



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 13, 2023 – 08:58 pm GMT

PDB ID : 4D42
Title : Crystal structure of *S. aureus* FabI in complex with NADP and 4-fluoro- 5-hexyl-2-phenoxyphenol
Authors : Schiebel, J.; Chang, A.; Tonge, P.J.; Sotriffer, C.A.; Kisker, C.
Deposited on : 2014-10-26
Resolution : 2.02 Å (reported)

This is a Full wwPDB X-ray Structure Validation 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 : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

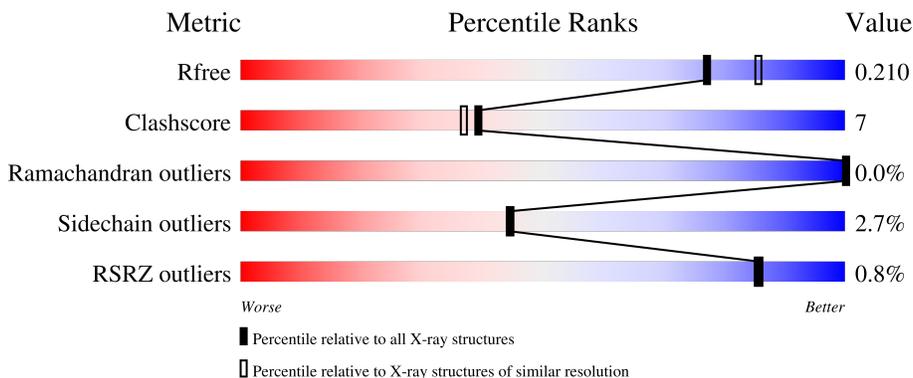
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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

Mol	Chain	Length	Quality of chain
1	A	282	 78% 12% 10%
1	B	282	 78% 11% 10%
1	C	282	 2% 78% 12% 10%
1	D	282	 2% 75% 14% 10%
1	E	282	 79% 11% 10%

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Mol	Chain	Length	Quality of chain
1	F	282	<p>% 79% 11% 10%</p>
1	G	282	<p>% 81% 8% 10%</p>
1	H	282	<p>% 78% 11% 10%</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GLU	A	1258	-	-	X	-
2	GLU	B	1259	-	-	X	-
2	GLU	C	1259	-	-	X	-
2	GLU	E	1259	-	-	X	-
2	GLU	F	1259	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18217 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
			Total	C	N	O	S			
1	A	255	Total 2049	C 1289	N 358	O 397	S 5	0	11	0
1	B	255	Total 2057	C 1293	N 357	O 402	S 5	0	13	0
1	C	255	Total 2045	C 1285	N 357	O 398	S 5	0	11	0
1	D	255	Total 2002	C 1261	N 350	O 387	S 4	0	6	0
1	E	254	Total 2044	C 1284	N 356	O 399	S 5	0	12	0
1	F	255	Total 2055	C 1294	N 359	O 397	S 5	0	12	0
1	G	254	Total 2001	C 1261	N 350	O 386	S 4	0	7	0
1	H	254	Total 1979	C 1246	N 343	O 386	S 4	0	4	0

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	expression tag	UNP Q7A6D8
A	-24	LYS	-	expression tag	UNP Q7A6D8
A	-23	HIS	-	expression tag	UNP Q7A6D8
A	-22	HIS	-	expression tag	UNP Q7A6D8
A	-21	HIS	-	expression tag	UNP Q7A6D8
A	-20	HIS	-	expression tag	UNP Q7A6D8
A	-19	HIS	-	expression tag	UNP Q7A6D8
A	-18	HIS	-	expression tag	UNP Q7A6D8
A	-17	PRO	-	expression tag	UNP Q7A6D8
A	-16	MET	-	expression tag	UNP Q7A6D8
A	-15	SER	-	expression tag	UNP Q7A6D8
A	-14	ASP	-	expression tag	UNP Q7A6D8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	TYR	-	expression tag	UNP Q7A6D8
A	-12	ASP	-	expression tag	UNP Q7A6D8
A	-11	ILE	-	expression tag	UNP Q7A6D8
A	-10	PRO	-	expression tag	UNP Q7A6D8
A	-9	THR	-	expression tag	UNP Q7A6D8
A	-8	THR	-	expression tag	UNP Q7A6D8
A	-7	GLU	-	expression tag	UNP Q7A6D8
A	-6	ASN	-	expression tag	UNP Q7A6D8
A	-5	LEU	-	expression tag	UNP Q7A6D8
A	-4	TYR	-	expression tag	UNP Q7A6D8
A	-3	PHE	-	expression tag	UNP Q7A6D8
A	-2	GLN	-	expression tag	UNP Q7A6D8
A	-1	GLY	-	expression tag	UNP Q7A6D8
A	0	ALA	-	expression tag	UNP Q7A6D8
A	2	VAL	LEU	engineered mutation	UNP Q7A6D8
B	-25	MET	-	expression tag	UNP Q7A6D8
B	-24	LYS	-	expression tag	UNP Q7A6D8
B	-23	HIS	-	expression tag	UNP Q7A6D8
B	-22	HIS	-	expression tag	UNP Q7A6D8
B	-21	HIS	-	expression tag	UNP Q7A6D8
B	-20	HIS	-	expression tag	UNP Q7A6D8
B	-19	HIS	-	expression tag	UNP Q7A6D8
B	-18	HIS	-	expression tag	UNP Q7A6D8
B	-17	PRO	-	expression tag	UNP Q7A6D8
B	-16	MET	-	expression tag	UNP Q7A6D8
B	-15	SER	-	expression tag	UNP Q7A6D8
B	-14	ASP	-	expression tag	UNP Q7A6D8
B	-13	TYR	-	expression tag	UNP Q7A6D8
B	-12	ASP	-	expression tag	UNP Q7A6D8
B	-11	ILE	-	expression tag	UNP Q7A6D8
B	-10	PRO	-	expression tag	UNP Q7A6D8
B	-9	THR	-	expression tag	UNP Q7A6D8
B	-8	THR	-	expression tag	UNP Q7A6D8
B	-7	GLU	-	expression tag	UNP Q7A6D8
B	-6	ASN	-	expression tag	UNP Q7A6D8
B	-5	LEU	-	expression tag	UNP Q7A6D8
B	-4	TYR	-	expression tag	UNP Q7A6D8
B	-3	PHE	-	expression tag	UNP Q7A6D8
B	-2	GLN	-	expression tag	UNP Q7A6D8
B	-1	GLY	-	expression tag	UNP Q7A6D8
B	0	ALA	-	expression tag	UNP Q7A6D8
B	2	VAL	LEU	engineered mutation	UNP Q7A6D8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-25	MET	-	expression tag	UNP Q7A6D8
C	-24	LYS	-	expression tag	UNP Q7A6D8
C	-23	HIS	-	expression tag	UNP Q7A6D8
C	-22	HIS	-	expression tag	UNP Q7A6D8
C	-21	HIS	-	expression tag	UNP Q7A6D8
C	-20	HIS	-	expression tag	UNP Q7A6D8
C	-19	HIS	-	expression tag	UNP Q7A6D8
C	-18	HIS	-	expression tag	UNP Q7A6D8
C	-17	PRO	-	expression tag	UNP Q7A6D8
C	-16	MET	-	expression tag	UNP Q7A6D8
C	-15	SER	-	expression tag	UNP Q7A6D8
C	-14	ASP	-	expression tag	UNP Q7A6D8
C	-13	TYR	-	expression tag	UNP Q7A6D8
C	-12	ASP	-	expression tag	UNP Q7A6D8
C	-11	ILE	-	expression tag	UNP Q7A6D8
C	-10	PRO	-	expression tag	UNP Q7A6D8
C	-9	THR	-	expression tag	UNP Q7A6D8
C	-8	THR	-	expression tag	UNP Q7A6D8
C	-7	GLU	-	expression tag	UNP Q7A6D8
C	-6	ASN	-	expression tag	UNP Q7A6D8
C	-5	LEU	-	expression tag	UNP Q7A6D8
C	-4	TYR	-	expression tag	UNP Q7A6D8
C	-3	PHE	-	expression tag	UNP Q7A6D8
C	-2	GLN	-	expression tag	UNP Q7A6D8
C	-1	GLY	-	expression tag	UNP Q7A6D8
C	0	ALA	-	expression tag	UNP Q7A6D8
C	2	VAL	LEU	engineered mutation	UNP Q7A6D8
D	-25	MET	-	expression tag	UNP Q7A6D8
D	-24	LYS	-	expression tag	UNP Q7A6D8
D	-23	HIS	-	expression tag	UNP Q7A6D8
D	-22	HIS	-	expression tag	UNP Q7A6D8
D	-21	HIS	-	expression tag	UNP Q7A6D8
D	-20	HIS	-	expression tag	UNP Q7A6D8
D	-19	HIS	-	expression tag	UNP Q7A6D8
D	-18	HIS	-	expression tag	UNP Q7A6D8
D	-17	PRO	-	expression tag	UNP Q7A6D8
D	-16	MET	-	expression tag	UNP Q7A6D8
D	-15	SER	-	expression tag	UNP Q7A6D8
D	-14	ASP	-	expression tag	UNP Q7A6D8
D	-13	TYR	-	expression tag	UNP Q7A6D8
D	-12	ASP	-	expression tag	UNP Q7A6D8
D	-11	ILE	-	expression tag	UNP Q7A6D8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-10	PRO	-	expression tag	UNP Q7A6D8
D	-9	THR	-	expression tag	UNP Q7A6D8
D	-8	THR	-	expression tag	UNP Q7A6D8
D	-7	GLU	-	expression tag	UNP Q7A6D8
D	-6	ASN	-	expression tag	UNP Q7A6D8
D	-5	LEU	-	expression tag	UNP Q7A6D8
D	-4	TYR	-	expression tag	UNP Q7A6D8
D	-3	PHE	-	expression tag	UNP Q7A6D8
D	-2	GLN	-	expression tag	UNP Q7A6D8
D	-1	GLY	-	expression tag	UNP Q7A6D8
D	0	ALA	-	expression tag	UNP Q7A6D8
D	2	VAL	LEU	engineered mutation	UNP Q7A6D8
E	-25	MET	-	expression tag	UNP Q7A6D8
E	-24	LYS	-	expression tag	UNP Q7A6D8
E	-23	HIS	-	expression tag	UNP Q7A6D8
E	-22	HIS	-	expression tag	UNP Q7A6D8
E	-21	HIS	-	expression tag	UNP Q7A6D8
E	-20	HIS	-	expression tag	UNP Q7A6D8
E	-19	HIS	-	expression tag	UNP Q7A6D8
E	-18	HIS	-	expression tag	UNP Q7A6D8
E	-17	PRO	-	expression tag	UNP Q7A6D8
E	-16	MET	-	expression tag	UNP Q7A6D8
E	-15	SER	-	expression tag	UNP Q7A6D8
E	-14	ASP	-	expression tag	UNP Q7A6D8
E	-13	TYR	-	expression tag	UNP Q7A6D8
E	-12	ASP	-	expression tag	UNP Q7A6D8
E	-11	ILE	-	expression tag	UNP Q7A6D8
E	-10	PRO	-	expression tag	UNP Q7A6D8
E	-9	THR	-	expression tag	UNP Q7A6D8
E	-8	THR	-	expression tag	UNP Q7A6D8
E	-7	GLU	-	expression tag	UNP Q7A6D8
E	-6	ASN	-	expression tag	UNP Q7A6D8
E	-5	LEU	-	expression tag	UNP Q7A6D8
E	-4	TYR	-	expression tag	UNP Q7A6D8
E	-3	PHE	-	expression tag	UNP Q7A6D8
E	-2	GLN	-	expression tag	UNP Q7A6D8
E	-1	GLY	-	expression tag	UNP Q7A6D8
E	0	ALA	-	expression tag	UNP Q7A6D8
E	2	VAL	LEU	engineered mutation	UNP Q7A6D8
F	-25	MET	-	expression tag	UNP Q7A6D8
F	-24	LYS	-	expression tag	UNP Q7A6D8
F	-23	HIS	-	expression tag	UNP Q7A6D8

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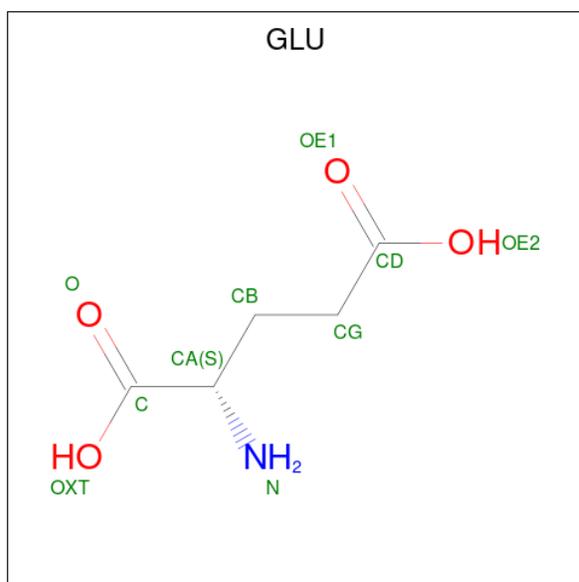
Chain	Residue	Modelled	Actual	Comment	Reference
F	-22	HIS	-	expression tag	UNP Q7A6D8
F	-21	HIS	-	expression tag	UNP Q7A6D8
F	-20	HIS	-	expression tag	UNP Q7A6D8
F	-19	HIS	-	expression tag	UNP Q7A6D8
F	-18	HIS	-	expression tag	UNP Q7A6D8
F	-17	PRO	-	expression tag	UNP Q7A6D8
F	-16	MET	-	expression tag	UNP Q7A6D8
F	-15	SER	-	expression tag	UNP Q7A6D8
F	-14	ASP	-	expression tag	UNP Q7A6D8
F	-13	TYR	-	expression tag	UNP Q7A6D8
F	-12	ASP	-	expression tag	UNP Q7A6D8
F	-11	ILE	-	expression tag	UNP Q7A6D8
F	-10	PRO	-	expression tag	UNP Q7A6D8
F	-9	THR	-	expression tag	UNP Q7A6D8
F	-8	THR	-	expression tag	UNP Q7A6D8
F	-7	GLU	-	expression tag	UNP Q7A6D8
F	-6	ASN	-	expression tag	UNP Q7A6D8
F	-5	LEU	-	expression tag	UNP Q7A6D8
F	-4	TYR	-	expression tag	UNP Q7A6D8
F	-3	PHE	-	expression tag	UNP Q7A6D8
F	-2	GLN	-	expression tag	UNP Q7A6D8
F	-1	GLY	-	expression tag	UNP Q7A6D8
F	0	ALA	-	expression tag	UNP Q7A6D8
F	2	VAL	LEU	engineered mutation	UNP Q7A6D8
G	-25	MET	-	expression tag	UNP Q7A6D8
G	-24	LYS	-	expression tag	UNP Q7A6D8
G	-23	HIS	-	expression tag	UNP Q7A6D8
G	-22	HIS	-	expression tag	UNP Q7A6D8
G	-21	HIS	-	expression tag	UNP Q7A6D8
G	-20	HIS	-	expression tag	UNP Q7A6D8
G	-19	HIS	-	expression tag	UNP Q7A6D8
G	-18	HIS	-	expression tag	UNP Q7A6D8
G	-17	PRO	-	expression tag	UNP Q7A6D8
G	-16	MET	-	expression tag	UNP Q7A6D8
G	-15	SER	-	expression tag	UNP Q7A6D8
G	-14	ASP	-	expression tag	UNP Q7A6D8
G	-13	TYR	-	expression tag	UNP Q7A6D8
G	-12	ASP	-	expression tag	UNP Q7A6D8
G	-11	ILE	-	expression tag	UNP Q7A6D8
G	-10	PRO	-	expression tag	UNP Q7A6D8
G	-9	THR	-	expression tag	UNP Q7A6D8
G	-8	THR	-	expression tag	UNP Q7A6D8

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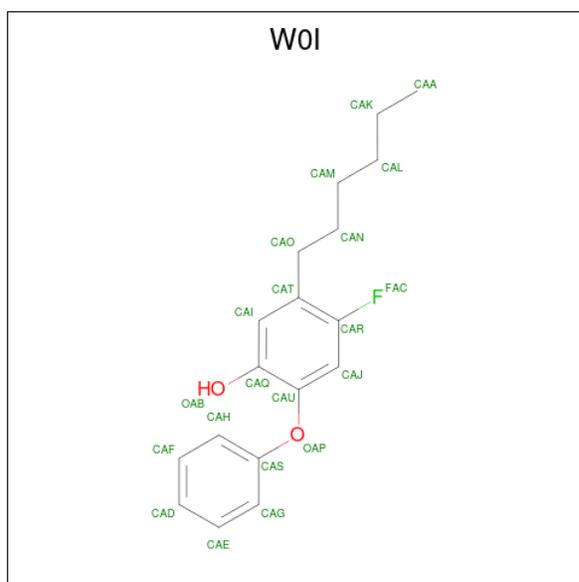
Chain	Residue	Modelled	Actual	Comment	Reference
G	-7	GLU	-	expression tag	UNP Q7A6D8
G	-6	ASN	-	expression tag	UNP Q7A6D8
G	-5	LEU	-	expression tag	UNP Q7A6D8
G	-4	TYR	-	expression tag	UNP Q7A6D8
G	-3	PHE	-	expression tag	UNP Q7A6D8
G	-2	GLN	-	expression tag	UNP Q7A6D8
G	-1	GLY	-	expression tag	UNP Q7A6D8
G	0	ALA	-	expression tag	UNP Q7A6D8
G	2	VAL	LEU	engineered mutation	UNP Q7A6D8
H	-25	MET	-	expression tag	UNP Q7A6D8
H	-24	LYS	-	expression tag	UNP Q7A6D8
H	-23	HIS	-	expression tag	UNP Q7A6D8
H	-22	HIS	-	expression tag	UNP Q7A6D8
H	-21	HIS	-	expression tag	UNP Q7A6D8
H	-20	HIS	-	expression tag	UNP Q7A6D8
H	-19	HIS	-	expression tag	UNP Q7A6D8
H	-18	HIS	-	expression tag	UNP Q7A6D8
H	-17	PRO	-	expression tag	UNP Q7A6D8
H	-16	MET	-	expression tag	UNP Q7A6D8
H	-15	SER	-	expression tag	UNP Q7A6D8
H	-14	ASP	-	expression tag	UNP Q7A6D8
H	-13	TYR	-	expression tag	UNP Q7A6D8
H	-12	ASP	-	expression tag	UNP Q7A6D8
H	-11	ILE	-	expression tag	UNP Q7A6D8
H	-10	PRO	-	expression tag	UNP Q7A6D8
H	-9	THR	-	expression tag	UNP Q7A6D8
H	-8	THR	-	expression tag	UNP Q7A6D8
H	-7	GLU	-	expression tag	UNP Q7A6D8
H	-6	ASN	-	expression tag	UNP Q7A6D8
H	-5	LEU	-	expression tag	UNP Q7A6D8
H	-4	TYR	-	expression tag	UNP Q7A6D8
H	-3	PHE	-	expression tag	UNP Q7A6D8
H	-2	GLN	-	expression tag	UNP Q7A6D8
H	-1	GLY	-	expression tag	UNP Q7A6D8
H	0	ALA	-	expression tag	UNP Q7A6D8
H	2	VAL	LEU	engineered mutation	UNP Q7A6D8

- Molecule 2 is GLUTAMIC ACID (three-letter code: GLU) (formula: C₅H₉NO₄).



