



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 01:11 PM UTC

PDB ID : 2V63 / pdb_00002v63
Title : Crystal structure of Rubisco from Chlamydomonas reinhardtii with a large-subunit V331A mutation
Authors : Karkehabadi, S.; Satagopagan, S.; Taylor, T.C.; Spreitzer, R.J.; Andersson, I.
Deposited on : 2007-07-13
Resolution : 1.80 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

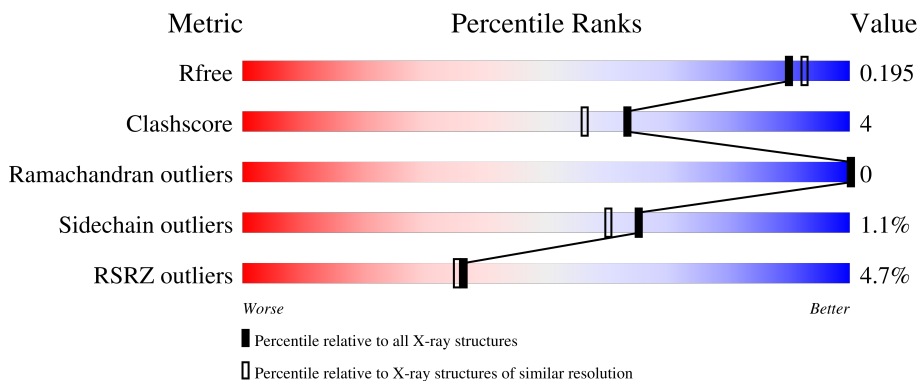
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	 4% 89% 9% .
1	B	475	 3% 87% 11% .
1	C	475	 4% 88% 10% .
1	D	475	 5% 87% 10% .
1	E	475	 4% 88% 9% .

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Mol	Chain	Length	Quality of chain
1	F	475	 4% 89% 8%
1	G	475	 5% 88% 10%
1	H	475	 5% 90% 8%
2	I	140	 11% 89% 10%
2	J	140	 6% 91% 9%
2	K	140	 3% 91% 9%
2	L	140	 6% 87% 12%
2	M	140	 7% 90% 9%
2	N	140	 3% 90% 9%
2	O	140	 6% 91% 9%
2	P	140	 4% 86% 13%

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	EDO	L	1142	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 41473 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
			Total	C	N	O	S			
1	A	466	Total 3643	C 2302	N 642	O 675	S 24	0	4	0
1	B	466	Total 3638	C 2296	N 642	O 675	S 25	0	4	0
1	C	466	Total 3639	C 2298	N 642	O 675	S 24	0	3	0
1	D	464	Total 3626	C 2291	N 640	O 671	S 24	0	2	0
1	E	464	Total 3626	C 2291	N 640	O 671	S 24	0	2	0
1	F	466	Total 3630	C 2294	N 639	O 673	S 24	0	1	0
1	G	466	Total 3634	C 2295	N 642	O 673	S 24	0	2	0
1	H	466	Total 3631	C 2294	N 641	O 672	S 24	0	1	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	PRO	LEU	variant	UNP P00877
A	331	ALA	VAL	engineered mutation	UNP P00877
B	46	PRO	LEU	variant	UNP P00877
B	331	ALA	VAL	engineered mutation	UNP P00877
C	46	PRO	LEU	variant	UNP P00877
C	331	ALA	VAL	engineered mutation	UNP P00877
D	46	PRO	LEU	variant	UNP P00877
D	331	ALA	VAL	engineered mutation	UNP P00877
E	46	PRO	LEU	variant	UNP P00877
E	331	ALA	VAL	engineered mutation	UNP P00877
F	46	PRO	LEU	variant	UNP P00877
F	331	ALA	VAL	engineered mutation	UNP P00877

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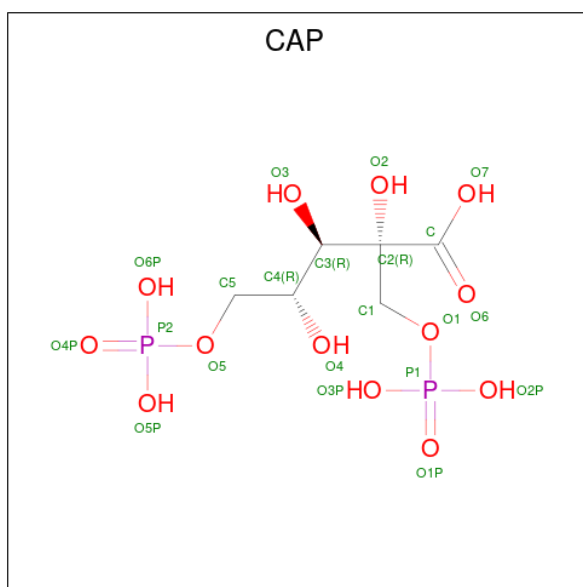
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Chain	Residue	Modelled	Actual	Comment	Reference
G	46	PRO	LEU	variant	UNP P00877
G	331	ALA	VAL	engineered mutation	UNP P00877
H	46	PRO	LEU	variant	UNP P00877
H	331	ALA	VAL	engineered mutation	UNP P00877

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	I	140	1143	739	190	203	11	0	0	0
2	J	140	1145	740	190	203	12	0	1	0
2	K	140	1145	740	190	203	12	0	1	0
2	L	140	1143	739	190	203	11	0	0	0
2	M	140	1146	740	190	204	12	0	2	0
2	N	140	1144	739	190	204	11	0	1	0
2	O	140	1145	740	190	203	12	0	1	0
2	P	140	1143	739	190	203	11	0	0	0

- Molecule 3 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (CCD ID: CAP) (formula: $C_6H_{14}O_{13}P_2$).



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

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

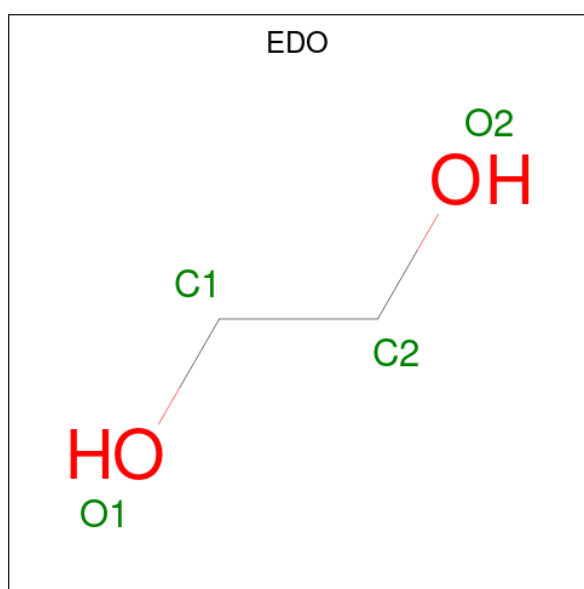
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total Mg 1 1	0	0
4	F	1	Total Mg 1 1	0	0
4	G	1	Total Mg 1 1	0	0
4	H	1	Total Mg 1 1	0	0

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
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
5	I	1	Total C O 4 2 2	0	0
5	J	1	Total C O 4 2 2	0	0
5	J	1	Total C O 4 2 2	0	0
5	K	1	Total C O 4 2 2	0	0
5	K	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0
5	M	1	Total C O 4 2 2	0	0
5	M	1	Total C O 4 2 2	0	0
5	N	1	Total C O 4 2 2	0	0
5	N	1	Total C O 4 2 2	0	0
5	O	1	Total C O 4 2 2	0	0
5	O	1	Total C O 4 2 2	0	0
5	P	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	296	Total O 296 296	0	0

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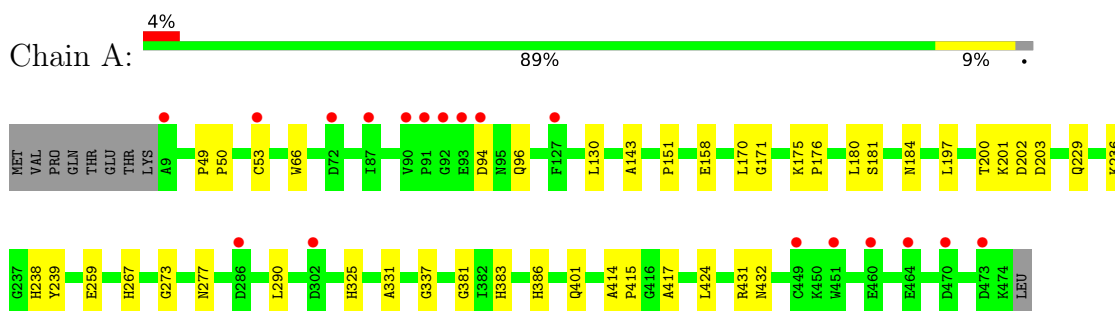
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	287	Total 287	O 287	0	0
6	C	282	Total 282	O 282	0	0
6	D	262	Total 262	O 262	0	0
6	E	262	Total 262	O 262	0	0
6	F	253	Total 253	O 253	0	0
6	G	287	Total 287	O 287	0	0
6	H	281	Total 281	O 281	0	0
6	I	75	Total 75	O 75	0	0
6	J	84	Total 84	O 84	0	0
6	K	91	Total 91	O 91	0	0
6	L	96	Total 96	O 96	0	0
6	M	106	Total 106	O 106	0	0
6	N	72	Total 72	O 72	0	0
6	O	81	Total 81	O 81	0	0
6	P	77	Total 77	O 77	0	0

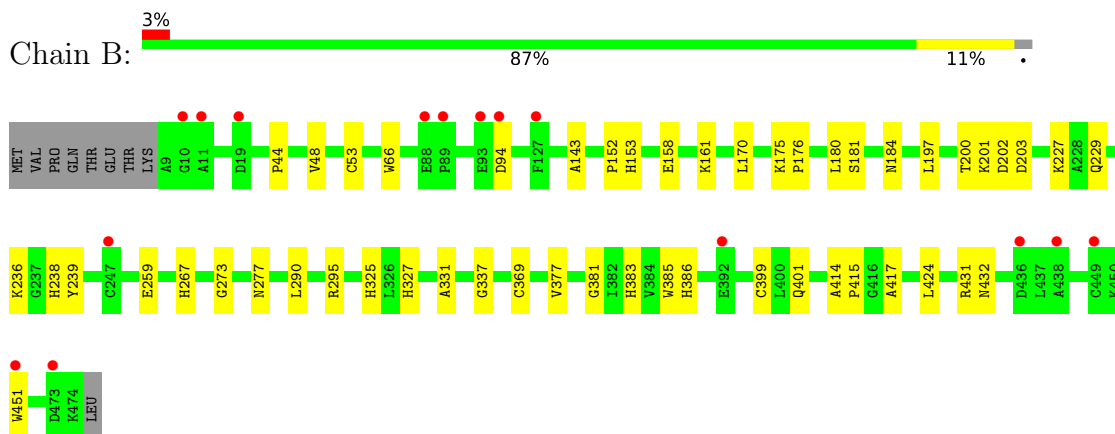
3 Residue-property plots [i](#)

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.

