Full wwPDB X-ray Structure Validation Report ⓘ

Dec 7, 2023 – 10:51 pm GMT

PDB ID	:	2VDI
Title	:	Crystal structure of Chlamydomonas reinhardtii Rubisco with a large- subunit C192S mutation
Authors	:	Garcia-Murria, M.-J.; Karkehabadi, S.; Marin-Navarro, J.; Satagopan, S.; Andersson, I.; Spreitzer, R.J.; Moreno, J.
Deposited on	:	2007-10-09
Resolution	:	2.65 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The 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:

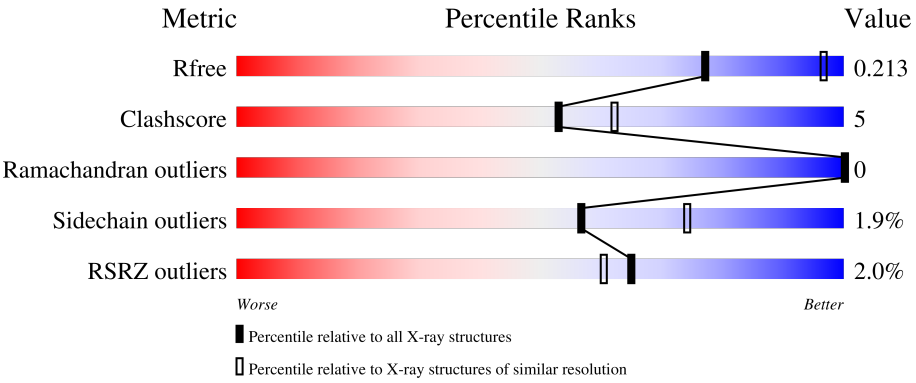
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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	475	86% 12%
1	B	475	87% 11%
1	C	475	88% 10%
1	D	475	3% 85% 12%

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Mol	Chain	Length	Quality of chain
1	E	475	2% 85% 13%
1	F	475	2% 85% 12%
1	G	475	% 86% 11%
1	H	475	% 87% 11%
2	I	140	4% 84% 15%
2	J	140	4% 86% 14%
2	K	140	4% 84% 15%
2	L	140	3% 88% 11%
2	M	140	% 86% 13%
2	N	140	4% 84% 16%
2	O	140	4% 89% 11%
2	P	140	2% 84% 15%

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
5	EDO	F	1479	-	-	X	-
5	EDO	G	1481	-	-	X	-
5	EDO	N	1141	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 40074 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 BISPHOSPHATE CARBOXYLASE LARGE CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	465	Total	C	N	O	S	0	0	0
			3628	2295	637	673	23			
1	B	468	Total	C	N	O	S	0	0	0
			3646	2306	641	676	23			
1	C	465	Total	C	N	O	S	0	0	0
			3628	2295	637	673	23			
1	D	465	Total	C	N	O	S	0	0	0
			3628	2295	637	673	23			
1	E	465	Total	C	N	O	S	0	0	0
			3627	2295	637	672	23			
1	F	465	Total	C	N	O	S	0	0	0
			3628	2295	637	673	23			
1	G	466	Total	C	N	O	S	0	0	0
			3632	2297	638	674	23			
1	H	465	Total	C	N	O	S	0	0	0
			3628	2295	637	673	23			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	46	PRO	LEU	conflict	UNP P00877
A	192	SER	CYS	engineered mutation	UNP P00877
B	46	PRO	LEU	conflict	UNP P00877
B	192	SER	CYS	engineered mutation	UNP P00877
C	46	PRO	LEU	conflict	UNP P00877
C	192	SER	CYS	engineered mutation	UNP P00877
D	46	PRO	LEU	conflict	UNP P00877
D	192	SER	CYS	engineered mutation	UNP P00877
E	46	PRO	LEU	conflict	UNP P00877
E	192	SER	CYS	engineered mutation	UNP P00877
F	46	PRO	LEU	conflict	UNP P00877
F	192	SER	CYS	engineered mutation	UNP P00877

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Chain	Residue	Modelled	Actual	Comment	Reference
G	46	PRO	LEU	conflict	UNP P00877
G	192	SER	CYS	engineered mutation	UNP P00877
H	46	PRO	LEU	conflict	UNP P00877
H	192	SER	CYS	engineered mutation	UNP P00877

- Molecule 2 is a protein called RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	I	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	J	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	K	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	L	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	M	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	N	140	Total	C	N	O	S	0	0	0
			1142	738	190	203	11			
2	O	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			
2	P	140	Total	C	N	O	S	0	0	0
			1143	739	190	203	11			

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

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

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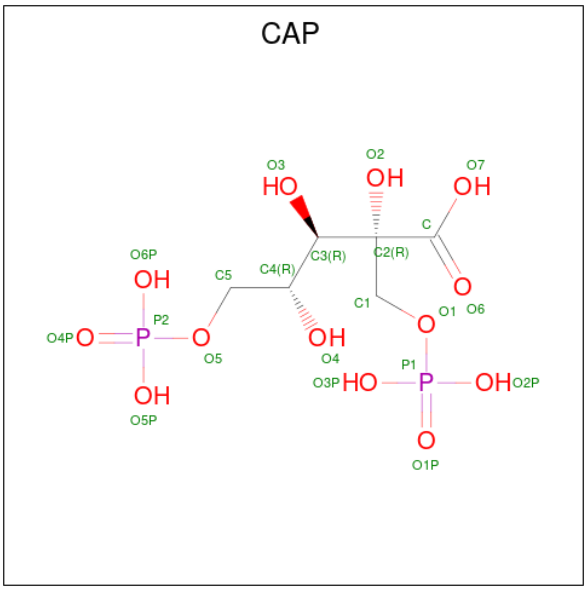
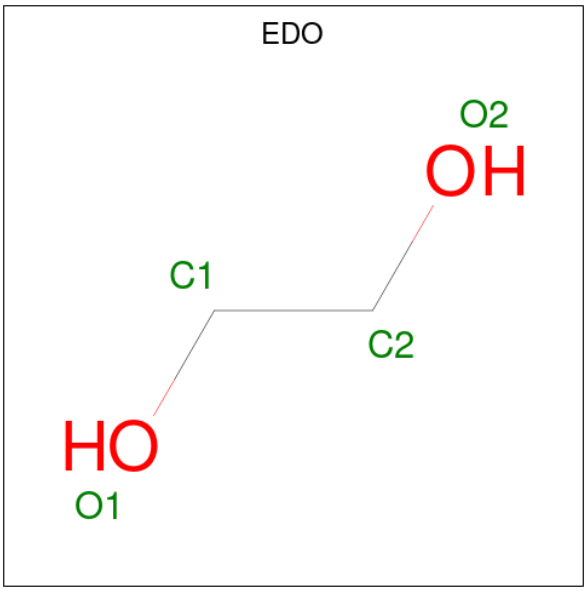
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Mg 1 1	0	0

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



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

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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		
5	D	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	E	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	F	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		
5	G	1	Total	C	O	0	0
			4	2	2		
5	H	1	Total	C	O	0	0
			4	2	2		
5	H	1	Total	C	O	0	0
			4	2	2		
5	H	1	Total	C	O	0	0
			4	2	2		
5	H	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total C O 4 2 2	0	0
5	J	1	Total C O 4 2 2	0	0
5	J	1	Total C O 4 2 2	0	0
5	K	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0
5	N	1	Total C O 4 2 2	0	0
5	O	1	Total C O 4 2 2	0	0
5	O	1	Total C O 4 2 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	154	Total O 154 154	0	0
6	B	154	Total O 154 154	0	0
6	C	146	Total O 146 146	0	0
6	D	158	Total O 158 158	0	0
6	E	159	Total O 159 159	0	0
6	F	132	Total O 132 132	0	0
6	G	162	Total O 162 162	0	0
6	H	150	Total O 150 150	0	0
6	I	47	Total O 47 47	0	0
6	J	36	Total O 36 36	0	0
6	K	37	Total O 37 37	0	0

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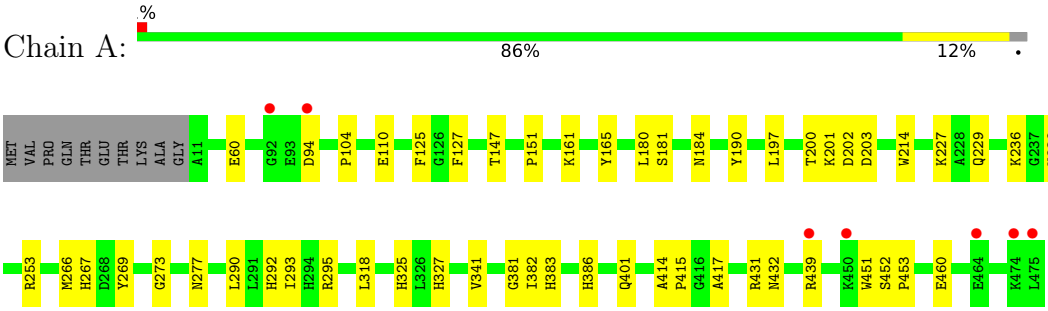
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	L	38	Total O 38 38	0	0
6	M	46	Total O 46 46	0	0
6	N	44	Total O 44 44	0	0
6	O	37	Total O 37 37	0	0
6	P	38	Total O 38 38	0	0

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.

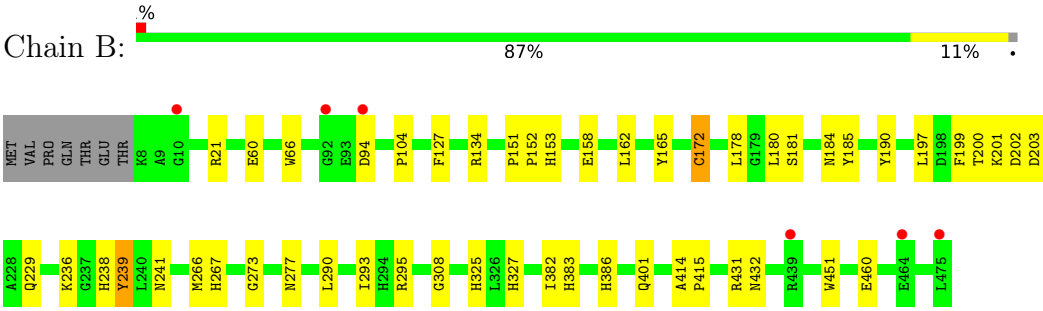
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain A:



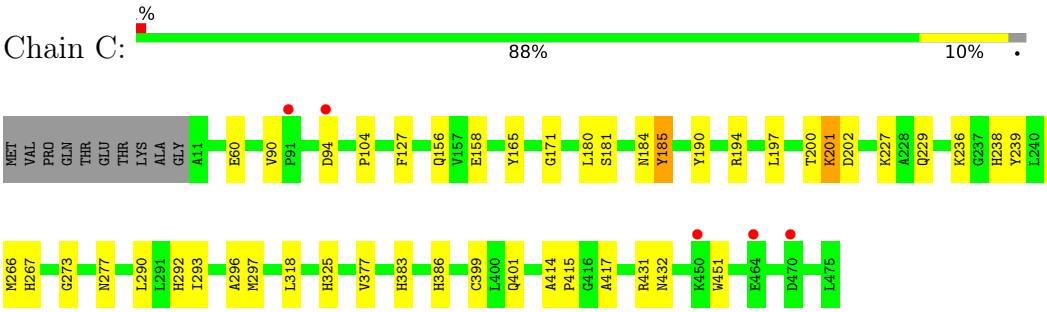
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain B:



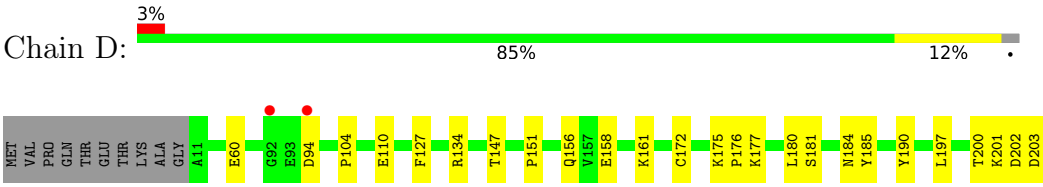
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

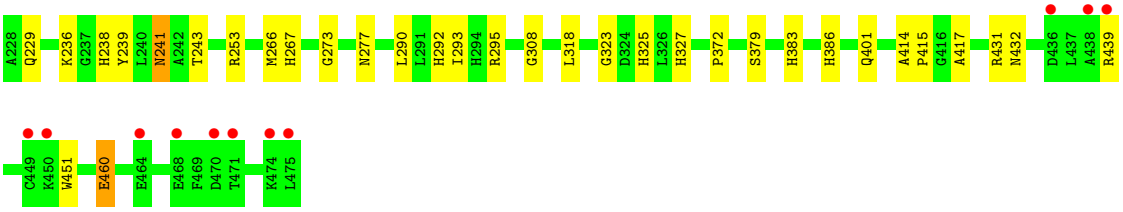
Chain C:



• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

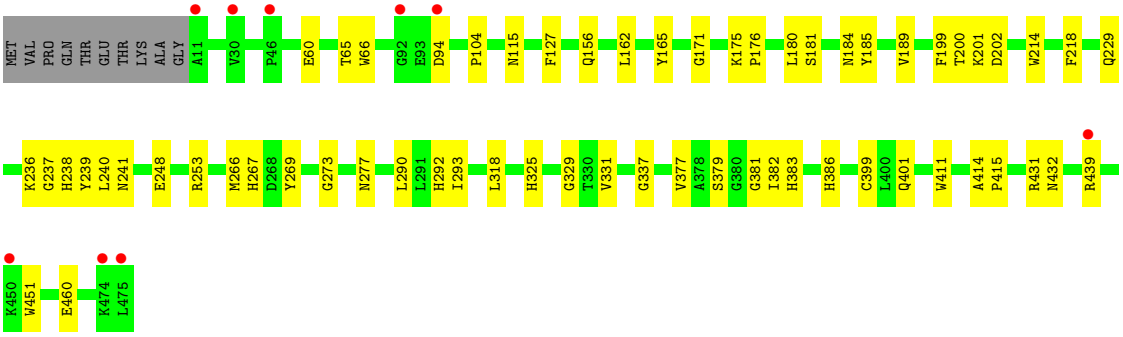
Chain D:





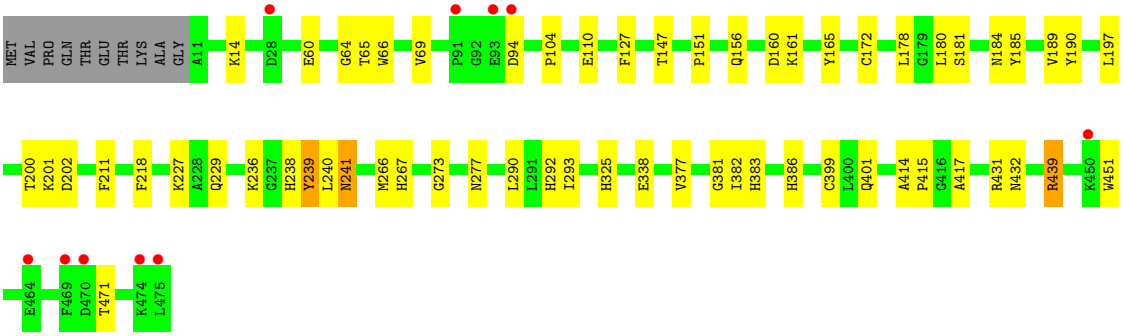
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain E:



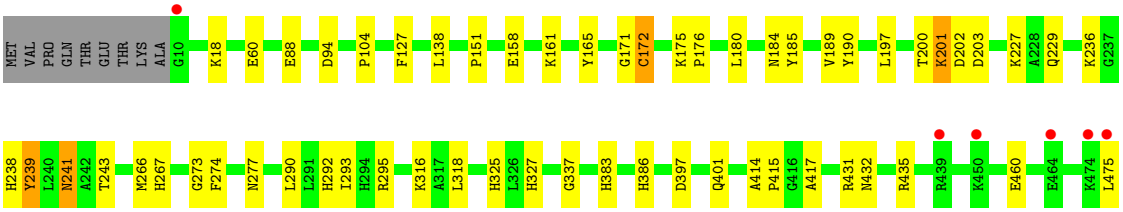
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain F:



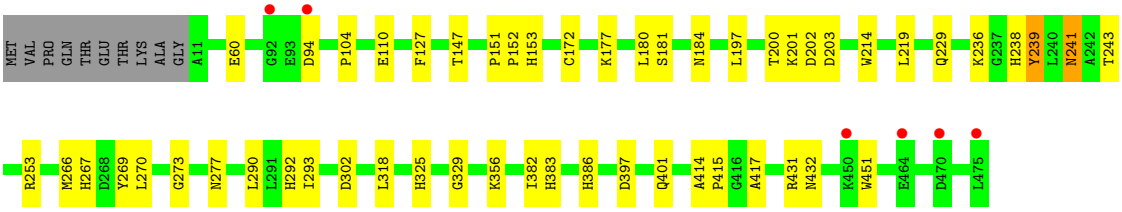
• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain G:



• Molecule 1: RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN

Chain H:

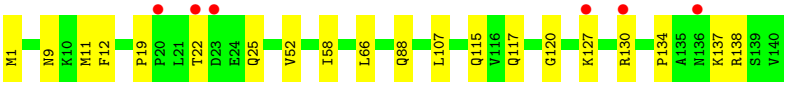


• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain I:

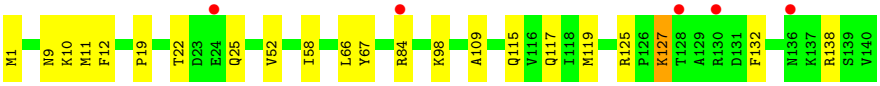
• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain J:



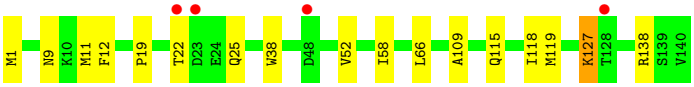
• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain K:



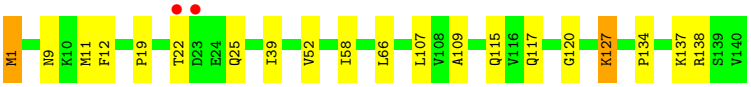
• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain L:



• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain M:

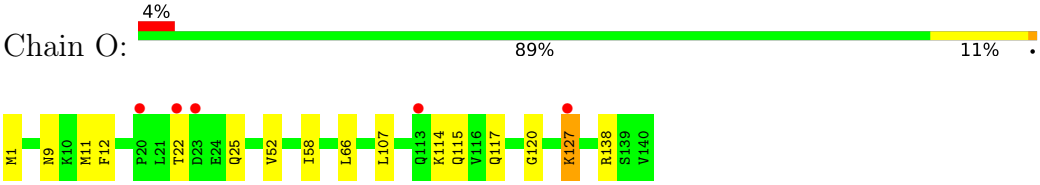


• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain N:

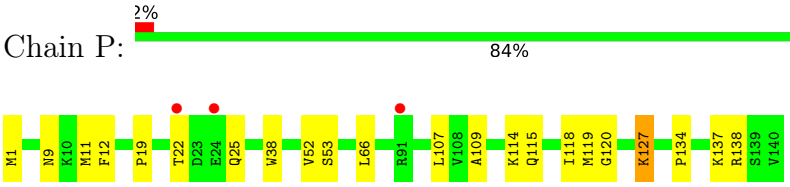
• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain O:



• Molecule 2: RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1

Chain P:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	120.83Å 178.21Å 122.92Å 90.00° 117.76° 90.00°	Depositor
Resolution (Å)	20.00 – 2.65 19.23 – 2.65	Depositor EDS
% Data completeness (in resolution range)	88.7 (20.00-2.65) 88.4 (19.23-2.65)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.78 (at 2.63Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.205 , 0.234 0.203 , 0.213	Depositor DCC
R_{free} test set	5941 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	20.1	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 32.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.000 for -h-l,k,h 0.000 for l,k,-h-l 0.000 for h,-k,-h-l 0.000 for -h-l,-k,l 0.086 for l,-k,h	Xtriage
F_o,F_c correlation	0.84	EDS
Total number of atoms	40074	wwPDB-VP
Average B, all atoms (Å^2)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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

5.1 Standard geometry

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

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	0.42	0/3666	0.52	0/4955
1	B	0.46	0/3684	0.55	0/4978
1	C	0.46	0/3666	0.56	0/4955
1	D	0.47	0/3666	0.56	0/4955
1	E	0.47	0/3665	0.56	0/4955
1	F	0.46	0/3666	0.54	0/4955
1	G	0.46	0/3670	0.56	0/4960
1	H	0.46	0/3666	0.55	0/4955
2	I	0.44	0/1166	0.53	0/1584
2	J	0.49	0/1166	0.56	0/1584
2	K	0.49	0/1166	0.56	0/1584
2	L	0.46	0/1166	0.57	0/1584
2	M	0.49	0/1166	0.57	0/1584
2	N	0.48	0/1164	0.56	0/1581
2	O	0.49	0/1166	0.55	0/1584
2	P	0.49	0/1166	0.55	0/1584
All	All	0.46	0/38675	0.55	0/52337

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3628	0	3538	39	0
1	B	3646	0	3559	38	0
1	C	3628	0	3537	38	0
1	D	3628	0	3537	42	1
1	E	3627	0	3537	48	0
1	F	3628	0	3537	46	1
1	G	3632	0	3540	49	0
1	H	3628	0	3537	39	0
2	I	1143	0	1122	17	0
2	J	1143	0	1122	13	0
2	K	1143	0	1122	18	0
2	L	1143	0	1122	14	0
2	M	1143	0	1122	15	0
2	N	1142	0	1119	20	0
2	O	1143	0	1122	11	0
2	P	1143	0	1122	14	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
4	A	21	0	7	0	0
4	B	21	0	7	0	0
4	C	21	0	8	0	0
4	D	21	0	7	0	0
4	E	21	0	8	0	0
4	F	21	0	8	0	0
4	G	21	0	7	0	0
4	H	21	0	7	0	0
5	A	20	0	30	0	0
5	B	16	0	24	0	0
5	C	12	0	18	0	0
5	D	12	0	18	0	0
5	E	20	0	30	0	0
5	F	24	0	36	5	0
5	G	20	0	30	10	0
5	H	20	0	30	0	0
5	J	8	0	12	0	0
5	K	4	0	6	0	0
5	L	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	N	4	0	6	5	0
5	O	8	0	12	0	0
6	A	154	0	0	6	0
6	B	154	0	0	4	0
6	C	146	0	0	3	0
6	D	158	0	0	3	0
6	E	159	0	0	5	0
6	F	132	0	0	5	0
6	G	162	0	0	3	0
6	H	150	0	0	3	0
6	I	47	0	0	2	0
6	J	36	0	0	1	0
6	K	37	0	0	1	0
6	L	38	0	0	1	0
6	M	46	0	0	1	0
6	N	44	0	0	2	0
6	O	37	0	0	0	0
6	P	38	0	0	1	0
All	All	40074	0	37612	401	1

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 5.

