



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 05:30 pm BST

PDB ID : 6FTL  
Title : Rubisco from *Skeletonema marinoi*  
Authors : Andersson, I.; Valegard, K.  
Deposited on : 2018-02-22  
Resolution : 2.60 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](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.

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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	:	2.11
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

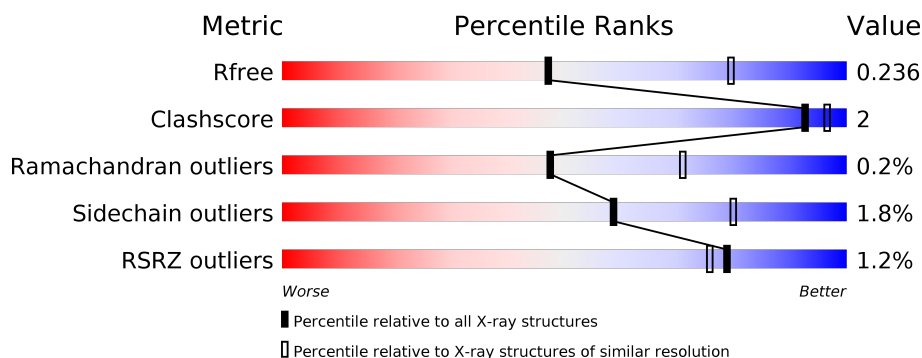
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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.



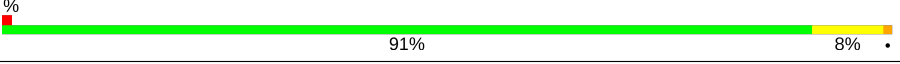
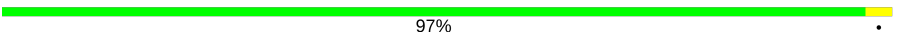
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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  $\geq 3$ , 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	484	<div> <div>2%</div> <div>89%</div> <div>10%</div> </div>
1	C	484	<div> <div>2%</div> <div>95%</div> <div>5%</div> </div>
1	E	484	<div> <div>%</div> <div>94%</div> <div>6%</div> </div>
1	G	484	<div> <div>96%</div> <div>.</div> </div>
2	I	139	<div> <div>%</div> <div>95%</div> <div>5%</div> </div>
2	J	139	<div> <div>%</div> <div>99%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
2	K	139	 91% 8%
2	L	139	 97%

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
1	HLU	E	174	-	X	-	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20045 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 biphosphate carboxylase large chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	0	0
			3768	2392	646	708	22			
1	C	482	Total	C	N	O	S	0	0	0
			3768	2392	646	708	22			
1	E	482	Total	C	N	O	S	0	0	0
			3768	2392	646	708	22			
1	G	482	Total	C	N	O	S	0	0	0
			3768	2392	646	708	22			

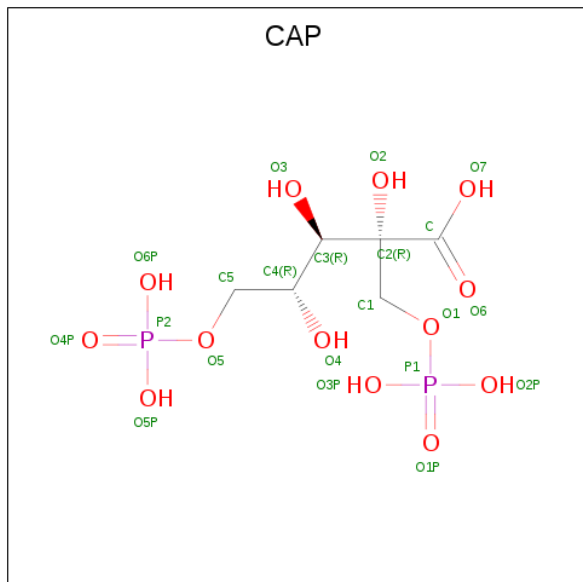
- Molecule 2 is a protein called Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	139	Total	C	N	O	S	0	0	0
			1115	709	187	211	8			
2	J	139	Total	C	N	O	S	0	0	0
			1115	709	187	211	8			
2	K	139	Total	C	N	O	S	0	0	0
			1115	709	187	211	8			
2	L	139	Total	C	N	O	S	0	0	0
			1115	709	187	211	8			

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

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

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



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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	I	1	Total	C	O	0	0
			4	2	2		
5	I	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	J	1	Total	C	O	0	0
			4	2	2		
5	J	1	Total	C	O	0	0
			4	2	2		
5	J	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	K	1	Total	C	O	0	0
			4	2	2		
5	K	1	Total	C	O	0	0
			4	2	2		
5	K	1	Total	C	O	0	0
			4	2	2		
5	K	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	G	1	Total	C	O	0	0
			4	2	2		
5	L	1	Total	C	O	0	0
			4	2	2		
5	L	1	Total	C	O	0	0
			4	2	2		
5	L	1	Total	C	O	0	0
			4	2	2		

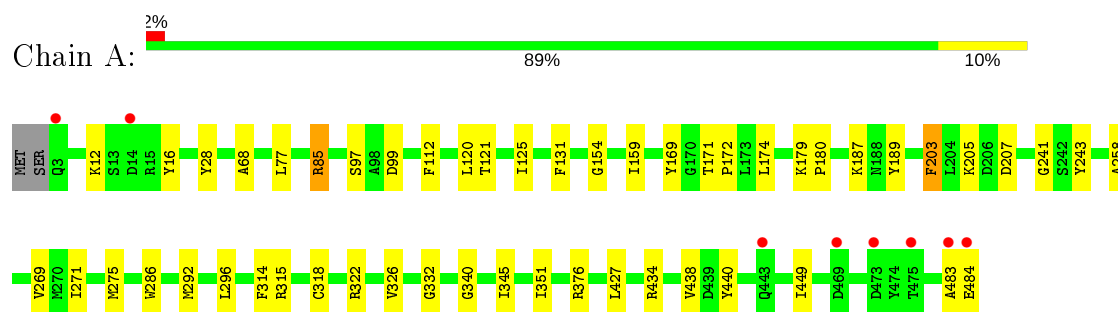
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	51	Total	O	0	0
			51	51		
6	I	22	Total	O	0	0
			22	22		
6	C	43	Total	O	0	0
			43	43		
6	J	21	Total	O	0	0
			21	21		
6	E	74	Total	O	0	0
			74	74		
6	K	34	Total	O	0	0
			34	34		
6	G	74	Total	O	0	0
			74	74		
6	L	34	Total	O	0	0
			34	34		

