



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 17, 2026 – 09:37 PM UTC

PDB ID : 3A13 / pdb_00003a13
Title : Crystal structure of Type III Rubisco SP4 mutant complexed with 2-CABP and activated with Ca
Authors : Nishitani, Y.; Fujihashi, M.; Doi, T.; Yoshida, S.; Atomi, H.; Imanaka, T.; Miki, K.
Deposited on : 2009-03-25
Resolution : 2.34 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

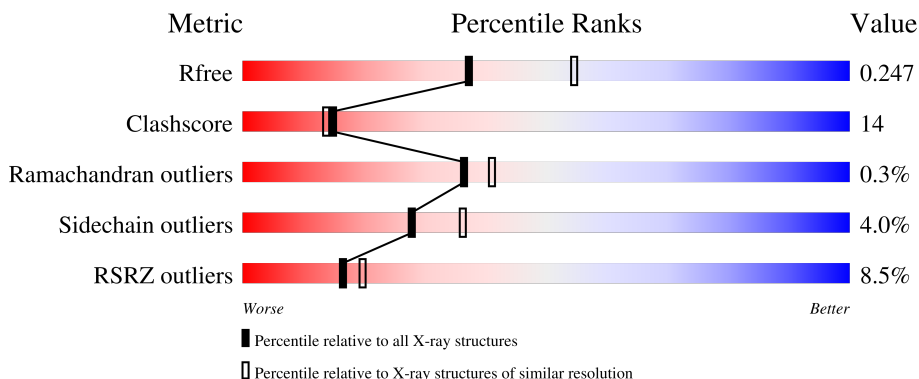
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 Å.

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



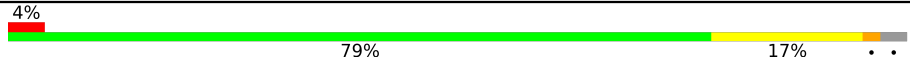

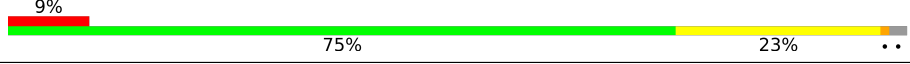
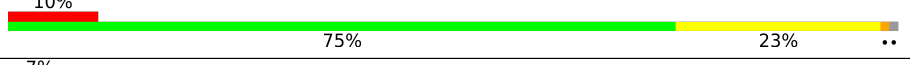

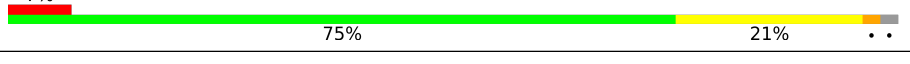
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	

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Mol	Chain	Length	Quality of chain
1	E	444	 4% 79% 17% ..
1	F	444	 9% 75% 23% ..
1	G	444	 9% 75% 23% ..
1	H	444	 10% 75% 23% ..
1	I	444	 7% 75% 21% ..
1	J	444	 7% 75% 21% ..

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 36193 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
			Total	C	N	O	S			
1	A	436	3408	2186	586	626	10	0	0	0
1	B	437	3412	2187	586	629	10	0	0	0
1	C	437	3399	2181	584	624	10	0	0	0
1	D	437	3392	2170	584	628	10	0	0	0
1	E	432	3379	2163	581	625	10	0	0	0
1	F	437	3405	2184	586	625	10	0	0	0
1	G	437	3413	2190	585	628	10	0	0	0
1	H	438	3412	2189	588	625	10	0	0	0
1	I	437	3423	2195	587	631	10	0	0	0
1	J	434	3379	2161	583	625	10	0	0	0

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

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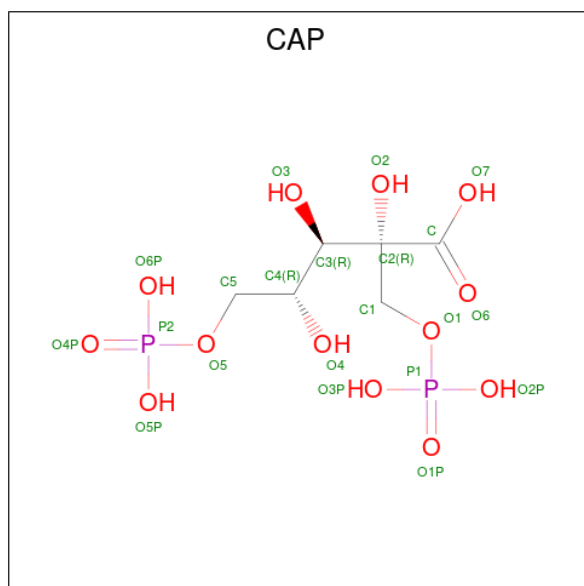
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Chain	Residue	Modelled	Actual	Comment	Reference
B	330	THR	VAL	engineered mutation	UNP O93627
C	326	GLU	GLY	engineered mutation	UNP O93627
C	327	ARG	LYS	engineered mutation	UNP O93627
C	328	ASP	TRP	engineered mutation	UNP O93627
C	329	ILE	ASP	engineered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

- Molecule 3 is 2-CARBOXYARABINITOL-1,5-DIPHOSPHATE (CCD ID: 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
3	B	1	Total C O P 21 6 13 2	0	0
3	C	1	Total C O P 21 6 13 2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
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 CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total	Ca	0	0
			1	1		
4	J	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	193	Total	O	0	0
			193	193		
5	B	204	Total	O	0	0
			204	204		
5	C	186	Total	O	0	0
			186	186		
5	D	210	Total	O	0	0
			210	210		
5	E	193	Total	O	0	0
			193	193		
5	F	176	Total	O	0	0
			176	176		
5	G	203	Total	O	0	0
			203	203		
5	H	180	Total	O	0	0
			180	180		

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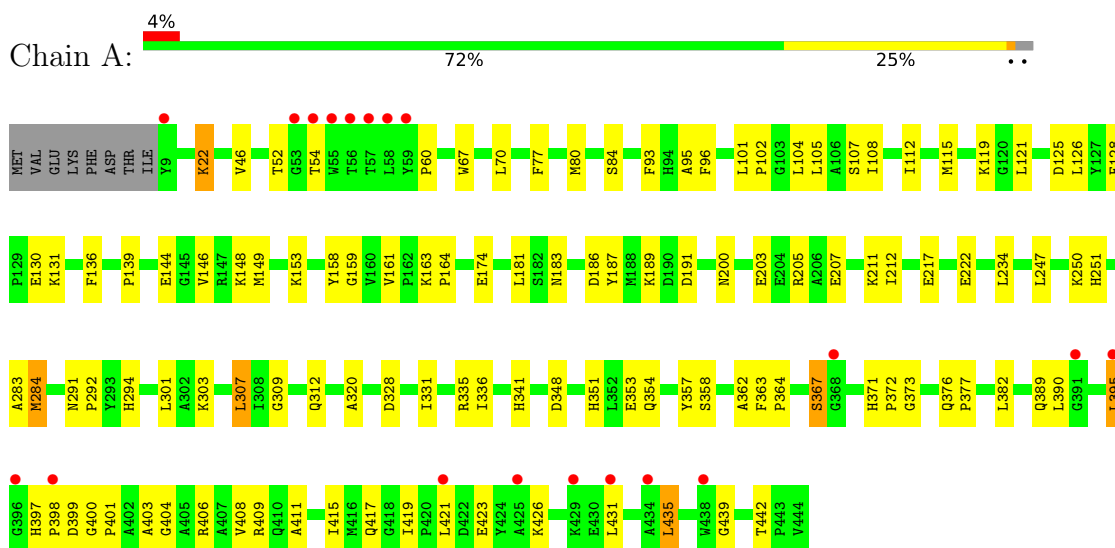
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	212	Total 212	O 212	0	0
5	J	194	Total 194	O 194	0	0

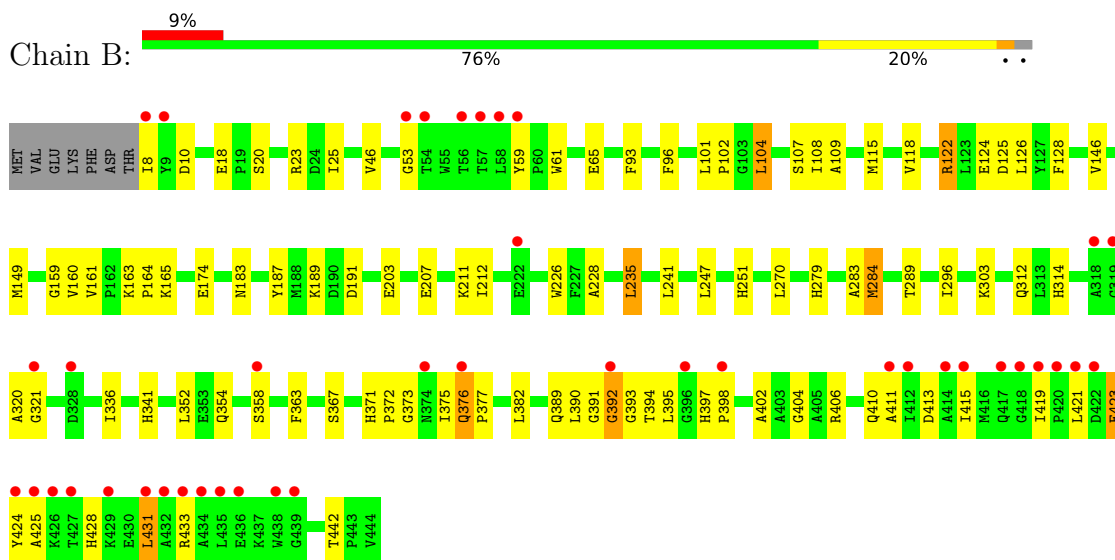
3 Residue-property plots [i](#)

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.

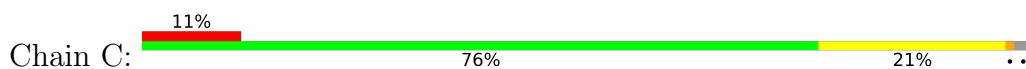
- Molecule 1: Ribulose biphosphate carboxylase

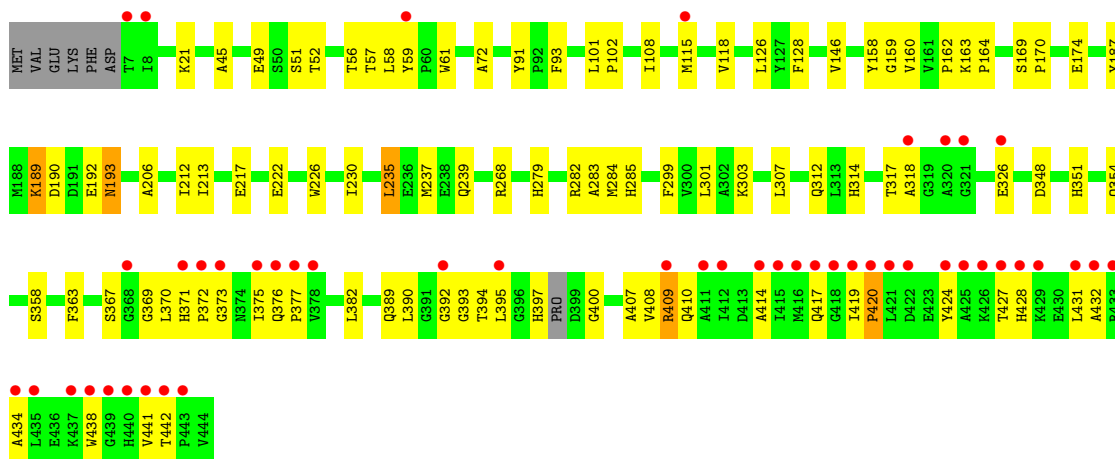


- Molecule 1: Ribulose biphosphate carboxylase

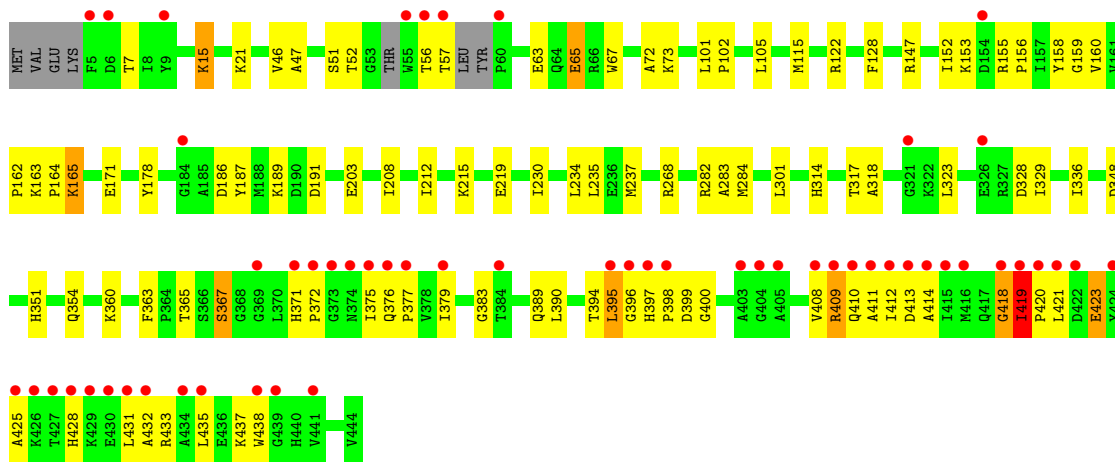
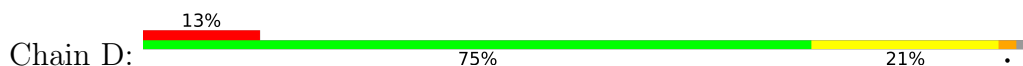


