



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 5, 2023 – 08:52 AM EST

PDB ID : 5HJY  
Title : Structure function studies of *R. palustris* RubisCO (I165T mutant; CABP-bound)  
Authors : Arbing, M.A.; Shin, A.; Cascio, D.; Satagopan, S.; North, J.A.; Tabita, F.R.  
Deposited on : 2016-01-13  
Resolution : 2.30 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](mailto: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>.

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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 : 2.36  
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) : 2.36

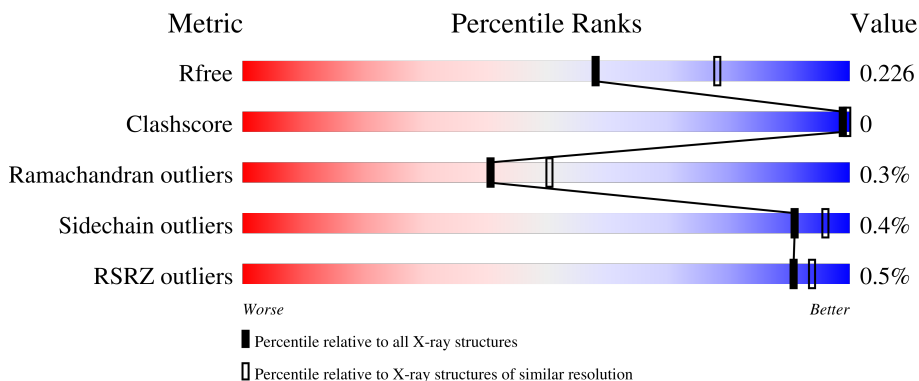
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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.



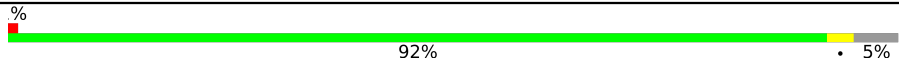
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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  $\geq 3$ , 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	94% • 5%
1	B	481	94% 5%
1	C	481	% 93% • 6%
1	D	481	92% • 5%
1	E	481	% 93% • 5%

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Mol	Chain	Length	Quality of chain
1	F	481	 <p>A horizontal bar chart representing the quality of the chain. The bar is primarily green, indicating a high quality score of 92%. A small yellow segment at the end indicates a lower quality score of 5%. The percentage values are printed below the bar.</p>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 42722 atoms, of which 20141 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	
			Total	C	H	N	O				S
1	A	455	6865	2231	3350	609	656	19	0	0	0
1	B	456	6855	2230	3344	609	653	19	0	0	0
1	C	453	6846	2222	3345	606	654	19	0	0	0
1	D	455	6879	2236	3356	612	656	19	0	1	0
1	E	455	6870	2229	3359	609	654	19	0	0	0
1	F	455	6860	2231	3345	609	656	19	0	0	0

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	165	THR	ILE	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	165	THR	ILE	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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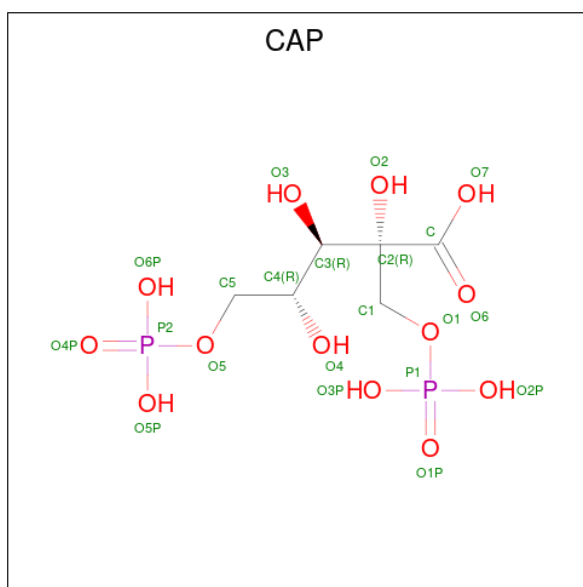
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP Q6N0W9
C	-1	SER	-	expression tag	UNP Q6N0W9
C	0	HIS	-	expression tag	UNP Q6N0W9
C	165	THR	ILE	engineered mutation	UNP Q6N0W9
D	-19	MET	-	initiating methionine	UNP Q6N0W9
D	-18	GLY	-	expression tag	UNP Q6N0W9
D	-17	SER	-	expression 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	165	THR	ILE	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	165	THR	ILE	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	165	THR	ILE	engineered mutation	UNP Q6N0W9

- Molecule 2 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>13</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	O	P		
2	A	1	28	6	7	13	2	0	0
2	B	1	28	6	7	13	2	0	0
2	C	1	28	6	7	13	2	0	0
2	D	1	28	6	7	13	2	0	0
2	E	1	28	6	7	13	2	0	0
2	F	1	28	6	7	13	2	0	0

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

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



- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total Cl 1 1	0	0

- Molecule 5 is water.

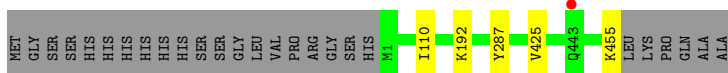
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	252	Total O 252 252	0	0
5	B	247	Total O 247 247	0	0
5	C	223	Total O 223 223	0	0
5	D	235	Total O 235 235	0	0
5	E	199	Total O 199 199	0	0
5	F	216	Total O 216 216	0	0

### 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.

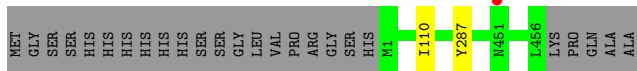
- Molecule 1: Ribulose biphosphate carboxylase

Chain A:  94% 5%

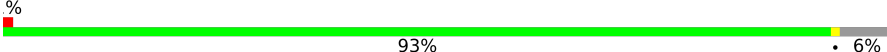


- Molecule 1: Ribulose biphosphate carboxylase

Chain B:  94% 5%



- Molecule 1: Ribulose biphosphate carboxylase

Chain C:  93% 6%

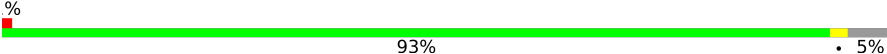


- Molecule 1: Ribulose biphosphate carboxylase

Chain D:  92% 5%



- Molecule 1: Ribulose biphosphate carboxylase

Chain E:  93% 5%



- Molecule 1: Ribulose biphosphate carboxylase

Chain F: % 92% 5%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.86Å 100.02Å 103.56Å 107.84° 113.77° 96.09°	Depositor
Resolution (Å)	91.85 – 2.30 91.85 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.3 (91.85-2.30) 93.4 (91.85-2.30)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.183 , 0.225 0.186 , 0.226	Depositor DCC
$R_{free}$ test set	10345 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.9	Xtrriage
Anisotropy	0.351	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 46.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	42722	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.28	0/3591	0.44	0/4860
1	B	0.28	0/3587	0.44	0/4857
1	C	0.27	0/3577	0.43	0/4842
1	D	0.27	0/3602	0.43	0/4874
1	E	0.27	0/3587	0.44	0/4855
1	F	0.27	0/3591	0.44	0/4860
All	All	0.27	0/21535	0.44	0/29148