All (401) 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:267:HIS:CD2	1:E:277:ASN:HD22	1.78	1.01
1:C:267:HIS:HD2	1:C:277:ASN:HD22	1.08	0.99
1:D:267:HIS:HD2	1:D:277:ASN:HD22	1.00	0.98
1:B:267:HIS:HD2	1:B:277:ASN:HD22	1.02	0.98
1:F:267:HIS:HD2	1:F:277:ASN:HD22	1.01	0.97
1:A:267:HIS:HD2	1:A:277:ASN:HD22	0.96	0.96
1:H:267:HIS:HD2	1:H:277:ASN:HD22	0.96	0.93
1:G:267:HIS:HD2	1:G:277:ASN:HD22	1.02	0.93
1:A:267:HIS:CD2	1:A:277:ASN:HD22	1.87	0.91
1:H:267:HIS:CD2	1:H:277:ASN:HD22	1.88	0.89
1:C:267:HIS:CD2	1:C:277:ASN:HD22	1.91	0.88
1:B:267:HIS:CD2	1:B:277:ASN:HD22	1.91	0.88
1:G:184:ASN:HD22	2:M:115:GLN:HE21	1.15	0.87
2:N:132:PHE:CE1	2:N:132:PHE:CE2	2.59	0.87
1:E:267:HIS:HD2	1:E:277:ASN:ND2	1.73	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:267:HIS:CD2	1:D:277:ASN:HD22	1.90	0.87
1:C:184:ASN:HD22	2:I:115:GLN:HE21	1.24	0.86
1:F:184:ASN:HD22	2:P:115:GLN:HE21	1.21	0.85
1:F:267:HIS:CD2	1:F:277:ASN:HD22	1.92	0.84
1:G:267:HIS:CD2	1:G:277:ASN:HD22	1.93	0.84
1:H:200:THR:OG1	1:H:238:HIS:HD2	1.61	0.84
1:B:383:HIS:H	1:B:386:HIS:HD2	1.27	0.82
1:E:267:HIS:HD2	1:E:277:ASN:HD22	0.88	0.81
1:B:184:ASN:HD22	2:L:115:GLN:HE21	1.30	0.79
1:G:295:ARG:HH22	5:G:1481:EDO:H11	1.45	0.79
1:H:184:ASN:HD22	2:J:115:GLN:HE21	1.28	0.79
1:A:184:ASN:HD22	2:O:115:GLN:HE21	1.31	0.78
1:D:431:ARG:HH21	1:D:432:ASN:HD21	1.30	0.77
1:D:383:HIS:H	1:D:386:HIS:HD2	1.32	0.77
1:F:431:ARG:HH21	1:F:432:ASN:HD21	1.32	0.77
1:H:267:HIS:HD2	1:H:277:ASN:ND2	1.80	0.77
1:F:200:THR:OG1	1:F:238:HIS:HD2	1.69	0.76
1:D:184:ASN:HD22	2:N:115:GLN:HE21	1.32	0.76
1:C:383:HIS:H	1:C:386:HIS:HD2	1.32	0.75
2:N:39:ILE:HG12	5:N:1141:EDO:H21	1.68	0.74
1:H:383:HIS:H	1:H:386:HIS:HD2	1.35	0.74
1:G:431:ARG:HH21	1:G:432:ASN:HD21	1.34	0.73
1:A:383:HIS:H	1:A:386:HIS:HD2	1.35	0.72
2:I:22:THR:H	2:I:25:GLN:HE21	1.38	0.72
1:E:431:ARG:HH21	1:E:432:ASN:HD21	1.38	0.71
1:C:431:ARG:HH21	1:C:432:ASN:HD21	1.37	0.71
1:A:200:THR:OG1	1:A:238:HIS:HD2	1.73	0.71
1:A:431:ARG:HH21	1:A:432:ASN:HD21	1.37	0.70
1:B:200:THR:OG1	1:B:238:HIS:HD2	1.74	0.70
1:E:383:HIS:H	1:E:386:HIS:HD2	1.39	0.70
2:P:22:THR:H	2:P:25:GLN:HE21	1.39	0.70
1:G:200:THR:OG1	1:G:238:HIS:HD2	1.74	0.70
2:O:22:THR:H	2:O:25:GLN:HE21	1.36	0.69
1:G:383:HIS:H	1:G:386:HIS:HD2	1.37	0.69
1:B:229:GLN:HE21	1:B:236:LYS:H	1.40	0.69
6:E:2100:HOH:O	1:F:267:HIS:HE1	1.75	0.69
1:F:383:HIS:H	1:F:386:HIS:HD2	1.41	0.69
1:E:184:ASN:HD22	2:K:115:GLN:HE21	1.38	0.68
2:N:22:THR:H	2:N:25:GLN:HE21	1.41	0.68
1:D:229:GLN:HE21	1:D:236:LYS:H	1.42	0.68
1:E:202:ASP:OD1	1:E:238:HIS:HE1	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:22:THR:H	2:J:25:GLN:HE21	1.42	0.67
2:M:22:THR:H	2:M:25:GLN:HE21	1.43	0.67
1:C:200:THR:OG1	1:C:238:HIS:HD2	1.78	0.67
1:G:229:GLN:HE21	1:G:236:LYS:H	1.40	0.66
5:F:1479:EDO:H21	6:F:2022:HOH:O	1.95	0.66
1:A:229:GLN:HE21	1:A:236:LYS:H	1.44	0.66
1:H:431:ARG:HH21	1:H:432:ASN:HD21	1.43	0.66
1:B:431:ARG:HH21	1:B:432:ASN:HD21	1.44	0.65
1:F:239:TYR:HE2	1:F:401:GLN:HE22	1.44	0.65
2:L:22:THR:H	2:L:25:GLN:HE21	1.44	0.65
1:G:202:ASP:OD1	1:G:238:HIS:HE1	1.79	0.65
1:F:439:ARG:NH1	6:F:2128:HOH:O	2.31	0.64
5:G:1482:EDO:H21	1:H:270:LEU:O	1.97	0.64
1:F:69:VAL:HG22	5:F:1479:EDO:H12	1.80	0.64
1:H:229:GLN:HE21	1:H:236:LYS:H	1.44	0.63
2:K:98:LYS:HE2	6:K:2031:HOH:O	1.98	0.63
2:N:82:GLY:H	5:N:1141:EDO:H22	1.64	0.63
1:E:229:GLN:HE21	1:E:236:LYS:H	1.47	0.63
1:D:200:THR:OG1	1:D:238:HIS:HD2	1.82	0.62
1:E:200:THR:OG1	1:E:238:HIS:HD2	1.80	0.62
2:K:22:THR:H	2:K:25:GLN:HE21	1.47	0.61
1:B:202:ASP:OD1	1:B:238:HIS:HE1	1.83	0.61
1:E:239:TYR:HE2	1:E:401:GLN:HE22	1.49	0.61
1:H:200:THR:OG1	1:H:238:HIS:CD2	2.50	0.60
1:G:337:GLY:HA3	5:G:1481:EDO:C2	2.31	0.60
1:C:229:GLN:HE21	1:C:236:LYS:H	1.48	0.60
1:C:202:ASP:OD1	1:C:238:HIS:HE1	1.84	0.59
1:D:414:ALA:HB3	1:D:415:PRO:HD3	1.83	0.59
1:E:156:GLN:HB2	6:E:2056:HOH:O	2.02	0.59
1:F:64:GLY:HA2	5:F:1479:EDO:H22	1.84	0.59
1:H:202:ASP:OD1	1:H:238:HIS:HE1	1.86	0.58
1:G:18:LYS:O	5:G:1479:EDO:H21	2.03	0.58
1:F:239:TYR:HB3	1:F:266:MET:HB3	1.86	0.58
1:B:239:TYR:HE2	1:B:401:GLN:HE22	1.51	0.58
1:D:292:HIS:HA	1:D:325:HIS:HB2	1.85	0.58
1:H:290:LEU:HG	2:P:66:LEU:HD11	1.86	0.58
1:A:202:ASP:OD1	1:A:238:HIS:HE1	1.87	0.57
1:F:290:LEU:HG	2:N:66:LEU:HD11	1.86	0.57
1:F:414:ALA:HB3	1:F:415:PRO:HD3	1.87	0.57
2:N:82:GLY:H	5:N:1141:EDO:C2	2.17	0.57
1:A:239:TYR:HE2	1:A:401:GLN:HE22	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:LEU:HG	2:L:66:LEU:HD11	1.87	0.56
1:G:290:LEU:HG	2:O:66:LEU:HD11	1.86	0.56
1:C:383:HIS:H	1:C:386:HIS:CD2	2.20	0.56
2:N:39:ILE:CG1	5:N:1141:EDO:H21	2.35	0.56
1:A:267:HIS:HD2	1:A:277:ASN:ND2	1.82	0.56
1:D:239:TYR:HE2	1:D:401:GLN:HE22	1.53	0.56
1:G:414:ALA:HB3	1:G:415:PRO:HD3	1.88	0.56
1:F:180:LEU:HA	2:P:115:GLN:HE22	1.71	0.55
1:F:277:ASN:HD21	1:F:293:ILE:HD12	1.72	0.55
1:G:267:HIS:HD2	1:G:277:ASN:ND2	1.87	0.55
2:M:127:LYS:HG2	6:M:2040:HOH:O	2.05	0.55
1:G:239:TYR:HE2	1:G:401:GLN:HE22	1.53	0.55
1:B:60:GLU:HG3	1:B:127:PHE:CZ	2.42	0.55
1:E:414:ALA:HB3	1:E:415:PRO:HD3	1.89	0.54
1:A:267:HIS:HE1	6:B:2081:HOH:O	1.89	0.54
1:G:200:THR:OG1	1:G:238:HIS:CD2	2.59	0.54
2:P:134:PRO:HG2	2:P:137:LYS:HB2	1.88	0.54
1:F:65:THR:HG22	5:F:1479:EDO:H11	1.90	0.54
1:F:229:GLN:HE21	1:F:236:LYS:H	1.53	0.54
1:F:60:GLU:HG3	1:F:127:PHE:CZ	2.43	0.54
1:A:414:ALA:HB3	1:A:415:PRO:HD3	1.90	0.54
1:H:414:ALA:HB3	1:H:415:PRO:HD3	1.88	0.54
1:G:295:ARG:HG2	1:G:327:HIS:HB2	1.90	0.54
1:G:337:GLY:CA	5:G:1481:EDO:H21	2.37	0.53
1:A:200:THR:OG1	1:A:238:HIS:CD2	2.59	0.53
1:A:341:VAL:HG21	6:A:2149:HOH:O	2.07	0.53
1:G:337:GLY:HA3	5:G:1481:EDO:H21	1.90	0.53
1:B:383:HIS:H	1:B:386:HIS:CD2	2.16	0.53
2:N:39:ILE:HG12	5:N:1141:EDO:C2	2.37	0.53
1:G:239:TYR:HB3	1:G:266:MET:HB3	1.90	0.52
1:H:239:TYR:HE2	1:H:401:GLN:HE22	1.56	0.52
1:D:60:GLU:HG3	1:D:127:PHE:CZ	2.44	0.52
1:E:273:GLY:HA3	1:F:273:GLY:HA3	1.90	0.52
2:J:58:ILE:HB	2:L:58:ILE:HD11	1.90	0.52
1:A:180:LEU:HA	2:O:115:GLN:HE22	1.74	0.52
1:A:451:TRP:CE2	2:I:19:PRO:HG3	2.45	0.52
1:E:329:GLY:HA3	6:E:2116:HOH:O	2.08	0.52
2:J:88:GLN:NE2	6:J:2028:HOH:O	2.42	0.52
1:A:290:LEU:HG	2:I:66:LEU:HD11	1.91	0.52
1:H:383:HIS:H	1:H:386:HIS:CD2	2.22	0.52
1:C:180:LEU:HA	2:I:115:GLN:HE22	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:267:HIS:HD2	1:C:277:ASN:ND2	1.92	0.52
2:J:11:MET:HE1	2:J:138:ARG:HD3	1.92	0.52
1:B:295:ARG:HG2	1:B:327:HIS:HB2	1.92	0.52
1:A:383:HIS:H	1:A:386:HIS:CD2	2.23	0.51
2:P:53:SER:HB3	6:P:2012:HOH:O	2.10	0.51
1:F:200:THR:OG1	1:F:238:HIS:CD2	2.56	0.51
1:G:435:ARG:HD3	6:G:2150:HOH:O	2.08	0.51
1:G:190:TYR:CZ	1:G:227:LYS:HE3	2.45	0.51
1:H:197:LEU:HG	1:H:417:ALA:HB1	1.93	0.51
1:G:273:GLY:HA3	1:H:273:GLY:HA3	1.92	0.51
1:H:269:TYR:CD2	1:H:318:LEU:HD23	2.46	0.51
2:L:11:MET:HE1	2:L:138:ARG:HD3	1.91	0.51
1:F:202:ASP:OD1	1:F:238:HIS:HE1	1.93	0.51
1:G:397:ASP:OD2	2:O:114:LYS:NZ	2.37	0.51
1:E:239:TYR:HE2	1:E:401:GLN:NE2	2.09	0.51
1:D:202:ASP:OD1	1:D:238:HIS:HE1	1.94	0.50
2:M:11:MET:HE1	2:M:138:ARG:HD3	1.91	0.50
1:A:273:GLY:HA3	1:B:273:GLY:HA3	1.94	0.50
1:D:177:LYS:HG2	1:D:203:ASP:OD2	2.11	0.50
1:D:239:TYR:HB3	1:D:266:MET:HB3	1.94	0.50
1:B:190:TYR:CZ	1:B:227:LYS:HE3	2.46	0.50
1:E:267:HIS:CD2	1:E:277:ASN:ND2	2.62	0.50
2:O:11:MET:HE1	2:O:138:ARG:HD3	1.93	0.50
1:B:180:LEU:HA	2:L:115:GLN:HE22	1.77	0.50
1:C:292:HIS:HA	1:C:325:HIS:HB2	1.94	0.50
1:E:180:LEU:HA	2:K:115:GLN:HE22	1.75	0.50
1:A:239:TYR:HB3	1:A:266:MET:HB3	1.94	0.49
1:E:60:GLU:HG3	1:E:127:PHE:CZ	2.47	0.49
1:H:292:HIS:HA	1:H:325:HIS:HB2	1.94	0.49
1:C:239:TYR:HE2	1:C:401:GLN:HE22	1.60	0.49
1:G:292:HIS:HA	1:G:325:HIS:HB2	1.93	0.49
1:C:451:TRP:CE2	2:K:19:PRO:HG3	2.47	0.49
1:F:292:HIS:HA	1:F:325:HIS:HB2	1.94	0.49
1:D:451:TRP:CE2	2:L:19:PRO:HG3	2.47	0.49
2:L:138:ARG:NH1	6:L:2037:HOH:O	2.46	0.49
1:D:190:TYR:CZ	1:D:227:LYS:HE3	2.48	0.49
1:A:277:ASN:HD21	1:A:293:ILE:HD12	1.77	0.49
1:E:185:TYR:O	1:E:189:VAL:HG23	2.12	0.48
1:H:239:TYR:HB3	1:H:266:MET:HB3	1.95	0.48
2:N:10:LYS:HE3	6:N:2006:HOH:O	2.12	0.48
1:C:239:TYR:HB3	1:C:266:MET:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:HIS:HA	1:A:325:HIS:HB2	1.95	0.48
2:P:107:LEU:O	2:P:120:GLY:HA2	2.13	0.48
2:I:11:MET:HE1	2:I:138:ARG:HD3	1.95	0.48
1:E:292:HIS:HA	1:E:325:HIS:HB2	1.95	0.48
1:A:60:GLU:HG3	1:A:127:PHE:CZ	2.48	0.48
2:I:22:THR:H	2:I:25:GLN:NE2	2.11	0.48
1:C:290:LEU:HG	2:K:66:LEU:HD11	1.95	0.48
1:C:383:HIS:N	1:C:386:HIS:HD2	2.07	0.48
1:E:239:TYR:HB3	1:E:266:MET:HB3	1.95	0.48
1:H:181:SER:H	2:J:115:GLN:NE2	2.12	0.48
6:B:2061:HOH:O	1:D:372:PRO:HG3	2.14	0.48
1:D:277:ASN:HD21	1:D:293:ILE:HD12	1.78	0.48
1:F:181:SER:H	2:P:115:GLN:NE2	2.12	0.47
1:G:172:CYS:HB3	1:G:197:LEU:HD13	1.94	0.47
1:G:383:HIS:H	1:G:386:HIS:CD2	2.25	0.47
1:G:475:LEU:HD22	6:G:2131:HOH:O	2.14	0.47
1:B:200:THR:OG1	1:B:238:HIS:CD2	2.62	0.47
1:B:267:HIS:HD2	1:B:277:ASN:ND2	1.87	0.47
6:D:2082:HOH:O	1:F:161:LYS:HE2	2.13	0.47
1:B:239:TYR:HB3	1:B:266:MET:HB3	1.95	0.47
1:C:90:VAL:HG11	6:C:2028:HOH:O	2.15	0.47
1:E:290:LEU:HG	2:M:66:LEU:HD11	1.96	0.47
1:F:185:TYR:O	1:F:189:VAL:HG23	2.13	0.47
1:H:180:LEU:HA	2:J:115:GLN:HE22	1.79	0.47
1:C:267:HIS:HE1	6:D:2106:HOH:O	1.98	0.47
1:D:241:ASN:ND2	1:D:243:THR:H	2.13	0.47
1:E:115:ASN:HB2	6:F:2059:HOH:O	2.15	0.47
1:F:165:TYR:CD1	2:N:117:GLN:HB3	2.50	0.47
1:F:197:LEU:HG	1:F:417:ALA:HB1	1.97	0.47
1:H:356:LYS:HD2	6:H:2121:HOH:O	2.14	0.47
2:P:38:TRP:CD2	2:P:118:ILE:HG21	2.49	0.47
1:B:290:LEU:HG	2:J:66:LEU:HD11	1.97	0.47
1:B:414:ALA:HB3	1:B:415:PRO:HD3	1.97	0.47
1:B:383:HIS:N	1:B:386:HIS:HD2	2.05	0.47
1:H:277:ASN:HD21	1:H:293:ILE:HD12	1.80	0.47
2:I:134:PRO:HG2	2:I:137:LYS:HB2	1.95	0.47
1:H:241:ASN:ND2	1:H:243:THR:H	2.13	0.46
1:D:180:LEU:HA	2:N:115:GLN:HE22	1.80	0.46
1:B:200:THR:O	1:B:238:HIS:HA	2.15	0.46
2:O:107:LEU:O	2:O:120:GLY:HA2	2.15	0.46
1:E:165:TYR:CD1	2:M:117:GLN:HB3	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:273:GLY:HA3	1:D:273:GLY:HA3	1.97	0.46
1:E:451:TRP:CE2	2:M:19:PRO:HG3	2.50	0.46
1:D:197:LEU:HG	1:D:417:ALA:HB1	1.97	0.46
1:D:379:SER:HB2	1:D:401:GLN:HB2	1.97	0.46
1:F:383:HIS:H	1:F:386:HIS:CD2	2.27	0.46
1:C:171:GLY:HA3	1:C:401:GLN:HG2	1.98	0.46
1:G:60:GLU:HG3	1:G:127:PHE:CZ	2.51	0.46
2:K:22:THR:H	2:K:25:GLN:NE2	2.13	0.46
1:A:190:TYR:CZ	1:A:227:LYS:HE3	2.51	0.46
1:C:165:TYR:CD1	2:K:117:GLN:HB3	2.51	0.46
1:H:397:ASP:OD2	2:P:114:LYS:NZ	2.41	0.46
1:H:451:TRP:CE2	2:P:19:PRO:HG3	2.50	0.46
1:D:383:HIS:H	1:D:386:HIS:CD2	2.22	0.45
1:F:110:GLU:HB3	1:F:147:THR:HB	1.97	0.45
1:E:377:VAL:HG22	1:E:399:CYS:HB3	1.99	0.45
1:D:241:ASN:HA	1:D:266:MET:HG2	1.98	0.45
1:E:383:HIS:H	1:E:386:HIS:CD2	2.26	0.45
1:F:386:HIS:HE1	6:F:2098:HOH:O	1.99	0.45
2:I:133:GLN:NE2	6:I:2045:HOH:O	2.43	0.45
1:B:277:ASN:HD21	1:B:293:ILE:HD12	1.81	0.45
1:F:190:TYR:CZ	1:F:227:LYS:HE3	2.51	0.45
1:G:277:ASN:HD21	1:G:293:ILE:HD12	1.82	0.45
2:J:22:THR:H	2:J:25:GLN:NE2	2.10	0.45
2:K:11:MET:HE1	2:K:138:ARG:HD3	1.99	0.45
1:A:381:GLY:HA2	1:B:66:TRP:CD1	2.52	0.45
2:N:110:PHE:HB3	6:N:2039:HOH:O	2.16	0.45
1:B:21:ARG:HD3	6:B:2007:HOH:O	2.16	0.45
1:C:190:TYR:CZ	1:C:227:LYS:HE3	2.52	0.45
1:F:382:ILE:HA	1:F:386:HIS:CD2	2.52	0.45
1:H:214:TRP:CD2	1:H:253:ARG:HG2	2.52	0.45
2:K:58:ILE:HD11	2:M:58:ILE:HB	1.99	0.45
2:M:22:THR:H	2:M:25:GLN:NE2	2.11	0.45
1:B:158:GLU:OE2	1:B:325:HIS:NE2	2.33	0.45
1:D:214:TRP:CE3	1:D:253:ARG:HG2	2.52	0.45
1:G:185:TYR:O	1:G:189:VAL:HG23	2.17	0.45
1:H:177:LYS:HG2	1:H:203:ASP:OD2	2.17	0.45
1:B:165:TYR:CD1	2:J:117:GLN:HB3	2.52	0.44
1:E:200:THR:OG1	1:E:238:HIS:CD2	2.66	0.44
1:E:248:GLU:OE2	6:E:2092:HOH:O	2.21	0.44
1:H:60:GLU:HG3	1:H:127:PHE:CZ	2.52	0.44
1:E:66:TRP:CD1	1:F:381:GLY:HA2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:127:LYS:H	2:I:127:LYS:HG2	1.61	0.44
2:P:11:MET:HE1	2:P:138:ARG:HD3	2.00	0.44
1:B:181:SER:H	2:L:115:GLN:NE2	2.15	0.44
1:C:200:THR:OG1	1:C:238:HIS:CD2	2.64	0.44
1:C:414:ALA:HB3	1:C:415:PRO:HD3	1.99	0.44
1:E:382:ILE:HA	1:E:386:HIS:CD2	2.52	0.44
2:K:127:LYS:H	2:K:127:LYS:HG2	1.66	0.44
1:A:197:LEU:HG	1:A:417:ALA:HB1	1.99	0.44
1:C:277:ASN:HD21	1:C:293:ILE:HD12	1.82	0.44
1:F:239:TYR:HE2	1:F:401:GLN:NE2	2.13	0.44
2:K:109:ALA:HB3	2:K:119:MET:HG3	1.99	0.44
1:E:218:PHE:CD1	1:E:240:LEU:HD22	2.52	0.44
2:M:107:LEU:O	2:M:120:GLY:HA2	2.18	0.44
1:A:181:SER:H	2:O:115:GLN:NE2	2.16	0.44
1:C:60:GLU:HG3	1:C:127:PHE:CZ	2.53	0.44
1:C:293:ILE:HG13	1:C:318:LEU:HD21	2.00	0.44
1:E:181:SER:H	2:K:115:GLN:NE2	2.16	0.44
1:E:383:HIS:N	1:E:386:HIS:HD2	2.13	0.44
1:D:241:ASN:HD22	1:D:243:THR:H	1.66	0.43
1:C:181:SER:H	2:I:115:GLN:NE2	2.15	0.43
1:G:158:GLU:CD	1:G:325:HIS:HE2	2.17	0.43
1:D:383:HIS:N	1:D:386:HIS:HD2	2.08	0.43
1:B:172:CYS:HB3	1:B:197:LEU:HD13	2.01	0.43
2:P:127:LYS:H	2:P:127:LYS:HG2	1.60	0.43
1:A:203:ASP:HB2	6:A:2054:HOH:O	2.18	0.43
1:F:241:ASN:HA	1:F:266:MET:HG2	2.00	0.43
1:C:190:TYR:CZ	1:C:194:ARG:HD3	2.54	0.43
1:C:451:TRP:NE1	2:K:19:PRO:HG3	2.34	0.43
2:I:58:ILE:HD11	2:K:58:ILE:HB	2.00	0.43
2:J:134:PRO:HG2	2:J:137:LYS:HB2	1.99	0.43
6:A:2091:HOH:O	1:B:267:HIS:HE1	2.01	0.43
1:B:162:LEU:HD11	1:B:199:PHE:HZ	1.84	0.43
1:D:158:GLU:OE2	1:D:325:HIS:NE2	2.39	0.43
1:D:295:ARG:HG2	1:D:327:HIS:HB2	2.00	0.43
1:B:158:GLU:CD	1:B:325:HIS:HE2	2.18	0.43
1:C:158:GLU:CD	1:C:325:HIS:HE2	2.21	0.43
1:E:381:GLY:HA2	1:F:66:TRP:CD1	2.54	0.43
1:G:180:LEU:HA	2:M:115:GLN:HE22	1.83	0.43
1:G:293:ILE:HG13	1:G:318:LEU:HD21	2.01	0.43
1:H:214:TRP:CE3	1:H:253:ARG:HG2	2.54	0.43
2:M:134:PRO:HG2	2:M:137:LYS:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:218:PHE:CD1	1:F:240:LEU:HD22	2.54	0.43
1:G:241:ASN:ND2	1:G:243:THR:H	2.17	0.43
1:C:156:GLN:HB2	6:C:2049:HOH:O	2.18	0.42
1:E:411:TRP:CD1	2:M:1:MME:HG3	2.54	0.42
1:F:65:THR:HG22	5:F:1479:EDO:C1	2.49	0.42
2:P:109:ALA:HB3	2:P:119:MET:HG3	2.00	0.42
2:L:22:THR:H	2:L:25:GLN:NE2	2.13	0.42
1:B:152:PRO:HB2	1:B:153:HIS:CD2	2.53	0.42
1:B:382:ILE:HA	1:B:386:HIS:CD2	2.54	0.42
2:I:114:LYS:HD2	6:I:2039:HOH:O	2.19	0.42
1:A:295:ARG:HG2	1:A:327:HIS:HB2	2.01	0.42
1:G:165:TYR:CD1	2:O:117:GLN:HB3	2.54	0.42
1:H:302:ASP:HA	6:H:2046:HOH:O	2.19	0.42
2:M:39:ILE:O	2:M:109:ALA:HA	2.19	0.42
1:F:156:GLN:HB2	6:F:2044:HOH:O	2.19	0.42
1:G:295:ARG:NH2	5:G:1481:EDO:H11	2.24	0.42
1:H:241:ASN:HD22	1:H:243:THR:H	1.67	0.42
2:I:107:LEU:O	2:I:120:GLY:HA2	2.19	0.42
1:B:451:TRP:CE2	2:J:19:PRO:HG3	2.54	0.42
1:C:197:LEU:HG	1:C:417:ALA:HB1	2.02	0.42
1:D:110:GLU:HB3	1:D:147:THR:HB	2.00	0.42
1:E:199:PHE:HA	1:E:237:GLY:O	2.20	0.42
1:E:331:VAL:HA	1:E:337:GLY:O	2.19	0.42
1:E:379:SER:HB2	1:E:401:GLN:HB2	2.01	0.42
1:G:175:LYS:HA	1:G:176:PRO:C	2.40	0.42
1:H:110:GLU:HB3	1:H:147:THR:HB	2.02	0.42
2:L:127:LYS:H	2:L:127:LYS:HG2	1.57	0.42
1:E:65:THR:HG22	6:E:2019:HOH:O	2.20	0.42
1:F:383:HIS:N	1:F:386:HIS:HD2	2.12	0.42
1:G:200:THR:O	1:G:238:HIS:HA	2.20	0.42
1:H:382:ILE:HA	1:H:386:HIS:CD2	2.54	0.42
1:C:377:VAL:HG22	1:C:399:CYS:HB3	2.02	0.42
1:H:383:HIS:N	1:H:386:HIS:HD2	2.10	0.42
2:O:127:LYS:H	2:O:127:LYS:HG2	1.60	0.42
1:A:214:TRP:CE3	1:A:253:ARG:HG2	2.55	0.42
1:A:431:ARG:HD3	6:A:2127:HOH:O	2.19	0.42
1:D:200:THR:OG1	1:D:238:HIS:CD2	2.66	0.42
2:K:67:TYR:CD2	2:K:67:TYR:C	2.92	0.42
6:B:2066:HOH:O	1:D:161:LYS:HE2	2.19	0.41
1:D:151:HYP:HB2	1:D:323:GLY:O	2.20	0.41
1:F:178:LEU:HD22	1:F:211:PHE:HZ	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:338:GLU:HB2	1:F:471:THR:HG21	2.02	0.41
1:B:134:ARG:HA	1:B:308:GLY:O	2.19	0.41
1:D:156:GLN:HB2	6:D:2064:HOH:O	2.19	0.41
1:G:88:GLU:HG3	6:G:2035:HOH:O	2.20	0.41
1:G:239:TYR:HE2	1:G:401:GLN:NE2	2.18	0.41
1:G:337:GLY:HA2	5:G:1481:EDO:H21	2.02	0.41
2:K:125:ARG:HD2	2:K:132:PHE:CE2	2.55	0.41
6:C:2072:HOH:O	2:K:10:LYS:HE3	2.20	0.41
1:A:239:TYR:HE2	1:A:401:GLN:NE2	2.16	0.41
1:A:382:ILE:HA	1:A:386:HIS:CD2	2.55	0.41
1:E:175:LYS:HA	1:E:176:PRO:C	2.40	0.41
1:E:229:GLN:NE2	1:E:236:LYS:H	2.16	0.41
1:F:451:TRP:CE2	2:N:19:PRO:HG3	2.55	0.41
1:G:295:ARG:HH12	5:G:1481:EDO:C1	2.33	0.41
2:N:67:TYR:CD2	2:N:67:TYR:C	2.93	0.41
1:A:125:PHE:HB2	6:A:2039:HOH:O	2.19	0.41
1:D:293:ILE:HG13	1:D:318:LEU:HD21	2.03	0.41
6:A:2068:HOH:O	1:G:161:LYS:HE2	2.20	0.41
1:C:201:KCX:HB2	1:C:239:TYR:CD2	2.56	0.41
1:E:171:GLY:HA2	1:E:199:PHE:O	2.20	0.41
1:G:171:GLY:HA3	1:G:401:GLN:HG2	2.03	0.41
2:J:107:LEU:O	2:J:120:GLY:HA2	2.21	0.41
1:A:452:SER:HA	1:A:453:PRO:HD3	1.94	0.41
1:E:171:GLY:HA3	1:E:401:GLN:HG2	2.03	0.41
1:G:197:LEU:HG	1:G:417:ALA:HB1	2.02	0.41
1:B:178:LEU:HD22	1:B:211:PHE:HZ	1.86	0.41
1:E:277:ASN:HD21	1:E:293:ILE:HD12	1.86	0.41
1:G:201:KCX:HB2	1:G:239:TYR:CD2	2.55	0.41
1:H:152:PRO:HB2	1:H:153:HIS:CD2	2.56	0.41
1:F:160:ASP:HA	1:F:165:TYR:OH	2.20	0.41
2:N:11:MET:HE1	2:N:138:ARG:HD3	2.03	0.41
2:N:22:THR:H	2:N:25:GLN:NE2	2.12	0.41
2:N:107:LEU:O	2:N:120:GLY:HA2	2.20	0.41
1:D:181:SER:H	2:N:115:GLN:NE2	2.19	0.41
2:N:109:ALA:HB3	2:N:119:MET:HG3	2.03	0.41
1:A:165:TYR:CD1	2:I:117:GLN:HB3	2.56	0.40
2:I:38:TRP:CD2	2:I:118:ILE:HG21	2.56	0.40
1:A:269:TYR:CD2	1:A:318:LEU:HD23	2.56	0.40
1:D:161:LYS:HD3	2:L:66:LEU:HD13	2.04	0.40
1:H:239:TYR:HE2	1:H:401:GLN:NE2	2.19	0.40
1:C:185:TYR:OH	1:C:202:ASP:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:134:ARG:HA	1:D:308:GLY:O	2.21	0.40
2:M:58:ILE:HD11	2:O:58:ILE:HB	2.03	0.40
1:A:110:GLU:HB3	1:A:147:THR:HB	2.04	0.40
1:C:296:ALA:O	1:C:297:MET:CB	2.70	0.40
1:D:175:LYS:HA	1:D:176:PRO:C	2.42	0.40
1:D:239:TYR:HE2	1:D:401:GLN:NE2	2.18	0.40
1:E:214:TRP:CE3	1:E:253:ARG:HG2	2.57	0.40
1:F:377:VAL:HG22	1:F:399:CYS:HB3	2.03	0.40
1:G:274:PHE:CD2	5:G:1482:EDO:H22	2.57	0.40
2:L:38:TRP:CD2	2:L:118:ILE:HG21	2.56	0.40
2:L:109:ALA:HB3	2:L:119:MET:HG3	2.04	0.40
1:A:161:LYS:HD3	2:I:66:LEU:HD13	2.03	0.40
1:B:277:ASN:HD21	1:B:293:ILE:CD1	2.35	0.40
1:E:162:LEU:HD11	1:E:199:PHE:HZ	1.87	0.40
1:E:269:TYR:CD2	1:E:318:LEU:HD23	2.57	0.40
1:G:138:LEU:O	1:G:316:LYS:NZ	2.48	0.40
1:H:329:GLY:HA3	6:H:2150:HOH:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:460:GLU:OE1	1:F:14:LYS:NZ[2_557]	1.89	0.31