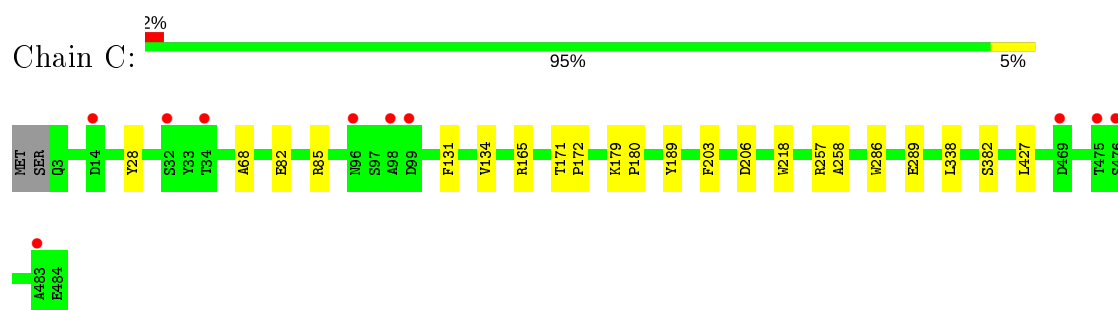
### 3 Residue-property plots [i](#)

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.

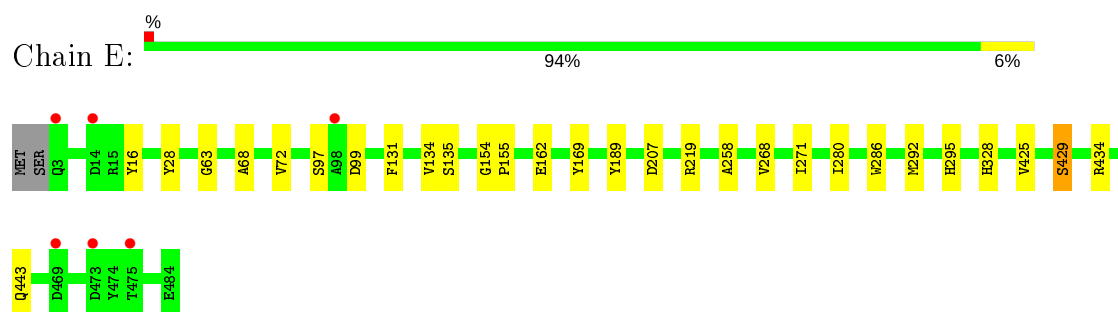
- Molecule 1: Ribulose biphosphate carboxylase large chain



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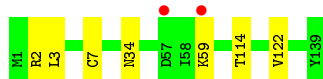
- Molecule 1: Ribulose biphosphate carboxylase large chain



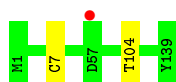




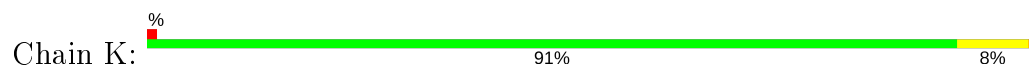
- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit



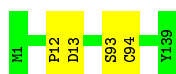
- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit



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- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.02Å 111.02Å 396.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.60 19.95 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.9 (19.96-2.60) 97.2 (19.95-2.60)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.68 (at 2.59Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, $R_{free}$	0.171 , 0.238 0.176 , 0.236	Depositor DCC
$R_{free}$ test set	3822 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.6	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 23.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	20045	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, LOH, CAP, EDO, KCX, HYP, M3L, LYO, HLU

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	0.60	0/3783	0.76	1/5123 (0.0%)
1	C	0.58	0/3783	0.77	2/5123 (0.0%)
1	E	0.59	0/3783	0.76	1/5123 (0.0%)
1	G	0.62	0/3783	0.81	4/5123 (0.1%)
2	I	0.59	0/1147	0.75	0/1558
2	J	0.58	0/1147	0.73	0/1558
2	K	0.61	0/1147	0.77	0/1558
2	L	0.59	0/1147	0.73	0/1558
All	All	0.60	0/19720	0.77	8/26724 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
2	I	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	315	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	G	110	ASP	CB-CG-OD1	5.71	123.44	118.30
1	G	110	ASP	CB-CG-OD2	-5.62	113.25	118.30
1	G	344	MET	CG-SD-CE	5.47	108.96	100.20
1	A	85	ARG	NE-CZ-NH2	-5.33	117.64	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	203	PHE	Peptide
1	C	203	PHE	Peptide
2	I	2	ARG	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3768	0	3686	24	0
1	C	3768	0	3686	9	0
1	E	3768	0	3686	13	0
1	G	3768	0	3686	5	0
2	I	1115	0	1057	2	0
2	J	1115	0	1057	1	0
2	K	1115	0	1057	6	0
2	L	1115	0	1057	2	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
4	A	21	0	9	0	0
4	C	21	0	8	0	0
4	E	21	0	8	0	0
4	G	21	0	9	0	0
5	C	4	0	6	0	0
5	E	8	0	12	0	0
5	G	8	0	12	0	0
5	I	8	0	12	0	0
5	J	12	0	18	1	0
5	K	20	0	30	0	0
5	L	12	0	18	0	0
6	A	51	0	0	0	0
6	C	43	0	0	0	0
6	E	74	0	0	0	0
6	G	74	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	I	22	0	0	0	0
6	J	21	0	0	0	0
6	K	34	0	0	0	0
6	L	34	0	0	0	0
All	All	20045	0	19114	59	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 2.

The worst 5 of 59 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:C:28:TYR:CZ	1:C:68:ALA:HB2	2.37	0.60
1:C:28:TYR:CE1	1:C:68:ALA:HB2	2.37	0.60
1:A:483:ALA:O	1:A:484:GLU:HB3	2.04	0.57
1:E:28:TYR:CZ	1:E:68:ALA:HB2	2.39	0.57
1:A:121:THR:O	1:A:125:ILE:HG12	2.06	0.56

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	474/484 (98%)	457 (96%)	16 (3%)	1 (0%)	47	71
1	C	474/484 (98%)	454 (96%)	20 (4%)	0	100	100
1	E	474/484 (98%)	454 (96%)	19 (4%)	1 (0%)	47	71
1	G	474/484 (98%)	453 (96%)	20 (4%)	1 (0%)	47	71
2	I	137/139 (99%)	131 (96%)	5 (4%)	1 (1%)	22	43
2	J	137/139 (99%)	135 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	K	137/139 (99%)	132 (96%)	5 (4%)	0	100	100
2	L	137/139 (99%)	134 (98%)	3 (2%)	0	100	100
All	All	2444/2492 (98%)	2350 (96%)	90 (4%)	4 (0%)	47	71