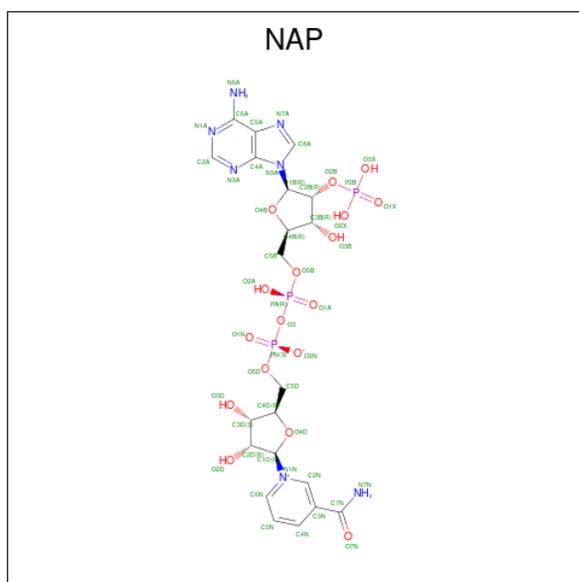
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	10	5	1	4	0	0
2	B	1	10	5	1	4	0	0
2	C	1	10	5	1	4	0	0
2	E	1	10	5	1	4	0	0
2	F	1	10	5	1	4	0	0
2	G	1	10	5	1	4	0	0

- Molecule 3 is 4-fluoro-5-hexyl-2-phenoxyphenol (three-letter code: WOI) (formula: $C_{18}H_{21}FO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	F	O		
3	A	1	21	18	1	2	0	0
3	B	1	21	18	1	2	0	0
3	C	1	21	18	1	2	0	0
3	D	1	21	18	1	2	0	0
3	E	1	21	18	1	2	0	0
3	F	1	21	18	1	2	0	0
3	G	1	21	18	1	2	0	0
3	H	1	21	18	1	2	0	0

- Molecule 4 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
			Total	C	N	O	P		
4	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	D	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	E	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	F	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	G	1	Total 48	C 21	N 7	O 17	P 3	0	0
4	H	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	215	Total 215	O 215	0	0
5	B	179	Total 179	O 179	0	0
5	C	189	Total 189	O 189	0	0
5	D	125	Total 125	O 125	0	0

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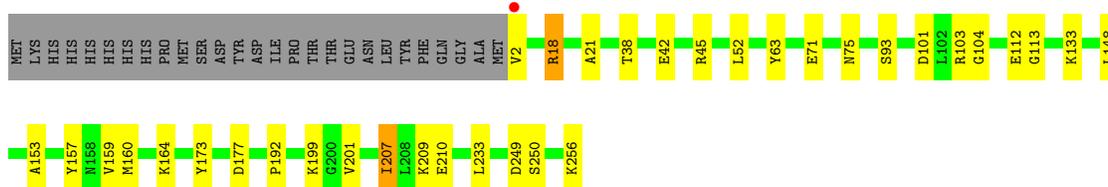
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	207	Total 207	O 207	0	0
5	F	169	Total 169	O 169	0	0
5	G	160	Total 160	O 160	0	0
5	H	129	Total 129	O 129	0	0

3 Residue-property plots

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.

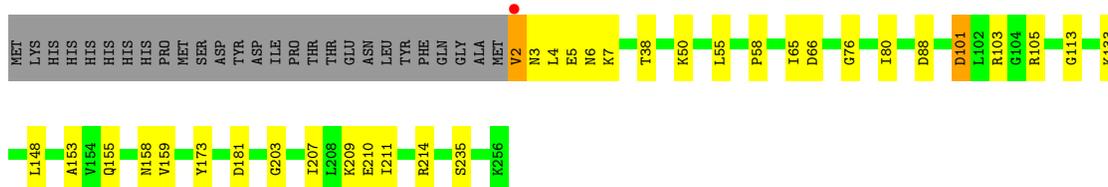
- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain A: 



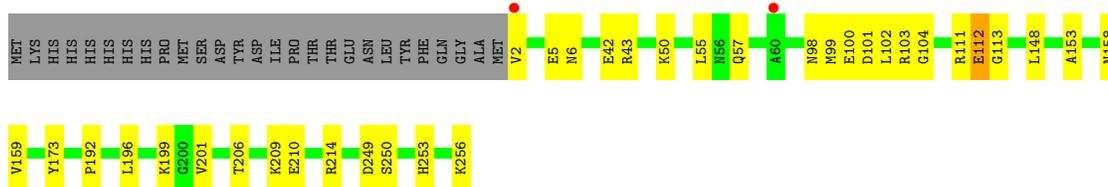
- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain B: 



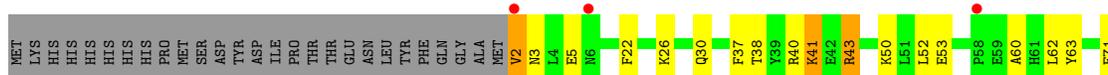
- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain C: 



- Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain D: 





• Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain E: 79% 11% 10%



• Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain F: 79% 11% 10%



• Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain G: 81% 8% 10%



• Molecule 1: ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADPH]

Chain H: 78% 11% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	90.35Å 94.86Å 94.90Å 98.19° 97.22° 112.46°	Depositor
Resolution (Å)	38.44 – 2.02 38.44 – 2.02	Depositor EDS
% Data completeness (in resolution range)	97.8 (38.44-2.02) 97.8 (38.44-2.02)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 2.01Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.145 , 0.185 0.177 , 0.210	Depositor DCC
R_{free} test set	9096 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtrriage
Anisotropy	0.578	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18217	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% 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: NAP, WOI

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	0.68	0/2088	0.87	4/2810 (0.1%)
1	B	0.65	0/2096	0.82	3/2821 (0.1%)
1	C	0.61	0/2078	0.79	0/2797
1	D	0.61	0/2041	0.81	0/2748
1	E	0.70	0/2080	0.84	0/2799
1	F	0.66	0/2097	0.83	1/2821 (0.0%)
1	G	0.61	0/2043	0.83	1/2749 (0.0%)
1	H	0.59	0/2012	0.81	1/2710 (0.0%)
All	All	0.64	0/16535	0.82	10/22255 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	18[A]	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	A	18[B]	ARG	NE-CZ-NH1	7.50	124.05	120.30
1	A	18[A]	ARG	NE-CZ-NH2	-6.97	116.82	120.30
1	A	18[B]	ARG	NE-CZ-NH2	-6.97	116.82	120.30
1	B	66	ASP	CB-CG-OD1	5.66	123.40	118.30
1	H	101	ASP	CB-CG-OD2	5.16	122.94	118.30
1	F	239	SER	C-N-CA	-5.03	111.74	122.30
1	B	101[A]	ASP	CB-CG-OD1	5.03	122.82	118.30
1	B	101[B]	ASP	CB-CG-OD1	5.03	122.82	118.30
1	G	43	ARG	NE-CZ-NH1	-5.01	117.80	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2049	0	2073	41	1
1	B	2057	0	2073	30	0
1	C	2045	0	2061	57	0
1	D	2002	0	2029	41	0
1	E	2044	0	2058	31	0
1	F	2055	0	2086	45	0
1	G	2001	0	2033	19	0
1	H	1979	0	1994	19	0
2	A	10	0	5	4	0
2	B	10	0	5	9	0
2	C	10	0	5	10	0
2	E	10	0	5	4	0
2	F	10	0	5	11	0
2	G	10	0	5	2	0
3	A	21	0	20	2	0
3	B	21	0	20	1	0
3	C	21	0	20	2	0
3	D	21	0	21	1	0
3	E	21	0	20	1	0
3	F	21	0	20	2	0
3	G	21	0	20	0	0
3	H	21	0	21	0	0
4	A	48	0	25	0	0
4	B	48	0	25	0	0
4	C	48	0	25	1	0
4	D	48	0	25	4	0
4	E	48	0	25	0	0
4	F	48	0	25	1	0
4	G	48	0	25	1	0
4	H	48	0	25	2	0
5	A	215	0	0	7	0
5	B	179	0	0	5	0
5	C	189	0	0	11	0
5	D	125	0	0	5	0
5	E	207	0	0	3	1
5	F	169	0	0	6	0
5	G	160	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	H	129	0	0	3	0
All	All	18217	0	16799	248	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (248) 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:C:104[B]:GLY:HA3	5:C:2104:HOH:O	1.30	1.31
1:A:2:VAL:HG12	1:D:2:VAL:HG13	1.16	1.15
1:B:103[A]:ARG:NH1	2:B:1259:GLU:HG3	1.70	1.07
1:C:98:ASN:HB3	1:C:100[B]:GLU:HG2	1.36	1.04
1:B:103[A]:ARG:NH1	2:B:1259:GLU:CG	2.29	0.95
1:A:18[A]:ARG:HH22	1:A:199:LYS:NZ	1.66	0.93
1:A:18[A]:ARG:HH22	1:A:199:LYS:HZ2	1.15	0.93
1:A:2:VAL:HG12	1:D:2:VAL:CG1	1.98	0.93
1:B:103[A]:ARG:HH12	2:B:1259:GLU:CG	1.81	0.92
1:A:101[B]:ASP:OD2	5:A:2093:HOH:O	1.89	0.91
1:C:100[B]:GLU:HG3	1:F:41:LYS:HZ3	1.37	0.90
1:B:101[A]:ASP:OD2	5:B:2092:HOH:O	1.90	0.89
1:A:103[B]:ARG:HH12	2:A:1258:GLU:CB	1.85	0.88
1:E:103[B]:ARG:HH12	2:E:1259:GLU:HG2	1.38	0.88
1:C:101[B]:ASP:OD2	5:C:2102:HOH:O	1.91	0.86
1:F:2:VAL:O	1:F:3:ASN:OD1	1.94	0.85
1:C:210:GLU:HG3	1:C:214[B]:ARG:HD2	1.56	0.84
1:C:103[A]:ARG:HH12	2:C:1259:GLU:CB	1.92	0.83
1:E:103[A]:ARG:NH1	2:E:1259:GLU:OXT	2.10	0.83
1:A:18[A]:ARG:NH2	1:A:199:LYS:NZ	2.25	0.83
1:D:210:GLU:HG3	1:D:214[B]:ARG:HD2	1.62	0.81
1:F:103[B]:ARG:HH12	2:F:1259:GLU:C	1.83	0.80
1:F:103[A]:ARG:HH12	2:F:1259:GLU:CA	1.95	0.79
1:B:101[A]:ASP:OD2	1:B:113:GLY:HA3	1.83	0.78
1:C:103[A]:ARG:HH12	2:C:1259:GLU:HB3	1.49	0.78
1:C:42[B]:GLU:OE2	5:C:2048:HOH:O	2.02	0.78
1:B:2:VAL:O	1:B:3:ASN:OD1	2.02	0.77
1:G:210:GLU:HG3	1:G:214[B]:ARG:HD2	1.66	0.77
1:A:103[B]:ARG:HH12	2:A:1258:GLU:HB2	1.50	0.76
1:C:100[B]:GLU:CG	1:F:41:LYS:HZ3	1.99	0.76
1:E:148:LEU:HD21	1:G:256:LYS:HD2	1.68	0.74
1:F:103[A]:ARG:HH12	2:F:1259:GLU:HA	1.50	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:60:ALA:HB1	1:D:62:LEU:HD11	1.69	0.74
1:A:2:VAL:CG1	1:D:2:VAL:HG13	2.09	0.73
1:F:101[A]:ASP:OD2	1:F:113:GLY:HA3	1.89	0.72
1:C:100[B]:GLU:CD	1:F:41:LYS:NZ	2.43	0.72
1:B:103[A]:ARG:HH12	2:B:1259:GLU:HG2	1.52	0.72
2:G:1259:GLU:OE2	5:G:2142:HOH:O	2.07	0.71
1:D:100:GLU:HG2	5:D:2060:HOH:O	1.89	0.70
1:F:2:VAL:HG12	1:F:3:ASN:H	1.55	0.70
1:C:100[B]:GLU:HG3	1:F:41:LYS:NZ	2.07	0.70
1:B:203:GLY:H	2:B:1259:GLU:HA	1.56	0.69
1:A:101[B]:ASP:OD2	1:A:113:GLY:HA3	1.92	0.69
1:F:253:HIS:HD2	5:F:2167:HOH:O	1.74	0.69
1:A:18[A]:ARG:NH2	1:A:199:LYS:HZ1	1.89	0.69
1:C:98:ASN:CB	1:C:100[B]:GLU:HG2	2.20	0.68
1:C:42[B]:GLU:OE1	5:C:2047:HOH:O	2.11	0.68
1:E:101[B]:ASP:OD2	5:E:2105:HOH:O	2.13	0.67
1:C:103[A]:ARG:NH1	2:C:1259:GLU:HB2	2.11	0.66
1:C:210:GLU:CG	1:C:214[B]:ARG:HD2	2.26	0.66
1:E:42[B]:GLU:OE1	1:E:45:ARG:NH2	2.23	0.66
1:D:50:LYS:O	1:D:53:GLU:HG3	1.96	0.65
1:A:199:LYS:HE3	5:A:2020:HOH:O	1.95	0.65
1:D:71:GLU:HG3	5:D:2043:HOH:O	1.95	0.65
1:E:218:LYS:NZ	5:E:2180:HOH:O	2.29	0.65
1:C:104[B]:GLY:CA	5:C:2104:HOH:O	2.08	0.64
1:C:103[A]:ARG:HH12	2:C:1259:GLU:HB2	1.62	0.64
2:B:1259:GLU:HG2	2:B:1259:GLU:O	1.98	0.64
1:E:207:ILE:HG13	3:E:1258:W0I:H1AL	1.82	0.61
1:F:103[B]:ARG:NH1	2:F:1259:GLU:OXT	2.26	0.61
1:A:42[B]:GLU:OE1	1:A:45:ARG:NH2	2.21	0.61
1:C:5:GLU:O	1:C:6:ASN:HB2	2.00	0.61
1:C:100[B]:GLU:CD	1:F:41:LYS:HZ1	2.04	0.61
1:C:100[B]:GLU:CG	1:F:41:LYS:NZ	2.61	0.60
1:C:103[A]:ARG:NH1	2:C:1259:GLU:CB	2.60	0.60
1:D:201:VAL:HG11	3:D:1258:W0I:H1AK	1.84	0.60
1:B:210:GLU:HG3	1:B:214:ARG:HD3	1.82	0.59
1:A:201:VAL:HG11	3:A:1257:W0I:H1AK	1.82	0.59
1:E:105[A]:ARG:NH2	1:F:181:ASP:OD2	2.34	0.59
1:A:177:ASP:O	1:B:105[A]:ARG:NH2	2.35	0.59
1:D:194[B]:ARG:HD2	5:D:2015:HOH:O	2.00	0.59
1:C:253:HIS:HD2	5:C:2089:HOH:O	1.86	0.58
1:E:194:ARG:HH11	1:E:194:ARG:HG2	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:42:GLU:O	1:H:45:ARG:N	2.35	0.58
1:A:256:LYS:HG2	1:C:148:LEU:HD21	1.86	0.58
1:F:101[A]:ASP:OD2	5:F:2085:HOH:O	2.16	0.58
1:E:101[B]:ASP:OD2	1:E:113:GLY:HA3	2.02	0.58
1:C:104[B]:GLY:C	5:C:2104:HOH:O	2.37	0.57
1:F:214:ARG:HH12	1:H:214[B]:ARG:CZ	2.16	0.57
1:D:2:VAL:CG2	5:D:2118:HOH:O	2.52	0.57
1:F:2:VAL:C	1:F:3:ASN:OD1	2.43	0.57
1:F:103[A]:ARG:NH1	2:F:1259:GLU:HA	2.18	0.56
1:C:199:LYS:HD3	2:F:1259:GLU:HA	1.87	0.56
1:D:60:ALA:HB1	1:D:62:LEU:CD1	2.34	0.56
1:E:253:HIS:HD2	5:H:2053:HOH:O	1.89	0.56
1:C:43:ARG:HH22	1:F:104[A]:GLY:HA3	1.71	0.56
1:H:253:HIS:HD2	5:H:2126:HOH:O	1.89	0.56
1:E:103[B]:ARG:HH12	2:E:1259:GLU:CG	2.14	0.56
1:E:101[A]:ASP:HB3	1:E:159:VAL:CG1	2.35	0.56
1:B:5:GLU:O	1:B:6:ASN:HB2	2.04	0.56
1:G:202:GLY:HA2	2:G:1259:GLU:HB2	1.88	0.56
1:B:103[B]:ARG:HH21	2:B:1259:GLU:HG3	1.71	0.56
1:D:188:ILE:HG21	1:D:226:VAL:HG13	1.88	0.56
1:D:209:LYS:HE3	1:D:213:GLU:OE2	2.06	0.56
1:H:15:ALA:O	1:H:47:GLU:HG2	2.06	0.55
1:C:201:VAL:HG11	3:C:1258:W0I:H2AK	1.88	0.55
1:C:2:VAL:HG22	1:C:2:VAL:O	2.07	0.55
1:E:103[B]:ARG:NH1	2:E:1259:GLU:HG2	2.15	0.55
2:B:1259:GLU:CG	2:B:1259:GLU:O	2.55	0.55
1:C:101[B]:ASP:OD2	1:C:113:GLY:HA3	2.07	0.55
1:C:201:VAL:CG1	3:C:1258:W0I:H2AK	2.37	0.55
1:H:40:ARG:HD3	4:H:1257:NAP:C6A	2.37	0.55
1:G:7:LYS:HE3	5:G:2005:HOH:O	2.05	0.54
1:B:148:LEU:HD21	1:D:256:LYS:HG2	1.90	0.54
1:A:2:VAL:CG1	1:D:2:VAL:CG1	2.78	0.54
1:F:201:VAL:HG11	3:F:1258:W0I:H2AK	1.89	0.54
5:A:2001:HOH:O	1:D:2:VAL:HG12	2.07	0.54
1:A:209:LYS:HG3	5:A:2177:HOH:O	2.06	0.54
1:C:100[B]:GLU:CD	1:F:41:LYS:HZ3	2.07	0.54
1:D:215:ALA:O	1:D:218:LYS:HD2	2.08	0.53
1:D:210:GLU:CG	1:D:214[B]:ARG:HD2	2.36	0.53
1:C:101[A]:ASP:HB3	1:C:159:VAL:CG1	2.39	0.52
1:C:42[B]:GLU:OE1	1:F:112:GLU:HB3	2.09	0.52
1:F:210:GLU:HG3	1:F:214:ARG:HD2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:2050:HOH:O	1:F:104[A]:GLY:HA2	2.08	0.52
1:F:5:GLU:HG3	5:F:2002:HOH:O	2.08	0.52
1:B:103[A]:ARG:HH12	2:B:1259:GLU:HG3	1.44	0.52
1:B:133:LYS:HE2	1:B:181:ASP:OD2	2.10	0.52
1:H:3:ASN:HD21	1:H:5:GLU:HG3	1.75	0.51
1:E:256:LYS:HG2	1:G:148:LEU:HD21	1.92	0.51
1:A:101[A]:ASP:HB3	1:A:159:VAL:CG1	2.41	0.51
1:E:256:LYS:HG2	1:G:148:LEU:CD2	2.40	0.51
1:F:214:ARG:HH12	1:H:214[B]:ARG:NH1	2.09	0.51
1:A:201:VAL:CG1	3:A:1257:WOL:H1AK	2.41	0.50
1:E:192:PRO:HG3	1:E:207:ILE:HG22	1.92	0.50
1:E:256:LYS:HE3	1:G:148:LEU:HD21	1.93	0.50
1:C:173:TYR:CZ	1:D:153:ALA:HA	2.47	0.49
1:E:5:GLU:O	1:E:6:ASN:HB2	2.12	0.49
1:C:112:GLU:HB3	1:F:42[B]:GLU:OE1	2.13	0.49
2:F:1259:GLU:CB	5:F:2138:HOH:O	2.61	0.49
1:G:80:ILE:O	1:G:84:VAL:HG22	2.13	0.49
1:E:207:ILE:O	1:E:211:ILE:HG12	2.13	0.49
1:B:207:ILE:O	1:B:211:ILE:HG12	2.13	0.48
1:C:101[A]:ASP:HB3	1:C:159:VAL:HG11	1.96	0.48
1:F:5:GLU:O	1:F:6:ASN:HB2	2.14	0.48
1:B:155:GLN:NE2	5:B:2122:HOH:O	2.08	0.47
1:C:103[A]:ARG:NH1	2:C:1259:GLU:HB3	2.24	0.47
1:F:103[A]:ARG:HH12	2:F:1259:GLU:CB	2.27	0.47
1:C:101[B]:ASP:HA	1:F:43:ARG:NH1	2.30	0.47
1:D:2:VAL:HG22	1:D:237:LEU:HG	1.97	0.47
1:D:41:LYS:HE2	1:D:43[A]:ARG:HH21	1.78	0.47
1:C:111:ARG:NH1	1:D:119:ASP:OD1	2.40	0.47
1:F:133[A]:LYS:HD3	5:F:2098:HOH:O	2.15	0.47
1:H:44:SER:O	1:H:48:LEU:HB2	2.15	0.46
1:D:2:VAL:HG23	5:D:2118:HOH:O	2.12	0.46
1:G:136:MET:N	1:G:137:PRO:HD3	2.31	0.46
1:D:40:ARG:HD3	4:D:1257:NAP:C6A	2.45	0.46
1:D:155:GLN:O	1:D:156:ASN:HB2	2.15	0.46
1:E:194:ARG:HG2	1:E:194:ARG:NH1	2.30	0.46
1:G:5:GLU:O	1:G:6:ASN:HB2	2.15	0.46
1:C:104[B]:GLY:O	1:C:158:ASN:ND2	2.49	0.46
1:A:160:MET:O	1:A:164:LYS:HG2	2.15	0.46
1:D:41:LYS:HD2	4:D:1257:NAP:P2B	2.55	0.46
1:H:210:GLU:CG	1:H:214[B]:ARG:HD2	2.45	0.46
1:C:199:LYS:CD	2:F:1259:GLU:HA	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:207:ILE:O	1:F:211:ILE:HG12	2.16	0.46
1:A:148:LEU:HD21	1:C:256:LYS:HE3	1.98	0.45
1:G:173:TYR:CZ	1:H:153:ALA:HA	2.50	0.45
1:A:256:LYS:HG2	1:C:148:LEU:CD2	2.45	0.45
1:D:22:PHE:O	1:D:26:LYS:HG3	2.16	0.45
1:E:173:TYR:CZ	1:F:153:ALA:HA	2.51	0.45
1:C:199:LYS:HE3	1:F:103[B]:ARG:NH1	2.31	0.45
1:A:153:ALA:HA	1:B:173:TYR:CZ	2.52	0.45
1:C:99[B]:MET:HA	1:C:102[B]:LEU:HB2	1.99	0.45
1:A:104[B]:GLY:C	5:A:2096:HOH:O	2.55	0.45
1:B:2:VAL:HG11	1:B:235:SER:CB	2.46	0.45
1:C:153:ALA:HA	1:D:173:TYR:CZ	2.52	0.45
5:F:2074:HOH:O	1:G:253:HIS:HD2	1.98	0.44
1:G:18[B]:ARG:HG2	1:G:18[B]:ARG:HH11	1.82	0.44
1:C:100[B]:GLU:OE1	1:F:41:LYS:NZ	2.50	0.44
1:A:103[B]:ARG:HH12	2:A:1258:GLU:CA	2.30	0.44
1:A:157:TYR:CZ	1:A:160:MET:HG3	2.52	0.44
1:D:2:VAL:HB	1:D:3:ASN:H	1.76	0.44
1:B:101[B]:ASP:HB3	1:B:159:VAL:CG1	2.48	0.44
1:A:71[B]:GLU:HG3	1:A:75:ASN:ND2	2.32	0.44
1:C:103[B]:ARG:HH12	2:C:1259:GLU:HB2	1.82	0.44
1:D:112[A]:GLU:H	1:D:112[A]:GLU:CD	2.22	0.44
1:C:192:PRO:HA	4:C:1257:NAP:O7N	2.18	0.44
1:G:100:GLU:H	1:G:100:GLU:CD	2.19	0.44
1:B:207:ILE:HG13	3:B:1258:W0I:H1AL	1.99	0.43
1:H:39:TYR:OH	1:H:45:ARG:NH1	2.45	0.43
1:A:103[B]:ARG:NH1	2:A:1258:GLU:HB2	2.27	0.43
2:C:1259:GLU:HB2	1:F:199:LYS:HE2	1.99	0.43
1:D:62:LEU:HD12	1:D:62:LEU:N	2.34	0.43
1:D:147:TYR:HB2	4:D:1257:NAP:C5N	2.48	0.43
1:B:2:VAL:HG11	1:B:235:SER:HB2	2.00	0.43
1:F:103[A]:ARG:NH1	2:F:1259:GLU:OXT	2.52	0.43
1:E:155:GLN:O	1:E:156:ASN:HB2	2.19	0.43
1:B:3:ASN:HB3	5:B:2006:HOH:O	2.18	0.43
1:C:158:ASN:HB3	5:C:2108:HOH:O	2.19	0.43
1:D:38:THR:HA	1:D:63:TYR:O	2.19	0.43
1:A:21:ALA:HB2	1:A:93:SER:CB	2.49	0.43
1:D:37:PHE:CE2	1:D:52:LEU:HD11	2.54	0.43
1:D:41:LYS:HE2	1:D:43[A]:ARG:HE	1.83	0.43
1:E:52:LEU:HD23	1:E:55:LEU:HD12	2.00	0.42
1:A:177:ASP:OD1	1:B:105[A]:ARG:NE	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:ASN:HB3	5:B:2098:HOH:O	2.19	0.42
1:C:103[B]:ARG:HH12	2:C:1259:GLU:CB	2.32	0.42
1:C:209:LYS:HE3	5:C:2171:HOH:O	2.18	0.42
1:G:233:LEU:HD23	1:G:233:LEU:HA	1.96	0.42
1:A:192:PRO:HG3	1:A:207:ILE:HG22	2.01	0.42
1:C:199:LYS:HD3	2:F:1259:GLU:CA	2.49	0.42
1:H:215:ALA:O	1:H:218:LYS:HD2	2.18	0.42
1:C:57:GLN:HB3	5:C:2062:HOH:O	2.19	0.42
1:E:38:THR:HA	1:E:63:TYR:O	2.19	0.42
1:G:45:ARG:NH2	5:G:2042:HOH:O	2.49	0.42
1:A:173:TYR:CZ	1:B:153:ALA:HA	2.55	0.42
1:C:43:ARG:HG2	1:F:100[B]:GLU:HG3	2.00	0.42
1:D:41:LYS:HB3	1:D:41:LYS:HE3	1.67	0.42
1:H:112[B]:GLU:HG2	5:H:2076:HOH:O	2.19	0.42
1:B:38:THR:HG21	1:B:65:ILE:HD12	2.02	0.42
1:E:7:LYS:HA	1:E:7:LYS:HD3	1.91	0.42
1:F:101[B]:ASP:HB3	1:F:159:VAL:CG1	2.50	0.42
1:A:207:ILE:HD12	1:A:207:ILE:HG23	1.64	0.41
1:B:76:GLY:O	1:B:80:ILE:HG13	2.20	0.41
1:E:101[A]:ASP:HB3	1:E:159:VAL:HG12	2.00	0.41
1:E:153:ALA:HA	1:F:173:TYR:CZ	2.54	0.41
1:A:101[B]:ASP:CG	5:A:2093:HOH:O	2.47	0.41
2:C:1259:GLU:HB2	1:F:199:LYS:CE	2.50	0.41
1:A:249:ASP:O	1:A:250:SER:HB2	2.20	0.41
1:C:249:ASP:O	1:C:250:SER:HB2	2.20	0.41
1:H:213:GLU:O	1:H:218:LYS:HE3	2.19	0.41
1:A:103[A]:ARG:CZ	1:A:103[A]:ARG:HB3	2.50	0.41
1:B:58:PRO:HD2	5:B:2055:HOH:O	2.19	0.41
1:D:3:ASN:OD1	1:D:5:GLU:HG3	2.20	0.41
1:D:41:LYS:HD2	4:D:1257:NAP:O3X	2.20	0.41
1:D:217:LEU:HB2	1:D:250:SER:HB3	2.03	0.41
1:F:155:GLN:O	1:F:156:ASN:HB2	2.20	0.41
1:G:30:GLN:O	1:G:30:GLN:HG3	2.21	0.41
1:H:155:GLN:O	1:H:156:ASN:HB2	2.20	0.41
1:H:193:ILE:HD13	1:H:193:ILE:HG21	1.90	0.41
1:A:101[A]:ASP:HB3	1:A:159:VAL:HG12	2.03	0.41
1:A:133:LYS:HD3	5:A:2118:HOH:O	2.21	0.41
1:C:196:LEU:CD2	1:F:100[A]:GLU:HG3	2.51	0.41
1:F:103[B]:ARG:CZ	1:F:103[B]:ARG:HB3	2.50	0.41
1:E:105[B]:ARG:HG3	5:E:2109:HOH:O	2.20	0.41
1:G:192:PRO:HA	4:G:1257:NAP:O7N	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:THR:HA	1:A:63:TYR:O	2.21	0.40
1:A:233:LEU:HA	1:A:233:LEU:HD23	1.85	0.40
1:B:7:LYS:HA	1:B:88:ASP:OD2	2.21	0.40
1:E:59:GLU:HG3	1:E:61:HIS:CE1	2.56	0.40
1:G:135:LEU:C	1:G:137:PRO:HD3	2.42	0.40
1:H:103:ARG:NH2	1:H:200:GLY:O	2.54	0.40
1:H:120:ILE:HD13	4:H:1257:NAP:H61A	1.85	0.40
1:H:41:LYS:H	1:H:41:LYS:HG2	1.72	0.40
1:D:207:ILE:HD12	1:D:207:ILE:HA	1.87	0.40
1:E:157:TYR:CZ	1:E:160:MET:HG3	2.56	0.40
4:F:1257:NAP:O2D	3:F:1258:W0I:OAB	2.30	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42[A]:GLU:OE2	5:E:2120:HOH:O[1_554]	1.95	0.25

