



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 31, 2021 – 05:12 AM EDT

PDB ID : 3KDO
Title : Crystal structure of Type III Rubisco SP6 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 : 2.36 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
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)	:	2.23.2

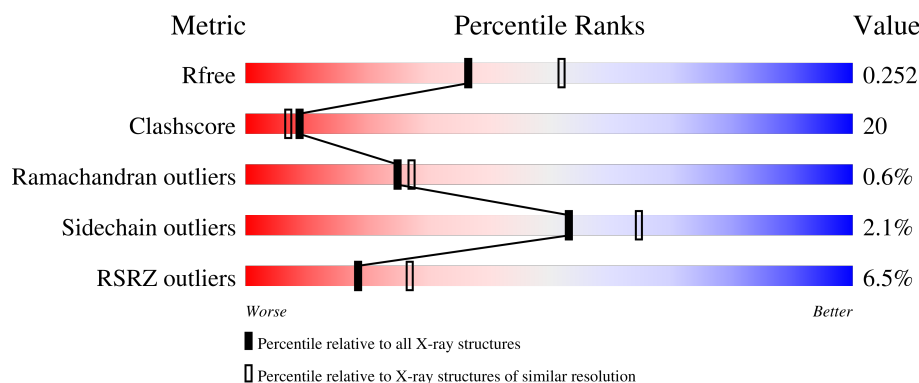
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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

Mol	Chain	Length	Quality of chain
1	A	444	
1	B	444	
1	C	444	
1	D	444	
1	E	444	

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Mol	Chain	Length	Quality of chain
1	F	444	<div><div>5%</div><div><div></div><div></div><div></div></div><div>71%</div><div>27%</div><div>..</div></div>
1	G	444	<div><div>2%</div><div><div></div><div></div><div></div></div><div>70%</div><div>27%</div><div>..</div></div>
1	H	444	<div><div>12%</div><div><div></div><div></div><div></div></div><div>60%</div><div>37%</div><div>..</div></div>
1	I	444	<div><div>5%</div><div><div></div><div></div><div></div></div><div>70%</div><div>28%</div><div>.</div></div>
1	J	444	<div><div>8%</div><div><div></div><div></div><div></div></div><div>69%</div><div>29%</div><div>..</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36065 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Ribulose biphosphate carboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	0	0
			3341	2146	569	616	10			
1	B	438	Total	C	N	O	S	0	0	0
			3391	2179	575	627	10			
1	C	440	Total	C	N	O	S	0	0	0
			3420	2196	580	634	10			
1	D	437	Total	C	N	O	S	0	0	0
			3419	2195	582	632	10			
1	E	440	Total	C	N	O	S	0	0	0
			3418	2198	582	628	10			
1	F	437	Total	C	N	O	S	0	0	0
			3415	2195	581	629	10			
1	G	437	Total	C	N	O	S	0	0	0
			3423	2200	582	631	10			
1	H	438	Total	C	N	O	S	0	0	0
			3382	2178	574	620	10			
1	I	438	Total	C	N	O	S	0	0	0
			3410	2190	582	628	10			
1	J	438	Total	C	N	O	S	0	0	0
			3415	2195	581	629	10			

There are 110 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
A	331	LEU	ILE	engineered mutation	UNP O93627
A	332	GLY	GLN	engineered mutation	UNP O93627
A	333	PHE	ASN	engineered mutation	UNP O93627
A	334	VAL	ALA	engineered mutation	UNP O93627

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Chain	Residue	Modelled	Actual	Comment	Reference
A	335	ASP	ARG	engineered mutation	UNP O93627
A	336	LEU	ILE	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
B	330	THR	VAL	engineered mutation	UNP O93627
B	331	LEU	ILE	engineered mutation	UNP O93627
B	332	GLY	GLN	engineered mutation	UNP O93627
B	333	PHE	ASN	engineered mutation	UNP O93627
B	334	VAL	ALA	engineered mutation	UNP O93627
B	335	ASP	ARG	engineered mutation	UNP O93627
B	336	LEU	ILE	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
C	331	LEU	ILE	engineered mutation	UNP O93627
C	332	GLY	GLN	engineered mutation	UNP O93627
C	333	PHE	ASN	engineered mutation	UNP O93627
C	334	VAL	ALA	engineered mutation	UNP O93627
C	335	ASP	ARG	engineered mutation	UNP O93627
C	336	LEU	ILE	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
D	331	LEU	ILE	engineered mutation	UNP O93627
D	332	GLY	GLN	engineered mutation	UNP O93627
D	333	PHE	ASN	engineered mutation	UNP O93627
D	334	VAL	ALA	engineered mutation	UNP O93627
D	335	ASP	ARG	engineered mutation	UNP O93627
D	336	LEU	ILE	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
E	331	LEU	ILE	engineered mutation	UNP O93627
E	332	GLY	GLN	engineered mutation	UNP O93627

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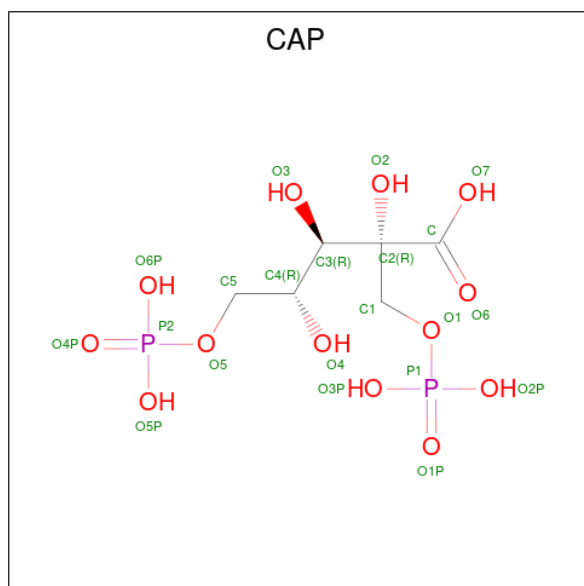
Chain	Residue	Modelled	Actual	Comment	Reference
E	333	PHE	ASN	engineered mutation	UNP O93627
E	334	VAL	ALA	engineered mutation	UNP O93627
E	335	ASP	ARG	engineered mutation	UNP O93627
E	336	LEU	ILE	engineered mutation	UNP O93627
F	326	GLU	GLY	engineered mutation	UNP O93627
F	327	ARG	LYS	engineered mutation	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
F	331	LEU	ILE	engineered mutation	UNP O93627
F	332	GLY	GLN	engineered mutation	UNP O93627
F	333	PHE	ASN	engineered mutation	UNP O93627
F	334	VAL	ALA	engineered mutation	UNP O93627
F	335	ASP	ARG	engineered mutation	UNP O93627
F	336	LEU	ILE	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
G	331	LEU	ILE	engineered mutation	UNP O93627
G	332	GLY	GLN	engineered mutation	UNP O93627
G	333	PHE	ASN	engineered mutation	UNP O93627
G	334	VAL	ALA	engineered mutation	UNP O93627
G	335	ASP	ARG	engineered mutation	UNP O93627
G	336	LEU	ILE	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
H	331	LEU	ILE	engineered mutation	UNP O93627
H	332	GLY	GLN	engineered mutation	UNP O93627
H	333	PHE	ASN	engineered mutation	UNP O93627
H	334	VAL	ALA	engineered mutation	UNP O93627
H	335	ASP	ARG	engineered mutation	UNP O93627
H	336	LEU	ILE	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

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Chain	Residue	Modelled	Actual	Comment	Reference
I	331	LEU	ILE	engineered mutation	UNP O93627
I	332	GLY	GLN	engineered mutation	UNP O93627
I	333	PHE	ASN	engineered mutation	UNP O93627
I	334	VAL	ALA	engineered mutation	UNP O93627
I	335	ASP	ARG	engineered mutation	UNP O93627
I	336	LEU	ILE	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
J	331	LEU	ILE	engineered mutation	UNP O93627
J	332	GLY	GLN	engineered mutation	UNP O93627
J	333	PHE	ASN	engineered mutation	UNP O93627
J	334	VAL	ALA	engineered mutation	UNP O93627
J	335	ASP	ARG	engineered mutation	UNP O93627
J	336	LEU	ILE	engineered mutation	UNP O93627

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



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

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

- 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		
3	H	1	Total	Mg	0	0
			1	1		
3	I	1	Total	Mg	0	0
			1	1		
3	J	1	Total	Mg	0	0
			1	1		

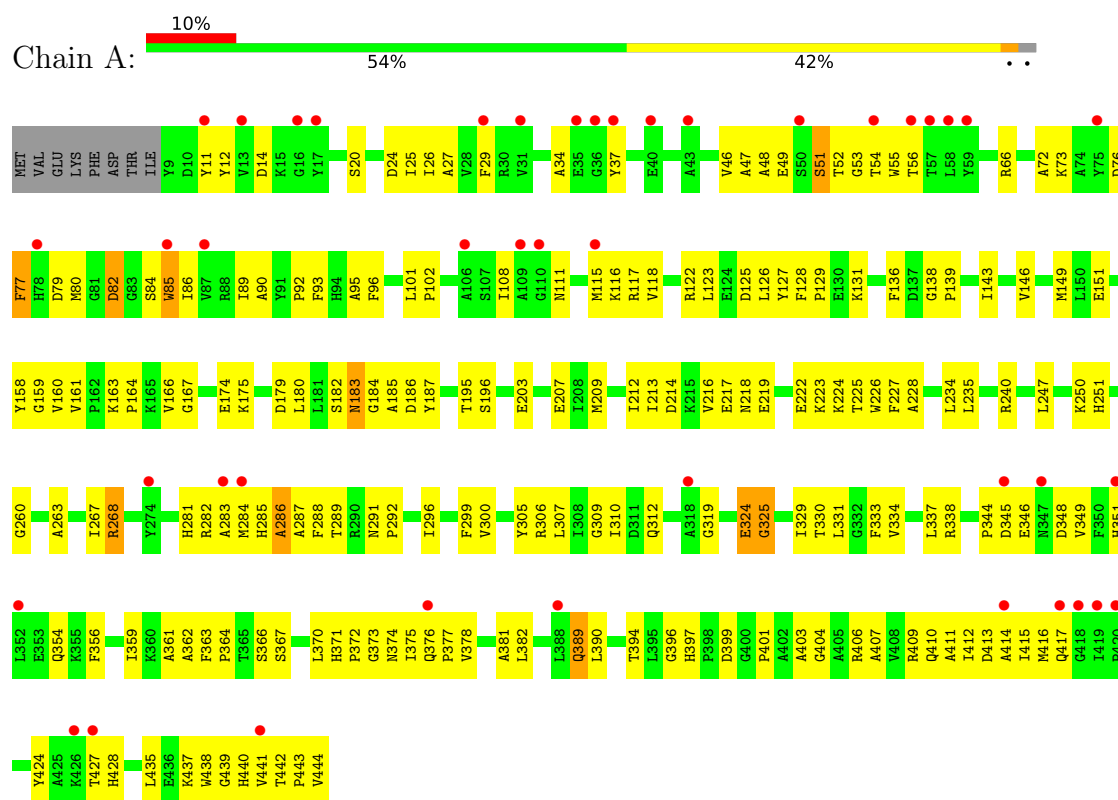
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	97	Total 97	O 97	0	0
4	B	175	Total 175	O 175	0	0
4	C	226	Total 226	O 226	0	0
4	D	239	Total 239	O 239	0	0
4	E	197	Total 197	O 197	0	0
4	F	179	Total 179	O 179	0	0
4	G	174	Total 174	O 174	0	0
4	H	123	Total 123	O 123	0	0
4	I	192	Total 192	O 192	0	0
4	J	209	Total 209	O 209	0	0

