



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:45 pm BST

PDB ID : 5HAO
Title : Structure function studies of R. palustris RubisCO (M331A mutant; CABP-bound)
Authors : Arbing, M.A.; Shin, A.; Satagopan, S.; North, J.A.; Tabita, F.R.
Deposited on : 2015-12-30
Resolution : 2.18 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

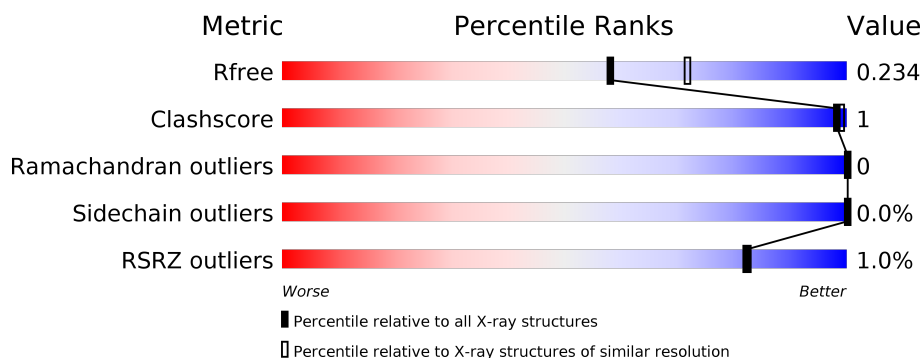
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	481	<div> <div style="width: 92%;"></div> <div>92%</div> <div>5%</div> </div>
1	B	481	<div> <div style="width: 94%;"></div> <div>94%</div> <div>5%</div> </div>
1	C	481	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>
1	D	481	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>
1	E	481	<div> <div style="width: 92%;"></div> <div>92%</div> <div>5%</div> </div>
1	F	481	<div> <div style="width: 93%;"></div> <div>93%</div> <div>5%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 42545 atoms, of which 20339 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 biphosphate carboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	455	Total	C	H	N	O	S	0	0	0
			6897	2233	3381	610	655	18			
1	B	455	Total	C	H	N	O	S	0	0	0
			6895	2233	3379	610	655	18			
1	C	455	Total	C	H	N	O	S	0	0	0
			6896	2233	3380	610	655	18			
1	D	455	Total	C	H	N	O	S	0	0	0
			6898	2233	3382	610	655	18			
1	E	455	Total	C	H	N	O	S	0	0	0
			6897	2233	3381	610	655	18			
1	F	455	Total	C	H	N	O	S	0	0	0
			6898	2233	3382	610	655	18			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q6N0W9
A	-18	GLY	-	expression tag	UNP Q6N0W9
A	-17	SER	-	expression tag	UNP Q6N0W9
A	-16	SER	-	expression tag	UNP Q6N0W9
A	-15	HIS	-	expression tag	UNP Q6N0W9
A	-14	HIS	-	expression tag	UNP Q6N0W9
A	-13	HIS	-	expression tag	UNP Q6N0W9
A	-12	HIS	-	expression tag	UNP Q6N0W9
A	-11	HIS	-	expression tag	UNP Q6N0W9
A	-10	HIS	-	expression tag	UNP Q6N0W9
A	-9	SER	-	expression tag	UNP Q6N0W9
A	-8	SER	-	expression tag	UNP Q6N0W9
A	-7	GLY	-	expression tag	UNP Q6N0W9
A	-6	LEU	-	expression tag	UNP Q6N0W9
A	-5	VAL	-	expression tag	UNP Q6N0W9
A	-4	PRO	-	expression tag	UNP Q6N0W9
A	-3	ARG	-	expression tag	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q6N0W9
A	-1	SER	-	expression tag	UNP Q6N0W9
A	0	HIS	-	expression tag	UNP Q6N0W9
A	331	ALA	MET	engineered mutation	UNP Q6N0W9
B	-19	MET	-	initiating methionine	UNP Q6N0W9
B	-18	GLY	-	expression tag	UNP Q6N0W9
B	-17	SER	-	expression tag	UNP Q6N0W9
B	-16	SER	-	expression tag	UNP Q6N0W9
B	-15	HIS	-	expression tag	UNP Q6N0W9
B	-14	HIS	-	expression tag	UNP Q6N0W9
B	-13	HIS	-	expression tag	UNP Q6N0W9
B	-12	HIS	-	expression tag	UNP Q6N0W9
B	-11	HIS	-	expression tag	UNP Q6N0W9
B	-10	HIS	-	expression tag	UNP Q6N0W9
B	-9	SER	-	expression tag	UNP Q6N0W9
B	-8	SER	-	expression tag	UNP Q6N0W9
B	-7	GLY	-	expression tag	UNP Q6N0W9
B	-6	LEU	-	expression tag	UNP Q6N0W9
B	-5	VAL	-	expression tag	UNP Q6N0W9
B	-4	PRO	-	expression tag	UNP Q6N0W9
B	-3	ARG	-	expression tag	UNP Q6N0W9
B	-2	GLY	-	expression tag	UNP Q6N0W9
B	-1	SER	-	expression tag	UNP Q6N0W9
B	0	HIS	-	expression tag	UNP Q6N0W9
B	331	ALA	MET	engineered mutation	UNP Q6N0W9
C	-19	MET	-	initiating methionine	UNP Q6N0W9
C	-18	GLY	-	expression tag	UNP Q6N0W9
C	-17	SER	-	expression tag	UNP Q6N0W9
C	-16	SER	-	expression tag	UNP Q6N0W9
C	-15	HIS	-	expression tag	UNP Q6N0W9
C	-14	HIS	-	expression tag	UNP Q6N0W9
C	-13	HIS	-	expression tag	UNP Q6N0W9
C	-12	HIS	-	expression tag	UNP Q6N0W9
C	-11	HIS	-	expression tag	UNP Q6N0W9
C	-10	HIS	-	expression tag	UNP Q6N0W9
C	-9	SER	-	expression tag	UNP Q6N0W9
C	-8	SER	-	expression tag	UNP Q6N0W9
C	-7	GLY	-	expression tag	UNP Q6N0W9
C	-6	LEU	-	expression tag	UNP Q6N0W9
C	-5	VAL	-	expression tag	UNP Q6N0W9
C	-4	PRO	-	expression tag	UNP Q6N0W9
C	-3	ARG	-	expression tag	UNP Q6N0W9