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	3515	3350	3377	2	0
1	B	3511	3344	3369	0	0
1	C	3501	3345	3359	2	0
1	D	3523	3356	3390	6	0
1	E	3511	3359	3373	4	0
1	F	3515	3345	3377	6	0
2	A	21	7	7	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	21	7	7	0	0
2	C	21	7	7	0	0
2	D	21	7	7	0	0
2	E	21	7	7	0	0
2	F	21	7	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	D	1	0	0	0	0
5	A	252	0	0	0	0
5	B	247	0	0	0	0
5	C	223	0	0	0	0
5	D	235	0	0	0	0
5	E	199	0	0	0	0
5	F	216	0	0	0	0
All	All	22581	20141	20287	18	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 0.

All (18) 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:425:VAL:HG11	1:A:455:LYS:HD3	1.66	0.76
1:D:250:GLU:OE2	1:F:206:LYS:NZ	2.27	0.62
1:D:217[A]:ARG:NH2	1:D:254:ASP:OD1	2.35	0.59
1:E:39:PHE:CG	1:E:77:GLU:HG3	2.44	0.53
1:E:145:LYS:HG3	1:E:155:VAL:HB	1.92	0.50
1:D:425:VAL:CG1	1:D:455:LYS:HG3	2.43	0.49
1:D:381:PHE:HB3	1:D:418:TRP:CE2	2.50	0.46
1:F:452:TRP:C	1:F:454:ALA:H	2.19	0.45
1:D:425:VAL:HG12	1:D:455:LYS:HG3	1.98	0.45
1:C:381:PHE:HB3	1:C:418:TRP:CE2	2.52	0.45
1:F:452:TRP:O	1:F:454:ALA:N	2.51	0.43
1:F:175:GLN:HB3	1:F:176:PRO:HD3	2.00	0.43
1:F:167:LYS:HA	1:F:168:PRO:C	2.40	0.42
1:D:138:ASP:HA	1:E:282:LYS:HE3	2.01	0.42
1:A:425:VAL:HG11	1:A:455:LYS:CD	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:LYS:HA	1:C:168:PRO:C	2.41	0.41
1:E:446:ASP:OD1	1:E:453:ARG:NH1	2.45	0.40
1:F:51:SER:OG	1:F:52:THR:N	2.54	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%)	15 (3%)	1 (0%)	47 58
1	B	453/481 (94%)	437 (96%)	15 (3%)	1 (0%)	47 58
1	C	450/481 (94%)	436 (97%)	13 (3%)	1 (0%)	47 58
1	D	453/481 (94%)	439 (97%)	13 (3%)	1 (0%)	47 58
1	E	452/481 (94%)	437 (97%)	14 (3%)	1 (0%)	47 58
1	F	452/481 (94%)	438 (97%)	12 (3%)	2 (0%)	34 42
All	All	2712/2886 (94%)	2623 (97%)	82 (3%)	7 (0%)	41 50

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	110	ILE
1	D	110	ILE
1	C	110	ILE
1	E	110	ILE
1	F	110	ILE
1	F	453	ARG
1	B	110	ILE

### 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	350/372 (94%)	349 (100%)	1 (0%)	92	97
1	B	348/372 (94%)	347 (100%)	1 (0%)	92	97
1	C	349/372 (94%)	348 (100%)	1 (0%)	92	97
1	D	351/372 (94%)	349 (99%)	2 (1%)	86	94
1	E	349/372 (94%)	347 (99%)	2 (1%)	86	94
1	F	350/372 (94%)	349 (100%)	1 (0%)	92	97
All	All	2097/2232 (94%)	2089 (100%)	8 (0%)	91	96

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	287	TYR
1	B	287	TYR
1	C	287	TYR
1	D	287	TYR
1	D	369	SER
1	E	287	TYR
1	E	455	LYS
1	F	287	TYR

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

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	E	192	1,3	9,11,12	0.73	0	5,12,14	0.83	0
1	KCX	D	192	1,3	9,11,12	2.17	1 (11%)	5,12,14	1.70	1 (20%)
1	KCX	B	192	1,3	9,11,12	0.67	0	5,12,14	1.11	0
1	KCX	C	192	1,3	9,11,12	0.66	0	5,12,14	0.96	0
1	KCX	A	192	1,3	9,11,12	2.18	1 (11%)	5,12,14	1.83	1 (20%)
1	KCX	F	192	1,3	9,11,12	2.24	1 (11%)	5,12,14	1.44	1 (20%)

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	E	192	1,3	-	0/9/10/12	-
1	KCX	D	192	1,3	-	0/9/10/12	-
1	KCX	B	192	1,3	-	1/9/10/12	-
1	KCX	C	192	1,3	-	0/9/10/12	-
1	KCX	A	192	1,3	-	0/9/10/12	-
1	KCX	F	192	1,3	-	0/9/10/12	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	192	KCX	OQ1-CX	6.44	1.33	1.21
1	A	192	KCX	OQ1-CX	6.25	1.33	1.21
1	D	192	KCX	OQ1-CX	6.20	1.33	1.21

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	192	KCX	OQ1-CX-NZ	-3.73	119.18	124.96
1	D	192	KCX	OQ1-CX-NZ	-3.64	119.31	124.96
1	F	192	KCX	OQ1-CX-NZ	-2.97	120.35	124.96