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	264/282 (94%)	252 (96%)	12 (4%)	0	100	100
1	B	266/282 (94%)	254 (96%)	12 (4%)	0	100	100
1	C	264/282 (94%)	256 (97%)	8 (3%)	0	100	100
1	D	259/282 (92%)	249 (96%)	10 (4%)	0	100	100
1	E	264/282 (94%)	256 (97%)	8 (3%)	0	100	100
1	F	265/282 (94%)	251 (95%)	14 (5%)	0	100	100
1	G	259/282 (92%)	251 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	256/282 (91%)	240 (94%)	15 (6%)	1 (0%)	34	28
All	All	2097/2256 (93%)	2009 (96%)	87 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	156	ASN

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	219/234 (94%)	215 (98%)	4 (2%)	59	61
1	B	220/234 (94%)	215 (98%)	5 (2%)	50	51
1	C	218/234 (93%)	214 (98%)	4 (2%)	59	61
1	D	214/234 (92%)	206 (96%)	8 (4%)	34	31
1	E	218/234 (93%)	215 (99%)	3 (1%)	67	70
1	F	220/234 (94%)	216 (98%)	4 (2%)	59	61
1	G	214/234 (92%)	209 (98%)	5 (2%)	50	51
1	H	211/234 (90%)	200 (95%)	11 (5%)	23	18
All	All	1734/1872 (93%)	1690 (98%)	44 (2%)	44	48

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LEU
1	A	112	GLU
1	A	207	ILE
1	A	210	GLU
1	B	2	VAL
1	B	4	LEU
1	B	50	LYS

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Mol	Chain	Res	Type
1	B	55	LEU
1	B	209	LYS
1	C	50	LYS
1	C	55	LEU
1	C	112	GLU
1	C	206	THR
1	D	2	VAL
1	D	30	GLN
1	D	41	LYS
1	D	43[A]	ARG
1	D	43[B]	ARG
1	D	84	VAL
1	D	99	MET
1	D	207	ILE
1	E	45	ARG
1	E	138	GLU
1	E	210	GLU
1	F	50	LYS
1	F	55	LEU
1	F	112	GLU
1	F	218	LYS
1	G	7	LYS
1	G	47	GLU
1	G	55	LEU
1	G	103	ARG
1	G	256	LYS
1	H	41	LYS
1	H	42	GLU
1	H	46	LYS
1	H	48	LEU
1	H	52	LEU
1	H	62	LEU
1	H	64	GLN
1	H	84	VAL
1	H	99	MET
1	H	138	GLU
1	H	208	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN

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Mol	Chain	Res	Type
1	A	75	ASN
1	E	253	HIS
1	H	30	GLN
1	H	64	GLN
1	H	253	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

22 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	W0I	F	1258	-	22,22,22	0.72	0	27,28,28	1.20	4 (14%)
4	NAP	G	1257	-	45,52,52	1.56	3 (6%)	56,80,80	1.55	9 (16%)
2	GLU	B	1259	-	8,9,9	1.01	0	10,11,11	1.23	1 (10%)
2	GLU	A	1258	-	8,9,9	1.14	0	10,11,11	1.15	0
3	W0I	E	1258	-	22,22,22	0.76	0	27,28,28	1.22	4 (14%)
3	W0I	A	1257	-	22,22,22	0.82	1 (4%)	27,28,28	1.19	2 (7%)
2	GLU	F	1259	-	8,9,9	1.10	0	10,11,11	1.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAP	E	1257	-	45,52,52	1.63	7 (15%)	56,80,80	1.77	6 (10%)
2	GLU	G	1259	-	8,9,9	1.10	0	10,11,11	1.10	0
3	W0I	G	1258	-	22,22,22	0.85	0	27,28,28	1.32	5 (18%)
2	GLU	E	1259	-	8,9,9	1.04	0	10,11,11	1.06	0
3	W0I	D	1258	-	22,22,22	0.68	0	27,28,28	1.23	3 (11%)
3	W0I	H	1258	-	22,22,22	0.81	0	27,28,28	1.23	4 (14%)
3	W0I	B	1258	-	22,22,22	0.76	0	27,28,28	1.21	5 (18%)
4	NAP	B	1257	-	45,52,52	1.56	4 (8%)	56,80,80	1.54	7 (12%)
4	NAP	D	1257	-	45,52,52	1.69	4 (8%)	56,80,80	1.35	8 (14%)
4	NAP	F	1257	-	45,52,52	1.62	4 (8%)	56,80,80	1.70	9 (16%)
4	NAP	A	1260	-	45,52,52	1.58	4 (8%)	56,80,80	1.58	10 (17%)
4	NAP	C	1257	-	45,52,52	1.56	4 (8%)	56,80,80	1.45	6 (10%)
2	GLU	C	1259	-	8,9,9	1.15	0	10,11,11	1.02	0
3	W0I	C	1258	-	22,22,22	0.98	0	27,28,28	1.42	5 (18%)
4	NAP	H	1257	-	45,52,52	1.60	3 (6%)	56,80,80	1.54	10 (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
3	W0I	F	1258	-	-	2/10/10/10	0/2/2/2
4	NAP	G	1257	-	-	6/31/67/67	0/5/5/5
2	GLU	B	1259	-	-	8/9/9/9	-
2	GLU	A	1258	-	-	2/9/9/9	-
3	W0I	E	1258	-	-	1/10/10/10	0/2/2/2
3	W0I	A	1257	-	-	3/10/10/10	0/2/2/2
2	GLU	F	1259	-	-	3/9/9/9	-
4	NAP	E	1257	-	-	7/31/67/67	0/5/5/5
2	GLU	G	1259	-	-	3/9/9/9	-
3	W0I	G	1258	-	-	2/10/10/10	0/2/2/2
2	GLU	E	1259	-	-	5/9/9/9	-
3	W0I	D	1258	-	-	2/10/10/10	0/2/2/2
3	W0I	H	1258	-	-	2/10/10/10	0/2/2/2
3	W0I	B	1258	-	-	0/10/10/10	0/2/2/2
4	NAP	B	1257	-	-	6/31/67/67	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAP	D	1257	-	-	6/31/67/67	0/5/5/5
4	NAP	F	1257	-	-	6/31/67/67	0/5/5/5
4	NAP	A	1260	-	-	6/31/67/67	0/5/5/5
4	NAP	C	1257	-	-	5/31/67/67	0/5/5/5
2	GLU	C	1259	-	-	4/9/9/9	-
3	W0I	C	1258	-	-	2/10/10/10	0/2/2/2
4	NAP	H	1257	-	-	6/31/67/67	0/5/5/5

