



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:32 PM UTC

PDB ID : 2V69 / pdb_00002v69
Title : Crystal structure of Chlamydomonas reinhardtii Rubisco with a large- subunit mutation D473E
Authors : Karkehabadi, S.; Satagopan, S.; Taylor, T.C.; Spreitzer, R.J.; Andersson, I.
Deposited on : 2007-07-14
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

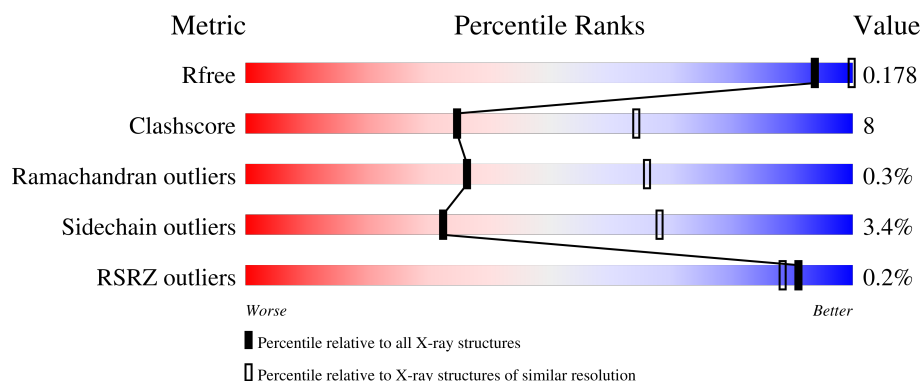
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

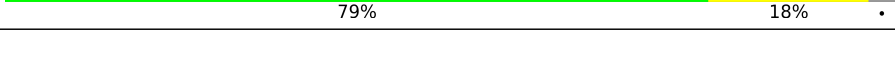
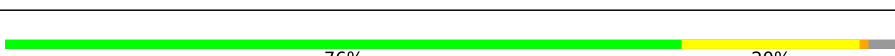
The reported resolution of this entry is 2.80 Å.

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	475	 80% 16% .
1	B	475	 79% 17% ..
1	C	475	 79% 18% .
1	D	475	 79% 18% ..
1	E	475	 76% 20% ..

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Mol	Chain	Length	Quality of chain
1	F	475	 78% 18% ..
1	G	475	 78% 18% ..
1	H	475	 79% 17% ..
2	I	140	 79% 19% ..
2	J	140	 80% 17% ..
2	K	140	 79% 19% ..
2	L	140	 84% 13% ..
2	M	140	 85% 12% ..
2	N	140	 77% 19% ..
2	O	140	 79% 19% ..
2	P	140	 76% 21% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 38504 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 RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	0	0	0
			3579	2265	630	660	24			
1	B	460	Total	C	N	O	S	0	0	0
			3583	2267	631	661	24			
1	C	459	Total	C	N	O	S	0	0	0
			3582	2266	630	662	24			
1	D	464	Total	C	N	O	S	0	0	0
			3620	2290	636	670	24			
1	E	459	Total	C	N	O	S	0	0	0
			3579	2265	630	660	24			
1	F	461	Total	C	N	O	S	0	0	0
			3588	2270	632	662	24			
1	G	461	Total	C	N	O	S	0	0	0
			3588	2270	632	662	24			
1	H	458	Total	C	N	O	S	0	0	0
			3574	2262	629	659	24			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	PRO	LEU	conflict	UNP P00877
A	473	GLU	ASP	engineered mutation	UNP P00877
B	46	PRO	LEU	conflict	UNP P00877
B	473	GLU	ASP	engineered mutation	UNP P00877
C	46	PRO	LEU	conflict	UNP P00877
C	473	GLU	ASP	engineered mutation	UNP P00877
D	46	PRO	LEU	conflict	UNP P00877
D	473	GLU	ASP	engineered mutation	UNP P00877
E	46	PRO	LEU	conflict	UNP P00877
E	473	GLU	ASP	engineered mutation	UNP P00877
F	46	PRO	LEU	conflict	UNP P00877
F	473	GLU	ASP	engineered mutation	UNP P00877

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Chain	Residue	Modelled	Actual	Comment	Reference
G	46	PRO	LEU	conflict	UNP P00877
G	473	GLU	ASP	engineered mutation	UNP P00877
H	46	PRO	LEU	conflict	UNP P00877
H	473	GLU	ASP	engineered mutation	UNP P00877

- Molecule 2 is a protein called RIBULOSE BISPHTHOSPHATE CARBOXYLASE SMALL CHAIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	J	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	K	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	L	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	M	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	N	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	O	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	P	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

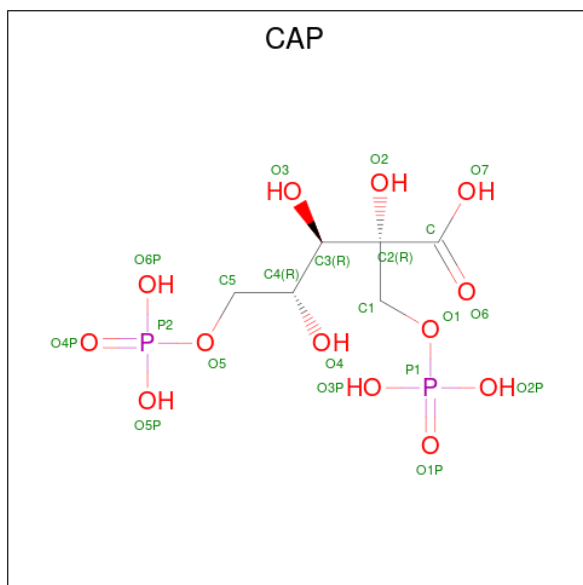
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		
3	G	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (CCD ID: CAP) (formula: $C_6H_{14}O_{13}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			21	6	13	2		
4	B	1	Total	C	O	P	0	0
			21	6	13	2		
4	C	1	Total	C	O	P	0	0
			21	6	13	2		
4	D	1	Total	C	O	P	0	0
			21	6	13	2		
4	E	1	Total	C	O	P	0	0
			21	6	13	2		
4	F	1	Total	C	O	P	0	0
			21	6	13	2		
4	G	1	Total	C	O	P	0	0
			21	6	13	2		
4	H	1	Total	C	O	P	0	0
			21	6	13	2		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	1	Total C O 4 2 2	0	0
5	F	1	Total C O 4 2 2	0	0
5	F	1	Total C O 4 2 2	0	0
5	G	1	Total C O 4 2 2	0	0
5	G	1	Total C O 4 2 2	0	0
5	G	1	Total C O 4 2 2	0	0
5	H	1	Total C O 4 2 2	0	0
5	H	1	Total C O 4 2 2	0	0
5	H	1	Total C O 4 2 2	0	0
5	H	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	52	Total O 52 52	0	0
6	B	29	Total O 29 29	0	0
6	C	57	Total O 57 57	0	0
6	D	39	Total O 39 39	0	0
6	E	54	Total O 54 54	0	0
6	F	41	Total O 41 41	0	0
6	G	45	Total O 45 45	0	0
6	H	43	Total O 43 43	0	0
6	I	6	Total O 6 6	0	0

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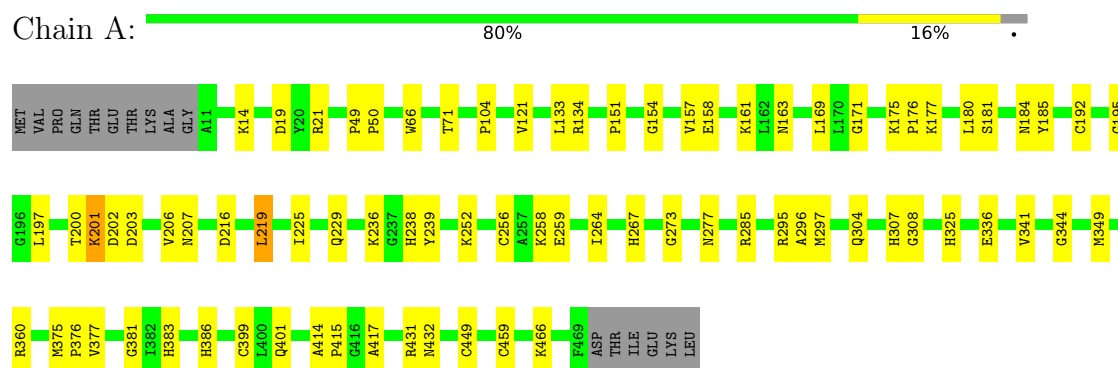
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	3	Total 3	O 3	0	0
6	K	6	Total 6	O 6	0	0
6	L	2	Total 2	O 2	0	0
6	M	4	Total 4	O 4	0	0
6	N	4	Total 4	O 4	0	0
6	O	5	Total 5	O 5	0	0
6	P	5	Total 5	O 5	0	0

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.

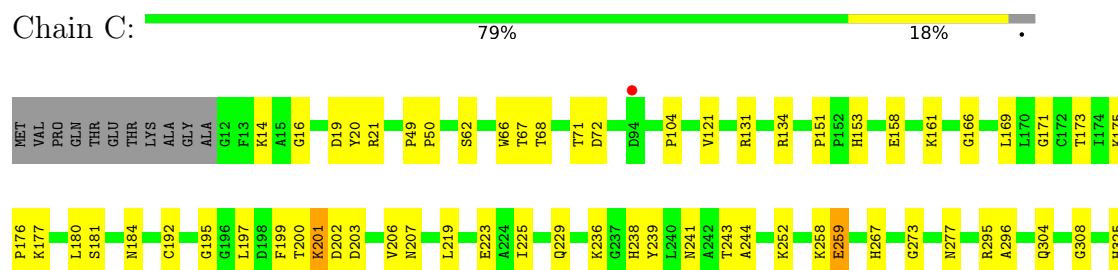
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

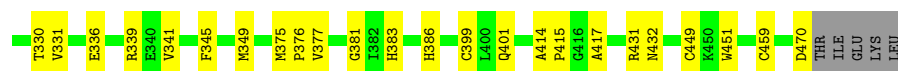


• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



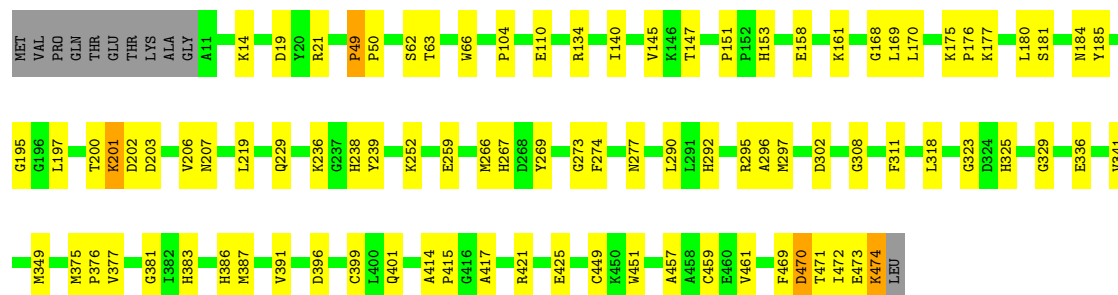
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN





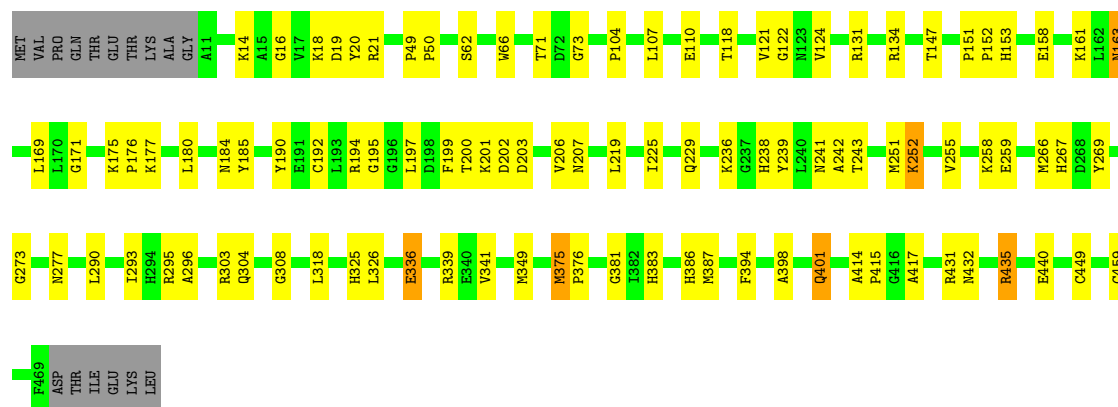
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain D: 79% 18% ..



