



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 15, 2026 – 02:00 AM UTC

PDB ID : 4ACF / pdb_00004acf
Title : CRYSTAL STRUCTURE OF MYCOBACTERIUM TUBERCULOSIS GLUTAMINE SYNTHETASE IN COMPLEX WITH IMIDAZOPYRIDINE INHIBITOR ((4-(6-BROMO-3-(BUTYLAMINO)IMIDAZO(1,2-A)PYRIDIN-2-YL)PHENOXY) ACETIC ACID) AND L-METHIONINE-S-SULFOXIMINE PHOSPHATE.
Authors : Nilsson, M.T.; Mowbray, S.L.
Deposited on : 2011-12-15
Resolution : 2.00 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)
Xtriage (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)

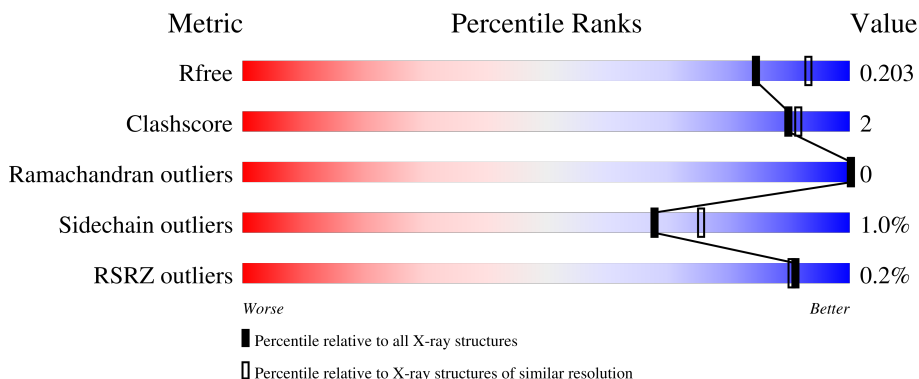
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

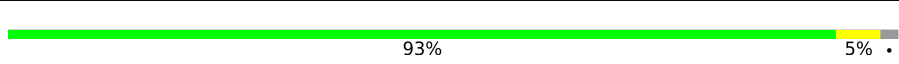
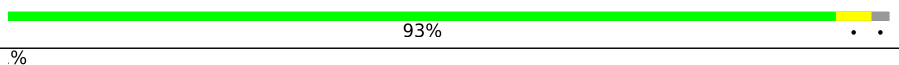
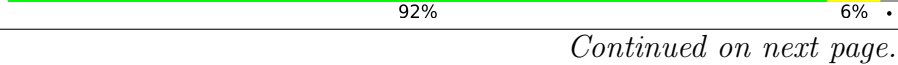
The reported resolution of this entry is 2.00 Å.

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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

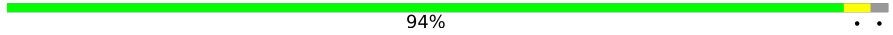
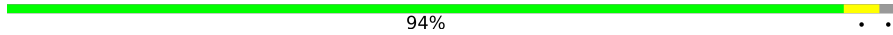
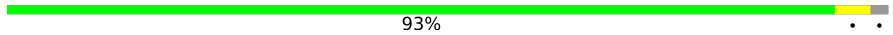
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	486	
1	B	486	
1	C	486	

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Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
1	D	486	 94%
1	E	486	 94%
1	F	486	 93%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 24804 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 GLUTAMINE SYNTHETASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	475	3762	2397	631	722	12	0	0	0
1	B	475	3762	2397	631	722	12	0	0	0
1	C	475	3762	2397	631	722	12	0	0	0
1	D	475	3762	2397	631	722	12	0	0	0
1	E	475	3762	2397	631	722	12	0	0	0
1	F	475	3762	2397	631	722	12	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

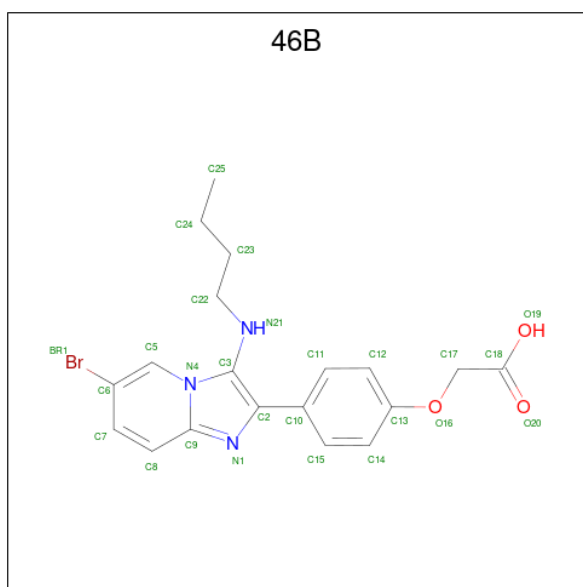
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP P0A590
A	-6	ALA	-	expression tag	UNP P0A590
A	-5	HIS	-	expression tag	UNP P0A590
A	-4	HIS	-	expression tag	UNP P0A590
A	-3	HIS	-	expression tag	UNP P0A590
A	-2	HIS	-	expression tag	UNP P0A590
A	-1	HIS	-	expression tag	UNP P0A590
A	0	HIS	-	expression tag	UNP P0A590
A	1	GLY	-	expression tag	UNP P0A590
B	-7	MET	-	expression tag	UNP P0A590
B	-6	ALA	-	expression tag	UNP P0A590
B	-5	HIS	-	expression tag	UNP P0A590
B	-4	HIS	-	expression tag	UNP P0A590
B	-3	HIS	-	expression tag	UNP P0A590
B	-2	HIS	-	expression tag	UNP P0A590
B	-1	HIS	-	expression tag	UNP P0A590
B	0	HIS	-	expression tag	UNP P0A590

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	-	expression tag	UNP P0A590
C	-7	MET	-	expression tag	UNP P0A590
C	-6	ALA	-	expression tag	UNP P0A590
C	-5	HIS	-	expression tag	UNP P0A590
C	-4	HIS	-	expression tag	UNP P0A590
C	-3	HIS	-	expression tag	UNP P0A590
C	-2	HIS	-	expression tag	UNP P0A590
C	-1	HIS	-	expression tag	UNP P0A590
C	0	HIS	-	expression tag	UNP P0A590
C	1	GLY	-	expression tag	UNP P0A590
D	-7	MET	-	expression tag	UNP P0A590
D	-6	ALA	-	expression tag	UNP P0A590
D	-5	HIS	-	expression tag	UNP P0A590
D	-4	HIS	-	expression tag	UNP P0A590
D	-3	HIS	-	expression tag	UNP P0A590
D	-2	HIS	-	expression tag	UNP P0A590
D	-1	HIS	-	expression tag	UNP P0A590
D	0	HIS	-	expression tag	UNP P0A590
D	1	GLY	-	expression tag	UNP P0A590
E	-7	MET	-	expression tag	UNP P0A590
E	-6	ALA	-	expression tag	UNP P0A590
E	-5	HIS	-	expression tag	UNP P0A590
E	-4	HIS	-	expression tag	UNP P0A590
E	-3	HIS	-	expression tag	UNP P0A590
E	-2	HIS	-	expression tag	UNP P0A590
E	-1	HIS	-	expression tag	UNP P0A590
E	0	HIS	-	expression tag	UNP P0A590
E	1	GLY	-	expression tag	UNP P0A590
F	-7	MET	-	expression tag	UNP P0A590
F	-6	ALA	-	expression tag	UNP P0A590
F	-5	HIS	-	expression tag	UNP P0A590
F	-4	HIS	-	expression tag	UNP P0A590
F	-3	HIS	-	expression tag	UNP P0A590
F	-2	HIS	-	expression tag	UNP P0A590
F	-1	HIS	-	expression tag	UNP P0A590
F	0	HIS	-	expression tag	UNP P0A590
F	1	GLY	-	expression tag	UNP P0A590

- Molecule 2 is {4-[6-BROMO-3-(BUTYLAMINO)IMIDAZO[1,2-A]PYRIDIN-2-YL]PHENOXY}ACETIC ACID (CCD ID: 46B) (formula: C₁₉H₂₀BrN₃O₃).

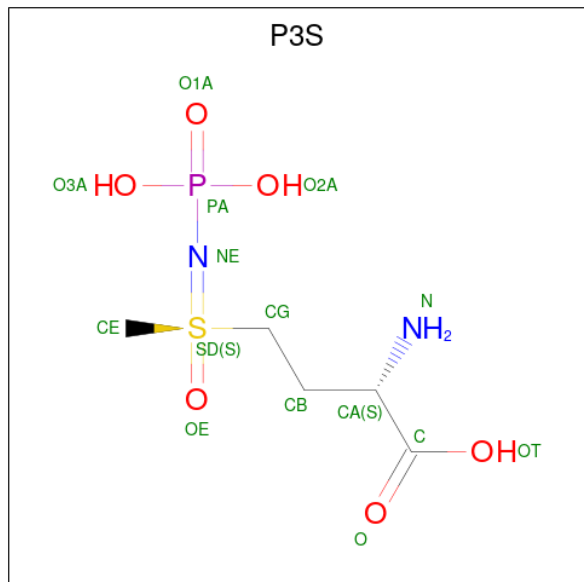


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	Br	C	N	O		
2	A	1	Total 26	Br 1	C 19	N 3	O 3	0	0
2	B	1	Total 26	Br 1	C 19	N 3	O 3	0	0
2	C	1	Total 26	Br 1	C 19	N 3	O 3	0	0
2	D	1	Total 26	Br 1	C 19	N 3	O 3	0	0
2	E	1	Total 26	Br 1	C 19	N 3	O 3	0	0
2	F	1	Total 26	Br 1	C 19	N 3	O 3	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

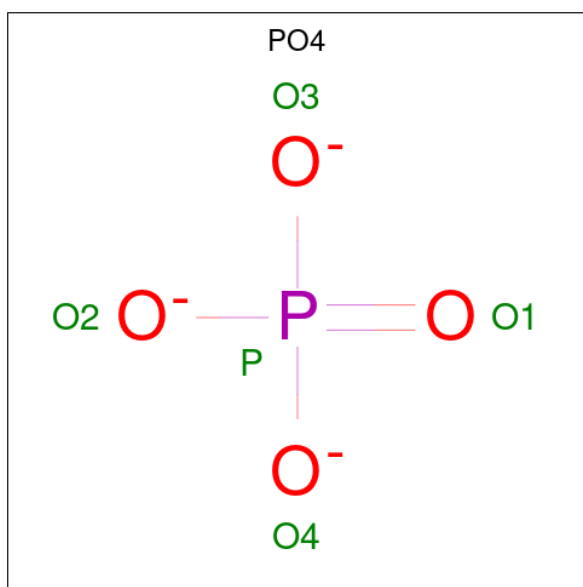
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	4	Total 4	Mg 4	0	0
3	B	4	Total 4	Mg 4	0	0
3	C	4	Total 4	Mg 4	0	0
3	D	4	Total 4	Mg 4	0	0
3	E	4	Total 4	Mg 4	0	0
3	F	4	Total 4	Mg 4	0	0

- Molecule 4 is L-METHIONINE-S-SULFOXIMINE PHOSPHATE (CCD ID: P3S) (formula: $C_5H_{13}N_2O_6PS$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
4	A	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	B	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	C	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	D	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	E	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	F	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0
6	B	1	Total Cl 1 1	0	0
6	C	1	Total Cl 1 1	0	0
6	D	1	Total Cl 1 1	0	0
6	E	1	Total Cl 1 1	0	0
6	F	1	Total Cl 1 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	349	Total 349	O 349	0	0
7	B	325	Total 325	O 325	0	0
7	C	320	Total 320	O 320	0	0
7	D	318	Total 318	O 318	0	0
7	E	320	Total 320	O 320	0	0
7	F	294	Total 294	O 294	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.

