wwPDB X-ray Structure Validation Summary Report (i)

Nov 1, 2023 – 05:26 PM EDT

PDB ID	:	3KDN
Title	:	Crystal structure of Type III Rubisco SP4 mutant complexed with 2-CABP
Authors	:	Nishitani, Y.; Fujihashi, M.; Doi, T.; Yoshida, S.; Atomi, H.; Imanaka, T.; Miki, K.
Deposited on	:	2009-10-23
Resolution	:	2.09 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:

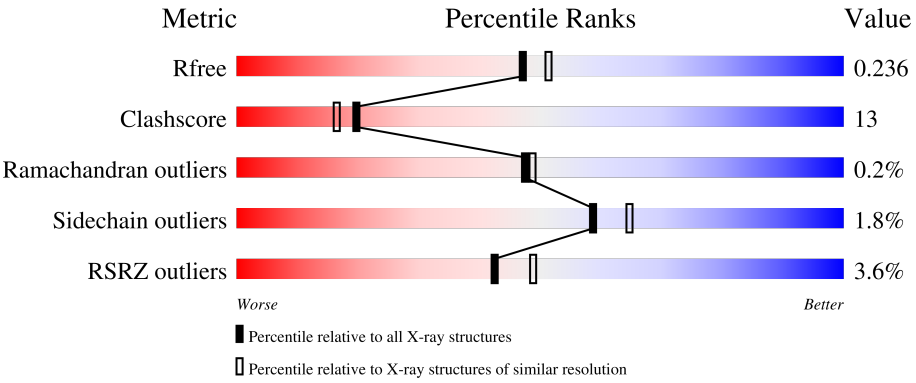
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.09 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.



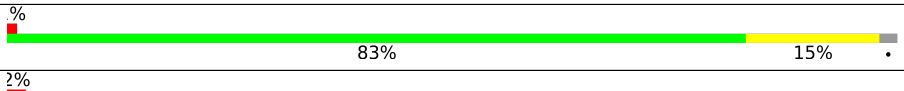
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	444	16% 58% 39%
1	B	444	% 80% 18%
1	C	444	% 79% 19%
1	D	444	2% 78% 20%
1	E	444	3% 79% 19%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	444	
1	G	444	
1	H	444	
1	I	444	
1	J	444	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 36999 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3349	2145	577	617	10			
1	B	437	Total	C	N	O	S	0	0	0
			3430	2201	588	631	10			
1	C	437	Total	C	N	O	S	0	0	0
			3417	2195	585	627	10			
1	D	437	Total	C	N	O	S	0	0	0
			3421	2196	586	629	10			
1	E	438	Total	C	N	O	S	0	0	0
			3428	2197	586	635	10			
1	F	437	Total	C	N	O	S	0	0	0
			3404	2185	586	623	10			
1	G	437	Total	C	N	O	S	0	0	0
			3433	2204	588	631	10			
1	H	438	Total	C	N	O	S	0	0	0
			3396	2182	584	620	10			
1	I	436	Total	C	N	O	S	0	0	0
			3421	2195	586	630	10			
1	J	437	Total	C	N	O	S	0	0	0
			3428	2199	586	633	10			

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	326	GLU	GLY	engineered mutation	UNP O93627
A	327	ARG	LYS	engineered mutation	UNP O93627
A	328	ASP	TRP	engineered mutation	UNP O93627
A	329	ILE	ASP	engineered mutation	UNP O93627
A	330	THR	VAL	engineered mutation	UNP O93627
B	326	GLU	GLY	engineered mutation	UNP O93627
B	327	ARG	LYS	engineered mutation	UNP O93627
B	328	ASP	TRP	engineered mutation	UNP O93627
B	329	ILE	ASP	engineered mutation	UNP O93627

Continued on next page...

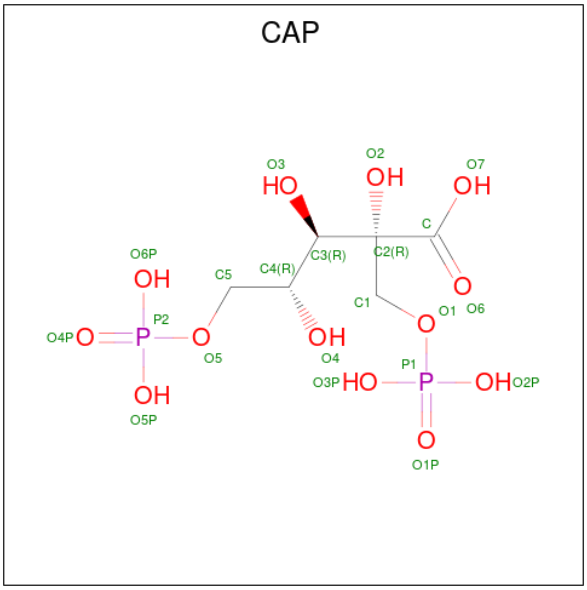
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	330	THR	VAL	engineered mutation	UNP O93627
C	326	GLU	GLY	engineered mutation	UNP O93627
C	327	ARG	LYS	engineered mutation	UNP O93627
C	328	ASP	TRP	engineered mutation	UNP O93627
C	329	ILE	ASP	engineered mutation	UNP O93627
C	330	THR	VAL	engineered mutation	UNP O93627
D	326	GLU	GLY	engineered mutation	UNP O93627
D	327	ARG	LYS	engineered mutation	UNP O93627
D	328	ASP	TRP	engineered mutation	UNP O93627
D	329	ILE	ASP	engineered mutation	UNP O93627
D	330	THR	VAL	engineered mutation	UNP O93627
E	326	GLU	GLY	engineered mutation	UNP O93627
E	327	ARG	LYS	engineered mutation	UNP O93627
E	328	ASP	TRP	engineered mutation	UNP O93627
E	329	ILE	ASP	engineered mutation	UNP O93627
E	330	THR	VAL	engineered mutation	UNP O93627
F	326	GLU	GLY	engineered mutation	UNP O93627
F	327	ARG	LYS	engineered mutation	UNP O93627
F	328	ASP	TRP	engineered mutation	UNP O93627
F	329	ILE	ASP	engineered mutation	UNP O93627
F	330	THR	VAL	engineered mutation	UNP O93627
G	326	GLU	GLY	engineered mutation	UNP O93627
G	327	ARG	LYS	engineered mutation	UNP O93627
G	328	ASP	TRP	engineered mutation	UNP O93627
G	329	ILE	ASP	engineered mutation	UNP O93627
G	330	THR	VAL	engineered mutation	UNP O93627
H	326	GLU	GLY	engineered mutation	UNP O93627
H	327	ARG	LYS	engineered mutation	UNP O93627
H	328	ASP	TRP	engineered mutation	UNP O93627
H	329	ILE	ASP	engineered mutation	UNP O93627
H	330	THR	VAL	engineered mutation	UNP O93627
I	326	GLU	GLY	engineered mutation	UNP O93627
I	327	ARG	LYS	engineered mutation	UNP O93627
I	328	ASP	TRP	engineered mutation	UNP O93627
I	329	ILE	ASP	engineered mutation	UNP O93627
I	330	THR	VAL	engineered mutation	UNP O93627
J	326	GLU	GLY	engineered mutation	UNP O93627
J	327	ARG	LYS	engineered mutation	UNP O93627
J	328	ASP	TRP	engineered mutation	UNP O93627
J	329	ILE	ASP	engineered mutation	UNP O93627
J	330	THR	VAL	engineered mutation	UNP O93627

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (three-letter code: CAP) (formula: $C_6H_{14}O_{13}P_2$).



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

Continued on next page...

Continued from previous page...

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

- Molecule 4 is water.

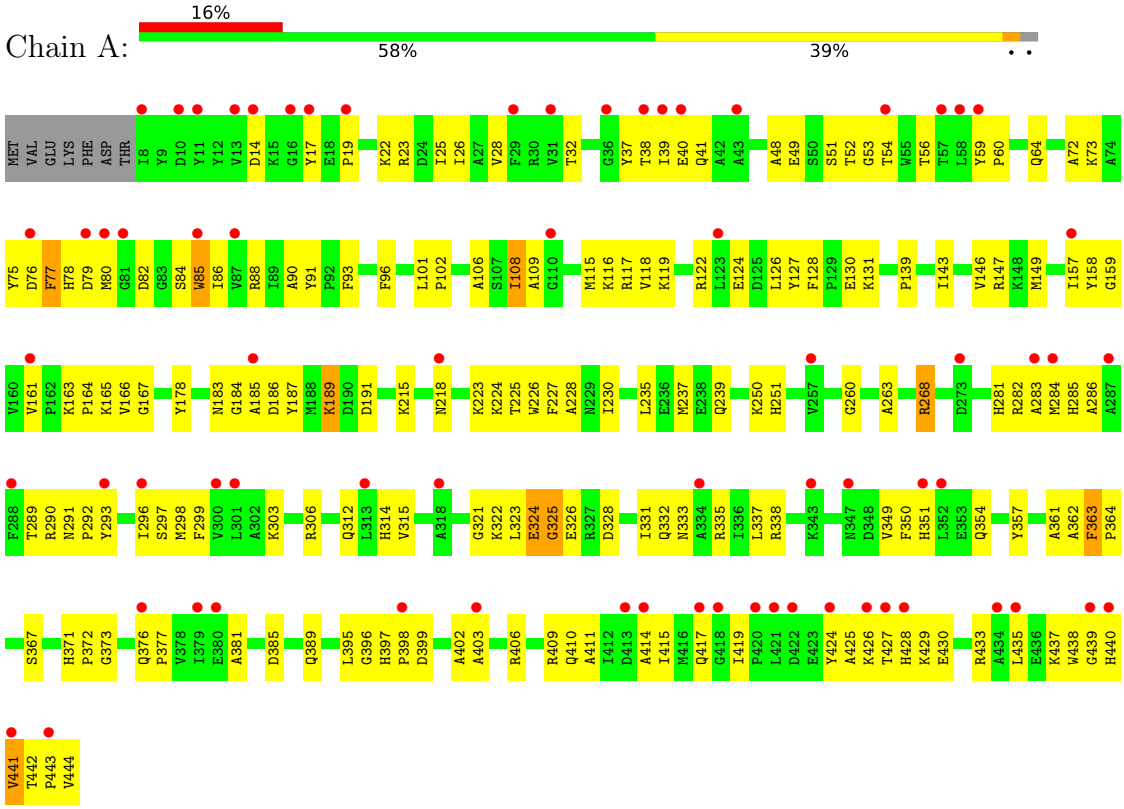
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	173	Total	O	0	0
			173	173		
4	B	290	Total	O	0	0
			290	290		
4	C	311	Total	O	0	0
			311	311		
4	D	308	Total	O	0	0
			308	308		
4	E	258	Total	O	0	0
			258	258		
4	F	268	Total	O	0	0
			268	268		
4	G	267	Total	O	0	0
			267	267		
4	H	185	Total	O	0	0
			185	185		
4	I	291	Total	O	0	0
			291	291		
4	J	301	Total	O	0	0
			301	301		

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.

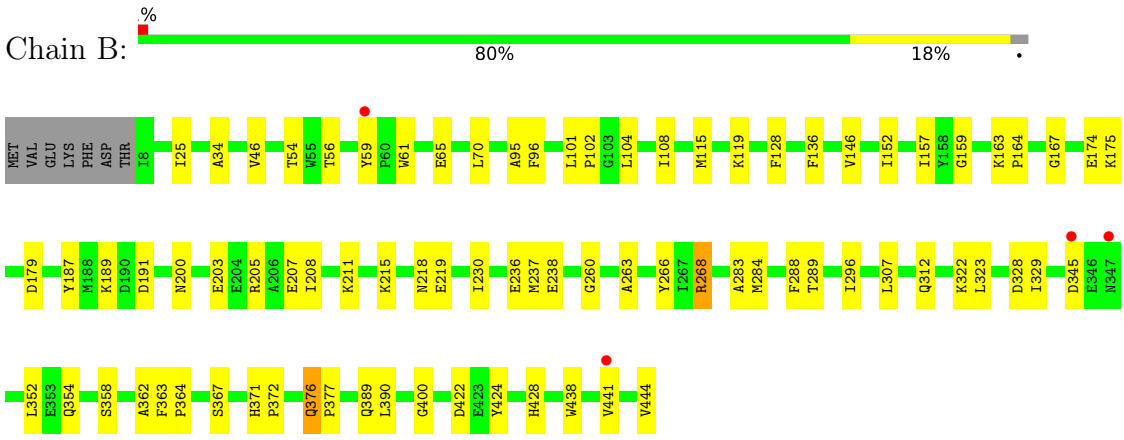
• Molecule 1: Ribulose bisphosphate carboxylase

Chain A:



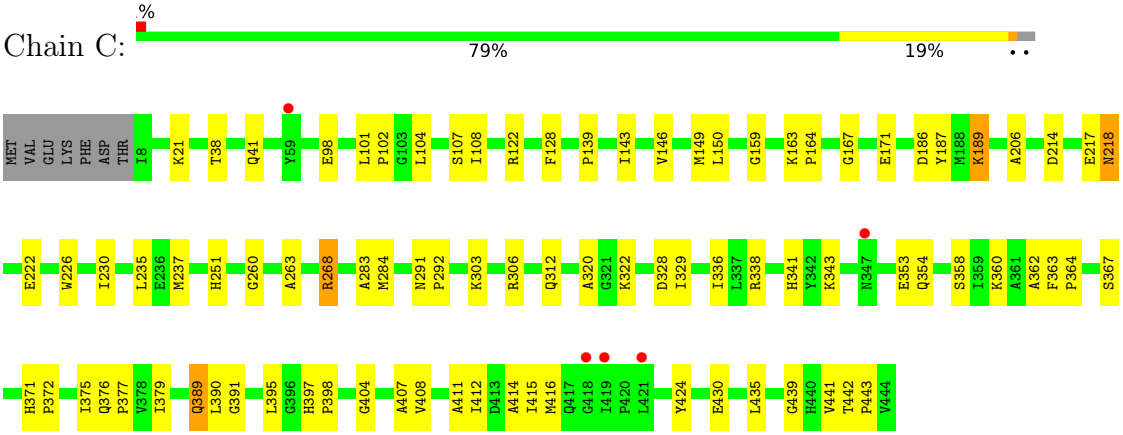
• Molecule 1: Ribulose bisphosphate carboxylase

Chain B:



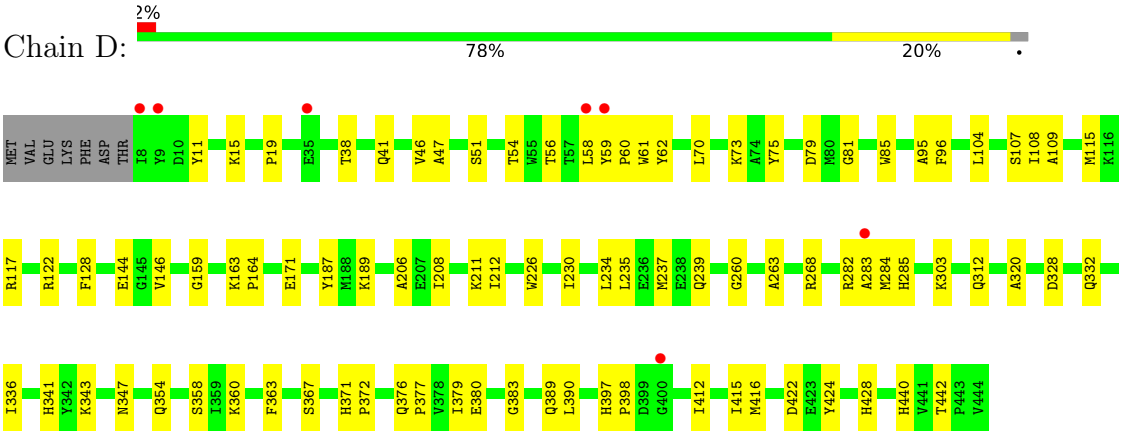
• Molecule 1: Ribulose bisphosphate carboxylase

Chain C:



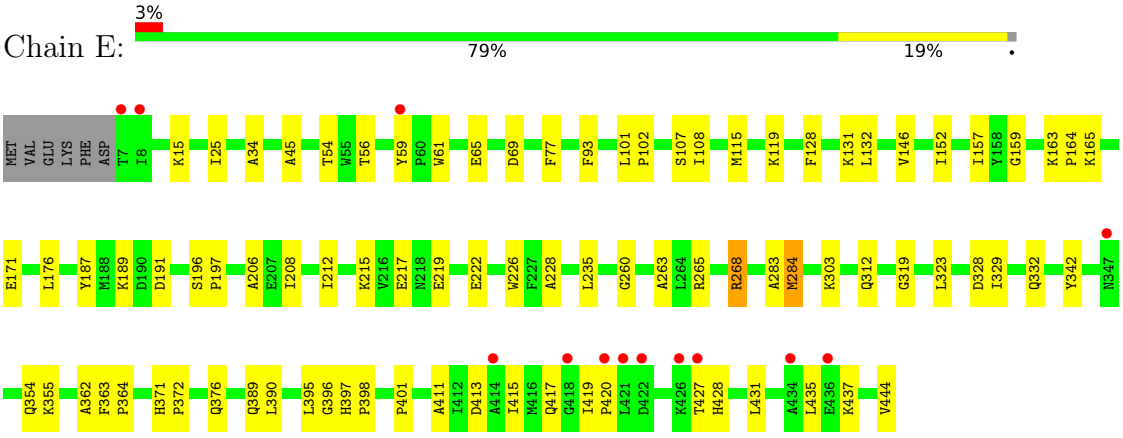
• Molecule 1: Ribulose bisphosphate carboxylase

Chain D:



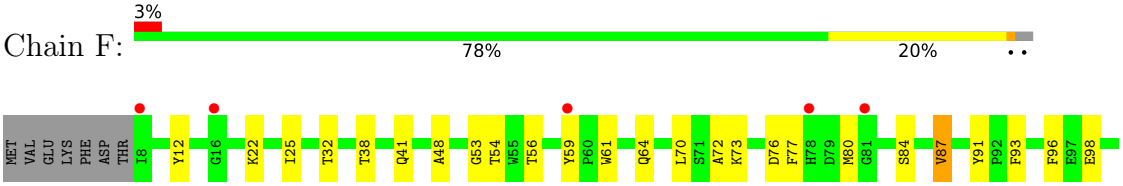
• Molecule 1: Ribulose bisphosphate carboxylase

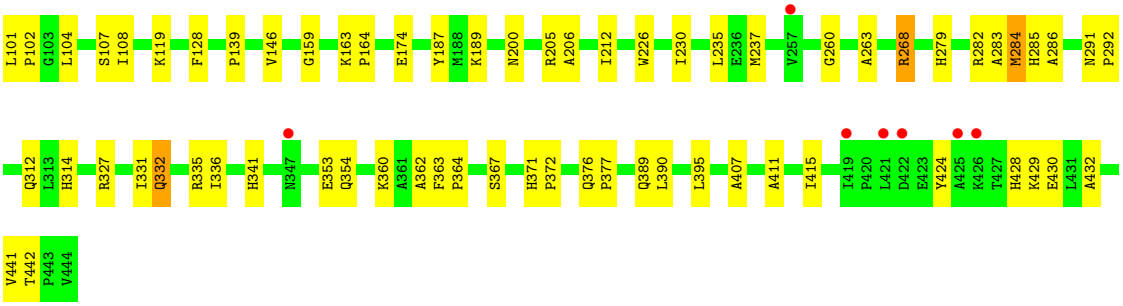
Chain E:



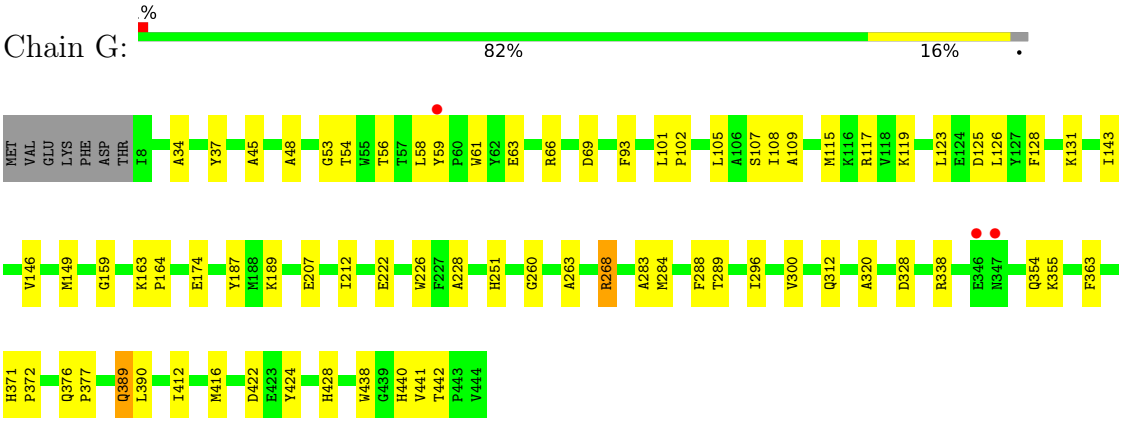
• Molecule 1: Ribulose bisphosphate carboxylase

Chain F:

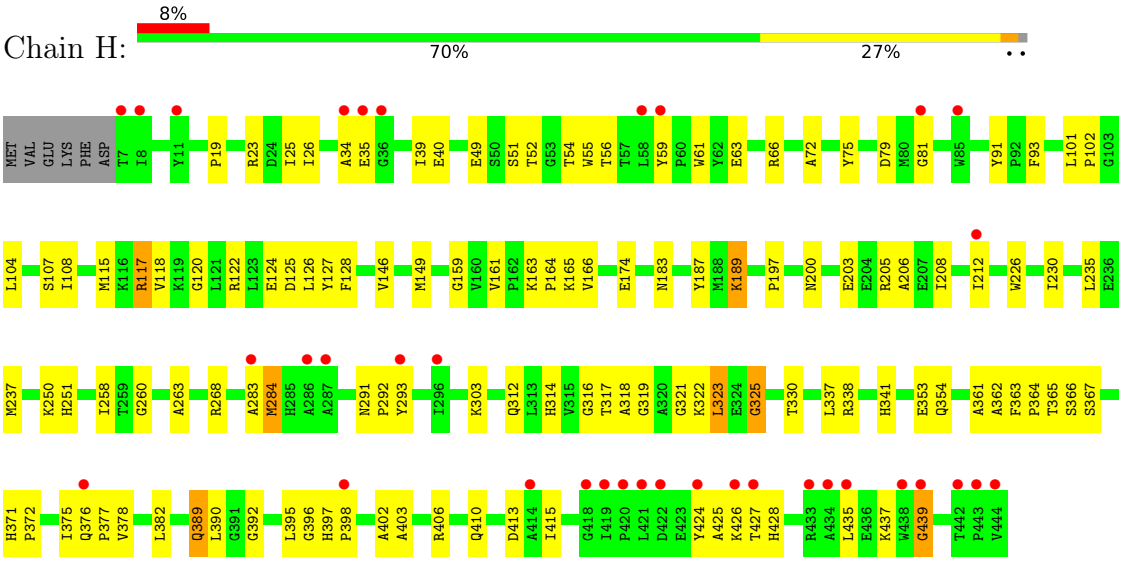




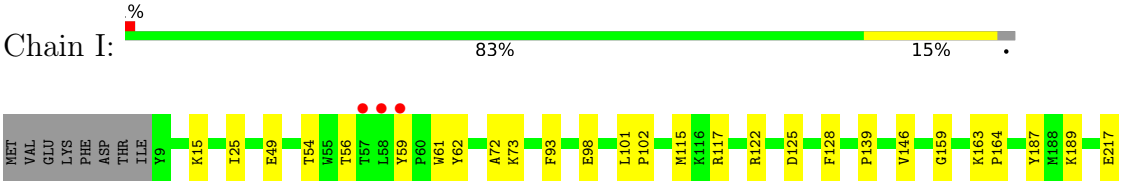
• Molecule 1: Ribulose bisphosphate carboxylase

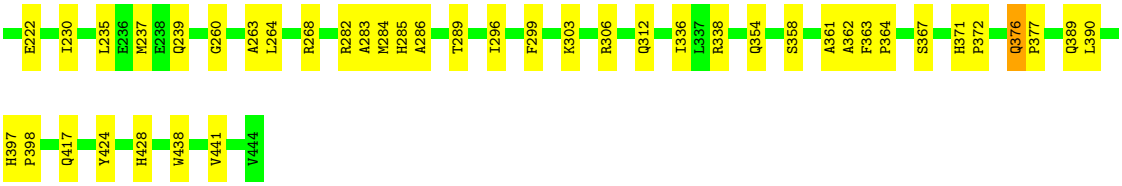


• Molecule 1: Ribulose bisphosphate carboxylase

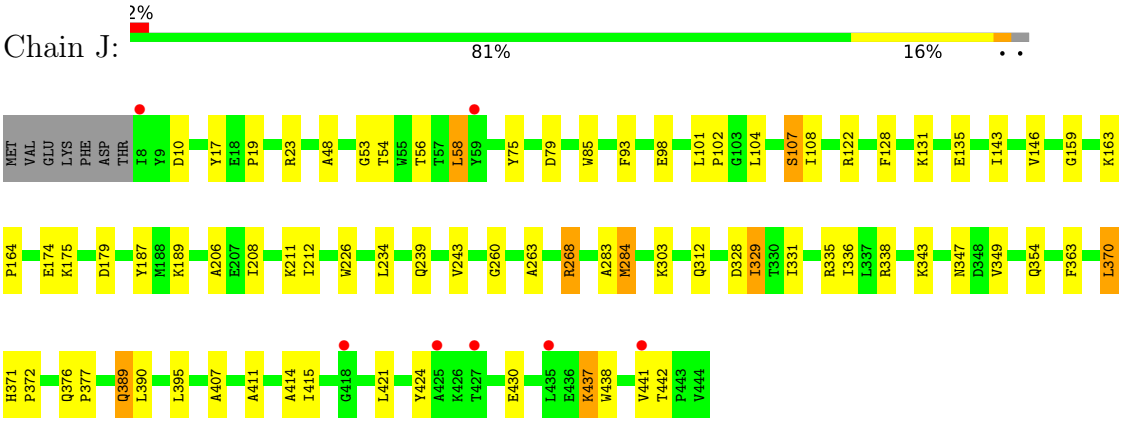


• Molecule 1: Ribulose bisphosphate carboxylase





• Molecule 1: Ribulose bisphosphate carboxylase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	97.47Å 246.24Å 133.08Å 90.00° 104.10° 90.00°	Depositor
Resolution (Å)	42.86 – 2.09 42.86 – 2.09	Depositor EDS
% Data completeness (in resolution range)	96.5 (42.86-2.09) 96.5 (42.86-2.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.76 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.213 , 0.253 0.202 , 0.236	Depositor DCC
R_{free} test set	17388 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	24.6	Xtriage
Anisotropy	0.556	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 55.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	36999	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CAP, KCX, 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	0.23	0/3421	0.40	0/4652
1	B	0.26	0/3505	0.42	0/4753
1	C	0.26	0/3492	0.42	0/4740
1	D	0.27	0/3496	0.44	0/4744
1	E	0.25	0/3503	0.42	0/4753
1	F	0.26	0/3478	0.43	0/4719
1	G	0.25	0/3508	0.43	0/4757
1	H	0.24	0/3471	0.41	0/4713
1	I	0.25	0/3496	0.42	0/4742
1	J	0.26	0/3503	0.43	0/4753
All	All	0.25	0/34873	0.42	0/47326

