



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2023 – 10:03 AM EDT

PDB ID : 5VG6
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 (NYSGRC)
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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

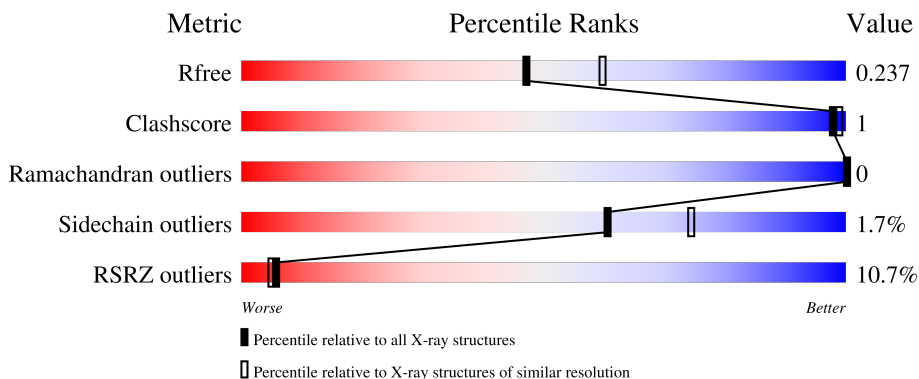
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	341	
1	B	341	
1	C	341	
1	D	341	

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Mol	Chain	Length	Quality of chain
1	E	341	<p>4% 90% 8%</p>
1	F	341	<p>24% 89% 9%</p>
1	G	341	<p>14% 70% 29%</p>
1	H	341	<p>14% 69% 29%</p>
1	I	341	<p>% 90% 8%</p>
1	J	341	<p>89% 8%</p>

2 Entry composition [i](#)

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

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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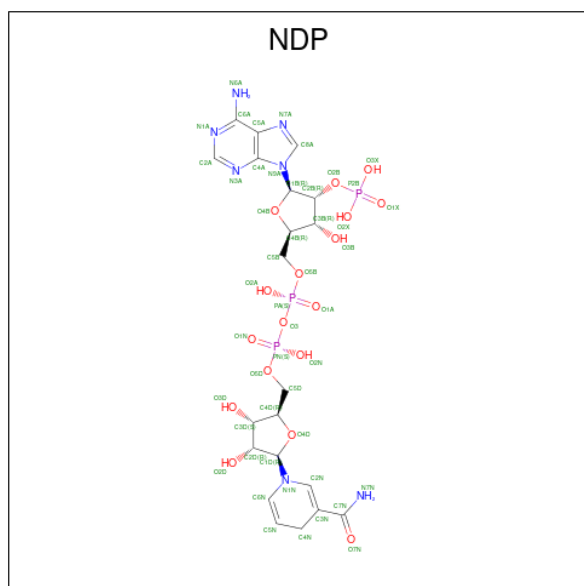
Chain	Residue	Modelled	Actual	Comment	Reference
I	-20	HIS	-	expression tag	UNP A7IIH0
I	-19	HIS	-	expression tag	UNP A7IIH0
I	-18	HIS	-	expression tag	UNP A7IIH0
I	-17	HIS	-	expression tag	UNP A7IIH0
I	-16	HIS	-	expression tag	UNP A7IIH0
I	-15	HIS	-	expression tag	UNP A7IIH0
I	-14	SER	-	expression tag	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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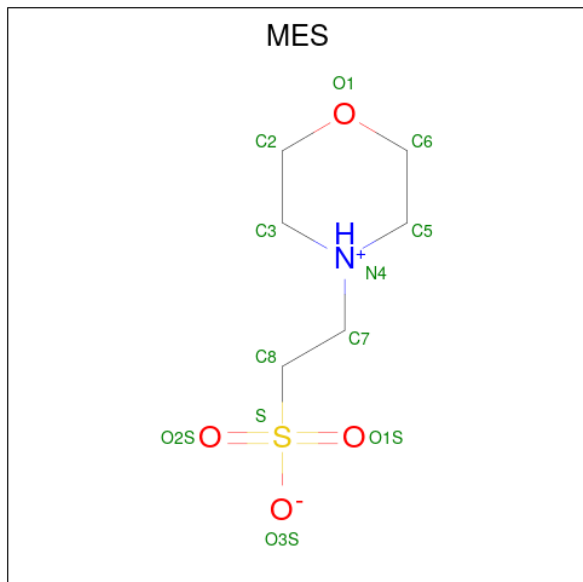
Chain	Residue	Modelled	Actual	Comment	Reference
J	0	SER	-	expression tag	UNP A7IIH0

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



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

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



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

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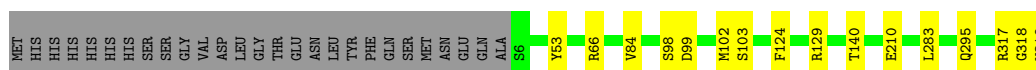
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	301	Total 301	O 301	0	0
4	C	420	Total 420	O 420	0	0
4	D	86	Total 86	O 86	0	0
4	E	304	Total 304	O 304	0	0
4	F	86	Total 86	O 86	0	0
4	G	75	Total 75	O 75	0	0
4	H	77	Total 77	O 77	0	0
4	I	422	Total 422	O 422	0	0
4	J	453	Total 453	O 453	0	0

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

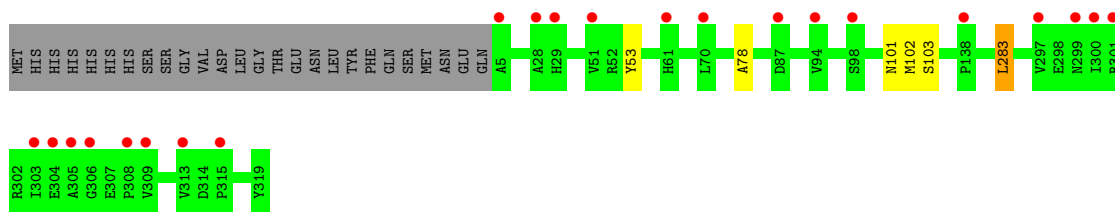
- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

Chain A: 




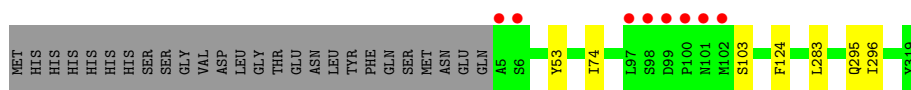
- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

Chain B: 




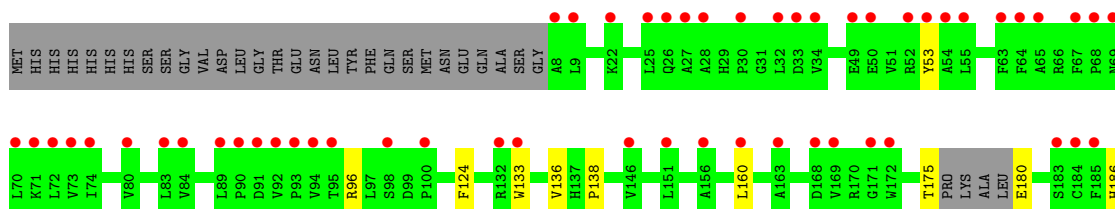
- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

Chain C: 



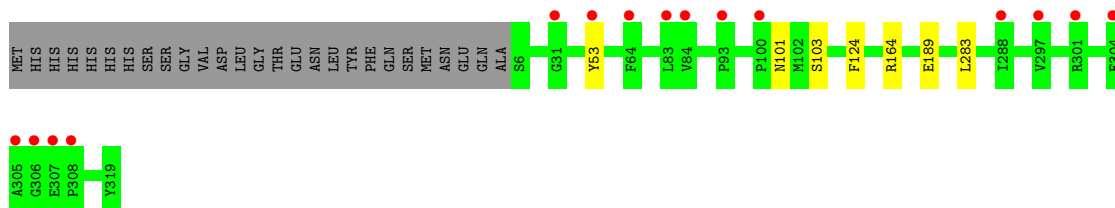
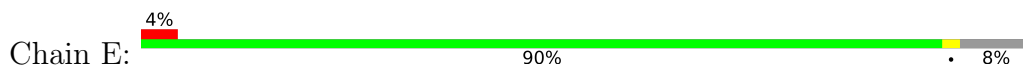
- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

Chain D: 

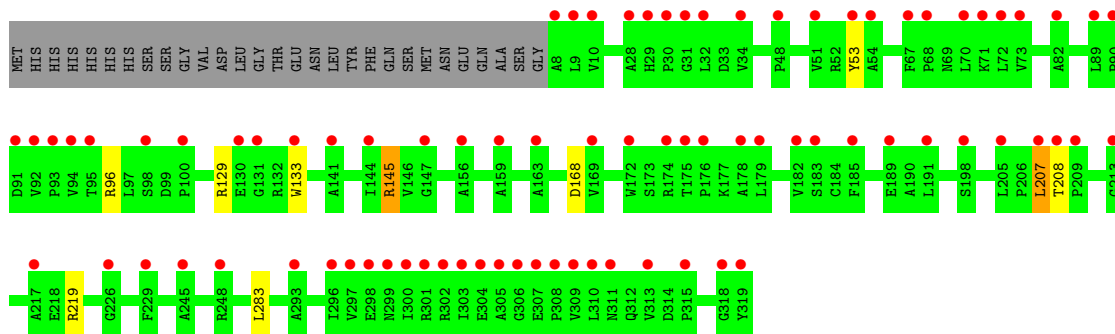
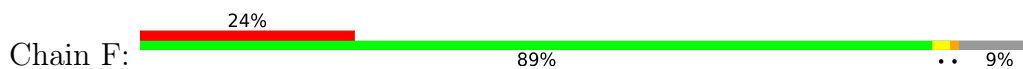