- Molecule 1: Ribulose biphosphate carboxylase

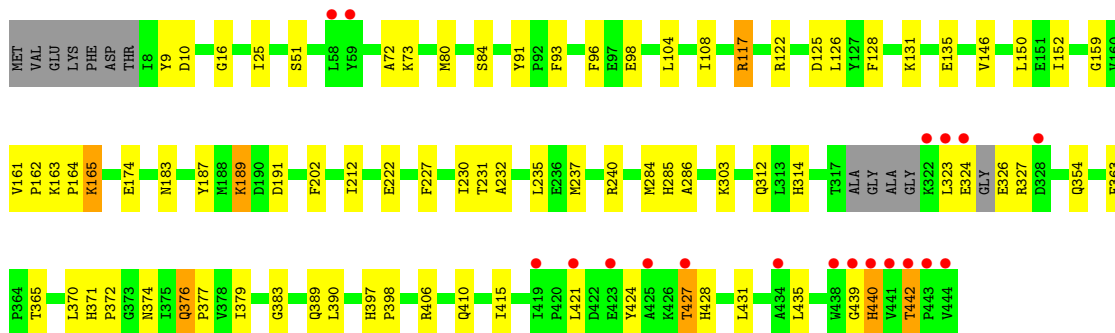
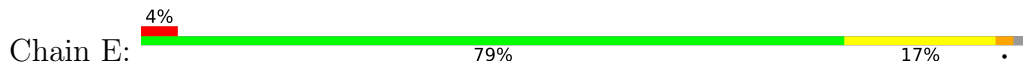




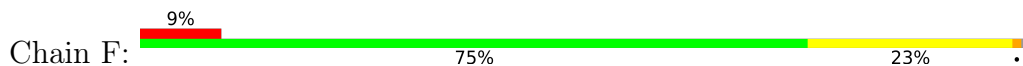
- Molecule 1: Ribulose biphosphate carboxylase

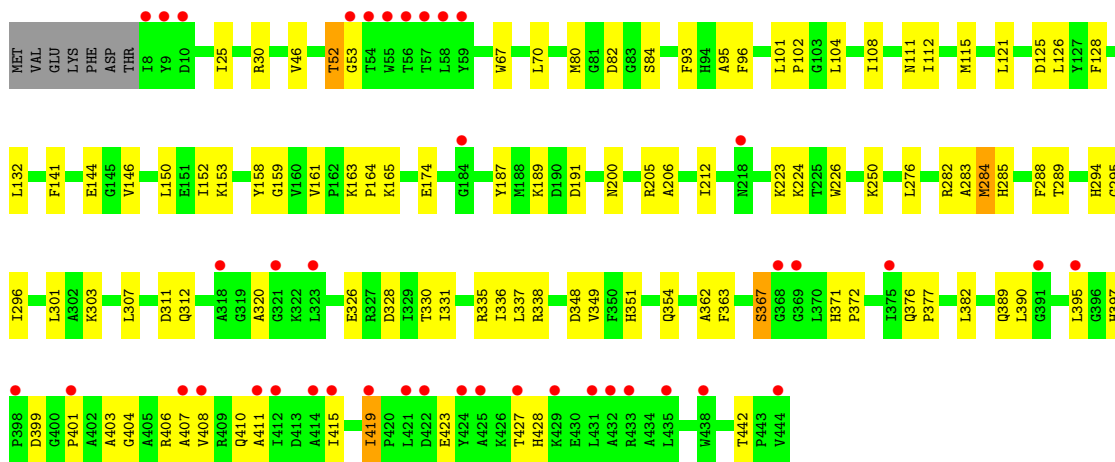


- Molecule 1: Ribulose biphosphate carboxylase

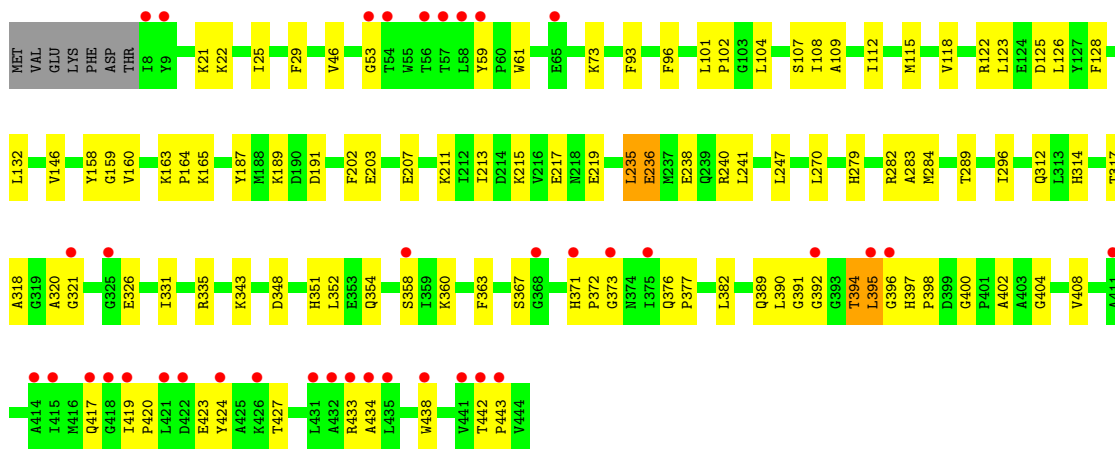
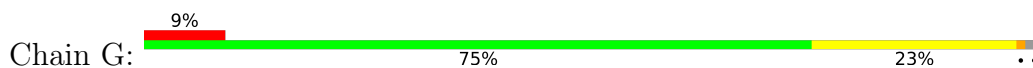


- Molecule 1: Ribulose biphosphate carboxylase

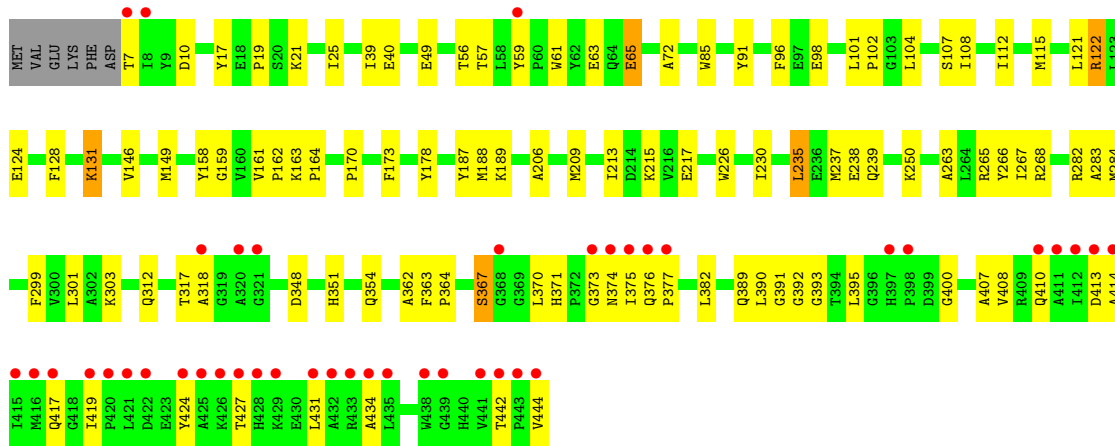
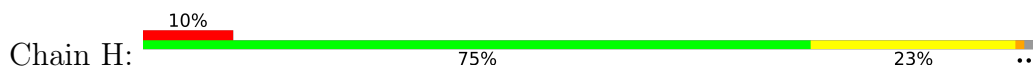




- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase



- Molecule 1: Ribulose biphosphate carboxylase

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	173.68Å 247.09Å 144.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.22 – 2.34 42.22 – 2.34	Depositor EDS
% Data completeness (in resolution range)	99.3 (42.22-2.34) 99.6 (42.22-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.34Å)	Xtrriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.205 , 0.250 0.206 , 0.247	Depositor DCC
R_{free} test set	13142 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.6	Xtrriage
Anisotropy	0.039	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	36193	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 49.31 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.5974e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, KCX, CAP, 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	0.46	0/3482	0.77	2/4722 (0.0%)
1	B	0.47	0/3486	0.77	1/4729 (0.0%)
1	C	0.46	0/3472	0.76	2/4711 (0.0%)
1	D	0.47	0/3463	0.76	4/4695 (0.1%)
1	E	0.47	0/3451	0.74	0/4680
1	F	0.46	0/3479	0.79	3/4719 (0.1%)
1	G	0.48	0/3488	0.78	4/4732 (0.1%)
1	H	0.46	0/3486	0.77	3/4729 (0.1%)
1	I	0.49	0/3495	0.76	0/4735
1	J	0.48	0/3451	0.77	4/4679 (0.1%)
All	All	0.47	0/34753	0.77	23/47131 (0.0%)

There are no bond length outliers.

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	53	GLY	N-CA-C	7.19	121.42	112.79
1	J	400	GLY	CA-C-N	6.28	125.77	119.24
1	J	400	GLY	C-N-CA	6.28	125.77	119.24
1	D	400	GLY	CA-C-N	6.12	127.49	119.84
1	D	400	GLY	C-N-CA	6.12	127.49	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3408	0	3311	89	0
1	B	3412	0	3307	122	0
1	C	3399	0	3284	94	0
1	D	3392	0	3267	94	0
1	E	3379	0	3253	76	0
1	F	3405	0	3301	76	0
1	G	3413	0	3303	93	0
1	H	3412	0	3315	96	0
1	I	3423	0	3330	88	0
1	J	3379	0	3235	89	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	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
3	A	21	0	7	1	0
3	B	21	0	7	1	0
3	C	21	0	7	3	0
3	D	21	0	7	0	0
3	E	21	0	9	1	0
3	F	21	0	8	2	0
3	G	21	0	7	1	0
3	H	21	0	8	2	0
3	I	21	0	7	0	0
3	J	21	0	9	1	0
4	E	1	0	0	0	0
4	J	1	0	0	0	0
5	A	193	0	0	16	0
5	B	204	0	0	14	0
5	C	186	0	0	9	0
5	D	210	0	0	16	0
5	E	193	0	0	12	0
5	F	176	0	0	9	0
5	G	203	0	0	15	0
5	H	180	0	0	6	0
5	I	212	0	0	14	0
5	J	194	0	0	11	0
All	All	36193	0	32982	925	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 14.

