



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:10 PM UTC

PDB ID : 5VG6 / pdb_00005vg6
Title : Crystal structure of D-isomer specific 2-hydroxyacid dehydrogenase from Xanthobacter autotrophicus Py2 in complex with NADPH and MES.
Authors : Lipowska, J.; Shabalin, I.G.; Kutner, J.; Gasiorowska, O.A.; Almo, S.C.; Minor, W.; New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2017-04-10
Resolution : 2.20 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:

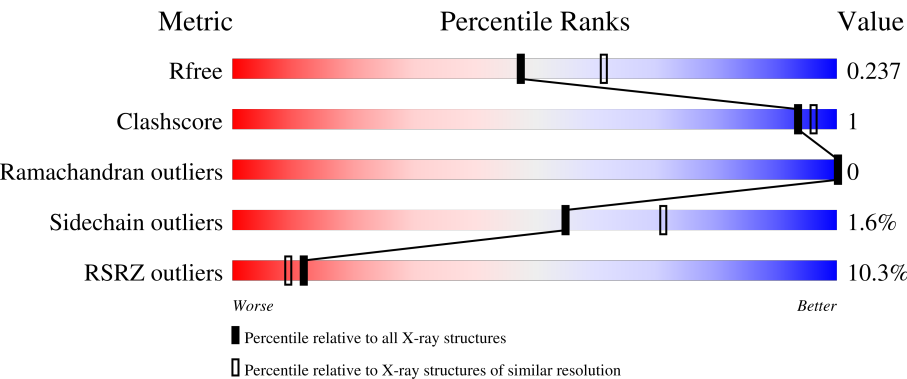
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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	341	% 88%8%
1	B	341	7% 89%8%
1	C	341	3% 89%8%
1	D	341	31% 84%6%10%

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Mol	Chain	Length	Quality of chain
1	E	341	3% 88% • 8%
1	F	341	19% 87% • • 9%
1	G	341	11% 68% • 29%
1	H	341	13% 68% • • 29%
1	I	341	% 88% • 8%
1	J	341	87% 5% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25838 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 D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	3	0
			2415	1537	445	425	8			
1	B	315	Total	C	N	O	S	0	0	0
			2387	1521	435	423	8			
1	C	315	Total	C	N	O	S	0	1	0
			2400	1530	433	429	8			
1	D	308	Total	C	N	O	S	0	0	0
			2274	1453	409	404	8			
1	E	314	Total	C	N	O	S	0	1	0
			2385	1520	432	425	8			
1	F	312	Total	C	N	O	S	0	0	0
			2284	1461	411	404	8			
1	G	242	Total	C	N	O	S	0	0	0
			1796	1142	323	323	8			
1	H	242	Total	C	N	O	S	0	0	0
			1789	1134	324	323	8			
1	I	315	Total	C	N	O	S	0	3	0
			2412	1537	437	430	8			
1	J	315	Total	C	N	O	S	0	3	0
			2428	1544	447	429	8			

There are 220 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	initiating methionine	UNP A7IIH0
A	-20	HIS	-	expression tag	UNP A7IIH0
A	-19	HIS	-	expression tag	UNP A7IIH0
A	-18	HIS	-	expression tag	UNP A7IIH0
A	-17	HIS	-	expression tag	UNP A7IIH0
A	-16	HIS	-	expression tag	UNP A7IIH0
A	-15	HIS	-	expression tag	UNP A7IIH0
A	-14	SER	-	expression tag	UNP A7IIH0
A	-13	SER	-	expression tag	UNP A7IIH0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	GLY	-	expression tag	UNP A7IIH0
A	-11	VAL	-	expression tag	UNP A7IIH0
A	-10	ASP	-	expression tag	UNP A7IIH0
A	-9	LEU	-	expression tag	UNP A7IIH0
A	-8	GLY	-	expression tag	UNP A7IIH0
A	-7	THR	-	expression tag	UNP A7IIH0
A	-6	GLU	-	expression tag	UNP A7IIH0
A	-5	ASN	-	expression tag	UNP A7IIH0
A	-4	LEU	-	expression tag	UNP A7IIH0
A	-3	TYR	-	expression tag	UNP A7IIH0
A	-2	PHE	-	expression tag	UNP A7IIH0
A	-1	GLN	-	expression tag	UNP A7IIH0
A	0	SER	-	expression tag	UNP A7IIH0
B	-21	MET	-	initiating methionine	UNP A7IIH0
B	-20	HIS	-	expression tag	UNP A7IIH0
B	-19	HIS	-	expression tag	UNP A7IIH0
B	-18	HIS	-	expression tag	UNP A7IIH0
B	-17	HIS	-	expression tag	UNP A7IIH0
B	-16	HIS	-	expression tag	UNP A7IIH0
B	-15	HIS	-	expression tag	UNP A7IIH0
B	-14	SER	-	expression tag	UNP A7IIH0
B	-13	SER	-	expression tag	UNP A7IIH0
B	-12	GLY	-	expression tag	UNP A7IIH0
B	-11	VAL	-	expression tag	UNP A7IIH0
B	-10	ASP	-	expression tag	UNP A7IIH0
B	-9	LEU	-	expression tag	UNP A7IIH0
B	-8	GLY	-	expression tag	UNP A7IIH0
B	-7	THR	-	expression tag	UNP A7IIH0
B	-6	GLU	-	expression tag	UNP A7IIH0
B	-5	ASN	-	expression tag	UNP A7IIH0
B	-4	LEU	-	expression tag	UNP A7IIH0
B	-3	TYR	-	expression tag	UNP A7IIH0
B	-2	PHE	-	expression tag	UNP A7IIH0
B	-1	GLN	-	expression tag	UNP A7IIH0
B	0	SER	-	expression tag	UNP A7IIH0
C	-21	MET	-	initiating methionine	UNP A7IIH0
C	-20	HIS	-	expression tag	UNP A7IIH0
C	-19	HIS	-	expression tag	UNP A7IIH0
C	-18	HIS	-	expression tag	UNP A7IIH0
C	-17	HIS	-	expression tag	UNP A7IIH0
C	-16	HIS	-	expression tag	UNP A7IIH0
C	-15	HIS	-	expression tag	UNP A7IIH0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	SER	-	expression tag	UNP A7IIH0
C	-13	SER	-	expression tag	UNP A7IIH0
C	-12	GLY	-	expression tag	UNP A7IIH0
C	-11	VAL	-	expression tag	UNP A7IIH0
C	-10	ASP	-	expression tag	UNP A7IIH0
C	-9	LEU	-	expression tag	UNP A7IIH0
C	-8	GLY	-	expression tag	UNP A7IIH0
C	-7	THR	-	expression tag	UNP A7IIH0
C	-6	GLU	-	expression tag	UNP A7IIH0
C	-5	ASN	-	expression tag	UNP A7IIH0
C	-4	LEU	-	expression tag	UNP A7IIH0
C	-3	TYR	-	expression tag	UNP A7IIH0
C	-2	PHE	-	expression tag	UNP A7IIH0
C	-1	GLN	-	expression tag	UNP A7IIH0
C	0	SER	-	expression tag	UNP A7IIH0
D	-21	MET	-	initiating methionine	UNP A7IIH0
D	-20	HIS	-	expression tag	UNP A7IIH0
D	-19	HIS	-	expression tag	UNP A7IIH0
D	-18	HIS	-	expression tag	UNP A7IIH0
D	-17	HIS	-	expression tag	UNP A7IIH0
D	-16	HIS	-	expression tag	UNP A7IIH0
D	-15	HIS	-	expression tag	UNP A7IIH0
D	-14	SER	-	expression tag	UNP A7IIH0
D	-13	SER	-	expression tag	UNP A7IIH0
D	-12	GLY	-	expression tag	UNP A7IIH0
D	-11	VAL	-	expression tag	UNP A7IIH0
D	-10	ASP	-	expression tag	UNP A7IIH0
D	-9	LEU	-	expression tag	UNP A7IIH0
D	-8	GLY	-	expression tag	UNP A7IIH0
D	-7	THR	-	expression tag	UNP A7IIH0
D	-6	GLU	-	expression tag	UNP A7IIH0
D	-5	ASN	-	expression tag	UNP A7IIH0
D	-4	LEU	-	expression tag	UNP A7IIH0
D	-3	TYR	-	expression tag	UNP A7IIH0
D	-2	PHE	-	expression tag	UNP A7IIH0
D	-1	GLN	-	expression tag	UNP A7IIH0
D	0	SER	-	expression tag	UNP A7IIH0
E	-21	MET	-	initiating methionine	UNP A7IIH0
E	-20	HIS	-	expression tag	UNP A7IIH0
E	-19	HIS	-	expression tag	UNP A7IIH0
E	-18	HIS	-	expression tag	UNP A7IIH0
E	-17	HIS	-	expression tag	UNP A7IIH0

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-16	HIS	-	expression tag	UNP A7IIH0
E	-15	HIS	-	expression tag	UNP A7IIH0
E	-14	SER	-	expression tag	UNP A7IIH0
E	-13	SER	-	expression tag	UNP A7IIH0
E	-12	GLY	-	expression tag	UNP A7IIH0
E	-11	VAL	-	expression tag	UNP A7IIH0
E	-10	ASP	-	expression tag	UNP A7IIH0
E	-9	LEU	-	expression tag	UNP A7IIH0
E	-8	GLY	-	expression tag	UNP A7IIH0
E	-7	THR	-	expression tag	UNP A7IIH0
E	-6	GLU	-	expression tag	UNP A7IIH0
E	-5	ASN	-	expression tag	UNP A7IIH0
E	-4	LEU	-	expression tag	UNP A7IIH0
E	-3	TYR	-	expression tag	UNP A7IIH0
E	-2	PHE	-	expression tag	UNP A7IIH0
E	-1	GLN	-	expression tag	UNP A7IIH0
E	0	SER	-	expression tag	UNP A7IIH0
F	-21	MET	-	initiating methionine	UNP A7IIH0
F	-20	HIS	-	expression tag	UNP A7IIH0
F	-19	HIS	-	expression tag	UNP A7IIH0
F	-18	HIS	-	expression tag	UNP A7IIH0
F	-17	HIS	-	expression tag	UNP A7IIH0
F	-16	HIS	-	expression tag	UNP A7IIH0
F	-15	HIS	-	expression tag	UNP A7IIH0
F	-14	SER	-	expression tag	UNP A7IIH0
F	-13	SER	-	expression tag	UNP A7IIH0
F	-12	GLY	-	expression tag	UNP A7IIH0
F	-11	VAL	-	expression tag	UNP A7IIH0
F	-10	ASP	-	expression tag	UNP A7IIH0
F	-9	LEU	-	expression tag	UNP A7IIH0
F	-8	GLY	-	expression tag	UNP A7IIH0
F	-7	THR	-	expression tag	UNP A7IIH0
F	-6	GLU	-	expression tag	UNP A7IIH0
F	-5	ASN	-	expression tag	UNP A7IIH0
F	-4	LEU	-	expression tag	UNP A7IIH0
F	-3	TYR	-	expression tag	UNP A7IIH0
F	-2	PHE	-	expression tag	UNP A7IIH0
F	-1	GLN	-	expression tag	UNP A7IIH0
F	0	SER	-	expression tag	UNP A7IIH0
G	-21	MET	-	initiating methionine	UNP A7IIH0
G	-20	HIS	-	expression tag	UNP A7IIH0
G	-19	HIS	-	expression tag	UNP A7IIH0

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-18	HIS	-	expression tag	UNP A7IIH0
G	-17	HIS	-	expression tag	UNP A7IIH0
G	-16	HIS	-	expression tag	UNP A7IIH0
G	-15	HIS	-	expression tag	UNP A7IIH0
G	-14	SER	-	expression tag	UNP A7IIH0
G	-13	SER	-	expression tag	UNP A7IIH0
G	-12	GLY	-	expression tag	UNP A7IIH0
G	-11	VAL	-	expression tag	UNP A7IIH0
G	-10	ASP	-	expression tag	UNP A7IIH0
G	-9	LEU	-	expression tag	UNP A7IIH0
G	-8	GLY	-	expression tag	UNP A7IIH0
G	-7	THR	-	expression tag	UNP A7IIH0
G	-6	GLU	-	expression tag	UNP A7IIH0
G	-5	ASN	-	expression tag	UNP A7IIH0
G	-4	LEU	-	expression tag	UNP A7IIH0
G	-3	TYR	-	expression tag	UNP A7IIH0
G	-2	PHE	-	expression tag	UNP A7IIH0
G	-1	GLN	-	expression tag	UNP A7IIH0
G	0	SER	-	expression tag	UNP A7IIH0
H	-21	MET	-	initiating methionine	UNP A7IIH0
H	-20	HIS	-	expression tag	UNP A7IIH0
H	-19	HIS	-	expression tag	UNP A7IIH0
H	-18	HIS	-	expression tag	UNP A7IIH0
H	-17	HIS	-	expression tag	UNP A7IIH0
H	-16	HIS	-	expression tag	UNP A7IIH0
H	-15	HIS	-	expression tag	UNP A7IIH0
H	-14	SER	-	expression tag	UNP A7IIH0
H	-13	SER	-	expression tag	UNP A7IIH0
H	-12	GLY	-	expression tag	UNP A7IIH0
H	-11	VAL	-	expression tag	UNP A7IIH0
H	-10	ASP	-	expression tag	UNP A7IIH0
H	-9	LEU	-	expression tag	UNP A7IIH0
H	-8	GLY	-	expression tag	UNP A7IIH0
H	-7	THR	-	expression tag	UNP A7IIH0
H	-6	GLU	-	expression tag	UNP A7IIH0
H	-5	ASN	-	expression tag	UNP A7IIH0
H	-4	LEU	-	expression tag	UNP A7IIH0
H	-3	TYR	-	expression tag	UNP A7IIH0
H	-2	PHE	-	expression tag	UNP A7IIH0
H	-1	GLN	-	expression tag	UNP A7IIH0
H	0	SER	-	expression tag	UNP A7IIH0
I	-21	MET	-	initiating methionine	UNP A7IIH0