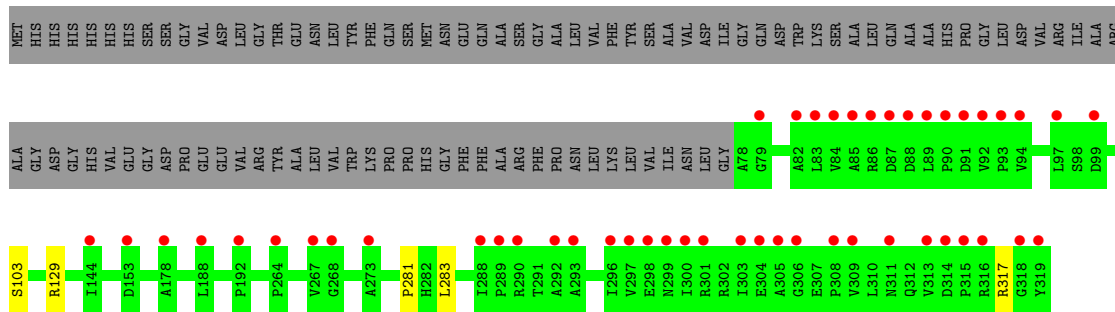
- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding



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

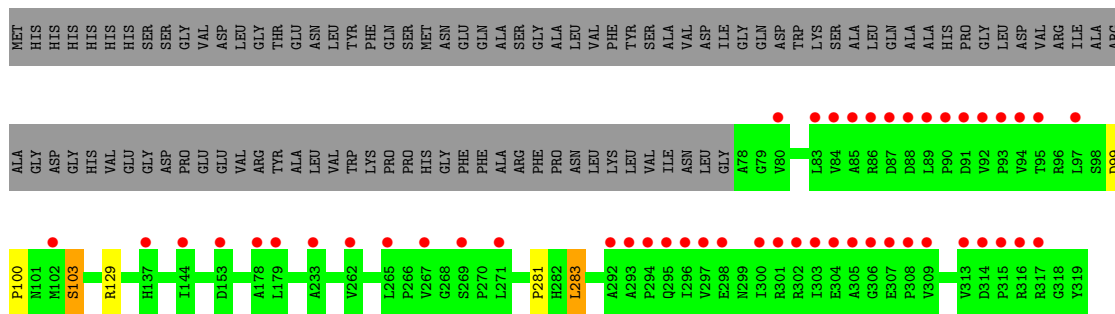


- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

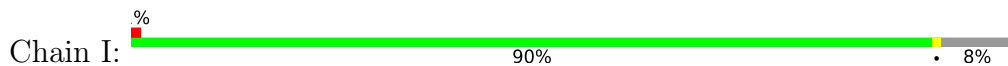


- Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding

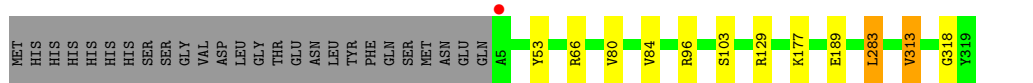
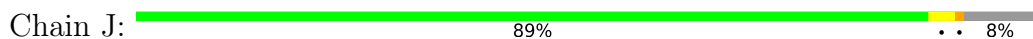




● Molecule 1: D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding



● 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 44.43 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.20) 99.8 (44.43-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 2.20Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200 , 0.233 0.203 , 0.237	Depositor DCC
R_{free} test set	10345 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtrriage
Anisotropy	0.481	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 61.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
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

Xtrriage'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 i

5.1 Standard geometry i

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

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	0.53	0/2489	0.72	2/3391 (0.1%)
1	B	0.44	0/2447	0.68	0/3338
1	C	0.49	0/2463	0.69	0/3360
1	D	0.43	0/2331	0.68	0/3187
1	E	0.43	0/2448	0.69	1/3341 (0.0%)
1	F	0.42	0/2341	0.68	1/3205 (0.0%)
1	G	0.42	0/1838	0.71	2/2512 (0.1%)
1	H	0.45	0/1831	0.71	3/2502 (0.1%)
1	I	0.47	0/2485	0.72	4/3388 (0.1%)
1	J	0.54	0/2497	0.73	2/3402 (0.1%)
All	All	0.47	0/23170	0.70	15/31626 (0.0%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	210[A]	GLU	CA-CB-CG	7.03	128.87	113.40
1	I	210[B]	GLU	CA-CB-CG	7.03	128.87	113.40
1	G	129	ARG	NE-CZ-NH2	6.88	123.74	120.30
1	H	129	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	H	99	ASP	CB-CG-OD1	-6.18	112.73	118.30
1	H	129	ARG	NE-CZ-NH1	-6.05	117.27	120.30
1	G	129	ARG	NE-CZ-NH1	-5.55	117.53	120.30
1	J	96	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	A	129	ARG	NE-CZ-NH2	5.46	123.03	120.30
1	F	129	ARG	NE-CZ-NH2	5.34	122.97	120.30
1	A	66	ARG	NE-CZ-NH2	5.29	122.94	120.30
1	E	189	GLU	CA-CB-CG	5.26	124.97	113.40
1	I	234	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	J	129	ARG	NE-CZ-NH2	5.16	122.88	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	86	ARG	NE-CZ-NH1	5.03	122.82	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2415	0	2428	7	0
1	B	2387	0	2375	3	0
1	C	2400	0	2397	2	0
1	D	2274	0	2198	9	0
1	E	2385	0	2372	2	0
1	F	2284	0	2215	6	0
1	G	1796	0	1773	1	0
1	H	1789	0	1743	3	0
1	I	2412	0	2414	3	0
1	J	2428	0	2442	5	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	456	0	0	1	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
4	J	453	0	0	2	0
All	All	25838	0	22734	34	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 (34) 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:D:208:THR:OG1	1:D:211:THR:HG23	1.66	0.93
1:A:99:ASP:H	1:A:102:MET:HE3	1.53	0.73
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:B:78:ALA:HB2	1:B:102:MET:HE3	1.74	0.69
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:A:99:ASP:H	1:A:102:MET:CE	2.16	0.57
1:B:78:ALA:HB2	1:B:102:MET:CE	2.33	0.57
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:A:84:VAL:HG21	1:A:318:GLY:HA2	1.91	0.52
1:F:133:TRP:CH2	1:G:281:PRO:HA	2.47	0.50
1:F:207:LEU:C	1:F:207:LEU:CD2	2.80	0.50
1:A:98:SER:N	1:A:102:MET:HE1	2.27	0.49
1:D:124:PHE:CZ	1:H:283:LEU:HD21	2.49	0.47
1:J:84:VAL:HG21	1:J:318:GLY:HA2	1.97	0.47
1:F:207:LEU:HD23	1:F:207:LEU:C	2.36	0.46
1:D:136:VAL:O	1:D:138:PRO:HD3	2.16	0.45
1:F:145:ARG:HD2	1:F:168:ASP:OD2	2.17	0.44
1:E:124:PHE:CZ	1:I:283:LEU:HD21	2.53	0.44
1:B:283:LEU:HD21	1:C:124:PHE:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:96:ARG:NH2	2:F:401:NDP:O1A	2.52	0.43
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:133:TRP:CH2	1:H:281:PRO:HA	2.55	0.41
1:J:66:ARG:NH2	4:J:518:HOH:O	2.53	0.41
1:C:74:ILE:HD13	1:C:296:ILE:HG23	2.02	0.40
1:A:124:PHE:CZ	1:J:283:LEU:HD21	2.56	0.40
1:H:100:PRO:HA	1:H:103:SER:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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 [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	248/270 (92%)	243 (98%)	5 (2%)	55	69
1	B	240/270 (89%)	236 (98%)	4 (2%)	60	74
1	C	245/270 (91%)	241 (98%)	4 (2%)	62	76
1	D	218/270 (81%)	215 (99%)	3 (1%)	67	80
1	E	242/270 (90%)	238 (98%)	4 (2%)	60	74
1	F	217/270 (80%)	212 (98%)	5 (2%)	50	63
1	G	179/270 (66%)	176 (98%)	3 (2%)	60	74
1	H	175/270 (65%)	173 (99%)	2 (1%)	73	85
1	I	247/270 (92%)	242 (98%)	5 (2%)	55	69
1	J	249/270 (92%)	244 (98%)	5 (2%)	55	69
All	All	2260/2700 (84%)	2220 (98%)	40 (2%)	60	72

