



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 15, 2024 – 07:43 PM EDT

PDB ID : 4QIJ
Title : Crystal structure of MenB from Mycobacteria tuberculosis in complex with 1-HNA-CoA
Authors : Song, H.G.; Sung, H.P.; Tse, Y.S.; Guo, Z.H.
Deposited on : 2014-05-31
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-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

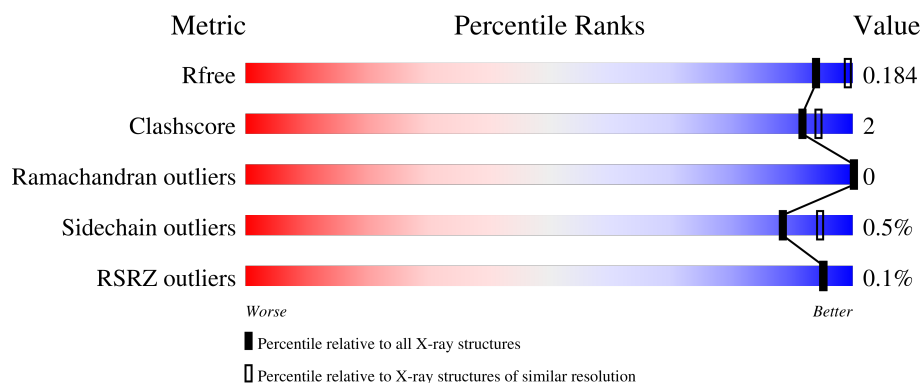
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	334	 89% 10%
1	B	334	 86% 10%
1	C	334	 85% 5% 10%
1	D	334	 85% 11%
1	E	334	 85% 11%

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Mol	Chain	Length	Quality of chain
1	F	334	 86% • 11%
1	G	334	 86% • 11%
1	H	334	 84% 5% 11%
1	I	334	 85% • 11%
1	J	334	 87% • 10%
1	K	334	 87% • 10%
1	L	334	 87% • 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 31323 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 1,4-Dihydroxy-2-naphthoyl-CoA synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	S	0	0	0
			2350	1480	425	436	9			
1	B	301	Total	C	N	O	S	0	0	0
			2349	1481	425	434	9			
1	C	301	Total	C	N	O	S	0	0	0
			2349	1481	425	434	9			
1	D	297	Total	C	N	O	S	0	0	0
			2323	1464	421	429	9			
1	E	298	Total	C	N	O	S	0	0	0
			2334	1470	425	430	9			
1	F	298	Total	C	N	O	S	0	0	0
			2333	1470	422	432	9			
1	G	297	Total	C	N	O	S	0	1	0
			2329	1468	421	431	9			
1	H	298	Total	C	N	O	S	0	0	0
			2331	1468	422	432	9			
1	I	298	Total	C	N	O	S	0	0	0
			2338	1472	425	432	9			
1	J	301	Total	C	N	O	S	0	0	0
			2351	1481	425	436	9			
1	K	301	Total	C	N	O	S	0	0	0
			2346	1479	422	436	9			
1	L	301	Total	C	N	O	S	0	0	0
			2347	1478	424	436	9			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P9WNP5
A	-18	GLY	-	expression tag	UNP P9WNP5
A	-17	SER	-	expression tag	UNP P9WNP5
A	-16	SER	-	expression tag	UNP P9WNP5
A	-15	HIS	-	expression tag	UNP P9WNP5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	HIS	-	expression tag	UNP P9WNP5
A	-13	HIS	-	expression tag	UNP P9WNP5
A	-12	HIS	-	expression tag	UNP P9WNP5
A	-11	HIS	-	expression tag	UNP P9WNP5
A	-10	HIS	-	expression tag	UNP P9WNP5
A	-9	SER	-	expression tag	UNP P9WNP5
A	-8	SER	-	expression tag	UNP P9WNP5
A	-7	GLY	-	expression tag	UNP P9WNP5
A	-6	LEU	-	expression tag	UNP P9WNP5
A	-5	VAL	-	expression tag	UNP P9WNP5
A	-4	PRO	-	expression tag	UNP P9WNP5
A	-3	ARG	-	expression tag	UNP P9WNP5
A	-2	GLY	-	expression tag	UNP P9WNP5
A	-1	SER	-	expression tag	UNP P9WNP5
A	0	HIS	-	expression tag	UNP P9WNP5
B	-19	MET	-	expression tag	UNP P9WNP5
B	-18	GLY	-	expression tag	UNP P9WNP5
B	-17	SER	-	expression tag	UNP P9WNP5
B	-16	SER	-	expression tag	UNP P9WNP5
B	-15	HIS	-	expression tag	UNP P9WNP5
B	-14	HIS	-	expression tag	UNP P9WNP5
B	-13	HIS	-	expression tag	UNP P9WNP5
B	-12	HIS	-	expression tag	UNP P9WNP5
B	-11	HIS	-	expression tag	UNP P9WNP5
B	-10	HIS	-	expression tag	UNP P9WNP5
B	-9	SER	-	expression tag	UNP P9WNP5
B	-8	SER	-	expression tag	UNP P9WNP5
B	-7	GLY	-	expression tag	UNP P9WNP5
B	-6	LEU	-	expression tag	UNP P9WNP5
B	-5	VAL	-	expression tag	UNP P9WNP5
B	-4	PRO	-	expression tag	UNP P9WNP5
B	-3	ARG	-	expression tag	UNP P9WNP5
B	-2	GLY	-	expression tag	UNP P9WNP5
B	-1	SER	-	expression tag	UNP P9WNP5
B	0	HIS	-	expression tag	UNP P9WNP5
C	-19	MET	-	expression tag	UNP P9WNP5
C	-18	GLY	-	expression tag	UNP P9WNP5
C	-17	SER	-	expression tag	UNP P9WNP5
C	-16	SER	-	expression tag	UNP P9WNP5
C	-15	HIS	-	expression tag	UNP P9WNP5
C	-14	HIS	-	expression tag	UNP P9WNP5
C	-13	HIS	-	expression tag	UNP P9WNP5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-12	HIS	-	expression tag	UNP P9WNP5
C	-11	HIS	-	expression tag	UNP P9WNP5
C	-10	HIS	-	expression tag	UNP P9WNP5
C	-9	SER	-	expression tag	UNP P9WNP5
C	-8	SER	-	expression tag	UNP P9WNP5
C	-7	GLY	-	expression tag	UNP P9WNP5
C	-6	LEU	-	expression tag	UNP P9WNP5
C	-5	VAL	-	expression tag	UNP P9WNP5
C	-4	PRO	-	expression tag	UNP P9WNP5
C	-3	ARG	-	expression tag	UNP P9WNP5
C	-2	GLY	-	expression tag	UNP P9WNP5
C	-1	SER	-	expression tag	UNP P9WNP5
C	0	HIS	-	expression tag	UNP P9WNP5
D	-19	MET	-	expression tag	UNP P9WNP5
D	-18	GLY	-	expression tag	UNP P9WNP5
D	-17	SER	-	expression tag	UNP P9WNP5
D	-16	SER	-	expression tag	UNP P9WNP5
D	-15	HIS	-	expression tag	UNP P9WNP5
D	-14	HIS	-	expression tag	UNP P9WNP5
D	-13	HIS	-	expression tag	UNP P9WNP5
D	-12	HIS	-	expression tag	UNP P9WNP5
D	-11	HIS	-	expression tag	UNP P9WNP5
D	-10	HIS	-	expression tag	UNP P9WNP5
D	-9	SER	-	expression tag	UNP P9WNP5
D	-8	SER	-	expression tag	UNP P9WNP5
D	-7	GLY	-	expression tag	UNP P9WNP5
D	-6	LEU	-	expression tag	UNP P9WNP5
D	-5	VAL	-	expression tag	UNP P9WNP5
D	-4	PRO	-	expression tag	UNP P9WNP5
D	-3	ARG	-	expression tag	UNP P9WNP5
D	-2	GLY	-	expression tag	UNP P9WNP5
D	-1	SER	-	expression tag	UNP P9WNP5
D	0	HIS	-	expression tag	UNP P9WNP5
E	-19	MET	-	expression tag	UNP P9WNP5
E	-18	GLY	-	expression tag	UNP P9WNP5
E	-17	SER	-	expression tag	UNP P9WNP5
E	-16	SER	-	expression tag	UNP P9WNP5
E	-15	HIS	-	expression tag	UNP P9WNP5
E	-14	HIS	-	expression tag	UNP P9WNP5
E	-13	HIS	-	expression tag	UNP P9WNP5
E	-12	HIS	-	expression tag	UNP P9WNP5
E	-11	HIS	-	expression tag	UNP P9WNP5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-10	HIS	-	expression tag	UNP P9WNP5
E	-9	SER	-	expression tag	UNP P9WNP5
E	-8	SER	-	expression tag	UNP P9WNP5
E	-7	GLY	-	expression tag	UNP P9WNP5
E	-6	LEU	-	expression tag	UNP P9WNP5
E	-5	VAL	-	expression tag	UNP P9WNP5
E	-4	PRO	-	expression tag	UNP P9WNP5
E	-3	ARG	-	expression tag	UNP P9WNP5
E	-2	GLY	-	expression tag	UNP P9WNP5
E	-1	SER	-	expression tag	UNP P9WNP5
E	0	HIS	-	expression tag	UNP P9WNP5
F	-19	MET	-	expression tag	UNP P9WNP5
F	-18	GLY	-	expression tag	UNP P9WNP5
F	-17	SER	-	expression tag	UNP P9WNP5
F	-16	SER	-	expression tag	UNP P9WNP5
F	-15	HIS	-	expression tag	UNP P9WNP5
F	-14	HIS	-	expression tag	UNP P9WNP5
F	-13	HIS	-	expression tag	UNP P9WNP5
F	-12	HIS	-	expression tag	UNP P9WNP5
F	-11	HIS	-	expression tag	UNP P9WNP5
F	-10	HIS	-	expression tag	UNP P9WNP5
F	-9	SER	-	expression tag	UNP P9WNP5
F	-8	SER	-	expression tag	UNP P9WNP5
F	-7	GLY	-	expression tag	UNP P9WNP5
F	-6	LEU	-	expression tag	UNP P9WNP5
F	-5	VAL	-	expression tag	UNP P9WNP5
F	-4	PRO	-	expression tag	UNP P9WNP5
F	-3	ARG	-	expression tag	UNP P9WNP5
F	-2	GLY	-	expression tag	UNP P9WNP5
F	-1	SER	-	expression tag	UNP P9WNP5
F	0	HIS	-	expression tag	UNP P9WNP5
G	-19	MET	-	expression tag	UNP P9WNP5
G	-18	GLY	-	expression tag	UNP P9WNP5
G	-17	SER	-	expression tag	UNP P9WNP5
G	-16	SER	-	expression tag	UNP P9WNP5
G	-15	HIS	-	expression tag	UNP P9WNP5
G	-14	HIS	-	expression tag	UNP P9WNP5
G	-13	HIS	-	expression tag	UNP P9WNP5
G	-12	HIS	-	expression tag	UNP P9WNP5
G	-11	HIS	-	expression tag	UNP P9WNP5
G	-10	HIS	-	expression tag	UNP P9WNP5
G	-9	SER	-	expression tag	UNP P9WNP5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-8	SER	-	expression tag	UNP P9WNP5
G	-7	GLY	-	expression tag	UNP P9WNP5
G	-6	LEU	-	expression tag	UNP P9WNP5
G	-5	VAL	-	expression tag	UNP P9WNP5
G	-4	PRO	-	expression tag	UNP P9WNP5
G	-3	ARG	-	expression tag	UNP P9WNP5
G	-2	GLY	-	expression tag	UNP P9WNP5
G	-1	SER	-	expression tag	UNP P9WNP5
G	0	HIS	-	expression tag	UNP P9WNP5
H	-19	MET	-	expression tag	UNP P9WNP5
H	-18	GLY	-	expression tag	UNP P9WNP5
H	-17	SER	-	expression tag	UNP P9WNP5
H	-16	SER	-	expression tag	UNP P9WNP5
H	-15	HIS	-	expression tag	UNP P9WNP5
H	-14	HIS	-	expression tag	UNP P9WNP5
H	-13	HIS	-	expression tag	UNP P9WNP5
H	-12	HIS	-	expression tag	UNP P9WNP5
H	-11	HIS	-	expression tag	UNP P9WNP5
H	-10	HIS	-	expression tag	UNP P9WNP5
H	-9	SER	-	expression tag	UNP P9WNP5
H	-8	SER	-	expression tag	UNP P9WNP5
H	-7	GLY	-	expression tag	UNP P9WNP5
H	-6	LEU	-	expression tag	UNP P9WNP5
H	-5	VAL	-	expression tag	UNP P9WNP5
H	-4	PRO	-	expression tag	UNP P9WNP5
H	-3	ARG	-	expression tag	UNP P9WNP5
H	-2	GLY	-	expression tag	UNP P9WNP5
H	-1	SER	-	expression tag	UNP P9WNP5
H	0	HIS	-	expression tag	UNP P9WNP5
I	-19	MET	-	expression tag	UNP P9WNP5
I	-18	GLY	-	expression tag	UNP P9WNP5
I	-17	SER	-	expression tag	UNP P9WNP5
I	-16	SER	-	expression tag	UNP P9WNP5
I	-15	HIS	-	expression tag	UNP P9WNP5
I	-14	HIS	-	expression tag	UNP P9WNP5
I	-13	HIS	-	expression tag	UNP P9WNP5
I	-12	HIS	-	expression tag	UNP P9WNP5
I	-11	HIS	-	expression tag	UNP P9WNP5
I	-10	HIS	-	expression tag	UNP P9WNP5
I	-9	SER	-	expression tag	UNP P9WNP5
I	-8	SER	-	expression tag	UNP P9WNP5
I	-7	GLY	-	expression tag	UNP P9WNP5