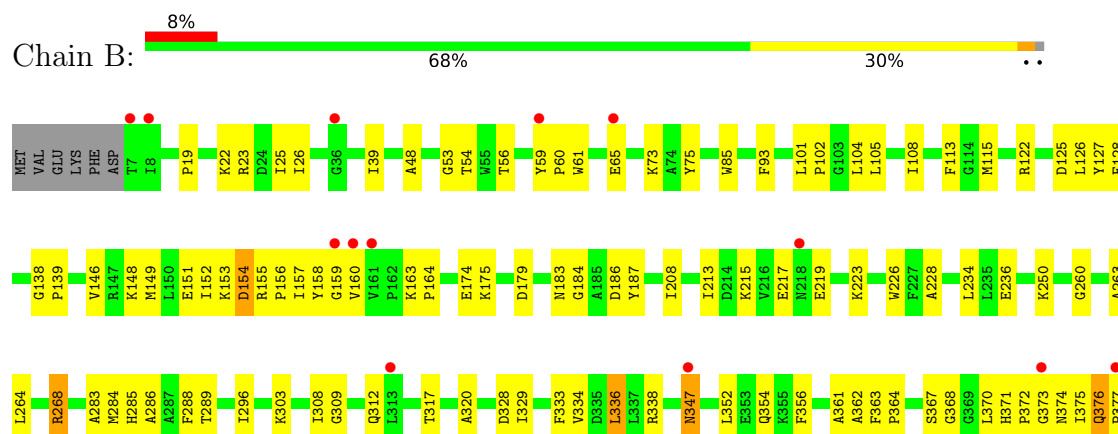
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Ribulose biphosphate carboxylase

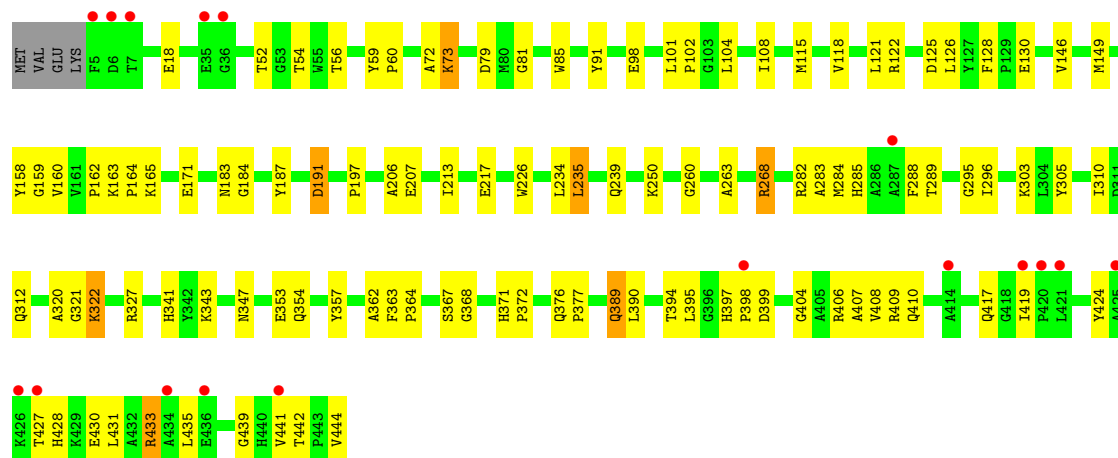
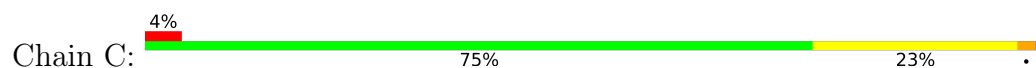


• Molecule 1: Ribulose biphosphate carboxylase

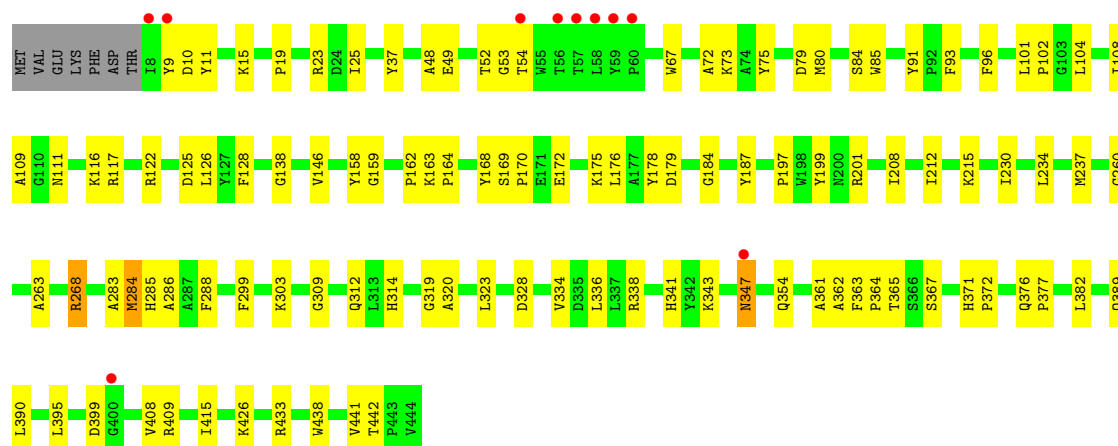
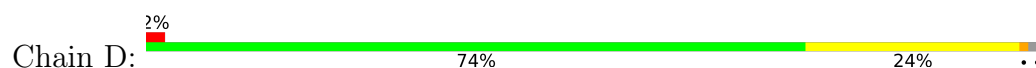




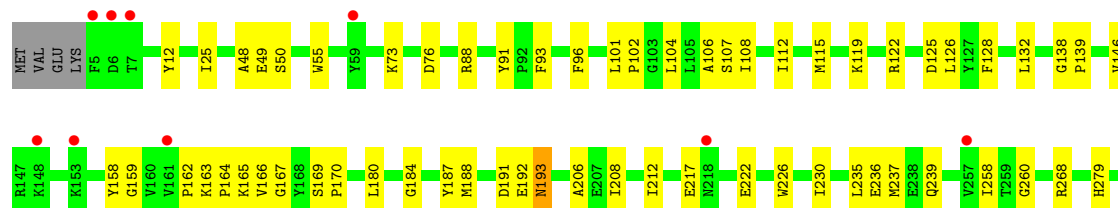
• Molecule 1: Ribulose biphosphate carboxylase

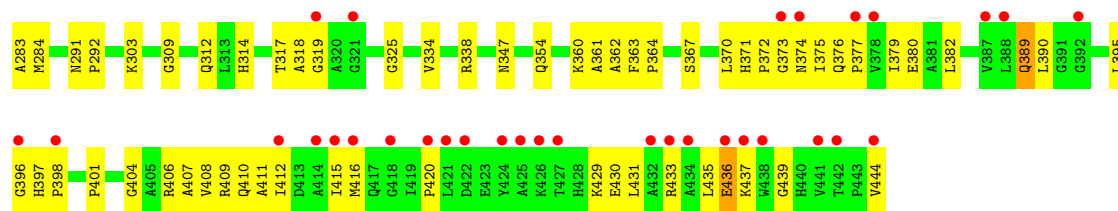


• Molecule 1: Ribulose biphosphate carboxylase

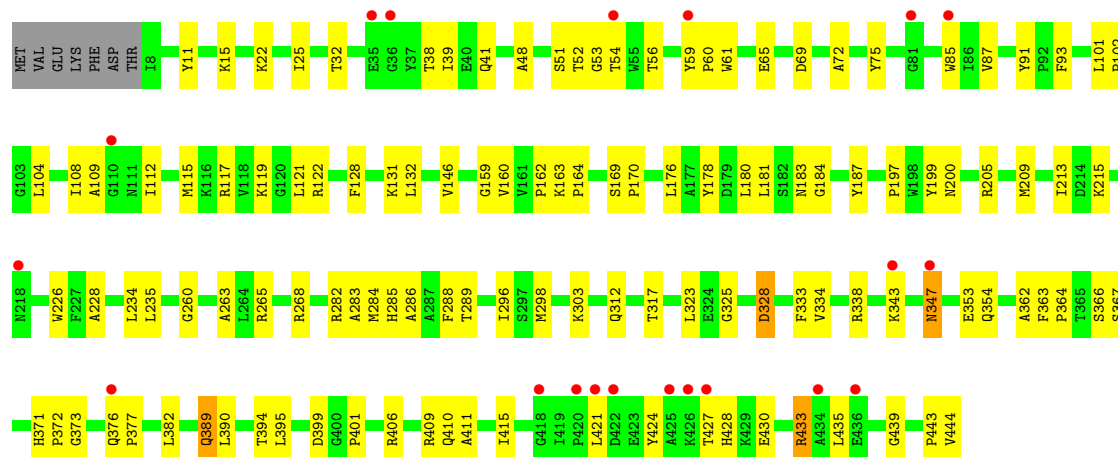


• Molecule 1: Ribulose biphosphate carboxylase

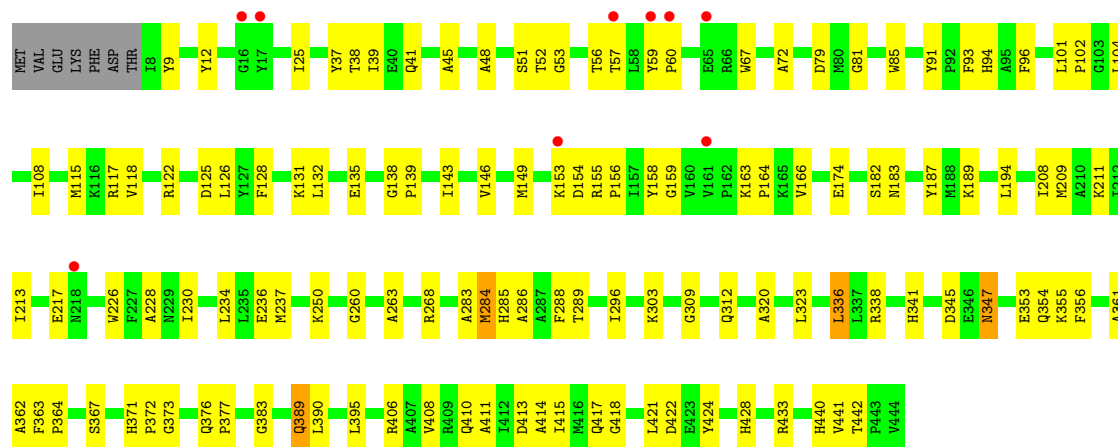




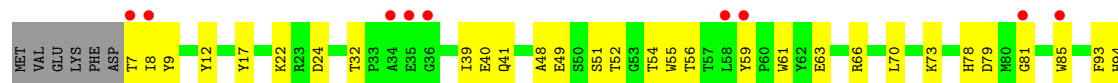
● Molecule 1: Ribulose biphosphate carboxylase