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	192	KCX	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 7 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	A	500	3	17,20,20	0.83	0	22,31,31	0.70	0
2	CAP	F	500	3	17,20,20	0.81	0	22,31,31	0.77	0
2	CAP	B	500	3	17,20,20	0.85	0	22,31,31	0.71	0
2	CAP	E	500	3	17,20,20	0.87	0	22,31,31	0.70	0
2	CAP	C	500	3	17,20,20	0.82	0	22,31,31	0.76	0
2	CAP	D	501	3	17,20,20	0.82	0	22,31,31	0.74	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	A	500	3	-	9/29/29/29	-
2	CAP	F	500	3	-	8/29/29/29	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CAP	B	500	3	-	9/29/29/29	-
2	CAP	E	500	3	-	8/29/29/29	-
2	CAP	C	500	3	-	7/29/29/29	-
2	CAP	D	501	3	-	6/29/29/29	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	CAP	O6-C-C2-C3
2	A	500	CAP	O6-C-C2-O2
2	A	500	CAP	O3-C3-C4-O4
2	B	500	CAP	O6-C-C2-C3
2	B	500	CAP	O6-C-C2-O2
2	B	500	CAP	O7-C-C2-O2
2	C	500	CAP	O6-C-C2-C1
2	C	500	CAP	O7-C-C2-C1
2	C	500	CAP	O6-C-C2-O2
2	C	500	CAP	O7-C-C2-O2
2	C	500	CAP	O3-C3-C4-O4
2	D	501	CAP	O6-C-C2-C1
2	D	501	CAP	O7-C-C2-C1
2	D	501	CAP	O6-C-C2-O2
2	D	501	CAP	O7-C-C2-O2
2	D	501	CAP	O3-C3-C4-O4
2	E	500	CAP	O6-C-C2-C3
2	E	500	CAP	O6-C-C2-O2
2	E	500	CAP	O3-C3-C4-O4
2	F	500	CAP	O6-C-C2-O2
2	F	500	CAP	O7-C-C2-O2
2	F	500	CAP	O3-C3-C4-O4
2	A	500	CAP	O7-C-C2-C1
2	B	500	CAP	O6-C-C2-C1
2	E	500	CAP	O7-C-C2-C1
2	F	500	CAP	O7-C-C2-C1
2	A	500	CAP	O2-C2-C3-C4
2	B	500	CAP	O2-C2-C3-C4
2	C	500	CAP	O2-C2-C3-C4

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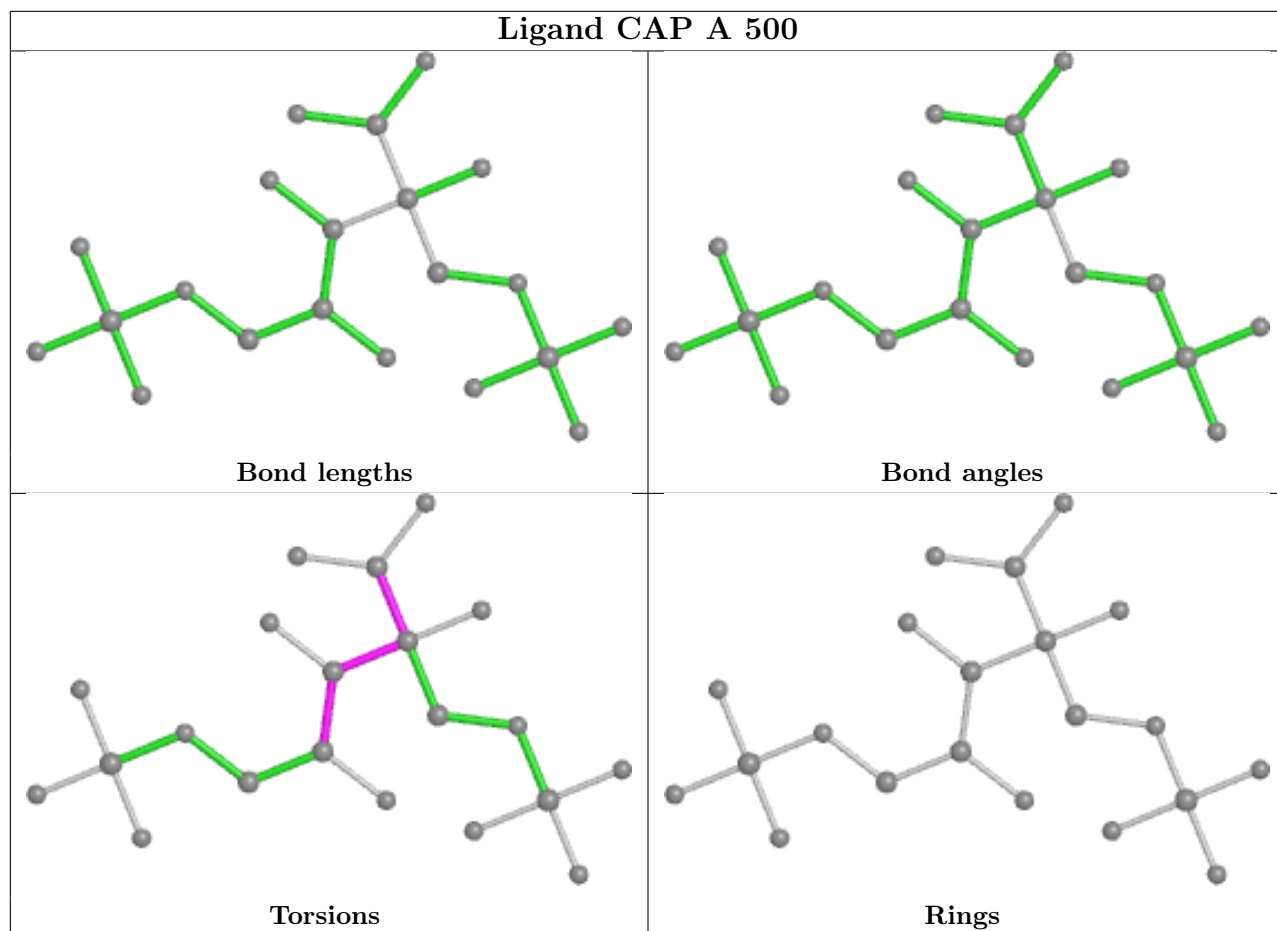
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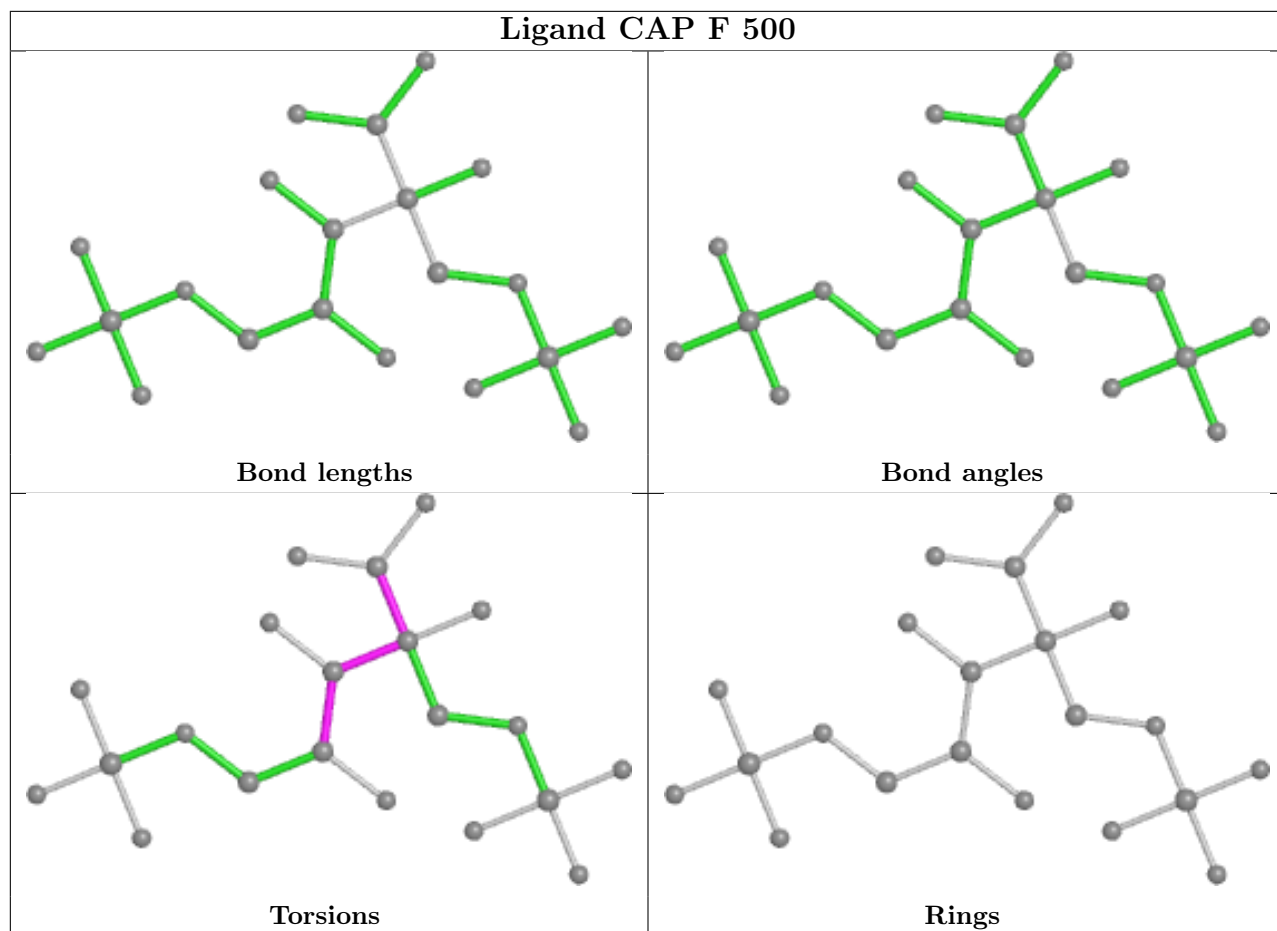
Mol	Chain	Res	Type	Atoms
2	D	501	CAP	O2-C2-C3-C4
2	E	500	CAP	O2-C2-C3-C4
2	F	500	CAP	O2-C2-C3-C4
2	A	500	CAP	O7-C-C2-O2
2	E	500	CAP	O7-C-C2-O2
2	B	500	CAP	O7-C-C2-C1
2	B	500	CAP	O3-C3-C4-O4
2	F	500	CAP	O6-C-C2-C3
2	F	500	CAP	O6-C-C2-C1
2	A	500	CAP	O7-C-C2-C3
2	B	500	CAP	O7-C-C2-C3
2	E	500	CAP	O7-C-C2-C3
2	F	500	CAP	O7-C-C2-C3
2	A	500	CAP	O6-C-C2-C1
2	E	500	CAP	O6-C-C2-C1
2	C	500	CAP	O4-C4-C5-O5
2	A	500	CAP	C2-C3-C4-O4
2	B	500	CAP	O4-C4-C5-O5