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	458/475 (96%)	443 (97%)	15 (3%)	0	100	100
1	B	461/475 (97%)	446 (97%)	15 (3%)	0	100	100
1	C	458/475 (96%)	444 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	458/475 (96%)	442 (96%)	16 (4%)	0	100	100
1	E	458/475 (96%)	444 (97%)	14 (3%)	0	100	100
1	F	458/475 (96%)	439 (96%)	19 (4%)	0	100	100
1	G	459/475 (97%)	447 (97%)	12 (3%)	0	100	100
1	H	458/475 (96%)	442 (96%)	16 (4%)	0	100	100
2	I	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
2	J	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
2	K	138/140 (99%)	130 (94%)	8 (6%)	0	100	100
2	L	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
2	M	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
2	N	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
2	O	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
2	P	138/140 (99%)	132 (96%)	6 (4%)	0	100	100
All	All	4772/4920 (97%)	4598 (96%)	174 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	368/376 (98%)	364 (99%)	4 (1%)	73	85
1	B	369/376 (98%)	362 (98%)	7 (2%)	57	74
1	C	368/376 (98%)	365 (99%)	3 (1%)	81	89
1	D	368/376 (98%)	362 (98%)	6 (2%)	62	78
1	E	368/376 (98%)	364 (99%)	4 (1%)	73	85
1	F	368/376 (98%)	363 (99%)	5 (1%)	67	81
1	G	368/376 (98%)	362 (98%)	6 (2%)	62	78
1	H	368/376 (98%)	363 (99%)	5 (1%)	67	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	I	122/122 (100%)	118 (97%)	4 (3%)	38	54
2	J	122/122 (100%)	117 (96%)	5 (4%)	30	46
2	K	122/122 (100%)	117 (96%)	5 (4%)	30	46
2	L	122/122 (100%)	118 (97%)	4 (3%)	38	54
2	M	122/122 (100%)	118 (97%)	4 (3%)	38	54
2	N	122/122 (100%)	118 (97%)	4 (3%)	38	54
2	O	122/122 (100%)	118 (97%)	4 (3%)	38	54
2	P	122/122 (100%)	118 (97%)	4 (3%)	38	54
All	All	3921/3984 (98%)	3847 (98%)	74 (2%)	57	74

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	ASP
1	A	241	ASN
1	A	439	ARG
1	A	460	GLU
1	B	94	ASP
1	B	172	CYS
1	B	185	TYR
1	B	203	ASP
1	B	239	TYR
1	B	241	ASN
1	B	460	GLU
1	C	94	ASP
1	C	185	TYR
1	C	241	ASN
1	D	94	ASP
1	D	172	CYS
1	D	185	TYR
1	D	241	ASN
1	D	439	ARG
1	D	460	GLU
1	E	94	ASP
1	E	241	ASN
1	E	439	ARG
1	E	460	GLU
1	F	94	ASP
1	F	172	CYS

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Mol	Chain	Res	Type
1	F	239	TYR
1	F	241	ASN
1	F	439	ARG
1	G	94	ASP
1	G	172	CYS
1	G	203	ASP
1	G	239	TYR
1	G	241	ASN
1	G	460	GLU
1	H	94	ASP
1	H	172	CYS
1	H	219	LEU
1	H	239	TYR
1	H	241	ASN
2	I	9	ASN
2	I	12	PHE
2	I	52	VAL
2	I	127	LYS
2	J	9	ASN
2	J	12	PHE
2	J	52	VAL
2	J	127	LYS
2	J	130	ARG
2	K	9	ASN
2	K	12	PHE
2	K	52	VAL
2	K	84	ARG
2	K	127	LYS
2	L	9	ASN
2	L	12	PHE
2	L	52	VAL
2	L	127	LYS
2	M	9	ASN
2	M	12	PHE
2	M	52	VAL
2	M	127	LYS
2	N	9	ASN
2	N	12	PHE
2	N	52	VAL
2	N	127	LYS
2	O	9	ASN
2	O	12	PHE

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Mol	Chain	Res	Type
2	O	52	VAL
2	O	127	LYS
2	P	9	ASN
2	P	12	PHE
2	P	52	VAL
2	P	127	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (127) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	HIS
1	A	156	GLN
1	A	229	GLN
1	A	238	HIS
1	A	241	ASN
1	A	267	HIS
1	A	277	ASN
1	A	386	HIS
1	A	401	GLN
1	A	432	ASN
1	B	153	HIS
1	B	229	GLN
1	B	238	HIS
1	B	241	ASN
1	B	267	HIS
1	B	277	ASN
1	B	304	GLN
1	B	386	HIS
1	B	401	GLN
1	B	432	ASN
1	C	156	GLN
1	C	229	GLN
1	C	238	HIS
1	C	241	ASN
1	C	267	HIS
1	C	277	ASN
1	C	304	GLN
1	C	386	HIS
1	C	401	GLN
1	C	420	ASN
1	C	432	ASN
1	D	153	HIS

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Mol	Chain	Res	Type
1	D	156	GLN
1	D	229	GLN
1	D	238	HIS
1	D	241	ASN
1	D	267	HIS
1	D	277	ASN
1	D	304	GLN
1	D	386	HIS
1	D	401	GLN
1	D	432	ASN
1	E	153	HIS
1	E	163	ASN
1	E	229	GLN
1	E	238	HIS
1	E	241	ASN
1	E	267	HIS
1	E	277	ASN
1	E	304	GLN
1	E	386	HIS
1	E	401	GLN
1	E	432	ASN
1	F	156	GLN
1	F	163	ASN
1	F	229	GLN
1	F	238	HIS
1	F	241	ASN
1	F	267	HIS
1	F	277	ASN
1	F	304	GLN
1	F	386	HIS
1	F	401	GLN
1	F	420	ASN
1	F	432	ASN
1	G	153	HIS
1	G	156	GLN
1	G	163	ASN
1	G	229	GLN
1	G	238	HIS
1	G	241	ASN
1	G	267	HIS
1	G	277	ASN
1	G	304	GLN

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Mol	Chain	Res	Type
1	G	386	HIS
1	G	401	GLN
1	G	432	ASN
1	H	153	HIS
1	H	156	GLN
1	H	163	ASN
1	H	207	ASN
1	H	229	GLN
1	H	238	HIS
1	H	241	ASN
1	H	267	HIS
1	H	277	ASN
1	H	304	GLN
1	H	386	HIS
1	H	401	GLN
1	H	432	ASN
2	I	8	ASN
2	I	9	ASN
2	I	25	GLN
2	I	29	GLN
2	I	115	GLN
2	I	133	GLN
2	J	9	ASN
2	J	25	GLN
2	J	29	GLN
2	J	88	GLN
2	J	115	GLN
2	K	9	ASN
2	K	25	GLN
2	K	29	GLN
2	K	115	GLN
2	L	9	ASN
2	L	25	GLN
2	L	29	GLN
2	L	115	GLN
2	M	8	ASN
2	M	9	ASN
2	M	25	GLN
2	M	29	GLN
2	M	115	GLN
2	N	9	ASN
2	N	25	GLN

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Mol	Chain	Res	Type
2	N	29	GLN
2	N	115	GLN
2	O	9	ASN
2	O	25	GLN
2	O	29	GLN
2	O	115	GLN
2	P	8	ASN
2	P	9	ASN
2	P	25	GLN
2	P	29	GLN
2	P	115	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

48 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	HYP	C	151	1	6,8,9	0.61	0	5,10,12	1.23	0
1	HYP	B	151	1	6,8,9	0.80	0	5,10,12	1.33	1 (20%)
1	SMC	C	256	1	5,6,7	0.56	0	2,6,8	1.80	1 (50%)
1	HYP	D	104	1	6,8,9	0.74	0	5,10,12	2.04	1 (20%)
1	HYP	H	151	1	6,8,9	0.61	0	5,10,12	1.40	2 (40%)
1	HYP	F	151	1	6,8,9	0.68	0	5,10,12	1.51	2 (40%)
1	HYP	C	104	1	6,8,9	0.64	0	5,10,12	1.89	1 (20%)
1	SMC	G	369	1	5,6,7	0.68	0	2,6,8	0.85	0
1	SMC	B	369	1	5,6,7	0.67	0	2,6,8	0.90	0
1	SMC	E	256	1	5,6,7	0.74	0	2,6,8	1.36	0
2	MME	K	1	2	7,8,9	2.88	2 (28%)	5,8,10	1.42	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	HYP	H	104	1	6,8,9	0.72	0	5,10,12	2.01	1 (20%)
1	KCX	E	201	3,1	9,11,12	0.70	0	5,12,14	1.97	1 (20%)
1	HYP	B	104	1	6,8,9	0.53	0	5,10,12	1.94	1 (20%)
1	SMC	A	369	1	5,6,7	0.67	0	2,6,8	0.75	0
1	SMC	D	256	1	5,6,7	0.71	0	2,6,8	1.45	0
1	SMC	H	256	1	5,6,7	0.61	0	2,6,8	1.24	0
1	SMC	G	256	1	5,6,7	0.55	0	2,6,8	0.34	0
1	KCX	B	201	3,1	9,11,12	0.84	0	5,12,14	1.83	1 (20%)
1	KCX	H	201	3,1	9,11,12	0.90	0	5,12,14	1.45	1 (20%)
1	HYP	D	151	1	6,8,9	0.65	0	5,10,12	1.18	0
1	HYP	E	151	1	6,8,9	0.62	0	5,10,12	1.24	0
1	KCX	G	201	3,1	9,11,12	0.86	0	5,12,14	1.43	1 (20%)
2	MME	P	1	2	7,8,9	2.92	1 (14%)	5,8,10	1.50	1 (20%)
2	MME	O	1	2	7,8,9	2.87	1 (14%)	5,8,10	1.35	1 (20%)
1	SMC	C	369	1	5,6,7	0.62	0	2,6,8	1.25	0
1	SMC	A	256	1	5,6,7	0.68	0	2,6,8	0.56	0
1	SMC	E	369	1	5,6,7	0.60	0	2,6,8	0.47	0
1	KCX	A	201	3,1	9,11,12	0.94	0	5,12,14	1.57	1 (20%)
2	MME	J	1	2	7,8,9	2.87	1 (14%)	5,8,10	1.19	1 (20%)
1	SMC	B	256	1	5,6,7	0.48	0	2,6,8	0.24	0
1	SMC	F	369	1	5,6,7	0.61	0	2,6,8	1.21	0
1	HYP	A	104	1	6,8,9	0.56	0	5,10,12	1.91	1 (20%)
1	SMC	D	369	1	5,6,7	0.49	0	2,6,8	0.84	0
2	MME	M	1	2	7,8,9	2.83	2 (28%)	5,8,10	1.53	1 (20%)
1	HYP	E	104	1	6,8,9	0.67	0	5,10,12	2.01	1 (20%)
2	MME	I	1	2	7,8,9	2.91	1 (14%)	5,8,10	1.34	1 (20%)
1	HYP	G	151	1	6,8,9	0.66	0	5,10,12	1.47	1 (20%)
1	HYP	A	151	1	6,8,9	0.65	0	5,10,12	1.51	1 (20%)
1	SMC	F	256	1	5,6,7	0.58	0	2,6,8	1.26	0
2	MME	N	1	2	7,8,9	2.91	1 (14%)	5,8,10	1.50	1 (20%)
1	HYP	G	104	1	6,8,9	0.62	0	5,10,12	1.94	1 (20%)
2	MME	L	1	2	7,8,9	2.87	1 (14%)	5,8,10	1.42	1 (20%)
1	HYP	F	104	1	6,8,9	0.54	0	5,10,12	2.05	1 (20%)
1	KCX	F	201	3,1	9,11,12	0.87	0	5,12,14	1.44	1 (20%)
1	SMC	H	369	1	5,6,7	0.61	0	2,6,8	0.78	0
1	KCX	D	201	3,1	9,11,12	0.93	0	5,12,14	1.46	1 (20%)
1	KCX	C	201	3,1	9,11,12	0.72	0	5,12,14	1.40	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	C	151	1	-	0/0/11/13	0/1/1/1
1	HYP	B	151	1	-	0/0/11/13	0/1/1/1
1	SMC	C	256	1	-	0/3/5/7	-
1	HYP	D	104	1	-	0/0/11/13	0/1/1/1
1	HYP	H	151	1	-	0/0/11/13	0/1/1/1
1	HYP	F	151	1	-	0/0/11/13	0/1/1/1
1	HYP	C	104	1	-	0/0/11/13	0/1/1/1
1	SMC	G	369	1	-	2/3/5/7	-
1	SMC	B	369	1	-	2/3/5/7	-
1	SMC	E	256	1	-	0/3/5/7	-
2	MME	K	1	2	-	3/5/8/10	-
1	HYP	H	104	1	-	0/0/11/13	0/1/1/1
1	KCX	E	201	3,1	-	0/9/10/12	-
1	HYP	B	104	1	-	0/0/11/13	0/1/1/1
1	SMC	A	369	1	-	2/3/5/7	-
1	SMC	D	256	1	-	0/3/5/7	-
1	SMC	H	256	1	-	1/3/5/7	-
1	SMC	G	256	1	-	0/3/5/7	-
1	KCX	B	201	3,1	-	0/9/10/12	-
1	KCX	H	201	3,1	-	0/9/10/12	-
1	HYP	D	151	1	-	0/0/11/13	0/1/1/1
1	HYP	E	151	1	-	0/0/11/13	0/1/1/1
1	KCX	G	201	3,1	-	0/9/10/12	-
2	MME	P	1	2	-	3/5/8/10	-
2	MME	O	1	2	-	3/5/8/10	-
1	SMC	C	369	1	-	2/3/5/7	-
1	SMC	A	256	1	-	0/3/5/7	-
1	SMC	E	369	1	-	2/3/5/7	-
1	KCX	A	201	3,1	-	0/9/10/12	-
2	MME	J	1	2	-	3/5/8/10	-
1	SMC	B	256	1	-	0/3/5/7	-
1	SMC	F	369	1	-	2/3/5/7	-
1	HYP	A	104	1	-	0/0/11/13	0/1/1/1
1	SMC	D	369	1	-	2/3/5/7	-
2	MME	M	1	2	-	3/5/8/10	-
1	HYP	E	104	1	-	0/0/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MME	I	1	2	-	3/5/8/10	-
1	HYP	G	151	1	-	0/0/11/13	0/1/1/1
1	HYP	A	151	1	-	0/0/11/13	0/1/1/1
1	SMC	F	256	1	-	0/3/5/7	-
2	MME	N	1	2	-	3/5/8/10	-
1	HYP	G	104	1	-	0/0/11/13	0/1/1/1
2	MME	L	1	2	-	3/5/8/10	-
1	HYP	F	104	1	-	0/0/11/13	0/1/1/1
1	KCX	F	201	3,1	-	0/9/10/12	-
1	SMC	H	369	1	-	2/3/5/7	-
1	KCX	D	201	3,1	-	0/9/10/12	-
1	KCX	C	201	3,1	-	0/9/10/12	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	1	MME	CM-N	-7.40	1.27	1.46
2	P	1	MME	CM-N	-7.35	1.27	1.46
2	J	1	MME	CM-N	-7.33	1.27	1.46
2	N	1	MME	CM-N	-7.33	1.27	1.46
2	O	1	MME	CM-N	-7.32	1.27	1.46
2	L	1	MME	CM-N	-7.26	1.27	1.46
2	K	1	MME	CM-N	-7.16	1.27	1.46
2	M	1	MME	CM-N	-7.00	1.28	1.46
2	M	1	MME	CA-N	2.32	1.51	1.47
2	K	1	MME	CA-N	2.26	1.51	1.47

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	201	KCX	OQ1-CX-NZ	-4.38	118.17	124.96
1	D	104	HYP	CB-CG-CD	4.10	108.29	103.27
1	H	104	HYP	CB-CG-CD	4.08	108.27	103.27
1	F	104	HYP	CB-CG-CD	4.06	108.25	103.27
1	B	201	KCX	OQ1-CX-NZ	-4.06	118.67	124.96
1	E	104	HYP	CB-CG-CD	4.04	108.22	103.27
1	B	104	HYP	CB-CG-CD	3.86	108.00	103.27
1	G	104	HYP	CB-CG-CD	3.82	107.95	103.27
1	A	104	HYP	CB-CG-CD	3.78	107.90	103.27
1	C	104	HYP	CB-CG-CD	3.73	107.83	103.27
1	A	201	KCX	OQ1-CX-NZ	-3.45	119.60	124.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	201	KCX	OQ1-CX-NZ	-3.24	119.93	124.96
1	H	201	KCX	OQ1-CX-NZ	-3.18	120.02	124.96
1	F	201	KCX	OQ1-CX-NZ	-3.05	120.23	124.96
1	G	201	KCX	OQ1-CX-NZ	-2.95	120.39	124.96
2	P	1	MME	CM-N-CA	2.84	122.48	113.64
2	M	1	MME	CM-N-CA	2.84	122.47	113.64
2	N	1	MME	CM-N-CA	2.82	122.41	113.64
1	A	151	HYP	CB-CG-CD	2.74	106.63	103.27
2	L	1	MME	CM-N-CA	2.73	122.14	113.64
1	C	201	KCX	OQ1-CX-NZ	-2.70	120.77	124.96
2	K	1	MME	CM-N-CA	2.66	121.92	113.64
2	O	1	MME	CM-N-CA	2.60	121.72	113.64
2	I	1	MME	CM-N-CA	2.55	121.56	113.64
1	G	151	HYP	CB-CG-CD	2.51	106.35	103.27
1	F	151	HYP	O-C-CA	-2.39	118.51	124.78
1	B	151	HYP	CB-CG-CD	2.21	105.98	103.27
2	J	1	MME	CM-N-CA	2.20	120.47	113.64
1	C	256	SMC	CS-SG-CB	2.17	105.29	101.30
1	F	151	HYP	CB-CG-CD	2.05	105.78	103.27
1	H	151	HYP	CB-CG-CD	2.04	105.77	103.27
1	H	151	HYP	O-C-CA	-2.02	119.49	124.78

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	369	SMC	N-CA-CB-SG
1	A	369	SMC	C-CA-CB-SG
1	B	369	SMC	N-CA-CB-SG
1	B	369	SMC	C-CA-CB-SG
1	C	369	SMC	N-CA-CB-SG
1	C	369	SMC	C-CA-CB-SG
1	D	369	SMC	N-CA-CB-SG
1	D	369	SMC	C-CA-CB-SG
1	E	369	SMC	N-CA-CB-SG
1	E	369	SMC	C-CA-CB-SG
1	F	369	SMC	N-CA-CB-SG
1	F	369	SMC	C-CA-CB-SG
1	G	369	SMC	C-CA-CB-SG
1	H	369	SMC	C-CA-CB-SG
2	I	1	MME	C-CA-CB-CG
2	J	1	MME	C-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
2	K	1	MME	C-CA-CB-CG
2	L	1	MME	C-CA-CB-CG
2	M	1	MME	C-CA-CB-CG
2	N	1	MME	C-CA-CB-CG
2	O	1	MME	C-CA-CB-CG
2	P	1	MME	C-CA-CB-CG
2	L	1	MME	CB-CG-SD-CE
2	M	1	MME	CB-CG-SD-CE
2	P	1	MME	CB-CG-SD-CE
2	I	1	MME	N-CA-CB-CG
2	J	1	MME	N-CA-CB-CG
2	K	1	MME	N-CA-CB-CG
2	L	1	MME	N-CA-CB-CG
2	N	1	MME	N-CA-CB-CG
2	O	1	MME	N-CA-CB-CG
2	P	1	MME	N-CA-CB-CG
2	I	1	MME	CB-CG-SD-CE
2	K	1	MME	CB-CG-SD-CE
2	N	1	MME	CB-CG-SD-CE
2	J	1	MME	CB-CG-SD-CE
2	O	1	MME	CB-CG-SD-CE
2	M	1	MME	N-CA-CB-CG
1	G	369	SMC	N-CA-CB-SG
1	H	369	SMC	N-CA-CB-SG
1	H	256	SMC	N-CA-CB-SG