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	I	3	LEU
1	E	97	SER
1	A	340	GLY
1	G	340	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	386/388 (100%)	378 (98%)	8 (2%)	53	77
1	C	386/388 (100%)	380 (98%)	6 (2%)	62	82
1	E	386/388 (100%)	377 (98%)	9 (2%)	50	75
1	G	386/388 (100%)	381 (99%)	5 (1%)	69	86
2	I	118/118 (100%)	116 (98%)	2 (2%)	60	81
2	J	118/118 (100%)	117 (99%)	1 (1%)	81	92
2	K	118/118 (100%)	112 (95%)	6 (5%)	24	46
2	L	118/118 (100%)	118 (100%)	0	100	100
All	All	2016/2024 (100%)	1979 (98%)	37 (2%)	59	80

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	104	THR
1	E	135	SER
1	G	189	TYR

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Mol	Chain	Res	Type
1	E	99	ASP
1	E	131	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	230	ASN
1	G	230	ASN
1	E	230	ASN
1	A	404	GLN
2	K	105	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

20 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	M3L	G	346	1	10,11,12	0.77	1 (10%)	9,14,16	0.84	0
1	M3L	A	346	1	10,11,12	0.51	0	9,14,16	1.16	0
1	KCX	G	205	1,3	7,11,12	0.75	0	4,12,14	0.59	0
1	HYP	E	155	1	6,8,9	0.75	0	5,10,12	2.58	2 (40%)
1	KCX	A	205	1,3	7,11,12	0.38	0	4,12,14	0.75	0
1	HYP	G	155	1	6,8,9	0.58	0	5,10,12	2.87	3 (60%)
1	HYP	A	155	1	6,8,9	0.51	0	5,10,12	3.19	1 (20%)
1	KCX	E	205	1,3	7,11,12	0.58	0	4,12,14	1.11	0
1	HYP	C	155	1	6,8,9	0.54	0	5,10,12	1.73	2 (40%)
1	HLU	A	174	1	7,8,9	0.69	0	7,10,12	1.35	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	LYO	E	198	1	7,9,10	0.29	0	6,10,12	0.99	0
1	HLU	C	174	1	7,8,9	0.61	0	7,10,12	1.43	1 (14%)
1	LYO	C	198	1	7,9,10	0.35	0	6,10,12	0.88	0
1	KCX	C	205	1,3	7,11,12	0.48	0	4,12,14	0.55	0
1	LYO	A	198	1	7,9,10	0.60	0	6,10,12	0.81	0
1	HLU	G	174	1	7,8,9	0.71	0	7,10,12	2.01	3 (42%)
1	HLU	E	174	1	7,8,9	0.84	0	7,10,12	2.33	4 (57%)
1	M3L	E	346	1	10,11,12	0.48	0	9,14,16	0.80	0
1	LYO	G	198	1	7,9,10	0.47	0	6,10,12	0.62	0
1	M3L	C	346	1	10,11,12	0.48	0	9,14,16	0.68	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	M3L	G	346	1	-	3/9/10/12	-
1	M3L	A	346	1	-	3/9/10/12	-
1	KCX	G	205	1,3	-	0/7/10/12	-
1	HYP	E	155	1	-	0/0/11/13	0/1/1/1
1	KCX	A	205	1,3	-	0/7/10/12	-
1	HYP	G	155	1	-	0/0/11/13	0/1/1/1
1	HYP	A	155	1	-	0/0/11/13	0/1/1/1
1	KCX	E	205	1,3	-	0/7/10/12	-
1	HYP	C	155	1	-	0/0/11/13	0/1/1/1
1	HLU	A	174	1	-	8/9/10/12	-
1	LYO	E	198	1	-	2/8/9/11	-
1	HLU	C	174	1	-	5/9/10/12	-
1	LYO	C	198	1	-	1/8/9/11	-
1	KCX	C	205	1,3	-	0/7/10/12	-
1	LYO	A	198	1	-	4/8/9/11	-
1	HLU	G	174	1	-	8/9/10/12	-
1	HLU	E	174	1	-	8/9/10/12	-
1	M3L	E	346	1	-	2/9/10/12	-
1	LYO	G	198	1	-	2/8/9/11	-
1	M3L	C	346	1	-	1/9/10/12	-

All (1) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	346	M3L	CB-CA	-2.01	1.50	1.53

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	155	HYP	OD1-CG-CD	-6.62	95.87	110.35
1	G	155	HYP	CB-CG-CD	4.71	109.04	103.27
1	E	155	HYP	OD1-CG-CD	-4.38	100.77	110.35
1	E	174	HLU	OH-CB-CG	3.98	118.21	109.89
1	G	155	HYP	CG-CB-CA	-3.47	99.58	103.96

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	174	HLU	N-CA-CB-CG
1	A	174	HLU	N-CA-CB-OH
1	A	174	HLU	C-CA-CB-CG
1	A	174	HLU	O-C-CA-CB
1	E	198	LYO	O-C-CA-CB

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	155	HYP	1	0
1	A	205	KCX	1	0
1	A	174	HLU	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 4 are monoatomic - leaving 22 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	J	203	-	3,3,3	0.29	0	2,2,2	0.68	0
5	EDO	L	202	-	3,3,3	0.63	0	2,2,2	0.23	0
5	EDO	I	201	-	3,3,3	0.68	0	2,2,2	0.13	0
5	EDO	C	503	-	3,3,3	0.39	0	2,2,2	0.48	0
5	EDO	I	202	-	3,3,3	0.50	0	2,2,2	0.22	0
4	CAP	A	501	3	15,20,20	0.65	0	20,31,31	1.36	3 (15%)
5	EDO	J	202	-	3,3,3	0.80	0	2,2,2	0.20	0
5	EDO	L	201	-	3,3,3	0.65	0	2,2,2	0.44	0
5	EDO	K	204	-	3,3,3	0.67	0	2,2,2	0.26	0
5	EDO	K	201	-	3,3,3	0.64	0	2,2,2	0.55	0
5	EDO	L	203	-	3,3,3	0.50	0	2,2,2	0.06	0
5	EDO	E	504	-	3,3,3	0.71	0	2,2,2	0.19	0
4	CAP	G	502	3	15,20,20	0.72	0	20,31,31	1.33	2 (10%)
5	EDO	G	503	-	3,3,3	0.42	0	2,2,2	0.45	0
5	EDO	K	203	-	3,3,3	0.49	0	2,2,2	0.18	0
5	EDO	K	202	-	3,3,3	0.55	0	2,2,2	0.33	0
5	EDO	E	503	-	3,3,3	0.49	0	2,2,2	0.68	0
4	CAP	C	502	3	15,20,20	0.59	0	20,31,31	1.34	2 (10%)
5	EDO	K	205	-	3,3,3	0.52	0	2,2,2	0.18	0
5	EDO	G	504	-	3,3,3	0.52	0	2,2,2	0.27	0
5	EDO	J	201	-	3,3,3	0.52	0	2,2,2	0.63	0
4	CAP	E	502	3	15,20,20	0.76	0	20,31,31	1.23	3 (15%)

