



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 27, 2026 – 01:21 AM UTC

PDB ID : 5N9Z / pdb_00005n9z
Title : Rubisco from *Thalassiosira hyalina*
Authors : Andersson, I.; Valegard, K.
Deposited on : 2017-02-27
Resolution : 1.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

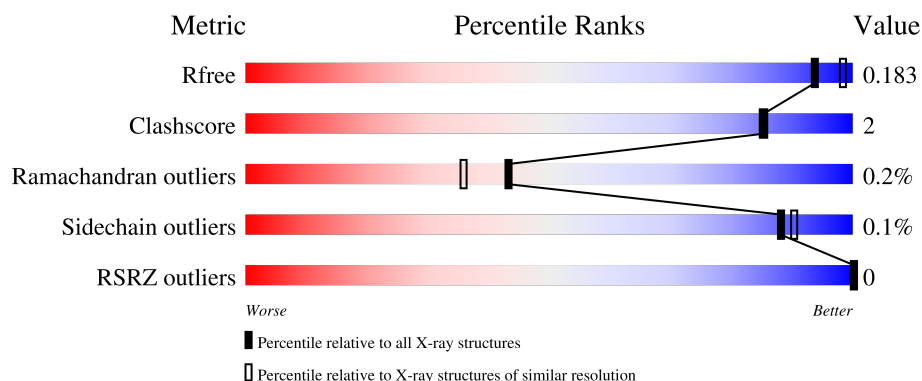
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

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



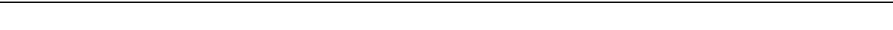
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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

Mol	Chain	Length	Quality of chain
1	A	490	92% 6% .
1	B	490	91% 7% .
1	C	490	91% 7% .
1	D	490	91% 7% .
1	E	490	92% 7% .

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Mol	Chain	Length	Quality of chain
1	F	490	 91% 7% .
1	G	490	 92% 6% .
1	H	490	 92% 7% .
2	I	139	 94% 6%
2	J	139	 93% 7%
2	K	139	 95% 5%
2	L	139	 96% .
2	M	139	 98% .
2	N	139	 94% 6%
2	O	139	 95% 5%
2	P	139	 95% 5%

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	A	174	-	X	-	-
1	HLU	B	174	-	X	-	-
1	HLU	C	174	-	X	-	-
1	HLU	D	174	-	X	-	-
1	HLU	E	174	-	X	-	-
1	HLU	F	174	-	X	-	-
1	HLU	G	174	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 42506 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	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	H	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	F	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	D	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	B	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	C	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	E	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			
1	G	481	Total	C	N	O	S	0	1	0
			3764	2389	647	707	21			

- 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	1	0
			1130	714	193	215	8			
2	O	139	Total	C	N	O	S	0	0	0
			1122	710	191	213	8			
2	N	139	Total	C	N	O	S	0	1	0
			1130	714	193	215	8			
2	M	139	Total	C	N	O	S	0	1	0
			1130	714	193	215	8			
2	P	139	Total	C	N	O	S	0	1	0
			1130	714	193	215	8			
2	J	139	Total	C	N	O	S	0	1	0
			1130	714	193	215	8			

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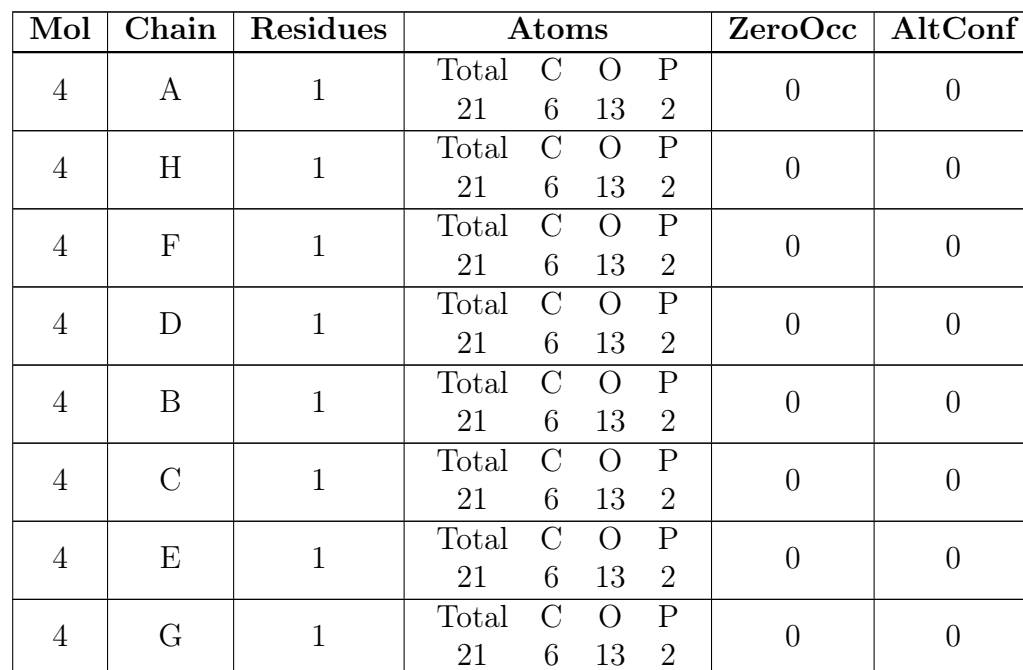
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	139	Total	C	N	O	S	0	1	0
			1130	714	193	215	8			
2	L	139	Total	C	N	O	S	0	1	0
			1130	714	193	215	8			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	I	1	Total	Mg	0	0
			1	1		
3	H	1	Total	Mg	0	0
			1	1		
3	F	1	Total	Mg	0	0
			1	1		
3	N	1	Total	Mg	0	0
			1	1		
3	D	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	E	1	Total	Mg	0	0
			1	1		
3	G	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (CCD ID: CAP) (formula: C₆H₁₄O₁₃P₂).



- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $\text{C}_2\text{H}_6\text{O}_2$).



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

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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	267	Total	O	0	0
			267	267		
6	I	93	Total	O	0	0
			93	93		
6	H	298	Total	O	0	0
			298	298		
6	O	103	Total	O	0	0
			103	103		
6	F	297	Total	O	0	0
			297	297		
6	N	97	Total	O	0	0
			97	97		
6	D	295	Total	O	0	0
			295	295		
6	M	101	Total	O	0	0
			101	101		
6	B	261	Total	O	0	0
			261	261		
6	P	93	Total	O	0	0
			93	93		
6	C	298	Total	O	0	0
			298	298		
6	J	96	Total	O	0	0
			96	96		
6	E	311	Total	O	0	0
			311	311		
6	K	95	Total	O	0	0
			95	95		

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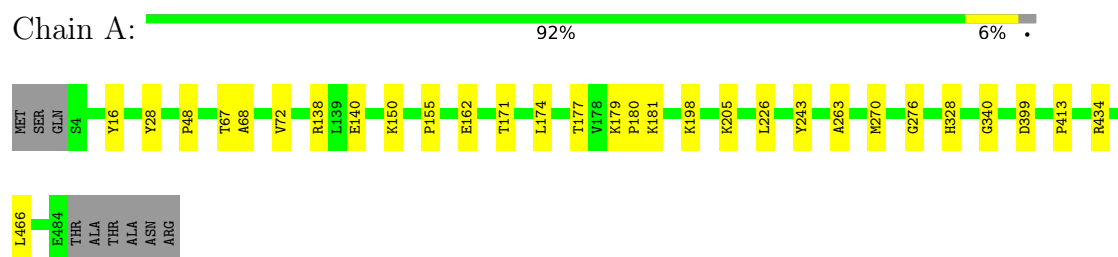
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	307	Total 307	O 307	0	0
6	L	96	Total 96	O 96	0	0

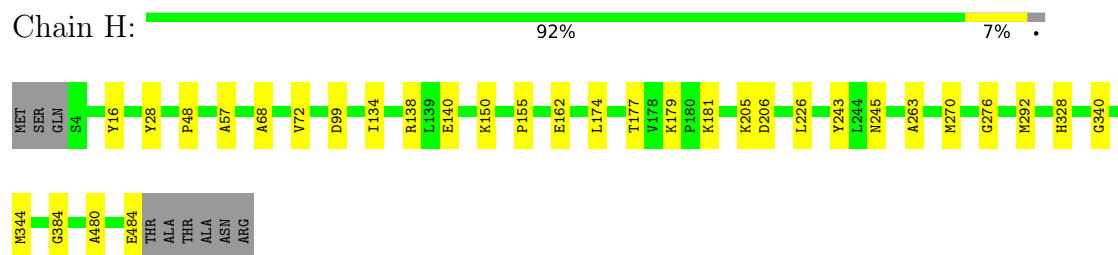
3 Residue-property plots [i](#)

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.

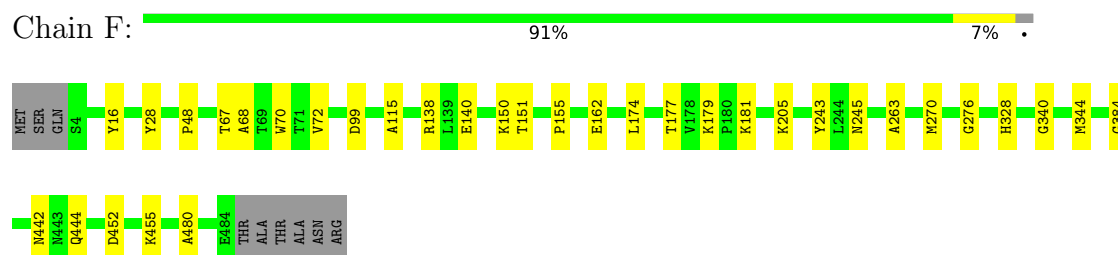
- Molecule 1: Ribulose biphosphate carboxylase large chain



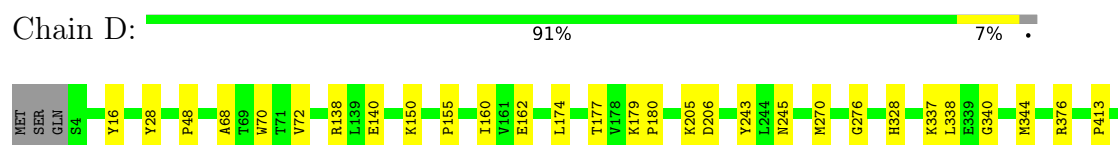
- Molecule 1: Ribulose biphosphate carboxylase large chain

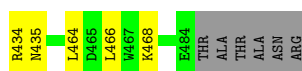


- Molecule 1: Ribulose biphosphate carboxylase large chain



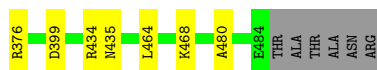
- Molecule 1: Ribulose biphosphate carboxylase large chain





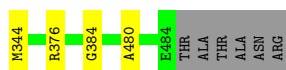
- Molecule 1: Ribulose biphosphate carboxylase large chain

Chain B: 91% 7%



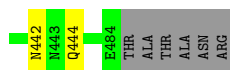
- Molecule 1: Ribulose biphosphate carboxylase large chain

Chain C: 91% 7%



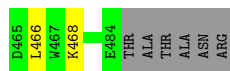
- Molecule 1: Ribulose biphosphate carboxylase large chain

Chain E: 92% 7%



- Molecule 1: Ribulose biphosphate carboxylase large chain

Chain G: 92% 6%

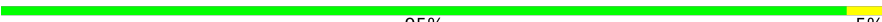


- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit

Chain I: 94% 6%



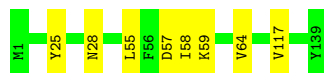
- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit

Chain O:  95% 5%

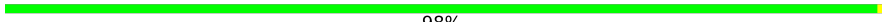


- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit

Chain N:  94% 6%

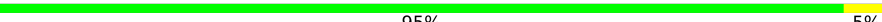


- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit

Chain M:  98% .



