



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 09:36 PM UTC

PDB ID : 6KE5 / pdb_00006ke5
Title : Structure of CavAb in complex with Diltiazem and Amlodipine
Authors : Tang, L.
Deposited on : 2019-07-03
Resolution : 2.80 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 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

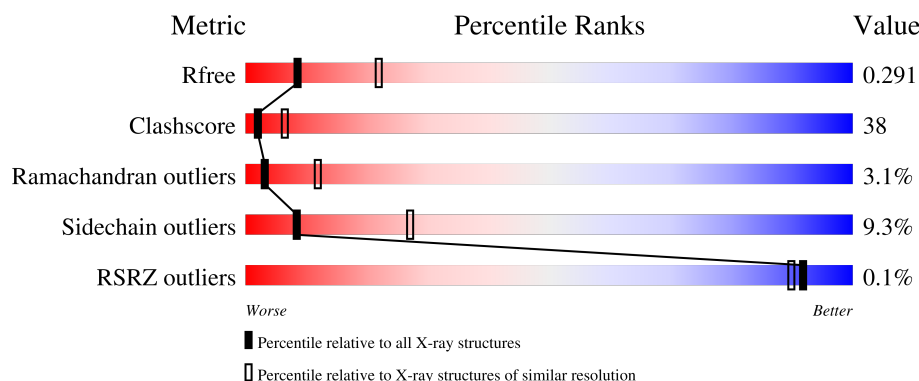
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 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	284	
1	B	284	
1	C	284	
1	D	284	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	6UB	B	1301	-	X	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7576 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1798	1225	268	295	10			
1	B	232	Total	C	N	O	S	0	0	0
			1903	1290	287	315	11			
1	C	219	Total	C	N	O	S	0	0	0
			1798	1225	268	295	10			
1	D	232	Total	C	N	O	S	0	0	0
			1903	1290	287	315	11			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	984	ASP	-	expression tag	UNP A8EVM5
A	985	TYR	-	expression tag	UNP A8EVM5
A	986	LYS	-	expression tag	UNP A8EVM5
A	987	ASP	-	expression tag	UNP A8EVM5
A	988	ASP	-	expression tag	UNP A8EVM5
A	989	ASP	-	expression tag	UNP A8EVM5
A	990	ASP	-	expression tag	UNP A8EVM5
A	991	LYS	-	expression tag	UNP A8EVM5
A	992	GLY	-	expression tag	UNP A8EVM5
A	993	SER	-	expression tag	UNP A8EVM5
A	994	LEU	-	expression tag	UNP A8EVM5
A	995	VAL	-	expression tag	UNP A8EVM5
A	996	PRO	-	expression tag	UNP A8EVM5
A	997	ARG	-	expression tag	UNP A8EVM5
A	998	GLY	-	expression tag	UNP A8EVM5
A	999	SER	-	expression tag	UNP A8EVM5
A	1000	HIS	-	expression tag	UNP A8EVM5
A	1177	ASP	GLU	conflict	UNP A8EVM5
A	1178	ASP	SER	conflict	UNP A8EVM5
A	1181	ASN	MET	conflict	UNP A8EVM5
A	1195	TYR	TRP	conflict	UNP A8EVM5

Continued on next page...

Continued from previous page...

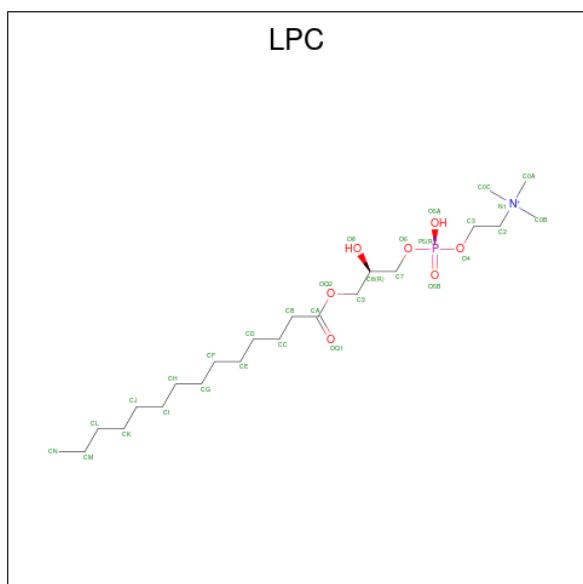
Chain	Residue	Modelled	Actual	Comment	Reference
B	984	ASP	-	expression tag	UNP A8EVM5
B	985	TYR	-	expression tag	UNP A8EVM5
B	986	LYS	-	expression tag	UNP A8EVM5
B	987	ASP	-	expression tag	UNP A8EVM5
B	988	ASP	-	expression tag	UNP A8EVM5
B	989	ASP	-	expression tag	UNP A8EVM5
B	990	ASP	-	expression tag	UNP A8EVM5
B	991	LYS	-	expression tag	UNP A8EVM5
B	992	GLY	-	expression tag	UNP A8EVM5
B	993	SER	-	expression tag	UNP A8EVM5
B	994	LEU	-	expression tag	UNP A8EVM5
B	995	VAL	-	expression tag	UNP A8EVM5
B	996	PRO	-	expression tag	UNP A8EVM5
B	997	ARG	-	expression tag	UNP A8EVM5
B	998	GLY	-	expression tag	UNP A8EVM5
B	999	SER	-	expression tag	UNP A8EVM5
B	1000	HIS	-	expression tag	UNP A8EVM5
B	1177	ASP	GLU	conflict	UNP A8EVM5
B	1178	ASP	SER	conflict	UNP A8EVM5
B	1181	ASN	MET	conflict	UNP A8EVM5
B	1195	TYR	TRP	conflict	UNP A8EVM5
C	984	ASP	-	expression tag	UNP A8EVM5
C	985	TYR	-	expression tag	UNP A8EVM5
C	986	LYS	-	expression tag	UNP A8EVM5
C	987	ASP	-	expression tag	UNP A8EVM5
C	988	ASP	-	expression tag	UNP A8EVM5
C	989	ASP	-	expression tag	UNP A8EVM5
C	990	ASP	-	expression tag	UNP A8EVM5
C	991	LYS	-	expression tag	UNP A8EVM5
C	992	GLY	-	expression tag	UNP A8EVM5
C	993	SER	-	expression tag	UNP A8EVM5
C	994	LEU	-	expression tag	UNP A8EVM5
C	995	VAL	-	expression tag	UNP A8EVM5
C	996	PRO	-	expression tag	UNP A8EVM5
C	997	ARG	-	expression tag	UNP A8EVM5
C	998	GLY	-	expression tag	UNP A8EVM5
C	999	SER	-	expression tag	UNP A8EVM5
C	1000	HIS	-	expression tag	UNP A8EVM5
C	1177	ASP	GLU	conflict	UNP A8EVM5
C	1178	ASP	SER	conflict	UNP A8EVM5
C	1181	ASN	MET	conflict	UNP A8EVM5
C	1195	TYR	TRP	conflict	UNP A8EVM5

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	984	ASP	-	expression tag	UNP A8EVM5
D	985	TYR	-	expression tag	UNP A8EVM5
D	986	LYS	-	expression tag	UNP A8EVM5
D	987	ASP	-	expression tag	UNP A8EVM5
D	988	ASP	-	expression tag	UNP A8EVM5
D	989	ASP	-	expression tag	UNP A8EVM5
D	990	ASP	-	expression tag	UNP A8EVM5
D	991	LYS	-	expression tag	UNP A8EVM5
D	992	GLY	-	expression tag	UNP A8EVM5
D	993	SER	-	expression tag	UNP A8EVM5
D	994	LEU	-	expression tag	UNP A8EVM5
D	995	VAL	-	expression tag	UNP A8EVM5
D	996	PRO	-	expression tag	UNP A8EVM5
D	997	ARG	-	expression tag	UNP A8EVM5
D	998	GLY	-	expression tag	UNP A8EVM5
D	999	SER	-	expression tag	UNP A8EVM5
D	1000	HIS	-	expression tag	UNP A8EVM5
D	1177	ASP	GLU	conflict	UNP A8EVM5
D	1178	ASP	SER	conflict	UNP A8EVM5
D	1181	ASN	MET	conflict	UNP A8EVM5
D	1195	TYR	TRP	conflict	UNP A8EVM5

- Molecule 2 is [1-MYRISTOYL-GLYCEROL-3-YL]PHOSPHONYLCHOLINE (CCD ID: LPC) (formula: C₂₂H₄₇NO₇P) (labeled as "Ligand of Interest" by depositor).

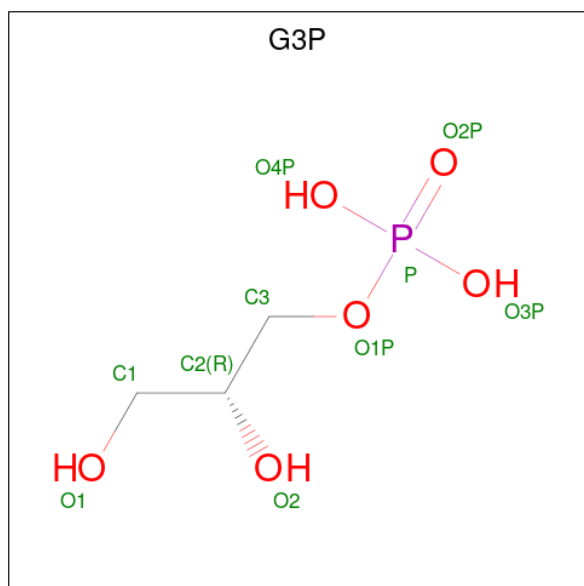


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			21	13	7	1		
2	C	1	Total	C	O	P	0	0
			21	13	7	1		
2	D	1	Total	C	O	P	0	0
			21	13	7	1		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 4 is SN-GLYCEROL-3-PHOSPHATE (CCD ID: G3P) (formula: C₃H₉O₆P) (labeled as "Ligand of Interest" by depositor).



