wwPDB X-ray Structure Validation Summary Report (i)

Mar 16, 2021 – 09:44 am GMT

PDB ID	:	6YUR
Title	:	Crystal structure of S. aureus FabI inhibited by SKTS1
Authors	:	Weinrich, J.D.; Eltschkner, S.; Schiebel, J.; Kehrein, J.; Le, T.A.; Davoodi, S.; Merget, B.; Tonge, P.J.; Engels, B.; Sotriffer, C.A.; Kisker, C.
Deposited on	:	2020-04-27
Resolution	:	1.96 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 following versions of software and data (see references (i)) were used in the production of this report:

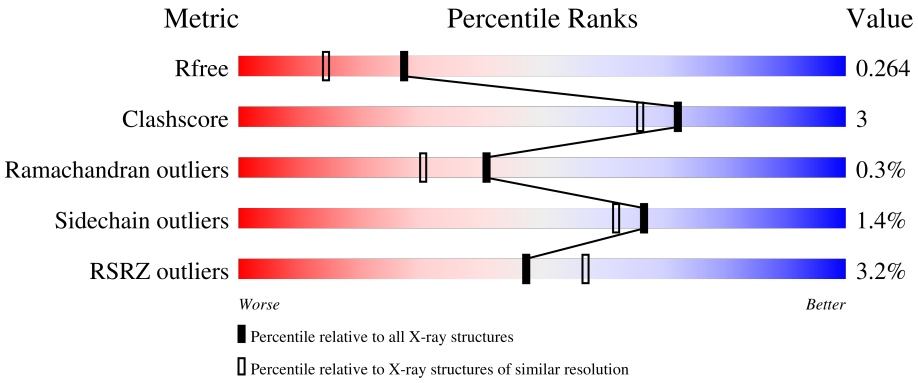
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.17.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.17.1

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 1.96 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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	282	2% 83% 7% 10%
1	B	282	2% 81% 9% • 9%
1	C	282	% 82% 7% • 10%
1	D	282	2% 82% 8% 9%
1	E	282	3% 80% 10% 9%

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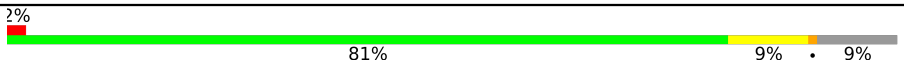
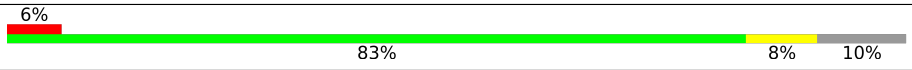
Mol	Chain	Length	Quality of chain
1	F	282	
1	G	282	
1	H	282	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17245 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 Enoyl-[acyl-carrier-protein] reductase [NADPH].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	255	Total	C	N	O	S	0	3	0
			1980	1247	344	385	4			
1	B	256	Total	C	N	O	S	0	2	0
			1980	1247	342	386	5			
1	C	255	Total	C	N	O	S	0	2	0
			1972	1242	341	385	4			
1	D	256	Total	C	N	O	S	0	4	0
			1994	1256	345	388	5			
1	E	256	Total	C	N	O	S	0	2	0
			1980	1247	342	386	5			
1	F	256	Total	C	N	O	S	0	3	0
			1988	1252	345	386	5			
1	G	254	Total	C	N	O	S	0	2	0
			1965	1237	340	384	4			
1	H	255	Total	C	N	O	S	0	2	0
			1972	1242	341	385	4			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
A	-24	LYS	-	expression tag	UNP A0A0J9X1X7
A	-23	HIS	-	expression tag	UNP A0A0J9X1X7
A	-22	HIS	-	expression tag	UNP A0A0J9X1X7
A	-21	HIS	-	expression tag	UNP A0A0J9X1X7
A	-20	HIS	-	expression tag	UNP A0A0J9X1X7
A	-19	HIS	-	expression tag	UNP A0A0J9X1X7
A	-18	HIS	-	expression tag	UNP A0A0J9X1X7
A	-17	PRO	-	expression tag	UNP A0A0J9X1X7
B	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
B	-24	LYS	-	expression tag	UNP A0A0J9X1X7
B	-23	HIS	-	expression tag	UNP A0A0J9X1X7
B	-22	HIS	-	expression tag	UNP A0A0J9X1X7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-21	HIS	-	expression tag	UNP A0A0J9X1X7
B	-20	HIS	-	expression tag	UNP A0A0J9X1X7
B	-19	HIS	-	expression tag	UNP A0A0J9X1X7
B	-18	HIS	-	expression tag	UNP A0A0J9X1X7
B	-17	PRO	-	expression tag	UNP A0A0J9X1X7
C	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
C	-24	LYS	-	expression tag	UNP A0A0J9X1X7
C	-23	HIS	-	expression tag	UNP A0A0J9X1X7
C	-22	HIS	-	expression tag	UNP A0A0J9X1X7
C	-21	HIS	-	expression tag	UNP A0A0J9X1X7
C	-20	HIS	-	expression tag	UNP A0A0J9X1X7
C	-19	HIS	-	expression tag	UNP A0A0J9X1X7
C	-18	HIS	-	expression tag	UNP A0A0J9X1X7
C	-17	PRO	-	expression tag	UNP A0A0J9X1X7
D	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
D	-24	LYS	-	expression tag	UNP A0A0J9X1X7
D	-23	HIS	-	expression tag	UNP A0A0J9X1X7
D	-22	HIS	-	expression tag	UNP A0A0J9X1X7
D	-21	HIS	-	expression tag	UNP A0A0J9X1X7
D	-20	HIS	-	expression tag	UNP A0A0J9X1X7
D	-19	HIS	-	expression tag	UNP A0A0J9X1X7
D	-18	HIS	-	expression tag	UNP A0A0J9X1X7
D	-17	PRO	-	expression tag	UNP A0A0J9X1X7
E	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
E	-24	LYS	-	expression tag	UNP A0A0J9X1X7
E	-23	HIS	-	expression tag	UNP A0A0J9X1X7
E	-22	HIS	-	expression tag	UNP A0A0J9X1X7
E	-21	HIS	-	expression tag	UNP A0A0J9X1X7
E	-20	HIS	-	expression tag	UNP A0A0J9X1X7
E	-19	HIS	-	expression tag	UNP A0A0J9X1X7
E	-18	HIS	-	expression tag	UNP A0A0J9X1X7
E	-17	PRO	-	expression tag	UNP A0A0J9X1X7
F	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
F	-24	LYS	-	expression tag	UNP A0A0J9X1X7
F	-23	HIS	-	expression tag	UNP A0A0J9X1X7
F	-22	HIS	-	expression tag	UNP A0A0J9X1X7
F	-21	HIS	-	expression tag	UNP A0A0J9X1X7
F	-20	HIS	-	expression tag	UNP A0A0J9X1X7
F	-19	HIS	-	expression tag	UNP A0A0J9X1X7
F	-18	HIS	-	expression tag	UNP A0A0J9X1X7
F	-17	PRO	-	expression tag	UNP A0A0J9X1X7
G	-25	MET	-	initiating methionine	UNP A0A0J9X1X7

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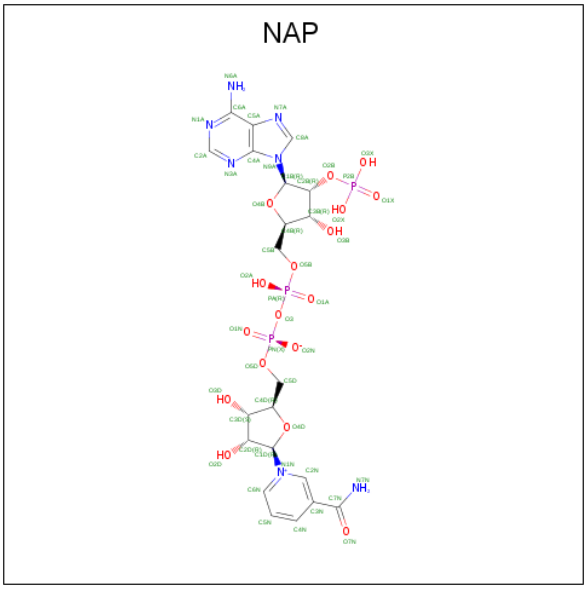
Chain	Residue	Modelled	Actual	Comment	Reference
G	-24	LYS	-	expression tag	UNP A0A0J9X1X7
G	-23	HIS	-	expression tag	UNP A0A0J9X1X7
G	-22	HIS	-	expression tag	UNP A0A0J9X1X7
G	-21	HIS	-	expression tag	UNP A0A0J9X1X7
G	-20	HIS	-	expression tag	UNP A0A0J9X1X7
G	-19	HIS	-	expression tag	UNP A0A0J9X1X7
G	-18	HIS	-	expression tag	UNP A0A0J9X1X7
G	-17	PRO	-	expression tag	UNP A0A0J9X1X7
H	-25	MET	-	initiating methionine	UNP A0A0J9X1X7
H	-24	LYS	-	expression tag	UNP A0A0J9X1X7
H	-23	HIS	-	expression tag	UNP A0A0J9X1X7
H	-22	HIS	-	expression tag	UNP A0A0J9X1X7
H	-21	HIS	-	expression tag	UNP A0A0J9X1X7
H	-20	HIS	-	expression tag	UNP A0A0J9X1X7
H	-19	HIS	-	expression tag	UNP A0A0J9X1X7
H	-18	HIS	-	expression tag	UNP A0A0J9X1X7
H	-17	PRO	-	expression tag	UNP A0A0J9X1X7

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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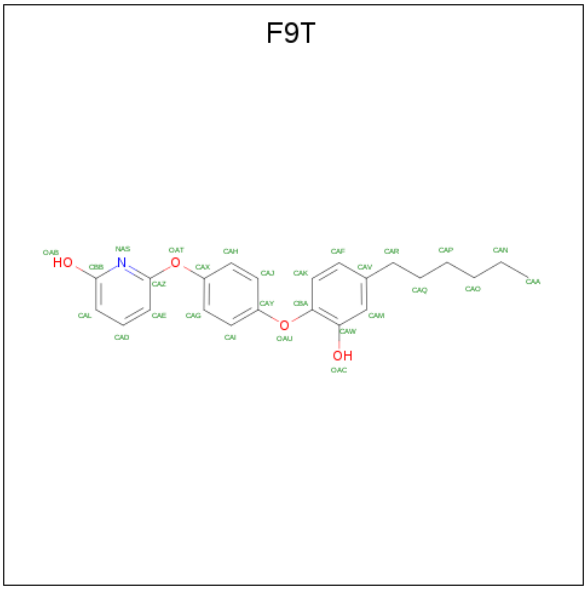
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	G	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	H	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 6-[4-(4-hexyl-2-oxidanyl-phenoxy)phenoxy]pyridin-2-ol (three-letter code: F9T) (formula: $C_{23}H_{25}NO_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			28	23	1	4		
3	B	1	Total	C	N	O	0	0
			28	23	1	4		
3	C	1	Total	C	N	O	0	0
			28	23	1	4		
3	D	1	Total	C	N	O	0	0
			28	23	1	4		
3	E	1	Total	C	N	O	0	0
			28	23	1	4		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	F	1	Total C N O 28 23 1 4	0	0
3	G	1	Total C N O 28 23 1 4	0	0
3	H	1	Total C N O 28 23 1 4	0	0

- Molecule 4 is water.

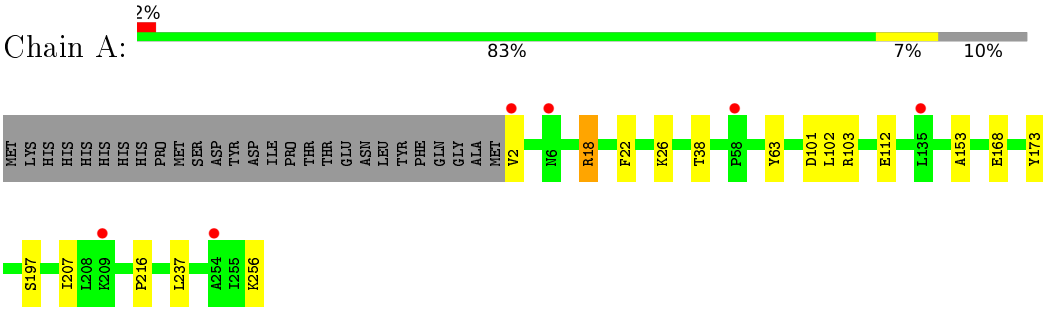
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	85	Total O 85 85	0	0
4	B	129	Total O 129 129	0	0
4	C	87	Total O 87 87	0	0
4	D	128	Total O 128 128	0	0
4	E	136	Total O 136 136	0	0
4	F	122	Total O 122 122	0	0
4	G	64	Total O 64 64	0	0
4	H	55	Total O 55 55	0	0

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.