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

Chain P:  95% 5%

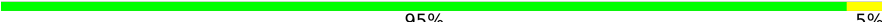


- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit

Chain J:  93% 7%

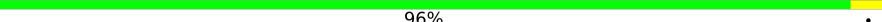


- Molecule 2: Ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit

Chain K:  95% 5%



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

Chain L:  96% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	117.99Å 219.99Å 124.27Å 90.00° 118.34° 90.00°	Depositor
Resolution (Å)	62.03 – 1.90 62.03 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.0 (62.03-1.90) 99.0 (62.03-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.83 (at 1.90Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.150 , 0.182 0.153 , 0.183	Depositor DCC
R_{free} test set	21717 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	17.0	Xtriage
Anisotropy	0.271	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 22.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.487 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	42506	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.08% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HLU, 8RE, HYP, MG, LYO, EDO, CAP, KCX, M3L, CSO

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	0.30	0/3763	0.48	0/5094
1	B	0.28	0/3763	0.49	0/5094
1	C	0.30	0/3763	0.51	0/5094
1	D	0.31	0/3763	0.52	0/5094
1	E	0.30	0/3763	0.52	0/5094
1	F	0.30	0/3763	0.52	0/5094
1	G	0.31	0/3763	0.54	1/5094 (0.0%)
1	H	0.31	0/3763	0.51	0/5094
2	I	0.27	0/1161	0.45	0/1576
2	J	0.29	0/1161	0.46	0/1576
2	K	0.29	0/1161	0.46	0/1576
2	L	0.29	0/1161	0.47	0/1576
2	M	0.27	0/1161	0.45	0/1576
2	N	0.29	0/1161	0.46	0/1576
2	O	0.27	0/1153	0.47	0/1565
2	P	0.28	0/1161	0.47	0/1576
All	All	0.30	0/39384	0.50	1/53349 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	203	PHE	CA-CB-CG	9.39	123.19	113.80

There are no chirality outliers.

There are no planarity outliers.

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	3764	0	3688	15	0
1	B	3764	0	3688	18	0
1	C	3764	0	3688	18	0
1	D	3764	0	3688	17	0
1	E	3764	0	3688	20	0
1	F	3764	0	3688	19	0
1	G	3764	0	3688	18	0
1	H	3764	0	3688	18	0
2	I	1130	0	1061	9	0
2	J	1130	0	1061	8	0
2	K	1130	0	1061	7	0
2	L	1130	0	1061	4	0
2	M	1130	0	1061	3	0
2	N	1130	0	1061	7	0
2	O	1122	0	1056	5	0
2	P	1130	0	1061	7	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	N	1	0	0	0	0
4	A	21	0	7	0	0
4	B	21	0	8	0	0
4	C	21	0	7	0	0
4	D	21	0	8	0	0
4	E	21	0	7	0	0
4	F	21	0	7	0	0
4	G	21	0	7	0	0
4	H	21	0	7	0	0
5	A	4	0	6	0	0
5	I	12	0	18	2	0
5	J	8	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	K	16	0	24	2	0
5	L	4	0	6	0	0
5	M	12	0	18	0	0
5	N	4	0	6	0	0
5	O	12	0	18	0	0
5	P	4	0	6	0	0
6	A	267	0	0	1	0
6	B	261	0	0	1	0
6	C	298	0	0	1	0
6	D	295	0	0	1	0
6	E	311	0	0	2	0
6	F	297	0	0	2	0
6	G	307	0	0	1	0
6	H	298	0	0	3	0
6	I	93	0	0	0	0
6	J	96	0	0	1	0
6	K	95	0	0	1	0
6	L	96	0	0	0	0
6	M	101	0	0	0	0
6	N	97	0	0	1	0
6	O	103	0	0	0	0
6	P	93	0	0	0	0
All	All	42506	0	38159	171	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 171 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)
2:N:25:TYR:O	2:N:28:ASN:OD1	1.74	1.03
1:A:276:GLY:HA3	1:B:276:GLY:HA3	1.59	0.83
1:H:276:GLY:HA3	1:G:276:GLY:HA3	1.62	0.81
1:C:160:ILE:HD11	1:C:376:ARG:HH11	1.47	0.78
1:D:276:GLY:HA3	1:C:276:GLY:HA3	1.64	0.78

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	472/490 (96%)	461 (98%)	10 (2%)	1 (0%)	43	36
1	B	472/490 (96%)	460 (98%)	11 (2%)	1 (0%)	43	36
1	C	472/490 (96%)	460 (98%)	11 (2%)	1 (0%)	43	36
1	D	472/490 (96%)	461 (98%)	10 (2%)	1 (0%)	43	36
1	E	472/490 (96%)	460 (98%)	11 (2%)	1 (0%)	43	36
1	F	472/490 (96%)	459 (97%)	12 (2%)	1 (0%)	43	36
1	G	472/490 (96%)	458 (97%)	13 (3%)	1 (0%)	43	36
1	H	472/490 (96%)	460 (98%)	11 (2%)	1 (0%)	43	36
2	I	138/139 (99%)	137 (99%)	1 (1%)	0	100	100
2	J	138/139 (99%)	136 (99%)	2 (1%)	0	100	100
2	K	138/139 (99%)	137 (99%)	1 (1%)	0	100	100
2	L	138/139 (99%)	136 (99%)	1 (1%)	1 (1%)	18	10
2	M	138/139 (99%)	136 (99%)	2 (1%)	0	100	100
2	N	138/139 (99%)	137 (99%)	1 (1%)	0	100	100
2	O	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
2	P	138/139 (99%)	137 (99%)	1 (1%)	0	100	100
All	All	4879/5032 (97%)	4771 (98%)	99 (2%)	9 (0%)	43	36

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	57	ASP
1	A	340	GLY
1	H	340	GLY
1	F	340	GLY
1	C	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	382/388 (98%)	380 (100%)	2 (0%)	81	84
1	B	382/388 (98%)	380 (100%)	2 (0%)	81	84
1	C	382/388 (98%)	379 (99%)	3 (1%)	73	75
1	D	382/388 (98%)	382 (100%)	0	100	100
1	E	382/388 (98%)	382 (100%)	0	100	100
1	F	382/388 (98%)	382 (100%)	0	100	100
1	G	382/388 (98%)	382 (100%)	0	100	100
1	H	382/388 (98%)	380 (100%)	2 (0%)	81	84
2	I	120/120 (100%)	120 (100%)	0	100	100
2	J	120/120 (100%)	120 (100%)	0	100	100
2	K	120/120 (100%)	120 (100%)	0	100	100
2	L	120/120 (100%)	120 (100%)	0	100	100
2	M	120/120 (100%)	120 (100%)	0	100	100
2	N	120/120 (100%)	120 (100%)	0	100	100
2	O	119/120 (99%)	119 (100%)	0	100	100
2	P	120/120 (100%)	120 (100%)	0	100	100
All	All	4015/4064 (99%)	4006 (100%)	9 (0%)	88	90

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	226[A]	LEU
1	C	226[B]	LEU
1	H	226[B]	LEU
1	B	226[A]	LEU
1	B	226[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	167	ASN
1	E	96	ASN
2	J	28	ASN
1	E	167	ASN
1	F	417	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

64 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	CSO	D	109	1	3,6,7	0.81	0	1,6,8	0.23	0
1	HLU	D	174	1	7,8,9	0.87	0	7,10,12	2.17	4 (57%)
1	M3L	H	346	1	10,11,12	0.53	0	9,14,16	0.49	0
1	HLU	F	174	1	7,8,9	0.76	0	7,10,12	2.74	5 (71%)
1	HYP	D	155	1	7,8,9	0.86	0	5,10,12	1.94	2 (40%)
1	M3L	B	346	1	10,11,12	0.50	0	9,14,16	0.38	0
1	LYO	C	198	1	7,9,10	0.38	0	7,10,12	0.87	0
1	LYO	A	198	1	7,9,10	0.50	0	7,10,12	1.57	1 (14%)
1	LYO	E	198	1	7,9,10	0.37	0	7,10,12	0.72	0
1	KCX	A	205	3,1	10,11,12	1.04	1 (10%)	6,12,14	1.55	1 (16%)
1	LYO	B	198	1	7,9,10	0.48	0	7,10,12	1.29	1 (14%)
1	M3L	D	346	1	10,11,12	0.55	0	9,14,16	0.49	0
1	HYP	C	155	1	7,8,9	0.89	0	5,10,12	1.65	2 (40%)
1	M3L	F	346	1	10,11,12	0.51	0	9,14,16	0.52	0
1	M3L	C	346	1	10,11,12	0.55	0	9,14,16	0.50	0
1	M3L	E	346	1	10,11,12	0.52	0	9,14,16	0.58	0
1	8RE	E	150	1	9,10,11	0.75	0	7,12,14	2.35	4 (57%)
1	HYP	E	155	1	7,8,9	0.87	0	5,10,12	1.29	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	HLU	C	174	1	7,8,9	0.80	0	7,10,12	2.22	4 (57%)
1	HYP	H	155	1	7,8,9	0.89	0	5,10,12	1.63	2 (40%)
1	CSO	A	109	1	3,6,7	0.79	0	1,6,8	0.37	0
1	HLU	G	174	1	7,8,9	0.87	0	7,10,12	2.33	4 (57%)
1	LYO	F	198	1	7,9,10	0.40	0	7,10,12	0.65	0
1	HYP	A	155	1	7,8,9	0.75	0	5,10,12	1.66	1 (20%)
1	CSO	H	109	1	3,6,7	0.85	0	1,6,8	0.37	0
1	M3L	A	346	1	10,11,12	0.54	0	9,14,16	0.39	0
1	HYP	C	48	1	7,8,9	0.79	0	5,10,12	2.35	3 (60%)
1	HLU	H	174	1	7,8,9	0.79	0	7,10,12	2.12	3 (42%)
1	CSO	C	109	1	3,6,7	0.83	0	1,6,8	0.26	0
1	LYO	G	198	1	7,9,10	0.42	0	7,10,12	0.84	0
1	HYP	E	48	1	7,8,9	0.98	0	5,10,12	1.88	2 (40%)
1	CSO	E	109	1	3,6,7	0.74	0	1,6,8	0.04	0
1	HLU	E	174	1	7,8,9	0.74	0	7,10,12	2.61	4 (57%)
1	HYP	B	155	1	7,8,9	0.83	0	5,10,12	1.54	1 (20%)
1	KCX	D	205	3,1	10,11,12	1.11	1 (10%)	6,12,14	1.59	1 (16%)
1	HYP	H	48	1	7,8,9	0.76	0	5,10,12	2.29	3 (60%)
1	KCX	C	205	3,1	10,11,12	1.07	0	6,12,14	0.89	1 (16%)
1	HYP	F	155	1	7,8,9	0.88	0	5,10,12	1.32	1 (20%)
1	HYP	B	48	1	7,8,9	0.98	0	5,10,12	2.26	2 (40%)
1	CSO	B	109	1	3,6,7	0.74	0	1,6,8	0.30	0
1	KCX	G	205	3,1	10,11,12	1.13	2 (20%)	6,12,14	1.58	1 (16%)
1	8RE	C	150	1	9,10,11	0.69	0	7,12,14	2.28	3 (42%)
1	HYP	A	48	1	7,8,9	0.91	0	5,10,12	2.19	3 (60%)
1	CSO	F	109	1	3,6,7	0.71	0	1,6,8	0.12	0
1	8RE	F	150	1	9,10,11	0.77	0	7,12,14	2.47	4 (57%)
1	HLU	B	174	1	7,8,9	0.82	0	7,10,12	2.25	4 (57%)
1	8RE	D	150	1	9,10,11	0.66	0	7,12,14	2.28	3 (42%)
1	8RE	G	150	1	9,10,11	0.68	0	7,12,14	2.19	3 (42%)
1	LYO	H	198	1	7,9,10	0.38	0	7,10,12	0.85	0
1	M3L	G	346	1	10,11,12	0.56	0	9,14,16	0.51	0
1	HYP	D	48	1	7,8,9	0.89	0	5,10,12	2.23	2 (40%)
1	8RE	H	150	1	9,10,11	0.72	0	7,12,14	2.29	4 (57%)
1	8RE	A	150	1	9,10,11	0.55	0	7,12,14	2.14	2 (28%)
1	8RE	B	150	1	9,10,11	0.57	0	7,12,14	2.07	2 (28%)
1	HYP	F	48	1	7,8,9	0.90	0	5,10,12	2.00	3 (60%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	KCX	E	205	3,1	10,11,12	1.01	0	6,12,14	0.86	1 (16%)
1	CSO	G	109	1	3,6,7	0.81	0	1,6,8	0.11	0
1	HLU	A	174	1	7,8,9	0.80	0	7,10,12	2.54	4 (57%)
1	LYO	D	198	1	7,9,10	0.39	0	7,10,12	0.93	0
1	KCX	H	205	3,1	10,11,12	1.04	1 (10%)	6,12,14	0.97	1 (16%)
1	KCX	B	205	3,1	10,11,12	1.01	1 (10%)	6,12,14	1.67	1 (16%)
1	HYP	G	48	1	7,8,9	0.86	0	5,10,12	2.24	3 (60%)
1	KCX	F	205	3,1	10,11,12	0.98	0	6,12,14	0.92	1 (16%)
1	HYP	G	155	1	7,8,9	0.89	0	5,10,12	1.69	2 (40%)