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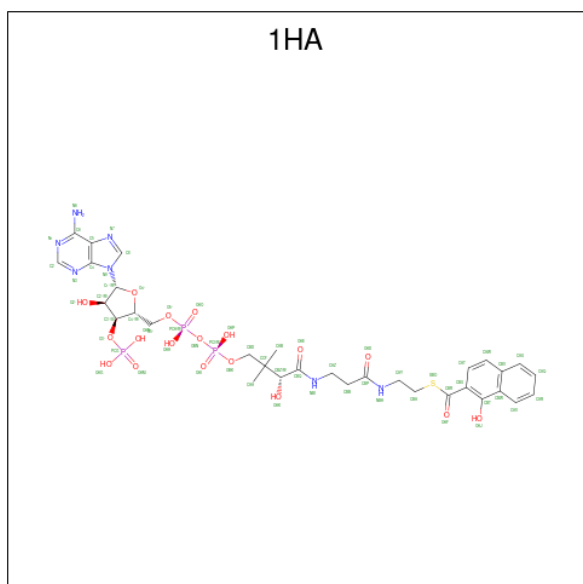
Chain	Residue	Modelled	Actual	Comment	Reference
I	-6	LEU	-	expression tag	UNP P9WNP5
I	-5	VAL	-	expression tag	UNP P9WNP5
I	-4	PRO	-	expression tag	UNP P9WNP5
I	-3	ARG	-	expression tag	UNP P9WNP5
I	-2	GLY	-	expression tag	UNP P9WNP5
I	-1	SER	-	expression tag	UNP P9WNP5
I	0	HIS	-	expression tag	UNP P9WNP5
J	-19	MET	-	expression tag	UNP P9WNP5
J	-18	GLY	-	expression tag	UNP P9WNP5
J	-17	SER	-	expression tag	UNP P9WNP5
J	-16	SER	-	expression tag	UNP P9WNP5
J	-15	HIS	-	expression tag	UNP P9WNP5
J	-14	HIS	-	expression tag	UNP P9WNP5
J	-13	HIS	-	expression tag	UNP P9WNP5
J	-12	HIS	-	expression tag	UNP P9WNP5
J	-11	HIS	-	expression tag	UNP P9WNP5
J	-10	HIS	-	expression tag	UNP P9WNP5
J	-9	SER	-	expression tag	UNP P9WNP5
J	-8	SER	-	expression tag	UNP P9WNP5
J	-7	GLY	-	expression tag	UNP P9WNP5
J	-6	LEU	-	expression tag	UNP P9WNP5
J	-5	VAL	-	expression tag	UNP P9WNP5
J	-4	PRO	-	expression tag	UNP P9WNP5
J	-3	ARG	-	expression tag	UNP P9WNP5
J	-2	GLY	-	expression tag	UNP P9WNP5
J	-1	SER	-	expression tag	UNP P9WNP5
J	0	HIS	-	expression tag	UNP P9WNP5
K	-19	MET	-	expression tag	UNP P9WNP5
K	-18	GLY	-	expression tag	UNP P9WNP5
K	-17	SER	-	expression tag	UNP P9WNP5
K	-16	SER	-	expression tag	UNP P9WNP5
K	-15	HIS	-	expression tag	UNP P9WNP5
K	-14	HIS	-	expression tag	UNP P9WNP5
K	-13	HIS	-	expression tag	UNP P9WNP5
K	-12	HIS	-	expression tag	UNP P9WNP5
K	-11	HIS	-	expression tag	UNP P9WNP5
K	-10	HIS	-	expression tag	UNP P9WNP5
K	-9	SER	-	expression tag	UNP P9WNP5
K	-8	SER	-	expression tag	UNP P9WNP5
K	-7	GLY	-	expression tag	UNP P9WNP5
K	-6	LEU	-	expression tag	UNP P9WNP5
K	-5	VAL	-	expression tag	UNP P9WNP5

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-4	PRO	-	expression tag	UNP P9WNP5
K	-3	ARG	-	expression tag	UNP P9WNP5
K	-2	GLY	-	expression tag	UNP P9WNP5
K	-1	SER	-	expression tag	UNP P9WNP5
K	0	HIS	-	expression tag	UNP P9WNP5
L	-19	MET	-	expression tag	UNP P9WNP5
L	-18	GLY	-	expression tag	UNP P9WNP5
L	-17	SER	-	expression tag	UNP P9WNP5
L	-16	SER	-	expression tag	UNP P9WNP5
L	-15	HIS	-	expression tag	UNP P9WNP5
L	-14	HIS	-	expression tag	UNP P9WNP5
L	-13	HIS	-	expression tag	UNP P9WNP5
L	-12	HIS	-	expression tag	UNP P9WNP5
L	-11	HIS	-	expression tag	UNP P9WNP5
L	-10	HIS	-	expression tag	UNP P9WNP5
L	-9	SER	-	expression tag	UNP P9WNP5
L	-8	SER	-	expression tag	UNP P9WNP5
L	-7	GLY	-	expression tag	UNP P9WNP5
L	-6	LEU	-	expression tag	UNP P9WNP5
L	-5	VAL	-	expression tag	UNP P9WNP5
L	-4	PRO	-	expression tag	UNP P9WNP5
L	-3	ARG	-	expression tag	UNP P9WNP5
L	-2	GLY	-	expression tag	UNP P9WNP5
L	-1	SER	-	expression tag	UNP P9WNP5
L	0	HIS	-	expression tag	UNP P9WNP5

- Molecule 2 is 1-hydroxy-2-naphthoyl-CoA (three-letter code: 1HA) (formula: $C_{32}H_{42}N_7O_{18}P_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	B	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	C	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	D	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	E	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	F	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	G	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	H	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	I	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	J	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	K	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0
2	L	1	Total 61	C 32	N 7	O 18	P 3	S 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	194	Total 194	O 194	0	0
3	B	214	Total 214	O 214	0	0
3	C	219	Total 219	O 219	0	0
3	D	188	Total 188	O 188	0	0
3	E	187	Total 187	O 187	0	0
3	F	187	Total 187	O 187	0	0
3	G	191	Total 191	O 191	0	0
3	H	202	Total 202	O 202	0	0

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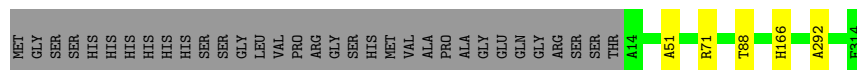
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	I	210	Total 210	O 210	0	0
3	J	227	Total 227	O 227	0	0
3	K	232	Total 232	O 232	0	0
3	L	260	Total 260	O 260	0	0

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.

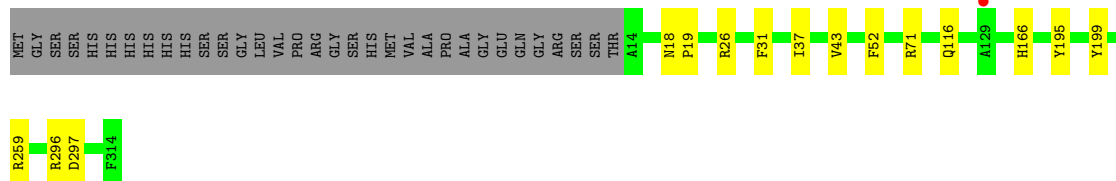
- Molecule 1: 1,4-Dihydroxy-2-naphthoyl-CoA synthase

Chain A: 




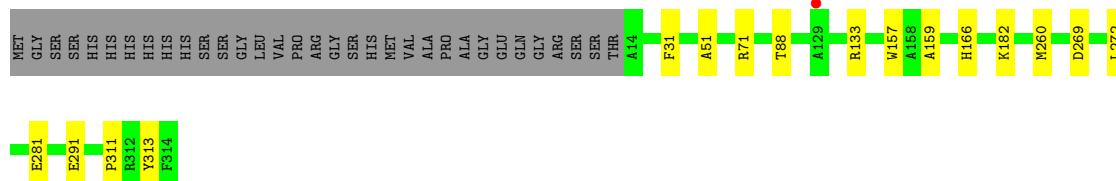
- Molecule 1: 1,4-Dihydroxy-2-naphthoyl-CoA synthase

Chain B: 



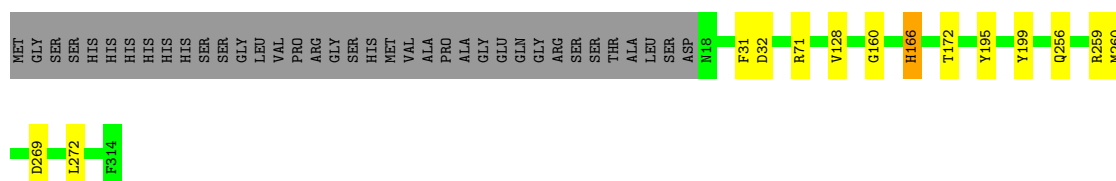
- Molecule 1: 1,4-Dihydroxy-2-naphthoyl-CoA synthase

Chain C: 



- Molecule 1: 1,4-Dihydroxy-2-naphthoyl-CoA synthase

Chain D: 



