wwPDB X-ray Structure Validation Summary Report (i)

Jan 7, 2024 – 06:09 pm GMT

PDB ID	:	5OYA
Title	:	Unusual posttranslational modifications revealed in crystal structures of diatom Rubisco.
Authors	:	Valegard, K.; Andersson, I.
Deposited on	:	2017-09-08
Resolution	:	1.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

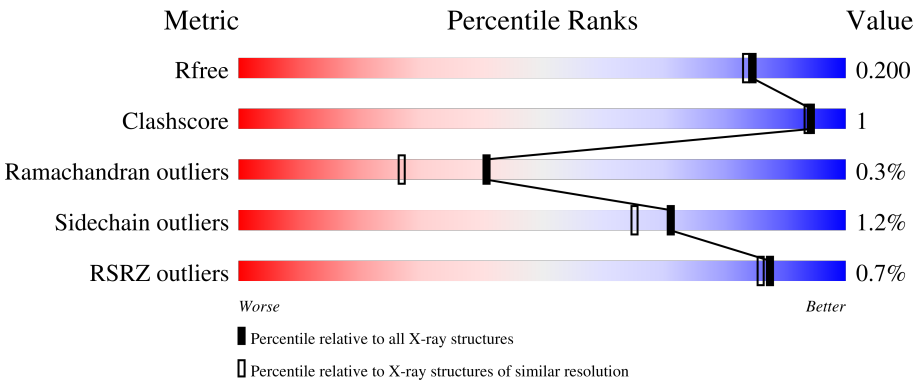
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	89% 7% •
1	B	490	89% 6% • •
1	D	490	.% 90% 6% •
1	E	490	.% 91% 5% •
1	F	490	.% 90% 6% •

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Mol	Chain	Length	Quality of chain
1	G	490	90% 5%
1	H	490	.% 91% 5%
2	C	490	.% 90% 6%
3	I	139	99%
3	J	139	.% 99%
3	K	139	.% 97%
3	L	139	.% 99%
3	M	139	.% 97%
3	N	139	.% 98%
3	O	139	.% 96%
3	P	139	.% 97%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 41512 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 Rubisco large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	468	3664	2335	624	684	21	0	2	0
1	B	469	3675	2341	628	685	21	0	2	0
1	D	468	3664	2335	624	684	21	0	2	0
1	E	469	3675	2341	628	685	21	0	2	0
1	F	469	3675	2341	628	685	21	0	2	0
1	G	469	3675	2341	628	685	21	0	2	0
1	H	468	3664	2335	624	684	21	0	2	0

- Molecule 2 is a protein called Rubisco large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	468	3663	2335	624	683	21	0	2	0

- Molecule 3 is a protein called Rubisco small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	I	139	1118	708	189	212	9	0	0	0
3	J	139	1117	708	189	211	9	0	0	0
3	K	139	1118	708	189	212	9	0	0	0
3	L	139	1118	708	189	212	9	0	0	0

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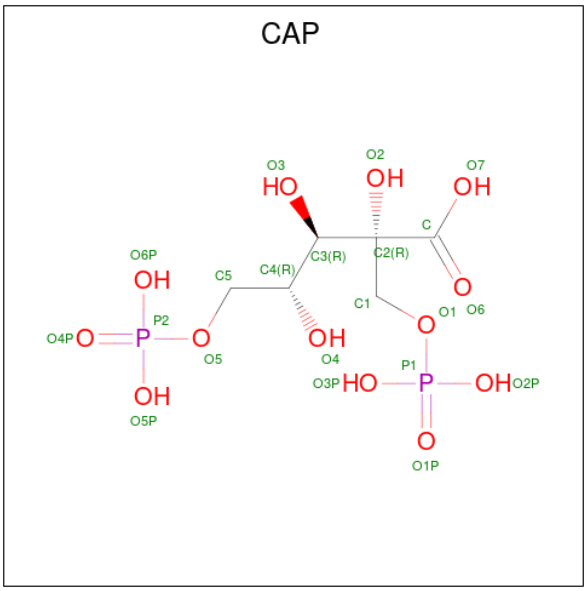
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	M	139	1118	708	189	212	9	0	0	0
			Total	C	N	O	S			
3	N	139	1118	708	189	212	9	0	0	0
			Total	C	N	O	S			
3	O	139	1118	708	189	212	9	0	0	0
			Total	C	N	O	S			
3	P	139	1118	708	189	212	9	0	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

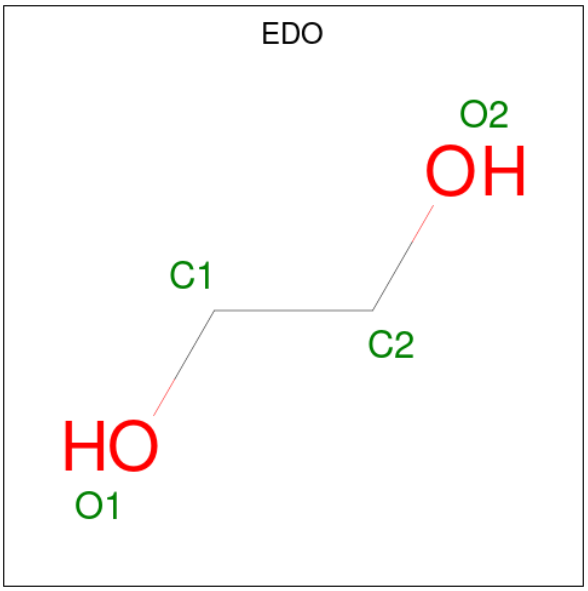
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0
			Total	Mg		
4	B	1	1	1	0	0
			Total	Mg		
4	C	1	1	1	0	0
			Total	Mg		
4	D	1	1	1	0	0
			Total	Mg		
4	E	1	1	1	0	0
			Total	Mg		
4	F	1	1	1	0	0
			Total	Mg		
4	G	1	1	1	0	0
			Total	Mg		
4	H	1	1	1	0	0
			Total	Mg		
4	J	1	1	1	0	0
			Total	Mg		
4	N	1	1	1	0	0

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



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

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	273	273	273	0	0
7	B	319	319	319	0	0
7	C	284	284	284	0	0
7	D	225	225	225	0	0
7	E	211	211	211	0	0
7	F	311	311	311	0	0
7	G	281	281	281	0	0
7	H	299	299	299	0	0
7	I	99	99	99	0	0

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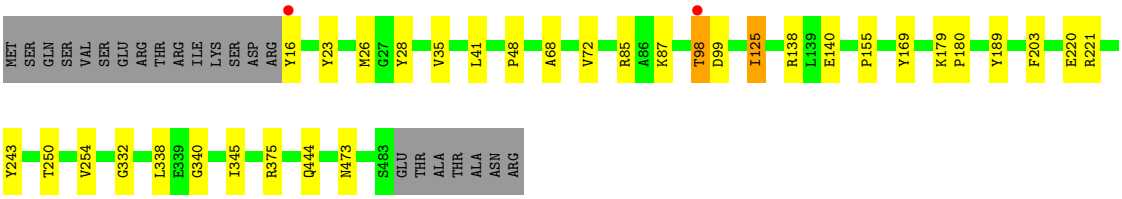
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	J	95	Total O 95 95	0	0
7	K	75	Total O 75 75	0	0
7	L	86	Total O 86 86	0	0
7	M	107	Total O 107 107	0	0
7	N	77	Total O 77 77	0	0
7	O	103	Total O 103 103	0	0
7	P	95	Total O 95 95	0	0

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.

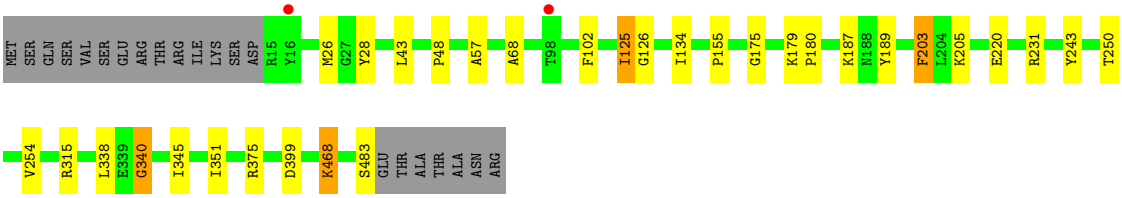
• Molecule 1: Rubisco large subunit

Chain A:



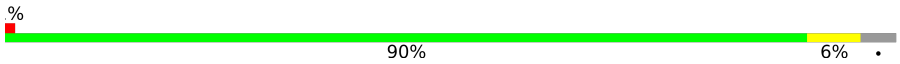
• Molecule 1: Rubisco large subunit

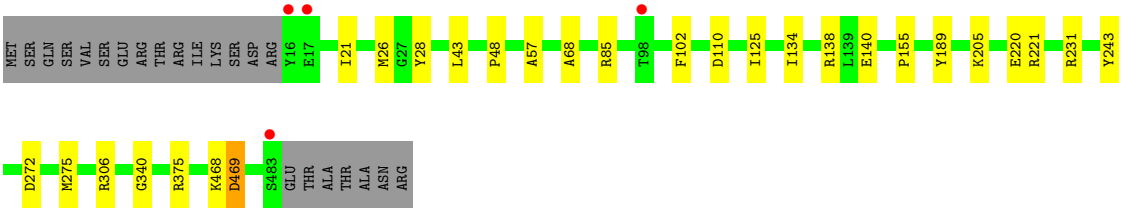
Chain B:



• Molecule 1: Rubisco large subunit

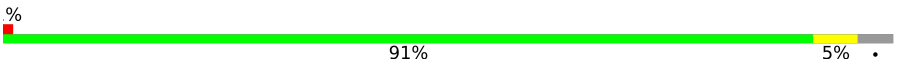
Chain D:

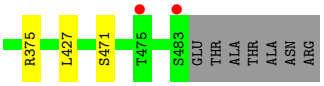




• Molecule 1: Rubisco large subunit

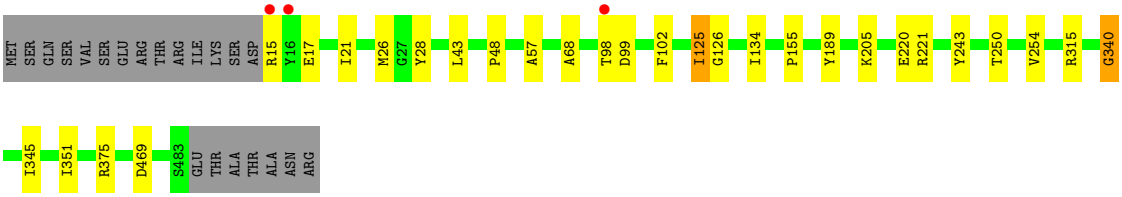
Chain E:





• Molecule 1: Rubisco large subunit

Chain F:

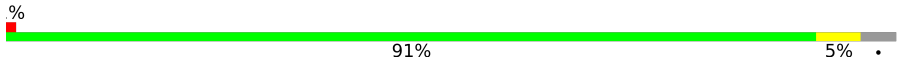


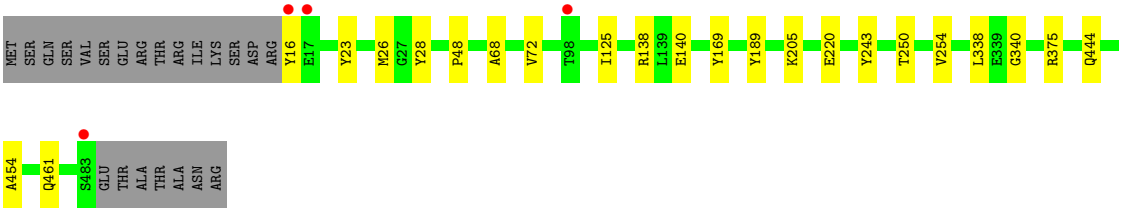
• Molecule 1: Rubisco large subunit

Chain G:

• Molecule 1: Rubisco large subunit

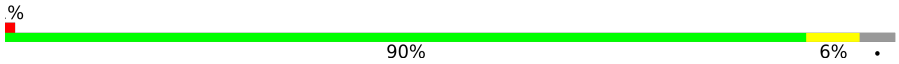
Chain H:

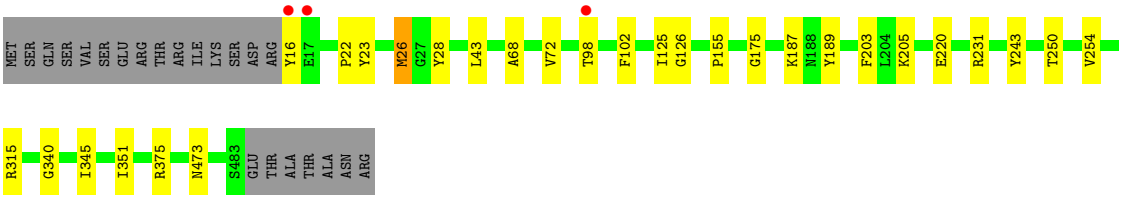




• Molecule 2: Rubisco large subunit

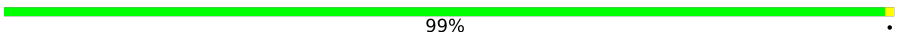
Chain C:





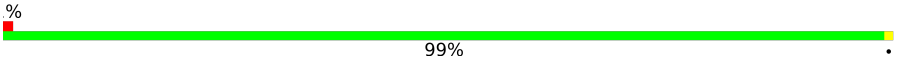
• Molecule 3: Rubisco small subunit

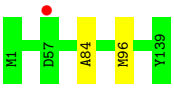
Chain I:



• Molecule 3: Rubisco small subunit

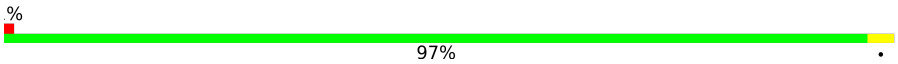
Chain J:

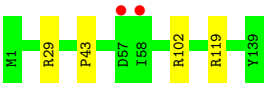




• Molecule 3: Rubisco small subunit

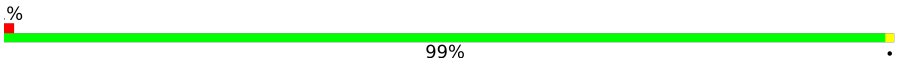
Chain K:

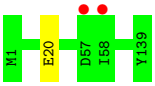




• Molecule 3: Rubisco small subunit

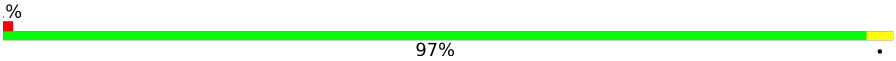
Chain L:

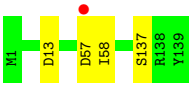




• Molecule 3: Rubisco small subunit

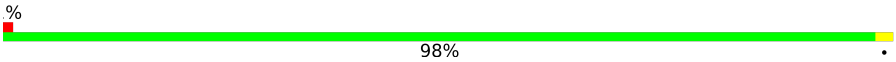
Chain M:

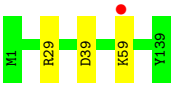




• Molecule 3: Rubisco small subunit

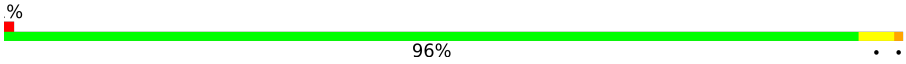
Chain N:





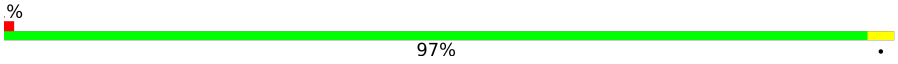
• Molecule 3: Rubisco small subunit

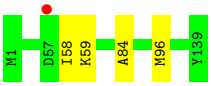
Chain O:



• Molecule 3: Rubisco small subunit

Chain P:




M1
D57
I58
K59
A84
M96
Y139

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	118.17Å 219.11Å 220.23Å 90.00° 90.19° 90.00°	Depositor
Resolution (Å)	49.19 – 1.80 49.19 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.1 (49.19-1.80) 95.3 (49.19-1.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.01 (at 1.79Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.167 , 0.192 0.177 , 0.200	Depositor DCC
R_{free} test set	24759 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	22.5	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 28.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.449 for h,-k,-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	41512	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.14% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: HYP, HL2, SNC, LOH, MG, CSO, KCX, CAP, EDO, M3L

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	0.62	1/3668 (0.0%)	0.79	3/4966 (0.1%)
1	B	0.64	1/3679 (0.0%)	0.81	4/4980 (0.1%)
1	D	0.59	1/3668 (0.0%)	0.79	11/4966 (0.2%)
1	E	0.61	1/3679 (0.0%)	0.78	2/4980 (0.0%)
1	F	0.65	1/3679 (0.0%)	0.80	3/4980 (0.1%)
1	G	0.65	1/3679 (0.0%)	0.80	4/4980 (0.1%)
1	H	0.62	1/3668 (0.0%)	0.78	1/4966 (0.0%)
2	C	0.64	1/3677 (0.0%)	0.79	3/4981 (0.1%)
3	I	0.57	0/1149	0.76	0/1558
3	J	0.60	0/1148	0.74	0/1558
3	K	0.56	0/1149	0.71	1/1558 (0.1%)
3	L	0.58	0/1149	0.72	0/1558
3	M	0.61	0/1149	0.75	1/1558 (0.1%)
3	N	0.56	0/1149	0.70	1/1558 (0.1%)
3	O	0.59	0/1149	0.71	0/1558
3	P	0.58	0/1149	0.76	0/1558
All	All	0.62	8/38588 (0.0%)	0.78	34/52263 (0.1%)

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	B	0	1
3	O	0	1
All	All	0	3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	220	GLU	CD-OE1	8.25	1.34	1.25
1	F	220	GLU	CD-OE1	7.86	1.34	1.25
1	A	220	GLU	CD-OE1	6.93	1.33	1.25
1	H	220	GLU	CD-OE1	6.46	1.32	1.25
1	B	220	GLU	CD-OE1	6.42	1.32	1.25

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	375	ARG	NE-CZ-NH2	-8.54	116.03	120.30
1	B	375	ARG	NE-CZ-NH2	-7.26	116.67	120.30
2	C	26	MET	CG-SD-CE	7.03	111.45	100.20
1	F	375	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	D	375	ARG	NE-CZ-NH2	-6.91	116.84	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	B	203	PHE	Peptide
3	O	57	ASP	Peptide

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	3664	0	3593	12	0
1	B	3675	0	3606	13	0
1	D	3664	0	3593	6	0
1	E	3675	0	3606	10	0
1	F	3675	0	3606	14	0
1	G	3675	0	3606	13	0
1	H	3664	0	3594	9	0
2	C	3663	0	3593	16	0
3	I	1118	0	1057	0	0
3	J	1117	0	1057	1	0
3	K	1118	0	1057	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	1118	0	1057	0	0
3	M	1118	0	1057	0	0
3	N	1118	0	1057	0	0
3	O	1118	0	1057	2	0
3	P	1118	0	1057	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	J	1	0	0	0	0
4	N	1	0	0	0	0
5	A	21	0	8	0	0
5	B	21	0	8	0	0
5	C	21	0	8	0	0
5	D	21	0	7	0	0
5	E	21	0	7	0	0
5	F	21	0	7	0	0
5	G	21	0	8	0	0
5	H	21	0	8	0	0
6	I	12	0	18	0	0
6	J	12	0	18	0	0
6	K	12	0	18	0	0
6	L	12	0	18	0	0
6	M	12	0	18	0	0
6	N	12	0	18	0	0
6	O	12	0	18	0	0
6	P	12	0	18	0	0
7	A	273	0	0	0	0
7	B	319	0	0	0	0
7	C	284	0	0	0	0
7	D	225	0	0	1	0
7	E	211	0	0	1	0
7	F	311	0	0	3	0
7	G	281	0	0	2	0
7	H	299	0	0	1	0
7	I	99	0	0	0	0
7	J	95	0	0	0	0
7	K	75	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	L	86	0	0	0	0
7	M	107	0	0	0	0
7	N	77	0	0	0	0
7	O	103	0	0	0	0
7	P	95	0	0	0	0
All	All	41512	0	37458	96	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

The worst 5 of 96 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:E:57:ALA:HB1	1:E:134:ILE:HD11	1.55	0.88
1:G:26:MET:CE	7:G:797:HOH:O	2.25	0.82
1:F:21:ILE:HD11	7:F:605:HOH:O	1.79	0.81
2:C:23:TYR:CD1	2:C:26:MET:HE3	2.33	0.63
1:G:254:VAL:HG11	1:G:275:MET:HE1	1.83	0.61

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	460/490 (94%)	447 (97%)	11 (2%)	2 (0%)	34	21
1	B	461/490 (94%)	447 (97%)	12 (3%)	2 (0%)	34	21
1	D	460/490 (94%)	445 (97%)	13 (3%)	2 (0%)	34	21
1	E	461/490 (94%)	445 (96%)	15 (3%)	1 (0%)	47	33
1	F	461/490 (94%)	446 (97%)	14 (3%)	1 (0%)	47	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	461/490 (94%)	447 (97%)	13 (3%)	1 (0%)	47	33
1	H	460/490 (94%)	447 (97%)	12 (3%)	1 (0%)	47	33
2	C	461/490 (94%)	446 (97%)	15 (3%)	0	100	100
3	I	137/139 (99%)	135 (98%)	1 (1%)	1 (1%)	22	10
3	J	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
3	K	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
3	L	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
3	M	137/139 (99%)	134 (98%)	1 (1%)	2 (2%)	10	2
3	N	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
3	O	137/139 (99%)	136 (99%)	1 (1%)	0	100	100
3	P	137/139 (99%)	135 (98%)	2 (2%)	0	100	100
All	All	4781/5032 (95%)	4652 (97%)	116 (2%)	13 (0%)	41	27

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	57	ASP
3	M	57	ASP
1	D	469	ASP
3	M	58	ILE
1	A	98	THR

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	371/389 (95%)	363 (98%)	8 (2%)	52	39
1	B	372/389 (96%)	365 (98%)	7 (2%)	57	46
1	D	371/389 (95%)	367 (99%)	4 (1%)	73	68
1	E	372/389 (96%)	367 (99%)	5 (1%)	69	62
1	F	372/389 (96%)	367 (99%)	5 (1%)	69	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	372/389 (96%)	366 (98%)	6 (2%)	62	54
1	H	371/389 (95%)	367 (99%)	4 (1%)	73	68
2	C	372/390 (95%)	370 (100%)	2 (0%)	88	87
3	I	118/118 (100%)	118 (100%)	0	100	100
3	J	118/118 (100%)	118 (100%)	0	100	100
3	K	118/118 (100%)	116 (98%)	2 (2%)	60	51
3	L	118/118 (100%)	117 (99%)	1 (1%)	81	78
3	M	118/118 (100%)	117 (99%)	1 (1%)	81	78
3	N	118/118 (100%)	116 (98%)	2 (2%)	60	51
3	O	118/118 (100%)	116 (98%)	2 (2%)	60	51
3	P	118/118 (100%)	117 (99%)	1 (1%)	81	78
All	All	3917/4057 (96%)	3867 (99%)	50 (1%)	71	62