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	CSO	D	109	1	-	0/1/5/7	-
1	HLU	D	174	1	-	8/9/10/12	-
1	M3L	H	346	1	-	2/9/10/12	-
1	HLU	F	174	1	-	8/9/10/12	-
1	HYP	D	155	1	-	0/0/11/13	0/1/1/1
1	M3L	B	346	1	-	2/9/10/12	-
1	LYO	C	198	1	-	1/8/9/11	-
1	LYO	A	198	1	-	2/8/9/11	-
1	LYO	E	198	1	-	1/8/9/11	-
1	KCX	A	205	3,1	-	0/9/10/12	-
1	LYO	B	198	1	-	2/8/9/11	-
1	M3L	D	346	1	-	1/9/10/12	-
1	HYP	C	155	1	-	0/0/11/13	0/1/1/1
1	M3L	F	346	1	-	2/9/10/12	-
1	M3L	C	346	1	-	1/9/10/12	-
1	M3L	E	346	1	-	1/9/10/12	-
1	8RE	E	150	1	-	9/12/13/15	-
1	HYP	E	155	1	-	0/0/11/13	0/1/1/1
1	HLU	C	174	1	-	8/9/10/12	-
1	HYP	H	155	1	-	0/0/11/13	0/1/1/1
1	CSO	A	109	1	-	0/1/5/7	-
1	HLU	G	174	1	-	8/9/10/12	-
1	LYO	F	198	1	-	1/8/9/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	A	155	1	-	0/0/11/13	0/1/1/1
1	CSO	H	109	1	-	0/1/5/7	-
1	M3L	A	346	1	-	2/9/10/12	-
1	HYP	C	48	1	-	0/0/11/13	0/1/1/1
1	HLU	H	174	1	-	8/9/10/12	-
1	CSO	C	109	1	-	0/1/5/7	-
1	LYO	G	198	1	-	1/8/9/11	-
1	HYP	E	48	1	-	0/0/11/13	0/1/1/1
1	CSO	E	109	1	-	0/1/5/7	-
1	HLU	E	174	1	-	8/9/10/12	-
1	HYP	B	155	1	-	0/0/11/13	0/1/1/1
1	KCX	D	205	3,1	-	0/9/10/12	-
1	HYP	H	48	1	-	0/0/11/13	0/1/1/1
1	KCX	C	205	3,1	-	0/9/10/12	-
1	HYP	F	155	1	-	0/0/11/13	0/1/1/1
1	HYP	B	48	1	-	0/0/11/13	0/1/1/1
1	CSO	B	109	1	-	0/1/5/7	-
1	KCX	G	205	3,1	-	0/9/10/12	-
1	8RE	C	150	1	-	9/12/13/15	-
1	HYP	A	48	1	-	0/0/11/13	0/1/1/1
1	CSO	F	109	1	-	0/1/5/7	-
1	8RE	F	150	1	-	9/12/13/15	-
1	HLU	B	174	1	-	8/9/10/12	-
1	8RE	D	150	1	-	9/12/13/15	-
1	8RE	G	150	1	-	9/12/13/15	-
1	LYO	H	198	1	-	1/8/9/11	-
1	M3L	G	346	1	-	2/9/10/12	-
1	HYP	D	48	1	-	0/0/11/13	0/1/1/1
1	8RE	H	150	1	-	9/12/13/15	-
1	8RE	A	150	1	-	9/12/13/15	-
1	8RE	B	150	1	-	9/12/13/15	-
1	HYP	F	48	1	-	0/0/11/13	0/1/1/1
1	KCX	E	205	3,1	-	0/9/10/12	-
1	CSO	G	109	1	-	0/1/5/7	-
1	HLU	A	174	1	-	8/9/10/12	-
1	LYO	D	198	1	-	1/8/9/11	-
1	KCX	H	205	3,1	-	0/9/10/12	-
1	KCX	B	205	3,1	-	0/9/10/12	-
1	HYP	G	48	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	F	205	3,1	-	0/9/10/12	-
1	HYP	G	155	1	-	0/0/11/13	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	205	KCX	CE-NZ	2.32	1.51	1.46
1	A	205	KCX	CE-NZ	2.16	1.51	1.46
1	G	205	KCX	CE-NZ	2.09	1.50	1.46
1	H	205	KCX	OQ1-CX	2.06	1.25	1.21
1	D	205	KCX	OQ1-CX	2.03	1.25	1.21

The worst 5 of 99 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	150	8RE	OH1-CB-CG	4.42	118.97	108.93
1	F	174	HLU	OH-CB-CG	4.36	118.98	109.92
1	E	174	HLU	OH-CB-CG	4.27	118.79	109.92
1	A	174	HLU	OH-CB-CG	4.26	118.77	109.92
1	E	150	8RE	OH1-CB-CG	4.18	118.43	108.93

There are no chirality outliers.

5 of 159 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	CA-CB-CG-CD1
1	A	174	HLU	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	G	205	KCX	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 37 ligands modelled in this entry, 10 are monoatomic - leaving 27 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
5	EDO	K	204	-	3,3,3	0.47	0	2,2,2	0.33	0
5	EDO	O	201	-	3,3,3	0.52	0	2,2,2	0.28	0
5	EDO	N	201	-	3,3,3	0.40	0	2,2,2	0.27	0
5	EDO	J	202	-	3,3,3	0.34	0	2,2,2	0.30	0
5	EDO	K	201	-	3,3,3	0.35	0	2,2,2	0.41	0
5	EDO	K	202	-	3,3,3	0.35	0	2,2,2	0.38	0
5	EDO	J	201	-	3,3,3	0.40	0	2,2,2	0.56	0
4	CAP	C	502	3	18,20,20	0.94	1 (5%)	23,31,31	1.21	2 (8%)
4	CAP	E	502	3	18,20,20	0.96	1 (5%)	23,31,31	0.98	0
4	CAP	A	502	3	18,20,20	0.89	0	23,31,31	1.11	2 (8%)
5	EDO	M	202	-	3,3,3	0.42	0	2,2,2	0.32	0
5	EDO	M	203	-	3,3,3	0.46	0	2,2,2	0.35	0
5	EDO	I	204	-	3,3,3	0.39	0	2,2,2	0.44	0
4	CAP	H	502	3	18,20,20	0.93	1 (5%)	23,31,31	1.15	2 (8%)
5	EDO	P	201	-	3,3,3	0.40	0	2,2,2	0.31	0
5	EDO	I	203	-	3,3,3	0.43	0	2,2,2	0.22	0
5	EDO	O	202	-	3,3,3	0.48	0	2,2,2	0.21	0
4	CAP	D	502	3	18,20,20	0.96	1 (5%)	23,31,31	1.38	2 (8%)
4	CAP	B	502	3	18,20,20	0.88	0	23,31,31	1.17	2 (8%)
4	CAP	F	502	3	18,20,20	0.97	1 (5%)	23,31,31	0.94	0
5	EDO	A	503	-	3,3,3	0.48	0	2,2,2	0.33	0
5	EDO	O	203	-	3,3,3	0.37	0	2,2,2	0.34	0
5	EDO	I	202	-	3,3,3	0.46	0	2,2,2	0.30	0
5	EDO	M	201	-	3,3,3	0.50	0	2,2,2	0.22	0
5	EDO	L	201	-	3,3,3	0.40	0	2,2,2	0.59	0
4	CAP	G	502	3	18,20,20	0.90	1 (5%)	23,31,31	1.26	2 (8%)
5	EDO	K	203	-	3,3,3	0.35	0	2,2,2	0.65	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	K	204	-	-	0/1/1/1	-
5	EDO	O	201	-	-	0/1/1/1	-
5	EDO	N	201	-	-	0/1/1/1	-
5	EDO	J	202	-	-	0/1/1/1	-
5	EDO	K	201	-	-	0/1/1/1	-
5	EDO	K	202	-	-	0/1/1/1	-
5	EDO	J	201	-	-	0/1/1/1	-
4	CAP	C	502	3	-	8/29/29/29	-
4	CAP	E	502	3	-	8/29/29/29	-
4	CAP	A	502	3	-	7/29/29/29	-
5	EDO	M	202	-	-	0/1/1/1	-
5	EDO	M	203	-	-	0/1/1/1	-
5	EDO	I	204	-	-	0/1/1/1	-
4	CAP	H	502	3	-	8/29/29/29	-
5	EDO	P	201	-	-	0/1/1/1	-
5	EDO	I	203	-	-	0/1/1/1	-
5	EDO	O	202	-	-	0/1/1/1	-
4	CAP	D	502	3	-	8/29/29/29	-
4	CAP	B	502	3	-	8/29/29/29	-
4	CAP	F	502	3	-	8/29/29/29	-
5	EDO	A	503	-	-	0/1/1/1	-
5	EDO	O	203	-	-	0/1/1/1	-
5	EDO	I	202	-	-	0/1/1/1	-
5	EDO	M	201	-	-	0/1/1/1	-
5	EDO	L	201	-	-	0/1/1/1	-
4	CAP	G	502	3	-	9/29/29/29	-
5	EDO	K	203	-	-	1/1/1/1	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	502	CAP	C2-C	-2.75	1.50	1.53
4	F	502	CAP	C2-C	-2.75	1.50	1.53
4	D	502	CAP	C2-C	-2.71	1.51	1.53
4	H	502	CAP	C2-C	-2.64	1.51	1.53
4	C	502	CAP	C2-C	-2.57	1.51	1.53

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	502	CAP	O6-C-C2	-3.96	114.95	122.32
4	G	502	CAP	O6-C-C2	-3.29	116.18	122.32
4	C	502	CAP	O6-C-C2	-3.02	116.70	122.32
4	G	502	CAP	O7-C-C2	2.98	119.04	114.06
4	D	502	CAP	O7-C-C2	2.89	118.91	114.06

There are no chirality outliers.