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	J	203	-	-	0/1/1/1	-
5	EDO	L	202	-	-	1/1/1/1	-
5	EDO	I	201	-	-	0/1/1/1	-
5	EDO	C	503	-	-	1/1/1/1	-
5	EDO	I	202	-	-	1/1/1/1	-
4	CAP	A	501	3	-	3/23/29/29	-
5	EDO	J	202	-	-	0/1/1/1	-
5	EDO	L	201	-	-	1/1/1/1	-
5	EDO	K	204	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	K	201	-	-	1/1/1/1	-
5	EDO	L	203	-	-	0/1/1/1	-
5	EDO	E	504	-	-	1/1/1/1	-
4	CAP	G	502	3	-	7/23/29/29	-
5	EDO	G	503	-	-	0/1/1/1	-
5	EDO	K	203	-	-	1/1/1/1	-
5	EDO	K	202	-	-	1/1/1/1	-
5	EDO	E	503	-	-	1/1/1/1	-
4	CAP	C	502	3	-	2/23/29/29	-
5	EDO	K	205	-	-	1/1/1/1	-
5	EDO	G	504	-	-	0/1/1/1	-
5	EDO	J	201	-	-	0/1/1/1	-
4	CAP	E	502	3	-	5/23/29/29	-

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	502	CAP	O3P-P1-O1	-3.32	97.91	106.73
4	E	502	CAP	O6P-P2-O5P	3.17	119.76	107.64
4	C	502	CAP	O4-C4-C5	-2.92	103.35	109.92
4	E	502	CAP	O6P-P2-O5	-2.68	99.59	106.73
4	A	501	CAP	O5-P2-O4P	-2.66	99.01	106.47

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

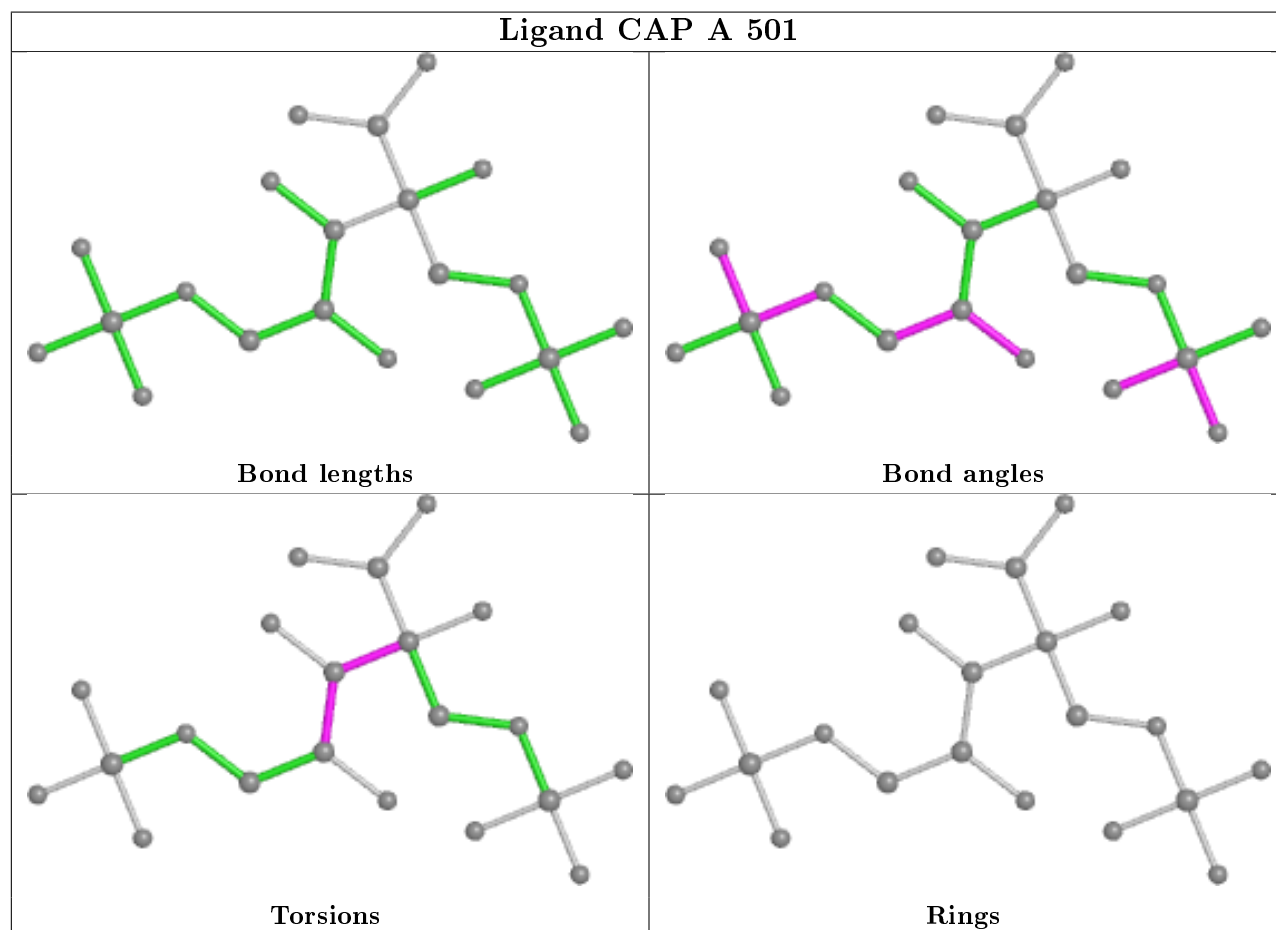
Mol	Chain	Res	Type	Atoms
4	A	501	CAP	O3-C3-C4-O4
4	G	502	CAP	O1-C1-C2-C
4	G	502	CAP	O1-C1-C2-O2
4	G	502	CAP	C2-C3-C4-O4
4	G	502	CAP	O3-C3-C4-O4