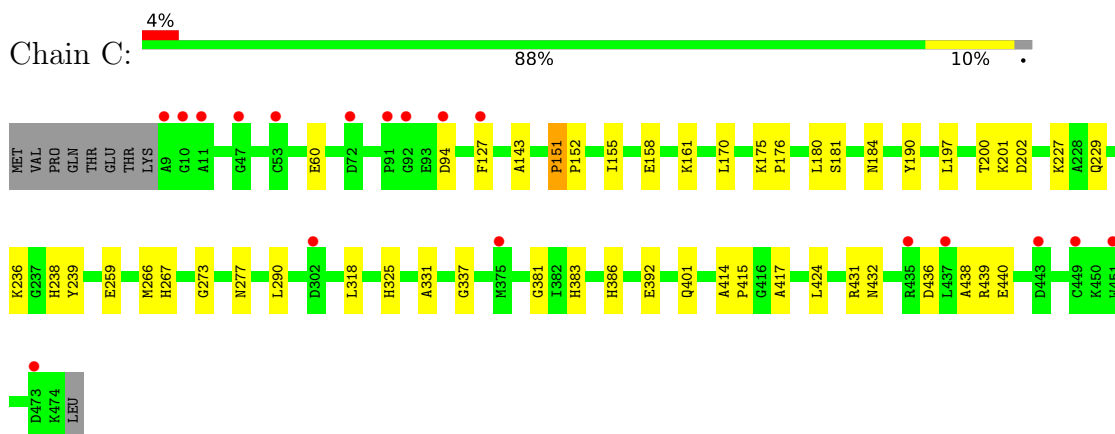
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



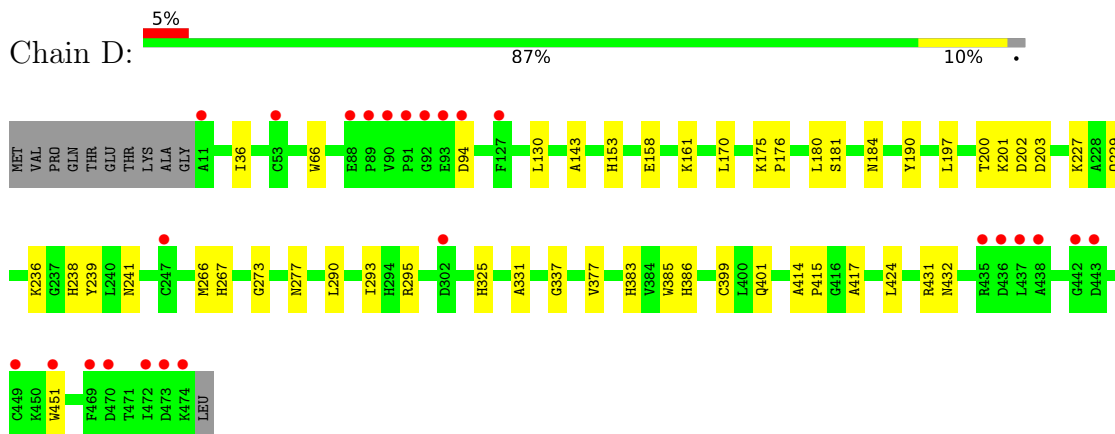
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



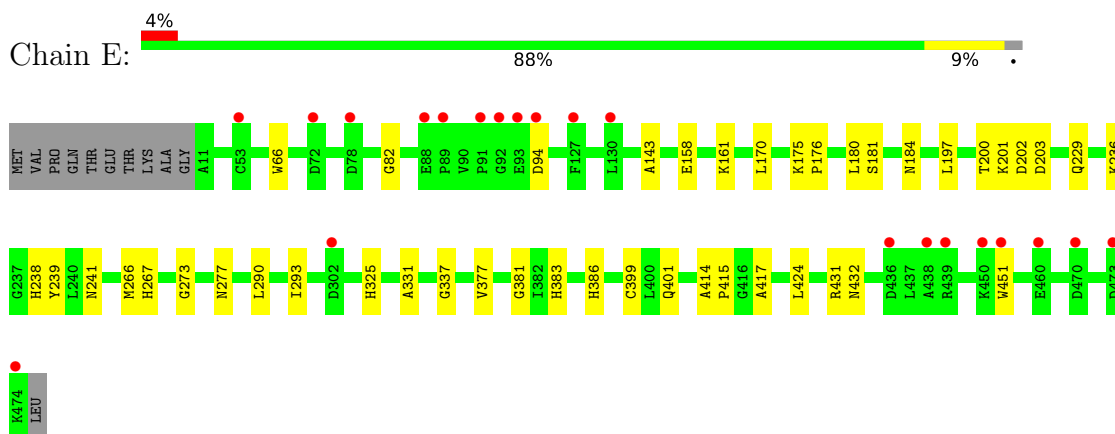
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



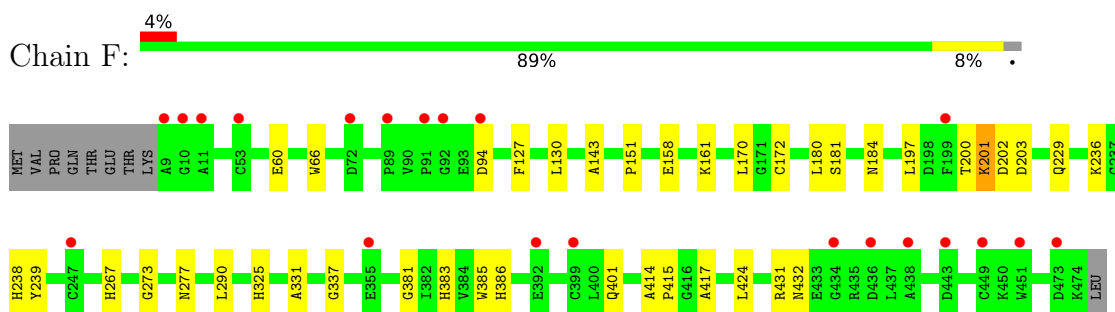
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



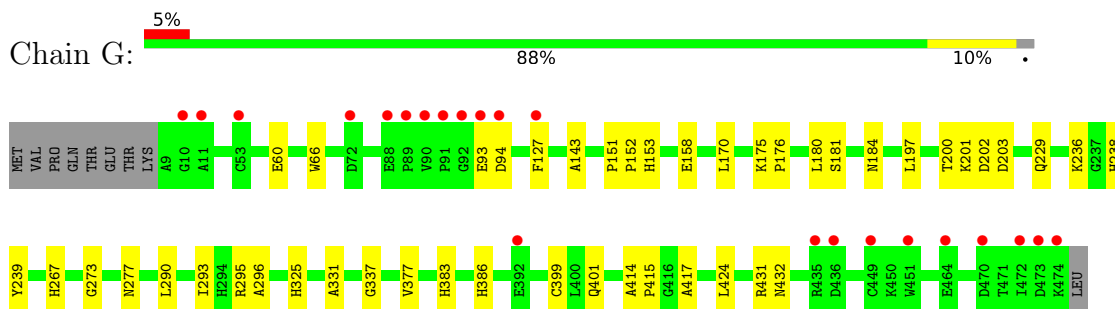
- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN



- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

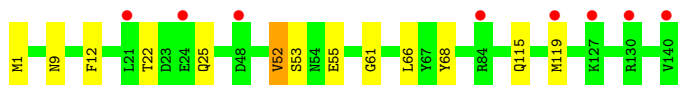
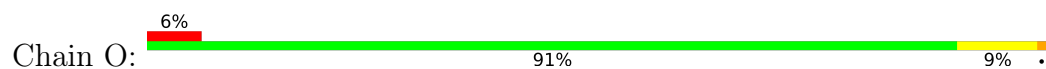


- Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

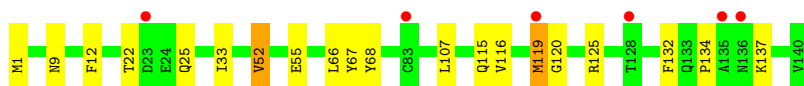
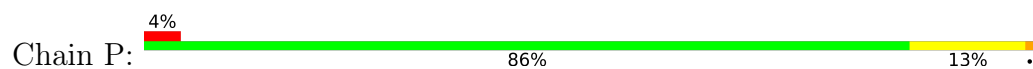




- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1



- Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	121.38Å 177.45Å 122.57Å 90.00° 117.65° 90.00°	Depositor
Resolution (Å)	30.00 – 1.80 30.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	92.1 (30.00-1.80) 92.1 (30.00-1.80)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.191 , 0.214 0.193 , 0.195	Depositor DCC
R_{free} test set	19570 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	13.6	Xtriage
Anisotropy	0.244	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.005 for -h-l,k,h 0.005 for l,k,-h-l 0.016 for h,-k,-h-l 0.014 for -h-l,-k,l 0.196 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	41473	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% 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: KCX, SMC, MG, HYP, CAP, MME, 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	0.49	0/3701	0.74	0/5002
1	B	0.52	0/3699	0.77	0/4999
1	C	0.52	0/3693	0.77	1/4991 (0.0%)
1	D	0.52	0/3675	0.77	0/4967
1	E	0.51	0/3675	0.76	1/4967 (0.0%)
1	F	0.52	0/3673	0.77	0/4965
1	G	0.53	0/3684	0.76	0/4979
1	H	0.53	0/3675	0.76	0/4967
2	I	0.47	0/1166	0.72	0/1584
2	J	0.48	0/1174	0.72	0/1594
2	K	0.49	0/1174	0.74	0/1594
2	L	0.49	0/1166	0.73	0/1584
2	M	0.48	0/1180	0.73	0/1602
2	N	0.49	0/1172	0.72	0/1592
2	O	0.48	0/1174	0.74	0/1594
2	P	0.49	0/1166	0.76	1/1584 (0.1%)
All	All	0.51	0/38847	0.76	3/52565 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	155	ILE	N-CA-C	5.40	116.03	110.36
2	P	55	GLU	N-CA-C	5.36	117.12	111.28
1	E	82	GLY	N-CA-C	-5.19	105.44	112.14

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	3643	0	3548	33	0
1	B	3638	0	3534	39	0
1	C	3639	0	3541	35	0
1	D	3626	0	3531	35	0
1	E	3626	0	3531	32	0
1	F	3630	0	3534	31	0
1	G	3634	0	3535	30	0
1	H	3631	0	3535	30	0
2	I	1143	0	1122	10	0
2	J	1145	0	1123	10	0
2	K	1145	0	1123	9	0
2	L	1143	0	1122	19	0
2	M	1146	0	1124	13	0
2	N	1144	0	1123	9	0
2	O	1145	0	1123	8	0
2	P	1143	0	1122	14	0
3	A	21	0	7	0	0
3	B	21	0	7	0	0
3	C	21	0	8	0	0
3	D	21	0	7	0	0
3	E	21	0	7	0	0
3	F	21	0	7	0	0
3	G	21	0	7	0	0
3	H	21	0	7	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	16	0	24	0	0
5	B	16	0	24	0	0
5	C	20	0	30	0	0
5	D	16	0	24	1	0
5	E	12	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	F	8	0	12	0	0
5	G	24	0	36	0	0
5	H	16	0	24	0	0
5	I	4	0	6	0	0
5	J	8	0	12	0	0
5	K	8	0	12	0	0
5	L	8	0	12	6	0
5	M	8	0	12	3	0
5	N	8	0	12	0	0
5	O	8	0	12	0	0
5	P	4	0	6	0	0
6	A	296	0	0	2	0
6	B	287	0	0	2	0
6	C	282	0	0	0	0
6	D	262	0	0	3	0
6	E	262	0	0	2	0
6	F	253	0	0	2	0
6	G	287	0	0	2	0
6	H	281	0	0	2	0
6	I	75	0	0	1	0
6	J	84	0	0	0	0
6	K	91	0	0	0	0
6	L	96	0	0	4	0
6	M	106	0	0	1	0
6	N	72	0	0	1	0
6	O	81	0	0	0	0
6	P	77	0	0	1	0
All	All	41473	0	37604	298	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 4.

The worst 5 of 298 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:A:53:CYS:SG	1:A:130[B]:LEU:HD21	1.30	1.66
1:A:53:CYS:SG	1:A:130[B]:LEU:CD2	2.12	1.38
2:L:82:GLY:H	5:L:1142:EDO:H12	1.13	1.10
1:A:267:HIS:HD2	1:A:277:ASN:HD22	1.08	1.02
1:D:267:HIS:HD2	1:D:277:ASN:HD22	1.06	1.01

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	463/475 (98%)	453 (98%)	10 (2%)	0	100	100
1	B	463/475 (98%)	454 (98%)	9 (2%)	0	100	100
1	C	462/475 (97%)	450 (97%)	12 (3%)	0	100	100
1	D	459/475 (97%)	448 (98%)	11 (2%)	0	100	100
1	E	459/475 (97%)	447 (97%)	12 (3%)	0	100	100
1	F	460/475 (97%)	450 (98%)	10 (2%)	0	100	100
1	G	461/475 (97%)	450 (98%)	11 (2%)	0	100	100
1	H	460/475 (97%)	449 (98%)	11 (2%)	0	100	100
2	I	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
2	J	139/140 (99%)	135 (97%)	4 (3%)	0	100	100
2	K	139/140 (99%)	133 (96%)	6 (4%)	0	100	100
2	L	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
2	M	140/140 (100%)	135 (96%)	5 (4%)	0	100	100
2	N	139/140 (99%)	131 (94%)	8 (6%)	0	100	100
2	O	139/140 (99%)	134 (96%)	5 (4%)	0	100	100
2	P	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
All	All	4797/4920 (98%)	4666 (97%)	131 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	370/375 (99%)	367 (99%)	3 (1%)	73	70
1	B	370/375 (99%)	368 (100%)	2 (0%)	81	80
1	C	369/375 (98%)	368 (100%)	1 (0%)	86	86
1	D	368/375 (98%)	365 (99%)	3 (1%)	73	70
1	E	368/375 (98%)	366 (100%)	2 (0%)	81	80
1	F	367/375 (98%)	364 (99%)	3 (1%)	73	70
1	G	368/375 (98%)	366 (100%)	2 (0%)	81	80
1	H	367/375 (98%)	365 (100%)	2 (0%)	81	80
2	I	122/122 (100%)	119 (98%)	3 (2%)	42	30
2	J	123/122 (101%)	119 (97%)	4 (3%)	33	21
2	K	123/122 (101%)	120 (98%)	3 (2%)	43	31
2	L	122/122 (100%)	119 (98%)	3 (2%)	42	30
2	M	124/122 (102%)	121 (98%)	3 (2%)	43	31
2	N	123/122 (101%)	120 (98%)	3 (2%)	43	31
2	O	123/122 (101%)	119 (97%)	4 (3%)	33	21
2	P	122/122 (100%)	119 (98%)	3 (2%)	42	30
All	All	3929/3976 (99%)	3885 (99%)	44 (1%)	65	60