All (40) 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	A	283	LEU
1	B	53	TYR
1	B	101	ASN
1	B	103	SER
1	B	283	LEU
1	C	53	TYR
1	C	103	SER
1	C	283	LEU
1	C	295	GLN
1	D	53	TYR

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Mol	Chain	Res	Type
1	D	211	THR
1	D	283	LEU
1	E	53	TYR
1	E	101	ASN
1	E	103	SER
1	E	283	LEU
1	F	53	TYR
1	F	145	ARG
1	F	207	LEU
1	F	219	ARG
1	F	283	LEU
1	G	103	SER
1	G	283	LEU
1	G	317	ARG
1	H	103	SER
1	H	283	LEU
1	I	53	TYR
1	I	103	SER
1	I	210[A]	GLU
1	I	210[B]	GLU
1	I	283	LEU
1	J	53	TYR
1	J	103	SER
1	J	189	GLU
1	J	283	LEU
1	J	313	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	295	GLN
1	I	295	GLN
1	I	311	ASN
1	J	295	GLN

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](#)

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
3	MES	B	402	-	12,12,12	2.07	1 (8%)	14,16,16	1.83	2 (14%)
3	MES	A	402	-	12,12,12	2.07	1 (8%)	14,16,16	1.78	4 (28%)
3	MES	A	403	-	12,12,12	2.35	1 (8%)	14,16,16	1.40	2 (14%)
3	MES	D	402	-	12,12,12	2.11	1 (8%)	14,16,16	1.59	2 (14%)
3	MES	I	402	-	12,12,12	2.08	1 (8%)	14,16,16	2.07	3 (21%)
3	MES	J	402	-	12,12,12	1.94	1 (8%)	14,16,16	2.37	4 (28%)
2	NDP	D	401	-	45,52,52	0.52	0	53,80,80	0.64	1 (1%)
2	NDP	J	401	-	45,52,52	0.65	0	53,80,80	0.81	2 (3%)
2	NDP	F	401	-	45,52,52	0.50	0	53,80,80	0.64	1 (1%)
2	NDP	E	401	-	45,52,52	0.47	0	53,80,80	0.78	2 (3%)
3	MES	C	402	-	12,12,12	2.03	1 (8%)	14,16,16	2.03	3 (21%)
2	NDP	B	401	-	45,52,52	0.50	0	53,80,80	0.66	1 (1%)
2	NDP	G	401	-	45,52,52	0.53	0	53,80,80	0.69	2 (3%)
2	NDP	H	401	-	45,52,52	0.49	0	53,80,80	0.71	2 (3%)
2	NDP	A	401	-	45,52,52	0.64	0	53,80,80	0.69	1 (1%)
3	MES	E	402	-	12,12,12	2.13	1 (8%)	14,16,16	1.91	1 (7%)
2	NDP	I	401	-	45,52,52	0.60	0	53,80,80	0.74	1 (1%)
2	NDP	C	401	-	45,52,52	0.60	0	53,80,80	0.74	1 (1%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MES	F	402	-	12,12,12	2.19	1 (8%)	14,16,16	1.52	2 (14%)

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	MES	B	402	-	-	3/6/14/14	0/1/1/1
3	MES	A	402	-	-	4/6/14/14	0/1/1/1
3	MES	A	403	-	-	0/6/14/14	0/1/1/1
3	MES	D	402	-	-	5/6/14/14	0/1/1/1
3	MES	I	402	-	-	4/6/14/14	0/1/1/1
3	MES	J	402	-	-	2/6/14/14	0/1/1/1
2	NDP	D	401	-	-	7/30/77/77	0/5/5/5
2	NDP	J	401	-	-	2/30/77/77	0/5/5/5
2	NDP	F	401	-	-	8/30/77/77	0/5/5/5
2	NDP	E	401	-	-	5/30/77/77	0/5/5/5
3	MES	C	402	-	-	1/6/14/14	0/1/1/1
2	NDP	B	401	-	-	6/30/77/77	0/5/5/5
2	NDP	G	401	-	-	4/30/77/77	0/5/5/5
2	NDP	H	401	-	-	9/30/77/77	0/5/5/5
2	NDP	A	401	-	-	5/30/77/77	0/5/5/5
3	MES	E	402	-	-	3/6/14/14	0/1/1/1
2	NDP	I	401	-	-	5/30/77/77	0/5/5/5
2	NDP	C	401	-	-	4/30/77/77	0/5/5/5
3	MES	F	402	-	-	0/6/14/14	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	-7.87	1.66	1.77
3	F	402	MES	C8-S	-7.32	1.67	1.77
3	E	402	MES	C8-S	-7.01	1.67	1.77
3	D	402	MES	C8-S	-6.87	1.67	1.77
3	B	402	MES	C8-S	-6.86	1.67	1.77
3	I	402	MES	C8-S	-6.68	1.68	1.77
3	A	402	MES	C8-S	-6.66	1.68	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	402	MES	C8-S	-6.55	1.68	1.77
3	J	402	MES	C8-S	-6.16	1.68	1.77

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	402	MES	O1S-S-C8	6.14	114.31	106.92
3	I	402	MES	O3S-S-C8	5.89	115.30	105.77
3	J	402	MES	O2S-S-C8	5.17	113.14	106.92
3	B	402	MES	O3S-S-C8	5.15	114.09	105.77
3	C	402	MES	O3S-S-C8	4.74	113.43	105.77
3	D	402	MES	O1S-S-C8	4.42	112.24	106.92
3	J	402	MES	O2S-S-O1S	-4.19	99.43	113.95
3	J	402	MES	O1S-S-C8	4.16	111.92	106.92
3	A	402	MES	O3S-S-C8	3.90	112.08	105.77
3	F	402	MES	O3S-S-C8	3.59	111.57	105.77
3	C	402	MES	C2-C3-N4	3.41	115.28	110.10
3	I	402	MES	C2-C3-N4	3.26	115.04	110.10
3	F	402	MES	O2S-S-C8	2.89	110.40	106.92
3	C	402	MES	O2S-S-C8	2.83	110.32	106.92
3	A	402	MES	C2-C3-N4	2.73	114.24	110.10
3	A	403	MES	O3S-S-C8	2.73	110.18	105.77
3	A	402	MES	O3S-S-O1S	-2.70	104.69	111.27
3	A	402	MES	O1S-S-C8	2.58	110.02	106.92
2	J	401	NDP	C5A-C6A-N6A	2.45	124.07	120.35
2	I	401	NDP	C5A-C6A-N6A	2.40	124.00	120.35
3	B	402	MES	O3S-S-O1S	-2.36	105.51	111.27
3	A	403	MES	O1-C2-C3	-2.36	106.61	111.80
2	B	401	NDP	C5A-C6A-N6A	2.35	123.92	120.35
2	E	401	NDP	C5A-C6A-N6A	2.31	123.86	120.35
2	F	401	NDP	C5A-C6A-N6A	2.30	123.84	120.35
2	G	401	NDP	C5A-C6A-N6A	2.27	123.81	120.35
2	G	401	NDP	O5D-PN-O1N	2.24	117.83	109.07
2	D	401	NDP	C5A-C6A-N6A	2.24	123.76	120.35
2	E	401	NDP	O5D-PN-O1N	2.24	117.82	109.07
3	J	402	MES	C7-N4-C5	2.23	116.93	111.23
2	H	401	NDP	O5D-PN-O1N	2.21	117.69	109.07
2	H	401	NDP	C5A-C6A-N6A	2.21	123.70	120.35
2	C	401	NDP	C5A-C6A-N6A	2.19	123.67	120.35
3	D	402	MES	O2S-S-C8	2.15	109.50	106.92
2	A	401	NDP	C5A-C6A-N6A	2.14	123.61	120.35
2	J	401	NDP	O5D-PN-O1N	2.08	117.19	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	402	MES	O3S-S-O1S	-2.06	106.23	111.27

There are no chirality outliers.