The worst 5 of 925 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:F:326:GLU:HG2	5:F:602:HOH:O	1.45	1.16
1:B:104:LEU:HD23	1:B:104:LEU:C	1.72	1.14
1:J:174:GLU:HG3	1:J:212:ILE:HD11	1.29	1.13
1:H:149:MET:HE3	1:H:250:LYS:HD2	1.18	1.12
1:J:391:GLY:O	1:J:395:LEU:HD12	1.49	1.12

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	433/444 (98%)	417 (96%)	13 (3%)	3 (1%)	18	18
1	B	434/444 (98%)	413 (95%)	19 (4%)	2 (0%)	24	26
1	C	432/444 (97%)	408 (94%)	23 (5%)	1 (0%)	43	50
1	D	430/444 (97%)	401 (93%)	26 (6%)	3 (1%)	18	18
1	E	425/444 (96%)	410 (96%)	14 (3%)	1 (0%)	43	50
1	F	434/444 (98%)	409 (94%)	23 (5%)	2 (0%)	24	26
1	G	434/444 (98%)	411 (95%)	23 (5%)	0	100	100
1	H	435/444 (98%)	415 (95%)	20 (5%)	0	100	100
1	I	430/444 (97%)	411 (96%)	18 (4%)	1 (0%)	43	50
1	J	427/444 (96%)	407 (95%)	19 (4%)	1 (0%)	43	50
All	All	4314/4440 (97%)	4102 (95%)	198 (5%)	14 (0%)	36	41

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	284	MET
1	E	284	MET
1	F	284	MET
1	F	401	PRO
1	I	284	MET

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	336/356 (94%)	319 (95%)	17 (5%)	21	26
1	B	336/356 (94%)	322 (96%)	14 (4%)	26	34
1	C	332/356 (93%)	322 (97%)	10 (3%)	36	47
1	D	332/356 (93%)	315 (95%)	17 (5%)	21	26
1	E	333/356 (94%)	322 (97%)	11 (3%)	33	43
1	F	334/356 (94%)	326 (98%)	8 (2%)	43	55
1	G	335/356 (94%)	322 (96%)	13 (4%)	28	37
1	H	335/356 (94%)	325 (97%)	10 (3%)	36	47
1	I	339/356 (95%)	318 (94%)	21 (6%)	16	19
1	J	329/356 (92%)	316 (96%)	13 (4%)	28	36
All	All	3341/3560 (94%)	3207 (96%)	134 (4%)	28	36

5 of 134 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	328	ASP
1	I	430	GLU
1	J	363	PHE
1	D	235	LEU
1	D	234	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	410	GLN
1	J	410	GLN
1	G	239	GLN
1	J	354	GLN
1	I	64	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	B	189	2,1	10,11,12	0.99	0	6,12,14	1.39	1 (16%)
1	KCX	E	189	4,1	10,11,12	0.93	0	6,12,14	1.36	1 (16%)
1	KCX	C	189	2,1	10,11,12	0.95	0	6,12,14	1.65	2 (33%)
1	KCX	A	189	2,1	10,11,12	0.89	0	6,12,14	1.24	1 (16%)
1	KCX	H	189	2,1	10,11,12	1.01	0	6,12,14	1.36	1 (16%)
1	KCX	J	189	4,1	10,11,12	0.96	0	6,12,14	1.66	1 (16%)
1	KCX	G	189	2,1	10,11,12	1.06	1 (10%)	6,12,14	1.19	1 (16%)
1	KCX	D	189	2,1	10,11,12	0.79	0	6,12,14	1.64	1 (16%)
1	KCX	F	189	2,1	10,11,12	0.93	0	6,12,14	1.40	1 (16%)
1	KCX	I	189	2,1	10,11,12	0.89	0	6,12,14	1.34	1 (16%)

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	B	189	2,1	-	0/9/10/12	-
1	KCX	E	189	4,1	-	0/9/10/12	-
1	KCX	C	189	2,1	-	0/9/10/12	-
1	KCX	A	189	2,1	-	1/9/10/12	-
1	KCX	H	189	2,1	-	2/9/10/12	-
1	KCX	J	189	4,1	-	0/9/10/12	-
1	KCX	G	189	2,1	-	1/9/10/12	-
1	KCX	D	189	2,1	-	0/9/10/12	-
1	KCX	F	189	2,1	-	1/9/10/12	-
1	KCX	I	189	2,1	-	0/9/10/12	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	189	KCX	OQ1-CX	2.24	1.25	1.21

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	189	KCX	OQ1-CX-NZ	-3.82	119.11	124.92
1	D	189	KCX	OQ1-CX-NZ	-3.77	119.19	124.92
1	F	189	KCX	OQ1-CX-NZ	-3.26	119.97	124.92
1	E	189	KCX	OQ1-CX-NZ	-3.07	120.26	124.92
1	C	189	KCX	OQ1-CX-NZ	-3.06	120.27	124.92

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	189	KCX	C-CA-CB-CG
1	G	189	KCX	C-CA-CB-CG
1	H	189	KCX	C-CA-CB-CG
1	H	189	KCX	O-C-CA-CB
1	F	189	KCX	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	A	446	2	18,20,20	1.00	1 (5%)	23,31,31	1.16	2 (8%)
3	CAP	F	446	2	18,20,20	1.05	1 (5%)	23,31,31	1.07	1 (4%)
3	CAP	I	446	2	18,20,20	0.92	0	23,31,31	1.24	2 (8%)
3	CAP	D	446	2	18,20,20	0.91	0	23,31,31	1.25	2 (8%)
3	CAP	H	446	2	18,20,20	0.97	0	23,31,31	1.45	4 (17%)
3	CAP	C	446	2	18,20,20	1.01	1 (5%)	23,31,31	1.50	3 (13%)
3	CAP	G	446	2	18,20,20	1.01	1 (5%)	23,31,31	1.27	2 (8%)
3	CAP	J	446	4	18,20,20	0.98	1 (5%)	23,31,31	1.01	2 (8%)
3	CAP	B	446	2	18,20,20	1.02	1 (5%)	23,31,31	1.28	3 (13%)
3	CAP	E	446	4	18,20,20	0.92	1 (5%)	23,31,31	1.13	2 (8%)

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	A	446	2	-	15/29/29/29	-
3	CAP	F	446	2	-	15/29/29/29	-
3	CAP	I	446	2	-	11/29/29/29	-
3	CAP	D	446	2	-	9/29/29/29	-
3	CAP	H	446	2	-	6/29/29/29	-
3	CAP	C	446	2	-	6/29/29/29	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CAP	G	446	2	-	6/29/29/29	-
3	CAP	J	446	4	-	0/29/29/29	-
3	CAP	B	446	2	-	3/29/29/29	-
3	CAP	E	446	4	-	0/29/29/29	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	446	CAP	C2-C	-2.33	1.51	1.53
3	B	446	CAP	C4-C3	-2.29	1.51	1.54
3	C	446	CAP	C4-C3	-2.25	1.51	1.54
3	G	446	CAP	C4-C3	-2.17	1.51	1.54
3	J	446	CAP	C2-C	-2.13	1.51	1.53

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	446	CAP	O7-C-C2	4.19	121.08	114.06
3	H	446	CAP	O7-C-C2	4.13	120.98	114.06
3	B	446	CAP	O7-C-C2	3.60	120.10	114.06
3	D	446	CAP	O7-C-C2	3.48	119.88	114.06
3	I	446	CAP	O7-C-C2	3.41	119.78	114.06

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	446	CAP	O1-C1-C2-C3
3	A	446	CAP	O1-C1-C2-C
3	A	446	CAP	O1-C1-C2-O2
3	A	446	CAP	O3-C3-C4-O4
3	A	446	CAP	C1-O1-P1-O2P

There are no ring outliers.

8 monomers are involved in 12 short contacts:

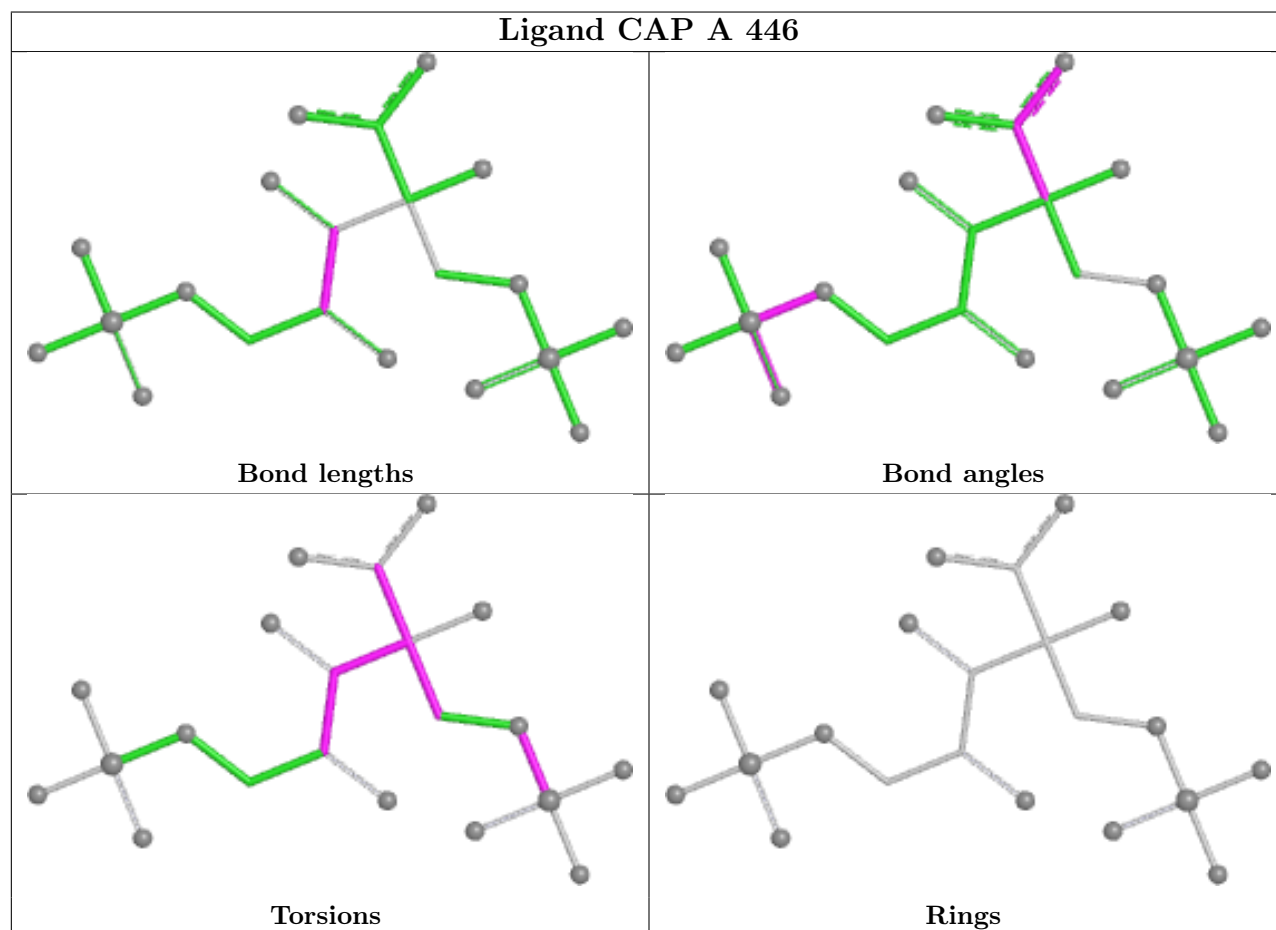
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	446	CAP	1	0
3	F	446	CAP	2	0
3	H	446	CAP	2	0

