wwPDB X-ray Structure Validation Summary Report (i)

Jun 25, 2024 – 10:07 AM EDT

PDB ID	:	8UAR
Title	:	Rhodococcus ruber Alcohol Dehydrogenase NADH Biomimetic Complex - Compound 4b
Authors	:	Wilson, L.A.; Schenk, G.; Guddat, L.W.; Scott, C.
Deposited on	:	2023-09-22
Resolution	:	2.99 Å(reported)

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

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

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

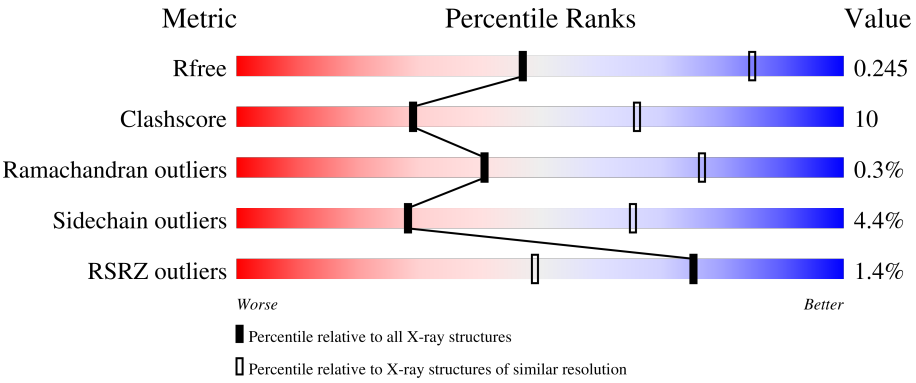
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.99 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 <=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	365	79% 15%
1	B	365	76% 18%
1	C	365	76% 17%
1	D	365	78% 17%
1	E	365	78% 17%

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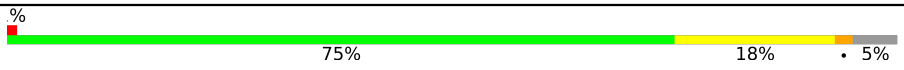
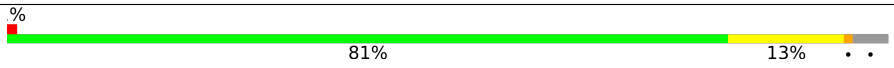
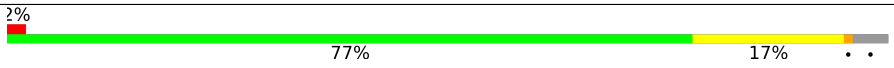
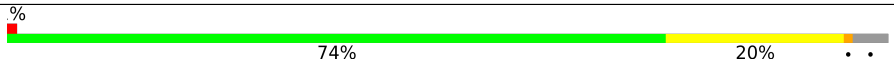
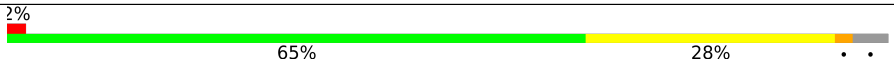
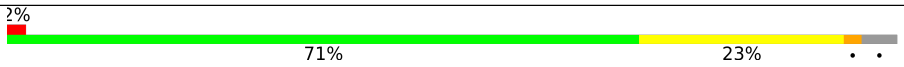
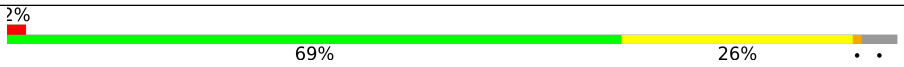
Mol	Chain	Length	Quality of chain
1	F	365	
1	G	365	
1	H	365	
1	I	365	
1	J	365	
1	K	365	
1	L	365	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 30414 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 Rhodococcus ruber ADH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	0	0
			2526	1594	445	475	12			
1	B	349	Total	C	N	O	S	0	1	0
			2511	1583	444	472	12			
1	C	349	Total	C	N	O	S	0	0	0
			2504	1578	442	472	12			
1	D	351	Total	C	N	O	S	0	0	0
			2518	1588	444	474	12			
1	E	349	Total	C	N	O	S	0	0	0
			2504	1578	442	472	12			
1	F	348	Total	C	N	O	S	0	0	0
			2493	1572	438	471	12			
1	G	350	Total	C	N	O	S	0	0	0
			2511	1583	443	473	12			
1	H	350	Total	C	N	O	S	0	0	0
			2511	1583	443	473	12			
1	I	349	Total	C	N	O	S	0	0	0
			2504	1578	442	472	12			
1	J	349	Total	C	N	O	S	0	0	0
			2504	1578	442	472	12			
1	K	349	Total	C	N	O	S	0	0	0
			2504	1578	442	472	12			
1	L	349	Total	C	N	O	S	0	0	0
			2504	1578	442	472	12			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		
2	B	2	Total	Zn	0	0
			2	2		

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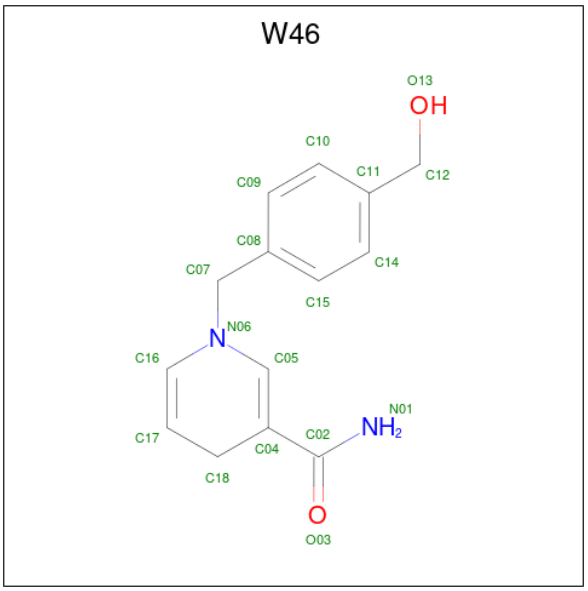
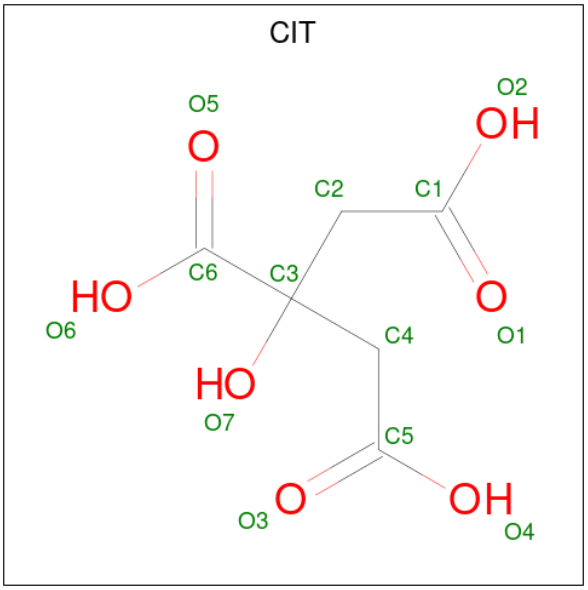
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	2	Total Zn 2 2	0	0
2	D	2	Total Zn 2 2	0	0
2	E	2	Total Zn 2 2	0	0
2	F	2	Total Zn 2 2	0	0
2	G	2	Total Zn 2 2	0	0
2	H	2	Total Zn 2 2	0	0
2	I	2	Total Zn 2 2	0	0
2	J	2	Total Zn 2 2	0	0
2	K	2	Total Zn 2 2	0	0
2	L	2	Total Zn 2 2	0	0

- Molecule 3 is 1-{[4-(hydroxymethyl)phenyl]methyl}-1,4-dihydropyridine-3-carboxamide (three-letter code: W46) (formula: $C_{14}H_{16}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



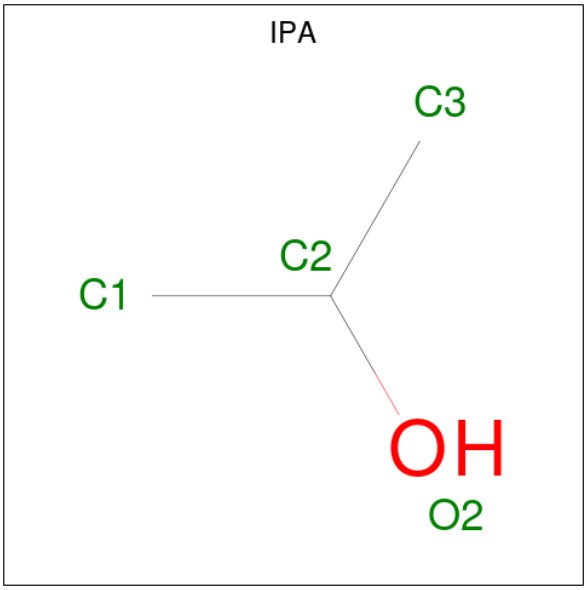
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	14	2	2		
3	B	1	Total	C	N	O	0	0
			18	14	2	2		
3	C	1	Total	C	N	O	0	0
			18	14	2	2		
3	D	1	Total	C	N	O	0	0
			18	14	2	2		
3	E	1	Total	C	N	O	0	0
			18	14	2	2		
3	F	1	Total	C	N	O	0	0
			18	14	2	2		
3	H	1	Total	C	N	O	0	0
			18	14	2	2		
3	I	1	Total	C	N	O	0	0
			18	14	2	2		
3	J	1	Total	C	N	O	0	0
			18	14	2	2		
3	K	1	Total	C	N	O	0	0
			18	14	2	2		
3	L	1	Total	C	N	O	0	0
			18	14	2	2		

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 13 6 7	0	0
4	H	1	Total C O 13 6 7	0	0
4	I	1	Total C O 13 6 7	0	0
4	K	1	Total C O 13 6 7	0	0
4	L	1	Total C O 13 6 7	0	0

- Molecule 5 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C O 4 3 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O 1 1	0	0
6	C	2	Total O 2 2	0	0
6	D	3	Total O 3 3	0	0
6	E	2	Total O 2 2	0	0

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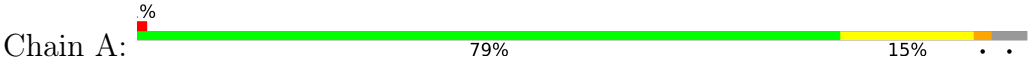
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	F	2	Total O 2 2	0	0
6	G	9	Total O 9 9	0	0
6	H	3	Total O 3 3	0	0
6	K	6	Total O 6 6	0	0
6	L	1	Total O 1 1	0	0

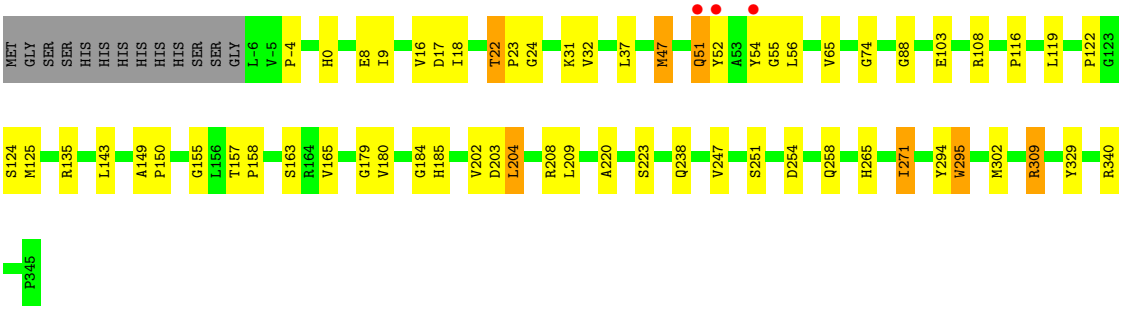
3 Residue-property plots (i)

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: Rhodococcus ruber ADH

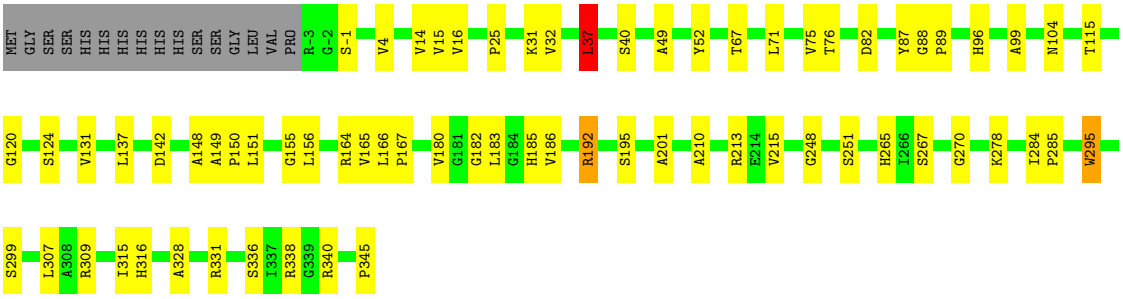
Chain A:





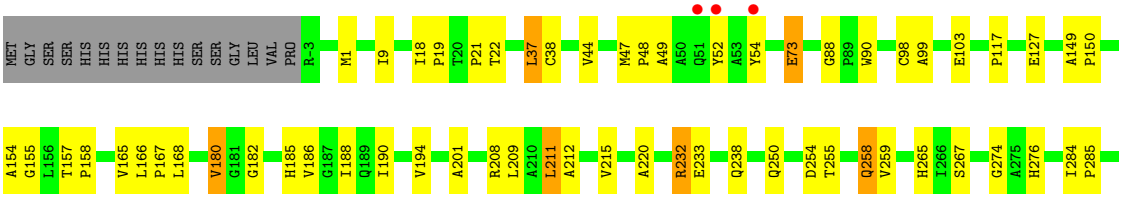
• Molecule 1: Rhodococcus ruber ADH

Chain B:



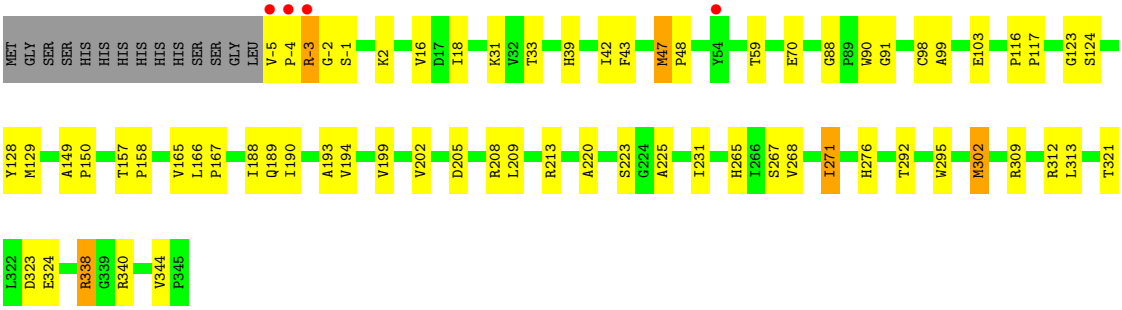
• Molecule 1: Rhodococcus ruber ADH

Chain C:



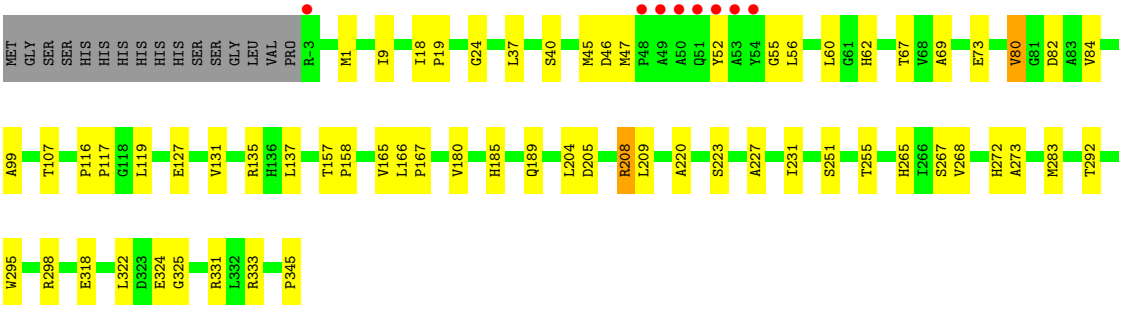
• Molecule 1: Rhodococcus ruber ADH

Chain D:



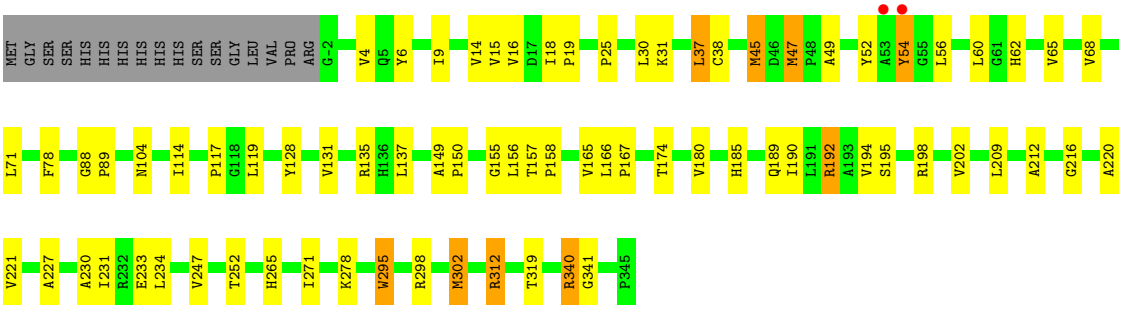
• Molecule 1: Rhodococcus ruber ADH

Chain E:



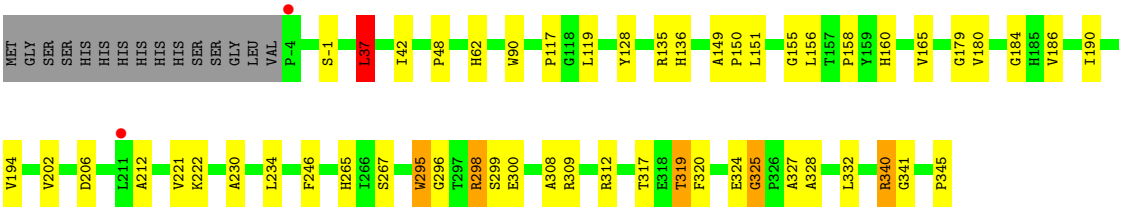
• Molecule 1: Rhodococcus ruber ADH

Chain F:



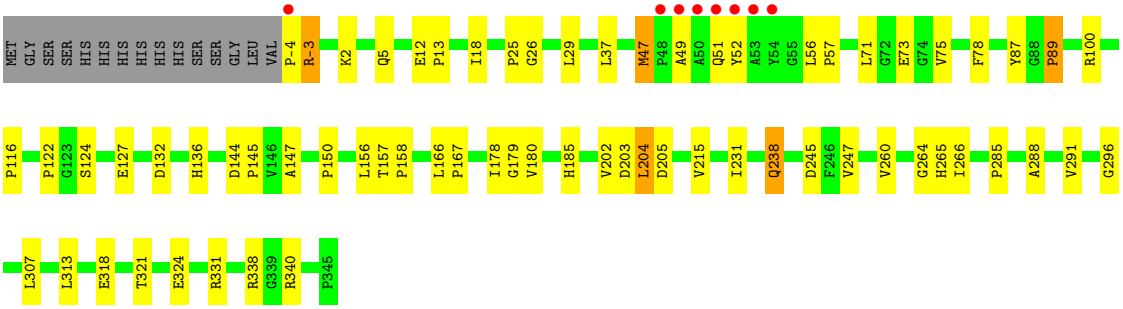
• Molecule 1: Rhodococcus ruber ADH

Chain G:



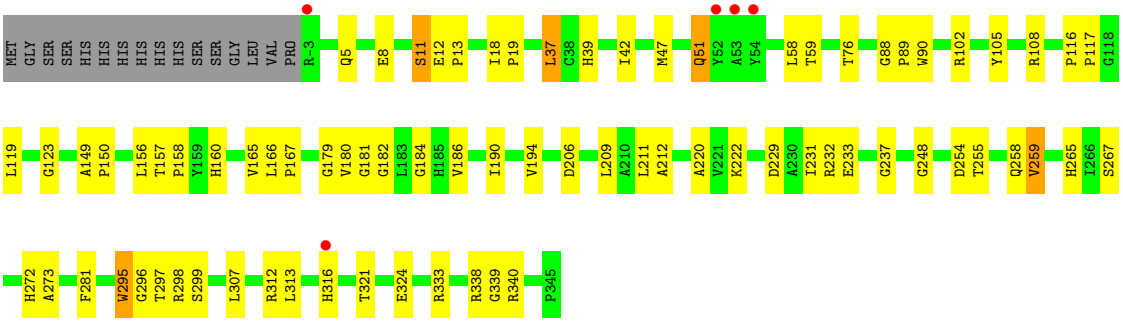
• Molecule 1: Rhodococcus ruber ADH

Chain H:



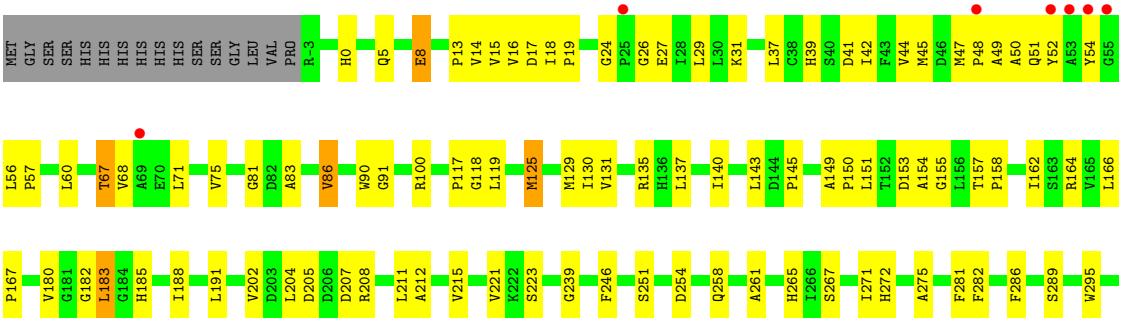
• Molecule 1: Rhodococcus ruber ADH

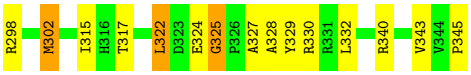
Chain I:



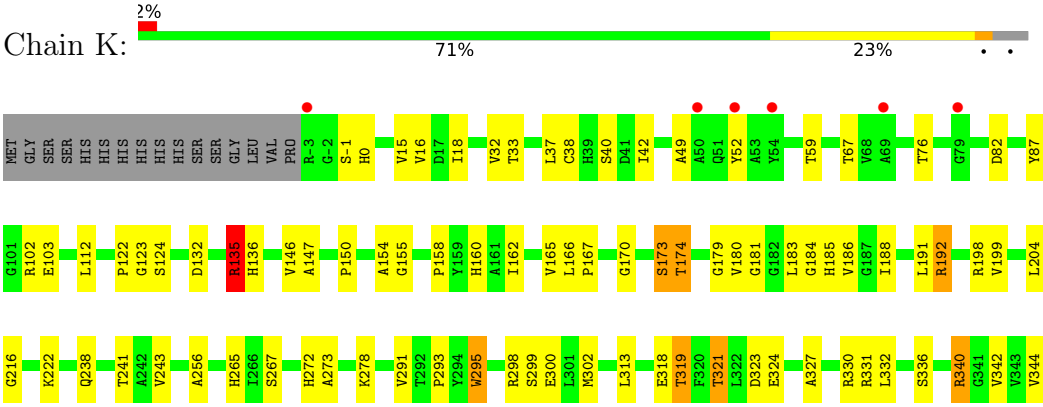
• Molecule 1: Rhodococcus ruber ADH

Chain J:

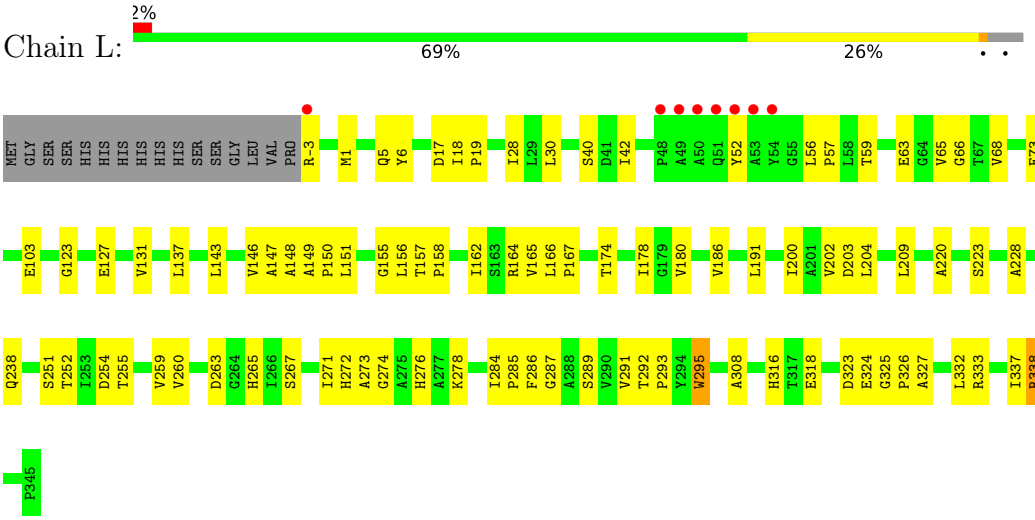




• Molecule 1: Rhodococcus ruber ADH



• Molecule 1: Rhodococcus ruber ADH



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	78.30Å 158.18Å 272.94Å 90.00° 91.05° 90.00°	Depositor
Resolution (Å)	49.18 – 2.99 49.18 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.4 (49.18-2.99) 99.4 (49.18-2.99)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.85 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.193 , 0.246 0.194 , 0.245	Depositor DCC
R_{free} test set	2006 reflections (1.50%)	wwPDB-VP
Wilson B-factor (Å^2)	42.8	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 39.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	30414	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.17% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IPA, ZN, CIT, W46

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.42	0/2579	0.93	4/3522 (0.1%)
1	B	0.42	0/2567	0.95	8/3504 (0.2%)
1	C	0.39	0/2556	0.90	5/3489 (0.1%)
1	D	0.41	0/2571	0.93	3/3511 (0.1%)
1	E	0.40	0/2556	0.88	2/3489 (0.1%)
1	F	0.39	0/2545	0.89	4/3475 (0.1%)
1	G	0.42	0/2564	0.92	5/3500 (0.1%)
1	H	0.40	0/2564	0.90	3/3500 (0.1%)
1	I	0.39	0/2556	0.86	1/3489 (0.0%)
1	J	0.38	0/2556	0.92	9/3489 (0.3%)
1	K	0.39	0/2556	0.88	3/3489 (0.1%)
1	L	0.37	0/2556	0.89	3/3489 (0.1%)
All	All	0.40	0/30726	0.91	50/41946 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	D	0	2
1	E	0	1
1	H	0	1
All	All	0	5

There are no bond length outliers.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	164	ARG	NE-CZ-NH2	-11.49	114.55	120.30
1	L	338	ARG	NE-CZ-NH1	10.46	125.53	120.30
1	L	338	ARG	CD-NE-CZ	9.48	136.87	123.60
1	G	37	LEU	CB-CG-CD2	-8.18	97.10	111.00
1	J	164	ARG	NE-CZ-NH1	-8.13	116.23	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	309	ARG	Sidechain
1	D	213	ARG	Sidechain
1	D	338	ARG	Sidechain
1	E	208	ARG	Sidechain
1	H	338	ARG	Sidechain

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	2526	0	2520	36	0
1	B	2511	0	2500	42	0
1	C	2504	0	2493	51	0
1	D	2518	0	2509	51	1
1	E	2504	0	2493	43	1
1	F	2493	0	2480	47	0
1	G	2511	0	2500	42	0
1	H	2511	0	2500	41	0
1	I	2504	0	2494	50	0
1	J	2504	0	2494	78	0
1	K	2504	0	2493	56	0
1	L	2504	0	2493	61	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	18	0	0	1	0
3	B	18	0	0	1	0
3	C	18	0	0	0	0
3	D	18	0	0	0	0
3	E	18	0	0	1	0
3	F	18	0	0	0	0
3	H	18	0	0	0	0
3	I	18	0	0	0	0
3	J	18	0	0	1	0
3	K	18	0	0	0	0
3	L	18	0	0	4	0
4	B	13	0	5	2	0
4	H	13	0	5	0	0
4	I	13	0	5	1	0
4	K	13	0	5	1	0
4	L	13	0	5	3	0
5	B	4	0	8	0	0
6	A	1	0	0	0	0
6	C	2	0	0	0	0
6	D	3	0	0	0	0
6	E	2	0	0	0	0
6	F	2	0	0	0	0
6	G	9	0	0	0	0
6	H	3	0	0	0	0
6	K	6	0	0	0	0
6	L	1	0	0	0	0
All	All	30414	0	30002	578	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 578 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:209:LEU:HD22	1:F:220:ALA:HB1	1.41	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:42:ILE:HD12	1:D:43:PHE:N	1.75	1.01
1:E:45:MET:CE	1:E:60:LEU:HD11	1.92	0.98
1:E:45:MET:HE2	1:E:60:LEU:HD11	1.44	0.97
1:E:318:GLU:OE2	1:E:331:ARG:NH1	1.99	0.95

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:338:ARG:NH2	1:E:324:GLU:OE1[1_455]	2.06	0.14

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	350/365 (96%)	330 (94%)	18 (5%)	2 (1%)	25	64
1	B	348/365 (95%)	328 (94%)	19 (6%)	1 (0%)	41	76
1	C	347/365 (95%)	331 (95%)	15 (4%)	1 (0%)	41	76
1	D	349/365 (96%)	327 (94%)	21 (6%)	1 (0%)	41	76
1	E	347/365 (95%)	327 (94%)	18 (5%)	2 (1%)	25	64
1	F	346/365 (95%)	329 (95%)	17 (5%)	0	100	100
1	G	348/365 (95%)	327 (94%)	20 (6%)	1 (0%)	41	76
1	H	348/365 (95%)	329 (94%)	19 (6%)	0	100	100
1	I	347/365 (95%)	327 (94%)	18 (5%)	2 (1%)	25	64
1	J	347/365 (95%)	315 (91%)	30 (9%)	2 (1%)	25	64
1	K	347/365 (95%)	331 (95%)	15 (4%)	1 (0%)	41	76
1	L	347/365 (95%)	324 (93%)	23 (7%)	0	100	100
All	All	4171/4380 (95%)	3925 (94%)	233 (6%)	13 (0%)	41	76

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	49	ALA
1	B	182	GLY
1	E	24	GLY
1	K	181	GLY
1	D	225	ALA

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	254/265 (96%)	242 (95%)	12 (5%)	26	63
1	B	252/265 (95%)	242 (96%)	10 (4%)	31	68
1	C	251/265 (95%)	236 (94%)	15 (6%)	19	53
1	D	253/265 (96%)	250 (99%)	3 (1%)	71	90
1	E	251/265 (95%)	243 (97%)	8 (3%)	39	74
1	F	250/265 (94%)	237 (95%)	13 (5%)	23	59
1	G	252/265 (95%)	243 (96%)	9 (4%)	35	70
1	H	252/265 (95%)	242 (96%)	10 (4%)	31	68
1	I	251/265 (95%)	238 (95%)	13 (5%)	23	59
1	J	251/265 (95%)	237 (94%)	14 (6%)	21	56
1	K	251/265 (95%)	234 (93%)	17 (7%)	16	48
1	L	251/265 (95%)	242 (96%)	9 (4%)	35	70
All	All	3019/3180 (95%)	2886 (96%)	133 (4%)	28	65

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	238	GLN
1	K	298	ARG
1	L	292	THR
1	F	37	LEU

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Mol	Chain	Res	Type
1	E	295	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	5	GLN
1	J	265	HIS
1	L	276	HIS
1	L	265	HIS
1	H	276	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 41 ligands modelled in this entry, 24 are monoatomic - leaving 17 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	W46	F	503	-	19,19,19	4.35	12 (63%)	18,25,25	2.67	7 (38%)
4	CIT	I	503	-	12,12,12	1.35	1 (8%)	17,17,17	1.15	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	W46	D	503	-	19,19,19	4.13	12 (63%)	18,25,25	2.25	7 (38%)
4	CIT	K	401	-	12,12,12	1.14	1 (8%)	17,17,17	1.54	2 (11%)
3	W46	L	504	-	19,19,19	4.05	11 (57%)	18,25,25	2.25	8 (44%)
3	W46	C	503	-	19,19,19	4.52	12 (63%)	18,25,25	2.61	8 (44%)
3	W46	K	404	-	19,19,19	4.59	12 (63%)	18,25,25	2.80	6 (33%)
3	W46	E	503	-	19,19,19	4.36	14 (73%)	18,25,25	2.83	7 (38%)
4	CIT	B	503	-	12,12,12	1.19	1 (8%)	17,17,17	1.63	2 (11%)
4	CIT	L	503	-	12,12,12	1.13	1 (8%)	17,17,17	1.40	2 (11%)
3	W46	J	503	-	19,19,19	4.51	12 (63%)	18,25,25	2.83	7 (38%)
3	W46	A	503	-	19,19,19	4.31	11 (57%)	18,25,25	2.32	4 (22%)
4	CIT	H	503	-	12,12,12	1.19	1 (8%)	17,17,17	1.46	2 (11%)
3	W46	H	504	-	19,19,19	4.35	12 (63%)	18,25,25	1.81	4 (22%)
3	W46	I	504	-	19,19,19	4.21	10 (52%)	18,25,25	2.32	4 (22%)
5	IPA	B	505	-	3,3,3	0.86	0	3,3,3	0.33	0
3	W46	B	504	-	19,19,19	4.15	10 (52%)	18,25,25	2.57	5 (27%)

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	W46	F	503	-	-	1/9/20/20	0/2/2/2
4	CIT	I	503	-	-	8/16/16/16	-
3	W46	D	503	-	-	0/9/20/20	0/2/2/2
4	CIT	K	401	-	-	8/16/16/16	-
3	W46	L	504	-	-	3/9/20/20	0/2/2/2
3	W46	C	503	-	-	0/9/20/20	0/2/2/2
3	W46	K	404	-	-	0/9/20/20	0/2/2/2
3	W46	E	503	-	-	0/9/20/20	0/2/2/2
4	CIT	B	503	-	-	7/16/16/16	-
4	CIT	L	503	-	-	0/16/16/16	-
3	W46	J	503	-	-	0/9/20/20	0/2/2/2
3	W46	A	503	-	-	1/9/20/20	0/2/2/2
4	CIT	H	503	-	-	10/16/16/16	-
3	W46	H	504	-	-	0/9/20/20	0/2/2/2
3	W46	I	504	-	-	0/9/20/20	0/2/2/2
3	W46	B	504	-	-	0/9/20/20	0/2/2/2

The worst 5 of 133 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	503	W46	C16-C17	13.64	1.57	1.33
3	J	503	W46	C16-C17	13.57	1.57	1.33
3	K	404	W46	C16-C17	13.35	1.57	1.33
3	F	503	W46	C16-C17	12.78	1.56	1.33
3	H	504	W46	C16-C17	12.72	1.56	1.33

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	J	503	W46	C08-C07-N06	-8.65	95.40	112.41
3	K	404	W46	O13-C12-C11	-6.79	87.03	112.03
3	B	504	W46	C08-C07-N06	-6.56	99.51	112.41
3	E	503	W46	C08-C07-N06	-6.40	99.83	112.41
3	A	503	W46	O13-C12-C11	-6.34	88.68	112.03

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	L	504	W46	N01-C02-C04-C05
3	L	504	W46	O03-C02-C04-C05
4	B	503	CIT	C1-C2-C3-O7
4	B	503	CIT	C1-C2-C3-C4
4	B	503	CIT	O7-C3-C6-O5

There are no ring outliers.