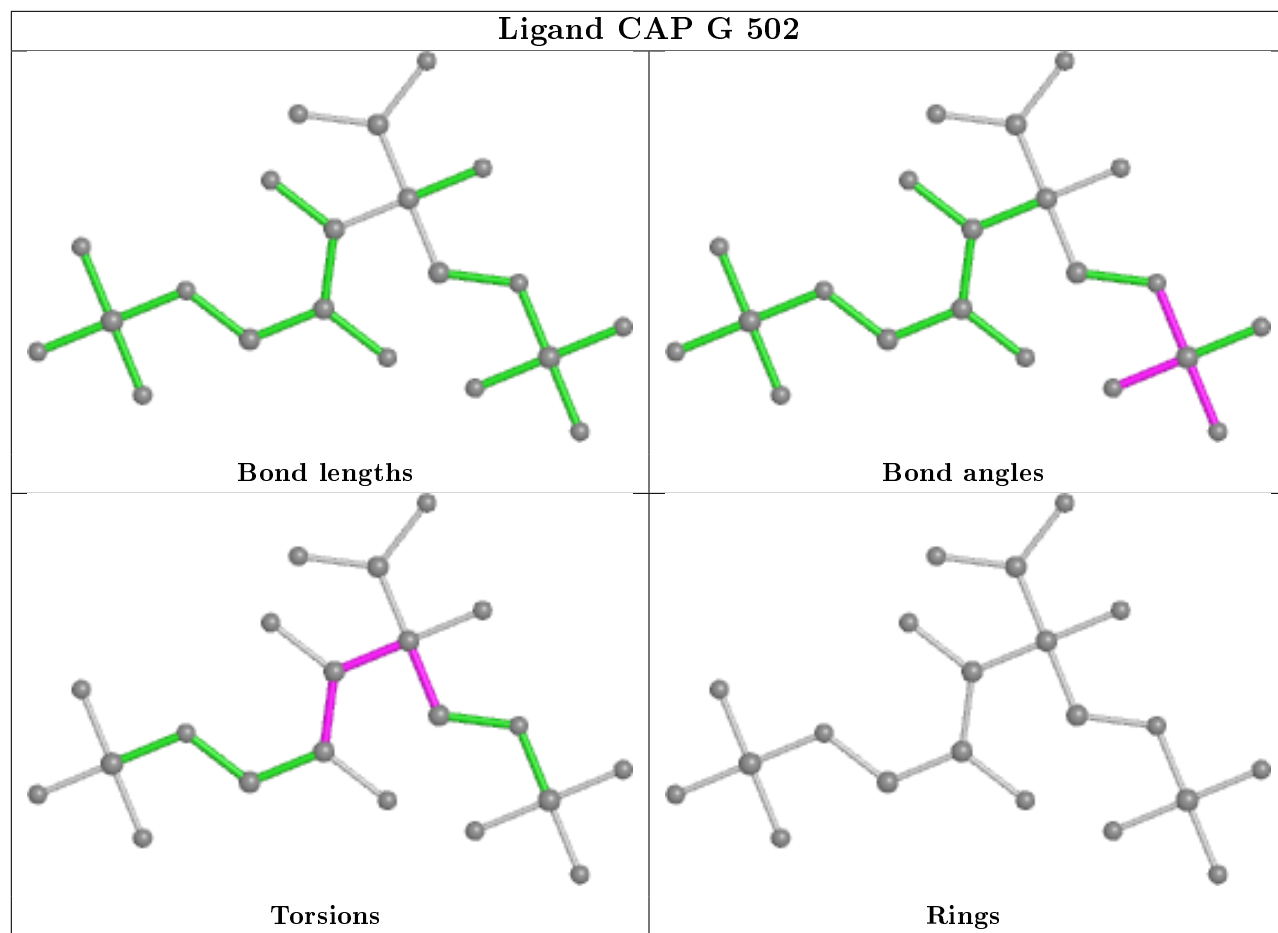
There are no ring outliers.

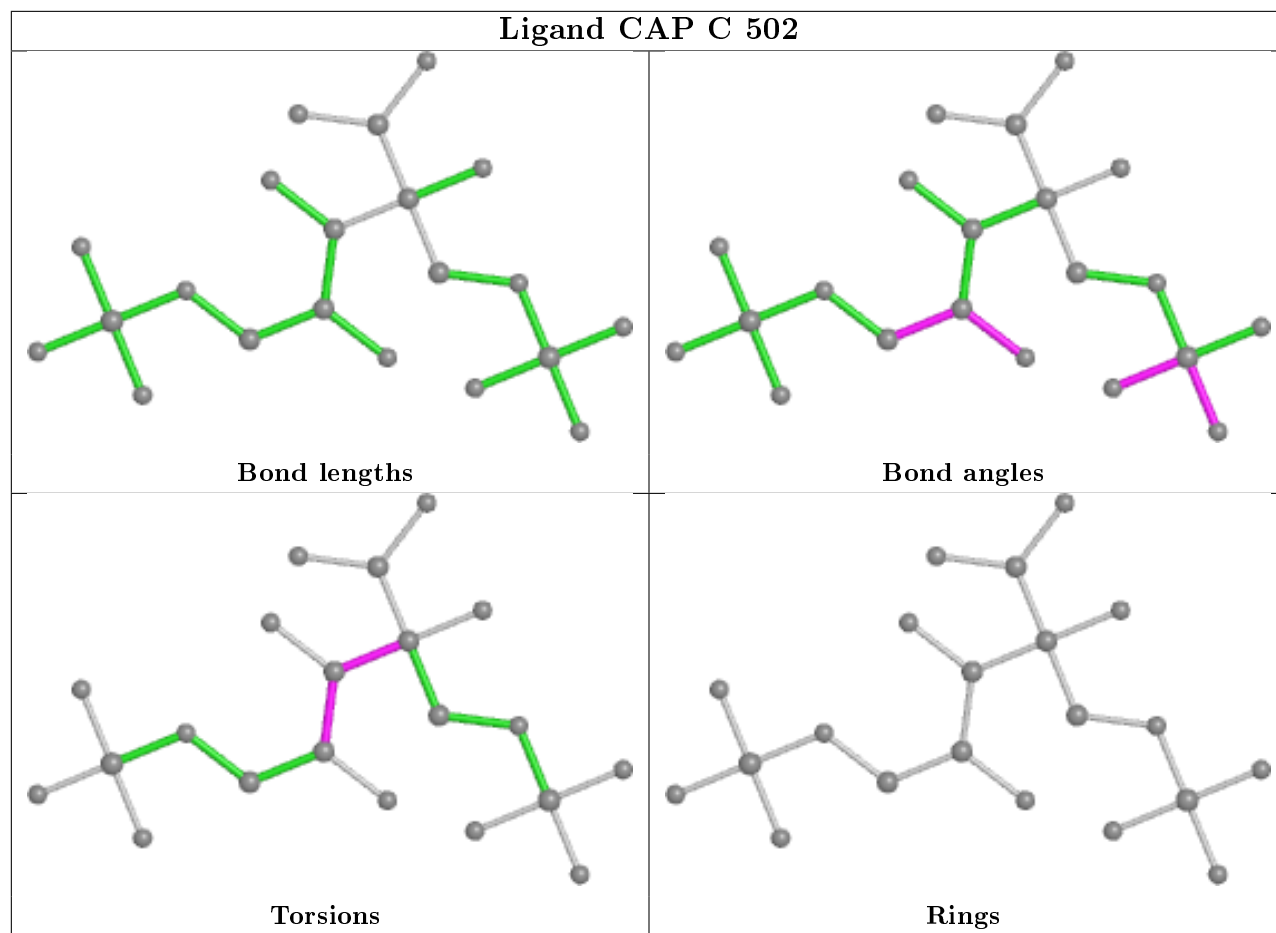
1 monomer is involved in 1 short contact:

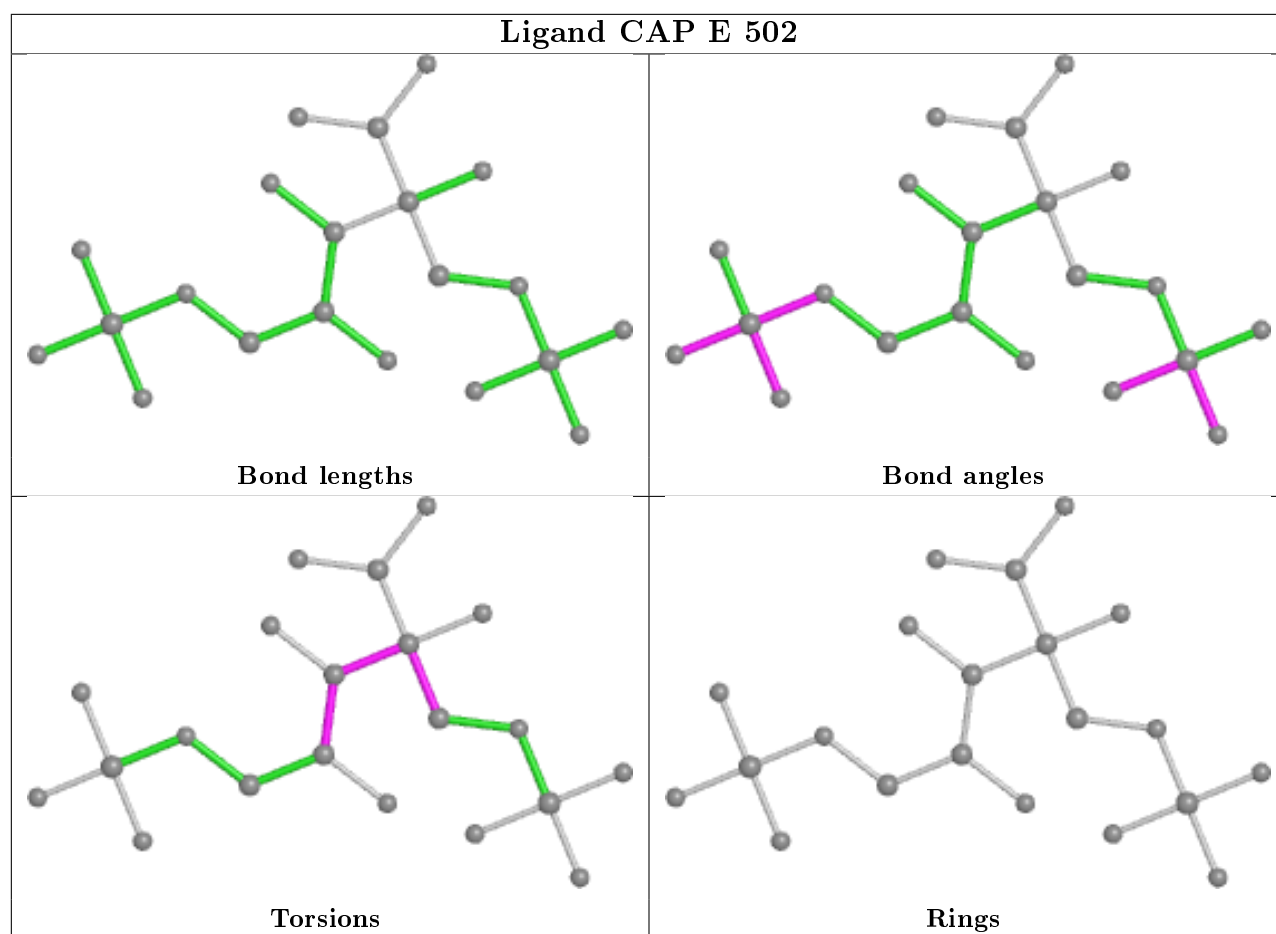
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	J	203	EDO	1	0

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, 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	476/484 (98%)	-0.62	8 (1%) 70 66	17, 29, 52, 73	0
1	C	476/484 (98%)	-0.51	10 (2%) 63 58	20, 34, 55, 71	0
1	E	476/484 (98%)	-0.66	6 (1%) 77 73	17, 27, 48, 65	0
1	G	476/484 (98%)	-0.81	0 100 100	13, 20, 40, 59	0
2	I	139/139 (100%)	-0.56	2 (1%) 75 71	17, 30, 44, 65	0
2	J	139/139 (100%)	-0.62	1 (0%) 87 86	20, 29, 44, 64	0
2	K	139/139 (100%)	-0.69	2 (1%) 75 71	19, 24, 37, 61	0
2	L	139/139 (100%)	-0.76	0 100 100	18, 24, 33, 47	0
All	All	2460/2492 (98%)	-0.65	29 (1%) 79 76	13, 27, 49, 73	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	96	ASN	4.3
1	C	475	THR	4.0
1	C	98	ALA	3.5
1	E	469	ASP	3.4
1	A	469	ASP	3.3