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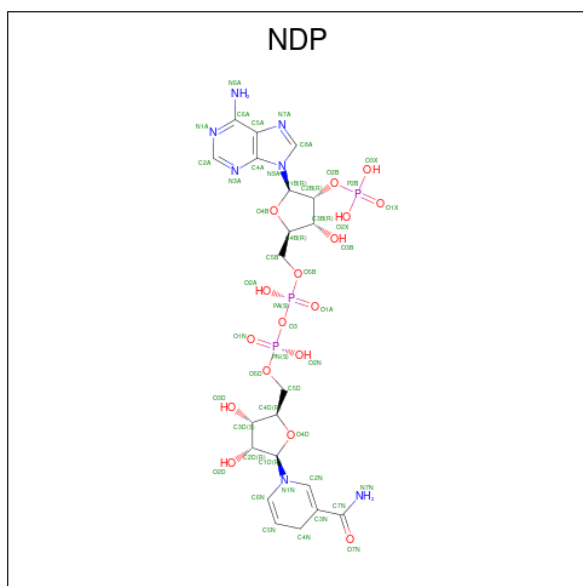
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I	-19	HIS	-	expression tag	UNP A7IIH0
I	-18	HIS	-	expression tag	UNP A7IIH0
I	-17	HIS	-	expression tag	UNP A7IIH0
I	-16	HIS	-	expression tag	UNP A7IIH0
I	-15	HIS	-	expression tag	UNP A7IIH0
I	-14	SER	-	expression tag	UNP A7IIH0
I	-13	SER	-	expression tag	UNP A7IIH0
I	-12	GLY	-	expression tag	UNP A7IIH0
I	-11	VAL	-	expression tag	UNP A7IIH0
I	-10	ASP	-	expression tag	UNP A7IIH0
I	-9	LEU	-	expression tag	UNP A7IIH0
I	-8	GLY	-	expression tag	UNP A7IIH0
I	-7	THR	-	expression tag	UNP A7IIH0
I	-6	GLU	-	expression tag	UNP A7IIH0
I	-5	ASN	-	expression tag	UNP A7IIH0
I	-4	LEU	-	expression tag	UNP A7IIH0
I	-3	TYR	-	expression tag	UNP A7IIH0
I	-2	PHE	-	expression tag	UNP A7IIH0
I	-1	GLN	-	expression tag	UNP A7IIH0
I	0	SER	-	expression tag	UNP A7IIH0
J	-21	MET	-	initiating methionine	UNP A7IIH0
J	-20	HIS	-	expression tag	UNP A7IIH0
J	-19	HIS	-	expression tag	UNP A7IIH0
J	-18	HIS	-	expression tag	UNP A7IIH0
J	-17	HIS	-	expression tag	UNP A7IIH0
J	-16	HIS	-	expression tag	UNP A7IIH0
J	-15	HIS	-	expression tag	UNP A7IIH0
J	-14	SER	-	expression tag	UNP A7IIH0
J	-13	SER	-	expression tag	UNP A7IIH0
J	-12	GLY	-	expression tag	UNP A7IIH0
J	-11	VAL	-	expression tag	UNP A7IIH0
J	-10	ASP	-	expression tag	UNP A7IIH0
J	-9	LEU	-	expression tag	UNP A7IIH0
J	-8	GLY	-	expression tag	UNP A7IIH0
J	-7	THR	-	expression tag	UNP A7IIH0
J	-6	GLU	-	expression tag	UNP A7IIH0
J	-5	ASN	-	expression tag	UNP A7IIH0
J	-4	LEU	-	expression tag	UNP A7IIH0
J	-3	TYR	-	expression tag	UNP A7IIH0
J	-2	PHE	-	expression tag	UNP A7IIH0
J	-1	GLN	-	expression tag	UNP A7IIH0

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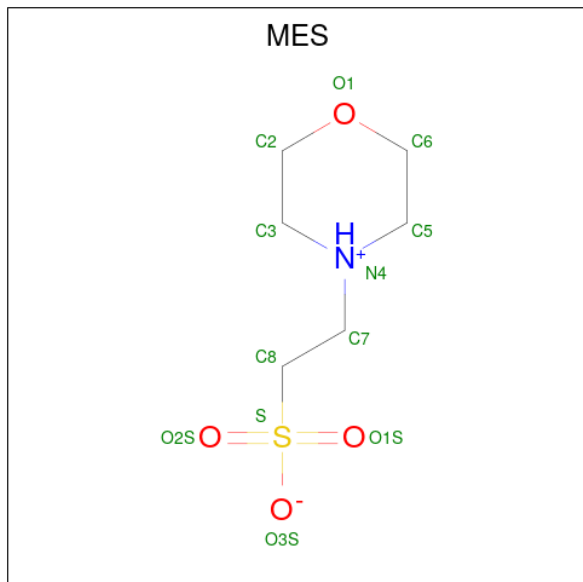
Chain	Residue	Modelled	Actual	Comment	Reference
J	0	SER	-	expression tag	UNP A7IIH0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



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

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	E	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	I	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	J	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 4 is water.

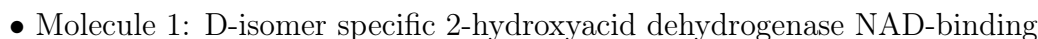
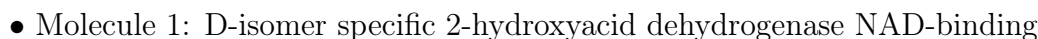
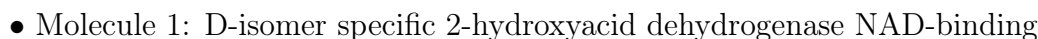
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	456	Total	O	0	0
			456	456		

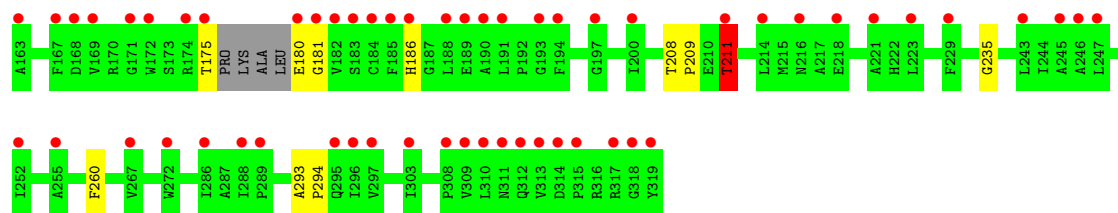
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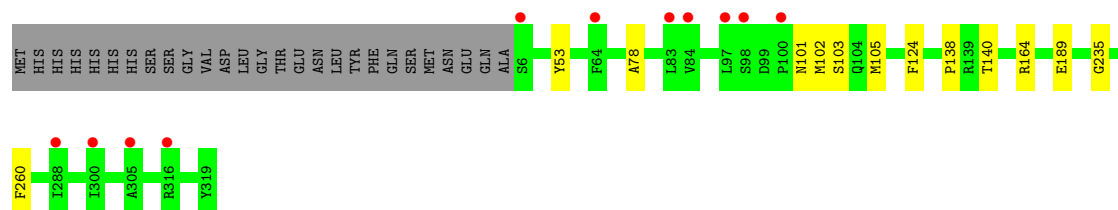
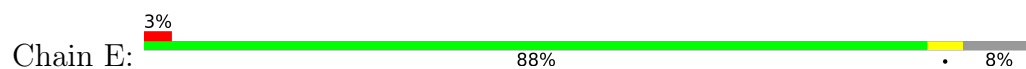
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	301	Total 301	O 301	0	0
4	C	420	Total 420	O 420	0	0
4	D	86	Total 86	O 86	0	0
4	E	304	Total 304	O 304	0	0
4	F	86	Total 86	O 86	0	0
4	G	75	Total 75	O 75	0	0
4	H	77	Total 77	O 77	0	0
4	I	422	Total 422	O 422	0	0
4	J	453	Total 453	O 453	0	0

- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

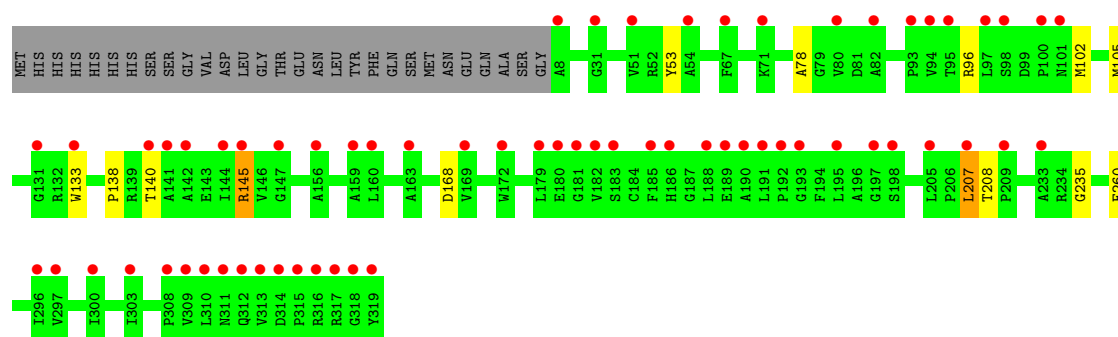
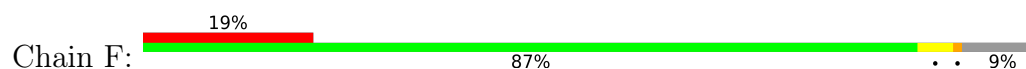




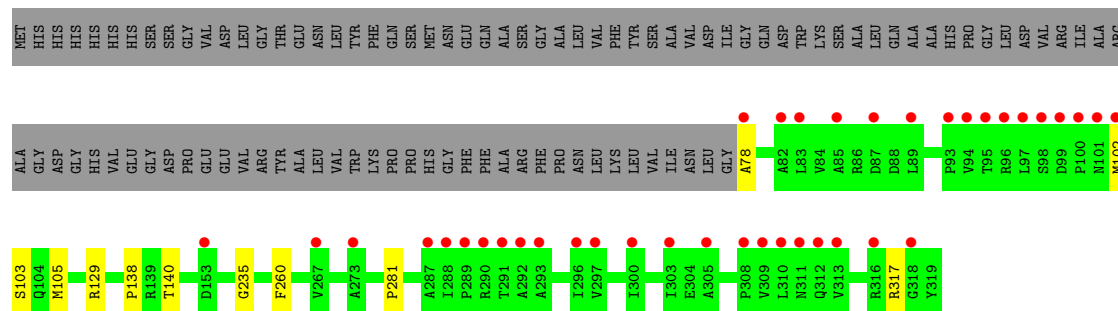
- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding



- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding



- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding



- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.51Å 311.04Å 98.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.20) 99.9 (50.00-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200 , 0.233 0.203 , 0.237	Depositor DCC
R_{free} test set	10345 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	25838	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.96 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6117e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MES, NDP

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	0.71	0/2489	0.80	0/3391
1	B	0.60	0/2447	0.78	0/3338
1	C	0.68	0/2463	0.78	0/3360
1	D	0.59	1/2331 (0.0%)	0.79	1/3187 (0.0%)
1	E	0.60	0/2448	0.77	1/3341 (0.0%)
1	F	0.59	0/2341	0.78	0/3205
1	G	0.60	0/1838	0.83	1/2512 (0.0%)
1	H	0.60	0/1831	0.81	1/2502 (0.0%)
1	I	0.65	0/2485	0.78	0/3388
1	J	0.71	0/2497	0.81	0/3402
All	All	0.64	1/23170 (0.0%)	0.79	4/31626 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	181	GLY	C-O	5.05	1.30	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	189	GLU	CA-CB-CG	5.43	124.97	114.10
1	D	211	THR	OG1-CB-CG2	-5.11	99.08	109.30
1	G	129	ARG	NE-CZ-NH2	5.04	123.74	119.20
1	H	98	SER	N-CA-C	5.02	115.62	107.23

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	2415	0	2428	11	0
1	B	2387	0	2375	6	0
1	C	2400	0	2397	5	0
1	D	2274	0	2198	14	0
1	E	2385	0	2372	6	0
1	F	2284	0	2215	11	0
1	G	1796	0	1773	6	0
1	H	1789	0	1743	8	0
1	I	2412	0	2414	8	0
1	J	2428	0	2442	10	0
2	A	48	0	26	0	0
2	B	48	0	26	0	0
2	C	48	0	26	0	0
2	D	48	0	26	1	0
2	E	48	0	26	0	0
2	F	48	0	26	1	0
2	G	48	0	26	0	0
2	H	48	0	26	0	0
2	I	48	0	26	0	0
2	J	48	0	26	0	0
3	A	24	0	26	0	0
3	B	12	0	13	0	0
3	C	12	0	13	0	0
3	D	12	0	13	0	0
3	E	12	0	13	0	0
3	F	12	0	13	0	0
3	I	12	0	13	0	0
3	J	12	0	13	0	0
4	A	456	0	0	2	0
4	B	301	0	0	0	0
4	C	420	0	0	0	0
4	D	86	0	0	0	0
4	E	304	0	0	0	0
4	F	86	0	0	0	0
4	G	75	0	0	0	0
4	H	77	0	0	0	0
4	I	422	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	J	453	0	0	2	0
All	All	25838	0	22734	66	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 1.