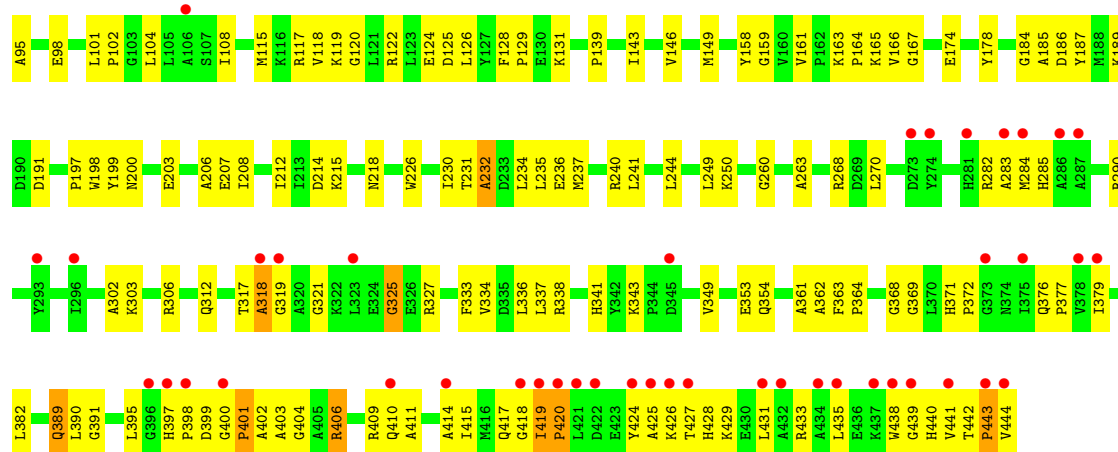


● Molecule 1: Ribulose biphosphate carboxylase

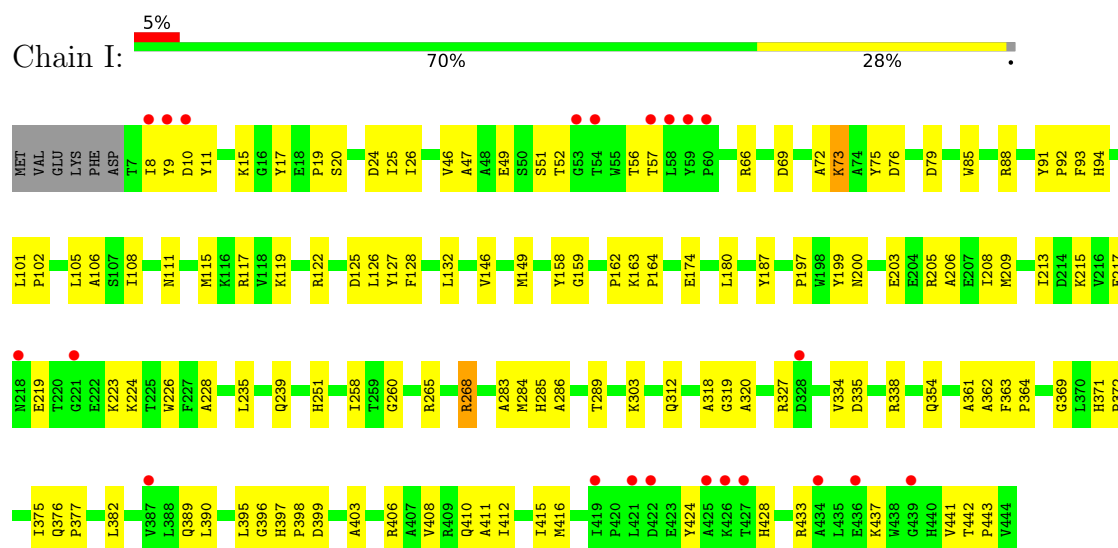


● Molecule 1: Ribulose biphosphate carboxylase

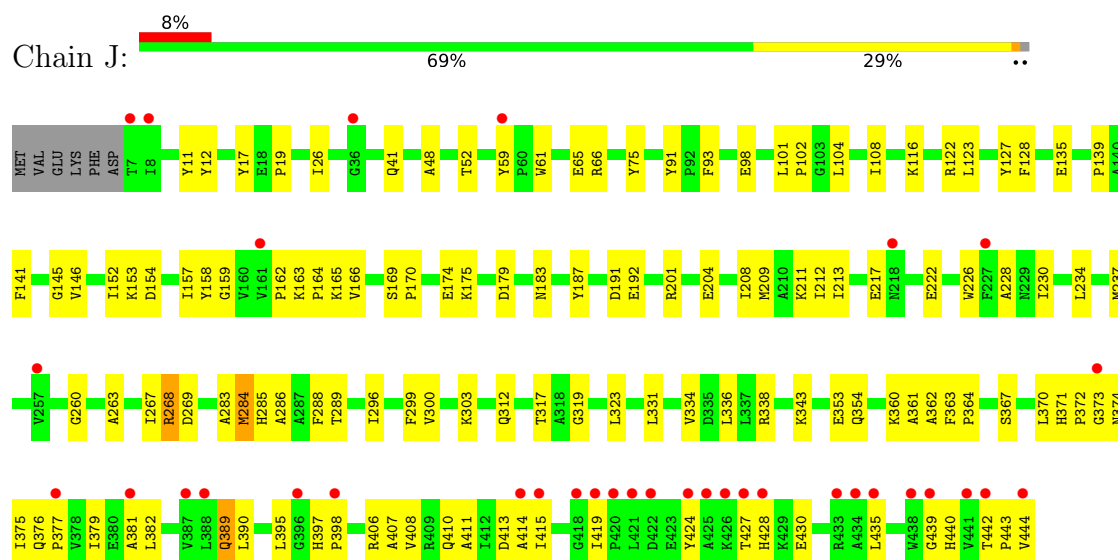




• Molecule 1: Ribulose biphosphate carboxylase



• Molecule 1: Ribulose biphosphate carboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	97.48Å 246.57Å 134.83Å 90.00° 104.73° 90.00°	Depositor
Resolution (Å)	38.46 – 2.36 38.46 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.4 (38.46-2.36) 99.4 (38.46-2.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.219 , 0.264 0.213 , 0.252	Depositor DCC
R_{free} test set	12530 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	36065	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.21	0/3415	0.36	0/4642
1	B	0.22	0/3467	0.37	0/4712
1	C	0.22	0/3496	0.38	0/4750
1	D	0.22	0/3494	0.39	0/4739
1	E	0.22	0/3494	0.38	0/4744
1	F	0.22	0/3491	0.38	0/4738
1	G	0.21	0/3499	0.38	0/4747
1	H	0.21	0/3458	0.37	0/4700
1	I	0.22	0/3485	0.38	0/4730
1	J	0.22	0/3491	0.39	0/4738
All	All	0.22	0/34790	0.38	0/47240

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	3341	0	3185	218	0
1	B	3391	0	3252	153	0
1	C	3420	0	3289	121	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3419	0	3317	102	0
1	E	3418	0	3303	121	0
1	F	3415	0	3313	126	0
1	G	3423	0	3328	129	0
1	H	3382	0	3257	207	0
1	I	3410	0	3301	112	0
1	J	3415	0	3310	143	0
2	A	21	0	8	0	0
2	B	21	0	7	1	0
2	C	21	0	9	1	0
2	D	21	0	8	0	0
2	E	21	0	8	2	0
2	F	21	0	8	0	0
2	G	21	0	8	1	0
2	H	21	0	8	0	0
2	I	21	0	8	0	0
2	J	21	0	7	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0
4	A	97	0	0	12	0
4	B	175	0	0	10	0
4	C	226	0	0	7	0
4	D	239	0	0	4	0
4	E	197	0	0	9	0
4	F	179	0	0	9	0
4	G	174	0	0	8	0
4	H	123	0	0	6	0
4	I	192	0	0	7	0
4	J	209	0	0	15	0
All	All	36065	0	32934	1362	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 20.

The worst 5 of 1362 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:H:397:HIS:ND1	1:H:398:PRO:HD2	1.29	1.44
1:H:397:HIS:CG	1:H:398:PRO:HD2	1.61	1.32
1:A:149:MET:HE3	1:A:250:LYS:CB	1.65	1.26
1:H:397:HIS:ND1	1:H:398:PRO:CD	2.06	1.18
1:I:72:ALA:O	1:I:73:LYS:HD2	1.43	1.17

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	433/444 (98%)	386 (89%)	40 (9%)	7 (2%)	9	8
1	B	435/444 (98%)	408 (94%)	25 (6%)	2 (0%)	29	32
1	C	437/444 (98%)	420 (96%)	16 (4%)	1 (0%)	47	56
1	D	434/444 (98%)	415 (96%)	18 (4%)	1 (0%)	47	56
1	E	437/444 (98%)	410 (94%)	25 (6%)	2 (0%)	29	32
1	F	434/444 (98%)	414 (95%)	19 (4%)	1 (0%)	47	56
1	G	434/444 (98%)	415 (96%)	18 (4%)	1 (0%)	47	56
1	H	435/444 (98%)	389 (89%)	39 (9%)	7 (2%)	9	8
1	I	435/444 (98%)	415 (95%)	18 (4%)	2 (0%)	29	32
1	J	435/444 (98%)	414 (95%)	20 (5%)	1 (0%)	47	56
All	All	4349/4440 (98%)	4086 (94%)	238 (6%)	25 (1%)	25	27

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	426	LYS
1	B	429	LYS
1	A	34	ALA

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Mol	Chain	Res	Type
1	A	82	ASP
1	A	117	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	321/356 (90%)	313 (98%)	8 (2%)	47	58
1	B	331/356 (93%)	322 (97%)	9 (3%)	44	55
1	C	336/356 (94%)	327 (97%)	9 (3%)	44	55
1	D	339/356 (95%)	333 (98%)	6 (2%)	59	70
1	E	335/356 (94%)	329 (98%)	6 (2%)	59	70
1	F	338/356 (95%)	329 (97%)	9 (3%)	44	55
1	G	340/356 (96%)	333 (98%)	7 (2%)	53	65
1	H	329/356 (92%)	322 (98%)	7 (2%)	53	65
1	I	336/356 (94%)	331 (98%)	5 (2%)	65	76
1	J	337/356 (95%)	333 (99%)	4 (1%)	71	82
All	All	3342/3560 (94%)	3272 (98%)	70 (2%)	53	65

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	363	PHE
1	H	406	ARG
1	I	363	PHE
1	C	389	GLN
1	C	363	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	312	GLN

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Mol	Chain	Res	Type
1	G	417	GLN
1	J	64	GLN
1	F	347	ASN
1	G	312	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	E	189	1,3	7,11,12	0.82	0	4,12,14	0.93	0
1	KCX	C	189	1,3	7,11,12	0.83	0	4,12,14	0.77	0
1	KCX	D	189	1,3	7,11,12	0.76	0	4,12,14	0.77	0
1	KCX	F	189	1,3	7,11,12	0.72	0	4,12,14	1.00	0
1	KCX	I	189	1,3	7,11,12	0.86	0	4,12,14	0.74	0
1	KCX	H	189	1,3	7,11,12	0.79	0	4,12,14	0.97	0
1	KCX	J	189	1,3	7,11,12	0.78	0	4,12,14	0.94	0
1	KCX	B	189	1,3	7,11,12	0.82	0	4,12,14	0.99	0
1	KCX	A	189	1,3	7,11,12	0.78	0	4,12,14	1.02	0
1	KCX	G	189	1,3	7,11,12	0.83	0	4,12,14	0.65	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	E	189	1,3	-	0/7/10/12	-
1	KCX	C	189	1,3	-	0/7/10/12	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	KCX	D	189	1,3	-	0/7/10/12	-
1	KCX	F	189	1,3	-	0/7/10/12	-
1	KCX	I	189	1,3	-	0/7/10/12	-
1	KCX	H	189	1,3	-	0/7/10/12	-
1	KCX	J	189	1,3	-	0/7/10/12	-
1	KCX	B	189	1,3	-	0/7/10/12	-
1	KCX	A	189	1,3	-	0/7/10/12	-
1	KCX	G	189	1,3	-	0/7/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	H	189	KCX	2	0
1	G	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	$\# Z > 2$
2	CAP	D	600	3	15,20,20	0.83	0	20,31,31	0.74	0
2	CAP	B	600	3	15,20,20	0.81	0	20,31,31	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CAP	G	600	3	15,20,20	0.81	0	20,31,31	0.76	0
2	CAP	H	600	3	15,20,20	0.80	0	20,31,31	0.72	0
2	CAP	E	600	3	15,20,20	0.85	0	20,31,31	0.77	0
2	CAP	C	600	3	15,20,20	0.80	0	20,31,31	0.73	0
2	CAP	I	600	3	15,20,20	0.80	0	20,31,31	0.76	0
2	CAP	F	600	3	15,20,20	0.81	0	20,31,31	0.76	0
2	CAP	J	600	3	15,20,20	0.85	0	20,31,31	0.77	0
2	CAP	A	600	3	15,20,20	0.83	0	20,31,31	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
2	CAP	D	600	3	-	2/23/29/29	-
2	CAP	B	600	3	-	3/23/29/29	-
2	CAP	G	600	3	-	2/23/29/29	-
2	CAP	H	600	3	-	5/23/29/29	-
2	CAP	E	600	3	-	8/23/29/29	-
2	CAP	C	600	3	-	3/23/29/29	-
2	CAP	I	600	3	-	2/23/29/29	-
2	CAP	F	600	3	-	2/23/29/29	-
2	CAP	J	600	3	-	2/23/29/29	-
2	CAP	A	600	3	-	2/23/29/29	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