5 of 65 torsion outliers are listed below:

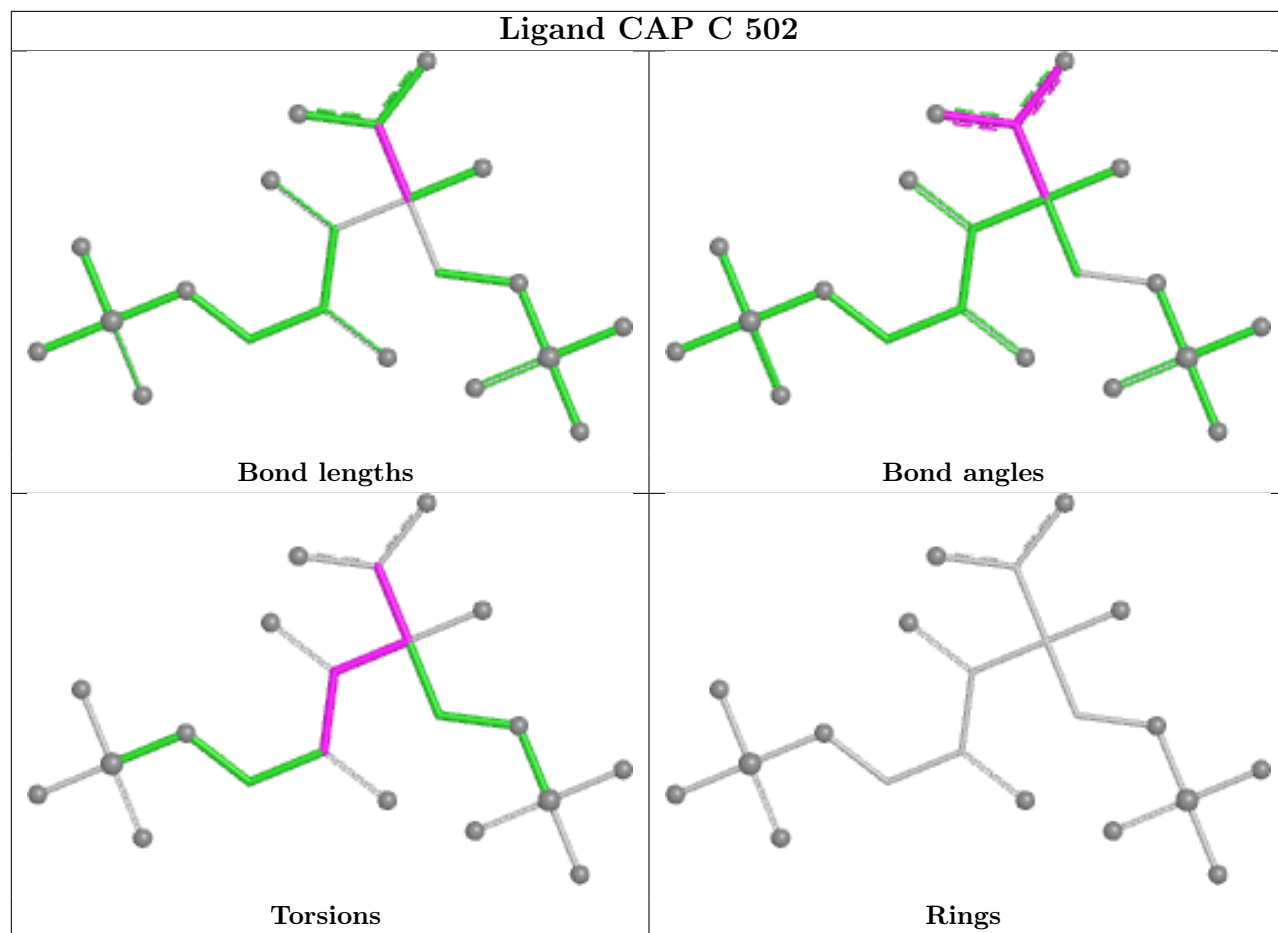
Mol	Chain	Res	Type	Atoms
4	A	502	CAP	O7-C-C2-C1
4	A	502	CAP	O6-C-C2-C3
4	A	502	CAP	O7-C-C2-O2
4	A	502	CAP	C2-C3-C4-O4
4	A	502	CAP	O3-C3-C4-O4

There are no ring outliers.

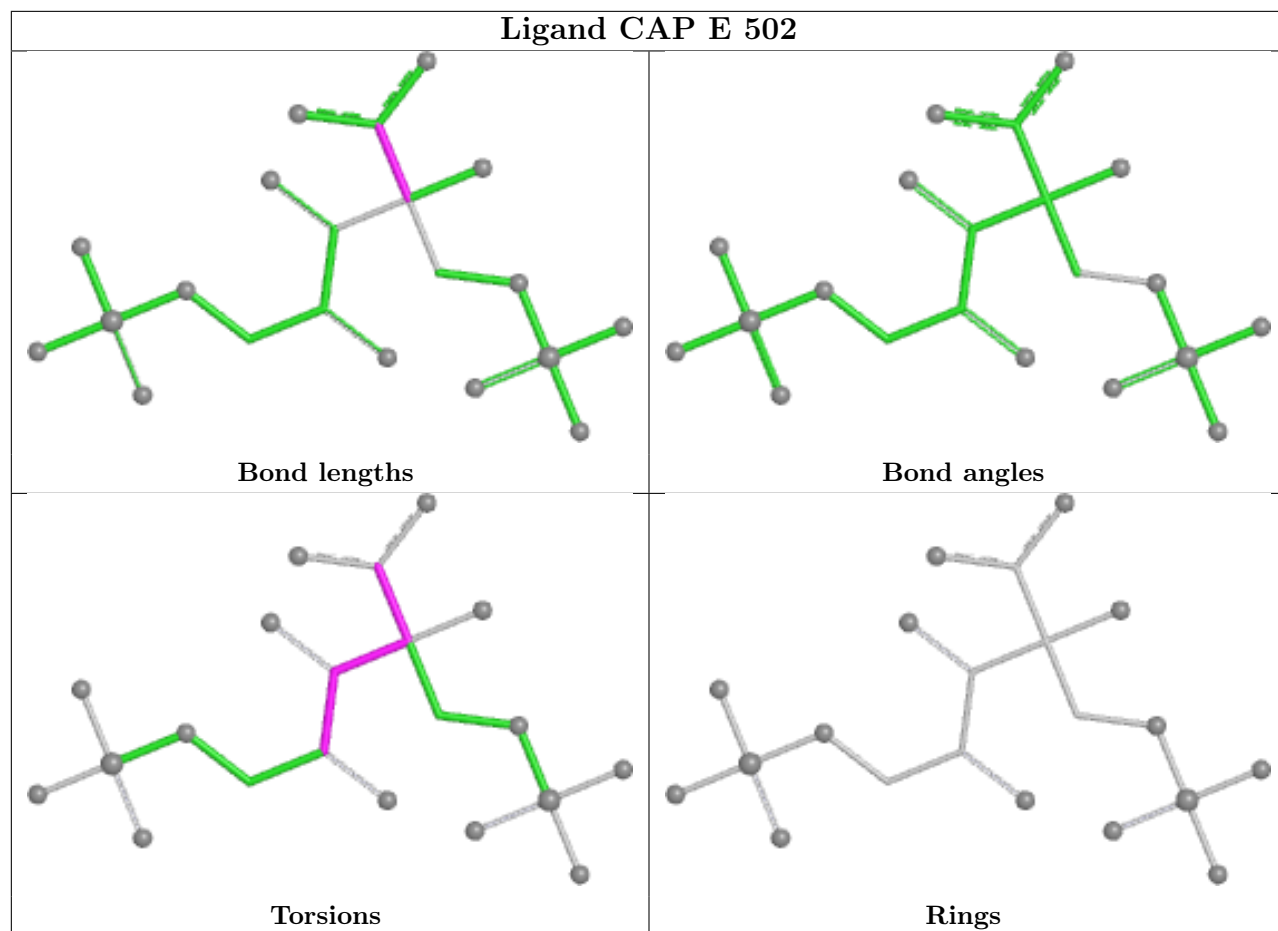
3 monomers are involved in 4 short contacts:

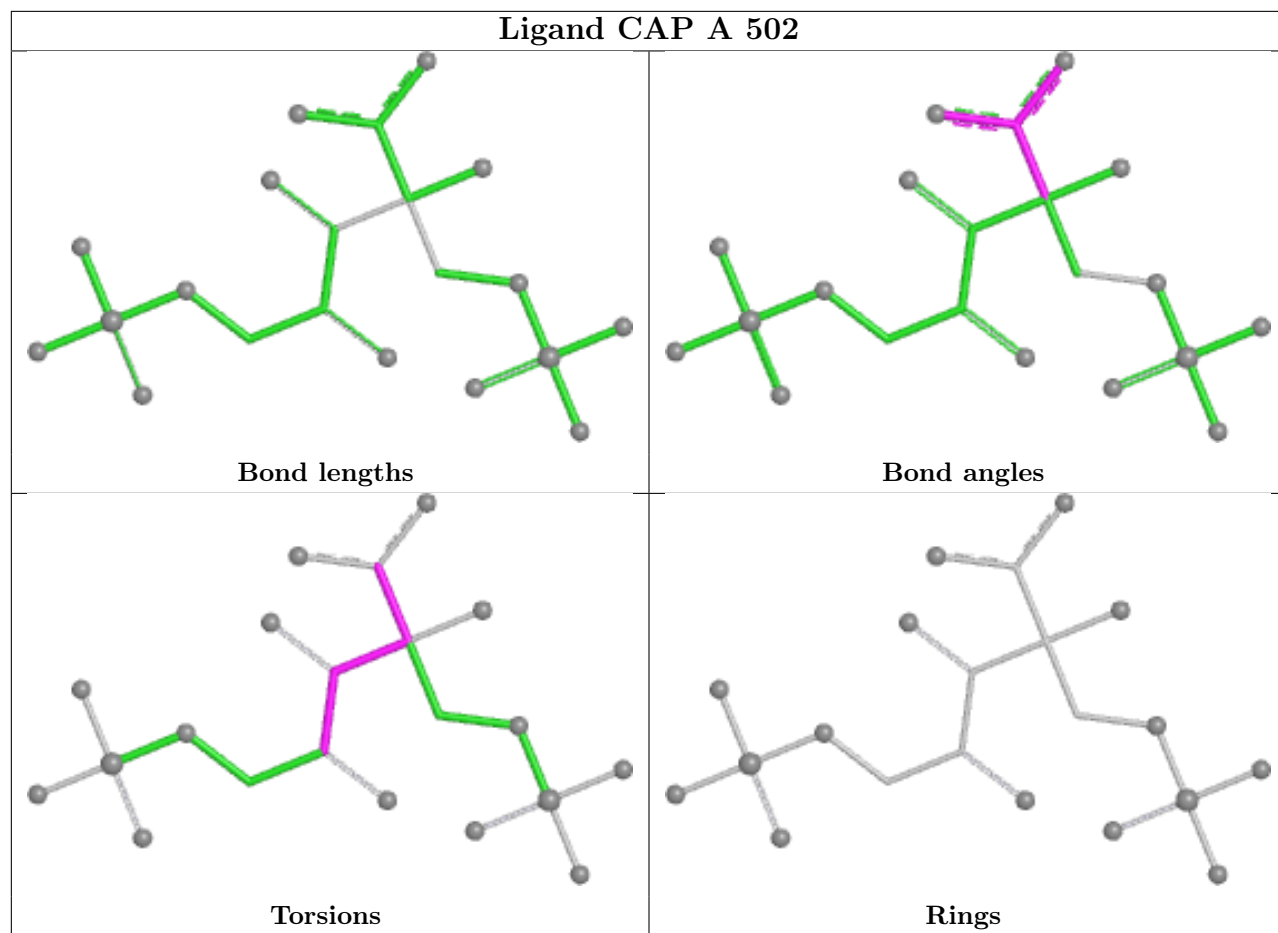
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	204	EDO	1	0
5	I	202	EDO	1	0
5	K	203	EDO	2	0