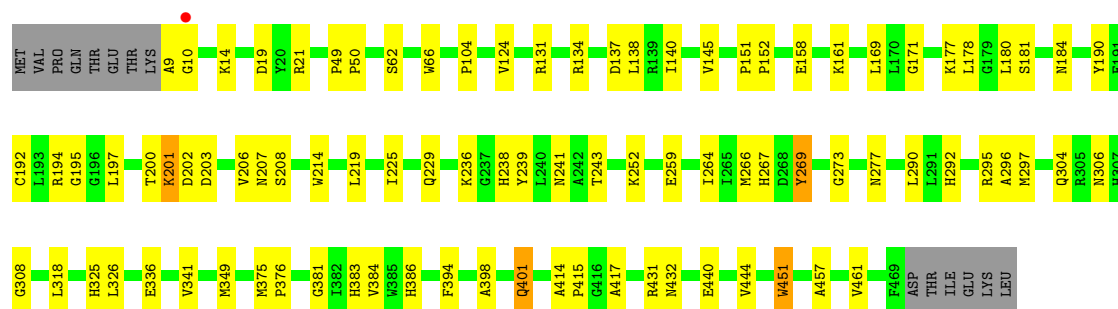
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain E: 76% 20% ..



• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

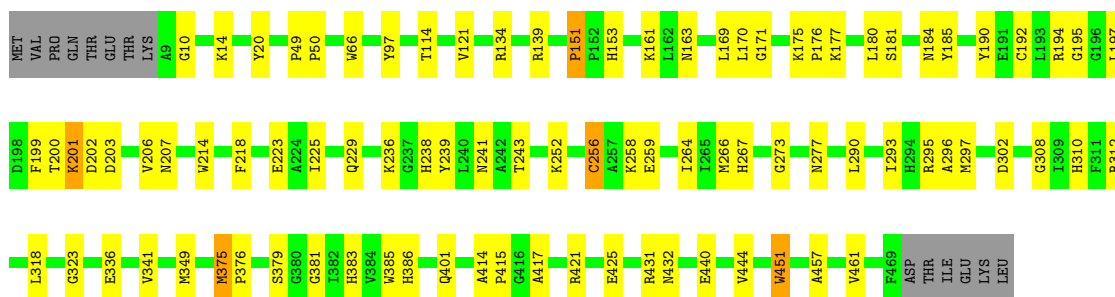
Chain F: 78% 18% ..



• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

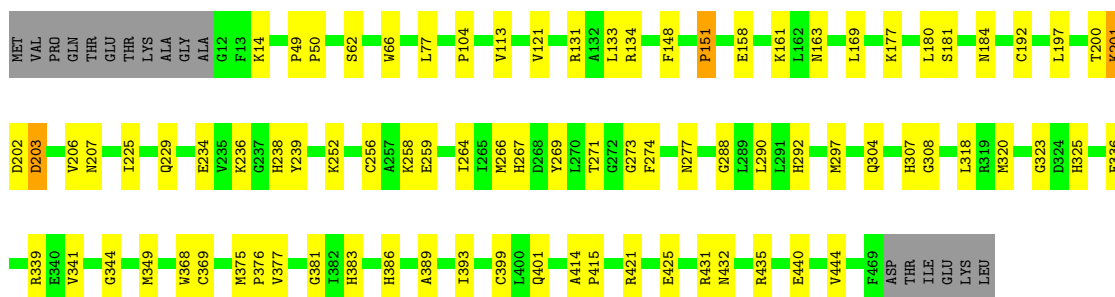
Chain G: 78% 18% ..





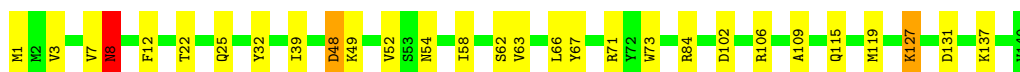
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain H: 79% 17% ..



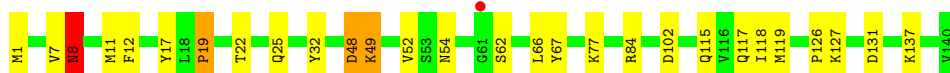
• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain I: 79% 19% ..



• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain J: 80% 17% ..



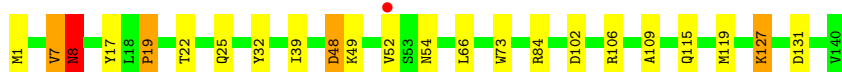
• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain K: 79% 19% ..



• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain L: 84% 13% ..



- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain M:  85% 12% ..



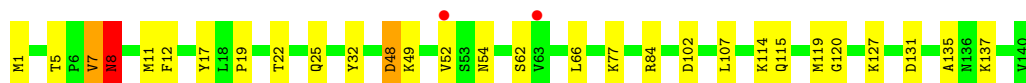
- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain N:  77% 19% ..



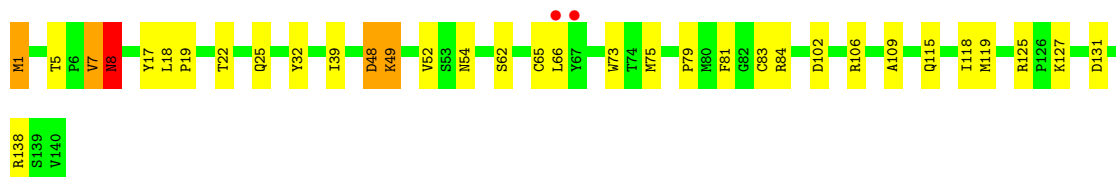
- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain O:  79% 19% ..



- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain P:  76% 21% ..



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	114.24Å 169.14Å 137.18Å 90.00° 96.24° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 20.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.4 (20.00-2.80) 98.1 (20.00-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.197 , 0.228 (Not available) , 0.178	Depositor DCC
R_{free} test set	6262 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.511	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 29.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	38504	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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: MG, CAP, MME, SMC, HYP, KCX, EDO

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	0.68	0/3617	0.86	1/4890 (0.0%)
1	B	0.79	0/3621	0.95	3/4895 (0.1%)
1	C	0.78	0/3620	0.93	2/4894 (0.0%)
1	D	0.77	0/3658	0.96	6/4945 (0.1%)
1	E	0.76	0/3617	0.93	4/4890 (0.1%)
1	F	0.78	0/3626	0.93	5/4902 (0.1%)
1	G	0.79	0/3626	0.95	2/4902 (0.0%)
1	H	0.76	0/3612	0.93	3/4883 (0.1%)
2	I	0.66	0/1166	0.89	2/1584 (0.1%)
2	J	0.75	0/1166	0.90	3/1584 (0.2%)
2	K	0.73	0/1166	0.92	2/1584 (0.1%)
2	L	0.79	0/1166	0.94	3/1584 (0.2%)
2	M	0.73	0/1166	0.94	2/1584 (0.1%)
2	N	0.67	0/1166	0.94	3/1584 (0.2%)
2	O	0.72	0/1166	0.95	5/1584 (0.3%)
2	P	0.73	0/1166	0.92	3/1584 (0.2%)
All	All	0.76	0/38325	0.93	49/51873 (0.1%)

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	D	0	2
2	I	0	1
2	J	0	1
2	K	0	1
2	L	0	1
2	M	0	1
2	N	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
2	O	0	1
2	P	0	1
All	All	0	10

There are no bond length outliers.

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	10	GLY	N-CA-C	8.29	119.93	111.56
2	L	8	ASN	N-CA-C	-6.42	93.04	111.00
2	J	12	PHE	N-CA-C	6.24	117.78	110.41
2	O	12	PHE	N-CA-C	6.13	117.64	110.41
1	C	16	GLY	N-CA-C	6.11	117.75	111.95

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	469	PHE	Peptide
1	D	470	ASP	Peptide
2	I	7	VAL	Peptide
2	J	7	VAL	Peptide
2	K	7	VAL	Peptide

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	3579	0	3487	57	0
1	B	3583	0	3490	65	0
1	C	3582	0	3486	62	0
1	D	3620	0	3528	61	0
1	E	3579	0	3487	68	0
1	F	3588	0	3495	65	0
1	G	3588	0	3495	67	0
1	H	3574	0	3482	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	1143	0	1122	18	0
2	J	1143	0	1122	19	0
2	K	1143	0	1122	18	0
2	L	1143	0	1122	14	0
2	M	1143	0	1122	17	0
2	N	1143	0	1122	18	0
2	O	1143	0	1122	18	0
2	P	1143	0	1122	30	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	21	0	7	0	0
4	B	21	0	8	0	0
4	C	21	0	7	0	0
4	D	21	0	9	0	0
4	E	21	0	7	0	0
4	F	21	0	7	0	0
4	G	21	0	8	0	0
4	H	21	0	8	0	0
5	A	12	0	18	1	0
5	B	8	0	12	0	0
5	C	12	0	18	5	0
5	D	12	0	18	0	0
5	E	16	0	24	1	0
5	F	8	0	12	0	0
5	G	12	0	18	3	0
5	H	16	0	24	0	0
6	A	52	0	0	7	0
6	B	29	0	0	4	0
6	C	57	0	0	5	0
6	D	39	0	0	4	0
6	E	54	0	0	4	0
6	F	41	0	0	2	0
6	G	45	0	0	3	0
6	H	43	0	0	2	0
6	I	6	0	0	0	0
6	J	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	K	6	0	0	0	0
6	L	2	0	0	0	0
6	M	4	0	0	0	0
6	N	4	0	0	0	0
6	O	5	0	0	1	0
6	P	5	0	0	0	0
All	All	38504	0	37131	560	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 8.

The worst 5 of 560 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:F:267:HIS:CD2	1:F:277:ASN:HD22	1.77	1.01
1:F:184:ASN:HD22	2:P:115:GLN:HE21	1.08	1.00
1:G:267:HIS:CD2	1:G:277:ASN:HD22	1.80	0.98
1:A:267:HIS:HD2	1:A:277:ASN:HD22	1.02	0.98
1:C:267:HIS:HD2	1:C:277:ASN:HD22	1.00	0.97

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	452/475 (95%)	432 (96%)	20 (4%)	0	100	100
1	B	453/475 (95%)	430 (95%)	22 (5%)	1 (0%)	43	72
1	C	452/475 (95%)	433 (96%)	19 (4%)	0	100	100
1	D	457/475 (96%)	430 (94%)	25 (6%)	2 (0%)	30	60
1	E	452/475 (95%)	431 (95%)	21 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	454/475 (96%)	434 (96%)	19 (4%)	1 (0%)	43	72
1	G	454/475 (96%)	429 (94%)	25 (6%)	0	100	100
1	H	451/475 (95%)	431 (96%)	20 (4%)	0	100	100
2	I	138/140 (99%)	125 (91%)	12 (9%)	1 (1%)	18	47
2	J	138/140 (99%)	123 (89%)	14 (10%)	1 (1%)	18	47
2	K	138/140 (99%)	126 (91%)	12 (9%)	0	100	100
2	L	138/140 (99%)	126 (91%)	11 (8%)	1 (1%)	18	47
2	M	138/140 (99%)	119 (86%)	18 (13%)	1 (1%)	18	47
2	N	138/140 (99%)	125 (91%)	11 (8%)	2 (1%)	9	30
2	O	138/140 (99%)	126 (91%)	11 (8%)	1 (1%)	18	47
2	P	138/140 (99%)	123 (89%)	14 (10%)	1 (1%)	18	47
All	All	4729/4920 (96%)	4443 (94%)	274 (6%)	12 (0%)	36	66

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	10	GLY
2	M	49	LYS
1	D	470	ASP
2	J	49	LYS
2	N	83	CYS