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	3349	0	3204	204	0
1	B	3430	0	3346	68	0
1	C	3417	0	3325	81	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3421	0	3329	75	0
1	E	3428	0	3319	78	0
1	F	3404	0	3312	70	0
1	G	3433	0	3355	60	0
1	H	3396	0	3282	118	0
1	I	3421	0	3333	56	0
1	J	3428	0	3335	82	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	21	0	7	3	0
3	B	21	0	7	0	0
3	C	21	0	8	1	0
3	D	21	0	8	0	0
3	E	21	0	7	0	0
3	F	21	0	8	0	0
3	G	21	0	8	0	0
3	H	21	0	8	1	0
3	I	21	0	7	0	0
3	J	21	0	7	0	0
4	A	173	0	0	9	0
4	B	290	0	0	5	0
4	C	311	0	0	7	0
4	D	308	0	0	6	0
4	E	258	0	0	9	0
4	F	268	0	0	10	0
4	G	267	0	0	4	0
4	H	185	0	0	9	0
4	I	291	0	0	8	0
4	J	301	0	0	9	0
All	All	36999	0	33215	856	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 13.

The worst 5 of 856 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:MET:HE3	1:A:250:LYS:CD	1.57	1.31
1:A:38:THR:HG23	1:A:41:GLN:OE1	1.53	1.07
1:A:149:MET:HE3	1:A:250:LYS:HD2	1.07	1.04
1:A:438:TRP:O	1:A:441:VAL:HG12	1.58	1.03
1:A:424:TYR:CE2	1:A:428:HIS:CE1	2.46	1.03

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	434/444 (98%)	394 (91%)	37 (8%)	3 (1%)	22	18
1	B	434/444 (98%)	418 (96%)	16 (4%)	0	100	100
1	C	434/444 (98%)	419 (96%)	15 (4%)	0	100	100
1	D	434/444 (98%)	422 (97%)	12 (3%)	0	100	100
1	E	435/444 (98%)	418 (96%)	16 (4%)	1 (0%)	47	49
1	F	434/444 (98%)	419 (96%)	14 (3%)	1 (0%)	47	49
1	G	434/444 (98%)	419 (96%)	15 (4%)	0	100	100
1	H	435/444 (98%)	399 (92%)	32 (7%)	4 (1%)	17	12
1	I	433/444 (98%)	418 (96%)	15 (4%)	0	100	100
1	J	434/444 (98%)	420 (97%)	13 (3%)	1 (0%)	47	49
All	All	4341/4440 (98%)	4146 (96%)	185 (4%)	10 (0%)	47	49

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	426	LYS
1	E	284	MET
1	J	284	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	117	ARG
1	A	325	GLY

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	323/356 (91%)	316 (98%)	7 (2%)	52	57
1	B	341/356 (96%)	336 (98%)	5 (2%)	65	71
1	C	338/356 (95%)	332 (98%)	6 (2%)	59	65
1	D	339/356 (95%)	333 (98%)	6 (2%)	59	65
1	E	339/356 (95%)	334 (98%)	5 (2%)	65	71
1	F	335/356 (94%)	328 (98%)	7 (2%)	53	59
1	G	342/356 (96%)	336 (98%)	6 (2%)	59	65
1	H	330/356 (93%)	323 (98%)	7 (2%)	53	59
1	I	340/356 (96%)	338 (99%)	2 (1%)	86	90
1	J	341/356 (96%)	331 (97%)	10 (3%)	42	46
All	All	3368/3560 (95%)	3307 (98%)	61 (2%)	59	65

5 of 61 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	363	PHE
1	J	268	ARG
1	F	363	PHE
1	J	122	ARG
1	J	389	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	312	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	354	GLN
1	I	376	GLN
1	C	376	GLN
1	C	354	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)

10 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	KCX	I	189	2,1	9,11,12	0.96	0	5,12,14	1.46	1 (20%)
1	KCX	G	189	2,1	9,11,12	0.93	0	5,12,14	1.46	1 (20%)
1	KCX	H	189	2,1	9,11,12	0.81	0	5,12,14	1.39	1 (20%)
1	KCX	A	189	2,1	9,11,12	0.88	0	5,12,14	1.41	1 (20%)
1	KCX	E	189	2,1	9,11,12	0.86	0	5,12,14	1.52	1 (20%)
1	KCX	J	189	2,1	9,11,12	0.85	0	5,12,14	1.46	1 (20%)
1	KCX	C	189	2,1	9,11,12	0.88	0	5,12,14	1.24	1 (20%)
1	KCX	B	189	2,1	9,11,12	0.91	0	5,12,14	1.27	1 (20%)
1	KCX	D	189	2,1	9,11,12	0.86	0	5,12,14	1.56	1 (20%)
1	KCX	F	189	2,1	9,11,12	0.95	0	5,12,14	1.48	1 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	I	189	2,1	-	0/9/10/12	-
1	KCX	G	189	2,1	-	0/9/10/12	-
1	KCX	H	189	2,1	-	0/9/10/12	-
1	KCX	A	189	2,1	-	0/9/10/12	-
1	KCX	E	189	2,1	-	0/9/10/12	-
1	KCX	J	189	2,1	-	0/9/10/12	-
1	KCX	C	189	2,1	-	0/9/10/12	-
1	KCX	B	189	2,1	-	0/9/10/12	-
1	KCX	D	189	2,1	-	0/9/10/12	-
1	KCX	F	189	2,1	-	0/9/10/12	-

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	189	KCX	OQ1-CX-NZ	-3.41	119.67	124.96
1	F	189	KCX	OQ1-CX-NZ	-3.19	120.02	124.96
1	G	189	KCX	OQ1-CX-NZ	-3.17	120.05	124.96
1	E	189	KCX	OQ1-CX-NZ	-3.16	120.06	124.96
1	J	189	KCX	OQ1-CX-NZ	-3.13	120.10	124.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	H	189	KCX	1	0
1	A	189	KCX	1	0
1	C	189	KCX	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
3	CAP	H	600	2	17,20,20	0.82	0	22,31,31	0.74	0
3	CAP	F	600	2	17,20,20	0.85	0	22,31,31	0.81	0
3	CAP	C	600	2	17,20,20	0.88	0	22,31,31	0.75	0
3	CAP	J	600	2	17,20,20	0.90	0	22,31,31	0.74	0
3	CAP	B	600	2	17,20,20	0.82	0	22,31,31	0.81	0
3	CAP	D	600	2	17,20,20	0.84	0	22,31,31	0.79	0
3	CAP	A	600	2	17,20,20	0.86	0	22,31,31	0.85	0
3	CAP	I	600	2	17,20,20	0.85	0	22,31,31	0.76	0
3	CAP	E	600	2	17,20,20	0.85	0	22,31,31	0.83	0
3	CAP	G	600	2	17,20,20	0.80	0	22,31,31	0.78	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
3	CAP	H	600	2	-	11/29/29/29	-
3	CAP	F	600	2	-	6/29/29/29	-
3	CAP	C	600	2	-	6/29/29/29	-
3	CAP	J	600	2	-	6/29/29/29	-
3	CAP	B	600	2	-	8/29/29/29	-
3	CAP	D	600	2	-	10/29/29/29	-
3	CAP	A	600	2	-	6/29/29/29	-
3	CAP	I	600	2	-	6/29/29/29	-
3	CAP	E	600	2	-	6/29/29/29	-
3	CAP	G	600	2	-	6/29/29/29	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	600	CAP	O6-C-C2-C1
3	A	600	CAP	O7-C-C2-C1
3	A	600	CAP	O6-C-C2-O2
3	A	600	CAP	O7-C-C2-O2
3	B	600	CAP	O6-C-C2-C1

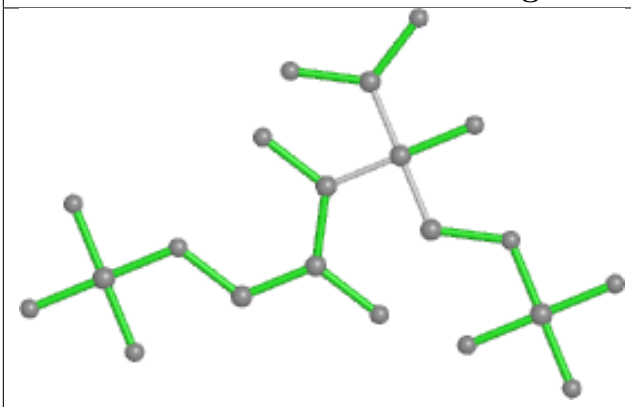
There are no ring outliers.

3 monomers are involved in 5 short contacts:

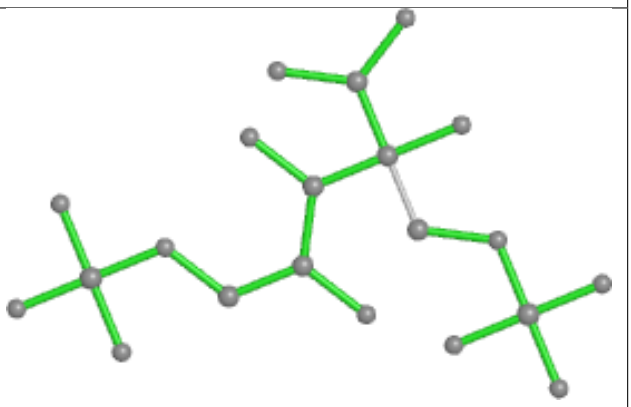
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	600	CAP	1	0
3	C	600	CAP	1	0
3	A	600	CAP	3	0

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.