All (66) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ASP:H	1:A:102:MET:HE3	1.30	0.95
1:D:208:THR:OG1	1:D:211:THR:HG23	1.66	0.93
1:B:78:ALA:HB2	1:B:102:MET:HE1	1.55	0.87
1:D:175:THR:O	1:D:186:HIS:ND1	2.23	0.72
1:I:210[B]:GLU:OE1	4:I:501:HOH:O	2.10	0.69
1:F:78:ALA:HB2	1:F:102:MET:HE1	1.81	0.62
1:D:78:ALA:HB2	1:D:102:MET:HE1	1.81	0.62
1:D:96:ARG:NH2	2:D:401:NDP:O1A	2.35	0.59
1:F:207:LEU:HD23	1:F:208:THR:N	2.17	0.59
1:E:164:ARG:NH1	1:I:164:ARG:NH1	2.50	0.58
1:F:207:LEU:C	1:F:207:LEU:CD2	2.80	0.55
1:A:138:PRO:HB2	1:J:105:MET:HE1	1.89	0.54
1:D:208:THR:HB	1:D:209:PRO:HD2	1.88	0.54
1:A:295:GLN:NE2	4:A:503:HOH:O	2.42	0.53
1:E:78:ALA:HB2	1:E:102:MET:HE1	1.89	0.53
1:A:105:MET:HE1	1:J:138:PRO:HB2	1.91	0.52
1:A:84:VAL:HG21	1:A:318:GLY:HA2	1.91	0.52
1:F:138:PRO:HB2	1:G:105:MET:HE1	1.90	0.52
1:C:78:ALA:HB2	1:C:102:MET:HE1	1.92	0.52
1:E:138:PRO:HB2	1:I:105:MET:HE1	1.92	0.52
1:F:207:LEU:HD23	1:F:207:LEU:C	2.36	0.50
1:A:99:ASP:OD2	1:A:102:MET:HE2	2.11	0.50
1:F:133:TRP:CH2	1:G:281:PRO:HA	2.47	0.50
1:G:78:ALA:HB2	1:G:102:MET:HE1	1.94	0.50
1:B:78:ALA:HB2	1:B:102:MET:CE	2.33	0.49
1:J:99:ASP:H	1:J:102:MET:HE3	1.78	0.48
1:I:99:ASP:H	1:I:102:MET:HE3	1.79	0.48
1:D:124:PHE:CZ	1:H:283:LEU:HD21	2.49	0.47
1:B:105:MET:HE1	1:C:138:PRO:HB2	1.96	0.47
1:J:84:VAL:HG21	1:J:318:GLY:HA2	1.97	0.47
1:E:105:MET:HE1	1:I:138:PRO:HB2	1.97	0.46
1:D:105:MET:HE1	1:H:138:PRO:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:136:VAL:O	1:D:138:PRO:HD3	2.16	0.45
1:A:228:LYS:NZ	4:A:506:HOH:O	2.48	0.45
1:F:145:ARG:HD2	1:F:168:ASP:OD2	2.17	0.44
1:D:138:PRO:CB	1:H:105:MET:HE1	2.48	0.44
1:E:124:PHE:CZ	1:I:283:LEU:HD21	2.53	0.44
1:F:105:MET:HE1	1:G:138:PRO:HB2	1.99	0.44
1:A:99:ASP:N	1:A:102:MET:HE3	2.14	0.43
1:H:98:SER:HA	1:H:102:MET:HE1	2.00	0.43
1:B:138:PRO:HB2	1:C:105:MET:HE1	2.01	0.43
1:B:283:LEU:HD21	1:C:124:PHE:CZ	2.54	0.43
1:F:96:ARG:NH2	2:F:401:NDP:O1A	2.52	0.43
1:A:99:ASP:H	1:A:102:MET:CE	2.16	0.42
1:D:293:ALA:N	1:D:294:PRO:HD2	2.34	0.42
1:D:160:LEU:HD21	1:D:180:GLU:CB	2.48	0.42
1:J:80:VAL:HG11	1:J:313:VAL:HG21	2.01	0.42
1:A:317:ARG:HG2	1:A:319:TYR:CE1	2.55	0.42
1:J:177:LYS:NZ	4:J:515:HOH:O	2.53	0.42
1:D:138:PRO:HB2	1:H:105:MET:HE1	2.02	0.42
1:D:133:TRP:CH2	1:H:281:PRO:HA	2.55	0.41
1:I:97:LEU:HB3	1:I:102:MET:HE1	2.03	0.41
1:F:138:PRO:CB	1:G:105:MET:HE1	2.51	0.41
1:E:235:GLY:HA3	1:E:260:PHE:C	2.46	0.41
1:H:235:GLY:HA3	1:H:260:PHE:C	2.46	0.41
1:I:235:GLY:HA3	1:I:260:PHE:C	2.46	0.41
1:J:66:ARG:NH2	4:J:518:HOH:O	2.53	0.41
1:J:235:GLY:HA3	1:J:260:PHE:C	2.46	0.41
1:C:74:ILE:HD13	1:C:296:ILE:HG23	2.02	0.40
1:J:97:LEU:HB3	1:J:102:MET:HE1	2.02	0.40
1:A:124:PHE:CZ	1:J:283:LEU:HD21	2.56	0.40
1:G:235:GLY:HA3	1:G:260:PHE:C	2.46	0.40
1:D:235:GLY:HA3	1:D:260:PHE:C	2.46	0.40
1:B:235:GLY:HA3	1:B:260:PHE:C	2.47	0.40
1:H:100:PRO:HA	1:H:103:SER:HB2	2.04	0.40
1:F:235:GLY:HA3	1:F:260:PHE:C	2.46	0.40

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	315/341 (92%)	309 (98%)	6 (2%)	0	100	100
1	B	313/341 (92%)	306 (98%)	7 (2%)	0	100	100
1	C	314/341 (92%)	307 (98%)	7 (2%)	0	100	100
1	D	304/341 (89%)	297 (98%)	7 (2%)	0	100	100
1	E	313/341 (92%)	306 (98%)	7 (2%)	0	100	100
1	F	310/341 (91%)	303 (98%)	7 (2%)	0	100	100
1	G	240/341 (70%)	235 (98%)	5 (2%)	0	100	100
1	H	240/341 (70%)	236 (98%)	4 (2%)	0	100	100
1	I	316/341 (93%)	310 (98%)	6 (2%)	0	100	100
1	J	316/341 (93%)	310 (98%)	6 (2%)	0	100	100
All	All	2981/3410 (87%)	2919 (98%)	62 (2%)	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	248/270 (92%)	244 (98%)	4 (2%)	55	71
1	B	240/270 (89%)	236 (98%)	4 (2%)	53	69
1	C	245/270 (91%)	242 (99%)	3 (1%)	63	78
1	D	218/270 (81%)	216 (99%)	2 (1%)	70	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	242/270 (90%)	238 (98%)	4 (2%)	53	69
1	F	217/270 (80%)	213 (98%)	4 (2%)	51	68
1	G	179/270 (66%)	176 (98%)	3 (2%)	53	69
1	H	175/270 (65%)	172 (98%)	3 (2%)	53	69
1	I	247/270 (92%)	241 (98%)	6 (2%)	43	58
1	J	249/270 (92%)	244 (98%)	5 (2%)	48	64
All	All	2260/2700 (84%)	2222 (98%)	38 (2%)	55	69

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	TYR
1	A	103	SER
1	A	140	THR
1	A	210	GLU
1	B	53	TYR
1	B	101	ASN
1	B	103	SER
1	B	140	THR
1	C	53	TYR
1	C	103	SER
1	C	140	THR
1	D	53	TYR
1	D	211	THR
1	E	53	TYR
1	E	101	ASN
1	E	103	SER
1	E	140	THR
1	F	53	TYR
1	F	140	THR
1	F	145	ARG
1	F	207	LEU
1	G	103	SER
1	G	140	THR
1	G	317	ARG
1	H	102	MET
1	H	103	SER
1	H	140	THR
1	I	53	TYR
1	I	101	ASN

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Mol	Chain	Res	Type
1	I	103	SER
1	I	140	THR
1	I	210[A]	GLU
1	I	210[B]	GLU
1	J	53	TYR
1	J	103	SER
1	J	140	THR
1	J	189	GLU
1	J	313	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	137	HIS
1	A	186	HIS
1	B	19	GLN
1	B	137	HIS
1	B	186	HIS
1	C	137	HIS
1	D	137	HIS
1	E	19	GLN
1	E	137	HIS
1	E	186	HIS
1	F	19	GLN
1	F	61	HIS
1	F	137	HIS
1	F	186	HIS
1	G	137	HIS
1	G	186	HIS
1	H	137	HIS
1	H	186	HIS
1	I	19	GLN
1	I	75	ASN
1	I	137	HIS
1	J	101	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

19 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	NDP	C	401	-	51,52,52	0.44	0	71,80,80	0.61	0
2	NDP	E	401	-	51,52,52	0.28	0	71,80,80	0.59	1 (1%)
2	NDP	H	401	-	51,52,52	0.30	0	71,80,80	0.59	1 (1%)
3	MES	I	402	-	12,12,12	2.13	1 (8%)	15,16,16	1.74	3 (20%)
3	MES	A	403	-	12,12,12	2.40	1 (8%)	15,16,16	1.27	2 (13%)
2	NDP	I	401	-	51,52,52	0.46	0	71,80,80	0.56	0
2	NDP	A	401	-	51,52,52	0.51	0	71,80,80	0.56	0
3	MES	A	402	-	12,12,12	2.12	1 (8%)	15,16,16	1.56	4 (26%)
2	NDP	G	401	-	51,52,52	0.36	0	71,80,80	0.51	1 (1%)
3	MES	C	402	-	12,12,12	2.08	1 (8%)	15,16,16	1.79	3 (20%)
2	NDP	F	401	-	51,52,52	0.31	0	71,80,80	0.49	0
3	MES	B	402	-	12,12,12	2.12	1 (8%)	15,16,16	1.55	2 (13%)
2	NDP	J	401	-	51,52,52	0.54	0	71,80,80	0.62	1 (1%)
2	NDP	B	401	-	51,52,52	0.33	0	71,80,80	0.49	0
3	MES	F	402	-	12,12,12	2.24	1 (8%)	15,16,16	1.29	2 (13%)
3	MES	J	402	-	12,12,12	1.99	1 (8%)	15,16,16	2.15	5 (33%)
3	MES	E	402	-	12,12,12	2.18	1 (8%)	15,16,16	1.60	1 (6%)
2	NDP	D	401	-	51,52,52	0.33	0	71,80,80	0.50	0
3	MES	D	402	-	12,12,12	2.16	1 (8%)	15,16,16	1.34	1 (6%)

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	NDP	C	401	-	-	4/34/77/77	0/5/5/5
2	NDP	E	401	-	-	5/34/77/77	0/5/5/5
2	NDP	H	401	-	-	9/34/77/77	0/5/5/5
3	MES	I	402	-	-	4/6/14/14	0/1/1/1
3	MES	A	403	-	-	0/6/14/14	0/1/1/1
2	NDP	I	401	-	-	5/34/77/77	0/5/5/5
2	NDP	A	401	-	-	4/34/77/77	0/5/5/5
3	MES	A	402	-	-	4/6/14/14	0/1/1/1
2	NDP	G	401	-	-	4/34/77/77	0/5/5/5
3	MES	C	402	-	-	1/6/14/14	0/1/1/1
2	NDP	F	401	-	-	8/34/77/77	0/5/5/5
3	MES	B	402	-	-	3/6/14/14	0/1/1/1
2	NDP	J	401	-	-	1/34/77/77	0/5/5/5
2	NDP	B	401	-	-	5/34/77/77	0/5/5/5
3	MES	F	402	-	-	0/6/14/14	0/1/1/1
3	MES	J	402	-	-	2/6/14/14	0/1/1/1
3	MES	E	402	-	-	3/6/14/14	0/1/1/1
2	NDP	D	401	-	-	5/34/77/77	0/5/5/5
3	MES	D	402	-	-	5/6/14/14	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	MES	C8-S	-8.03	1.66	1.77
3	F	402	MES	C8-S	-7.47	1.67	1.77
3	E	402	MES	C8-S	-7.16	1.67	1.77
3	D	402	MES	C8-S	-7.03	1.67	1.77
3	B	402	MES	C8-S	-7.01	1.67	1.77
3	I	402	MES	C8-S	-6.83	1.68	1.77
3	A	402	MES	C8-S	-6.81	1.68	1.77
3	C	402	MES	C8-S	-6.69	1.68	1.77
3	J	402	MES	C8-S	-6.30	1.68	1.77

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	402	MES	O1S-S-C8	5.02	114.31	106.73
3	I	402	MES	O3S-S-C8	4.75	115.30	106.00
3	J	402	MES	O2S-S-O1S	-4.42	99.43	113.82
3	J	402	MES	O2S-S-C8	4.25	113.14	106.73
3	B	402	MES	O3S-S-C8	4.13	114.09	106.00
3	C	402	MES	O3S-S-C8	3.79	113.43	106.00
3	D	402	MES	O1S-S-C8	3.65	112.24	106.73
3	J	402	MES	O1S-S-C8	3.44	111.92	106.73
3	C	402	MES	C2-C3-N4	3.40	115.28	110.12
3	I	402	MES	C2-C3-N4	3.24	115.04	110.12
3	A	402	MES	O3S-S-C8	3.11	112.08	106.00
3	F	402	MES	O3S-S-C8	2.85	111.57	106.00
3	A	402	MES	C2-C3-N4	2.71	114.24	110.12
3	A	402	MES	O3S-S-O1S	-2.68	104.69	111.40
3	F	402	MES	O2S-S-C8	2.43	110.40	106.73
3	A	403	MES	O1-C2-C3	-2.40	106.61	111.77
3	C	402	MES	O2S-S-C8	2.38	110.32	106.73
3	B	402	MES	O3S-S-O1S	-2.35	105.51	111.40
2	G	401	NDP	O5D-PN-O1N	2.24	117.83	108.94
2	E	401	NDP	O5D-PN-O1N	2.24	117.82	108.94
2	H	401	NDP	O5D-PN-O1N	2.21	117.69	108.94
3	A	402	MES	O1S-S-C8	2.18	110.02	106.73
3	J	402	MES	C7-N4-C5	2.14	116.93	111.24
3	A	403	MES	O3S-S-C8	2.13	110.18	106.00
2	J	401	NDP	O5D-PN-O1N	2.08	117.19	108.94
3	I	402	MES	O3S-S-O1S	-2.07	106.23	111.40
3	J	402	MES	C6-O1-C2	2.06	116.56	109.88

There are no chirality outliers.