- | | |
|------|-----|
| H166 | Met |
| | Gly |
| R259 | Ser |
| F314 | Ser |
| | His |
| | His |
| | His |
| | His |
| | Ser |
| | Ser |
| | Gly |
| | Leu |
| | Val |
| | Pro |
| | Arg |
| | Gly |
| | Ser |
| | His |
| | Met |
| | Val |
| | Ala |
| | Pro |
| | Ala |
| | Gly |
| | Glu |
| | Gln |
| | Gly |
| | Arg |
| | Ser |
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| | Thr |
| | Ala |
| | Leu |
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| | Leu |
| | Asp |
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| | Asp |
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| | Glu |
| | Gln |
| | Gly |
| | Arg |
| | Ser |
| | Ser |
| | Thr |
| | Ala |
| | Leu |
| | Ser |
| | Leu |
| | Asp |
| | Met |
| | Asp |
| | Val |
| | Pro |
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| | Val |
| | Pro |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|
| MET | GLY | SER | HIS | HIS | HIS | HIS | HIS | HIS | SER | SER | GLY | LEU | VAL | PRO | ARG | GLY | SER | HIS | MET | VAL | ALA | PRO | ALA | GLY | GLU | GLN | GLY | ARG | SER | SER | THR | THR | Al4 | Tl22 | Al23 | Dl24 | Wl57 | HL66 | Tl72 | R202 | R259 | M260 | D269 | E281 | M288 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.50Å 148.31Å 141.00Å 90.00° 103.47° 90.00°	Depositor
Resolution (Å)	46.58 – 2.20 46.58 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.9 (46.58-2.20) 93.7 (46.58-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.25 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.127 , 0.184 0.129 , 0.184	Depositor DCC
R_{free} test set	8824 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.178	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	31323	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 1HA

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	0.41	0/2407	0.52	0/3264
1	B	0.42	0/2406	0.52	0/3262
1	C	0.40	0/2406	0.52	0/3262
1	D	0.36	0/2380	0.52	0/3227
1	E	0.38	0/2391	0.52	0/3241
1	F	0.38	0/2390	0.52	0/3240
1	G	0.39	0/2389	0.53	0/3239
1	H	0.40	0/2388	0.53	0/3238
1	I	0.40	0/2395	0.53	0/3246
1	J	0.41	0/2408	0.52	0/3265
1	K	0.41	0/2403	0.53	0/3259
1	L	0.42	0/2404	0.54	0/3261
All	All	0.40	0/28767	0.53	0/39004

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [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	2350	0	2247	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2349	0	2249	8	0
1	C	2349	0	2249	11	0
1	D	2323	0	2222	10	0
1	E	2334	0	2235	9	0
1	F	2333	0	2230	8	0
1	G	2329	0	2228	6	0
1	H	2331	0	2226	9	0
1	I	2338	0	2239	9	0
1	J	2351	0	2249	6	0
1	K	2346	0	2240	8	0
1	L	2347	0	2238	9	0
2	A	61	0	38	0	0
2	B	61	0	38	0	0
2	C	61	0	37	1	0
2	D	61	0	38	1	0
2	E	61	0	37	4	0
2	F	61	0	37	0	0
2	G	61	0	38	1	0
2	H	61	0	38	0	0
2	I	61	0	38	0	0
2	J	61	0	37	0	0
2	K	61	0	38	0	0
2	L	61	0	37	2	0
3	A	194	0	0	1	0
3	B	214	0	0	2	0
3	C	219	0	0	1	0
3	D	188	0	0	2	0
3	E	187	0	0	3	0
3	F	187	0	0	0	0
3	G	191	0	0	1	0
3	H	202	0	0	0	0
3	I	210	0	0	3	0
3	J	227	0	0	2	0
3	K	232	0	0	1	0
3	L	260	0	0	1	0
All	All	31323	0	27303	92	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 92 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:L:122:THR:OG1	1:L:124:ASP:OD1	2.00	0.77
3:G:676:HOH:O	1:L:288:MET:SD	2.50	0.70
1:E:184:THR:OG1	3:E:568:HOH:O	2.04	0.69
2:E:401:1HA:H8	3:E:568:HOH:O	1.91	0.69
1:B:259:ARG:NH2	3:B:698:HOH:O	2.27	0.67

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	299/334 (90%)	292 (98%)	7 (2%)	0	100	100
1	B	299/334 (90%)	290 (97%)	9 (3%)	0	100	100
1	C	299/334 (90%)	291 (97%)	8 (3%)	0	100	100
1	D	295/334 (88%)	287 (97%)	8 (3%)	0	100	100
1	E	296/334 (89%)	288 (97%)	8 (3%)	0	100	100
1	F	296/334 (89%)	288 (97%)	8 (3%)	0	100	100
1	G	296/334 (89%)	288 (97%)	8 (3%)	0	100	100
1	H	296/334 (89%)	288 (97%)	8 (3%)	0	100	100
1	I	296/334 (89%)	288 (97%)	8 (3%)	0	100	100
1	J	299/334 (90%)	292 (98%)	7 (2%)	0	100	100
1	K	299/334 (90%)	291 (97%)	8 (3%)	0	100	100
1	L	299/334 (90%)	291 (97%)	8 (3%)	0	100	100
All	All	3569/4008 (89%)	3474 (97%)	95 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	236/264 (89%)	235 (100%)	1 (0%)	91	96
1	B	235/264 (89%)	234 (100%)	1 (0%)	91	96
1	C	235/264 (89%)	234 (100%)	1 (0%)	91	96
1	D	233/264 (88%)	232 (100%)	1 (0%)	91	96
1	E	234/264 (89%)	233 (100%)	1 (0%)	91	96
1	F	234/264 (89%)	233 (100%)	1 (0%)	91	96
1	G	234/264 (89%)	232 (99%)	2 (1%)	78	88
1	H	234/264 (89%)	232 (99%)	2 (1%)	78	88
1	I	235/264 (89%)	234 (100%)	1 (0%)	91	96
1	J	236/264 (89%)	235 (100%)	1 (0%)	91	96
1	K	235/264 (89%)	234 (100%)	1 (0%)	91	96
1	L	235/264 (89%)	234 (100%)	1 (0%)	91	96
All	All	2816/3168 (89%)	2802 (100%)	14 (0%)	88	94

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	166	HIS
1	H	32	ASP
1	L	166	HIS
1	J	166	HIS
1	K	166	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	166	HIS
1	J	166	HIS
1	L	166	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

12 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	$\# Z > 2$
2	1HA	J	401	-	57,65,65	3.24	16 (28%)	74,97,97	1.73	11 (14%)
2	1HA	C	401	-	57,65,65	3.17	17 (29%)	74,97,97	1.89	11 (14%)
2	1HA	A	401	-	57,65,65	3.22	17 (29%)	74,97,97	1.89	12 (16%)
2	1HA	E	401	-	57,65,65	3.25	17 (29%)	74,97,97	2.03	13 (17%)
2	1HA	I	401	-	57,65,65	3.22	18 (31%)	74,97,97	1.83	11 (14%)
2	1HA	L	401	-	57,65,65	3.31	21 (36%)	74,97,97	1.87	14 (18%)
2	1HA	H	401	-	57,65,65	3.27	20 (35%)	74,97,97	1.99	13 (17%)
2	1HA	K	401	-	57,65,65	3.21	16 (28%)	74,97,97	1.84	13 (17%)
2	1HA	F	401	-	57,65,65	3.22	18 (31%)	74,97,97	1.80	11 (14%)
2	1HA	G	401	-	57,65,65	3.25	19 (33%)	74,97,97	1.91	14 (18%)
2	1HA	D	401	-	57,65,65	3.24	18 (31%)	74,97,97	1.86	12 (16%)
2	1HA	B	401	-	57,65,65	3.25	17 (29%)	74,97,97	1.90	13 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	1HA	J	401	-	-	14/51/71/71	0/5/5/5
2	1HA	C	401	-	-	13/51/71/71	0/5/5/5
2	1HA	A	401	-	-	14/51/71/71	0/5/5/5
2	1HA	E	401	-	-	11/51/71/71	0/5/5/5
2	1HA	I	401	-	-	7/51/71/71	0/5/5/5
2	1HA	L	401	-	-	15/51/71/71	0/5/5/5
2	1HA	H	401	-	-	8/51/71/71	0/5/5/5
2	1HA	K	401	-	-	13/51/71/71	0/5/5/5
2	1HA	F	401	-	-	10/51/71/71	0/5/5/5
2	1HA	G	401	-	-	10/51/71/71	0/5/5/5
2	1HA	D	401	-	-	9/51/71/71	0/5/5/5
2	1HA	B	401	-	-	8/51/71/71	0/5/5/5

The worst 5 of 214 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	401	1HA	C2'-C1'	-13.36	1.33	1.53
2	E	401	1HA	C2'-C1'	-13.36	1.33	1.53
2	D	401	1HA	O4'-C1'	13.28	1.59	1.41
2	L	401	1HA	C2'-C1'	-13.26	1.33	1.53
2	K	401	1HA	C2'-C1'	-13.22	1.33	1.53

The worst 5 of 148 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	401	1HA	CBA-SBO-CBR	10.07	112.45	99.80
2	H	401	1HA	CBA-SBO-CBR	9.37	111.57	99.80
2	G	401	1HA	CBA-SBO-CBR	8.63	110.65	99.80
2	B	401	1HA	CBA-SBO-CBR	7.70	109.48	99.80
2	I	401	1HA	CBA-SBO-CBR	7.65	109.41	99.80

There are no chirality outliers.

5 of 132 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	1HA	OAF-CBR-SBO-CBA
2	A	401	1HA	OBK-CBD-CCF-CBZ

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Mol	Chain	Res	Type	Atoms
2	A	401	1HA	CBD-OBK-PCI-OAP
2	B	401	1HA	OAF-CBR-SBO-CBA
2	B	401	1HA	PCH-OBN-PCI-OBK

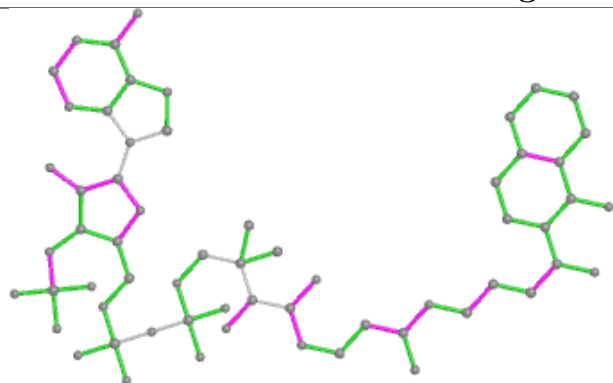
There are no ring outliers.