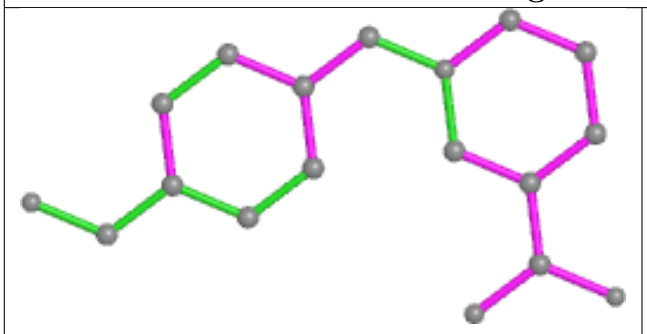
9 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	503	CIT	1	0
4	K	401	CIT	1	0
3	L	504	W46	4	0
3	E	503	W46	1	0
4	B	503	CIT	2	0
4	L	503	CIT	3	0
3	J	503	W46	1	0
3	A	503	W46	1	0
3	B	504	W46	1	0

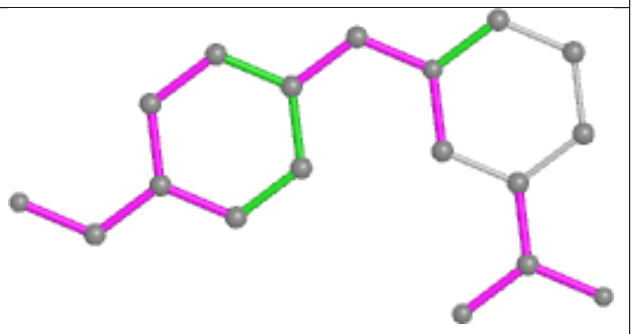
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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

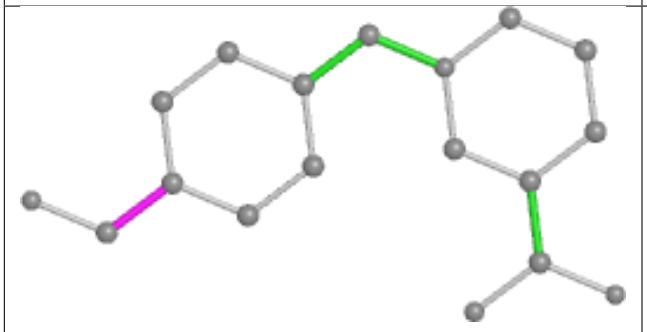
Ligand W46 F 503



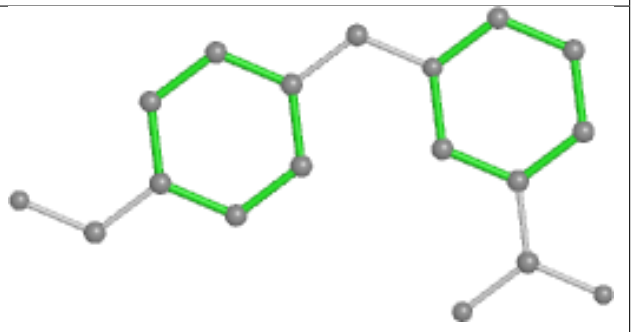
Bond lengths



Bond angles

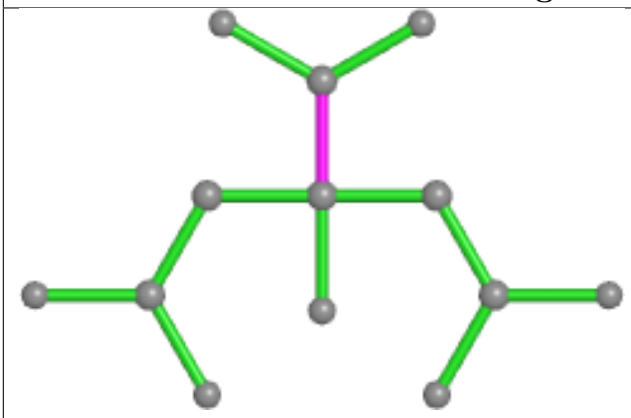


Torsions



Rings

Ligand CIT I 503



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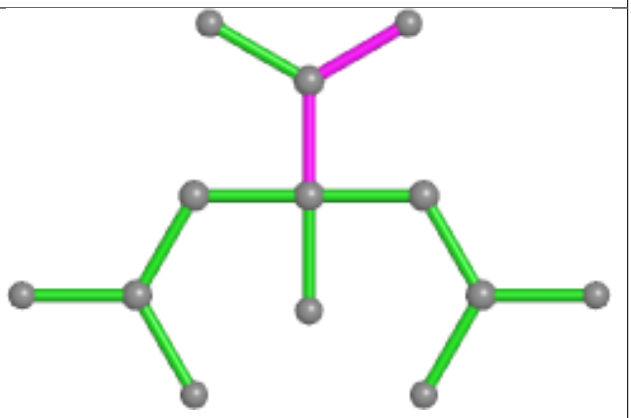

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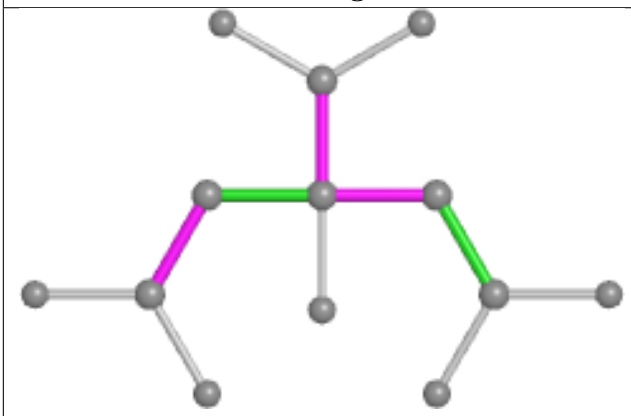

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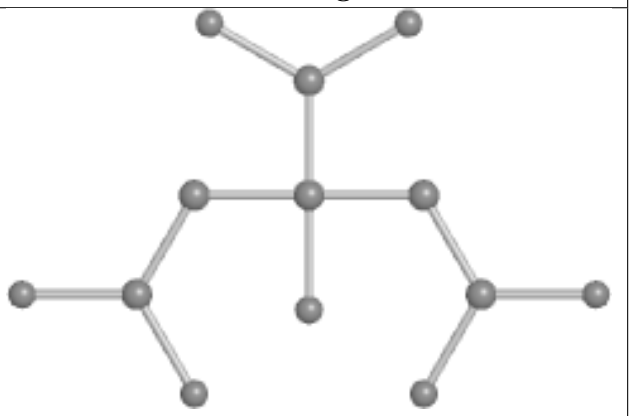
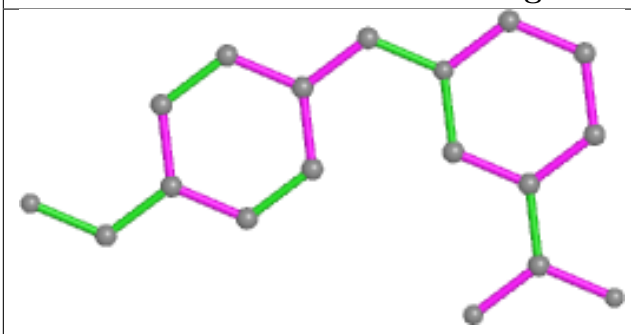


Rings

Ligand W46 D 503



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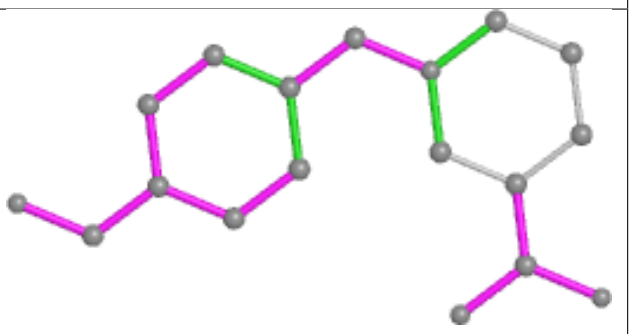
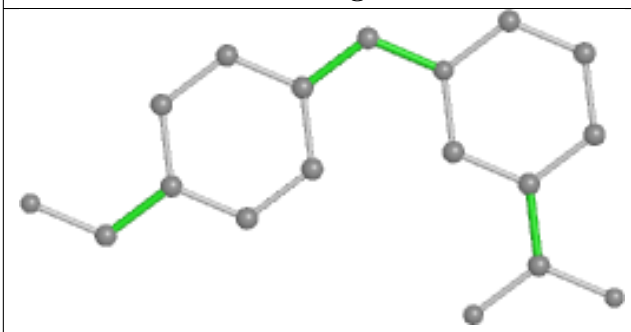


Bond angles



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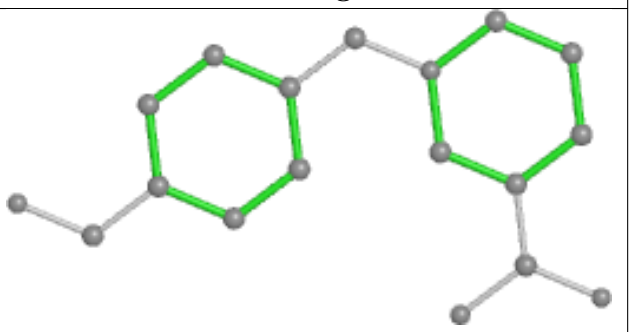
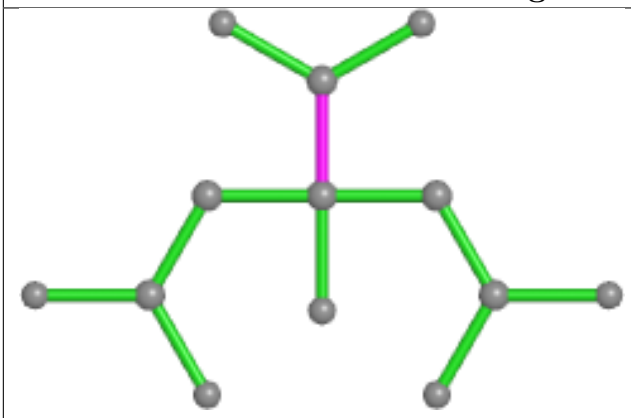


Rings

Ligand CIT K 401



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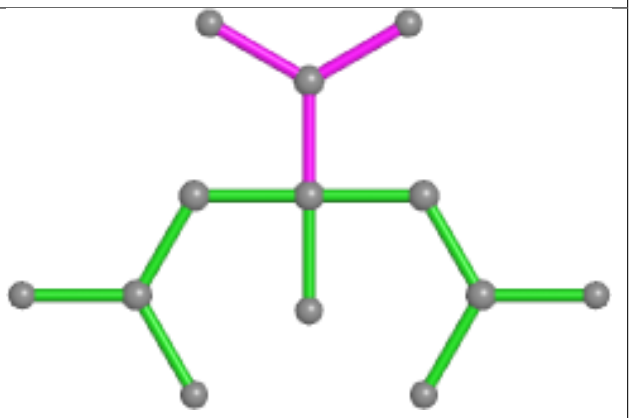

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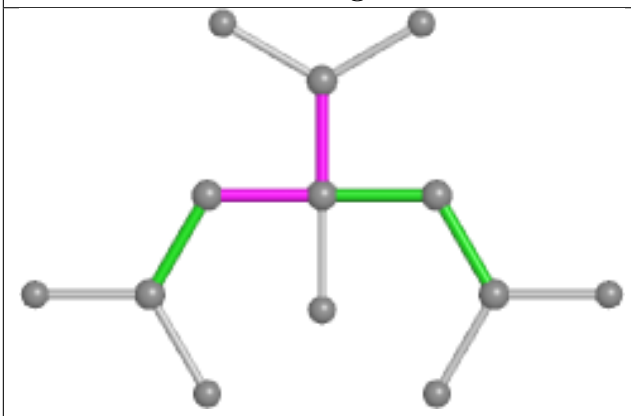

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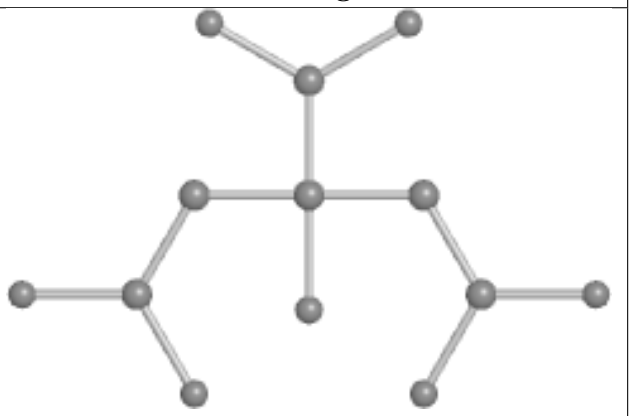
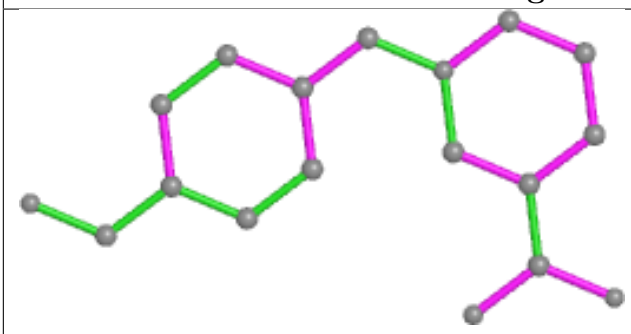


Rings

Ligand W46 L 504



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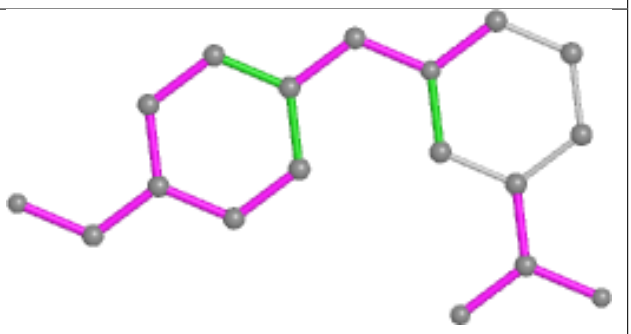
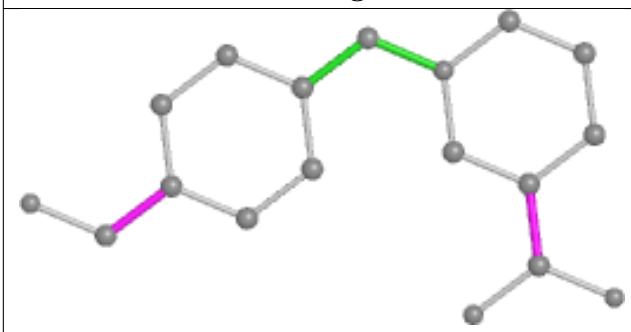