All (72) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	H	401	NDP	C5B-O5B-PA-O3
2	H	401	NDP	C3B-C2B-O2B-P2B
2	H	401	NDP	O4D-C1D-N1N-C2N
2	H	401	NDP	C2N-C3N-C7N-N7N
3	A	402	MES	C7-C8-S-O2S
3	A	402	MES	C7-C8-S-O3S
3	B	402	MES	C7-C8-S-O1S
3	B	402	MES	C7-C8-S-O2S
3	B	402	MES	C7-C8-S-O3S
3	C	402	MES	C8-C7-N4-C5
3	D	402	MES	C7-C8-S-O2S

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Mol	Chain	Res	Type	Atoms
3	D	402	MES	C7-C8-S-O3S
3	E	402	MES	C7-C8-S-O2S
3	E	402	MES	C7-C8-S-O3S
3	I	402	MES	C8-C7-N4-C5
3	I	402	MES	C7-C8-S-O1S
3	I	402	MES	C7-C8-S-O3S
3	J	402	MES	C8-C7-N4-C5
2	H	401	NDP	O4B-C4B-C5B-O5B
2	F	401	NDP	O4D-C4D-C5D-O5D
2	F	401	NDP	C3D-C4D-C5D-O5D
2	H	401	NDP	C3B-C4B-C5B-O5B
2	E	401	NDP	C1B-C2B-O2B-P2B
2	A	401	NDP	C3B-C2B-O2B-P2B
2	B	401	NDP	C3B-C2B-O2B-P2B
2	C	401	NDP	C3B-C2B-O2B-P2B
2	E	401	NDP	C3B-C2B-O2B-P2B
2	F	401	NDP	C3B-C2B-O2B-P2B
2	G	401	NDP	C3B-C2B-O2B-P2B
2	I	401	NDP	C3B-C2B-O2B-P2B
2	B	401	NDP	C1B-C2B-O2B-P2B
2	C	401	NDP	C1B-C2B-O2B-P2B
2	F	401	NDP	C1B-C2B-O2B-P2B
2	G	401	NDP	C1B-C2B-O2B-P2B
2	I	401	NDP	C1B-C2B-O2B-P2B
3	A	402	MES	N4-C7-C8-S
2	D	401	NDP	O4D-C4D-C5D-O5D
2	F	401	NDP	O4B-C4B-C5B-O5B
2	A	401	NDP	C1B-C2B-O2B-P2B
3	J	402	MES	C8-C7-N4-C3
2	G	401	NDP	O4D-C1D-N1N-C2N
2	G	401	NDP	O4B-C4B-C5B-O5B
2	D	401	NDP	C3D-C4D-C5D-O5D
2	H	401	NDP	PN-O3-PA-O5B
3	A	402	MES	C7-C8-S-O1S
3	D	402	MES	C7-C8-S-O1S
3	E	402	MES	C7-C8-S-O1S
3	I	402	MES	C7-C8-S-O2S
2	B	401	NDP	O4D-C1D-N1N-C2N
2	J	401	NDP	O4D-C1D-N1N-C2N
2	A	401	NDP	O4D-C1D-N1N-C2N
2	C	401	NDP	O4D-C1D-N1N-C2N
2	I	401	NDP	O4D-C1D-N1N-C2N

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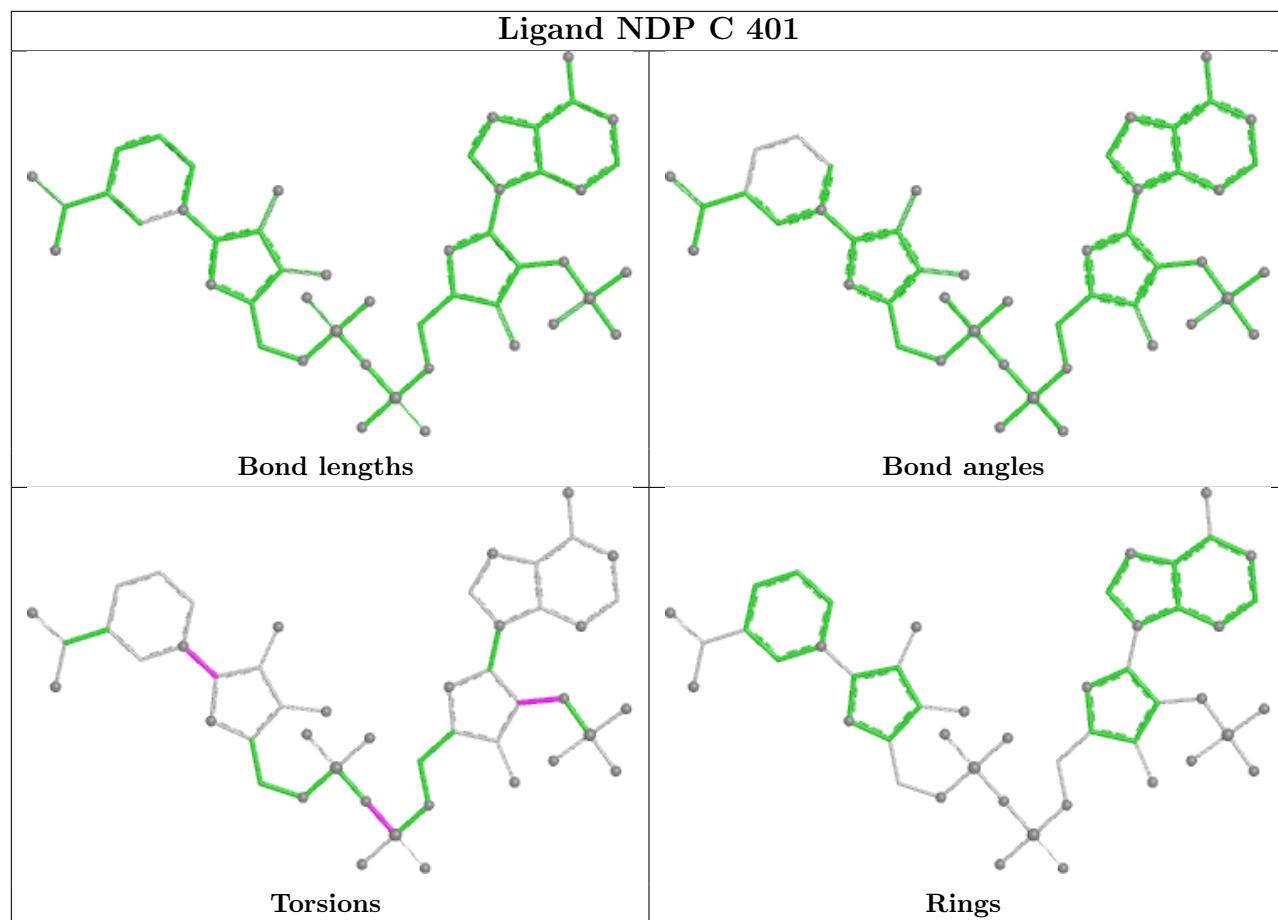
Mol	Chain	Res	Type	Atoms
2	A	401	NDP	C5D-O5D-PN-O1N
2	H	401	NDP	C5B-O5B-PA-O1A
2	I	401	NDP	C5D-O5D-PN-O1N
2	H	401	NDP	C1B-C2B-O2B-P2B
3	D	402	MES	C8-C7-N4-C3
3	D	402	MES	C8-C7-N4-C5
2	E	401	NDP	O4D-C1D-N1N-C2N
2	B	401	NDP	C2B-O2B-P2B-O2X
2	D	401	NDP	O4D-C1D-N1N-C2N
2	F	401	NDP	O4D-C1D-N1N-C2N
2	B	401	NDP	C2B-O2B-P2B-O1X
2	D	401	NDP	C2B-O2B-P2B-O1X
2	F	401	NDP	C2B-O2B-P2B-O1X
2	D	401	NDP	C3B-C2B-O2B-P2B
2	E	401	NDP	O4B-C4B-C5B-O5B
2	E	401	NDP	C2B-O2B-P2B-O2X
2	F	401	NDP	C2D-C1D-N1N-C2N
2	C	401	NDP	PN-O3-PA-O2A
2	I	401	NDP	PN-O3-PA-O2A

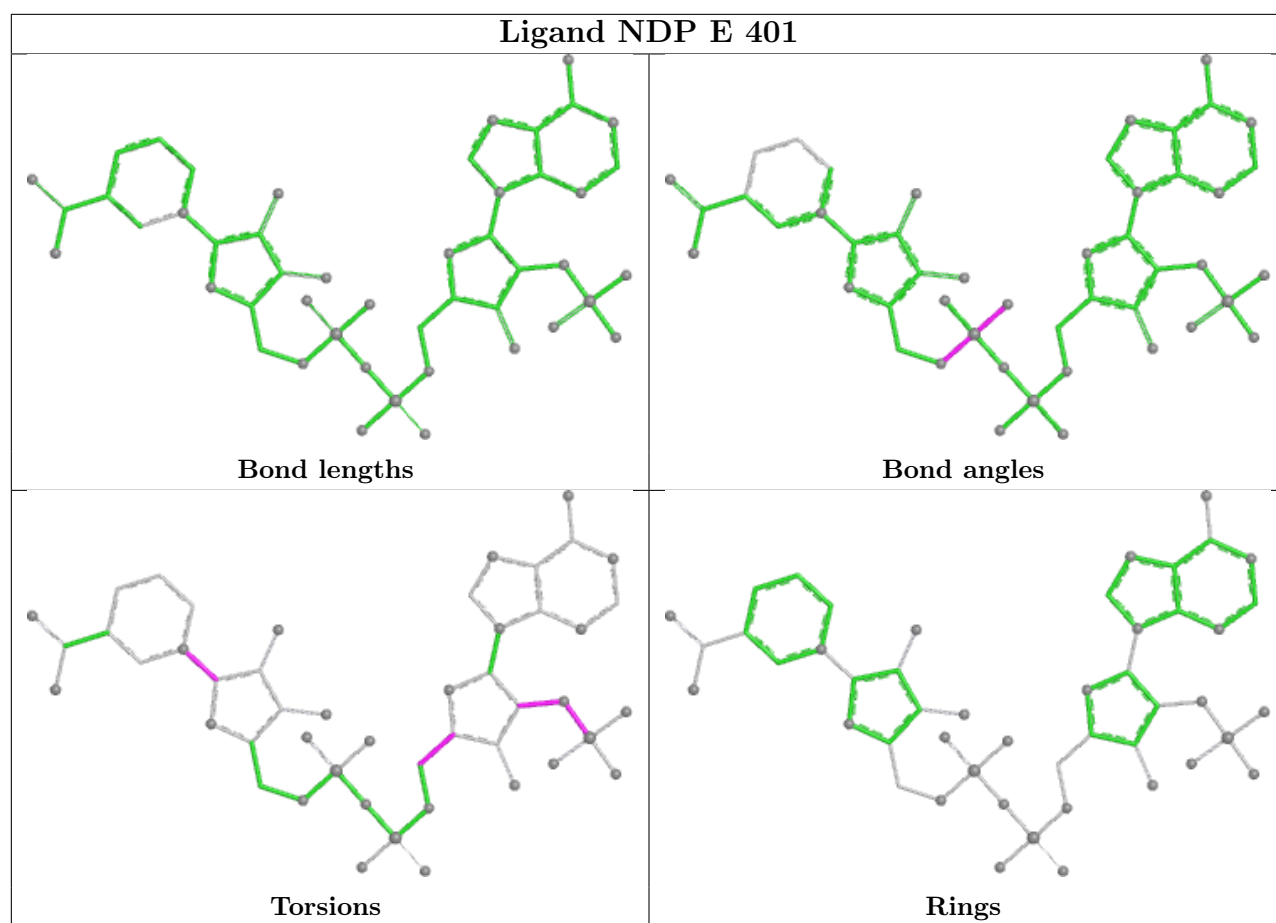
There are no ring outliers.