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	125[B]	ILE
1	G	243	TYR
3	P	59	LYS
1	F	189	TYR
1	G	125[A]	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	461	GLN
2	C	211	ASN
1	E	443	ASN
1	E	444	GLN
1	H	461	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

55 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	0.78	0	9,14,16	0.52	0
1	HL2	A	174	1	7,8,9	0.74	0	7,10,12	0.56	0
1	HYP	A	155	1	6,8,9	0.44	0	5,10,12	1.93	2 (40%)
1	M3L	A	346	1	10,11,12	0.60	0	9,14,16	0.61	0
1	HL2	E	174	1	7,8,9	0.70	0	7,10,12	0.86	0
1	KCX	A	205	4,1	9,11,12	0.86	0	5,12,14	0.77	0
1	HYP	G	155	1	6,8,9	0.83	0	5,10,12	1.95	2 (40%)
1	SNC	H	457	1	4,7,8	0.85	0	1,7,9	0.18	0
1	HYP	D	155	1	6,8,9	1.17	1 (16%)	5,10,12	1.93	2 (40%)
1	HYP	H	48	1	6,8,9	0.63	0	5,10,12	1.54	2 (40%)
1	HL2	D	174	1	7,8,9	0.62	0	7,10,12	0.63	0
1	KCX	E	205	4,1	9,11,12	2.22	1 (11%)	5,12,14	2.08	1 (20%)
1	CSO	A	109	1	3,6,7	0.99	0	0,6,8	-	-
1	HYP	E	48	1	6,8,9	0.72	0	5,10,12	1.92	2 (40%)
1	M3L	E	346	1	10,11,12	0.64	0	9,14,16	0.60	0
1	M3L	F	346	1	10,11,12	0.46	0	9,14,16	0.65	0
1	M3L	H	346	1	10,11,12	0.55	0	9,14,16	0.72	0
1	SNC	D	457	1	4,7,8	1.00	0	1,7,9	0.39	0
2	HL2	C	174	2	7,8,9	0.65	0	7,10,12	0.82	0
1	SNC	G	457	1	4,7,8	1.20	1 (25%)	1,7,9	0.54	0
1	CSO	F	109	1	3,6,7	0.45	0	0,6,8	-	-
1	HYP	D	48	1	6,8,9	0.55	0	5,10,12	1.16	1 (20%)
1	HYP	F	48	1	6,8,9	0.70	0	5,10,12	1.47	1 (20%)
1	HL2	B	174	1	7,8,9	0.61	0	7,10,12	0.59	0
1	SNC	B	457	1	4,7,8	0.77	0	1,7,9	0.52	0
2	KCX	C	205	4,2	9,11,12	0.96	0	5,12,14	1.01	0
2	SNC	C	457	2	4,7,8	1.07	0	1,7,9	0.66	0
2	M3L	C	346	2	10,11,12	0.57	0	9,14,16	0.78	0
1	M3L	B	346	1	10,11,12	0.83	0	9,14,16	0.60	0
1	SNC	A	457	1	4,7,8	0.88	0	1,7,9	0.22	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	HYP	F	155	1	6,8,9	0.82	0	5,10,12	1.30	1 (20%)
1	HL2	H	174	1	7,8,9	0.54	0	7,10,12	0.64	0
1	KCX	G	205	4,1	9,11,12	2.05	2 (22%)	5,12,14	2.44	1 (20%)
1	HYP	E	155	1	6,8,9	0.78	0	5,10,12	2.51	3 (60%)
2	CSO	C	109	2	3,6,7	0.67	0	0,6,8	-	-
1	HYP	A	48	1	6,8,9	0.61	0	5,10,12	1.63	1 (20%)
1	CSO	E	109	1	3,6,7	0.61	0	0,6,8	-	-
1	KCX	D	205	4,1	9,11,12	0.69	0	5,12,14	1.13	1 (20%)
1	SNC	F	457	1	4,7,8	0.93	0	1,7,9	1.12	0
1	KCX	B	205	4,1	9,11,12	2.30	1 (11%)	5,12,14	2.35	2 (40%)
1	SNC	E	457	1	4,7,8	0.98	0	1,7,9	0.71	0
1	KCX	H	205	4,1	9,11,12	2.23	1 (11%)	5,12,14	1.62	1 (20%)
1	HL2	F	174	1	7,8,9	0.81	0	7,10,12	0.37	0
1	HYP	B	155	1	6,8,9	0.66	0	5,10,12	2.23	3 (60%)
1	HYP	G	48	1	6,8,9	0.50	0	5,10,12	1.74	2 (40%)
2	HYP	C	155	2	6,8,9	0.53	0	5,10,12	1.79	2 (40%)
1	HL2	G	174	1	7,8,9	0.70	0	7,10,12	0.65	0
1	HYP	B	48	1	6,8,9	0.59	0	5,10,12	1.61	2 (40%)
1	CSO	H	109	1	3,6,7	0.90	0	0,6,8	-	-
1	CSO	G	109	1	3,6,7	0.70	0	0,6,8	-	-
1	KCX	F	205	4,1	9,11,12	0.67	0	5,12,14	1.05	1 (20%)
1	M3L	D	346	1	10,11,12	0.67	0	9,14,16	0.46	0
1	CSO	B	109	1	3,6,7	0.61	0	0,6,8	-	-
1	CSO	D	109	1	3,6,7	0.45	0	0,6,8	-	-
1	HYP	H	155	1	6,8,9	0.73	0	5,10,12	0.90	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	-	1/9/10/12	-
1	HL2	A	174	1	-	2/9/10/12	-
1	HYP	A	155	1	-	0/0/11/13	0/1/1/1
1	M3L	A	346	1	-	1/9/10/12	-
1	HL2	E	174	1	-	1/9/10/12	-
1	KCX	A	205	4,1	-	0/9/10/12	-
1	HYP	G	155	1	-	0/0/11/13	0/1/1/1
1	SNC	H	457	1	-	0/0/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	D	155	1	-	0/0/11/13	0/1/1/1
1	HYP	H	48	1	-	0/0/11/13	0/1/1/1
1	HL2	D	174	1	-	1/9/10/12	-
1	KCX	E	205	4,1	-	0/9/10/12	-
1	CSO	A	109	1	-	0/1/5/7	-
1	HYP	E	48	1	-	0/0/11/13	0/1/1/1
1	M3L	E	346	1	-	1/9/10/12	-
1	M3L	F	346	1	-	4/9/10/12	-
1	M3L	H	346	1	-	1/9/10/12	-
1	SNC	D	457	1	-	0/0/6/8	-
2	HL2	C	174	2	-	1/9/10/12	-
1	SNC	G	457	1	-	0/0/6/8	-
1	CSO	F	109	1	-	0/1/5/7	-
1	HYP	D	48	1	-	0/0/11/13	0/1/1/1
1	HYP	F	48	1	-	0/0/11/13	0/1/1/1
1	HL2	B	174	1	-	1/9/10/12	-
1	SNC	B	457	1	-	0/0/6/8	-
2	KCX	C	205	4,2	-	0/9/10/12	-
2	SNC	C	457	2	-	0/0/6/8	-
2	M3L	C	346	2	-	1/9/10/12	-
1	M3L	B	346	1	-	1/9/10/12	-
1	SNC	A	457	1	-	0/0/6/8	-
1	HYP	F	155	1	-	0/0/11/13	0/1/1/1
1	HL2	H	174	1	-	2/9/10/12	-
1	KCX	G	205	4,1	-	0/9/10/12	-
1	HYP	E	155	1	-	0/0/11/13	0/1/1/1
2	CSO	C	109	2	-	0/1/5/7	-
1	HYP	A	48	1	-	0/0/11/13	0/1/1/1
1	CSO	E	109	1	-	0/1/5/7	-
1	KCX	D	205	4,1	-	0/9/10/12	-
1	SNC	F	457	1	-	0/0/6/8	-
1	KCX	B	205	4,1	-	0/9/10/12	-
1	SNC	E	457	1	-	0/0/6/8	-
1	KCX	H	205	4,1	-	0/9/10/12	-
1	HL2	F	174	1	-	1/9/10/12	-
1	HYP	B	155	1	-	0/0/11/13	0/1/1/1
1	HYP	G	48	1	-	0/0/11/13	0/1/1/1
2	HYP	C	155	2	-	0/0/11/13	0/1/1/1
1	HL2	G	174	1	-	1/9/10/12	-
1	HYP	B	48	1	-	0/0/11/13	0/1/1/1
1	CSO	H	109	1	-	0/1/5/7	-
1	CSO	G	109	1	-	0/1/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	F	205	4,1	-	0/9/10/12	-
1	M3L	D	346	1	-	1/9/10/12	-
1	CSO	B	109	1	-	0/1/5/7	-
1	CSO	D	109	1	-	0/1/5/7	-
1	HYP	H	155	1	-	0/0/11/13	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	205	KCX	OQ1-CX	6.54	1.33	1.21
1	E	205	KCX	OQ1-CX	6.41	1.33	1.21
1	H	205	KCX	OQ1-CX	6.28	1.33	1.21
1	G	205	KCX	OQ1-CX	5.40	1.31	1.21
1	D	155	HYP	CB-CA	-2.54	1.48	1.54

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	205	KCX	OQ1-CX-NZ	-5.43	116.53	124.96
1	E	205	KCX	OQ1-CX-NZ	-4.59	117.84	124.96
1	B	205	KCX	OQ1-CX-NZ	-4.52	117.95	124.96
1	H	205	KCX	OQ1-CX-NZ	-3.54	119.46	124.96
1	E	155	HYP	CB-CG-CD	3.42	107.46	103.27