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	362/376 (96%)	354 (98%)	8 (2%)	45	78
1	B	362/376 (96%)	354 (98%)	8 (2%)	45	78
1	C	363/376 (96%)	354 (98%)	9 (2%)	42	76
1	D	367/376 (98%)	359 (98%)	8 (2%)	45	78
1	E	362/376 (96%)	352 (97%)	10 (3%)	38	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	362/376 (96%)	354 (98%)	8 (2%)	45	78
1	G	362/376 (96%)	354 (98%)	8 (2%)	45	78
1	H	362/376 (96%)	354 (98%)	8 (2%)	45	78
2	I	122/122 (100%)	114 (93%)	8 (7%)	15	43
2	J	122/122 (100%)	114 (93%)	8 (7%)	15	43
2	K	122/122 (100%)	114 (93%)	8 (7%)	15	43
2	L	122/122 (100%)	115 (94%)	7 (6%)	18	49
2	M	122/122 (100%)	115 (94%)	7 (6%)	18	49
2	N	122/122 (100%)	112 (92%)	10 (8%)	10	33
2	O	122/122 (100%)	114 (93%)	8 (7%)	15	43
2	P	122/122 (100%)	114 (93%)	8 (7%)	15	43
All	All	3878/3984 (97%)	3747 (97%)	131 (3%)	32	68

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	8	ASN
2	O	84	ARG
2	P	127	LYS
1	F	336	GLU
1	F	259	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 135 such sidechains are listed below:

Mol	Chain	Res	Type
2	L	29	GLN
2	M	25	GLN
2	O	115	GLN
1	E	156	GLN
1	E	153	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

48 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
1	HYP	G	151	1	7,8,9	0.86	0	5,10,12	1.28	1 (20%)
1	HYP	H	151	1	7,8,9	0.81	0	5,10,12	1.48	1 (20%)
1	KCX	G	201	1,3	10,11,12	0.99	1 (10%)	6,12,14	1.20	1 (16%)
1	HYP	F	104	1	7,8,9	0.86	0	5,10,12	1.50	1 (20%)
1	HYP	F	151	1	7,8,9	0.94	0	5,10,12	1.21	0
1	SMC	D	256	1	5,6,7	0.65	0	3,6,8	0.55	0
2	MME	O	1	2	7,8,9	3.13	2 (28%)	5,8,10	1.80	1 (20%)
2	MME	P	1	2	7,8,9	3.09	2 (28%)	5,8,10	1.66	1 (20%)
1	SMC	C	369	1	5,6,7	0.53	0	3,6,8	0.51	0
1	HYP	A	151	1	7,8,9	0.81	0	5,10,12	1.49	2 (40%)
1	SMC	E	369	1	5,6,7	0.58	0	3,6,8	0.76	0
1	HYP	C	151	1	7,8,9	0.98	1 (14%)	5,10,12	2.03	2 (40%)
1	SMC	H	369	1	5,6,7	0.55	0	3,6,8	0.29	0
2	MME	K	1	2	7,8,9	3.10	2 (28%)	5,8,10	1.72	1 (20%)
1	KCX	H	201	1,3	10,11,12	1.06	1 (10%)	6,12,14	1.73	1 (16%)
1	HYP	H	104	1	7,8,9	0.77	0	5,10,12	1.61	1 (20%)
1	KCX	D	201	1,3	10,11,12	0.97	0	6,12,14	1.78	1 (16%)
2	MME	N	1	2	7,8,9	3.08	2 (28%)	5,8,10	1.71	1 (20%)
1	KCX	F	201	1,3	10,11,12	1.06	0	6,12,14	1.66	1 (16%)
1	HYP	E	151	1	7,8,9	1.27	1 (14%)	5,10,12	1.65	1 (20%)
2	MME	J	1	2	7,8,9	3.10	2 (28%)	5,8,10	1.57	1 (20%)
1	SMC	G	256	1	5,6,7	0.80	0	3,6,8	1.48	1 (33%)
1	HYP	E	104	1	7,8,9	0.81	0	5,10,12	1.65	2 (40%)
2	MME	L	1	2	7,8,9	3.20	2 (28%)	5,8,10	1.45	1 (20%)
1	SMC	B	369	1	5,6,7	0.51	0	3,6,8	0.63	0
1	SMC	F	256	1	5,6,7	0.74	0	3,6,8	0.53	0
1	HYP	B	104	1	7,8,9	0.65	0	5,10,12	1.86	2 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MME	I	1	2	7,8,9	3.17	2 (28%)	5,8,10	1.64	1 (20%)
1	HYP	G	104	1	7,8,9	1.04	0	5,10,12	1.10	0
1	HYP	D	151	1	7,8,9	1.06	0	5,10,12	1.37	0
1	HYP	D	104	1	7,8,9	0.66	0	5,10,12	1.76	3 (60%)
1	SMC	H	256	1	5,6,7	0.63	0	3,6,8	2.29	1 (33%)
1	KCX	E	201	1,3	10,11,12	0.87	0	6,12,14	1.67	1 (16%)
1	HYP	C	104	1	7,8,9	0.84	0	5,10,12	1.91	1 (20%)
1	KCX	B	201	1,3	10,11,12	1.04	1 (10%)	6,12,14	1.15	1 (16%)
1	SMC	A	256	1	5,6,7	0.58	0	3,6,8	1.40	1 (33%)
1	SMC	F	369	1	5,6,7	0.53	0	3,6,8	0.75	0
1	SMC	G	369	1	5,6,7	0.59	0	3,6,8	0.32	0
1	SMC	D	369	1	5,6,7	0.57	0	3,6,8	0.60	0
1	KCX	A	201	1,3	10,11,12	0.95	0	6,12,14	1.25	1 (16%)
1	SMC	B	256	1	5,6,7	0.77	0	3,6,8	1.67	1 (33%)
1	HYP	B	151	1	7,8,9	0.84	0	5,10,12	1.82	2 (40%)
1	HYP	A	104	1	7,8,9	0.84	0	5,10,12	1.67	1 (20%)
1	SMC	C	256	1	5,6,7	0.60	0	3,6,8	1.15	0
2	MME	M	1	2	7,8,9	3.16	2 (28%)	5,8,10	1.63	1 (20%)
1	KCX	C	201	1,3	10,11,12	1.22	1 (10%)	6,12,14	1.06	1 (16%)
1	SMC	A	369	1	5,6,7	0.44	0	3,6,8	0.53	0
1	SMC	E	256	1	5,6,7	0.62	0	3,6,8	1.17	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
1	HYP	G	151	1	-	0/0/11/13	0/1/1/1
1	HYP	H	151	1	-	0/0/11/13	0/1/1/1
1	KCX	G	201	1,3	-	0/9/10/12	-
1	HYP	F	104	1	-	0/0/11/13	0/1/1/1
1	HYP	F	151	1	-	0/0/11/13	0/1/1/1
1	SMC	D	256	1	-	0/3/5/7	-
2	MME	O	1	2	-	4/5/8/10	-
2	MME	P	1	2	-	3/5/8/10	-
1	SMC	C	369	1	-	1/3/5/7	-
1	HYP	A	151	1	-	0/0/11/13	0/1/1/1
1	SMC	E	369	1	-	1/3/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	C	151	1	-	0/0/11/13	0/1/1/1
1	SMC	H	369	1	-	1/3/5/7	-
2	MME	K	1	2	-	3/5/8/10	-
1	KCX	H	201	1,3	-	0/9/10/12	-
1	HYP	H	104	1	-	0/0/11/13	0/1/1/1
1	KCX	D	201	1,3	-	0/9/10/12	-
2	MME	N	1	2	-	3/5/8/10	-
1	KCX	F	201	1,3	-	0/9/10/12	-
1	HYP	E	151	1	-	0/0/11/13	0/1/1/1
2	MME	J	1	2	-	3/5/8/10	-
1	SMC	G	256	1	-	0/3/5/7	-
1	HYP	E	104	1	-	0/0/11/13	0/1/1/1
2	MME	L	1	2	-	4/5/8/10	-
1	SMC	B	369	1	-	1/3/5/7	-
1	SMC	F	256	1	-	0/3/5/7	-
1	HYP	B	104	1	-	0/0/11/13	0/1/1/1
2	MME	I	1	2	-	3/5/8/10	-
1	HYP	G	104	1	-	0/0/11/13	0/1/1/1
1	HYP	D	151	1	-	0/0/11/13	0/1/1/1
1	HYP	D	104	1	-	0/0/11/13	0/1/1/1
1	SMC	H	256	1	-	0/3/5/7	-
1	KCX	E	201	1,3	-	0/9/10/12	-
1	HYP	C	104	1	-	0/0/11/13	0/1/1/1
1	KCX	B	201	1,3	-	0/9/10/12	-
1	SMC	A	256	1	-	0/3/5/7	-
1	SMC	F	369	1	-	1/3/5/7	-
1	SMC	G	369	1	-	1/3/5/7	-
1	SMC	D	369	1	-	1/3/5/7	-
1	KCX	A	201	1,3	-	0/9/10/12	-
1	SMC	B	256	1	-	0/3/5/7	-
1	HYP	B	151	1	-	0/0/11/13	0/1/1/1
1	HYP	A	104	1	-	0/0/11/13	0/1/1/1
1	SMC	C	256	1	-	0/3/5/7	-
2	MME	M	1	2	-	4/5/8/10	-
1	KCX	C	201	1,3	-	0/9/10/12	-
1	SMC	A	369	1	-	1/3/5/7	-
1	SMC	E	256	1	-	0/3/5/7	-

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	1	MME	CM-N	-7.91	1.27	1.46
2	M	1	MME	CM-N	-7.88	1.27	1.46
2	K	1	MME	CM-N	-7.84	1.27	1.46
2	I	1	MME	CM-N	-7.83	1.27	1.46
2	O	1	MME	CM-N	-7.81	1.27	1.46

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	201	KCX	OQ1-CX-NZ	-4.23	118.50	124.92
1	H	256	SMC	CA-CB-SG	-3.93	107.68	114.04
1	F	201	KCX	OQ1-CX-NZ	-3.91	118.99	124.92
1	E	201	KCX	OQ1-CX-NZ	-3.85	119.08	124.92
1	H	201	KCX	OQ1-CX-NZ	-3.76	119.21	124.92

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	I	1	MME	N-CA-CB-CG
2	I	1	MME	C-CA-CB-CG
2	J	1	MME	N-CA-CB-CG
2	J	1	MME	C-CA-CB-CG
2	K	1	MME	N-CA-CB-CG

There are no ring outliers.