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	12	PHE
2	N	52	VAL
2	L	52	VAL
2	M	52	VAL
2	O	9	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
2	N	25	GLN
2	O	9	ASN
1	E	241	ASN
1	E	238	HIS

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Mol	Chain	Res	Type
2	O	29	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	SMC	B	369	1	5,6,7	0.58	0	3,6,8	1.49	1 (33%)
2	MME	I	1	2	7,8,9	3.07	1 (14%)	5,8,10	1.31	1 (20%)
1	KCX	E	201	1,4	10,11,12	0.86	0	6,12,14	1.20	1 (16%)
1	HYP	G	104	1	7,8,9	0.79	0	5,10,12	1.13	0
1	KCX	G	201	1,4	10,11,12	0.97	0	6,12,14	1.67	1 (16%)
1	SMC	D	369	1	5,6,7	0.55	0	3,6,8	1.21	0
1	SMC	G	256	1	5,6,7	0.58	0	3,6,8	0.64	0
1	HYP	C	151	1	7,8,9	0.79	0	5,10,12	1.62	1 (20%)
1	HYP	G	151	1	7,8,9	0.68	0	5,10,12	1.51	1 (20%)
1	HYP	F	104	1	7,8,9	0.84	0	5,10,12	0.88	0
1	KCX	F	201	1,4	10,11,12	0.93	0	6,12,14	1.53	1 (16%)
1	SMC	F	256	1	5,6,7	0.46	0	3,6,8	0.70	0
1	KCX	D	201	1,4	10,11,12	1.11	0	6,12,14	1.35	1 (16%)
1	KCX	C	201	1,4	10,11,12	1.06	1 (10%)	6,12,14	1.39	1 (16%)
1	HYP	F	151	1	7,8,9	0.68	0	5,10,12	1.58	2 (40%)
1	HYP	B	104	1	7,8,9	0.78	0	5,10,12	0.95	0
1	SMC	B	256	1	5,6,7	0.69	0	3,6,8	0.39	0
2	MME	L	1	2	7,8,9	3.07	1 (14%)	5,8,10	1.32	1 (20%)
2	MME	N	1	2	7,8,9	3.06	1 (14%)	5,8,10	1.31	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MME	O	1	2	7,8,9	3.08	1 (14%)	5,8,10	1.19	0
1	HYP	A	104	1	7,8,9	0.74	0	5,10,12	1.01	0
1	SMC	C	369	1	5,6,7	0.54	0	3,6,8	0.66	0
2	MME	K	1	2	7,8,9	3.07	1 (14%)	5,8,10	1.39	1 (20%)
1	SMC	H	369	1	5,6,7	0.57	0	3,6,8	1.18	0
2	MME	J	1	2	7,8,9	3.07	1 (14%)	5,8,10	1.34	1 (20%)
1	KCX	A	201	1,4	10,11,12	1.03	1 (10%)	6,12,14	1.45	1 (16%)
1	HYP	E	151	1	7,8,9	0.82	0	5,10,12	1.57	0
1	HYP	A	151	1	7,8,9	0.78	0	5,10,12	1.53	1 (20%)
2	MME	P	1	2	7,8,9	3.07	1 (14%)	5,8,10	1.32	1 (20%)
1	HYP	E	104	1	7,8,9	0.78	0	5,10,12	1.19	0
1	SMC	E	256	1	5,6,7	0.51	0	3,6,8	0.43	0
1	SMC	F	369	1	5,6,7	0.60	0	3,6,8	1.17	0
1	KCX	H	201	1,4	10,11,12	1.03	1 (10%)	6,12,14	1.43	1 (16%)
1	HYP	D	151	1	7,8,9	0.79	0	5,10,12	1.28	0
1	SMC	H	256	1	5,6,7	0.64	0	3,6,8	0.60	0
1	SMC	G	369	1	5,6,7	0.55	0	3,6,8	0.80	0
1	SMC	C	256	1	5,6,7	0.51	0	3,6,8	0.85	0
1	HYP	C	104	1	7,8,9	0.76	0	5,10,12	1.00	0
1	SMC	A	256	1	5,6,7	0.59	0	3,6,8	0.57	0
1	HYP	D	104	1	7,8,9	0.64	0	5,10,12	1.26	0
1	SMC	D	256	1	5,6,7	0.54	0	3,6,8	1.17	0
1	HYP	H	104	1	7,8,9	0.70	0	5,10,12	1.13	0
1	SMC	A	369	1	5,6,7	0.58	0	3,6,8	1.09	0
1	KCX	B	201	1,4	10,11,12	0.88	0	6,12,14	1.66	1 (16%)
1	HYP	B	151	1	7,8,9	0.95	0	5,10,12	1.56	0
1	SMC	E	369	1	5,6,7	0.63	0	3,6,8	1.16	0
2	MME	M	1	2	7,8,9	3.10	1 (14%)	5,8,10	1.30	1 (20%)
1	HYP	H	151	1	7,8,9	0.84	0	5,10,12	1.52	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	SMC	B	369	1	-	1/3/5/7	-
2	MME	I	1	2	-	3/5/8/10	-
1	KCX	E	201	1,4	-	0/9/10/12	-
1	HYP	G	104	1	-	0/0/11/13	0/1/1/1

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

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SMC	E	369	1	-	1/3/5/7	-
2	MME	M	1	2	-	3/5/8/10	-
1	HYP	H	151	1	-	0/0/11/13	0/1/1/1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	M	1	MME	CM-N	-7.97	1.27	1.46
2	O	1	MME	CM-N	-7.93	1.27	1.46
2	L	1	MME	CM-N	-7.91	1.27	1.46
2	I	1	MME	CM-N	-7.90	1.27	1.46
2	P	1	MME	CM-N	-7.88	1.27	1.46

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	201	KCX	OQ1-CX-NZ	-4.04	118.79	124.92
1	G	201	KCX	OQ1-CX-NZ	-3.93	118.95	124.92
1	F	201	KCX	OQ1-CX-NZ	-3.70	119.31	124.92
1	A	201	KCX	OQ1-CX-NZ	-3.51	119.58	124.92
1	H	201	KCX	OQ1-CX-NZ	-3.44	119.70	124.92

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	369	SMC	C-CA-CB-SG
2	I	1	MME	C-CA-CB-CG
2	J	1	MME	C-CA-CB-CG
2	K	1	MME	C-CA-CB-CG
2	L	1	MME	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	151	HYP	1	0
1	F	201	KCX	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 62 ligands modelled in this entry, 8 are monoatomic - leaving 54 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	K	1142	-	3,3,3	0.45	0	2,2,2	0.32	0
5	EDO	G	1476	-	3,3,3	0.40	0	2,2,2	0.33	0
5	EDO	C	1478	-	3,3,3	0.51	0	2,2,2	0.28	0
5	EDO	E	1477	-	3,3,3	0.40	0	2,2,2	0.43	0
5	EDO	D	1478	-	3,3,3	0.43	0	2,2,2	0.43	0
5	EDO	E	1475	-	3,3,3	0.50	0	2,2,2	0.27	0
5	EDO	D	1476	-	3,3,3	0.45	0	2,2,2	0.29	0
5	EDO	N	1141	-	3,3,3	0.43	0	2,2,2	0.36	0
5	EDO	A	1480	-	3,3,3	0.49	0	2,2,2	0.33	0
3	CAP	F	477	4	18,20,20	0.86	0	23,31,31	0.92	2 (8%)
5	EDO	J	1142	-	3,3,3	0.38	0	2,2,2	0.48	0
5	EDO	F	1475	-	3,3,3	0.44	0	2,2,2	0.30	0
5	EDO	F	1476	-	3,3,3	0.47	0	2,2,2	0.33	0
5	EDO	O	1141	-	3,3,3	0.46	0	2,2,2	0.33	0
5	EDO	M	1142	-	3,3,3	0.47	0	2,2,2	0.19	0
3	CAP	E	477	4	18,20,20	0.81	0	23,31,31	0.95	1 (4%)
3	CAP	B	477	4	18,20,20	0.80	0	23,31,31	0.93	1 (4%)
5	EDO	B	1478	-	3,3,3	0.44	0	2,2,2	0.28	0
5	EDO	H	1476	-	3,3,3	0.50	0	2,2,2	0.28	0
5	EDO	B	1476	-	3,3,3	0.45	0	2,2,2	0.30	0
5	EDO	P	1141	-	3,3,3	0.42	0	2,2,2	0.39	0
5	EDO	A	1477	-	3,3,3	0.42	0	2,2,2	0.33	0
5	EDO	B	1477	-	3,3,3	0.43	0	2,2,2	0.38	0
5	EDO	D	1477	-	3,3,3	0.54	0	2,2,2	0.22	0
3	CAP	A	476	4	18,20,20	0.88	0	23,31,31	0.87	1 (4%)
5	EDO	C	1475	-	3,3,3	0.43	0	2,2,2	0.28	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	A	1478	-	3,3,3	0.50	0	2,2,2	0.33	0
5	EDO	H	1475	-	3,3,3	0.40	0	2,2,2	0.31	0
5	EDO	K	1141	-	3,3,3	0.43	0	2,2,2	0.36	0
5	EDO	B	1475	-	3,3,3	0.58	0	2,2,2	0.09	0
5	EDO	D	1475	-	3,3,3	0.47	0	2,2,2	0.25	0
3	CAP	H	477	4	18,20,20	0.90	0	23,31,31	0.99	1 (4%)
5	EDO	G	1479	-	3,3,3	0.48	0	2,2,2	0.17	0
5	EDO	G	1477	-	3,3,3	0.44	0	2,2,2	0.30	0
5	EDO	L	1142	-	3,3,3	0.44	0	2,2,2	0.21	0
5	EDO	H	1477	-	3,3,3	0.46	0	2,2,2	0.28	0
3	CAP	C	477	4	18,20,20	0.91	0	23,31,31	0.83	1 (4%)
3	CAP	D	477	4	18,20,20	0.88	0	23,31,31	0.87	1 (4%)
5	EDO	G	1475	-	3,3,3	0.52	0	2,2,2	0.23	0
5	EDO	L	1141	-	3,3,3	0.42	0	2,2,2	0.24	0
5	EDO	C	1479	-	3,3,3	0.44	0	2,2,2	0.35	0
5	EDO	C	1477	-	3,3,3	0.42	0	2,2,2	0.35	0
5	EDO	C	1476	-	3,3,3	0.49	0	2,2,2	0.17	0
5	EDO	M	1141	-	3,3,3	0.41	0	2,2,2	0.34	0
5	EDO	I	1141	-	3,3,3	0.46	0	2,2,2	0.25	0
5	EDO	O	1142	-	3,3,3	0.45	0	2,2,2	0.39	0
5	EDO	N	1142	-	3,3,3	0.45	0	2,2,2	0.37	0
5	EDO	G	1478	-	3,3,3	0.48	0	2,2,2	0.32	0
3	CAP	G	477	4	18,20,20	0.90	0	23,31,31	0.89	1 (4%)
5	EDO	E	1476	-	3,3,3	0.46	0	2,2,2	0.26	0
5	EDO	A	1479	-	3,3,3	0.43	0	2,2,2	0.34	0
5	EDO	G	1480	-	3,3,3	0.47	0	2,2,2	0.34	0
5	EDO	H	1478	-	3,3,3	0.42	0	2,2,2	0.39	0
5	EDO	J	1141	-	3,3,3	0.43	0	2,2,2	0.38	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	K	1142	-	-	0/1/1/1	-
5	EDO	G	1476	-	-	0/1/1/1	-
5	EDO	C	1478	-	-	0/1/1/1	-
5	EDO	E	1477	-	-	1/1/1/1	-
5	EDO	D	1478	-	-	0/1/1/1	-
5	EDO	E	1475	-	-	0/1/1/1	-
5	EDO	D	1476	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	N	1141	-	-	1/1/1/1	-
5	EDO	A	1480	-	-	0/1/1/1	-
3	CAP	F	477	4	-	7/29/29/29	-
5	EDO	J	1142	-	-	0/1/1/1	-
5	EDO	F	1475	-	-	0/1/1/1	-
5	EDO	F	1476	-	-	0/1/1/1	-
5	EDO	O	1141	-	-	0/1/1/1	-
5	EDO	M	1142	-	-	1/1/1/1	-
3	CAP	E	477	4	-	7/29/29/29	-
3	CAP	B	477	4	-	7/29/29/29	-
5	EDO	B	1478	-	-	0/1/1/1	-
5	EDO	H	1476	-	-	0/1/1/1	-
5	EDO	B	1476	-	-	1/1/1/1	-
5	EDO	P	1141	-	-	0/1/1/1	-
5	EDO	A	1477	-	-	1/1/1/1	-
5	EDO	B	1477	-	-	1/1/1/1	-
5	EDO	D	1477	-	-	0/1/1/1	-
3	CAP	A	476	4	-	7/29/29/29	-
5	EDO	C	1475	-	-	1/1/1/1	-
5	EDO	A	1478	-	-	0/1/1/1	-
5	EDO	H	1475	-	-	1/1/1/1	-
5	EDO	K	1141	-	-	0/1/1/1	-
5	EDO	B	1475	-	-	0/1/1/1	-
5	EDO	D	1475	-	-	1/1/1/1	-
3	CAP	H	477	4	-	7/29/29/29	-
5	EDO	G	1479	-	-	1/1/1/1	-
5	EDO	G	1477	-	-	0/1/1/1	-
5	EDO	L	1142	-	-	1/1/1/1	-
5	EDO	H	1477	-	-	0/1/1/1	-
3	CAP	C	477	4	-	7/29/29/29	-
3	CAP	D	477	4	-	7/29/29/29	-
5	EDO	G	1475	-	-	0/1/1/1	-
5	EDO	L	1141	-	-	1/1/1/1	-
5	EDO	C	1479	-	-	1/1/1/1	-
5	EDO	C	1477	-	-	0/1/1/1	-
5	EDO	C	1476	-	-	1/1/1/1	-
5	EDO	M	1141	-	-	0/1/1/1	-
5	EDO	I	1141	-	-	1/1/1/1	-
5	EDO	O	1142	-	-	0/1/1/1	-
5	EDO	N	1142	-	-	0/1/1/1	-
5	EDO	G	1478	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CAP	G	477	4	-	6/29/29/29	-
5	EDO	E	1476	-	-	1/1/1/1	-
5	EDO	A	1479	-	-	1/1/1/1	-
5	EDO	G	1480	-	-	0/1/1/1	-
5	EDO	H	1478	-	-	1/1/1/1	-
5	EDO	J	1141	-	-	0/1/1/1	-