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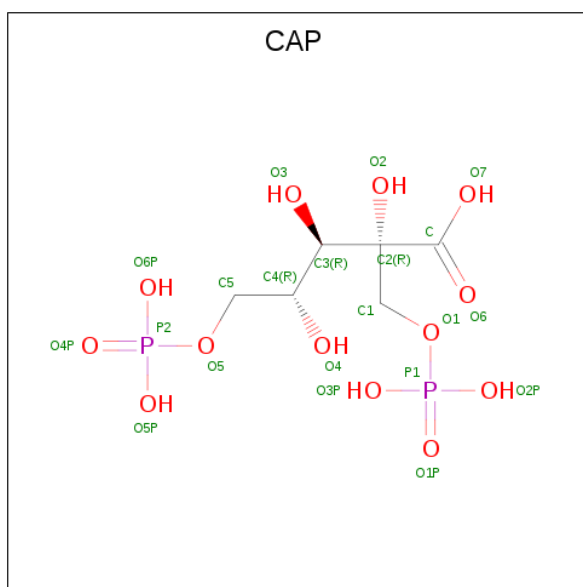
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q6N0W9
C	-1	SER	-	expression tag	UNP Q6N0W9
C	0	HIS	-	expression tag	UNP Q6N0W9
C	331	ALA	MET	engineered mutation	UNP Q6N0W9
D	-19	MET	-	initiating methionine	UNP Q6N0W9
D	-18	GLY	-	expression tag	UNP Q6N0W9
D	-17	SER	-	expression tag	UNP Q6N0W9
D	-16	SER	-	expression tag	UNP Q6N0W9
D	-15	HIS	-	expression tag	UNP Q6N0W9
D	-14	HIS	-	expression tag	UNP Q6N0W9
D	-13	HIS	-	expression tag	UNP Q6N0W9
D	-12	HIS	-	expression tag	UNP Q6N0W9
D	-11	HIS	-	expression tag	UNP Q6N0W9
D	-10	HIS	-	expression tag	UNP Q6N0W9
D	-9	SER	-	expression tag	UNP Q6N0W9
D	-8	SER	-	expression tag	UNP Q6N0W9
D	-7	GLY	-	expression tag	UNP Q6N0W9
D	-6	LEU	-	expression tag	UNP Q6N0W9
D	-5	VAL	-	expression tag	UNP Q6N0W9
D	-4	PRO	-	expression tag	UNP Q6N0W9
D	-3	ARG	-	expression tag	UNP Q6N0W9
D	-2	GLY	-	expression tag	UNP Q6N0W9
D	-1	SER	-	expression tag	UNP Q6N0W9
D	0	HIS	-	expression tag	UNP Q6N0W9
D	331	ALA	MET	engineered mutation	UNP Q6N0W9
E	-19	MET	-	initiating methionine	UNP Q6N0W9
E	-18	GLY	-	expression tag	UNP Q6N0W9
E	-17	SER	-	expression tag	UNP Q6N0W9
E	-16	SER	-	expression tag	UNP Q6N0W9
E	-15	HIS	-	expression tag	UNP Q6N0W9
E	-14	HIS	-	expression tag	UNP Q6N0W9
E	-13	HIS	-	expression tag	UNP Q6N0W9
E	-12	HIS	-	expression tag	UNP Q6N0W9
E	-11	HIS	-	expression tag	UNP Q6N0W9
E	-10	HIS	-	expression tag	UNP Q6N0W9
E	-9	SER	-	expression tag	UNP Q6N0W9
E	-8	SER	-	expression tag	UNP Q6N0W9
E	-7	GLY	-	expression tag	UNP Q6N0W9
E	-6	LEU	-	expression tag	UNP Q6N0W9
E	-5	VAL	-	expression tag	UNP Q6N0W9
E	-4	PRO	-	expression tag	UNP Q6N0W9
E	-3	ARG	-	expression tag	UNP Q6N0W9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP Q6N0W9
E	-1	SER	-	expression tag	UNP Q6N0W9
E	0	HIS	-	expression tag	UNP Q6N0W9
E	331	ALA	MET	engineered mutation	UNP Q6N0W9
F	-19	MET	-	initiating methionine	UNP Q6N0W9
F	-18	GLY	-	expression tag	UNP Q6N0W9
F	-17	SER	-	expression tag	UNP Q6N0W9
F	-16	SER	-	expression tag	UNP Q6N0W9
F	-15	HIS	-	expression tag	UNP Q6N0W9
F	-14	HIS	-	expression tag	UNP Q6N0W9
F	-13	HIS	-	expression tag	UNP Q6N0W9
F	-12	HIS	-	expression tag	UNP Q6N0W9
F	-11	HIS	-	expression tag	UNP Q6N0W9
F	-10	HIS	-	expression tag	UNP Q6N0W9
F	-9	SER	-	expression tag	UNP Q6N0W9
F	-8	SER	-	expression tag	UNP Q6N0W9
F	-7	GLY	-	expression tag	UNP Q6N0W9
F	-6	LEU	-	expression tag	UNP Q6N0W9
F	-5	VAL	-	expression tag	UNP Q6N0W9
F	-4	PRO	-	expression tag	UNP Q6N0W9
F	-3	ARG	-	expression tag	UNP Q6N0W9
F	-2	GLY	-	expression tag	UNP Q6N0W9
F	-1	SER	-	expression tag	UNP Q6N0W9
F	0	HIS	-	expression tag	UNP Q6N0W9
F	331	ALA	MET	engineered mutation	UNP Q6N0W9

- Molecule 2 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: $C_6H_{14}O_{13}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	B	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	C	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	D	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	E	1	Total	C	H	O	P	0	0
			30	6	9	13	2		
2	F	1	Total	C	H	O	P	0	0
			30	6	9	13	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

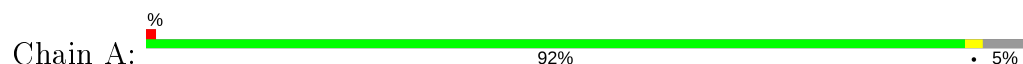
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	158	Total 158	O 158	0	0
4	B	193	Total 193	O 193	0	0
4	C	171	Total 171	O 171	0	0
4	D	142	Total 142	O 142	0	0
4	E	162	Total 162	O 162	0	0
4	F	152	Total 152	O 152	0	0

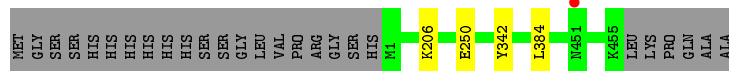
3 Residue-property plots [i](#)

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

- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



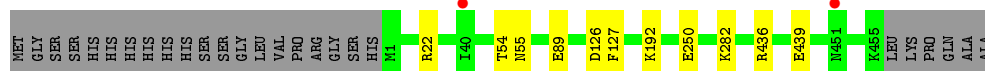
- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



MET	GLY	SER	SER	HIS	HIS	HIS	HIS	HIS	SER	SER	GLY	LEU	VAL	PRO	ARG	GLY	SER	HIS	P1	V56	E57	D126	F127	Q175	P176	K206	E250	Y342	L384	Q420	K447	L448	Y449	P450	H451	A454	K455	LEU	LYS	PRO	GLN	ALA	ALA
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.75Å 100.12Å 100.31Å 112.82° 108.14° 88.76°	Depositor
Resolution (Å)	91.69 – 2.18 91.69 – 2.18	Depositor EDS
% Data completeness (in resolution range)	91.4 (91.69-2.18) 91.4 (91.69-2.18)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.96 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.201 , 0.233 0.204 , 0.234	Depositor DCC
R_{free} test set	12200 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.135	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	42545	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CAP, KCX

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	0.24	0/3592	0.41	0/4861
1	B	0.24	0/3592	0.40	0/4861
1	C	0.24	0/3592	0.40	0/4861
1	D	0.24	0/3592	0.41	0/4861
1	E	0.23	0/3592	0.40	0/4861
1	F	0.23	0/3592	0.39	0/4861
All	All	0.24	0/21552	0.40	0/29166

There are no bond length outliers.

There are no bond angle outliers.

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	3516	3381	3386	6	0
1	B	3516	3379	3386	3	0
1	C	3516	3380	3386	4	0
1	D	3516	3382	3386	4	0
1	E	3516	3381	3386	7	0
1	F	3516	3382	3386	5	0
2	A	21	9	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	21	9	7	0	0
2	C	21	9	7	0	0
2	D	21	9	7	0	0
2	E	21	9	7	1	0
2	F	21	9	7	0	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
4	A	158	0	0	0	0
4	B	193	0	0	0	0
4	C	171	0	0	0	0
4	D	142	0	0	0	0
4	E	162	0	0	1	0
4	F	152	0	0	0	0
All	All	22206	20339	20359	24	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 1.