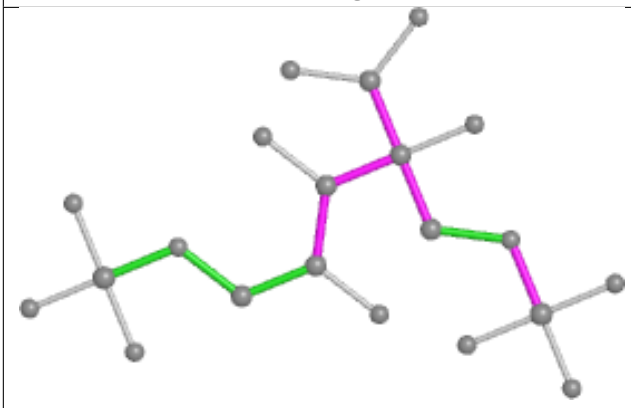
Ligand CAP H 600



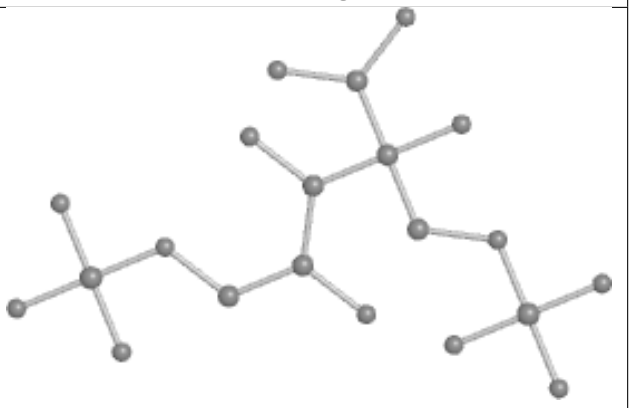
Bond lengths



Bond angles

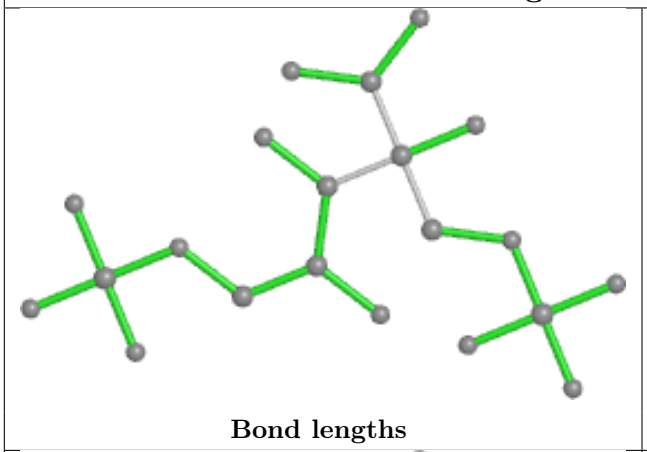


Torsions

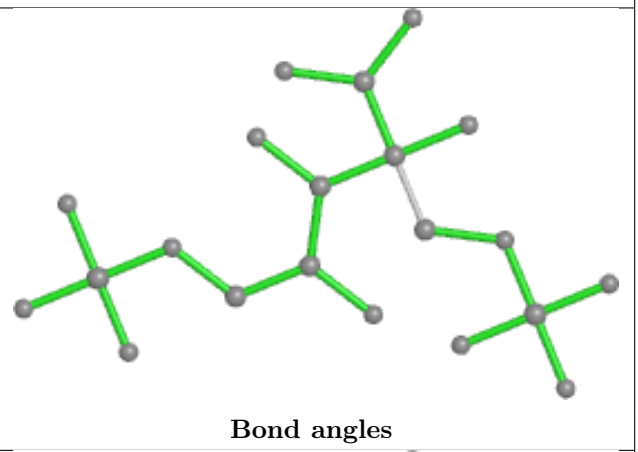


Rings

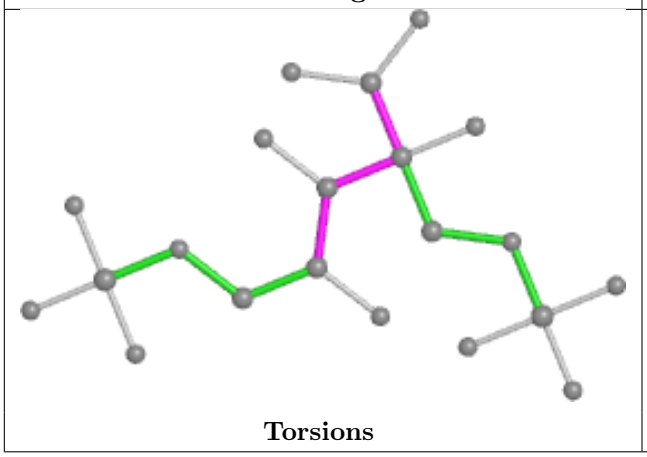
Ligand CAP F 600



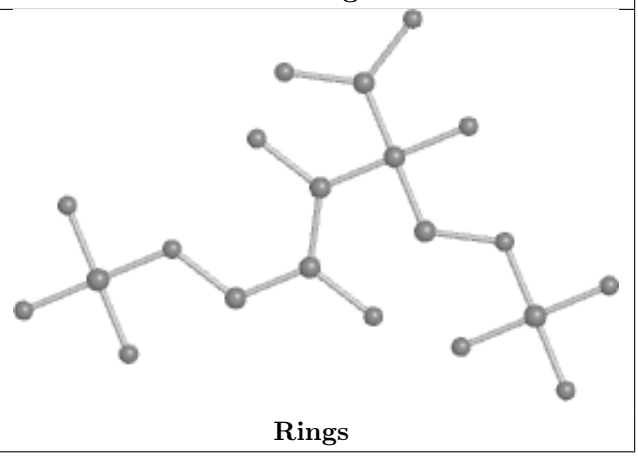
Bond lengths



Bond angles

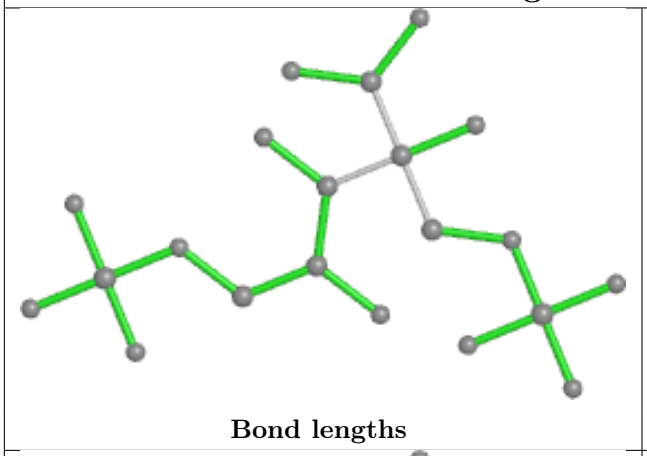


Torsions

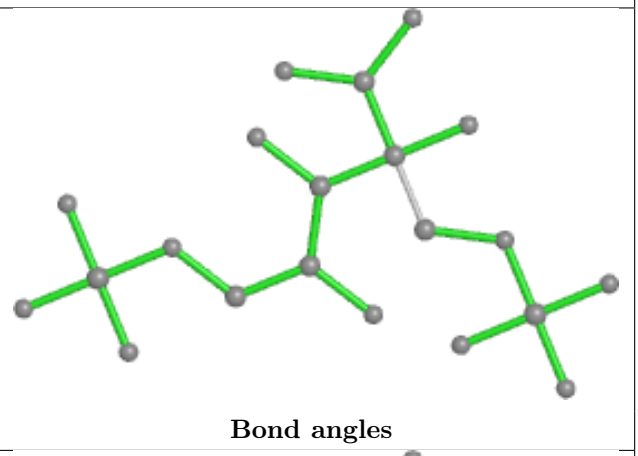


Rings

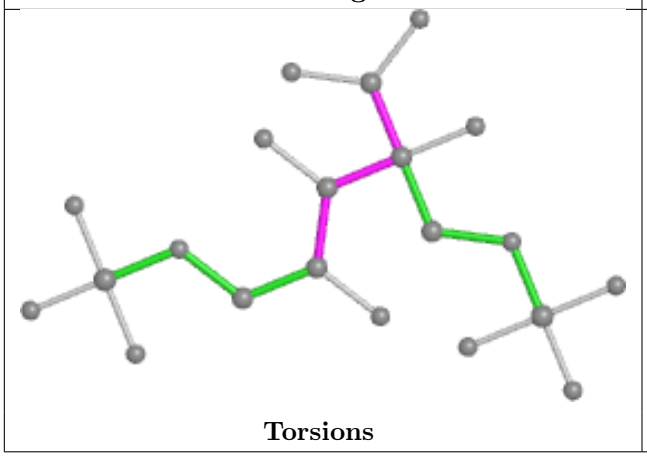
Ligand CAP C 600



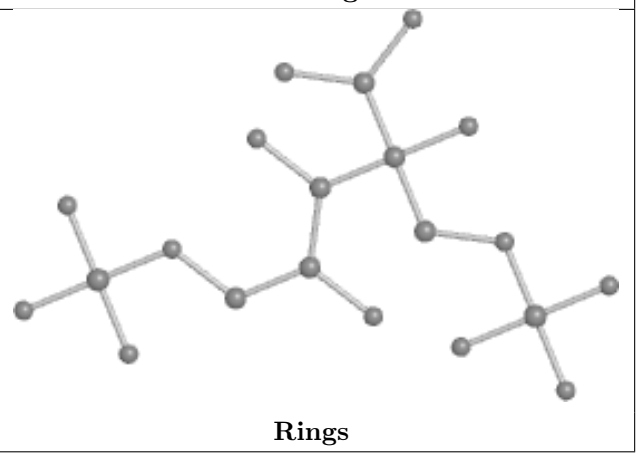
Bond lengths



Bond angles

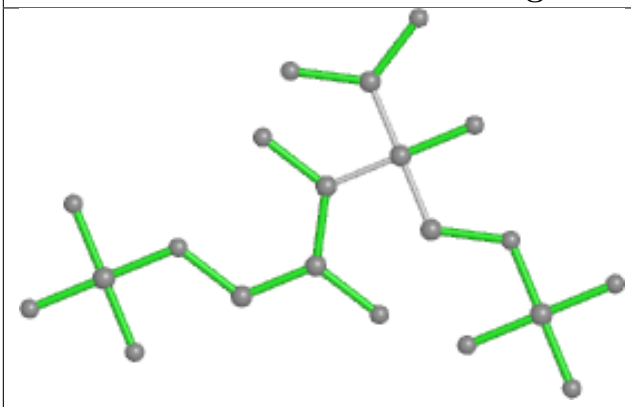


Torsions

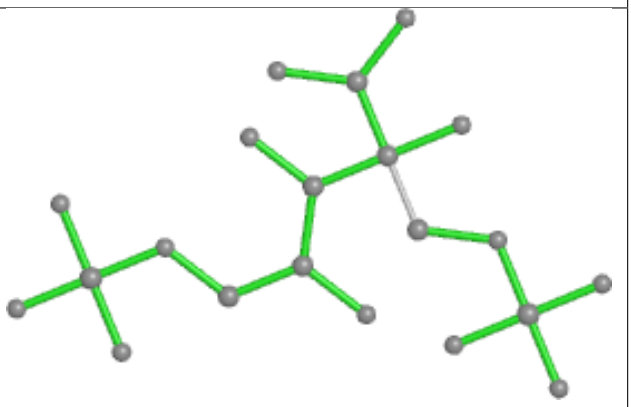


Rings

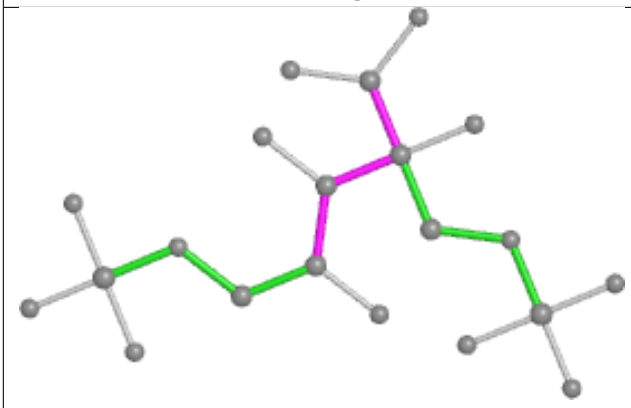
Ligand CAP J 600



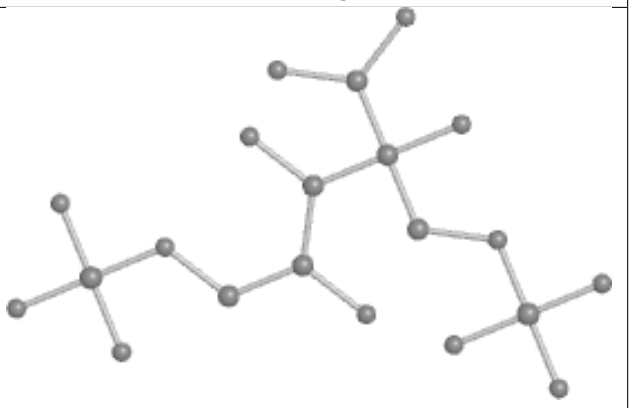
Bond lengths



Bond angles

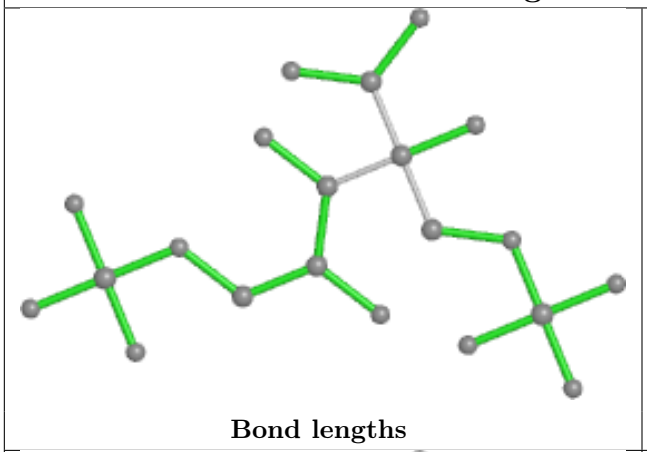


Torsions

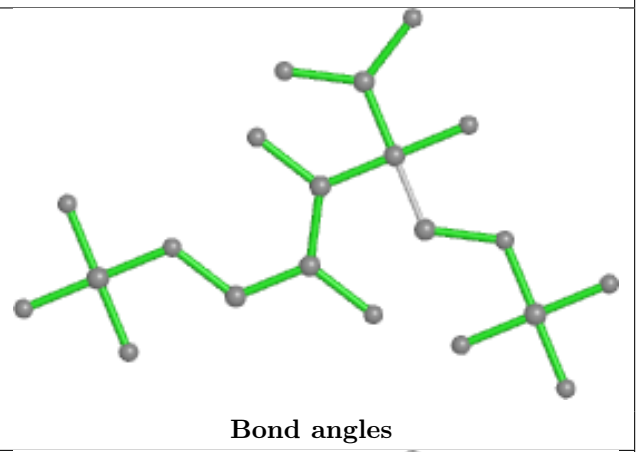


Rings

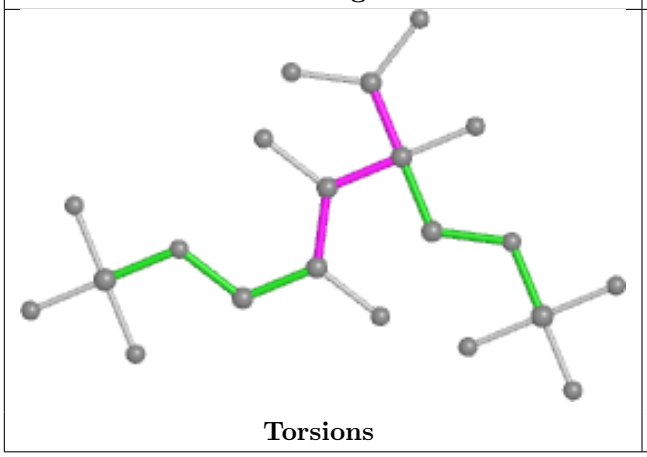
Ligand CAP B 600



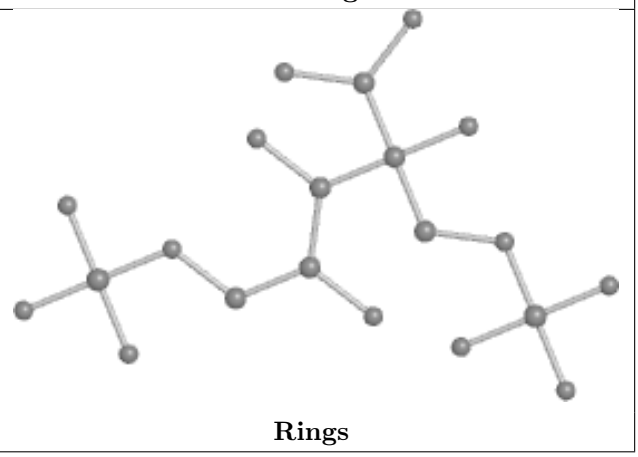
Bond lengths



Bond angles

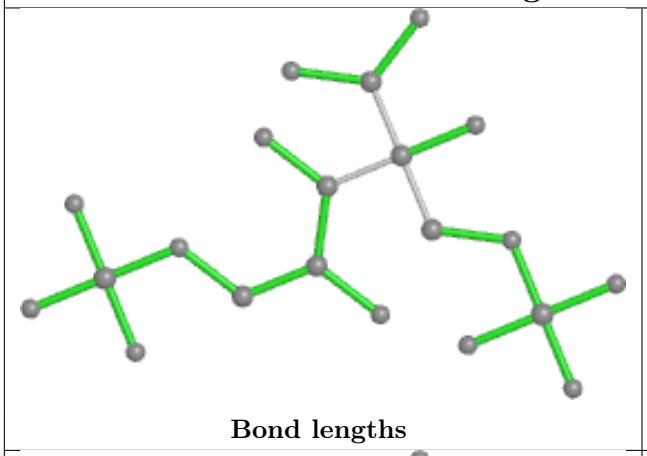


Torsions

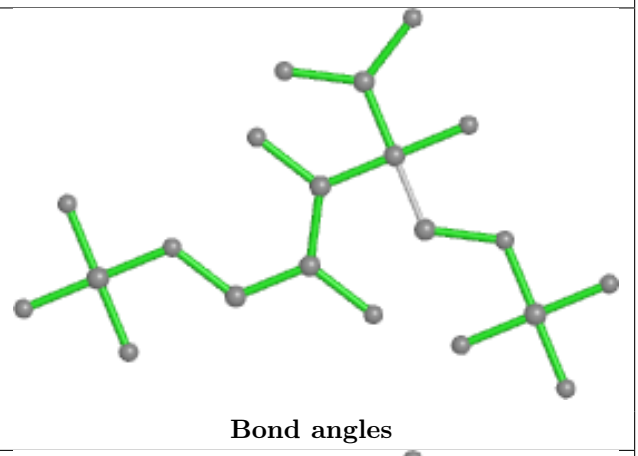


Rings

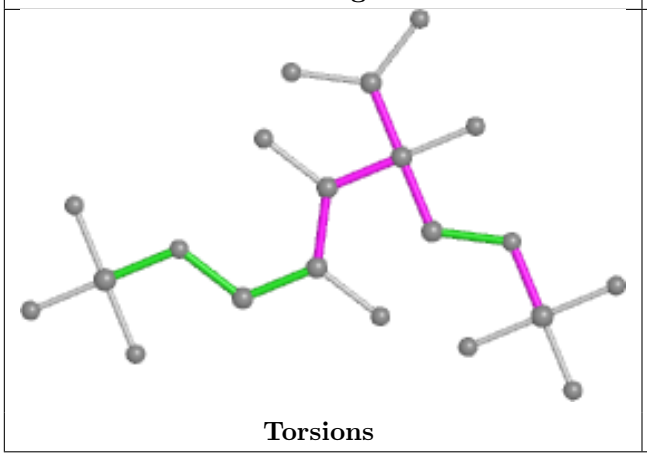
Ligand CAP D 600



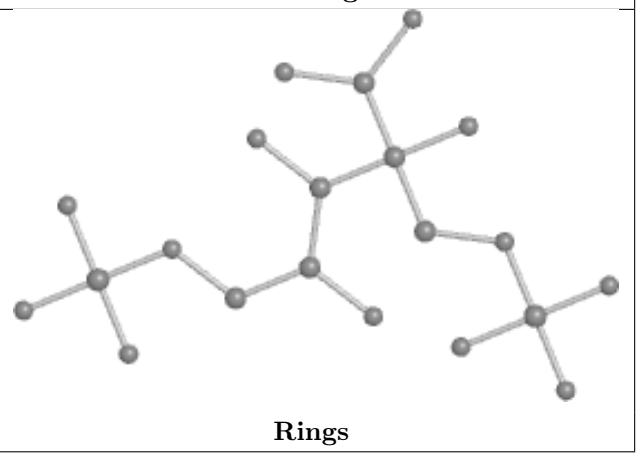
Bond lengths



Bond angles

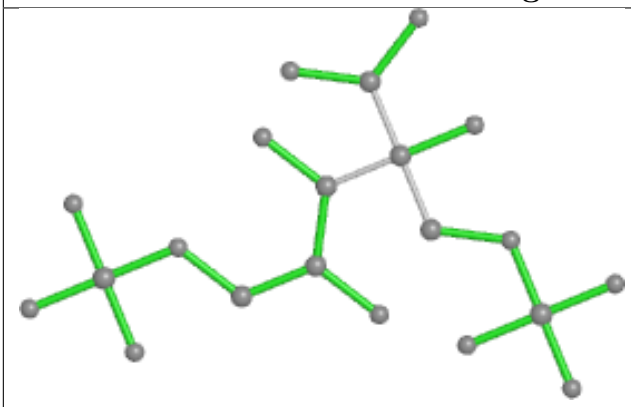


Torsions

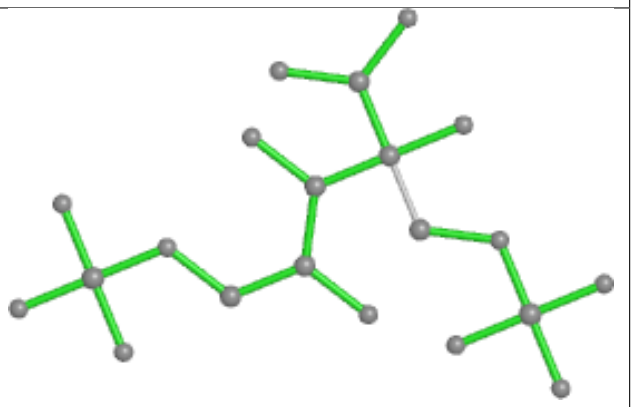


Rings

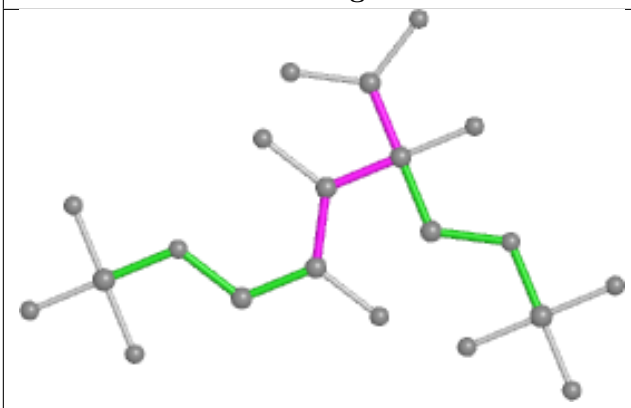
Ligand CAP A 600