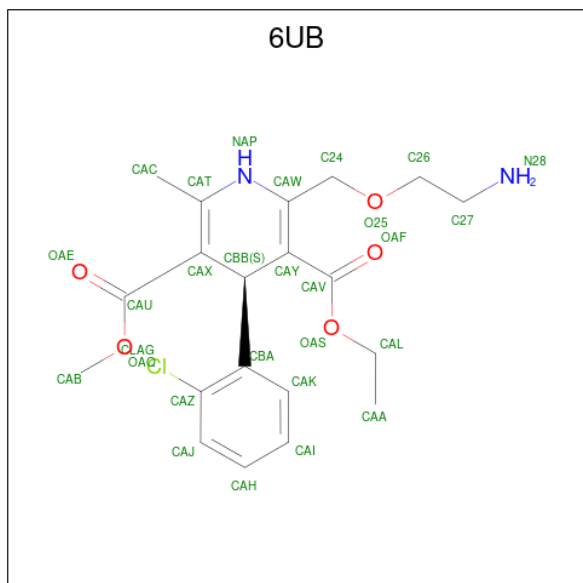
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			10	3	6	1		
4	A	1	Total	C	O	P	0	0
			10	3	6	1		
4	B	1	Total	C	O	P	0	0
			10	3	6	1		

Continued on next page...

Continued from previous page...

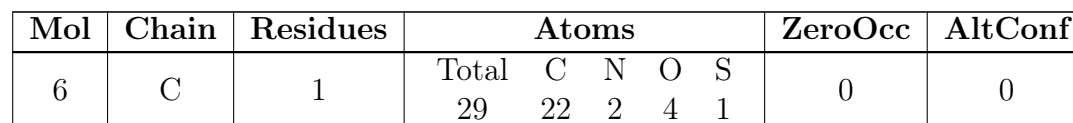
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	O	P	0	0
			10	3	6	1		
4	D	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 5 is amlodipine (CCD ID: 6UB) (formula: $C_{20}H_{25}ClN_2O_5$) (labeled as "Ligand of Interest" by depositor).



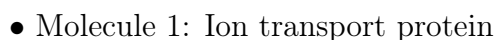
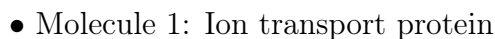
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	Cl	N	O	0
			28	20	1	2	5	

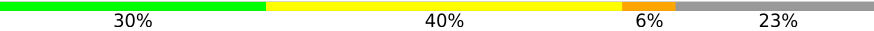
- Molecule 6 is [(2 {S},3 {R})-5-[2-(dimethylamino)ethyl]-2-(4-methoxyphenyl)-4-oxidanylidene-2,3-dihydro-1,5-benzothiazepin-3-yl] ethanoate (CCD ID: D6C) (formula: $C_{22}H_{26}N_2O_4S$) (labeled as "Ligand of Interest" by depositor).

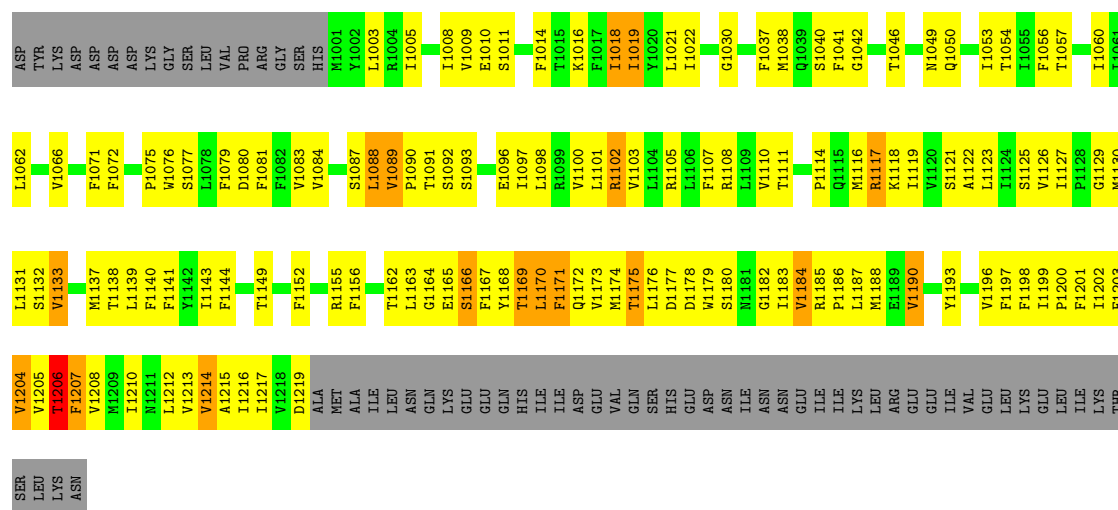


- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|----------------|---------|---------|
| 7 | C | 1 | Total O
1 1 | 0 | 0 |

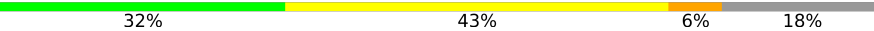
- Molecule 1: Ion transport protein

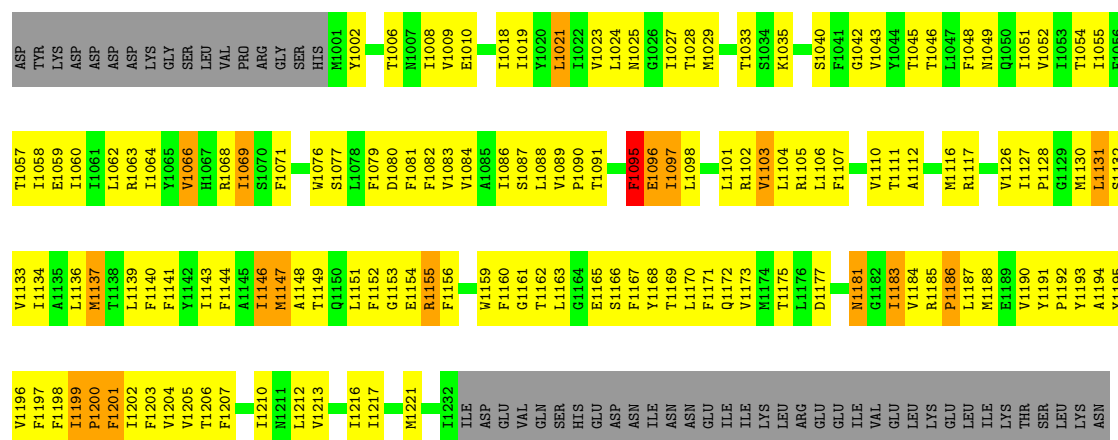


Chain C:  30% 40% 6% 23%



• Molecule 1: Ion transport protein

Chain D:  32% 43% 6% 18%



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	124.73Å 124.99Å 191.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.71 – 2.80 44.71 – 2.80	Depositor EDS
% Data completeness (in resolution range)	90.0 (44.71-2.80) 89.5 (44.71-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.249 , 0.292 0.248 , 0.291	Depositor DCC
R_{free} test set	3285 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å ²)	67.1	Xtriage
Anisotropy	0.487	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 87.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.460 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7576	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: D6C, G3P, 6UB, LPC, CA

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	1.02	3/1848 (0.2%)	1.11	11/2515 (0.4%)
1	B	0.91	0/1954	0.98	10/2657 (0.4%)
1	C	1.10	6/1848 (0.3%)	1.03	8/2515 (0.3%)
1	D	0.94	2/1954 (0.1%)	0.98	5/2657 (0.2%)
All	All	0.99	11/7604 (0.1%)	1.03	34/10344 (0.3%)

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1180	SER	CA-C	-9.20	1.41	1.52
1	A	1183	ILE	C-O	-6.52	1.16	1.24
1	C	1178	ASP	CA-C	-6.46	1.46	1.53
1	C	1206	THR	C-O	-6.25	1.16	1.24
1	C	1205	VAL	C-O	-5.78	1.17	1.24

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1184	VAL	N-CA-C	9.59	119.55	110.53
1	B	1004	ARG	N-CA-C	-9.29	101.23	111.36
1	A	1180	SER	N-CA-C	8.77	120.61	111.14
1	A	1096	GLU	N-CA-C	8.74	129.41	110.80
1	B	1159	TRP	N-CA-C	7.79	120.90	111.40

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	1798	0	1868	167	0
1	B	1903	0	1974	133	0
1	C	1798	0	1868	153	0
1	D	1903	0	1974	175	0
2	A	21	0	20	3	0
2	C	21	0	20	2	0
2	D	21	0	20	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	20	0	14	2	0
4	B	10	0	7	3	0
4	C	10	0	7	0	0
4	D	10	0	7	3	0
5	B	28	0	0	6	0
6	C	29	0	0	1	0
7	C	1	0	0	0	0
All	All	7576	0	7779	586	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 38.