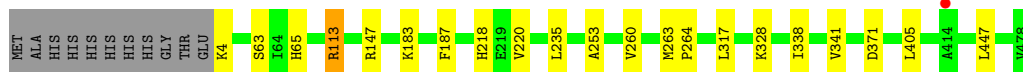
- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain A:  93% 5%

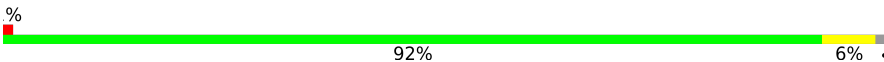


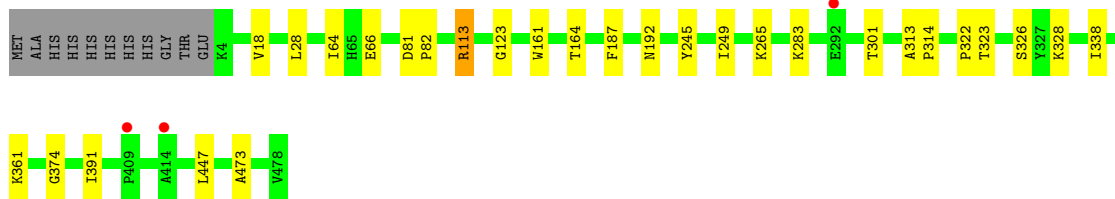
- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain B:  93%



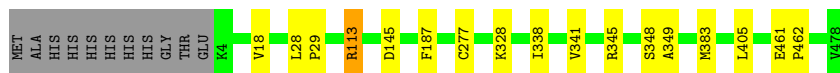
- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain C:  % 92% 6%



- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain D:  94%



- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain E:  94%



● Molecule 1: GLUTAMINE SYNTHETASE 1

Chain F:  93%

4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	132.59Å 227.39Å 202.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.1 (20.00-2.00) 99.0 (20.00-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 2.01Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.165 , 0.198 0.172 , 0.203	Depositor DCC
R_{free} test set	10190 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtrriage
Anisotropy	0.505	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.015 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.020 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	24804	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CL, 46B, PO4, MG, P3S

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	0.82	0/3868	0.87	0/5257
1	B	0.80	0/3868	0.85	1/5257 (0.0%)
1	C	0.81	1/3868 (0.0%)	0.87	0/5257
1	D	0.81	0/3868	0.87	0/5257
1	E	0.83	1/3868 (0.0%)	0.87	1/5257 (0.0%)
1	F	0.84	0/3868	0.86	1/5257 (0.0%)
All	All	0.82	2/23208 (0.0%)	0.86	3/31542 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	473	ALA	CA-CB	5.39	1.61	1.53
1	E	148	ALA	CA-CB	5.23	1.61	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	221	GLY	N-CA-C	5.28	117.54	111.36
1	F	327	TYR	CA-CB-CG	-5.13	104.67	113.90
1	B	218	HIS	N-CA-C	-5.06	103.37	110.50

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	3762	0	3591	13	0
1	B	3762	0	3591	13	0
1	C	3762	0	3591	16	0
1	D	3762	0	3591	14	0
1	E	3762	0	3591	9	0
1	F	3762	0	3591	15	0
2	A	26	0	19	0	0
2	B	26	0	19	0	0
2	C	26	0	19	1	0
2	D	26	0	19	0	0
2	E	26	0	19	0	0
2	F	26	0	19	1	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
3	C	4	0	0	0	0
3	D	4	0	0	0	0
3	E	4	0	0	0	0
3	F	4	0	0	0	0
4	A	15	0	10	0	0
4	B	15	0	10	0	0
4	C	15	0	10	0	0
4	D	15	0	10	0	0
4	E	15	0	10	0	0
4	F	15	0	10	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
5	E	5	0	0	0	0
5	F	5	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
7	A	349	0	0	2	0
7	B	325	0	0	4	0
7	C	320	0	0	2	0
7	D	318	0	0	2	0
7	E	320	0	0	2	0
7	F	294	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	24804	0	21720	78	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 2.

The worst 5 of 78 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:D:328:LYS:NZ	7:D:2248:HOH:O	2.26	0.68
1:B:328:LYS:NZ	7:B:2253:HOH:O	2.30	0.63
1:F:28:LEU:HD11	1:F:447:LEU:HD11	1.82	0.61
1:F:328:LYS:NZ	7:F:2223:HOH:O	2.27	0.59
1:B:341:VAL:CG2	1:B:405:LEU:HD11	2.34	0.57

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	473/486 (97%)	464 (98%)	9 (2%)	0	100	100
1	B	473/486 (97%)	465 (98%)	8 (2%)	0	100	100
1	C	473/486 (97%)	465 (98%)	8 (2%)	0	100	100
1	D	473/486 (97%)	462 (98%)	11 (2%)	0	100	100
1	E	473/486 (97%)	468 (99%)	5 (1%)	0	100	100
1	F	473/486 (97%)	465 (98%)	8 (2%)	0	100	100
All	All	2838/2916 (97%)	2789 (98%)	49 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	402/411 (98%)	399 (99%)	3 (1%)	76 82
1	B	402/411 (98%)	397 (99%)	5 (1%)	63 70
1	C	402/411 (98%)	397 (99%)	5 (1%)	63 70
1	D	402/411 (98%)	398 (99%)	4 (1%)	68 75
1	E	402/411 (98%)	397 (99%)	5 (1%)	63 70
1	F	402/411 (98%)	399 (99%)	3 (1%)	76 82
All	All	2412/2466 (98%)	2387 (99%)	25 (1%)	68 75

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	113	ARG
1	E	18	VAL
1	F	192	ASN
1	D	338	ILE
1	E	187	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	321	ASN
1	E	62	GLN
1	D	422	GLN
1	E	321	ASN
1	B	321	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 30 are monoatomic - leaving 18 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	46B	A	1479	-	28,28,28	1.91	6 (21%)	37,38,38	1.60	7 (18%)
5	PO4	B	1484	3	4,4,4	0.68	0	6,6,6	1.01	1 (16%)
4	P3S	A	1483	3	11,14,14	2.23	3 (27%)	9,21,21	1.09	0
4	P3S	B	1483	3	11,14,14	1.76	3 (27%)	9,21,21	0.95	0
5	PO4	A	1484	3	4,4,4	0.77	0	6,6,6	1.12	0
4	P3S	C	1483	3	11,14,14	1.91	2 (18%)	9,21,21	0.93	1 (11%)
5	PO4	D	1484	3	4,4,4	1.04	0	6,6,6	0.90	0
2	46B	E	1479	-	28,28,28	1.89	6 (21%)	37,38,38	1.55	8 (21%)
4	P3S	D	1483	3	11,14,14	1.76	2 (18%)	9,21,21	1.14	0
5	PO4	E	1484	3	4,4,4	1.13	0	6,6,6	0.66	0
4	P3S	E	1483	3	11,14,14	1.76	2 (18%)	9,21,21	1.04	0
4	P3S	F	1483	3	11,14,14	1.82	4 (36%)	9,21,21	1.01	1 (11%)
2	46B	F	1479	-	28,28,28	2.01	6 (21%)	37,38,38	1.55	7 (18%)
2	46B	C	1479	-	28,28,28	1.90	6 (21%)	37,38,38	1.56	8 (21%)
5	PO4	C	1484	3	4,4,4	0.83	0	6,6,6	1.09	0
5	PO4	F	1484	3	4,4,4	1.26	1 (25%)	6,6,6	1.15	1 (16%)
2	46B	D	1479	-	28,28,28	1.87	6 (21%)	37,38,38	1.71	7 (18%)
2	46B	B	1479	-	28,28,28	1.90	6 (21%)	37,38,38	1.76	8 (21%)

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	46B	A	1479	-	-	5/14/14/14	0/3/3/3
4	P3S	A	1483	3	-	4/9/16/16	-
4	P3S	B	1483	3	-	4/9/16/16	-
4	P3S	C	1483	3	-	4/9/16/16	-
2	46B	E	1479	-	-	5/14/14/14	0/3/3/3
4	P3S	D	1483	3	-	4/9/16/16	-
4	P3S	E	1483	3	-	4/9/16/16	-
4	P3S	F	1483	3	-	4/9/16/16	-
2	46B	F	1479	-	-	5/14/14/14	0/3/3/3
2	46B	C	1479	-	-	5/14/14/14	0/3/3/3
2	46B	D	1479	-	-	5/14/14/14	0/3/3/3
2	46B	B	1479	-	-	5/14/14/14	0/3/3/3

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1479	46B	C3-N4	-6.80	1.32	1.39
2	C	1479	46B	C3-N4	-6.26	1.32	1.39
2	E	1479	46B	C3-N4	-6.16	1.32	1.39
2	B	1479	46B	C3-N4	-5.87	1.33	1.39
2	A	1479	46B	C3-N4	-5.45	1.33	1.39