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	477	CAP	O7-C-C2	3.17	119.37	114.06
3	E	477	CAP	O7-C-C2	3.15	119.34	114.06
3	B	477	CAP	O7-C-C2	2.98	119.05	114.06
3	A	476	CAP	O7-C-C2	2.84	118.82	114.06
3	G	477	CAP	O7-C-C2	2.67	118.54	114.06

There are no chirality outliers.

5 of 74 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	476	CAP	O6-C-C2-C1
3	A	476	CAP	O7-C-C2-C1
3	A	476	CAP	O6-C-C2-O2
3	A	476	CAP	O7-C-C2-O2
3	A	476	CAP	O3-C3-C4-O4

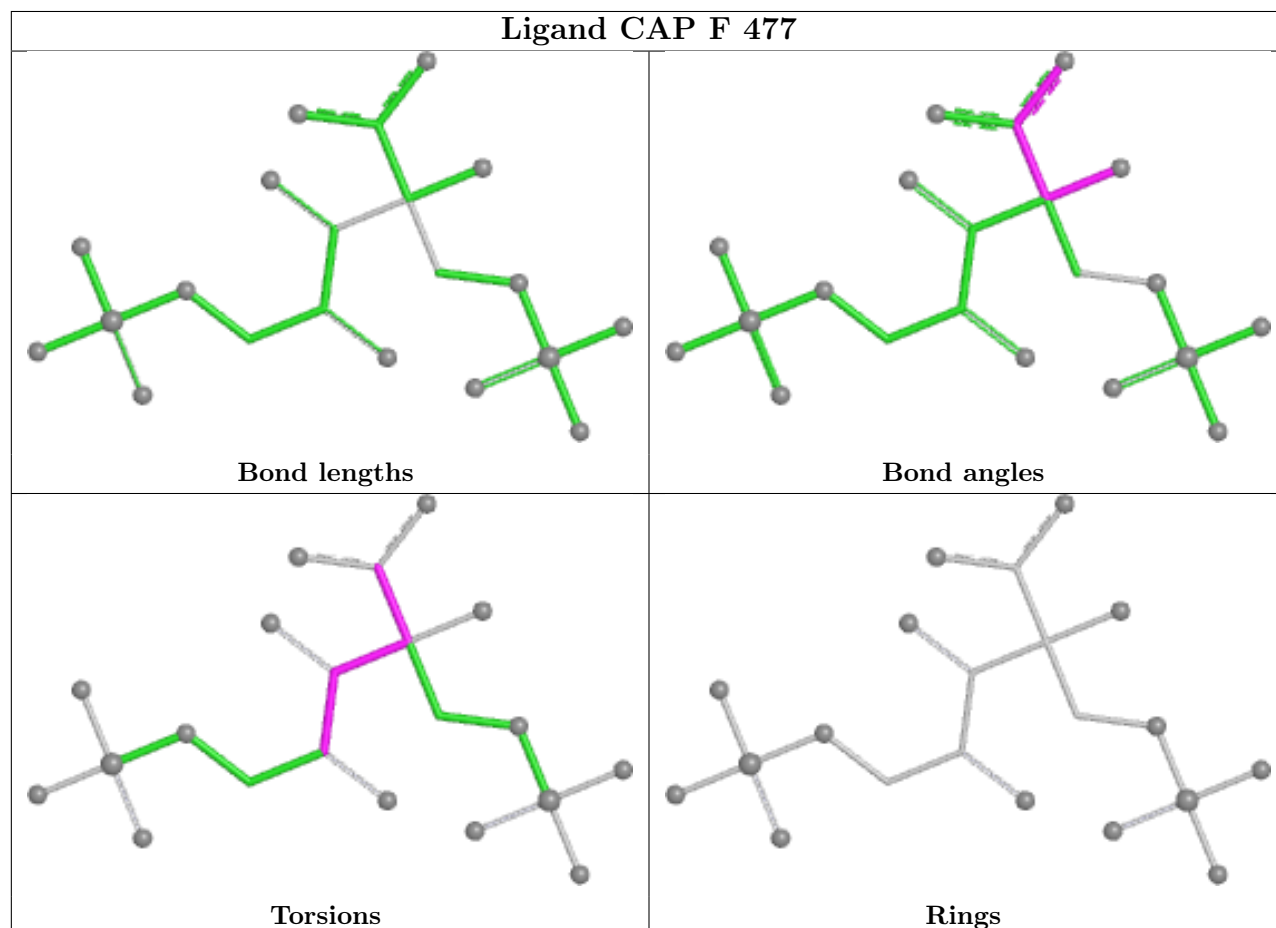
There are no ring outliers.

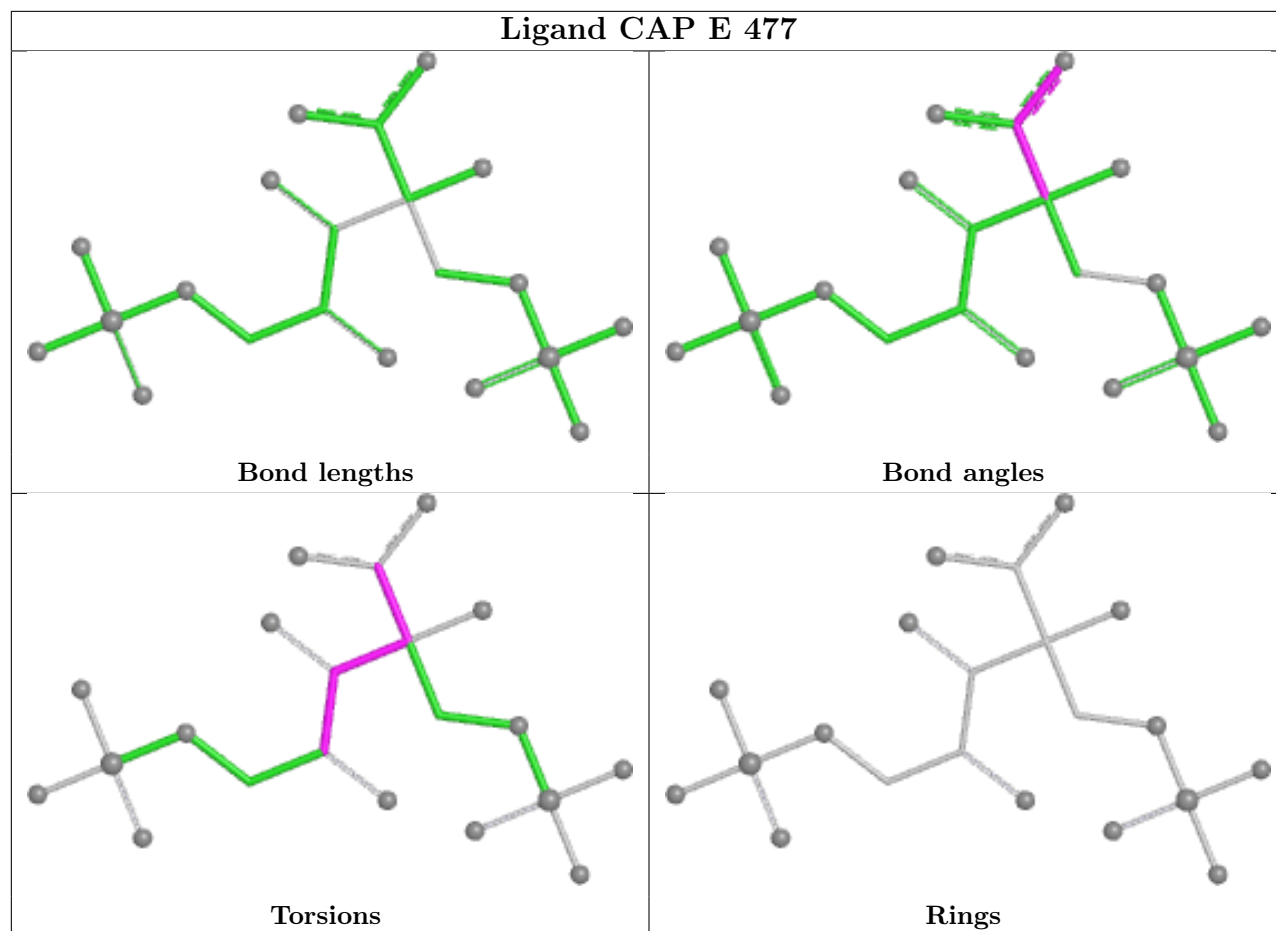
4 monomers are involved in 10 short contacts:

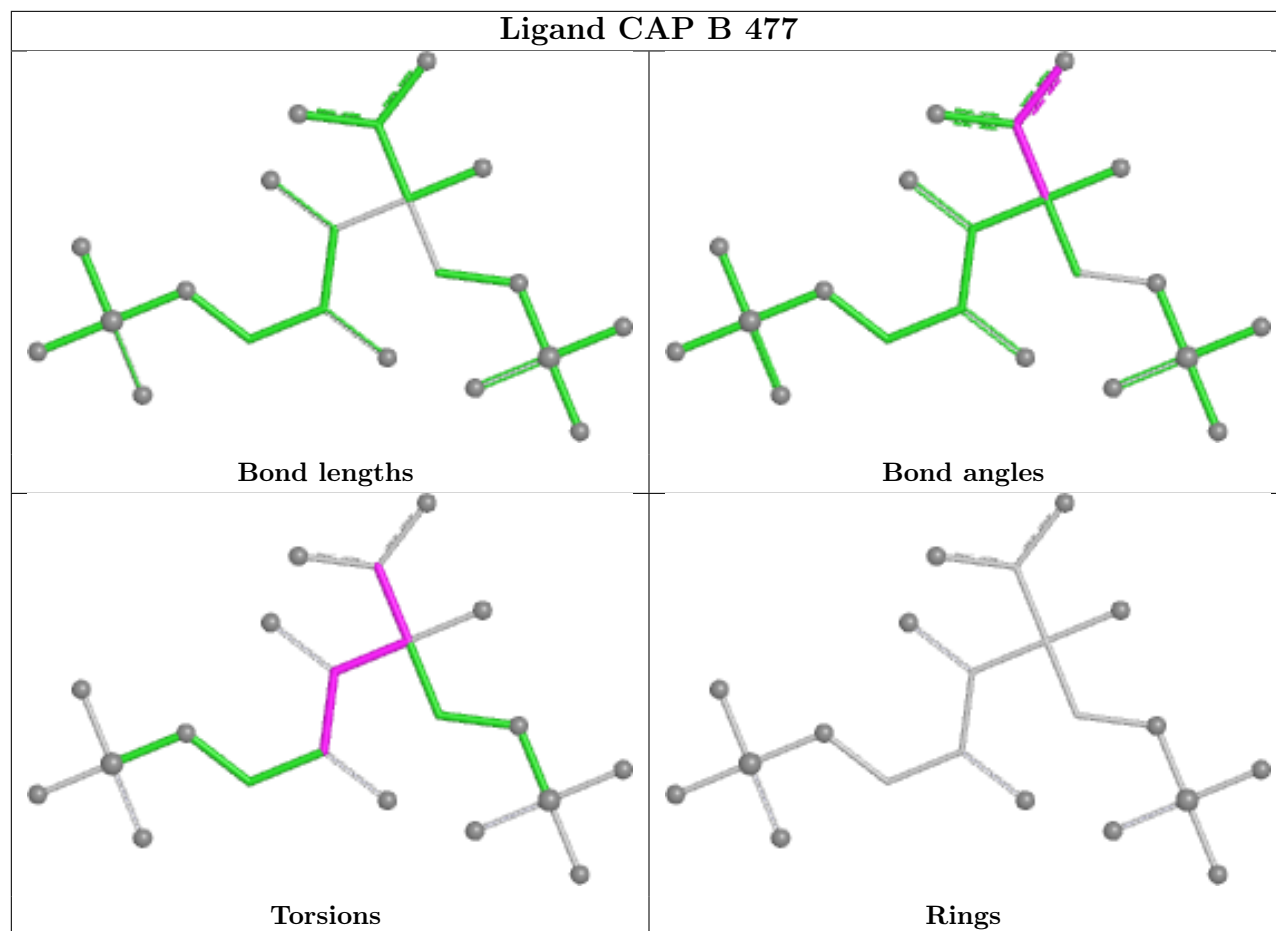
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1478	EDO	1	0
5	M	1142	EDO	3	0
5	L	1142	EDO	4	0
5	L	1141	EDO	2	0