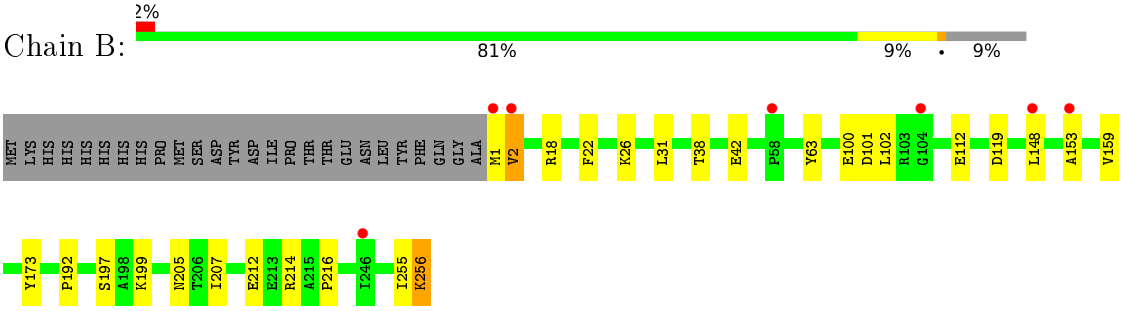
- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

Chain A:



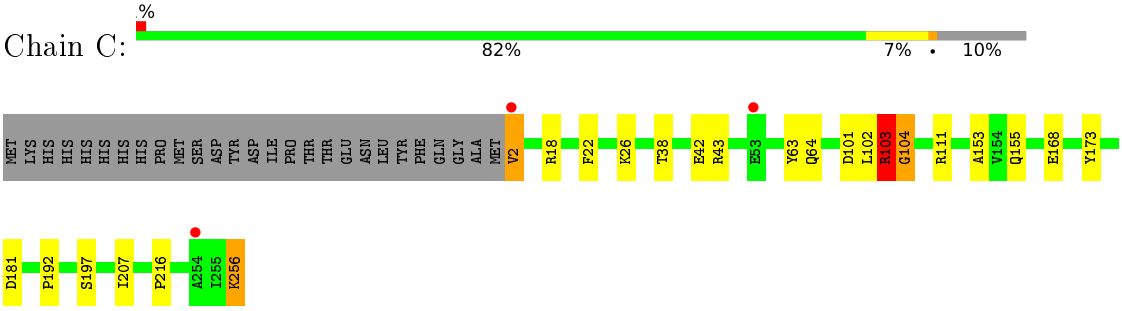
- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

Chain B:



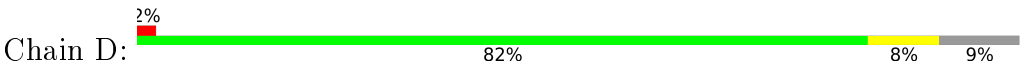
- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

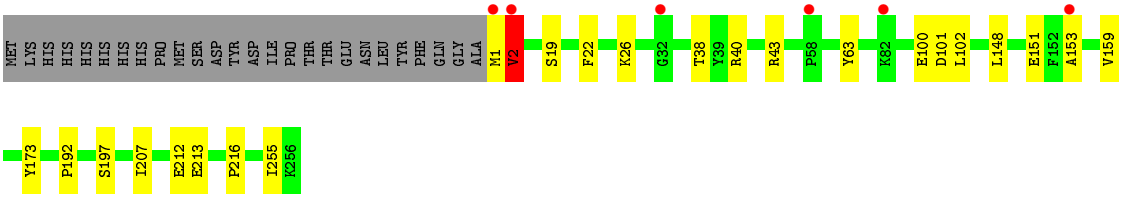
Chain C:



- Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

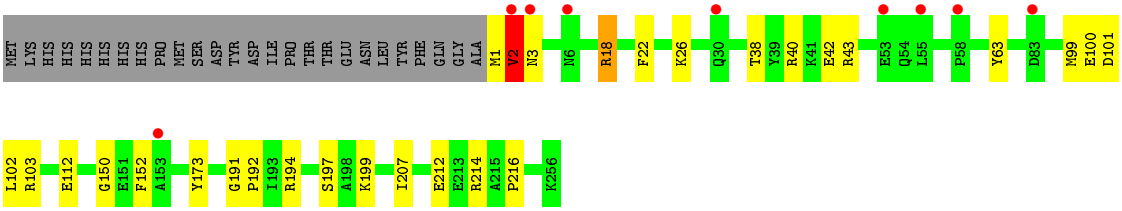
Chain D:





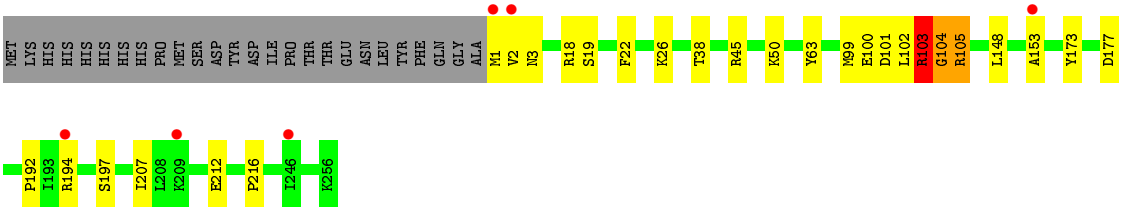
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

Chain E:



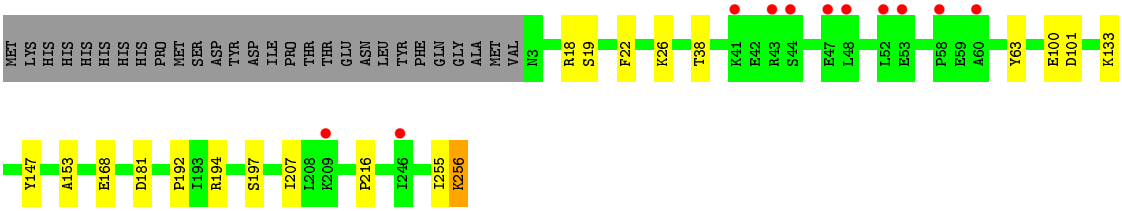
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

Chain F:



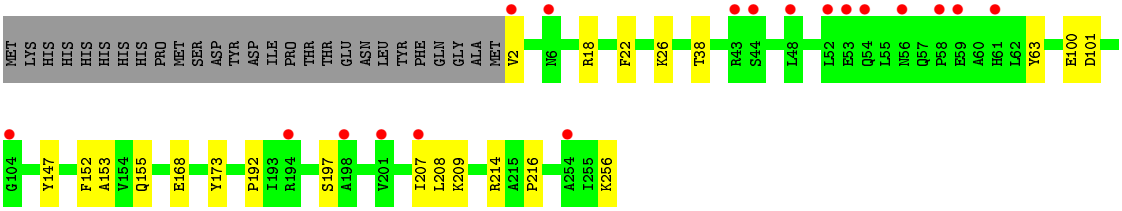
• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

Chain G:



• Molecule 1: Enoyl-[acyl-carrier-protein] reductase [NADPH]

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	90.35Å 94.56Å 94.78Å 98.47° 111.71° 97.42°	Depositor
Resolution (Å)	49.55 – 1.96 49.55 – 1.96	Depositor EDS
% Data completeness (in resolution range)	91.6 (49.55-1.96) 91.6 (49.55-1.96)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 1.97Å)	Xtriage
Refinement program	REFMAC 5.8.0222	Depositor
R, R_{free}	0.230 , 0.260 0.236 , 0.264	Depositor DCC
R_{free} test set	9068 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å^2)	27.4	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 35.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.000 for -l,-k,-h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	17245	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.01 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.5520e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: F9T, NAP

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	0.80	3/2010 (0.1%)	0.84	2/2708 (0.1%)
1	B	0.85	2/2007 (0.1%)	0.88	2/2704 (0.1%)
1	C	0.82	3/1999 (0.2%)	0.85	3/2694 (0.1%)
1	D	0.84	3/2027 (0.1%)	0.88	2/2730 (0.1%)
1	E	0.84	3/2007 (0.1%)	0.89	6/2704 (0.2%)
1	F	0.86	2/2018 (0.1%)	0.89	3/2718 (0.1%)
1	G	0.77	1/1992 (0.1%)	0.81	4/2684 (0.1%)
1	H	0.76	1/1999 (0.1%)	0.80	1/2694 (0.0%)
All	All	0.82	18/16059 (0.1%)	0.86	23/21636 (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	A	0	2
1	B	0	3
1	C	0	4
1	D	0	2
1	E	0	4
1	F	0	4
1	G	0	2
1	H	0	2
All	All	0	23

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	102	LEU	C-O	7.23	1.37	1.23
1	G	168	GLU	CD-OE1	7.06	1.33	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	102	LEU	C-O	6.60	1.35	1.23
1	F	102	LEU	C-O	6.16	1.35	1.23
1	D	102	LEU	C-O	6.14	1.35	1.23

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	101	ASP	CB-CG-OD1	11.00	128.20	118.30
1	G	101	ASP	CB-CG-OD1	10.55	127.80	118.30
1	A	101	ASP	CB-CG-OD1	10.38	127.64	118.30
1	C	101	ASP	CB-CG-OD1	10.07	127.36	118.30
1	F	101	ASP	CB-CG-OD1	9.90	127.21	118.30

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	103	ARG	Sidechain
1	A	18	ARG	Sidechain
1	B	18	ARG	Sidechain
1	B	2	VAL	Peptide
1	B	214	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	1980	0	1997	13	0
1	B	1980	0	1996	22	0
1	C	1972	0	1984	14	0
1	D	1994	0	2015	16	0
1	E	1980	0	1996	15	0
1	F	1988	0	2009	17	0
1	G	1965	0	1975	12	0
1	H	1972	0	1984	14	0
2	A	48	0	25	1	0
2	B	48	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	48	0	25	1	0
2	D	48	0	25	4	0
2	E	48	0	25	4	0
2	F	48	0	25	3	0
2	G	48	0	25	4	0
2	H	48	0	25	3	0
3	A	28	0	0	1	0
3	B	28	0	0	1	0
3	C	28	0	0	1	0
3	D	28	0	0	2	0
3	E	28	0	0	3	0
3	F	28	0	0	2	0
3	G	28	0	0	1	0
3	H	28	0	0	2	0
4	A	85	0	0	2	0
4	B	129	0	0	6	0
4	C	87	0	0	2	0
4	D	128	0	0	2	0
4	E	136	0	0	4	0
4	F	122	0	0	5	0
4	G	64	0	0	1	0
4	H	55	0	0	0	0
All	All	17245	0	16156	111	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 3.

