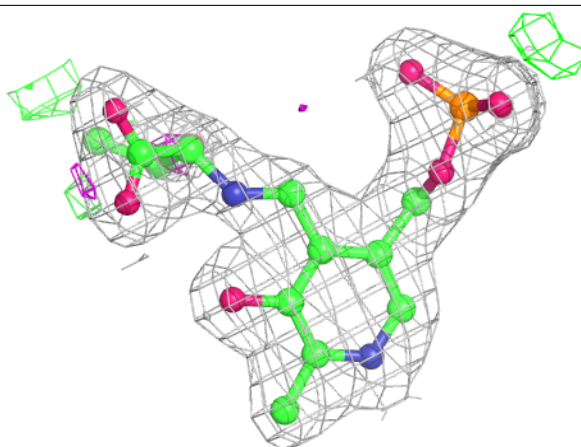
Electron density around 2BO A 501 (A):

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



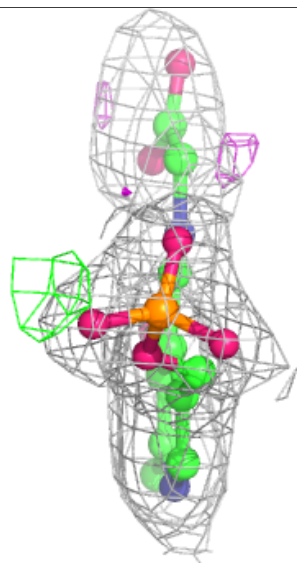
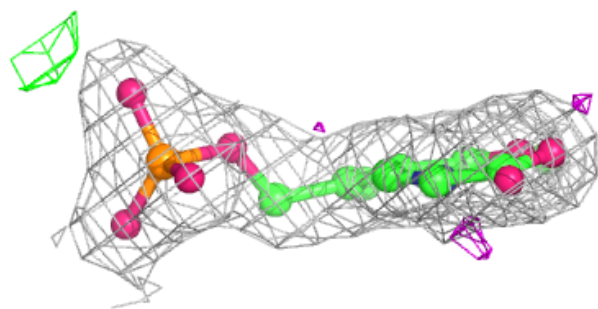
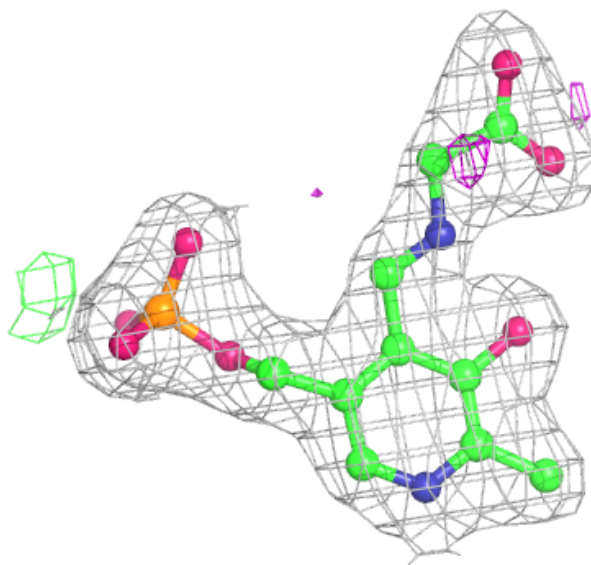
Electron density around 2BO C 501 (A):

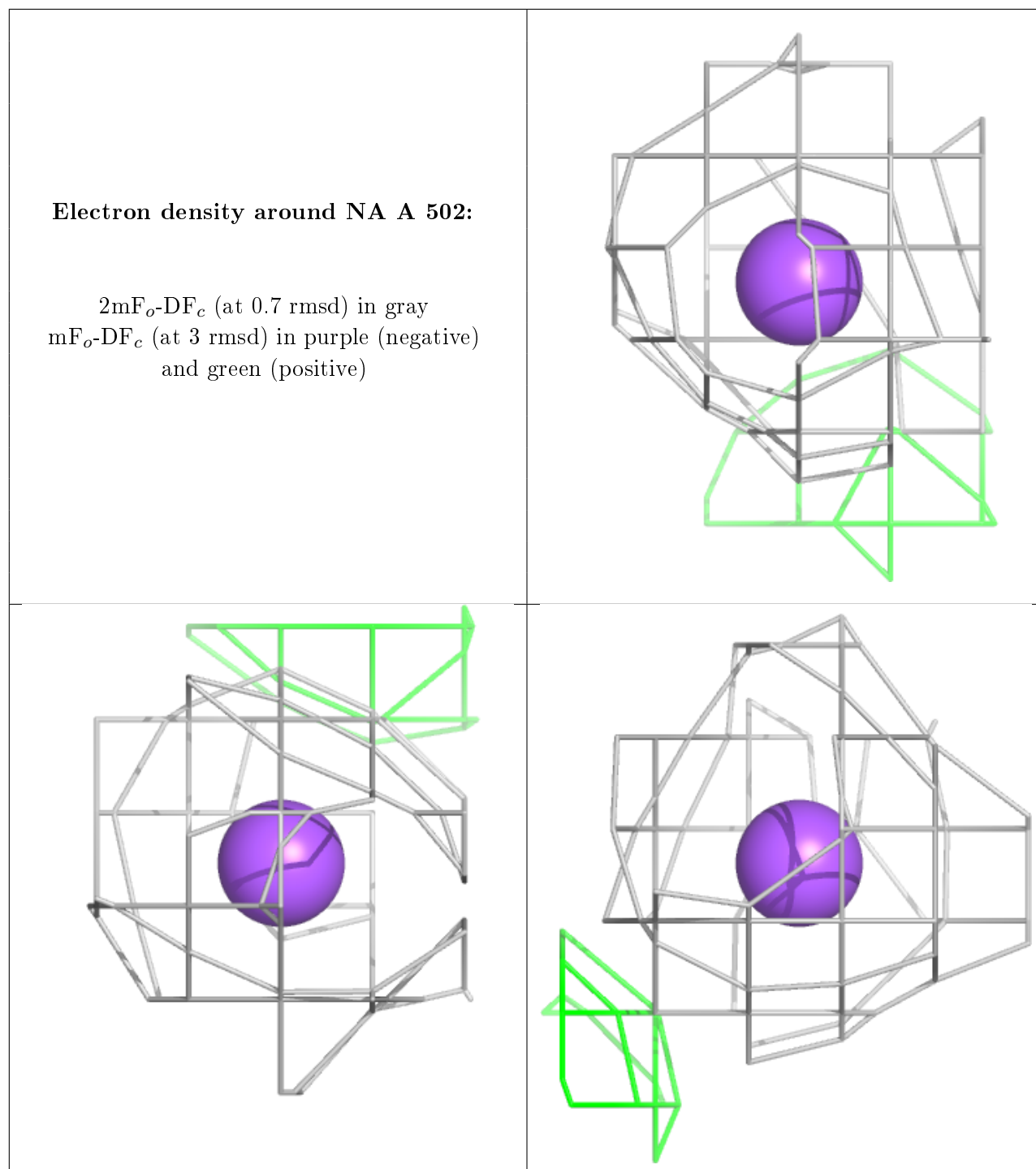
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 2BO C 501 (B):

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





6.5 Other polymers ⓘ

There are no such residues in this entry.