5 monomers are involved in 9 short contacts:

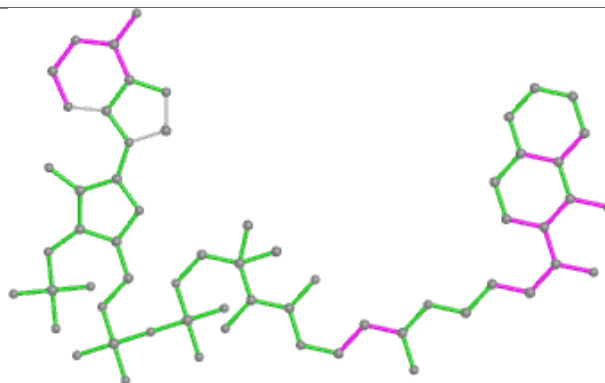
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	1HA	1	0
2	E	401	1HA	4	0
2	L	401	1HA	2	0
2	G	401	1HA	1	0
2	D	401	1HA	1	0

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

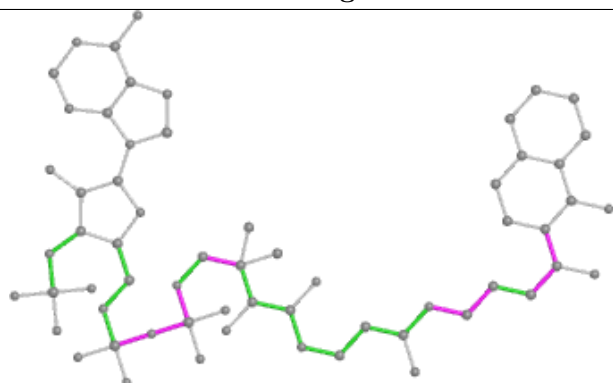
Ligand 1HA J 401



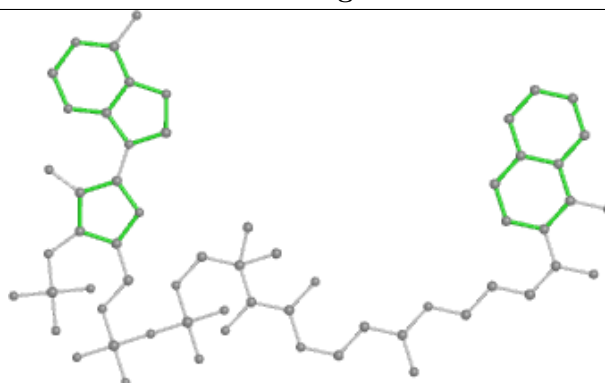
Bond lengths



Bond angles

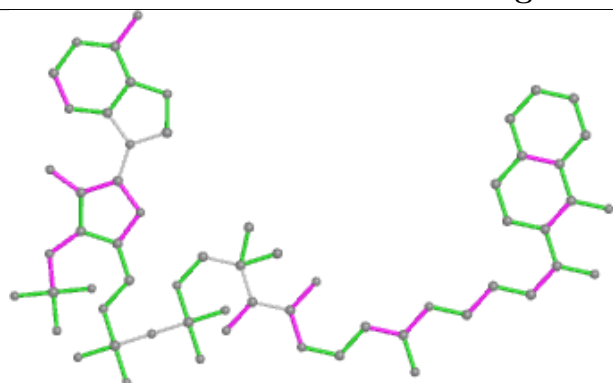


Torsions

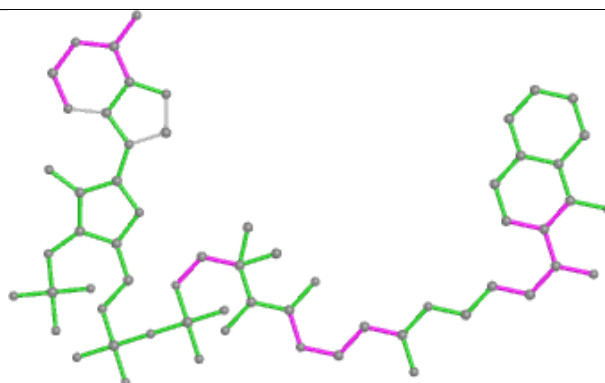


Rings