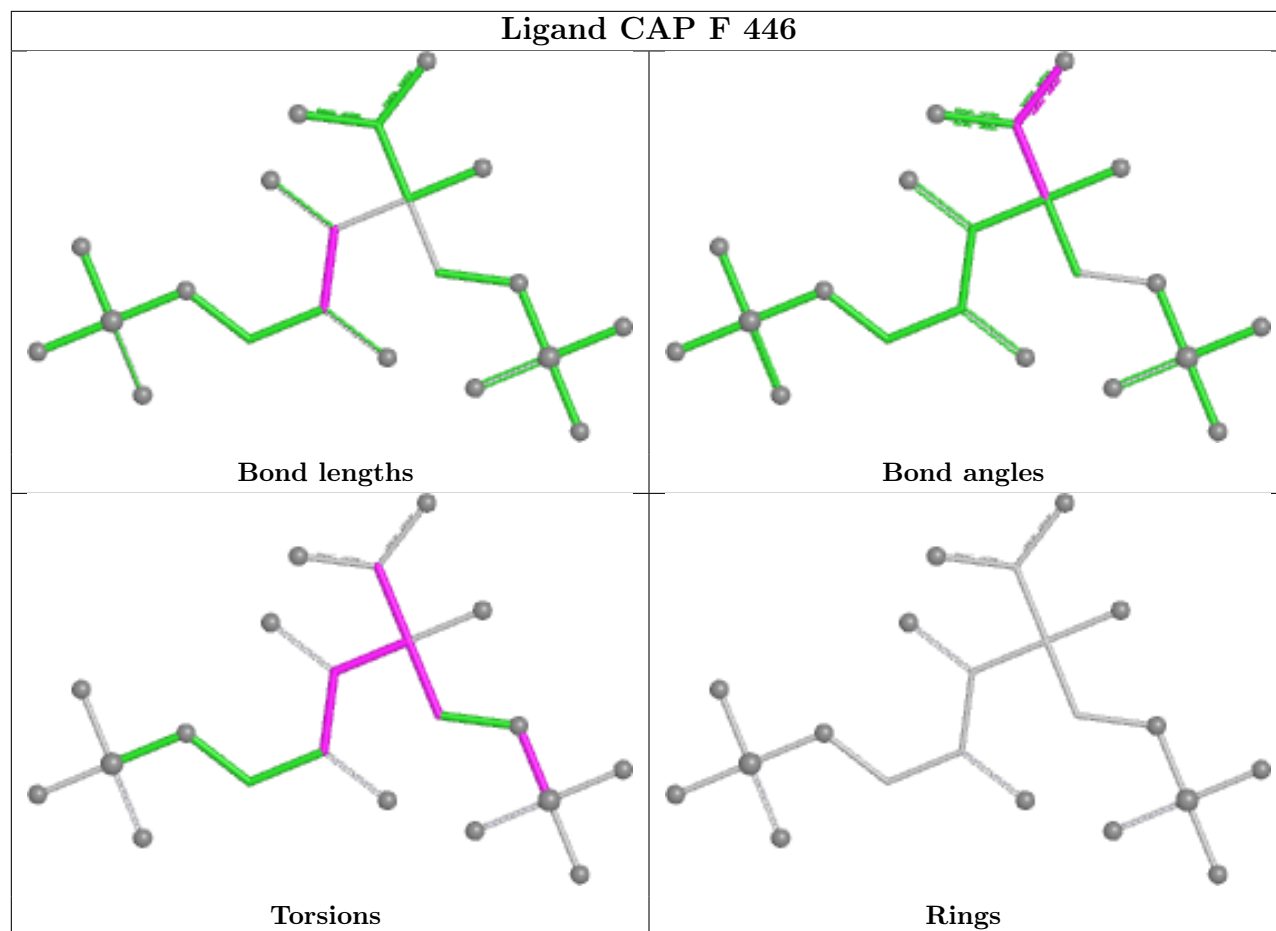
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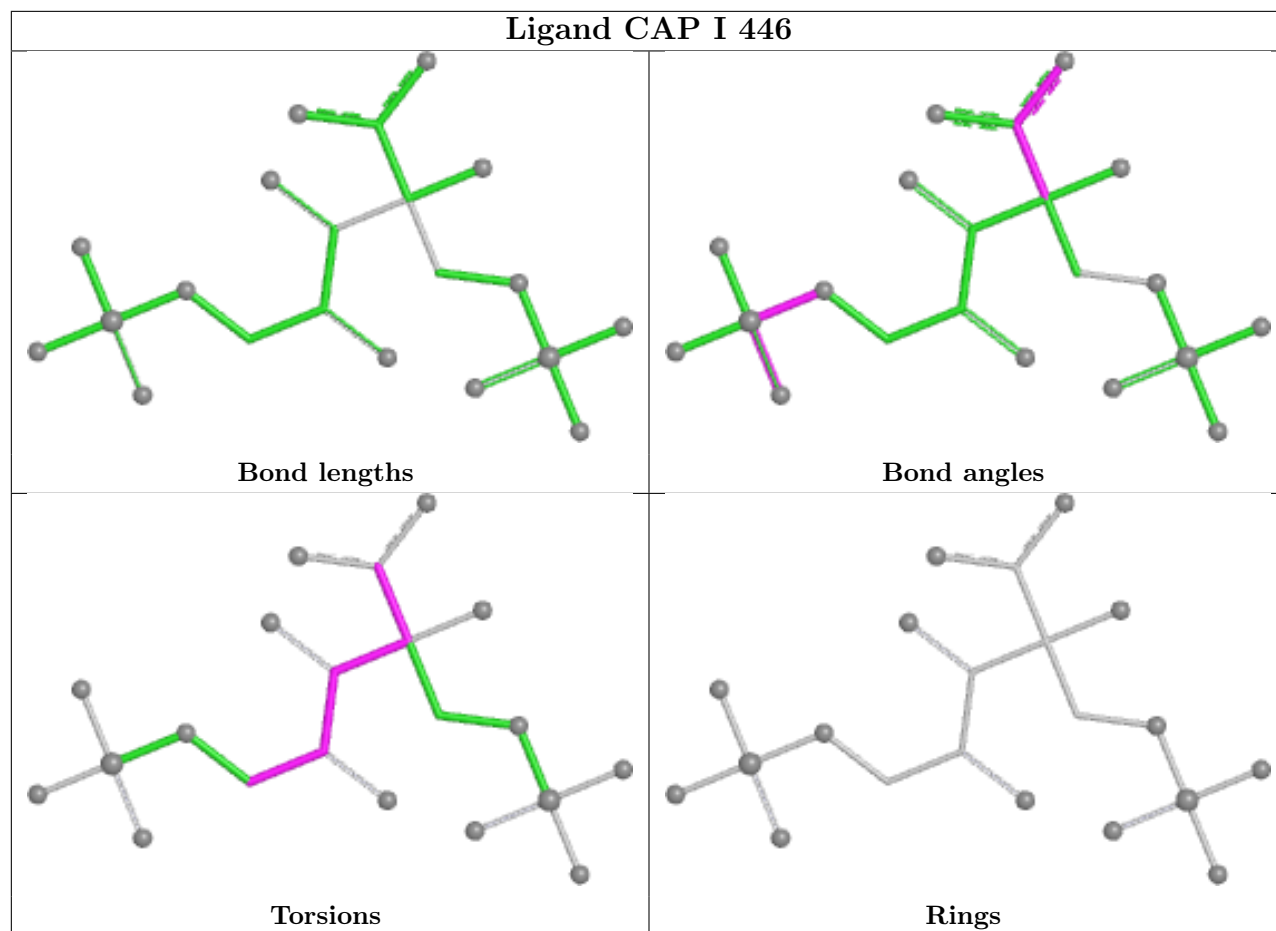
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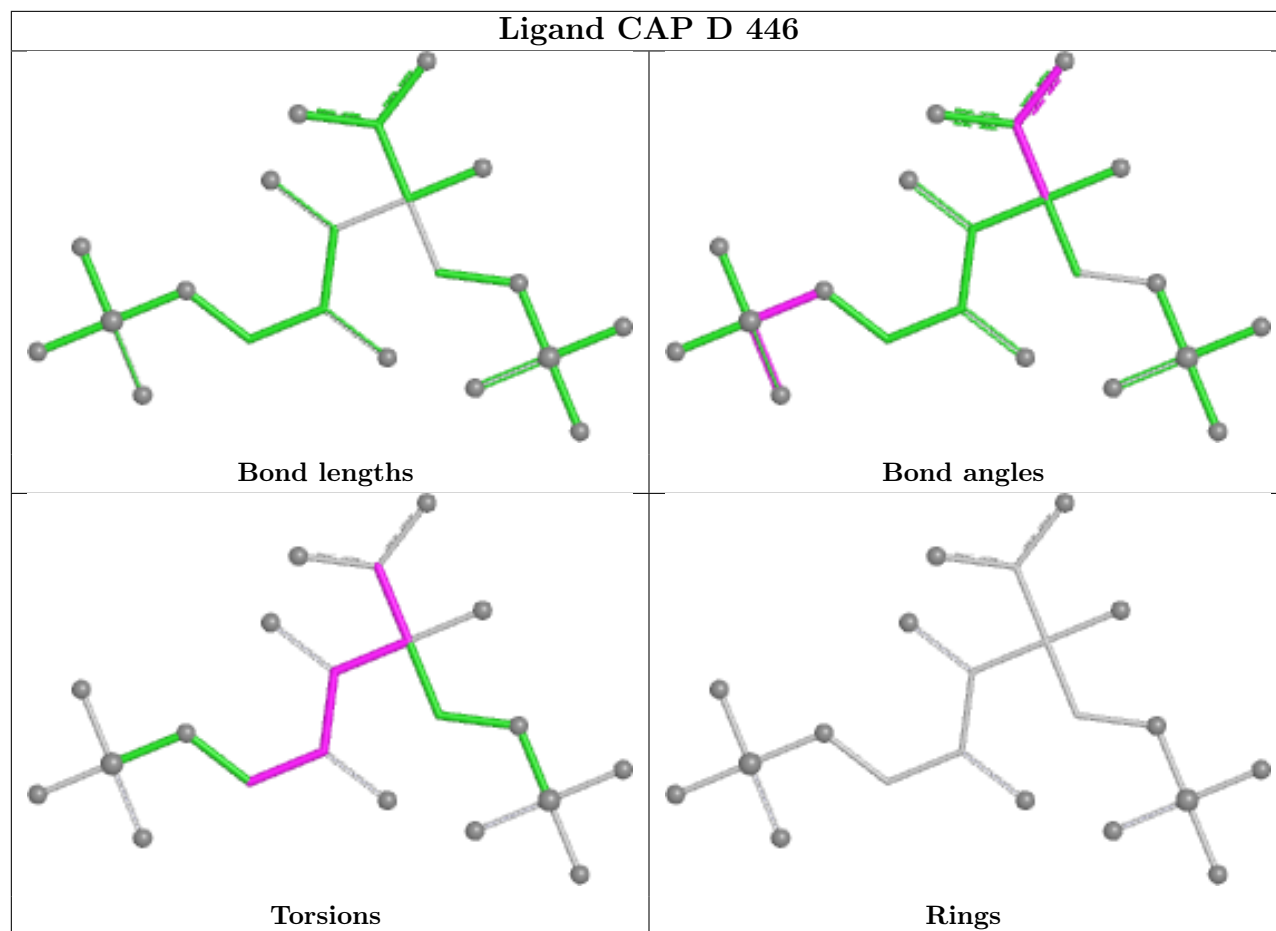
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	446	CAP	3	0
3	G	446	CAP	1	0
3	J	446	CAP	1	0
3	B	446	CAP	1	0
3	E	446	CAP	1	0

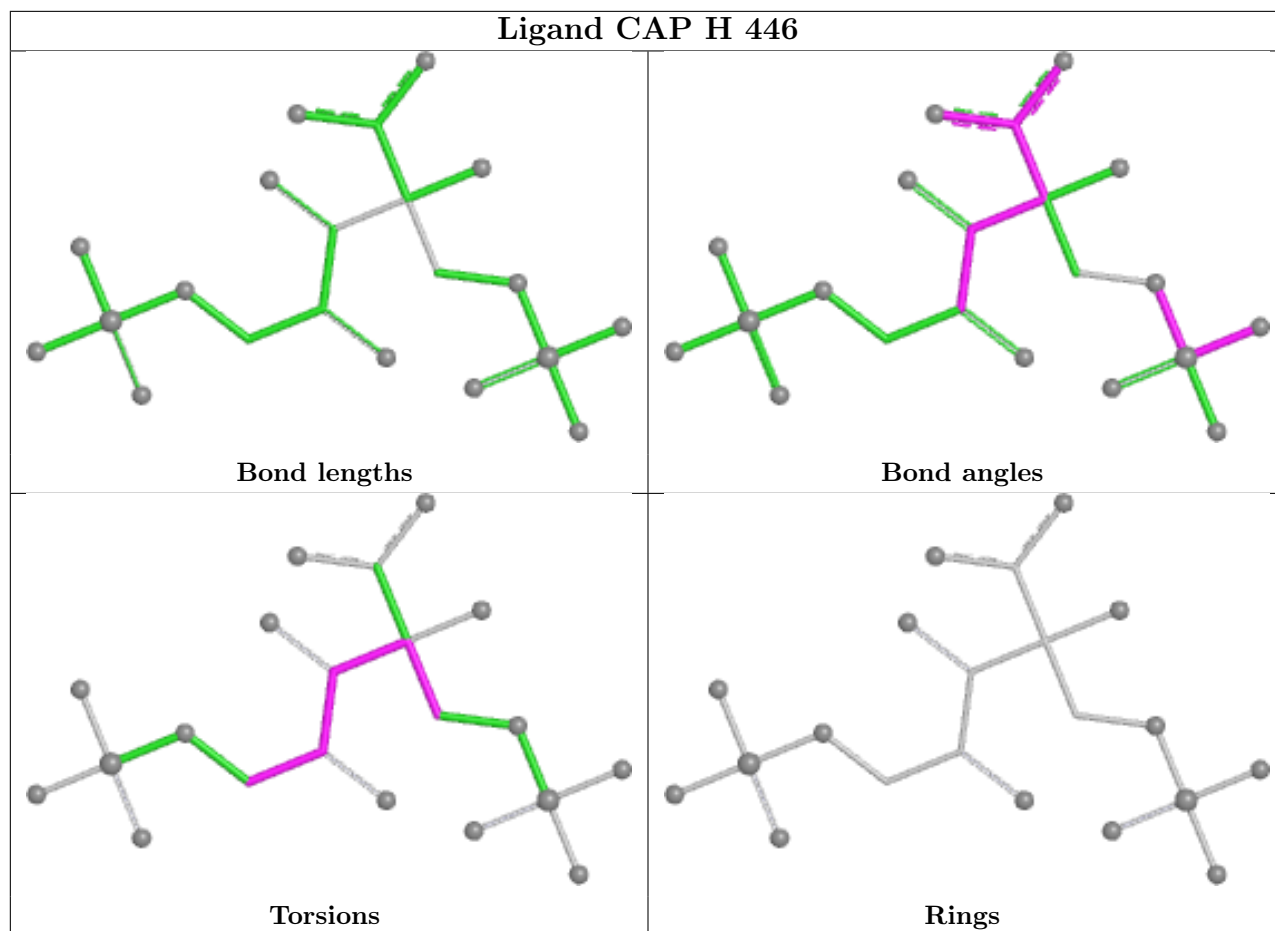
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