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1479	46B	C2-C3-N4	5.07	108.41	104.96
2	A	1479	46B	C2-C3-N4	4.76	108.20	104.96
2	D	1479	46B	C2-C3-N4	4.53	108.04	104.96
2	E	1479	46B	N4-C9-N1	-4.44	107.25	111.26
2	F	1479	46B	N4-C9-N1	-4.11	107.55	111.26

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

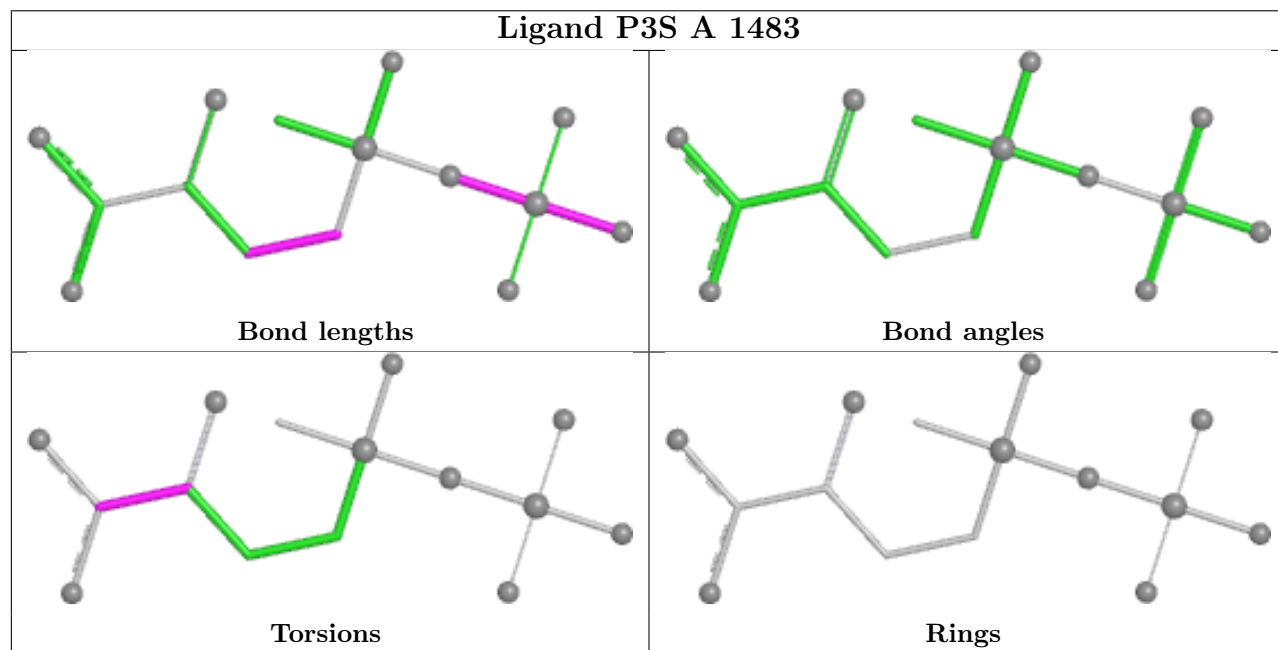
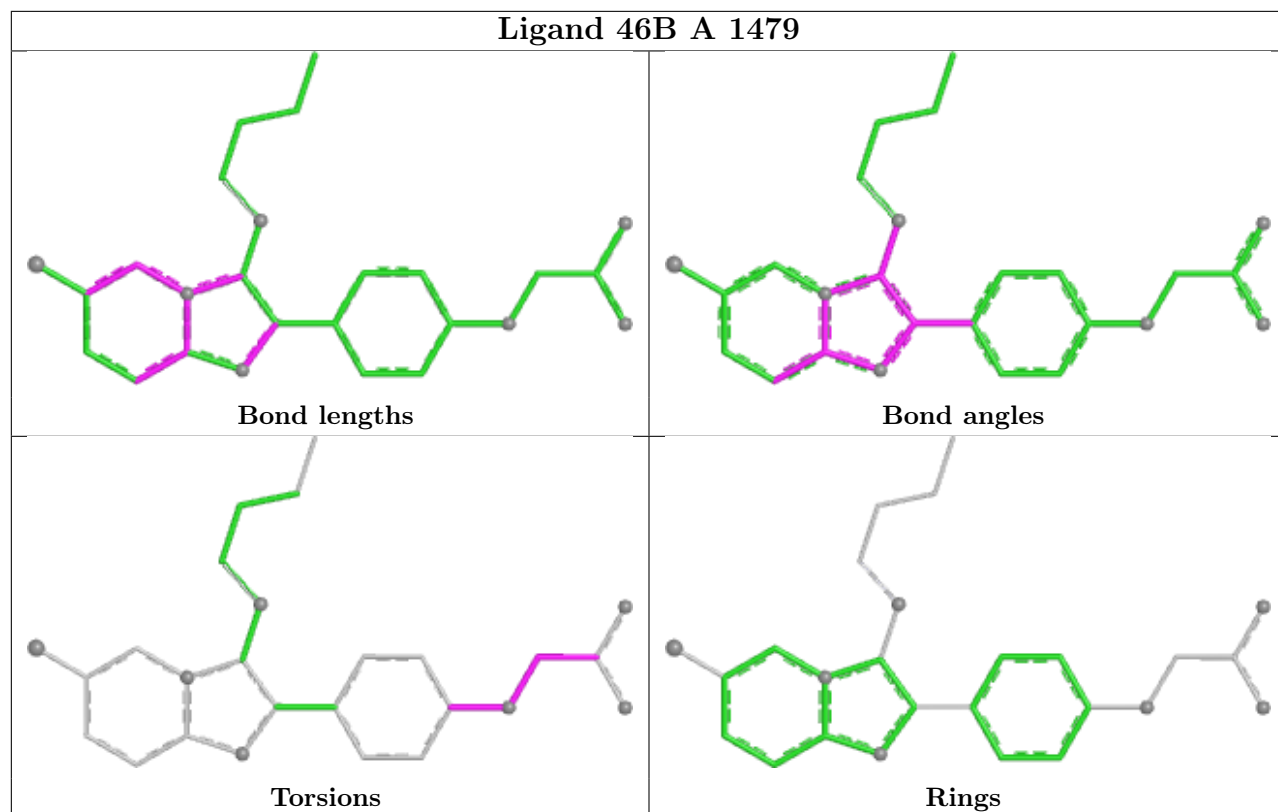
Mol	Chain	Res	Type	Atoms
4	A	1483	P3S	O-C-CA-N
4	B	1483	P3S	O-C-CA-N
4	F	1483	P3S	O-C-CA-N
4	A	1483	P3S	OT-C-CA-CB
4	C	1483	P3S	OT-C-CA-CB

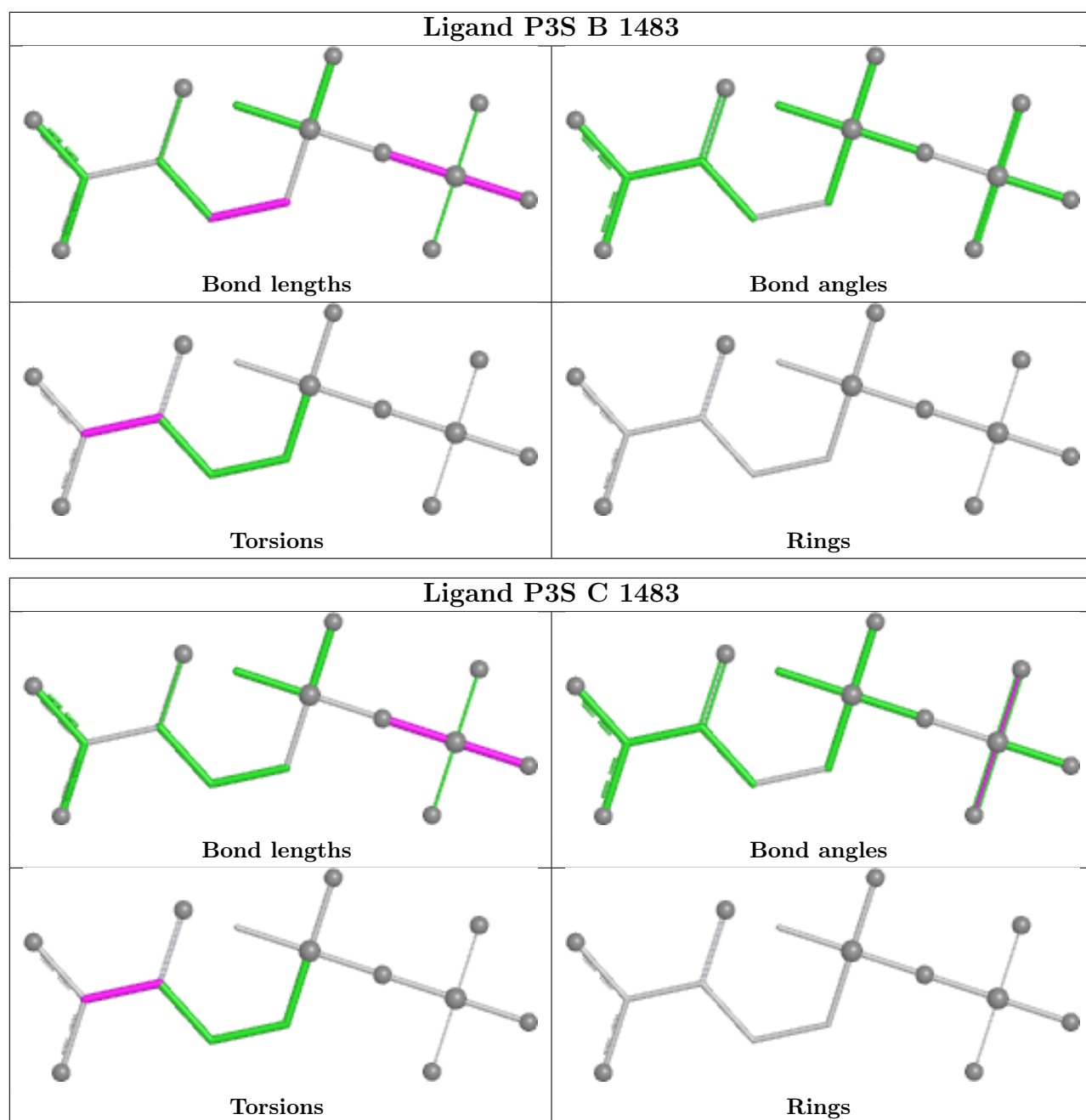
There are no ring outliers.