The worst 5 of 586 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1149:THR:HG22	1:D:1162:THR:N	1.42	1.29
1:C:1199:ILE:CG2	1:C:1203:PHE:HE2	1.51	1.21
1:A:1080:ASP:O	1:A:1084:VAL:HG23	1.46	1.14
1:D:1153:GLY:HA3	1:D:1161:GLY:HA3	1.27	1.14
1:D:1159:TRP:O	1:D:1160:PHE:CD2	1.99	1.14

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	217/284 (76%)	179 (82%)	32 (15%)	6 (3%)	4	14
1	B	230/284 (81%)	197 (86%)	28 (12%)	5 (2%)	5	19
1	C	217/284 (76%)	180 (83%)	28 (13%)	9 (4%)	2	8
1	D	230/284 (81%)	196 (85%)	26 (11%)	8 (4%)	3	10
All	All	894/1136 (79%)	752 (84%)	114 (13%)	28 (3%)	3	12

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1096	GLU
1	C	1131	LEU
1	A	1006	THR
1	A	1145	ALA
1	B	1114	PRO

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	202/263 (77%)	173 (86%)	29 (14%)	3	11
1	B	213/263 (81%)	200 (94%)	13 (6%)	17	46
1	C	202/263 (77%)	187 (93%)	15 (7%)	13	37
1	D	213/263 (81%)	193 (91%)	20 (9%)	8	27
All	All	830/1052 (79%)	753 (91%)	77 (9%)	8	27

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	1008	ILE
1	D	1155	ARG
1	D	1018	ILE
1	D	1095	PHE
1	D	1199	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1025	ASN
1	B	1039	GLN
1	C	1067	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 3 are monoatomic - leaving 10 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
4	G3P	C	1304	-	9,9,9	2.09	2 (22%)	10,12,12	1.39	2 (20%)
2	LPC	C	1301	-	20,20,30	2.24	5 (25%)	22,24,37	1.61	3 (13%)
2	LPC	A	1301	-	20,20,30	1.73	4 (20%)	22,24,37	1.95	2 (9%)
2	LPC	D	1301	-	20,20,30	1.71	4 (20%)	22,24,37	1.81	2 (9%)
4	G3P	B	1302	-	9,9,9	1.05	0	10,12,12	1.06	1 (10%)
4	G3P	A	1303	-	9,9,9	1.18	1 (11%)	10,12,12	0.92	0
4	G3P	D	1303	-	9,9,9	1.20	2 (22%)	10,12,12	0.63	0
5	6UB	B	1301	-	28,29,29	3.22	13 (46%)	38,39,39	3.40	18 (47%)
4	G3P	A	1304	-	9,9,9	1.00	1 (11%)	10,12,12	1.26	1 (10%)
6	D6C	C	1302	-	31,31,31	2.38	6 (19%)	43,43,43	2.83	16 (37%)

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
4	G3P	C	1304	-	-	1/8/8/8	-
2	LPC	C	1301	-	-	14/22/22/32	-
2	LPC	A	1301	-	-	10/22/22/32	-
2	LPC	D	1301	-	-	13/22/22/32	-
4	G3P	B	1302	-	-	1/8/8/8	-
4	G3P	A	1303	-	-	5/8/8/8	-
4	G3P	D	1303	-	-	4/8/8/8	-
5	6UB	B	1301	-	-	15/22/42/42	0/2/2/2
4	G3P	A	1304	-	-	2/8/8/8	-
6	D6C	C	1302	-	-	6/15/35/35	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1301	6UB	CAW-NAP	9.67	1.52	1.37
5	B	1301	6UB	CAU-CAX	7.46	1.61	1.47
6	C	1302	D6C	C16-N17	7.45	1.50	1.43
2	C	1301	LPC	OQ1-CA	7.44	1.44	1.22
5	B	1301	6UB	CAT-NAP	6.59	1.47	1.38

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1301	6UB	CAT-NAP-CAW	-9.97	113.97	122.35
5	B	1301	6UB	CAZ-CBA-CBB	-9.56	111.30	123.97
2	D	1301	LPC	OQ2-CA-OQ1	-7.38	105.16	123.63
5	B	1301	6UB	CAC-CAT-CAX	-7.35	120.31	127.61
2	A	1301	LPC	OQ2-CA-OQ1	-7.01	106.09	123.63

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

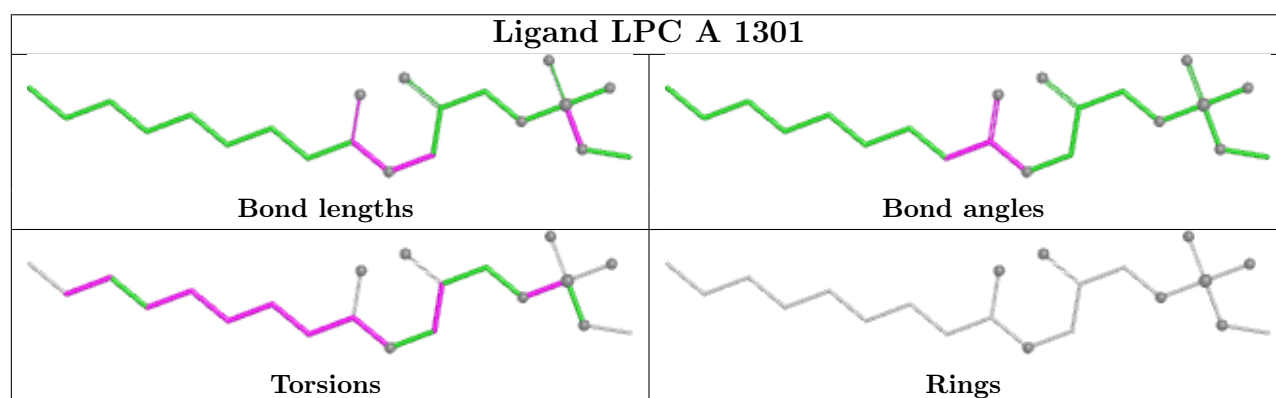
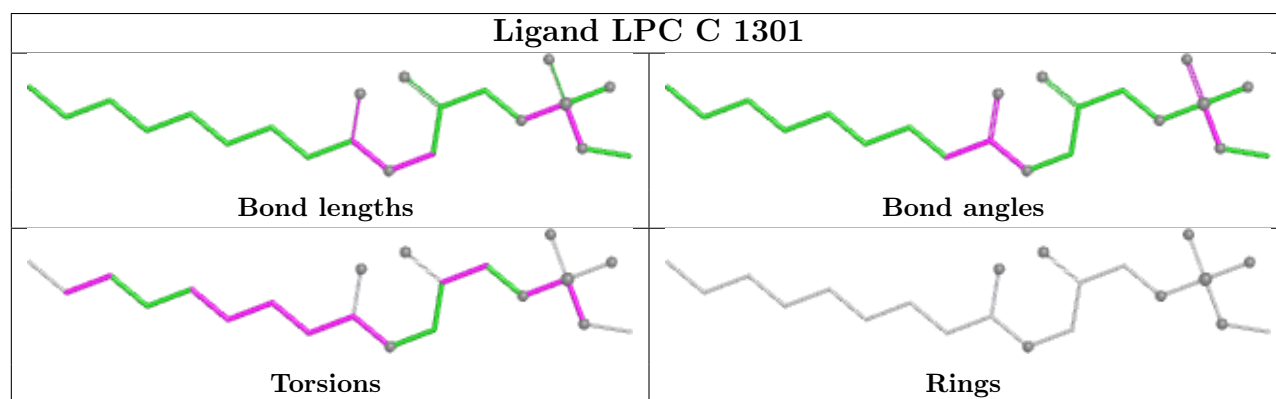
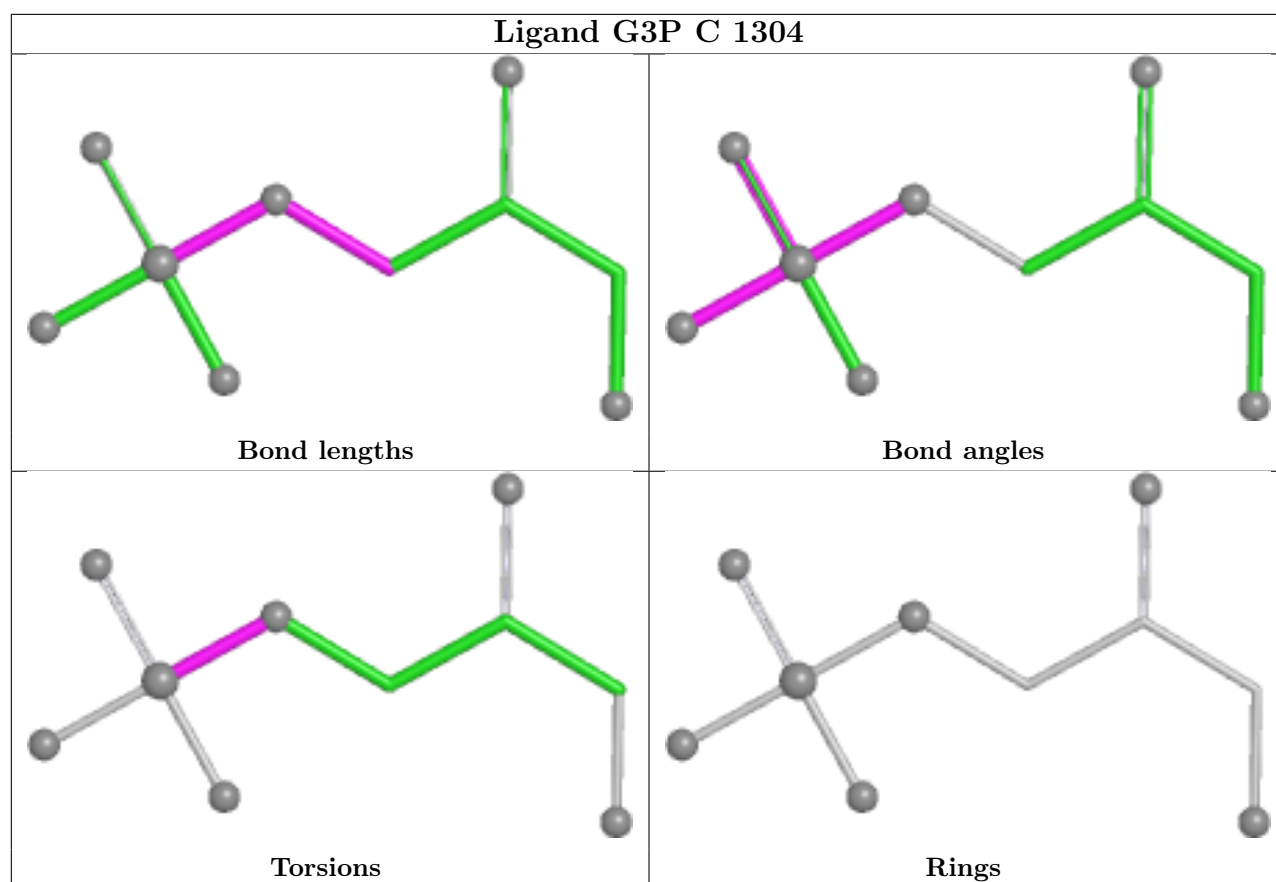
Mol	Chain	Res	Type	Atoms
2	A	1301	LPC	C7-O6-P5-O5B
2	A	1301	LPC	O8-C8-C9-OQ2
2	C	1301	LPC	C3-O4-P5-O5A
2	C	1301	LPC	C7-O6-P5-O4
2	C	1301	LPC	C7-O6-P5-O5B