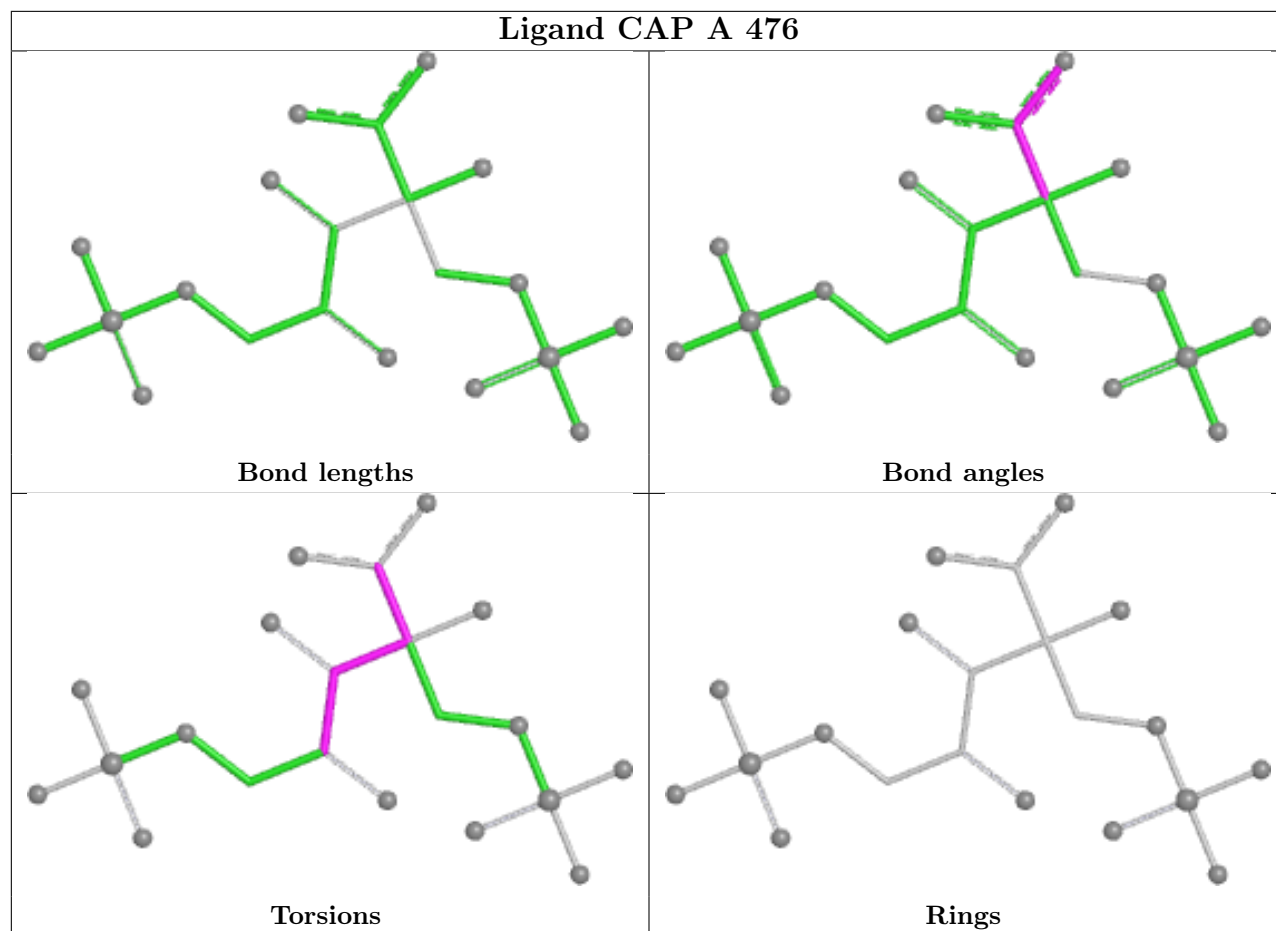
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

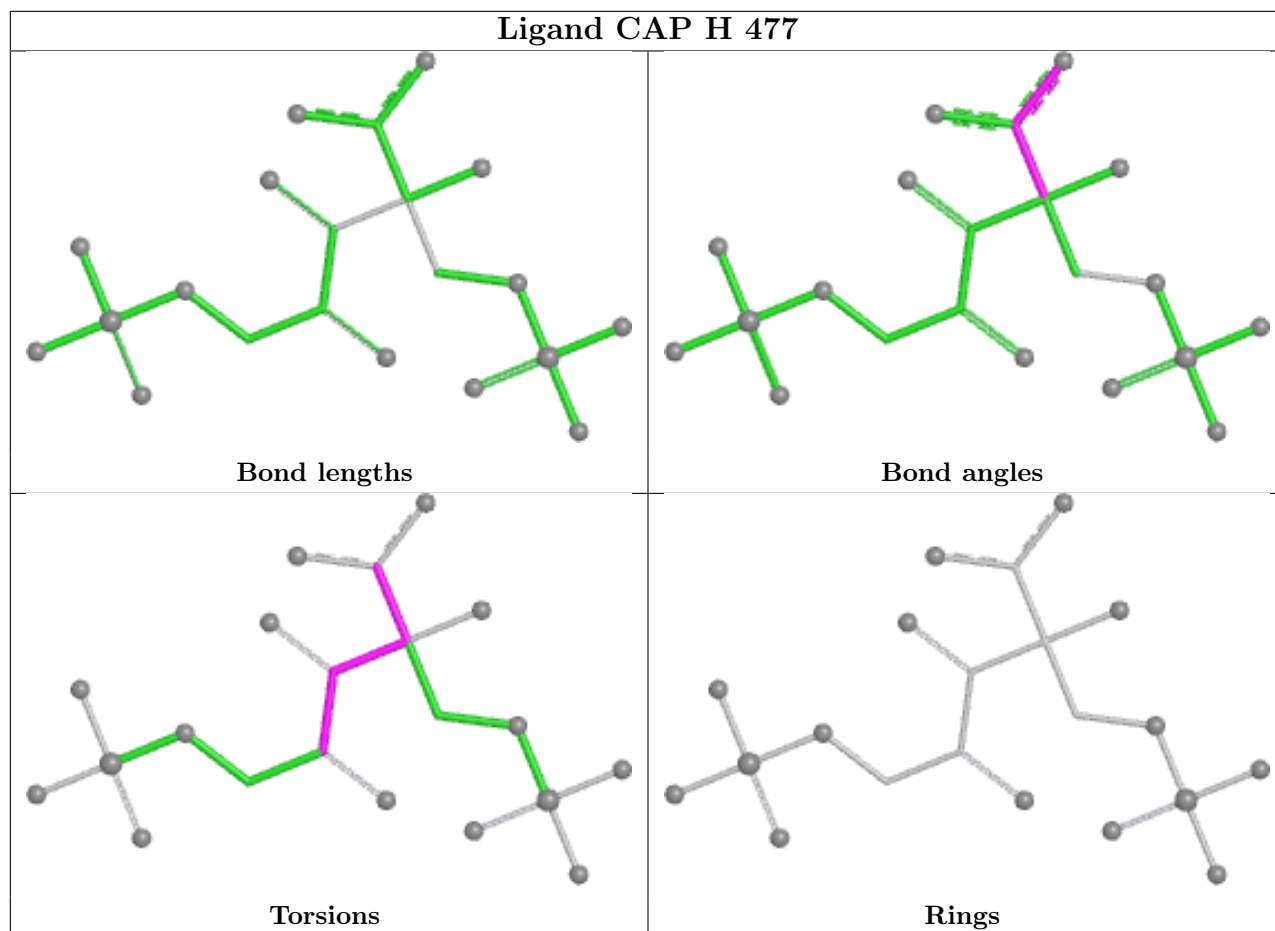
Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD 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.