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1257	NAP	O7N-C7N	8.44	1.40	1.24
4	G	1257	NAP	O7N-C7N	7.99	1.39	1.24
4	C	1257	NAP	O7N-C7N	7.96	1.39	1.24
4	H	1257	NAP	O7N-C7N	7.86	1.39	1.24
4	F	1257	NAP	O7N-C7N	7.31	1.38	1.24
4	A	1260	NAP	O7N-C7N	7.25	1.38	1.24
4	B	1257	NAP	O7N-C7N	7.22	1.38	1.24
4	E	1257	NAP	O7N-C7N	7.06	1.37	1.24
4	A	1260	NAP	C2A-N3A	4.35	1.39	1.32
4	H	1257	NAP	C2A-N3A	4.08	1.38	1.32
4	D	1257	NAP	C2A-N3A	4.07	1.38	1.32
4	F	1257	NAP	C2A-N3A	4.04	1.38	1.32
4	E	1257	NAP	C2A-N3A	4.02	1.38	1.32
4	B	1257	NAP	C2A-N3A	3.60	1.37	1.32
4	E	1257	NAP	C2A-N1A	3.59	1.40	1.33
4	C	1257	NAP	P2B-O2B	3.21	1.65	1.59
4	G	1257	NAP	C2A-N3A	3.05	1.37	1.32
4	F	1257	NAP	P2B-O2B	2.95	1.64	1.59
4	A	1260	NAP	P2B-O2B	2.81	1.64	1.59
4	D	1257	NAP	C2A-N1A	2.74	1.39	1.33
4	E	1257	NAP	P2B-O2B	2.57	1.64	1.59
4	C	1257	NAP	C2A-N3A	2.51	1.36	1.32
4	D	1257	NAP	C2N-N1N	2.49	1.38	1.35
4	B	1257	NAP	P2B-O2B	2.46	1.63	1.59
4	F	1257	NAP	C2A-N1A	2.44	1.38	1.33
4	G	1257	NAP	C2A-N1A	2.41	1.38	1.33
4	H	1257	NAP	C2A-N1A	2.36	1.38	1.33
4	A	1260	NAP	C2A-N1A	2.22	1.38	1.33
4	C	1257	NAP	C2N-N1N	2.19	1.37	1.35
4	B	1257	NAP	C2N-N1N	2.12	1.37	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1257	NAP	PN-O2N	-2.11	1.45	1.55
3	A	1257	W0I	OAP-CAS	-2.09	1.35	1.39
4	E	1257	NAP	PA-O2A	-2.01	1.45	1.55
4	E	1257	NAP	C2N-N1N	2.01	1.37	1.35

All (98) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1257	NAP	C3N-C7N-N7N	7.44	126.68	117.75
4	F	1257	NAP	C3N-C7N-N7N	6.40	125.43	117.75
4	H	1257	NAP	N3A-C2A-N1A	-6.13	119.10	128.68
4	A	1260	NAP	C3N-C7N-N7N	6.10	125.08	117.75
4	F	1257	NAP	N3A-C2A-N1A	-5.96	119.36	128.68
4	B	1257	NAP	N3A-C2A-N1A	-5.61	119.91	128.68
4	E	1257	NAP	N3A-C2A-N1A	-5.59	119.94	128.68
4	C	1257	NAP	N3A-C2A-N1A	-5.48	120.11	128.68
4	G	1257	NAP	N3A-C2A-N1A	-5.44	120.18	128.68
4	B	1257	NAP	C3N-C7N-N7N	5.01	123.76	117.75
4	G	1257	NAP	C3N-C7N-N7N	4.85	123.57	117.75
4	E	1257	NAP	O7N-C7N-N7N	-4.48	116.21	122.58
4	A	1260	NAP	N3A-C2A-N1A	-4.48	121.68	128.68
4	D	1257	NAP	N3A-C2A-N1A	-4.32	121.92	128.68
3	C	1258	W0I	OAP-CAU-CAQ	3.84	123.40	116.22
4	B	1257	NAP	O7N-C7N-N7N	-3.81	117.17	122.58
4	C	1257	NAP	O4B-C1B-C2B	-3.60	100.35	106.59
4	H	1257	NAP	C3N-C7N-N7N	3.43	121.87	117.75
3	A	1257	W0I	OAP-CAU-CAQ	3.42	122.62	116.22
4	F	1257	NAP	O7N-C7N-N7N	-3.41	117.73	122.58
4	A	1260	NAP	O7N-C7N-C3N	-3.35	115.62	119.63
4	G	1257	NAP	C1B-N9A-C4A	-3.32	120.81	126.64
3	C	1258	W0I	CAI-CAQ-CAU	3.31	123.20	119.81
3	D	1258	W0I	OAP-CAU-CAQ	3.26	122.32	116.22
3	G	1258	W0I	CAI-CAQ-CAU	3.19	123.07	119.81
4	F	1257	NAP	C1B-N9A-C4A	-3.13	121.15	126.64
3	G	1258	W0I	OAP-CAU-CAQ	3.04	121.90	116.22
4	D	1257	NAP	C3N-C7N-N7N	3.01	121.37	117.75
4	G	1257	NAP	O7N-C7N-C3N	-3.01	116.03	119.63
4	D	1257	NAP	O4B-C1B-C2B	-2.93	101.51	106.59
4	H	1257	NAP	C3N-C2N-N1N	-2.92	117.57	120.43
3	B	1258	W0I	CAI-CAQ-CAU	2.89	122.77	119.81
3	H	1258	W0I	FAC-CAR-CAT	2.87	122.65	117.96
4	H	1257	NAP	C1B-N9A-C4A	-2.79	121.75	126.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1258	W0I	CAN-CAO-CAT	-2.76	105.79	114.10
3	H	1258	W0I	OAP-CAU-CAQ	2.74	121.35	116.22
4	C	1257	NAP	C3N-C2N-N1N	-2.72	117.77	120.43
3	A	1257	W0I	CAN-CAO-CAT	-2.71	105.92	114.10
4	H	1257	NAP	O4B-C1B-C2B	-2.69	101.93	106.59
4	E	1257	NAP	O4B-C1B-C2B	-2.68	101.93	106.59
4	B	1257	NAP	C6N-N1N-C2N	-2.66	119.55	121.97
4	F	1257	NAP	O2N-PN-O1N	2.62	125.20	112.24
3	H	1258	W0I	CAJ-CAR-CAT	-2.59	120.59	123.98
4	C	1257	NAP	C3N-C7N-N7N	2.58	120.84	117.75
4	G	1257	NAP	C2N-C3N-C4N	2.55	121.15	118.26
4	C	1257	NAP	C2N-C3N-C4N	2.53	121.13	118.26
4	H	1257	NAP	O3X-P2B-O2X	2.53	117.32	107.64
4	B	1257	NAP	O4B-C1B-C2B	-2.50	102.25	106.59
4	A	1260	NAP	C1B-N9A-C4A	-2.50	122.25	126.64
3	G	1258	W0I	CAN-CAO-CAT	-2.49	106.59	114.10
4	G	1257	NAP	O4B-C1B-C2B	-2.49	102.27	106.59
3	B	1258	W0I	CAJ-CAU-CAQ	-2.47	117.39	120.06
4	F	1257	NAP	O7N-C7N-C3N	-2.44	116.71	119.63
4	A	1260	NAP	C3D-C2D-C1D	-2.43	97.32	100.98
3	C	1258	W0I	CAJ-CAU-CAQ	-2.43	117.44	120.06
4	G	1257	NAP	N6A-C6A-N1A	2.42	123.59	118.57
3	E	1258	W0I	CAI-CAT-CAR	2.42	119.39	116.58
4	B	1257	NAP	O4D-C1D-C2D	-2.41	103.40	106.93
4	D	1257	NAP	C1B-N9A-C4A	-2.40	122.43	126.64
3	D	1258	W0I	CAJ-CAR-CAT	-2.38	120.86	123.98
3	G	1258	W0I	CAJ-CAU-CAQ	-2.38	117.49	120.06
4	A	1260	NAP	O4D-C1D-C2D	-2.38	103.45	106.93
4	D	1257	NAP	O2N-PN-O1N	2.37	123.95	112.24
3	F	1258	W0I	CAN-CAO-CAT	-2.36	106.99	114.10
3	F	1258	W0I	CAI-CAT-CAR	2.36	119.32	116.58
4	A	1260	NAP	O7N-C7N-N7N	-2.35	119.25	122.58
3	F	1258	W0I	OAP-CAU-CAQ	2.34	120.60	116.22
3	E	1258	W0I	OAP-CAU-CAQ	2.32	120.56	116.22
4	G	1257	NAP	C6N-N1N-C2N	-2.31	119.86	121.97
4	A	1260	NAP	C6N-N1N-C2N	-2.31	119.87	121.97
4	H	1257	NAP	O2N-PN-O1N	2.31	123.65	112.24
4	F	1257	NAP	O3B-C3B-C2B	-2.29	104.67	111.17
4	D	1257	NAP	O3X-P2B-O2X	2.29	116.37	107.64
4	F	1257	NAP	C2N-C3N-C4N	2.28	120.85	118.26
3	E	1258	W0I	CAN-CAO-CAT	-2.28	107.22	114.10
3	D	1258	W0I	CAN-CAO-CAT	-2.26	107.30	114.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1257	NAP	O4D-C1D-C2D	-2.25	103.63	106.93
4	B	1257	NAP	O2N-PN-O1N	2.24	123.30	112.24
4	C	1257	NAP	C4A-C5A-N7A	-2.23	107.07	109.40
4	A	1260	NAP	O3B-C3B-C2B	-2.23	104.82	111.17
3	B	1258	W0I	OAP-CAU-CAQ	2.23	120.38	116.22
4	H	1257	NAP	C2N-C3N-C4N	2.21	120.76	118.26
4	A	1260	NAP	C4A-C5A-N7A	-2.19	107.12	109.40
4	F	1257	NAP	C2A-N1A-C6A	2.13	122.41	118.75
3	H	1258	W0I	CAN-CAO-CAT	-2.13	107.67	114.10
4	E	1257	NAP	O3X-P2B-O2X	2.13	115.77	107.64
4	E	1257	NAP	O7N-C7N-C3N	-2.13	117.09	119.63
3	G	1258	W0I	CAU-OAP-CAS	-2.12	112.71	118.00
2	B	1259	GLU	OE1-CD-CG	-2.11	116.29	123.08
3	E	1258	W0I	CAQ-CAI-CAT	-2.09	118.57	121.55
4	D	1257	NAP	O2X-P2B-O1X	2.08	118.83	110.68
4	H	1257	NAP	C2A-N1A-C6A	2.08	122.31	118.75
3	C	1258	W0I	CAQ-CAI-CAT	-2.06	118.61	121.55
4	H	1257	NAP	O7N-C7N-N7N	-2.06	119.65	122.58
3	F	1258	W0I	CAJ-CAR-CAT	-2.01	121.34	123.98
3	B	1258	W0I	CAQ-CAI-CAT	-2.01	118.68	121.55
3	B	1258	W0I	CAN-CAO-CAT	-2.00	108.07	114.10
4	G	1257	NAP	C3D-C2D-C1D	-2.00	97.97	100.98

There are no chirality outliers.

All (87) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1258	GLU	N-CA-CB-CG
2	B	1259	GLU	O-C-CA-N
2	B	1259	GLU	N-CA-CB-CG
2	B	1259	GLU	C-CA-CB-CG
2	C	1259	GLU	N-CA-CB-CG
2	G	1259	GLU	N-CA-CB-CG
2	G	1259	GLU	C-CA-CB-CG
4	A	1260	NAP	PN-O3-PA-O5B
4	A	1260	NAP	C5D-O5D-PN-O1N
4	A	1260	NAP	C5D-O5D-PN-O2N
4	A	1260	NAP	O4D-C1D-N1N-C2N
4	B	1257	NAP	C5D-O5D-PN-O1N
4	B	1257	NAP	C5D-O5D-PN-O2N
4	B	1257	NAP	O4D-C1D-N1N-C2N
4	C	1257	NAP	C5D-O5D-PN-O1N

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Mol	Chain	Res	Type	Atoms
4	C	1257	NAP	C5D-O5D-PN-O2N
4	D	1257	NAP	PN-O3-PA-O5B
4	D	1257	NAP	C2B-O2B-P2B-O3X
4	D	1257	NAP	C5D-O5D-PN-O1N
4	D	1257	NAP	C5D-O5D-PN-O2N
4	E	1257	NAP	PN-O3-PA-O5B
4	E	1257	NAP	C2B-O2B-P2B-O3X
4	E	1257	NAP	C5D-O5D-PN-O1N
4	E	1257	NAP	C5D-O5D-PN-O2N
4	E	1257	NAP	O4D-C1D-N1N-C2N
4	F	1257	NAP	PN-O3-PA-O5B
4	F	1257	NAP	C5D-O5D-PN-O1N
4	F	1257	NAP	C5D-O5D-PN-O2N
4	F	1257	NAP	O4D-C1D-N1N-C2N
4	G	1257	NAP	PN-O3-PA-O5B
4	G	1257	NAP	C5D-O5D-PN-O1N
4	G	1257	NAP	C5D-O5D-PN-O2N
4	G	1257	NAP	O4D-C1D-N1N-C2N
4	H	1257	NAP	PN-O3-PA-O5B
4	H	1257	NAP	C5D-O5D-PN-O1N
4	H	1257	NAP	O4D-C1D-N1N-C2N
3	D	1258	W0I	CAK-CAL-CAM-CAN
3	E	1258	W0I	CAK-CAL-CAM-CAN
2	B	1259	GLU	OXT-C-CA-N
3	H	1258	W0I	CAM-CAN-CAO-CAT
3	G	1258	W0I	CAK-CAL-CAM-CAN
3	F	1258	W0I	CAL-CAM-CAN-CAO
3	C	1258	W0I	CAK-CAL-CAM-CAN
3	G	1258	W0I	CAL-CAM-CAN-CAO
3	C	1258	W0I	CAL-CAM-CAN-CAO
3	A	1257	W0I	CAK-CAL-CAM-CAN
4	B	1257	NAP	PN-O3-PA-O5B
4	C	1257	NAP	PN-O3-PA-O5B
3	A	1257	W0I	CAL-CAM-CAN-CAO
3	A	1257	W0I	CAM-CAN-CAO-CAT
2	A	1258	GLU	C-CA-CB-CG
2	C	1259	GLU	C-CA-CB-CG
4	C	1257	NAP	C5D-O5D-PN-O3
4	D	1257	NAP	O4B-C4B-C5B-O5B
2	C	1259	GLU	OXT-C-CA-CB
4	H	1257	NAP	C5D-O5D-PN-O2N
2	F	1259	GLU	N-CA-CB-CG

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Mol	Chain	Res	Type	Atoms
2	B	1259	GLU	O-C-CA-CB
2	B	1259	GLU	OXT-C-CA-CB
2	C	1259	GLU	O-C-CA-CB
3	D	1258	W0I	CAM-CAN-CAO-CAT
2	F	1259	GLU	CA-CB-CG-CD
3	F	1258	W0I	CAK-CAL-CAM-CAN
3	H	1258	W0I	CAL-CAM-CAN-CAO
2	E	1259	GLU	CA-CB-CG-CD
4	A	1260	NAP	O4B-C4B-C5B-O5B
2	E	1259	GLU	O-C-CA-N
2	B	1259	GLU	OE2-CD-CG-CB
2	E	1259	GLU	OE2-CD-CG-CB
2	B	1259	GLU	OE1-CD-CG-CB
4	C	1257	NAP	O4B-C4B-C5B-O5B
4	G	1257	NAP	O4B-C4B-C5B-O5B
2	F	1259	GLU	C-CA-CB-CG
2	E	1259	GLU	OXT-C-CA-N
2	E	1259	GLU	OE1-CD-CG-CB
2	G	1259	GLU	CA-CB-CG-CD
4	A	1260	NAP	C5D-O5D-PN-O3
4	B	1257	NAP	C5D-O5D-PN-O3
4	D	1257	NAP	C5D-O5D-PN-O3
4	E	1257	NAP	C5D-O5D-PN-O3
4	F	1257	NAP	C5D-O5D-PN-O3
4	G	1257	NAP	C5D-O5D-PN-O3
4	H	1257	NAP	C5D-O5D-PN-O3
4	H	1257	NAP	O4B-C4B-C5B-O5B
4	B	1257	NAP	O4B-C4B-C5B-O5B
4	E	1257	NAP	O4B-C4B-C5B-O5B
4	F	1257	NAP	O4B-C4B-C5B-O5B

There are no ring outliers.

17 monomers are involved in 57 short contacts:

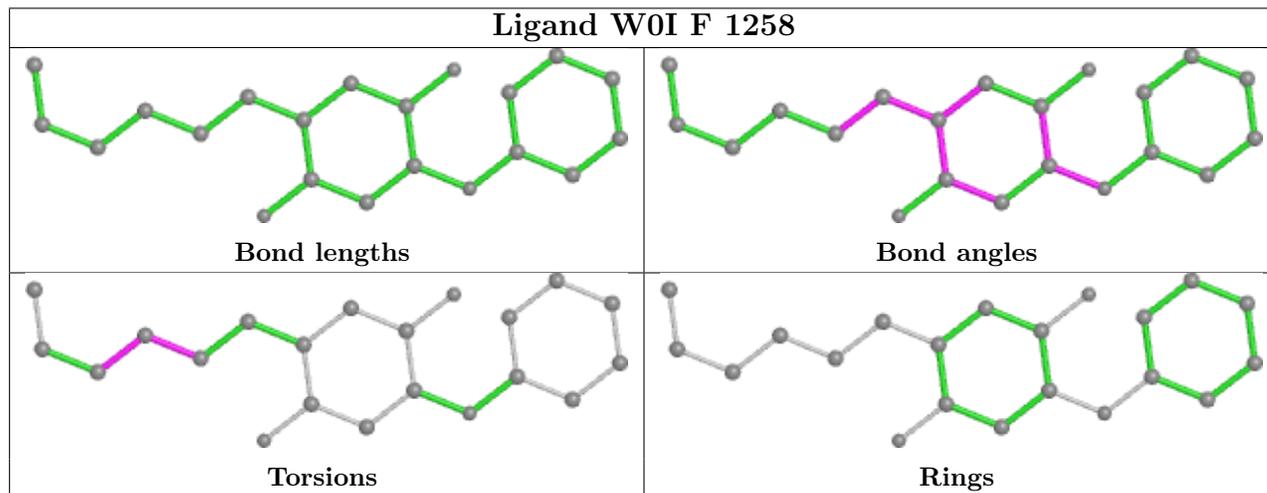
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1258	W0I	2	0
4	G	1257	NAP	1	0
2	B	1259	GLU	9	0
2	A	1258	GLU	4	0
3	E	1258	W0I	1	0
3	A	1257	W0I	2	0
2	F	1259	GLU	11	0