The worst 5 of 111 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:ASP:OD1	1:F:105:ARG:HD2	1.72	0.89
1:F:194:ARG:NH1	4:F:401:HOH:O	2.18	0.76
2:E:301:NAP:N3A	4:E:401:HOH:O	2.24	0.71
1:C:256:LYS:HE2	1:D:255:ILE:O	1.97	0.64
1:E:2:VAL:HG22	1:E:3:ASN:HB2	1.79	0.64

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	256/282 (91%)	246 (96%)	10 (4%)	0	100 100
1	B	256/282 (91%)	245 (96%)	11 (4%)	0	100 100
1	C	255/282 (90%)	244 (96%)	9 (4%)	2 (1%)	19 9
1	D	258/282 (92%)	248 (96%)	9 (4%)	1 (0%)	34 22
1	E	256/282 (91%)	246 (96%)	9 (4%)	1 (0%)	34 22
1	F	257/282 (91%)	245 (95%)	9 (4%)	3 (1%)	13 4
1	G	254/282 (90%)	244 (96%)	10 (4%)	0	100 100
1	H	255/282 (90%)	245 (96%)	10 (4%)	0	100 100
All	All	2047/2256 (91%)	1963 (96%)	77 (4%)	7 (0%)	41 30

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	104	GLY
1	F	3	ASN
1	F	103	ARG
1	F	104	GLY
1	D	2	VAL

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	211/234 (90%)	209 (99%)	2 (1%)	78 77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	211/234 (90%)	208 (99%)	3 (1%)	67 62
1	C	210/234 (90%)	207 (99%)	3 (1%)	67 62
1	D	213/234 (91%)	209 (98%)	4 (2%)	57 50
1	E	211/234 (90%)	209 (99%)	2 (1%)	78 77
1	F	212/234 (91%)	209 (99%)	3 (1%)	67 62
1	G	209/234 (89%)	207 (99%)	2 (1%)	76 74
1	H	210/234 (90%)	205 (98%)	5 (2%)	49 40
All	All	1687/1872 (90%)	1663 (99%)	24 (1%)	67 62

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	50	LYS
1	G	100	GLU
1	F	216	PRO
1	G	216	PRO
1	C	103	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	75	ASN
1	G	75	ASN
1	F	75	ASN
1	E	54	GLN
1	F	156	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

16 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	F9T	H	302	-	30,30,30	1.44	3 (10%)	39,39,39	1.45	4 (10%)
2	NAP	D	301	-	45,52,52	1.77	8 (17%)	56,80,80	2.09	16 (28%)
3	F9T	G	302	-	30,30,30	1.40	3 (10%)	39,39,39	1.47	5 (12%)
3	F9T	C	302	-	30,30,30	1.68	5 (16%)	39,39,39	1.71	4 (10%)
2	NAP	E	301	-	45,52,52	1.80	11 (24%)	56,80,80	1.95	13 (23%)
2	NAP	G	301	-	45,52,52	1.78	6 (13%)	56,80,80	1.61	10 (17%)
2	NAP	H	301	-	45,52,52	1.59	3 (6%)	56,80,80	1.58	8 (14%)
2	NAP	B	401	-	45,52,52	1.63	7 (15%)	56,80,80	1.93	15 (26%)
2	NAP	C	301	-	45,52,52	1.79	6 (13%)	56,80,80	1.75	8 (14%)
3	F9T	A	302	-	30,30,30	1.61	3 (10%)	39,39,39	2.26	5 (12%)
3	F9T	B	402	-	30,30,30	1.46	5 (16%)	39,39,39	1.92	5 (12%)
3	F9T	E	302	-	30,30,30	1.56	3 (10%)	39,39,39	1.80	6 (15%)
2	NAP	F	301	-	45,52,52	1.65	8 (17%)	56,80,80	1.90	9 (16%)
2	NAP	A	301	-	45,52,52	1.75	6 (13%)	56,80,80	1.66	10 (17%)
3	F9T	F	302	-	30,30,30	1.60	5 (16%)	39,39,39	1.77	3 (7%)
3	F9T	D	302	-	30,30,30	1.97	5 (16%)	39,39,39	1.94	4 (10%)

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	F9T	H	302	-	-	2/14/14/14	0/3/3/3
2	NAP	D	301	-	-	7/31/67/67	0/5/5/5
3	F9T	G	302	-	-	2/14/14/14	0/3/3/3
3	F9T	C	302	-	-	3/14/14/14	0/3/3/3
2	NAP	E	301	-	-	5/31/67/67	0/5/5/5
2	NAP	G	301	-	-	5/31/67/67	0/5/5/5
2	NAP	H	301	-	-	6/31/67/67	0/5/5/5
2	NAP	B	401	-	-	5/31/67/67	0/5/5/5
2	NAP	C	301	-	-	5/31/67/67	0/5/5/5
3	F9T	A	302	-	-	1/14/14/14	0/3/3/3
3	F9T	B	402	-	-	1/14/14/14	0/3/3/3
3	F9T	E	302	-	-	2/14/14/14	0/3/3/3
2	NAP	F	301	-	-	7/31/67/67	0/5/5/5
2	NAP	A	301	-	-	4/31/67/67	0/5/5/5
3	F9T	F	302	-	-	3/14/14/14	0/3/3/3
3	F9T	D	302	-	-	4/14/14/14	0/3/3/3

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	301	NAP	O7N-C7N	9.09	1.41	1.24
2	H	301	NAP	O7N-C7N	8.14	1.39	1.24
2	C	301	NAP	O7N-C7N	7.22	1.38	1.24
2	A	301	NAP	O7N-C7N	7.22	1.38	1.24
2	D	301	NAP	O7N-C7N	6.40	1.36	1.24

The worst 5 of 125 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	302	F9T	CBB-NAS-CAZ	10.27	125.58	115.70
3	D	302	F9T	CBB-NAS-CAZ	7.96	123.36	115.70
3	B	402	F9T	CBB-NAS-CAZ	7.94	123.34	115.70
3	F	302	F9T	CBB-NAS-CAZ	7.46	122.88	115.70
3	E	302	F9T	CBB-NAS-CAZ	7.43	122.85	115.70

There are no chirality outliers.

5 of 62 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	NAP	C5D-O5D-PN-O1N
2	A	301	NAP	C5D-O5D-PN-O2N
2	B	401	NAP	C5D-O5D-PN-O1N
2	B	401	NAP	C5D-O5D-PN-O2N
2	C	301	NAP	C5D-O5D-PN-O1N

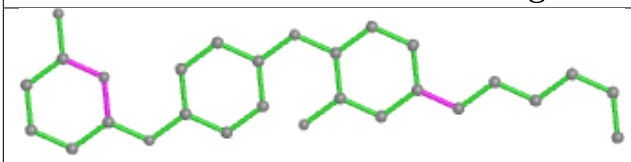
There are no ring outliers.

15 monomers are involved in 29 short contacts:

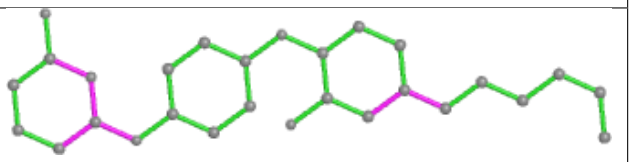
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	302	F9T	2	0
2	D	301	NAP	4	0
3	G	302	F9T	1	0
3	C	302	F9T	1	0
2	E	301	NAP	4	0
2	G	301	NAP	4	0
2	H	301	NAP	3	0
2	C	301	NAP	1	0
3	A	302	F9T	1	0
3	B	402	F9T	1	0
3	E	302	F9T	3	0
2	F	301	NAP	3	0
2	A	301	NAP	1	0
3	F	302	F9T	2	0
3	D	302	F9T	2	0

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.

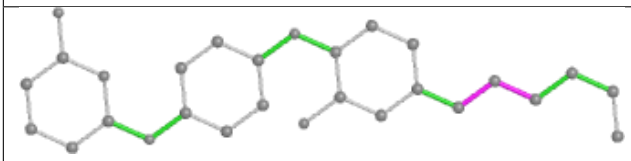
Ligand F9T H 302



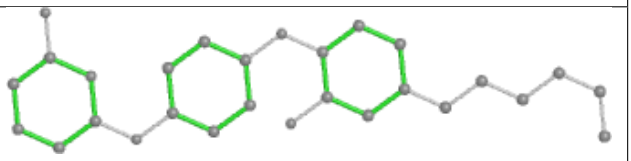
Bond lengths



Bond angles

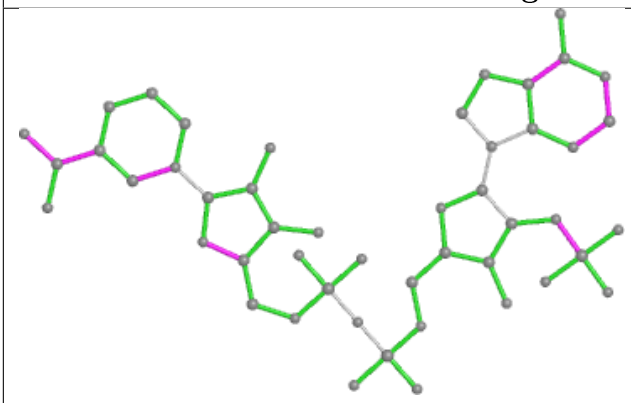


Torsions



Rings

Ligand NAP D 301



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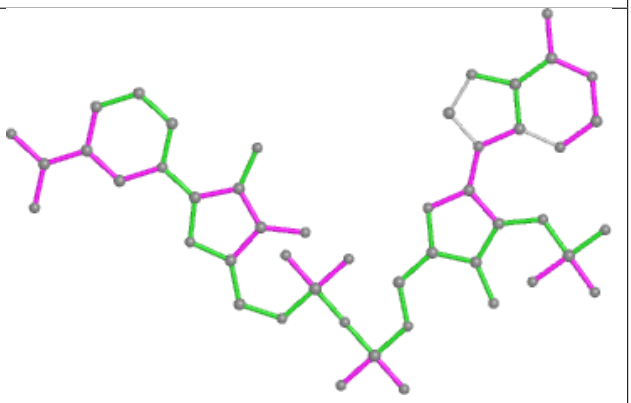

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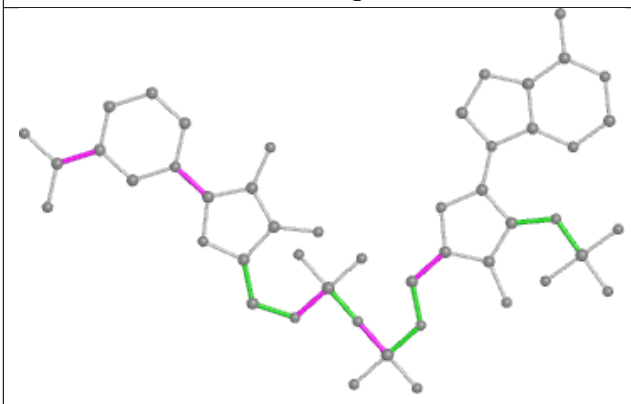

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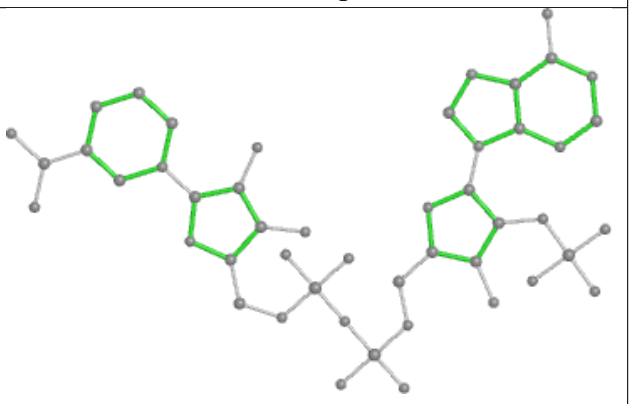
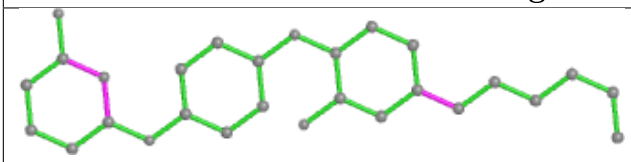
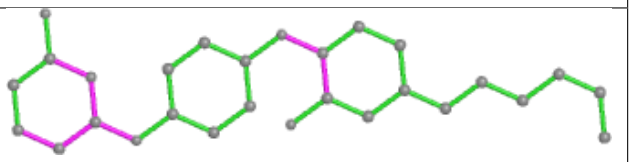
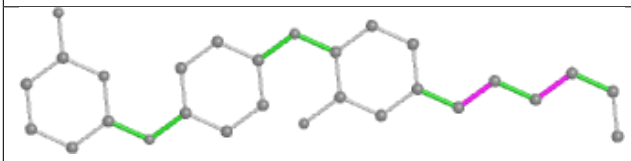
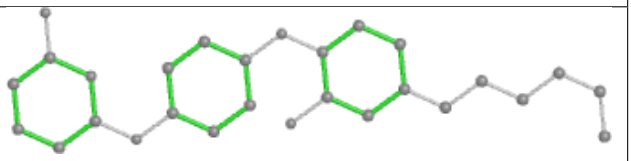
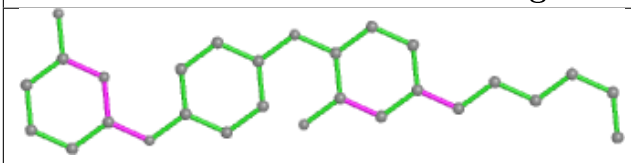
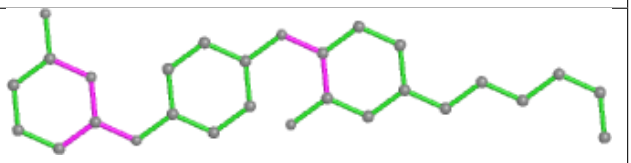
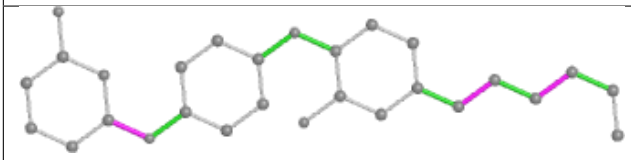
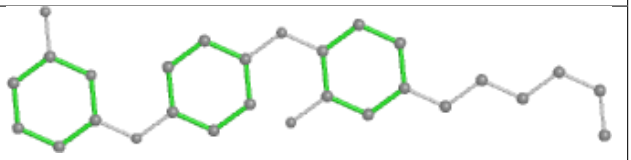
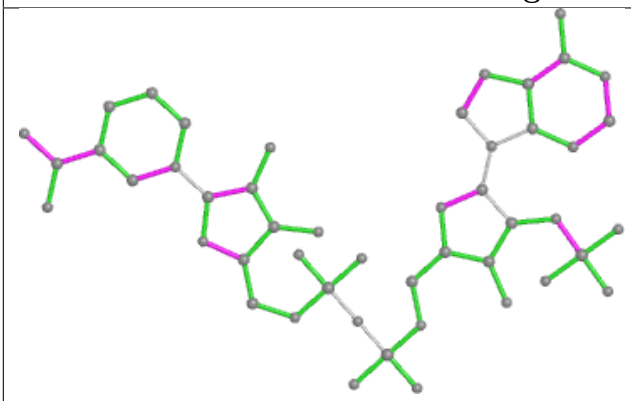