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	151	HYP	1	0
1	G	201	KCX	1	0
2	M	1	MME	1	0
1	C	201	KCX	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 59 ligands modelled in this entry, 8 are monoatomic - leaving 51 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	G	1482	-	3,3,3	0.46	0	2,2,2	0.25	0
5	EDO	F	1482	-	3,3,3	0.59	0	2,2,2	0.10	0
5	EDO	A	1482	-	3,3,3	0.83	0	2,2,2	0.31	0
4	CAP	E	1477	3	17,20,20	0.85	0	22,31,31	0.87	0
5	EDO	F	1483	-	3,3,3	0.48	0	2,2,2	0.26	0
5	EDO	B	1480	-	3,3,3	0.52	0	2,2,2	0.31	0
5	EDO	E	1478	-	3,3,3	0.55	0	2,2,2	0.18	0
5	EDO	H	1481	-	3,3,3	0.54	0	2,2,2	0.11	0
5	EDO	E	1481	-	3,3,3	0.57	0	2,2,2	0.32	0
5	EDO	N	1141	-	3,3,3	0.53	0	2,2,2	0.21	0
5	EDO	C	1478	-	3,3,3	0.62	0	2,2,2	0.09	0
5	EDO	F	1480	-	3,3,3	0.43	0	2,2,2	0.34	0
5	EDO	H	1480	-	3,3,3	0.60	0	2,2,2	0.29	0
5	EDO	H	1478	-	3,3,3	0.58	0	2,2,2	0.20	0
5	EDO	E	1479	-	3,3,3	0.48	0	2,2,2	0.34	0
5	EDO	G	1481	-	3,3,3	0.55	0	2,2,2	0.13	0
5	EDO	F	1481	-	3,3,3	0.51	0	2,2,2	0.24	0
5	EDO	C	1479	-	3,3,3	0.46	0	2,2,2	0.28	0
5	EDO	E	1482	-	3,3,3	0.50	0	2,2,2	0.28	0
5	EDO	J	1142	-	3,3,3	0.45	0	2,2,2	0.44	0
5	EDO	G	1479	-	3,3,3	0.46	0	2,2,2	0.32	0
5	EDO	A	1480	-	3,3,3	0.54	0	2,2,2	0.35	0
5	EDO	A	1479	-	3,3,3	0.43	0	2,2,2	0.38	0
4	CAP	A	1477	3	17,20,20	0.83	0	22,31,31	0.84	0
5	EDO	G	1478	-	3,3,3	0.50	0	2,2,2	0.24	0
5	EDO	A	1478	-	3,3,3	0.57	0	2,2,2	0.15	0
5	EDO	H	1482	-	3,3,3	0.47	0	2,2,2	0.39	0
5	EDO	O	1141	-	3,3,3	0.51	0	2,2,2	0.11	0
5	EDO	K	1141	-	3,3,3	0.56	0	2,2,2	0.07	0
5	EDO	B	1481	-	3,3,3	0.51	0	2,2,2	0.20	0
5	EDO	D	1478	-	3,3,3	0.51	0	2,2,2	0.16	0
4	CAP	C	1477	3	17,20,20	0.82	0	22,31,31	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	EDO	C	1480	-	3,3,3	0.47	0	2,2,2	0.14	0
4	CAP	B	1477	3	17,20,20	0.89	0	22,31,31	0.98	0
5	EDO	B	1478	-	3,3,3	0.59	0	2,2,2	0.05	0
5	EDO	G	1480	-	3,3,3	0.49	0	2,2,2	0.29	0
4	CAP	G	1477	3	17,20,20	0.80	0	22,31,31	1.09	2 (9%)
4	CAP	H	1477	3	17,20,20	0.91	0	22,31,31	0.86	1 (4%)
5	EDO	D	1479	-	3,3,3	0.48	0	2,2,2	0.45	0
4	CAP	F	1477	3	17,20,20	0.84	0	22,31,31	0.97	2 (9%)
5	EDO	D	1480	-	3,3,3	0.65	0	2,2,2	0.11	0
5	EDO	E	1480	-	3,3,3	0.45	0	2,2,2	0.32	0
4	CAP	D	1477	3	17,20,20	0.79	0	22,31,31	0.96	0
5	EDO	F	1478	-	3,3,3	0.42	0	2,2,2	0.36	0
5	EDO	F	1479	-	3,3,3	0.51	0	2,2,2	0.18	0
5	EDO	O	1142	-	3,3,3	0.45	0	2,2,2	0.45	0
5	EDO	B	1479	-	3,3,3	0.41	0	2,2,2	0.40	0
5	EDO	A	1481	-	3,3,3	0.47	0	2,2,2	0.35	0
5	EDO	H	1479	-	3,3,3	0.43	0	2,2,2	0.39	0
5	EDO	L	1141	-	3,3,3	0.50	0	2,2,2	0.29	0
5	EDO	J	1141	-	3,3,3	0.46	0	2,2,2	0.30	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	G	1482	-	-	0/1/1/1	-
5	EDO	F	1482	-	-	1/1/1/1	-
5	EDO	A	1482	-	-	0/1/1/1	-
4	CAP	E	1477	3	-	7/29/29/29	-
5	EDO	F	1483	-	-	1/1/1/1	-
5	EDO	B	1480	-	-	0/1/1/1	-
5	EDO	E	1478	-	-	0/1/1/1	-
5	EDO	H	1481	-	-	1/1/1/1	-
5	EDO	E	1481	-	-	0/1/1/1	-
5	EDO	N	1141	-	-	1/1/1/1	-
5	EDO	C	1478	-	-	1/1/1/1	-
5	EDO	F	1480	-	-	0/1/1/1	-
5	EDO	H	1480	-	-	0/1/1/1	-
5	EDO	H	1478	-	-	0/1/1/1	-
5	EDO	E	1479	-	-	1/1/1/1	-
5	EDO	G	1481	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	F	1481	-	-	0/1/1/1	-
5	EDO	C	1479	-	-	0/1/1/1	-
5	EDO	E	1482	-	-	0/1/1/1	-
5	EDO	J	1142	-	-	1/1/1/1	-
5	EDO	G	1479	-	-	1/1/1/1	-
5	EDO	A	1480	-	-	1/1/1/1	-
5	EDO	A	1479	-	-	0/1/1/1	-
4	CAP	A	1477	3	-	7/29/29/29	-
5	EDO	G	1478	-	-	0/1/1/1	-
5	EDO	A	1478	-	-	1/1/1/1	-
5	EDO	H	1482	-	-	1/1/1/1	-
5	EDO	O	1141	-	-	1/1/1/1	-
5	EDO	K	1141	-	-	0/1/1/1	-
5	EDO	B	1481	-	-	1/1/1/1	-
5	EDO	D	1478	-	-	1/1/1/1	-
4	CAP	C	1477	3	-	7/29/29/29	-
5	EDO	C	1480	-	-	1/1/1/1	-
4	CAP	B	1477	3	-	7/29/29/29	-
5	EDO	B	1478	-	-	0/1/1/1	-
5	EDO	G	1480	-	-	1/1/1/1	-
4	CAP	G	1477	3	-	7/29/29/29	-
4	CAP	H	1477	3	-	7/29/29/29	-
5	EDO	D	1479	-	-	0/1/1/1	-
4	CAP	F	1477	3	-	8/29/29/29	-
5	EDO	D	1480	-	-	0/1/1/1	-
5	EDO	E	1480	-	-	0/1/1/1	-
4	CAP	D	1477	3	-	7/29/29/29	-
5	EDO	F	1478	-	-	0/1/1/1	-
5	EDO	F	1479	-	-	0/1/1/1	-
5	EDO	O	1142	-	-	1/1/1/1	-
5	EDO	B	1479	-	-	0/1/1/1	-
5	EDO	A	1481	-	-	1/1/1/1	-
5	EDO	H	1479	-	-	0/1/1/1	-
5	EDO	L	1141	-	-	1/1/1/1	-
5	EDO	J	1141	-	-	0/1/1/1	-

There are no bond length outliers.

All (5) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	G	1477	CAP	O2-C2-C	-2.72	104.01	108.97
4	H	1477	CAP	O6P-P2-O5	2.12	112.38	106.73
4	F	1477	CAP	O2-C2-C	-2.06	105.21	108.97
4	G	1477	CAP	O5P-P2-O5	2.05	112.18	106.73
4	F	1477	CAP	O6P-P2-O5	2.04	112.16	106.73

There are no chirality outliers.

All (77) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1477	CAP	O6-C-C2-C1
4	A	1477	CAP	O7-C-C2-C1
4	A	1477	CAP	O6-C-C2-O2
4	A	1477	CAP	O7-C-C2-O2
4	A	1477	CAP	C2-C3-C4-O4
4	A	1477	CAP	O3-C3-C4-O4
4	B	1477	CAP	O6-C-C2-C1
4	B	1477	CAP	O7-C-C2-C1
4	B	1477	CAP	O6-C-C2-O2
4	B	1477	CAP	O7-C-C2-O2
4	B	1477	CAP	C2-C3-C4-O4
4	B	1477	CAP	O3-C3-C4-O4
4	C	1477	CAP	O6-C-C2-C1
4	C	1477	CAP	O7-C-C2-C1
4	C	1477	CAP	O6-C-C2-O2
4	C	1477	CAP	O7-C-C2-O2
4	C	1477	CAP	C2-C3-C4-O4
4	C	1477	CAP	O3-C3-C4-O4
4	D	1477	CAP	O6-C-C2-C1
4	D	1477	CAP	O7-C-C2-C1
4	D	1477	CAP	O6-C-C2-O2
4	D	1477	CAP	O7-C-C2-O2
4	D	1477	CAP	C2-C3-C4-O4
4	D	1477	CAP	O3-C3-C4-O4
4	E	1477	CAP	O6-C-C2-C1
4	E	1477	CAP	O7-C-C2-C1
4	E	1477	CAP	O6-C-C2-O2
4	E	1477	CAP	O7-C-C2-O2
4	E	1477	CAP	C2-C3-C4-O4
4	E	1477	CAP	O3-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
4	F	1477	CAP	O6-C-C2-C1
4	F	1477	CAP	O7-C-C2-C1
4	F	1477	CAP	O6-C-C2-O2
4	F	1477	CAP	O7-C-C2-O2
4	F	1477	CAP	C2-C3-C4-O4
4	F	1477	CAP	O3-C3-C4-O4
4	G	1477	CAP	O6-C-C2-C1
4	G	1477	CAP	O7-C-C2-C1
4	G	1477	CAP	O6-C-C2-O2
4	G	1477	CAP	O7-C-C2-O2
4	G	1477	CAP	C2-C3-C4-O4
4	G	1477	CAP	O3-C3-C4-O4
4	H	1477	CAP	O6-C-C2-C1
4	H	1477	CAP	O7-C-C2-C1
4	H	1477	CAP	O6-C-C2-O2
4	H	1477	CAP	O7-C-C2-O2
4	H	1477	CAP	C2-C3-C4-O4
4	H	1477	CAP	O3-C3-C4-O4
5	E	1479	EDO	O1-C1-C2-O2
5	D	1478	EDO	O1-C1-C2-O2
5	G	1479	EDO	O1-C1-C2-O2
5	H	1481	EDO	O1-C1-C2-O2
5	H	1482	EDO	O1-C1-C2-O2
5	O	1142	EDO	O1-C1-C2-O2
4	A	1477	CAP	O2-C2-C3-C4
4	B	1477	CAP	O2-C2-C3-C4
4	C	1477	CAP	O2-C2-C3-C4
4	D	1477	CAP	O2-C2-C3-C4
4	E	1477	CAP	O2-C2-C3-C4
4	F	1477	CAP	O2-C2-C3-C4
4	G	1477	CAP	O2-C2-C3-C4
4	H	1477	CAP	O2-C2-C3-C4
5	G	1481	EDO	O1-C1-C2-O2
5	A	1481	EDO	O1-C1-C2-O2
5	B	1481	EDO	O1-C1-C2-O2
5	F	1482	EDO	O1-C1-C2-O2
5	G	1480	EDO	O1-C1-C2-O2
5	L	1141	EDO	O1-C1-C2-O2
5	N	1141	EDO	O1-C1-C2-O2
5	A	1478	EDO	O1-C1-C2-O2
5	A	1480	EDO	O1-C1-C2-O2
5	C	1478	EDO	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
5	F	1483	EDO	O1-C1-C2-O2
5	C	1480	EDO	O1-C1-C2-O2
5	J	1142	EDO	O1-C1-C2-O2
5	O	1141	EDO	O1-C1-C2-O2
4	F	1477	CAP	C2-C3-C4-C5

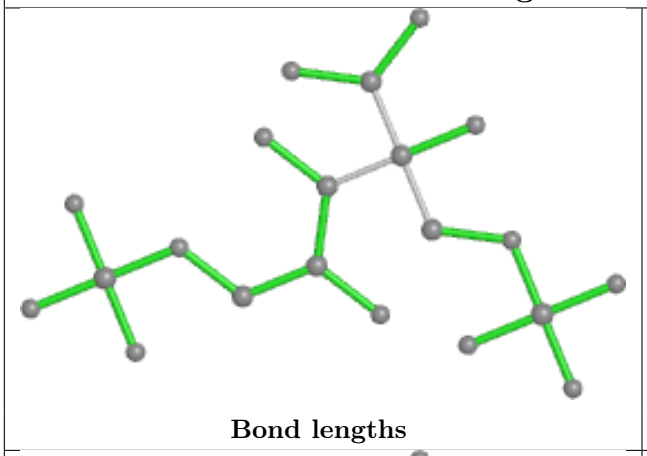
There are no ring outliers.

5 monomers are involved in 20 short contacts:

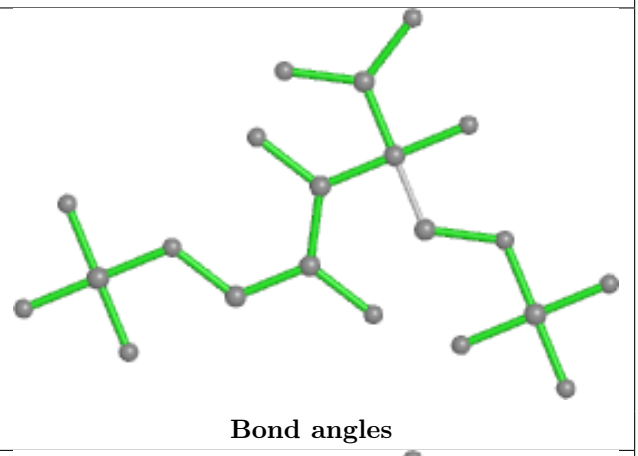
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	G	1482	EDO	2	0
5	N	1141	EDO	5	0
5	G	1481	EDO	7	0
5	G	1479	EDO	1	0
5	F	1479	EDO	5	0

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 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.