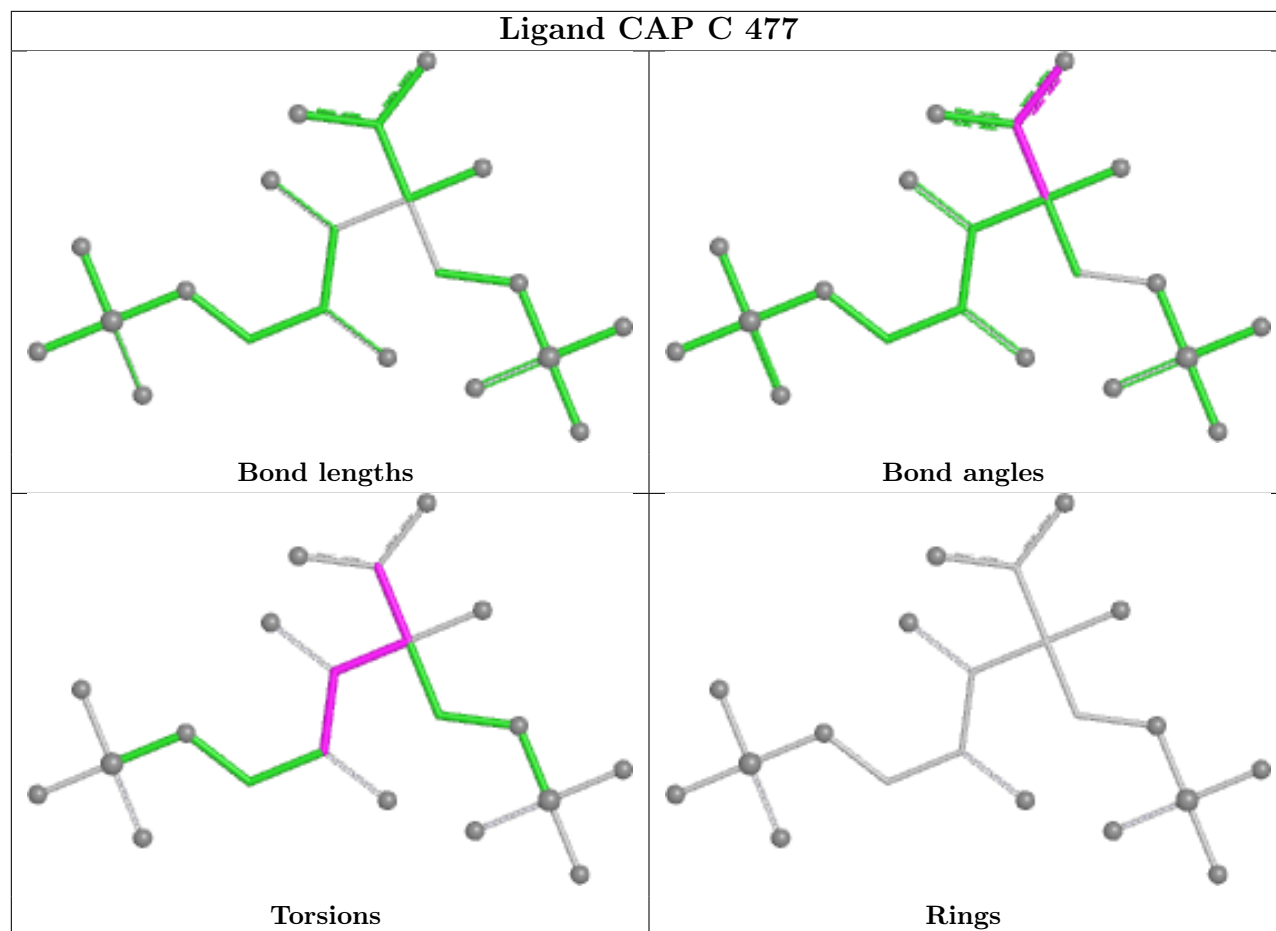


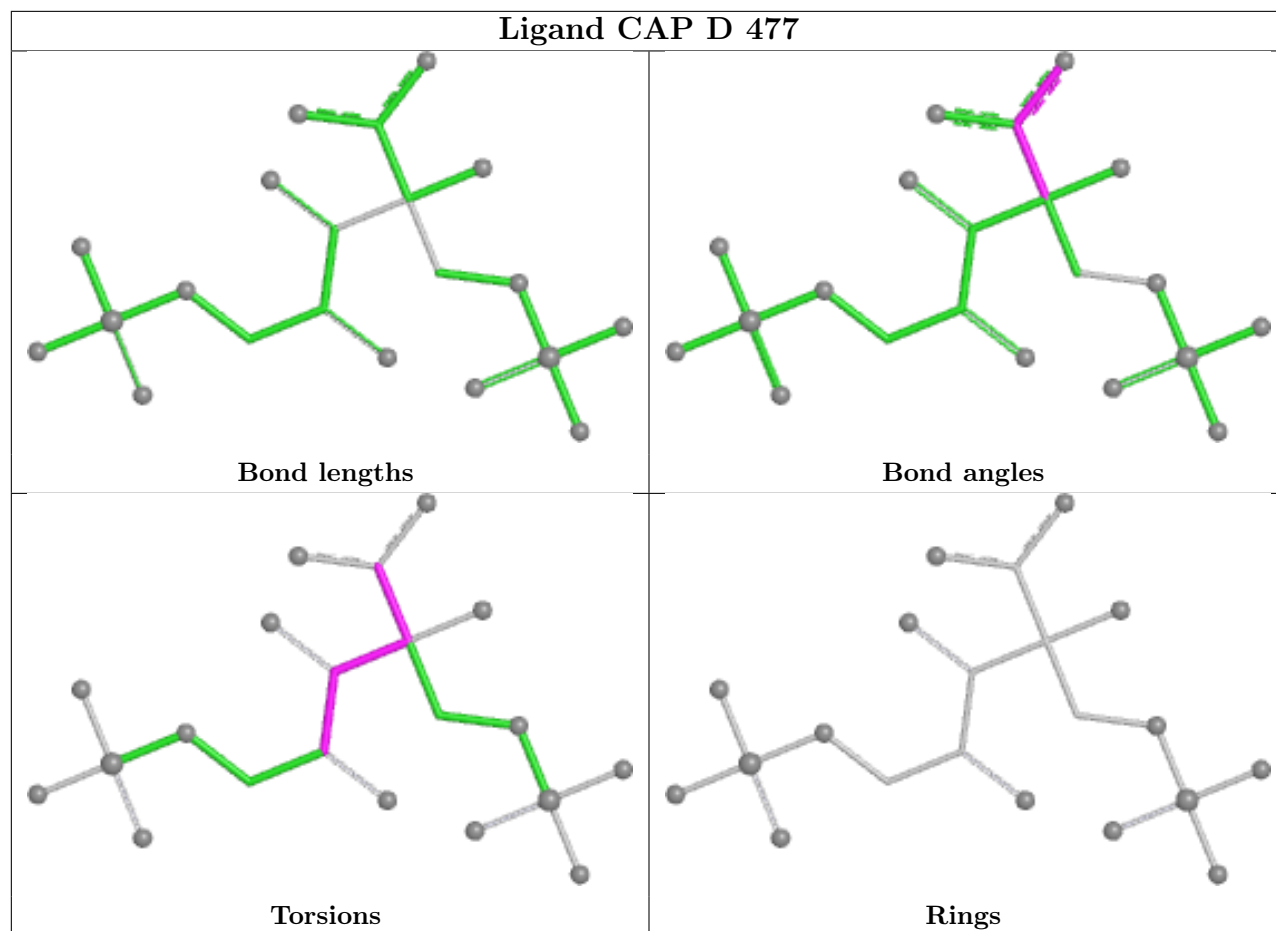


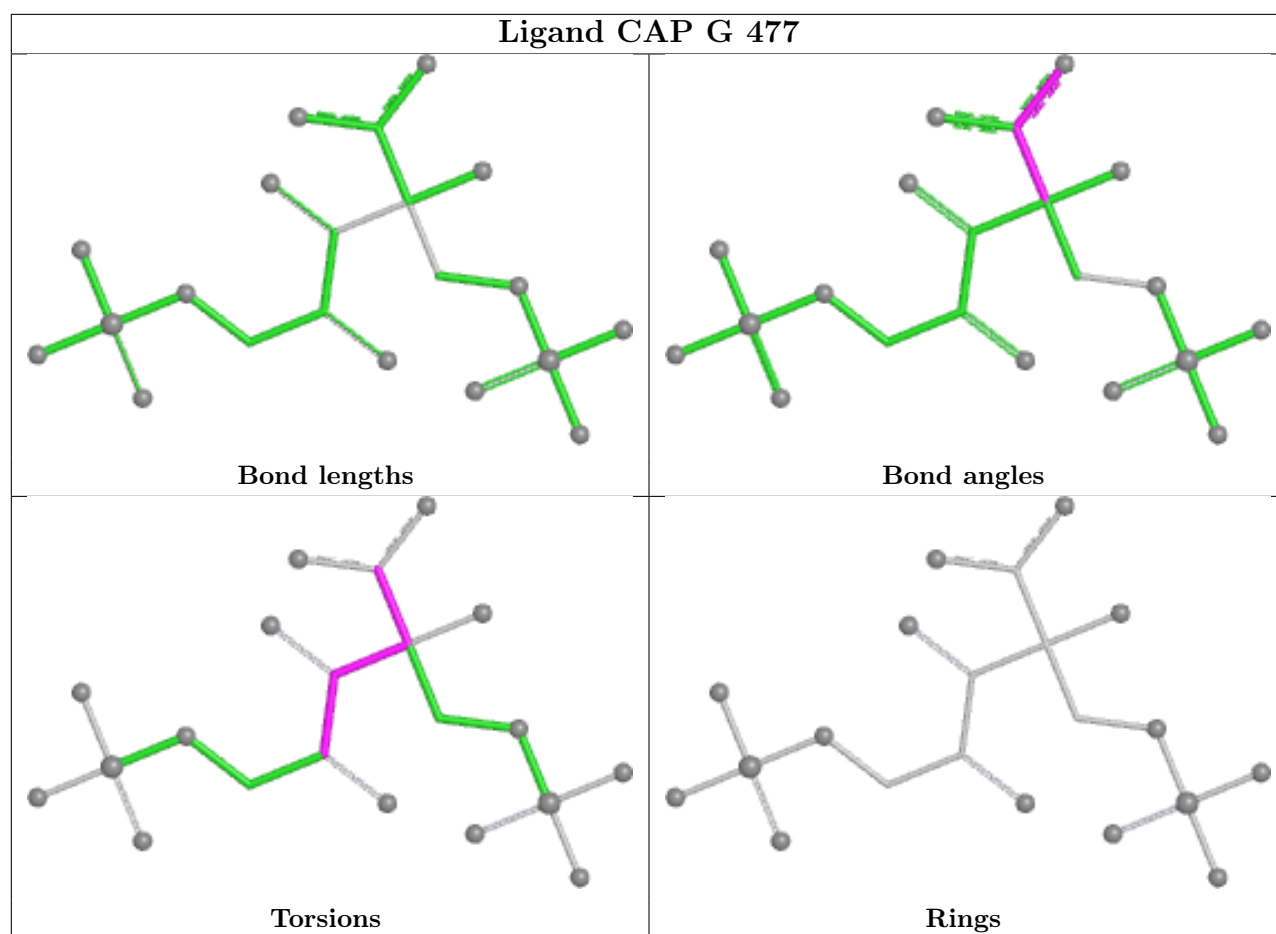












5.7 Other polymers [i](#)

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	461/475 (97%)	0.20	18 (3%) 43 43	5, 12, 25, 37	4 (0%)
1	B	461/475 (97%)	0.13	15 (3%) 49 49	5, 12, 25, 37	4 (0%)
1	C	461/475 (97%)	0.18	18 (3%) 43 43	5, 12, 25, 37	3 (0%)
1	D	459/475 (96%)	0.20	25 (5%) 31 30	5, 12, 25, 37	2 (0%)
1	E	459/475 (96%)	0.23	21 (4%) 37 36	5, 12, 25, 37	2 (0%)
1	F	461/475 (97%)	0.21	21 (4%) 37 36	5, 12, 26, 37	1 (0%)
1	G	461/475 (97%)	0.14	22 (4%) 35 34	5, 11, 25, 37	2 (0%)
1	H	461/475 (97%)	0.16	23 (4%) 34 33	5, 12, 25, 37	2 (0%)
2	I	139/140 (99%)	0.72	15 (10%) 11 9	9, 16, 28, 31	0
2	J	139/140 (99%)	0.55	8 (5%) 29 27	9, 17, 28, 31	1 (0%)
2	K	139/140 (99%)	0.50	4 (2%) 53 53	9, 16, 27, 31	1 (0%)
2	L	139/140 (99%)	0.57	9 (6%) 25 23	9, 16, 27, 31	0
2	M	139/140 (99%)	0.65	10 (7%) 21 20	9, 16, 26, 31	2 (1%)
2	N	139/140 (99%)	0.55	4 (2%) 53 53	10, 17, 30, 32	1 (0%)
2	O	139/140 (99%)	0.51	8 (5%) 29 27	9, 16, 28, 31	1 (0%)
2	P	139/140 (99%)	0.56	6 (4%) 40 39	10, 17, 27, 31	0
All	All	4796/4920 (97%)	0.27	227 (4%) 36 35	5, 13, 26, 37	26 (0%)

The worst 5 of 227 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	127	PHE	4.8
1	E	93	GLU	4.7
1	A	94	ASP	4.6
1	C	11	ALA	4.5
1	E	92	GLY	4.4