15 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	151	HYP	1	0
1	H	151	HYP	1	0
1	G	201	KCX	1	0
1	F	151	HYP	1	0
2	P	1	MME	1	0
1	H	369	SMC	1	0
1	H	201	KCX	1	0
1	D	201	KCX	1	0
1	F	201	KCX	1	0
1	G	256	SMC	1	0
1	B	369	SMC	1	0
1	D	151	HYP	1	0
1	B	201	KCX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	201	KCX	1	0
1	C	201	KCX	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 40 ligands modelled in this entry, 8 are monoatomic - leaving 32 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	$\# Z > 2$
5	EDO	E	1475	-	3,3,3	0.38	0	2,2,2	0.68	0
5	EDO	C	1474	-	3,3,3	0.45	0	2,2,2	0.25	0
5	EDO	E	1474	-	3,3,3	0.38	0	2,2,2	0.71	0
4	CAP	F	1471	3	18,20,20	0.83	0	23,31,31	1.21	2 (8%)
4	CAP	D	1476	3	18,20,20	1.05	1 (5%)	23,31,31	1.11	2 (8%)
5	EDO	A	1472	-	3,3,3	0.48	0	2,2,2	0.36	0
5	EDO	C	1473	-	3,3,3	0.62	0	2,2,2	0.09	0
5	EDO	H	1475	-	3,3,3	0.52	0	2,2,2	0.18	0
5	EDO	B	1473	-	3,3,3	0.54	0	2,2,2	0.31	0
5	EDO	G	1474	-	3,3,3	0.69	0	2,2,2	0.10	0
5	EDO	B	1472	-	3,3,3	0.61	0	2,2,2	0.12	0
5	EDO	H	1472	-	3,3,3	0.48	0	2,2,2	0.21	0
4	CAP	C	1472	3	18,20,20	0.93	0	23,31,31	1.26	4 (17%)
5	EDO	A	1473	-	3,3,3	0.56	0	2,2,2	0.13	0
5	EDO	A	1474	-	3,3,3	0.48	0	2,2,2	0.39	0
5	EDO	H	1473	-	3,3,3	0.53	0	2,2,2	0.33	0
4	CAP	B	1471	3	18,20,20	1.13	1 (5%)	23,31,31	1.44	4 (17%)
4	CAP	A	1471	3	18,20,20	0.94	0	23,31,31	1.21	2 (8%)
4	CAP	H	1471	3	18,20,20	1.12	1 (5%)	23,31,31	0.98	0
5	EDO	D	1479	-	3,3,3	0.64	0	2,2,2	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	E	1473	-	3,3,3	0.50	0	2,2,2	0.02	0
5	EDO	D	1477	-	3,3,3	0.56	0	2,2,2	0.24	0
5	EDO	G	1473	-	3,3,3	0.46	0	2,2,2	0.23	0
5	EDO	H	1474	-	3,3,3	0.32	0	2,2,2	0.81	0
5	EDO	E	1472	-	3,3,3	0.64	0	2,2,2	0.07	0
5	EDO	F	1472	-	3,3,3	0.51	0	2,2,2	0.35	0
4	CAP	G	1471	3	18,20,20	0.86	0	23,31,31	1.42	4 (17%)
5	EDO	G	1472	-	3,3,3	0.45	0	2,2,2	0.53	0
4	CAP	E	1471	3	18,20,20	0.89	0	23,31,31	1.51	3 (13%)
5	EDO	F	1473	-	3,3,3	0.55	0	2,2,2	0.09	0
5	EDO	D	1478	-	3,3,3	0.50	0	2,2,2	0.62	0
5	EDO	C	1475	-	3,3,3	0.50	0	2,2,2	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	E	1475	-	-	1/1/1/1	-
5	EDO	C	1474	-	-	0/1/1/1	-
5	EDO	E	1474	-	-	0/1/1/1	-
4	CAP	F	1471	3	-	10/29/29/29	-
4	CAP	D	1476	3	-	9/29/29/29	-
5	EDO	A	1472	-	-	1/1/1/1	-
5	EDO	C	1473	-	-	0/1/1/1	-
5	EDO	H	1475	-	-	1/1/1/1	-
5	EDO	B	1473	-	-	1/1/1/1	-
5	EDO	G	1474	-	-	1/1/1/1	-
5	EDO	B	1472	-	-	0/1/1/1	-
5	EDO	H	1472	-	-	1/1/1/1	-
4	CAP	C	1472	3	-	8/29/29/29	-
5	EDO	A	1473	-	-	1/1/1/1	-
5	EDO	A	1474	-	-	1/1/1/1	-
5	EDO	H	1473	-	-	1/1/1/1	-
4	CAP	B	1471	3	-	10/29/29/29	-
4	CAP	A	1471	3	-	9/29/29/29	-
4	CAP	H	1471	3	-	7/29/29/29	-
5	EDO	D	1479	-	-	1/1/1/1	-
5	EDO	E	1473	-	-	1/1/1/1	-
5	EDO	D	1477	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	G	1473	-	-	0/1/1/1	-
5	EDO	H	1474	-	-	1/1/1/1	-
5	EDO	E	1472	-	-	0/1/1/1	-
5	EDO	F	1472	-	-	0/1/1/1	-
4	CAP	G	1471	3	-	10/29/29/29	-
5	EDO	G	1472	-	-	1/1/1/1	-
4	CAP	E	1471	3	-	10/29/29/29	-
5	EDO	F	1473	-	-	0/1/1/1	-
5	EDO	D	1478	-	-	0/1/1/1	-
5	EDO	C	1475	-	-	1/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1471	CAP	C2-C	-2.86	1.50	1.53
4	B	1471	CAP	C5-C4	2.39	1.55	1.51
4	D	1476	CAP	C2-C	-2.27	1.51	1.53

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1471	CAP	O7-C-C2	3.79	120.40	114.06
4	E	1471	CAP	O3P-P1-O1	3.04	114.59	106.67
4	G	1471	CAP	O2-C2-C	-3.01	103.42	109.07
4	C	1472	CAP	O7-C-C2	2.85	118.83	114.06
4	A	1471	CAP	O7-C-C2	2.72	118.61	114.06

There are no chirality outliers.

5 of 88 torsion outliers are listed below:

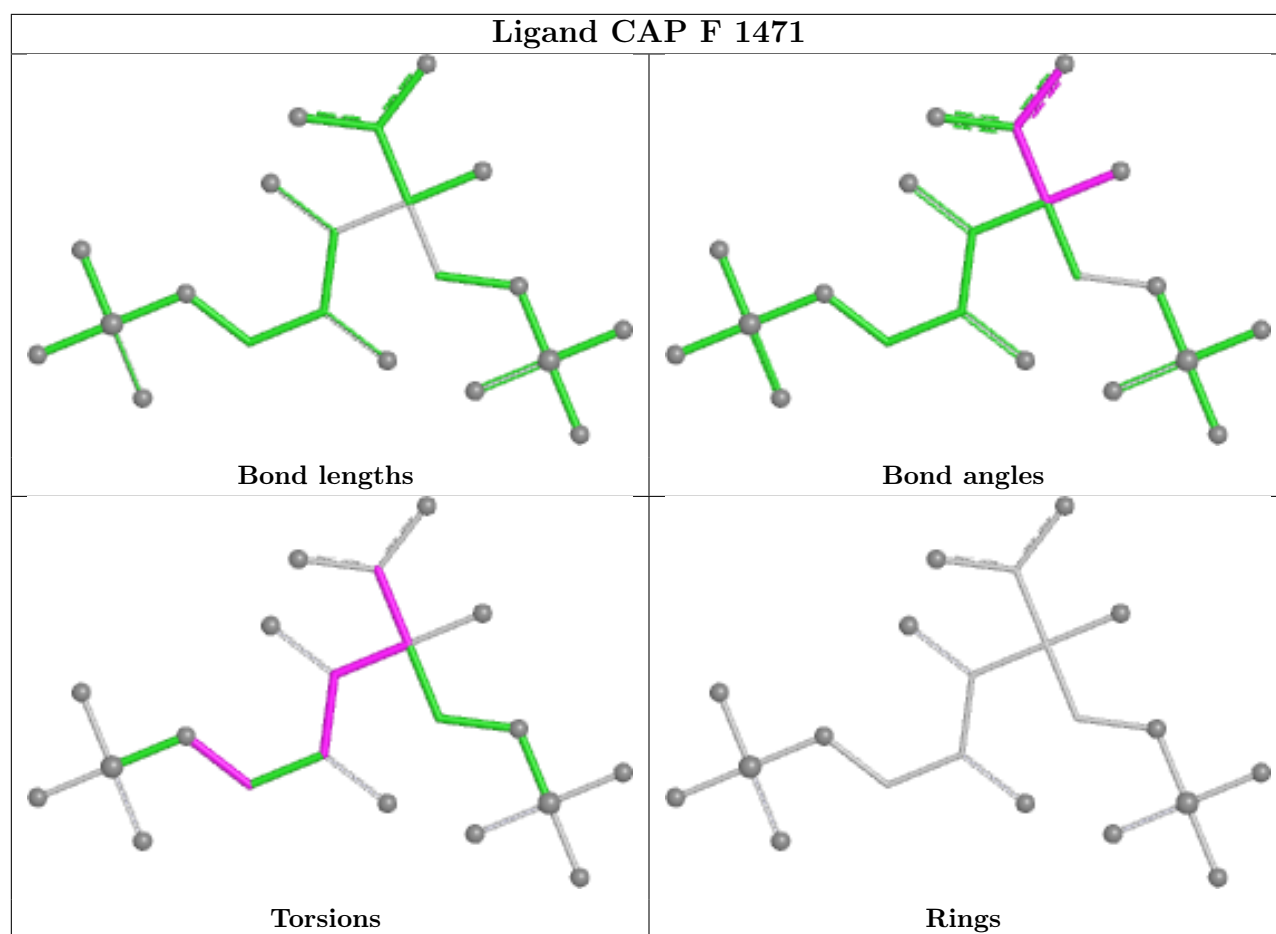
Mol	Chain	Res	Type	Atoms
4	A	1471	CAP	O6-C-C2-C1
4	A	1471	CAP	O7-C-C2-C1
4	A	1471	CAP	O6-C-C2-O2
4	A	1471	CAP	O7-C-C2-O2
4	A	1471	CAP	C2-C3-C4-O4

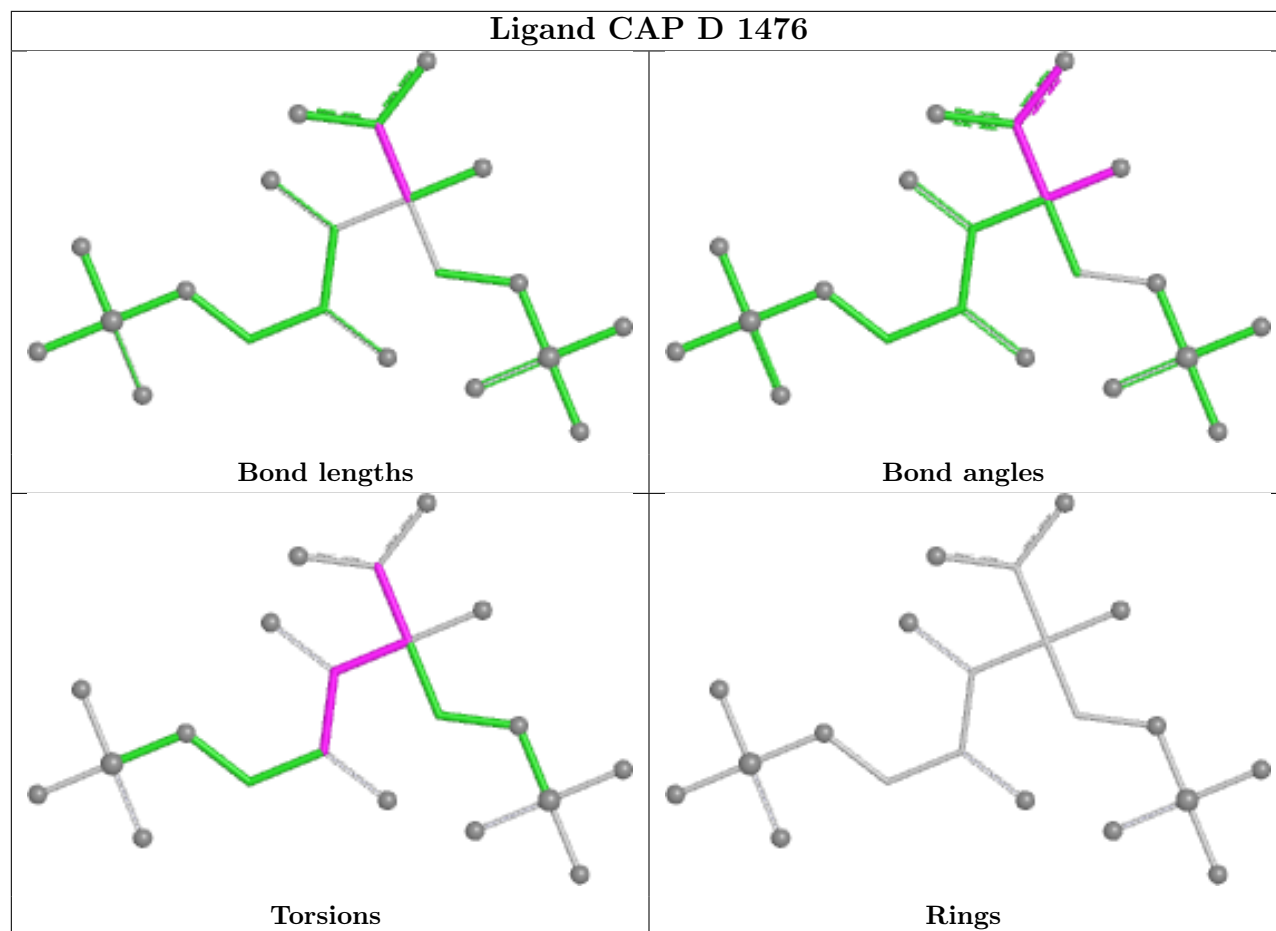
There are no ring outliers.