Rings

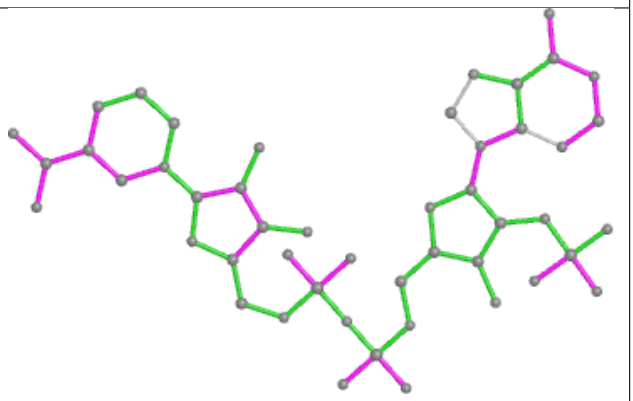
Ligand F9T G 302	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand F9T C 302	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NAP E 301



Bond lengths



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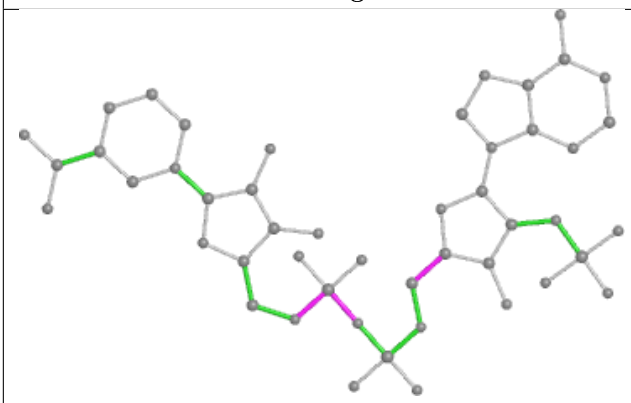

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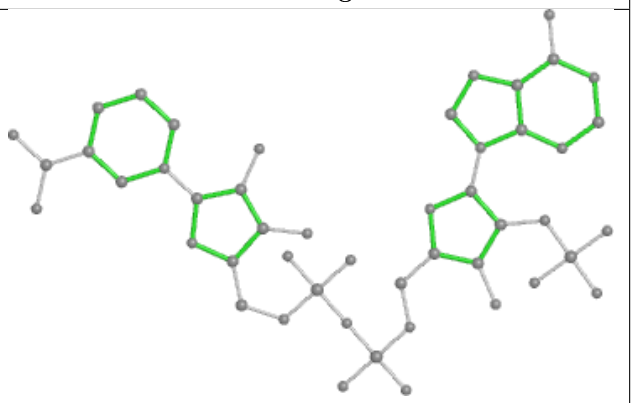
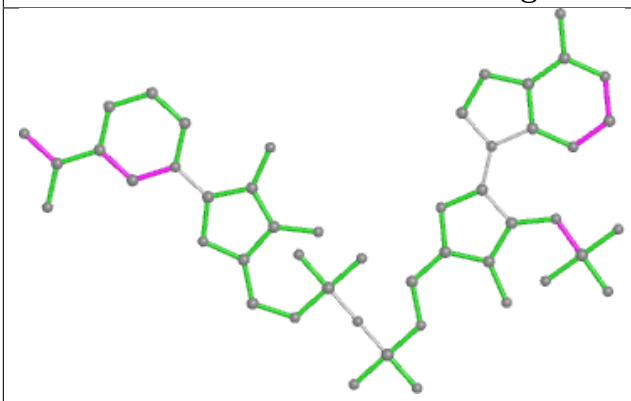


Rings

Ligand NAP G 301



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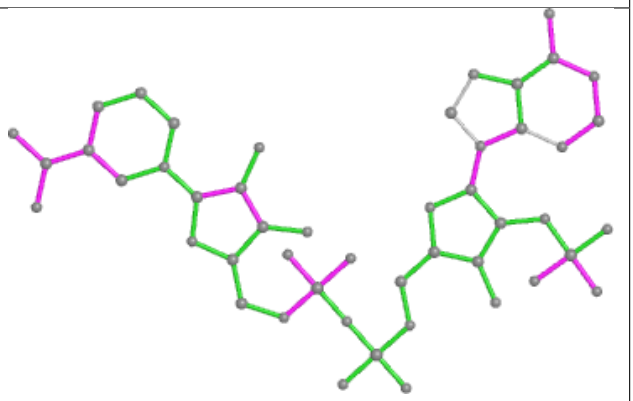
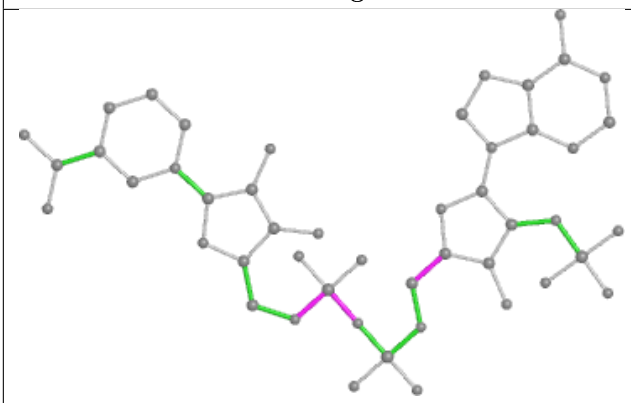


Bond angles



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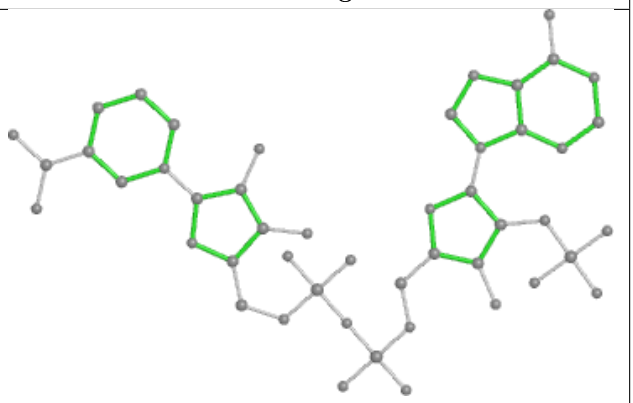
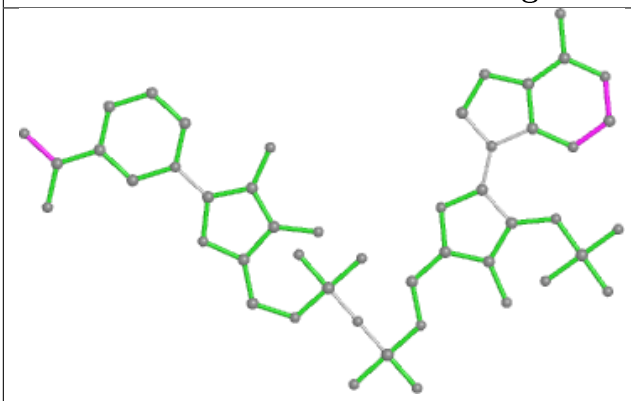
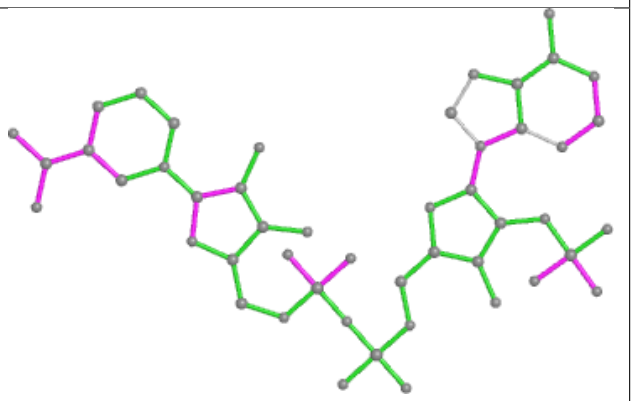