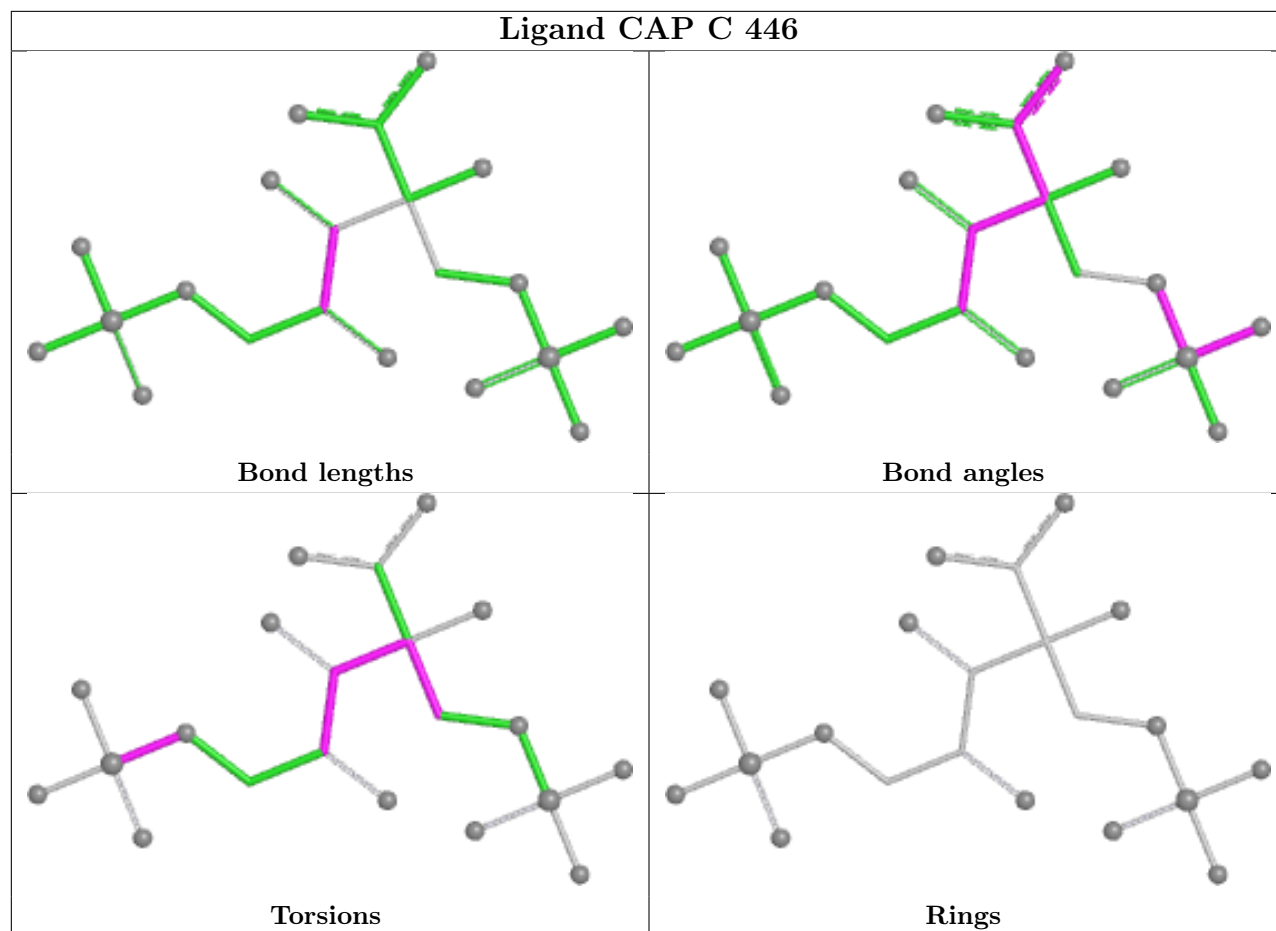


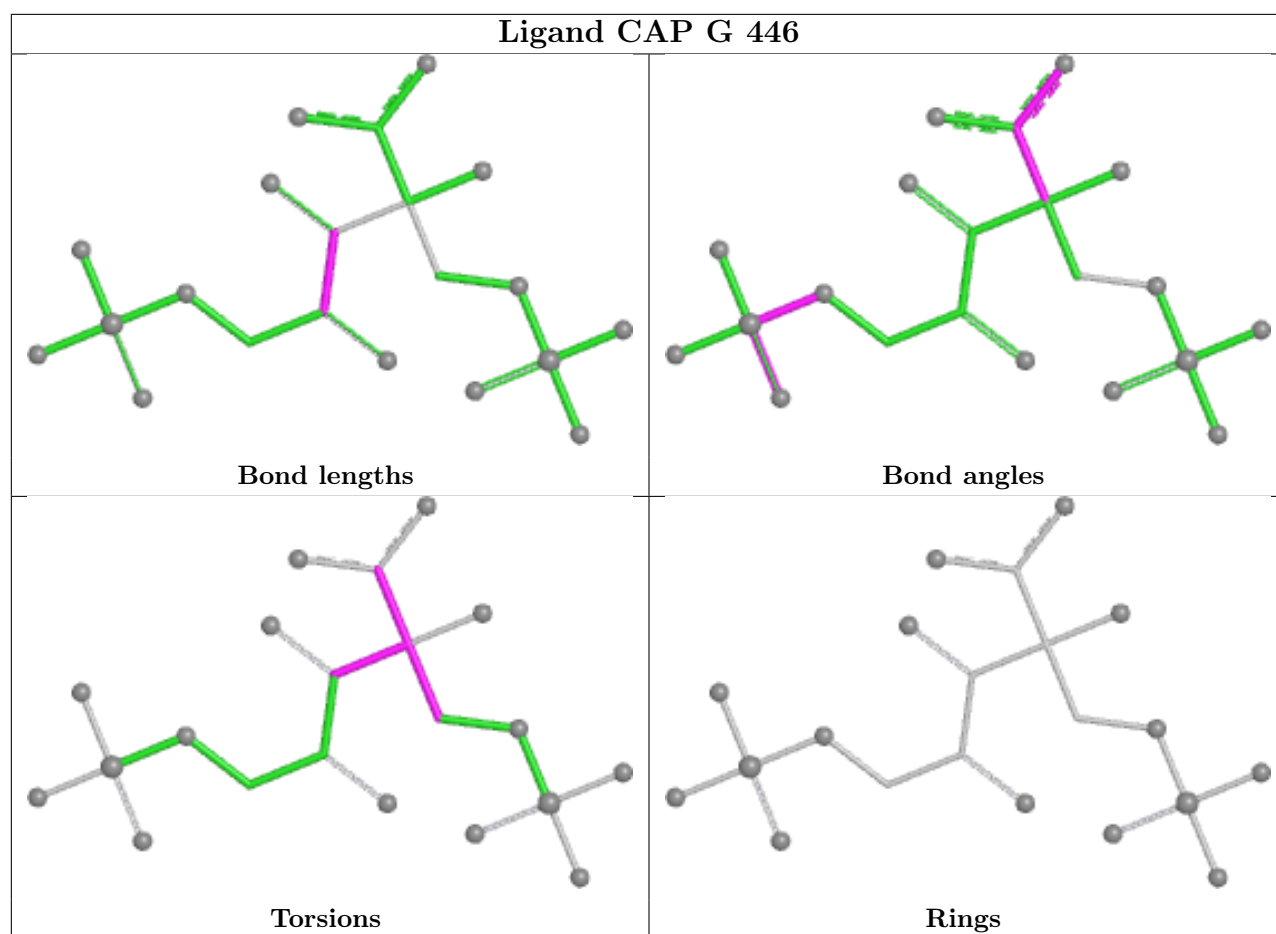


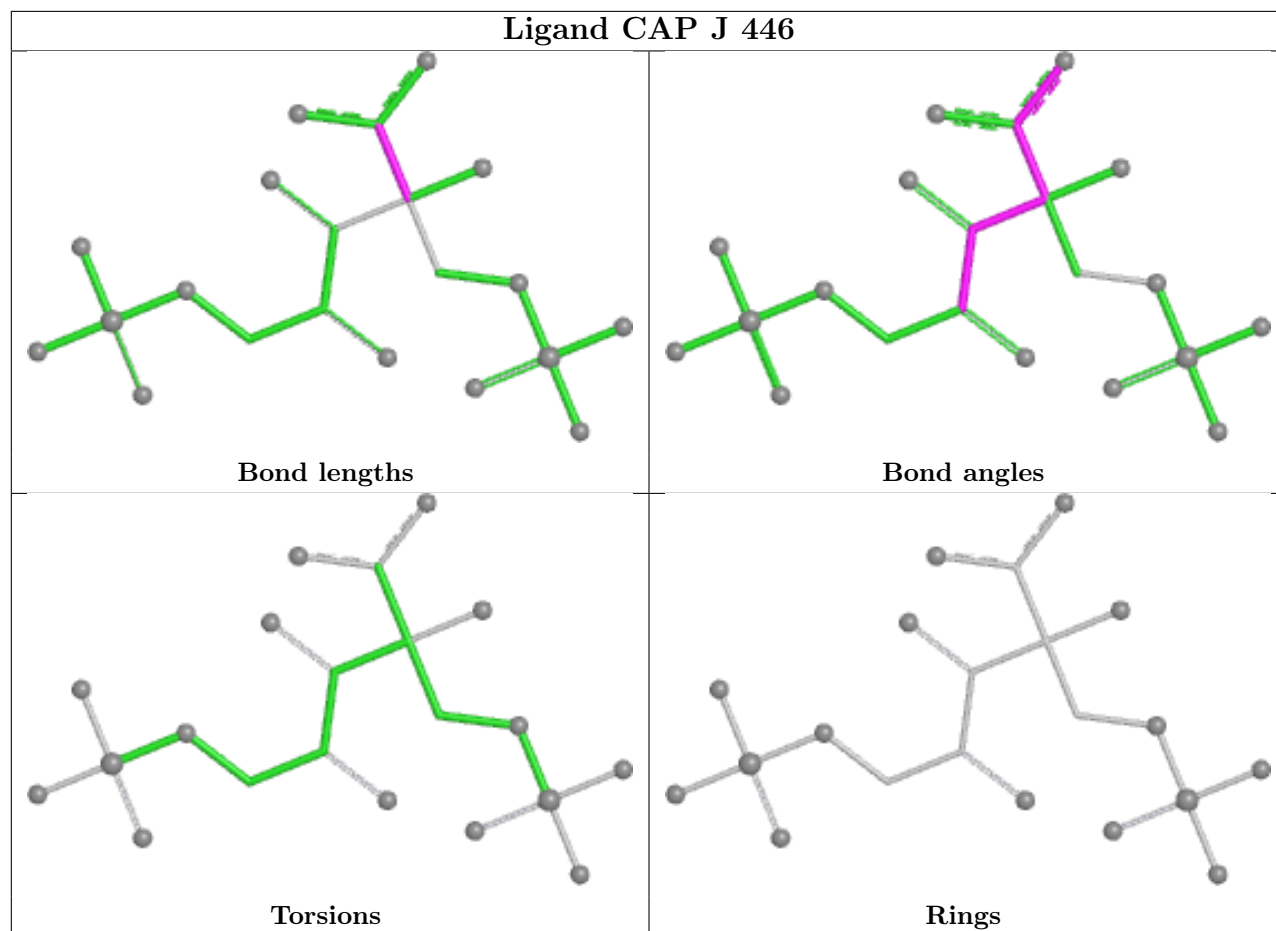


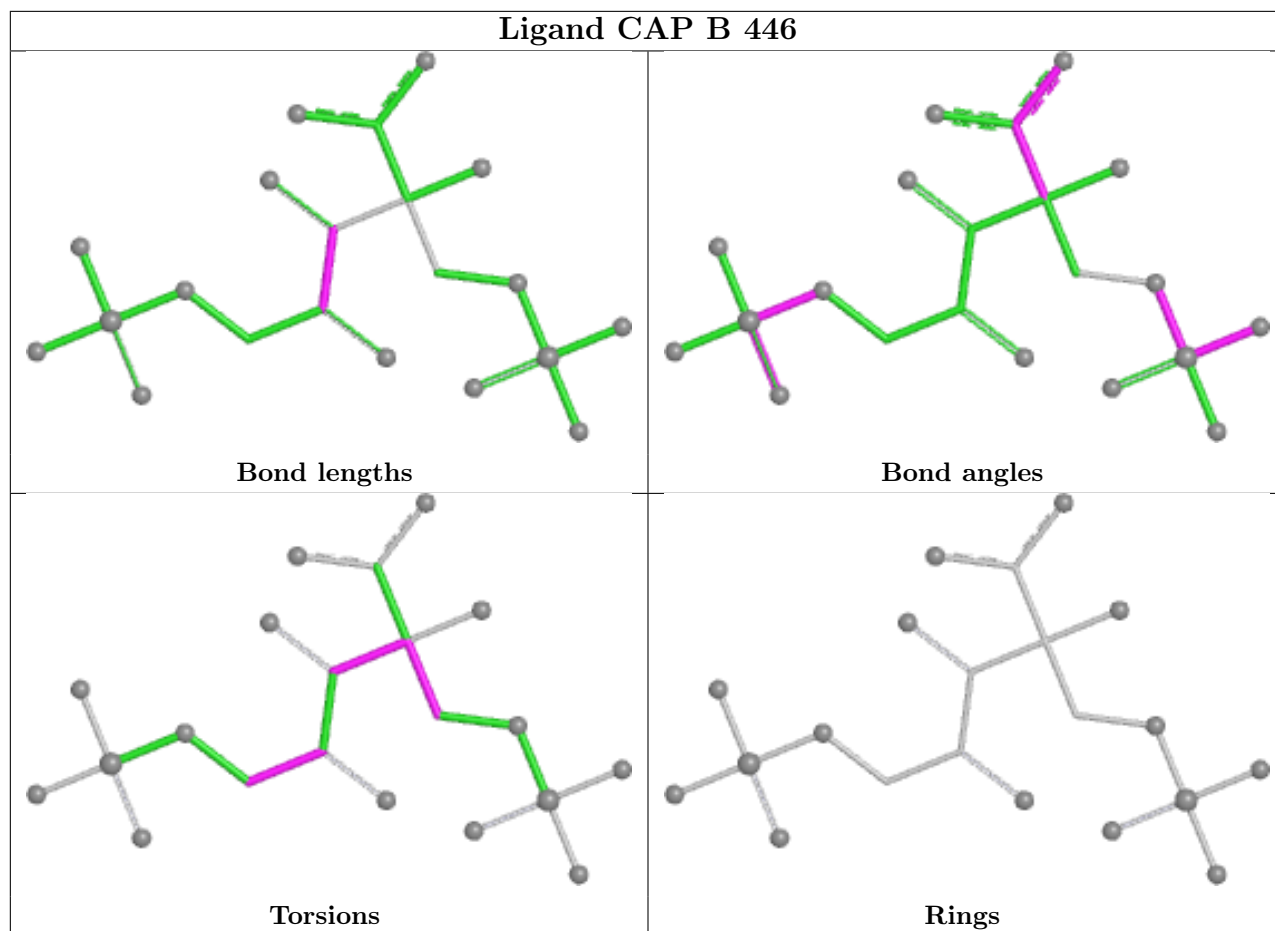


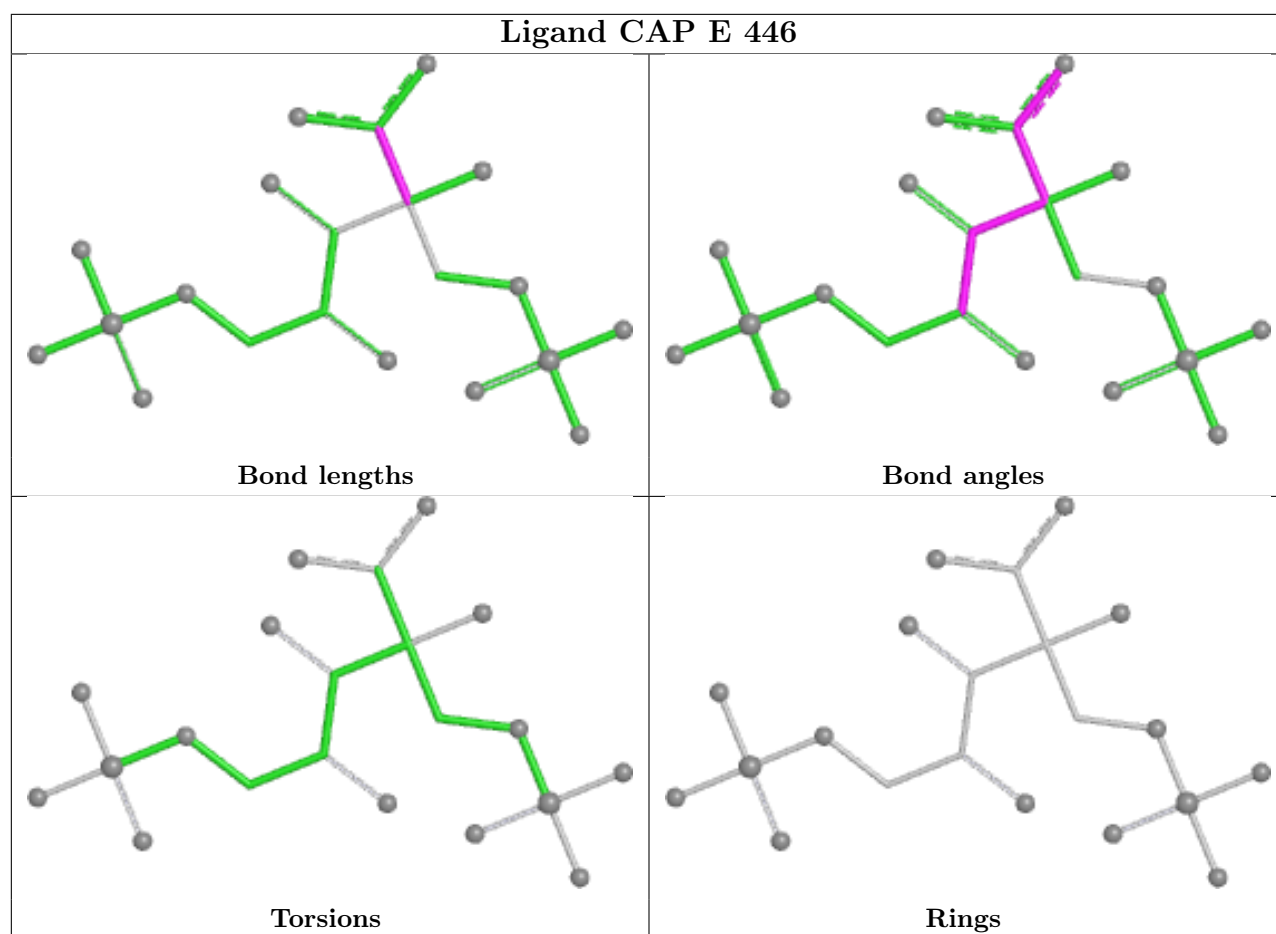












5.7 Other polymers [i](#)

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%)	0.14	19 (4%) 39 45	17, 28, 49, 58	0
1	B	436/444 (98%)	0.23	42 (9%) 13 16	14, 26, 56, 62	0
1	C	436/444 (98%)	0.24	48 (11%) 10 12	16, 27, 60, 66	0
1	D	436/444 (98%)	0.31	56 (12%) 7 9	15, 26, 58, 85	0
1	E	431/444 (97%)	0.07	19 (4%) 39 45	15, 25, 53, 70	0
1	F	436/444 (98%)	0.39	41 (9%) 14 17	17, 30, 57, 64	0
1	G	436/444 (98%)	0.21	38 (8%) 16 19	13, 25, 52, 58	0
1	H	437/444 (98%)	0.27	43 (9%) 13 16	16, 28, 58, 61	0
1	I	436/444 (98%)	0.09	30 (6%) 23 27	13, 24, 52, 70	0
1	J	433/444 (97%)	0.16	33 (7%) 20 24	14, 25, 57, 74	0
All	All	4352/4440 (98%)	0.21	369 (8%) 16 20	13, 27, 56, 85	0

The worst 5 of 369 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	57	THR	8.0
1	G	434	ALA	7.5
1	J	444	VAL	7.3
1	D	421	LEU	6.7
1	E	444	VAL	6.4

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	B	189	12/13	0.95	0.08	18,20,21,22	0
1	KCX	F	189	12/13	0.95	0.08	23,25,27,27	0
1	KCX	I	189	12/13	0.95	0.08	19,21,25,25	0
1	KCX	G	189	12/13	0.96	0.07	16,19,20,20	0
1	KCX	A	189	12/13	0.96	0.07	20,23,24,24	0
1	KCX	J	189	12/13	0.96	0.08	19,19,24,26	0
1	KCX	D	189	12/13	0.97	0.06	21,22,24,25	0
1	KCX	H	189	12/13	0.97	0.06	20,21,25,26	0
1	KCX	E	189	12/13	0.97	0.07	18,19,23,24	0
1	KCX	C	189	12/13	0.97	0.06	21,22,26,28	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