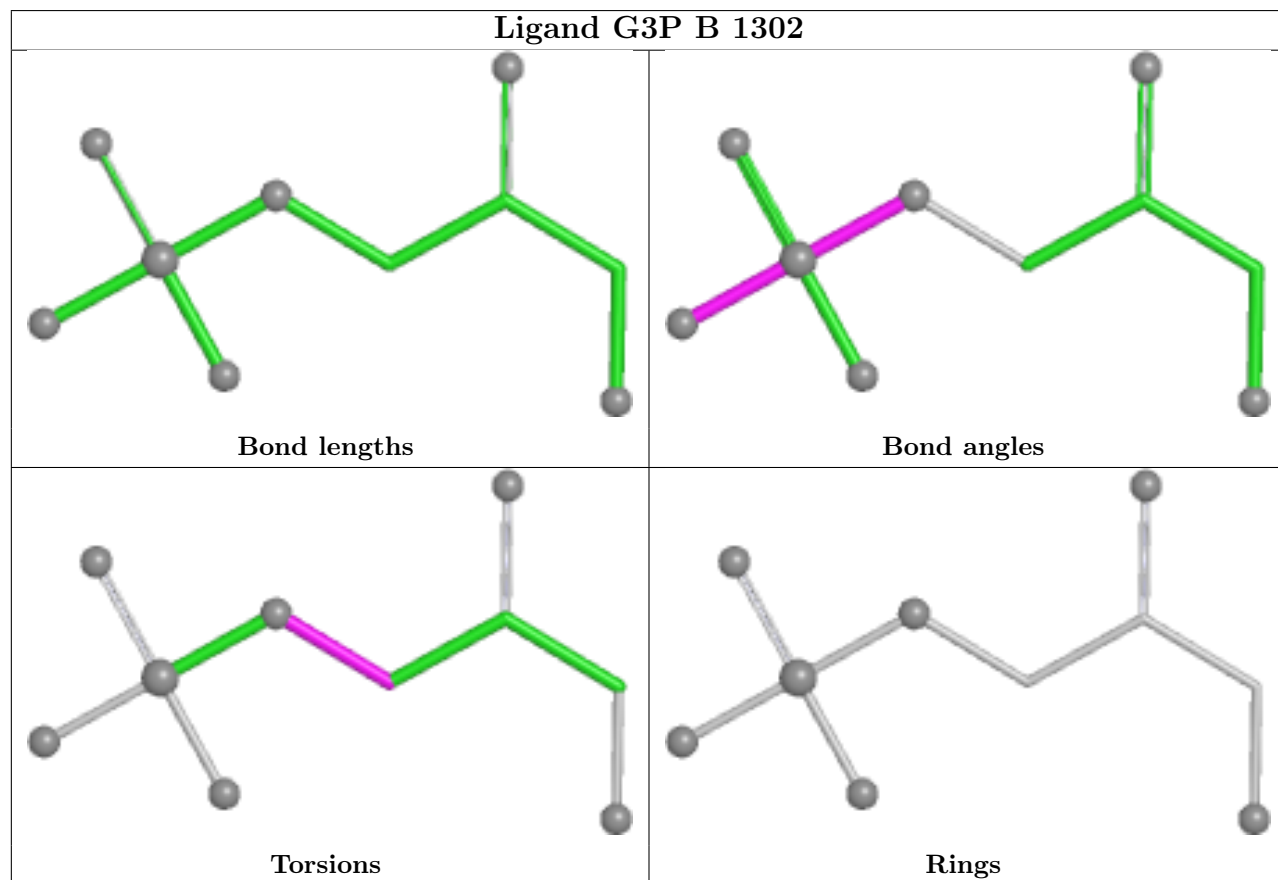
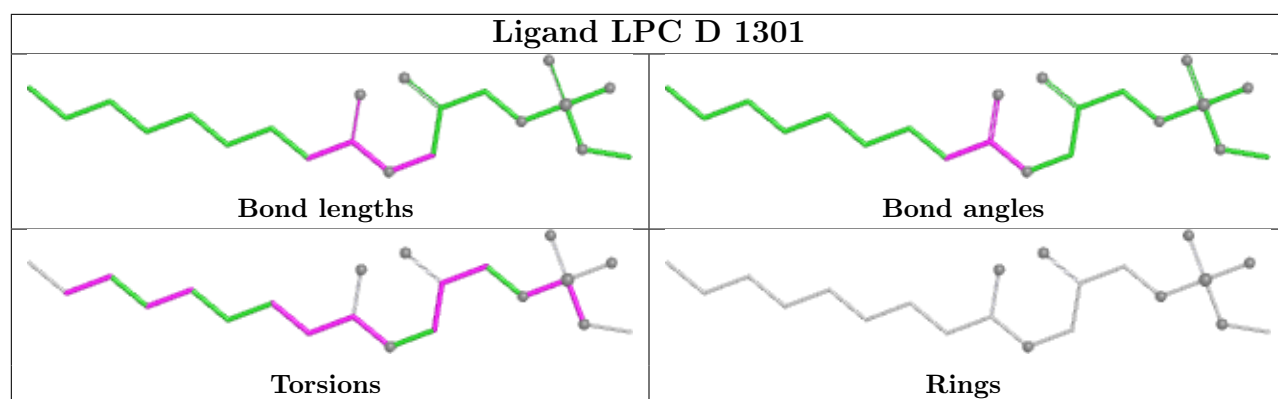
There are no ring outliers.