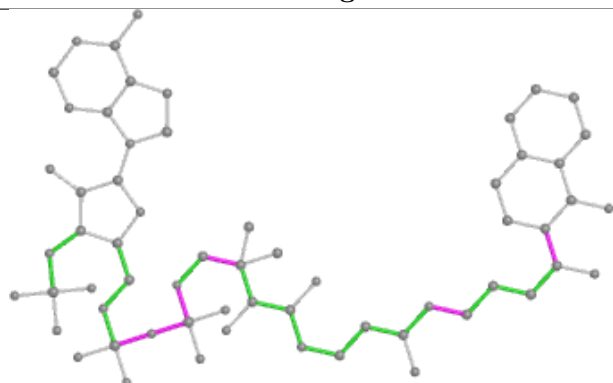
Ligand 1HA C 401



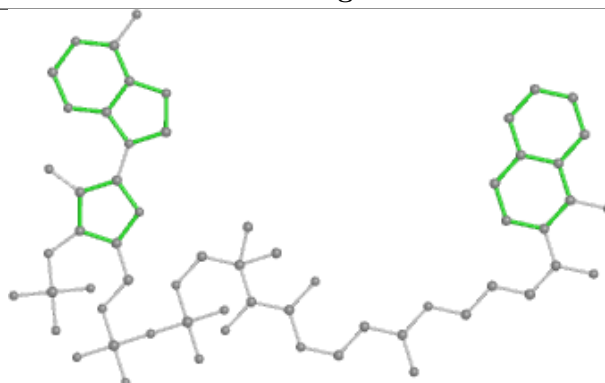
Bond lengths



Bond angles

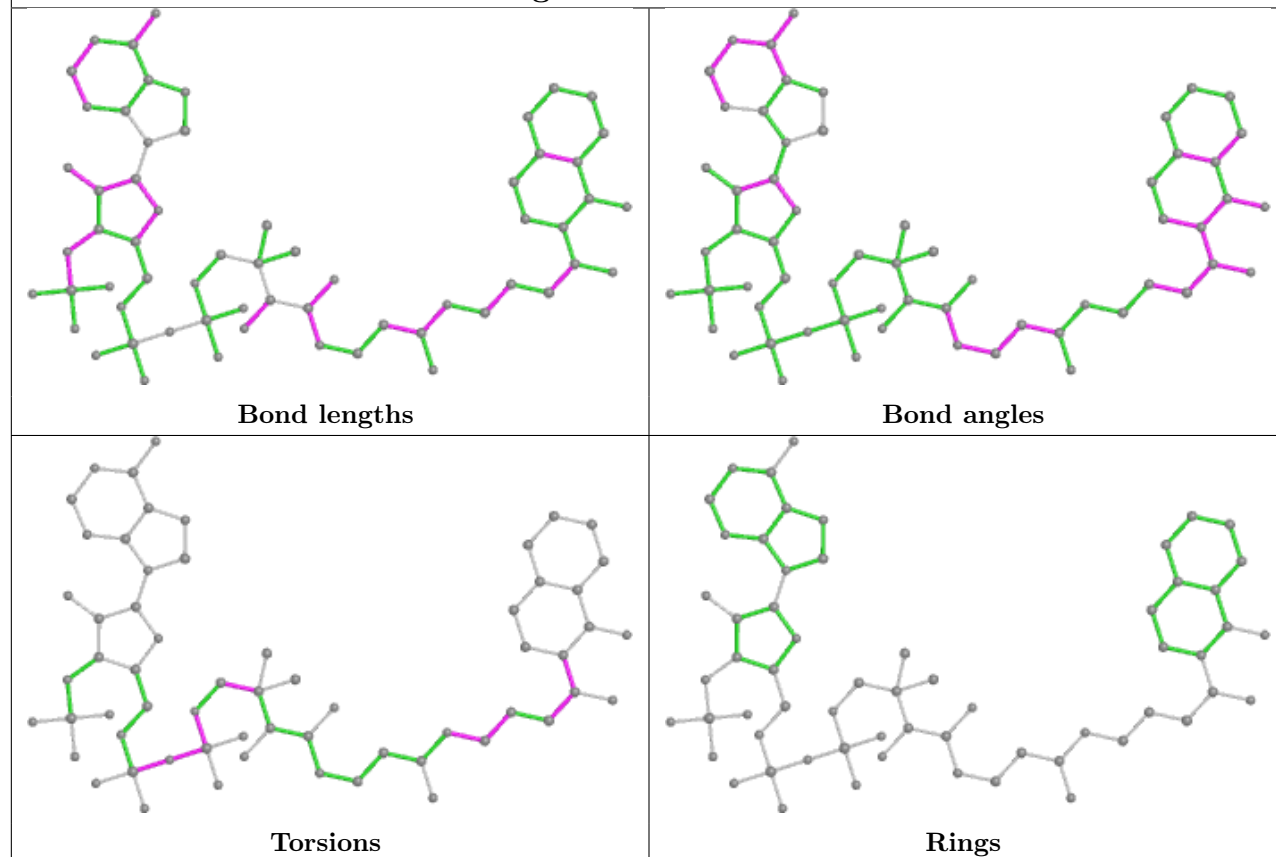


Torsions

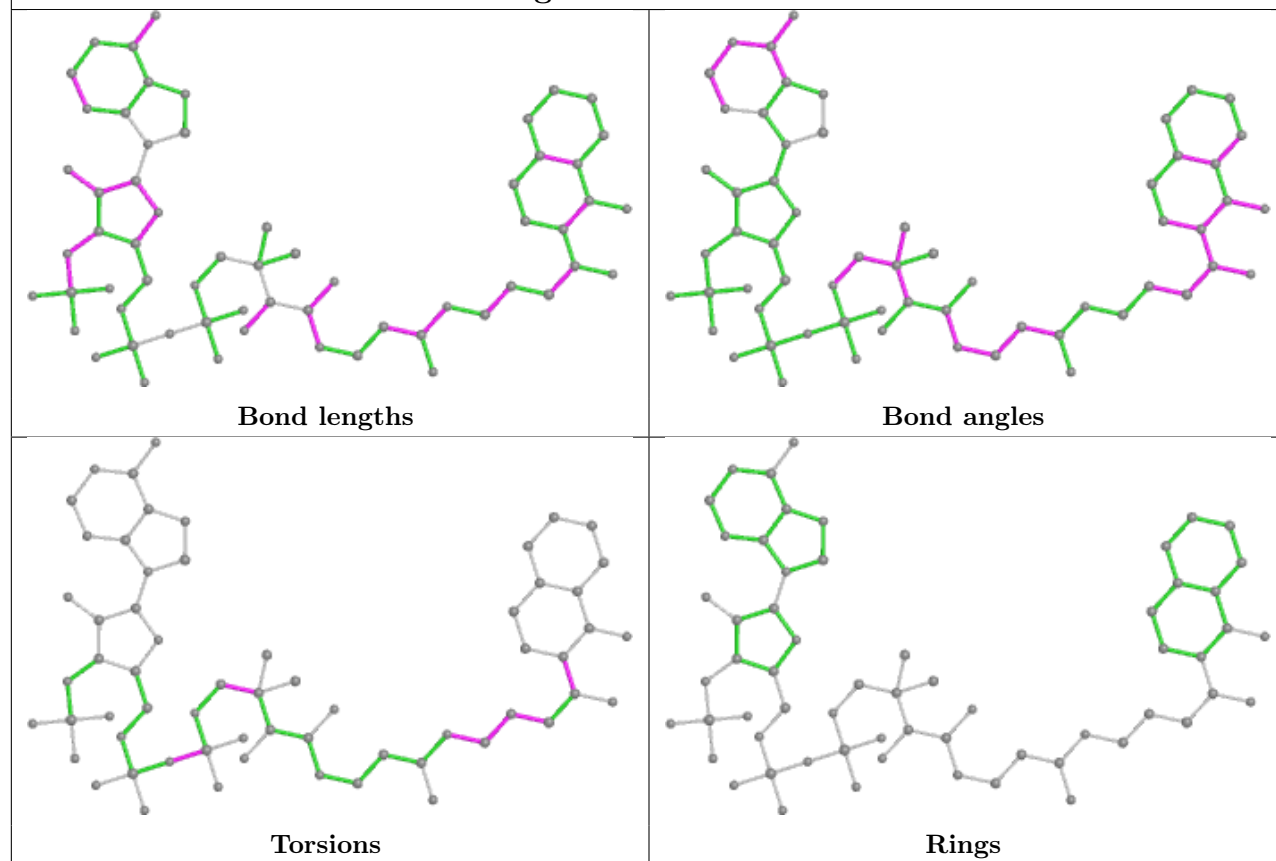


Rings

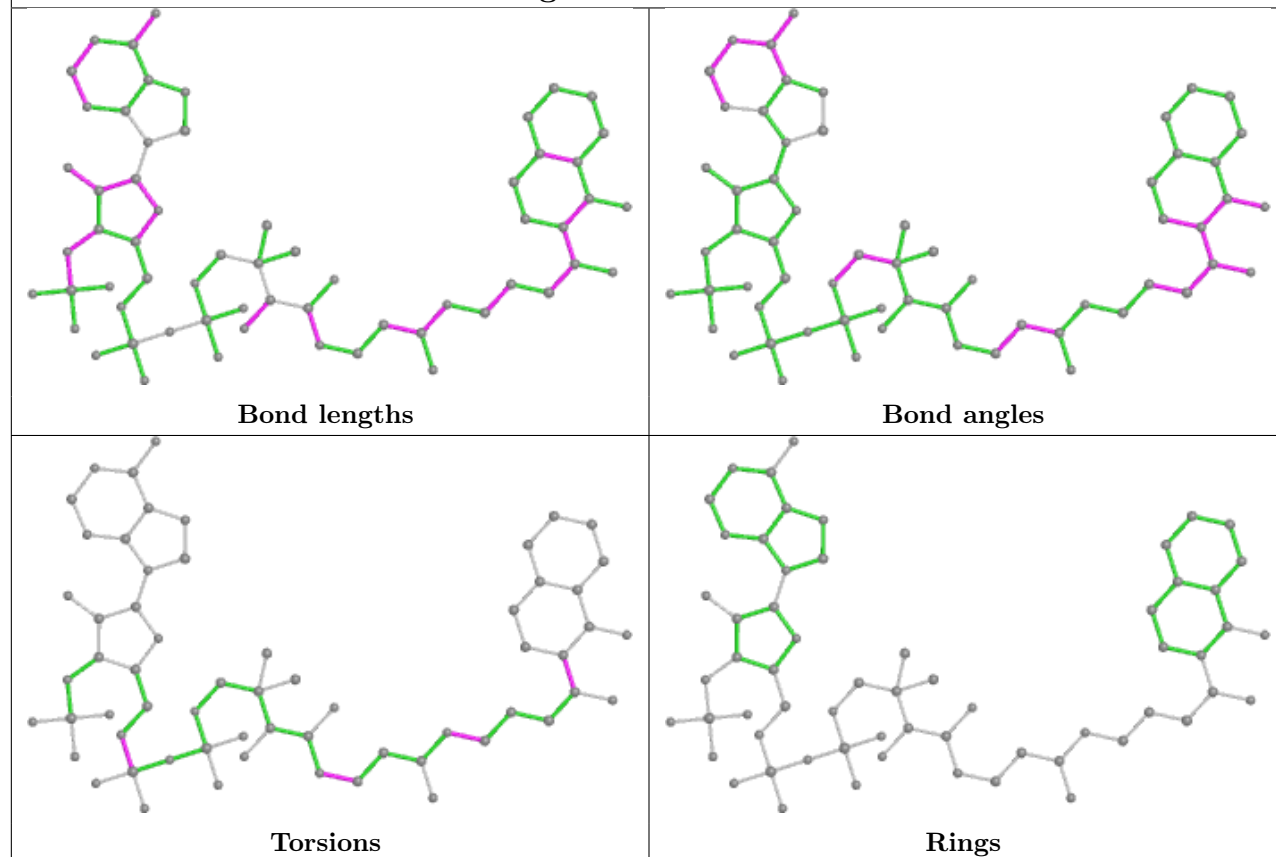
Ligand 1HA A 401



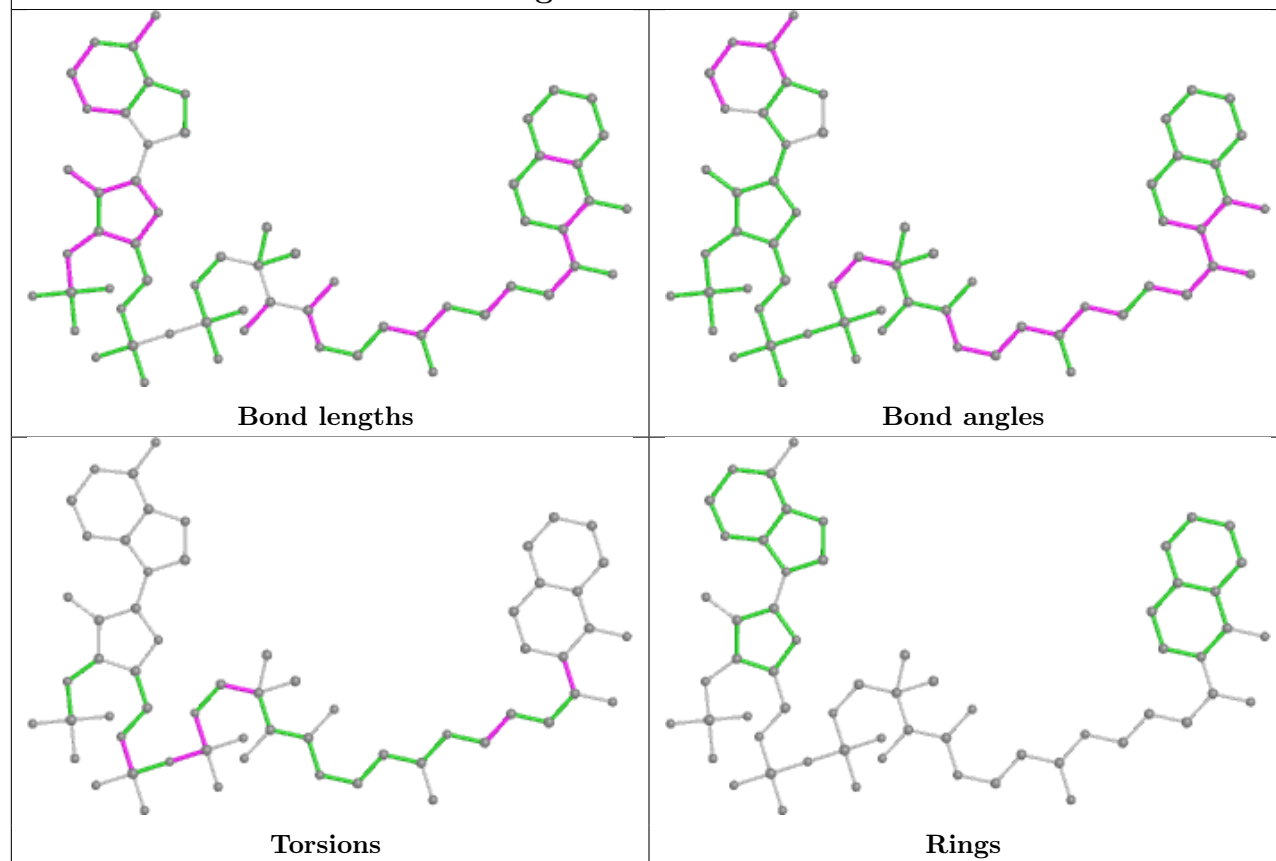
Ligand 1HA E 401



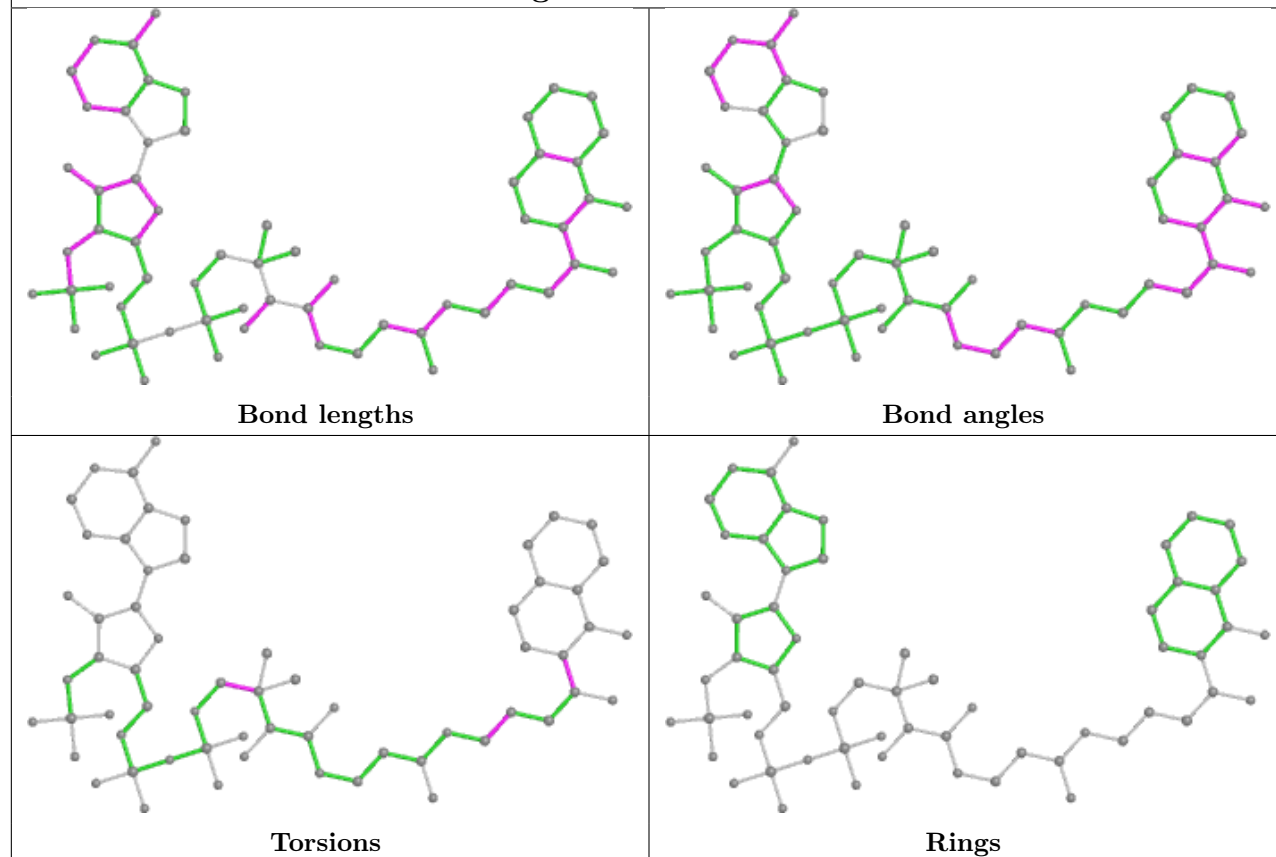
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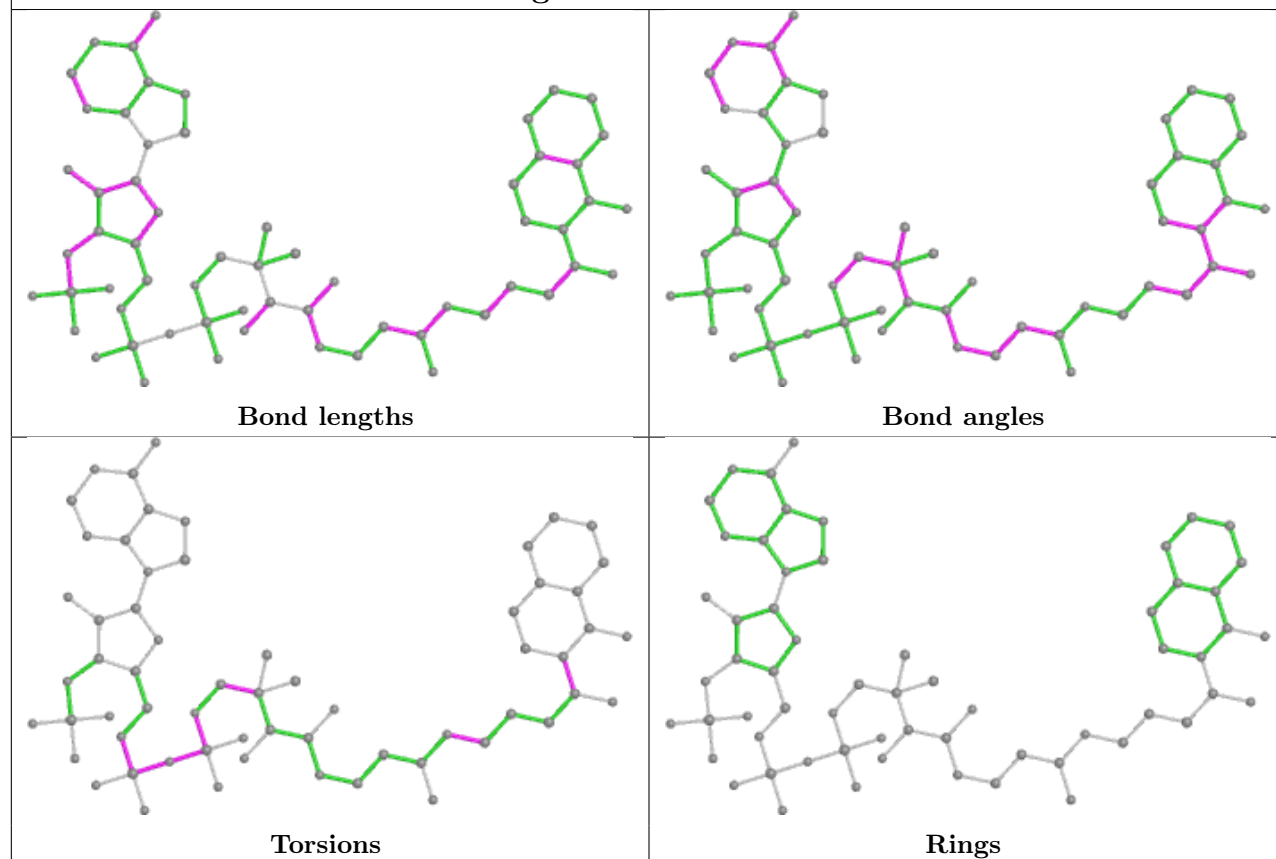
Ligand 1HA L 401