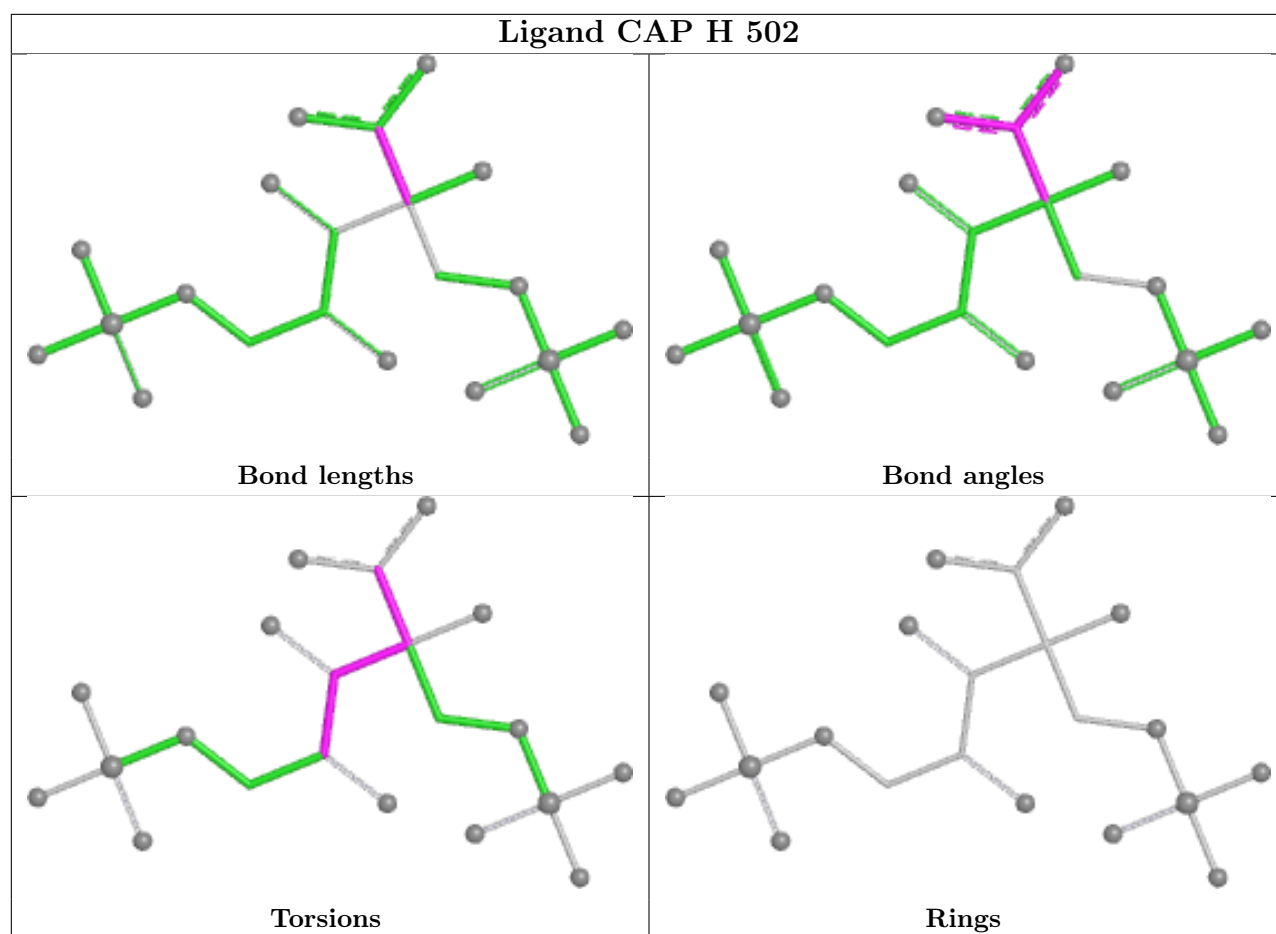
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