All (24) 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:B:206:LYS:NZ	1:F:250:GLU:OE2	2.20	0.72
1:D:250:GLU:OE1	1:F:206:LYS:NZ	2.22	0.72
1:A:206:LYS:NZ	1:C:250:GLU:OE2	2.17	0.72
1:C:206:LYS:NZ	1:E:250:GLU:OE2	2.30	0.52
1:B:250:GLU:OE1	1:D:206:LYS:NZ	2.24	0.51
1:F:342:TYR:OH	1:F:384:LEU:O	2.25	0.49
1:E:436:ARG:NH1	1:E:439:GLU:OE1	2.46	0.48
1:E:192:KCX:OQ1	2:E:500:CAP:O3	2.32	0.47
1:E:54:THR:OG1	1:E:55:ASN:N	2.46	0.45
1:E:22:ARG:NH2	1:E:89:GLU:OE2	2.49	0.44
1:D:126:ASP:OD1	1:D:127:PHE:N	2.51	0.43
1:E:126:ASP:OD1	1:E:127:PHE:N	2.51	0.43
1:A:381:PHE:HB3	1:A:418:TRP:CE2	2.53	0.43
1:A:175:GLN:HB3	1:A:176:PRO:HD3	2.01	0.42
1:A:54:THR:OG1	1:A:55:ASN:N	2.52	0.42
1:C:126:ASP:OD1	1:C:127:PHE:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:54:THR:OG1	1:D:55:ASN:N	2.50	0.41
1:A:145:LYS:HG3	1:A:155:VAL:HB	2.03	0.41
1:E:282:LYS:NZ	4:E:627:HOH:O	2.53	0.41
1:C:175:GLN:HB3	1:C:176:PRO:HD3	2.02	0.41
1:F:126:ASP:OD1	1:F:127:PHE:N	2.54	0.41
1:A:164:THR:HB	1:A:184:PHE:CE1	2.55	0.41
1:F:175:GLN:HB3	1:F:176:PRO:HD3	2.03	0.41
1:B:342:TYR:OH	1:B:384:LEU:O	2.26	0.40

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	452/481 (94%)	436 (96%)	16 (4%)	0	100	100
1	B	452/481 (94%)	435 (96%)	17 (4%)	0	100	100
1	C	452/481 (94%)	436 (96%)	16 (4%)	0	100	100
1	D	452/481 (94%)	435 (96%)	17 (4%)	0	100	100
1	E	452/481 (94%)	437 (97%)	15 (3%)	0	100	100
1	F	452/481 (94%)	437 (97%)	15 (3%)	0	100	100
All	All	2712/2886 (94%)	2616 (96%)	96 (4%)	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	350/371 (94%)	350 (100%)	0	100	100
1	B	350/371 (94%)	350 (100%)	0	100	100
1	C	350/371 (94%)	349 (100%)	1 (0%)	92	96
1	D	350/371 (94%)	350 (100%)	0	100	100
1	E	350/371 (94%)	350 (100%)	0	100	100
1	F	350/371 (94%)	350 (100%)	0	100	100
All	All	2100/2226 (94%)	2099 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	455	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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	KCX	B	192	1,3	7,11,12	0.64	0	4,12,14	0.44	0
1	KCX	D	192	1,3	7,11,12	0.70	0	4,12,14	0.50	0
1	KCX	F	192	1,3	7,11,12	0.63	0	4,12,14	0.26	0
1	KCX	C	192	1,3	7,11,12	0.68	0	4,12,14	0.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	KCX	A	192	1,3	7,11,12	0.67	0	4,12,14	0.64	0
1	KCX	E	192	1,3	7,11,12	0.67	0	4,12,14	0.51	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	KCX	B	192	1,3	-	1/7/10/12	-
1	KCX	D	192	1,3	-	2/7/10/12	-
1	KCX	F	192	1,3	-	1/7/10/12	-
1	KCX	C	192	1,3	-	0/7/10/12	-
1	KCX	A	192	1,3	-	1/7/10/12	-
1	KCX	E	192	1,3	-	1/7/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	192	KCX	O-C-CA-CB
1	D	192	KCX	C-CA-CB-CG
1	F	192	KCX	O-C-CA-CB
1	A	192	KCX	O-C-CA-CB
1	D	192	KCX	CE-CD-CG-CB
1	E	192	KCX	CG-CD-CE-NZ

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	192	KCX	1	0

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CAP	E	500	3	15,20,20	0.75	0	20,31,31	0.79	0
2	CAP	C	500	3	15,20,20	0.76	0	20,31,31	0.82	0
2	CAP	A	500	3	15,20,20	0.73	0	20,31,31	0.79	0
2	CAP	F	500	3	15,20,20	0.77	0	20,31,31	0.84	0
2	CAP	B	500	3	15,20,20	0.75	0	20,31,31	0.79	0
2	CAP	D	500	3	15,20,20	0.75	0	20,31,31	0.97	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
2	CAP	E	500	3	-	3/23/29/29	-
2	CAP	C	500	3	-	3/23/29/29	-
2	CAP	A	500	3	-	3/23/29/29	-
2	CAP	F	500	3	-	3/23/29/29	-
2	CAP	B	500	3	-	2/23/29/29	-
2	CAP	D	500	3	-	3/23/29/29	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	500	CAP	O3-C3-C4-O4
2	C	500	CAP	O3-C3-C4-O4

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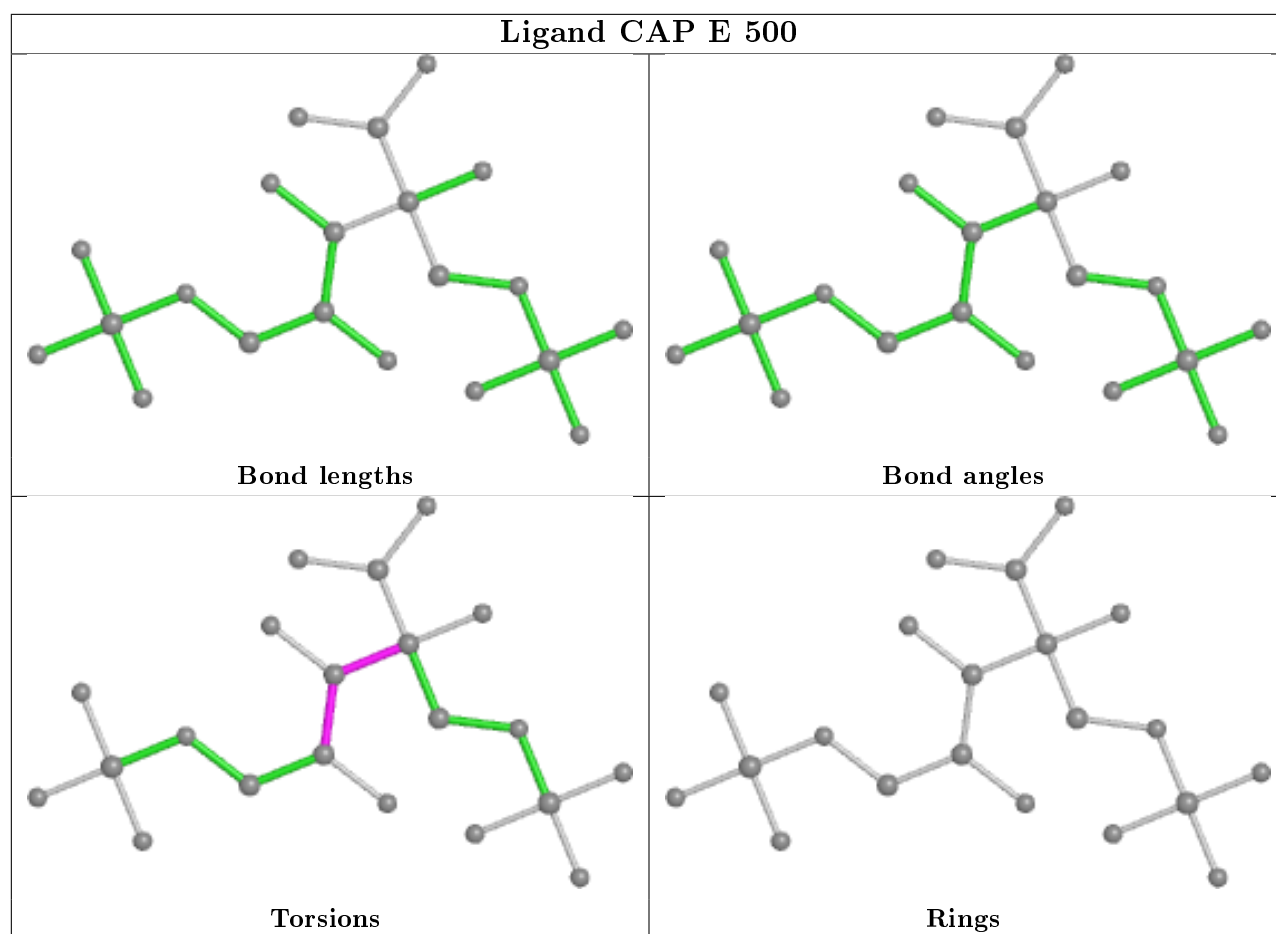
Mol	Chain	Res	Type	Atoms
2	A	500	CAP	O3-C3-C4-O4
2	F	500	CAP	O3-C3-C4-O4
2	B	500	CAP	O3-C3-C4-O4
2	D	500	CAP	C2-C3-C4-O4
2	D	500	CAP	O3-C3-C4-O4
2	E	500	CAP	O2-C2-C3-C4
2	C	500	CAP	O2-C2-C3-C4
2	A	500	CAP	O2-C2-C3-C4
2	F	500	CAP	O2-C2-C3-C4
2	B	500	CAP	O2-C2-C3-C4
2	D	500	CAP	O2-C2-C3-C4
2	F	500	CAP	C2-C3-C4-O4
2	A	500	CAP	O1-C1-C2-O2
2	E	500	CAP	C2-C3-C4-O4
2	C	500	CAP	C2-C3-C4-O4