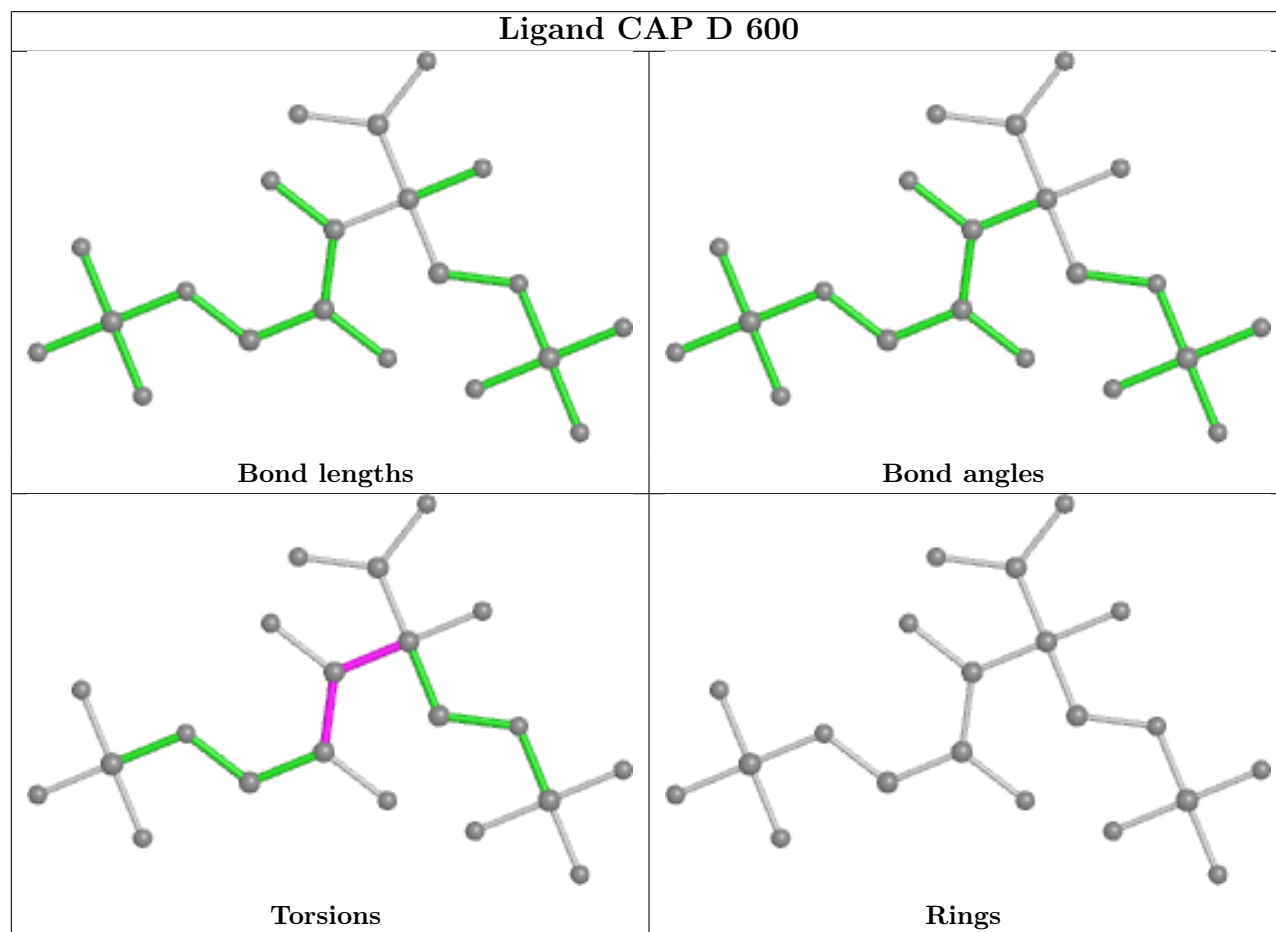
Mol	Chain	Res	Type	Atoms
2	A	600	CAP	O3-C3-C4-O4
2	B	600	CAP	O3-C3-C4-O4
2	C	600	CAP	C2-C3-C4-O4
2	C	600	CAP	O3-C3-C4-O4
2	E	600	CAP	O1-C1-C2-C

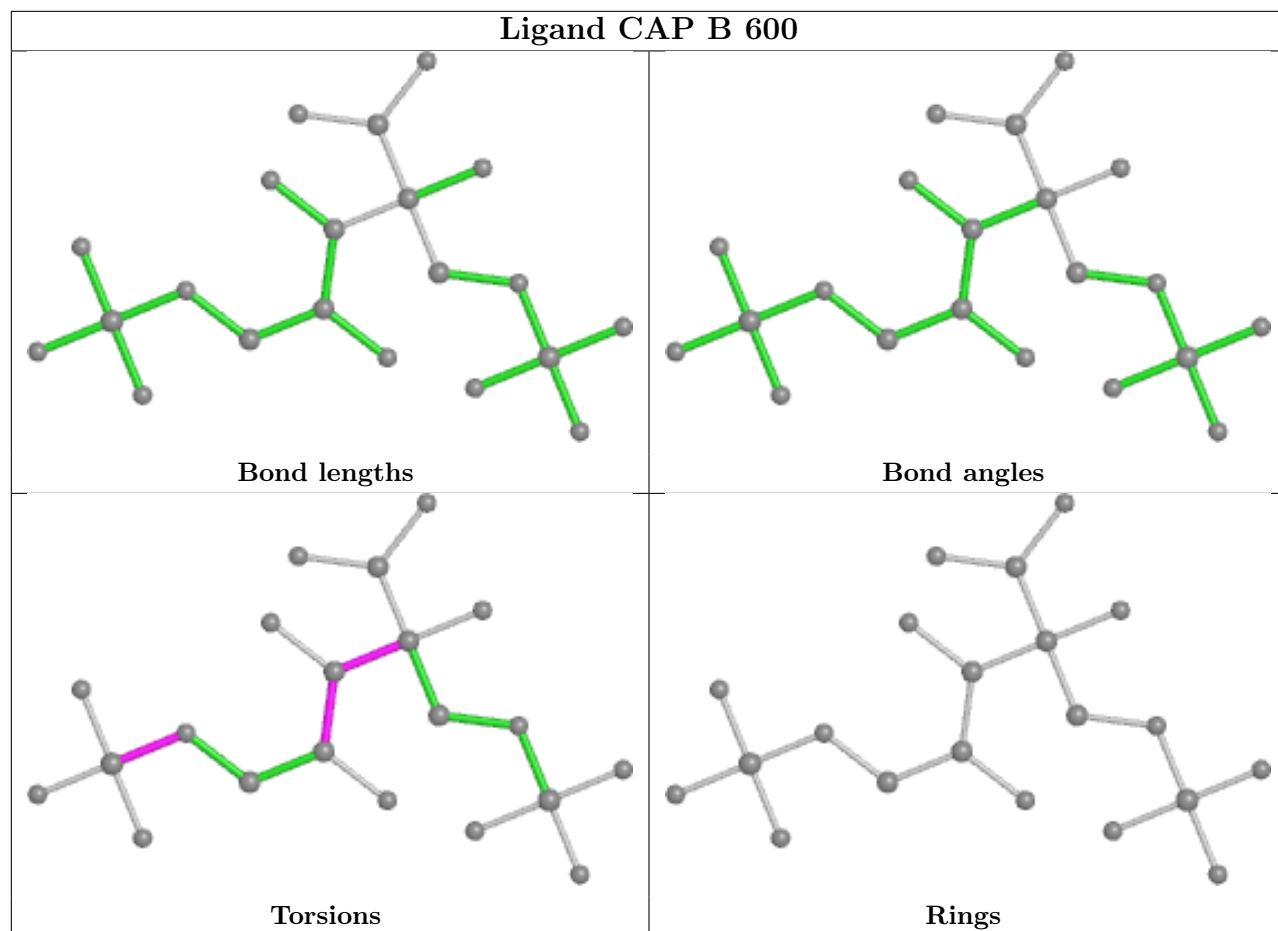
There are no ring outliers.

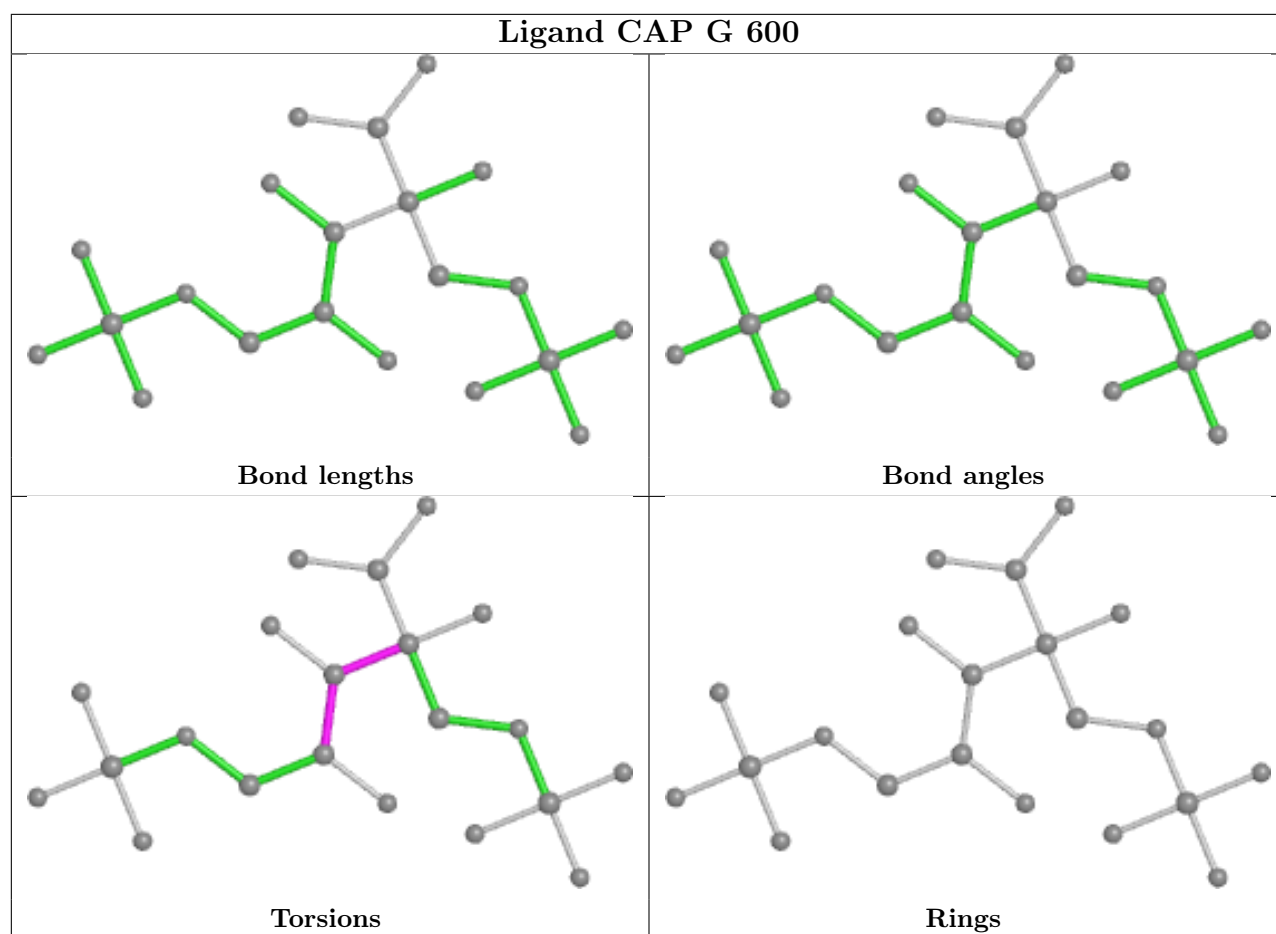
4 monomers are involved in 5 short contacts:

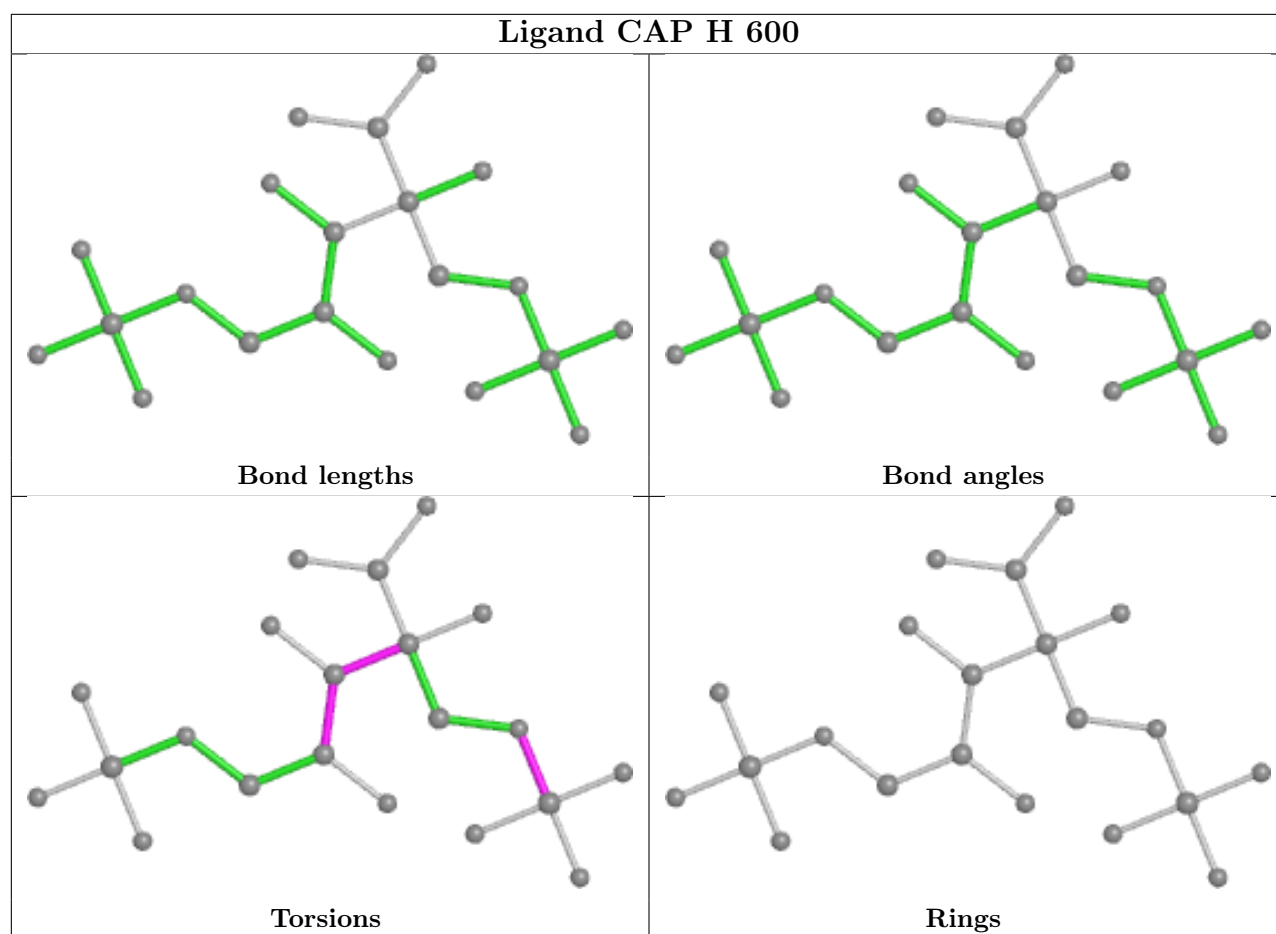
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	600	CAP	1	0
2	G	600	CAP	1	0
2	E	600	CAP	2	0
2	C	600	CAP	1	0

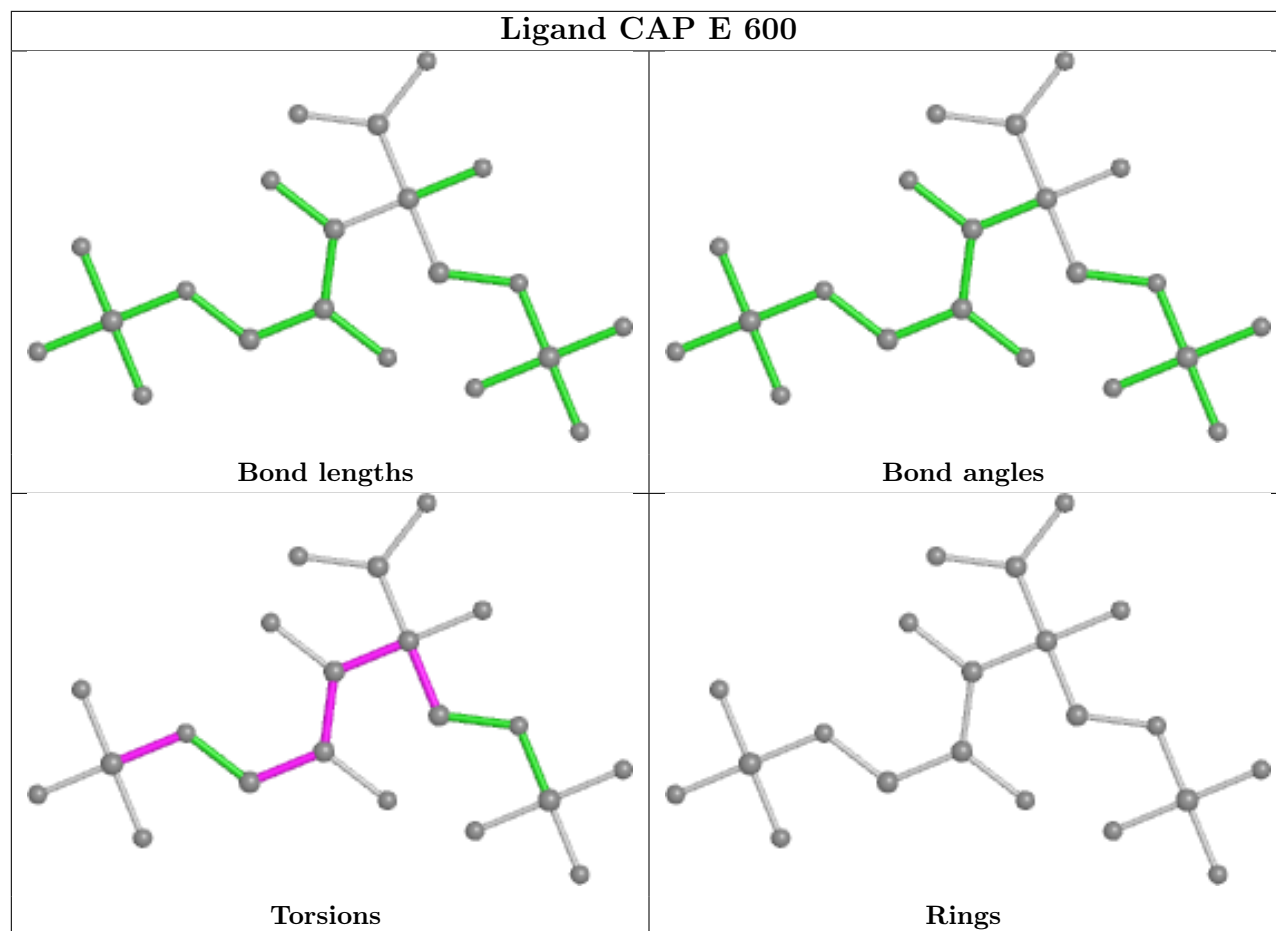
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