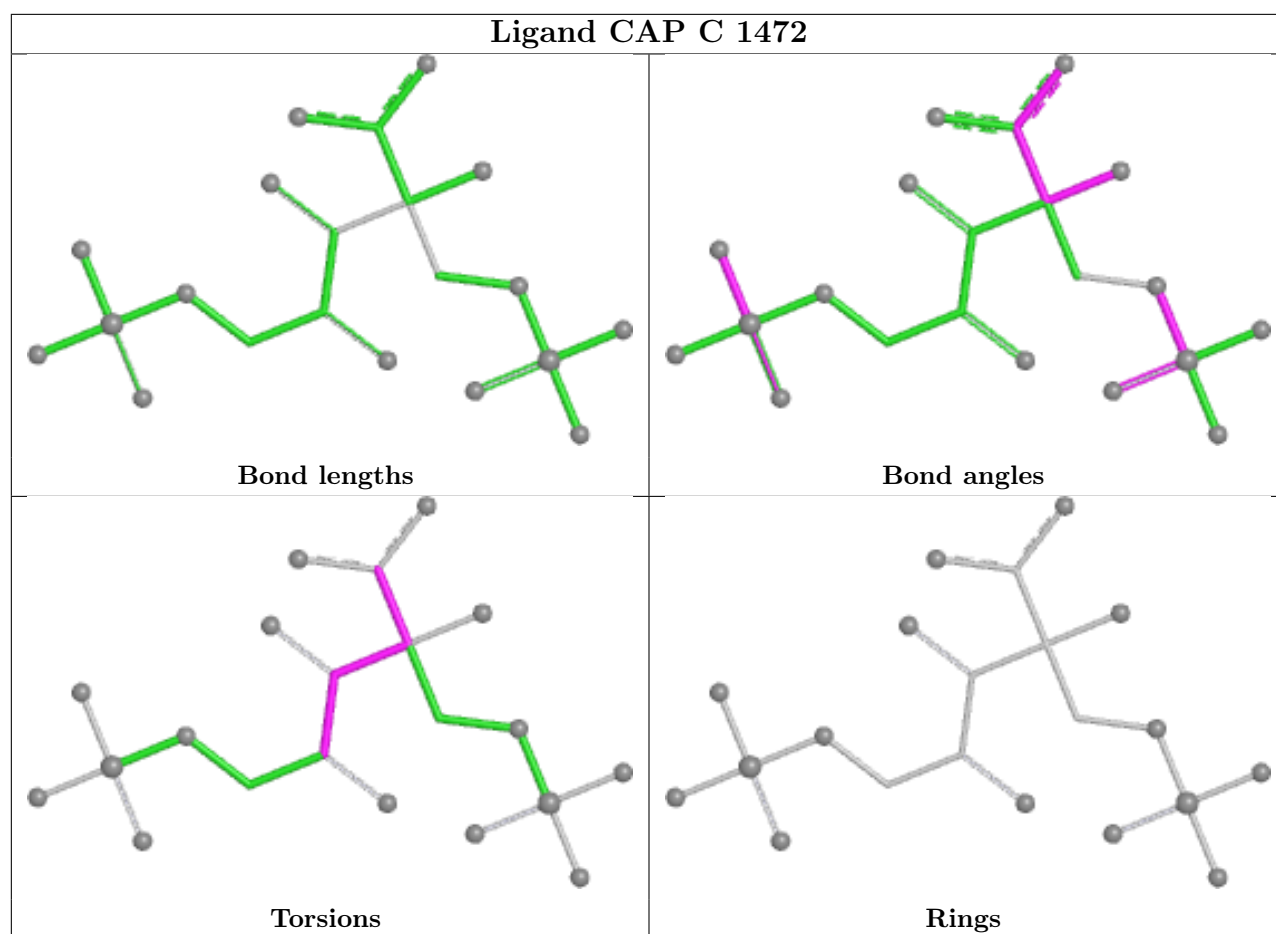
8 monomers are involved in 10 short contacts:

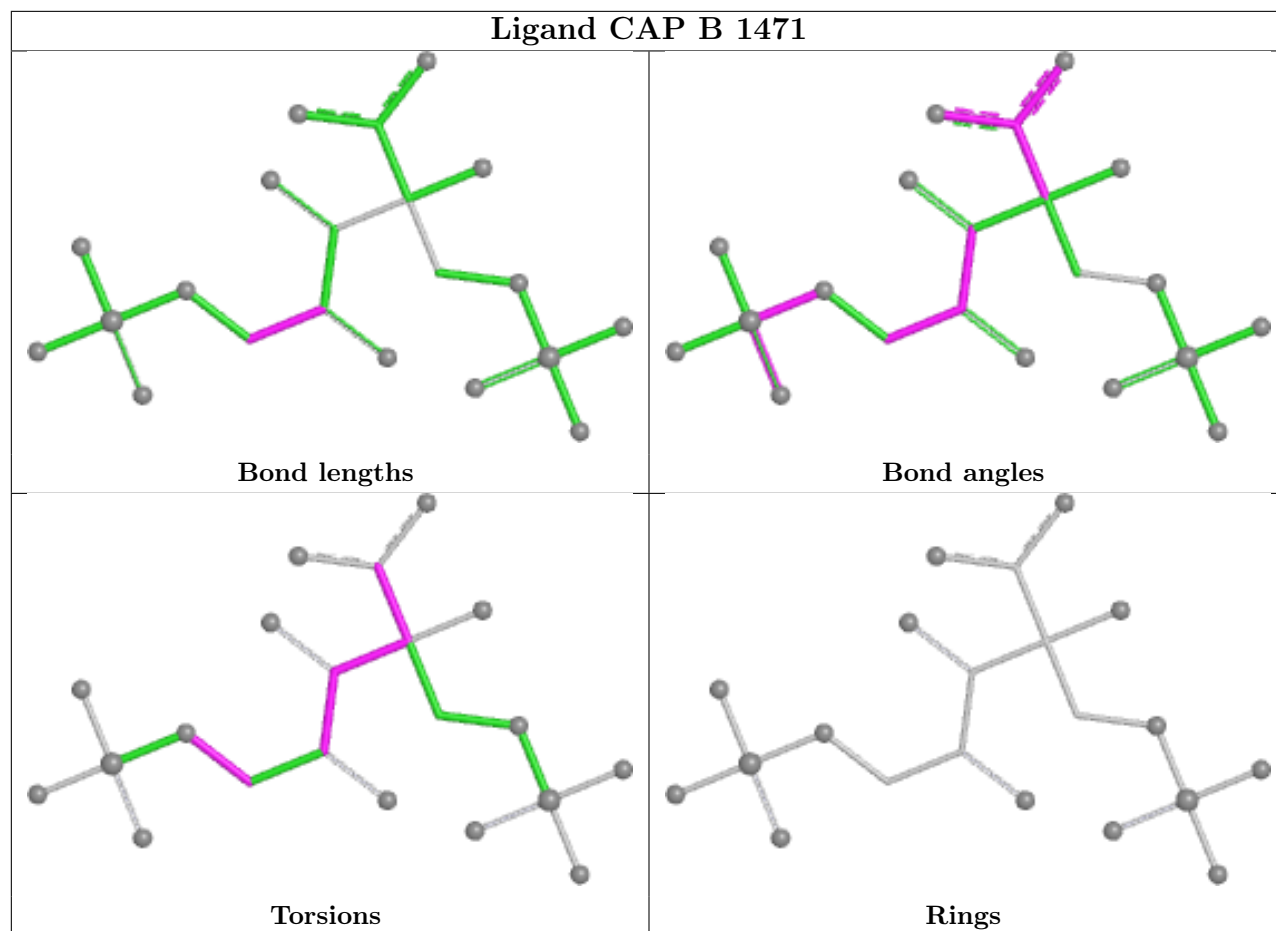
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1474	EDO	1	0
5	C	1473	EDO	2	0
5	G	1474	EDO	1	0
5	A	1473	EDO	1	0
5	E	1473	EDO	1	0
5	G	1473	EDO	2	0
5	G	1472	EDO	1	0
5	C	1475	EDO	2	0

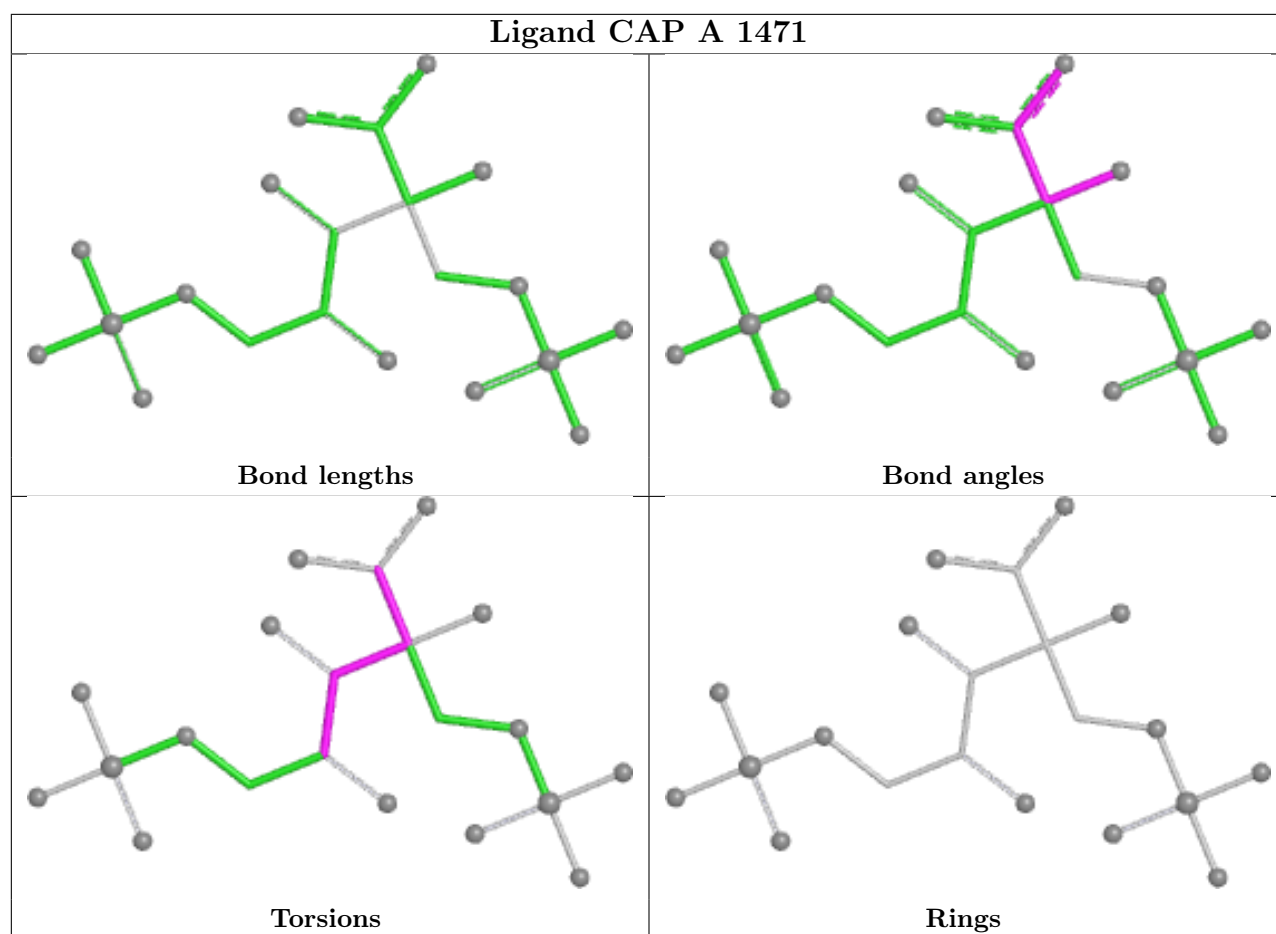
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