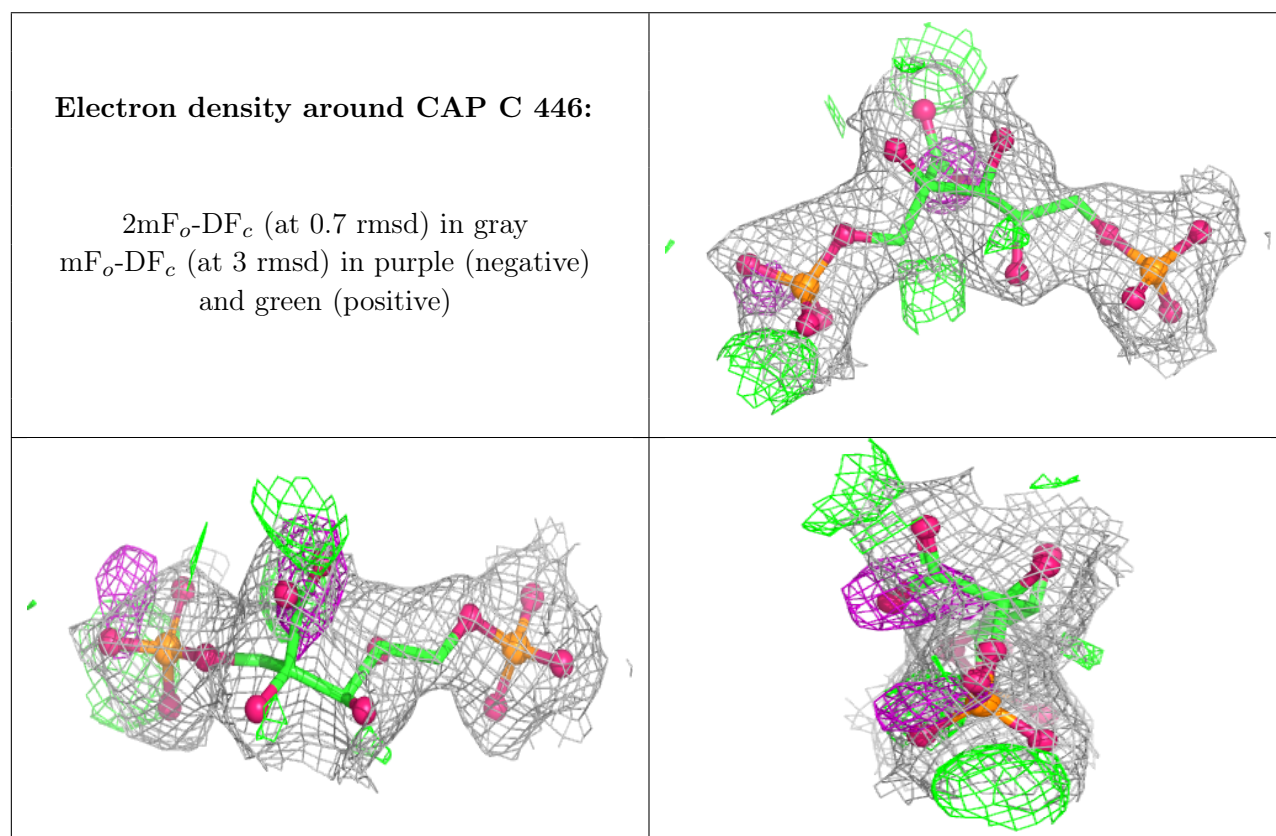
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CAP	C	446	21/21	0.91	0.11	23,34,37,39	0
3	CAP	H	446	21/21	0.93	0.10	24,35,37,39	0
3	CAP	D	446	21/21	0.94	0.09	18,28,31,32	0
3	CAP	F	446	21/21	0.94	0.09	24,33,34,35	0
3	CAP	G	446	21/21	0.94	0.10	16,29,33,34	0
3	CAP	B	446	21/21	0.94	0.09	18,29,35,36	0
3	CAP	J	446	21/21	0.94	0.10	20,28,40,40	0
3	CAP	I	446	21/21	0.95	0.08	15,25,27,28	0
3	CAP	E	446	21/21	0.95	0.09	16,27,37,38	0
2	MG	C	445	1/1	0.96	0.10	23,23,23,23	0
3	CAP	A	446	21/21	0.97	0.07	21,30,31,32	0
4	CA	J	445	1/1	0.97	0.05	27,27,27,27	0
2	MG	H	445	1/1	0.98	0.09	22,22,22,22	0
4	CA	E	445	1/1	0.98	0.03	27,27,27,27	0
2	MG	F	445	1/1	0.98	0.09	36,36,36,36	0
2	MG	G	445	1/1	0.99	0.05	22,22,22,22	0
2	MG	A	445	1/1	0.99	0.03	32,32,32,32	0
2	MG	I	445	1/1	0.99	0.02	21,21,21,21	0
2	MG	D	445	1/1	0.99	0.03	27,27,27,27	0

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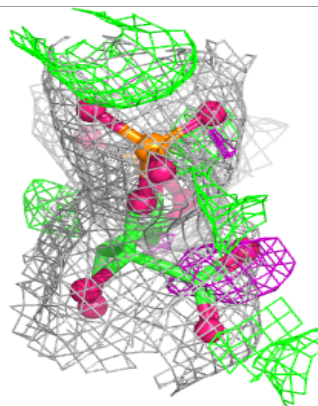
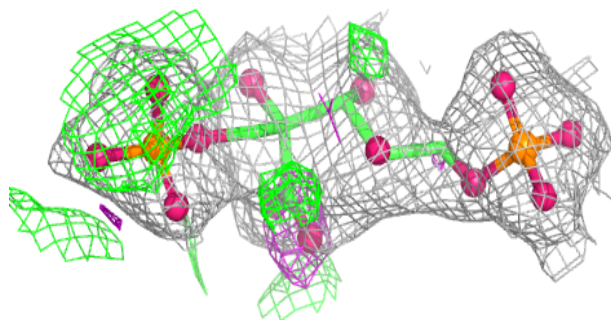
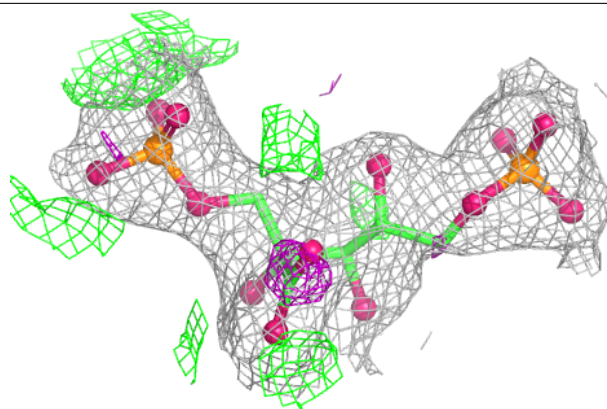
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MG	B	445	1/1	0.99	0.05	19,19,19,19	0

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.

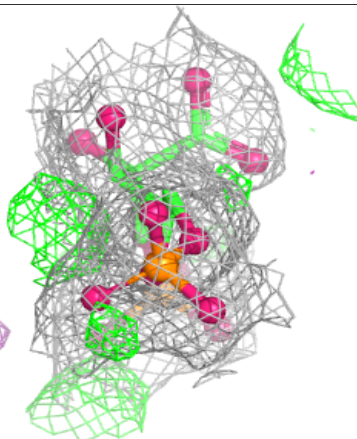
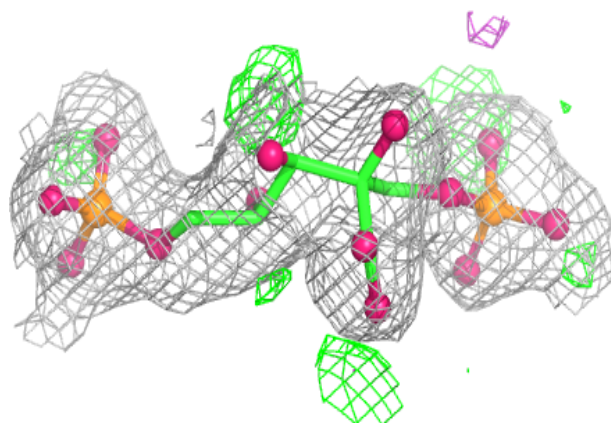
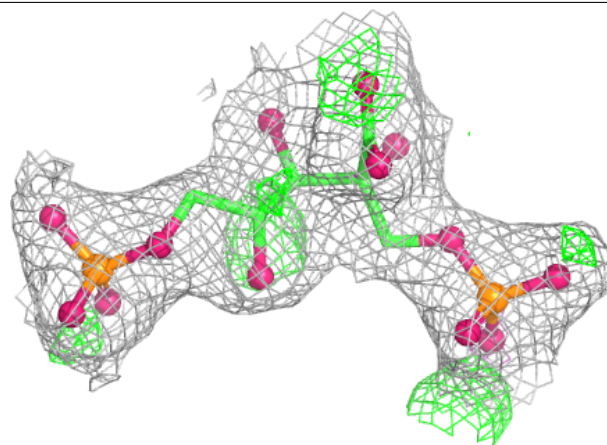


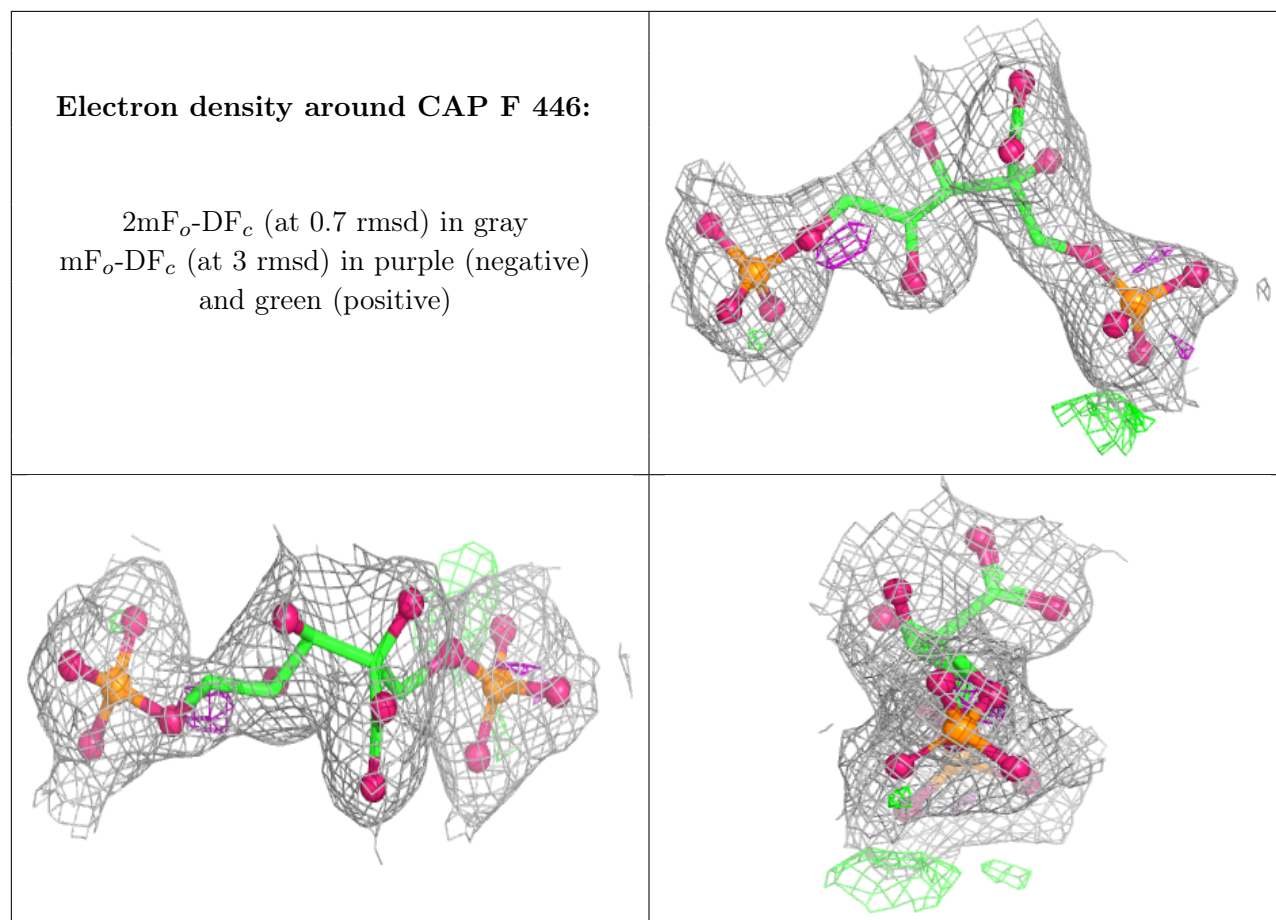
Electron density around CAP H 446:

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

**Electron density around CAP D 446:**

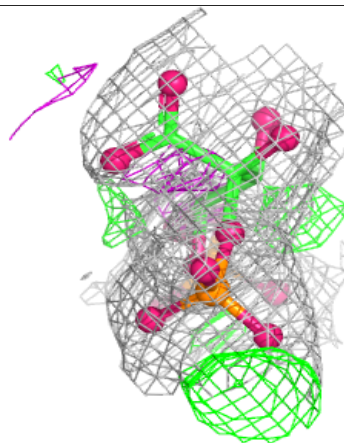
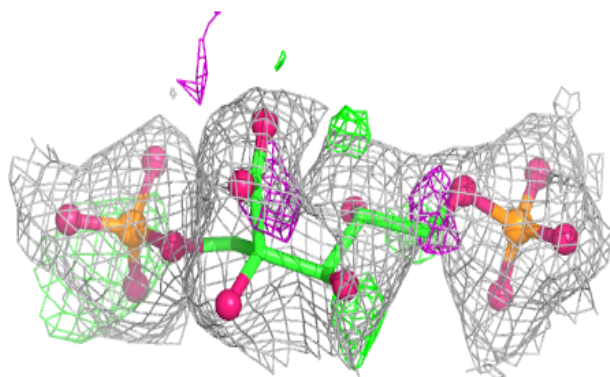
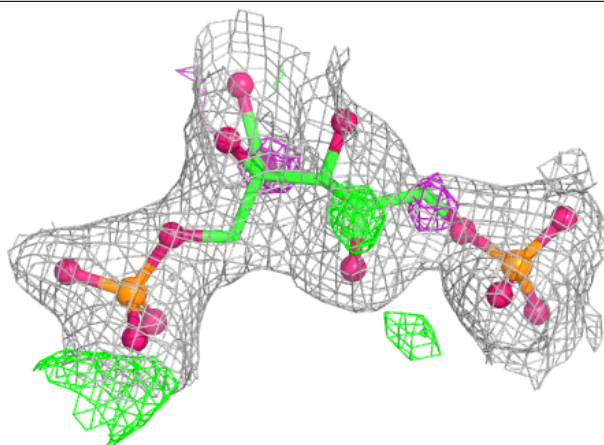
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