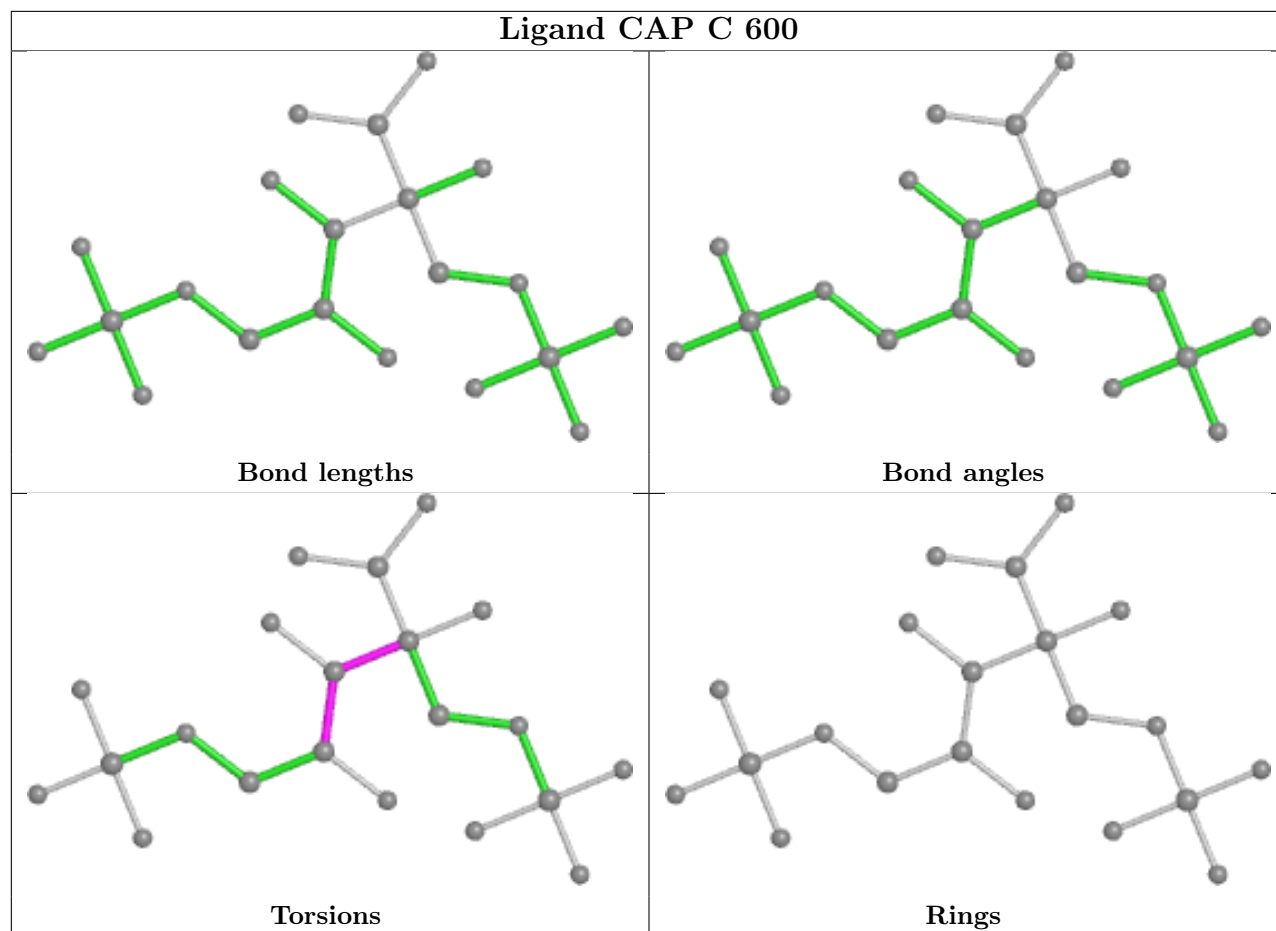


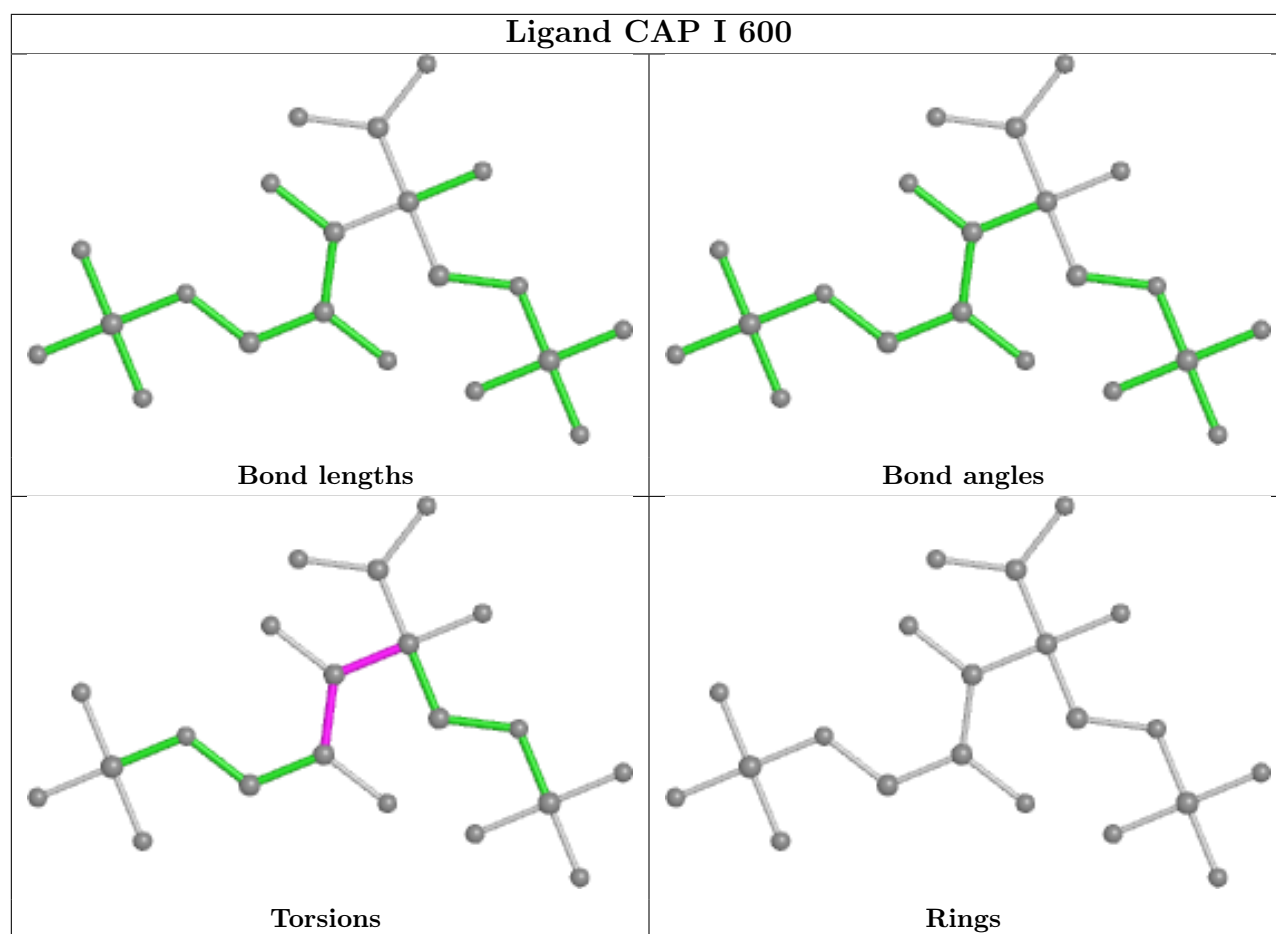


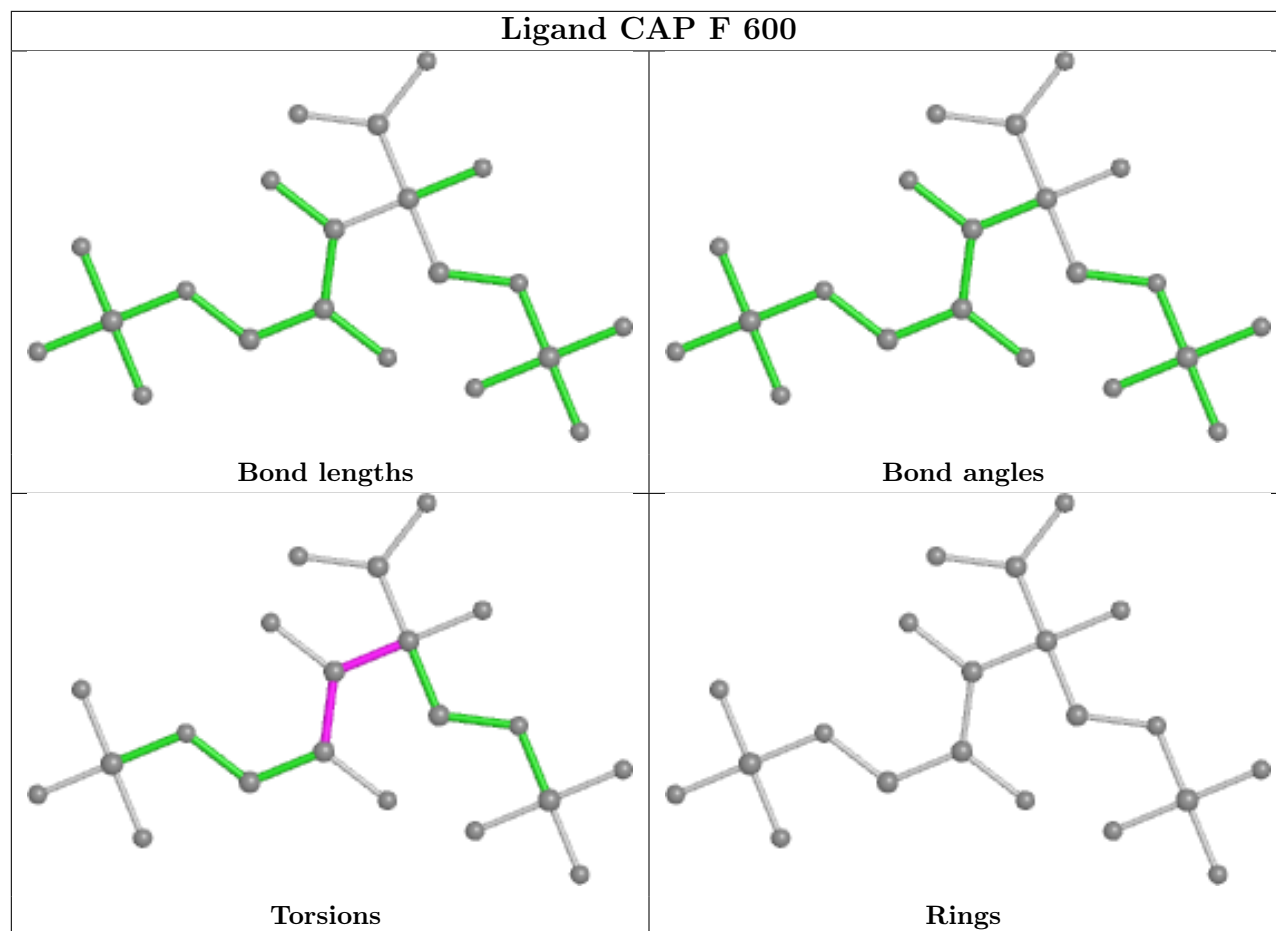


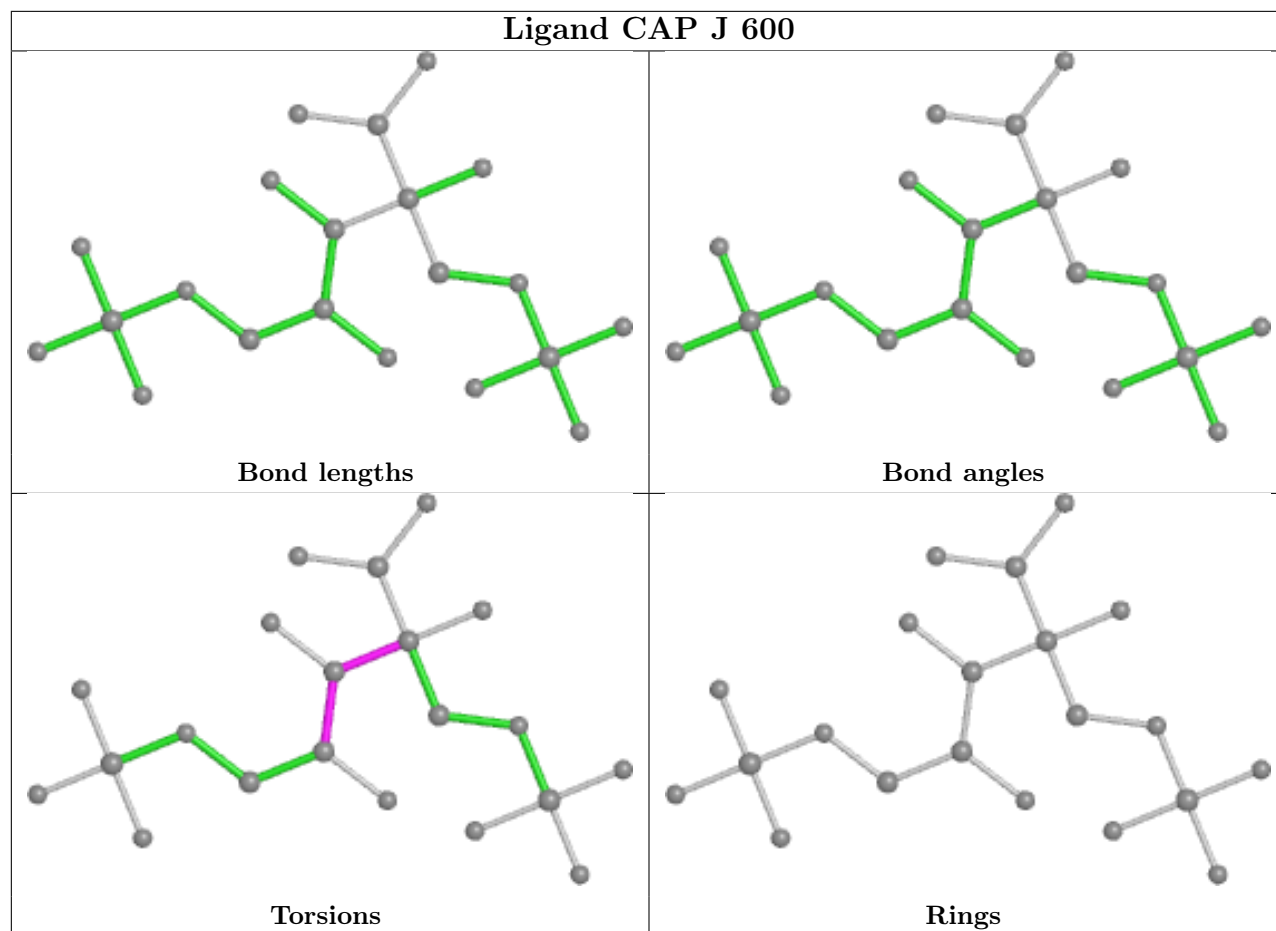


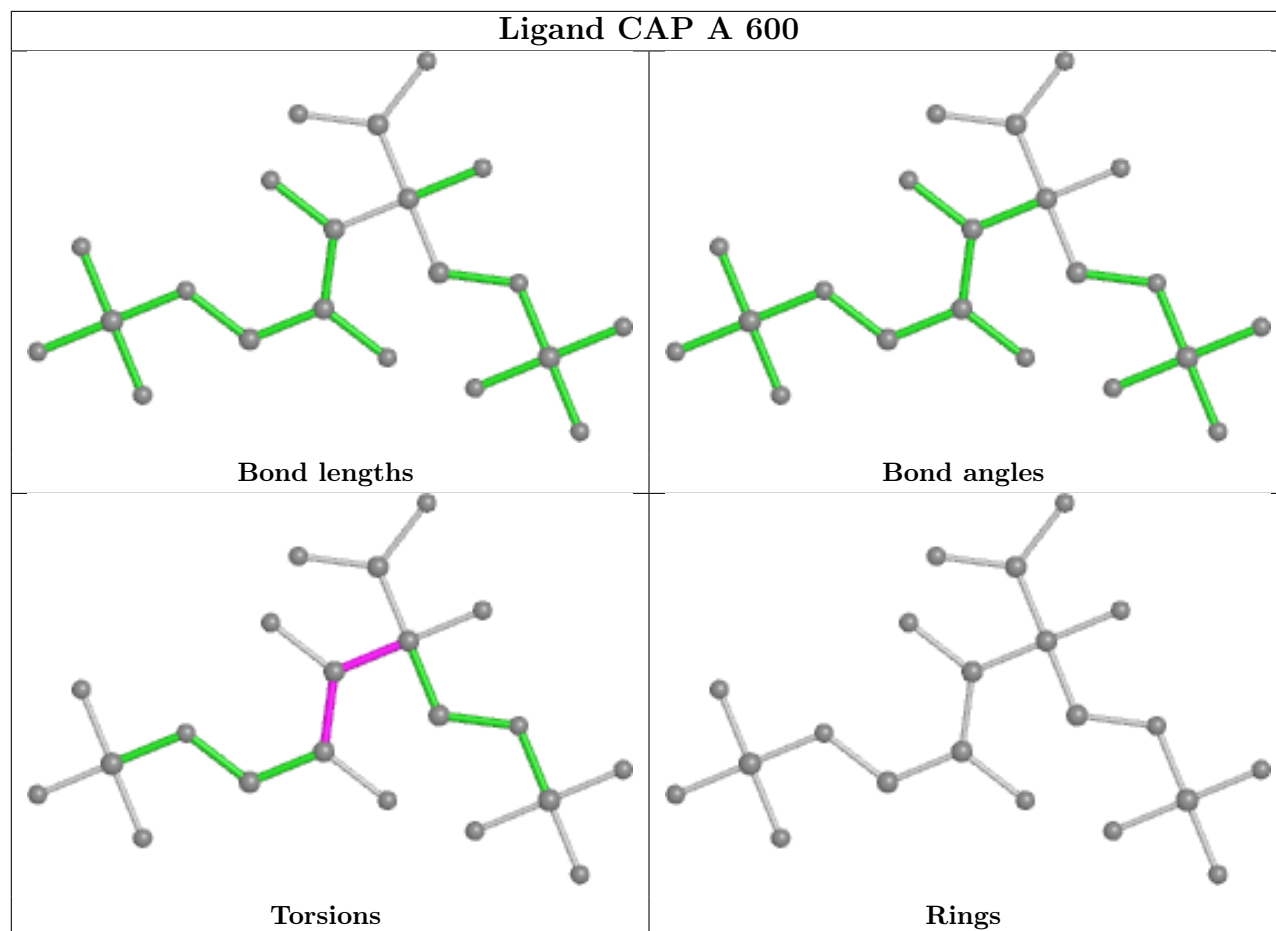












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	435/444 (97%)	0.83	43 (9%) 7 11	28, 41, 56, 60	0
1	B	437/444 (98%)	0.50	35 (8%) 12 18	19, 32, 62, 65	0
1	C	439/444 (98%)	0.27	17 (3%) 39 52	17, 27, 49, 52	0
1	D	436/444 (98%)	0.11	10 (2%) 60 70	16, 24, 35, 42	0
1	E	439/444 (98%)	0.46	41 (9%) 8 14	18, 28, 58, 60	0
1	F	436/444 (98%)	0.32	20 (4%) 32 45	18, 29, 45, 51	0
1	G	436/444 (98%)	0.26	9 (2%) 63 74	18, 31, 44, 48	0
1	H	437/444 (98%)	0.79	52 (11%) 4 7	27, 37, 66, 66	0
1	I	437/444 (98%)	0.23	22 (5%) 28 41	17, 28, 47, 53	0
1	J	437/444 (98%)	0.39	35 (8%) 12 18	16, 25, 59, 60	0
All	All	4369/4440 (98%)	0.42	284 (6%) 18 27	16, 30, 52, 66	0