All (77) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	NDP	C2B-O2B-P2B-O1X
2	B	401	NDP	C2B-O2B-P2B-O2X
2	D	401	NDP	C2B-O2B-P2B-O1X
2	F	401	NDP	C2B-O2B-P2B-O1X
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
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	F	401	NDP	O4B-C4B-C5B-O5B
2	H	401	NDP	O4B-C4B-C5B-O5B
2	H	401	NDP	C3B-C4B-C5B-O5B
2	F	401	NDP	O4D-C4D-C5D-O5D
2	F	401	NDP	C3D-C4D-C5D-O5D
2	G	401	NDP	O4B-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

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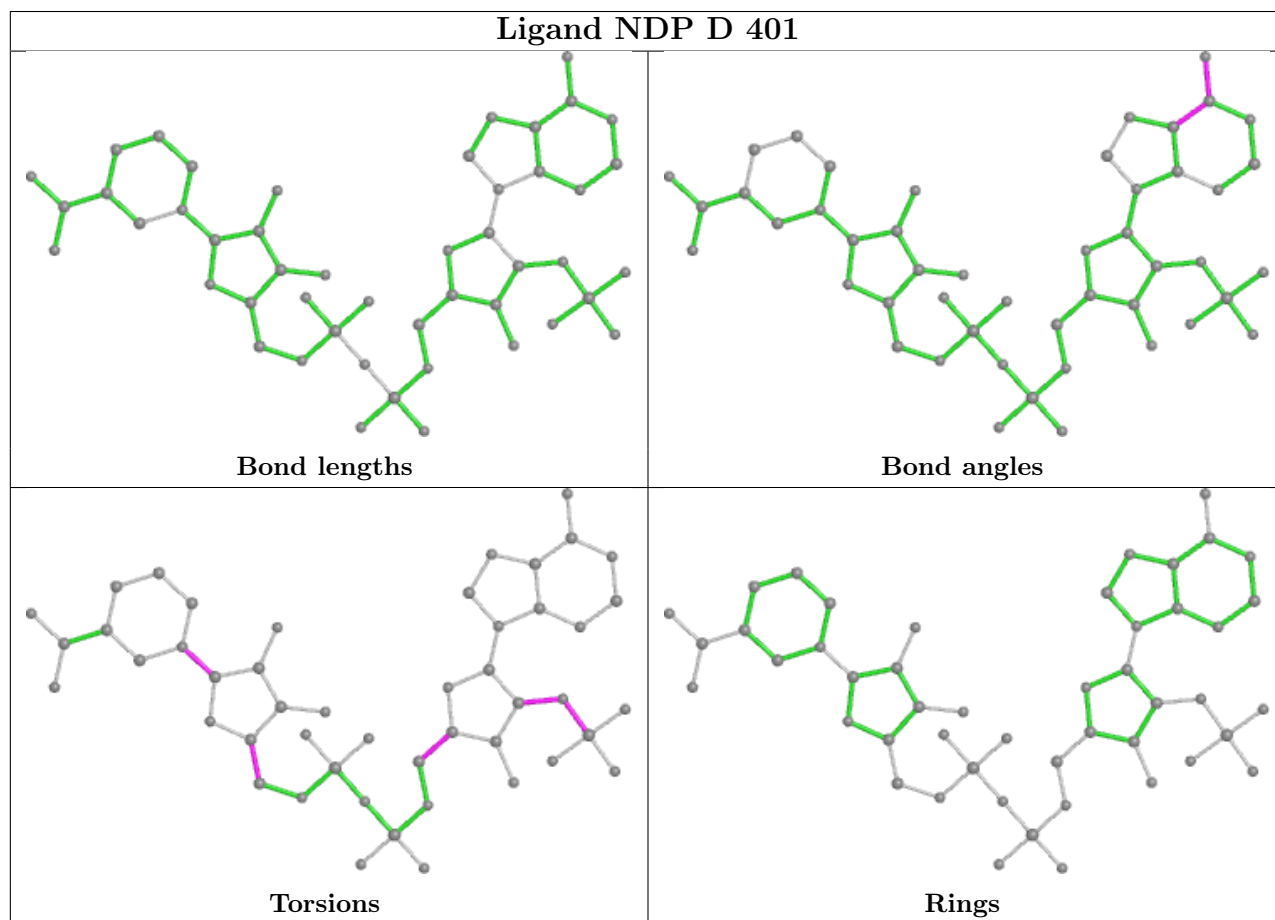
Mol	Chain	Res	Type	Atoms
2	B	401	NDP	C1B-C2B-O2B-P2B
2	C	401	NDP	C1B-C2B-O2B-P2B
2	F	401	NDP	C1B-C2B-O2B-P2B
2	G	401	NDP	C1B-C2B-O2B-P2B
2	I	401	NDP	C1B-C2B-O2B-P2B
2	D	401	NDP	O4D-C4D-C5D-O5D
2	A	401	NDP	C1B-C2B-O2B-P2B
3	A	402	MES	N4-C7-C8-S
3	J	402	MES	C8-C7-N4-C3
2	G	401	NDP	O4D-C1D-N1N-C2N
2	H	401	NDP	PN-O3-PA-O5B
2	D	401	NDP	C3D-C4D-C5D-O5D
2	E	401	NDP	C2B-O2B-P2B-O2X
2	B	401	NDP	O4D-C1D-N1N-C2N
2	J	401	NDP	O4D-C1D-N1N-C2N
2	H	401	NDP	C5B-O5B-PA-O1A
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	A	401	NDP	O4D-C1D-N1N-C2N
2	C	401	NDP	O4D-C1D-N1N-C2N
2	I	401	NDP	O4D-C1D-N1N-C2N
2	H	401	NDP	C1B-C2B-O2B-P2B
2	E	401	NDP	O4D-C1D-N1N-C2N
2	E	401	NDP	O4B-C4B-C5B-O5B
2	F	401	NDP	O4D-C1D-N1N-C2N
3	D	402	MES	C8-C7-N4-C3
3	D	402	MES	C8-C7-N4-C5
2	D	401	NDP	O4D-C1D-N1N-C2N
2	F	401	NDP	C2D-C1D-N1N-C2N
2	D	401	NDP	C3B-C2B-O2B-P2B
2	D	401	NDP	C2B-O2B-P2B-O2X
2	A	401	NDP	O4B-C4B-C5B-O5B
2	C	401	NDP	O4B-C4B-C5B-O5B
2	D	401	NDP	O4B-C4B-C5B-O5B
2	I	401	NDP	O4B-C4B-C5B-O5B
2	J	401	NDP	O4B-C4B-C5B-O5B
2	A	401	NDP	C5D-O5D-PN-O1N
2	I	401	NDP	C5D-O5D-PN-O1N
2	B	401	NDP	O4B-C4B-C5B-O5B

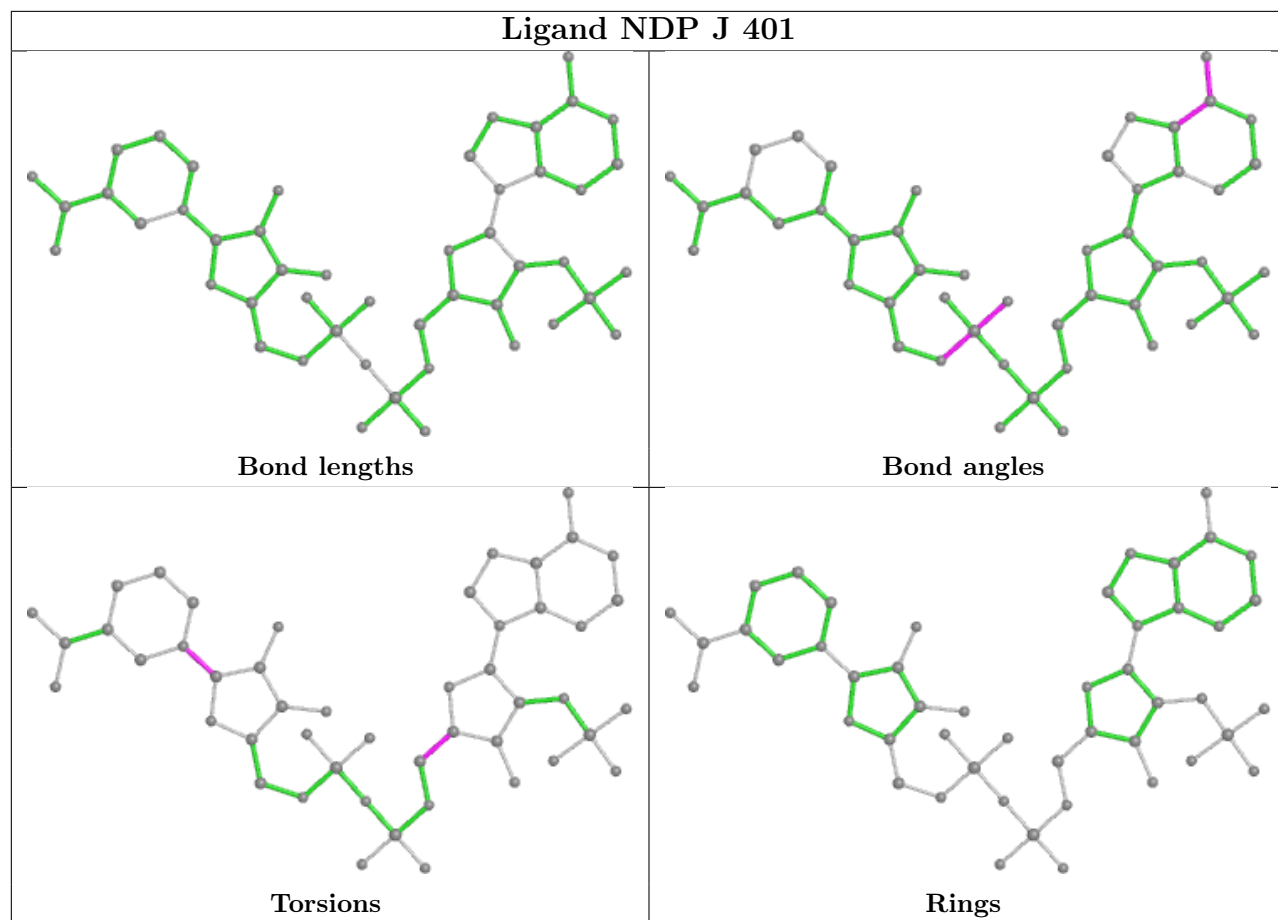
There are no ring outliers.