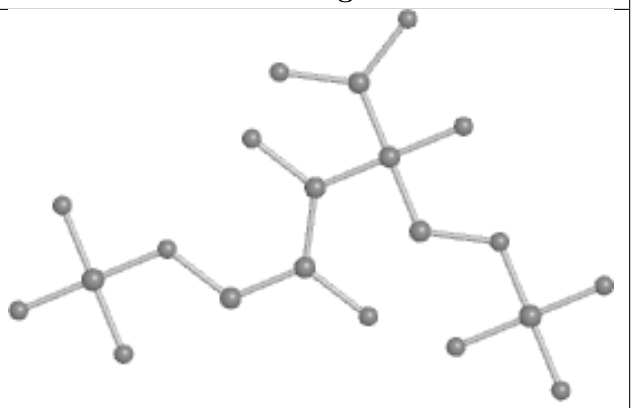
Bond lengths



Bond angles

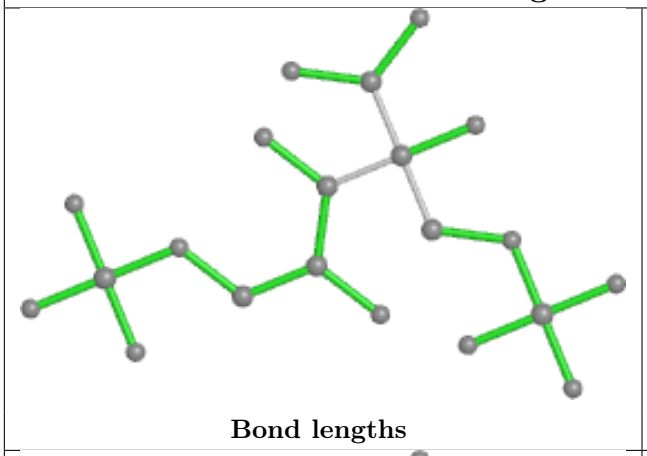


Torsions

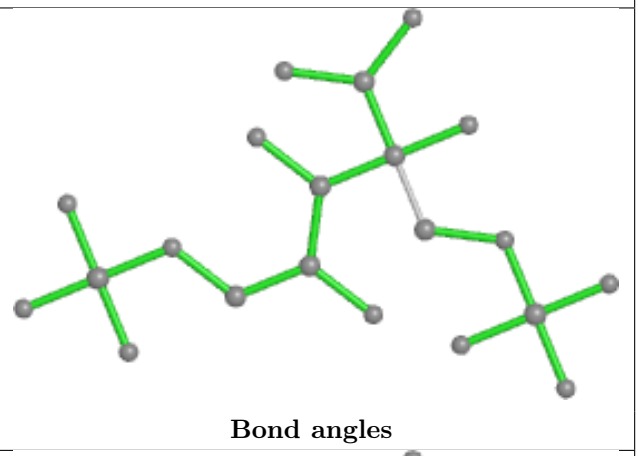


Rings

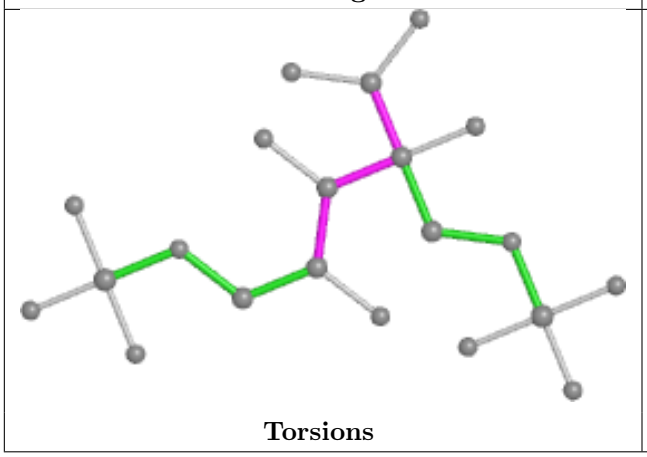
Ligand CAP I 600



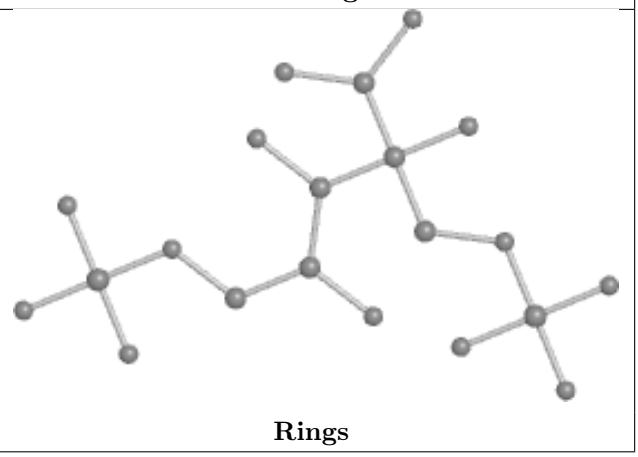
Bond lengths



Bond angles

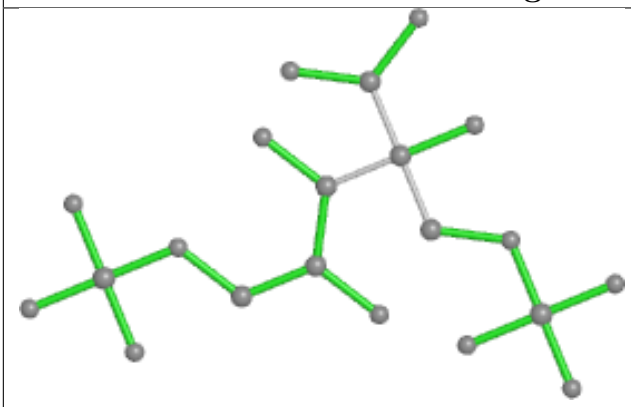


Torsions

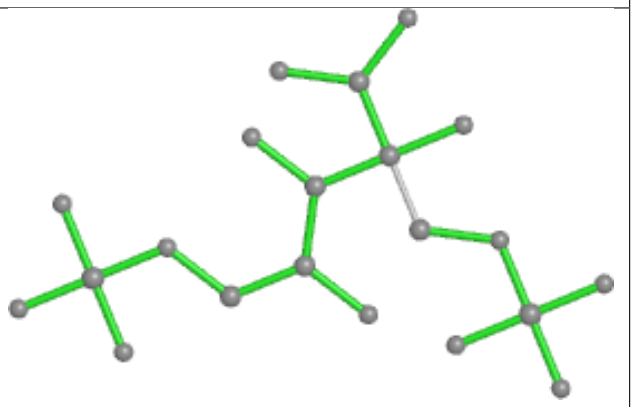


Rings

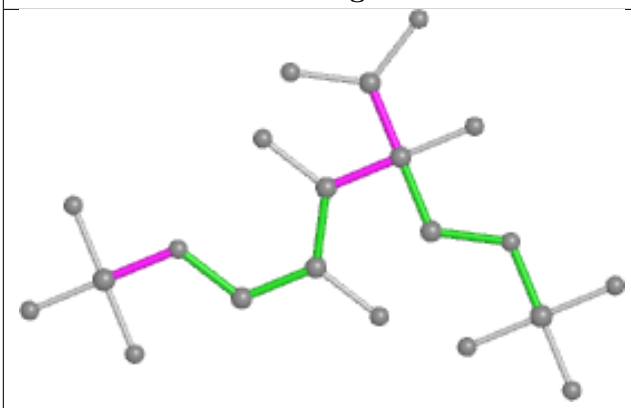
Ligand CAP E 600



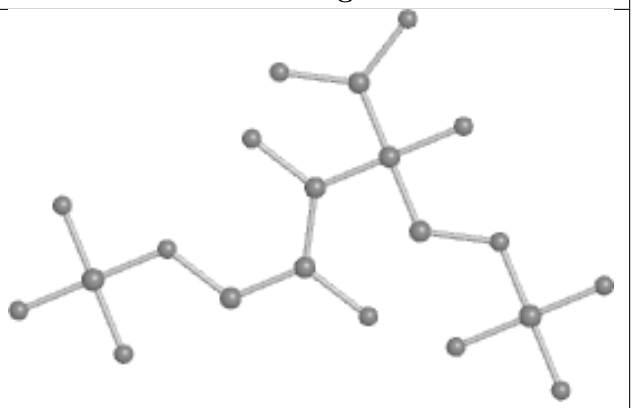
Bond lengths



Bond angles

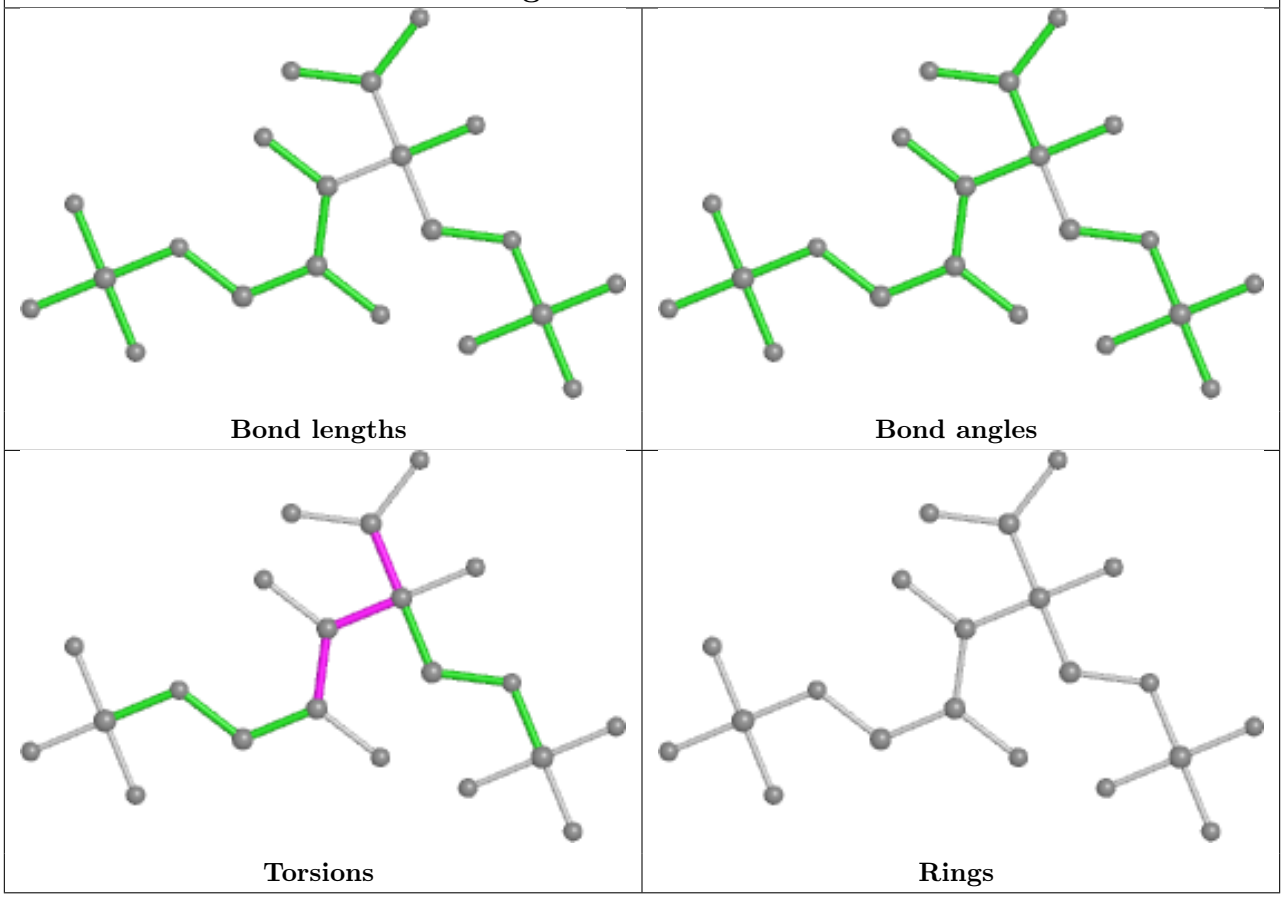


Torsions



Rings

Ligand CAP G 600



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	436/444 (98%)	0.92	70 (16%) 1 2	22, 36, 52, 58	0
1	B	436/444 (98%)	-0.15	4 (0%) 84 86	13, 22, 34, 37	0
1	C	436/444 (98%)	-0.05	5 (1%) 80 84	12, 21, 40, 45	0
1	D	436/444 (98%)	-0.09	7 (1%) 72 75	11, 20, 32, 39	0
1	E	437/444 (98%)	-0.01	13 (2%) 50 56	15, 24, 47, 51	0
1	F	436/444 (98%)	0.14	12 (2%) 53 59	12, 24, 38, 46	0
1	G	436/444 (98%)	-0.05	3 (0%) 87 89	13, 24, 36, 41	0
1	H	437/444 (98%)	0.57	35 (8%) 12 16	22, 32, 57, 61	0
1	I	435/444 (97%)	-0.13	3 (0%) 87 89	15, 23, 34, 40	0
1	J	436/444 (98%)	-0.07	7 (1%) 72 75	11, 20, 41, 47	0
All	All	4361/4440 (98%)	0.11	159 (3%) 42 49	11, 24, 42, 61	0

The worst 5 of 159 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	59	TYR	5.8
1	A	59	TYR	5.4
1	E	7	THR	4.7
1	D	59	TYR	4.6
1	F	59	TYR	4.6