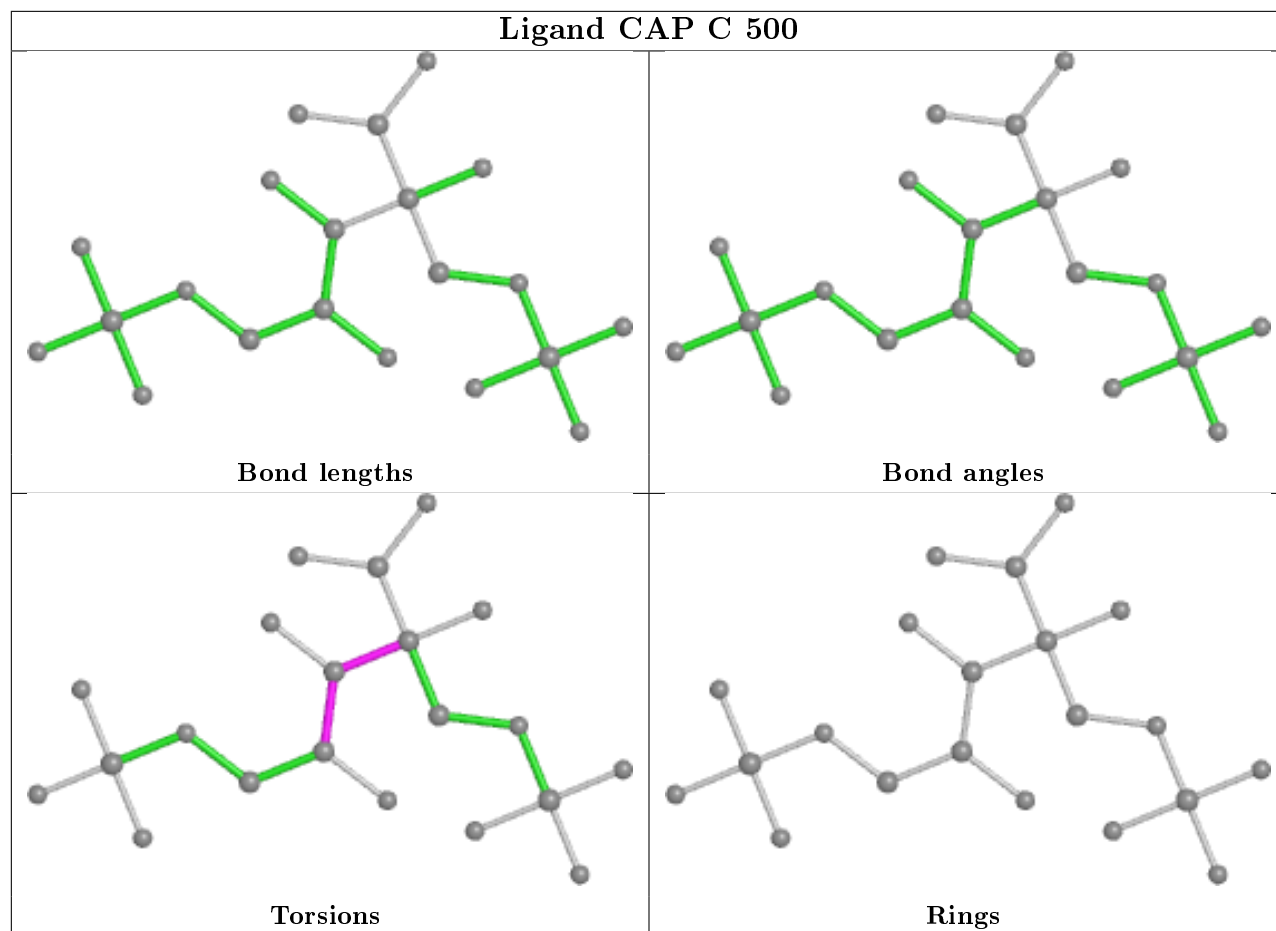
There are no ring outliers.

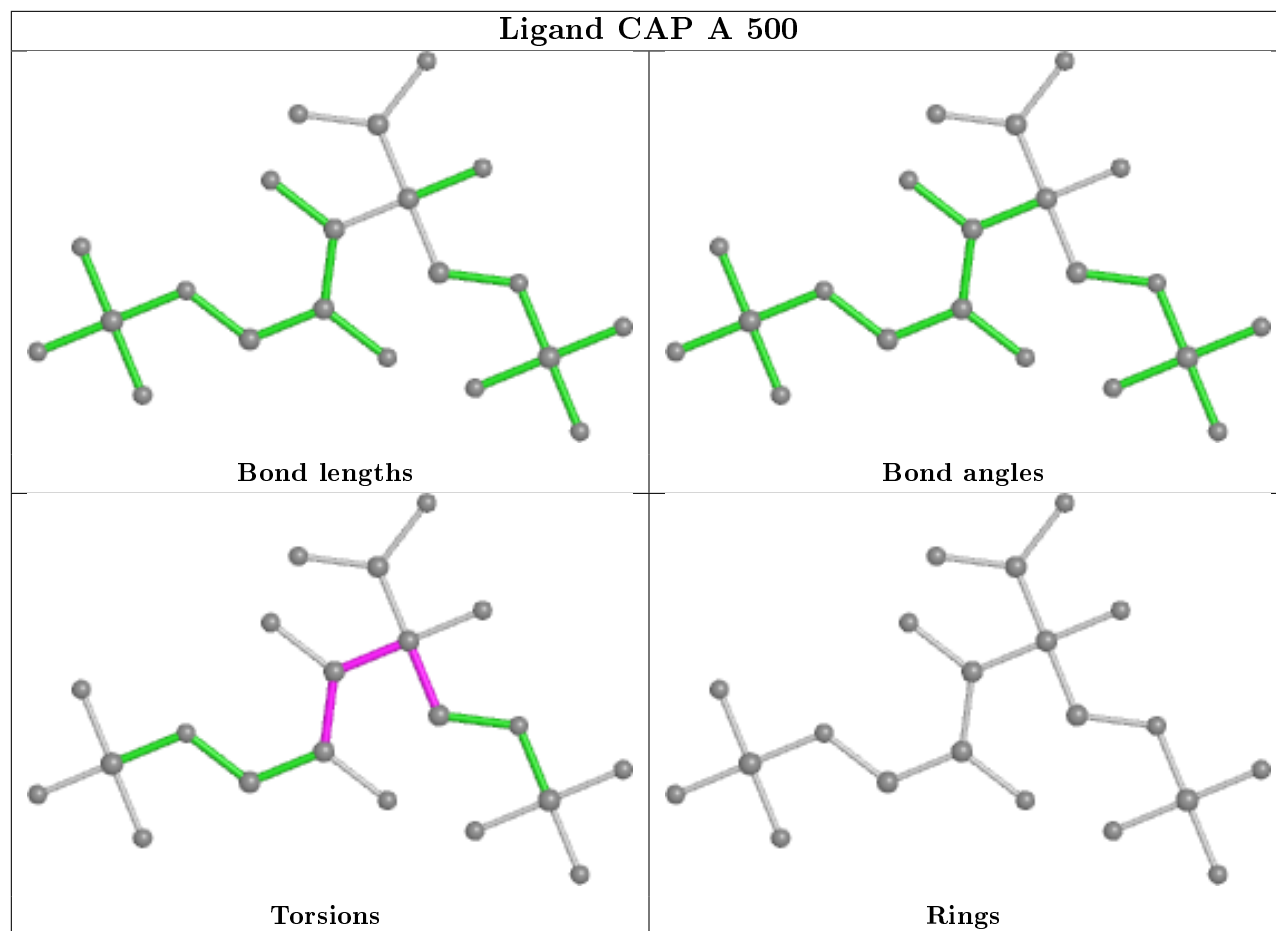
1 monomer is involved in 1 short contact:

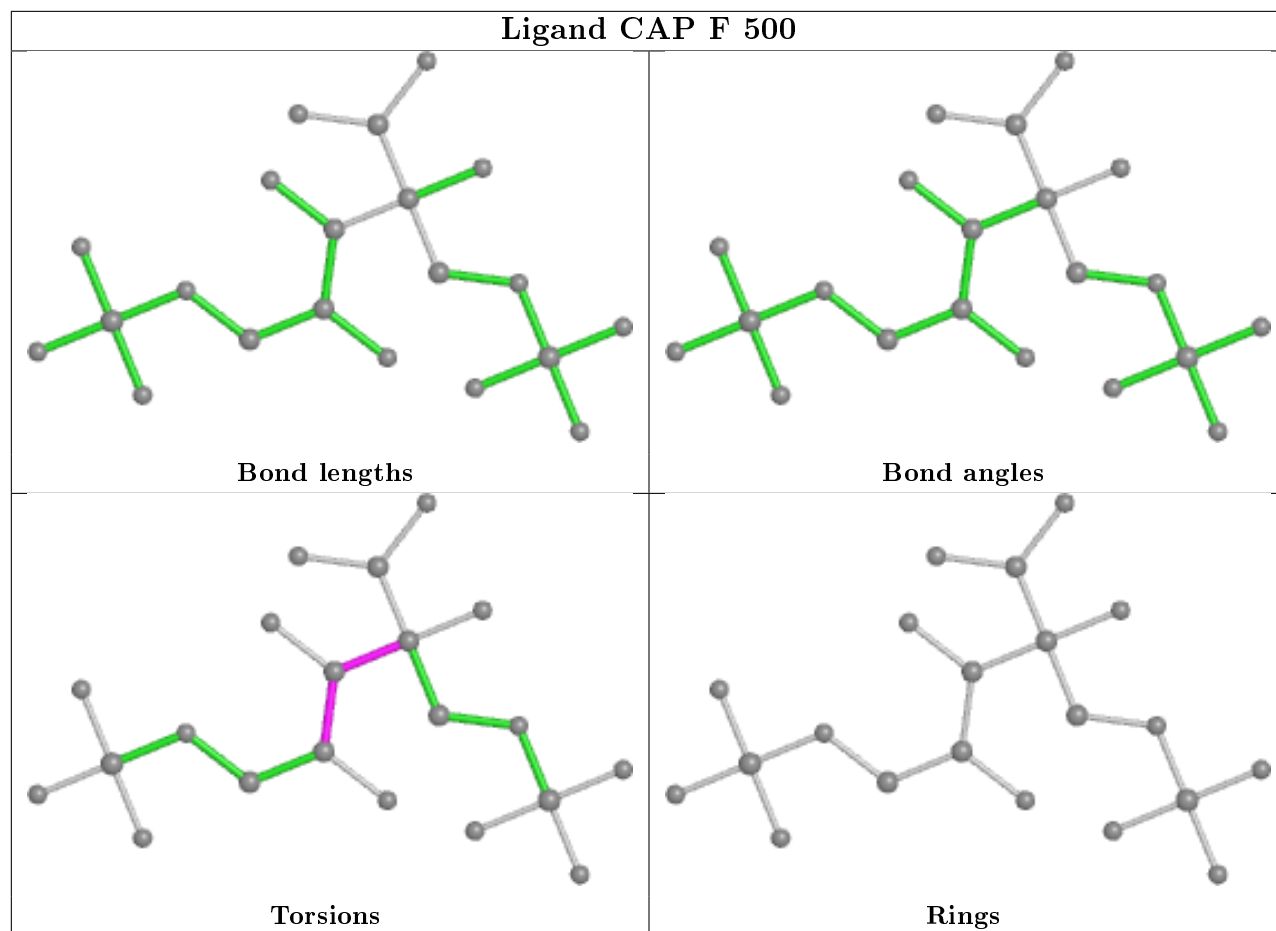
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	500	CAP	1	0

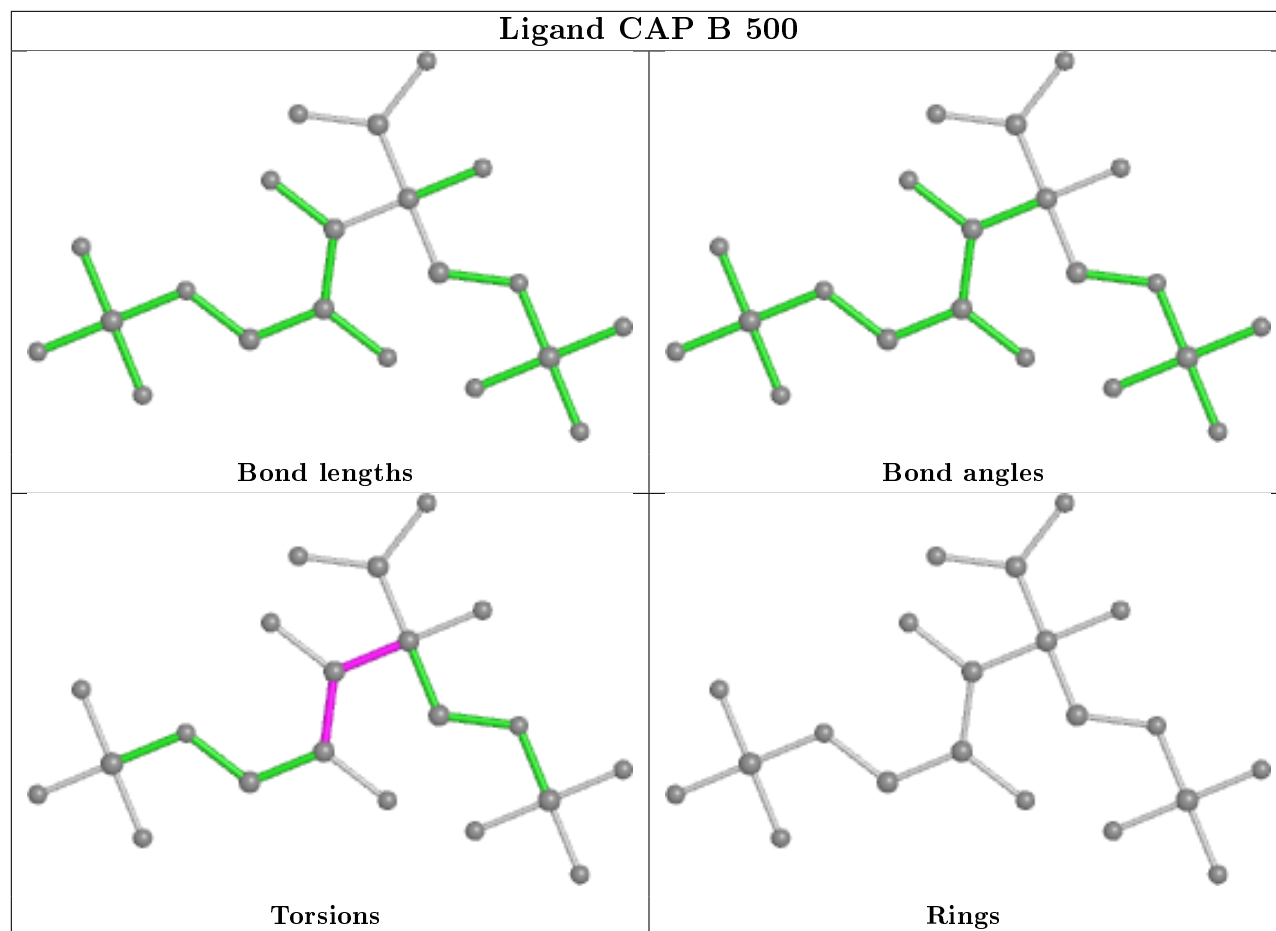
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