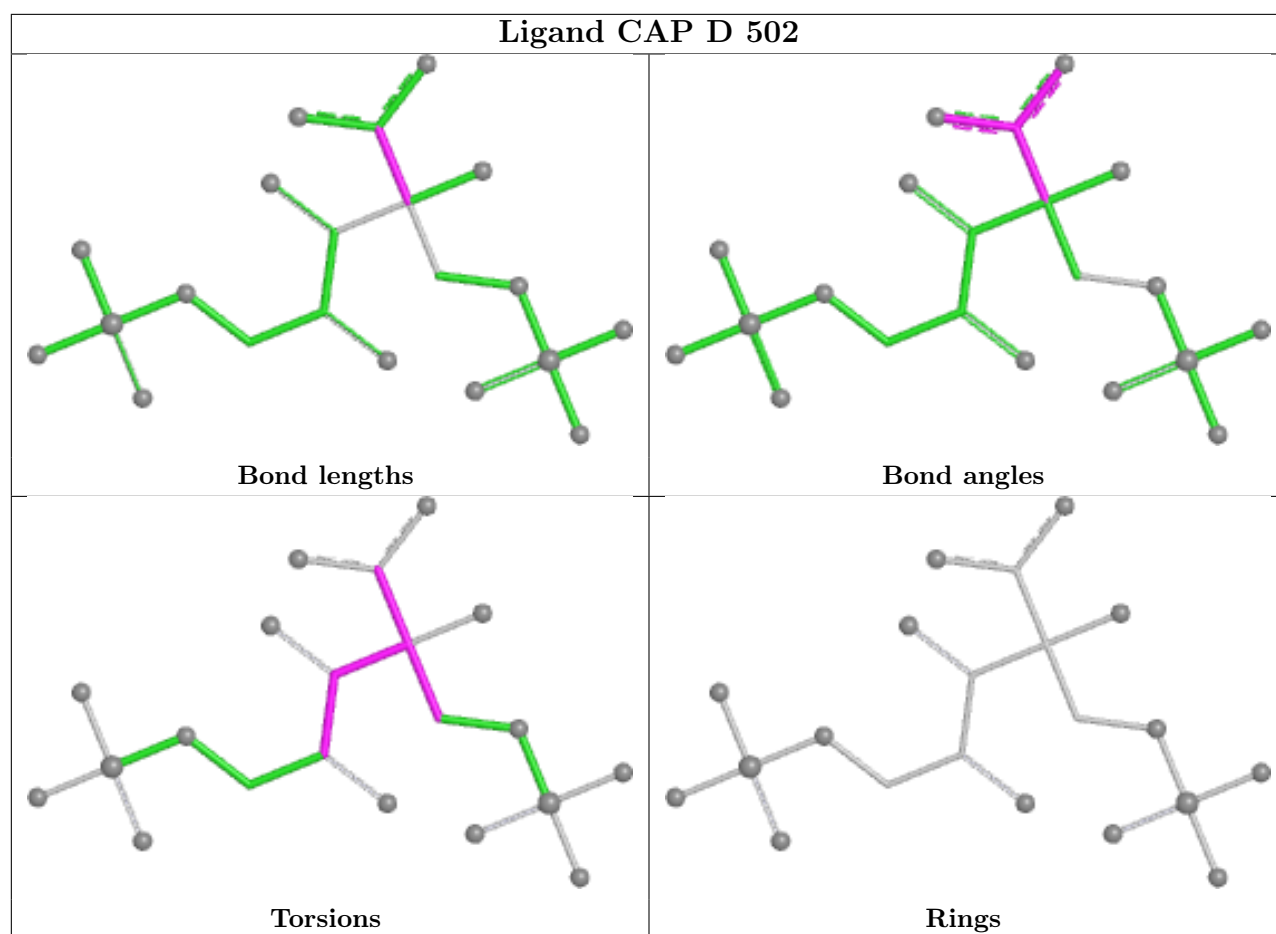


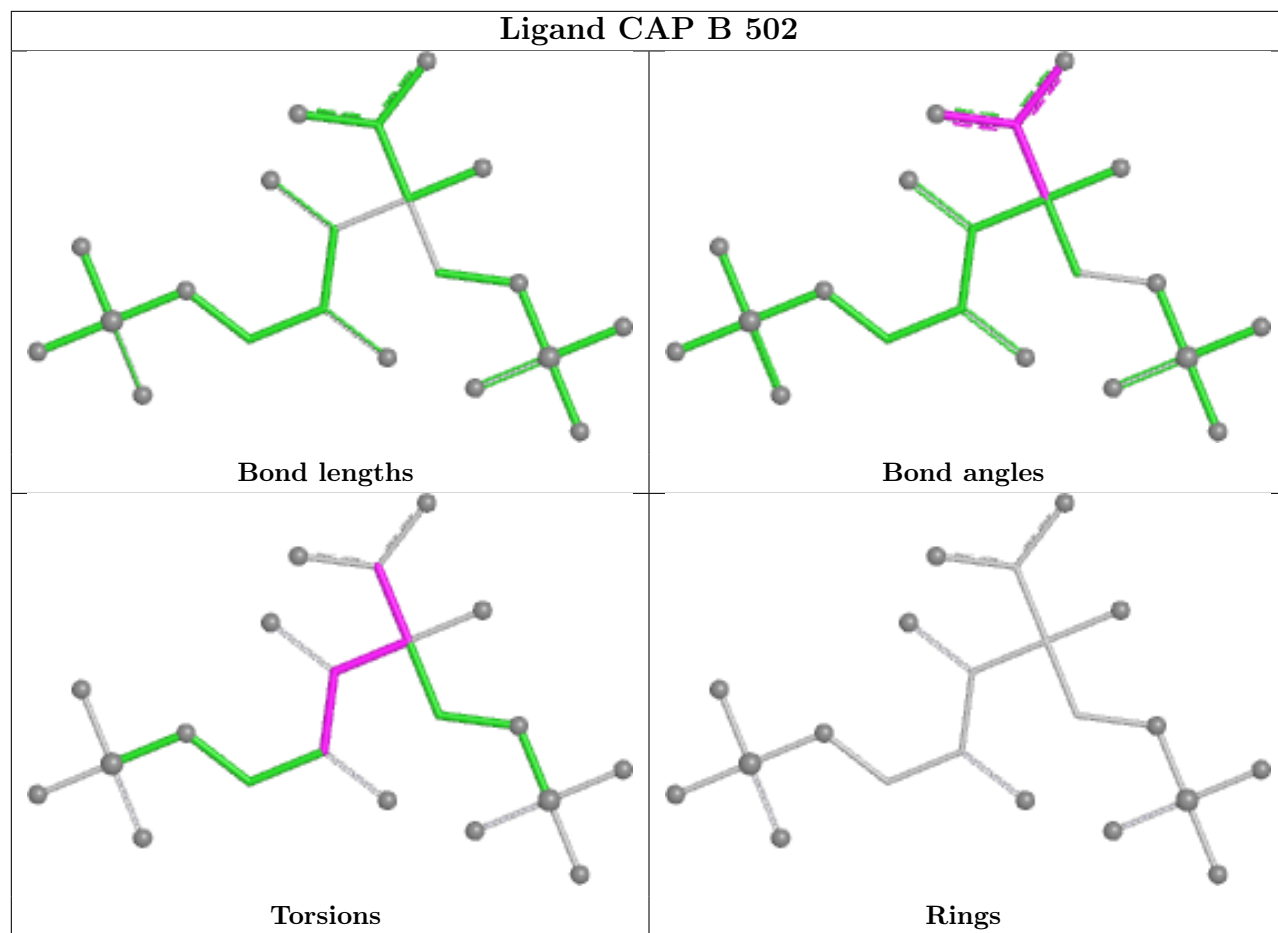
Ligand CAP E 502



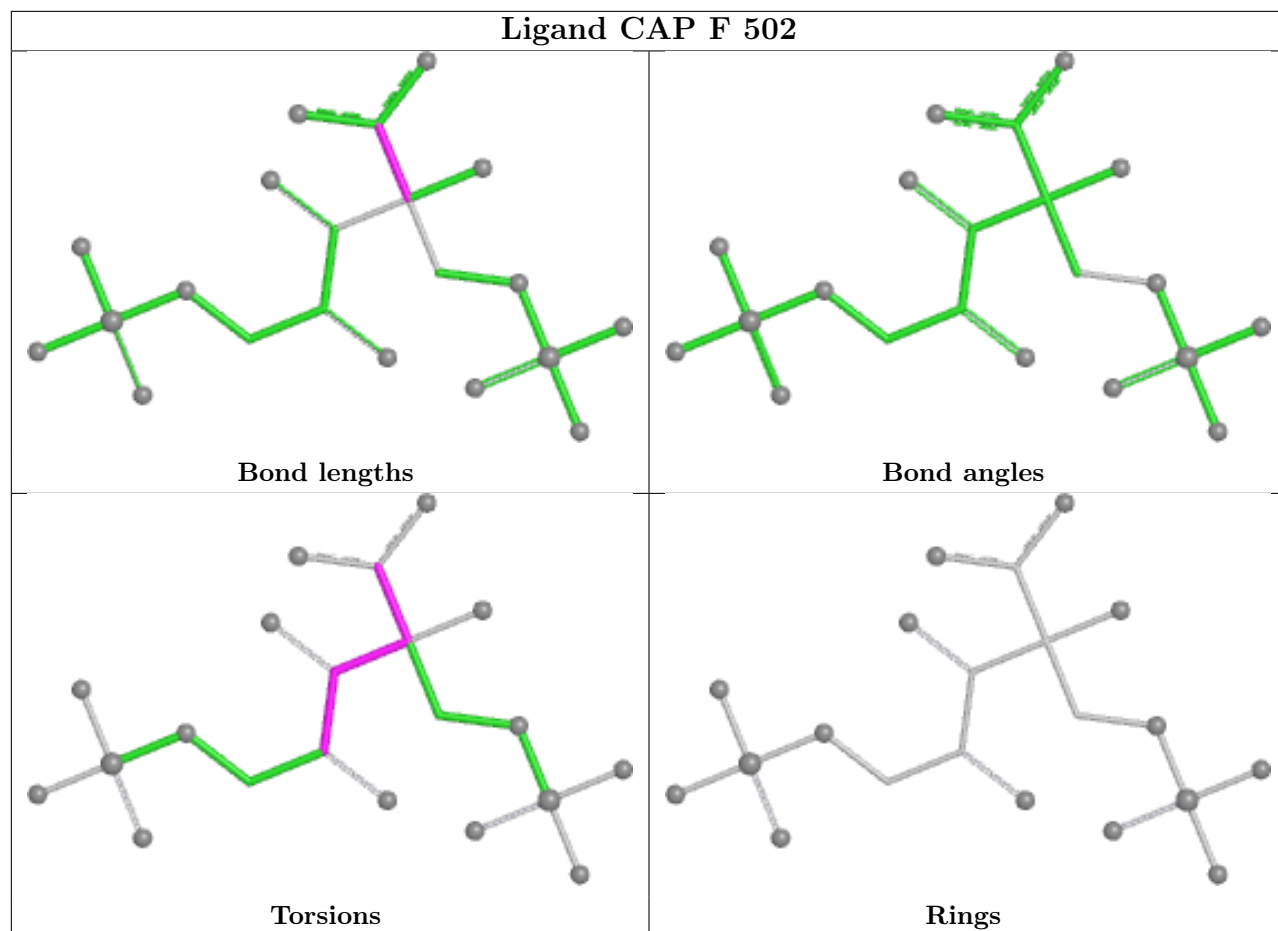


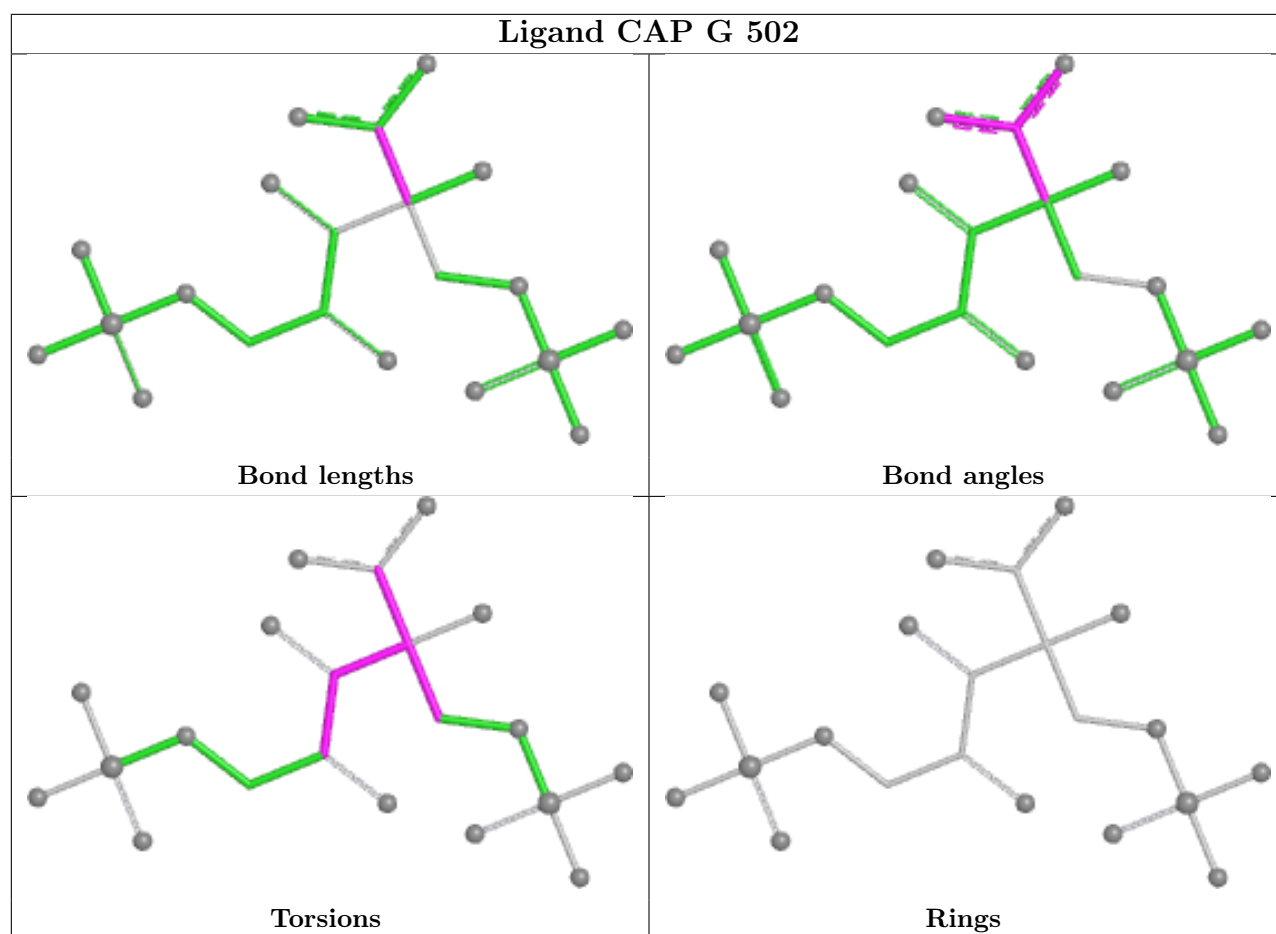






Ligand CAP F 502





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	473/490 (96%)	-1.39	0 100 100	7, 16, 31, 56	1 (0%)
1	B	473/490 (96%)	-1.39	0 100 100	7, 16, 30, 57	1 (0%)
1	C	473/490 (96%)	-1.46	0 100 100	7, 14, 27, 41	1 (0%)
1	D	473/490 (96%)	-1.48	0 100 100	7, 14, 27, 43	1 (0%)
1	E	473/490 (96%)	-1.46	0 100 100	7, 14, 28, 41	1 (0%)
1	F	473/490 (96%)	-1.46	0 100 100	7, 14, 28, 44	1 (0%)
1	G	473/490 (96%)	-1.48	0 100 100	7, 14, 27, 41	1 (0%)
1	H	473/490 (96%)	-1.49	0 100 100	7, 14, 27, 43	1 (0%)
2	I	139/139 (100%)	-1.34	0 100 100	10, 19, 31, 49	1 (0%)
2	J	139/139 (100%)	-1.41	0 100 100	9, 18, 29, 49	1 (0%)
2	K	139/139 (100%)	-1.39	0 100 100	11, 18, 30, 46	1 (0%)
2	L	139/139 (100%)	-1.37	0 100 100	9, 18, 30, 58	1 (0%)
2	M	139/139 (100%)	-1.41	0 100 100	10, 18, 30, 50	1 (0%)
2	N	139/139 (100%)	-1.41	0 100 100	10, 18, 29, 49	1 (0%)
2	O	139/139 (100%)	-1.43	0 100 100	12, 19, 30, 48	0
2	P	139/139 (100%)	-1.39	0 100 100	10, 19, 29, 49	1 (0%)
All	All	4896/5032 (97%)	-1.44	0 100 100	7, 16, 29, 58	15 (0%)

There are no RSRZ outliers to report.