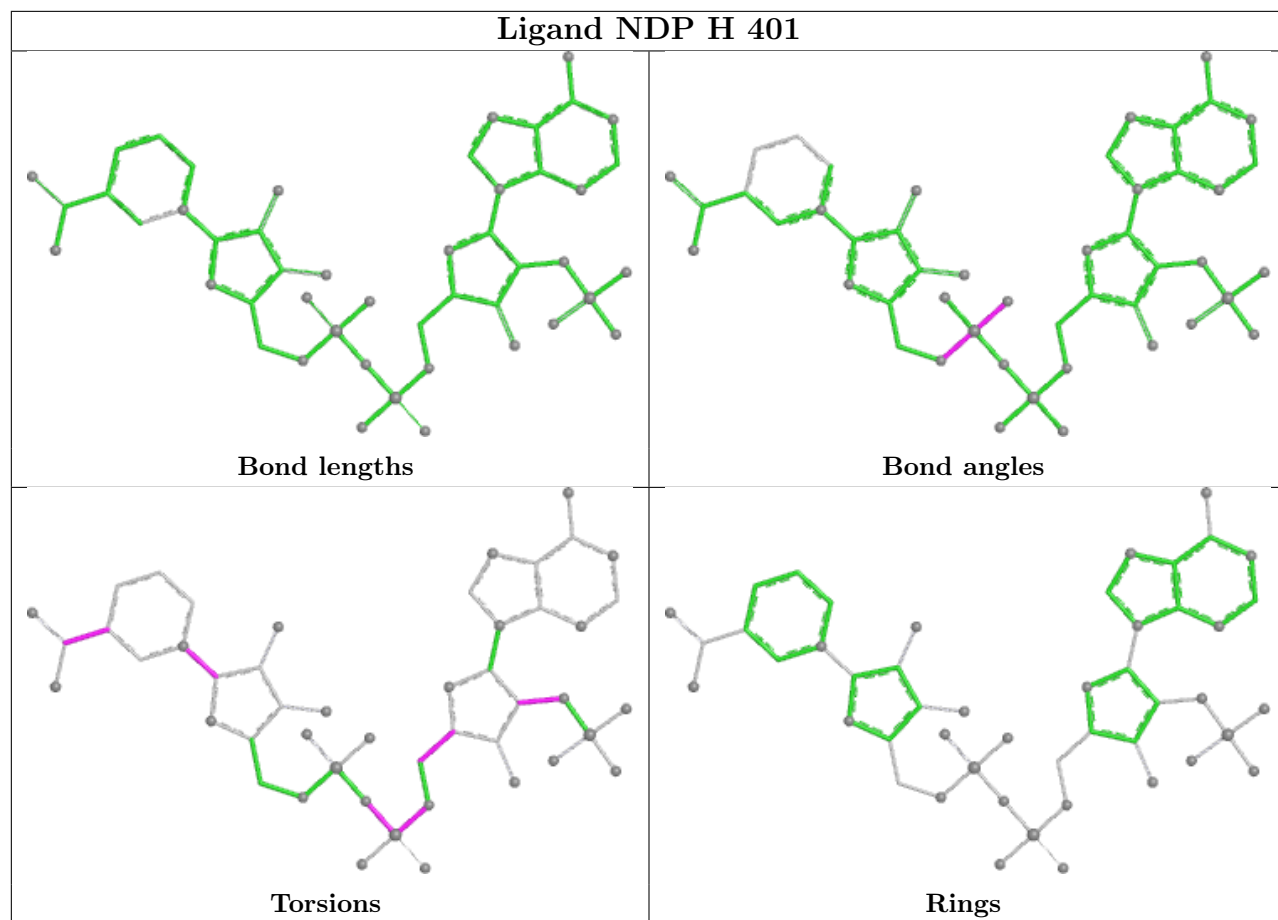
2 monomers are involved in 2 short contacts:

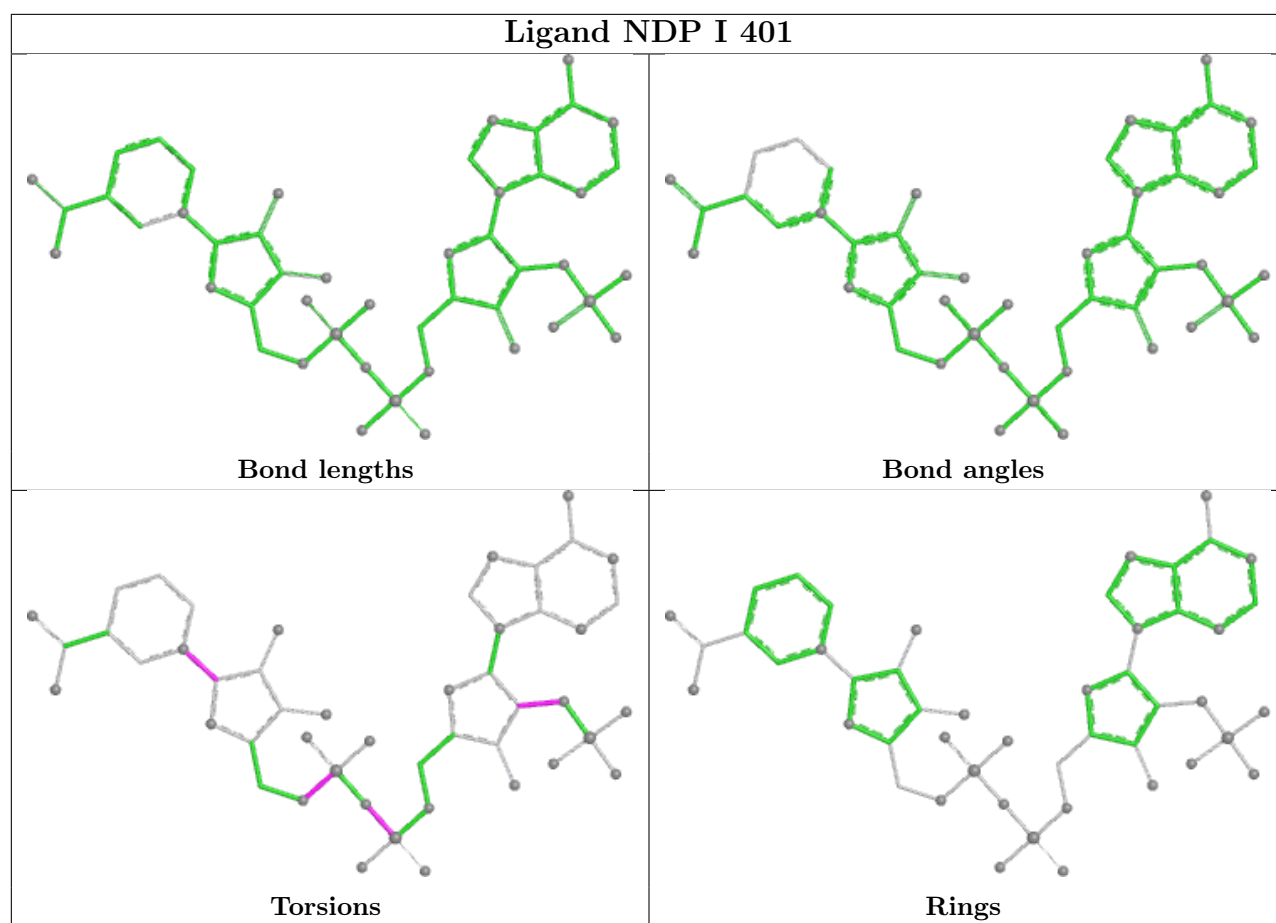
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	401	NDP	1	0
2	D	401	NDP	1	0

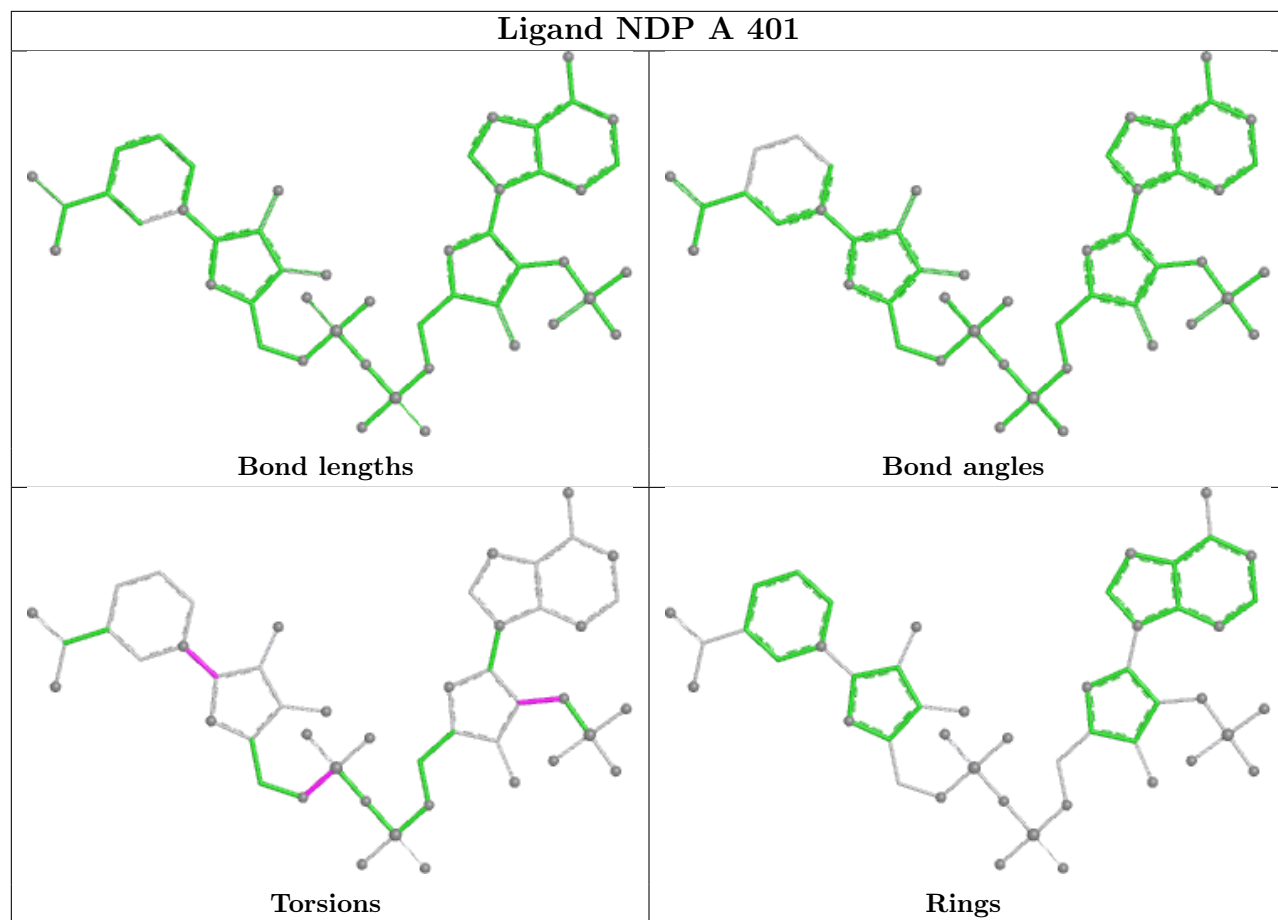
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