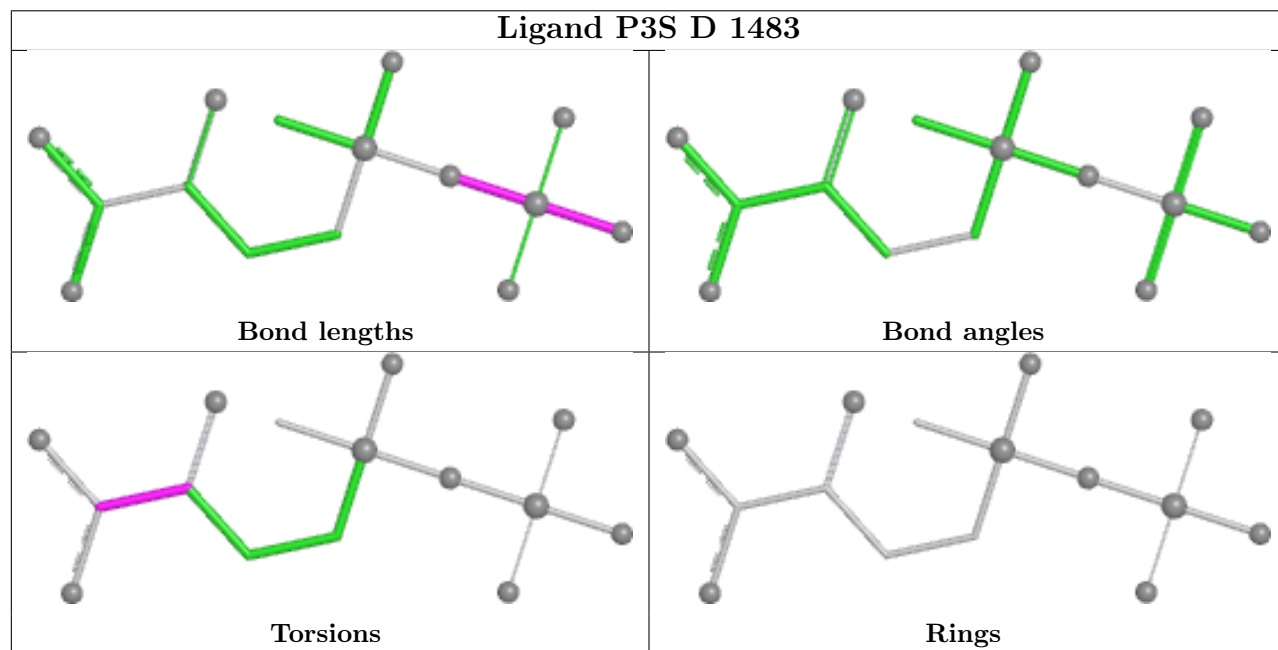
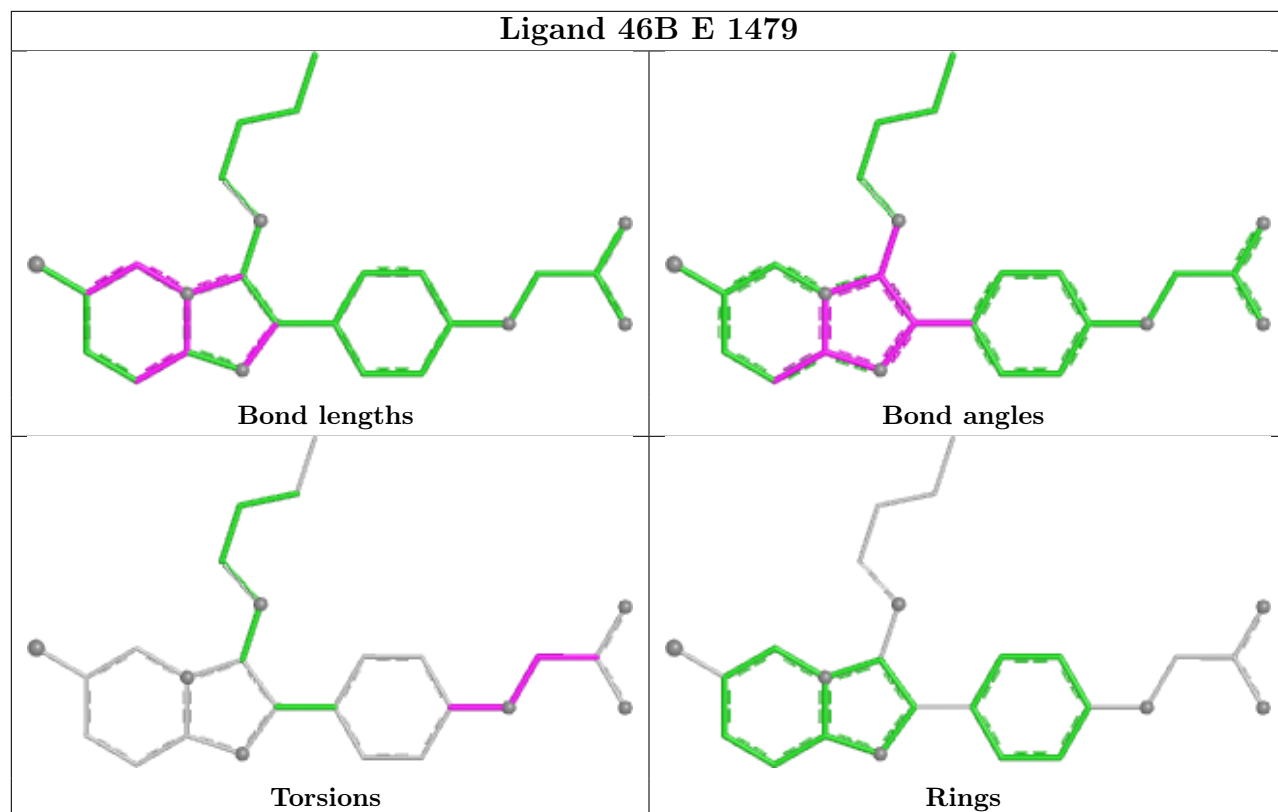
2 monomers are involved in 2 short contacts:

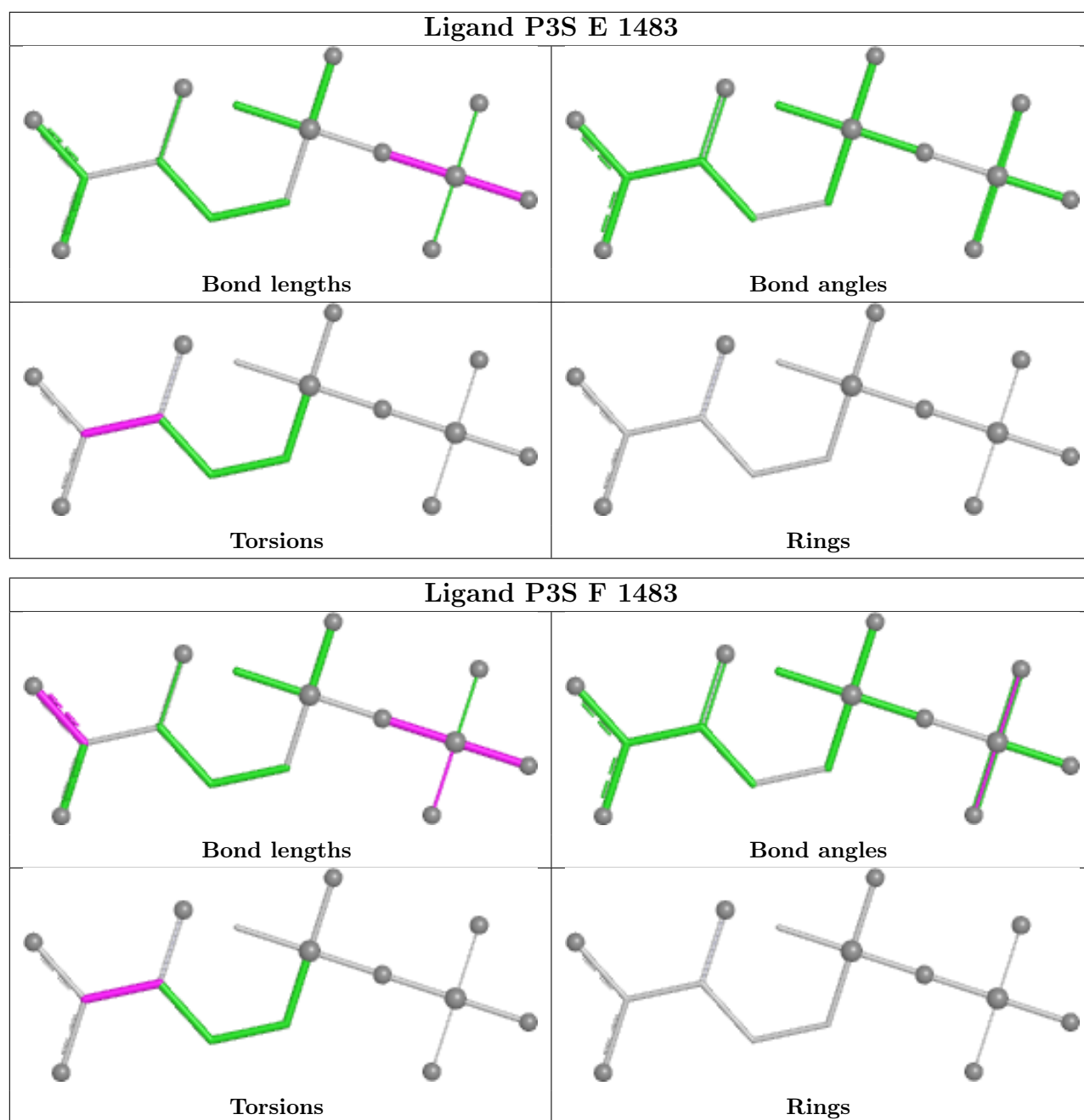
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1479	46B	1	0
2	C	1479	46B	1	0