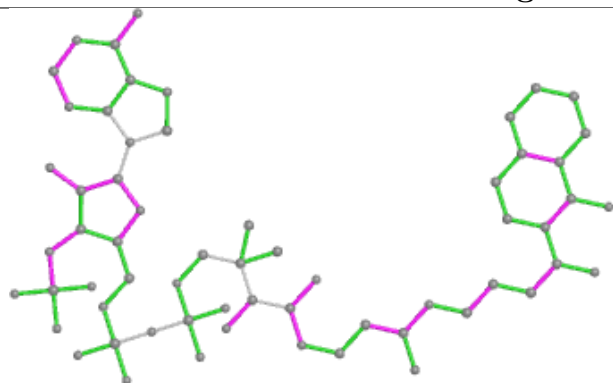
Ligand 1HA H 401



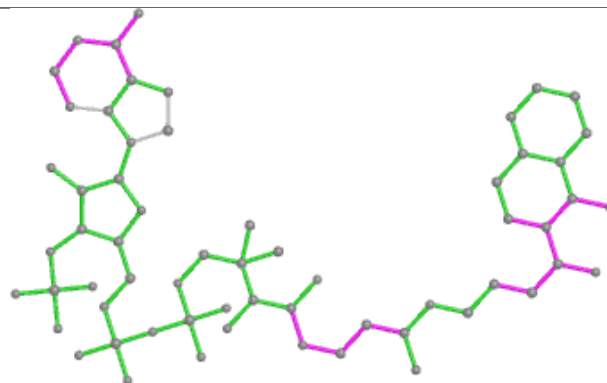
Ligand 1HA K 401



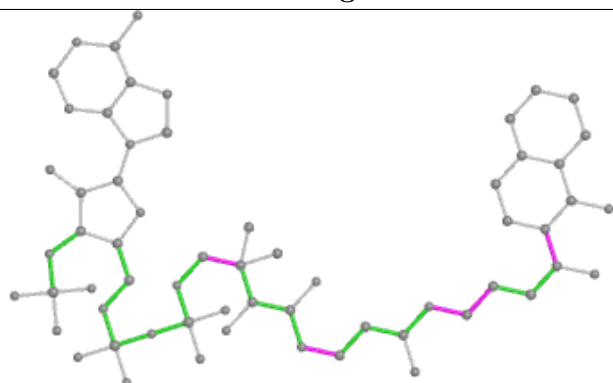
Ligand 1HA F 401



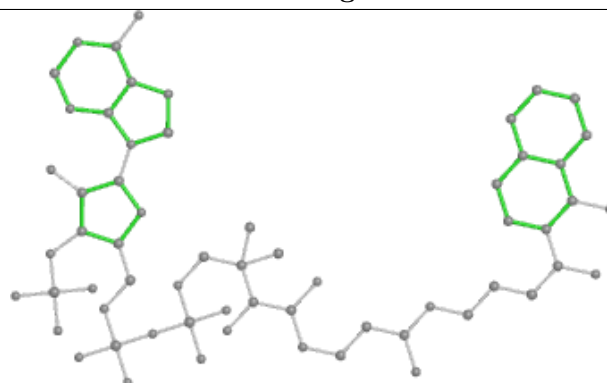
Bond lengths



Bond angles

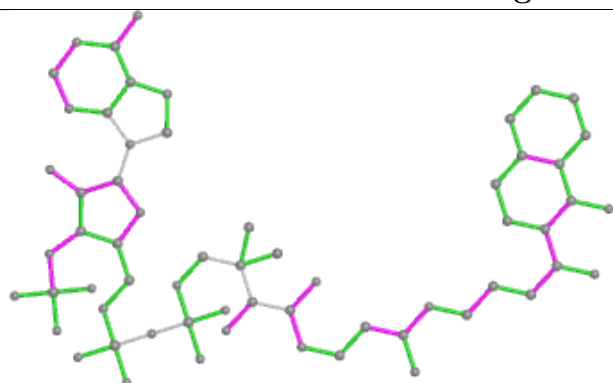


Torsions

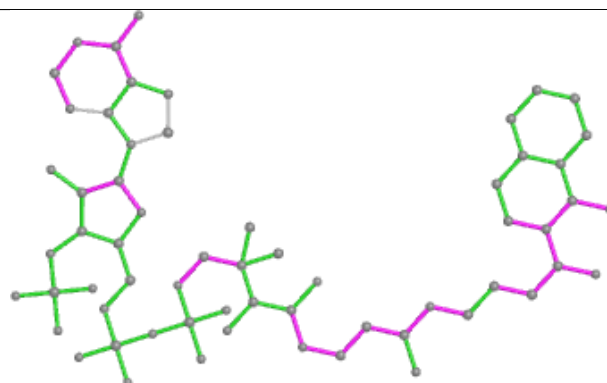


Rings

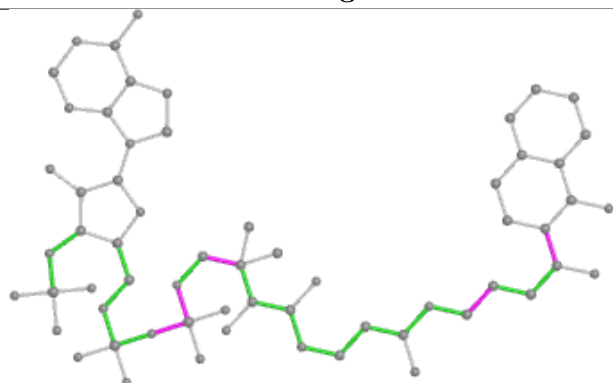
Ligand 1HA G 401



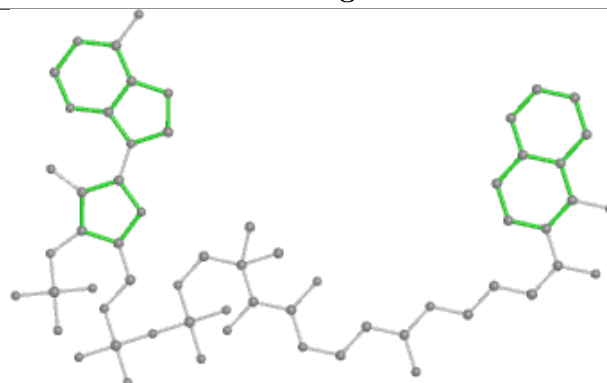
Bond lengths



Bond angles

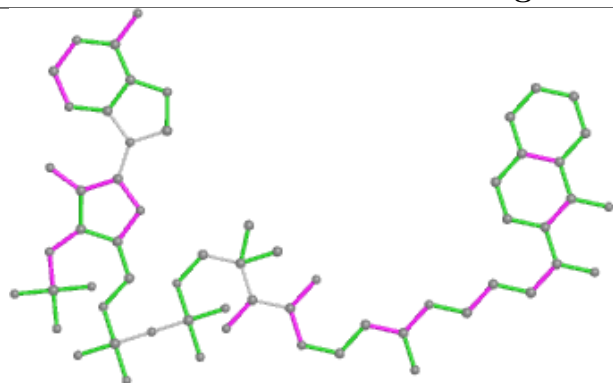


Torsions

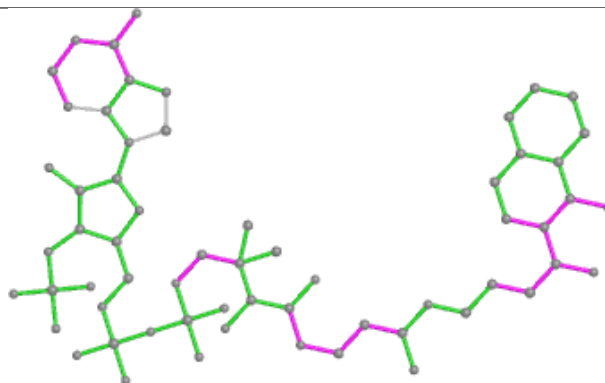


Rings

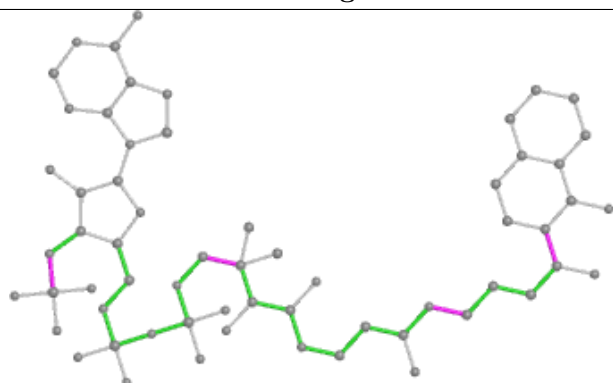
Ligand 1HA D 401



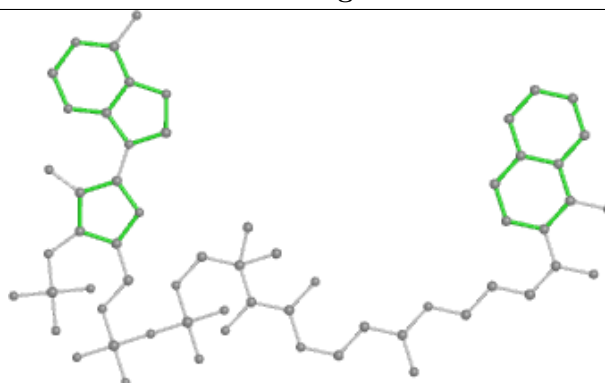
Bond lengths



Bond angles

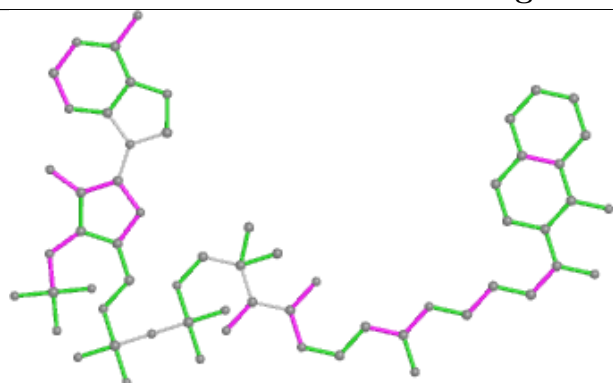


Torsions

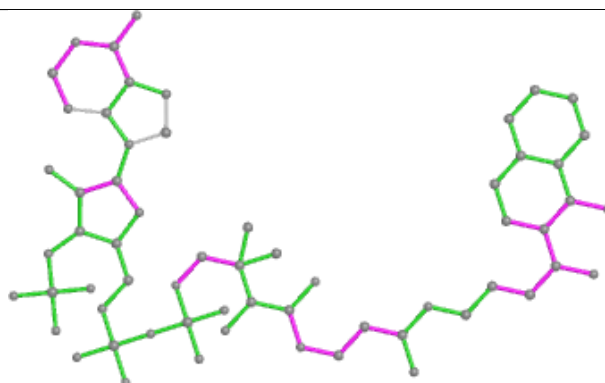


Rings

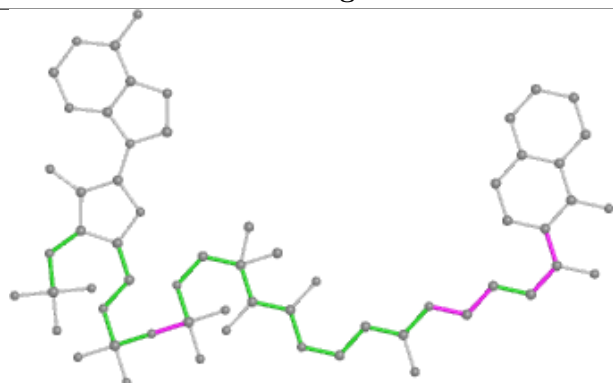
Ligand 1HA B 401



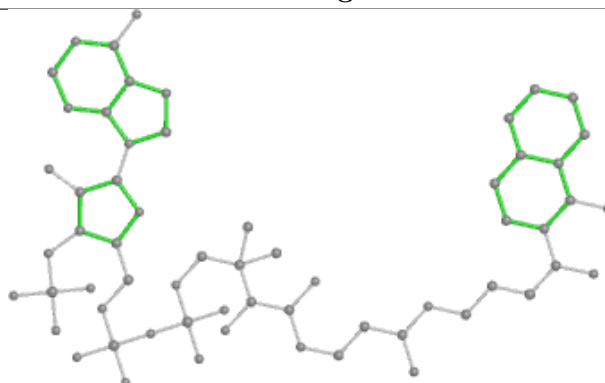
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	301/334 (90%)	-0.71	0 100 100	7, 16, 31, 48	0
1	B	301/334 (90%)	-0.72	1 (0%) 94 93	7, 16, 29, 52	0
1	C	301/334 (90%)	-0.74	1 (0%) 94 93	9, 16, 30, 49	0
1	D	297/334 (88%)	-0.62	0 100 100	11, 20, 37, 62	0
1	E	298/334 (89%)	-0.70	0 100 100	11, 18, 34, 56	0
1	F	298/334 (89%)	-0.79	0 100 100	10, 18, 32, 49	0
1	G	297/334 (88%)	-0.76	0 100 100	10, 18, 32, 55	0
1	H	298/334 (89%)	-0.76	0 100 100	7, 17, 30, 56	0
1	I	298/334 (89%)	-0.82	0 100 100	9, 16, 29, 55	0
1	J	301/334 (90%)	-0.81	1 (0%) 94 93	8, 15, 33, 50	0
1	K	301/334 (90%)	-0.83	0 100 100	8, 16, 33, 52	0