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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	M3L	C	346	12/13	0.91	0.20	35,40,45,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
1	M3L	A	346	12/13	0.92	0.17	31,33,37,37	0
1	LYO	A	198	10/11	0.93	0.16	25,26,26,27	0
1	HYP	E	155	8/9	0.93	0.13	18,18,18,18	0
1	M3L	E	346	12/13	0.94	0.16	29,32,34,35	0
1	M3L	G	346	12/13	0.94	0.13	21,23,26,26	0
1	HLU	A	174	9/10	0.95	0.13	28,29,31,31	0
1	LYO	E	198	10/11	0.95	0.15	24,25,27,27	0
1	HYP	G	155	8/9	0.95	0.11	16,16,16,16	0
1	HYP	A	155	8/9	0.95	0.10	23,23,24,24	0
1	HYP	C	155	8/9	0.95	0.11	24,25,26,27	0
1	KCX	E	205	12/13	0.96	0.12	22,22,23,23	0
1	LYO	C	198	10/11	0.96	0.12	28,30,31,31	0
1	LYO	G	198	10/11	0.96	0.10	18,19,20,20	0
1	KCX	C	205	12/13	0.96	0.12	25,25,26,26	0
1	HLU	G	174	9/10	0.97	0.11	20,20,21,21	0
1	HLU	E	174	9/10	0.97	0.11	24,24,25,26	0
1	KCX	G	205	12/13	0.97	0.10	16,16,17,17	0
1	KCX	A	205	12/13	0.97	0.10	22,23,23,24	0
1	HLU	C	174	9/10	0.97	0.13	29,30,31,31	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, 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.

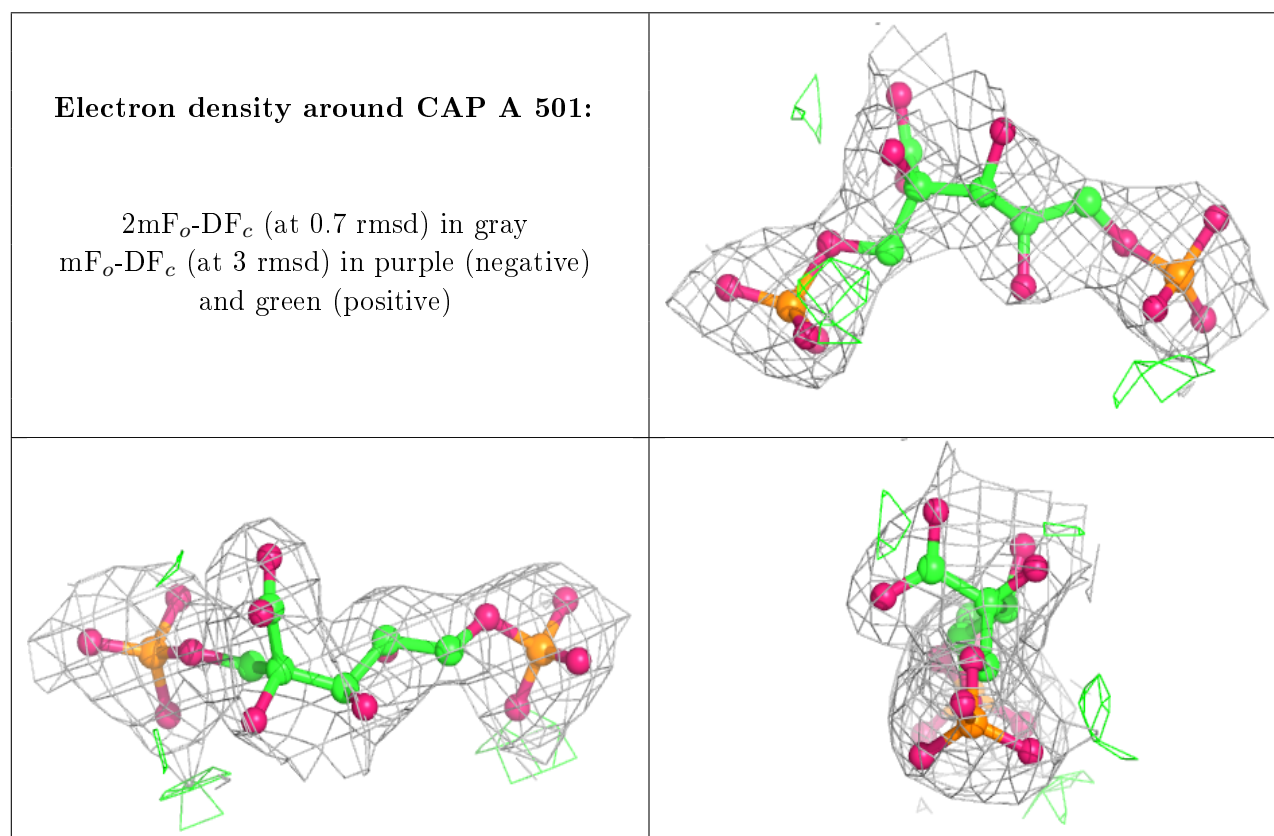
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	EDO	K	204	4/4	0.81	0.20	32,32,32,32	0
5	EDO	E	503	4/4	0.84	0.18	35,36,36,36	0
5	EDO	J	202	4/4	0.91	0.20	22,22,22,23	0
5	EDO	J	203	4/4	0.92	0.12	22,23,23,23	0
5	EDO	K	201	4/4	0.92	0.14	33,33,34,35	0
5	EDO	K	205	4/4	0.93	0.20	35,35,36,36	0
5	EDO	G	503	4/4	0.94	0.14	28,28,29,29	0
5	EDO	E	504	4/4	0.94	0.30	33,33,33,33	0
3	MG	C	501	1/1	0.95	0.05	34,34,34,34	0