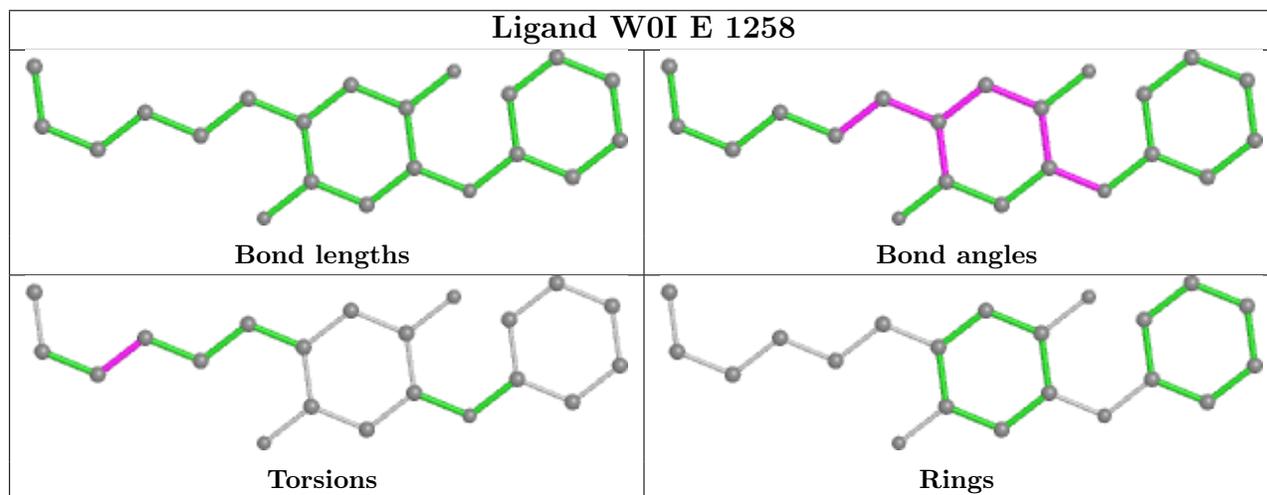
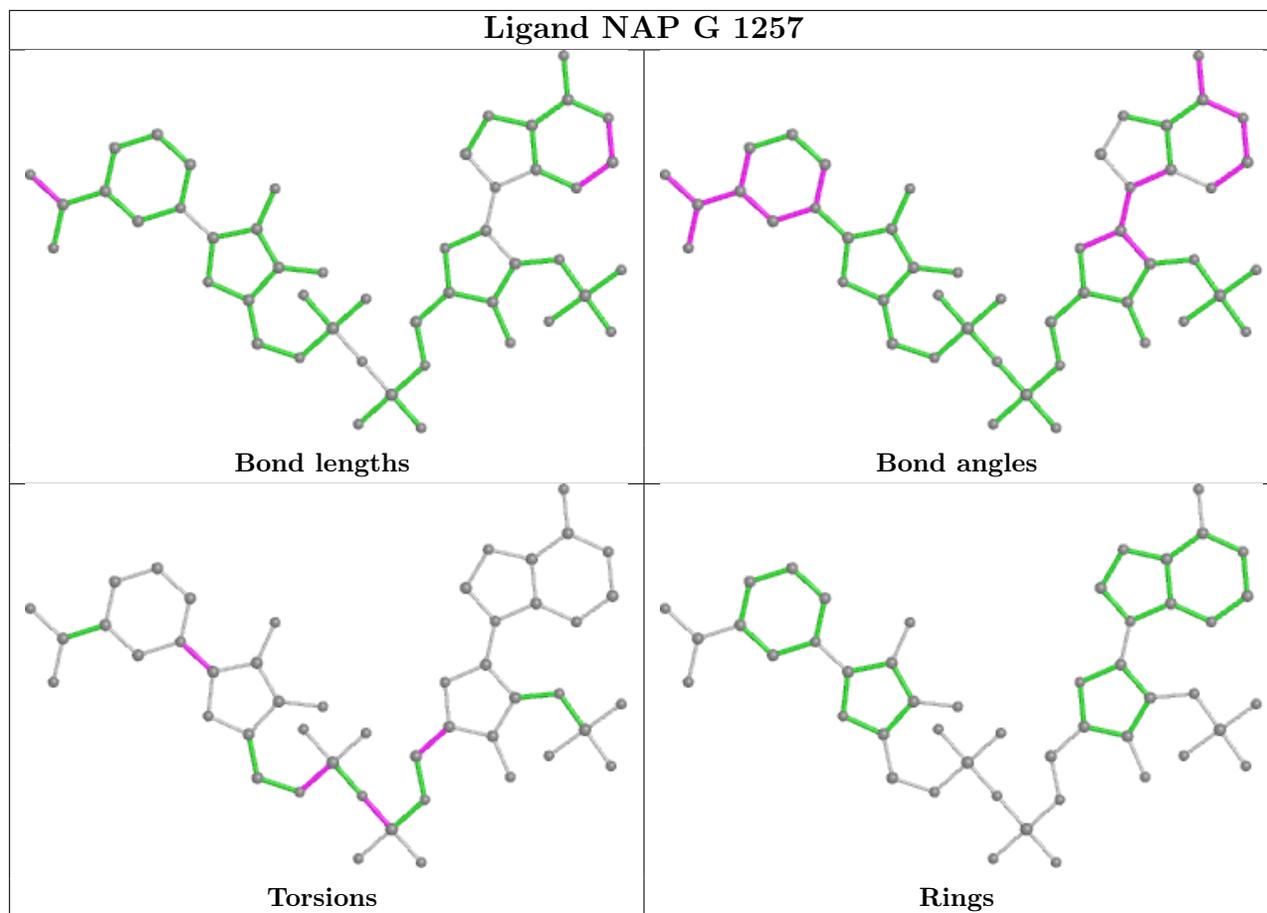
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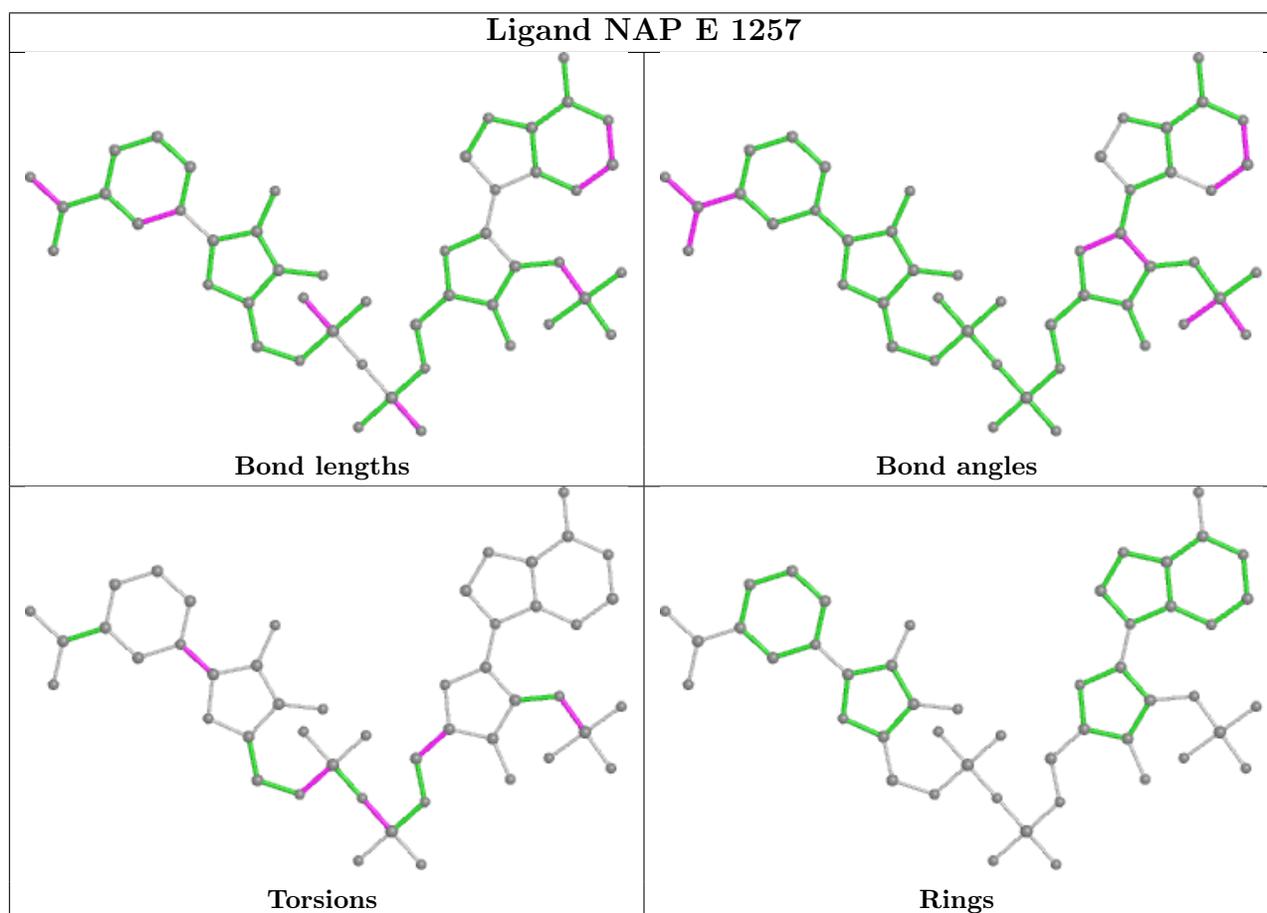
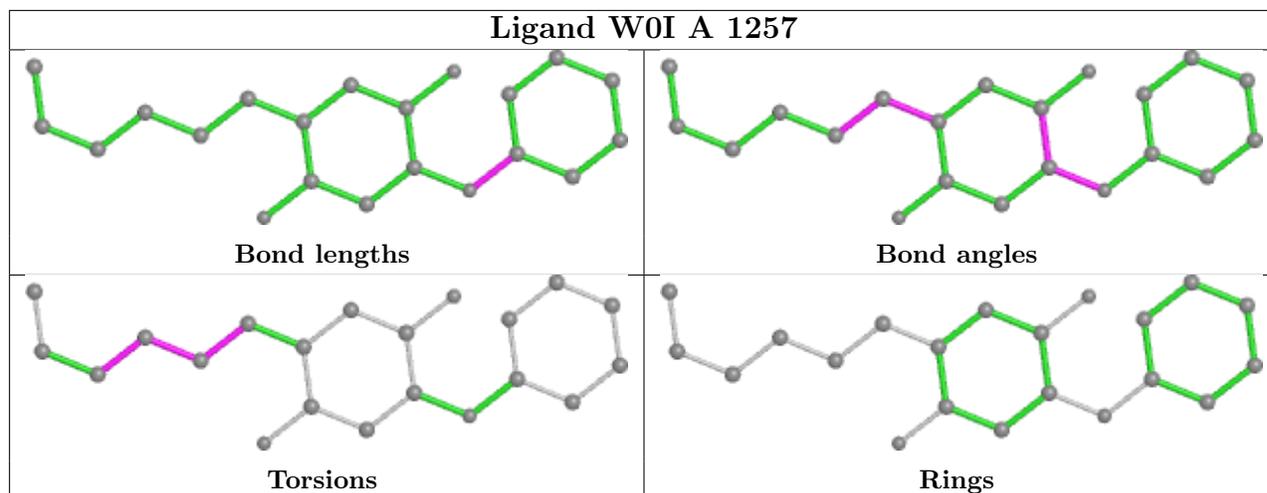
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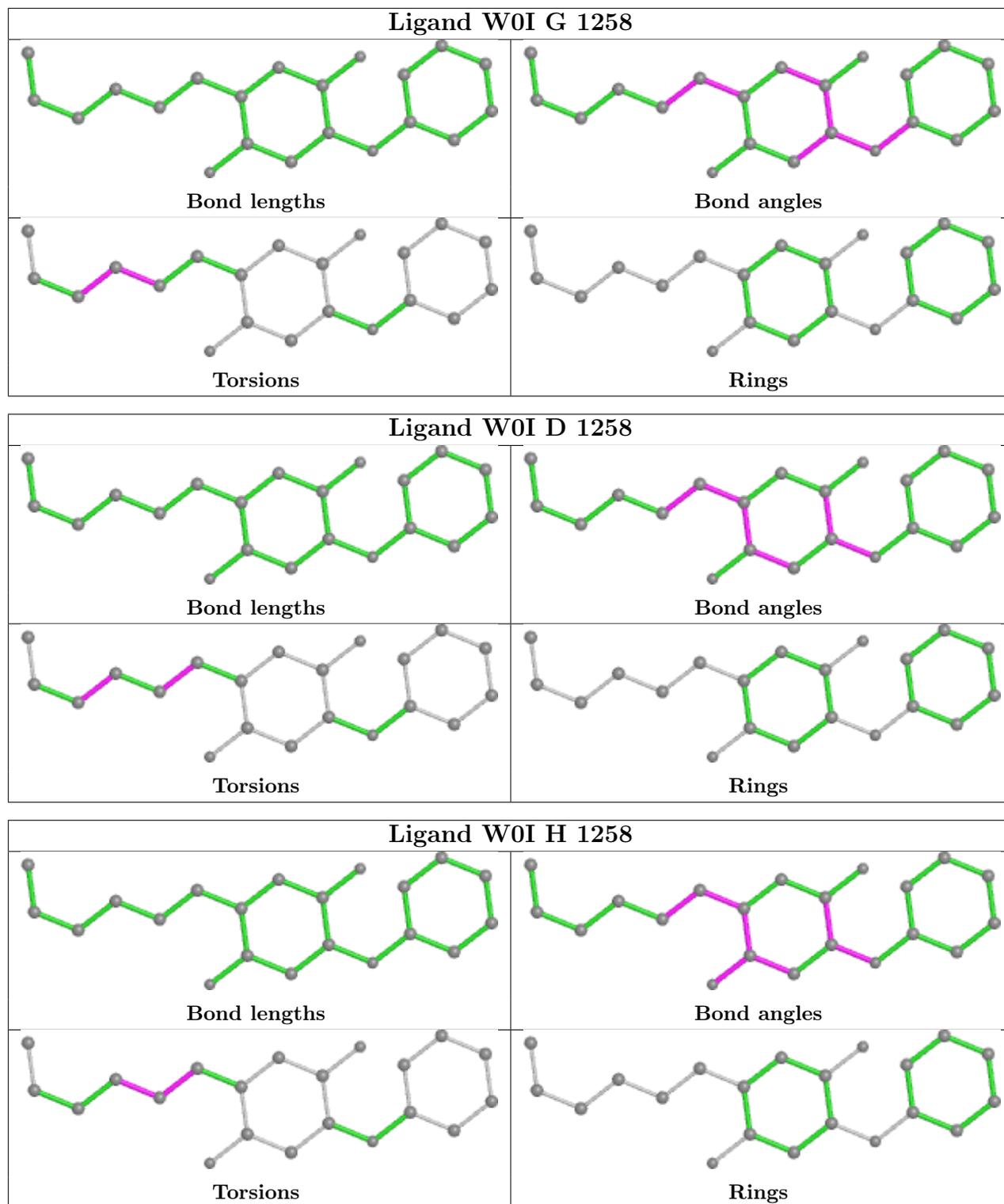
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1259	GLU	2	0
2	E	1259	GLU	4	0
3	D	1258	W0I	1	0
3	B	1258	W0I	1	0
4	D	1257	NAP	4	0
4	F	1257	NAP	1	0
4	C	1257	NAP	1	0
2	C	1259	GLU	10	0
3	C	1258	W0I	2	0
4	H	1257	NAP	2	0

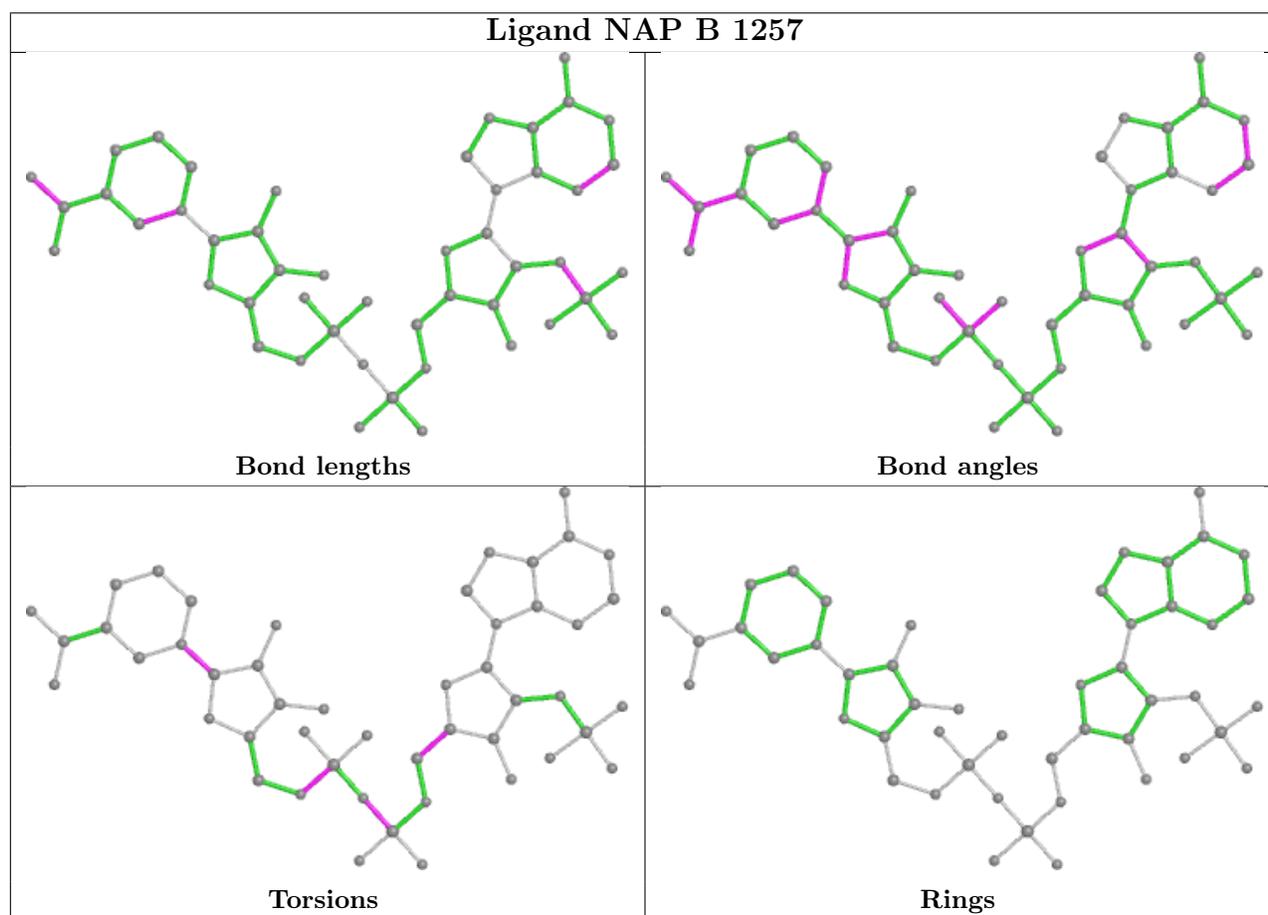
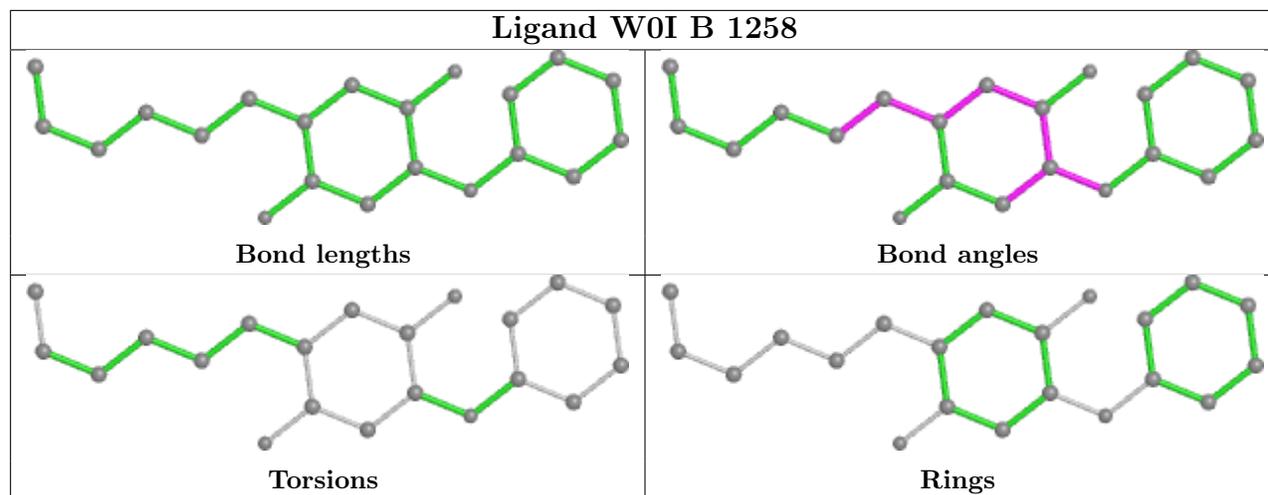
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