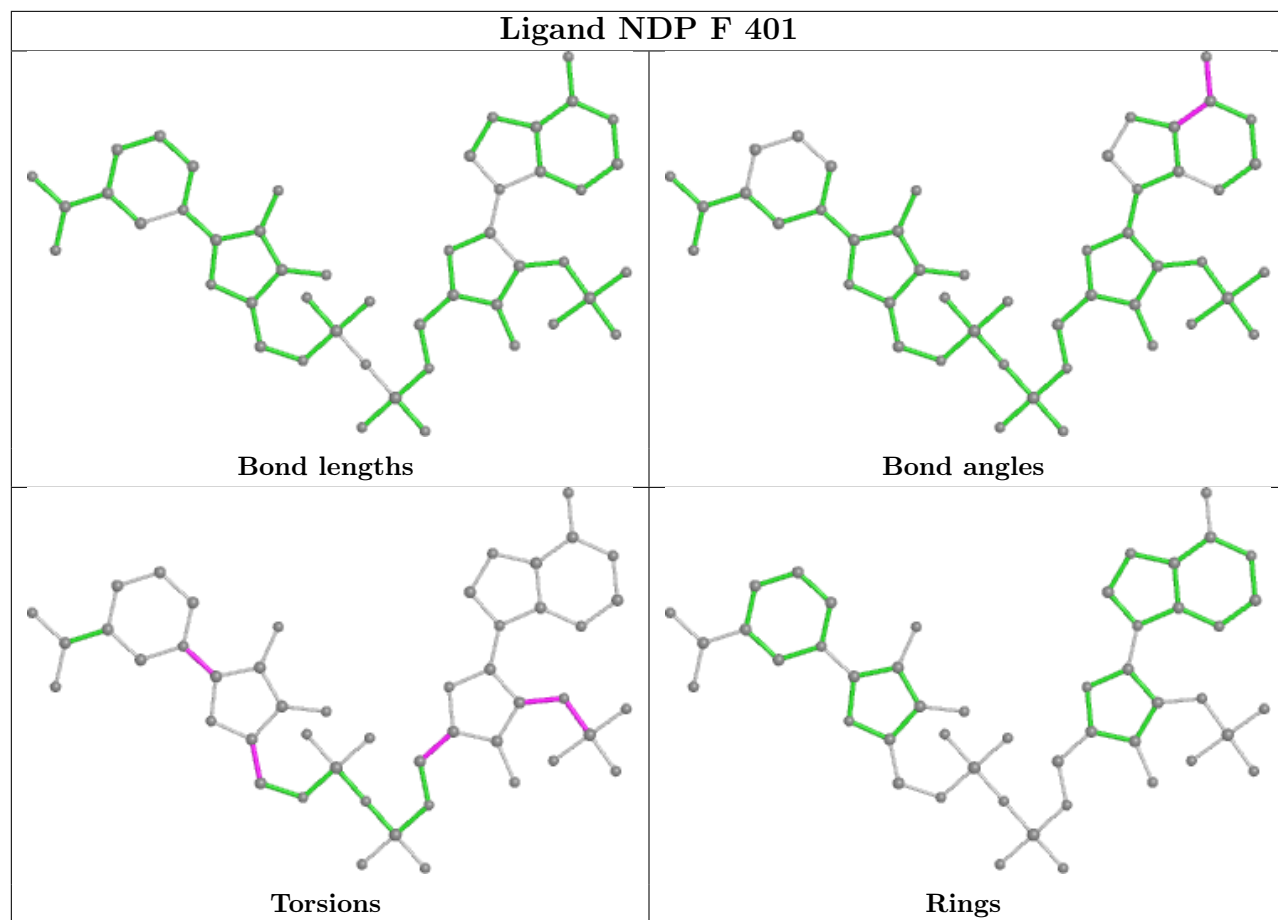
2 monomers are involved in 2 short contacts:

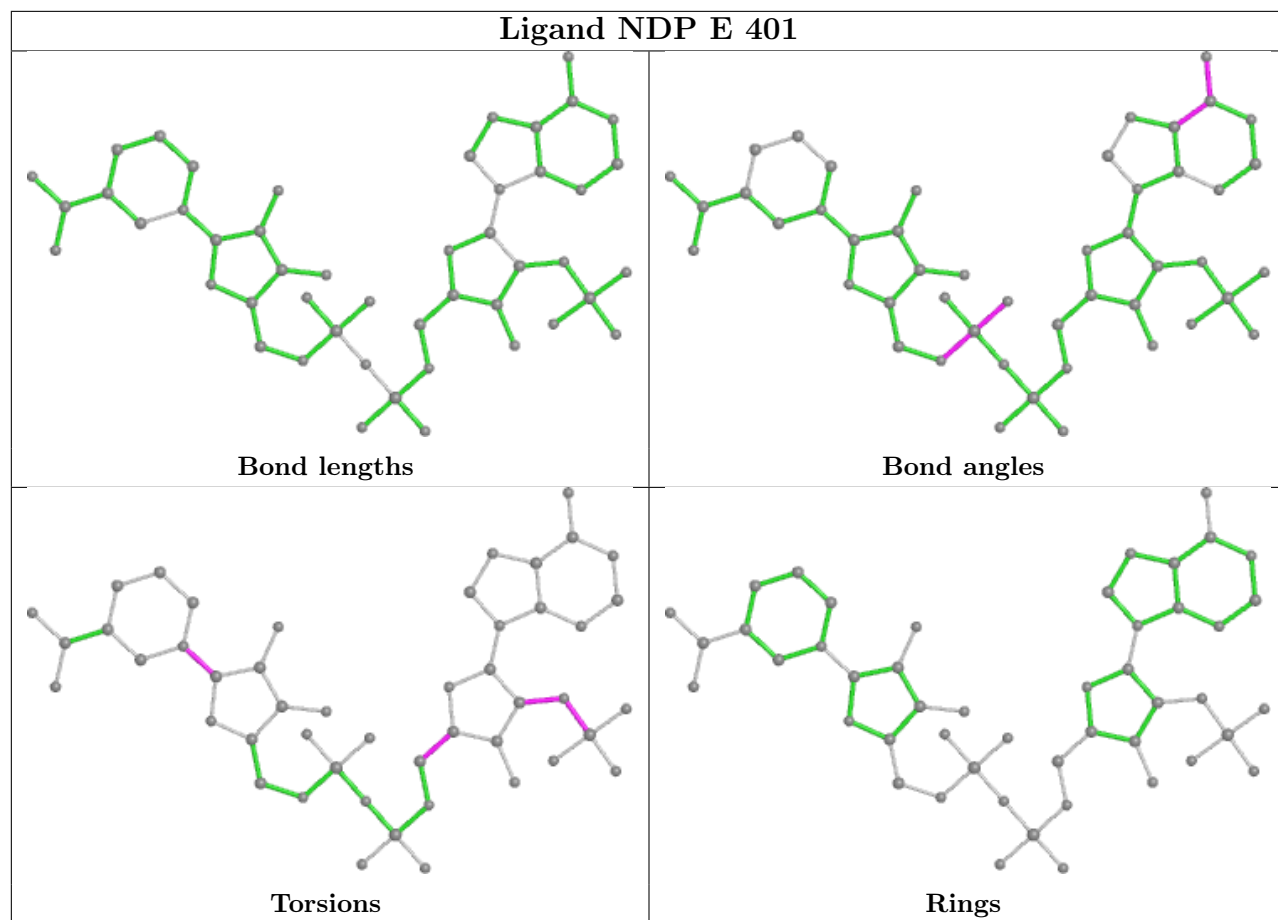
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	NDP	1	0
2	F	401	NDP	1	0