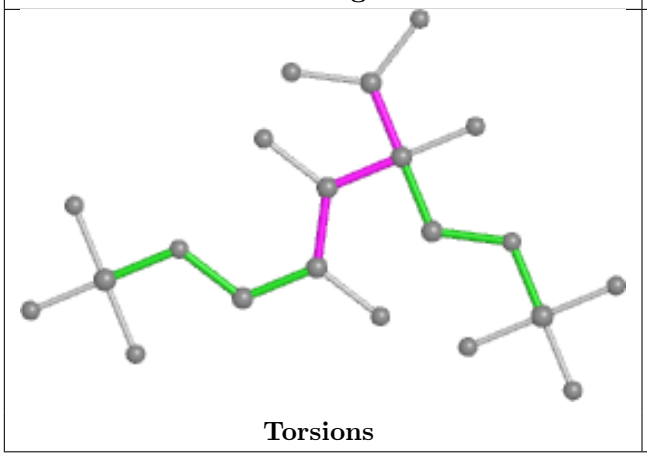
Ligand CAP E 1477



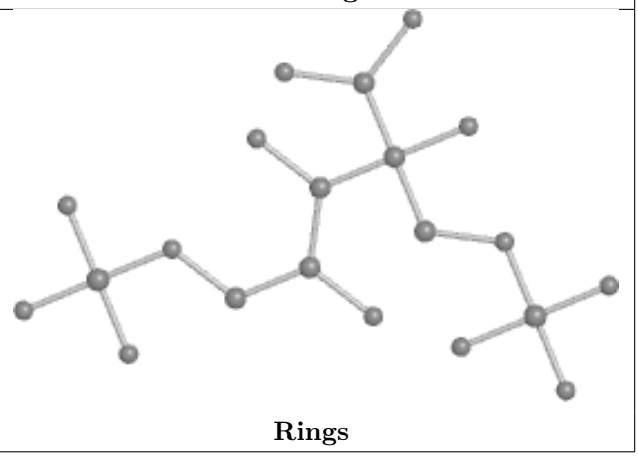
Bond lengths



Bond angles

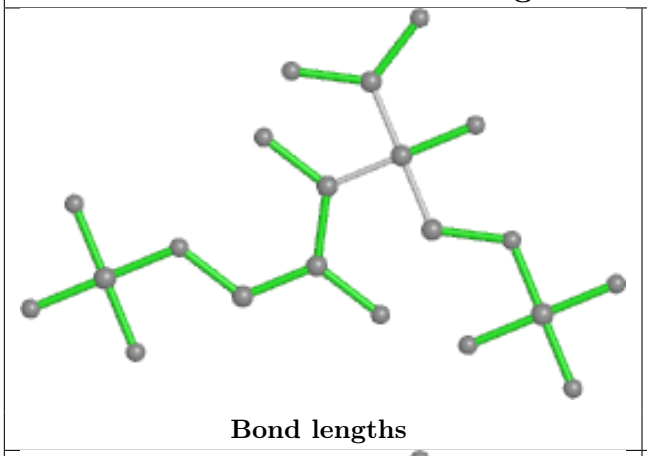


Torsions

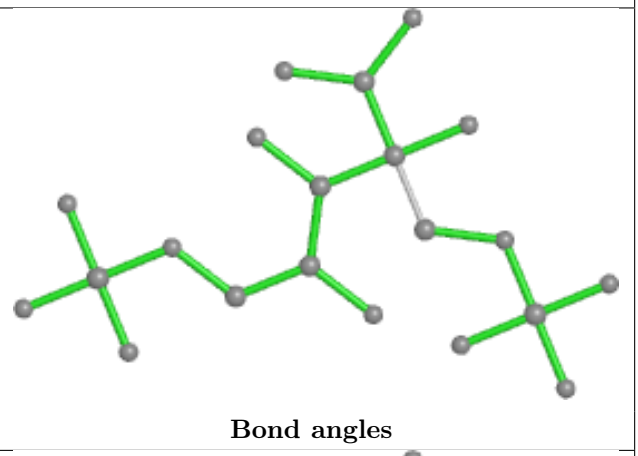


Rings

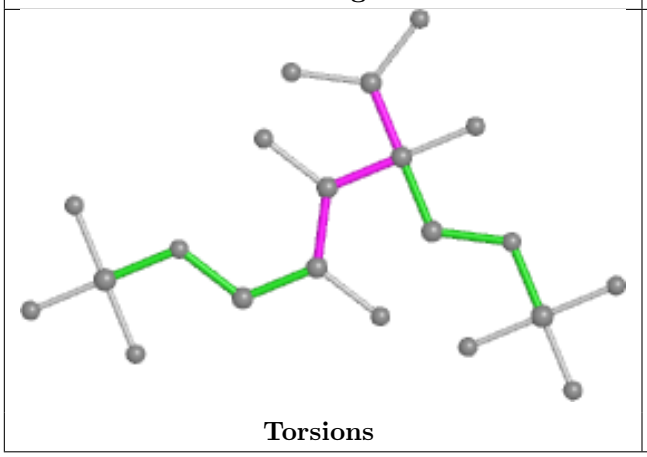
Ligand CAP A 1477



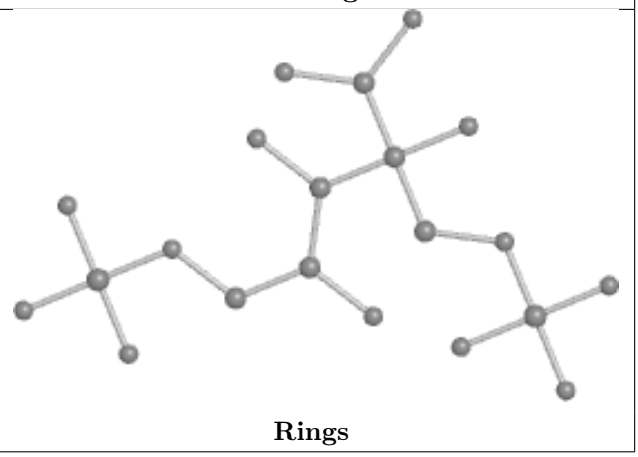
Bond lengths



Bond angles

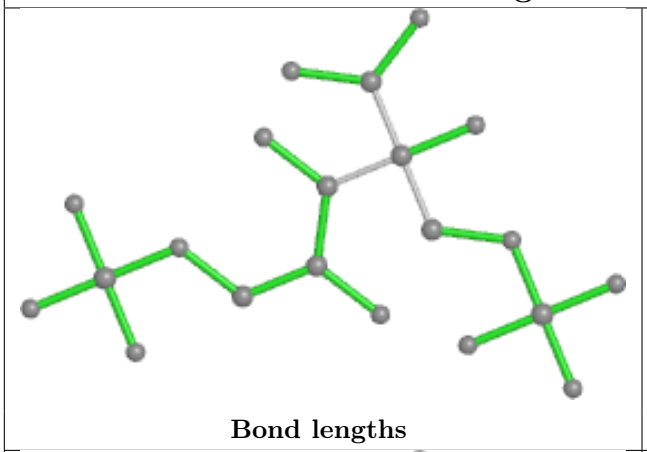


Torsions

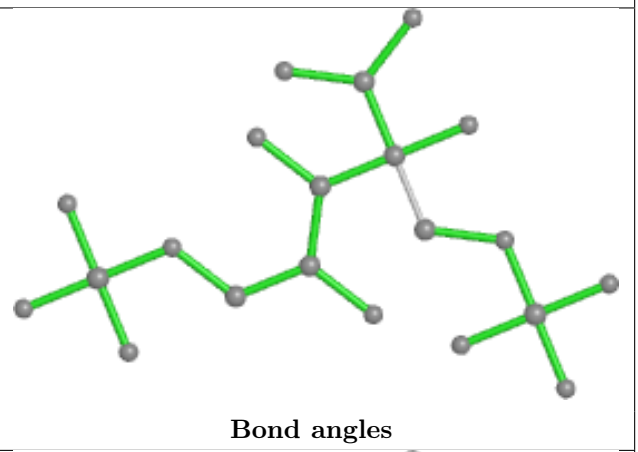


Rings

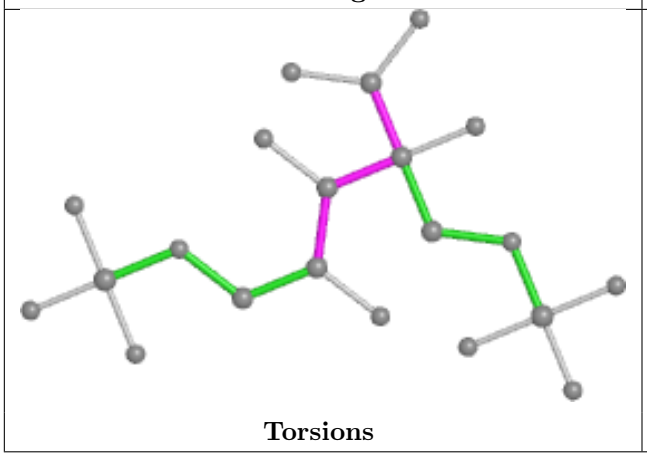
Ligand CAP C 1477



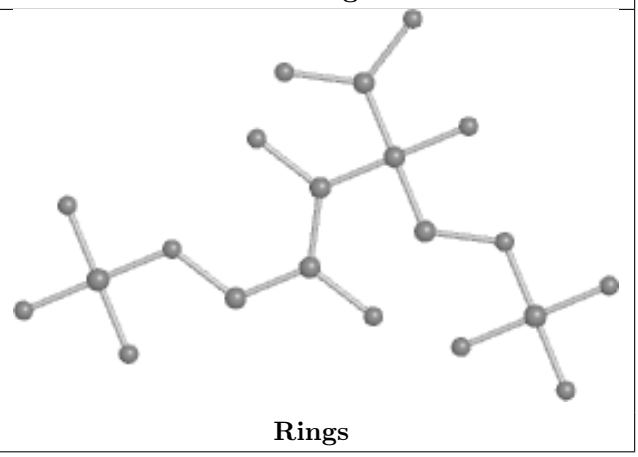
Bond lengths



Bond angles

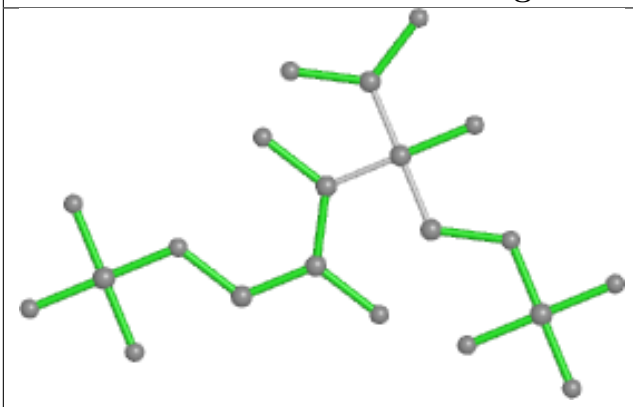


Torsions

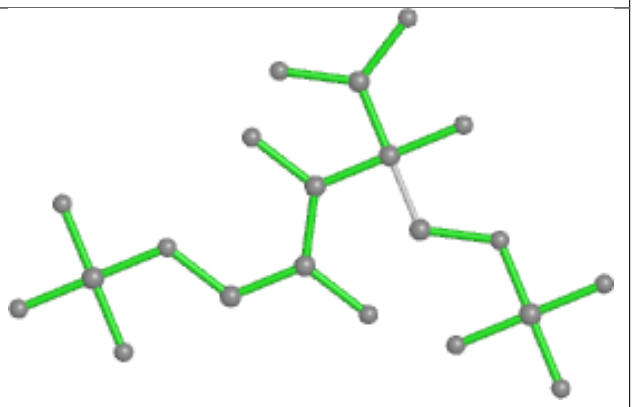


Rings

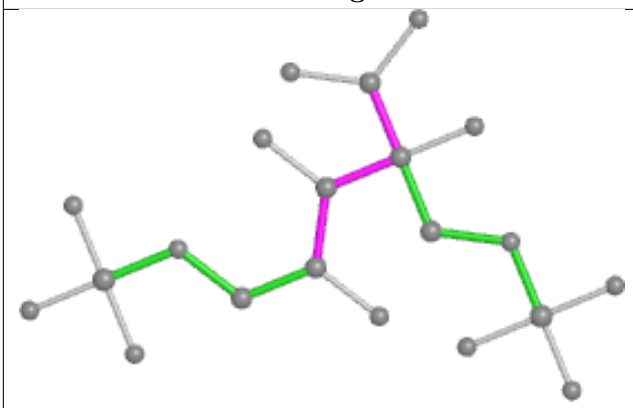
Ligand CAP B 1477



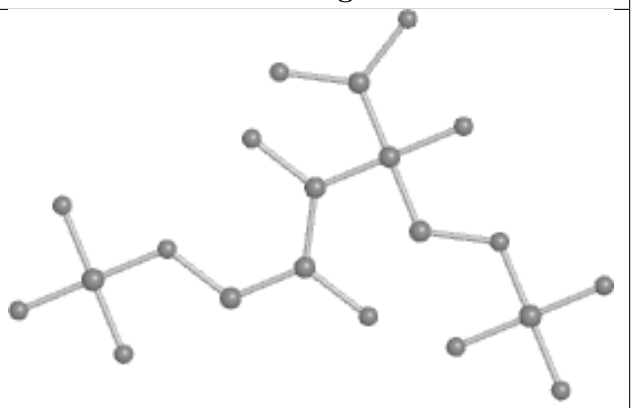
Bond lengths



Bond angles

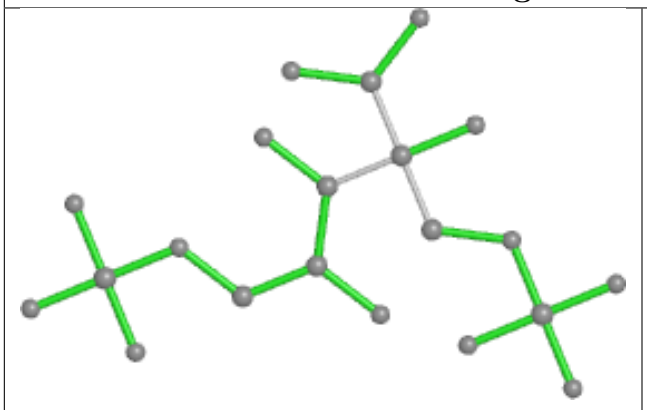


Torsions

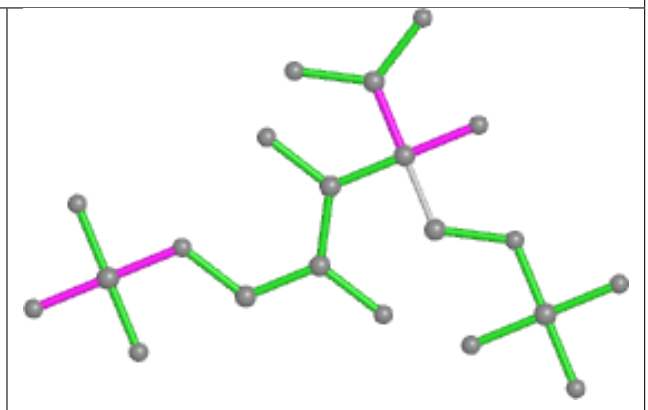


Rings

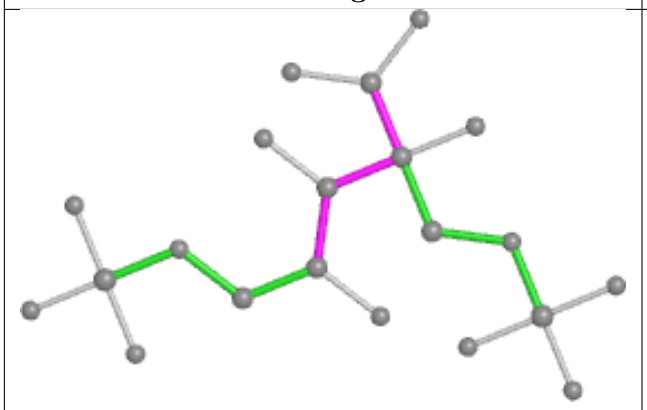
Ligand CAP G 1477



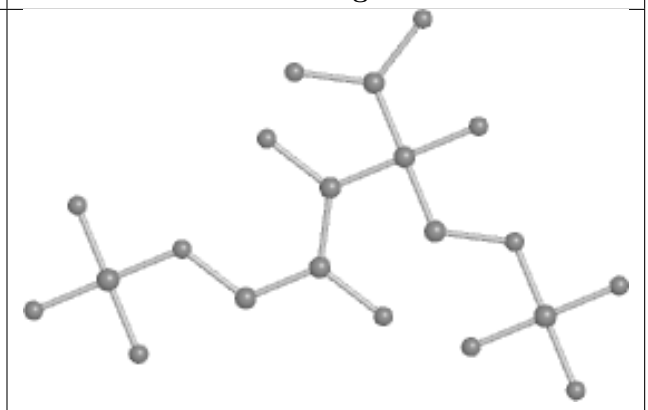
Bond lengths



Bond angles

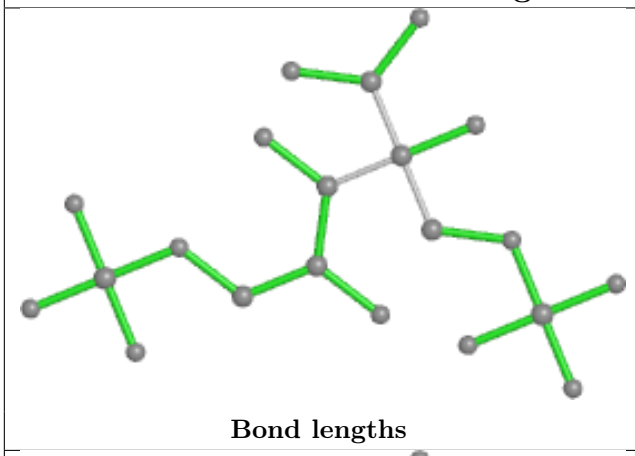


Torsions

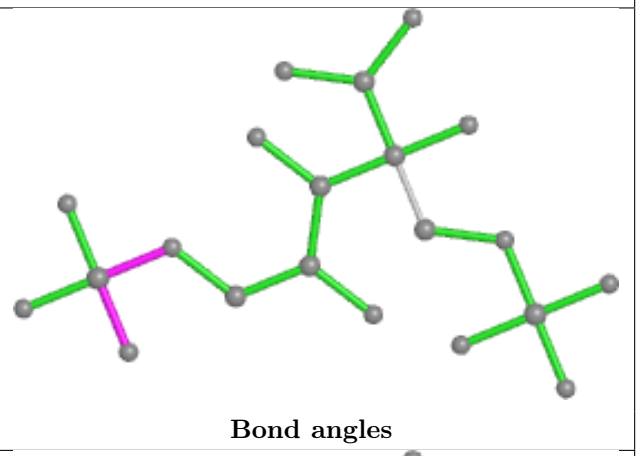


Rings

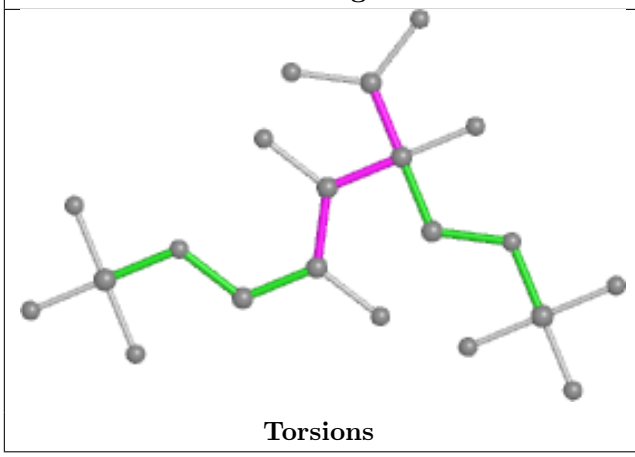
Ligand CAP H 1477



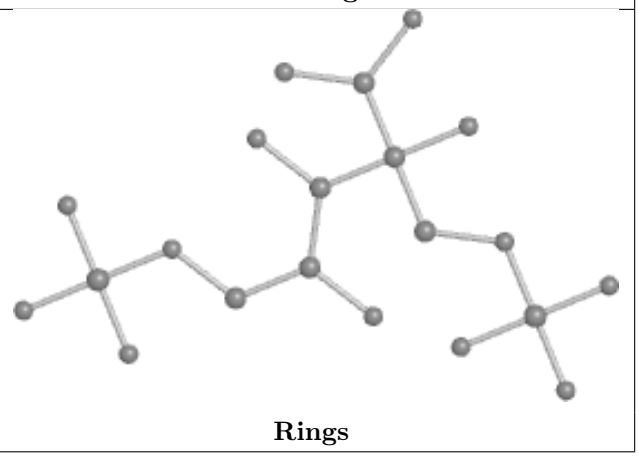
Bond lengths



Bond angles

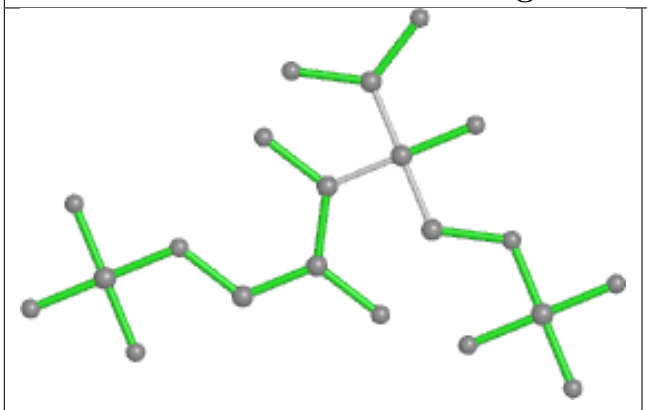


Torsions

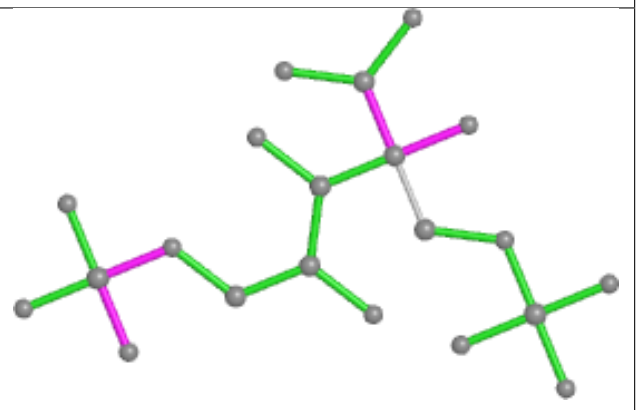


Rings

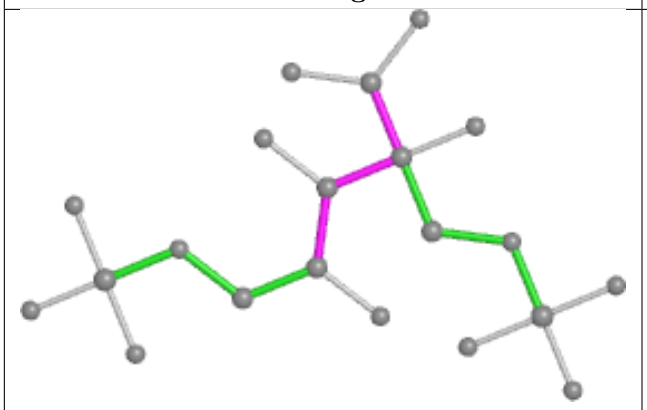
Ligand CAP F 1477



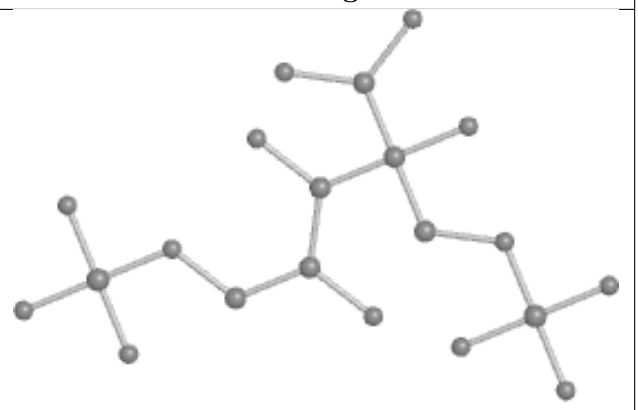
Bond lengths



Bond angles

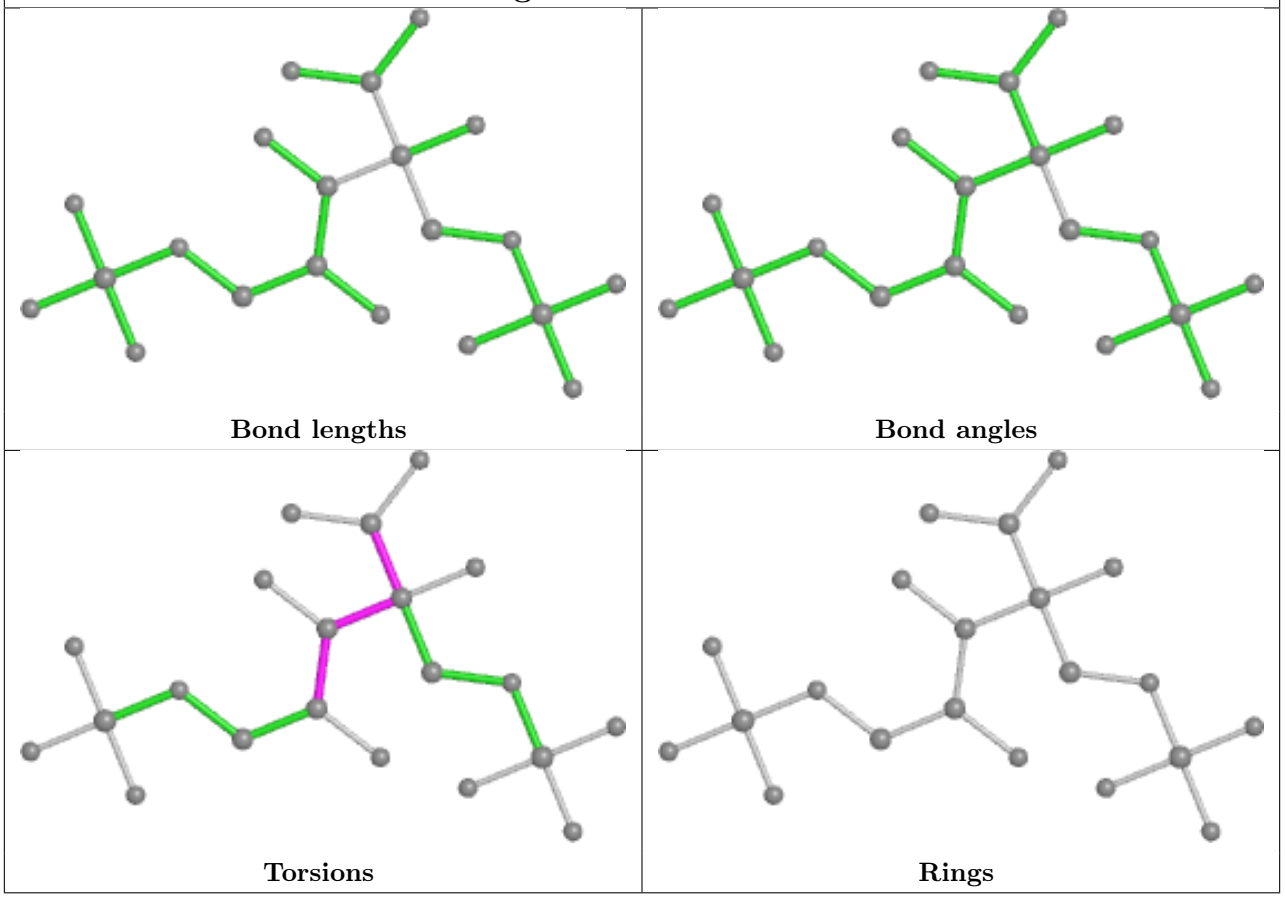


Torsions



Rings

Ligand CAP D 1477



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	460/475 (96%)	-0.46	7 (1%)	73	71	5, 12, 29, 44	0
1	B	463/475 (97%)	-0.52	6 (1%)	77	75	5, 12, 30, 44	0
1	C	460/475 (96%)	-0.53	5 (1%)	80	79	5, 12, 29, 44	0
1	D	460/475 (96%)	-0.50	13 (2%)	53	49	5, 12, 29, 44	0
1	E	460/475 (96%)	-0.53	9 (1%)	65	60	5, 12, 29, 44	0
1	F	460/475 (96%)	-0.50	10 (2%)	62	57	5, 12, 29, 44	0
1	G	461/475 (97%)	-0.54	6 (1%)	77	75	5, 12, 29, 44	0
1	H	460/475 (96%)	-0.54	6 (1%)	77	75	5, 12, 29, 44	0
2	I	139/140 (99%)	-0.11	5 (3%)	42	39	9, 18, 31, 36	0
2	J	139/140 (99%)	-0.12	6 (4%)	35	31	9, 18, 31, 37	0
2	K	139/140 (99%)	-0.17	5 (3%)	42	39	9, 18, 31, 36	0
2	L	139/140 (99%)	-0.22	4 (2%)	51	48	9, 18, 31, 35	0
2	M	139/140 (99%)	-0.28	2 (1%)	75	73	9, 18, 31, 34	0
2	N	139/140 (99%)	-0.20	5 (3%)	42	39	9, 18, 31, 37	0
2	O	139/140 (99%)	-0.17	5 (3%)	42	39	9, 18, 31, 35	0
2	P	139/140 (99%)	-0.15	3 (2%)	62	57	9, 18, 31, 35	0
All	All	4796/4920 (97%)	-0.44	97 (2%)	65	60	5, 13, 30, 44	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	94	ASP	4.4
1	A	92	GLY	4.3
1	D	94	ASP	4.3
1	E	92	GLY	4.0
1	D	439	ARG	4.0

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Mol	Chain	Res	Type	RSRZ
2	O	22	THR	4.0
1	A	450	LYS	4.0
1	B	475	LEU	4.0
1	C	94	ASP	3.9
1	F	450	LYS	3.8
1	H	94	ASP	3.7
2	O	23	ASP	3.7
1	D	470	ASP	3.6
1	E	94	ASP	3.5
1	D	450	LYS	3.5
1	G	450	LYS	3.4
1	B	464	GLU	3.3
1	A	439	ARG	3.3
1	E	450	LYS	3.3
2	I	22	THR	3.2
1	H	92	GLY	3.2
2	M	23	ASP	3.2
1	G	439	ARG	3.1
1	B	439	ARG	3.1
2	J	130	ARG	3.1
1	G	10	GLY	3.0
2	N	130	ARG	3.0
1	E	475	LEU	3.0
1	H	475	LEU	3.0
1	F	475	LEU	2.9
2	J	136	ASN	2.9
1	C	91	PRO	2.8
1	D	474	LYS	2.8
2	N	136	ASN	2.8
1	G	475	LEU	2.8
2	J	127	LYS	2.8
2	P	22	THR	2.8
2	J	23	ASP	2.7
1	D	471	THR	2.7
1	D	475	LEU	2.7
2	L	23	ASP	2.6
1	F	94	ASP	2.6
1	D	438	ALA	2.6
1	C	470	ASP	2.6
2	L	22	THR	2.6
1	E	11	ALA	2.6
1	H	450	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
2	K	24	GLU	2.6
1	A	474	LYS	2.5
1	B	10	GLY	2.5
1	A	94	ASP	2.5
1	C	450	LYS	2.5
1	D	464	GLU	2.5
2	K	136	ASN	2.5
1	D	92	GLY	2.4
1	G	464	GLU	2.4
2	P	24	GLU	2.4
2	K	130	ARG	2.4
2	O	20	PRO	2.4
2	L	48	ASP	2.4
2	O	113	GLN	2.3
1	D	436	ASP	2.3
2	I	24	GLU	2.3
1	A	464	GLU	2.3
1	D	449	CYS	2.3
1	E	439	ARG	2.3
1	F	474	LYS	2.3
1	E	46	PRO	2.3
1	H	464	GLU	2.3
2	P	91	ARG	2.3
2	N	82	GLY	2.3
1	E	474	LYS	2.3
1	F	28	ASP	2.3
1	D	468	GLU	2.2
1	G	474	LYS	2.2
2	N	134	PRO	2.2
1	A	475	LEU	2.2
2	M	22	THR	2.2
1	F	470	ASP	2.2
2	J	22	THR	2.2
1	B	92	GLY	2.1
2	O	127	LYS	2.1
2	L	128	THR	2.1
2	I	113	GLN	2.1
1	E	30	VAL	2.1
2	I	127	LYS	2.1
1	C	464	GLU	2.1
2	K	84	ARG	2.1
2	N	24	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	93	GLU	2.1
2	J	20	PRO	2.1
1	F	464	GLU	2.1
1	H	470	ASP	2.1
2	I	130	ARG	2.0
1	F	91	PRO	2.0
1	F	469	PHE	2.0
2	K	128	THR	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} 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
2	MME	M	1	9/10	0.91	0.18	22,24,28,28	0
2	MME	O	1	9/10	0.91	0.20	22,23,27,28	0