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($\text{\AA}^2$)	Q<0.9
1	HYP	A	48	8/9	0.99	0.03	18,20,24,29	0
1	HYP	A	155	8/9	0.99	0.02	11,12,16,16	0
1	HLU	A	174	9/10	0.99	0.03	14,17,20,21	0
1	M3L	A	346	12/13	0.99	0.04	15,22,27,30	0
1	HYP	H	48	8/9	0.99	0.02	11,16,18,22	0
1	HYP	H	155	8/9	0.99	0.02	8,11,13,14	0
1	HLU	H	174	9/10	0.99	0.03	13,15,19,22	0
1	KCX	H	205	12/13	0.99	0.02	10,12,14,14	0
1	M3L	H	346	12/13	0.99	0.03	12,16,22,24	0
1	HYP	F	48	8/9	0.99	0.03	14,16,22,27	0
1	HYP	F	155	8/9	0.99	0.03	8,10,13,15	0
1	HLU	F	174	9/10	0.99	0.03	10,14,17,20	0
1	KCX	F	205	12/13	0.99	0.03	11,12,13,14	0
1	HYP	D	48	8/9	0.99	0.03	13,15,20,28	0
1	HYP	D	155	8/9	0.99	0.03	10,12,13,18	0
1	HLU	D	174	9/10	0.99	0.03	10,13,18,20	0
1	M3L	D	346	12/13	0.99	0.04	10,17,22,23	0
1	HYP	B	48	8/9	0.99	0.04	18,19,24,30	0
1	HYP	B	155	8/9	0.99	0.03	12,12,15,15	0
1	HLU	B	174	9/10	0.99	0.03	13,18,20,22	0
1	M3L	B	346	12/13	0.99	0.04	15,22,29,30	0
1	HYP	C	48	8/9	0.99	0.03	12,16,21,25	0
1	HYP	C	155	8/9	0.99	0.02	8,11,13,14	0
1	HLU	C	174	9/10	0.99	0.02	12,14,18,20	0
1	HYP	E	48	8/9	0.99	0.03	14,16,22,28	0
1	HYP	E	155	8/9	0.99	0.02	9,10,14,15	0
1	HLU	E	174	9/10	0.99	0.03	12,15,18,19	0
1	M3L	E	346	12/13	0.99	0.03	12,17,25,25	0
1	HYP	G	48	8/9	0.99	0.03	12,14,19,29	0
1	HYP	G	155	8/9	0.99	0.02	10,11,13,17	0
1	HLU	G	174	9/10	0.99	0.03	9,13,17,20	0
1	KCX	G	205	12/13	0.99	0.03	9,10,12,13	0
1	M3L	G	346	12/13	0.99	0.03	11,18,23,24	0
1	8RE	A	150	11/12	0.99	0.02	10,12,19,19	0
1	8RE	H	150	11/12	0.99	0.03	7,11,15,17	0
1	8RE	D	150	11/12	0.99	0.02	8,12,17,17	0
1	8RE	C	150	11/12	0.99	0.03	8,10,17,18	0
1	LYO	A	198	10/11	0.99	0.04	12,18,25,28	0
1	LYO	F	198	10/11	0.99	0.03	10,15,23,26	0
1	LYO	D	198	10/11	0.99	0.03	9,16,24,26	0
1	LYO	B	198	10/11	0.99	0.03	12,16,25,27	0
1	LYO	C	198	10/11	0.99	0.03	10,15,24,28	0
1	LYO	E	198	10/11	0.99	0.03	11,16,21,21	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	LYO	G	198	10/11	0.99	0.03	10,16,24,25	0
1	CSO	H	109	7/8	1.00	0.02	10,12,13,19	0
1	CSO	A	109	7/8	1.00	0.03	12,15,17,25	0
1	CSO	C	109	7/8	1.00	0.02	11,12,13,19	0
1	KCX	D	205	12/13	1.00	0.02	8,10,12,13	0
1	KCX	A	205	12/13	1.00	0.02	12,14,16,17	0
1	KCX	C	205	12/13	1.00	0.02	10,11,13,14	0
1	8RE	F	150	11/12	1.00	0.02	8,10,16,17	0
1	M3L	C	346	12/13	1.00	0.03	13,16,25,25	0
1	8RE	B	150	11/12	1.00	0.02	10,11,19,20	0
1	M3L	F	346	12/13	1.00	0.02	12,18,27,27	0
1	8RE	E	150	11/12	1.00	0.02	9,11,15,17	0
1	8RE	G	150	11/12	1.00	0.03	7,12,17,19	0
1	CSO	E	109	7/8	1.00	0.02	9,12,14,21	0
1	LYO	H	198	10/11	1.00	0.02	10,14,22,27	0
1	CSO	B	109	7/8	1.00	0.02	13,14,16,25	0
1	CSO	F	109	7/8	1.00	0.02	10,12,13,20	0
1	KCX	E	205	12/13	1.00	0.02	11,11,14,14	0
1	CSO	D	109	7/8	1.00	0.02	11,11,15,21	0
1	KCX	B	205	12/13	1.00	0.02	13,14,15,18	0
1	CSO	G	109	7/8	1.00	0.02	10,12,15,22	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	I	204	4/4	0.98	0.06	26,31,32,37	0
5	EDO	I	202	4/4	0.99	0.05	20,24,25,28	0
5	EDO	I	203	4/4	0.99	0.02	16,21,21,22	0
5	EDO	A	503	4/4	0.99	0.06	19,22,25,32	0
5	EDO	O	201	4/4	0.99	0.05	21,21,25,31	0
5	EDO	O	202	4/4	0.99	0.05	20,22,25,31	0
5	EDO	O	203	4/4	0.99	0.03	15,17,21,24	0

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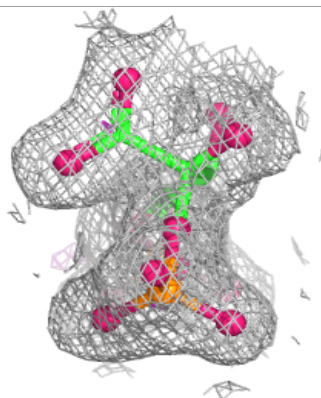
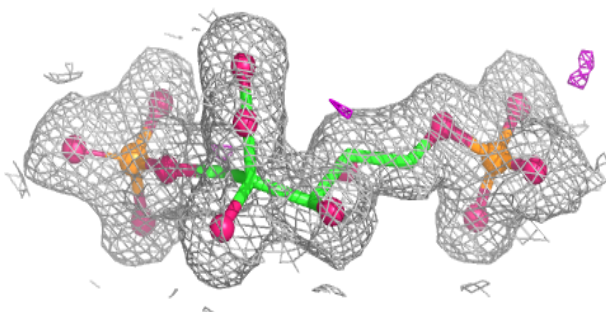
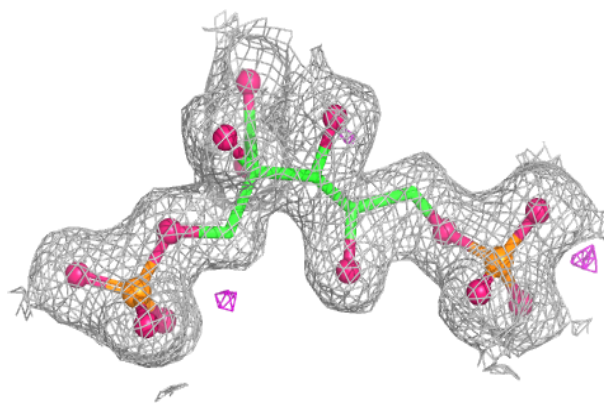
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	N	201	4/4	0.99	0.04	14,17,20,24	0
5	EDO	M	201	4/4	0.99	0.04	19,23,23,29	0
5	EDO	M	202	4/4	0.99	0.03	17,20,21,22	0
5	EDO	M	203	4/4	0.99	0.04	21,23,25,29	0
5	EDO	P	201	4/4	0.99	0.03	16,20,21,22	0
5	EDO	J	202	4/4	0.99	0.03	13,16,20,26	0
5	EDO	K	203	4/4	0.99	0.05	17,22,28,32	0
5	EDO	K	204	4/4	0.99	0.05	20,22,25,29	0
5	EDO	L	201	4/4	0.99	0.03	18,18,18,21	0
4	CAP	E	502	21/21	1.00	0.02	10,13,14,16	0
4	CAP	G	502	21/21	1.00	0.01	9,12,13,14	0
3	MG	A	501	1/1	1.00	0.02	14,14,14,14	0
3	MG	I	201	1/1	1.00	0.07	21,21,21,21	0
3	MG	H	501	1/1	1.00	0.01	13,13,13,13	0
3	MG	F	501	1/1	1.00	0.03	13,13,13,13	0
3	MG	N	202	1/1	1.00	0.06	20,20,20,20	0
3	MG	D	501	1/1	1.00	0.02	13,13,13,13	0
3	MG	B	501	1/1	1.00	0.02	14,14,14,14	0
3	MG	C	501	1/1	1.00	0.03	14,14,14,14	0
3	MG	E	501	1/1	1.00	0.03	13,13,13,13	0
3	MG	G	501	1/1	1.00	0.01	12,12,12,12	0
4	CAP	A	502	21/21	1.00	0.02	13,15,17,19	0
4	CAP	H	502	21/21	1.00	0.02	10,12,13,16	0
5	EDO	J	201	4/4	1.00	0.03	11,14,20,24	0
4	CAP	F	502	21/21	1.00	0.02	10,13,14,15	0
5	EDO	K	201	4/4	1.00	0.02	15,15,20,23	0
5	EDO	K	202	4/4	1.00	0.02	15,15,18,24	0
4	CAP	D	502	21/21	1.00	0.02	9,12,13,15	0
4	CAP	B	502	21/21	1.00	0.02	13,15,16,18	0
4	CAP	C	502	21/21	1.00	0.02	10,12,13,15	0

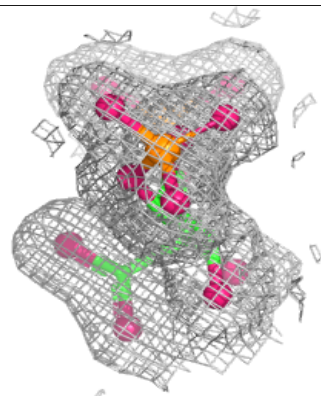
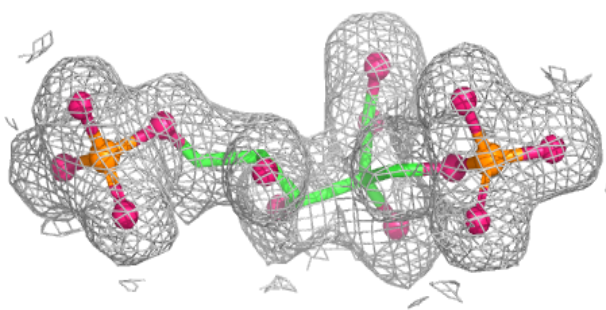
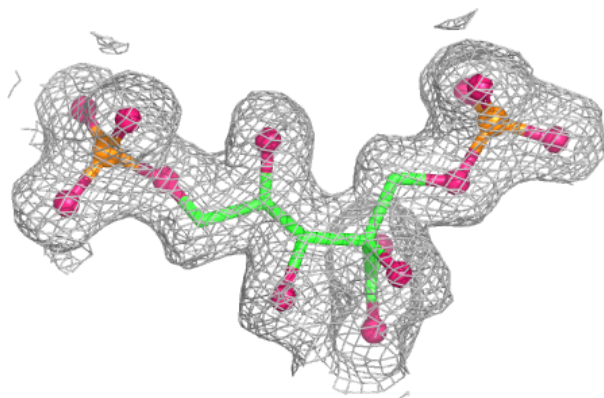
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CAP 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)