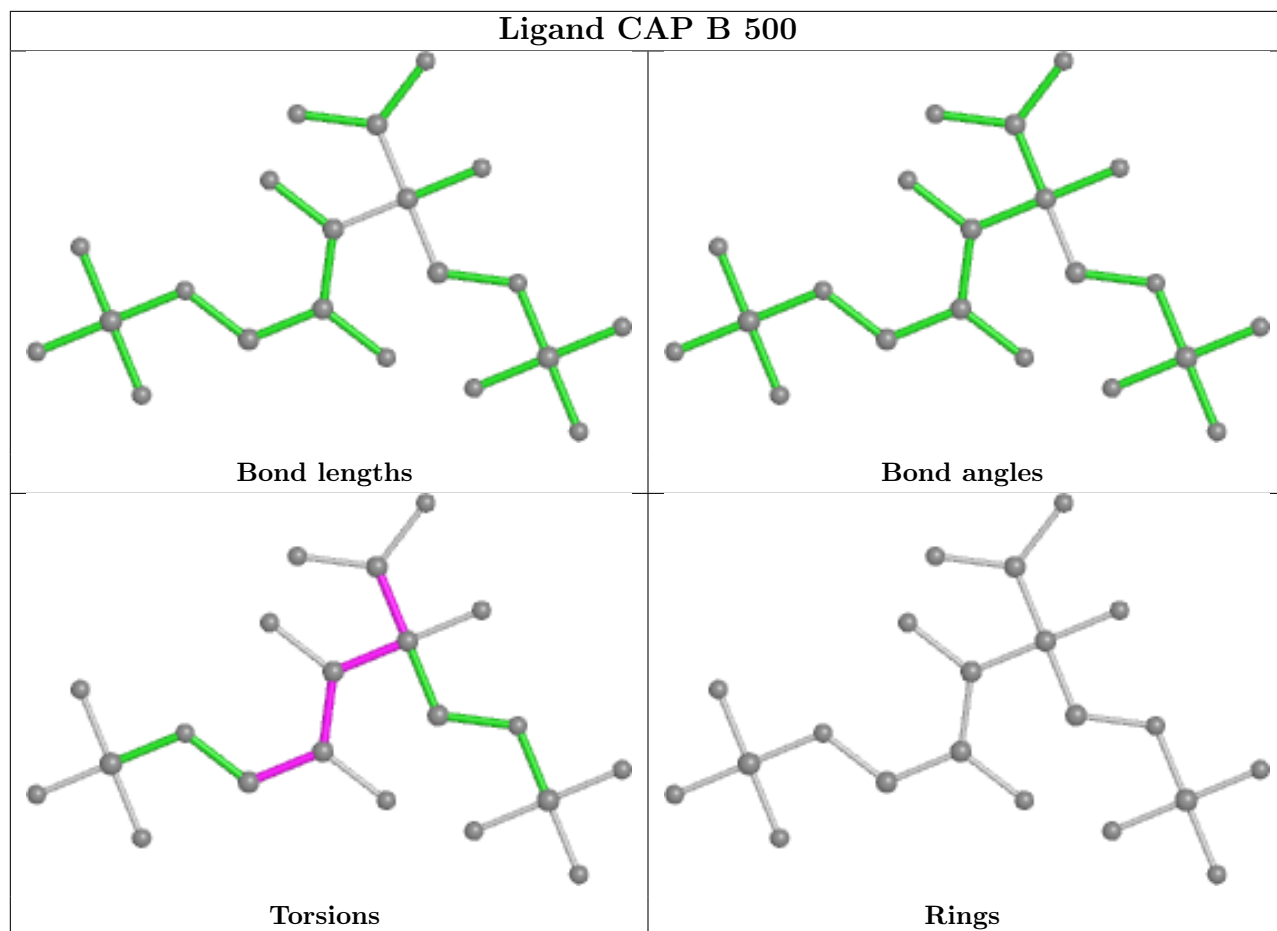
There are no ring outliers.