Bond angles



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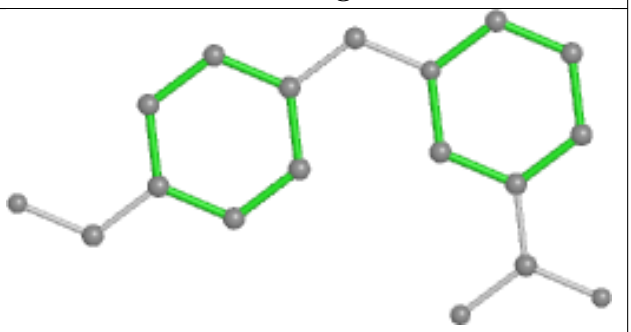
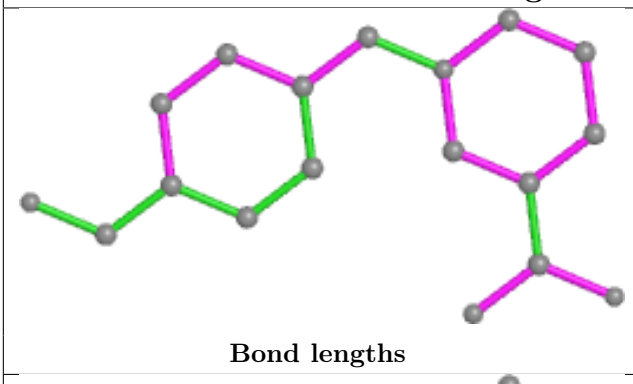


Rings

Ligand W46 C 503



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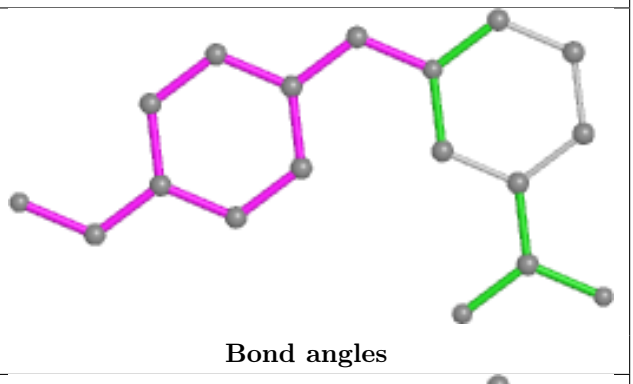
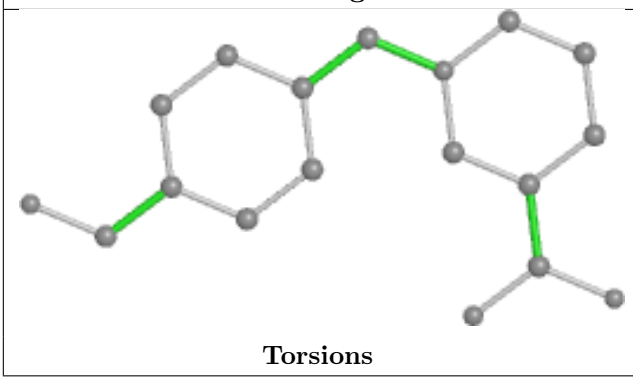
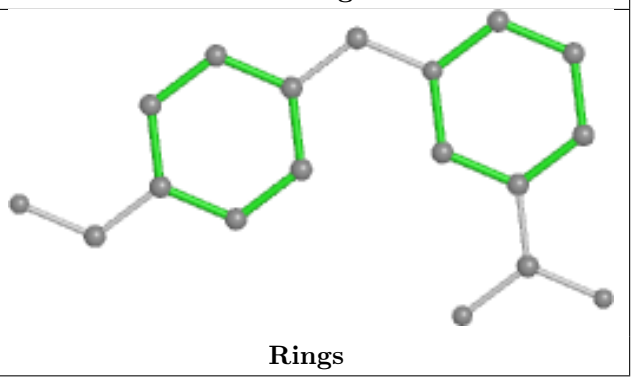


Bond angles

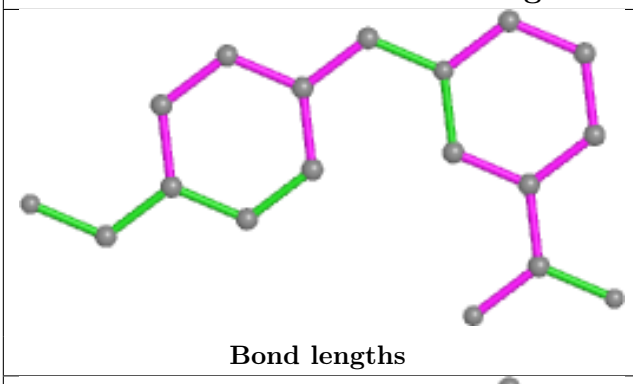


Torsions

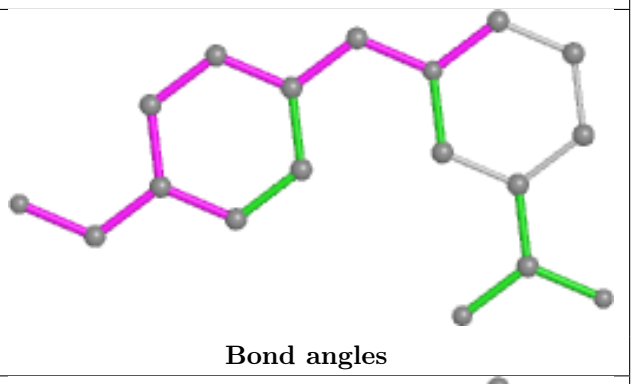


Rings

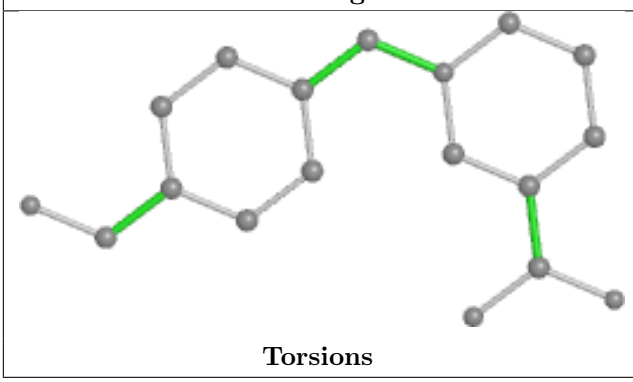
Ligand W46 K 404



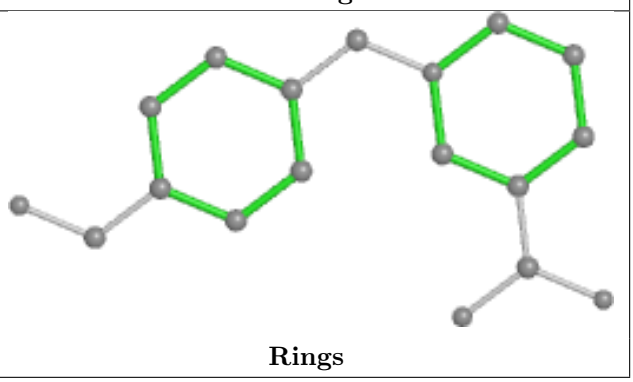
Bond lengths



Bond angles

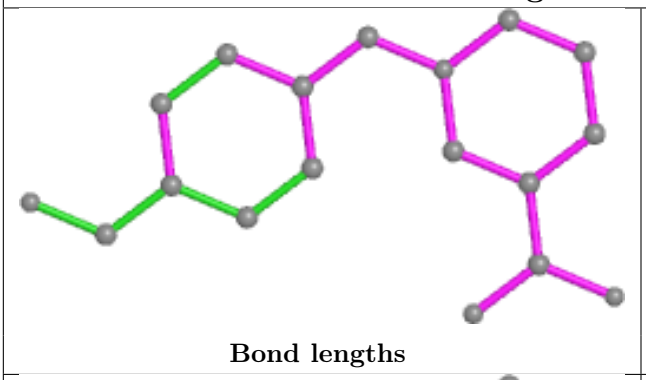


Torsions



Rings

Ligand W46 E 503



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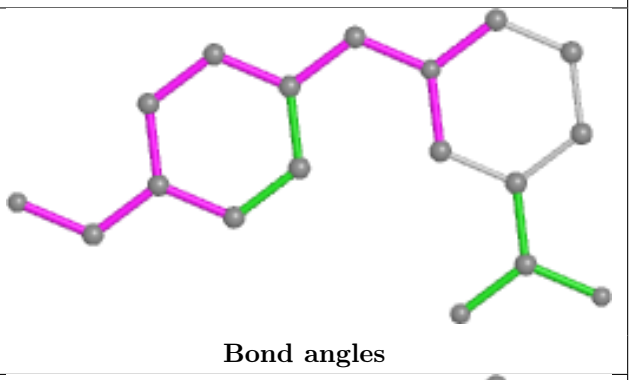
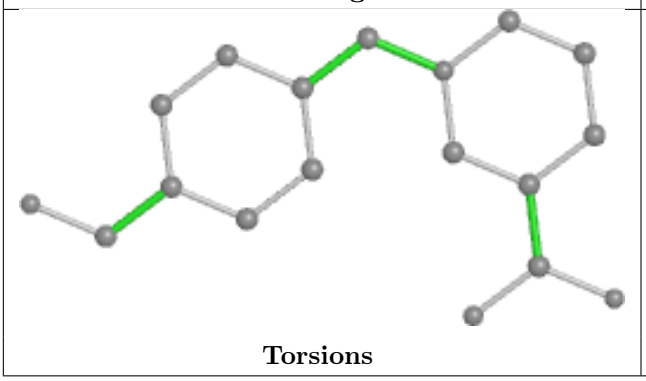
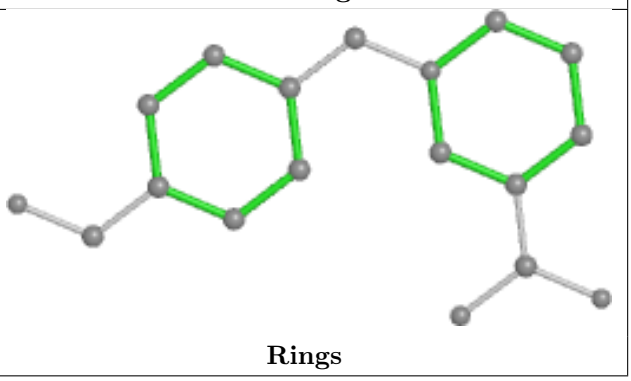