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	174	HL2	O-C-CA-CB
1	B	174	HL2	O-C-CA-CB
1	D	174	HL2	O-C-CA-CB
1	E	174	HL2	O-C-CA-CB
1	F	174	HL2	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	174	HL2	1	0
2	C	205	KCX	1	0
1	G	205	KCX	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 42 ligands modelled in this entry, 10 are monoatomic - leaving 32 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	$\#\|Z\| > 2$
6	EDO	M	202	-	3,3,3	0.44	0	2,2,2	0.38	0
5	CAP	E	502	4	17,20,20	0.83	0	22,31,31	1.32	3 (13%)
6	EDO	O	202	-	3,3,3	0.44	0	2,2,2	0.56	0
5	CAP	C	502	4	17,20,20	0.92	0	22,31,31	1.00	1 (4%)
6	EDO	P	203	-	3,3,3	0.53	0	2,2,2	0.34	0
6	EDO	N	203	-	3,3,3	0.40	0	2,2,2	0.71	0
6	EDO	N	204	-	3,3,3	0.45	0	2,2,2	0.37	0
6	EDO	L	201	-	3,3,3	0.56	0	2,2,2	0.19	0
6	EDO	K	203	-	3,3,3	0.44	0	2,2,2	0.50	0
6	EDO	K	201	-	3,3,3	0.49	0	2,2,2	0.08	0
6	EDO	M	203	-	3,3,3	0.59	0	2,2,2	0.27	0
6	EDO	L	202	-	3,3,3	0.46	0	2,2,2	0.53	0
6	EDO	L	203	-	3,3,3	0.50	0	2,2,2	0.28	0
6	EDO	J	203	-	3,3,3	0.41	0	2,2,2	0.21	0
6	EDO	I	202	-	3,3,3	0.39	0	2,2,2	0.51	0
6	EDO	M	201	-	3,3,3	0.46	0	2,2,2	0.10	0
5	CAP	A	502	4	17,20,20	0.77	0	22,31,31	1.13	3 (13%)
5	CAP	F	502	4	17,20,20	0.89	0	22,31,31	0.89	0
6	EDO	P	202	-	3,3,3	0.29	0	2,2,2	0.58	0
6	EDO	K	202	-	3,3,3	0.44	0	2,2,2	0.69	0
5	CAP	B	502	4	17,20,20	0.85	0	22,31,31	1.12	1 (4%)
6	EDO	O	203	-	3,3,3	0.58	0	2,2,2	0.36	0
5	CAP	G	502	4	17,20,20	0.83	0	22,31,31	0.94	1 (4%)
5	CAP	D	502	4	17,20,20	0.83	0	22,31,31	1.25	3 (13%)
6	EDO	I	203	-	3,3,3	0.54	0	2,2,2	0.29	0
6	EDO	N	202	-	3,3,3	0.60	0	2,2,2	0.14	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	CAP	H	502	4	17,20,20	0.76	0	22,31,31	1.23	3 (13%)
6	EDO	P	201	-	3,3,3	0.52	0	2,2,2	0.32	0
6	EDO	I	201	-	3,3,3	0.51	0	2,2,2	0.03	0
6	EDO	J	202	-	3,3,3	0.46	0	2,2,2	0.12	0
6	EDO	O	201	-	3,3,3	0.54	0	2,2,2	0.05	0
6	EDO	J	204	-	3,3,3	0.57	0	2,2,2	0.39	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
6	EDO	M	202	-	-	0/1/1/1	-
5	CAP	E	502	4	-	8/29/29/29	-
6	EDO	O	202	-	-	0/1/1/1	-
5	CAP	C	502	4	-	8/29/29/29	-
6	EDO	P	203	-	-	0/1/1/1	-
6	EDO	N	203	-	-	0/1/1/1	-
6	EDO	N	204	-	-	0/1/1/1	-
6	EDO	L	201	-	-	0/1/1/1	-
6	EDO	K	203	-	-	0/1/1/1	-
6	EDO	K	201	-	-	1/1/1/1	-
6	EDO	M	203	-	-	0/1/1/1	-
6	EDO	L	202	-	-	0/1/1/1	-
6	EDO	L	203	-	-	0/1/1/1	-
6	EDO	J	203	-	-	0/1/1/1	-
6	EDO	I	202	-	-	0/1/1/1	-
6	EDO	M	201	-	-	0/1/1/1	-
5	CAP	A	502	4	-	7/29/29/29	-
5	CAP	F	502	4	-	9/29/29/29	-
6	EDO	P	202	-	-	0/1/1/1	-
6	EDO	K	202	-	-	0/1/1/1	-
5	CAP	B	502	4	-	7/29/29/29	-
6	EDO	O	203	-	-	0/1/1/1	-
5	CAP	G	502	4	-	9/29/29/29	-
5	CAP	D	502	4	-	8/29/29/29	-
6	EDO	I	203	-	-	0/1/1/1	-
6	EDO	N	202	-	-	0/1/1/1	-
5	CAP	H	502	4	-	7/29/29/29	-
6	EDO	P	201	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	I	201	-	-	0/1/1/1	-
6	EDO	J	202	-	-	0/1/1/1	-
6	EDO	O	201	-	-	0/1/1/1	-
6	EDO	J	204	-	-	0/1/1/1	-

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	502	CAP	O2P-P1-O1	-2.94	98.91	106.73
5	B	502	CAP	O6P-P2-O5P	2.75	118.16	107.64
5	E	502	CAP	O3P-P1-O2P	2.66	117.79	107.64
5	C	502	CAP	O6P-P2-O5P	2.57	117.47	107.64
5	D	502	CAP	O3P-P1-O2P	2.54	117.36	107.64

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

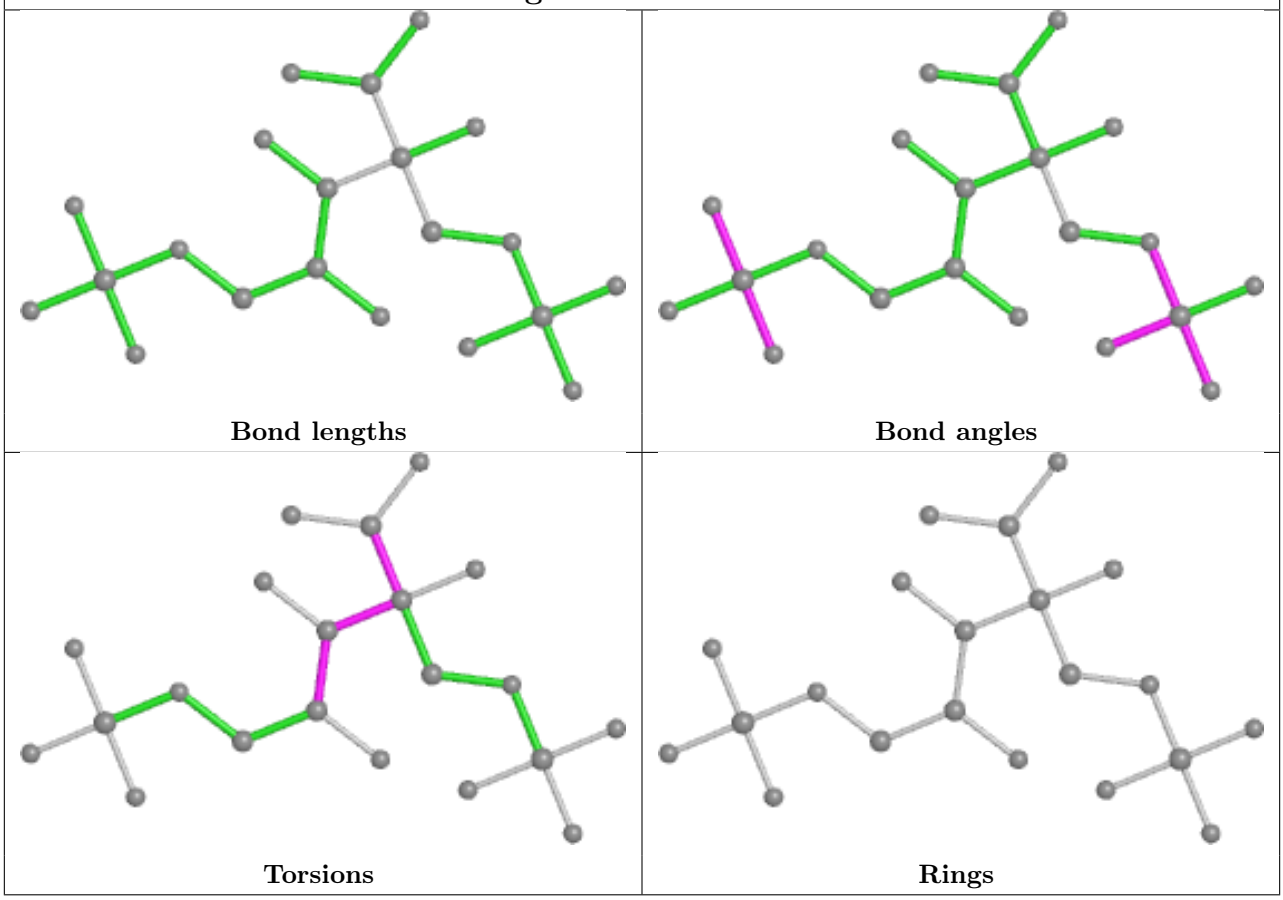
Mol	Chain	Res	Type	Atoms
5	A	502	CAP	O6-C-C2-C1
5	A	502	CAP	O7-C-C2-C1
5	A	502	CAP	O6-C-C2-O2
5	A	502	CAP	O7-C-C2-O2
5	A	502	CAP	C2-C3-C4-O4

There are no ring outliers.

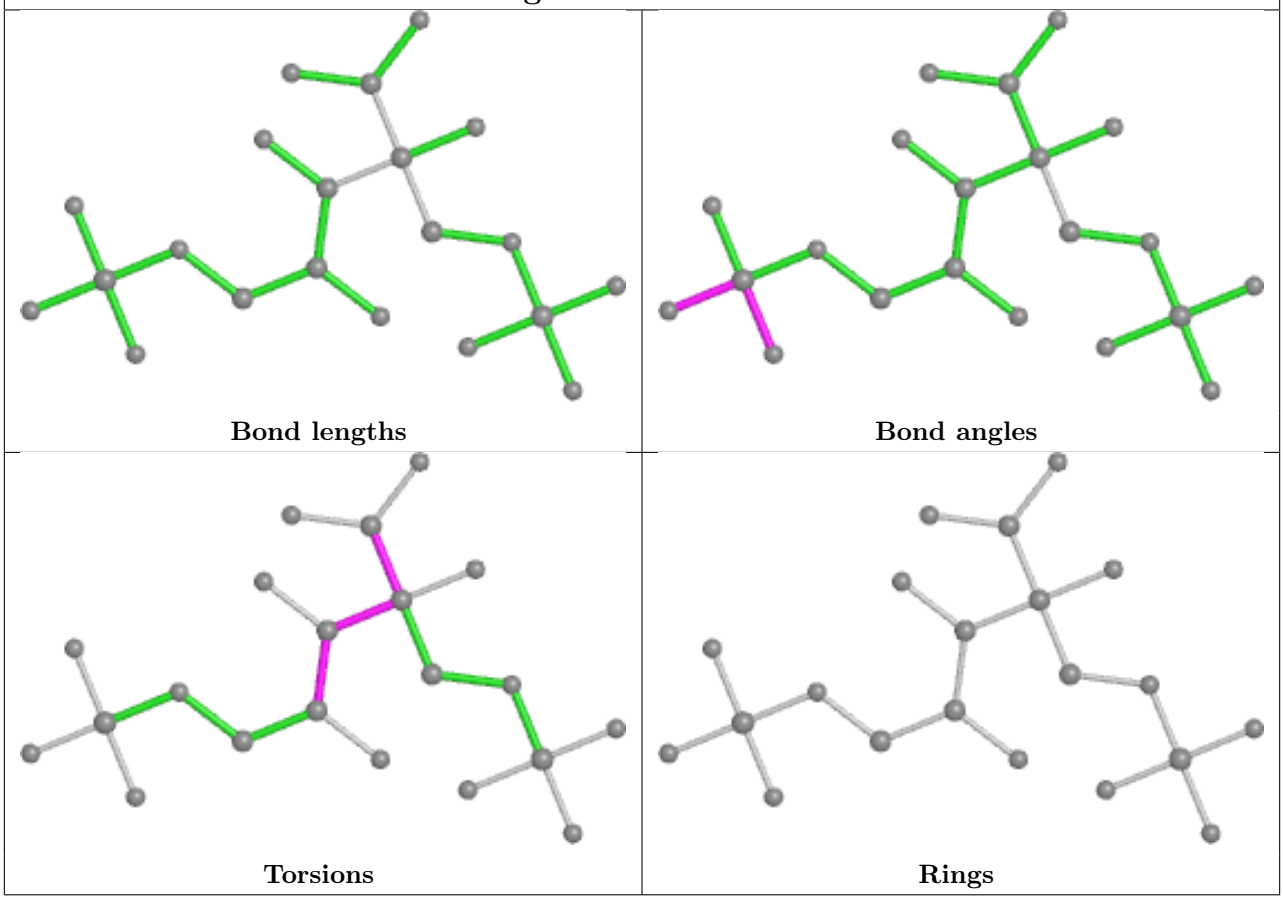
No monomer is involved in short contacts.

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 then 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.