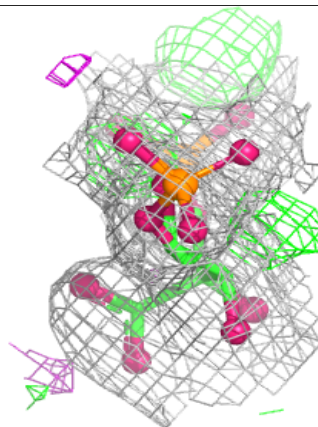
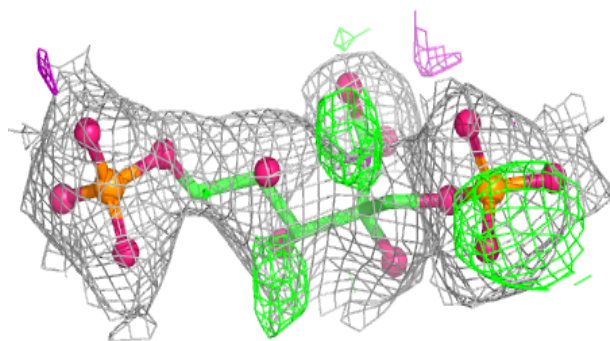
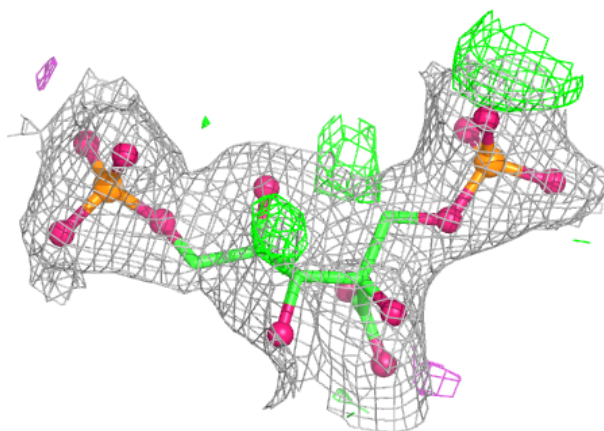
Electron density around CAP G 446:

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

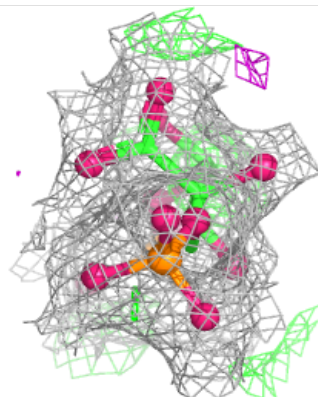
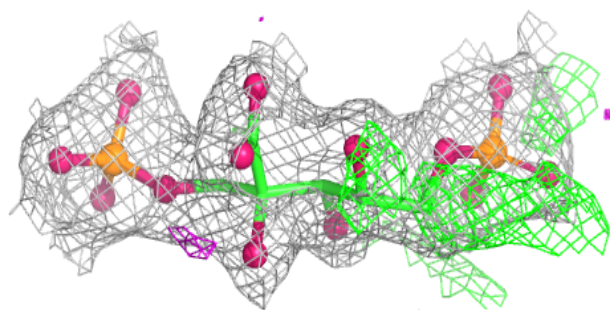
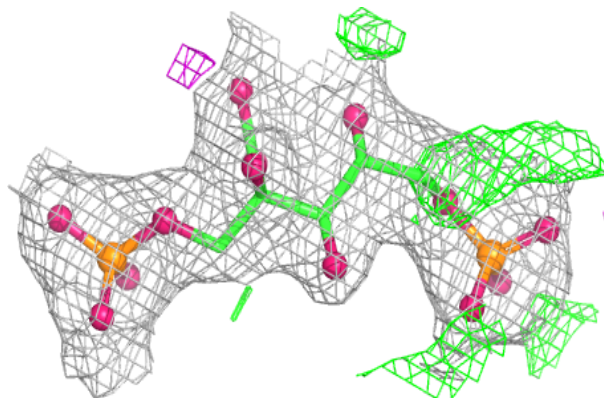


Electron density around CAP B 446:

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

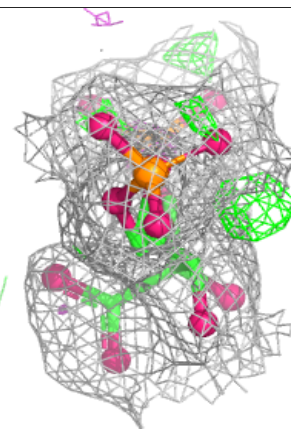
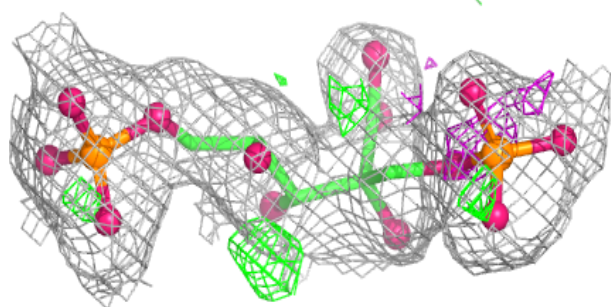
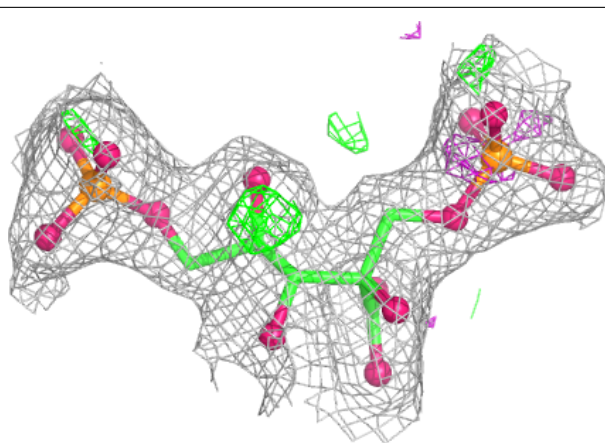
**Electron density around CAP J 446:**

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

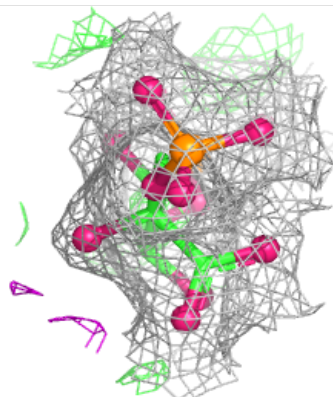
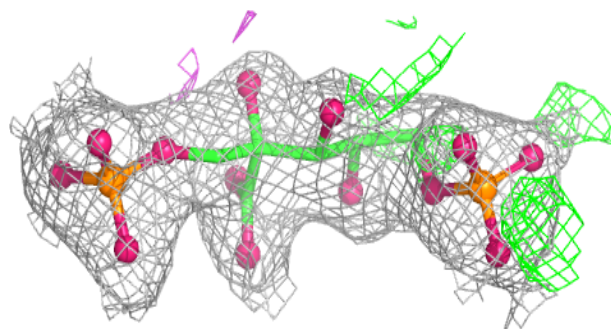
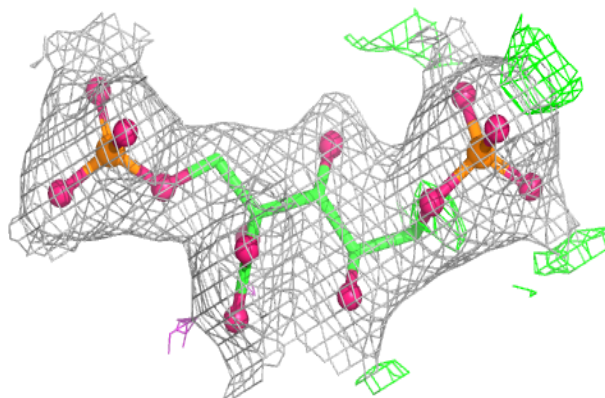


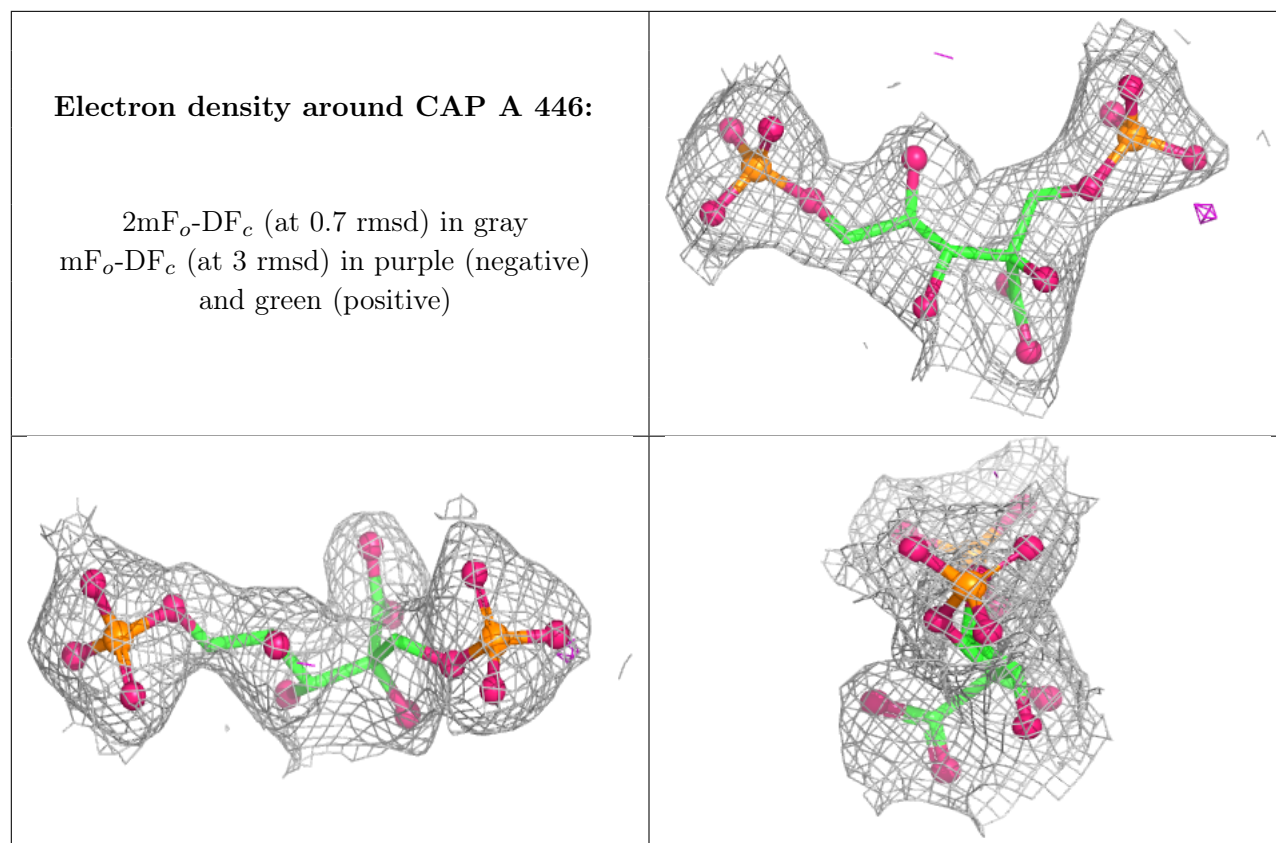
Electron density around CAP I 446:

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

**Electron density around CAP E 446:**

$2mF_o-DF_c$ (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.