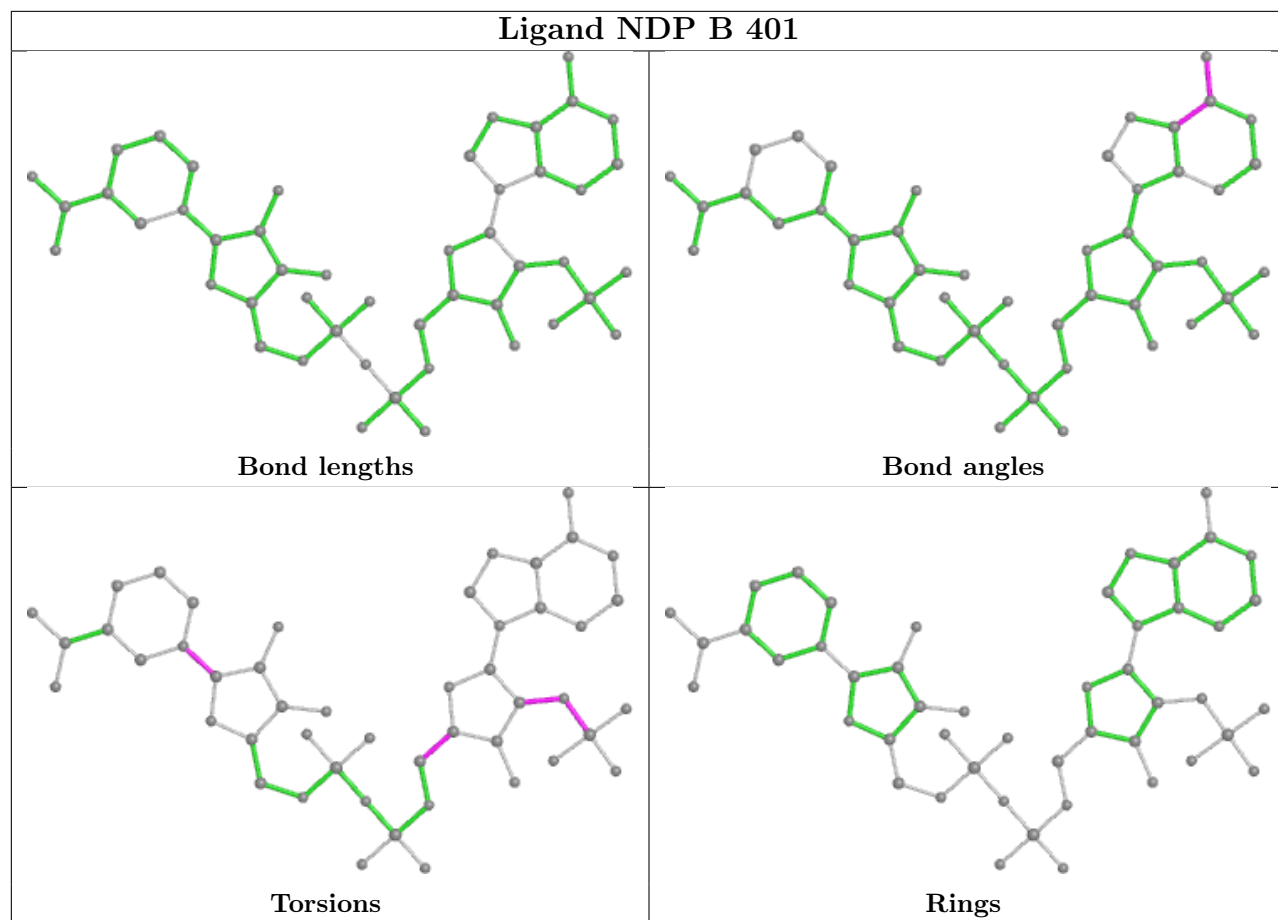
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