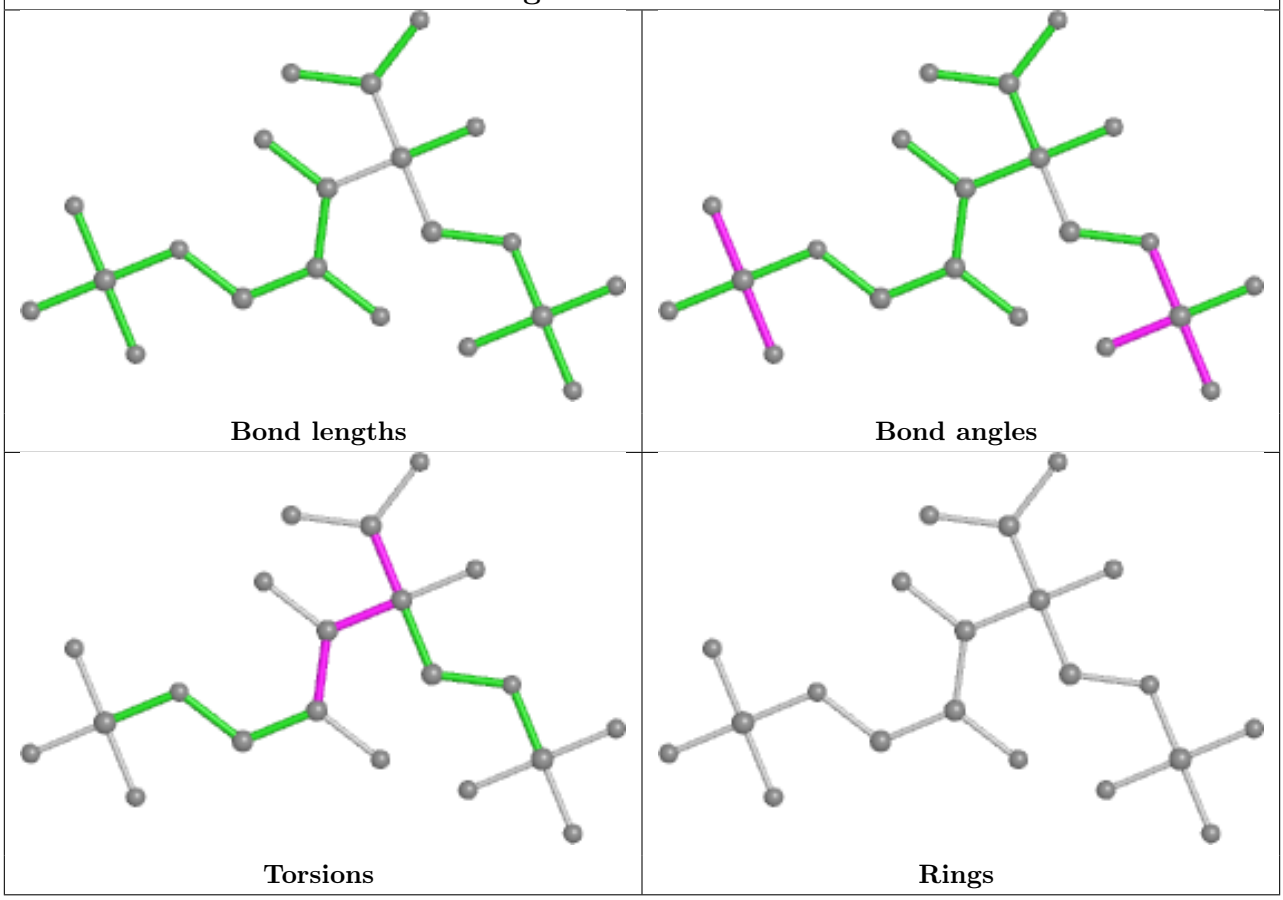
Ligand CAP E 502



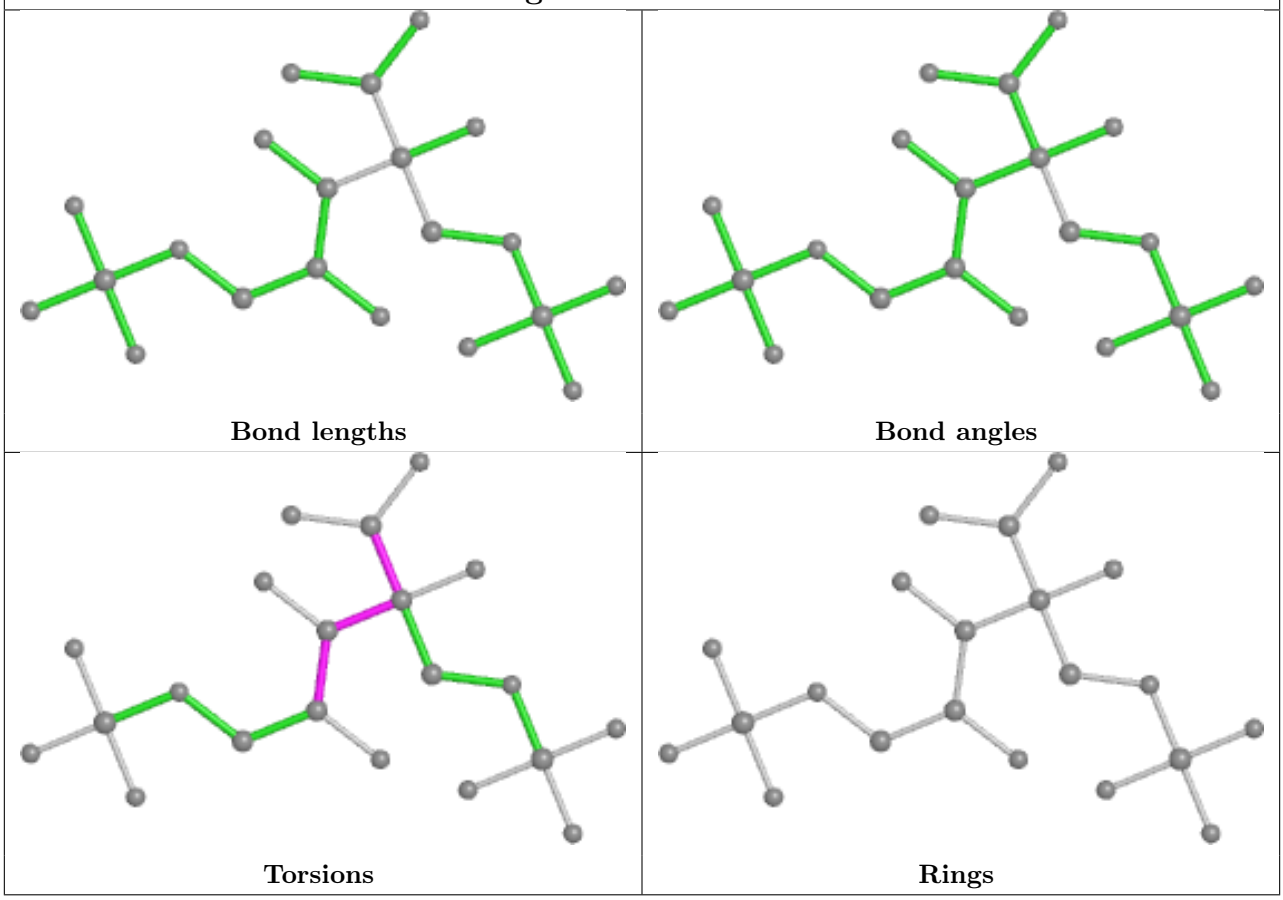
Ligand CAP C 502



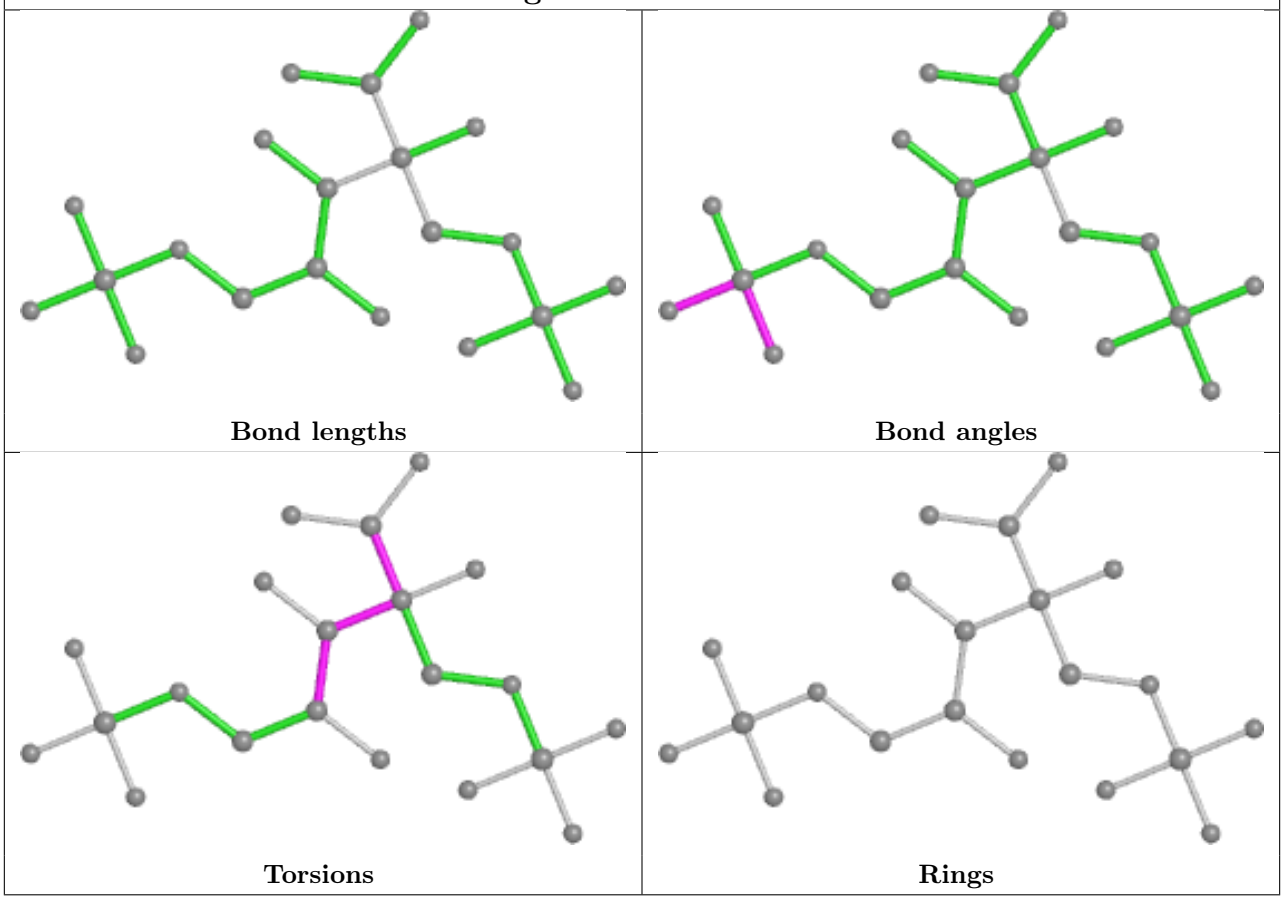
Ligand CAP A 502



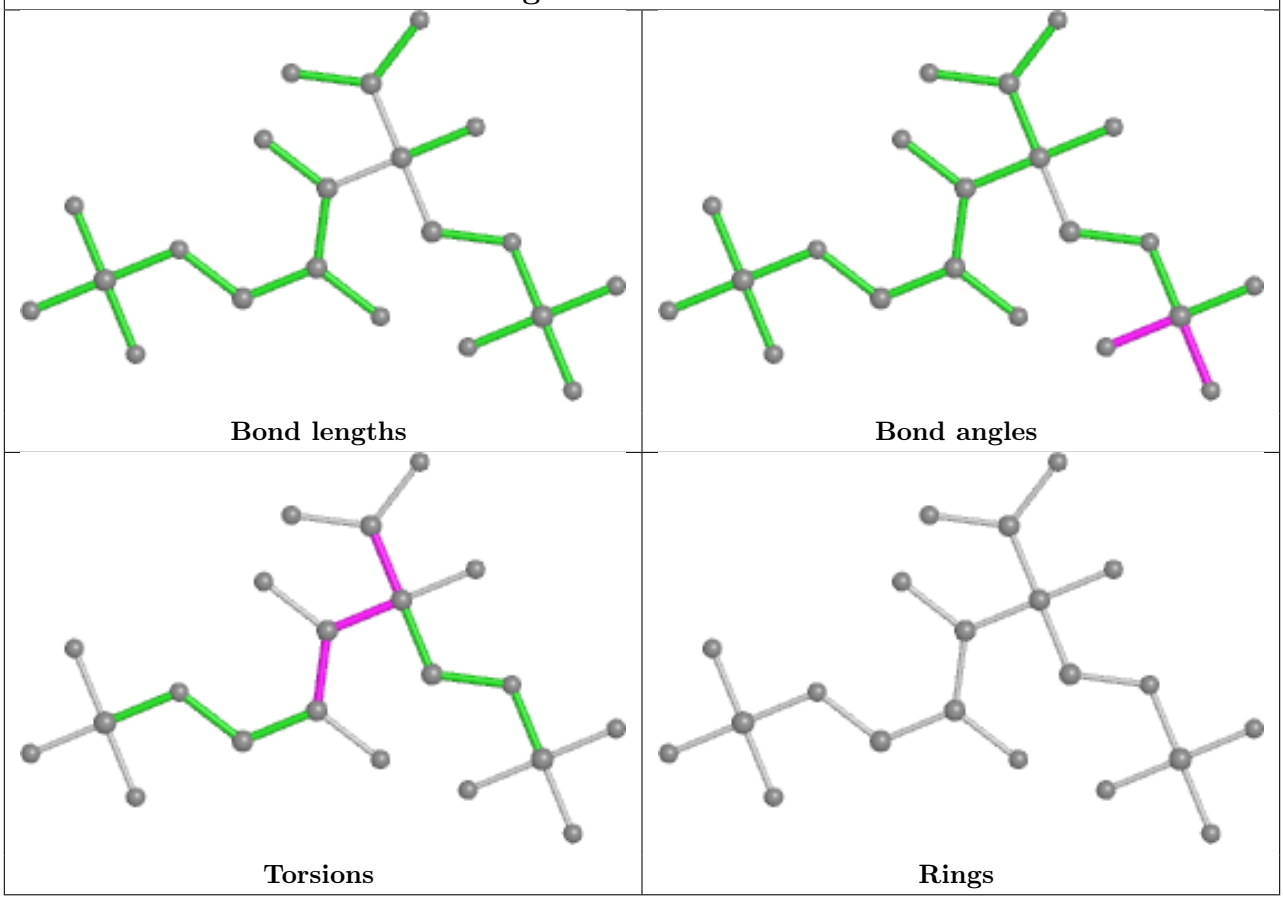
Ligand CAP F 502



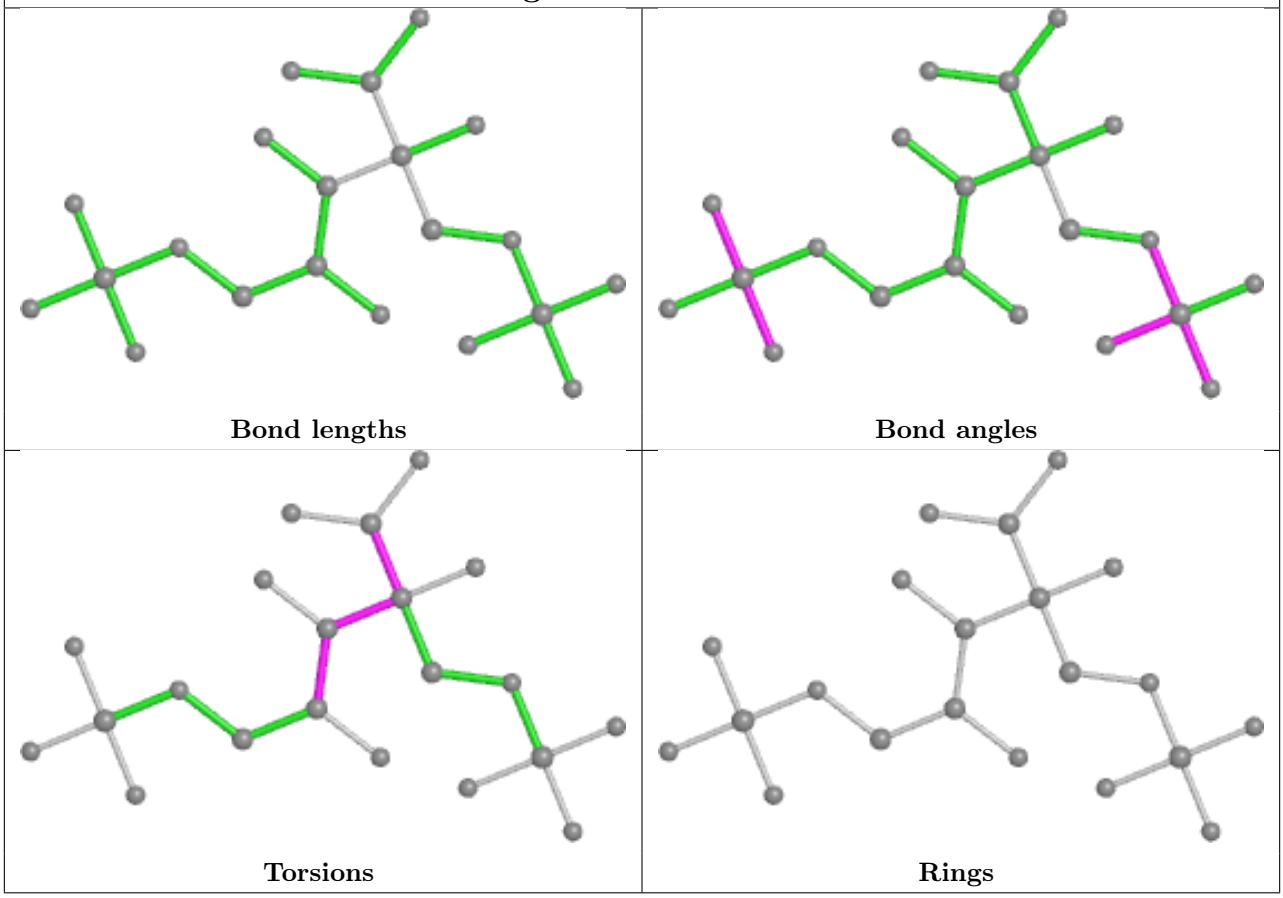
Ligand CAP B 502



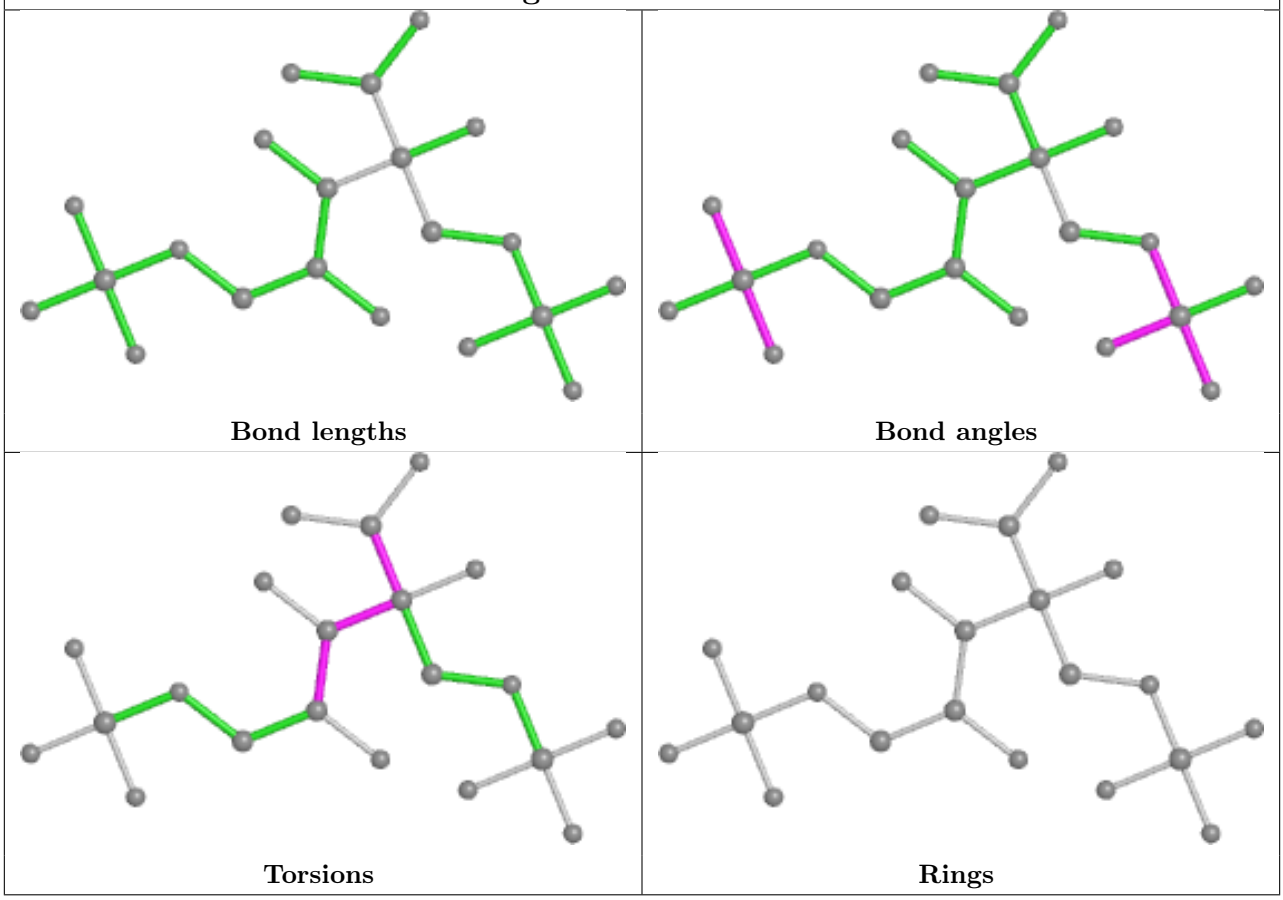
Ligand CAP G 502



Ligand CAP D 502



Ligand CAP H 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	460/490 (93%)	-0.74	2 (0%)	92	90	14, 23, 42, 59	0
1	B	461/490 (94%)	-0.78	2 (0%)	92	90	14, 22, 35, 62	0
1	D	460/490 (93%)	-0.61	4 (0%)	84	82	17, 31, 50, 65	0
1	E	461/490 (94%)	-0.55	5 (1%)	80	78	18, 30, 49, 66	0
1	F	461/490 (94%)	-0.79	3 (0%)	87	86	15, 23, 39, 66	0
1	G	461/490 (94%)	-0.77	2 (0%)	92	90	15, 23, 40, 54	0