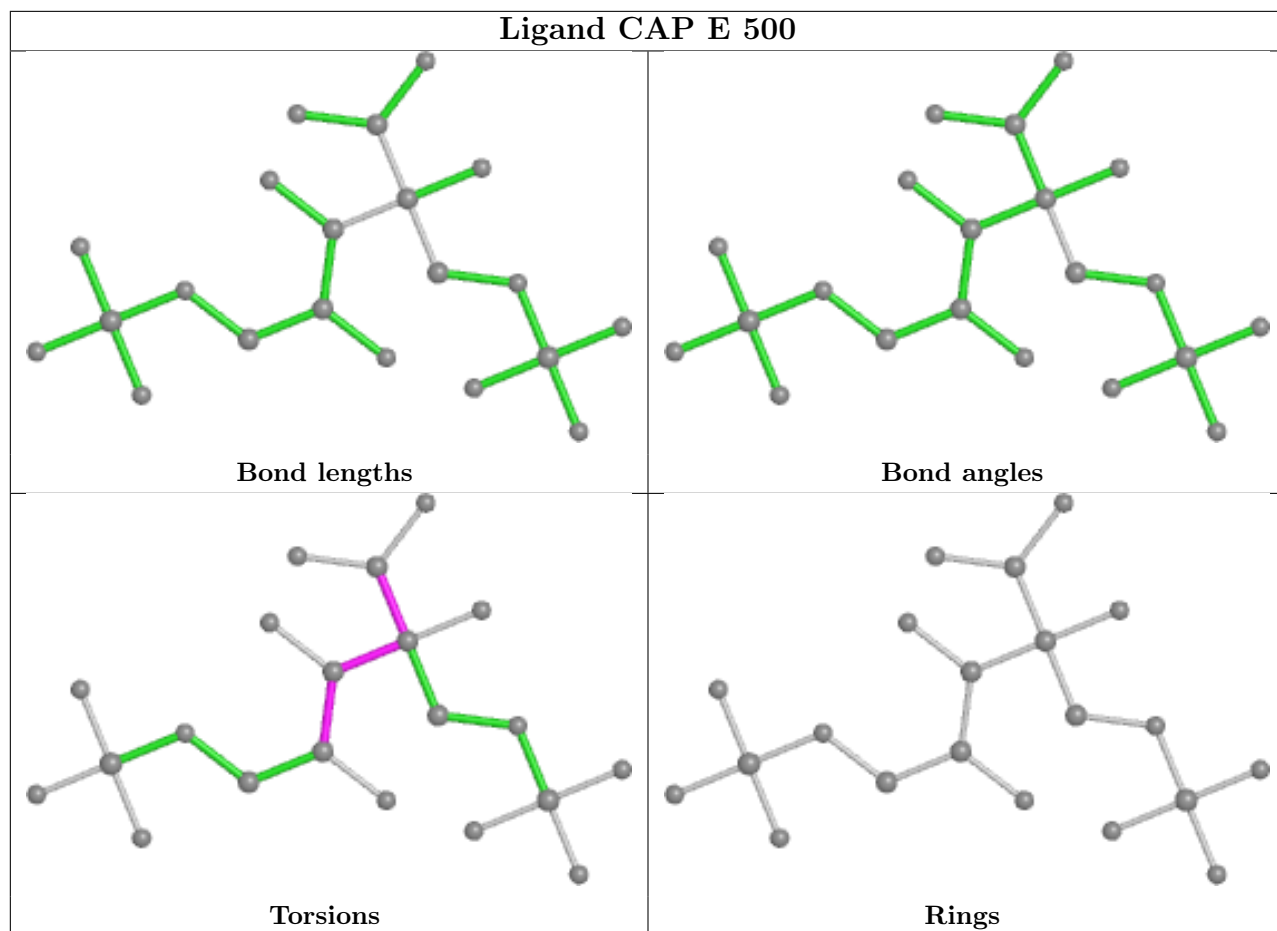
No monomer is involved in short contacts.