Bond angles

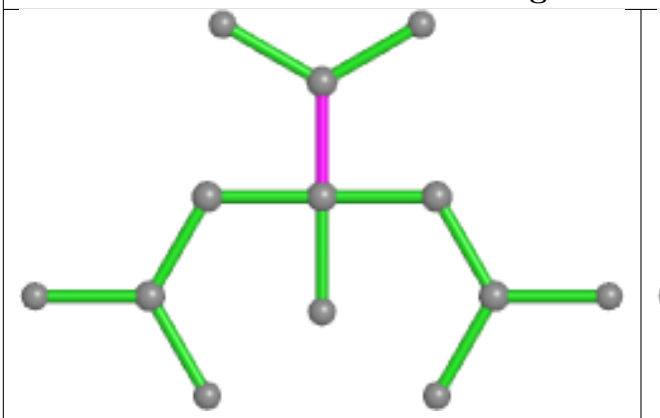


Torsions

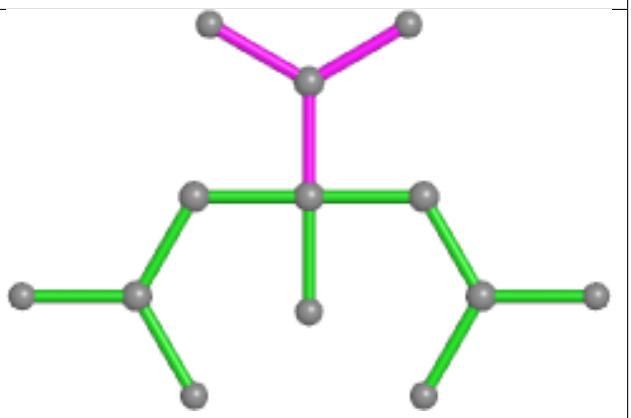


Rings

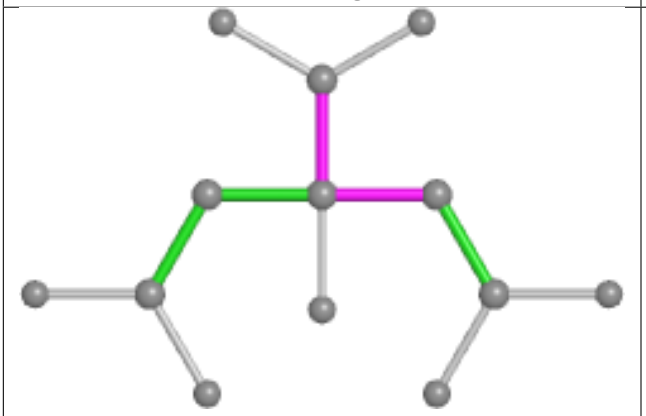
Ligand CIT B 503



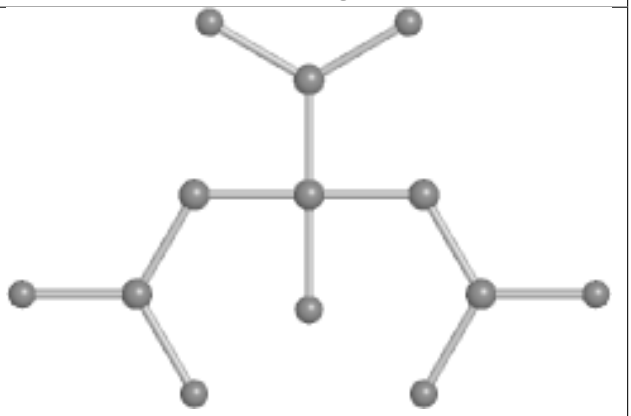
Bond lengths



Bond angles

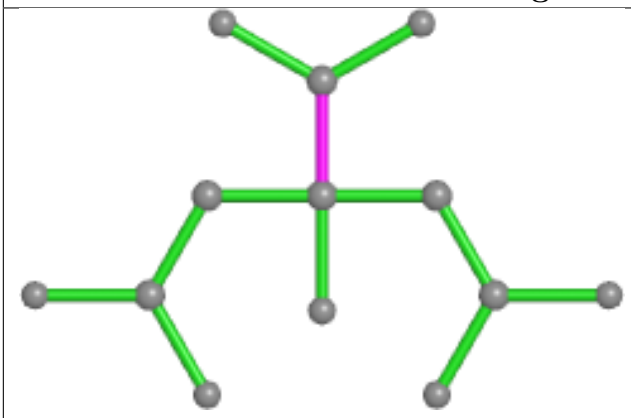


Torsions

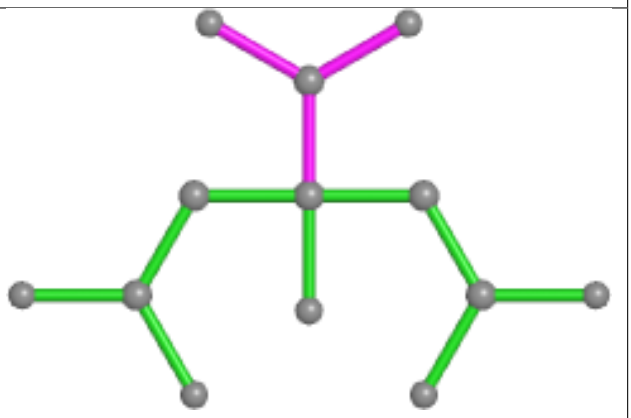


Rings

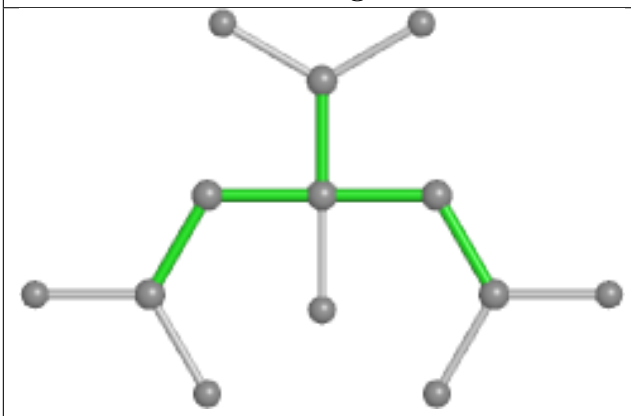
Ligand CIT L 503



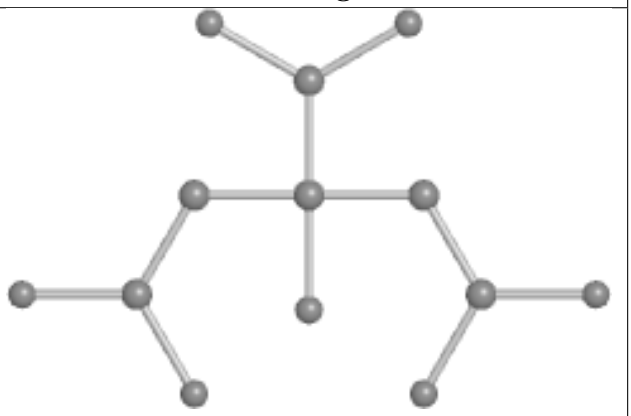
Bond lengths



Bond angles

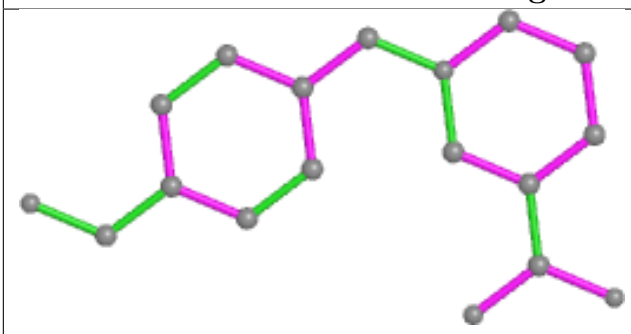


Torsions

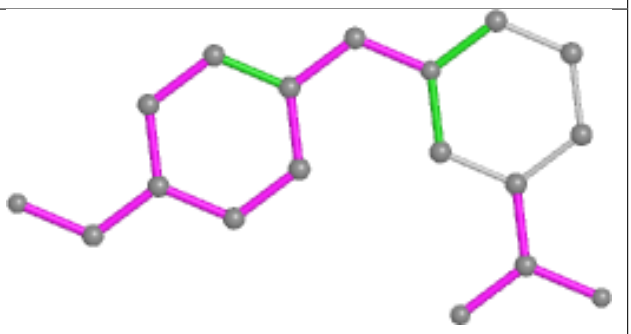


Rings

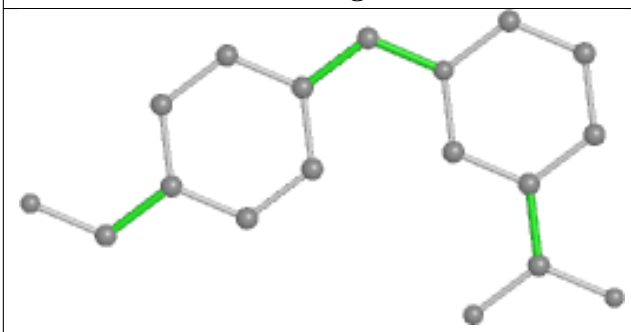
Ligand W46 J 503



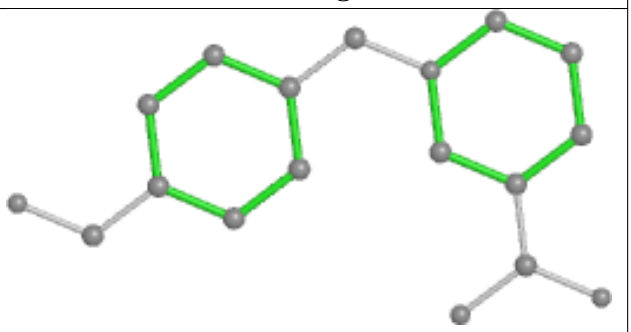
Bond lengths



Bond angles

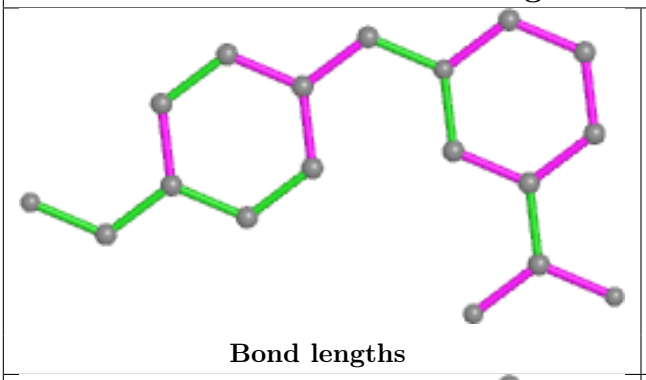


Torsions



Rings

Ligand W46 A 503



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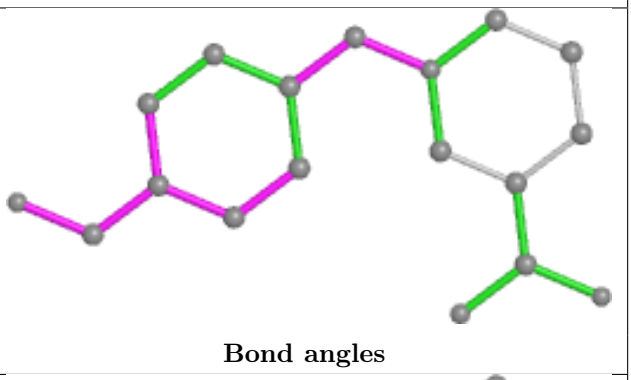
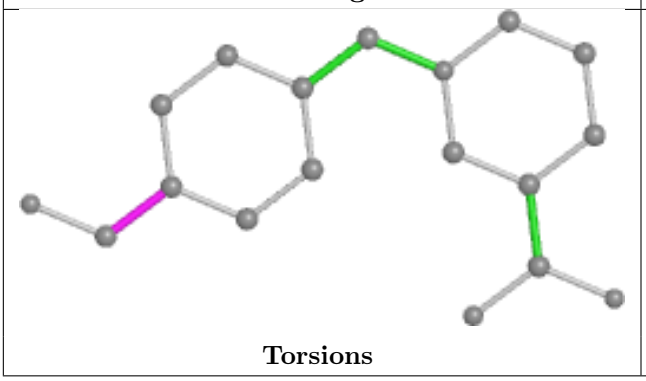
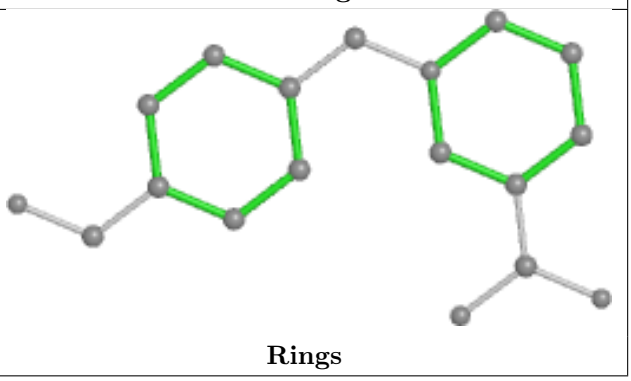