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	K	1	9/10	0.75	0.15	23,24,32,32	0
2	MME	L	1	9/10	0.84	0.17	23,24,32,32	0
2	MME	J	1	9/10	0.86	0.15	23,24,32,33	0
2	MME	N	1	9/10	0.88	0.12	23,24,32,32	0
2	MME	P	1	9/10	0.88	0.12	23,24,32,33	0
2	MME	I	1	9/10	0.89	0.12	23,24,32,33	0
2	MME	M	1	9/10	0.89	0.14	23,23,32,32	0
2	MME	O	1	9/10	0.90	0.12	23,24,32,33	0
1	SMC	G	369	7/8	0.90	0.11	11,12,16,17	0
1	SMC	B	369	7/8	0.91	0.11	11,12,16,16	0
1	SMC	H	369	7/8	0.92	0.09	11,12,16,17	0
1	SMC	C	369	7/8	0.92	0.10	11,12,17,17	0
1	SMC	A	369	7/8	0.92	0.09	11,12,16,17	0
1	SMC	D	369	7/8	0.93	0.09	11,12,16,17	0
1	SMC	F	369	7/8	0.93	0.09	11,12,16,17	0
1	HYP	D	151	8/9	0.93	0.06	9,9,9,9	0
1	HYP	A	151	8/9	0.94	0.07	8,9,9,9	0
1	HYP	E	104	8/9	0.94	0.06	8,9,9,9	0
1	HYP	E	151	8/9	0.94	0.07	8,9,9,9	0
1	KCX	E	201	12/13	0.94	0.07	7,9,10,10	0
1	SMC	E	369	7/8	0.94	0.09	11,12,16,17	0
1	HYP	F	104	8/9	0.94	0.07	8,8,9,10	0
1	HYP	D	104	8/9	0.94	0.07	8,8,9,10	0
1	KCX	A	201	12/13	0.94	0.07	8,9,10,11	0
1	HYP	H	151	8/9	0.94	0.07	8,9,9,9	0
1	HYP	C	151	8/9	0.95	0.06	8,9,9,9	0
1	HYP	F	151	8/9	0.95	0.06	9,9,9,9	0
1	KCX	F	201	12/13	0.95	0.06	8,9,10,11	0
1	KCX	C	201	12/13	0.95	0.06	7,9,10,10	0
1	HYP	G	104	8/9	0.95	0.06	8,8,8,9	0
1	KCX	G	201	12/13	0.95	0.07	7,9,10,11	0
1	KCX	D	201	12/13	0.95	0.06	8,9,10,11	0
1	HYP	H	104	8/9	0.95	0.06	8,8,8,9	0
1	KCX	B	201	12/13	0.95	0.06	7,9,10,11	0
1	HYP	B	104	8/9	0.96	0.06	8,8,9,9	0
1	HYP	C	104	8/9	0.96	0.05	8,8,9,10	0
1	KCX	H	201	12/13	0.96	0.06	8,9,10,11	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	HYP	G	151	8/9	0.96	0.06	8,9,9,9	0
1	HYP	B	151	8/9	0.96	0.07	8,9,9,9	0
1	HYP	A	104	8/9	0.96	0.06	8,8,9,9	0
1	SMC	B	256	7/8	0.97	0.06	6,6,7,8	0
1	SMC	E	256	7/8	0.97	0.06	6,6,7,8	0
1	SMC	H	256	7/8	0.97	0.06	5,5,7,8	0
1	SMC	A	256	7/8	0.97	0.06	5,5,7,8	0
1	SMC	D	256	7/8	0.98	0.05	6,6,7,8	0
1	SMC	G	256	7/8	0.98	0.06	5,6,7,8	0
1	SMC	C	256	7/8	0.98	0.05	5,5,7,9	0
1	SMC	F	256	7/8	0.98	0.05	6,6,7,9	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(\AA^2)	Q<0.9
5	EDO	C	1477	4/4	0.59	0.37	29,29,29,29	4
5	EDO	I	1141	4/4	0.62	0.26	19,20,20,20	4
5	EDO	H	1476	4/4	0.63	0.19	36,37,38,38	0
5	EDO	F	1476	4/4	0.64	0.22	17,17,17,18	4
5	EDO	D	1478	4/4	0.67	0.26	22,22,23,24	4
5	EDO	M	1141	4/4	0.67	0.23	22,23,23,24	4
5	EDO	L	1142	4/4	0.70	0.28	25,25,26,26	4
5	EDO	H	1478	4/4	0.71	0.26	49,50,51,51	0
5	EDO	C	1479	4/4	0.71	0.27	46,47,47,47	0
5	EDO	G	1480	4/4	0.71	0.20	41,42,42,42	0
5	EDO	A	1478	4/4	0.71	0.17	35,36,36,36	0
5	EDO	E	1477	4/4	0.72	0.18	50,51,51,52	0
5	EDO	G	1478	4/4	0.72	0.23	41,43,43,45	0
5	EDO	B	1477	4/4	0.73	0.23	51,51,52,52	0
5	EDO	J	1141	4/4	0.74	0.19	43,43,43,44	0
5	EDO	L	1141	4/4	0.74	0.21	38,38,39,39	1
5	EDO	O	1141	4/4	0.74	0.20	33,33,33,34	0

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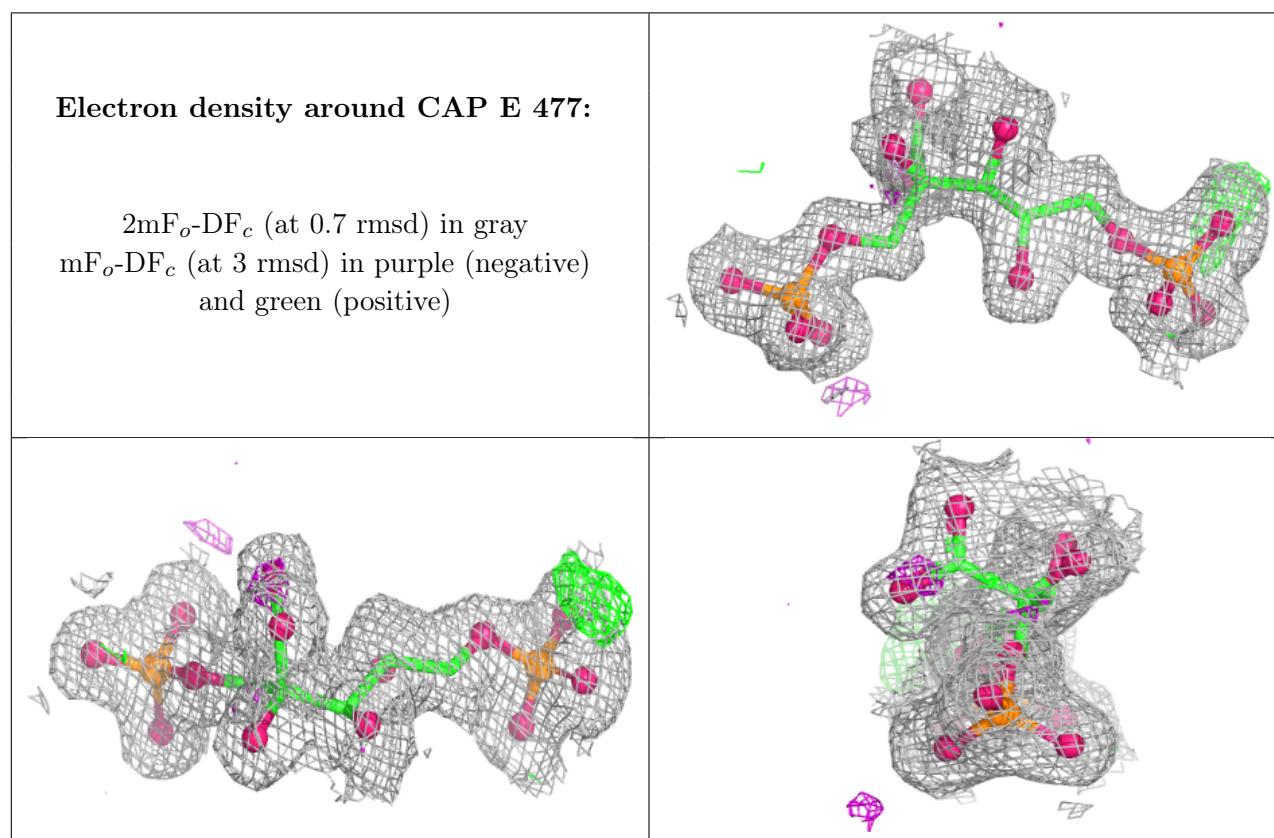
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	M	1142	4/4	0.76	0.18	18,18,18,19	4
5	EDO	K	1142	4/4	0.77	0.18	36,37,37,38	0
5	EDO	E	1475	4/4	0.77	0.18	31,31,32,32	0
5	EDO	P	1141	4/4	0.78	0.16	36,37,37,37	0
5	EDO	N	1142	4/4	0.79	0.17	28,29,31,32	0
5	EDO	B	1475	4/4	0.80	0.17	17,19,21,21	0
5	EDO	D	1476	4/4	0.80	0.15	38,38,39,39	0
5	EDO	N	1141	4/4	0.81	0.16	40,40,40,40	0
5	EDO	B	1478	4/4	0.81	0.15	30,32,32,32	0
5	EDO	G	1479	4/4	0.82	0.17	8,11,11,13	4
5	EDO	A	1479	4/4	0.83	0.16	37,38,38,39	0
5	EDO	C	1478	4/4	0.83	0.16	26,27,27,27	0
5	EDO	E	1476	4/4	0.85	0.12	25,26,27,27	0
5	EDO	G	1475	4/4	0.85	0.14	19,20,22,22	0
5	EDO	F	1475	4/4	0.85	0.11	23,24,25,25	0
5	EDO	A	1480	4/4	0.86	0.13	26,26,27,27	0
5	EDO	K	1141	4/4	0.88	0.13	33,33,33,34	0
5	EDO	C	1476	4/4	0.88	0.13	12,13,15,15	4
5	EDO	D	1475	4/4	0.90	0.09	21,21,21,22	0
5	EDO	D	1477	4/4	0.90	0.12	21,22,23,24	0
5	EDO	H	1477	4/4	0.91	0.09	21,23,23,23	0
5	EDO	O	1142	4/4	0.91	0.09	24,24,25,25	0
5	EDO	G	1476	4/4	0.91	0.09	20,20,21,22	0
5	EDO	J	1142	4/4	0.92	0.08	23,24,25,26	0
5	EDO	C	1475	4/4	0.92	0.08	19,19,20,21	0
5	EDO	A	1477	4/4	0.92	0.07	19,19,19,20	0
5	EDO	B	1476	4/4	0.93	0.09	18,19,20,20	0
5	EDO	G	1477	4/4	0.93	0.08	25,25,26,27	0
5	EDO	H	1475	4/4	0.95	0.06	19,19,20,20	0
3	CAP	E	477	21/21	0.95	0.07	10,13,15,17	0
3	CAP	F	477	21/21	0.96	0.06	11,13,15,17	0
3	CAP	H	477	21/21	0.96	0.07	9,13,14,17	0
3	CAP	D	477	21/21	0.96	0.06	10,13,15,17	0
3	CAP	A	476	21/21	0.96	0.07	10,13,14,17	0
3	CAP	G	477	21/21	0.97	0.06	10,13,14,16	0
3	CAP	C	477	21/21	0.97	0.06	10,13,14,16	0
4	MG	A	477	1/1	0.97	0.02	9,9,9,9	0
4	MG	D	476	1/1	0.97	0.03	9,9,9,9	0
4	MG	E	476	1/1	0.97	0.04	10,10,10,10	0
4	MG	F	476	1/1	0.97	0.03	10,10,10,10	0
4	MG	G	476	1/1	0.97	0.04	8,8,8,8	0
4	MG	H	476	1/1	0.97	0.02	9,9,9,9	0

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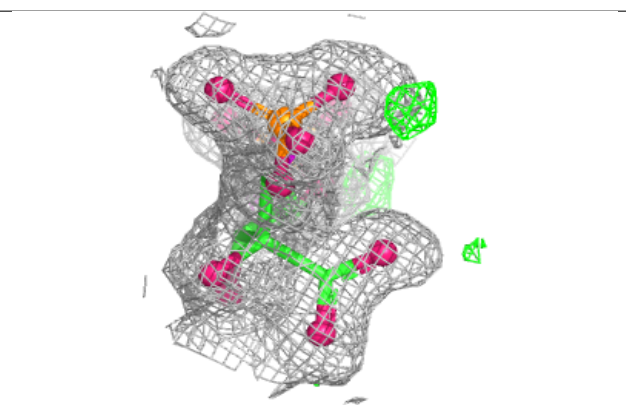
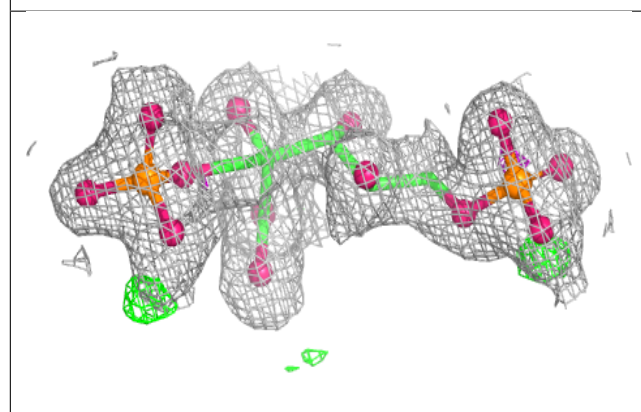
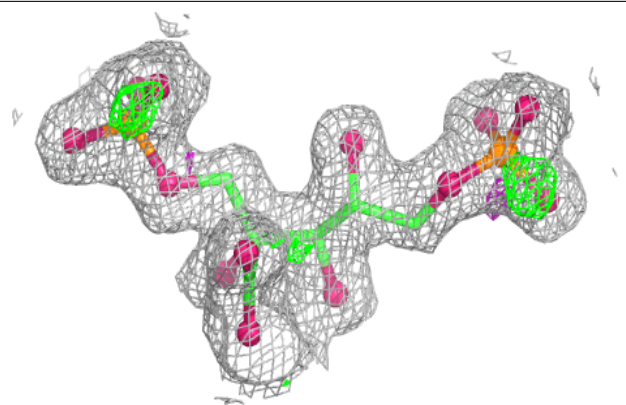
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CAP	B	477	21/21	0.97	0.05	10,13,14,17	0
4	MG	C	476	1/1	0.98	0.02	9,9,9,9	0
4	MG	B	476	1/1	0.99	0.02	9,9,9,9	0

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.