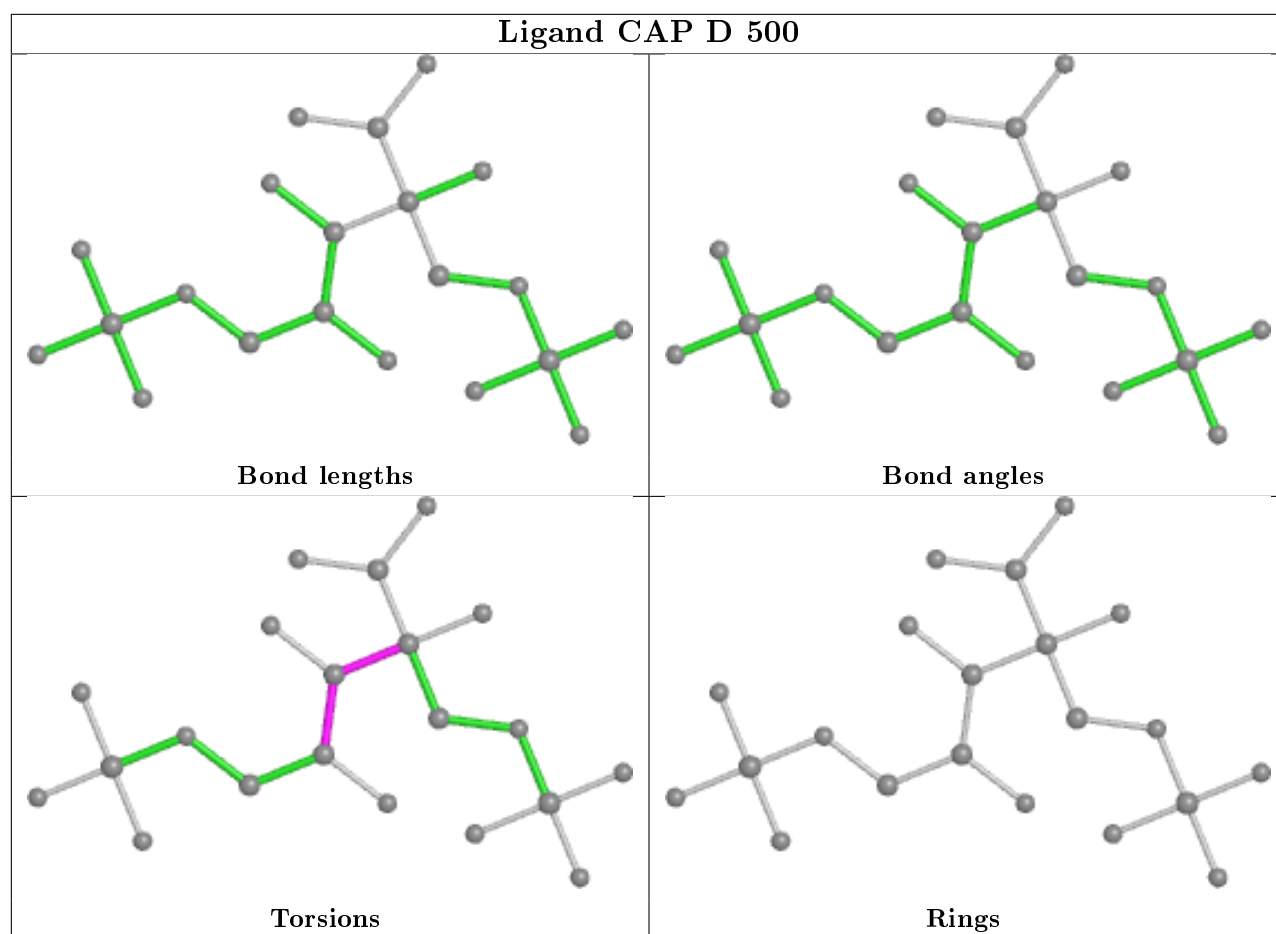












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	454/481 (94%)	0.14	4 (0%) 84 84	18, 37, 66, 89	0
1	B	454/481 (94%)	0.05	1 (0%) 95 95	16, 35, 57, 69	0
1	C	454/481 (94%)	0.15	6 (1%) 77 77	20, 41, 73, 103	0
1	D	454/481 (94%)	0.17	5 (1%) 80 80	18, 39, 69, 94	0
1	E	454/481 (94%)	0.13	2 (0%) 92 92	18, 38, 63, 73	0
1	F	454/481 (94%)	0.21	8 (1%) 68 69	19, 40, 73, 100	0
All	All	2724/2886 (94%)	0.14	26 (0%) 82 82	16, 39, 66, 103	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	449	TYR	4.4
1	D	449	TYR	3.6
1	C	422	ALA	3.5
1	F	450	PRO	3.4
1	C	449	TYR	3.2
1	C	450	PRO	3.1
1	C	427	PHE	2.9
1	D	451	ASN	2.8
1	C	448	LEU	2.7
1	F	420	GLN	2.6
1	F	451	ASN	2.5
1	A	454	ALA	2.5
1	A	420	GLN	2.4
1	F	447	LYS	2.3
1	D	448	LEU	2.3
1	E	451	ASN	2.3
1	A	451	ASN	2.2
1	D	452	TRP	2.2
1	F	56	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	451	ASN	2.2
1	C	378	PRO	2.1
1	F	57	GLU	2.1
1	D	450	PRO	2.1
1	E	40	ILE	2.1
1	F	454	ALA	2.0
1	A	450	PRO	2.0

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
1	KCX	F	192	12/13	0.92	0.12	30,36,38,39	0
1	KCX	E	192	12/13	0.92	0.14	27,30,37,37	0
1	KCX	C	192	12/13	0.93	0.12	30,33,38,38	0
1	KCX	D	192	12/13	0.95	0.11	26,29,34,35	0
1	KCX	A	192	12/13	0.96	0.13	29,32,36,37	0
1	KCX	B	192	12/13	0.96	0.13	23,27,30,30	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