Bond angles

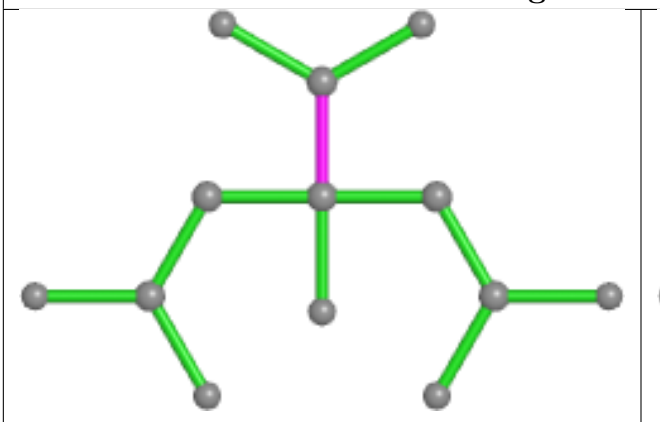


Torsions

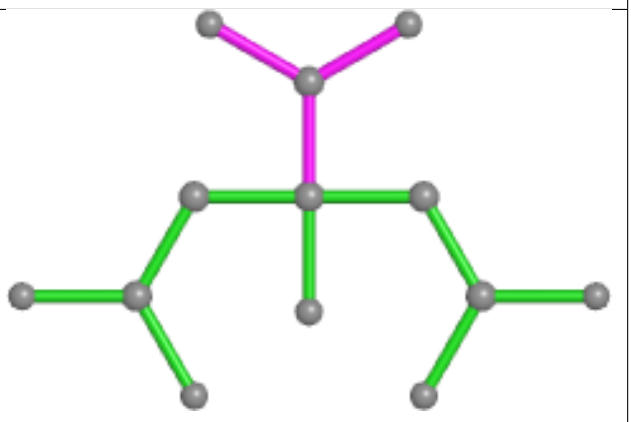


Rings

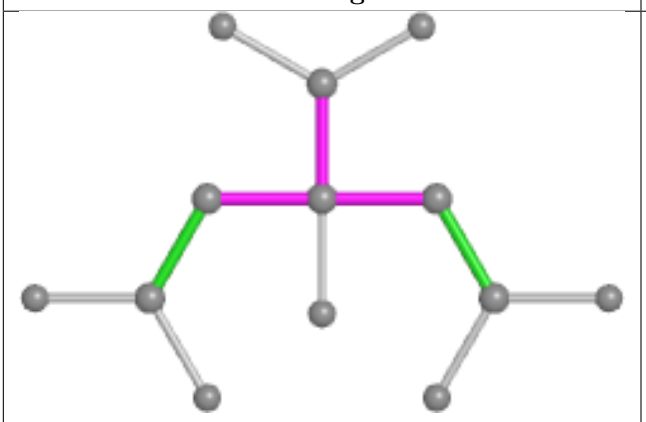
Ligand CIT H 503



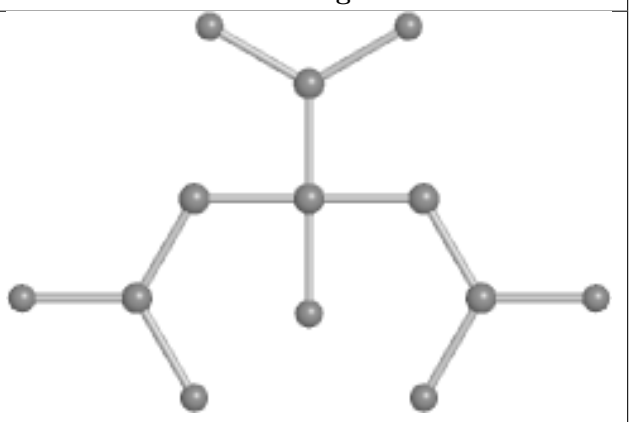
Bond lengths



Bond angles

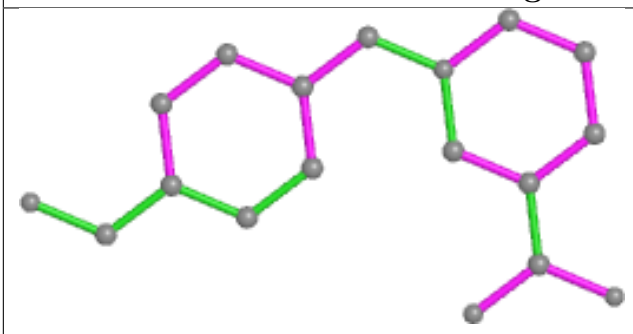


Torsions

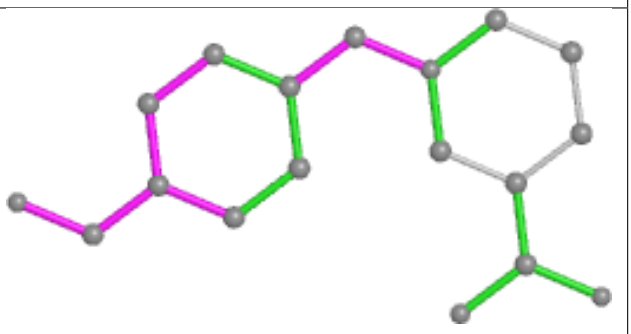


Rings

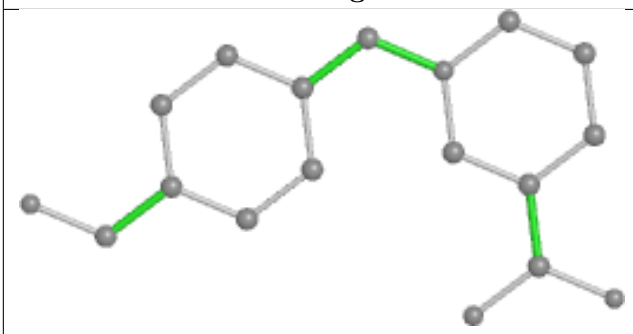
Ligand W46 H 504



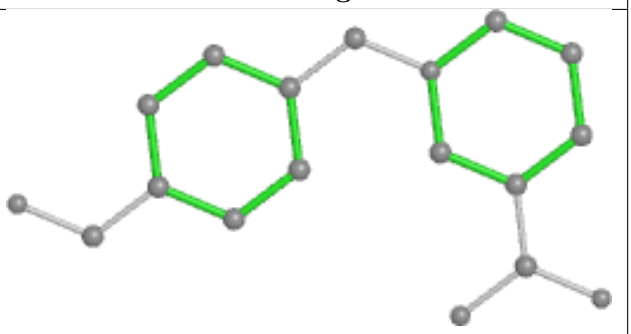
Bond lengths



Bond angles

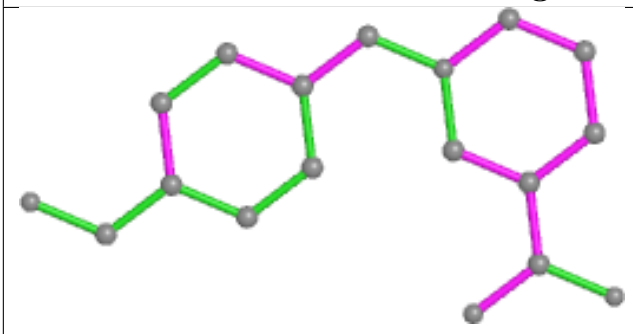


Torsions

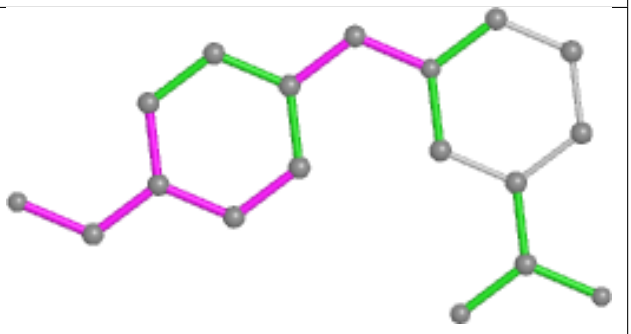


Rings

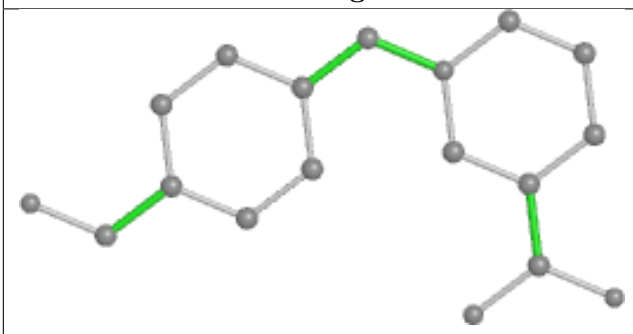
Ligand W46 I 504



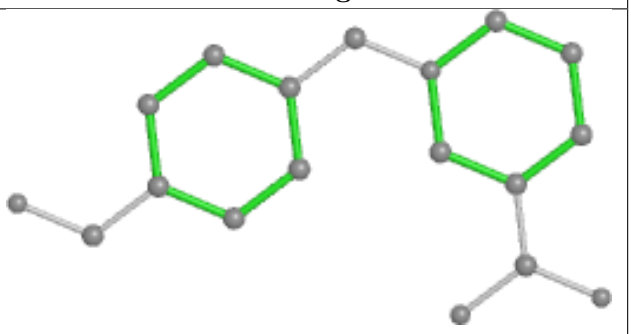
Bond lengths



Bond angles

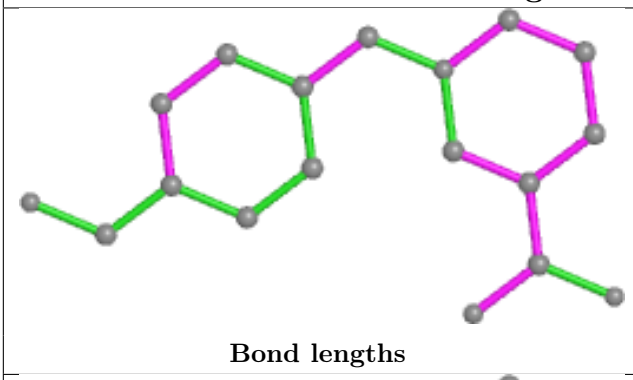


Torsions

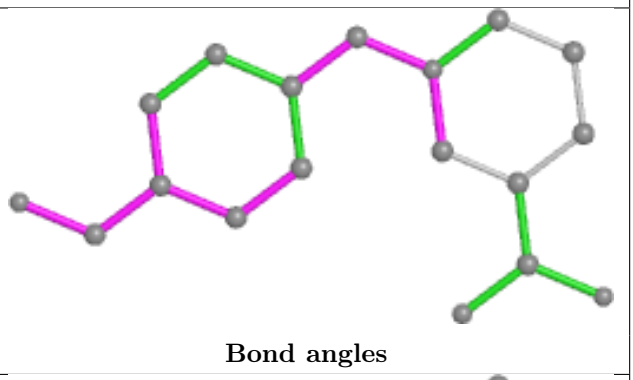


Rings

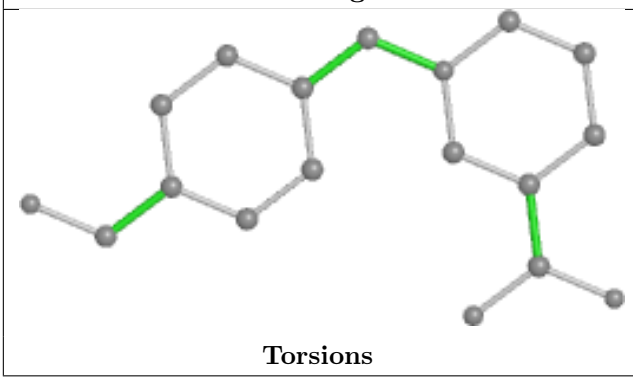
Ligand W46 B 504



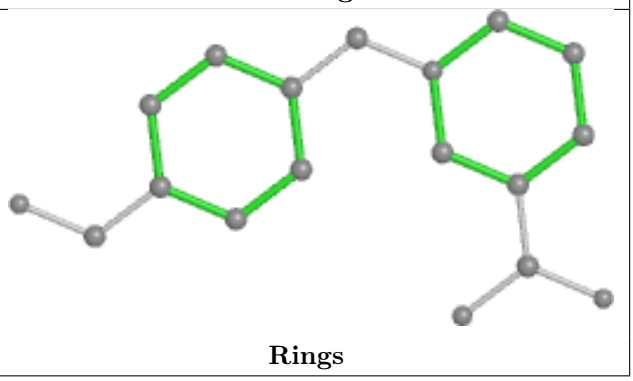
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	352/365 (96%)	-0.55	3 (0%) 84 63	13, 26, 59, 96	0
1	B	349/365 (95%)	-0.51	0 100 100	13, 26, 55, 80	0
1	C	349/365 (95%)	-0.38	4 (1%) 80 56	16, 33, 69, 123	0
1	D	351/365 (96%)	-0.47	4 (1%) 80 56	15, 30, 60, 101	0
1	E	349/365 (95%)	-0.38	8 (2%) 60 31	16, 35, 65, 106	0
1	F	348/365 (95%)	-0.31	2 (0%) 89 72	24, 39, 73, 109	0
1	G	350/365 (95%)	-0.49	2 (0%) 89 72	12, 26, 53, 92	0
1	H	350/365 (95%)	-0.44	8 (2%) 60 31	13, 30, 67, 110	0
1	I	349/365 (95%)	-0.25	5 (1%) 75 49	22, 43, 77, 116	0
1	J	349/365 (95%)	-0.13	7 (2%) 65 36	22, 48, 91, 150	0
1	K	349/365 (95%)	-0.25	6 (1%) 70 41	19, 40, 76, 108	0
1	L	349/365 (95%)	-0.20	9 (2%) 56 27	21, 46, 78, 123	0
All	All	4194/4380 (95%)	-0.36	58 (1%) 75 49	12, 35, 73, 150	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	-5	VAL	9.2
1	J	52	TYR	6.0
1	C	52	TYR	5.4
1	J	54	TYR	5.1
1	D	-4	PRO	5.1

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	CIT	I	503	13/13	0.85	0.29	63,79,88,88	0
4	CIT	K	401	13/13	0.85	0.25	63,89,98,101	0
4	CIT	L	503	13/13	0.86	0.31	80,93,105,108	0
4	CIT	B	503	13/13	0.89	0.22	67,72,77,81	0
3	W46	J	503	18/18	0.92	0.21	44,61,75,75	0
3	W46	C	503	18/18	0.92	0.24	36,46,71,87	0
4	CIT	H	503	13/13	0.92	0.27	70,78,88,101	0
3	W46	K	404	18/18	0.94	0.21	39,47,51,56	0
3	W46	L	504	18/18	0.94	0.18	44,50,60,61	0
3	W46	D	503	18/18	0.94	0.20	32,38,60,83	0
3	W46	E	503	18/18	0.94	0.19	35,43,50,52	0
3	W46	F	503	18/18	0.94	0.20	37,45,54,55	0
3	W46	I	504	18/18	0.94	0.20	56,61,72,78	0
3	W46	B	504	18/18	0.94	0.21	33,38,56,77	0
5	IPA	B	505	4/4	0.94	0.18	25,26,28,29	0
3	W46	A	503	18/18	0.95	0.21	36,44,53,68	0
3	W46	H	504	18/18	0.95	0.26	42,54,73,88	0
2	ZN	J	502	1/1	0.97	0.06	95,95,95,95	0
2	ZN	L	502	1/1	0.98	0.08	73,73,73,73	0
2	ZN	I	502	1/1	0.98	0.07	57,57,57,57	0
2	ZN	A	502	1/1	0.98	0.06	61,61,61,61	0
2	ZN	D	501	1/1	0.99	0.08	31,31,31,31	0
2	ZN	D	502	1/1	0.99	0.07	44,44,44,44	0
2	ZN	E	501	1/1	0.99	0.08	40,40,40,40	0
2	ZN	E	502	1/1	0.99	0.07	49,49,49,49	0
2	ZN	F	501	1/1	0.99	0.09	50,50,50,50	0
2	ZN	F	502	1/1	0.99	0.07	48,48,48,48	0
2	ZN	H	501	1/1	0.99	0.08	23,23,23,23	0
2	ZN	H	502	1/1	0.99	0.07	52,52,52,52	0
2	ZN	I	501	1/1	0.99	0.07	38,38,38,38	0
2	ZN	A	501	1/1	0.99	0.09	30,30,30,30	0
2	ZN	B	502	1/1	0.99	0.07	39,39,39,39	0

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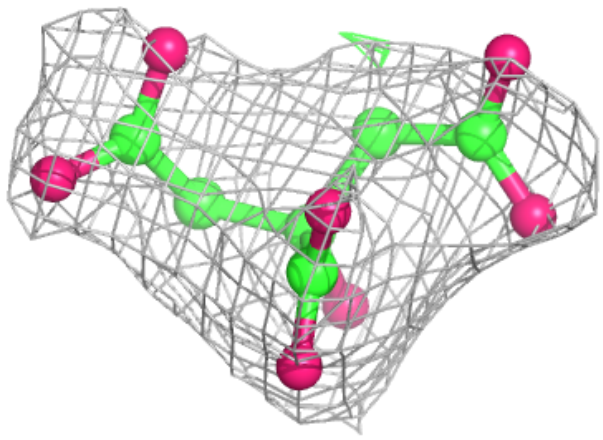
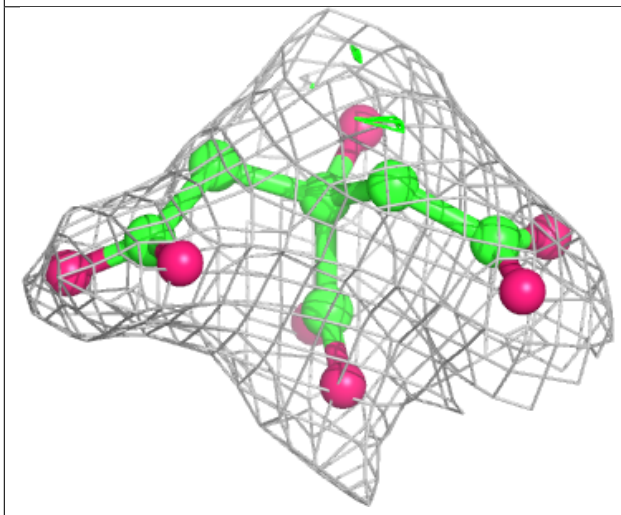
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ZN	K	402	1/1	0.99	0.07	35,35,35,35	0
2	ZN	K	403	1/1	0.99	0.05	53,53,53,53	0
2	ZN	L	501	1/1	0.99	0.08	42,42,42,42	0
2	ZN	C	501	1/1	0.99	0.09	41,41,41,41	0
2	ZN	C	502	1/1	0.99	0.07	56,56,56,56	0
2	ZN	B	501	1/1	1.00	0.10	28,28,28,28	0
2	ZN	J	501	1/1	1.00	0.08	34,34,34,34	0
2	ZN	G	501	1/1	1.00	0.09	28,28,28,28	0
2	ZN	G	502	1/1	1.00	0.07	30,30,30,30	0

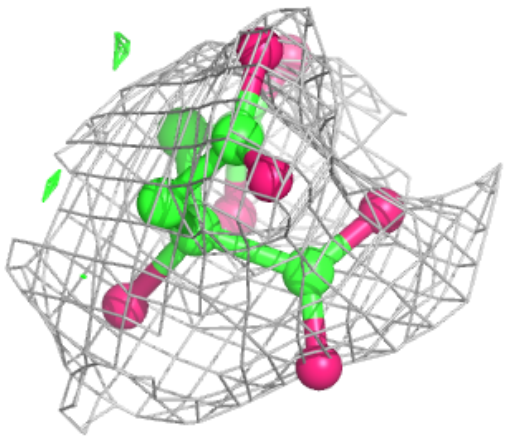
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CIT I 503:

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

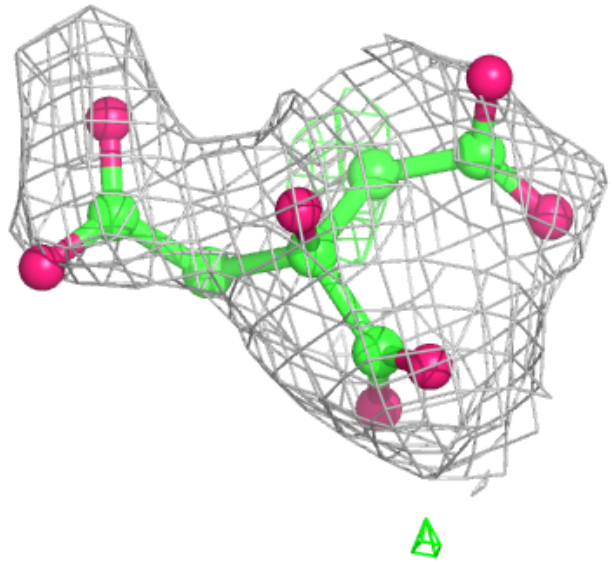


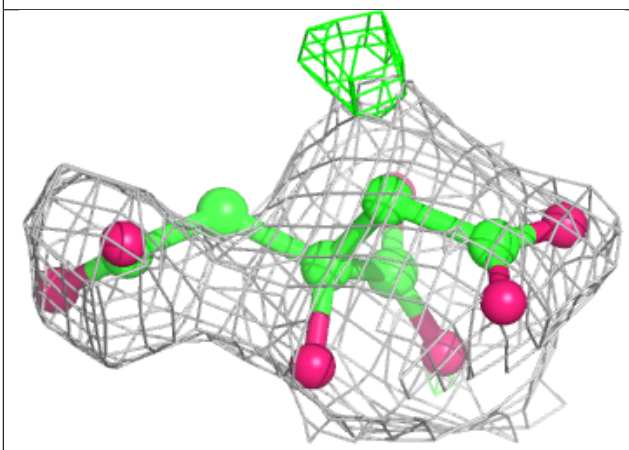


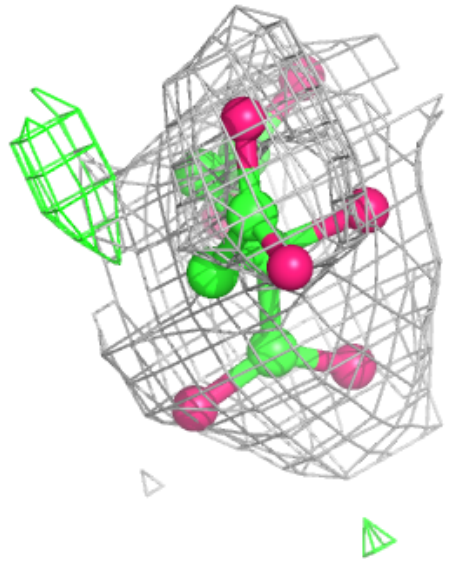


Electron density around CIT K 401:

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

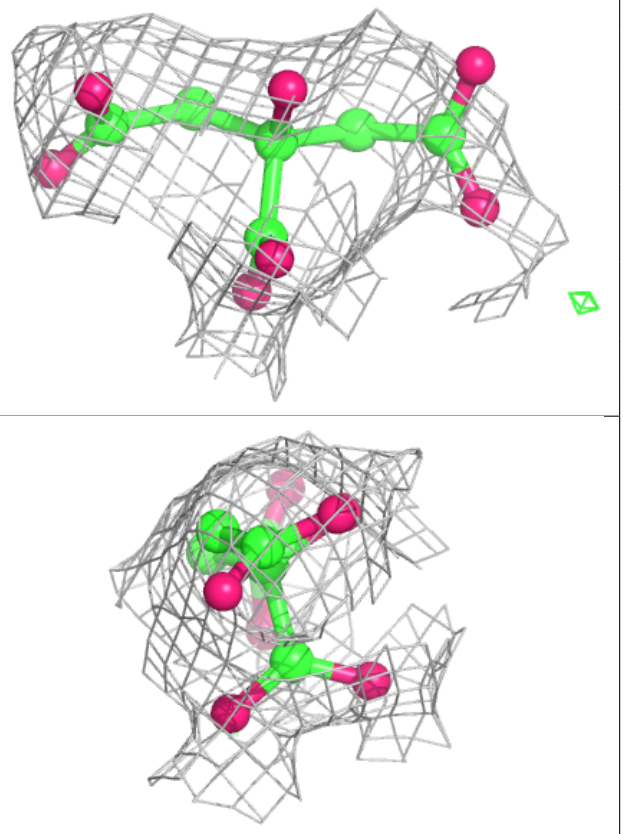






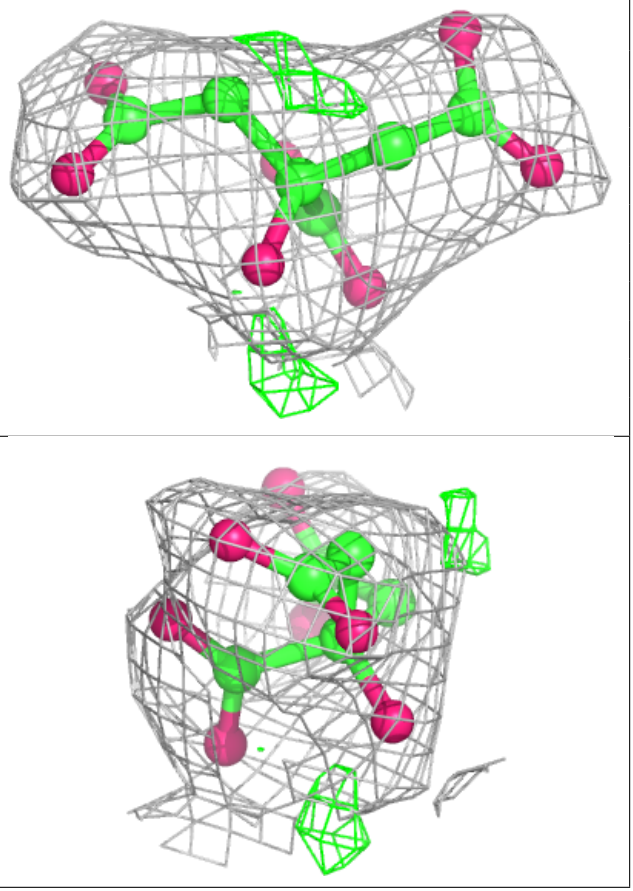
Electron density around CIT L 503:

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



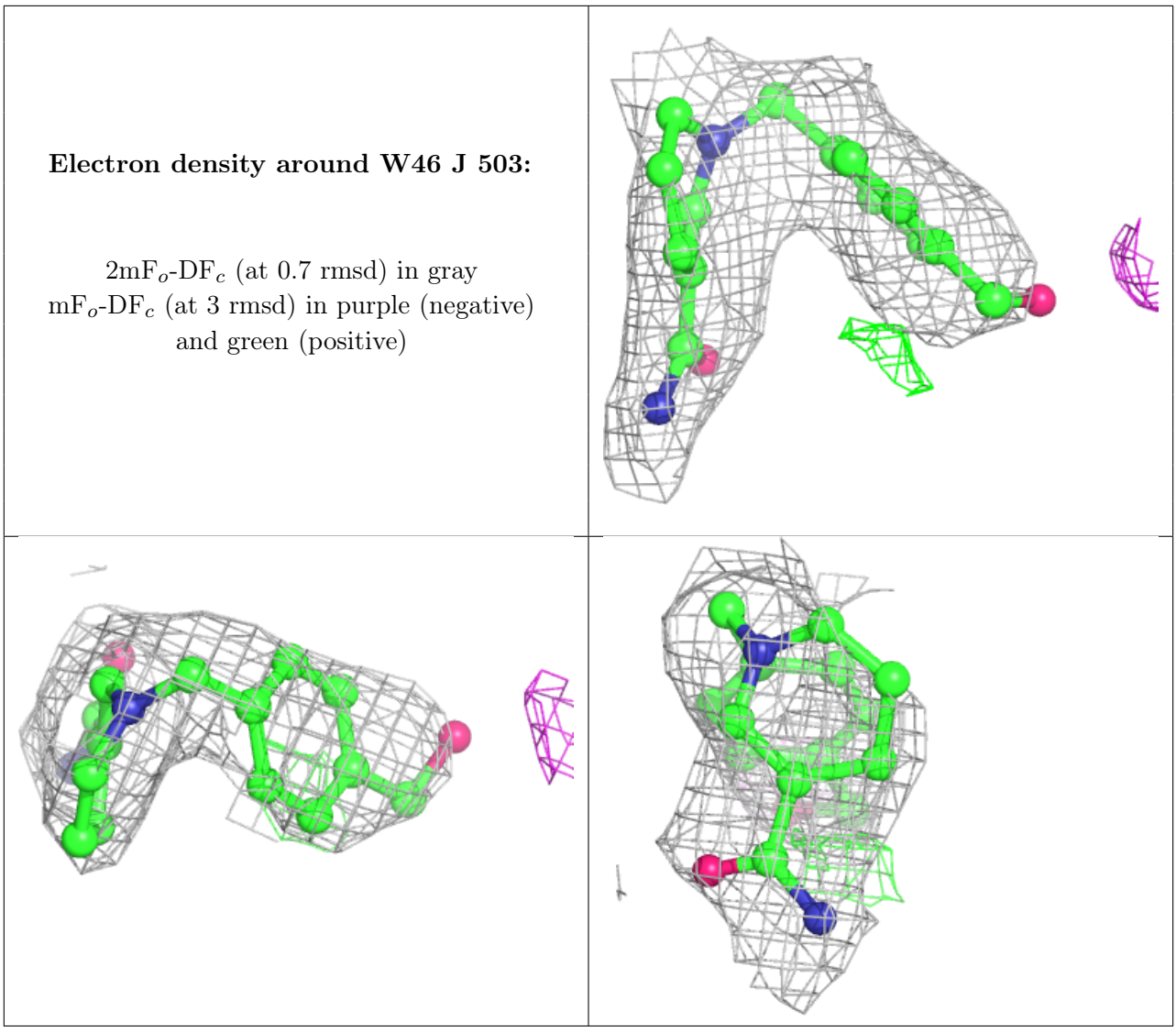
Electron density around CIT B 503:

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



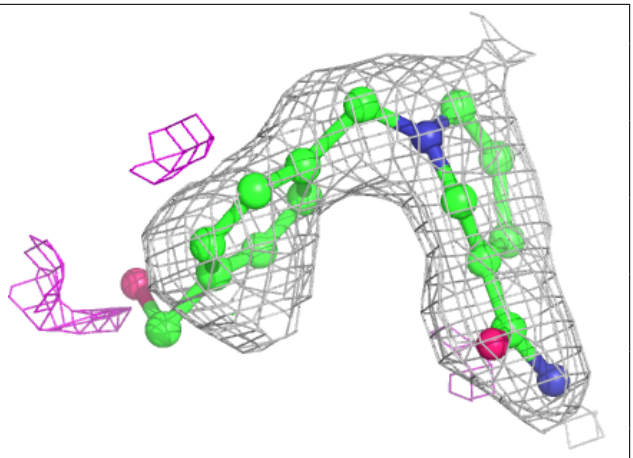
Electron density around W46 J 503:

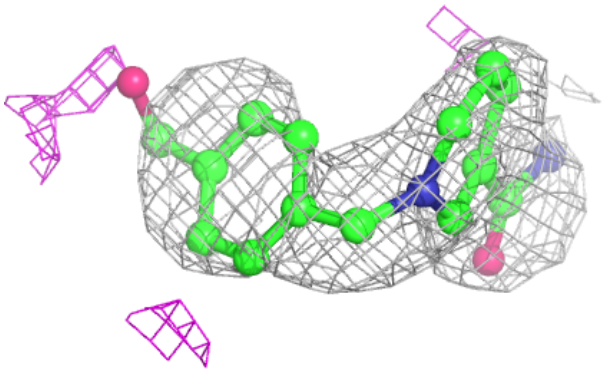
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

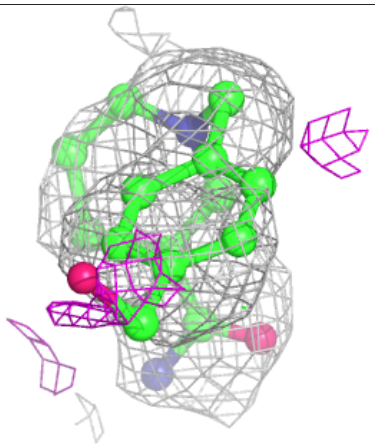


Electron density around W46 C 503:

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

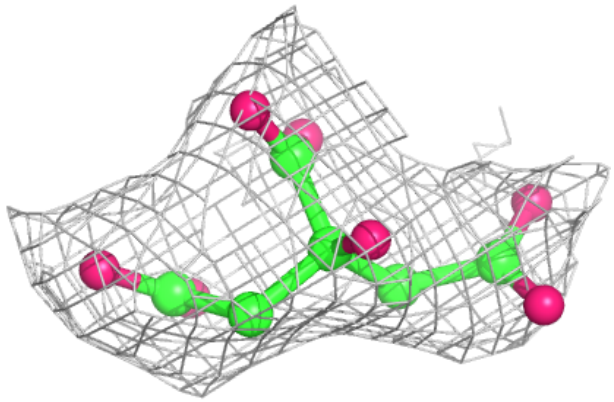


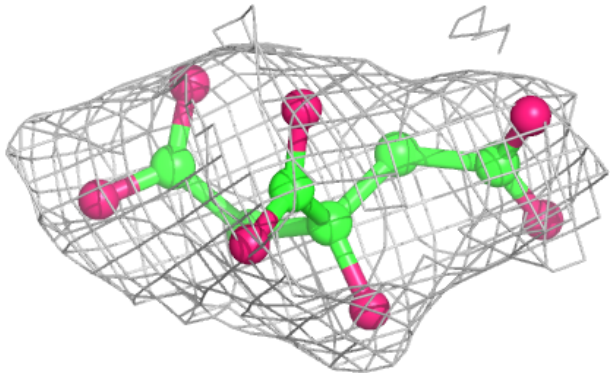


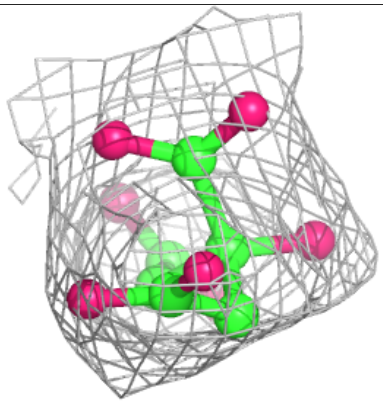


Electron density around CIT H 503:

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

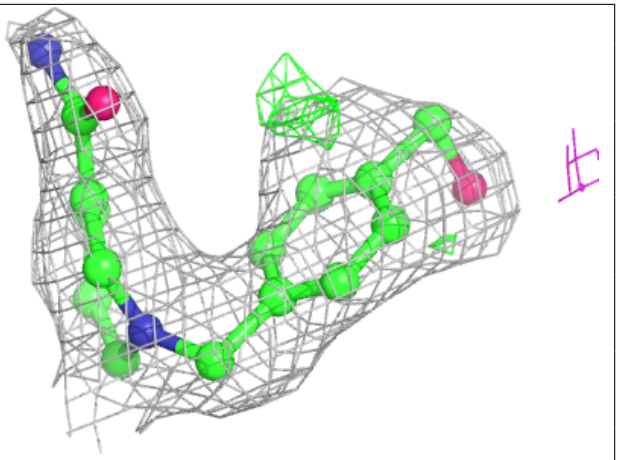


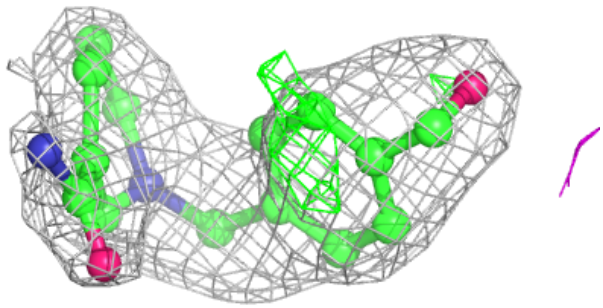


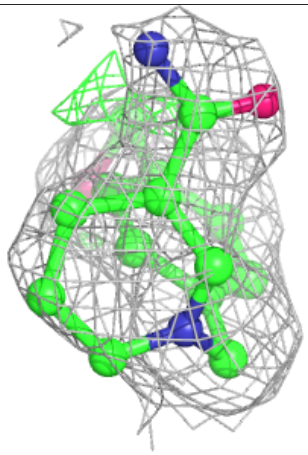


Electron density around W46 K 404:

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

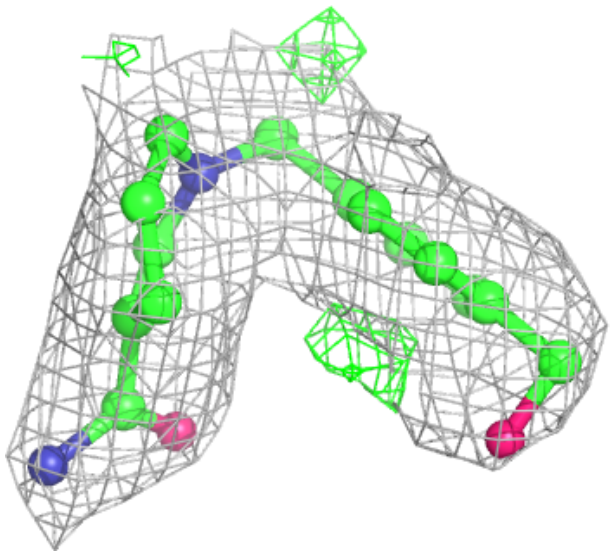


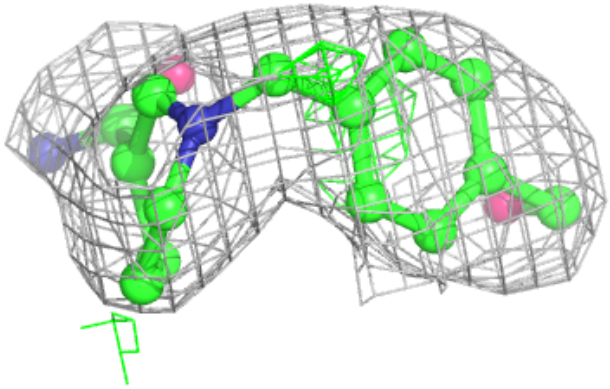


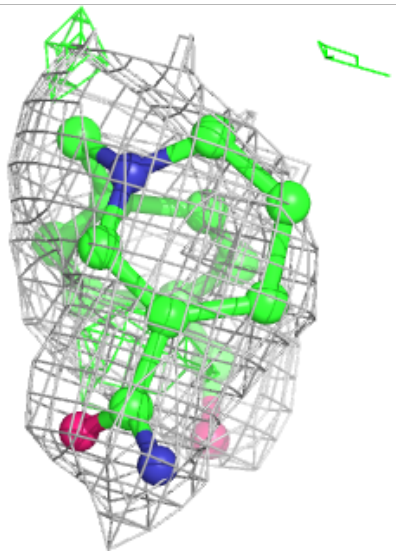


Electron density around W46 L 504:

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

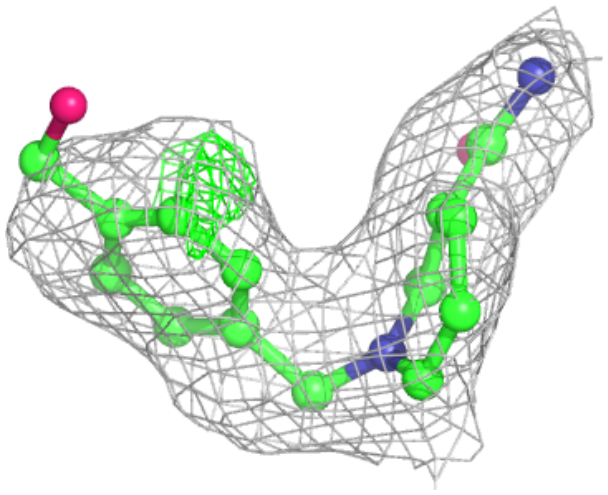


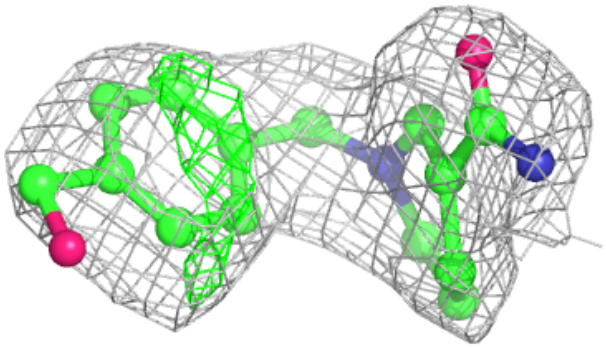


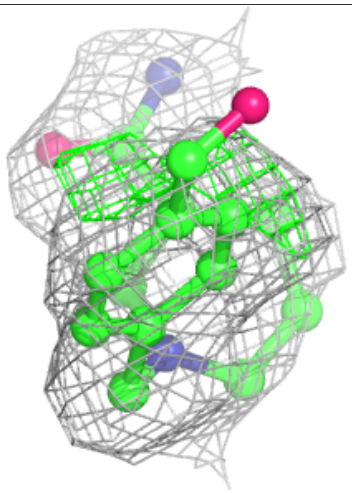


Electron density around W46 D 503:

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

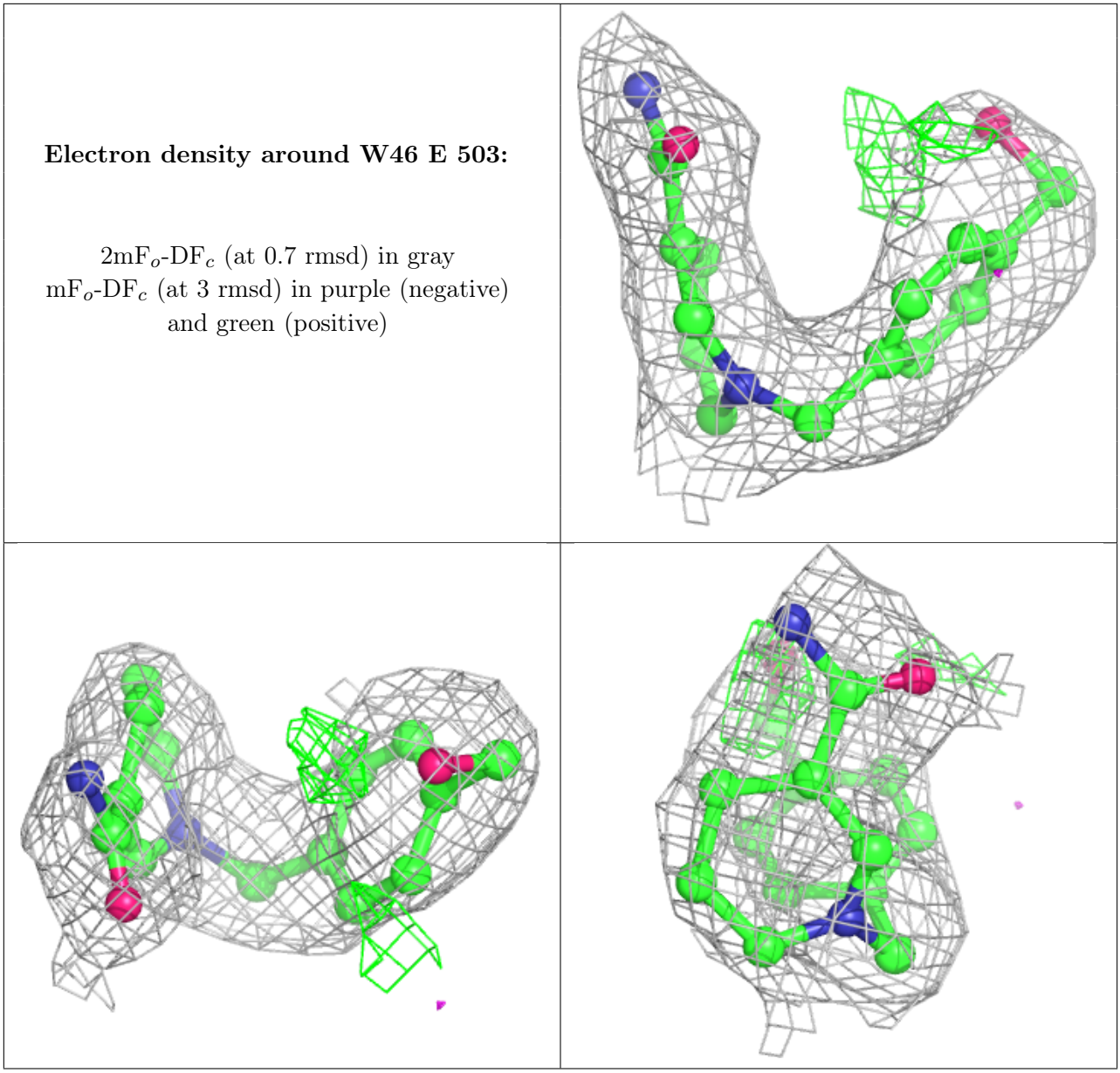






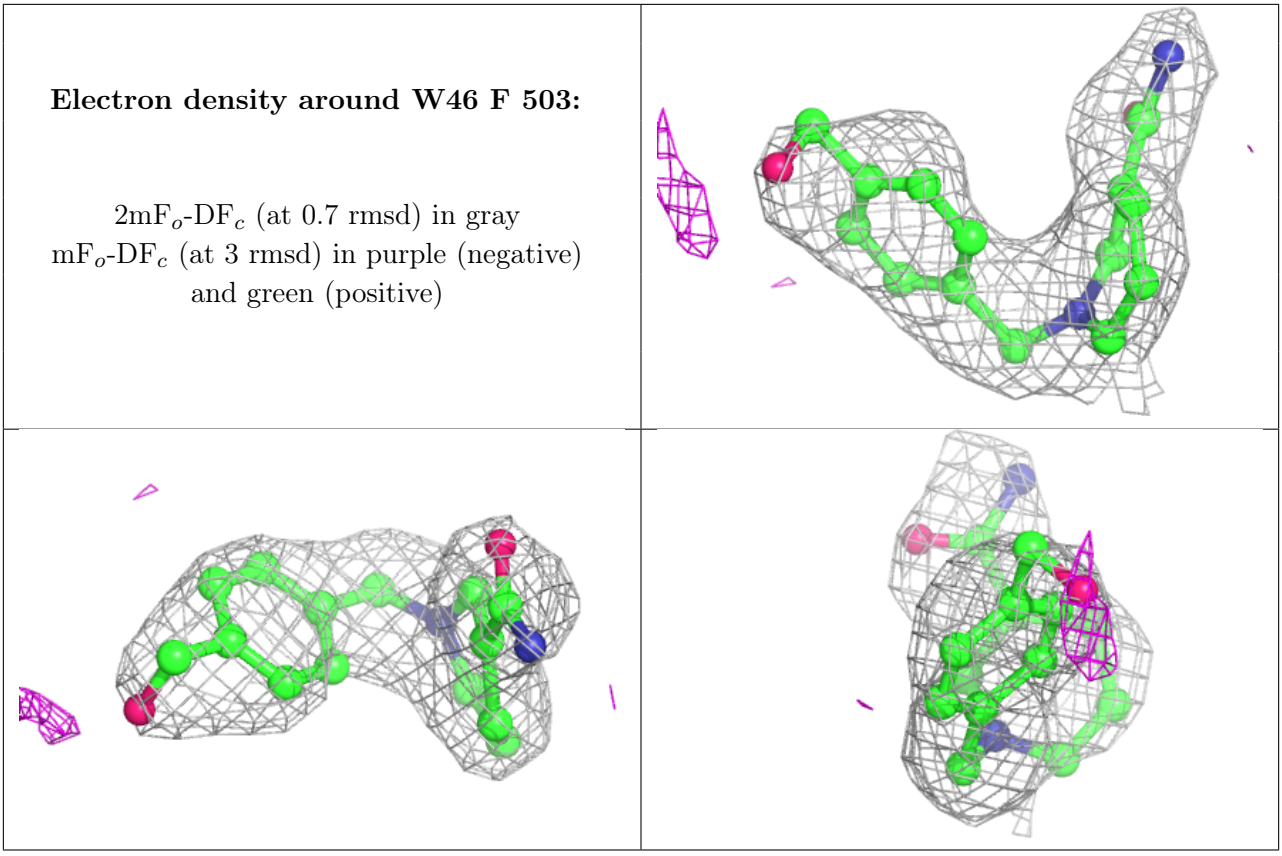
Electron density around W46 E 503:

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



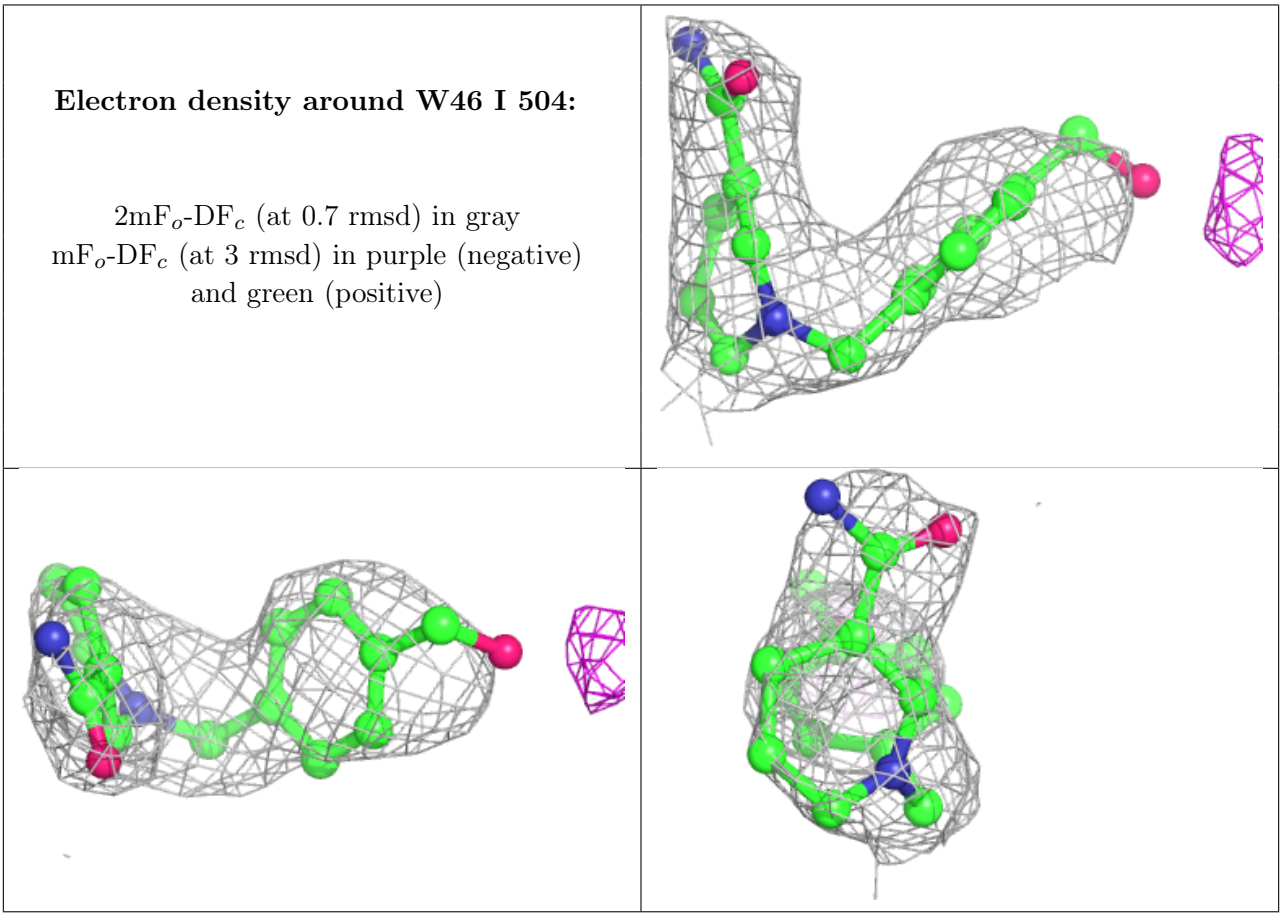
Electron density around W46 F 503:

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



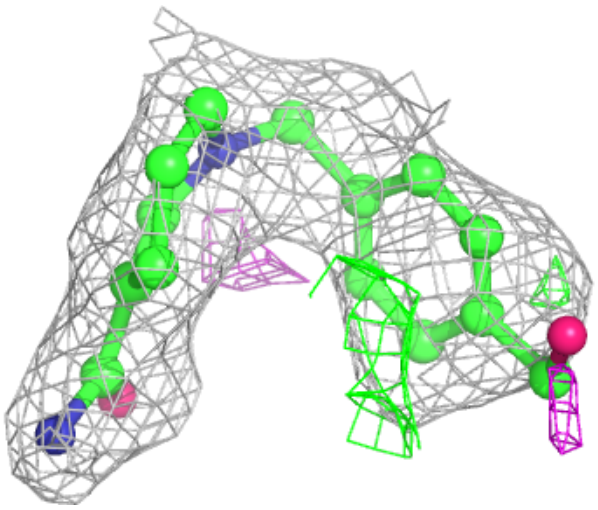
Electron density around W46 I 504:

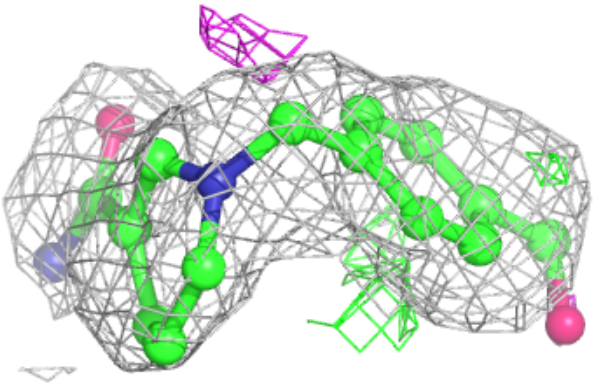
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

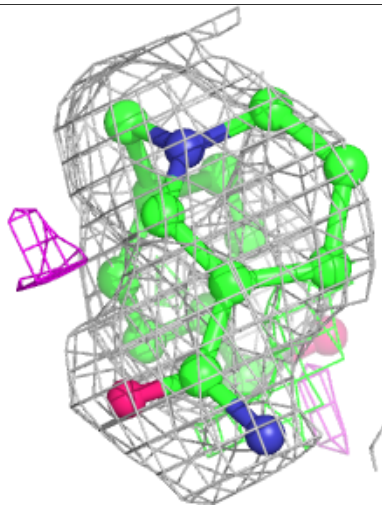


Electron density around W46 B 504:

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

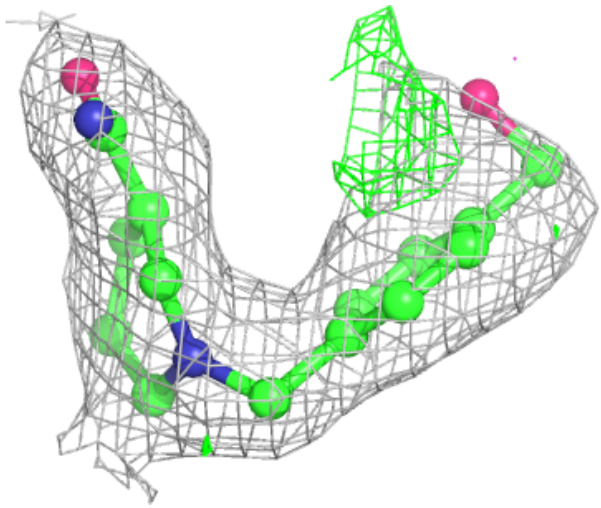


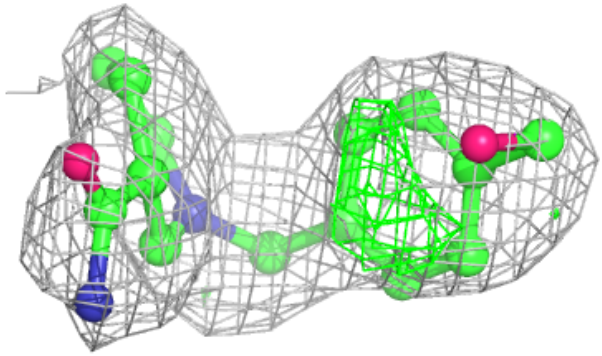


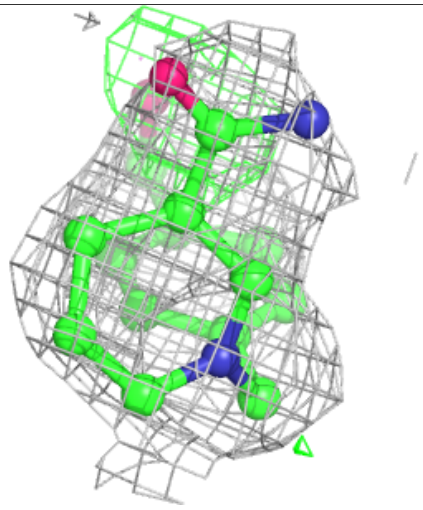


Electron density around W46 A 503:

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

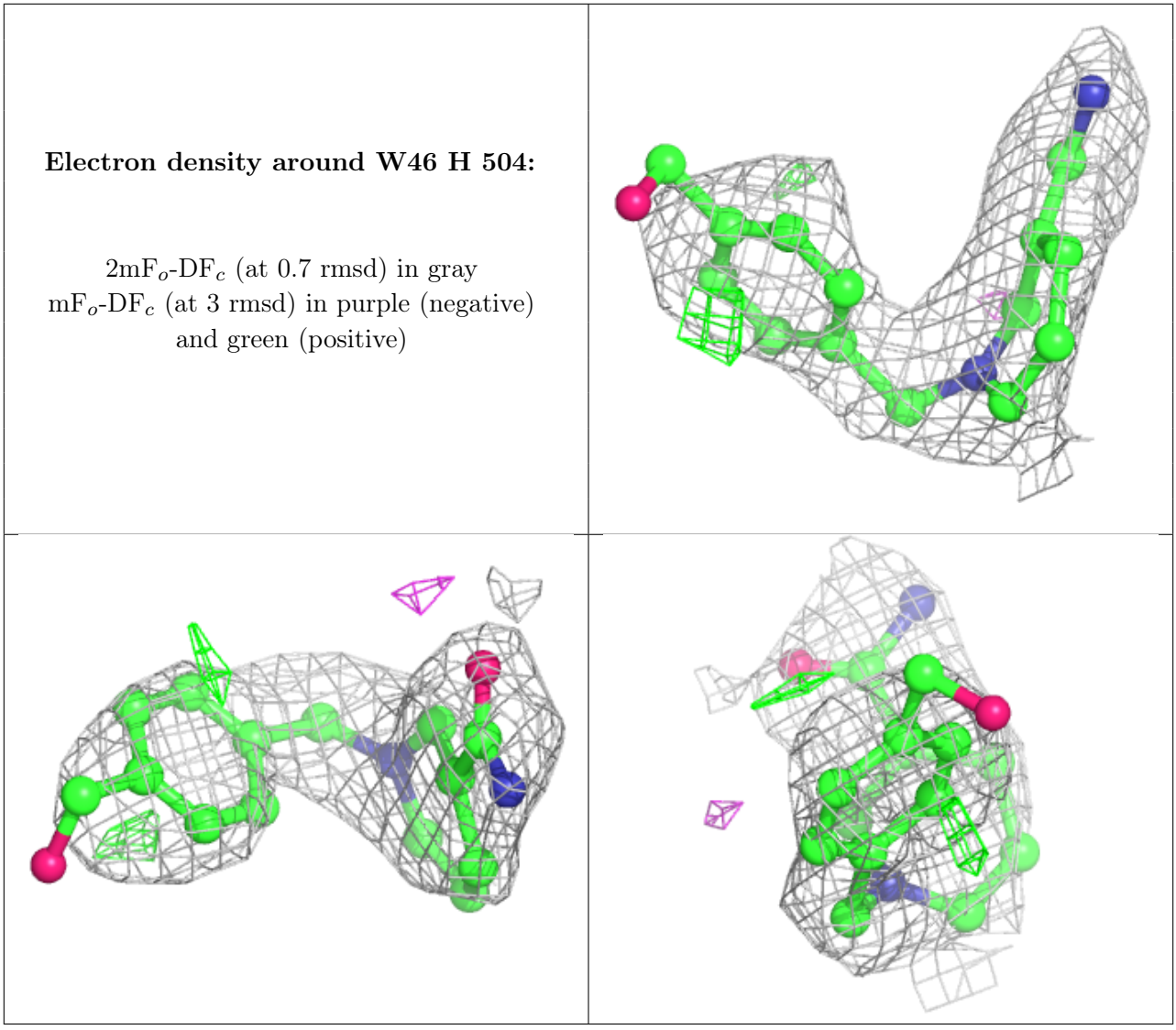






Electron density around W46 H 504:

$2mF_o$-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.