The worst 5 of 284 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	444	VAL	7.3
1	J	434	ALA	6.6
1	E	441	VAL	6.4
1	E	425	ALA	6.2
1	E	415	ILE	6.1

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	KCX	C	189	12/13	0.96	0.20	24,24,24,24	0
1	KCX	H	189	12/13	0.96	0.20	35,36,37,37	0
1	KCX	A	189	12/13	0.97	0.22	33,33,33,34	0
1	KCX	E	189	12/13	0.97	0.21	22,23,24,24	0
1	KCX	B	189	12/13	0.97	0.23	30,31,32,33	0
1	KCX	I	189	12/13	0.97	0.19	24,25,26,26	0
1	KCX	J	189	12/13	0.97	0.23	22,23,23,24	0
1	KCX	D	189	12/13	0.98	0.20	16,18,19,19	0
1	KCX	F	189	12/13	0.98	0.20	22,22,22,22	0
1	KCX	G	189	12/13	0.98	0.21	21,21,22,23	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.

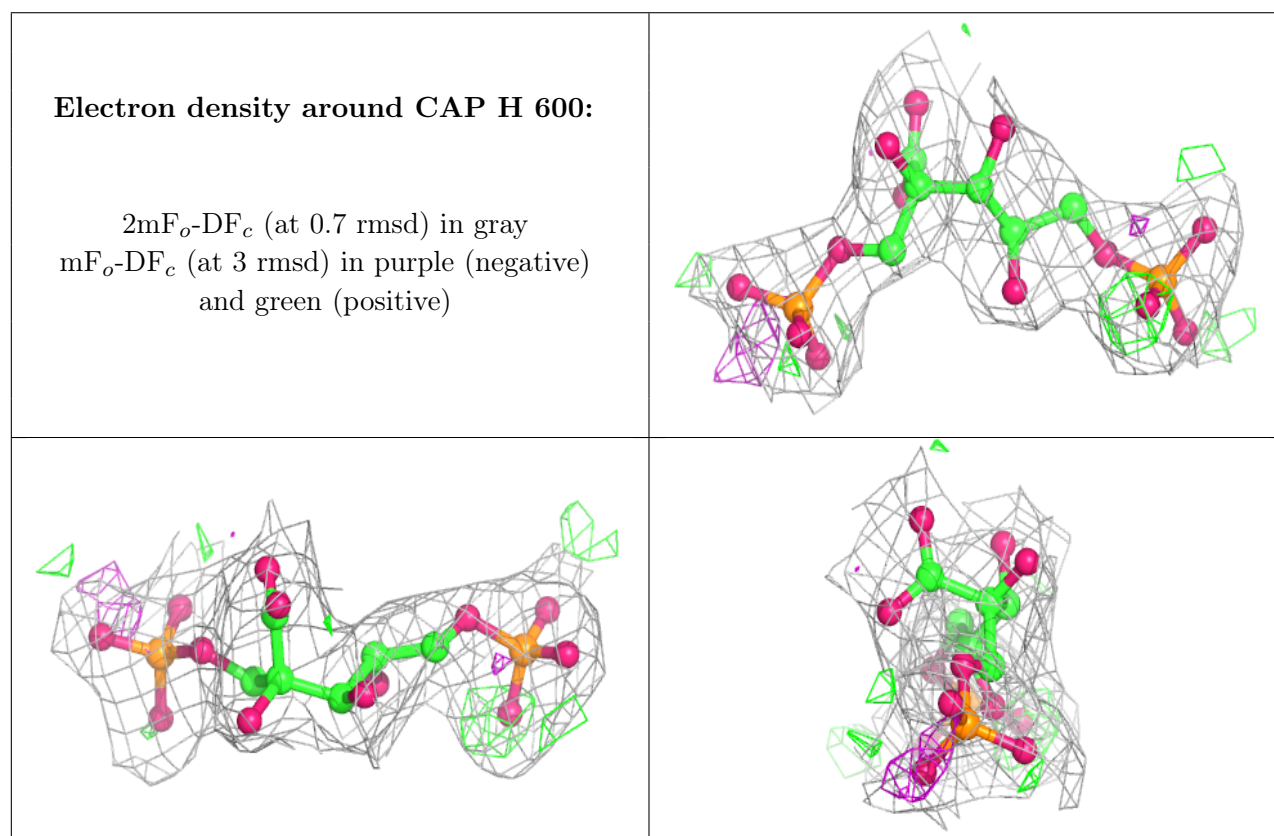
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	CAP	H	600	21/21	0.89	0.22	41,42,42,43	0
2	CAP	E	600	21/21	0.92	0.24	31,37,40,41	0
3	MG	B	500	1/1	0.93	0.10	31,31,31,31	0
2	CAP	A	600	21/21	0.94	0.17	36,38,38,39	0
3	MG	C	500	1/1	0.94	0.17	28,28,28,28	0
3	MG	H	500	1/1	0.94	0.16	37,37,37,37	0
3	MG	I	500	1/1	0.94	0.10	20,20,20,20	0
2	CAP	J	600	21/21	0.95	0.21	31,35,38,38	0
3	MG	G	500	1/1	0.97	0.09	20,20,20,20	0
2	CAP	C	600	21/21	0.97	0.18	30,31,32,32	0
2	CAP	B	600	21/21	0.97	0.16	31,35,36,37	0
2	CAP	G	600	21/21	0.98	0.17	22,25,26,26	0
2	CAP	D	600	21/21	0.98	0.13	16,20,21,21	0
3	MG	E	500	1/1	0.98	0.23	26,26,26,26	0
2	CAP	I	600	21/21	0.98	0.10	18,21,21,22	0
2	CAP	F	600	21/21	0.98	0.12	22,24,24,25	0
3	MG	A	500	1/1	0.98	0.14	28,28,28,28	0
3	MG	F	500	1/1	0.99	0.10	25,25,25,25	0
3	MG	D	500	1/1	0.99	0.08	15,15,15,15	0

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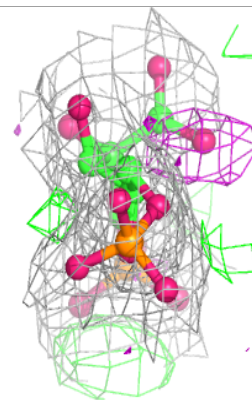
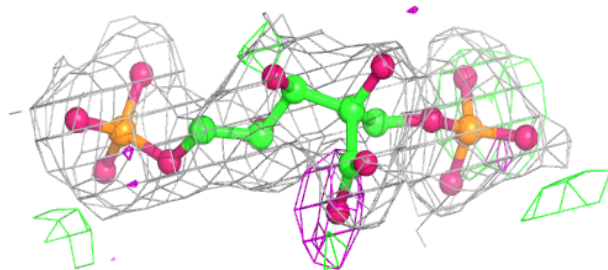
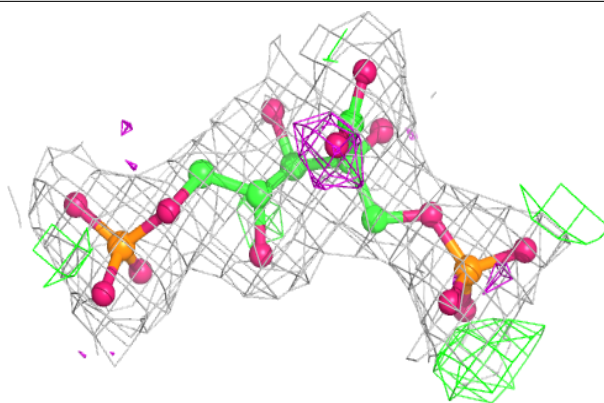
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	J	500	1/1	0.99	0.13	19,19,19,19	0

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.

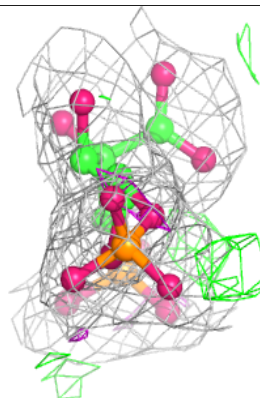
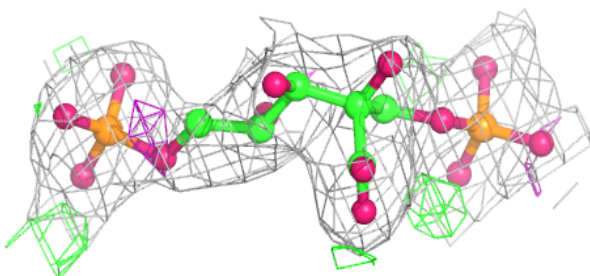
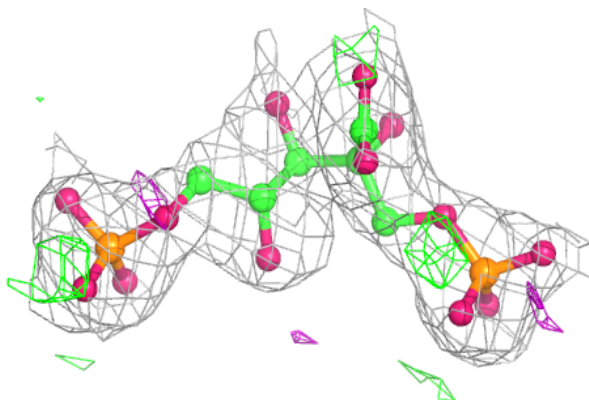


Electron density around CAP E 600:

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

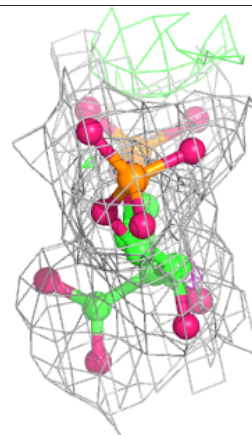
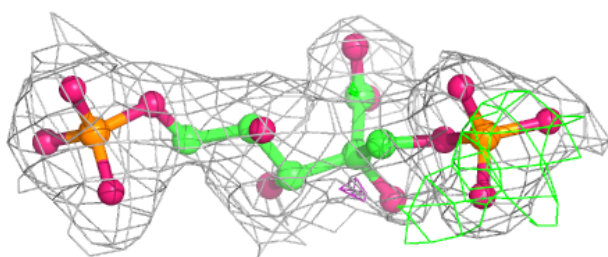
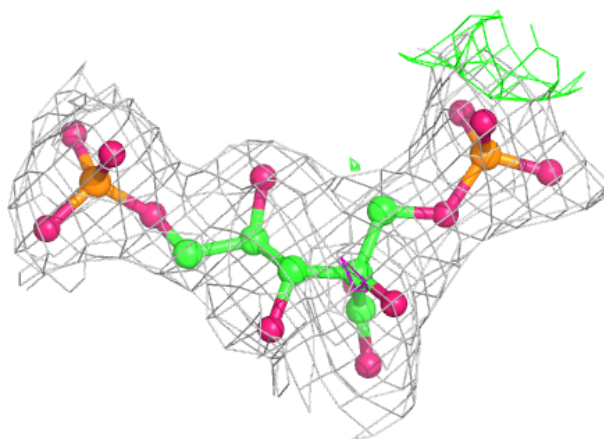
**Electron density around CAP A 600:**