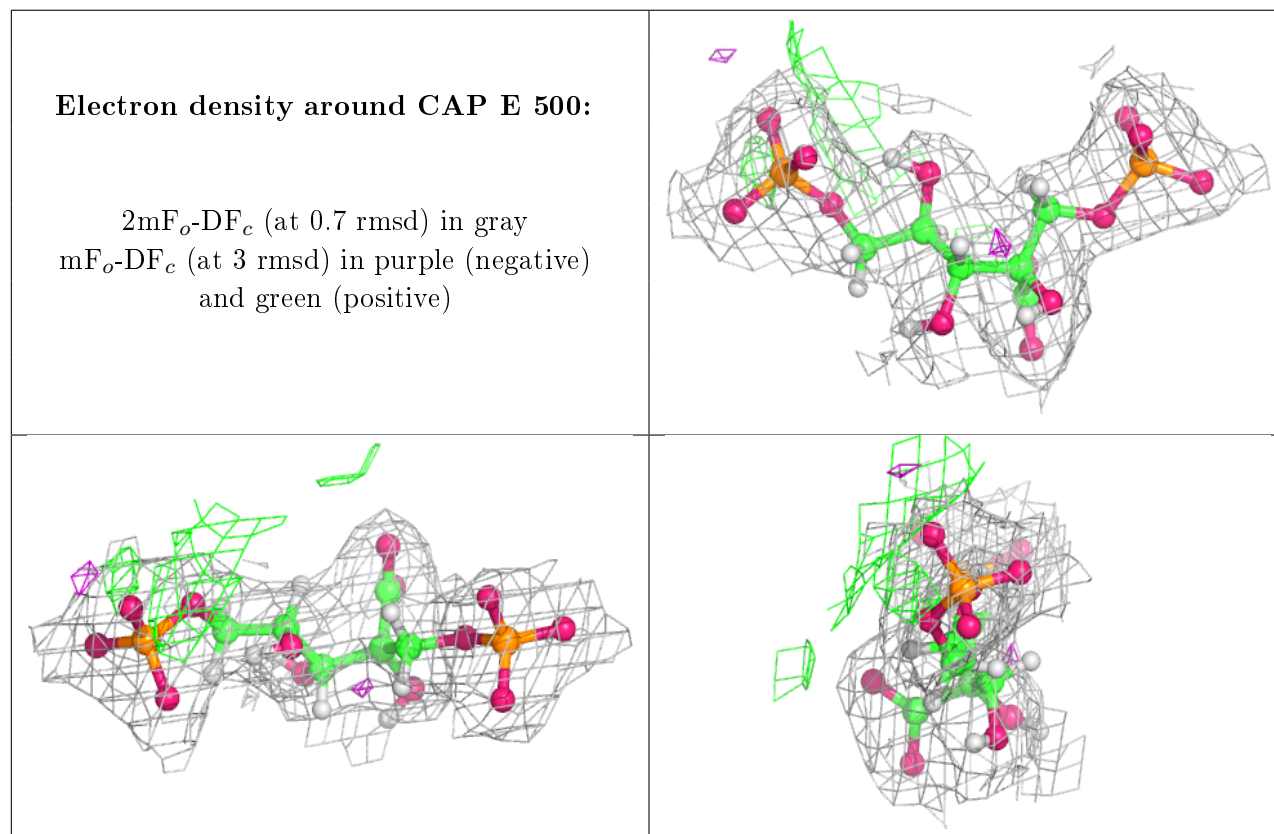
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	E	501	1/1	0.86	0.08	30,30,30,30	0
3	MG	C	501	1/1	0.92	0.05	43,43,43,43	0
2	CAP	E	500	21/21	0.95	0.12	27,31,45,48	0
3	MG	A	501	1/1	0.96	0.05	28,28,28,28	0
3	MG	B	501	1/1	0.96	0.05	29,29,29,29	0

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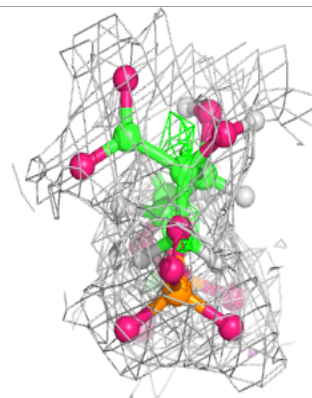
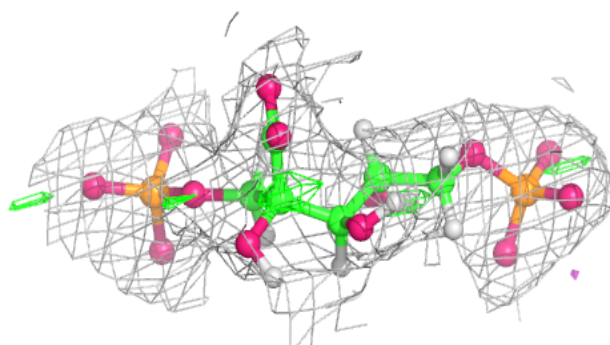
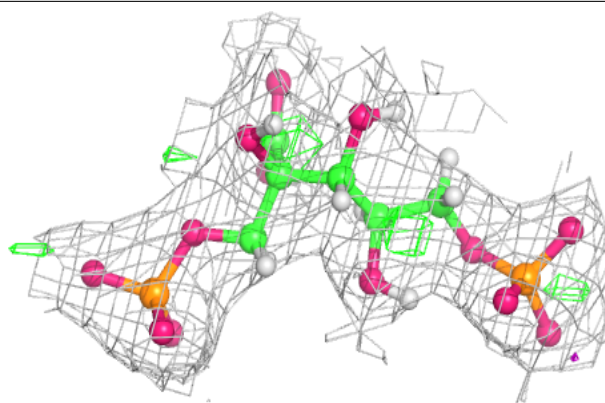
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CAP	A	500	21/21	0.97	0.14	30,37,45,50	0
2	CAP	F	500	21/21	0.97	0.11	35,41,50,54	0
3	MG	D	501	1/1	0.97	0.10	31,31,31,31	0
2	CAP	C	500	21/21	0.97	0.11	37,42,49,51	0
2	CAP	D	500	21/21	0.97	0.14	34,40,48,48	0
2	CAP	B	500	21/21	0.98	0.09	24,30,37,38	0
3	MG	F	501	1/1	0.99	0.06	33,33,33,33	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.

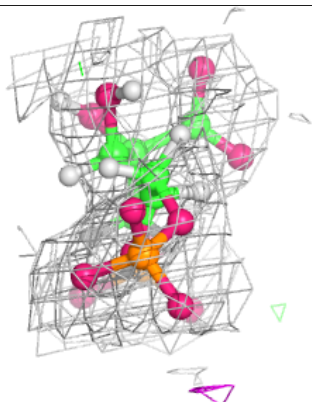
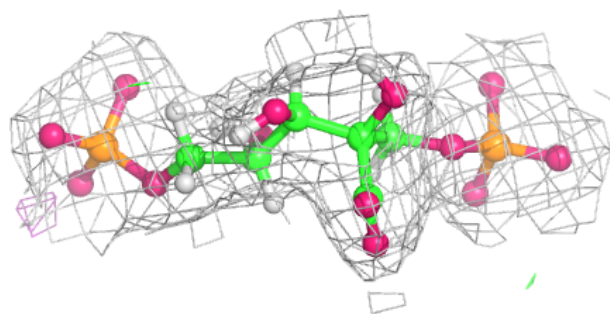
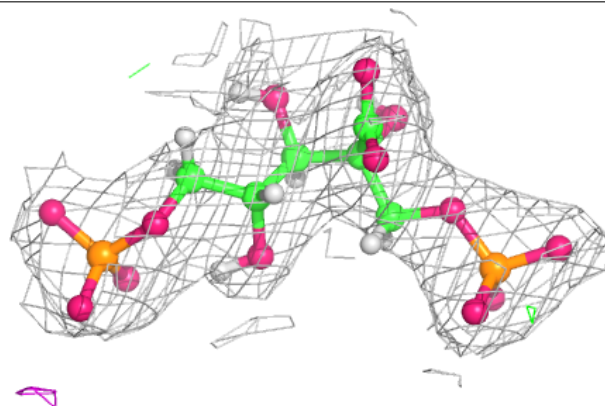