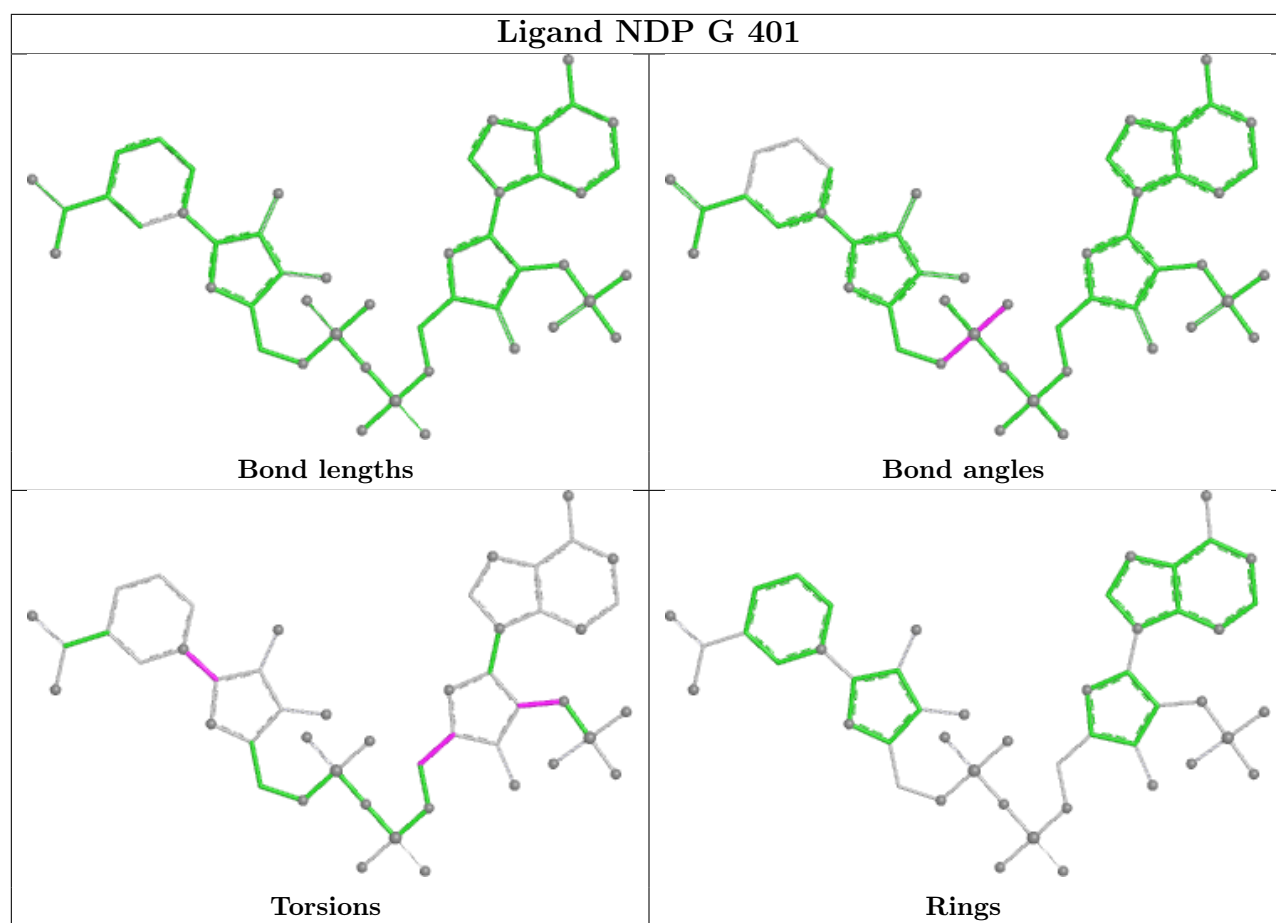


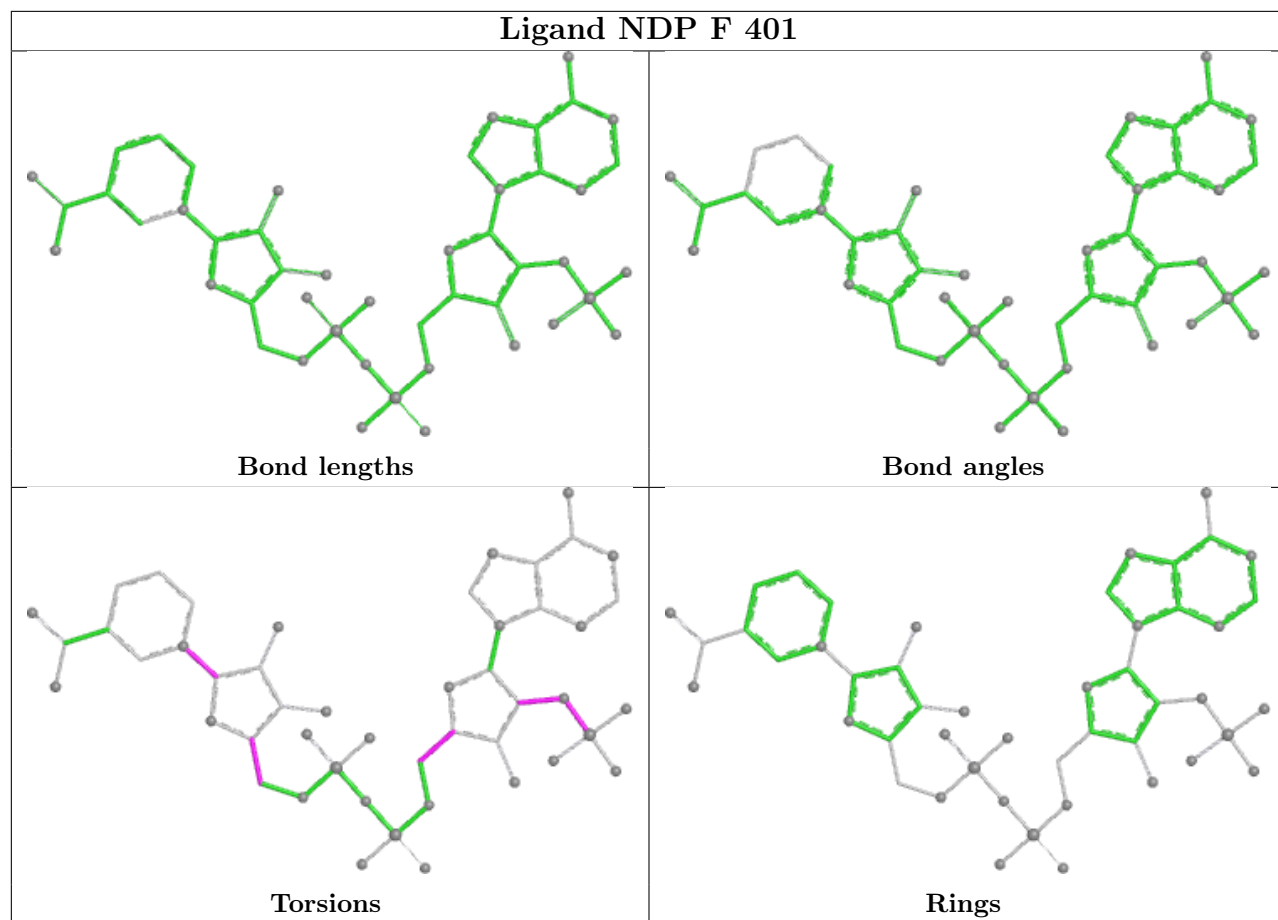


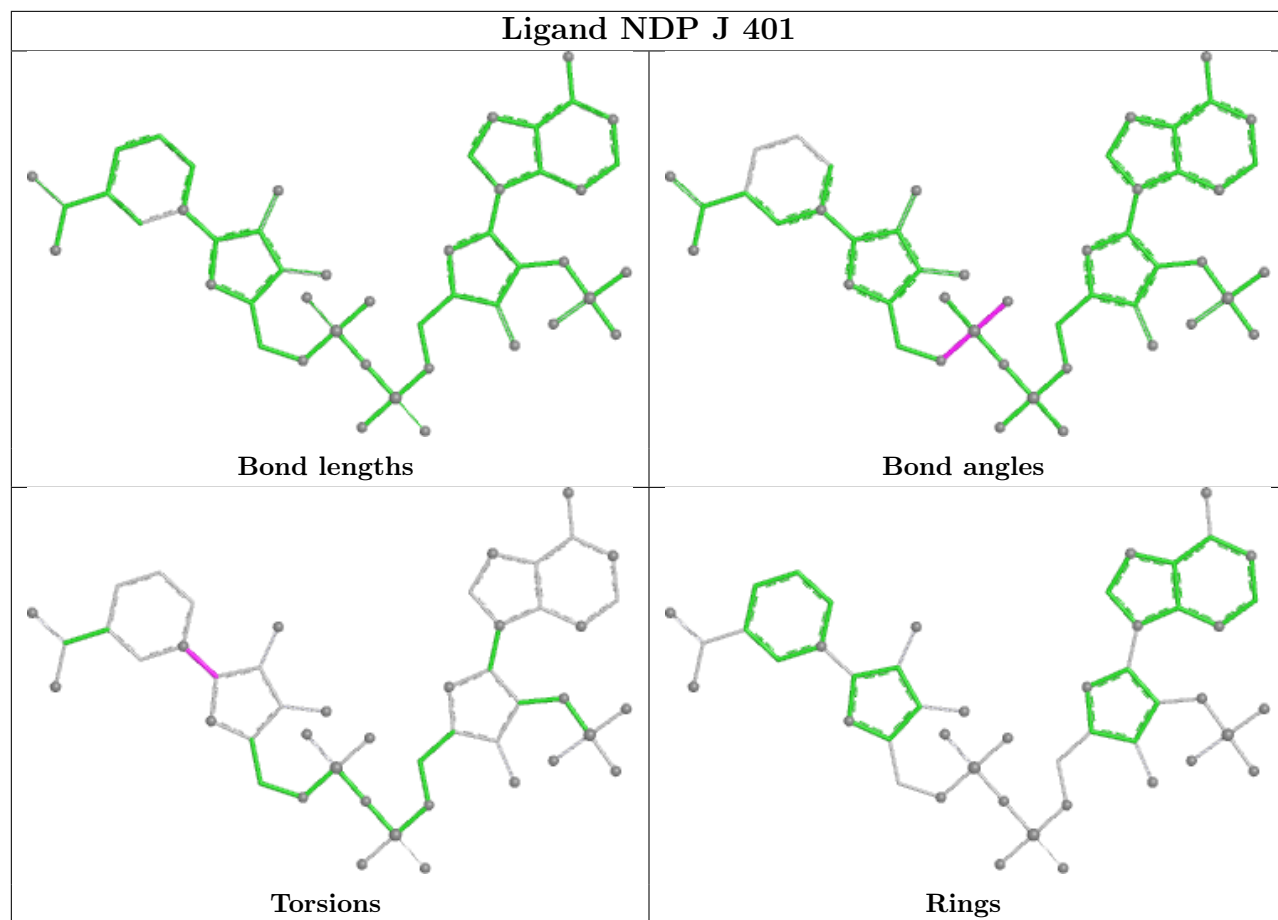


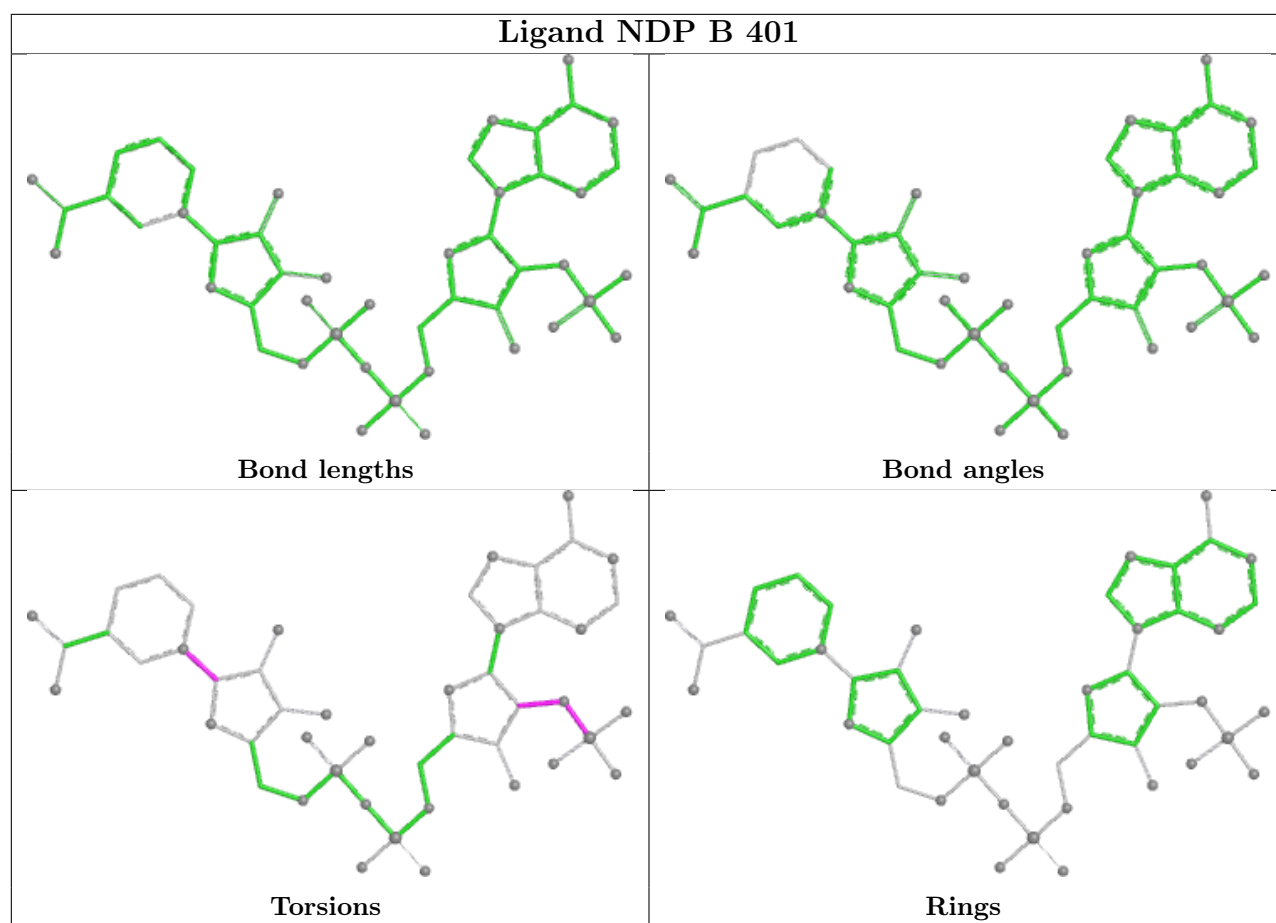


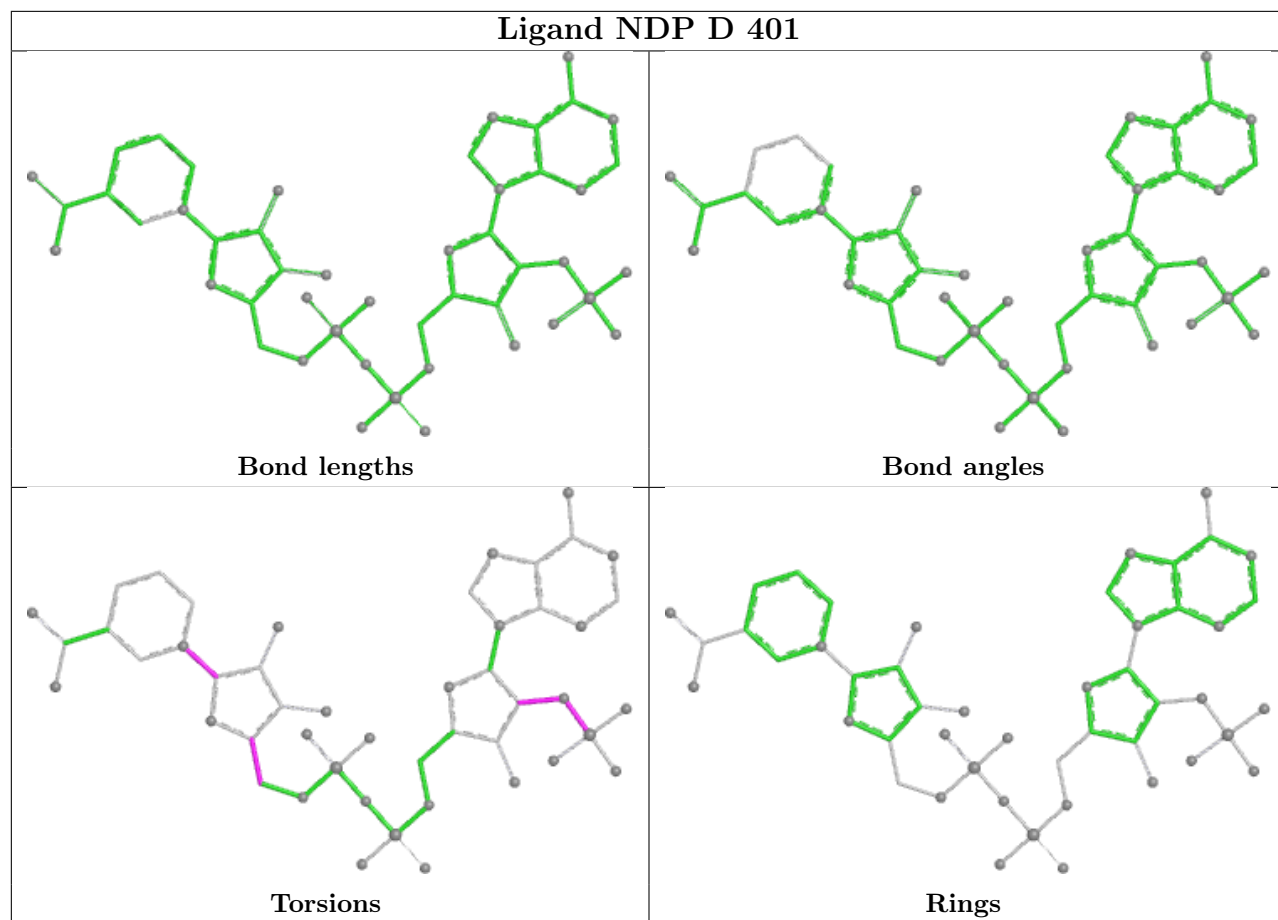












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	314/341 (92%)	-0.13	2 (0%) 85 83	21, 31, 50, 73	3 (0%)
1	B	315/341 (92%)	0.53	23 (7%) 21 18	24, 46, 104, 137	0
1	C	315/341 (92%)	-0.03	11 (3%) 47 44	22, 31, 57, 125	1 (0%)
1	D	308/341 (90%)	1.70	105 (34%) 1 0	41, 103, 150, 179	0
1	E	314/341 (92%)	0.34	11 (3%) 47 44	17, 44, 94, 118	1 (0%)
1	F	312/341 (91%)	1.34	65 (20%) 2 2	40, 88, 129, 160	0
1	G	242/341 (70%)	0.95	39 (16%) 4 3	43, 69, 134, 153	0
1	H	242/341 (70%)	1.12	45 (18%) 3 2	43, 75, 138, 191	0
1	I	315/341 (92%)	-0.11	5 (1%) 70 67	19, 31, 52, 98	3 (0%)
1	J	315/341 (92%)	-0.06	1 (0%) 90 88	19, 32, 52, 88	3 (0%)
All	All	2992/3410 (87%)	0.54	307 (10%) 12 9	17, 47, 126, 191	11 (0%)