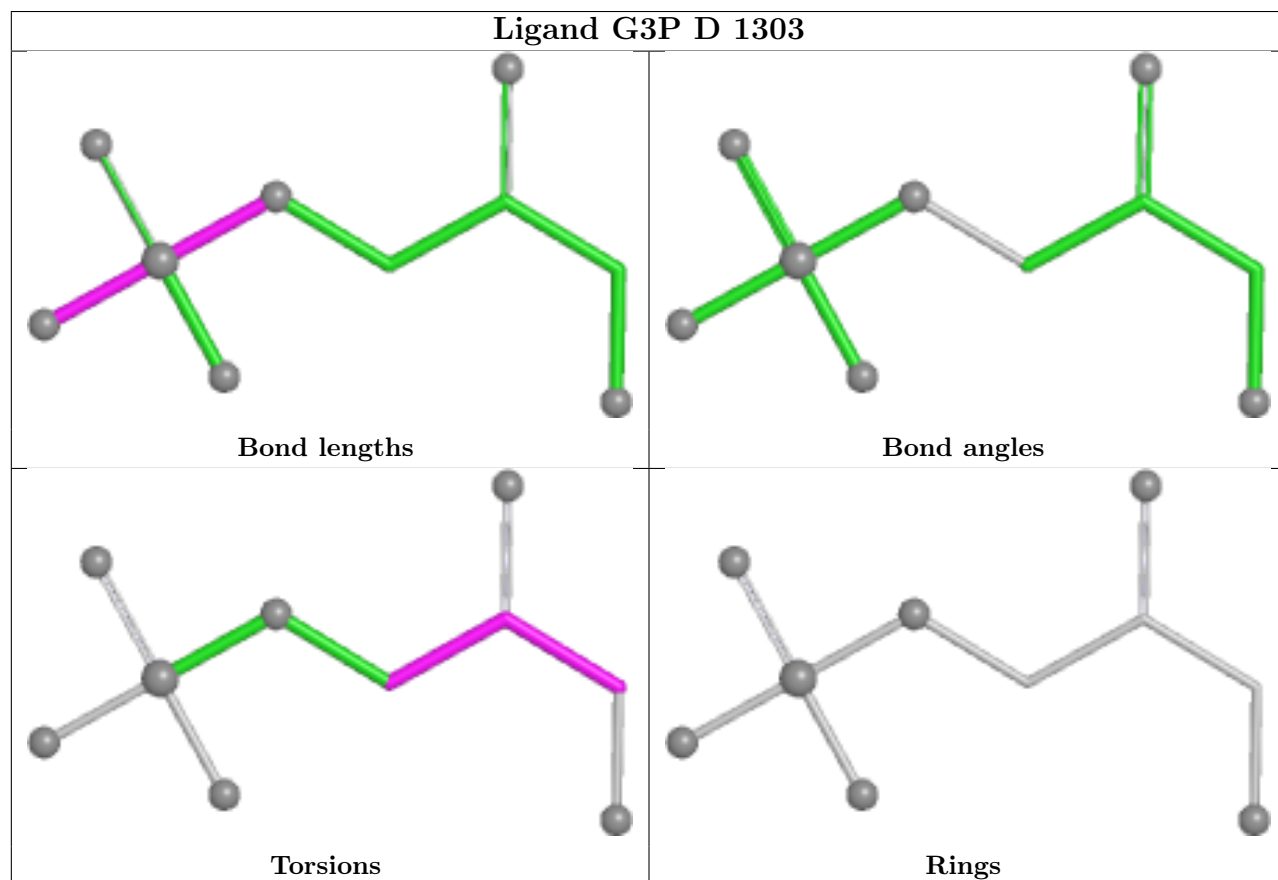
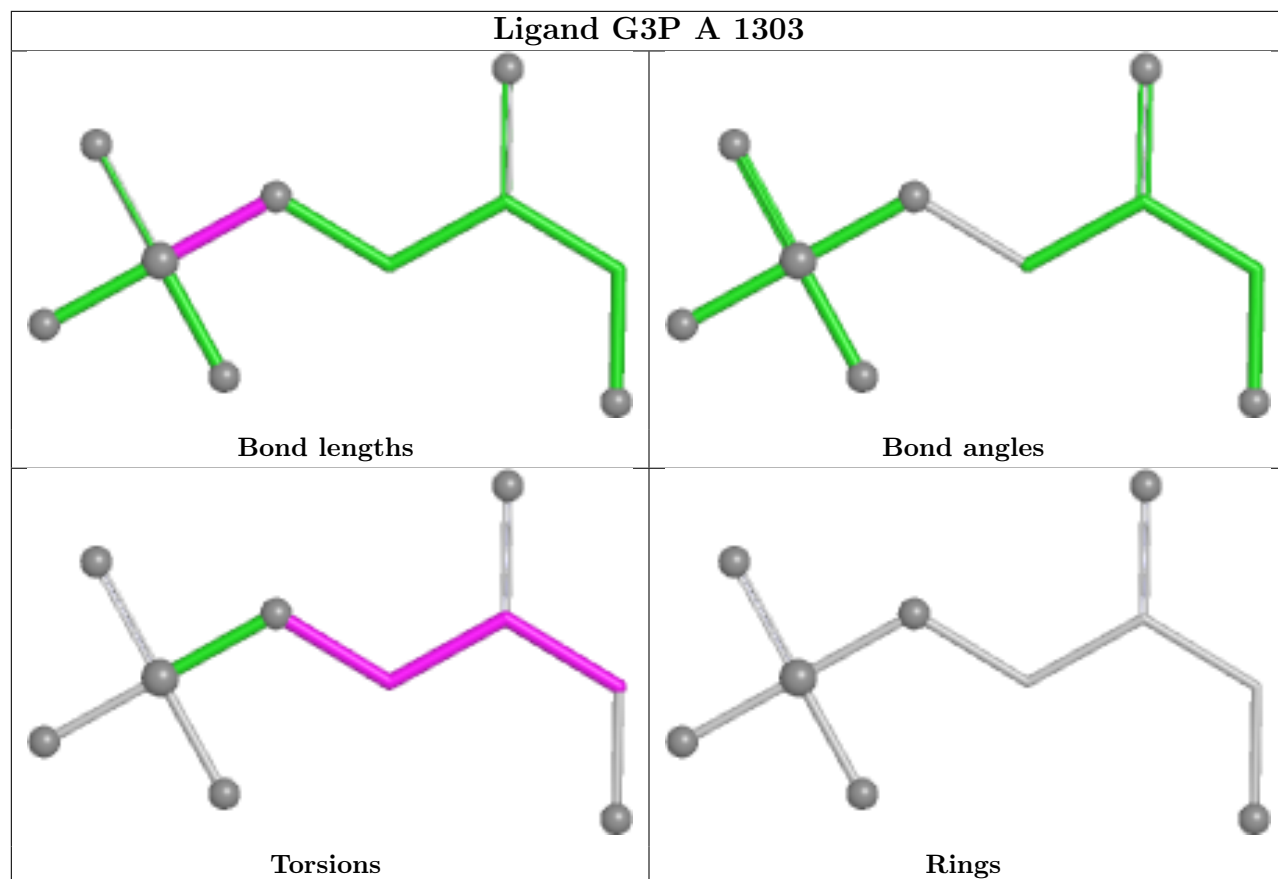
7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1301	LPC	2	0
2	A	1301	LPC	3	0
4	B	1302	G3P	3	0
4	A	1303	G3P	2	0
4	D	1303	G3P	3	0
5	B	1301	6UB	6	0
6	C	1302	D6C	1	0

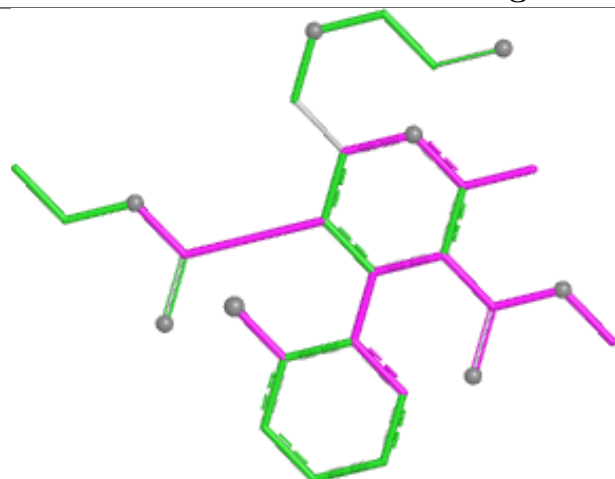
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