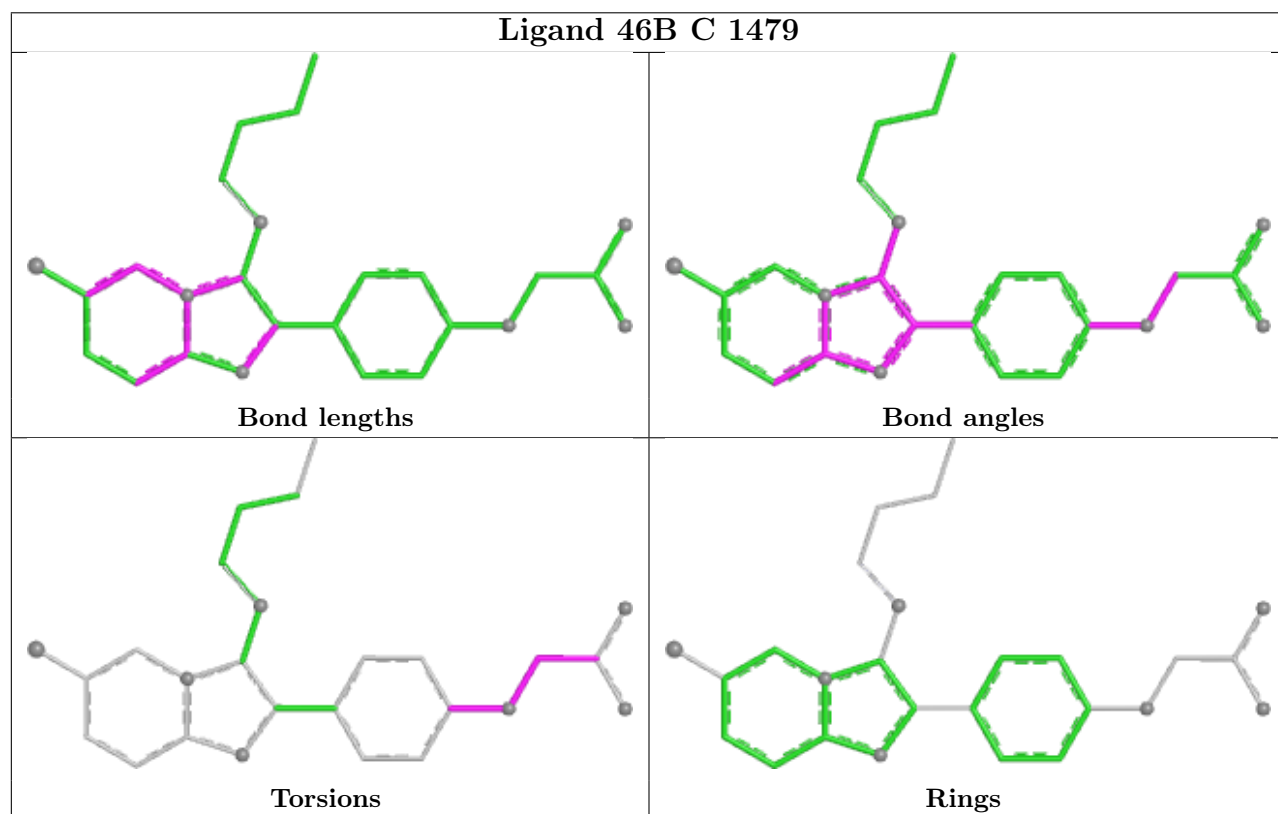
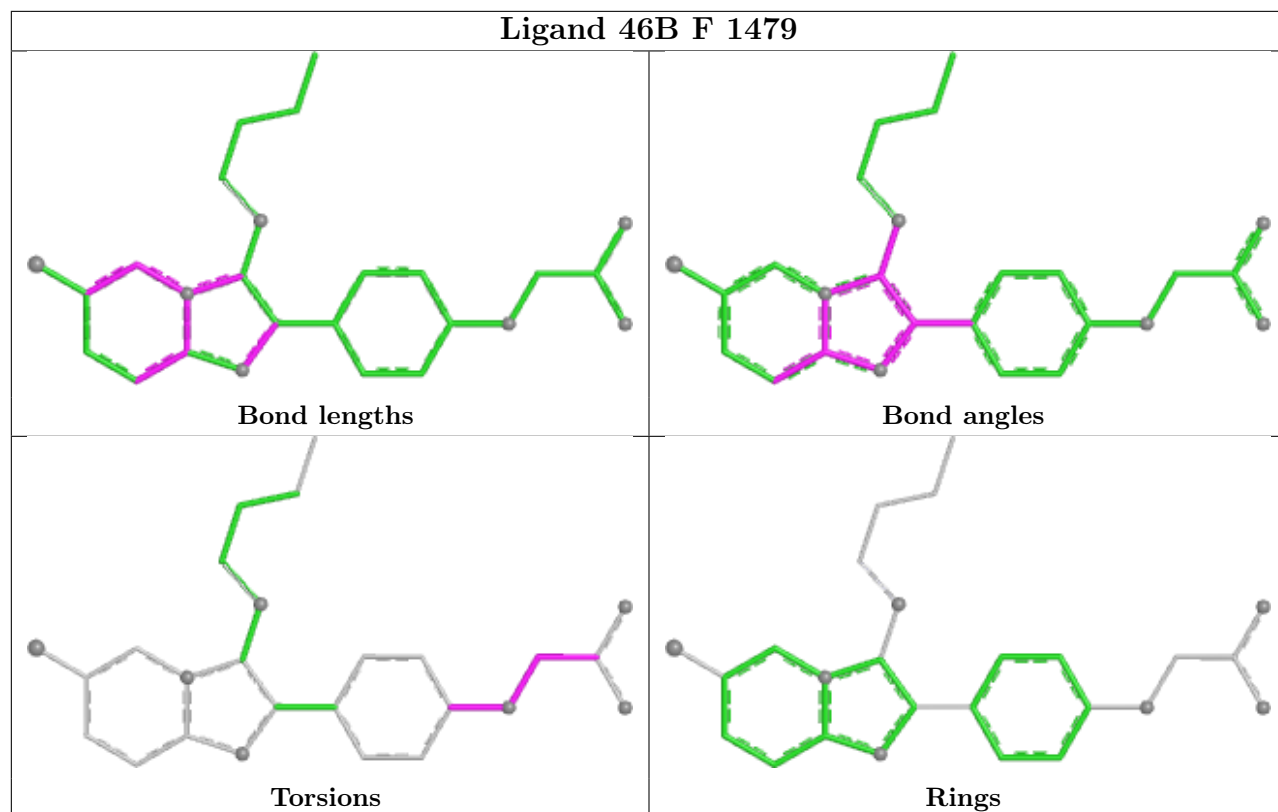
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

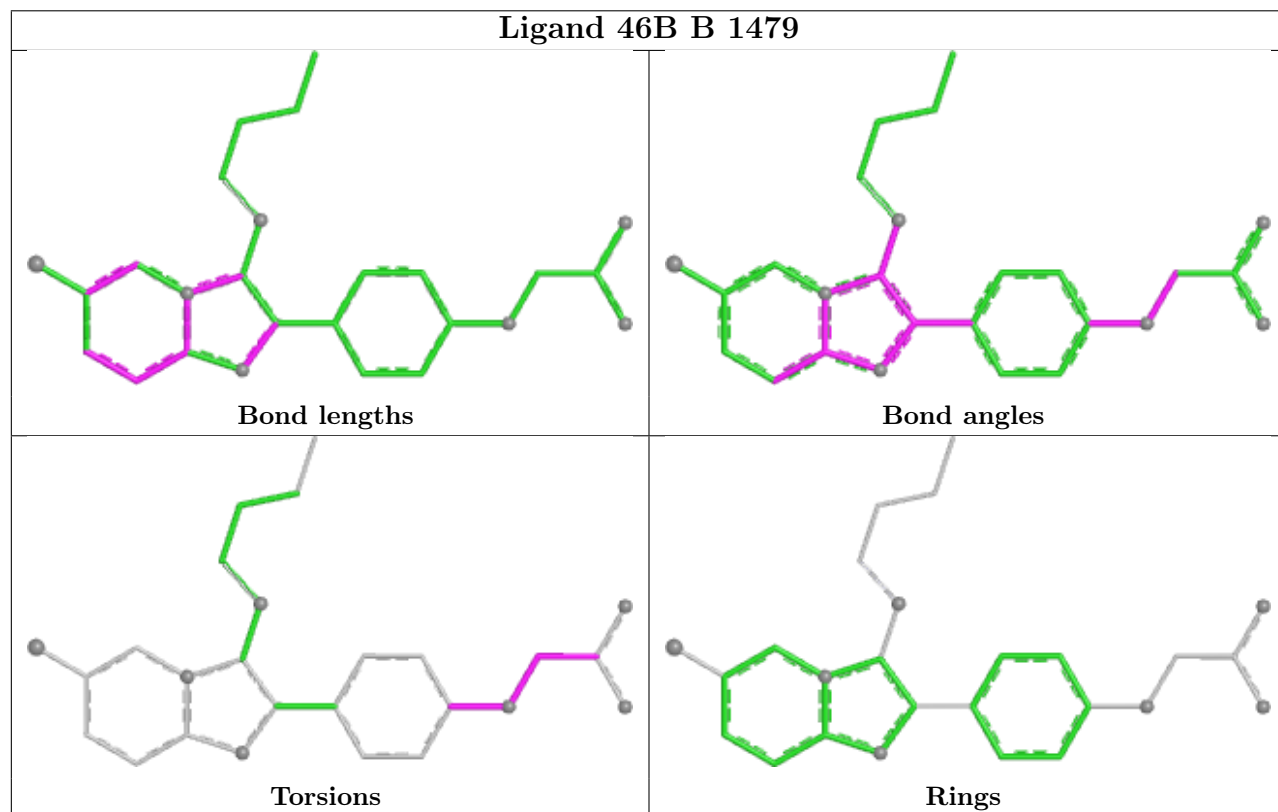
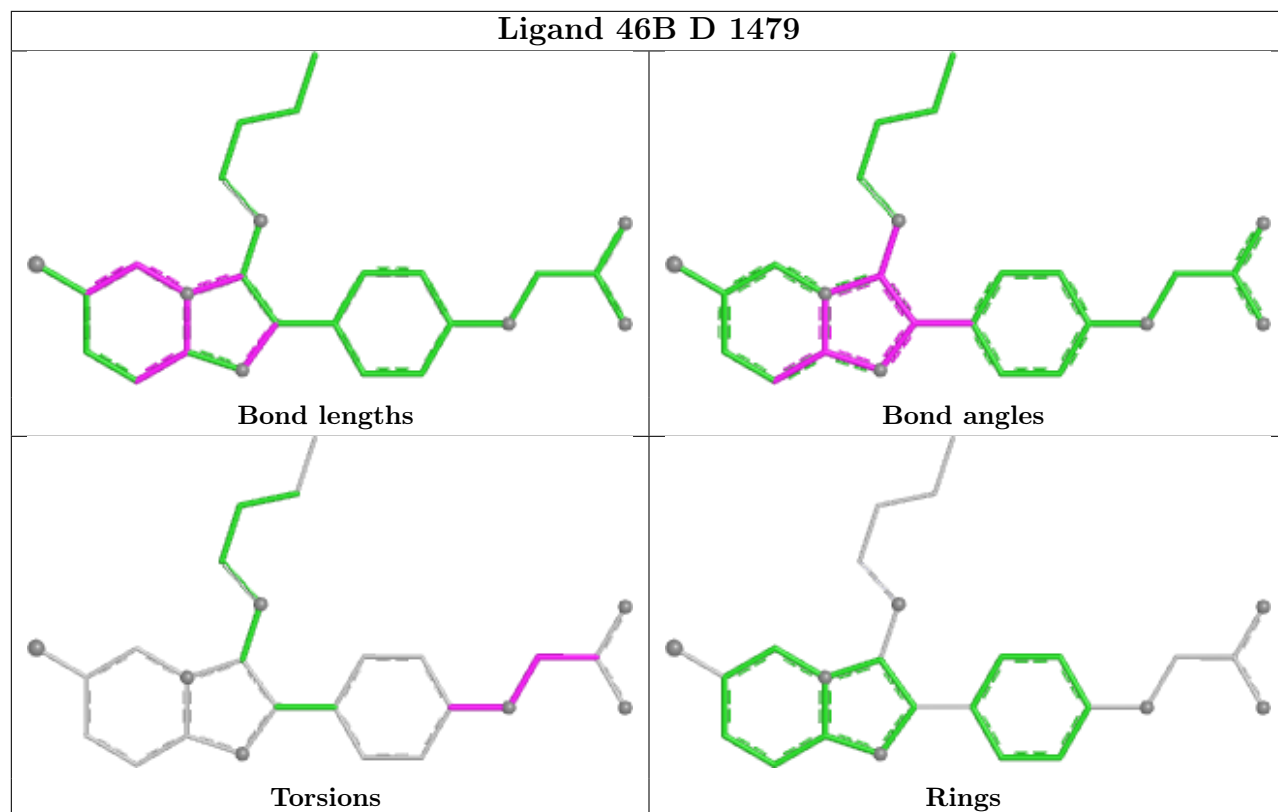