Rings

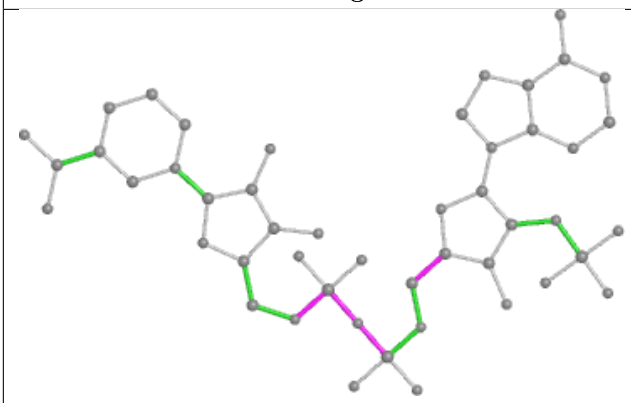
Ligand NAP H 301



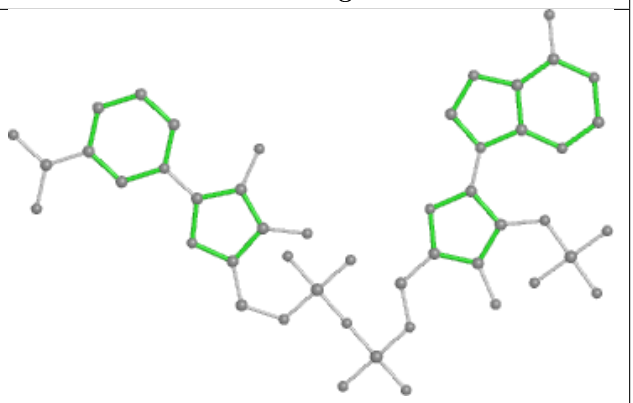
Bond lengths



Bond angles

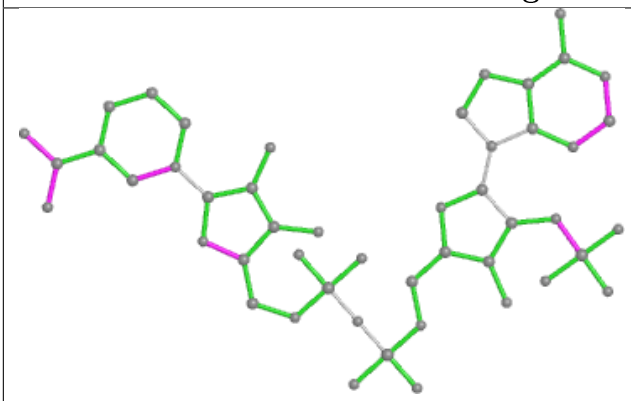


Torsions

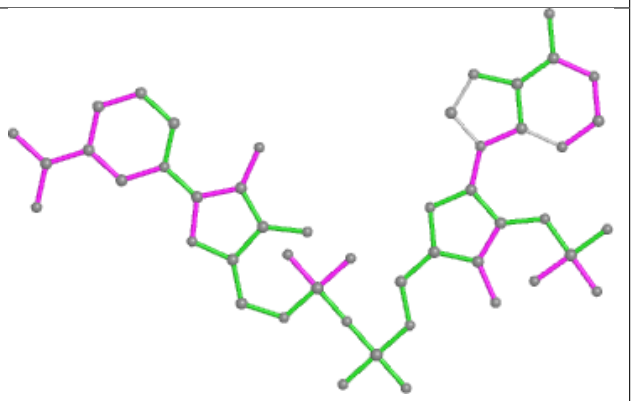


Rings

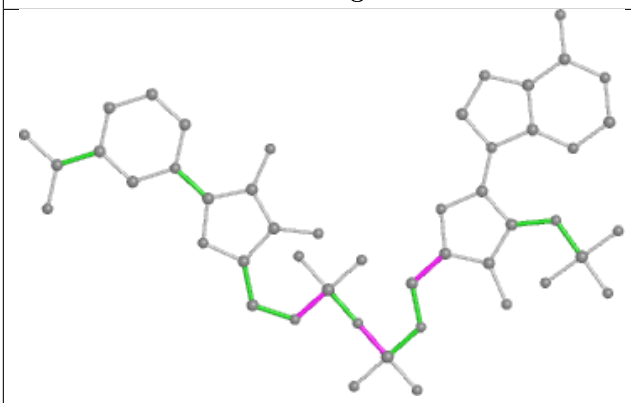
Ligand NAP B 401



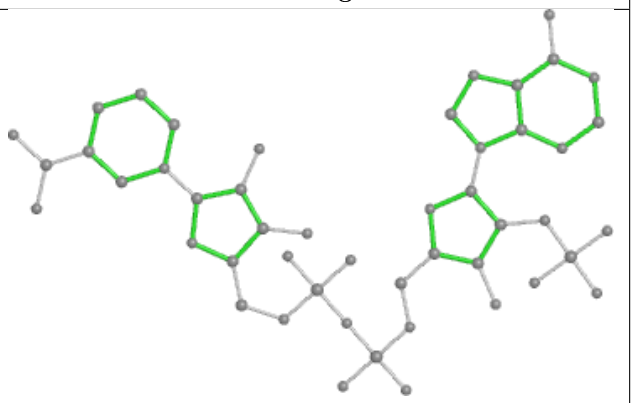
Bond lengths



Bond angles

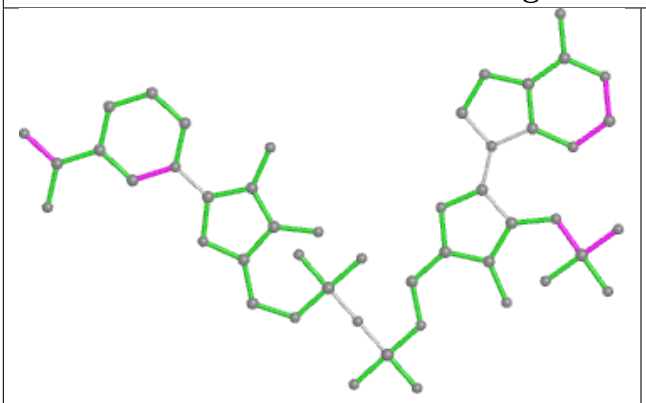


Torsions

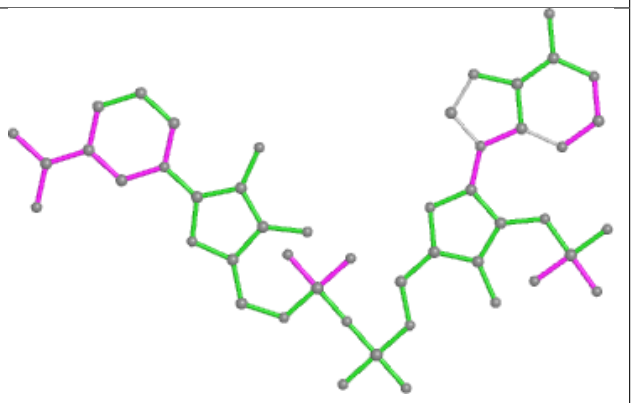


Rings

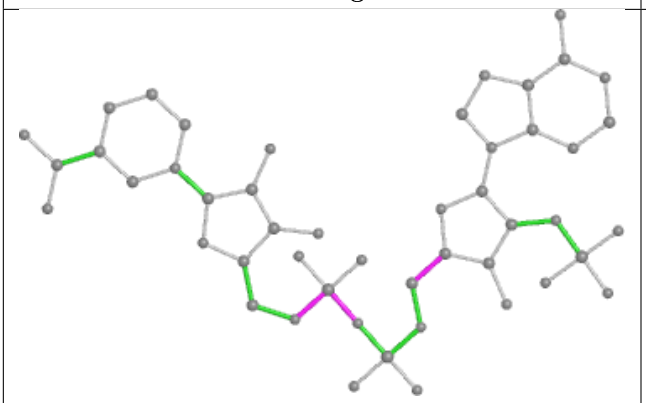
Ligand NAP C 301



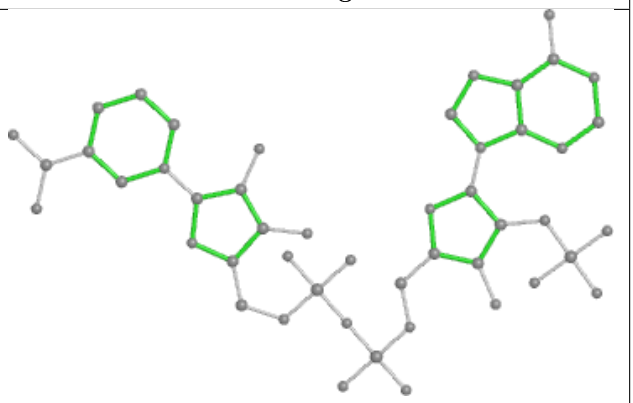
Bond lengths



Bond angles

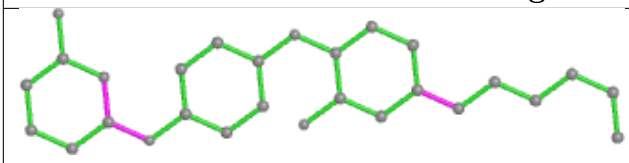


Torsions

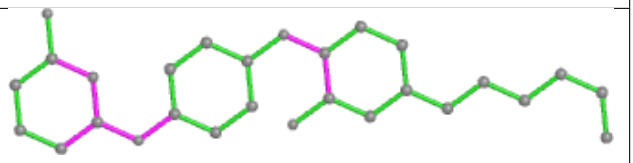


Rings

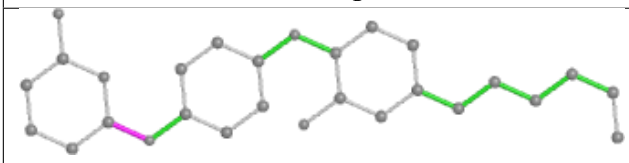
Ligand F9T A 302



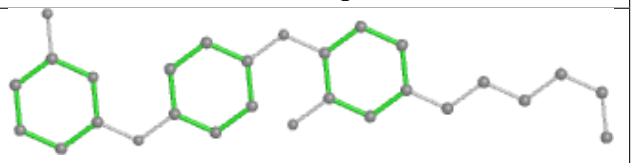
Bond lengths



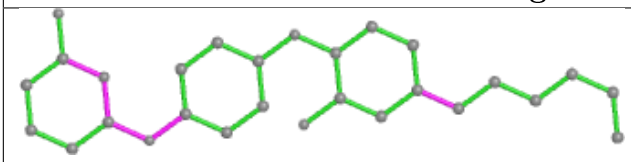
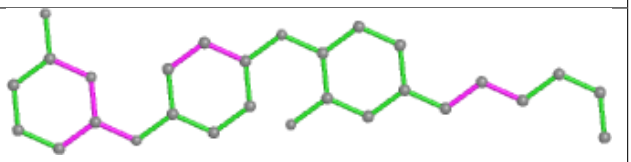
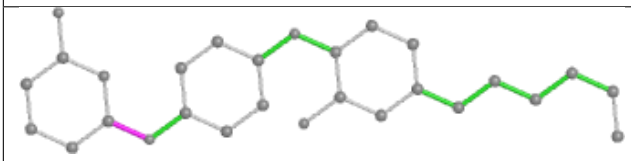
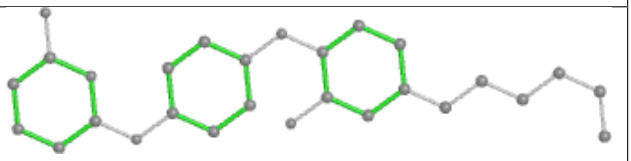
Bond angles

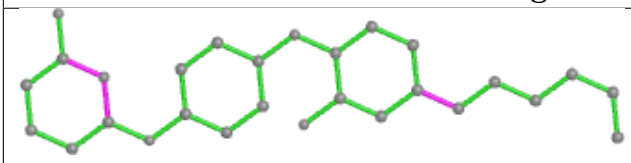
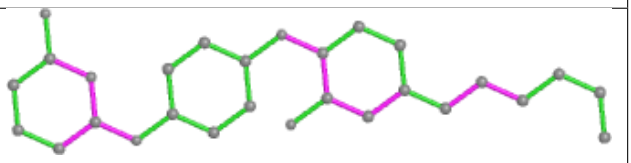
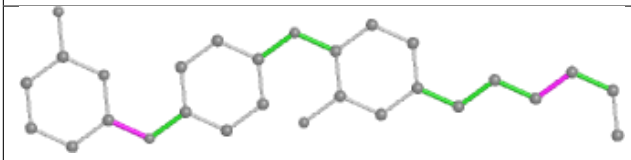
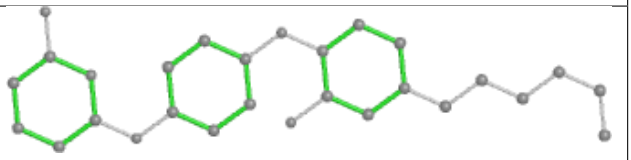


Torsions

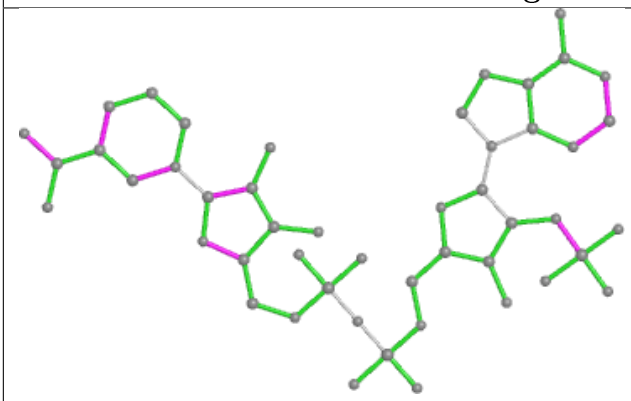


Rings

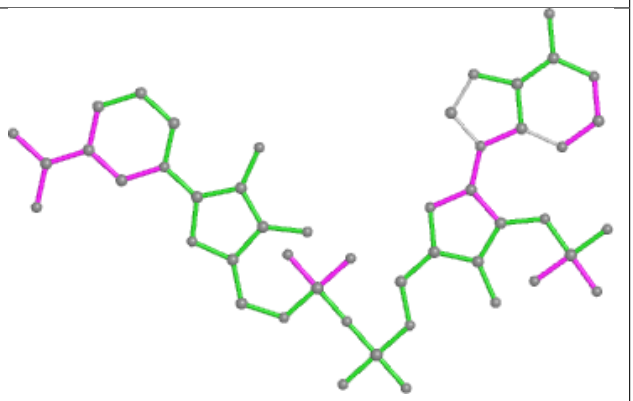
Ligand F9T B 402	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand F9T E 302	
 Bond lengths	 Bond angles
 Torsions	 Rings