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

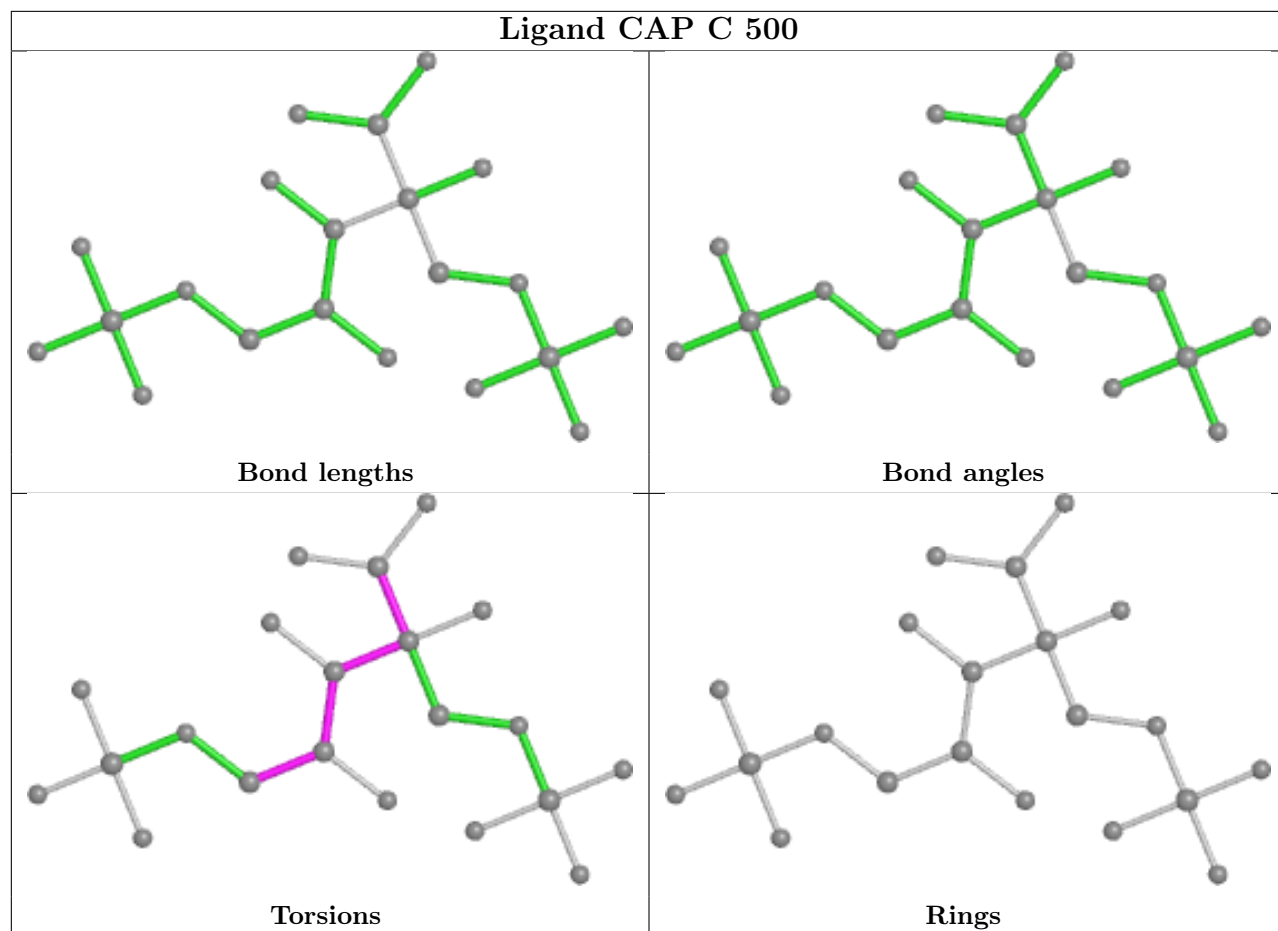


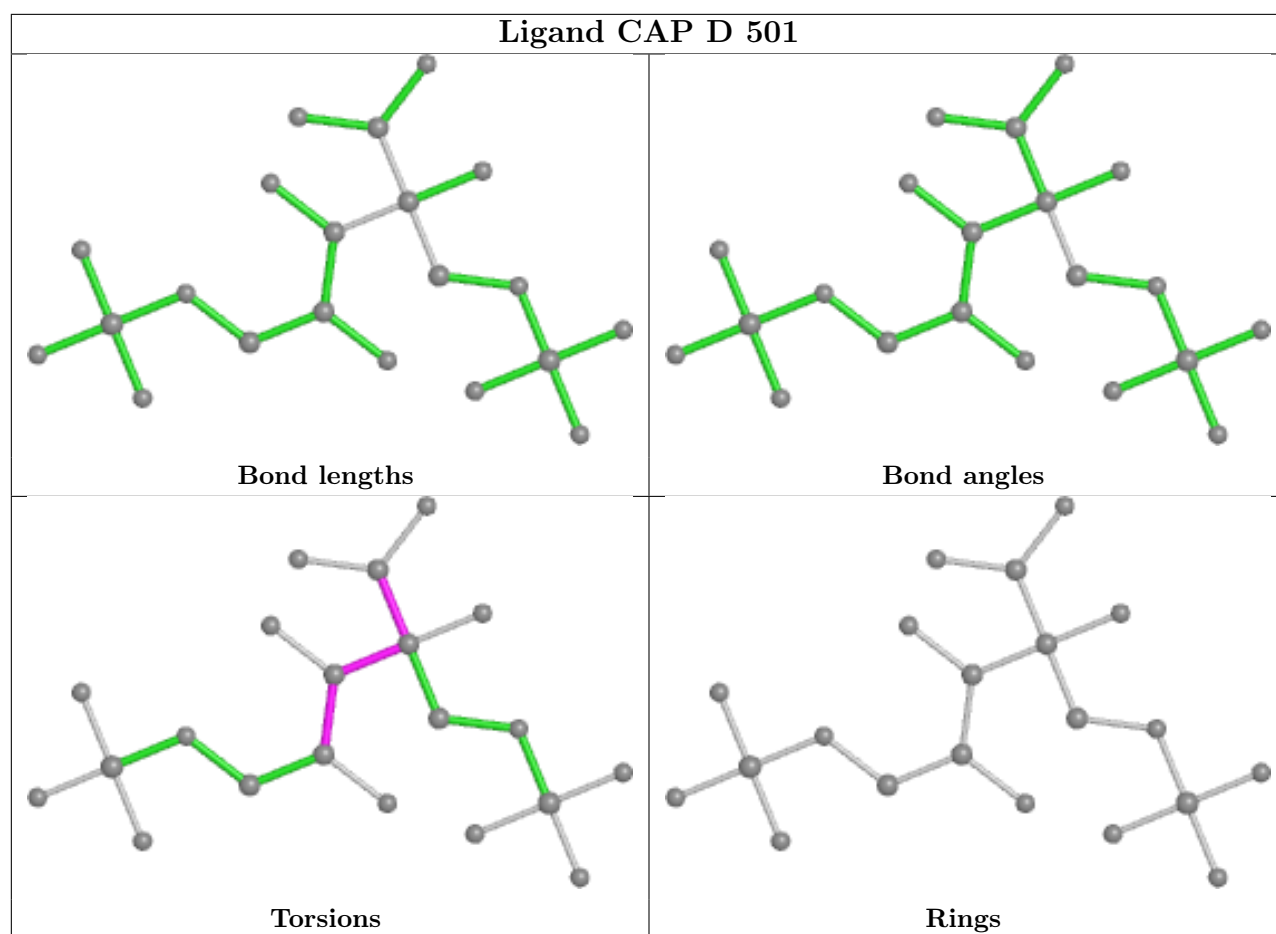












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	454/481 (94%)	-0.40	1 (0%) 95 96	18, 27, 38, 55	0
1	B	455/481 (94%)	-0.35	1 (0%) 95 96	18, 26, 39, 57	0
1	C	452/481 (93%)	-0.26	4 (0%) 84 88	18, 29, 46, 70	0
1	D	454/481 (94%)	-0.29	0 100 100	18, 29, 42, 62	0
1	E	454/481 (94%)	-0.24	5 (1%) 80 85	20, 31, 50, 72	0
1	F	454/481 (94%)	-0.30	3 (0%) 87 91	19, 30, 46, 64	0
All	All	2723/2886 (94%)	-0.31	14 (0%) 91 94	18, 29, 44, 72	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	MET	4.0
1	E	35	GLY	3.8
1	F	1	MET	3.8
1	E	451	ASN	3.4
1	F	450	PRO	3.1
1	E	10	LEU	2.8
1	A	443	GLN	2.4
1	B	451	ASN	2.4
1	C	419	LYS	2.3
1	F	448	LEU	2.3
1	E	2	ASP	2.2
1	C	449	TYR	2.1
1	C	432	ARG	2.1
1	C	448	LEU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	KCX	C	192	12/13	0.92	0.09	20,24,25,26	0
1	KCX	F	192	12/13	0.92	0.12	20,25,27,27	0
1	KCX	A	192	12/13	0.93	0.09	16,19,22,22	0
1	KCX	B	192	12/13	0.94	0.12	14,17,20,21	0
1	KCX	E	192	12/13	0.95	0.08	20,25,25,27	0
1	KCX	D	192	12/13	0.96	0.08	16,19,22,26	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides 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, 95<sup>th</sup> 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.