1	HYP	H	151	8/9	0.92	0.13	9,9,9,12	0
2	MME	N	1	9/10	0.92	0.20	22,23,27,28	0
2	MME	J	1	9/10	0.92	0.18	22,23,27,28	0
2	MME	I	1	9/10	0.93	0.24	22,23,28,28	0
1	HYP	F	104	8/9	0.93	0.14	10,11,11,15	0
2	MME	L	1	9/10	0.93	0.19	22,23,27,28	0
2	MME	P	1	9/10	0.93	0.23	22,23,28,28	0
1	HYP	E	104	8/9	0.94	0.15	11,11,11,15	0
1	KCX	B	201	12/13	0.95	0.15	8,9,9,11	0
1	KCX	C	201	12/13	0.95	0.12	8,9,9,10	0
1	HYP	D	104	8/9	0.95	0.15	10,11,11,15	0
2	MME	K	1	9/10	0.95	0.12	22,23,27,28	0
1	HYP	A	104	8/9	0.95	0.15	11,11,11,15	0
1	HYP	E	151	8/9	0.95	0.13	9,9,9,12	0
1	HYP	A	151	8/9	0.95	0.09	9,9,9,13	0
1	SMC	F	369	7/8	0.95	0.13	14,15,17,18	0
1	HYP	G	104	8/9	0.95	0.14	10,11,11,15	0
1	SMC	E	369	7/8	0.96	0.10	14,14,17,17	0
1	HYP	D	151	8/9	0.96	0.11	8,9,9,12	0
1	HYP	F	151	8/9	0.96	0.12	8,9,9,12	0
1	SMC	A	369	7/8	0.96	0.12	14,15,17,17	0
1	HYP	C	104	8/9	0.96	0.11	10,11,12,15	0
1	HYP	G	151	8/9	0.96	0.10	8,9,9,12	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	HYP	H	104	8/9	0.96	0.11	10,11,11,15	0
1	KCX	E	201	12/13	0.96	0.12	8,9,9,10	0
1	KCX	A	201	12/13	0.97	0.10	8,9,9,10	0
1	SMC	E	256	7/8	0.97	0.10	6,7,7,7	0
1	SMC	H	256	7/8	0.97	0.09	6,7,7,7	0
1	SMC	H	369	7/8	0.97	0.09	14,15,17,17	0
1	SMC	B	369	7/8	0.97	0.11	14,14,17,17	0
1	KCX	D	201	12/13	0.97	0.12	8,9,9,11	0
1	SMC	D	256	7/8	0.97	0.08	5,7,7,8	0
1	SMC	D	369	7/8	0.97	0.09	14,15,17,17	0
1	HYP	B	104	8/9	0.97	0.12	10,11,11,15	0
1	HYP	B	151	8/9	0.97	0.10	8,9,9,12	0
1	SMC	G	256	7/8	0.97	0.10	6,7,7,7	0
1	SMC	G	369	7/8	0.97	0.10	14,14,17,17	0
1	KCX	F	201	12/13	0.98	0.08	8,9,9,10	0
1	HYP	C	151	8/9	0.98	0.09	9,9,9,12	0
1	SMC	A	256	7/8	0.98	0.08	6,7,7,7	0
1	KCX	H	201	12/13	0.98	0.09	8,9,10,10	0
1	SMC	C	256	7/8	0.98	0.09	6,6,7,7	0
1	KCX	G	201	12/13	0.98	0.13	8,9,9,10	0
1	SMC	C	369	7/8	0.98	0.09	14,15,17,17	0
1	SMC	F	256	7/8	0.99	0.08	6,7,7,7	0
1	SMC	B	256	7/8	0.99	0.07	6,7,7,7	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
5	EDO	H	1480	4/4	0.76	0.25	23,24,24,25	0
5	EDO	E	1482	4/4	0.79	0.33	42,43,43,43	0
5	EDO	B	1480	4/4	0.80	0.22	24,25,25,26	0
5	EDO	B	1481	4/4	0.80	0.31	45,45,45,46	0
5	EDO	G	1482	4/4	0.81	0.46	2,2,2,2	4

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	EDO	G	1481	4/4	0.81	0.27	34,34,34,35	0
5	EDO	F	1482	4/4	0.83	0.27	28,29,30,30	0
5	EDO	N	1141	4/4	0.83	0.26	20,20,21,22	0
5	EDO	E	1480	4/4	0.84	0.20	45,45,45,45	0
5	EDO	D	1480	4/4	0.85	0.35	28,28,28,29	0
5	EDO	G	1480	4/4	0.85	0.24	29,29,30,30	0
5	EDO	L	1141	4/4	0.85	0.30	54,54,54,55	0
5	EDO	F	1479	4/4	0.85	0.30	30,32,32,33	0
5	EDO	O	1142	4/4	0.85	0.22	31,32,32,33	0
5	EDO	E	1481	4/4	0.86	0.29	30,31,32,32	0
5	EDO	E	1478	4/4	0.87	0.18	19,22,23,25	0
5	EDO	C	1478	4/4	0.87	0.21	29,30,31,31	0
5	EDO	A	1481	4/4	0.87	0.32	47,48,48,49	0
5	EDO	H	1478	4/4	0.87	0.17	17,17,19,20	0
5	EDO	A	1482	4/4	0.88	0.21	20,21,22,22	0
5	EDO	F	1481	4/4	0.90	0.20	38,38,39,39	0
5	EDO	A	1480	4/4	0.90	0.15	17,19,19,19	0
5	EDO	J	1142	4/4	0.91	0.20	37,38,38,40	0
5	EDO	K	1141	4/4	0.91	0.22	24,25,26,26	0
5	EDO	B	1478	4/4	0.91	0.22	11,12,13,13	0
5	EDO	H	1481	4/4	0.91	0.22	26,27,27,27	0
5	EDO	H	1482	4/4	0.91	0.19	25,27,27,28	0
3	MG	F	1476	1/1	0.92	0.06	8,8,8,8	0
5	EDO	O	1141	4/4	0.93	0.28	21,22,23,23	0
5	EDO	A	1478	4/4	0.93	0.13	13,15,15,15	0
5	EDO	D	1479	4/4	0.94	0.13	23,24,24,24	0
5	EDO	G	1478	4/4	0.94	0.15	13,13,13,14	0
5	EDO	H	1479	4/4	0.94	0.17	23,24,24,24	0
3	MG	G	1476	1/1	0.95	0.06	8,8,8,8	0
5	EDO	B	1479	4/4	0.95	0.19	10,11,11,12	0
5	EDO	F	1483	4/4	0.95	0.17	32,33,34,34	0
5	EDO	C	1480	4/4	0.96	0.57	2,2,2,2	4
5	EDO	D	1478	4/4	0.96	0.14	15,16,17,18	0
5	EDO	J	1141	4/4	0.96	0.25	33,35,35,36	0
4	CAP	B	1477	21/21	0.96	0.14	8,12,13,14	0
5	EDO	F	1478	4/4	0.96	0.49	2,2,2,2	4
5	EDO	A	1479	4/4	0.96	0.13	19,20,21,21	0
5	EDO	F	1480	4/4	0.96	0.18	16,16,17,18	0
5	EDO	C	1479	4/4	0.96	0.09	19,19,20,20	0
5	EDO	E	1479	4/4	0.96	0.12	32,32,32,32	0
4	CAP	F	1477	21/21	0.97	0.12	9,12,14,14	0
4	CAP	G	1477	21/21	0.97	0.12	8,12,13,14	0

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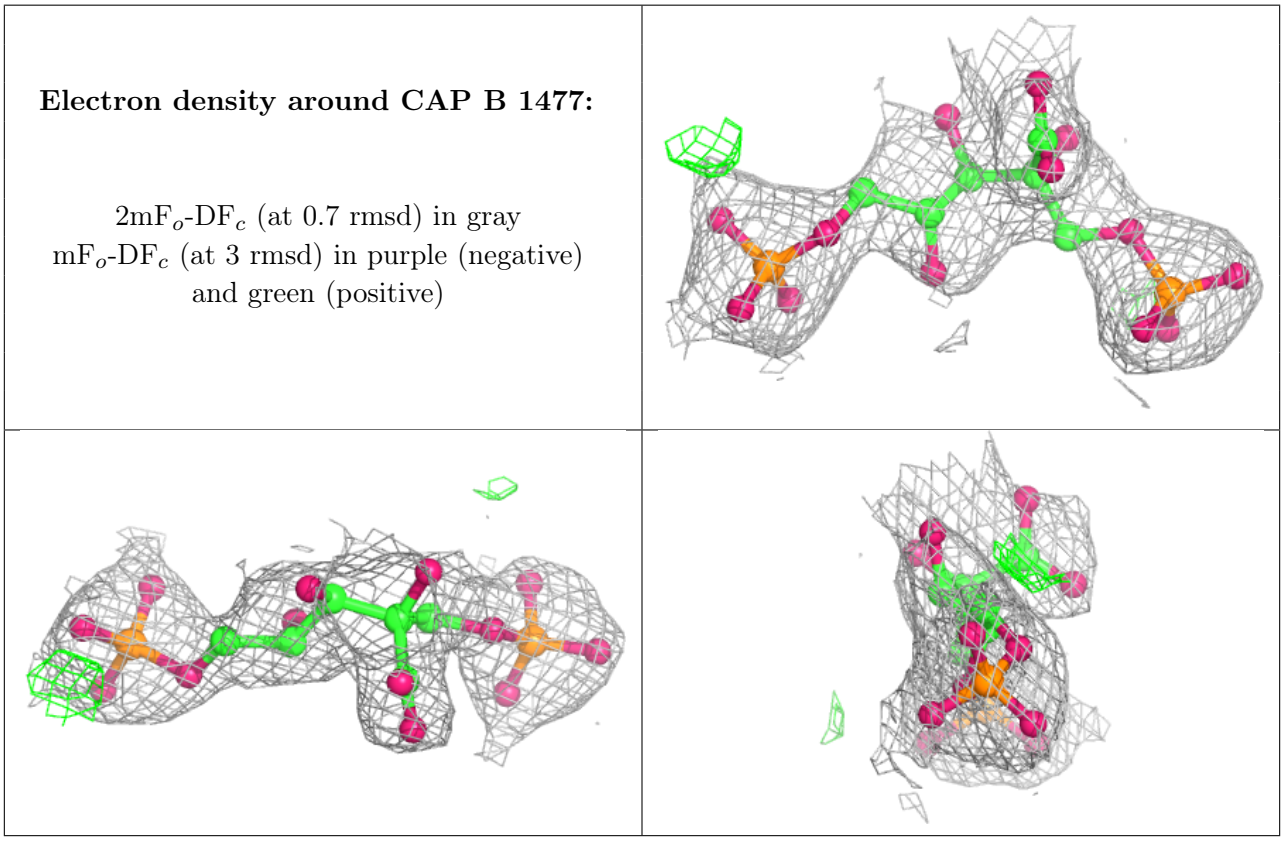
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	H	1476	1/1	0.97	0.06	8,8,8,8	0
4	CAP	A	1477	21/21	0.97	0.11	8,12,14,14	0
3	MG	E	1476	1/1	0.97	0.04	8,8,8,8	0
5	EDO	G	1479	4/4	0.97	0.13	15,15,15,16	0
4	CAP	C	1477	21/21	0.97	0.12	9,12,13,14	0
3	MG	A	1476	1/1	0.98	0.04	8,8,8,8	0
4	CAP	H	1477	21/21	0.98	0.10	9,12,13,14	0
4	CAP	D	1477	21/21	0.98	0.09	8,12,13,14	0
4	CAP	E	1477	21/21	0.98	0.10	8,12,14,14	0
3	MG	B	1476	1/1	0.98	0.03	8,8,8,8	0
3	MG	D	1476	1/1	0.99	0.07	8,8,8,8	0
3	MG	C	1476	1/1	0.99	0.06	9,9,9,9	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.