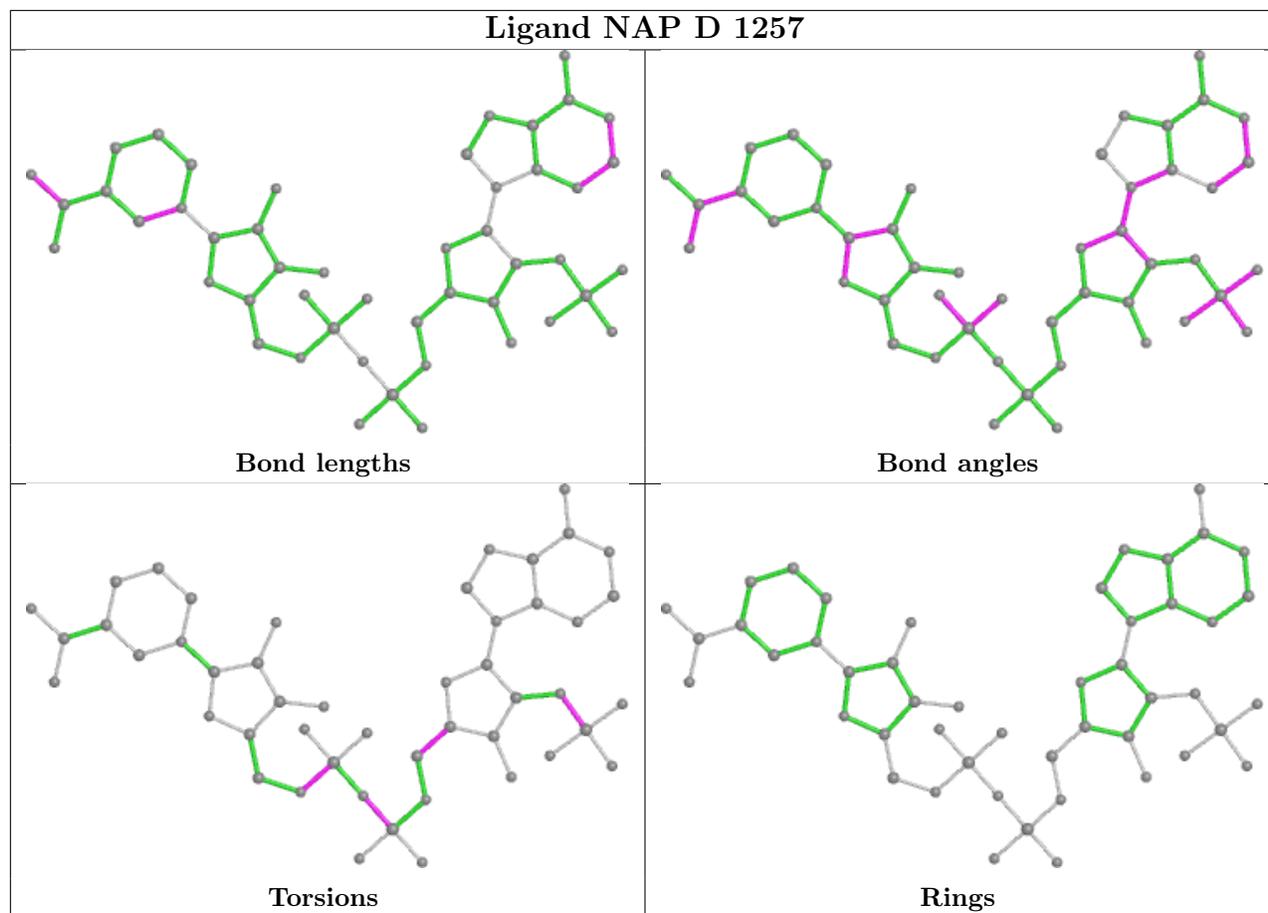


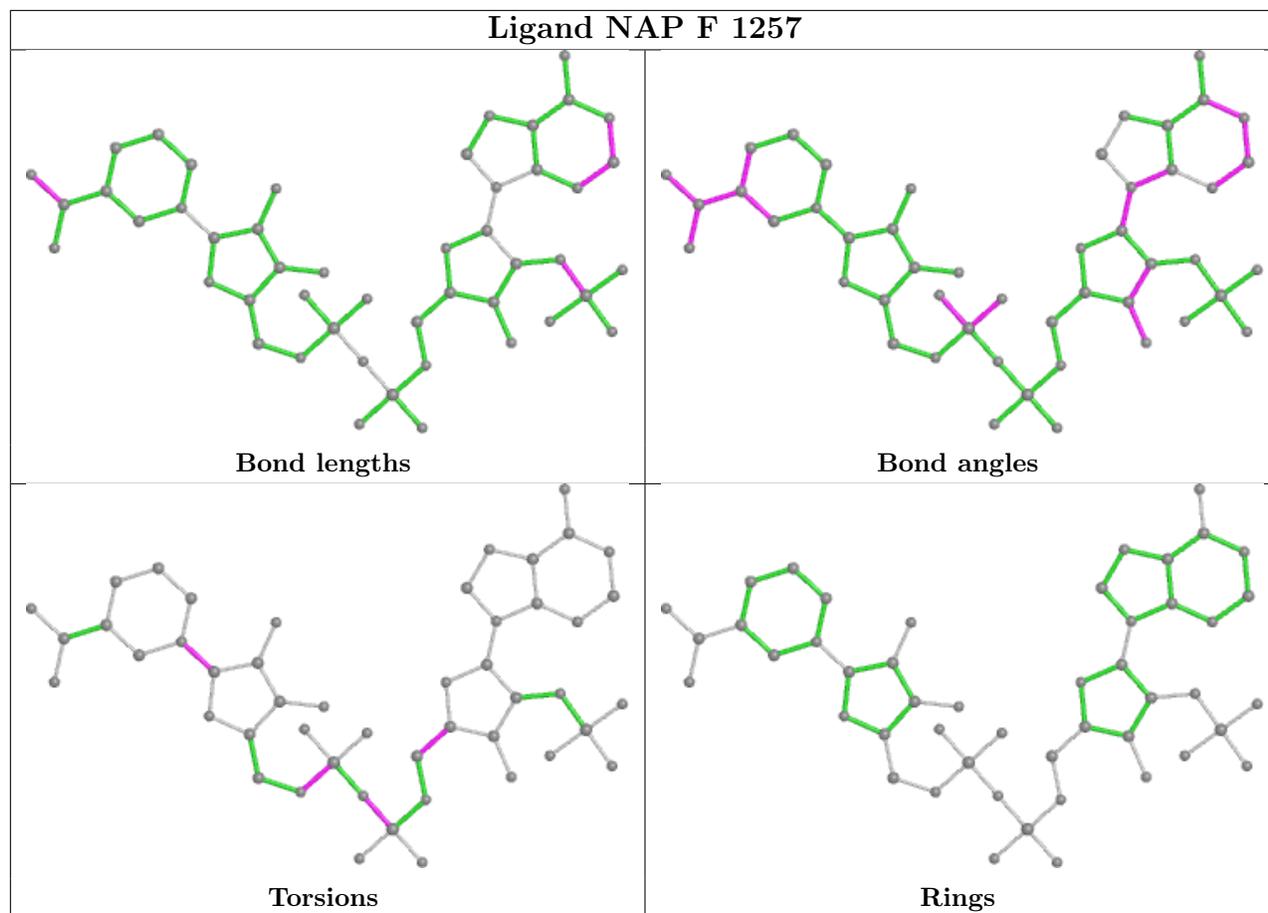


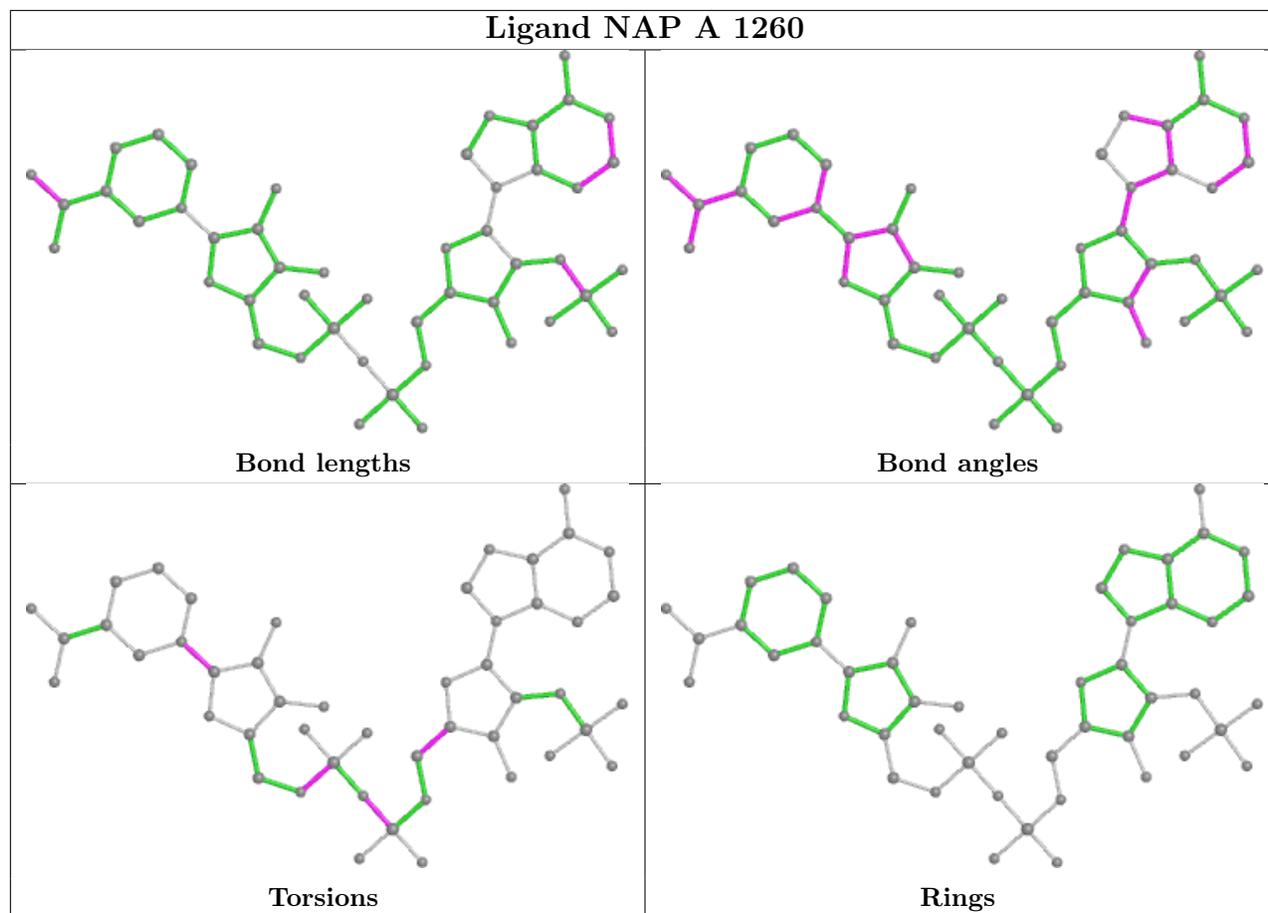


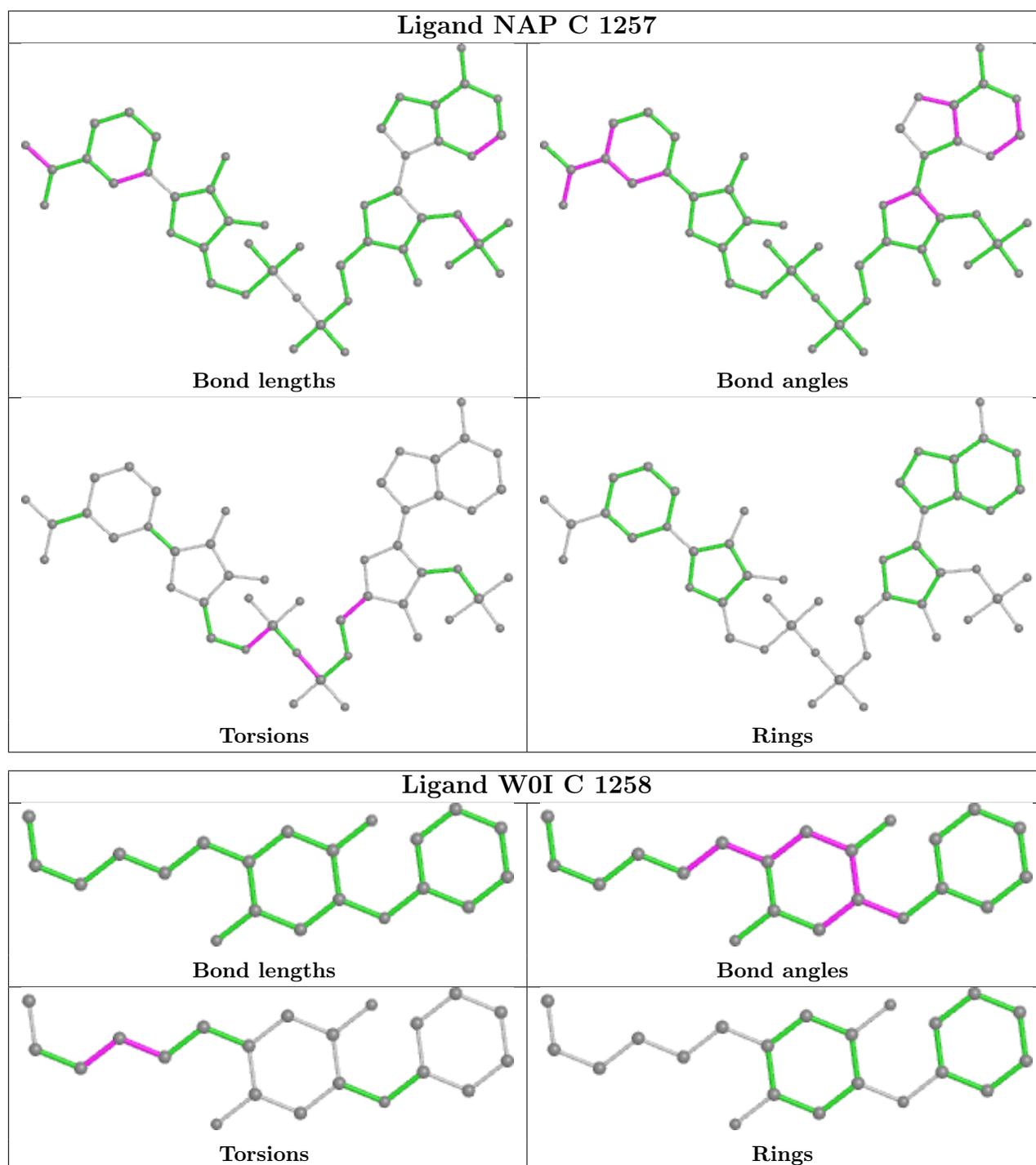


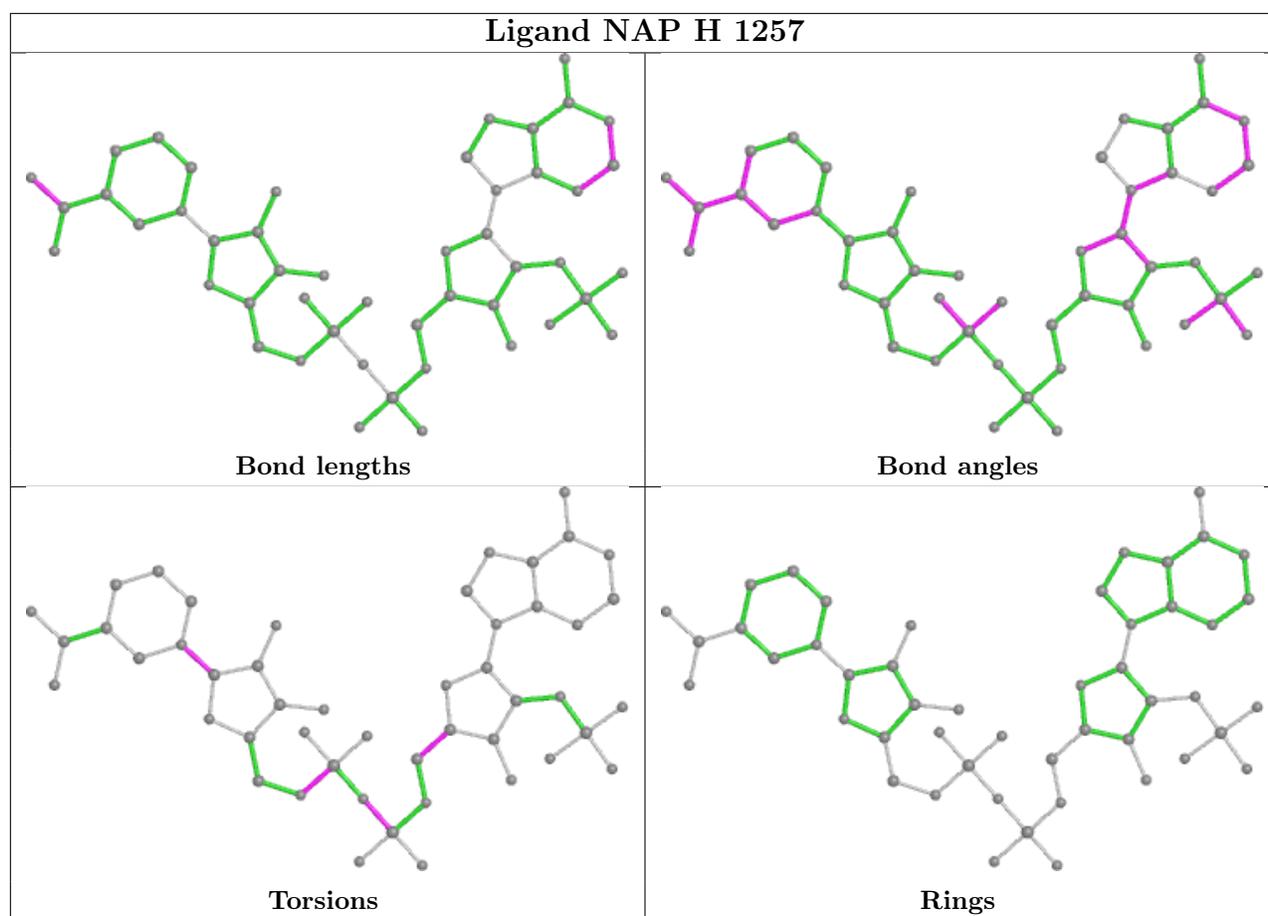












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [\(i\)](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	255/282 (90%)	-0.41	1 (0%) 92 92	14, 27, 51, 71	0
1	B	255/282 (90%)	-0.54	1 (0%) 92 92	17, 28, 54, 68	0
1	C	255/282 (90%)	-0.34	2 (0%) 86 85	18, 30, 55, 71	0
1	D	255/282 (90%)	-0.33	5 (1%) 65 64	20, 34, 68, 80	0
1	E	254/282 (90%)	-0.52	0 100 100	15, 27, 51, 61	0
1	F	255/282 (90%)	-0.47	3 (1%) 79 78	18, 30, 55, 72	0
1	G	254/282 (90%)	-0.33	2 (0%) 86 85	18, 30, 54, 72	0
1	H	254/282 (90%)	-0.44	3 (1%) 79 78	20, 33, 65, 92	0
All	All	2037/2256 (90%)	-0.42	17 (0%) 86 85	14, 30, 57, 92	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	2	VAL	4.5
1	C	2	VAL	3.8
1	F	2	VAL	3.4
1	D	58	PRO	2.9
1	F	6	ASN	2.8
1	A	2	VAL	2.4
1	D	246	ILE	2.4
1	H	58	PRO	2.4
1	D	6	ASN	2.3
1	F	246	ILE	2.2
1	H	56	ASN	2.2
1	C	60	ALA	2.2
1	G	82	LYS	2.1
1	G	143	VAL	2.1
1	B	2	VAL	2.1
1	H	104	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	99	MET	2.0