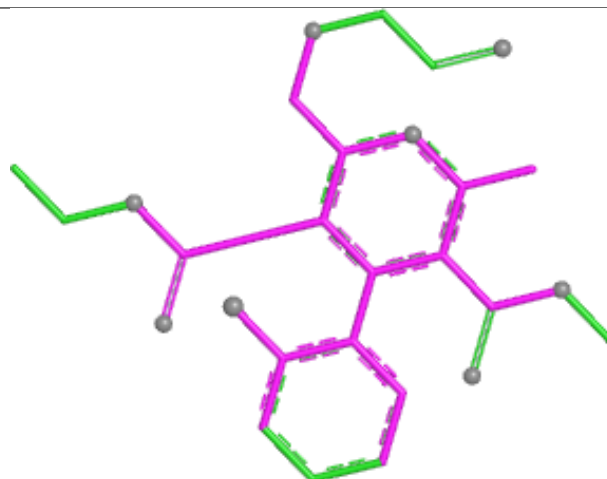




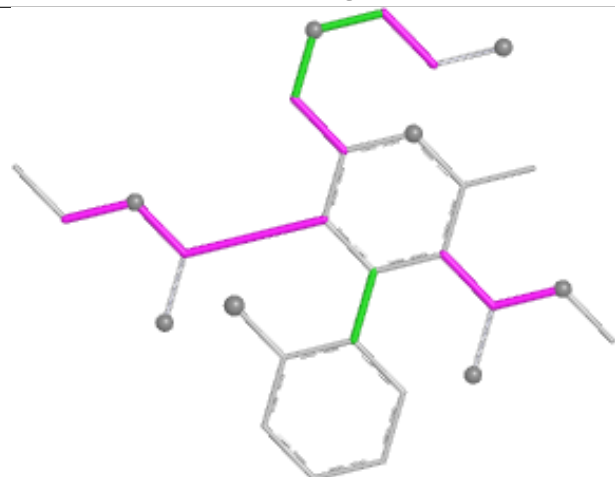
Ligand 6UB B 1301



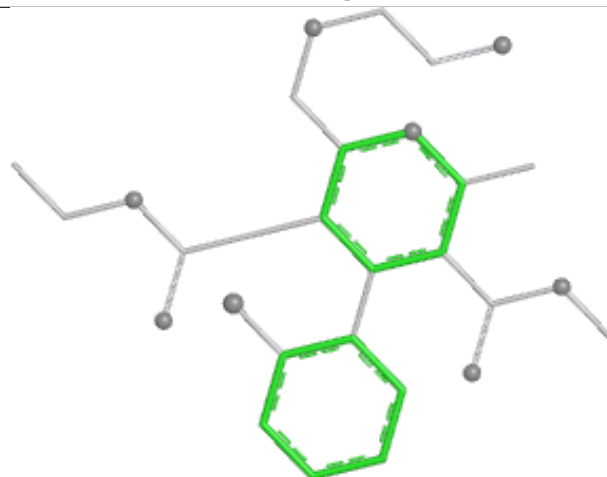
Bond lengths



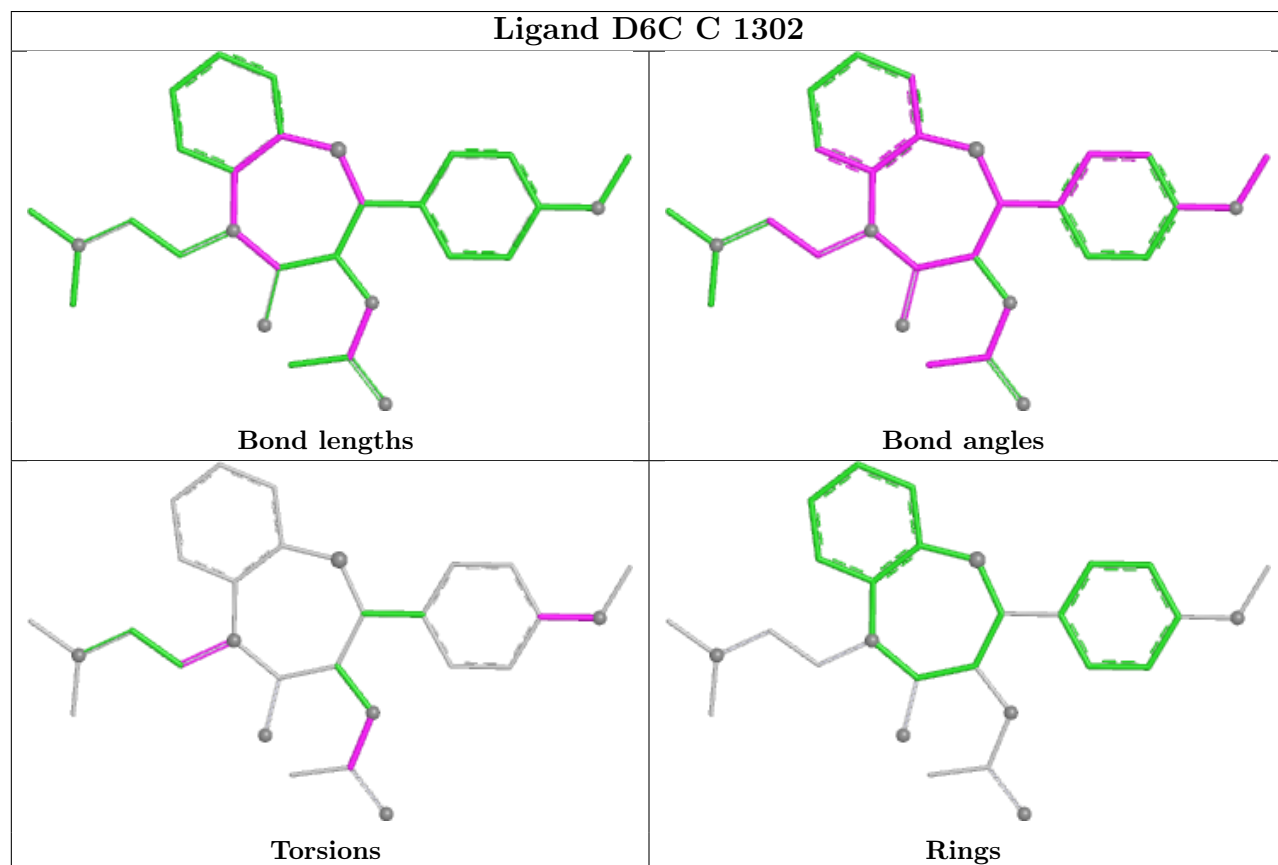
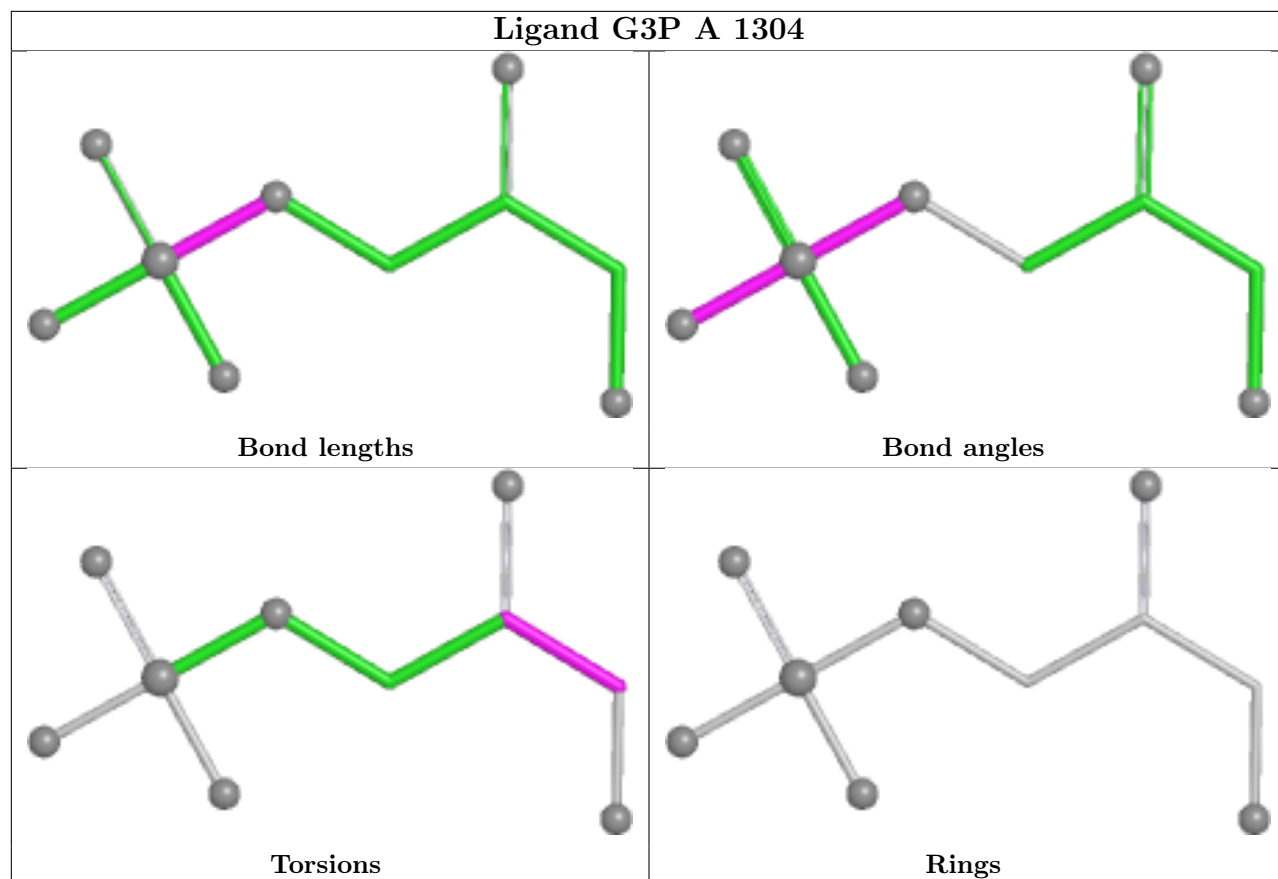
Bond angles



Torsions



Rings



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	219/284 (77%)	-0.99	0 100 100	28, 80, 143, 168	0
1	B	232/284 (81%)	-0.97	1 (0%) 88 84	29, 84, 152, 222	0
1	C	219/284 (77%)	-1.01	0 100 100	26, 86, 121, 137	0
1	D	232/284 (81%)	-0.99	0 100 100	26, 79, 136, 166	0
All	All	902/1136 (79%)	-0.99	1 (0%) 92 90	26, 83, 135, 222	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1223	ILE	2.9

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	LPC	A	1301	21/31	0.98	0.07	46,62,88,97	0

Continued on next page...

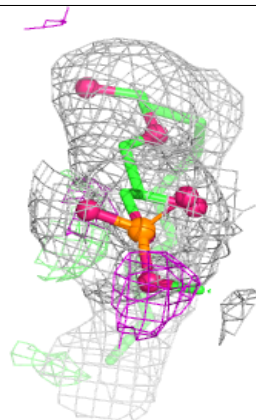
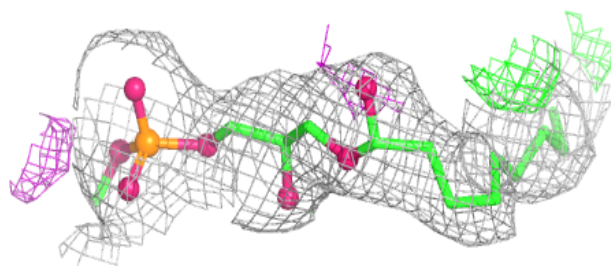
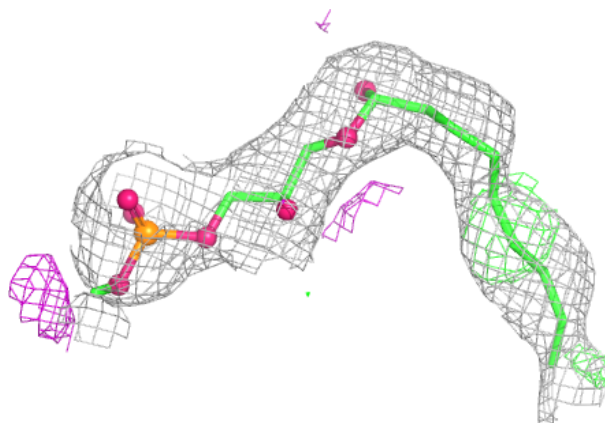
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	LPC	C	1301	21/31	0.98	0.08	38,49,63,64	0
4	G3P	A	1303	10/10	0.98	0.05	43,55,68,69	0
4	G3P	A	1304	10/10	0.98	0.06	88,96,103,105	0
4	G3P	C	1304	10/10	0.98	0.04	35,41,53,53	0
4	G3P	D	1303	10/10	0.98	0.05	42,45,60,65	0
5	6UB	B	1301	28/28	0.98	0.06	56,65,71,74	0
6	D6C	C	1302	29/29	0.98	0.06	47,56,78,79	0
4	G3P	B	1302	10/10	0.99	0.05	60,66,76,78	0
3	CA	C	1303	1/1	0.99	0.04	55,55,55,55	0
3	CA	D	1302	1/1	0.99	0.03	54,54,54,54	0
2	LPC	D	1301	21/31	0.99	0.05	37,43,48,50	0
3	CA	A	1302	1/1	0.99	0.03	50,50,50,50	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.