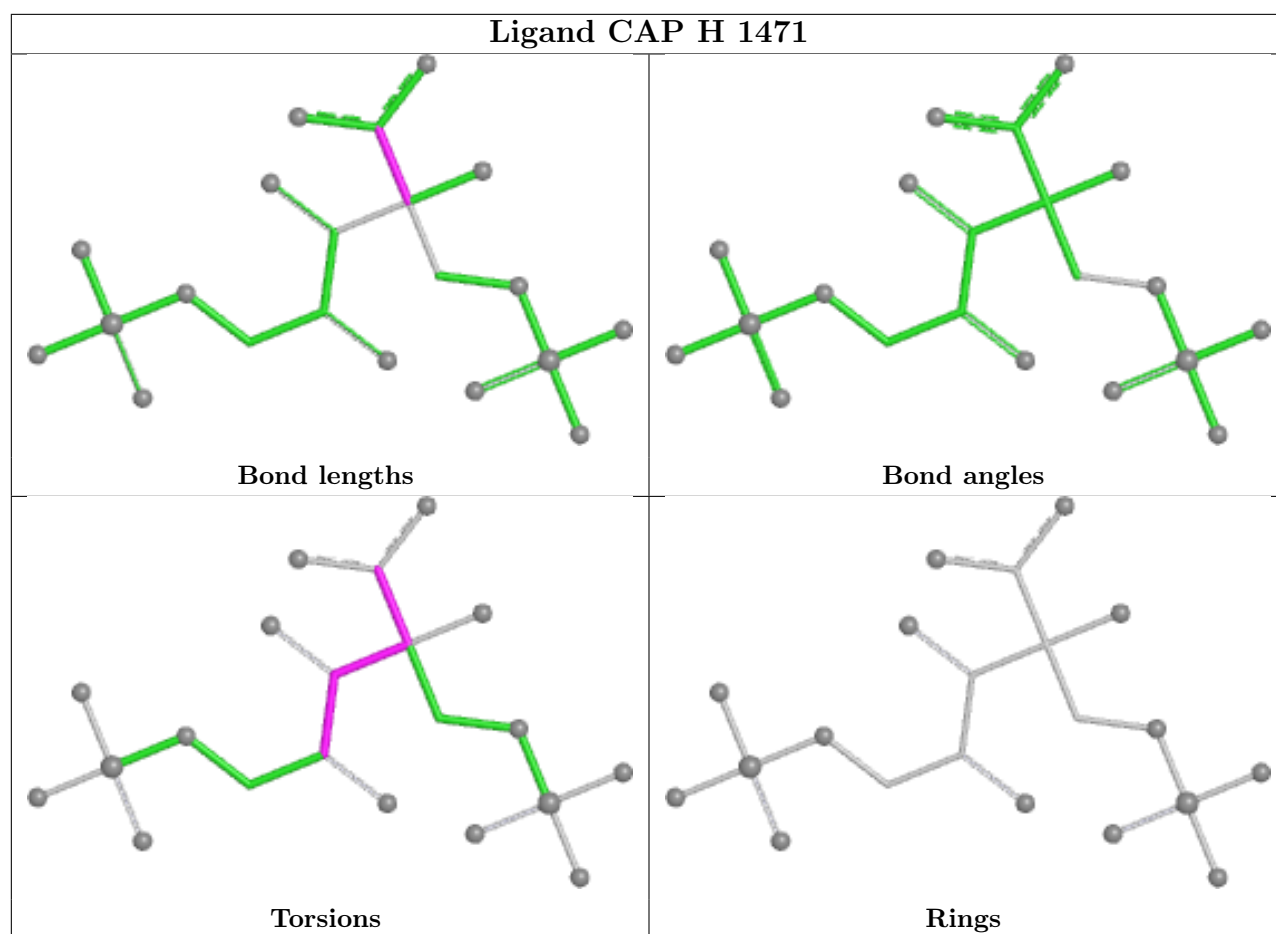


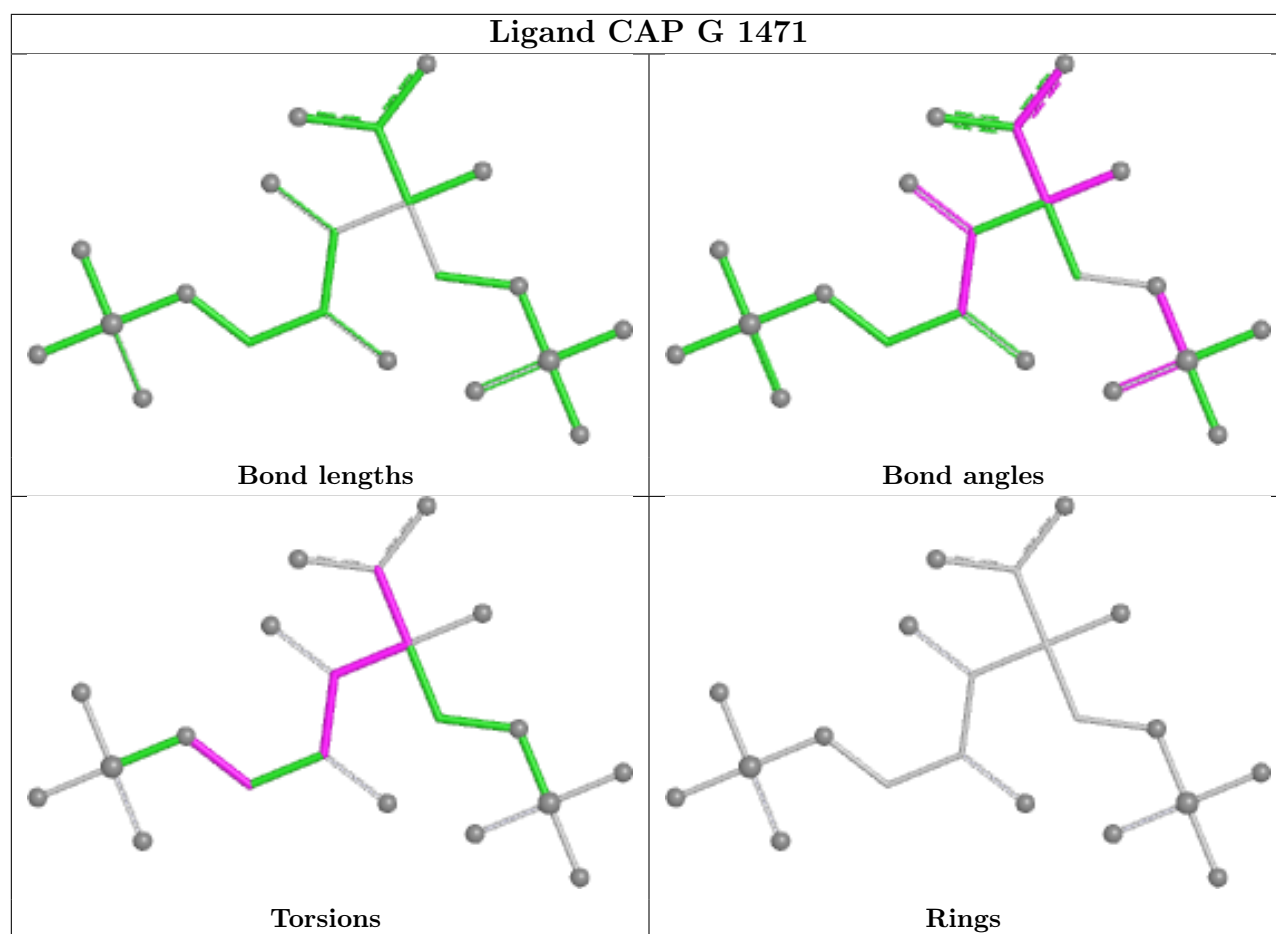


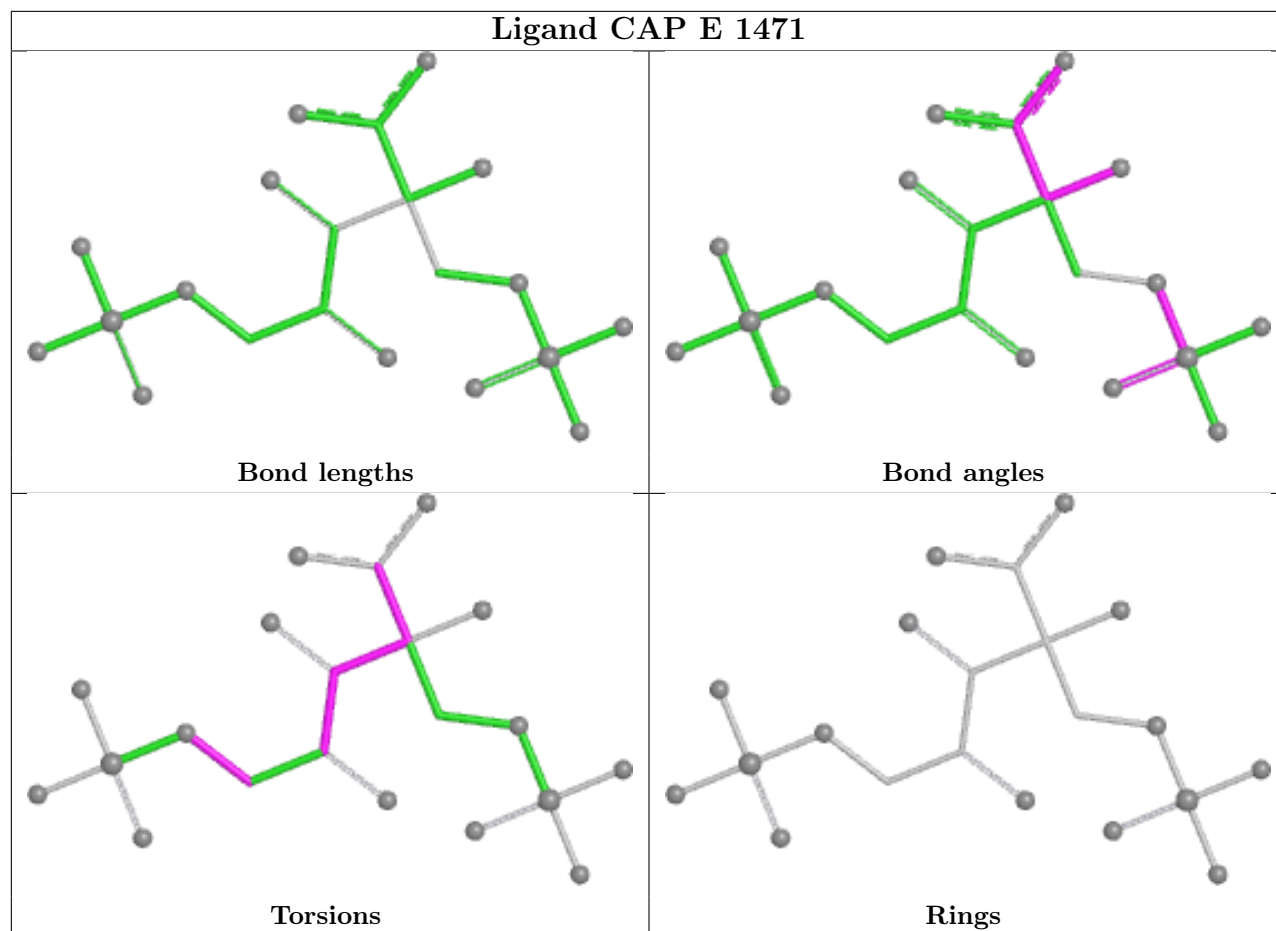












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	454/475 (95%)	-0.49	0 100 100	31, 52, 82, 90	0
1	B	455/475 (95%)	-0.58	0 100 100	32, 52, 82, 90	0
1	C	454/475 (95%)	-0.61	1 (0%) 91 88	31, 52, 82, 91	0
1	D	459/475 (96%)	-0.58	0 100 100	31, 52, 83, 98	0
1	E	454/475 (95%)	-0.64	0 100 100	31, 52, 82, 90	0
1	F	456/475 (96%)	-0.57	1 (0%) 91 88	31, 52, 82, 90	0
1	G	456/475 (96%)	-0.52	0 100 100	31, 52, 82, 90	0
1	H	453/475 (95%)	-0.62	0 100 100	31, 52, 82, 90	0
2	I	139/140 (99%)	0.12	0 100 100	57, 74, 99, 101	0
2	J	139/140 (99%)	0.02	1 (0%) 84 77	57, 74, 99, 101	0
2	K	139/140 (99%)	-0.07	0 100 100	56, 74, 99, 101	0
2	L	139/140 (99%)	0.05	1 (0%) 84 77	57, 74, 99, 101	0
2	M	139/140 (99%)	-0.05	0 100 100	57, 74, 99, 101	0
2	N	139/140 (99%)	-0.09	0 100 100	57, 74, 99, 101	0
2	O	139/140 (99%)	-0.00	2 (1%) 73 64	57, 74, 99, 101	0
2	P	139/140 (99%)	-0.03	2 (1%) 73 64	57, 74, 99, 101	0
All	All	4753/4920 (96%)	-0.44	8 (0%) 91 88	31, 57, 93, 101	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	10	GLY	3.3
2	J	61	GLY	2.3
1	C	94	ASP	2.3
2	O	52	VAL	2.2
2	O	63	VAL	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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	MME	O	1	9/10	0.83	0.14	75,76,78,78	0
2	MME	J	1	9/10	0.86	0.11	75,76,78,79	0
2	MME	P	1	9/10	0.87	0.11	75,76,78,78	0
2	MME	L	1	9/10	0.88	0.10	75,76,78,78	0
2	MME	N	1	9/10	0.88	0.12	75,76,78,78	0
2	MME	K	1	9/10	0.89	0.12	75,76,78,78	0
1	HYP	A	104	8/9	0.90	0.08	45,45,46,47	0
2	MME	I	1	9/10	0.90	0.12	75,76,78,78	0
1	HYP	D	104	8/9	0.92	0.08	45,46,46,47	0
2	MME	M	1	9/10	0.93	0.09	75,76,77,78	0
1	HYP	H	104	8/9	0.94	0.07	46,46,46,46	0
1	KCX	H	201	12/13	0.94	0.08	46,46,53,53	0
1	HYP	B	104	8/9	0.94	0.07	45,45,46,47	0
1	KCX	A	201	12/13	0.94	0.10	46,46,53,53	0
1	HYP	D	151	8/9	0.94	0.07	38,38,38,38	0
1	HYP	E	104	8/9	0.95	0.06	45,46,46,47	0
1	SMC	E	369	7/8	0.95	0.08	48,49,52,52	0
1	HYP	C	104	8/9	0.95	0.07	45,45,45,46	0
1	HYP	B	151	8/9	0.96	0.06	37,38,38,38	0
1	SMC	D	369	7/8	0.96	0.08	49,49,52,53	0
1	KCX	B	201	12/13	0.96	0.07	46,47,53,54	0
1	SMC	A	256	7/8	0.96	0.07	34,36,37,37	0
1	HYP	F	104	8/9	0.96	0.05	45,45,45,46	0
1	KCX	F	201	12/13	0.96	0.07	46,46,52,53	0
1	HYP	G	104	8/9	0.96	0.07	45,45,46,47	0
1	HYP	G	151	8/9	0.96	0.06	37,38,39,39	0
1	HYP	A	151	8/9	0.96	0.06	37,38,38,38	0
1	HYP	F	151	8/9	0.97	0.05	37,38,38,39	0
1	KCX	C	201	12/13	0.97	0.08	45,46,53,53	0
1	SMC	A	369	7/8	0.97	0.06	48,49,51,52	0
1	KCX	E	201	12/13	0.97	0.07	46,46,52,52	0
1	KCX	G	201	12/13	0.97	0.06	46,46,52,53	0
1	SMC	G	369	7/8	0.97	0.06	48,49,51,52	0
1	HYP	C	151	8/9	0.97	0.05	37,38,38,38	0
1	KCX	D	201	12/13	0.97	0.06	46,46,52,53	0
1	SMC	H	369	7/8	0.98	0.05	48,49,51,52	0