5.7 Other polymers [i](#)

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	475/486 (97%)	-0.40	0 100 100	12, 20, 33, 52	0
1	B	475/486 (97%)	-0.42	1 (0%) 91 90	12, 20, 33, 49	0
1	C	475/486 (97%)	-0.37	3 (0%) 85 85	13, 21, 33, 51	0
1	D	475/486 (97%)	-0.51	0 100 100	11, 19, 32, 49	0
1	E	475/486 (97%)	-0.55	0 100 100	12, 18, 30, 45	0
1	F	475/486 (97%)	-0.48	1 (0%) 91 90	11, 19, 31, 45	0
All	All	2850/2916 (97%)	-0.45	5 (0%) 91 90	11, 19, 32, 52	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	435	GLU	2.5
1	C	292	GLU	2.3
1	C	409	PRO	2.1
1	B	414	ALA	2.1
1	C	414	ALA	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

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

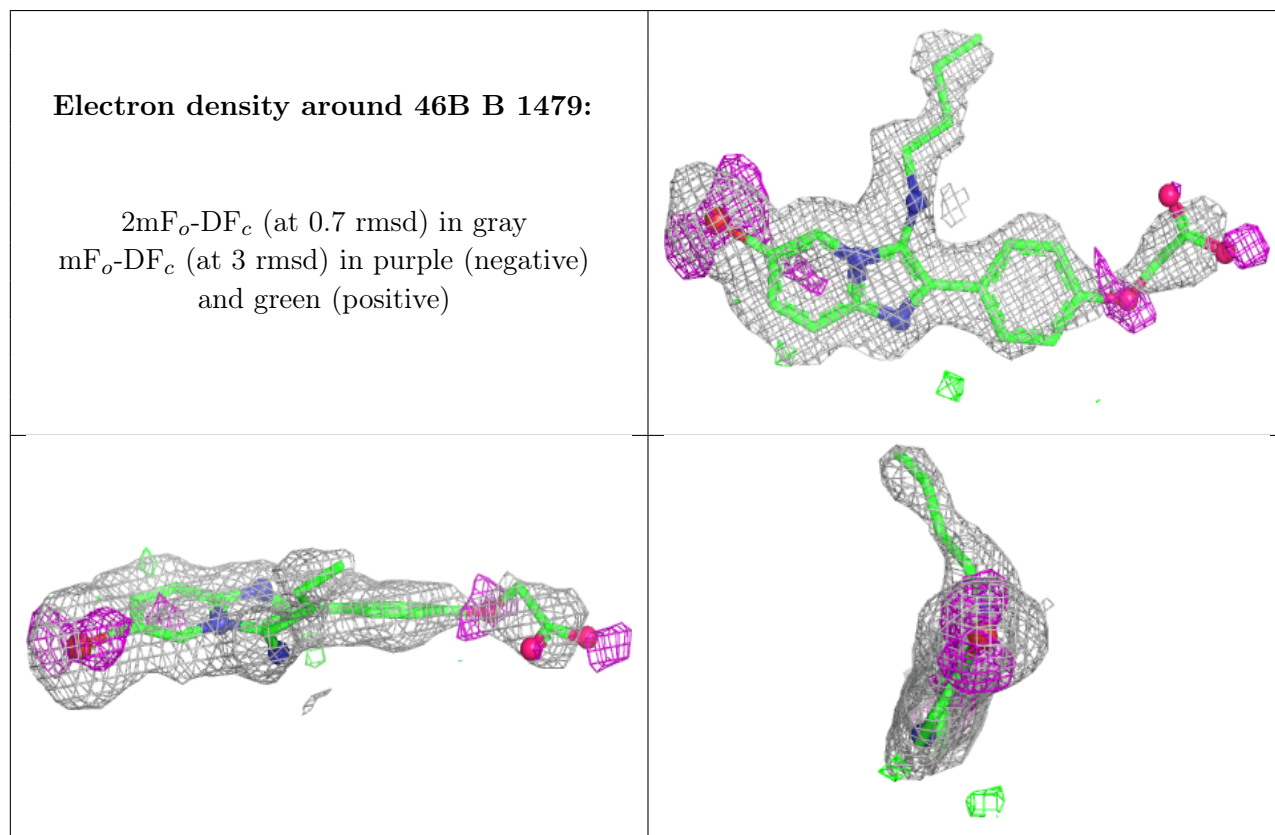
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	E	1486	1/1	0.90	0.11	42,42,42,42	0
3	MG	A	1486	1/1	0.91	0.11	42,42,42,42	0
2	46B	B	1479	26/26	0.92	0.13	39,42,55,57	0
2	46B	E	1479	26/26	0.93	0.14	39,41,55,57	0
2	46B	C	1479	26/26	0.94	0.13	39,42,55,57	0
3	MG	B	1486	1/1	0.94	0.11	42,42,42,42	0
2	46B	A	1479	26/26	0.94	0.12	39,42,54,57	0
3	MG	F	1486	1/1	0.94	0.10	42,42,42,42	0
2	46B	D	1479	26/26	0.95	0.12	39,41,55,57	0
2	46B	F	1479	26/26	0.95	0.12	37,42,55,57	0
3	MG	C	1486	1/1	0.96	0.07	42,42,42,42	0
5	PO4	B	1484	5/5	0.96	0.08	19,20,23,25	0
4	P3S	A	1483	15/15	0.97	0.08	14,16,17,19	0
4	P3S	C	1483	15/15	0.97	0.07	14,16,17,19	0
5	PO4	A	1484	5/5	0.97	0.12	19,21,24,25	0
3	MG	D	1486	1/1	0.97	0.05	42,42,42,42	0
5	PO4	C	1484	5/5	0.97	0.11	19,21,24,25	0
5	PO4	D	1484	5/5	0.97	0.07	19,20,23,25	0
3	MG	B	1480	1/1	0.98	0.03	15,15,15,15	0
3	MG	E	1481	1/1	0.98	0.02	16,16,16,16	0
3	MG	B	1482	1/1	0.98	0.11	17,17,17,17	0
3	MG	A	1482	1/1	0.98	0.07	16,16,16,16	0
3	MG	C	1480	1/1	0.98	0.02	16,16,16,16	0
4	P3S	B	1483	15/15	0.98	0.07	14,16,17,18	0
3	MG	C	1481	1/1	0.98	0.07	17,17,17,17	0
3	MG	C	1482	1/1	0.98	0.04	17,17,17,17	0
3	MG	A	1481	1/1	0.98	0.05	17,17,17,17	0
3	MG	D	1481	1/1	0.98	0.04	16,16,16,16	0
3	MG	D	1482	1/1	0.98	0.02	16,16,16,16	0
5	PO4	E	1484	5/5	0.98	0.05	18,20,22,25	0
5	PO4	F	1484	5/5	0.98	0.05	18,19,24,25	0
6	CL	B	1485	1/1	0.98	0.05	23,23,23,23	0
6	CL	C	1485	1/1	0.98	0.06	23,23,23,23	0
6	CL	D	1485	1/1	0.98	0.04	22,22,22,22	0
4	P3S	E	1483	15/15	0.99	0.04	14,15,16,16	0
4	P3S	F	1483	15/15	0.99	0.04	13,15,16,16	0
3	MG	B	1481	1/1	0.99	0.03	17,17,17,17	0