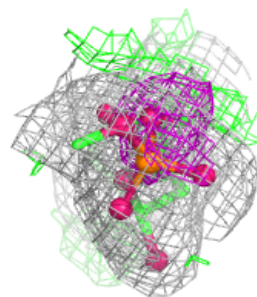
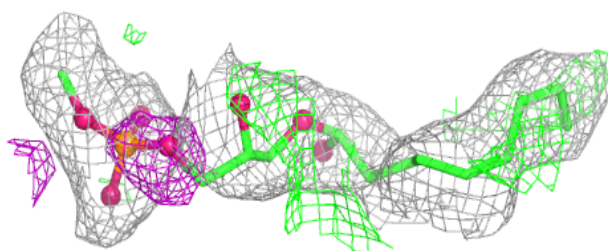
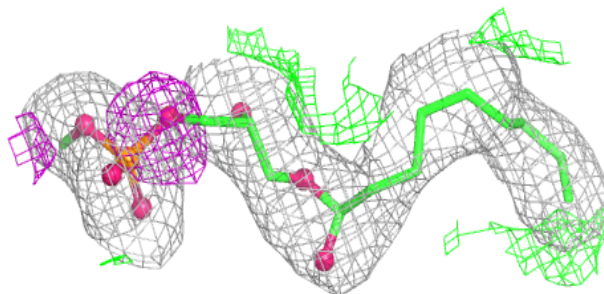
Electron density around LPC A 1301:

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

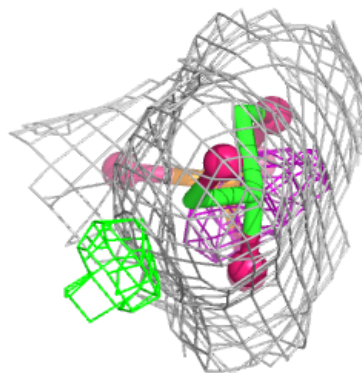
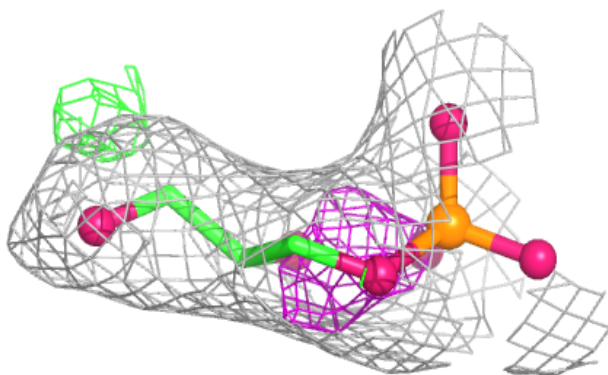
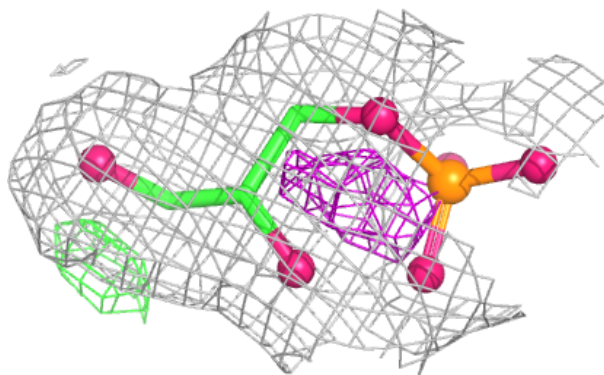


Electron density around LPC C 1301:

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

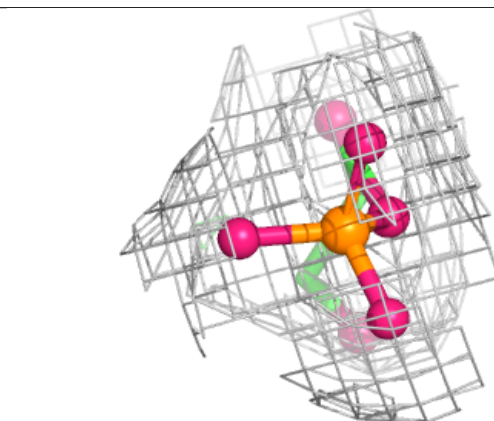
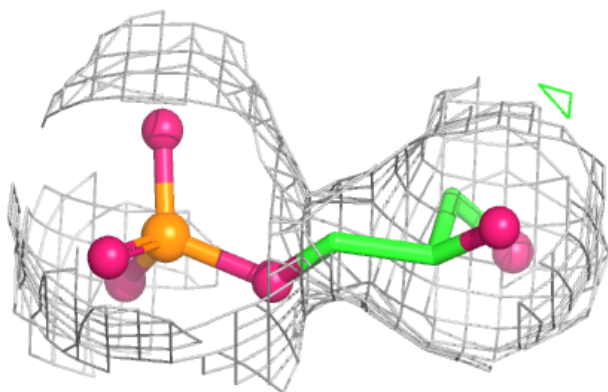
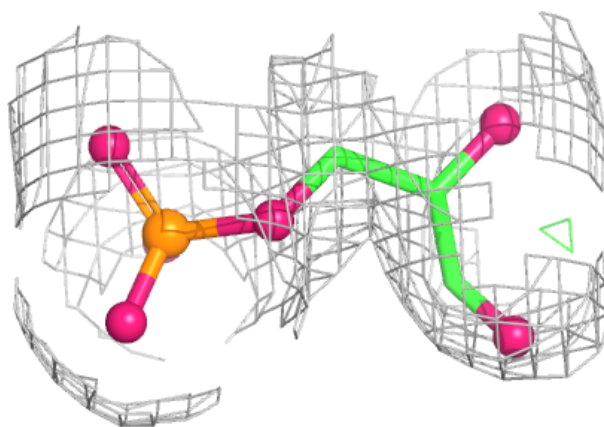
**Electron density around G3P A 1303:**

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

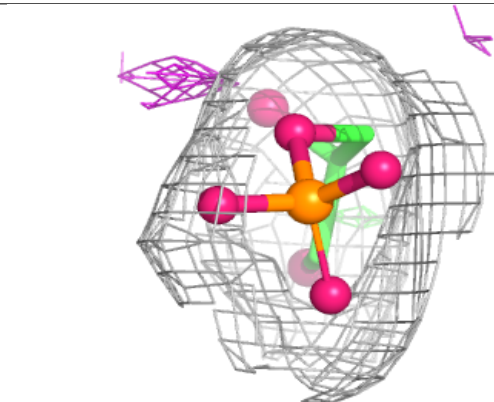
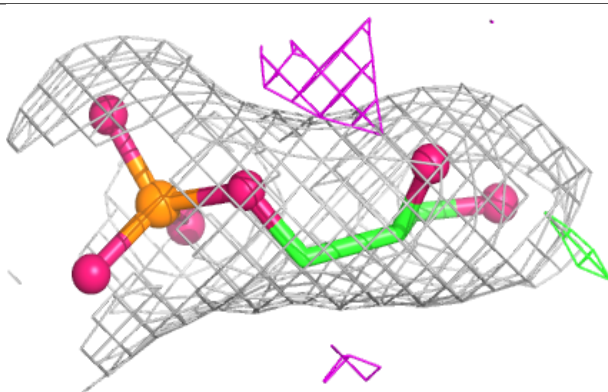
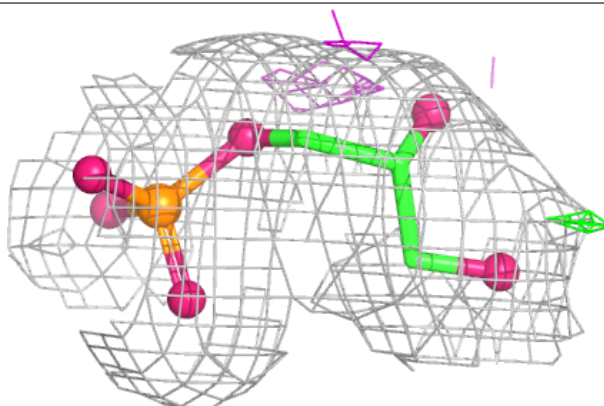


Electron density around G3P A 1304:

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

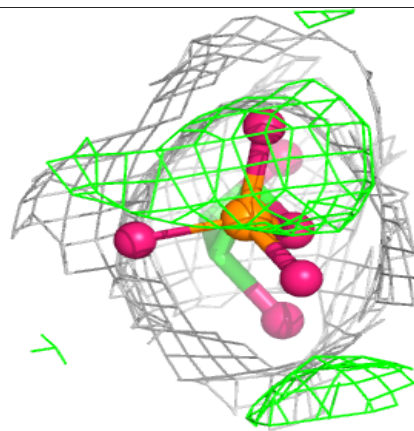
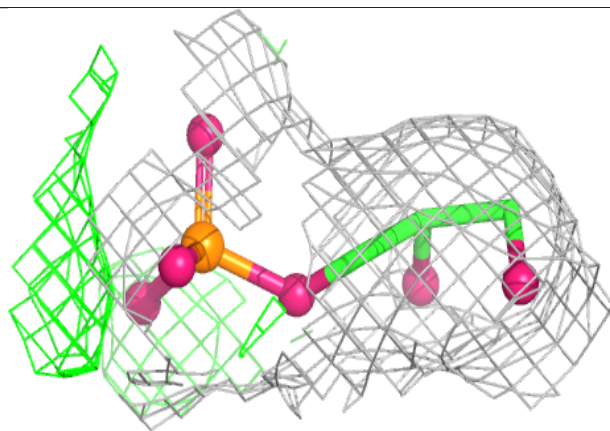
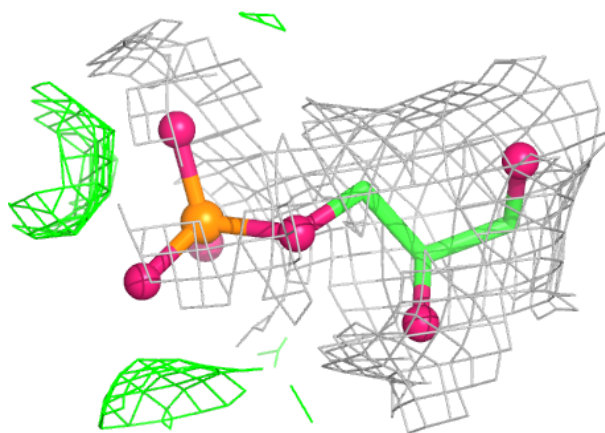
**Electron density around G3P C 1304:**