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{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
1	KCX	A	189	12/13	0.93	0.20	29,30,31,31	0
1	KCX	H	189	12/13	0.93	0.13	30,30,31,31	0
1	KCX	E	189	12/13	0.96	0.11	21,22,23,23	0
1	KCX	F	189	12/13	0.96	0.19	17,18,20,20	0
1	KCX	C	189	12/13	0.96	0.11	14,16,17,17	0
1	KCX	D	189	12/13	0.97	0.14	11,14,15,15	0
1	KCX	I	189	12/13	0.97	0.11	17,18,18,18	0
1	KCX	B	189	12/13	0.98	0.11	18,19,19,20	0
1	KCX	G	189	12/13	0.98	0.13	16,17,17,17	0
1	KCX	J	189	12/13	0.98	0.13	18,18,19,20	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{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
3	CAP	H	600	21/21	0.90	0.16	31,34,36,37	0
3	CAP	A	600	21/21	0.92	0.15	27,33,34,35	0
2	MG	A	500	1/1	0.94	0.11	29,29,29,29	0
3	CAP	J	600	21/21	0.96	0.13	17,21,22,22	0
3	CAP	B	600	21/21	0.97	0.09	17,20,21,22	0
3	CAP	E	600	21/21	0.97	0.10	21,24,26,26	0
3	CAP	G	600	21/21	0.97	0.11	17,17,18,18	0
2	MG	H	500	1/1	0.97	0.09	29,29,29,29	0
2	MG	G	500	1/1	0.97	0.05	16,16,16,16	0
2	MG	B	500	1/1	0.98	0.07	18,18,18,18	0
2	MG	C	500	1/1	0.98	0.07	16,16,16,16	0
3	CAP	C	600	21/21	0.98	0.10	19,21,22,23	0
3	CAP	I	600	21/21	0.98	0.11	16,18,18,19	0
3	CAP	D	600	21/21	0.98	0.10	13,14,15,16	0
2	MG	J	500	1/1	0.99	0.09	16,16,16,16	0
2	MG	E	500	1/1	0.99	0.07	21,21,21,21	0
2	MG	I	500	1/1	0.99	0.07	13,13,13,13	0
3	CAP	F	600	21/21	0.99	0.12	15,17,17,18	0
2	MG	D	500	1/1	1.00	0.06	11,11,11,11	0

Continued on next page...

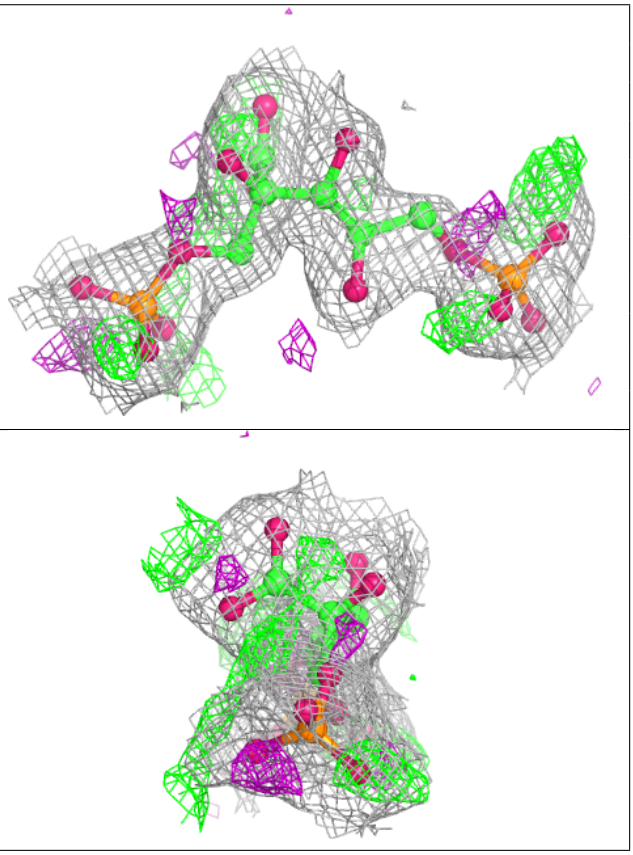
Continued from previous page...