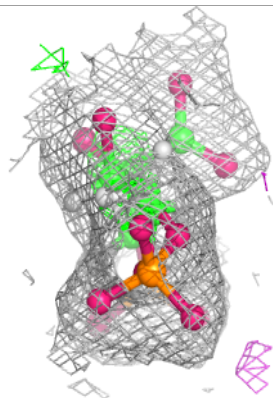
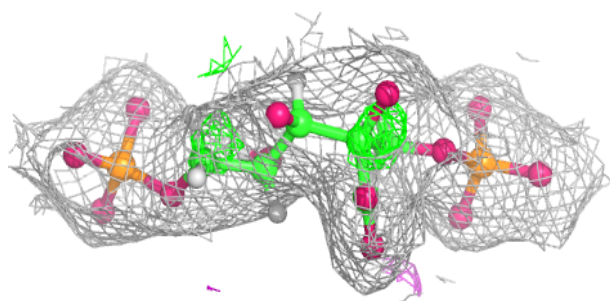
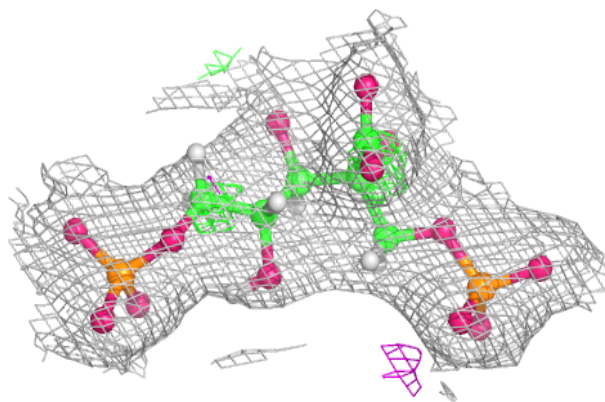
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	D	502	1/1	0.81	0.07	29,29,29,29	0
3	MG	E	501	1/1	0.88	0.05	27,27,27,27	0
3	MG	C	501	1/1	0.93	0.07	29,29,29,29	0
3	MG	B	501	1/1	0.96	0.06	22,22,22,22	0
4	CL	D	503	1/1	0.96	0.07	50,50,50,50	0
2	CAP	F	500	21/21	0.97	0.13	24,28,34,34	0
2	CAP	A	500	21/21	0.97	0.14	22,26,31,32	0
2	CAP	B	500	21/21	0.97	0.12	19,22,26,28	0
2	CAP	C	500	21/21	0.97	0.08	23,25,30,31	0
2	CAP	D	501	21/21	0.97	0.10	24,27,31,33	0
3	MG	F	501	1/1	0.97	0.11	29,29,29,29	0
2	CAP	E	500	21/21	0.97	0.11	23,26,31,32	0
3	MG	A	501	1/1	0.98	0.06	28,28,28,28	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.

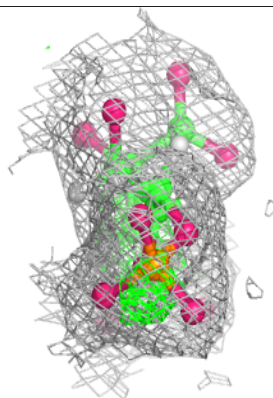
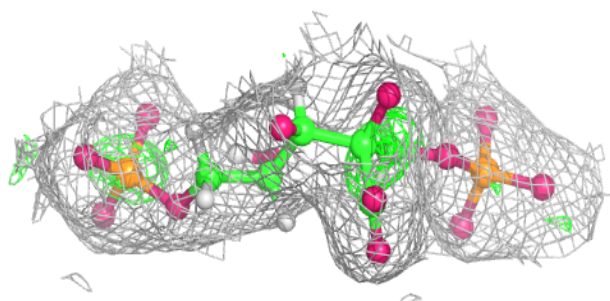
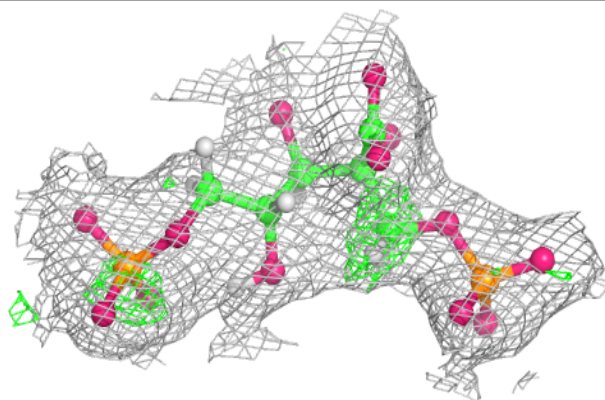
**Electron density around CAP F 500:**

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



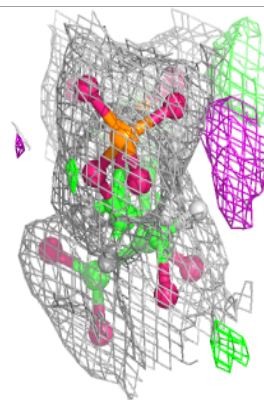
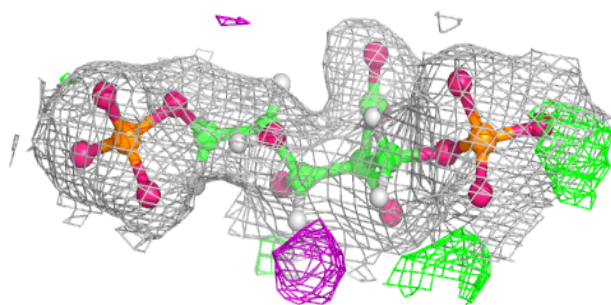
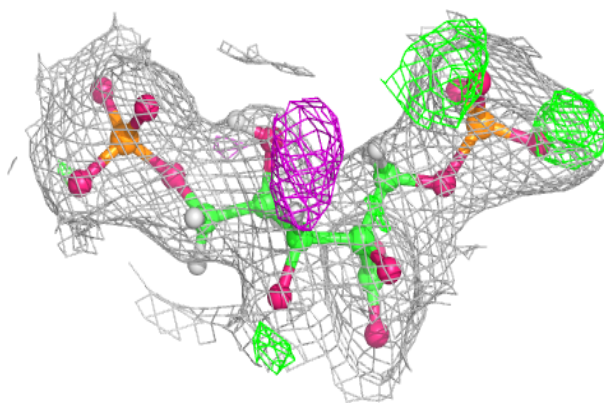
**Electron density around CAP A 500:**