1	H	460/490 (93%)	-0.68	4 (0%)	84	82	15, 25, 43, 57	0
2	C	461/490 (94%)	-0.80	3 (0%)	87	86	14, 22, 35, 56	0
3	I	139/139 (100%)	-0.64	0	100	100	15, 28, 42, 62	0
3	J	139/139 (100%)	-0.63	1 (0%)	87	86	16, 30, 46, 72	0
3	K	139/139 (100%)	-0.49	2 (1%)	75	72	19, 35, 50, 59	0
3	L	139/139 (100%)	-0.57	2 (1%)	75	72	19, 32, 46, 58	0
3	M	139/139 (100%)	-0.60	1 (0%)	87	86	17, 31, 45, 59	0
3	N	139/139 (100%)	-0.55	1 (0%)	87	86	16, 34, 51, 66	0
3	O	139/139 (100%)	-0.57	2 (1%)	75	72	19, 31, 49, 78	0
3	P	139/139 (100%)	-0.59	1 (0%)	87	86	18, 29, 42, 57	0
All	All	4797/5032 (95%)	-0.68	35 (0%)	87	86	14, 27, 45, 78	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	16	TYR	5.2
3	O	57	ASP	5.0
1	E	98	THR	4.8
1	F	16	TYR	4.4
1	A	16	TYR	4.3