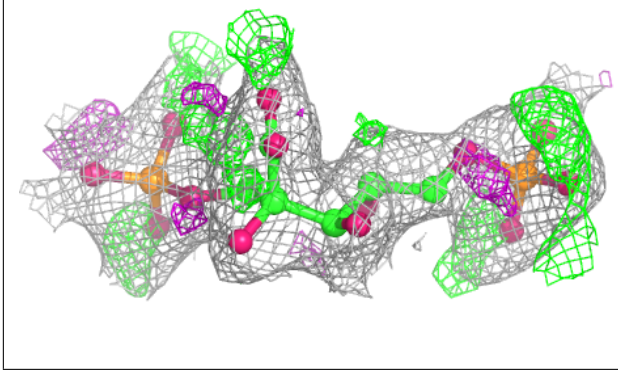
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MG	F	500	1/1	1.00	0.09	19,19,19,19	0

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

Electron density around CAP H 600:

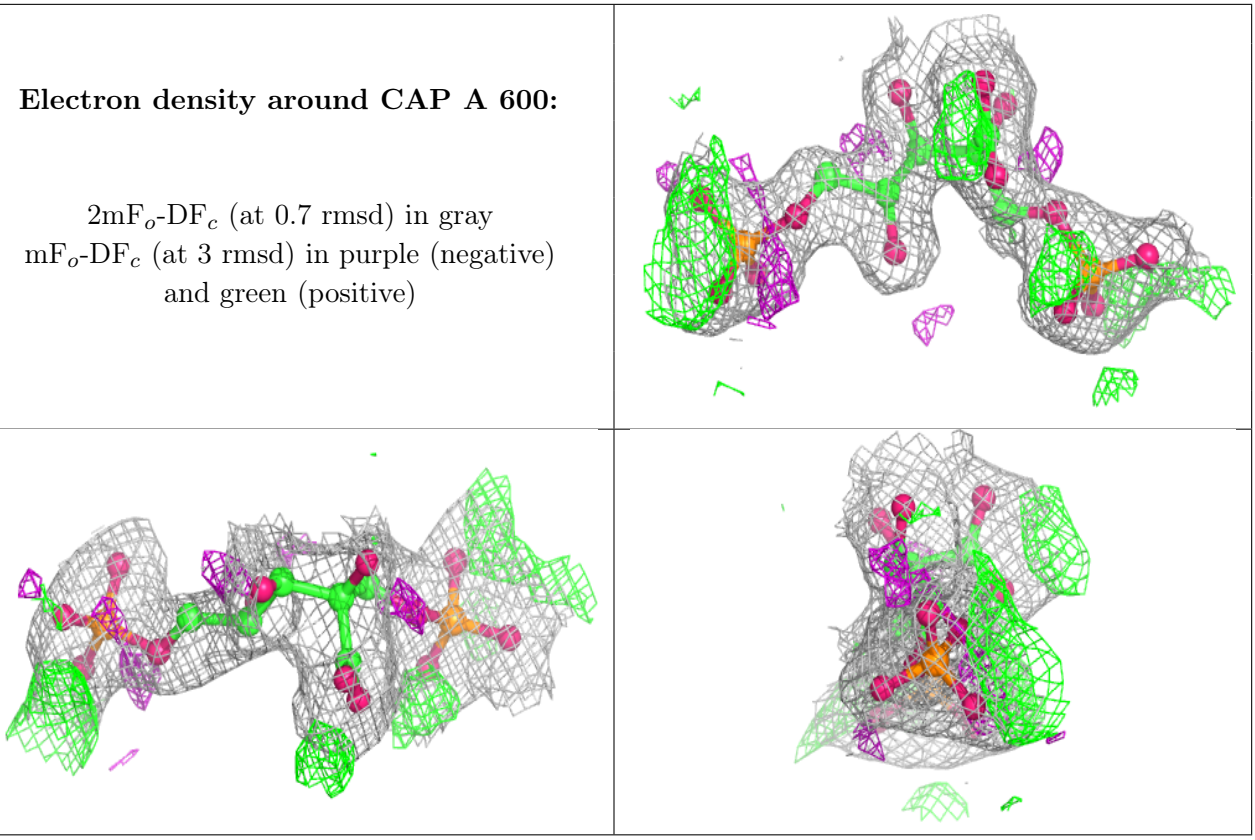
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





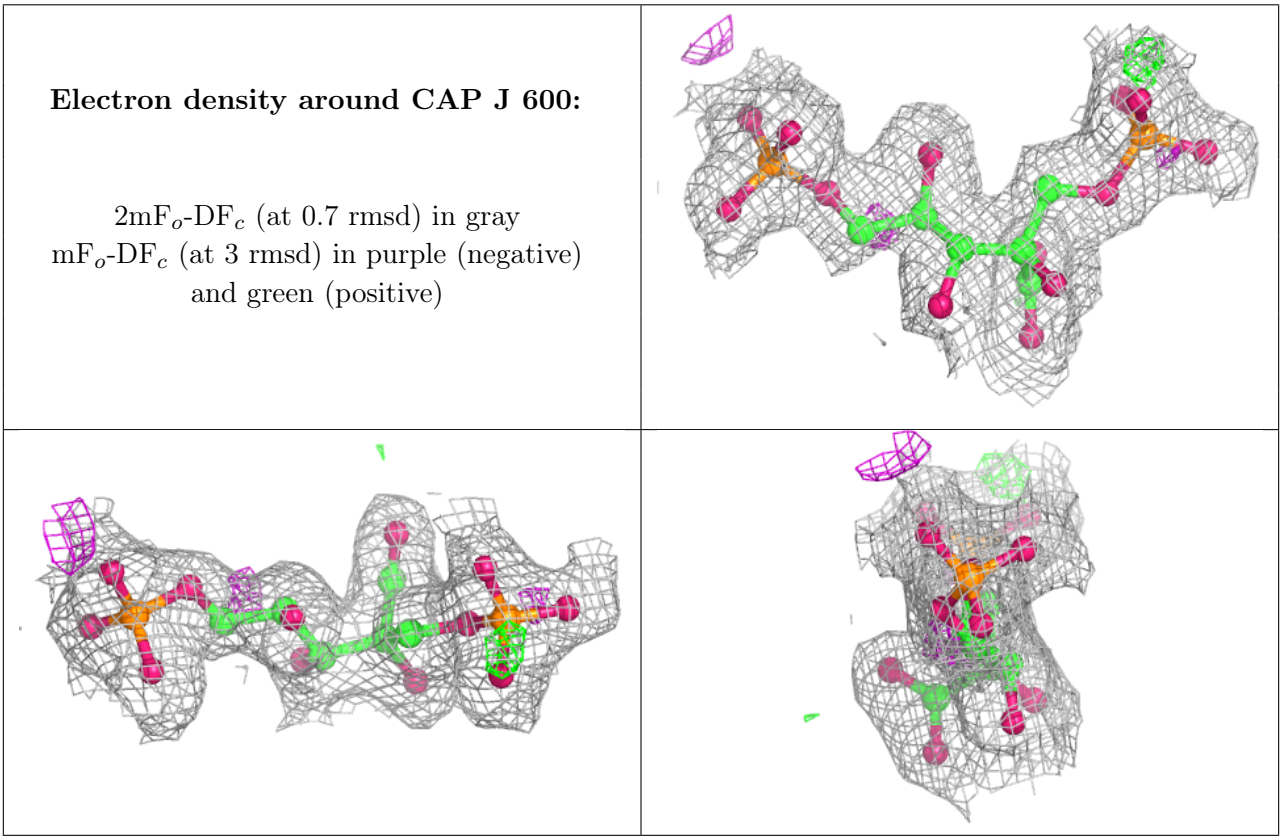
Electron density around CAP A 600:

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



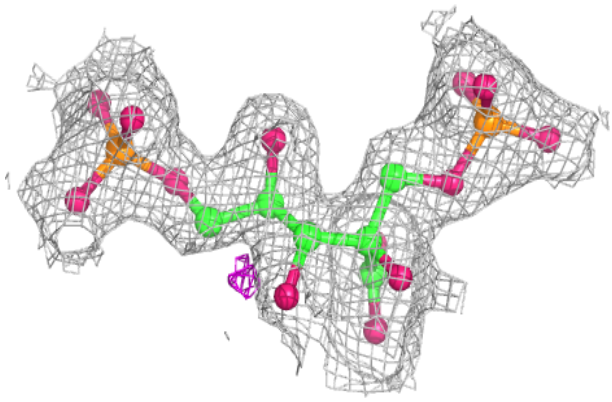
Electron density around CAP J 600:

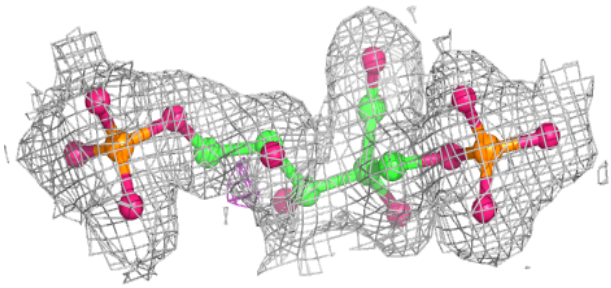
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

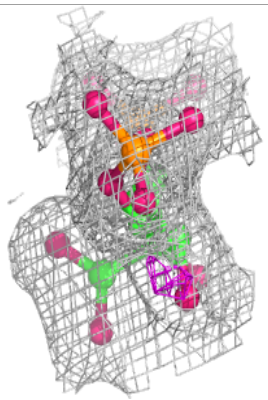


Electron density around CAP B 600:

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

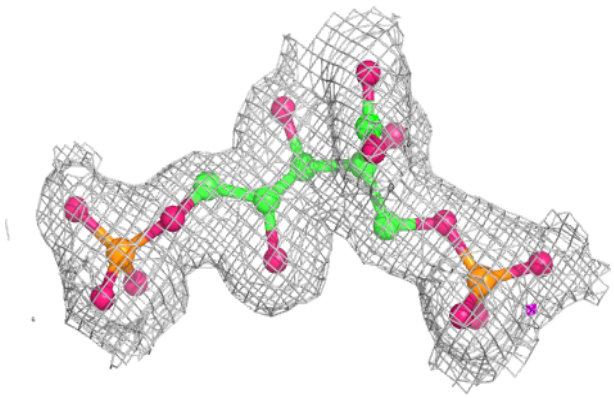


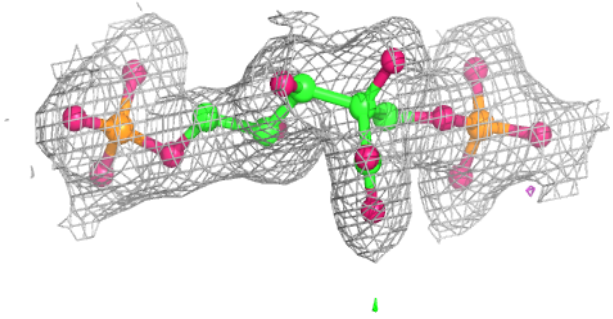


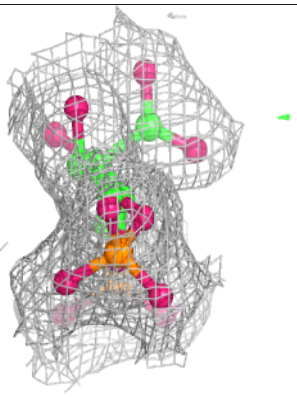


Electron density around CAP E 600:

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

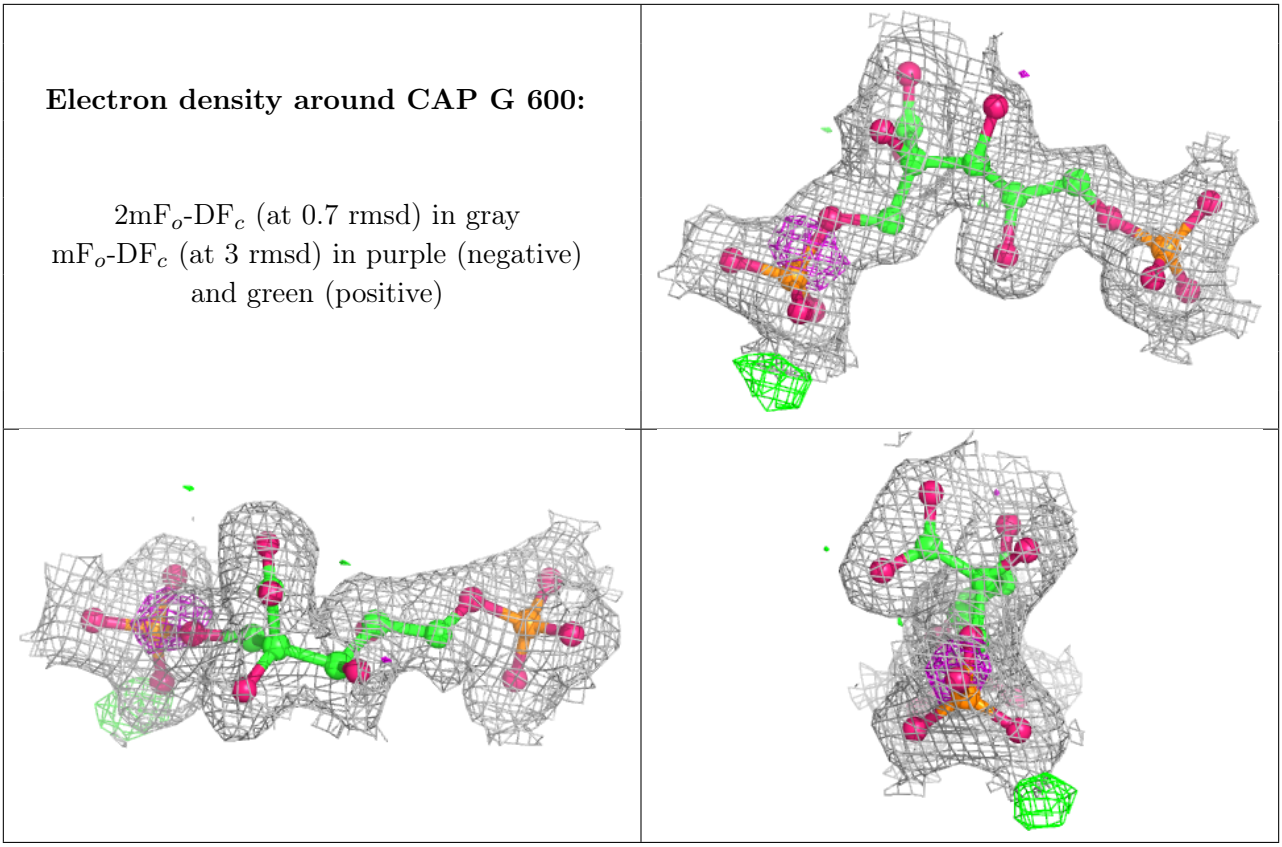






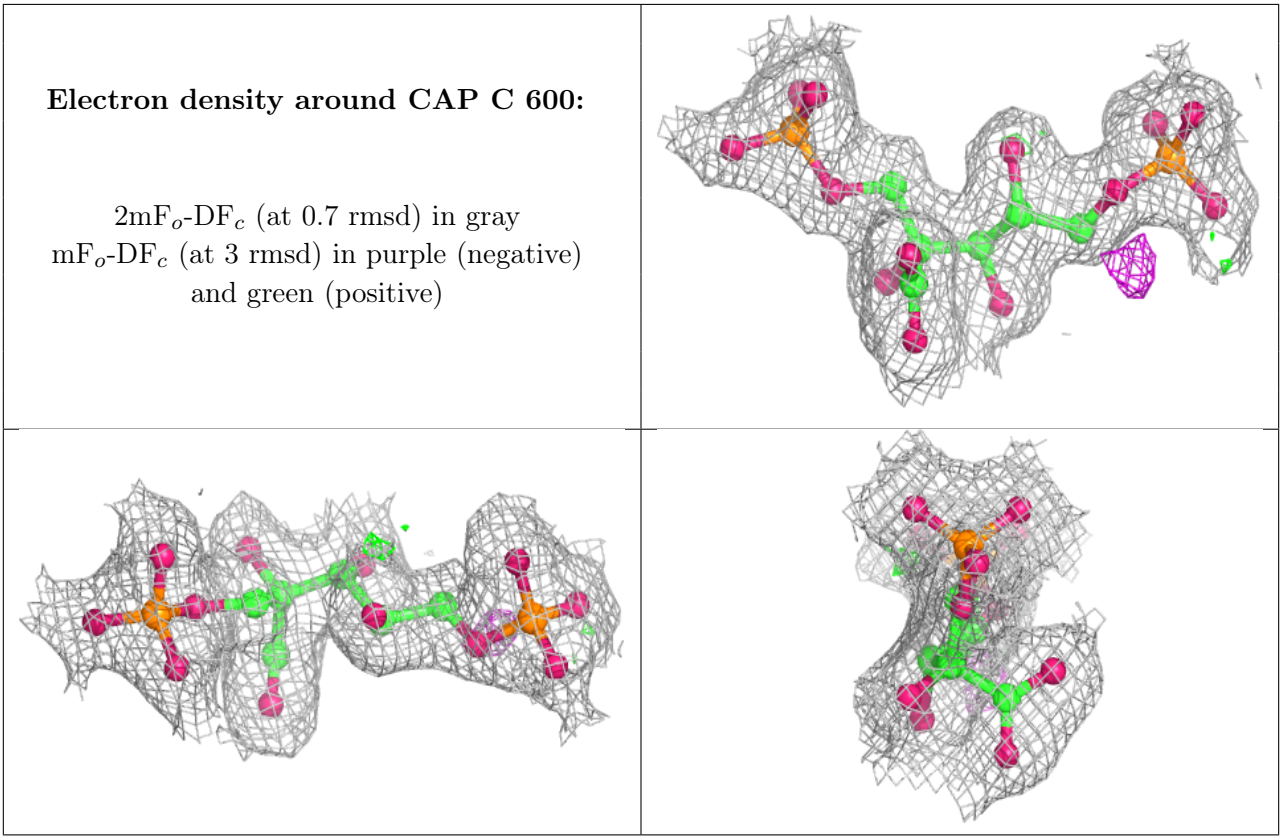
Electron density around CAP G 600:

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



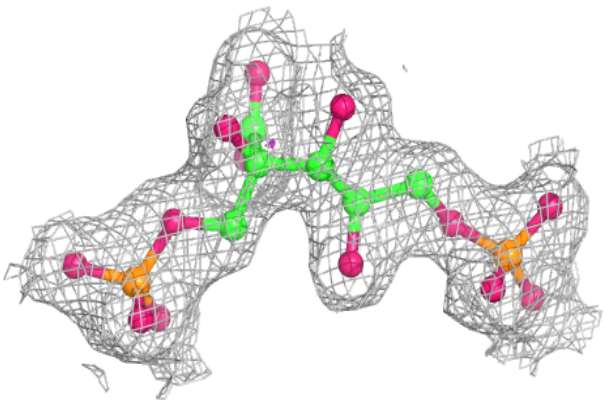
Electron density around CAP C 600:

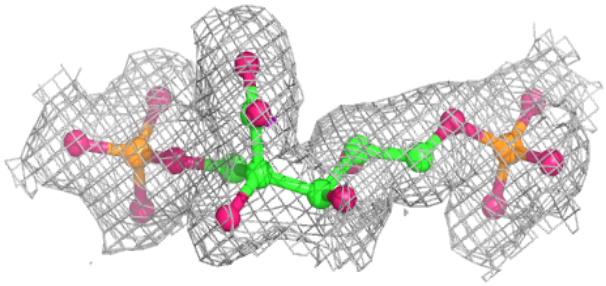
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

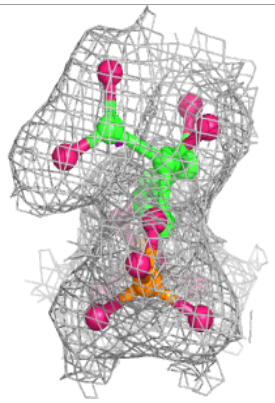


Electron density around CAP I 600:

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

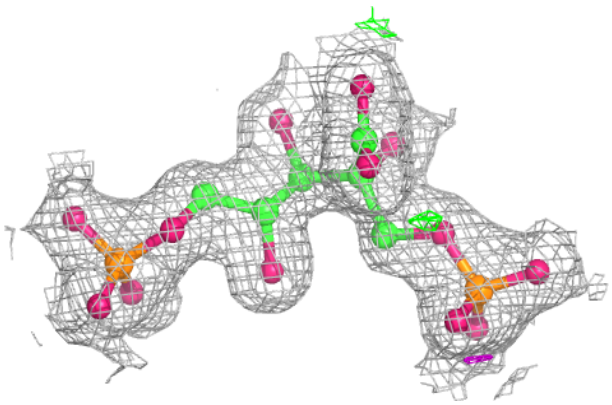


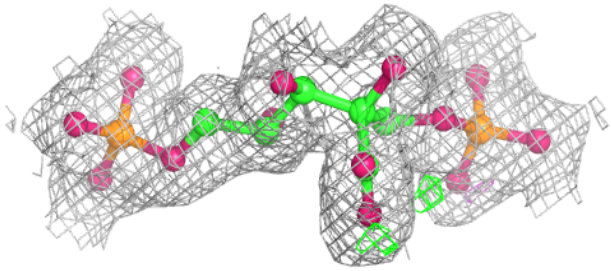


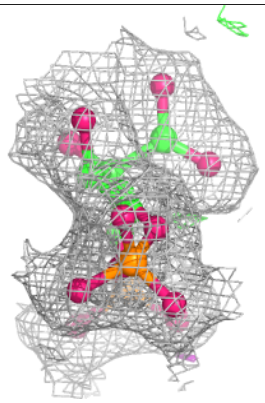


Electron density around CAP D 600:

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

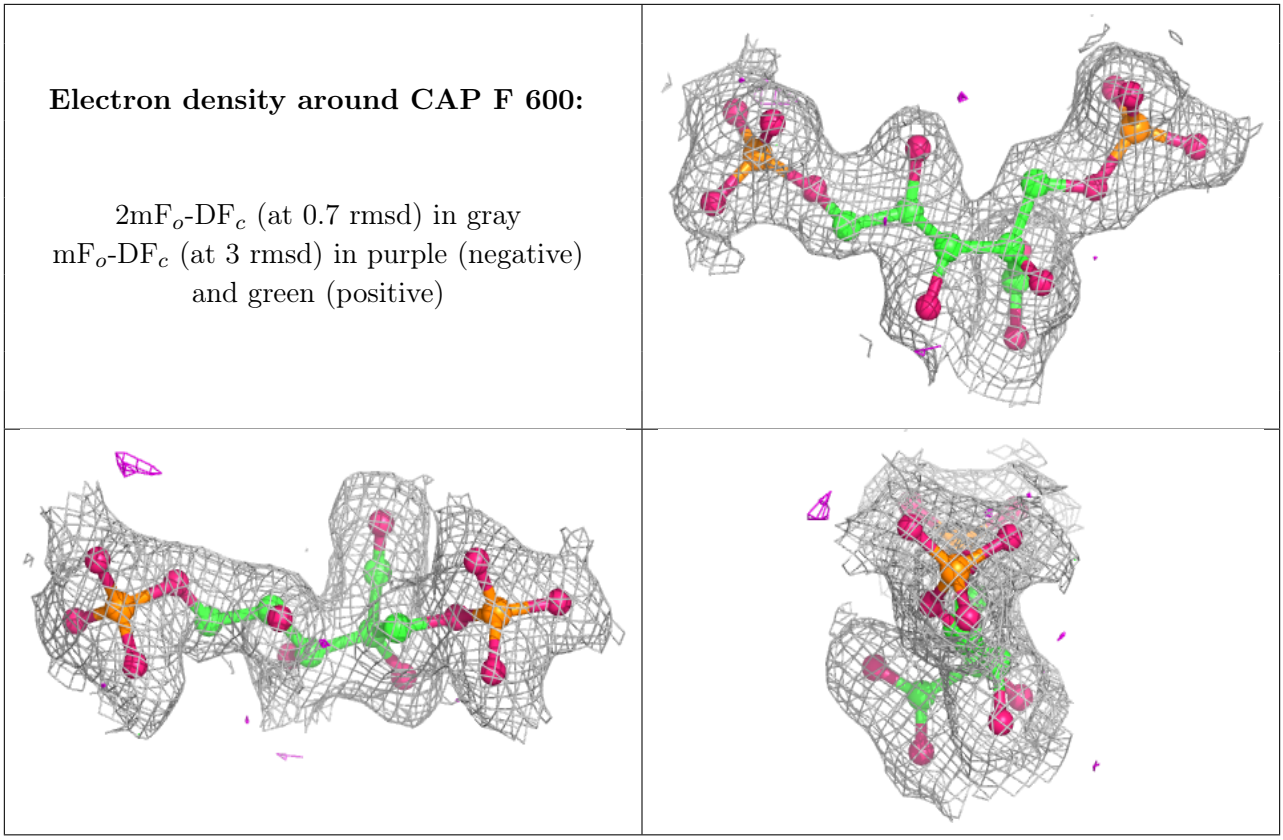






Electron density around CAP F 600:

$2mF_o$-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.