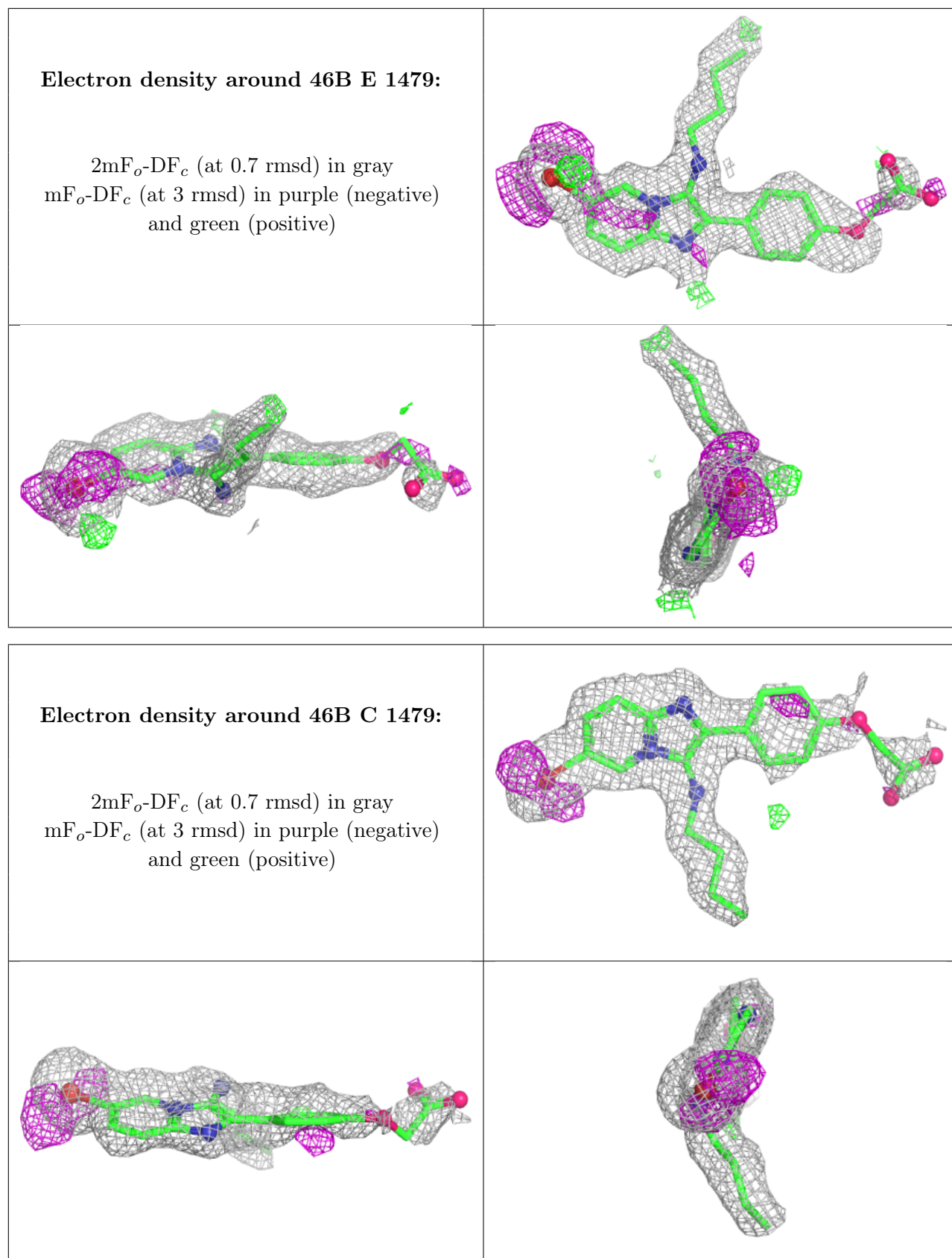
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	F	1480	1/1	0.99	0.02	14,14,14,14	0
3	MG	F	1481	1/1	0.99	0.03	16,16,16,16	0
3	MG	F	1482	1/1	0.99	0.02	16,16,16,16	0
3	MG	D	1480	1/1	0.99	0.02	15,15,15,15	0
3	MG	E	1480	1/1	0.99	0.03	14,14,14,14	0
6	CL	A	1485	1/1	0.99	0.03	22,22,22,22	0
3	MG	A	1480	1/1	0.99	0.02	15,15,15,15	0
3	MG	E	1482	1/1	0.99	0.04	15,15,15,15	0
4	P3S	D	1483	15/15	0.99	0.04	14,16,17,18	0
6	CL	E	1485	1/1	0.99	0.02	22,22,22,22	0
6	CL	F	1485	1/1	0.99	0.03	22,22,22,22	0

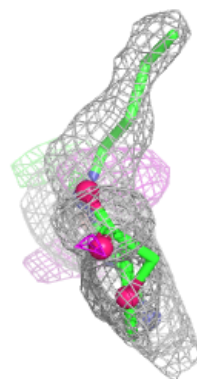
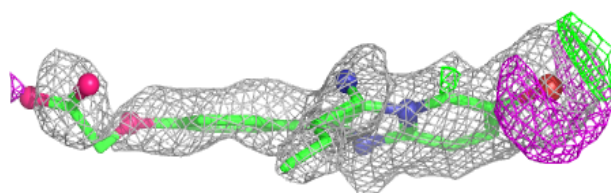
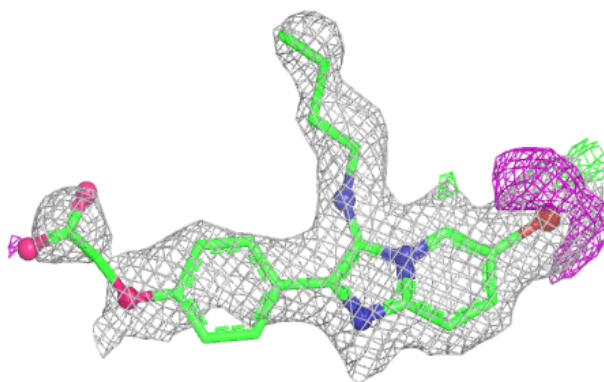
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



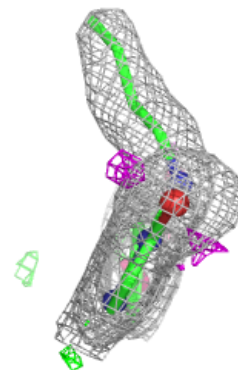
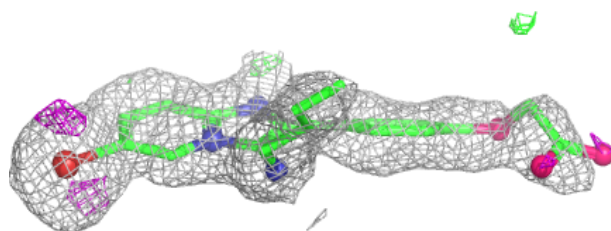
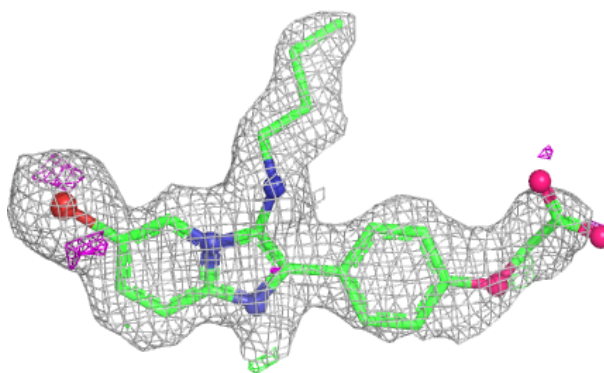


Electron density around 46B A 1479:

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

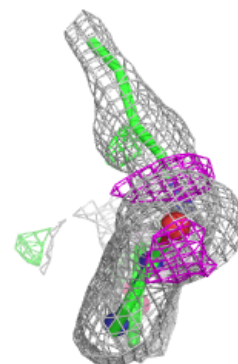
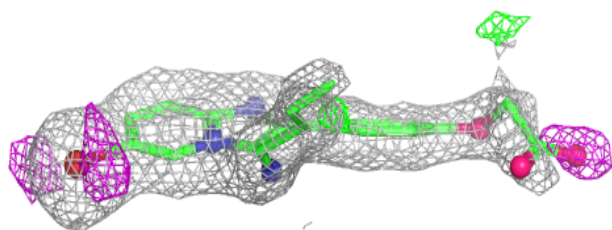
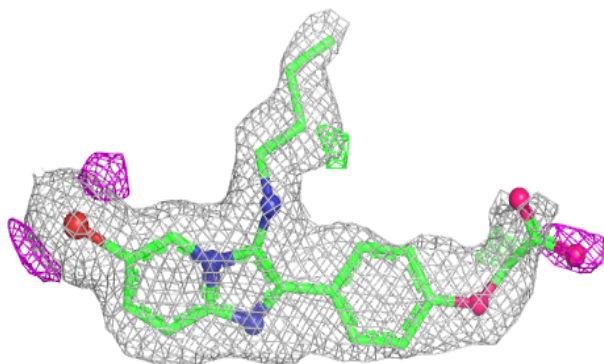
**Electron density around 46B D 1479:**

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

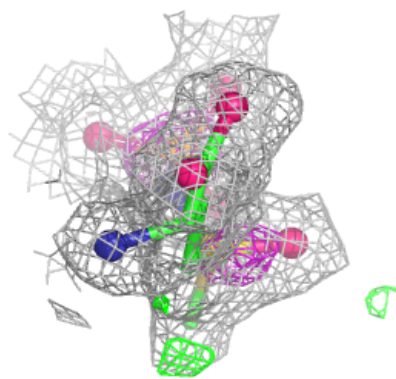
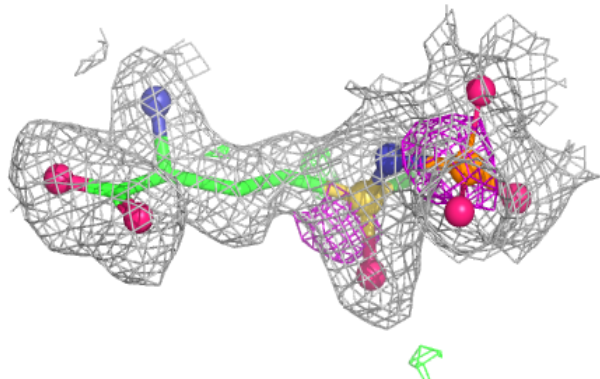
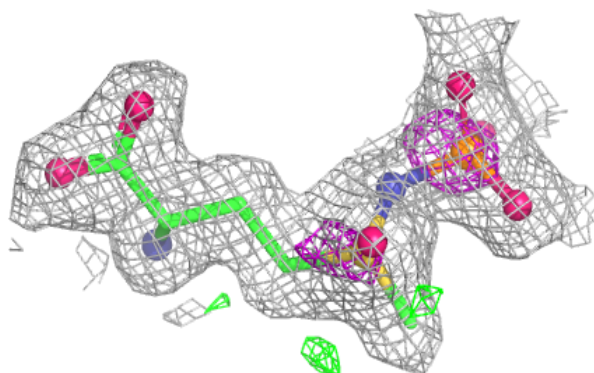


Electron density around 46B F 1479:

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

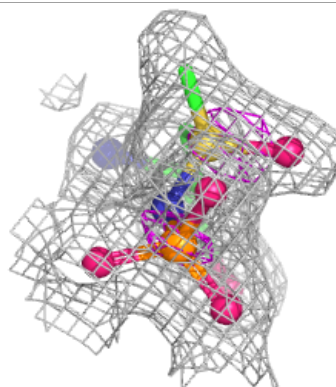
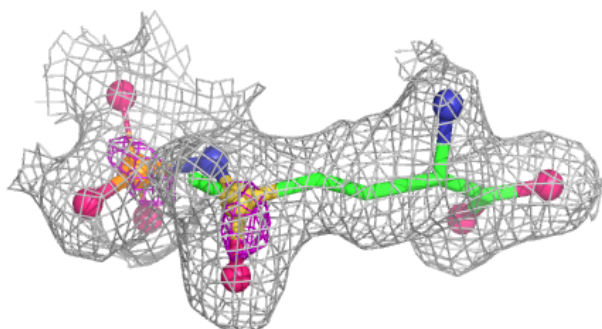
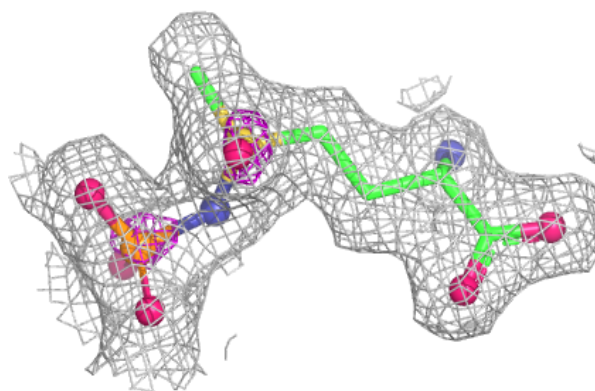
**Electron density around P3S A 1483:**

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

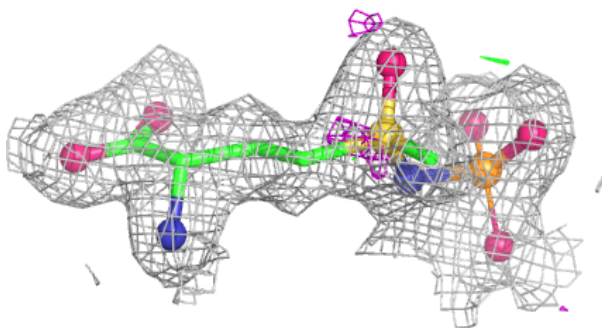
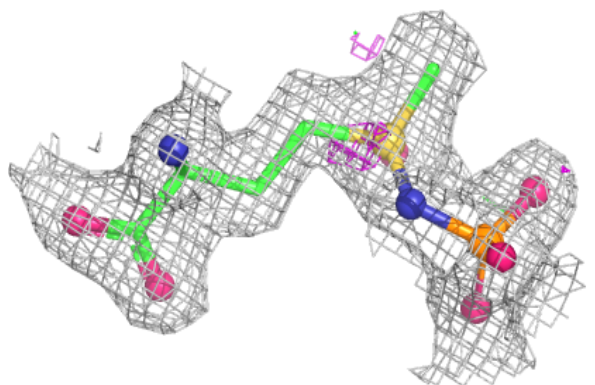


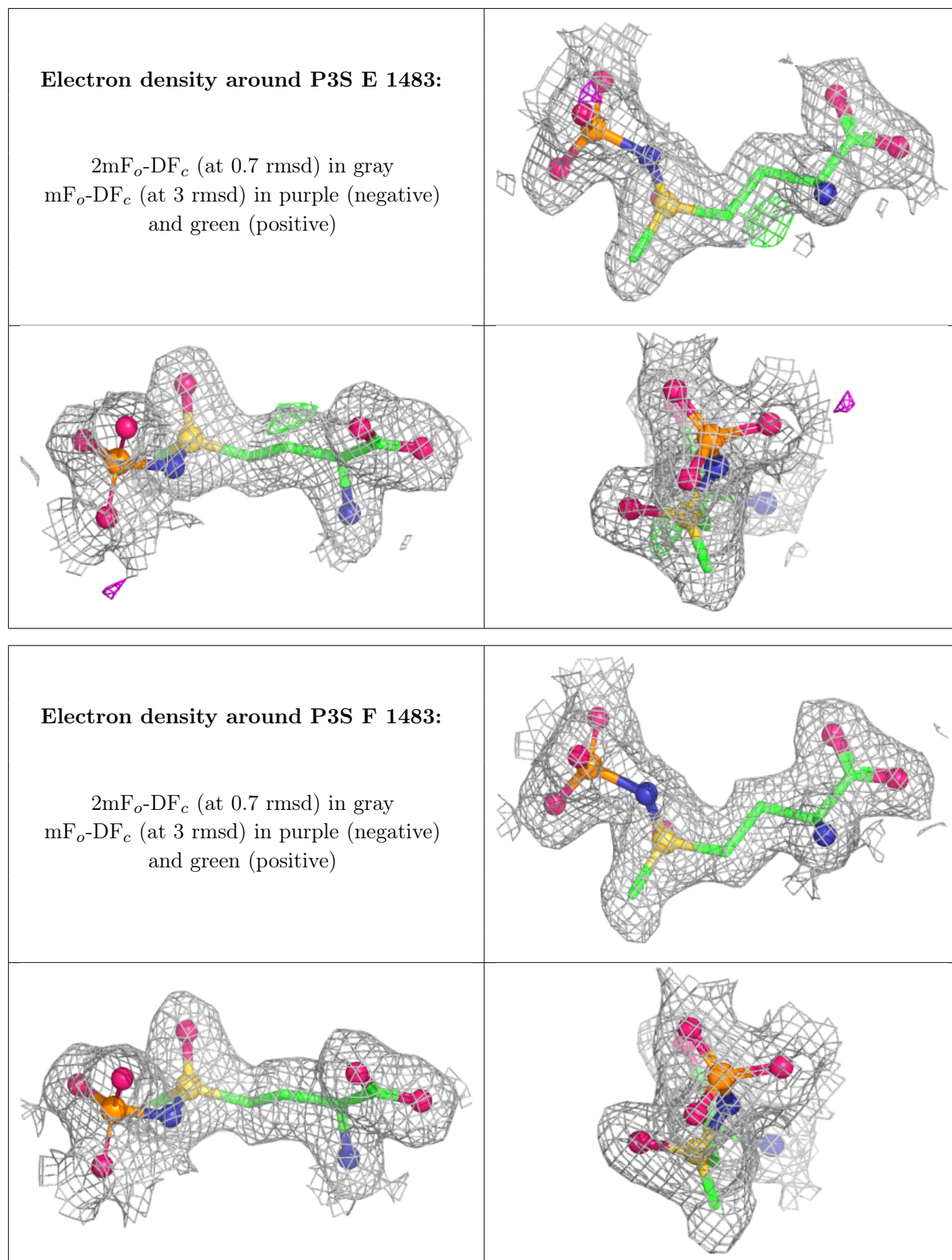
Electron density around P3S C 1483:

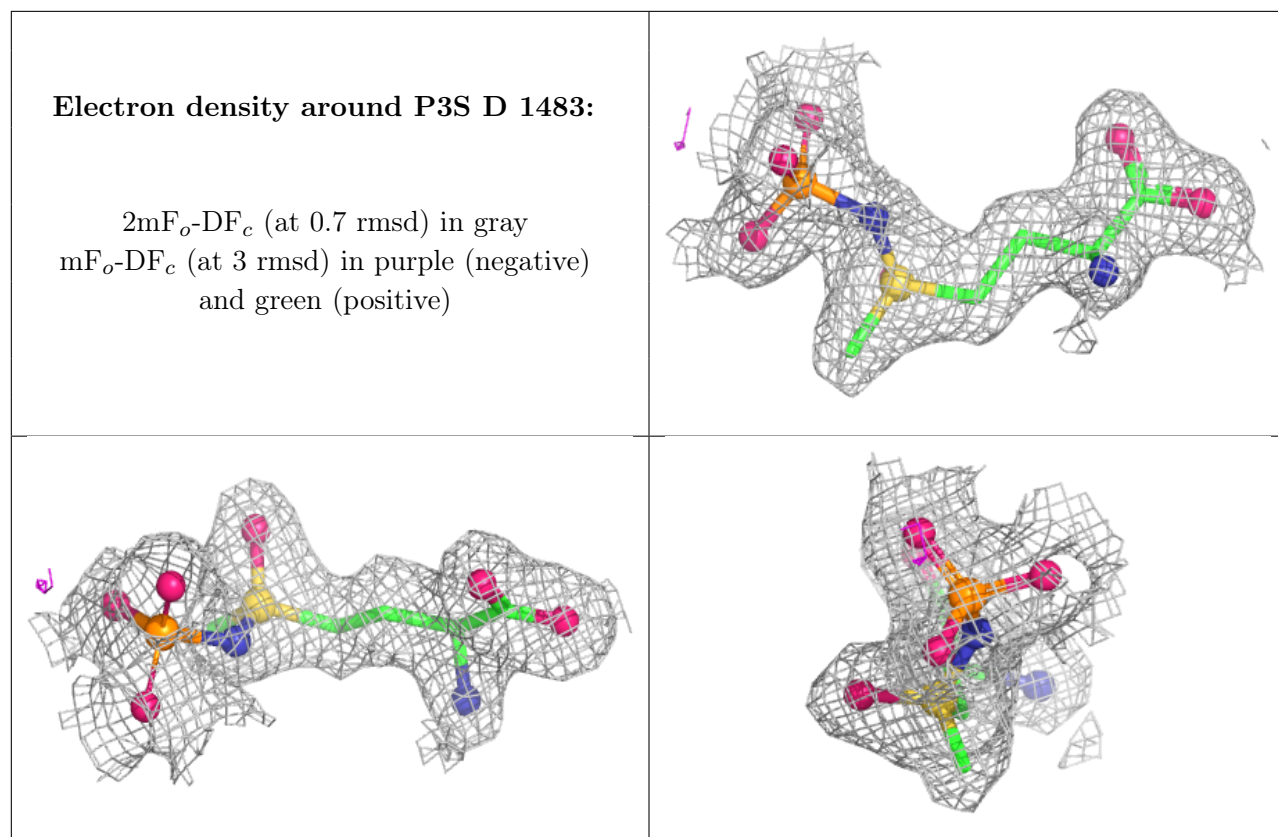
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around P3S B 1483:**

$2mF_o-DF_c$ (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.