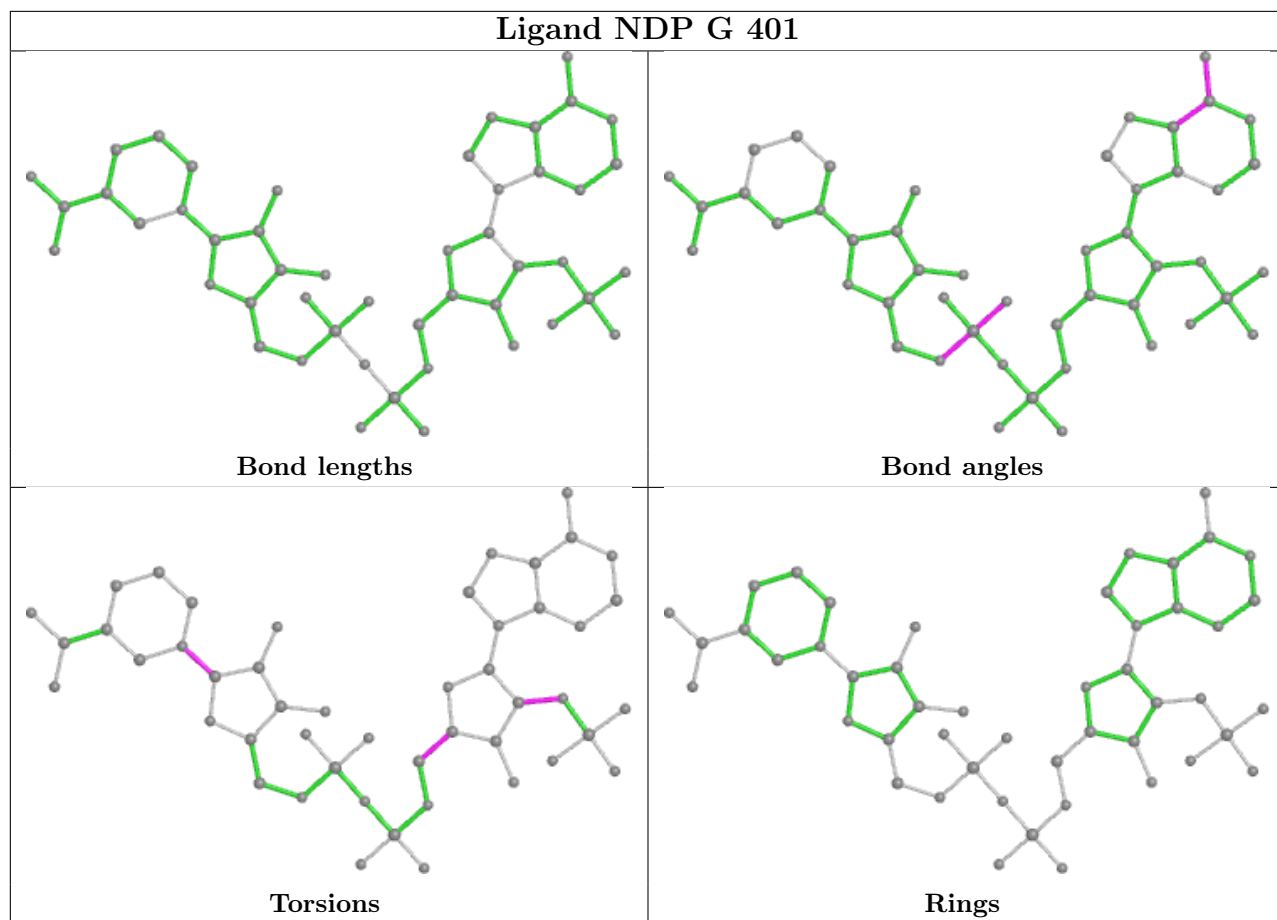


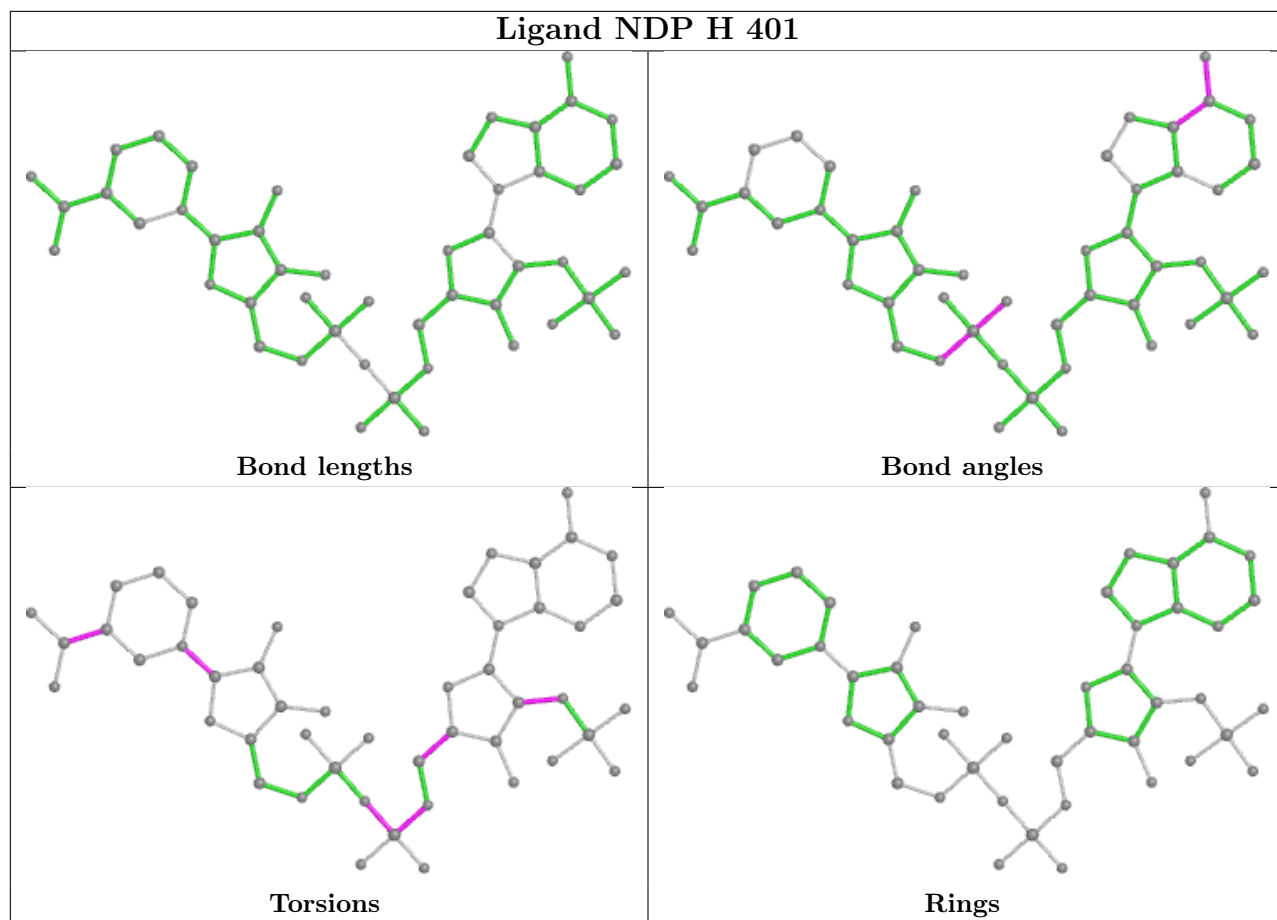


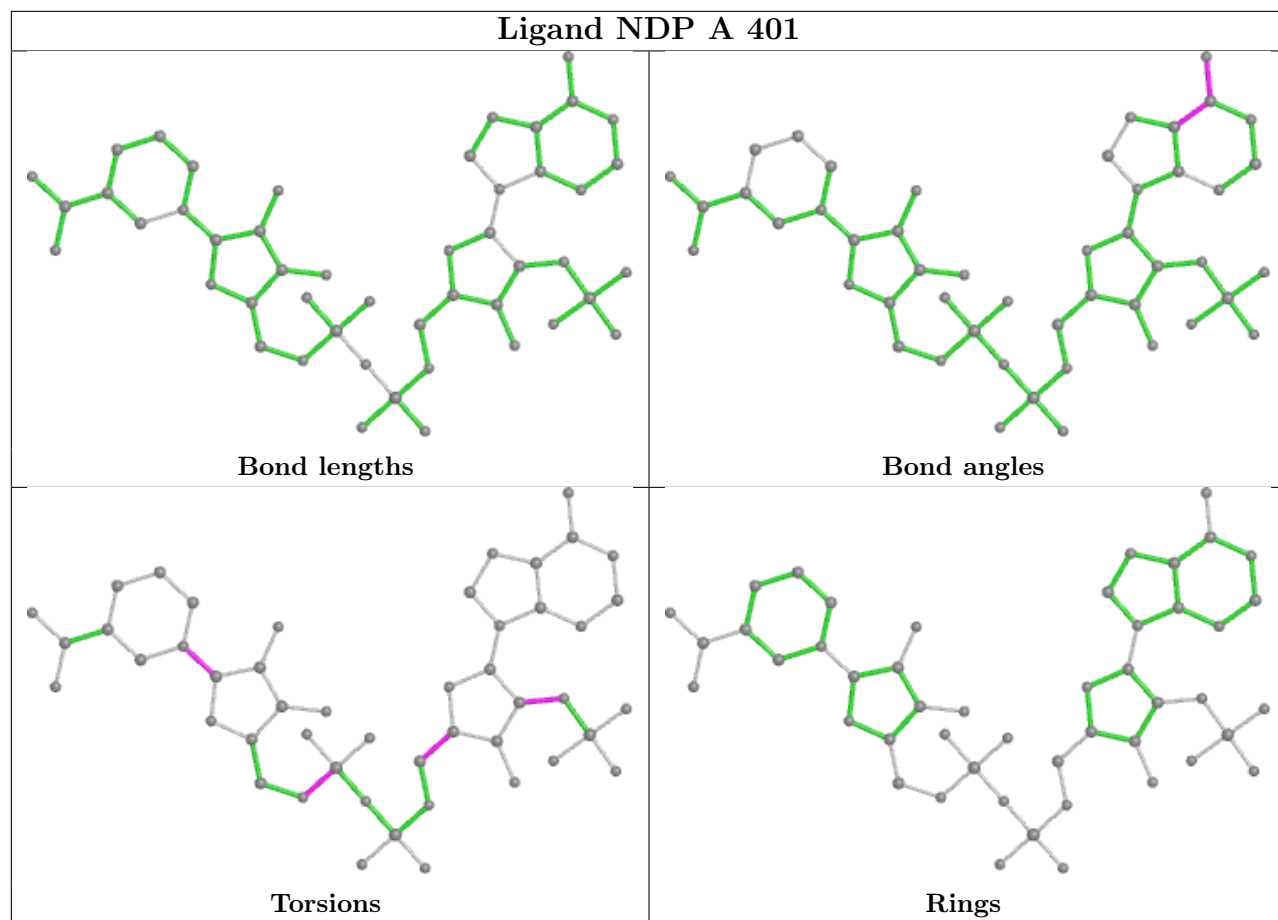


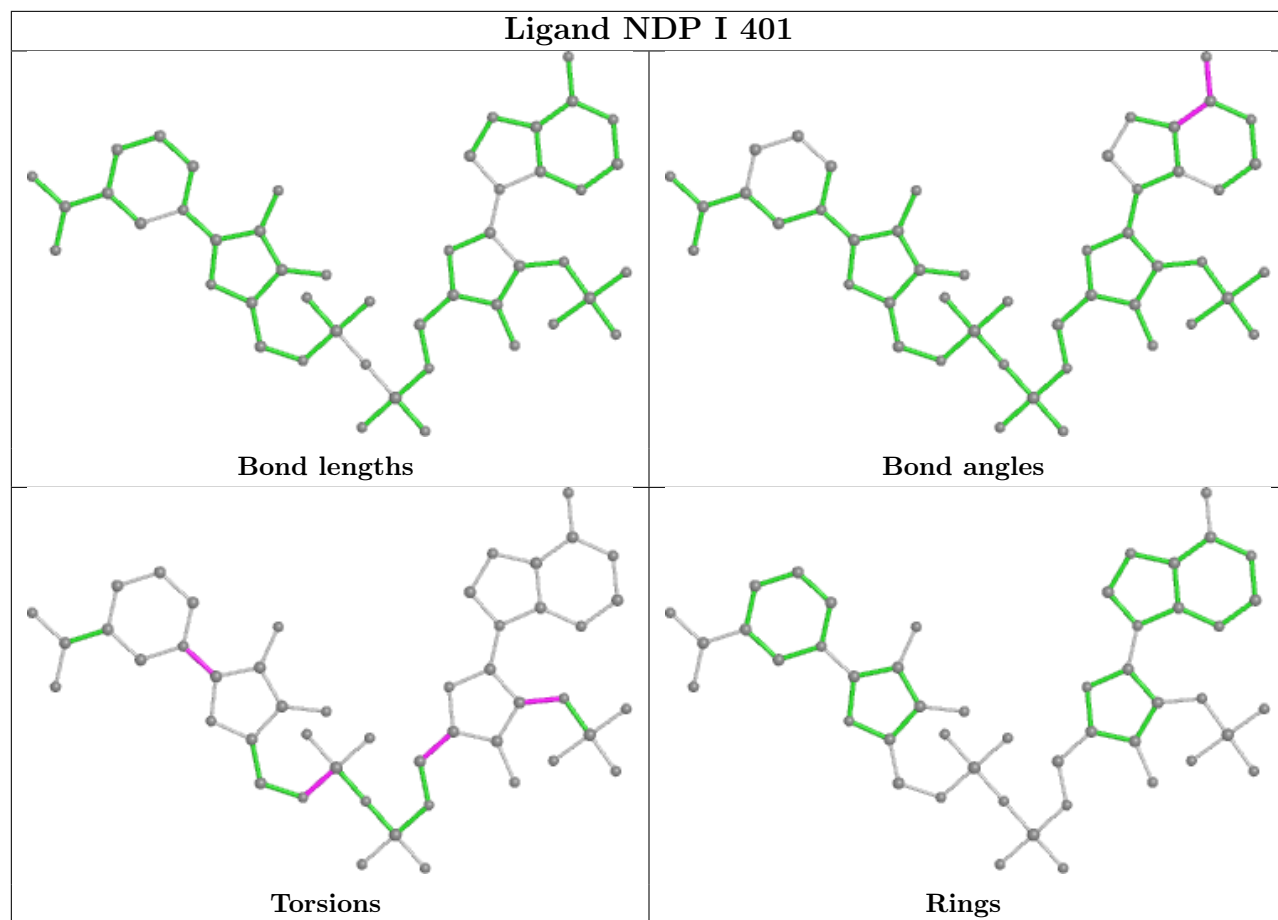


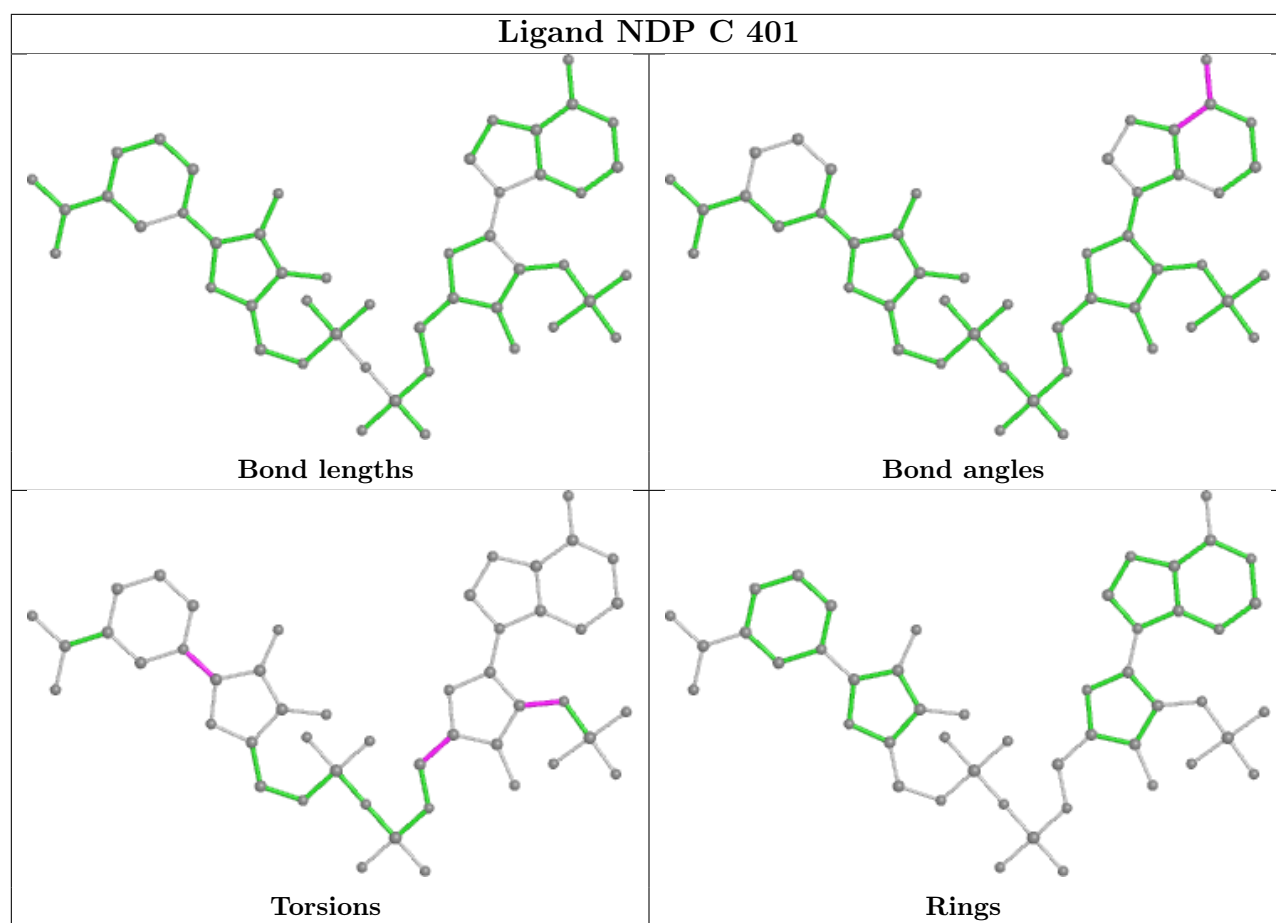












5.7 Other polymers [\(i\)](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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%)	-0.31	0 100 100	21, 31, 50, 73	0
1	B	315/341 (92%)	0.24	22 (6%) 16 15	24, 46, 104, 137	0
1	C	315/341 (92%)	-0.17	8 (2%) 57 55	22, 31, 57, 125	0
1	D	308/341 (90%)	1.46	93 (30%) 0 0	41, 103, 150, 179	0
1	E	314/341 (92%)	0.05	15 (4%) 30 29	24, 44, 94, 118	0
1	F	312/341 (91%)	1.19	82 (26%) 0 0	40, 88, 129, 160	0
1	G	242/341 (70%)	0.92	49 (20%) 1 1	43, 69, 134, 153	0
1	H	242/341 (70%)	0.97	49 (20%) 1 1	43, 75, 138, 191	0
1	I	315/341 (92%)	-0.25	2 (0%) 89 88	20, 32, 52, 98	0
1	J	315/341 (92%)	-0.29	1 (0%) 94 93	22, 32, 52, 88	0
All	All	2992/3410 (87%)	0.35	321 (10%) 6 5	20, 47, 126, 191	0

All (321) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	308	PRO	10.8
1	D	309	VAL	8.6
1	F	303	ILE	8.3
1	D	156	ALA	8.2
1	G	305	ALA	8.1
1	D	72	LEU	7.9
1	F	300	ILE	7.3
1	F	310	LEU	7.2
1	H	83	LEU	6.9
1	G	85	ALA	6.9
1	G	308	PRO	6.8
1	G	94	VAL	6.7
1	D	93	PRO	6.6

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Mol	Chain	Res	Type	RSRZ
1	F	309	VAL	6.6
1	H	306	GLY	6.6
1	G	300	ILE	6.5
1	G	293	ALA	6.5
1	D	53	TYR	6.4
1	D	90	PRO	6.4
1	G	309	VAL	6.2
1	G	93	PRO	6.2
1	G	297	VAL	6.2
1	F	315	PRO	6.1
1	D	310	LEU	6.0
1	D	171	GLY	6.0
1	F	296	ILE	5.9
1	G	92	VAL	5.9
1	D	151	LEU	5.8
1	H	94	VAL	5.8
1	G	288	ILE	5.8
1	H	93	PRO	5.7
1	F	94	VAL	5.6
1	D	300	ILE	5.5
1	E	305	ALA	5.5
1	C	5	ALA	5.4
1	F	53	TYR	5.4
1	D	297	VAL	5.4
1	F	179	LEU	5.3
1	F	172	TRP	5.3
1	F	91	ASP	5.2
1	D	172	TRP	5.2
1	D	193	GLY	5.2
1	G	315	PRO	5.2