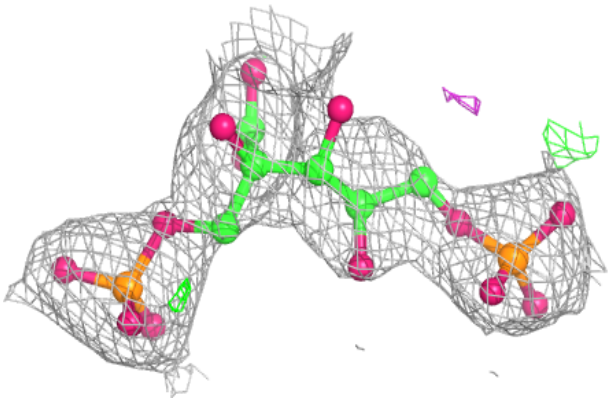
Electron density around CAP B 1477:

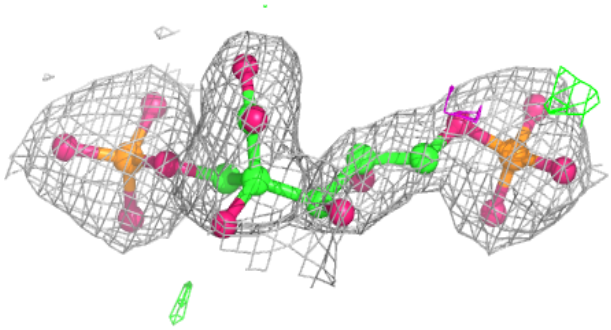
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

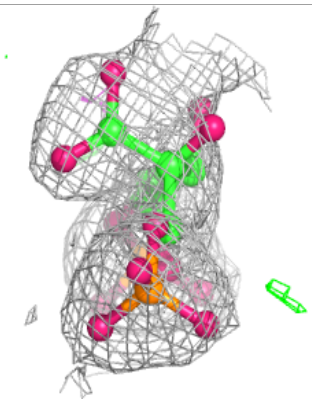


Electron density around CAP F 1477:

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

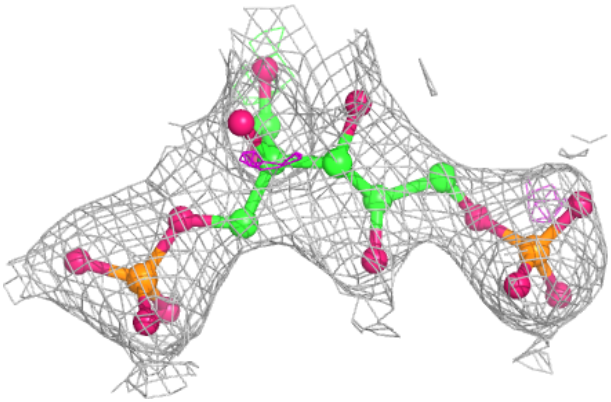


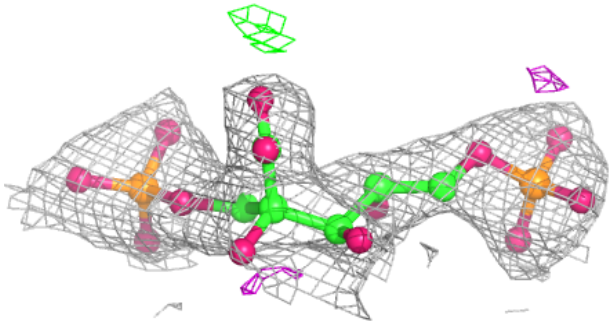


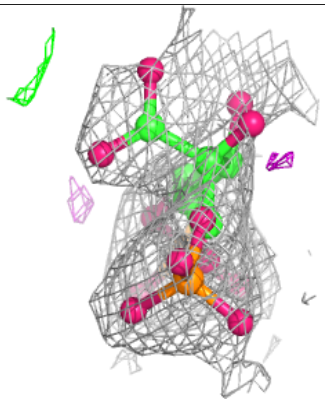


Electron density around CAP G 1477:

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

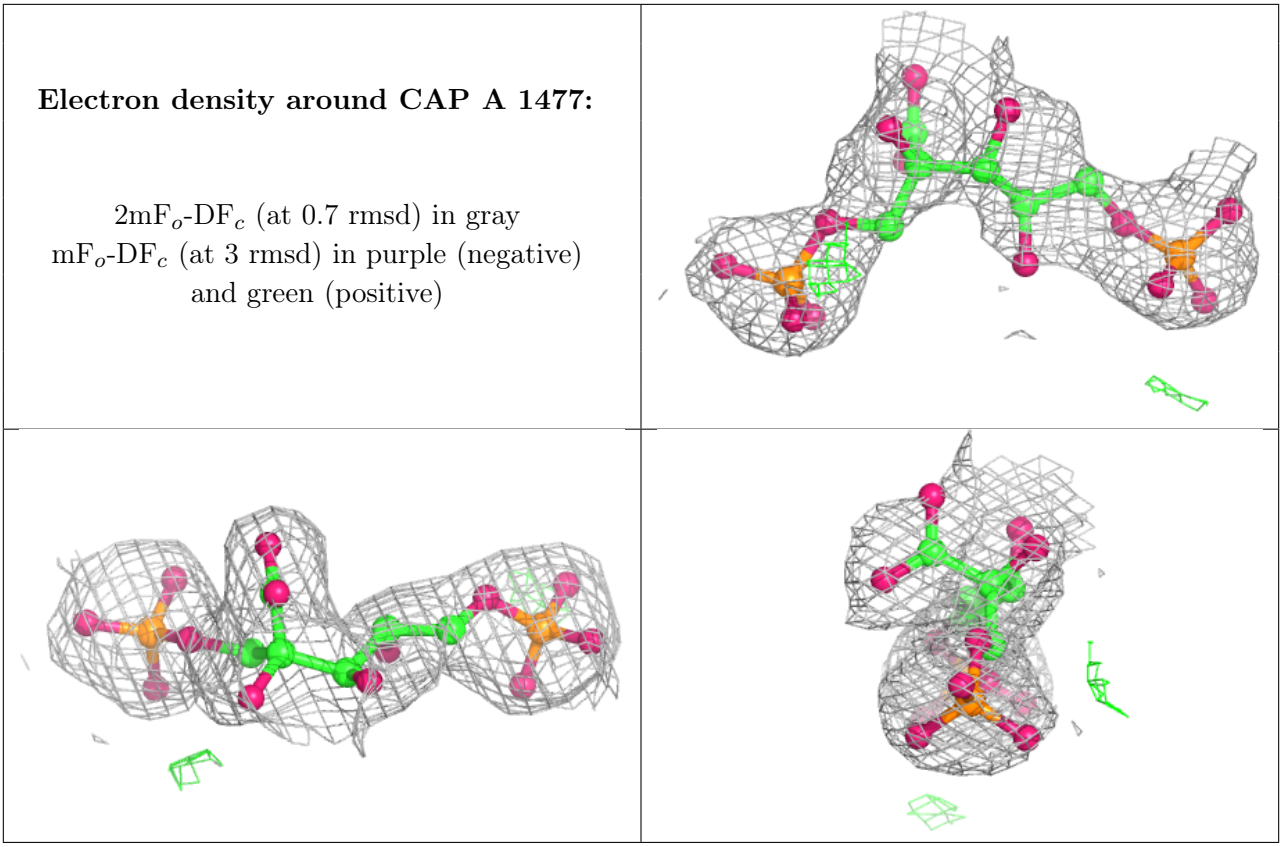






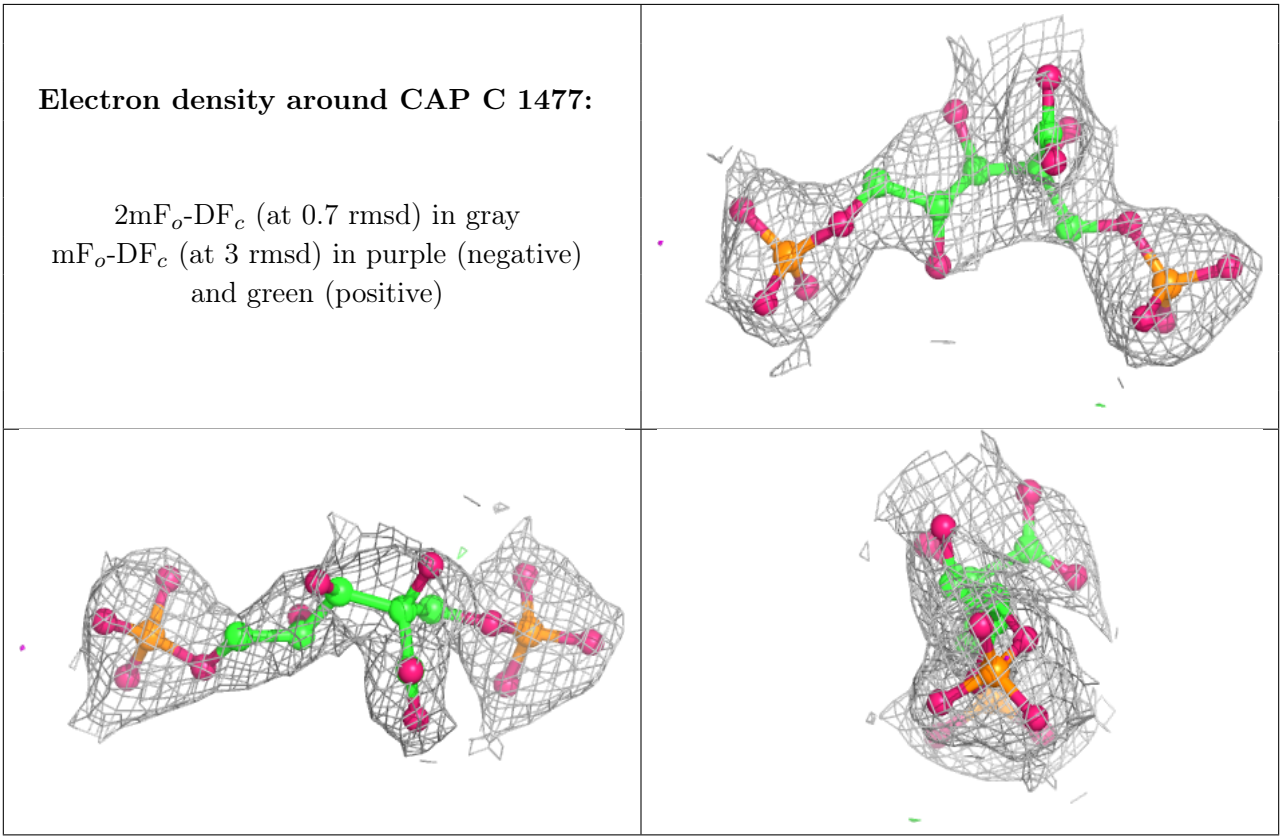
Electron density around CAP A 1477:

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



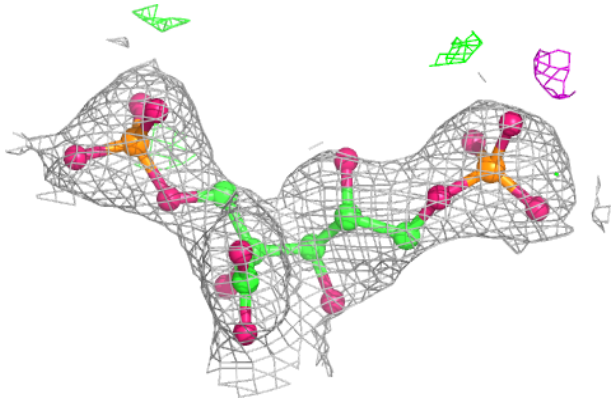
Electron density around CAP C 1477:

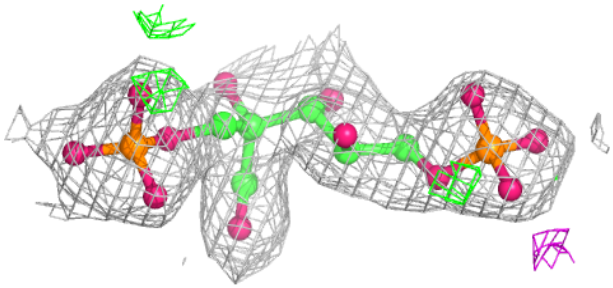
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

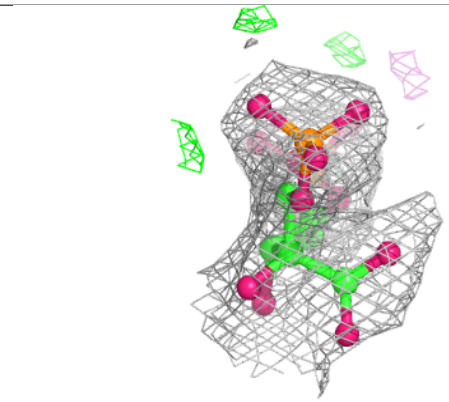


Electron density around CAP H 1477:

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

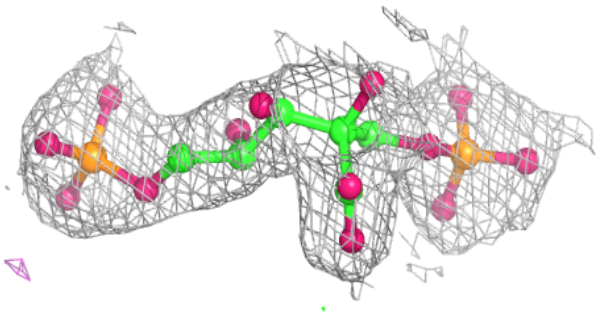


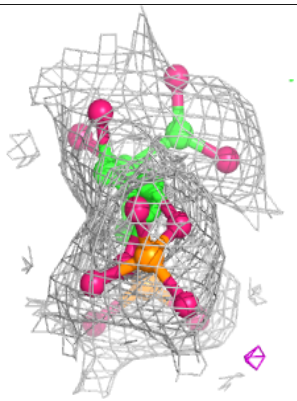




Electron density around CAP D 1477:

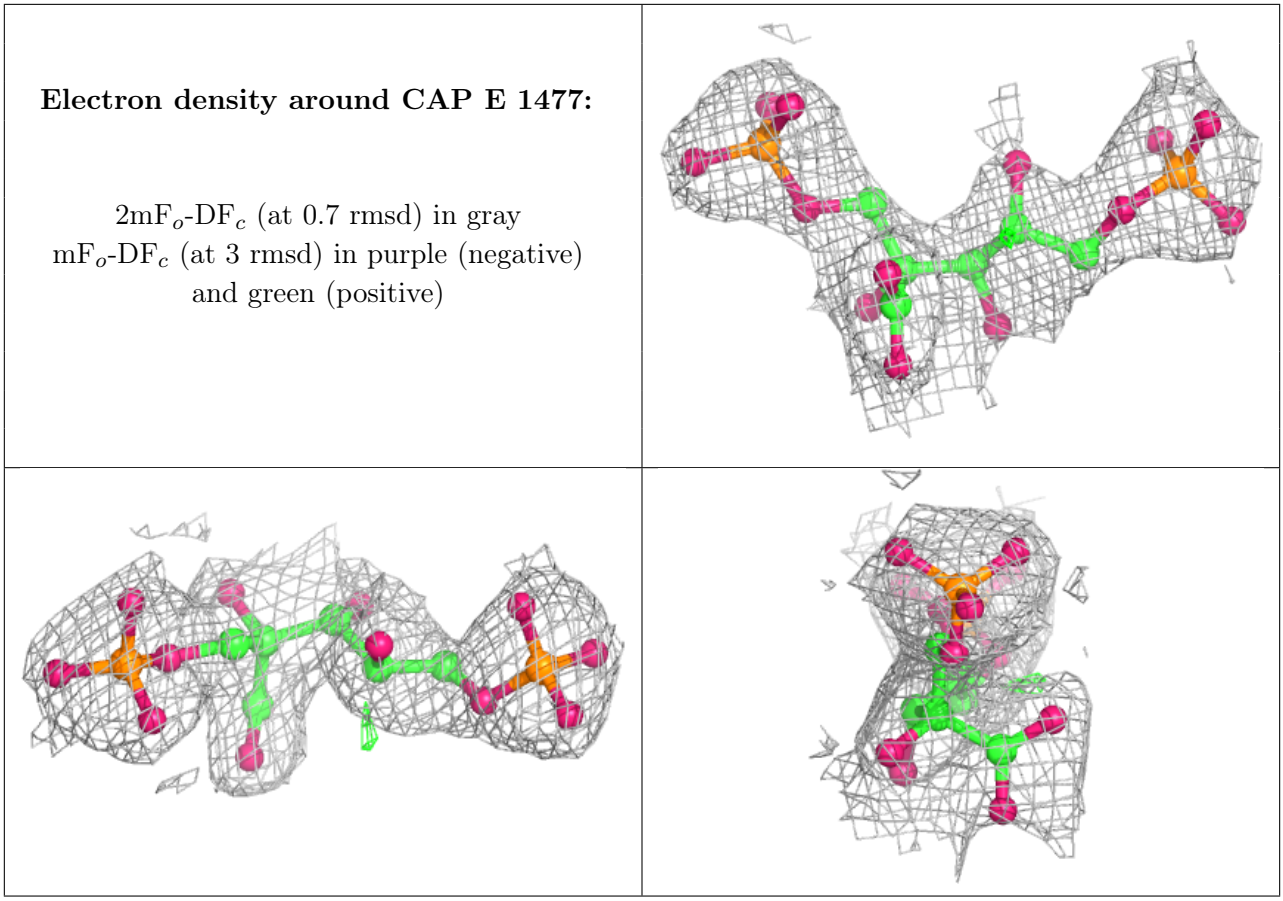
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





Electron density around CAP E 1477:

$2mF_o$-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.