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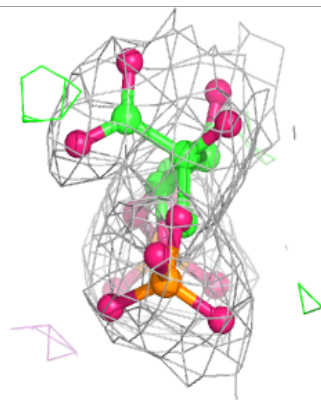
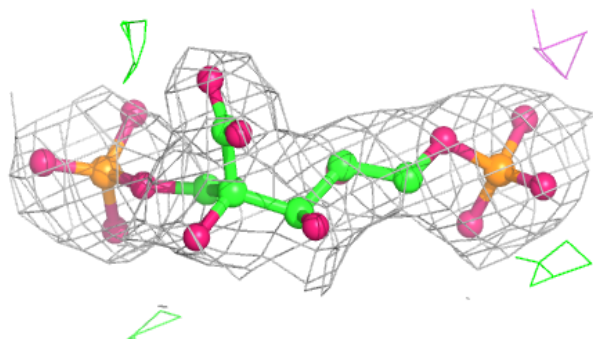
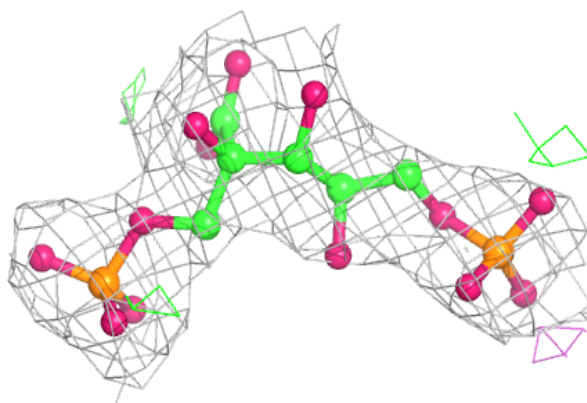
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	EDO	L	202	4/4	0.95	0.17	21,21,21,22	0
5	EDO	J	201	4/4	0.95	0.14	27,27,28,28	0
5	EDO	L	203	4/4	0.96	0.12	17,18,18,18	0
5	EDO	I	201	4/4	0.96	0.13	29,30,30,30	0
5	EDO	L	201	4/4	0.96	0.11	27,27,28,28	0
5	EDO	G	504	4/4	0.96	0.10	41,42,42,42	0
5	EDO	K	203	4/4	0.96	0.14	22,23,23,23	0
5	EDO	K	202	4/4	0.97	0.11	19,19,19,19	0
3	MG	G	501	1/1	0.97	0.03	16,16,16,16	0
5	EDO	I	202	4/4	0.97	0.20	20,20,20,20	0
4	CAP	A	501	21/21	0.98	0.08	25,26,27,27	0
5	EDO	C	503	4/4	0.98	0.12	21,21,21,22	0
3	MG	E	501	1/1	0.98	0.08	33,33,33,33	0
4	CAP	C	502	21/21	0.98	0.09	31,32,33,34	0
4	CAP	E	502	21/21	0.98	0.08	26,27,28,28	0
3	MG	A	500	1/1	0.99	0.04	27,27,27,27	0
4	CAP	G	502	21/21	0.99	0.09	18,18,19,19	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.

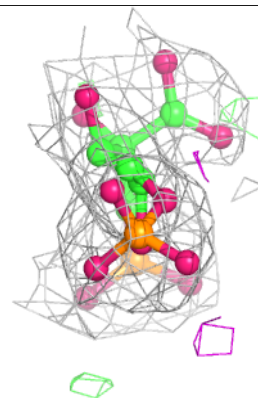
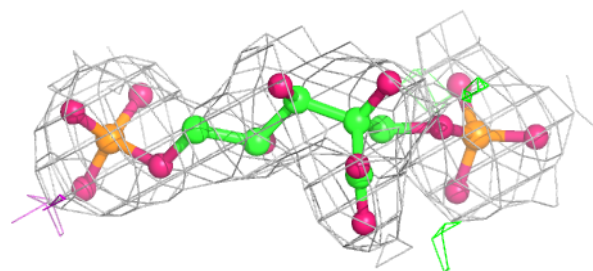
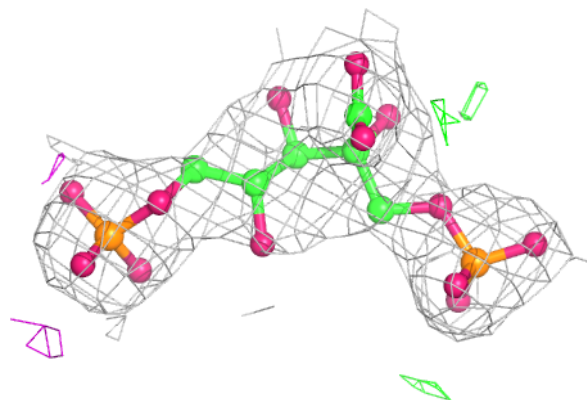


**Electron density around CAP C 502:**

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

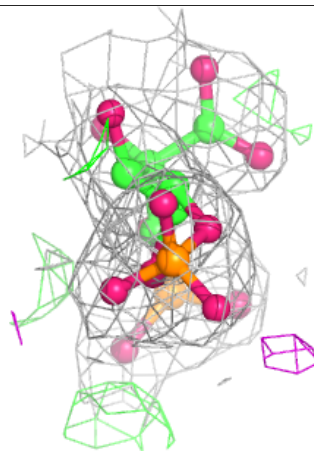
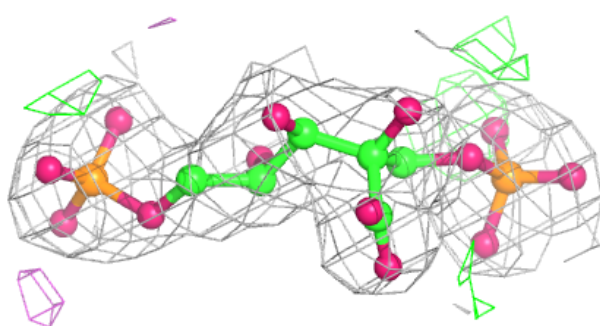
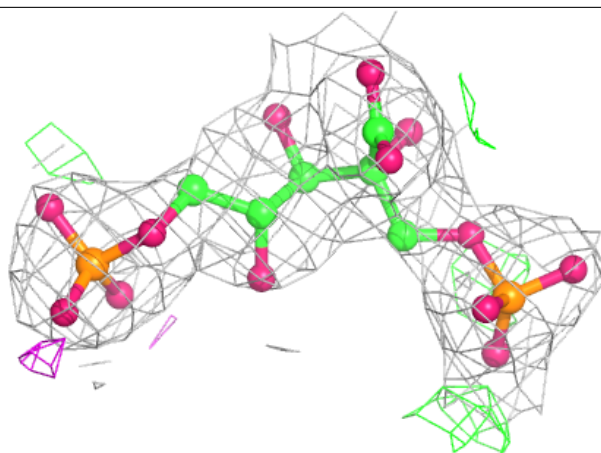
**Electron density around CAP E 502:**

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



**Electron density around CAP G 502:**

$2mF_o-DF_c$  (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.