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and green (positive)

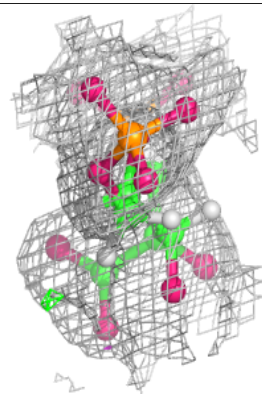
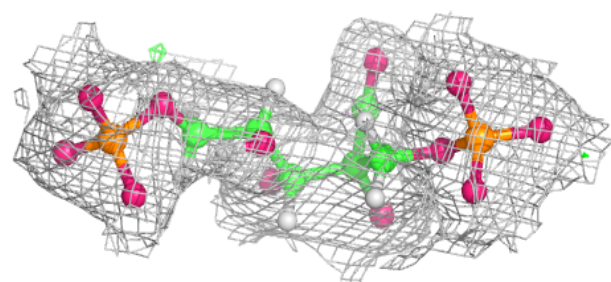
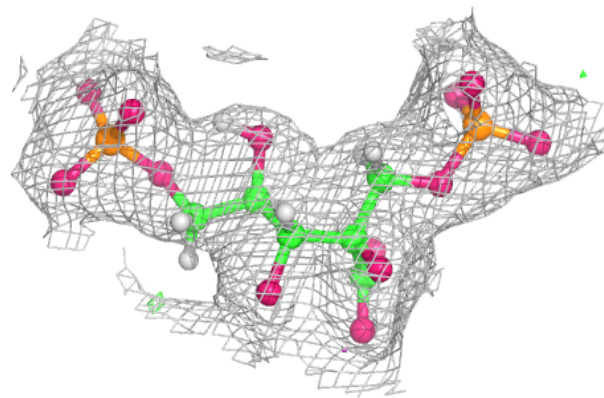


**Electron density around CAP B 500:**

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

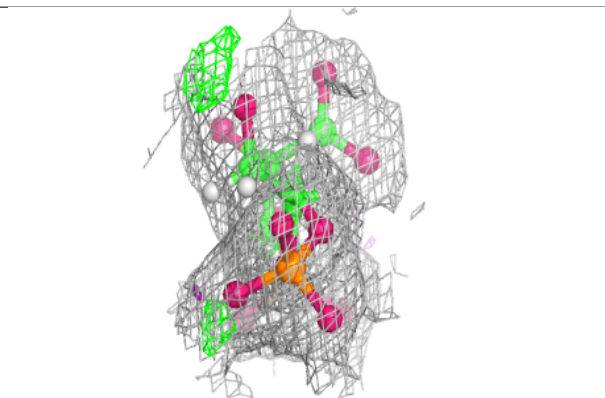
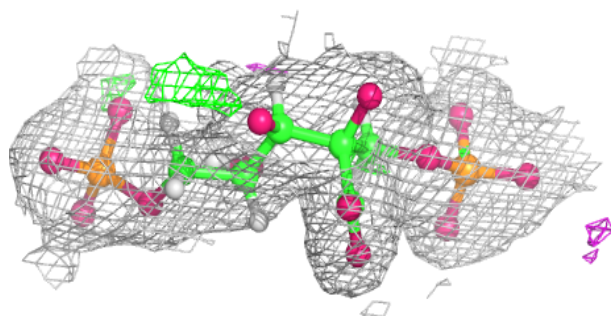
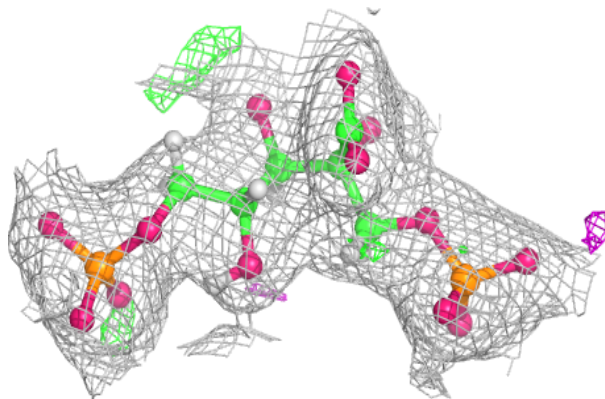
**Electron density around CAP C 500:**

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

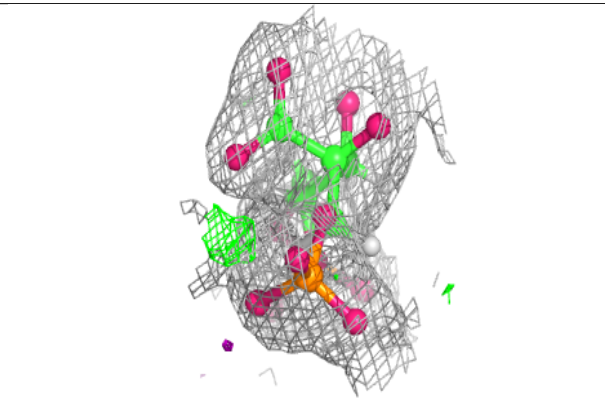
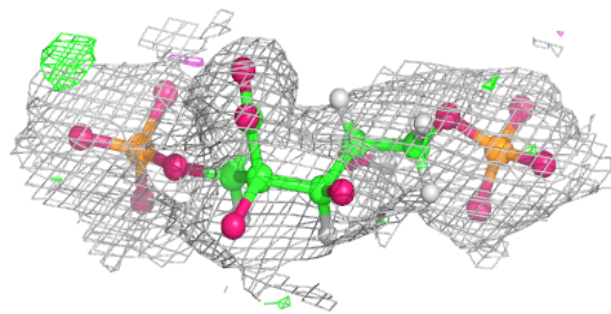
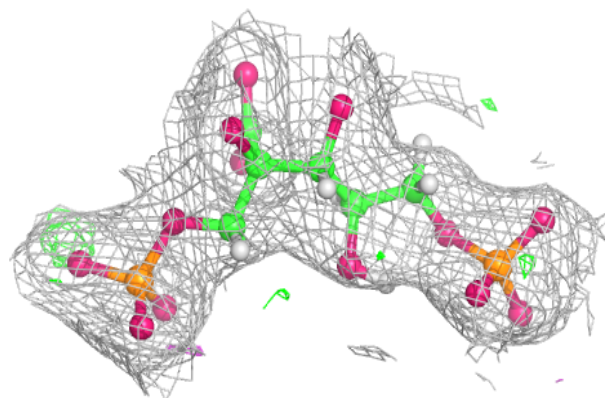


**Electron density around CAP D 501:**

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

**Electron density around CAP E 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.