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

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

6.3 Carbohydrates [i](#)

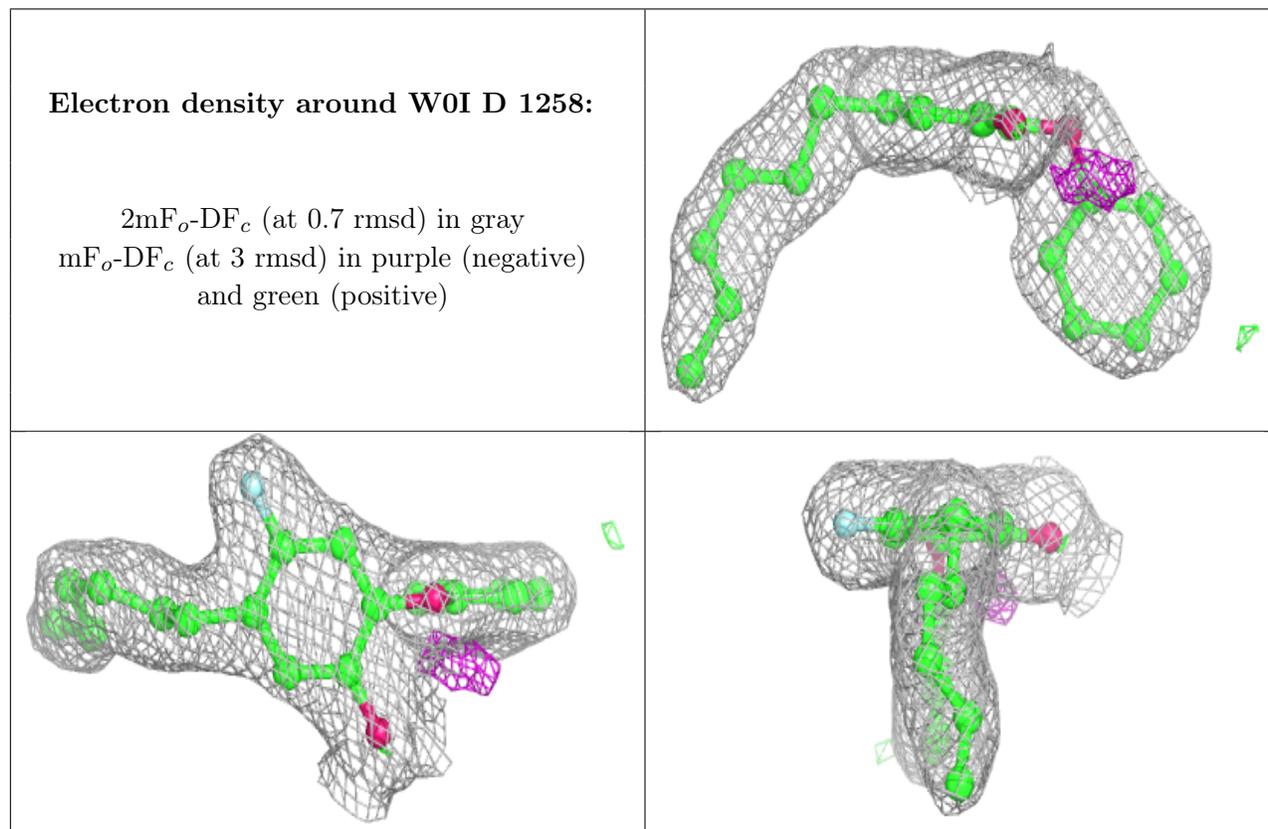
There are no monosaccharides in this entry.

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.

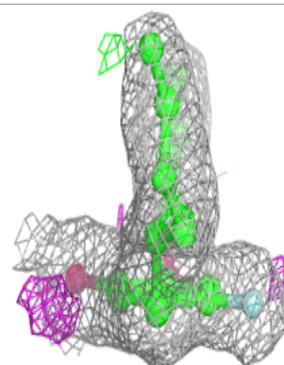
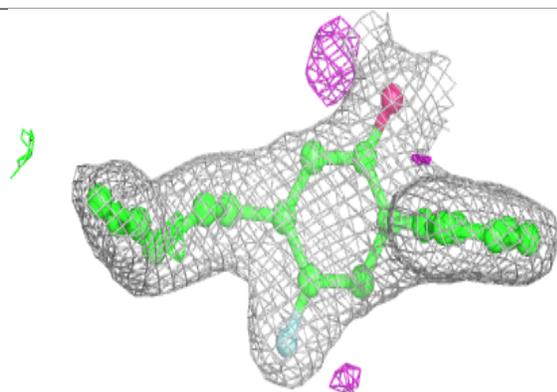
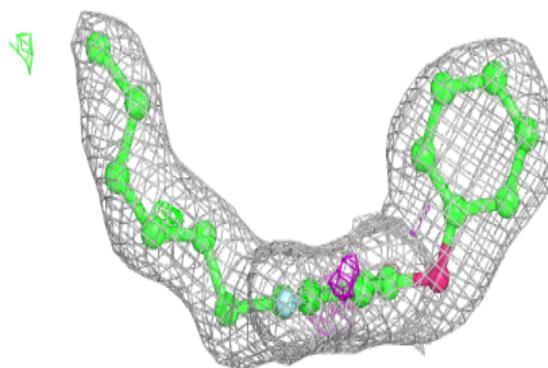
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLU	B	1259	10/10	0.68	0.20	89,90,93,96	0
2	GLU	F	1259	10/10	0.68	0.25	102,103,103,103	0
2	GLU	E	1259	10/10	0.70	0.24	98,109,110,110	0
2	GLU	A	1258	10/10	0.70	0.30	99,101,102,104	0
2	GLU	C	1259	10/10	0.73	0.20	89,92,94,94	0
2	GLU	G	1259	10/10	0.77	0.18	100,102,102,102	0
3	W0I	D	1258	21/21	0.93	0.11	35,39,43,44	0
3	W0I	H	1258	21/21	0.93	0.10	30,36,40,42	0
4	NAP	D	1257	48/48	0.96	0.08	29,33,49,52	0
3	W0I	A	1257	21/21	0.97	0.09	21,25,34,41	0
3	W0I	E	1258	21/21	0.97	0.08	22,25,32,33	0
3	W0I	G	1258	21/21	0.97	0.11	23,28,38,40	0
3	W0I	B	1258	21/21	0.97	0.07	24,28,36,37	0
3	W0I	C	1258	21/21	0.97	0.09	24,29,38,42	0
4	NAP	H	1257	48/48	0.97	0.07	26,32,47,50	0
4	NAP	B	1257	48/48	0.98	0.09	20,27,31,33	0
4	NAP	C	1257	48/48	0.98	0.10	22,28,35,37	0
3	W0I	F	1258	21/21	0.98	0.10	23,29,43,45	0
4	NAP	E	1257	48/48	0.98	0.10	18,24,30,35	0
4	NAP	F	1257	48/48	0.98	0.10	22,27,33,34	0
4	NAP	G	1257	48/48	0.98	0.10	18,28,33,41	0
4	NAP	A	1260	48/48	0.98	0.10	17,25,29,33	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.

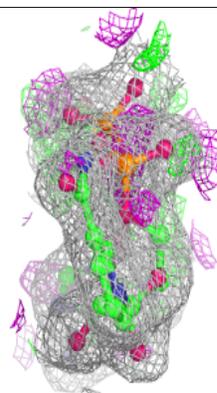
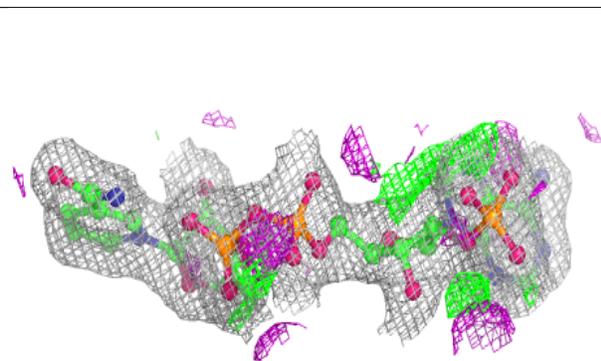
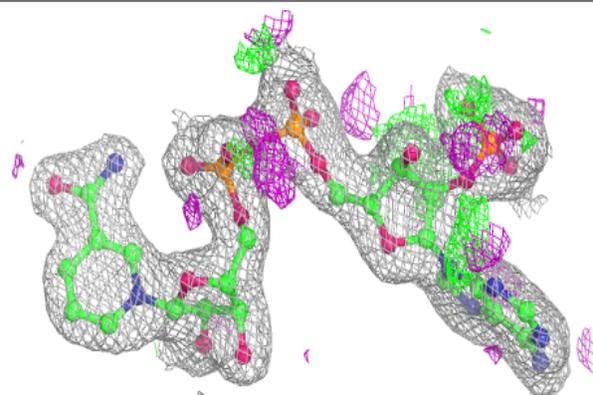


Electron density around WOI H 1258:

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

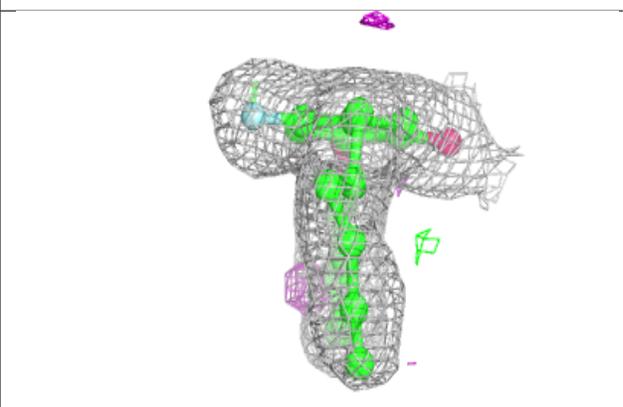
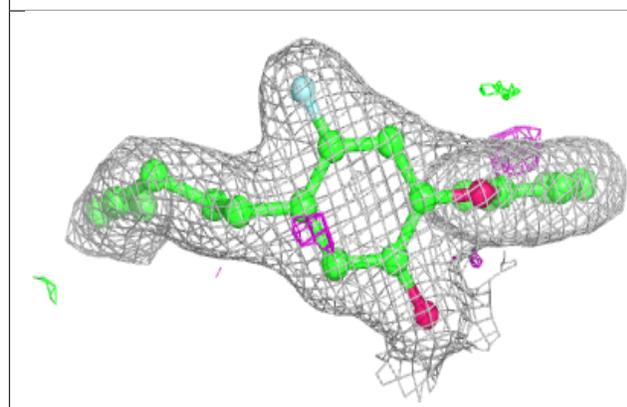
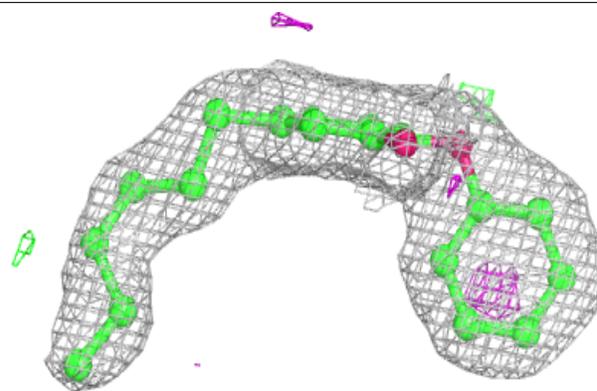
**Electron density around NAP D 1257:**

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

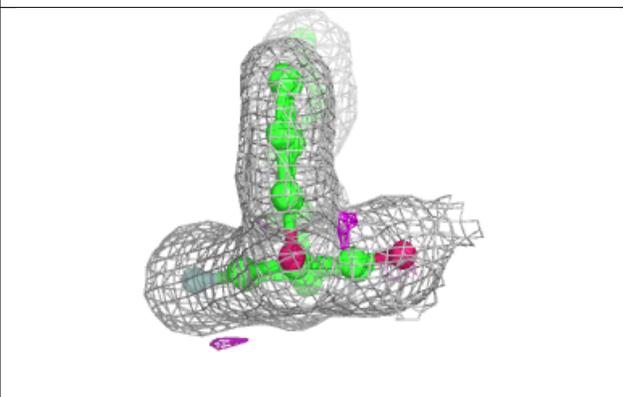
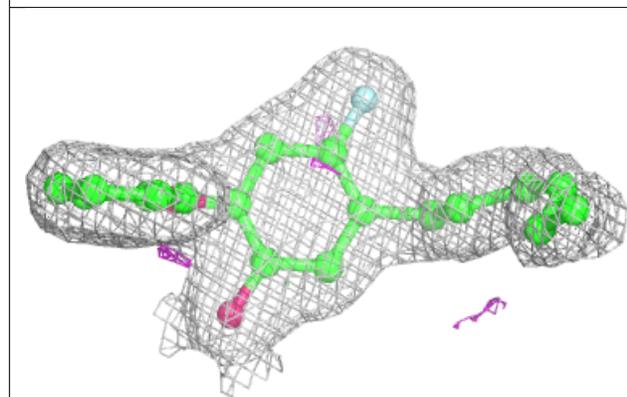
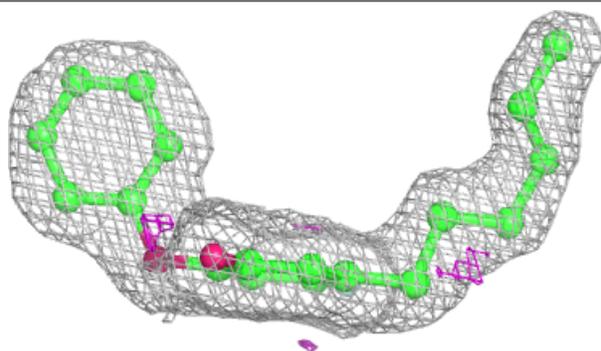


Electron density around WOI A 1257:

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

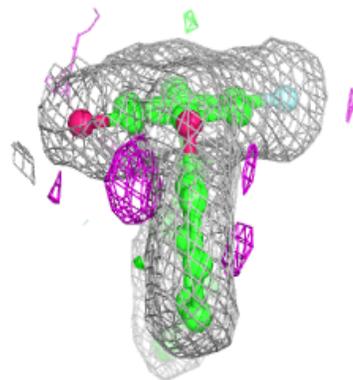
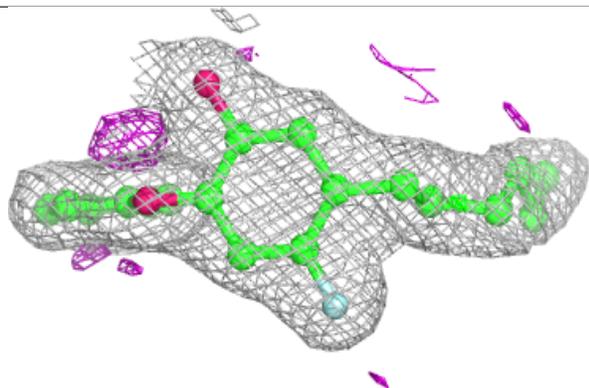
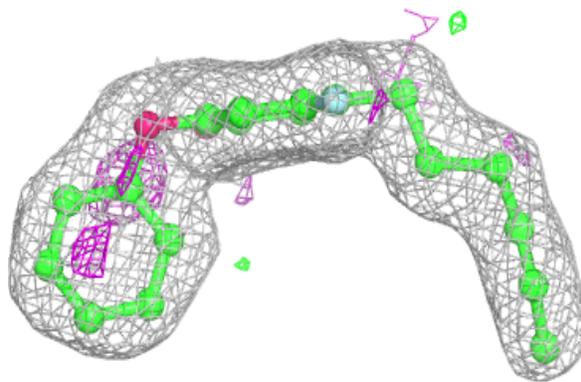
**Electron density around WOI E 1258:**

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

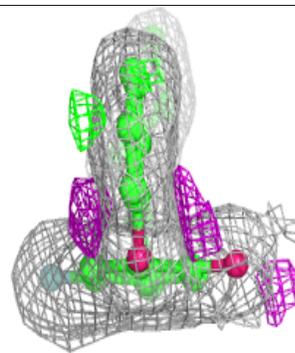
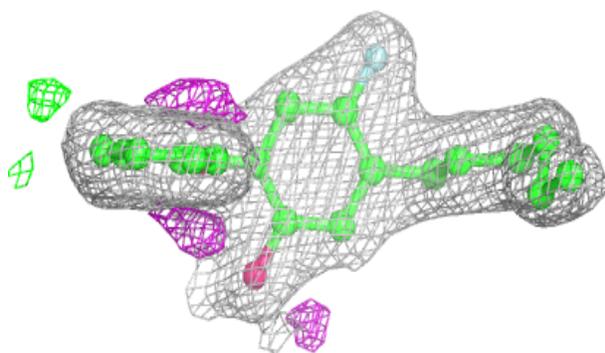
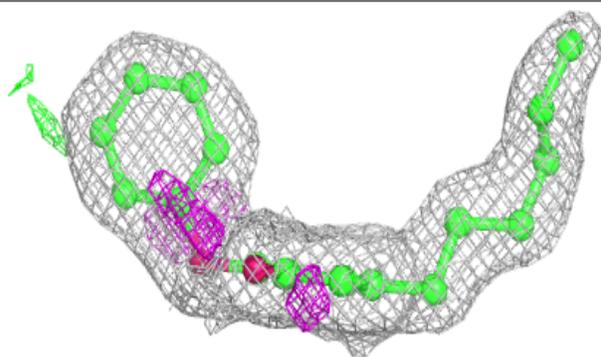