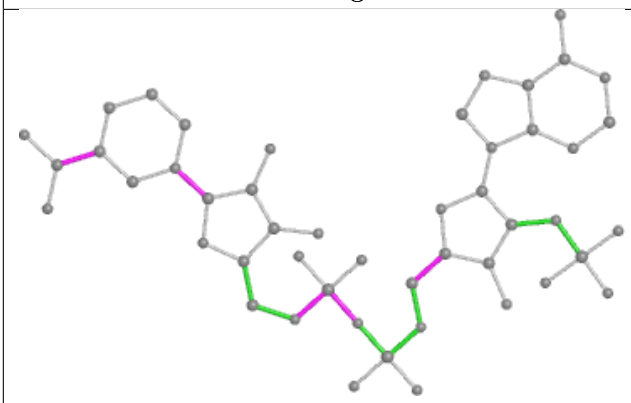
Ligand NAP F 301



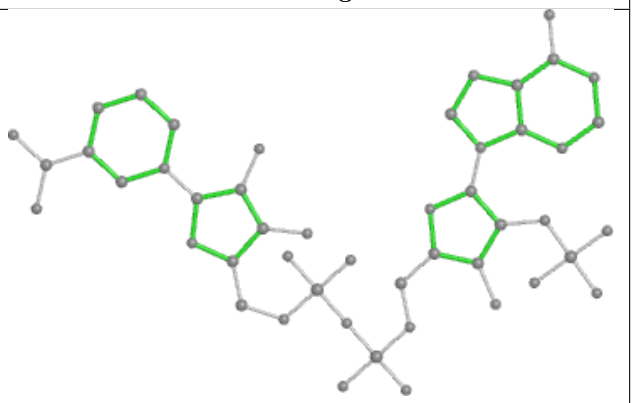
Bond lengths



Bond angles

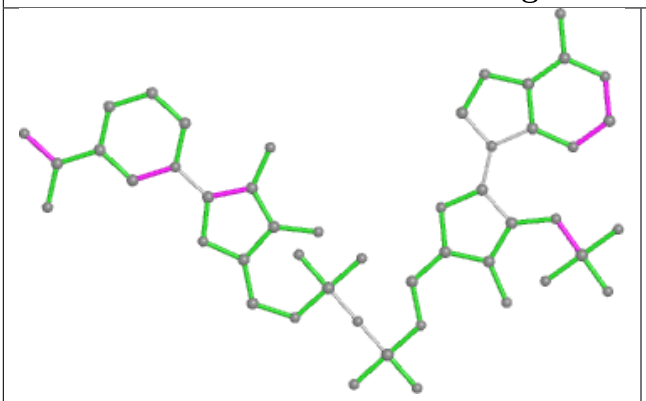


Torsions

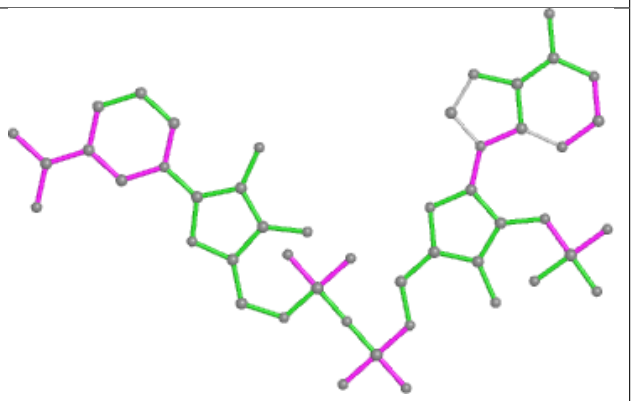


Rings

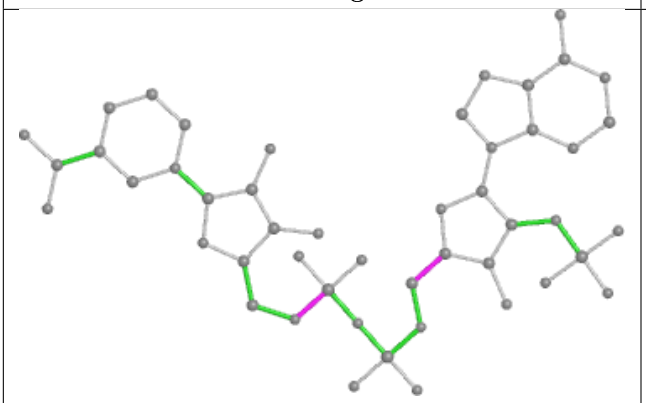
Ligand NAP A 301



Bond lengths



Bond angles



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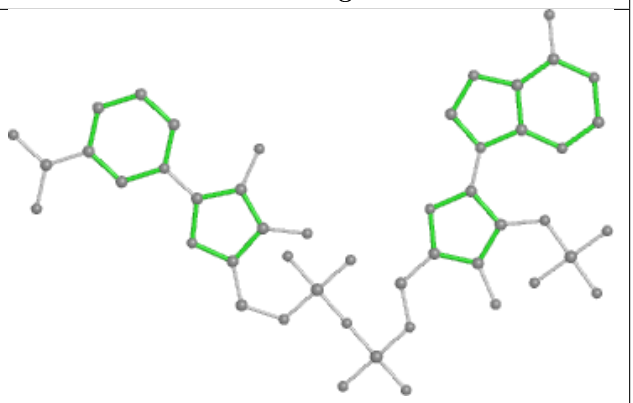
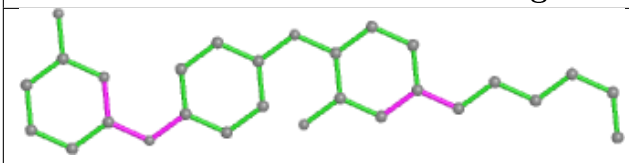
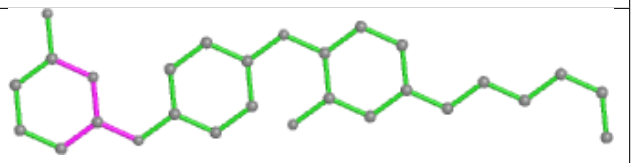


Rings

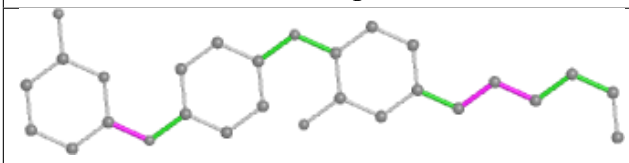
Ligand F9T F 302



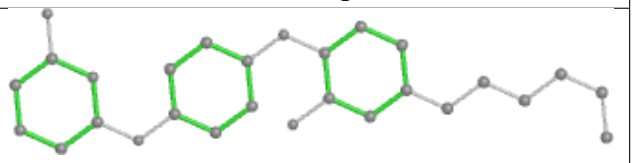
Bond lengths



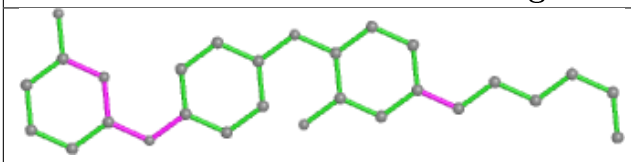
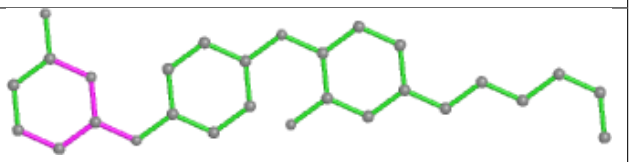
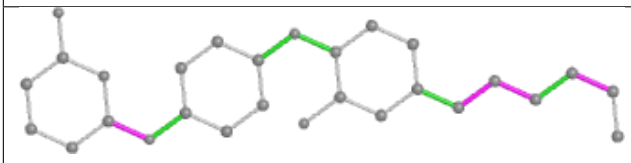
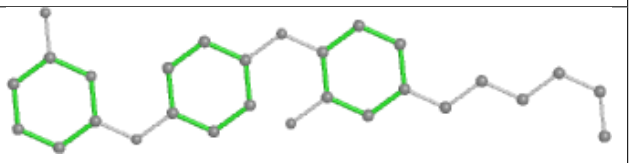
Bond angles



Torsions



Rings

Ligand F9T D 302	
 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	255/282 (90%)	-0.06	6 (2%)	59	68	23, 34, 57, 73	0
1	B	256/282 (90%)	0.15	7 (2%)	54	63	24, 35, 55, 98	0
1	C	255/282 (90%)	-0.14	3 (1%)	79	84	24, 34, 57, 72	0
1	D	256/282 (90%)	0.11	6 (2%)	60	69	26, 37, 57, 104	0
1	E	256/282 (90%)	0.17	9 (3%)	44	53	25, 37, 56, 94	0
1	F	256/282 (90%)	0.15	6 (2%)	60	69	24, 35, 58, 113	0
1	G	254/282 (90%)	0.15	11 (4%)	35	45	26, 41, 75, 113	0
1	H	255/282 (90%)	0.25	18 (7%)	16	24	26, 42, 75, 90	0
All	All	2043/2256 (90%)	0.10	66 (3%)	47	57	23, 37, 65, 113	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	44	SER	7.5
1	H	43	ARG	4.4
1	F	2	VAL	4.4
1	G	43	ARG	4.2
1	G	47	GLU	3.9

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

There are no monosaccharides in this entry.

6.4 Ligands (i)

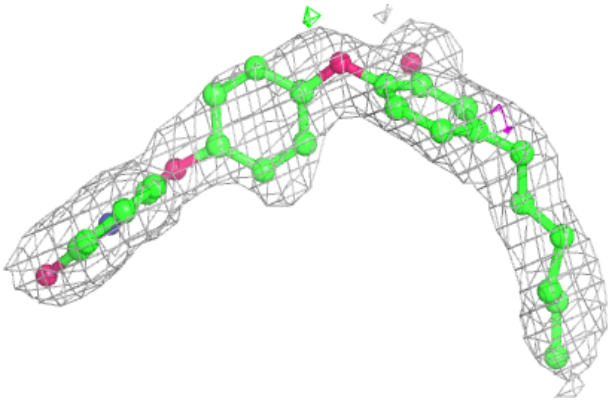
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

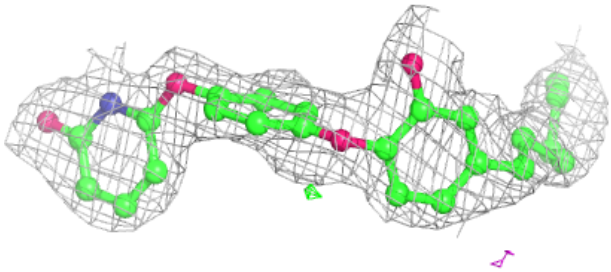
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	F9T	H	302	28/28	0.86	0.16	45,65,71,72	0
3	F9T	G	302	28/28	0.91	0.10	41,48,56,57	0
3	F9T	D	302	28/28	0.91	0.12	30,38,42,44	0
3	F9T	E	302	28/28	0.93	0.10	27,38,40,41	0
3	F9T	F	302	28/28	0.93	0.10	31,37,43,44	0
3	F9T	C	302	28/28	0.93	0.10	29,34,40,42	0
3	F9T	B	402	28/28	0.93	0.13	33,36,43,45	0
3	F9T	A	302	28/28	0.94	0.08	28,32,36,37	0
2	NAP	H	301	48/48	0.94	0.10	30,46,58,64	0
2	NAP	G	301	48/48	0.95	0.08	29,39,54,60	0
2	NAP	D	301	48/48	0.96	0.08	20,27,32,36	0
2	NAP	E	301	48/48	0.96	0.09	21,28,34,36	0
2	NAP	B	401	48/48	0.97	0.08	20,27,32,35	0
2	NAP	F	301	48/48	0.97	0.08	21,28,34,36	0
2	NAP	C	301	48/48	0.97	0.08	21,27,35,36	0
2	NAP	A	301	48/48	0.97	0.08	21,27,35,36	0

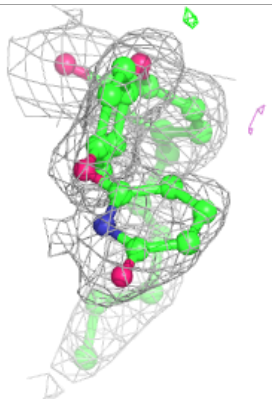
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around F9T H 302:

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

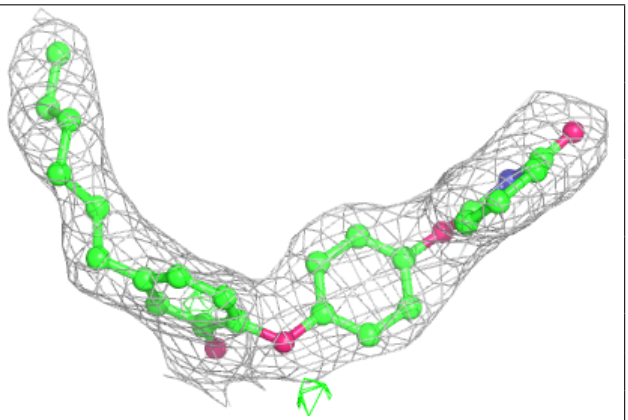


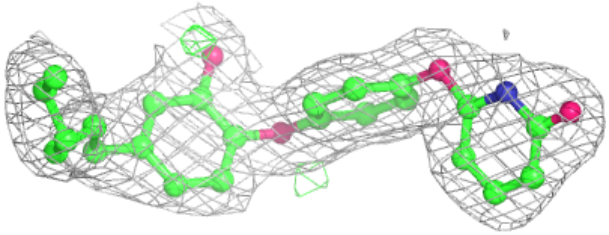




Electron density around F9T G 302:

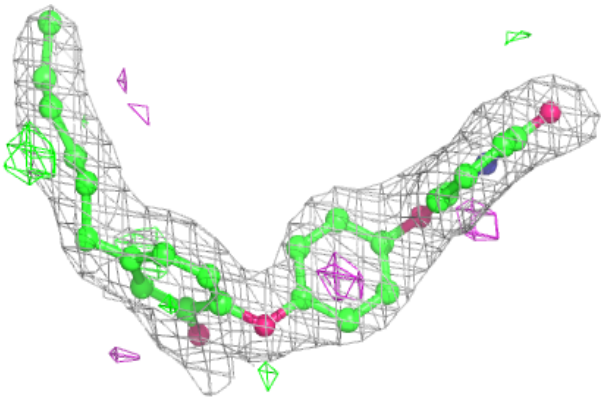
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

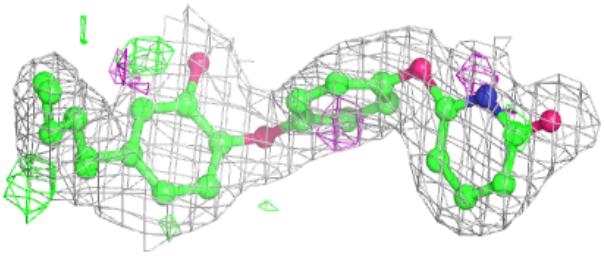


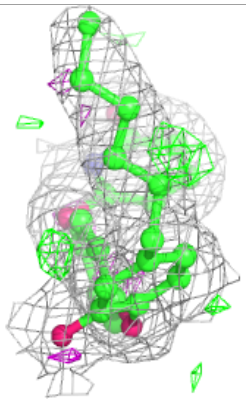


Electron density around F9T D 302:

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

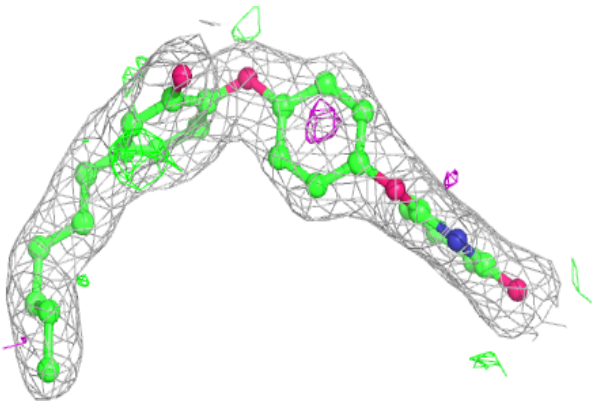


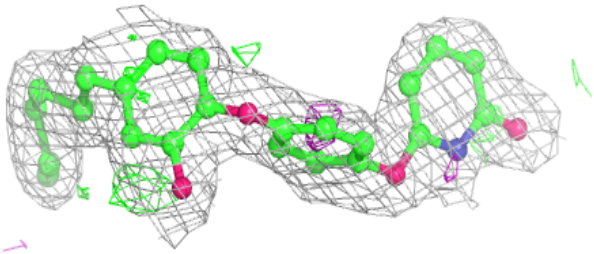


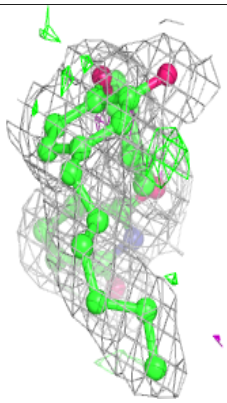


Electron density around F9T E 302:

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

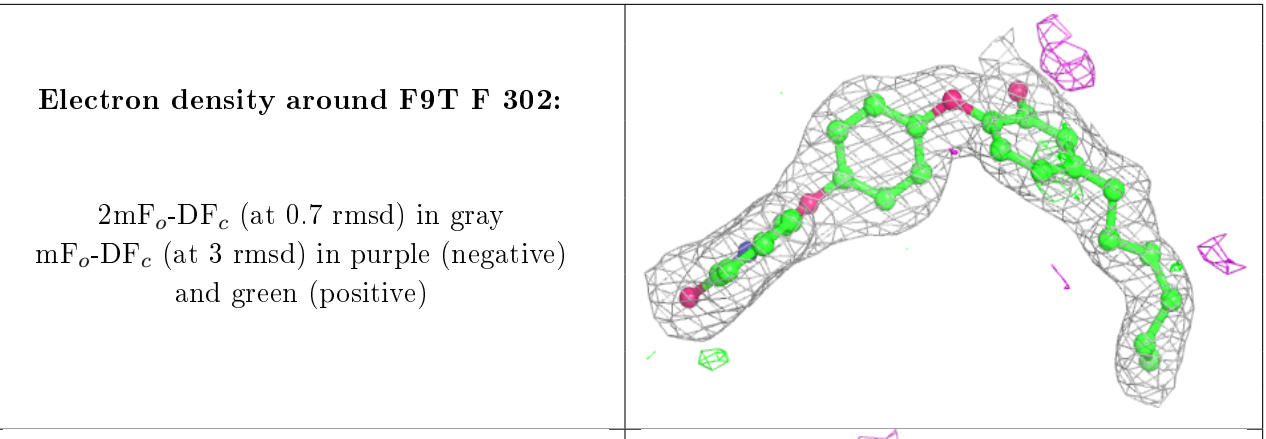






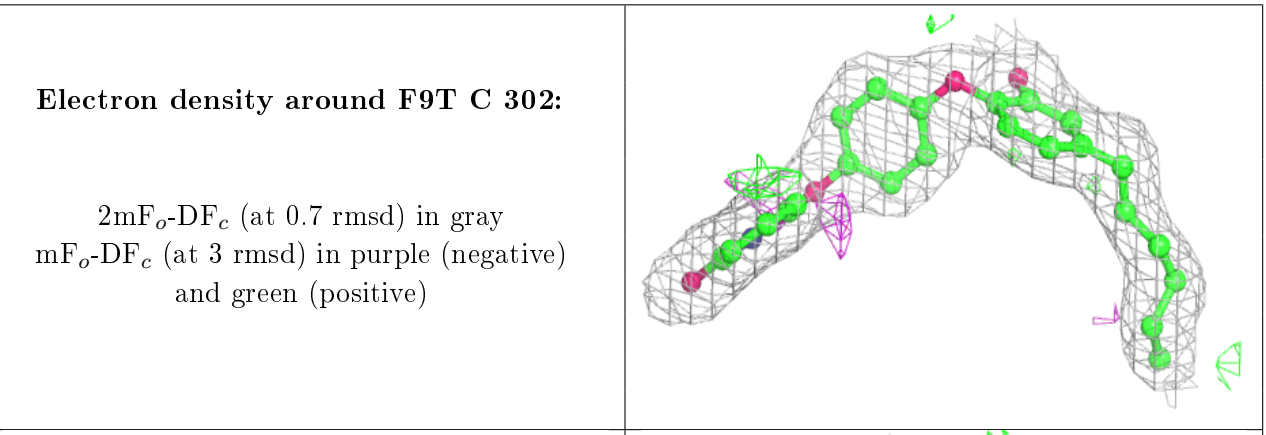
Electron density around F9T F 302:

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



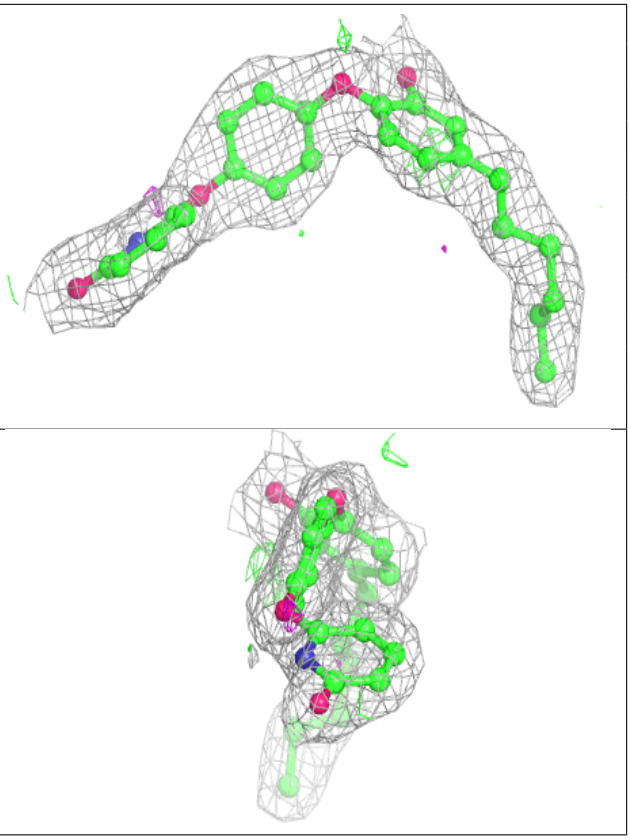
Electron density around F9T C 302:

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



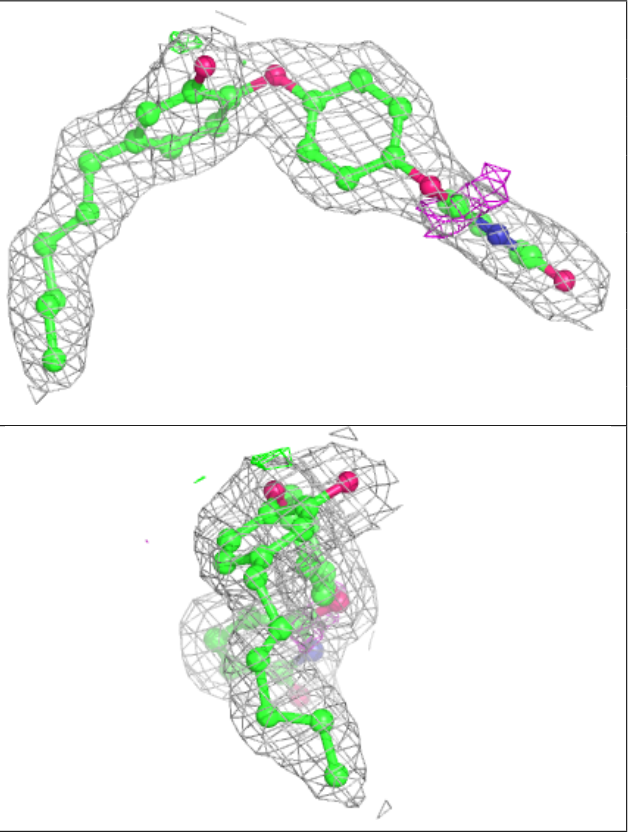
Electron density around F9T B 402:

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



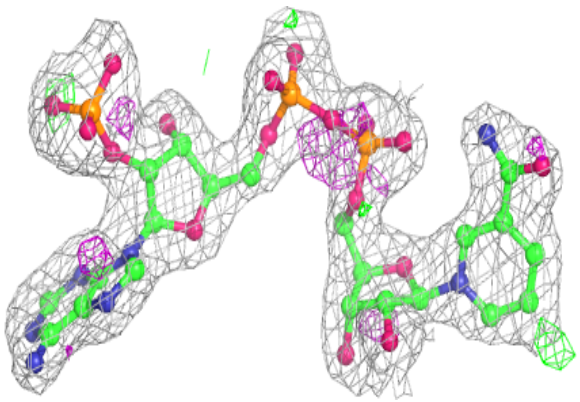
Electron density around F9T A 302:

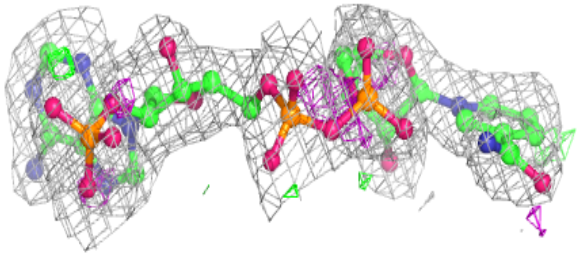
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

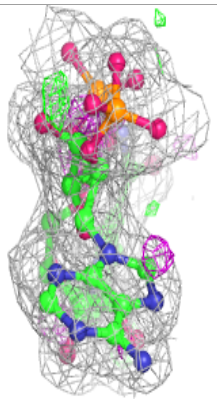


Electron density around NAP H 301:

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

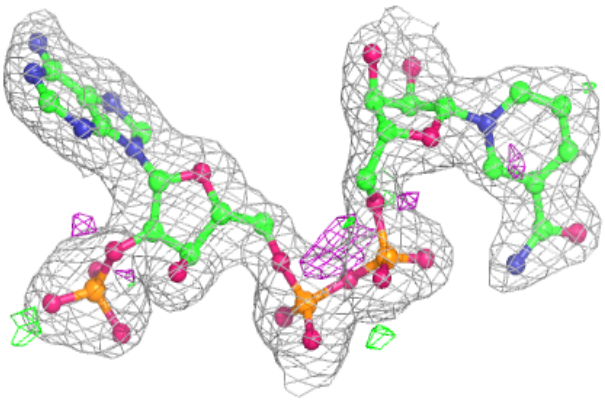


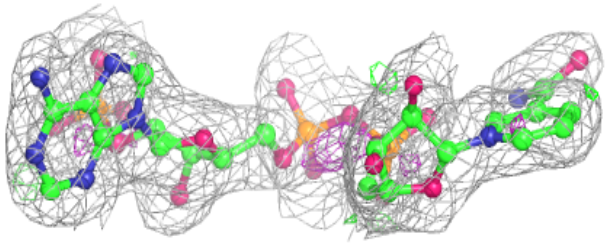


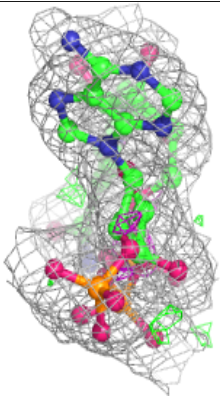


Electron density around NAP G 301:

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

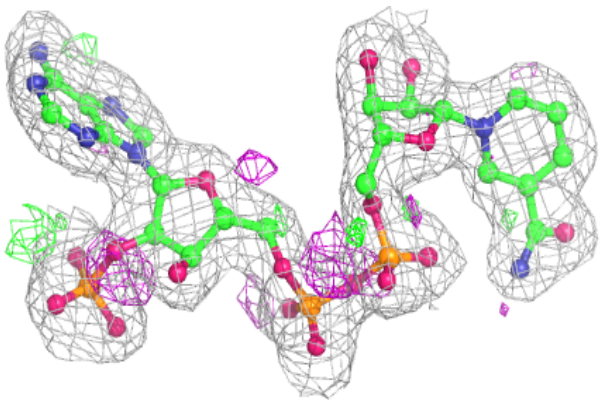


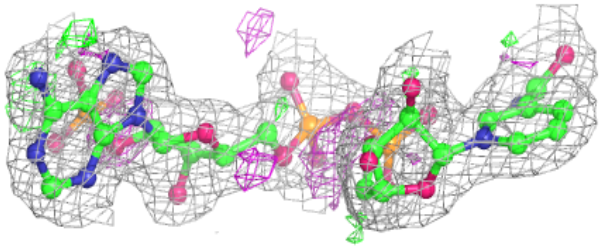


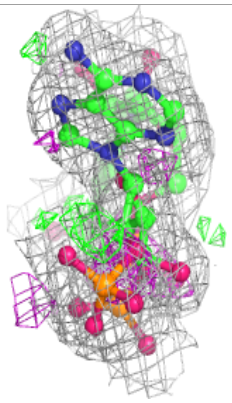


Electron density around NAP D 301:

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

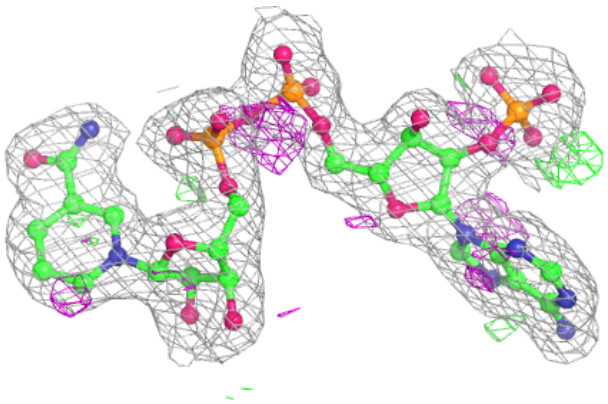


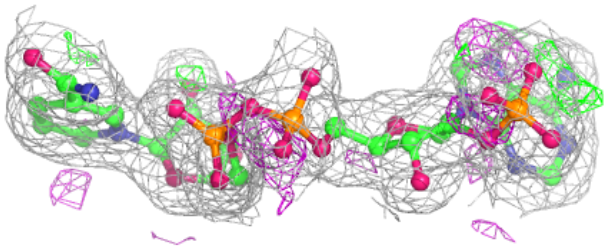




Electron density around NAP E 301:

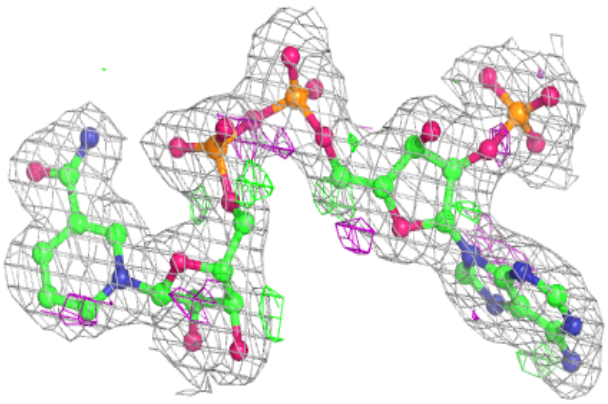
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

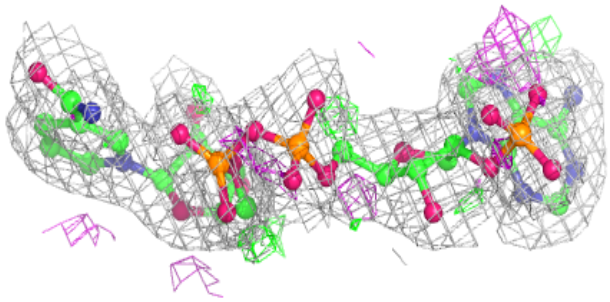


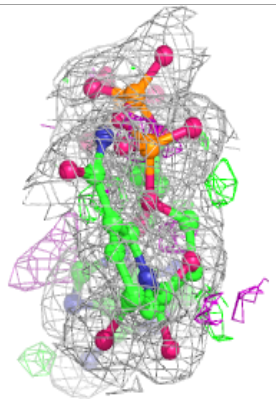


Electron density around NAP B 401:

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

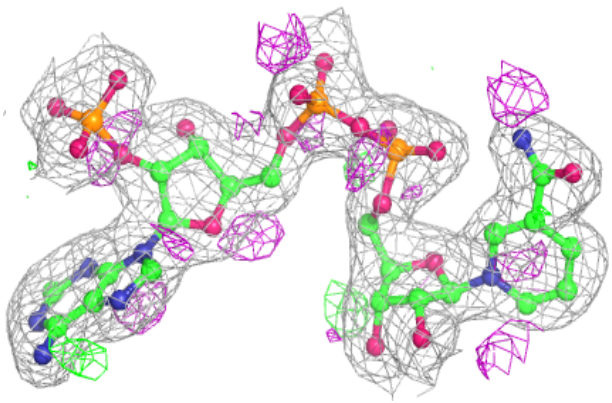


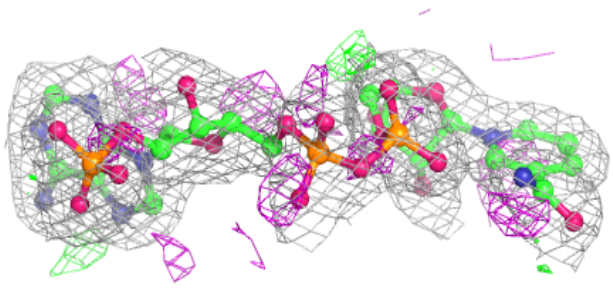


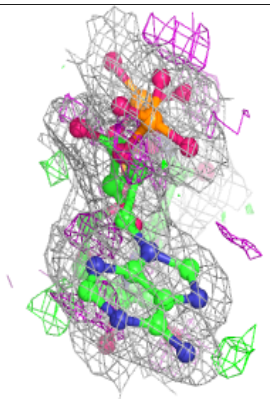


Electron density around NAP F 301:

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

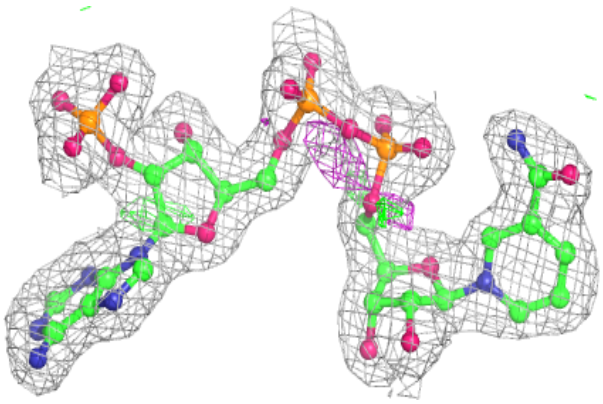


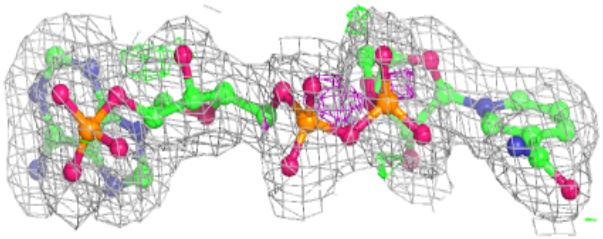


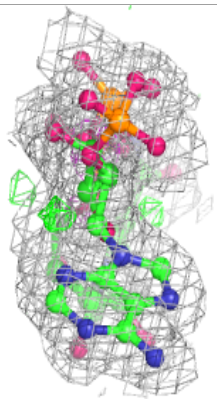


Electron density around NAP C 301:

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

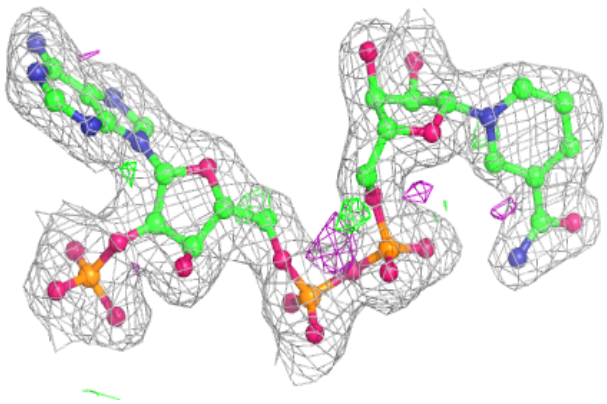


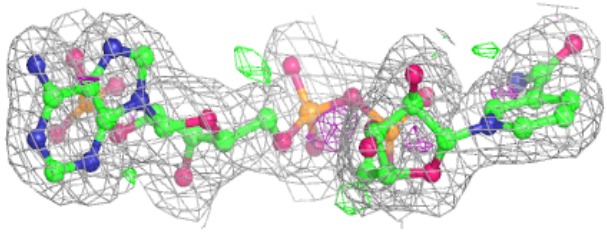


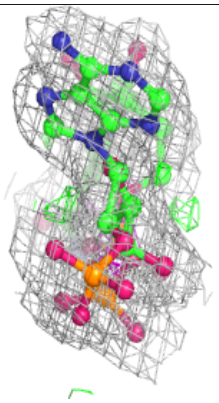


Electron density around NAP A 301:

$2mF_o$-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.