1	L	301/334 (90%)	-0.73	0 100 100	7, 15, 31, 59	0
All	All	3592/4008 (89%)	-0.75	3 (0%) 95 95	7, 17, 32, 62	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	129	ALA	2.2
1	C	129	ALA	2.1
1	J	268	LEU	2.1

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](#)

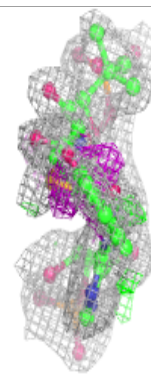
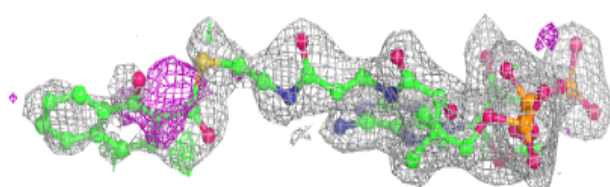
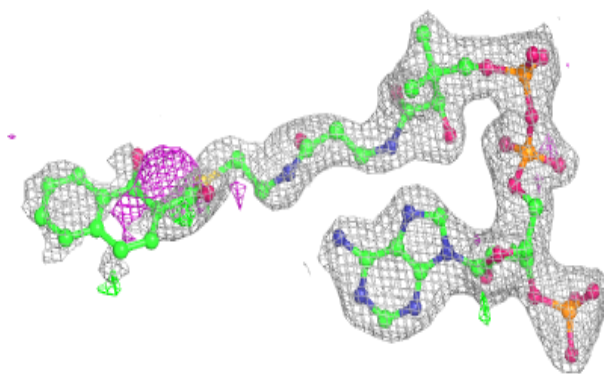
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	1HA	D	401	61/61	0.96	0.12	18,29,67,77	0
2	1HA	E	401	61/61	0.96	0.12	11,24,69,95	0
2	1HA	G	401	61/61	0.96	0.13	15,28,63,71	0
2	1HA	J	401	61/61	0.96	0.11	15,23,61,78	0
2	1HA	L	401	61/61	0.96	0.12	12,28,67,73	0
2	1HA	F	401	61/61	0.97	0.11	13,24,73,90	0
2	1HA	C	401	61/61	0.97	0.10	11,23,66,89	0
2	1HA	H	401	61/61	0.97	0.11	9,20,58,77	0
2	1HA	I	401	61/61	0.97	0.12	10,22,61,80	0
2	1HA	A	401	61/61	0.97	0.11	9,22,67,88	0
2	1HA	K	401	61/61	0.97	0.10	9,22,72,101	0
2	1HA	B	401	61/61	0.97	0.10	8,20,64,97	0

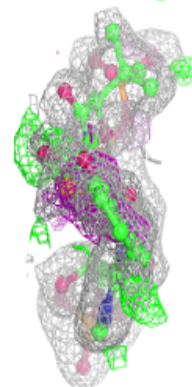
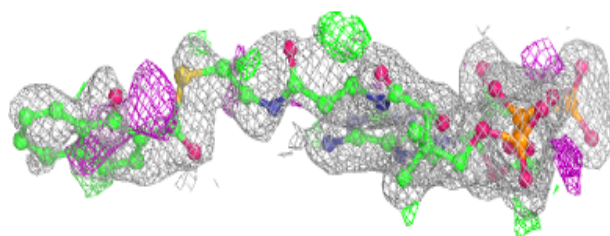
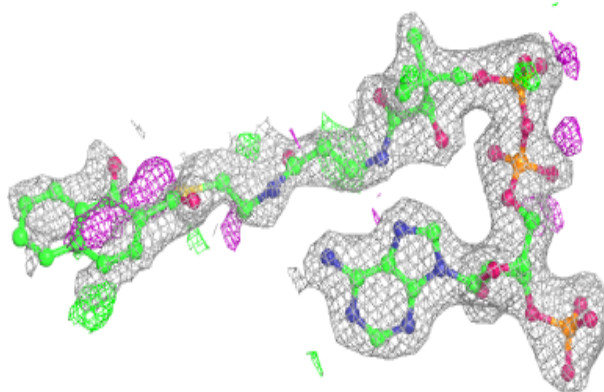
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 1HA D 401:

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

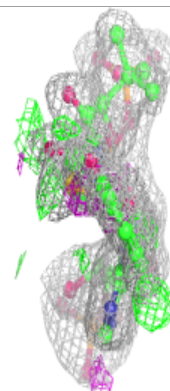
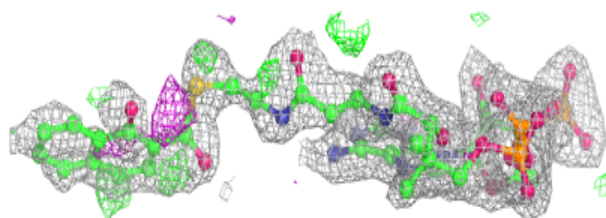
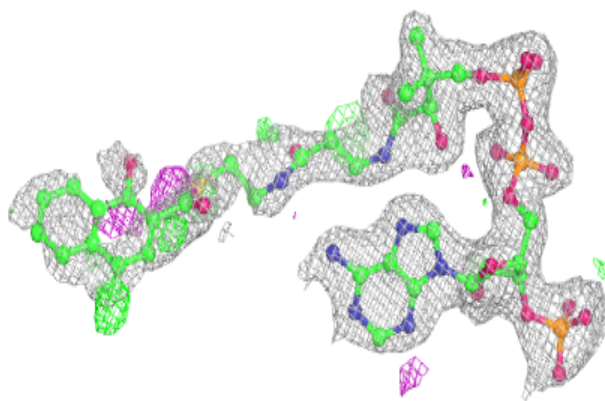
**Electron density around 1HA E 401:**

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

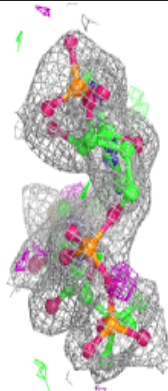
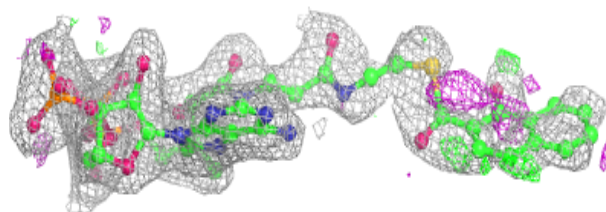
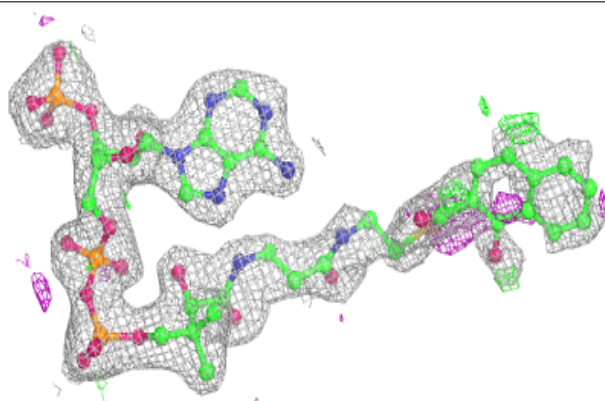


Electron density around 1HA G 401:

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

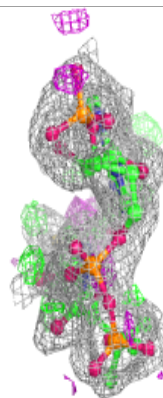
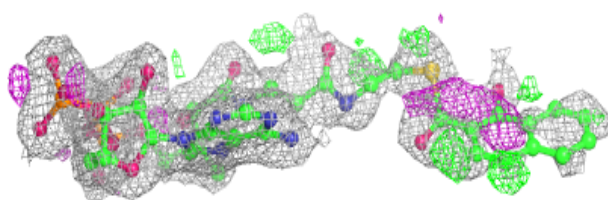
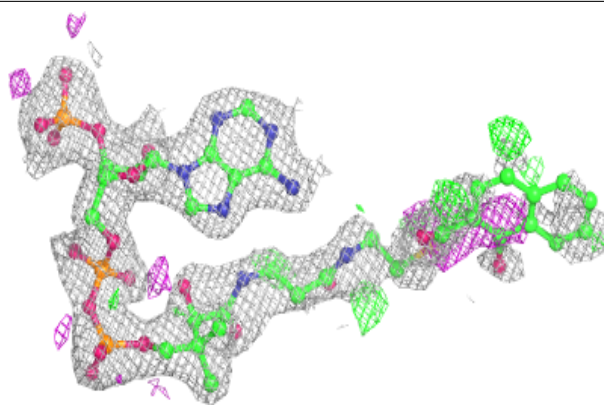
**Electron density around 1HA J 401:**

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

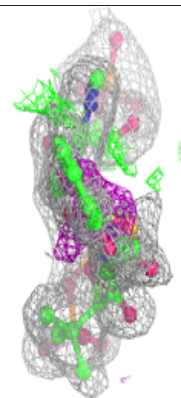
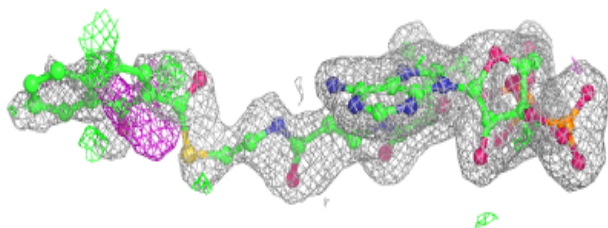
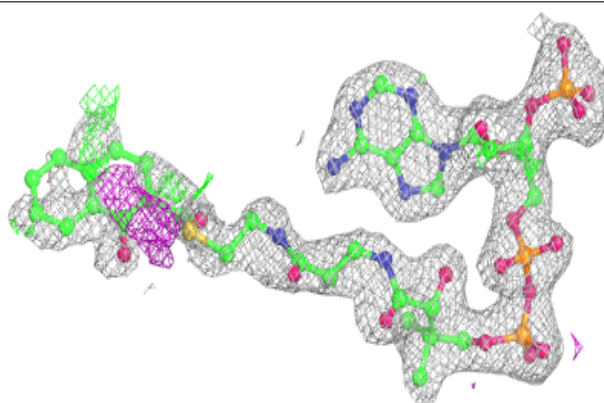


Electron density around 1HA L 401:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

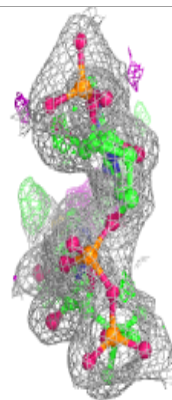
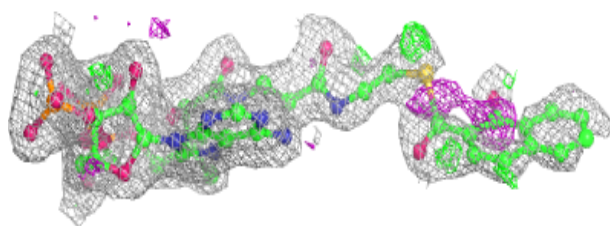
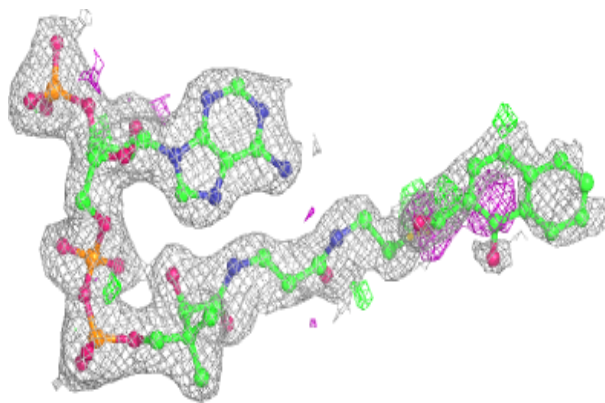
**Electron density around 1HA F 401:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

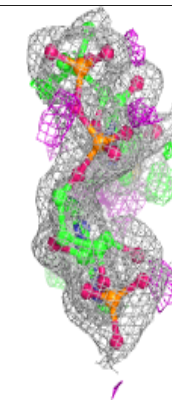
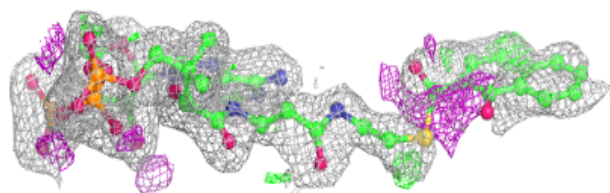
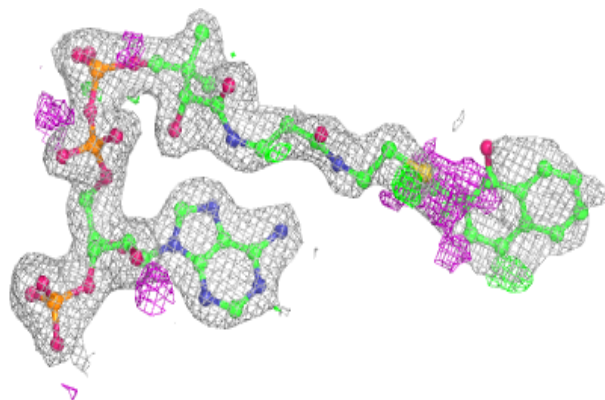


Electron density around 1HA C 401:

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

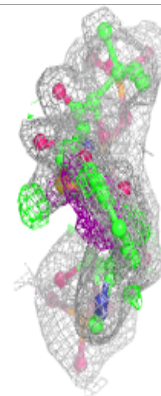
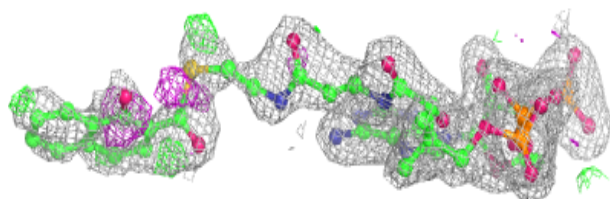
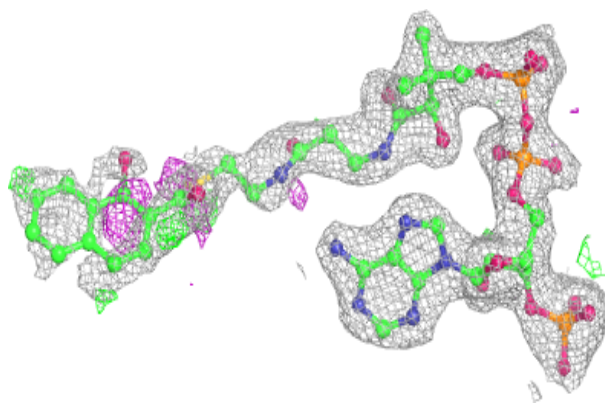
**Electron density around 1HA H 401:**

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

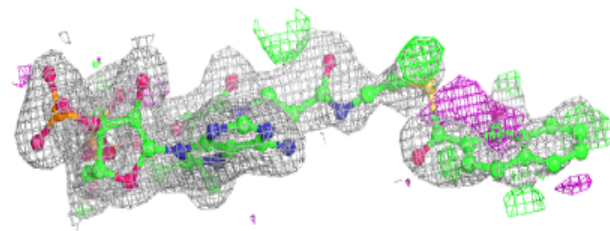
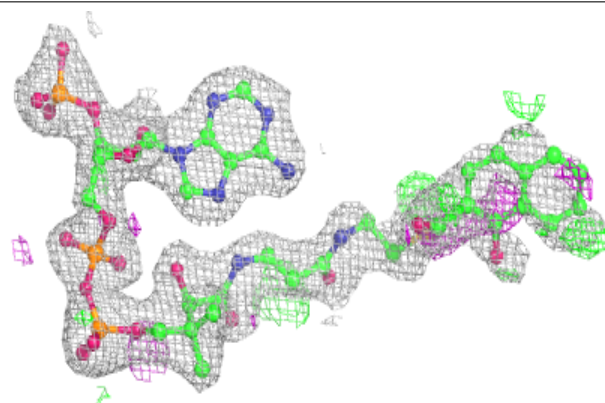


Electron density around 1HA I 401:

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

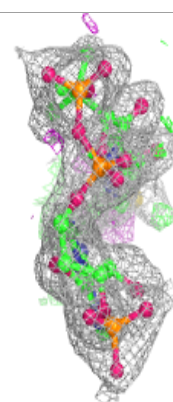
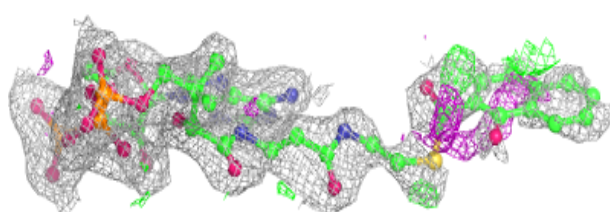
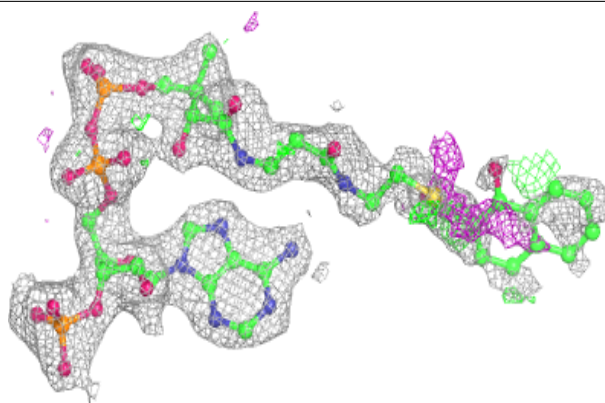
**Electron density around 1HA A 401:**

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

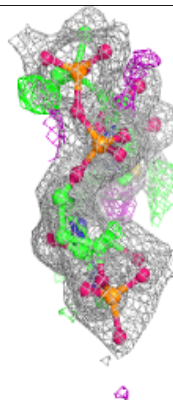
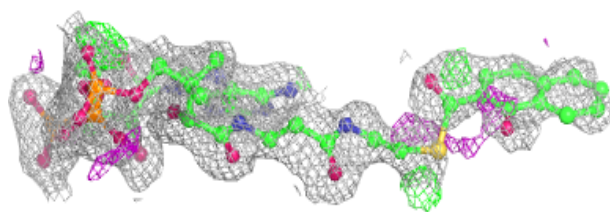
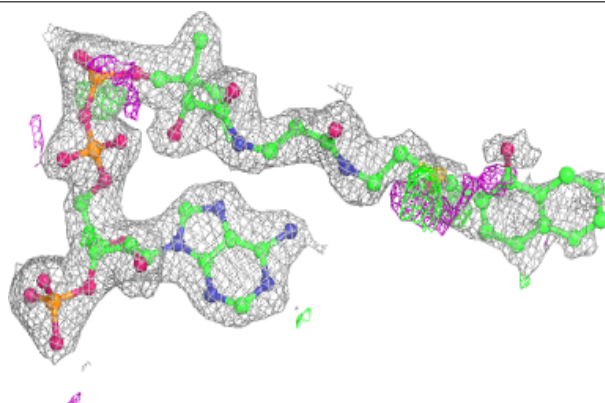


Electron density around 1HA K 401:

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

**Electron density around 1HA 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.