Electron density around CAP A 500:

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

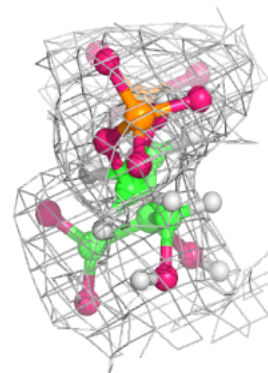
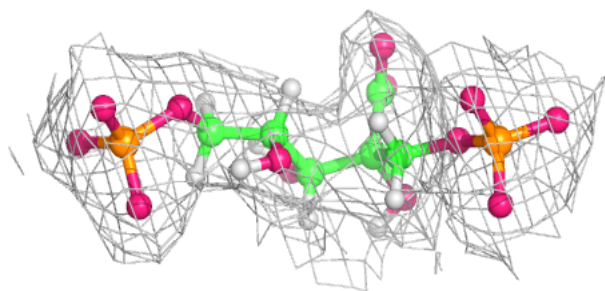
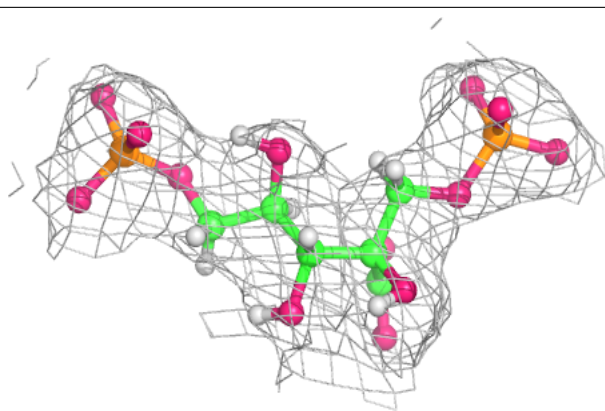
**Electron density around CAP F 500:**

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

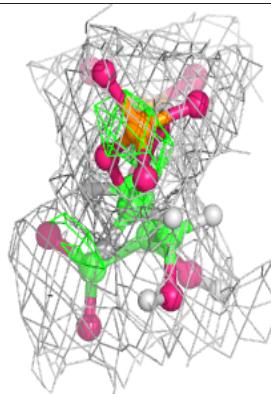
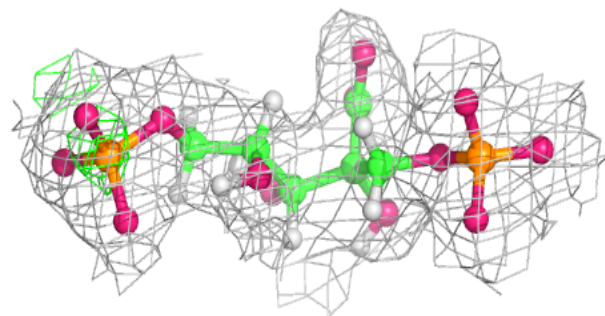
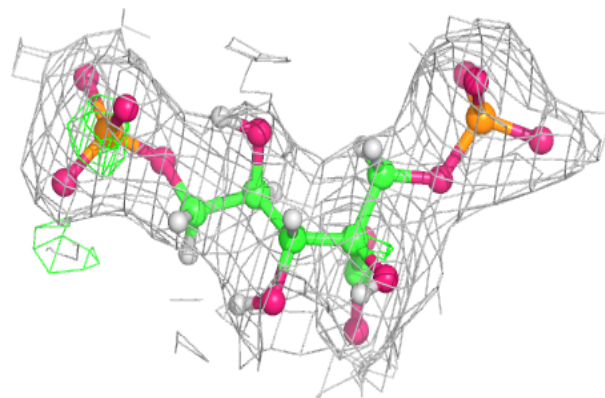


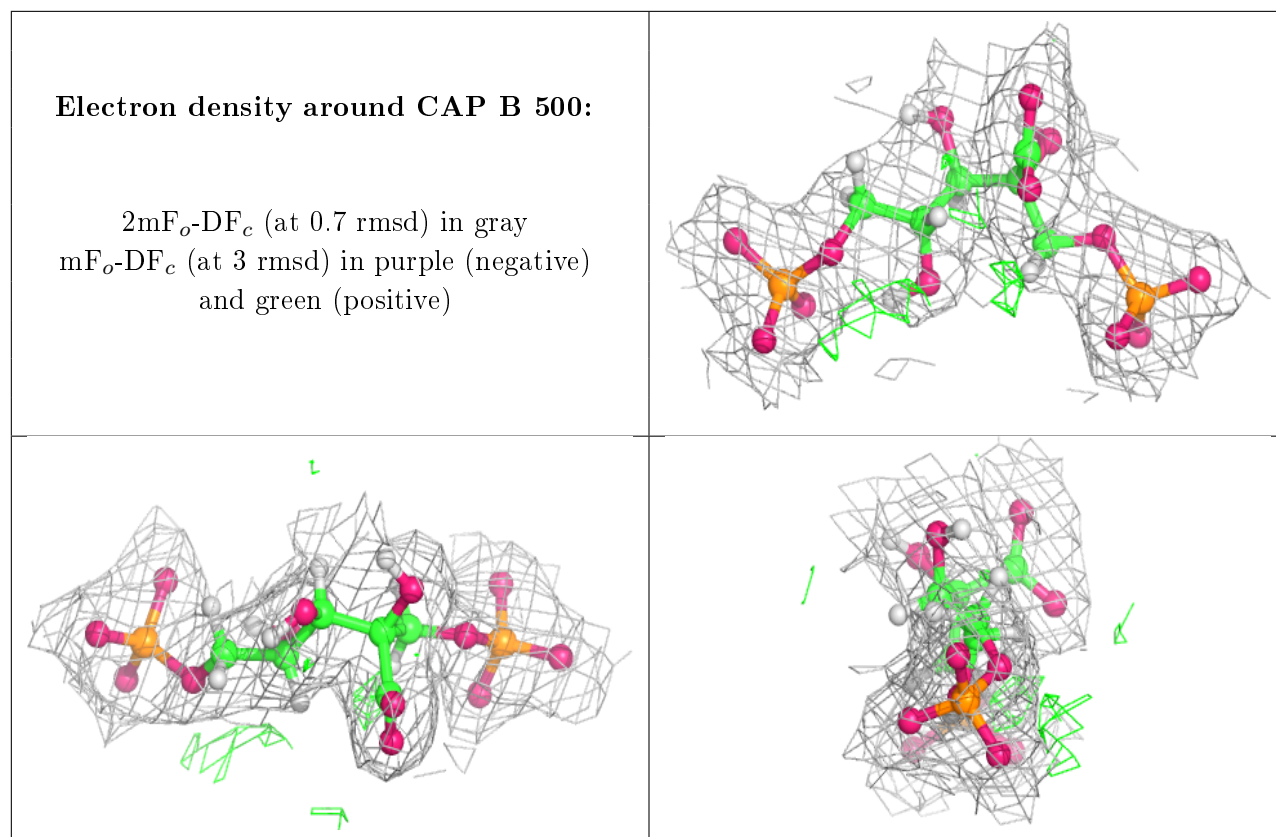
Electron density around CAP C 500:

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

**Electron density around CAP D 500:**

$2mF_o-DF_c$ (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.