1	SMC	B	369	7/8	0.98	0.05	48,49,50,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	SMC	B	256	7/8	0.98	0.04	34,36,37,38	0
1	HYP	E	151	8/9	0.98	0.07	37,38,38,38	0
1	SMC	G	256	7/8	0.98	0.04	34,36,37,37	0
1	SMC	C	369	7/8	0.98	0.06	48,49,50,51	0
1	SMC	F	256	7/8	0.98	0.04	34,36,37,37	0
1	HYP	H	151	8/9	0.98	0.04	36,38,38,38	0
1	SMC	F	369	7/8	0.98	0.06	48,49,51,52	0
1	SMC	C	256	7/8	0.99	0.04	33,36,37,37	0
1	SMC	D	256	7/8	0.99	0.05	34,36,37,37	0
1	SMC	H	256	7/8	0.99	0.05	33,36,37,37	0
1	SMC	E	256	7/8	0.99	0.03	33,36,37,37	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	D	1479	4/4	0.77	0.14	44,45,47,48	0
5	EDO	A	1472	4/4	0.78	0.13	79,81,82,83	0
5	EDO	A	1473	4/4	0.80	0.10	75,75,76,76	0
5	EDO	D	1477	4/4	0.83	0.13	59,60,60,61	0
5	EDO	G	1472	4/4	0.84	0.18	80,82,83,83	0
5	EDO	G	1474	4/4	0.84	0.11	49,50,51,51	0
5	EDO	H	1473	4/4	0.87	0.12	54,54,55,57	0
5	EDO	H	1475	4/4	0.87	0.11	71,74,77,77	0
5	EDO	F	1473	4/4	0.88	0.14	70,71,72,74	0
5	EDO	B	1473	4/4	0.89	0.12	68,68,68,69	0
5	EDO	C	1473	4/4	0.90	0.09	58,60,60,60	0
5	EDO	C	1475	4/4	0.90	0.12	57,57,57,59	0
5	EDO	B	1472	4/4	0.90	0.14	67,68,68,69	0
5	EDO	E	1474	4/4	0.91	0.11	73,74,76,77	0
5	EDO	D	1478	4/4	0.91	0.08	46,48,54,59	0
5	EDO	G	1473	4/4	0.92	0.07	50,51,53,55	0
5	EDO	E	1472	4/4	0.92	0.11	59,60,60,61	0

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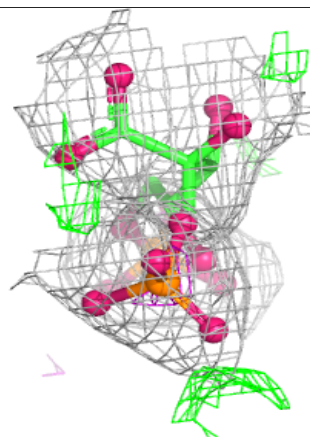
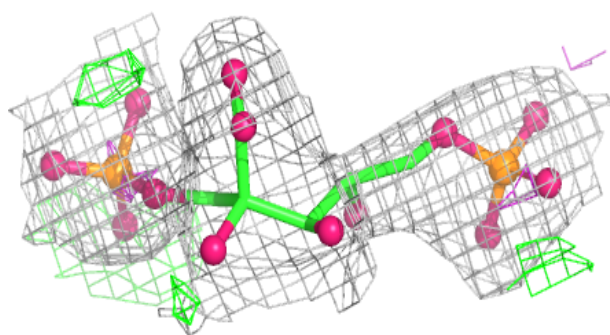
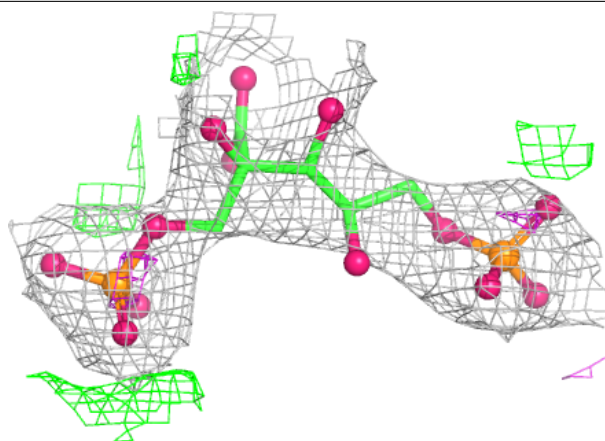
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CAP	B	1471	21/21	0.93	0.09	50,55,56,57	0
5	EDO	A	1474	4/4	0.94	0.08	42,44,45,45	0
5	EDO	C	1474	4/4	0.94	0.10	55,55,57,59	0
5	EDO	F	1472	4/4	0.94	0.09	51,53,53,55	0
4	CAP	G	1471	21/21	0.95	0.07	48,54,56,56	0
5	EDO	H	1472	4/4	0.95	0.06	40,40,41,42	0
4	CAP	A	1471	21/21	0.95	0.06	49,54,56,56	0
4	CAP	D	1476	21/21	0.95	0.07	48,54,56,56	0
4	CAP	E	1471	21/21	0.96	0.06	48,54,56,57	0
5	EDO	E	1475	4/4	0.96	0.08	45,47,48,50	0
4	CAP	C	1472	21/21	0.96	0.06	49,54,56,56	0
4	CAP	H	1471	21/21	0.96	0.06	48,54,56,57	0
5	EDO	H	1474	4/4	0.96	0.06	47,48,49,49	0
5	EDO	E	1473	4/4	0.96	0.06	51,52,52,53	0
4	CAP	F	1471	21/21	0.97	0.06	49,54,56,56	0
3	MG	H	1470	1/1	0.98	0.04	47,47,47,47	0
3	MG	F	1470	1/1	0.99	0.03	47,47,47,47	0
3	MG	G	1470	1/1	0.99	0.06	46,46,46,46	0
3	MG	A	1470	1/1	0.99	0.02	47,47,47,47	0
3	MG	B	1470	1/1	0.99	0.04	47,47,47,47	0
3	MG	E	1470	1/1	0.99	0.02	46,46,46,46	0
3	MG	C	1471	1/1	1.00	0.02	46,46,46,46	0
3	MG	D	1475	1/1	1.00	0.02	47,47,47,47	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.

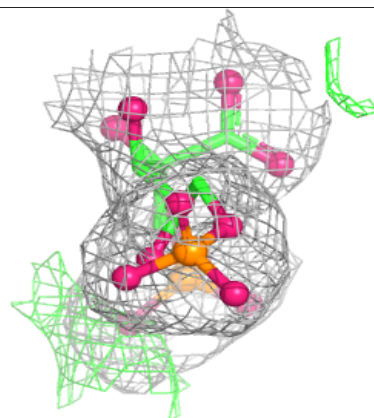
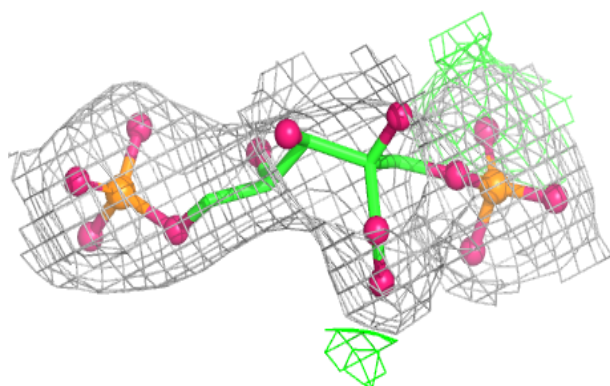
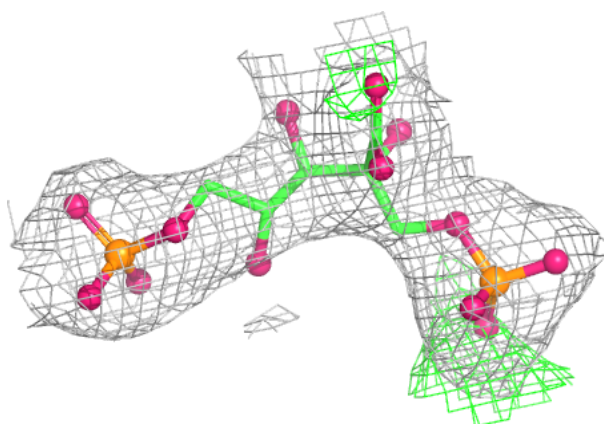
Electron density around CAP B 1471:

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

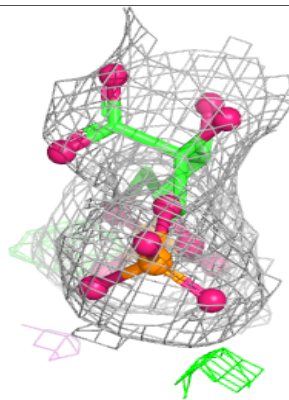
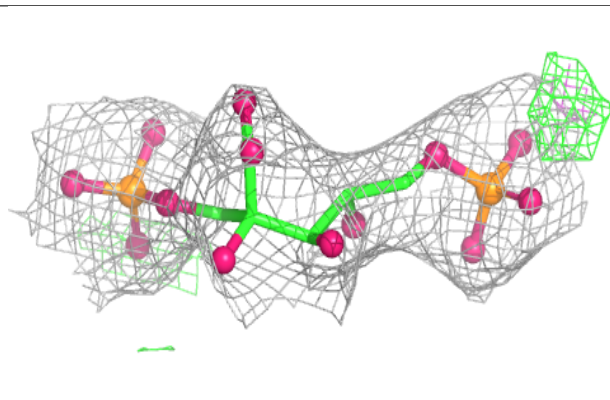
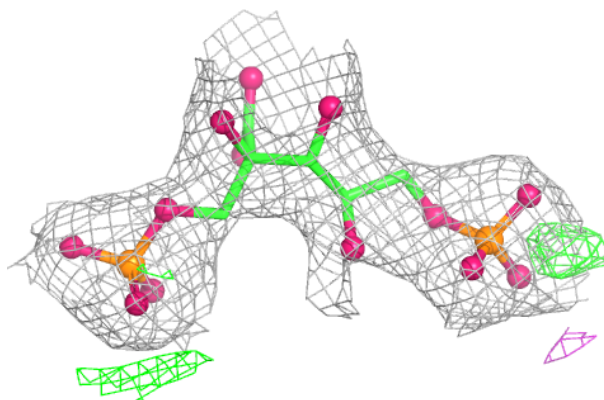