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



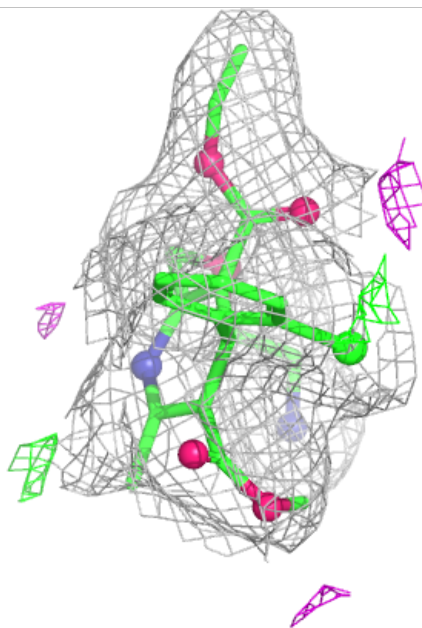
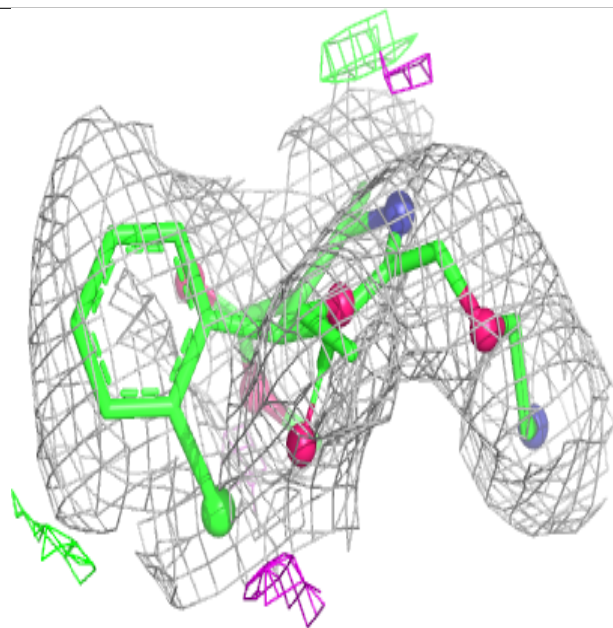
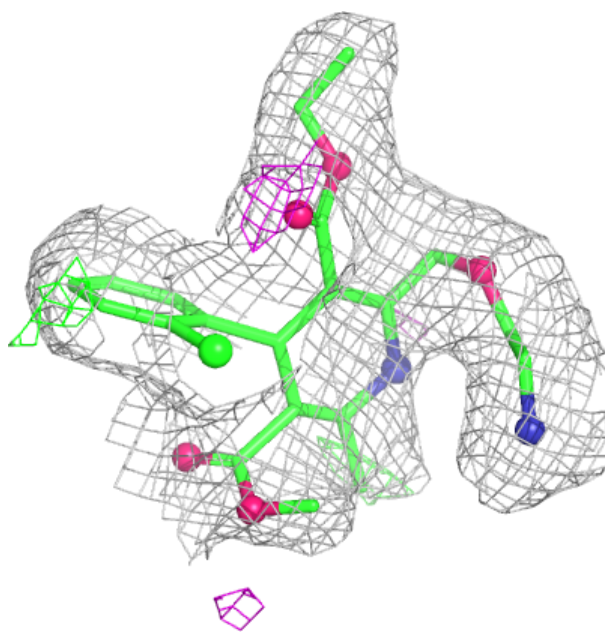
Electron density around G3P D 1303:

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



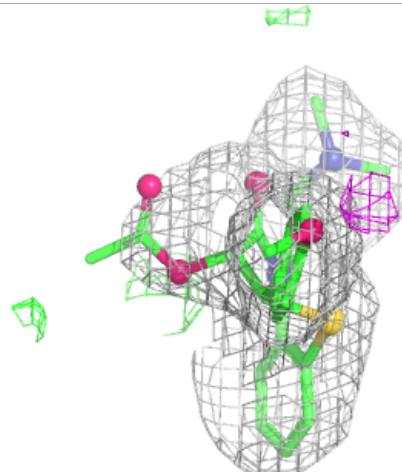
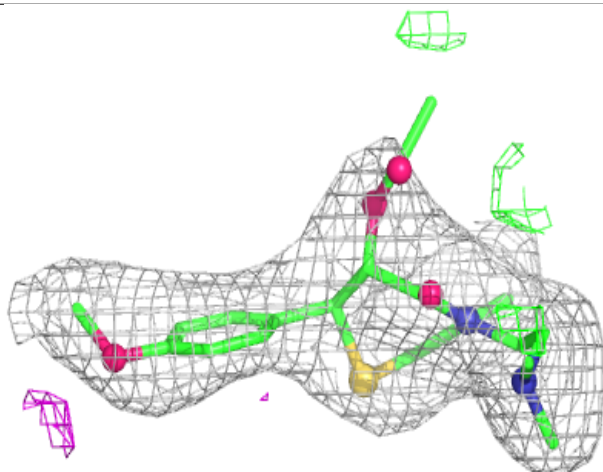
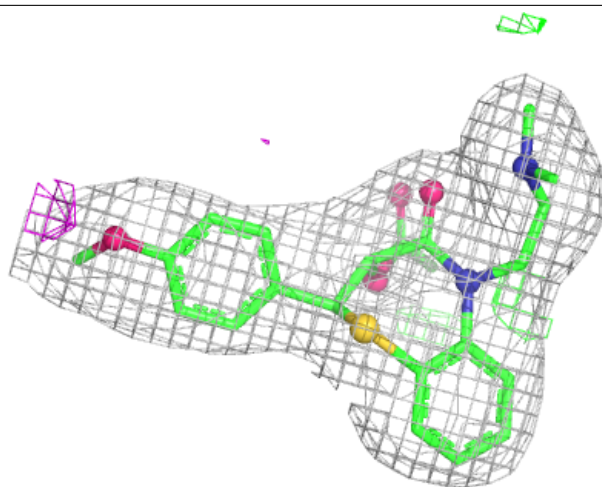
Electron density around 6UB B 1301:

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



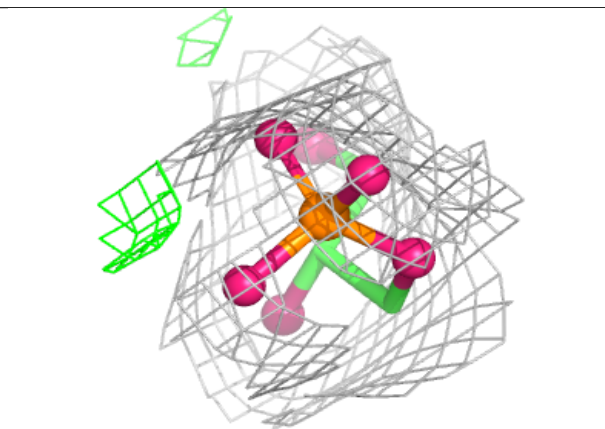
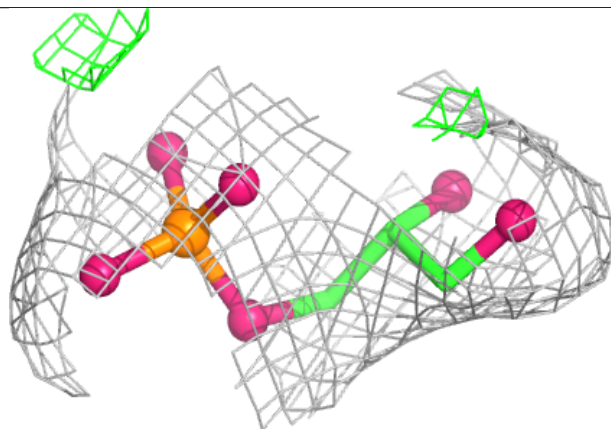
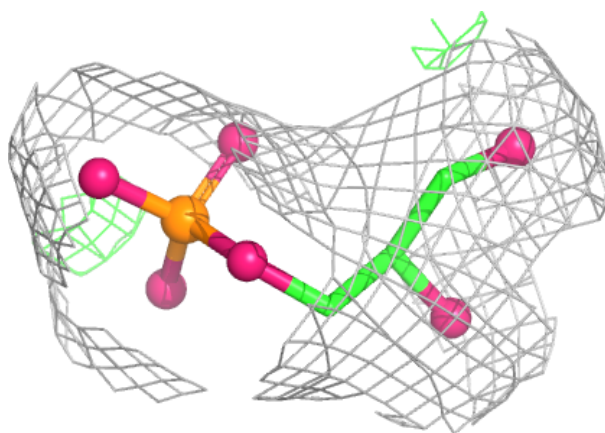
Electron density around D6C C 1302:

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

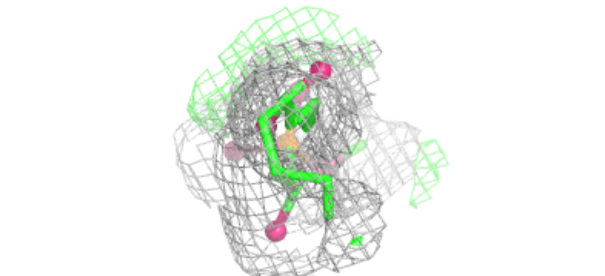
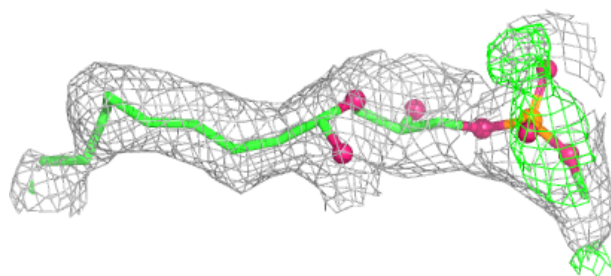
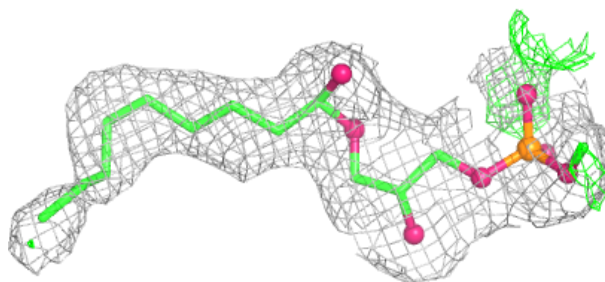


Electron density around G3P B 1302:

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

**Electron density around LPC D 1301:**

$2mF_o-DF_c$ (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.