All (307) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	288	ILE	5.7
1	G	293	ALA	5.6
1	D	156	ALA	5.4
1	H	83	LEU	5.3
1	H	97	LEU	5.3
1	G	97	LEU	5.1
1	D	151	LEU	5.0
1	H	101	ASN	5.0
1	I	315	PRO	4.9
1	H	94	VAL	4.9
1	C	5	ALA	4.9
1	D	309	VAL	4.9
1	H	78	ALA	4.8

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Mol	Chain	Res	Type	RSRZ
1	C	98	SER	4.8
1	C	100	PRO	4.7
1	C	101	ASN	4.6
1	C	99	ASP	4.6
1	D	180	GLU	4.6
1	I	5	ALA	4.5
1	F	189	GLU	4.5
1	D	146	VAL	4.5
1	D	193	GLY	4.5
1	G	289	PRO	4.4
1	C	97	LEU	4.4
1	G	297	VAL	4.4
1	G	95	THR	4.3
1	H	308	PRO	4.3
1	D	84	VAL	4.3
1	H	289	PRO	4.3
1	G	288	ILE	4.3
1	F	172	TRP	4.3
1	F	191	LEU	4.2
1	D	171	GLY	4.2
1	D	100	PRO	4.2
1	D	97	LEU	4.2
1	E	84	VAL	4.1
1	G	101	ASN	4.1
1	G	99	ASP	4.1
1	G	83	LEU	4.0
1	D	200	ILE	4.0
1	D	286	ILE	4.0
1	F	94	VAL	4.0
1	H	291	THR	4.0
1	H	309	VAL	4.0
1	F	100	PRO	3.9
1	G	290	ARG	3.9
1	H	292	ALA	3.9
1	D	144	ILE	3.9
1	H	313	VAL	3.9
1	D	184	CYS	3.9
1	D	197	GLY	3.8
1	D	172	TRP	3.8
1	F	316	ARG	3.7
1	G	300	ILE	3.7
1	G	102	MET	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	185	PHE	3.7
1	G	94	VAL	3.7
1	F	163	ALA	3.7
1	F	319	TYR	3.7
1	F	310	LEU	3.6
1	D	181	GLY	3.6
1	H	84	VAL	3.6
1	D	118	ALA	3.6
1	D	221	ALA	3.6
1	G	313	VAL	3.6
1	D	190	ALA	3.6
1	B	318	GLY	3.5
1	D	315	PRO	3.5
1	B	5	ALA	3.5
1	B	98	SER	3.5
1	D	310	LEU	3.5
1	F	185	PHE	3.5
1	H	290	ARG	3.5
1	D	186	HIS	3.4
1	G	100	PRO	3.4
1	D	169	VAL	3.4
1	F	179	LEU	3.4
1	H	306	GLY	3.4
1	J	5	ALA	3.4
1	D	308	PRO	3.3
1	G	318	GLY	3.3
1	F	93	PRO	3.3
1	H	267	VAL	3.3
1	D	131	GLY	3.3
1	G	87	ASP	3.3
1	H	99	ASP	3.3
1	H	300	ILE	3.3
1	F	183	SER	3.3
1	D	314	ASP	3.2
1	D	129	ARG	3.2
1	H	79	GLY	3.2
1	D	101	ASN	3.2
1	G	308	PRO	3.2
1	F	140	THR	3.2
1	F	98	SER	3.2
1	G	292	ALA	3.2
1	D	95	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	183	SER	3.1
1	B	99	ASP	3.1
1	D	163	ALA	3.1
1	D	318	GLY	3.1
1	F	101	ASN	3.1
1	B	6	SER	3.1
1	D	80	VAL	3.1
1	F	308	PRO	3.1
1	C	316	ARG	3.1
1	D	142	ALA	3.1
1	H	293	ALA	3.1
1	F	309	VAL	3.1
1	D	114	VAL	3.1
1	D	313	VAL	3.1
1	F	188	LEU	3.1
1	F	205	LEU	3.1
1	B	309	VAL	3.0
1	D	160	LEU	3.0
1	H	303	ILE	3.0
1	H	295	GLN	3.0
1	H	305	ALA	3.0
1	F	197	GLY	3.0
1	G	303	ILE	3.0
1	D	145	ARG	3.0
1	F	317	ARG	3.0
1	G	93	PRO	3.0
1	B	28	ALA	2.9
1	F	315	PRO	2.9
1	D	223	LEU	2.9
1	H	80	VAL	2.9
1	D	295	GLN	2.9
1	D	102	MET	2.9
1	D	72	LEU	2.9
1	D	149	LEU	2.9
1	D	246	ALA	2.9
1	F	97	LEU	2.9
1	F	159	ALA	2.9
1	F	300	ILE	2.9
1	F	54	ALA	2.8
1	D	74	ILE	2.8
1	D	194	PHE	2.8
1	F	51	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	296	ILE	2.8
1	F	190	ALA	2.8
1	G	305	ALA	2.8
1	D	140	THR	2.8
1	E	100	PRO	2.8
1	D	98	SER	2.7
1	H	98	SER	2.7
1	F	192	PRO	2.7
1	D	148	VAL	2.7
1	G	267	VAL	2.7
1	D	147	GLY	2.7
1	D	133	TRP	2.7
1	B	317	ARG	2.7
1	E	305	ALA	2.7
1	D	267	VAL	2.7
1	F	180	GLU	2.7
1	D	83	LEU	2.7
1	H	89	LEU	2.7
1	F	233	ALA	2.7
1	D	319	TYR	2.7
1	F	169	VAL	2.7
1	D	288	ILE	2.7
1	D	296	ILE	2.7
1	H	296	ILE	2.7
1	D	93	PRO	2.7
1	F	198	SER	2.7
1	D	162	LEU	2.7
1	H	233	ALA	2.6
1	H	81	ASP	2.6
1	D	252	ILE	2.6
1	G	96	ARG	2.6
1	H	93	PRO	2.6
1	H	82	ALA	2.6
1	D	132	ARG	2.6
1	D	182	VAL	2.6
1	F	209	PRO	2.6
1	F	82	ALA	2.6
1	H	87	ASP	2.6
1	D	175	THR	2.6
1	B	315	PRO	2.6
1	G	316	ARG	2.6
1	F	141	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	78	ALA	2.6
1	H	102	MET	2.6
1	C	315	PRO	2.6
1	D	46	GLY	2.6
1	D	297	VAL	2.6
1	I	100	PRO	2.6
1	D	191	LEU	2.5
1	F	80	VAL	2.5
1	F	144	ILE	2.5
1	G	98	SER	2.5
1	F	312	GLN	2.5
1	D	189	GLU	2.5
1	D	25	LEU	2.5
1	F	67	PHE	2.5
1	C	102	MET	2.5
1	H	311	ASN	2.5
1	I	101	ASN	2.5
1	D	137	HIS	2.5
1	G	309	VAL	2.5
1	D	214	LEU	2.5
1	E	83	LEU	2.5
1	C	314	ASP	2.5
1	F	314	ASP	2.5
1	H	85	ALA	2.5
1	D	211	THR	2.4
1	E	6	SER	2.4
1	G	296	ILE	2.4
1	G	311	ASN	2.4
1	H	287	ALA	2.4
1	F	95	THR	2.4
1	D	188	LEU	2.4
1	B	319	TYR	2.4
1	I	314	ASP	2.4
1	B	178	ALA	2.4
1	F	156	ALA	2.4
1	B	313	VAL	2.4
1	D	167	PHE	2.4
1	D	229	PHE	2.4
1	F	313	VAL	2.4
1	D	174	ARG	2.4
1	B	310	LEU	2.4
1	F	207	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	216	ASN	2.3
1	D	245	ALA	2.3
1	B	303	ILE	2.3
1	D	303	ILE	2.3
1	F	182	VAL	2.3
1	D	218	GLU	2.3
1	D	312	GLN	2.3
1	B	100	PRO	2.3
1	D	36	ILE	2.3
1	B	44	VAL	2.3
1	D	70	LEU	2.3
1	D	138	PRO	2.3
1	D	289	PRO	2.3
1	F	318	GLY	2.3
1	G	82	ALA	2.3
1	E	98	SER	2.3
1	F	145	ARG	2.3
1	D	130	GLU	2.3
1	F	71	LYS	2.3
1	G	310	LEU	2.3
1	F	147	GLY	2.3
1	B	316	ARG	2.3
1	D	272	TRP	2.3
1	G	273	ALA	2.3
1	D	34	VAL	2.3
1	E	64	PHE	2.2
1	F	297	VAL	2.3
1	F	131	GLY	2.2
1	H	181	GLY	2.2
1	B	45	GLU	2.2
1	F	8	ALA	2.2
1	G	85	ALA	2.2
1	F	133	TRP	2.2
1	D	55	LEU	2.2
1	H	271	LEU	2.2
1	F	311	ASN	2.2
1	F	31	GLY	2.2
1	D	255	ALA	2.2
1	G	287	ALA	2.2
1	G	291	THR	2.2
1	F	303	ILE	2.2
1	D	247	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	195	LEU	2.2
1	B	94	VAL	2.2
1	D	11	PHE	2.2
1	D	31	GLY	2.2
1	D	154	LEU	2.2
1	H	86	ARG	2.2
1	A	308	PRO	2.2
1	G	312	GLN	2.2
1	E	316	ARG	2.1
1	E	288	ILE	2.1
1	H	90	PRO	2.1
1	B	305	ALA	2.1
1	D	58	LYS	2.1
1	D	89	LEU	2.1
1	G	89	LEU	2.1
1	H	286	ILE	2.1
1	D	311	ASN	2.1
1	H	95	THR	2.1
1	D	28	ALA	2.1
1	F	142	ALA	2.1
1	H	178	ALA	2.1
1	F	160	LEU	2.1
1	B	101	ASN	2.1
1	D	168	ASP	2.1
1	F	186	HIS	2.1
1	F	193	GLY	2.1
1	C	317	ARG	2.1
1	A	6	SER	2.1
1	D	159	ALA	2.1
1	D	115	LEU	2.1
1	E	97	LEU	2.1
1	B	93	PRO	2.1
1	B	61	HIS	2.0
1	H	312	GLN	2.0
1	D	76	LEU	2.0
1	D	243	LEU	2.0
1	E	300	ILE	2.0
1	D	317	ARG	2.0
1	H	297	VAL	2.0
1	F	181	GLY	2.0
1	D	134	HIS	2.0
1	G	153	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

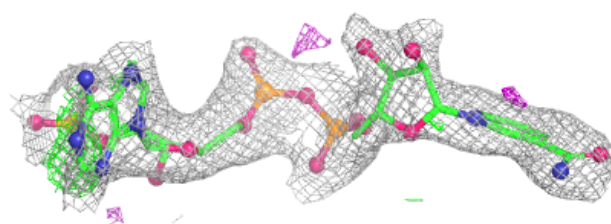
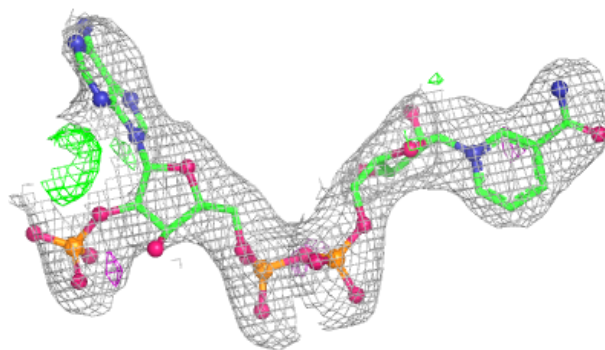
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MES	B	402	12/12	0.80	0.23	61,89,100,111	0
3	MES	D	402	12/12	0.83	0.16	61,93,109,135	0
3	MES	C	402	12/12	0.84	0.18	43,59,72,73	0
2	NDP	D	401	48/48	0.85	0.13	48,84,121,139	0
3	MES	F	402	12/12	0.85	0.20	54,97,113,113	0
2	NDP	F	401	48/48	0.86	0.13	40,79,107,120	0
3	MES	A	403	12/12	0.86	0.21	43,73,96,108	0
2	NDP	H	401	48/48	0.89	0.13	44,72,92,105	0
3	MES	E	402	12/12	0.91	0.14	53,72,91,99	0
2	NDP	G	401	48/48	0.93	0.10	44,63,90,101	0
3	MES	J	402	12/12	0.93	0.13	28,43,55,62	0
3	MES	I	402	12/12	0.94	0.12	33,51,60,69	0
3	MES	A	402	12/12	0.94	0.13	32,43,64,65	0
2	NDP	B	401	48/48	0.95	0.07	29,39,49,55	0
2	NDP	E	401	48/48	0.95	0.07	27,36,43,47	0
2	NDP	A	401	48/48	0.97	0.06	20,27,35,44	0
2	NDP	I	401	48/48	0.97	0.05	19,26,32,36	0
2	NDP	J	401	48/48	0.97	0.06	17,27,37,40	0
2	NDP	C	401	48/48	0.98	0.05	18,25,29,32	0