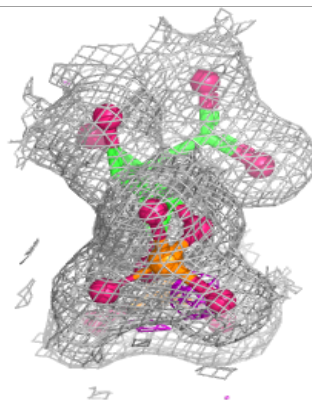
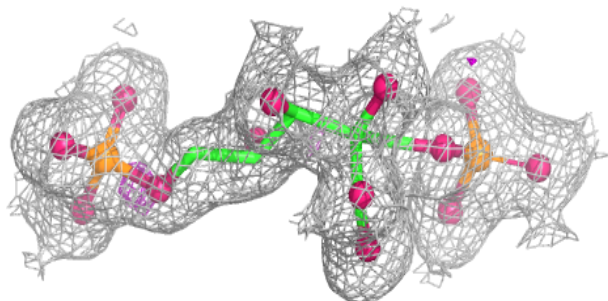
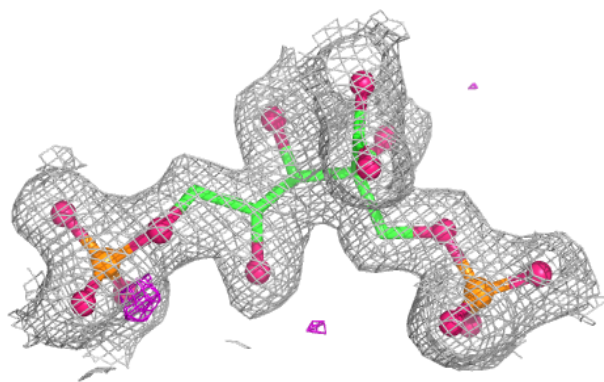
**Electron density around CAP G 502:**

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

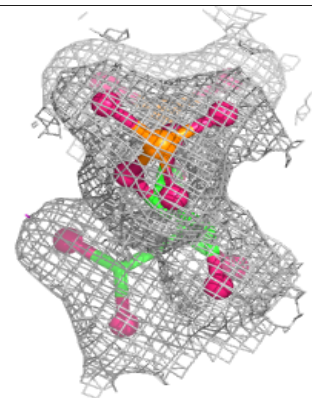
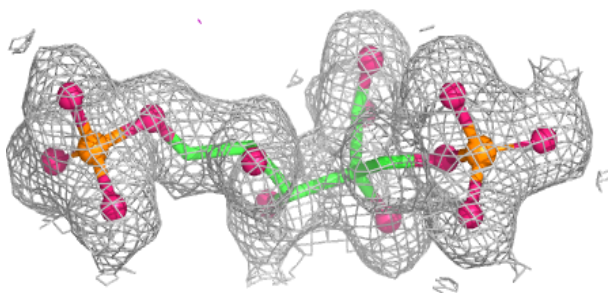
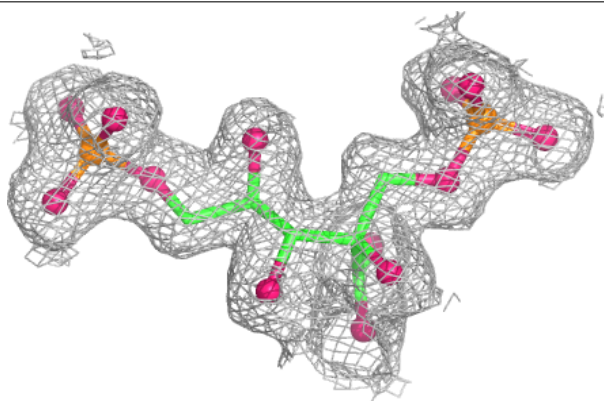


Electron density around CAP A 502:

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

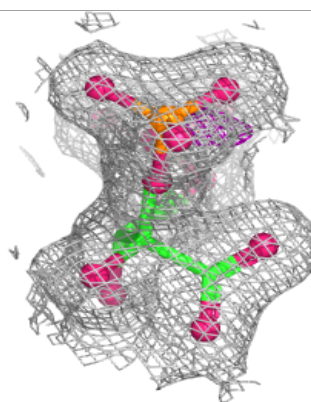
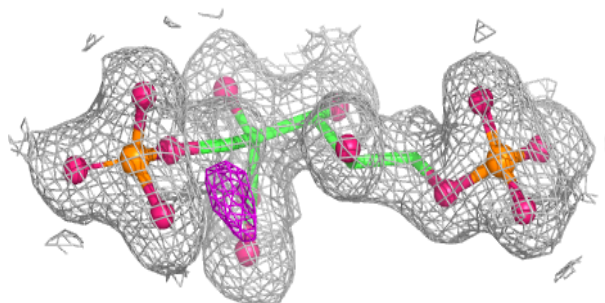
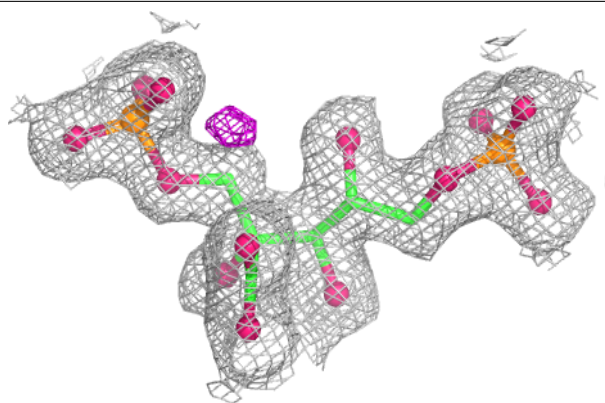
**Electron density around CAP H 502:**

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

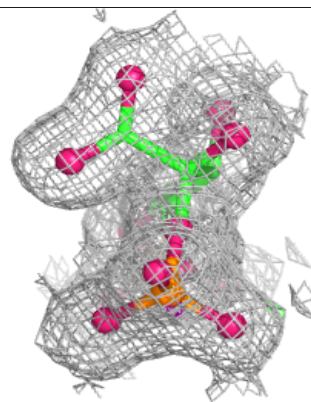
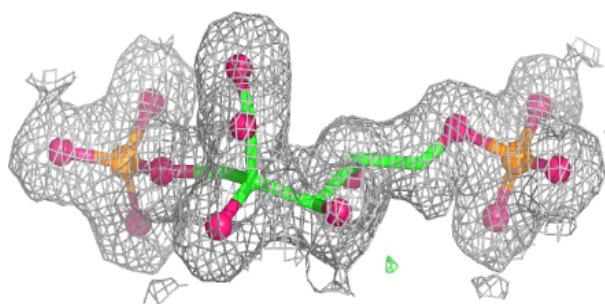
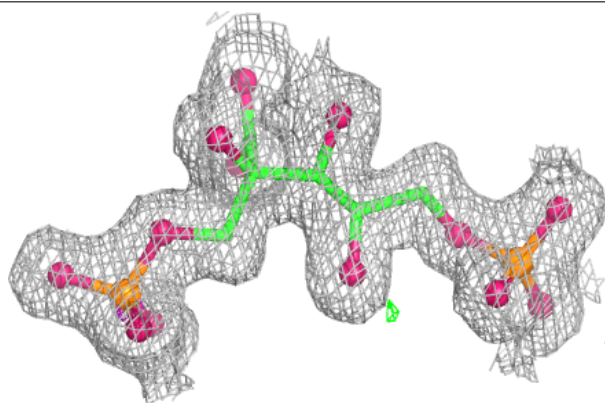


Electron density around CAP F 502:

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

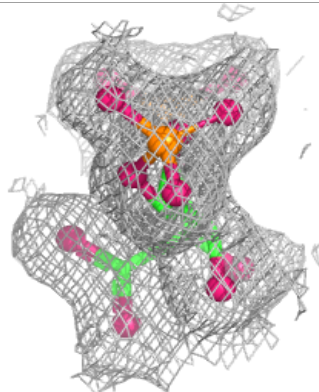
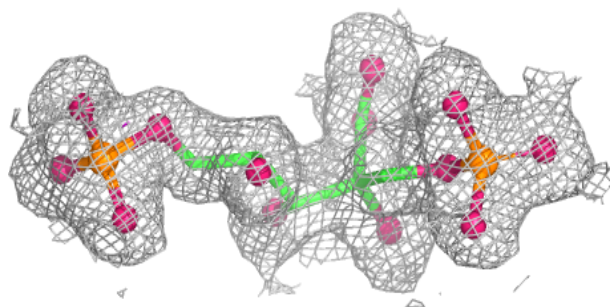
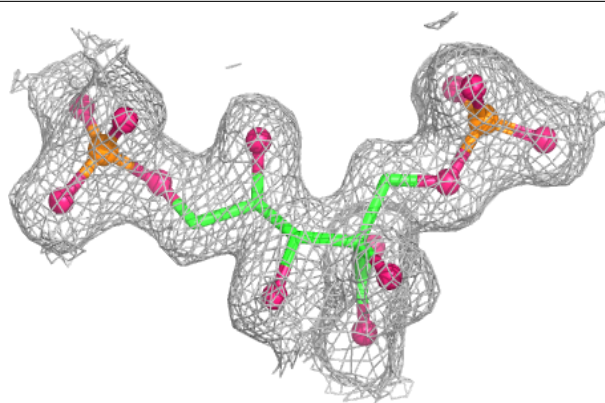
**Electron density around CAP D 502:**

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

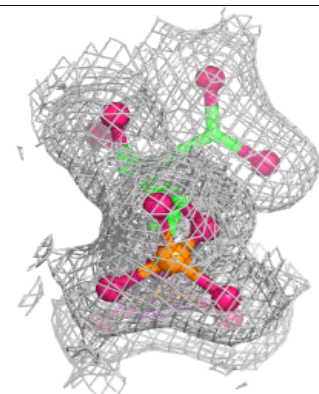
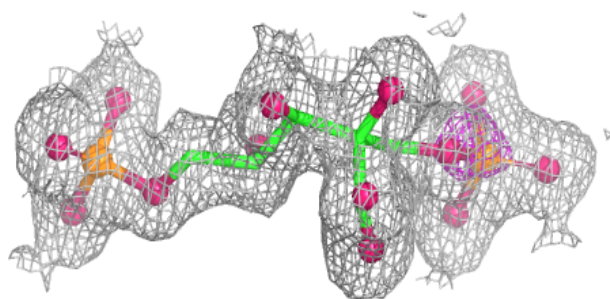
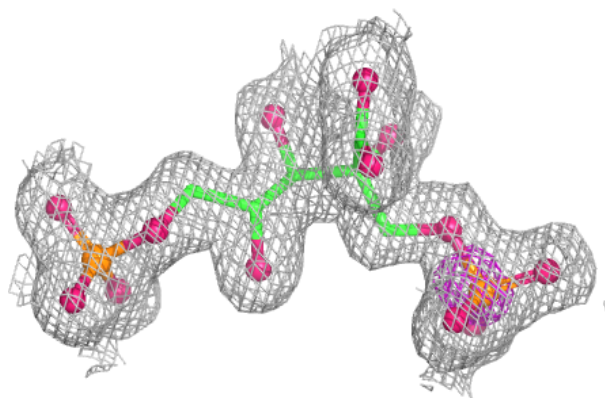


Electron density around CAP B 502:

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

**Electron density around CAP 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.