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

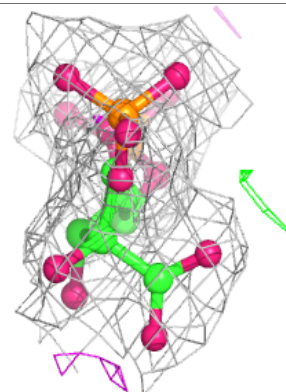
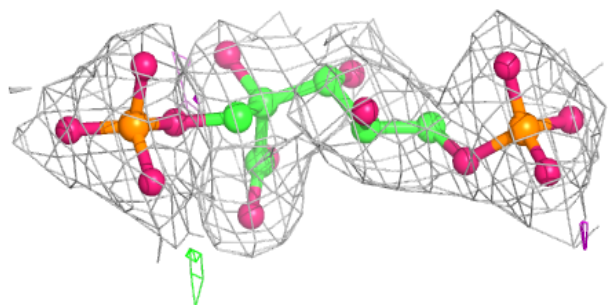
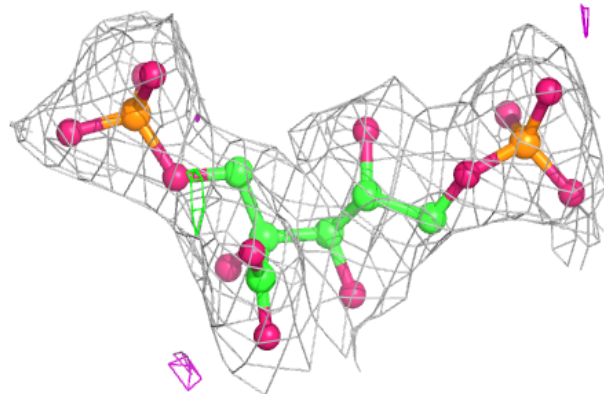


Electron density around CAP J 600:

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

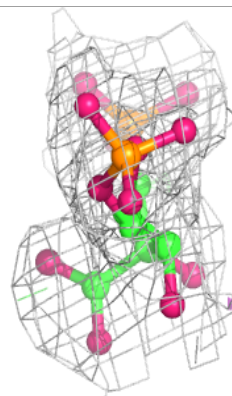
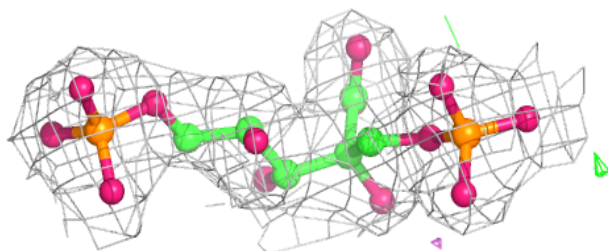
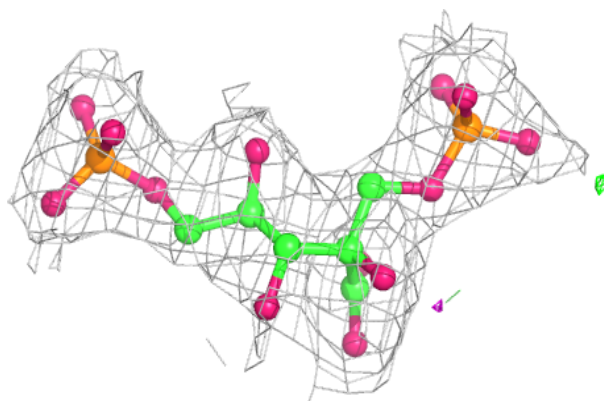
**Electron density around CAP C 600:**

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

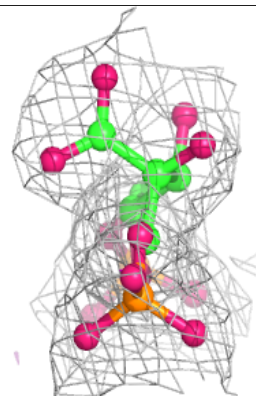
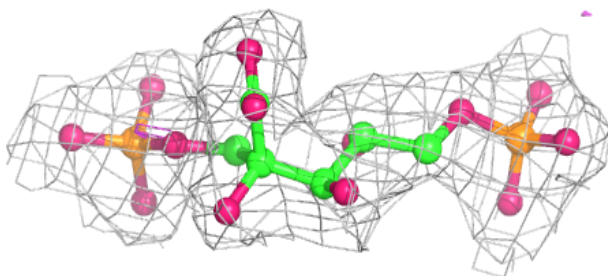
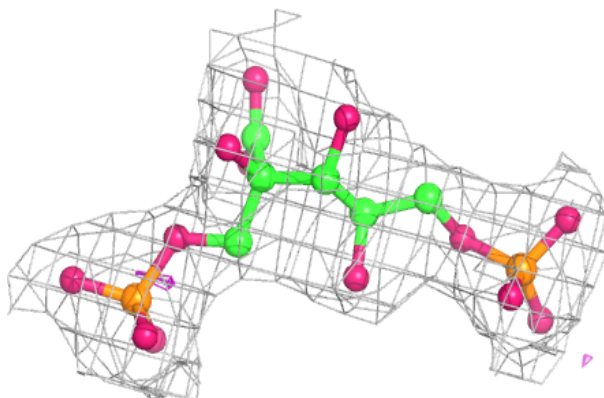


Electron density around CAP B 600:

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

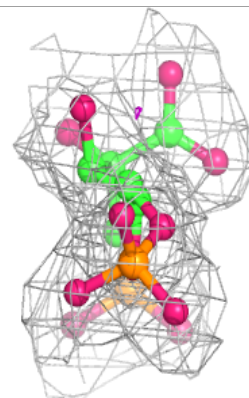
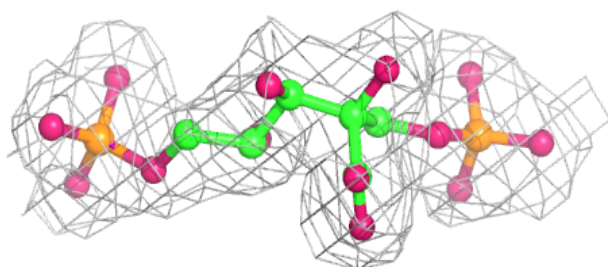
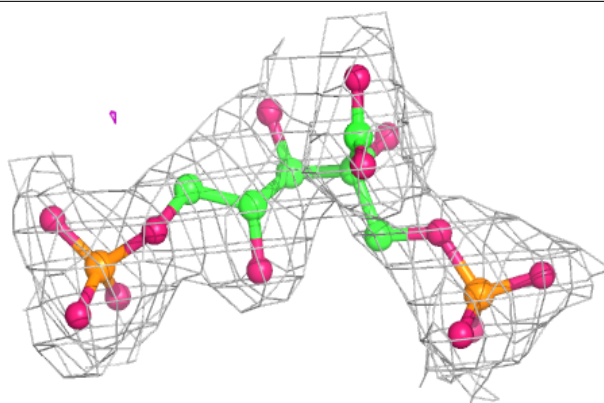
**Electron density around CAP G 600:**

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

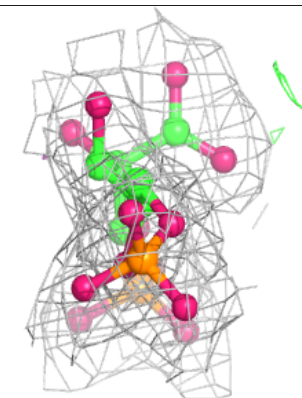
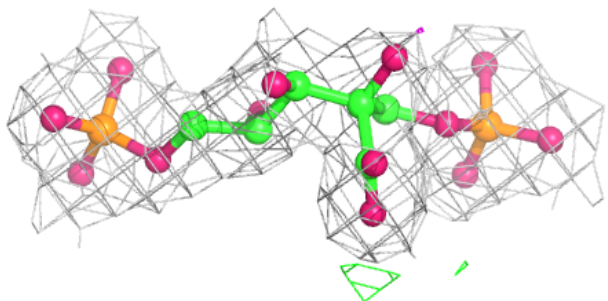
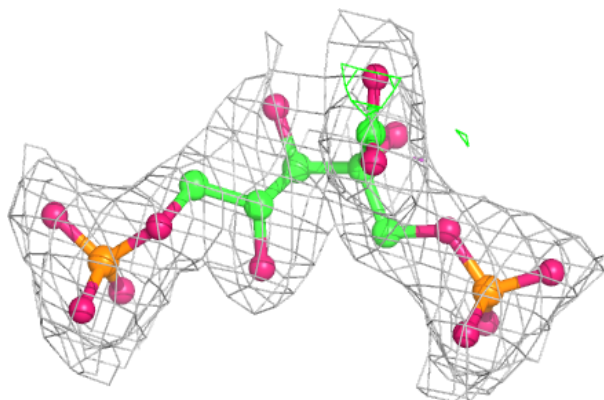


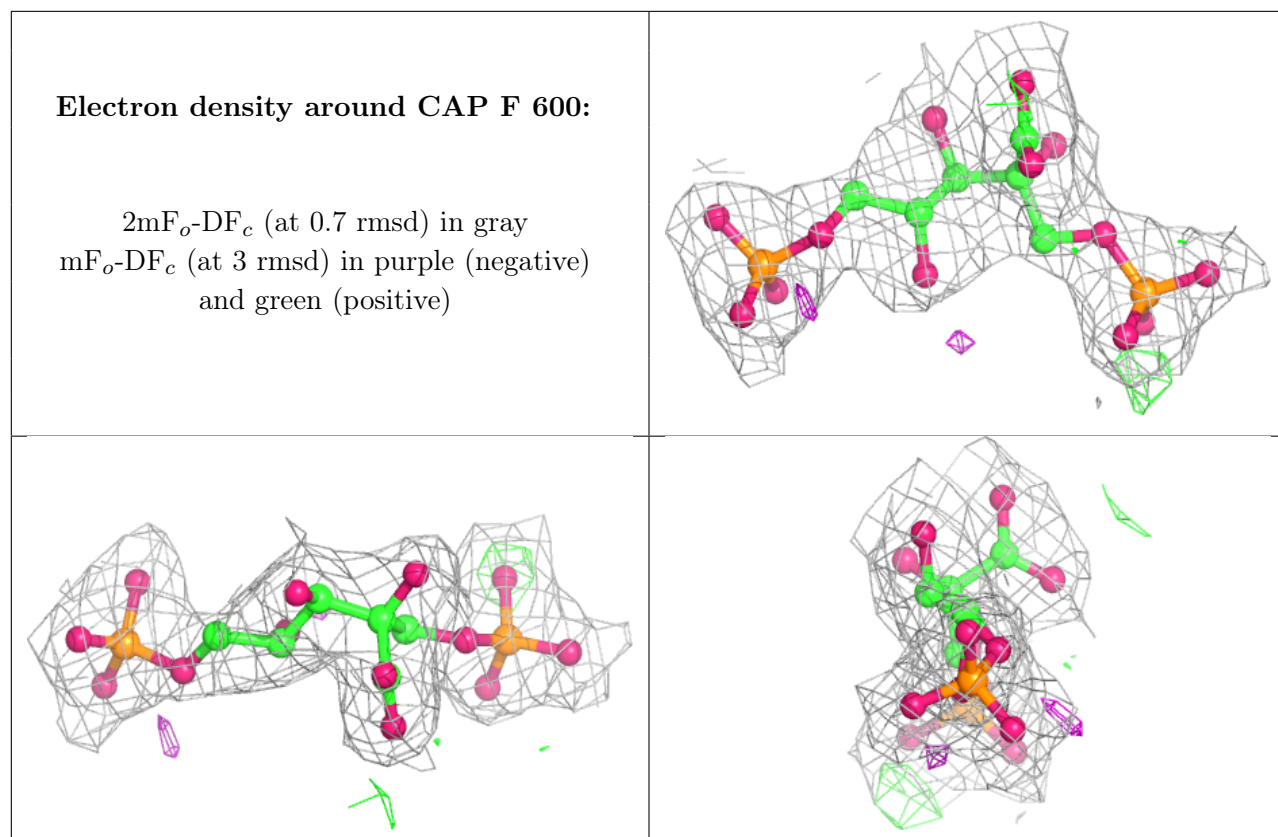
Electron density around CAP D 600:

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

**Electron density around CAP 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.