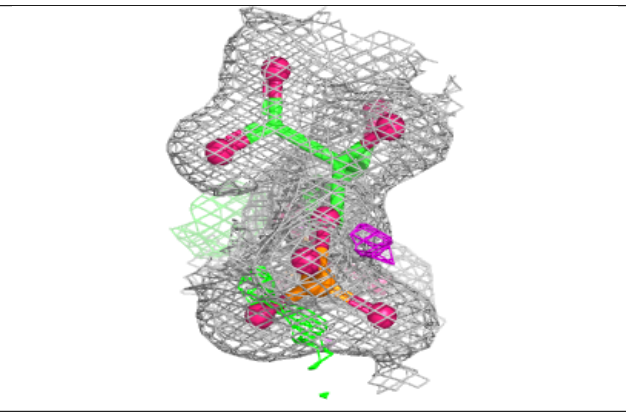
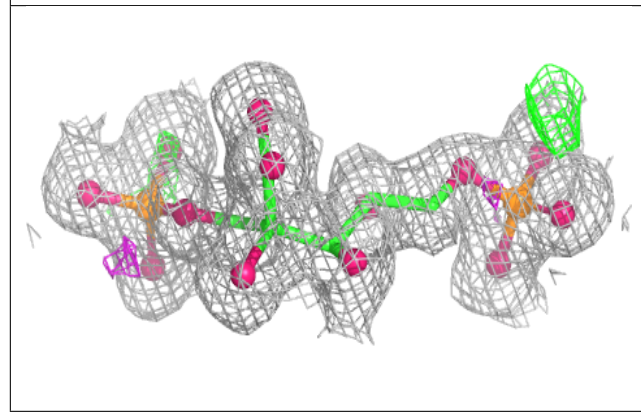
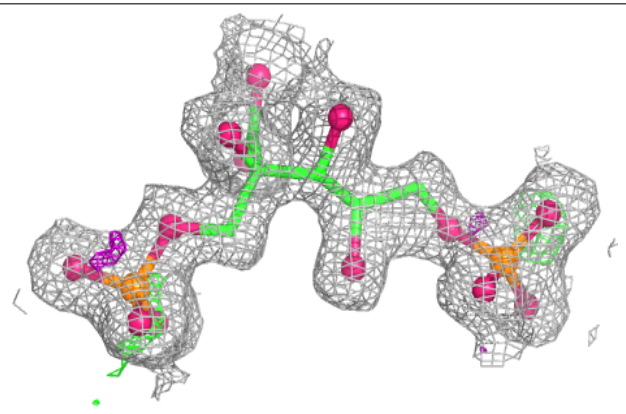


Electron density around CAP F 477:

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

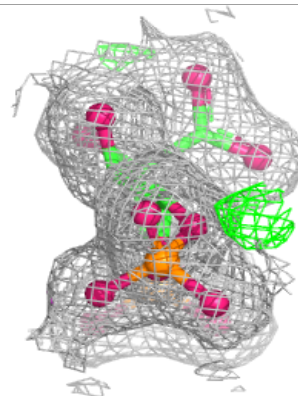
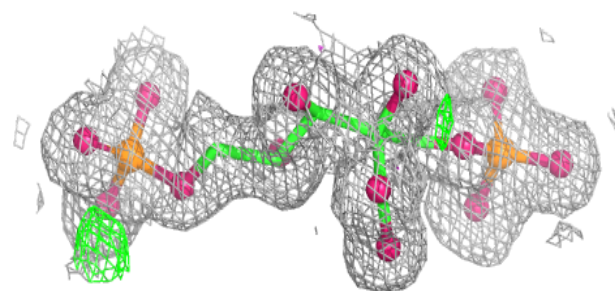
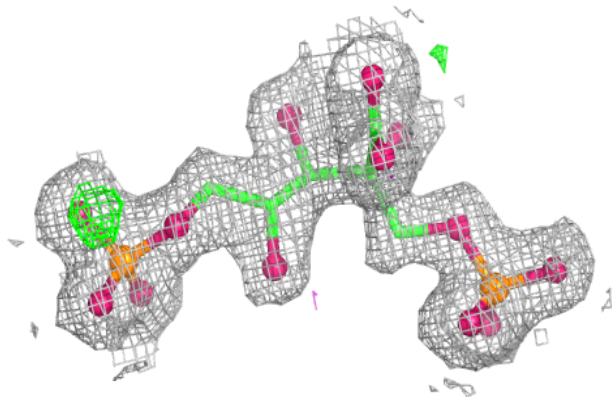
**Electron density around CAP H 477:**

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

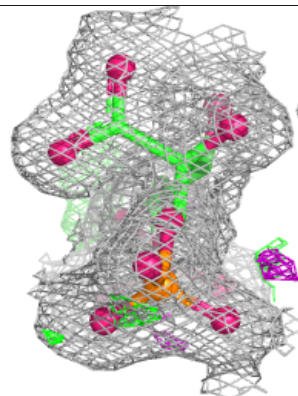
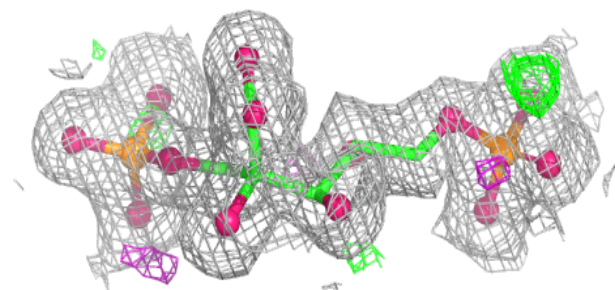
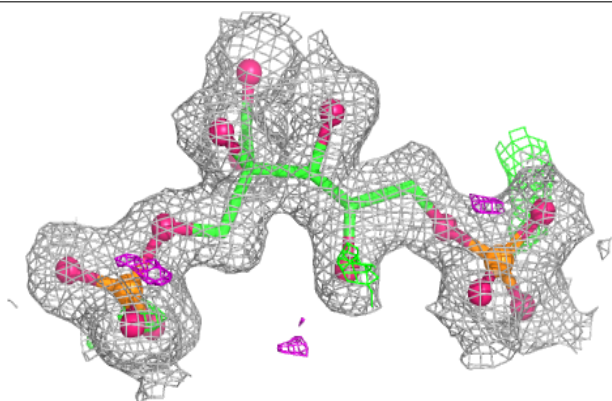


Electron density around CAP D 477:

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

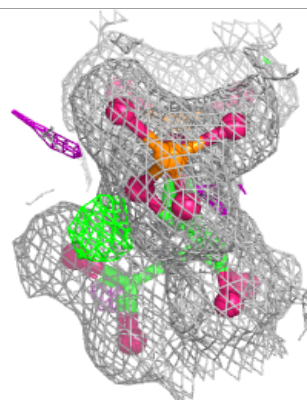
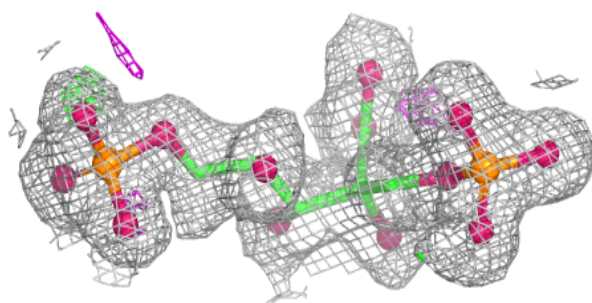
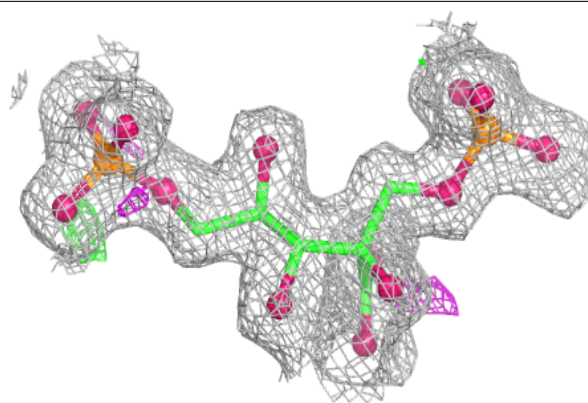
**Electron density around CAP A 476:**

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

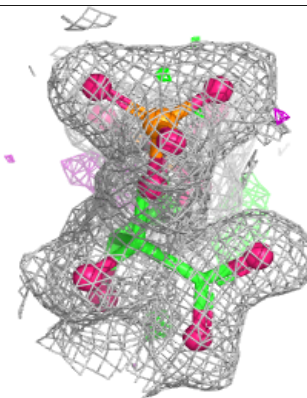
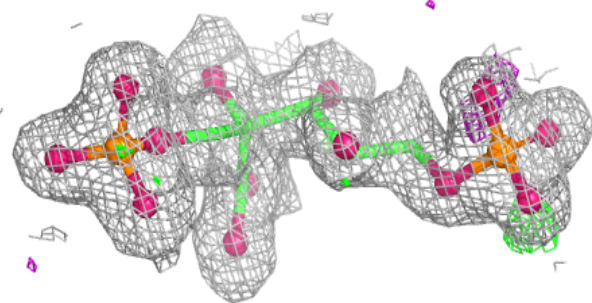
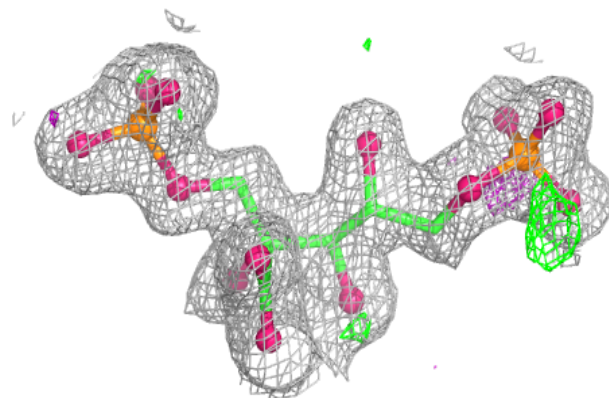


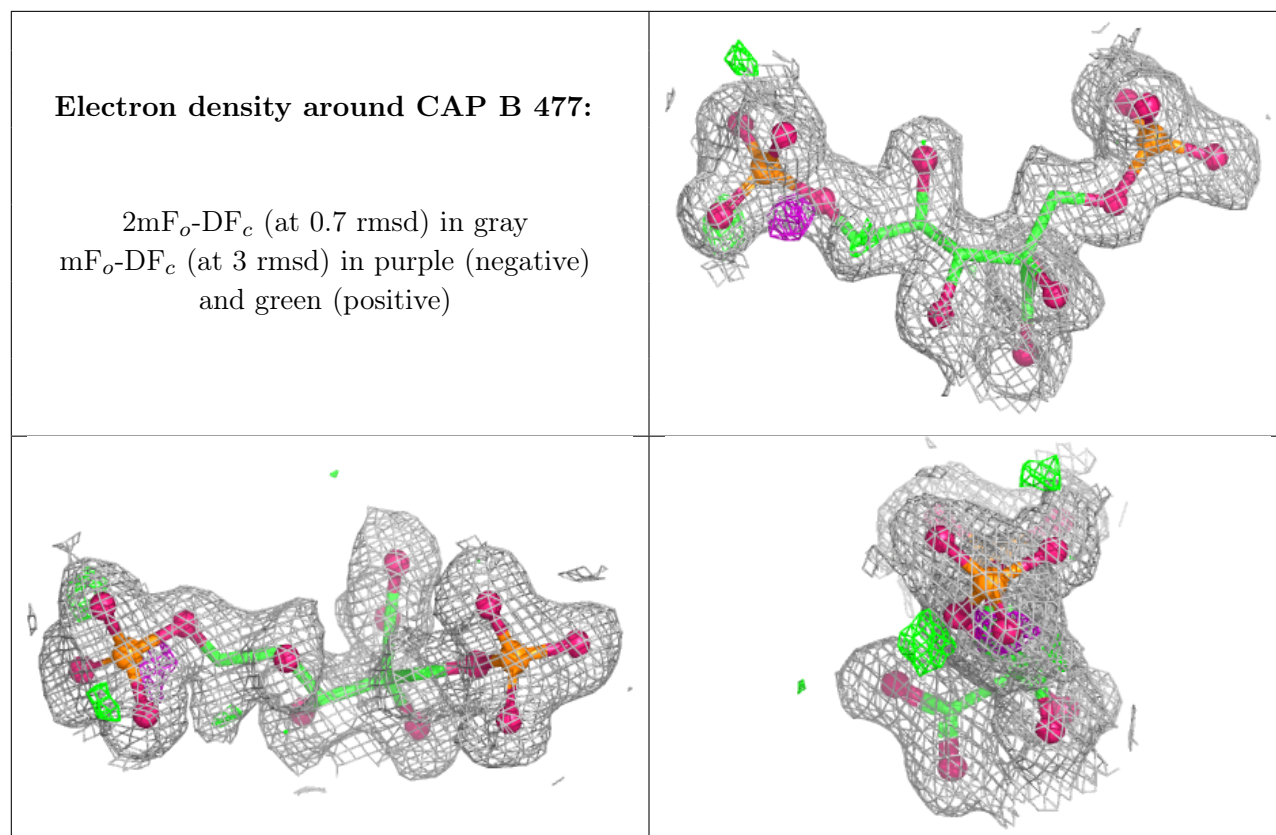
Electron density around CAP G 477:

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

**Electron density around CAP C 477:**

$2mF_o-DF_c$ (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.