Electron density around CAP G 1471:

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

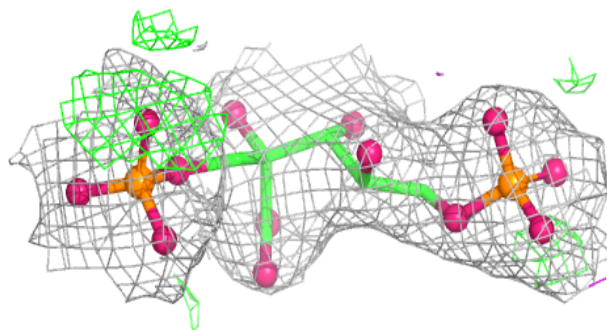
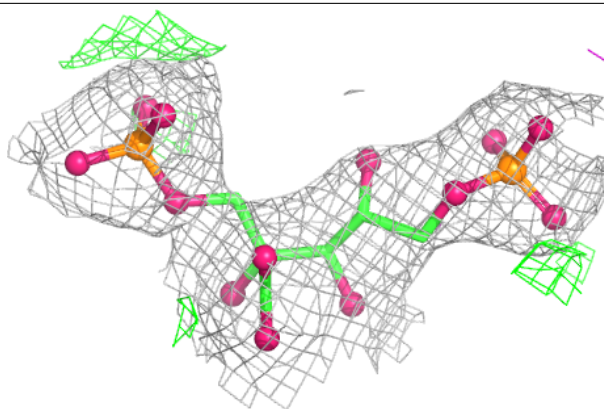
**Electron density around CAP A 1471:**

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

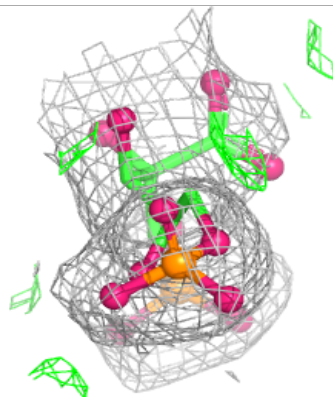
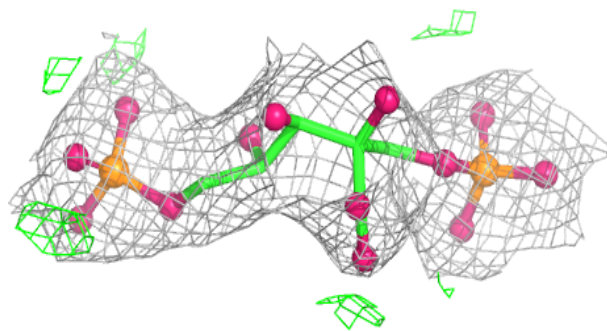
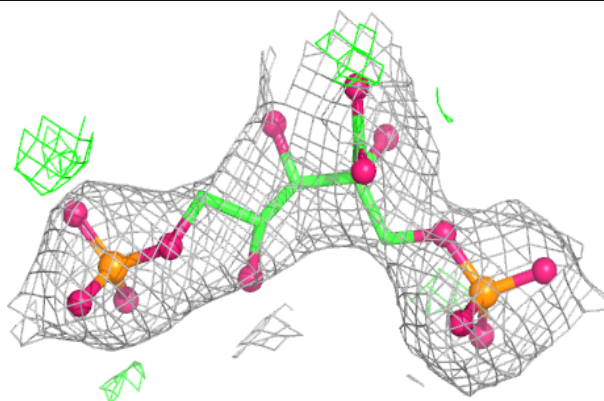


Electron density around CAP D 1476:

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

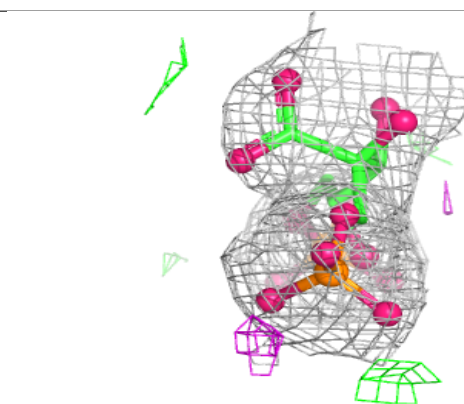
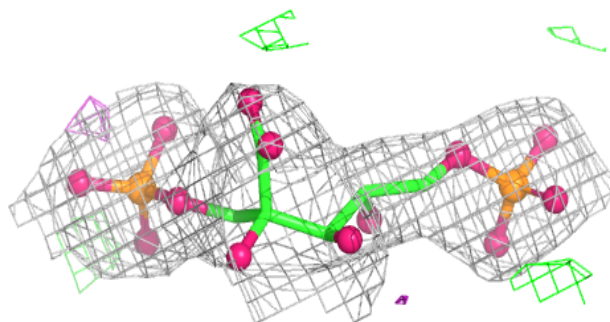
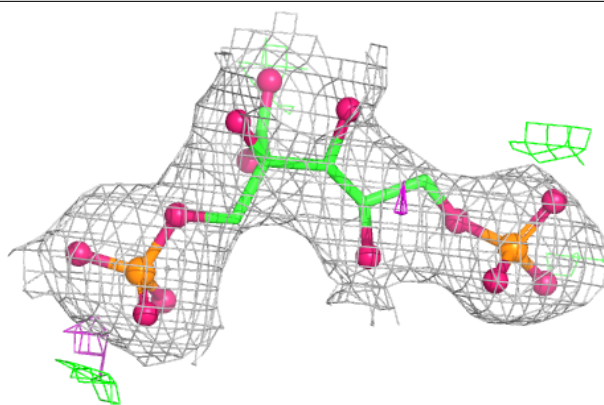
**Electron density around CAP E 1471:**

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

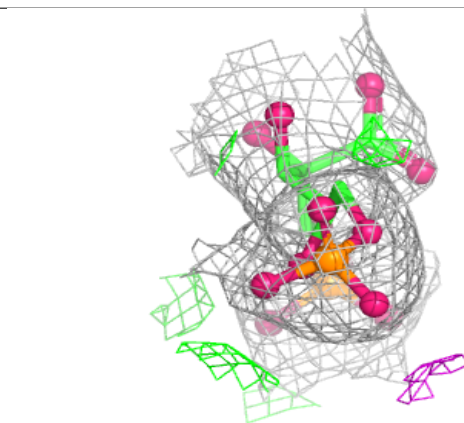
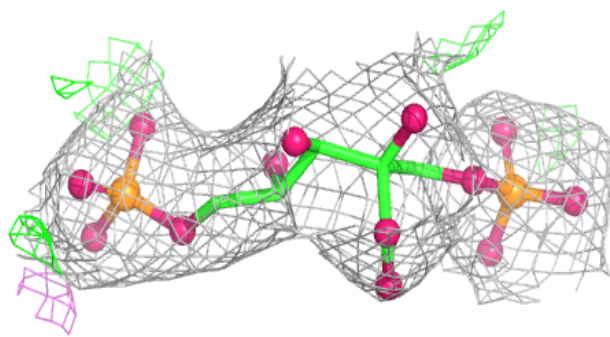
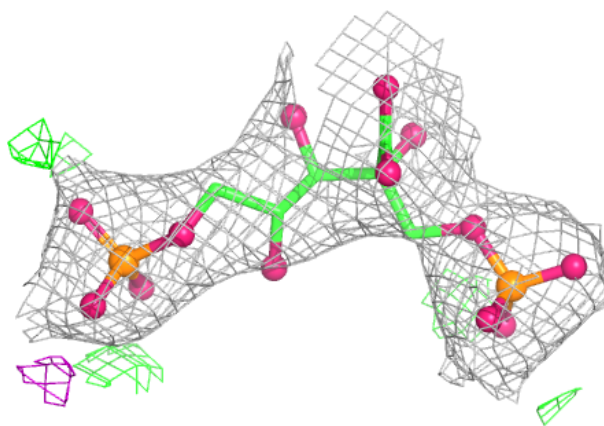


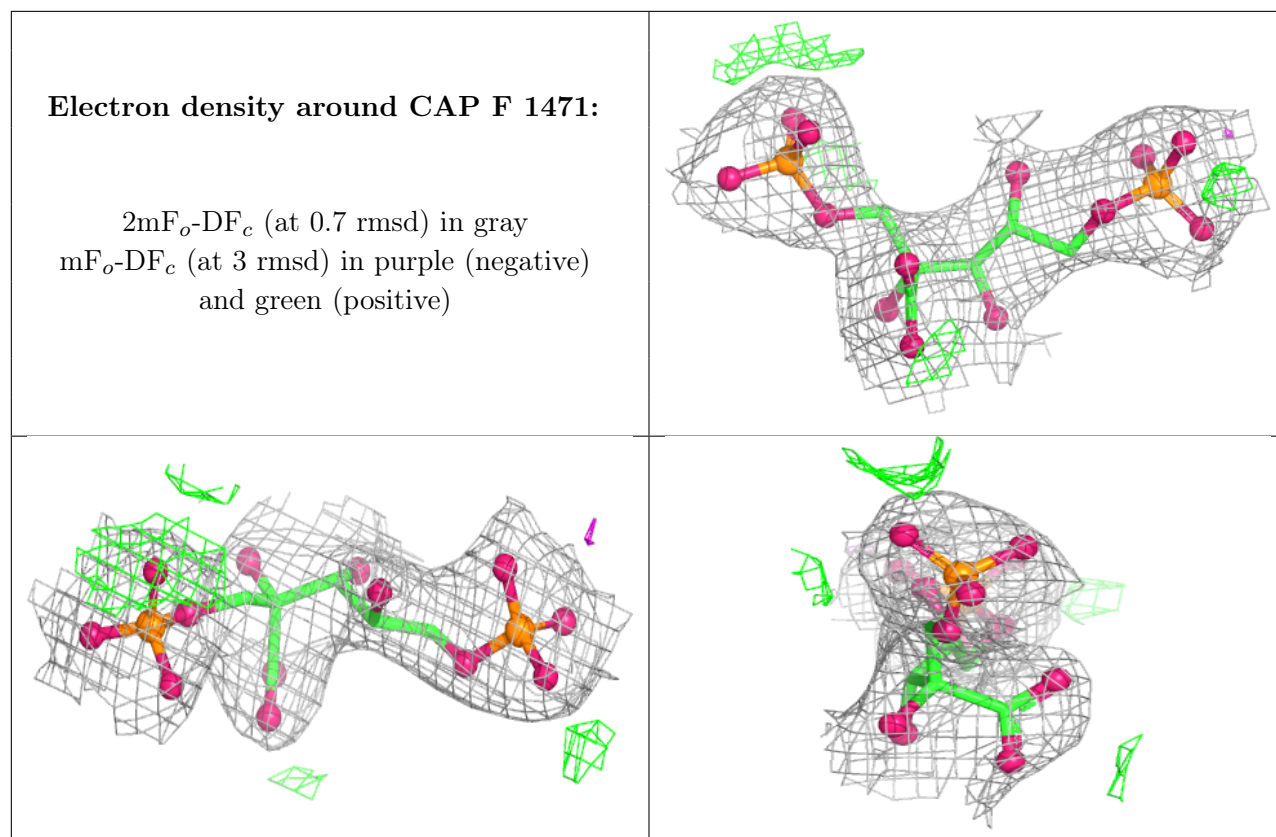
Electron density around CAP C 1472:

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

**Electron density around CAP H 1471:**

$2mF_o-DF_c$ (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.