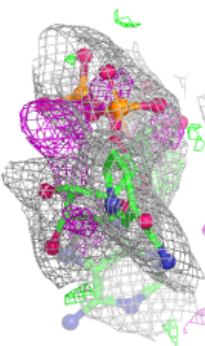
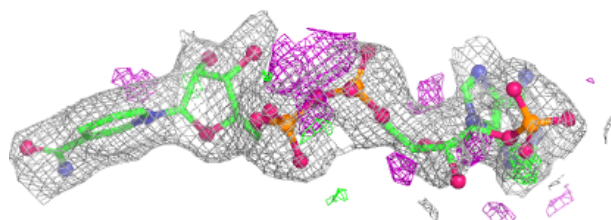
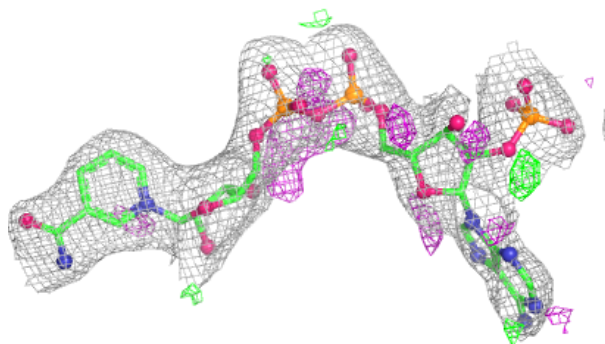
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NDP 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)

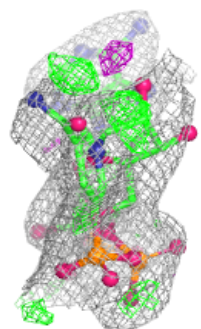
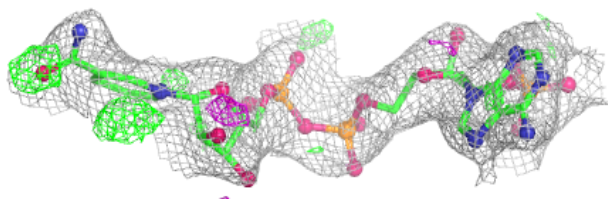
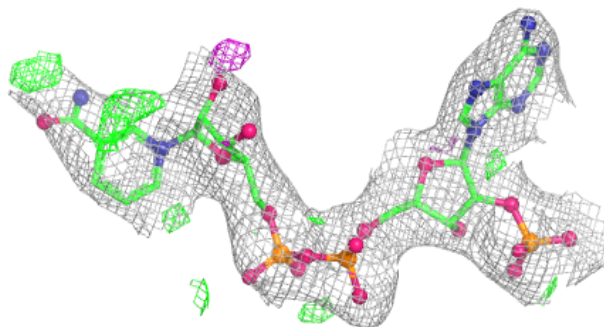
**Electron density around NDP F 401:**

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

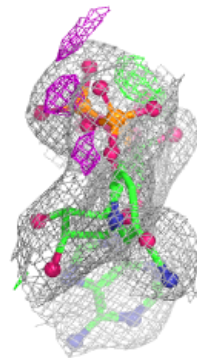
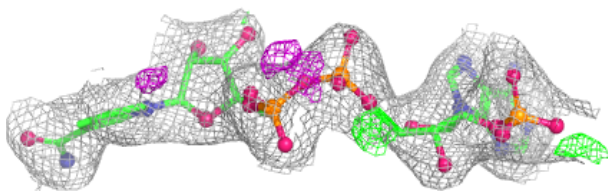
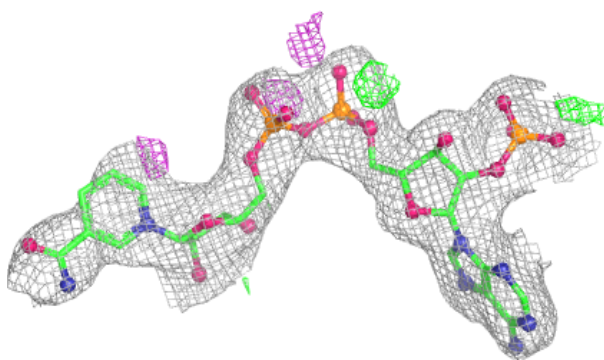


Electron density around NDP H 401:

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

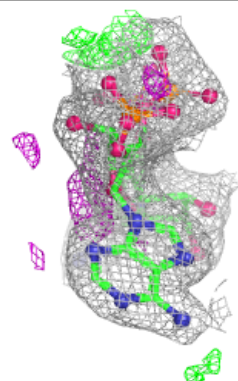
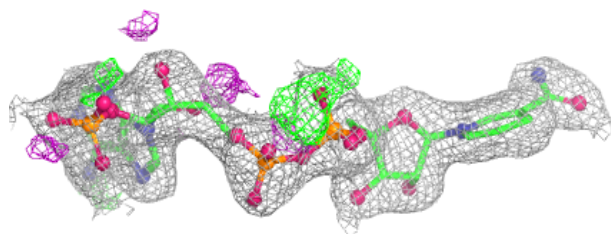
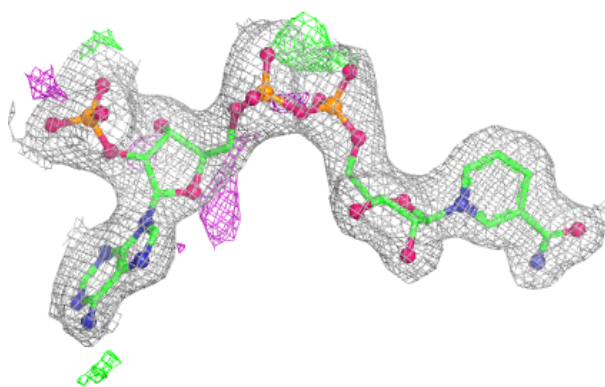
**Electron density around NDP G 401:**

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

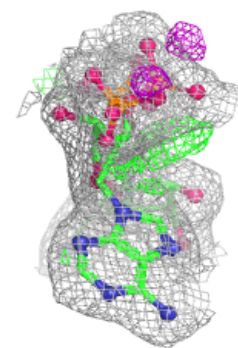
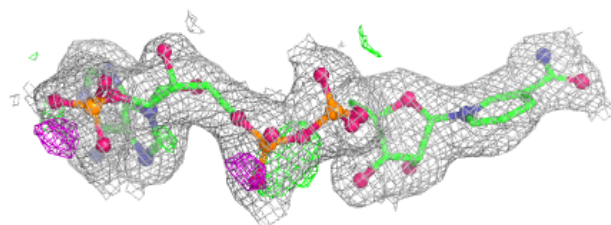
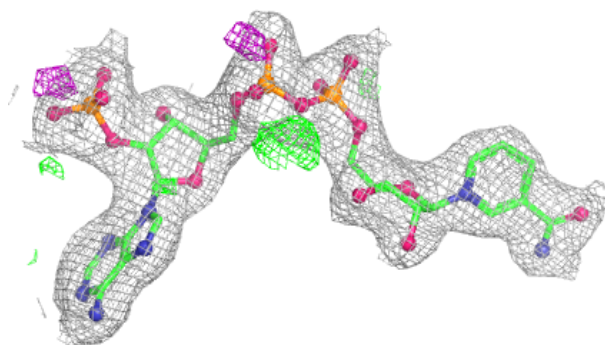


Electron density around NDP B 401:

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

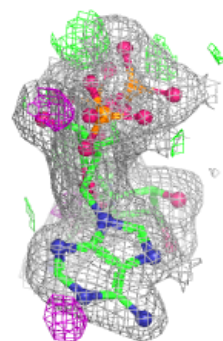
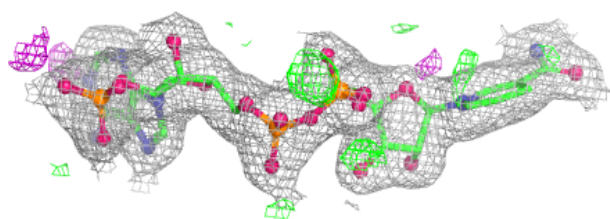
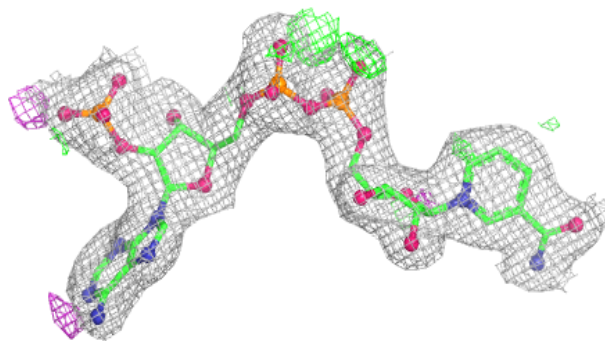
**Electron density around NDP E 401:**

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

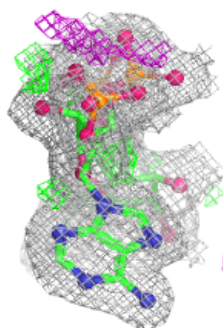
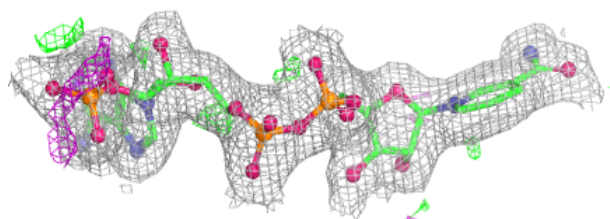
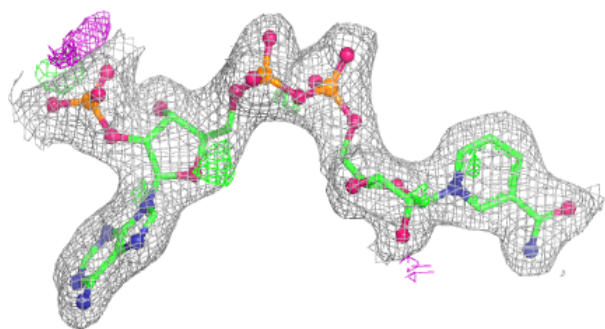


Electron density around NDP A 401:

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

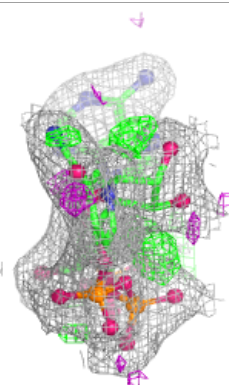
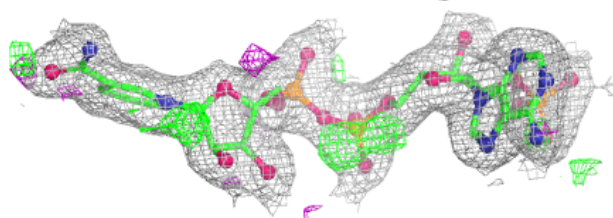
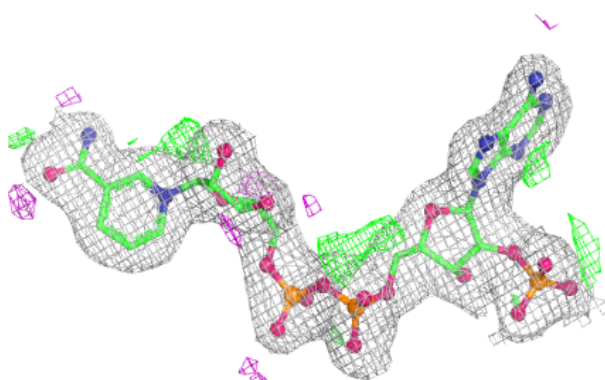
**Electron density around NDP I 401:**

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

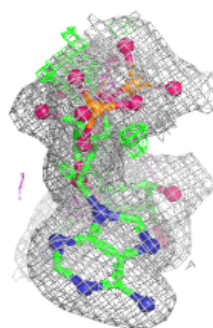
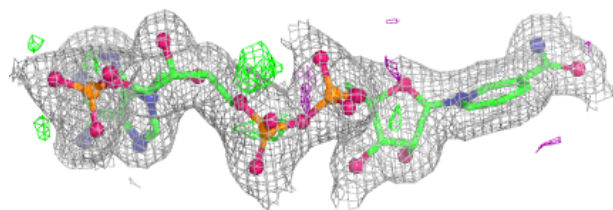
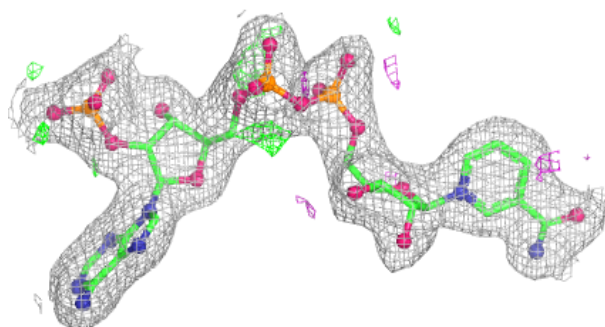


Electron density around NDP J 401:

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

**Electron density around NDP 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.