Electron density around WOI G 1258:

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

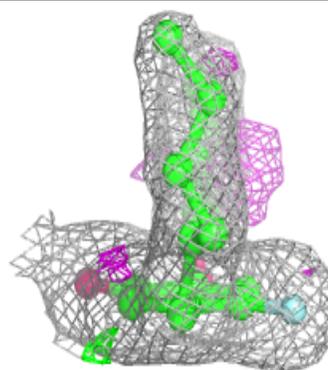
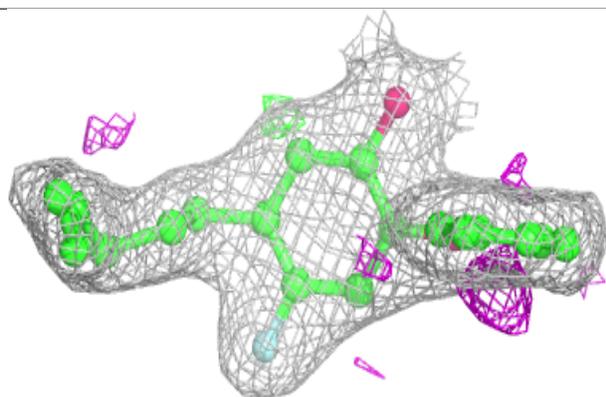
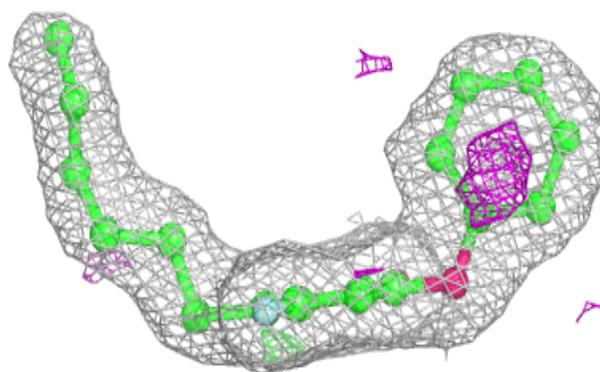
**Electron density around WOI B 1258:**

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

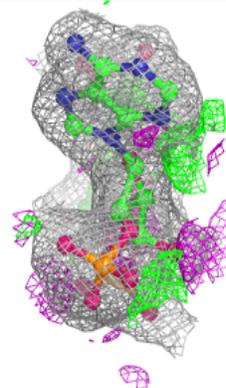
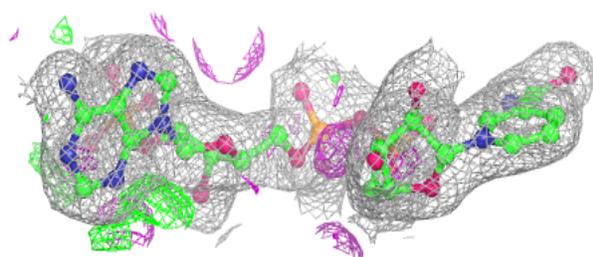
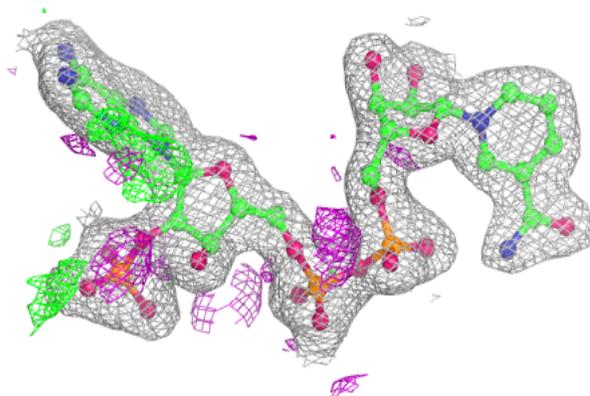


Electron density around WOI C 1258:

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

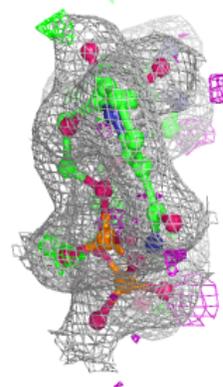
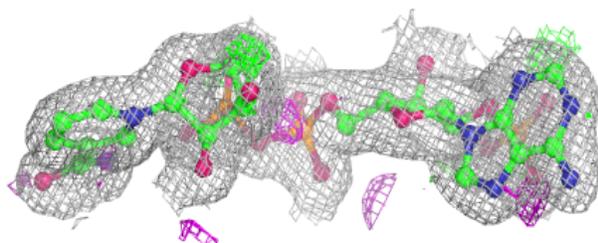
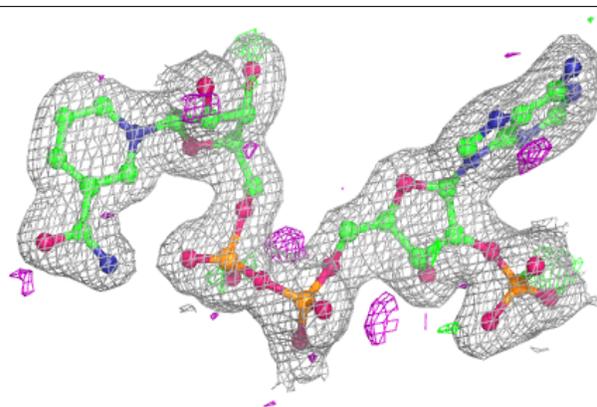
**Electron density around NAP H 1257:**

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

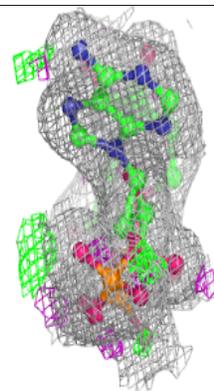
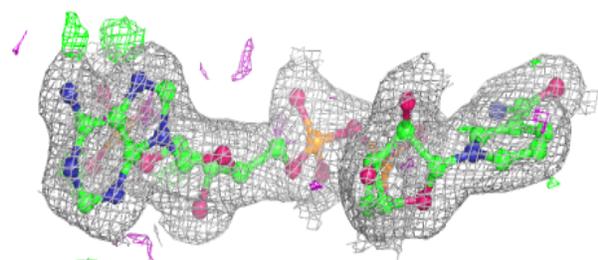
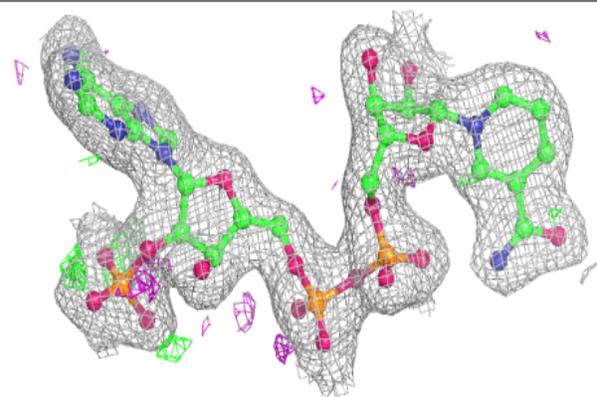


Electron density around NAP B 1257:

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

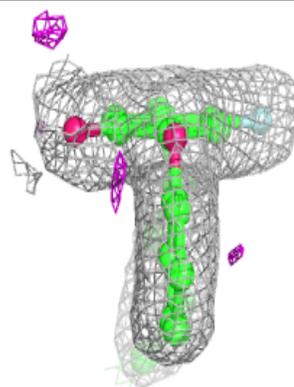
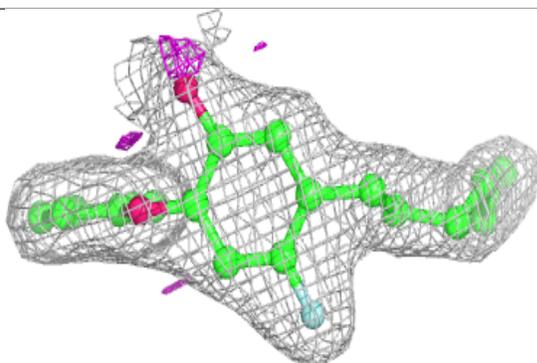
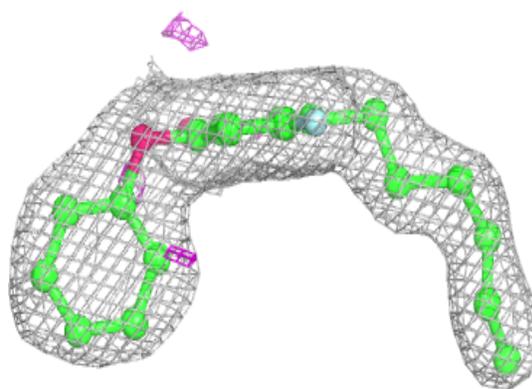
**Electron density around NAP C 1257:**

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

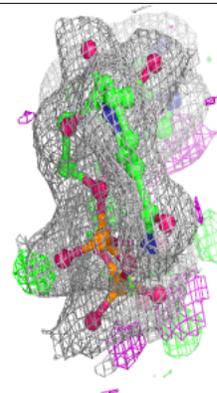
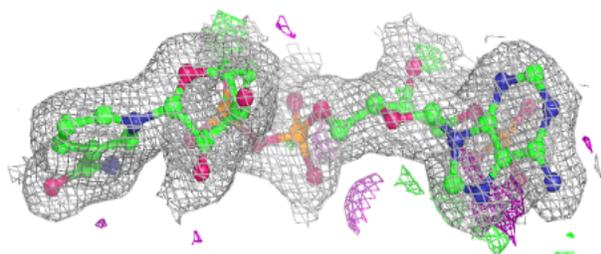
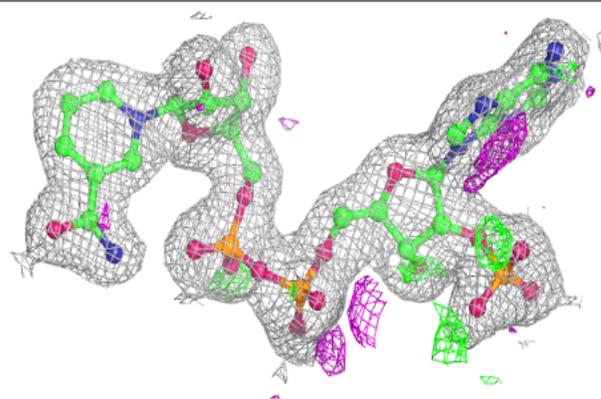


Electron density around WOI F 1258:

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

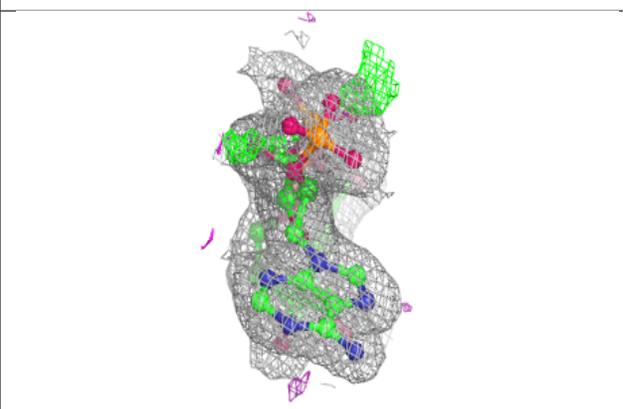
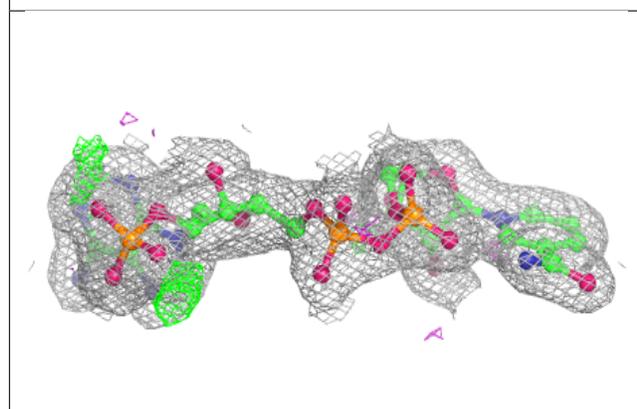
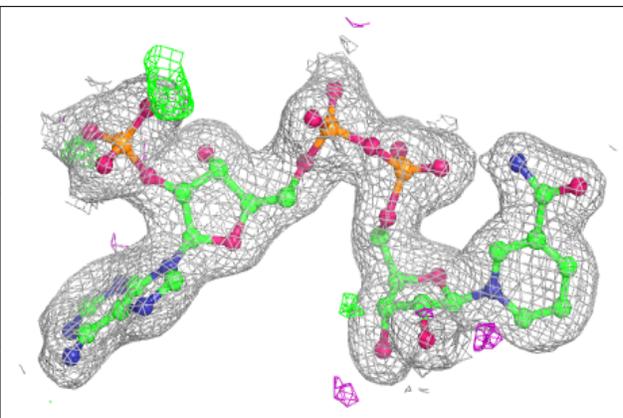
**Electron density around NAP E 1257:**

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

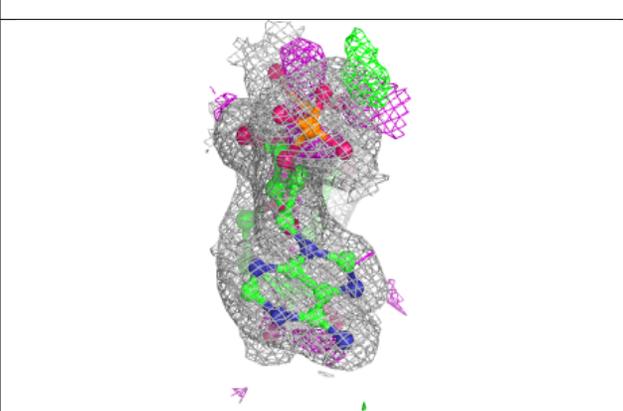
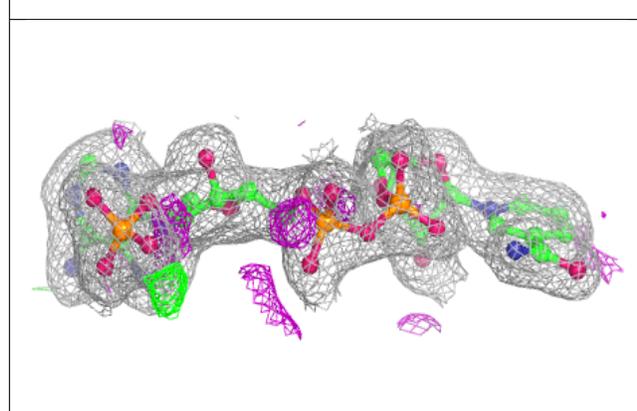
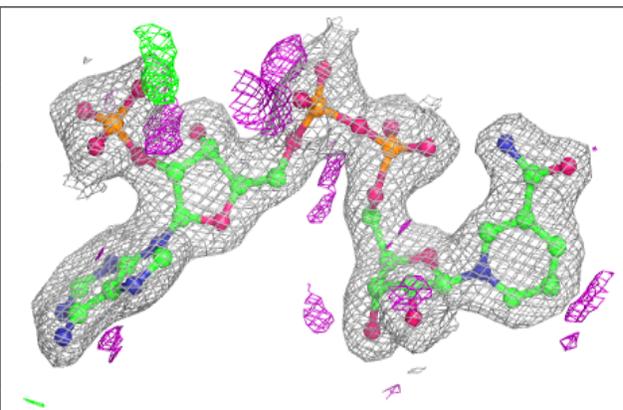


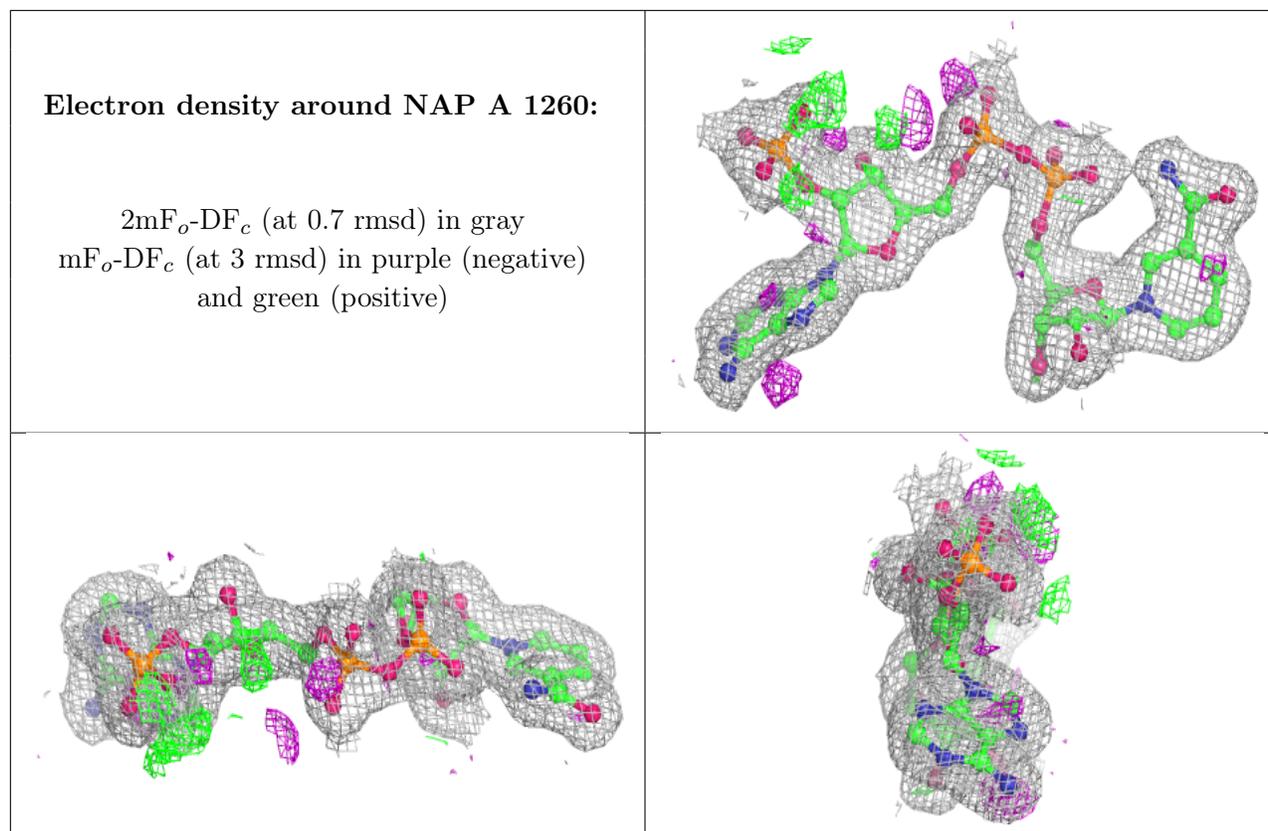
Electron density around NAP F 1257:

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

**Electron density around NAP G 1257:**

$2mF_o-DF_c$ (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.