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	M3L	E	346	12/13	0.91	0.11	34,37,41,41	0
1	HYP	E	48	8/9	0.92	0.08	42,43,43,44	0
1	HYP	A	48	8/9	0.92	0.09	29,30,30,31	0
1	M3L	D	346	12/13	0.93	0.11	33,40,46,46	0
1	M3L	H	346	12/13	0.93	0.12	24,28,32,32	0
1	SNC	F	457	8/9	0.93	0.10	36,39,41,43	0
1	M3L	A	346	12/13	0.94	0.12	23,29,34,35	0
1	HYP	D	48	8/9	0.94	0.08	43,43,44,45	0
1	HYP	G	48	8/9	0.94	0.07	23,24,24,24	0
1	M3L	G	346	12/13	0.94	0.09	23,27,31,31	0
1	HYP	H	48	8/9	0.94	0.09	31,32,32,33	0
1	HYP	D	155	8/9	0.94	0.08	21,22,22,22	0
1	M3L	F	346	12/13	0.95	0.08	22,27,32,33	0
1	SNC	A	457	8/9	0.95	0.07	36,38,39,41	0
1	SNC	B	457	8/9	0.95	0.07	28,28,29,30	0
1	SNC	D	457	8/9	0.95	0.07	40,42,43,46	0
1	HYP	E	155	8/9	0.95	0.07	21,22,23,23	0
1	SNC	G	457	8/9	0.95	0.07	39,40,41,43	0
2	SNC	C	457	8/9	0.95	0.08	28,29,29,30	0
1	M3L	B	346	12/13	0.96	0.09	22,25,28,28	0
1	HL2	E	174	9/10	0.96	0.07	26,28,29,29	0
1	KCX	B	205	12/13	0.96	0.07	16,17,17,17	0
1	SNC	E	457	8/9	0.96	0.07	38,40,40,42	0
1	KCX	E	205	12/13	0.96	0.06	24,25,26,27	0
1	KCX	F	205	12/13	0.96	0.06	19,19,20,21	0
1	SNC	H	457	8/9	0.96	0.07	37,39,40,41	0
1	HYP	B	48	8/9	0.96	0.06	26,27,27,27	0
1	HL2	G	174	9/10	0.97	0.07	23,24,25,26	0
1	HYP	F	48	8/9	0.97	0.06	23,23,24,24	0
1	KCX	D	205	12/13	0.97	0.06	25,26,28,29	0
1	CSO	D	109	7/8	0.97	0.07	24,26,27,29	0
1	HYP	F	155	8/9	0.97	0.07	17,17,17,18	0
1	KCX	G	205	12/13	0.97	0.06	19,20,20,20	0
1	KCX	H	205	12/13	0.97	0.05	20,20,21,21	0
1	HL2	B	174	9/10	0.97	0.06	19,20,21,22	0
1	HL2	D	174	9/10	0.97	0.07	26,28,30,30	0
1	HYP	A	155	8/9	0.97	0.06	16,16,16,16	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	HYP	C	155	8/9	0.97	0.07	17,18,18,19	0
2	KCX	C	205	12/13	0.97	0.07	16,16,16,16	0
2	M3L	C	346	12/13	0.97	0.07	21,25,30,31	0
1	HL2	F	174	9/10	0.97	0.05	22,23,24,25	0
1	HYP	G	155	8/9	0.98	0.07	16,17,17,17	0
1	HL2	A	174	9/10	0.98	0.06	20,21,23,24	0
1	HL2	H	174	9/10	0.98	0.05	22,23,24,25	0
2	CSO	C	109	7/8	0.98	0.07	22,23,25,25	0
1	KCX	A	205	12/13	0.98	0.06	18,19,21,21	0
2	HL2	C	174	9/10	0.98	0.06	18,20,21,21	0
1	CSO	E	109	7/8	0.98	0.06	25,26,26,27	0
1	CSO	B	109	7/8	0.98	0.05	22,23,24,24	0
1	HYP	B	155	8/9	0.98	0.08	17,18,18,18	0
1	HYP	H	155	8/9	0.99	0.05	16,16,17,17	0
1	CSO	G	109	7/8	0.99	0.07	17,18,19,19	0
1	CSO	H	109	7/8	0.99	0.06	19,20,20,21	0
1	CSO	A	109	7/8	0.99	0.06	18,20,21,24	0
1	CSO	F	109	7/8	0.99	0.07	17,18,19,21	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	EDO	K	202	4/4	0.95	0.08	26,26,27,28	0
6	EDO	N	203	4/4	0.95	0.08	26,26,27,27	0
6	EDO	P	203	4/4	0.95	0.08	20,20,20,20	0
6	EDO	L	203	4/4	0.96	0.06	18,19,19,20	0
6	EDO	M	203	4/4	0.96	0.06	18,19,19,19	0
5	CAP	E	502	21/21	0.96	0.08	23,28,30,31	0
6	EDO	O	202	4/4	0.96	0.07	24,25,27,28	0
6	EDO	O	203	4/4	0.96	0.06	18,20,21,22	0
6	EDO	P	202	4/4	0.96	0.05	24,25,25,27	0
5	CAP	D	502	21/21	0.96	0.07	22,28,28,29	0

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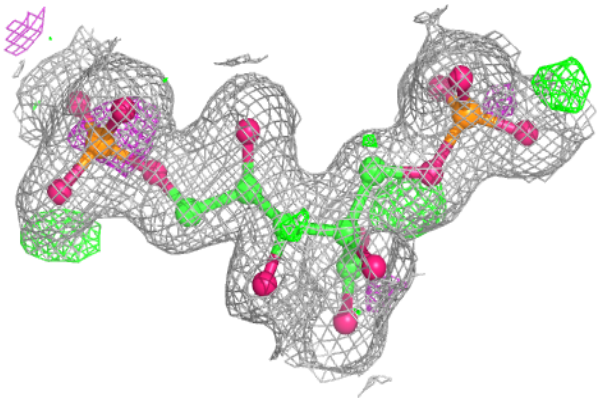
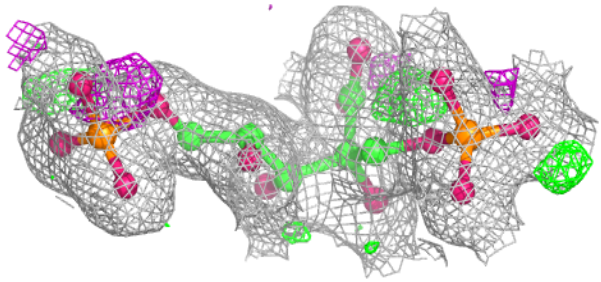
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	EDO	N	204	4/4	0.97	0.06	18,18,19,19	0
6	EDO	J	203	4/4	0.97	0.11	26,27,28,28	0
6	EDO	J	204	4/4	0.97	0.06	19,20,21,21	0
6	EDO	N	202	4/4	0.97	0.07	17,19,19,19	0
6	EDO	I	203	4/4	0.97	0.08	19,19,19,19	0
4	MG	E	501	1/1	0.98	0.04	28,28,28,28	0
6	EDO	K	203	4/4	0.98	0.05	19,19,19,19	0
6	EDO	L	201	4/4	0.98	0.05	21,21,22,22	0
6	EDO	L	202	4/4	0.98	0.05	21,22,23,25	0
4	MG	J	201	1/1	0.98	0.05	21,21,21,21	0
6	EDO	M	202	4/4	0.98	0.07	25,25,26,26	0
5	CAP	F	502	21/21	0.98	0.06	19,22,24,25	0
5	CAP	G	502	21/21	0.98	0.06	19,21,22,22	0
5	CAP	H	502	21/21	0.98	0.05	21,24,25,25	0
6	EDO	I	201	4/4	0.98	0.07	18,18,18,19	0
6	EDO	I	202	4/4	0.98	0.07	24,25,27,27	0
4	MG	N	201	1/1	0.98	0.06	23,23,23,23	0
6	EDO	P	201	4/4	0.98	0.07	17,17,18,18	0
5	CAP	A	502	21/21	0.98	0.07	19,23,24,25	0
5	CAP	B	502	21/21	0.98	0.05	17,18,19,20	0
4	MG	D	501	1/1	0.99	0.02	27,27,27,27	0
6	EDO	K	201	4/4	0.99	0.06	16,17,17,18	0
4	MG	A	501	1/1	0.99	0.07	21,21,21,21	0
5	CAP	C	502	21/21	0.99	0.05	16,18,19,21	0
6	EDO	O	201	4/4	0.99	0.04	20,20,21,21	0
4	MG	F	501	1/1	0.99	0.05	21,21,21,21	0
4	MG	B	501	1/1	0.99	0.04	16,16,16,16	0
6	EDO	J	202	4/4	0.99	0.05	17,17,18,18	0
6	EDO	M	201	4/4	0.99	0.05	17,17,18,19	0
4	MG	C	501	1/1	0.99	0.04	17,17,17,17	0
4	MG	G	501	1/1	1.00	0.04	21,21,21,21	0
4	MG	H	501	1/1	1.00	0.03	22,22,22,22	0

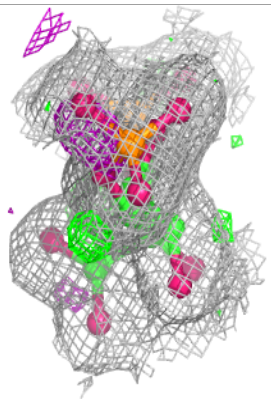
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

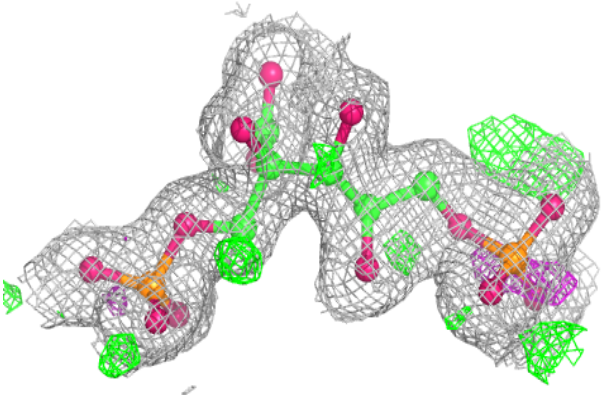


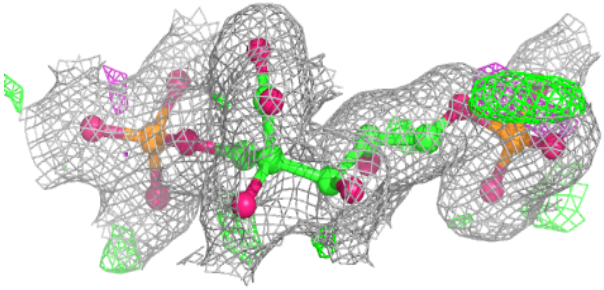


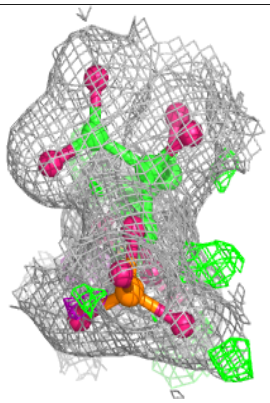


Electron density around CAP D 502:

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

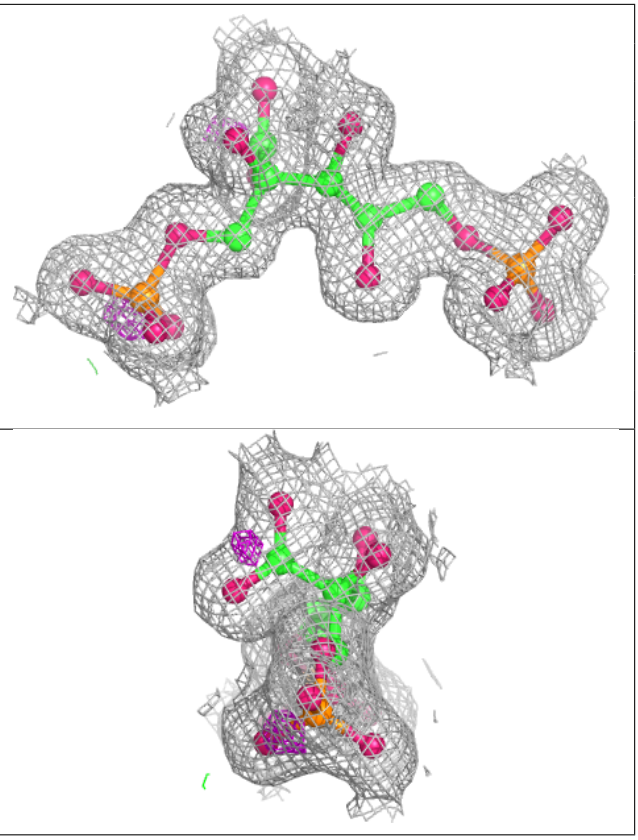






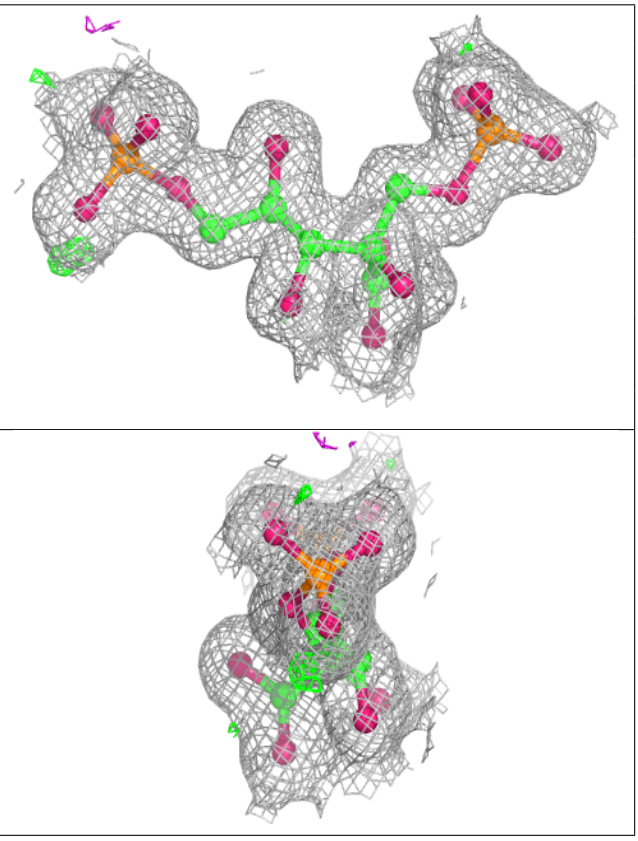
Electron density around CAP F 502:

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



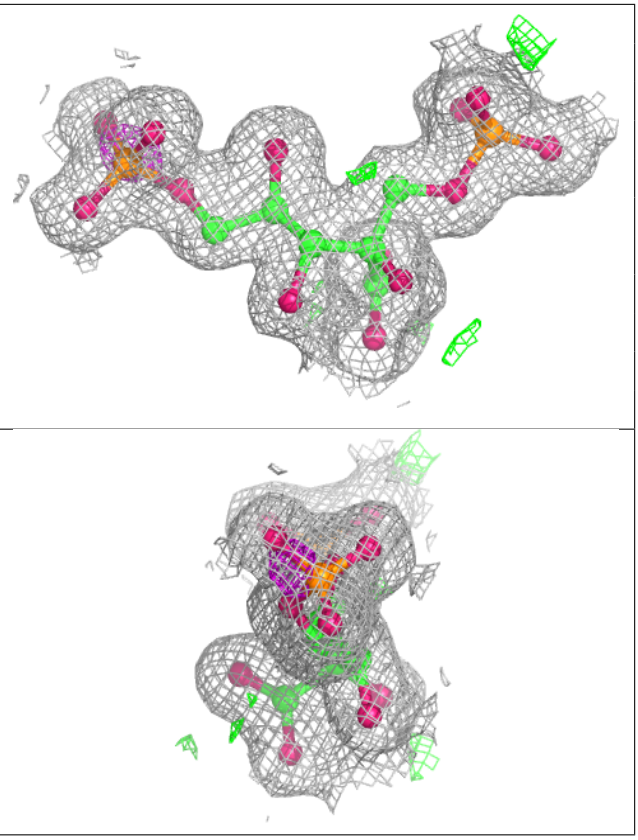
Electron density around CAP G 502:

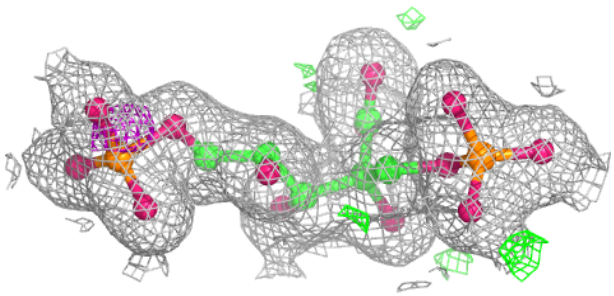
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around CAP H 502:

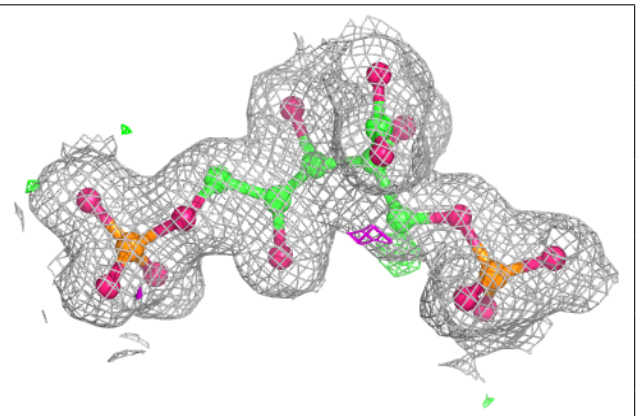
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

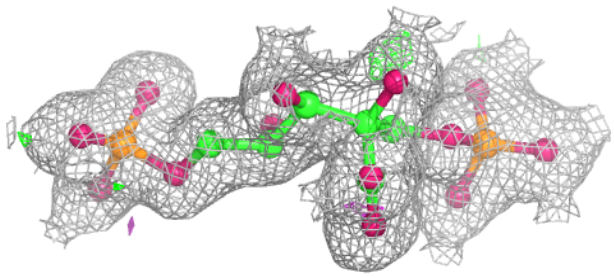


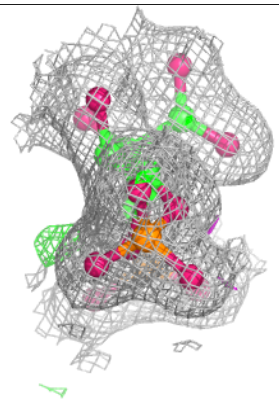


Electron density around CAP A 502:

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

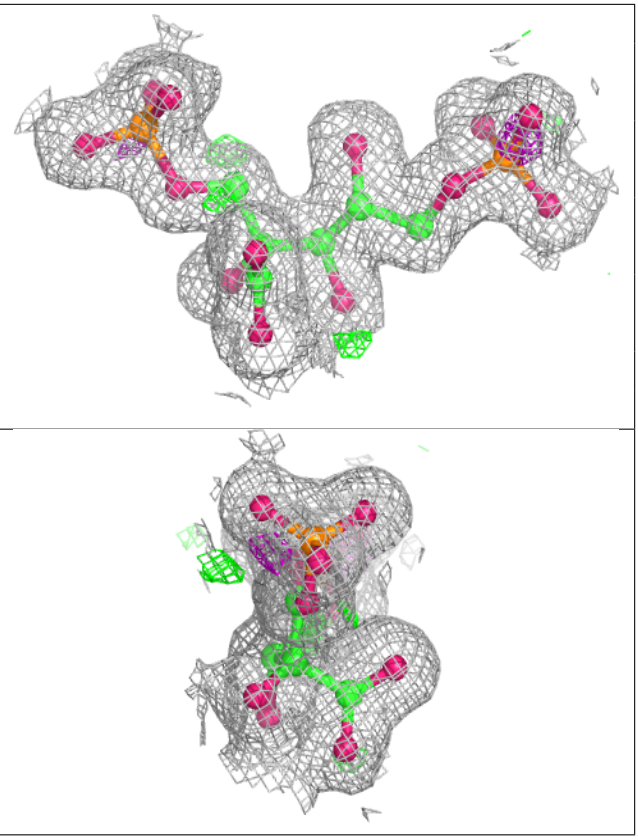


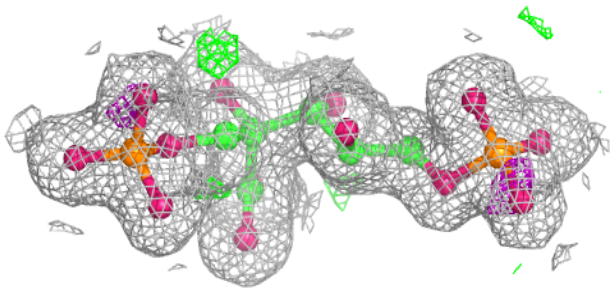




Electron density around CAP B 502:

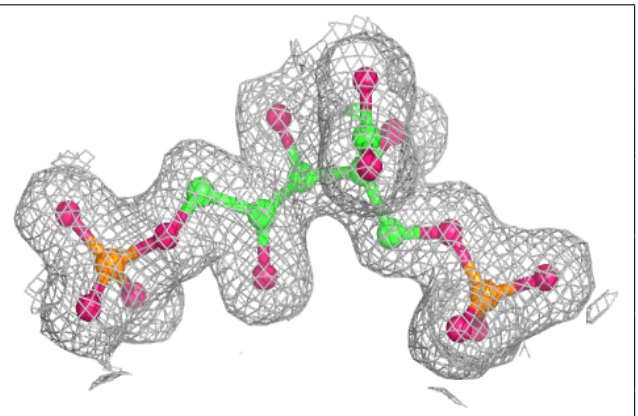
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

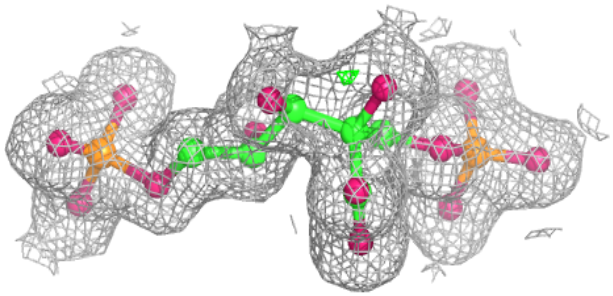


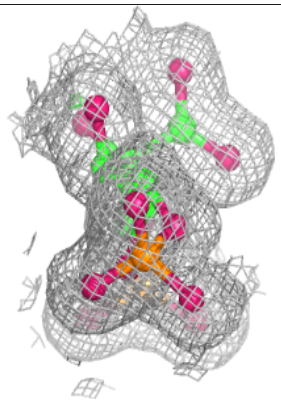


Electron density around CAP C 502:

$2mF_o$-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.