1	H	300	ILE	5.1
1	G	83	LEU	5.1
1	D	95	THR	5.1
1	H	92	VAL	5.1
1	F	163	ALA	5.1
1	F	54	ALA	5.1
1	D	247	LEU	5.1
1	F	51	VAL	5.0
1	H	89	LEU	5.0
1	F	297	VAL	5.0
1	D	64	PHE	4.9
1	D	71	LYS	4.9

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Mol	Chain	Res	Type	RSRZ
1	G	303	ILE	4.9
1	F	67	PHE	4.8
1	D	74	ILE	4.8
1	B	28	ALA	4.8
1	D	303	ILE	4.8
1	D	189	GLU	4.7
1	F	92	VAL	4.7
1	D	305	ALA	4.7
1	F	313	VAL	4.7
1	F	205	LEU	4.6
1	H	295	GLN	4.6
1	D	194	PHE	4.6
1	H	309	VAL	4.5
1	D	89	LEU	4.4
1	H	305	ALA	4.4
1	D	185	PHE	4.4
1	D	8	ALA	4.4
1	G	301	ARG	4.4
1	G	318	GLY	4.4
1	F	130	GLU	4.4
1	D	298	GLU	4.4
1	G	90	PRO	4.4
1	H	315	PRO	4.4
1	H	262	VAL	4.3
1	F	95	THR	4.3
1	H	303	ILE	4.3
1	F	178	ALA	4.3
1	F	131	GLY	4.3
1	H	293	ALA	4.3
1	D	304	GLU	4.3
1	D	94	VAL	4.3
1	G	97	LEU	4.3
1	D	84	VAL	4.2
1	D	286	ILE	4.2
1	G	88	ASP	4.2
1	D	70	LEU	4.1
1	F	34	VAL	4.1
1	G	268	GLY	4.1
1	D	163	ALA	4.1
1	D	69	ASN	4.1
1	H	87	ASP	4.1
1	G	267	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	301	ARG	4.0
1	G	313	VAL	4.0
1	B	61	HIS	4.0
1	F	305	ALA	3.9
1	C	101	ASN	3.8
1	C	102	MET	3.8
1	D	308	PRO	3.8
1	D	306	GLY	3.8
1	F	159	ALA	3.8
1	D	91	ASP	3.8
1	D	92	VAL	3.8
1	D	54	ALA	3.7
1	G	89	LEU	3.7
1	H	298	GLU	3.7
1	B	306	GLY	3.7
1	H	84	VAL	3.7
1	H	292	ALA	3.7
1	D	211	THR	3.7
1	D	243	LEU	3.6
1	G	87	ASP	3.6
1	D	100	PRO	3.6
1	H	233	ALA	3.6
1	F	93	PRO	3.6
1	F	189	GLU	3.6
1	F	308	PRO	3.6
1	F	72	LEU	3.6
1	H	297	VAL	3.6
1	D	319	TYR	3.6
1	F	8	ALA	3.5
1	I	5	ALA	3.5
1	H	267	VAL	3.5
1	H	304	GLU	3.5
1	D	270	PRO	3.5
1	G	264	PRO	3.5
1	H	316	ARG	3.5
1	B	303	ILE	3.5
1	F	90	PRO	3.4
1	F	209	PRO	3.4
1	F	31	GLY	3.4
1	D	214	LEU	3.4
1	F	306	GLY	3.4
1	E	308	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
1	G	91	ASP	3.3
1	F	32	LEU	3.3
1	F	70	LEU	3.3
1	H	317	ARG	3.3
1	D	223	LEU	3.3
1	D	183	SER	3.3
1	F	82	ALA	3.3
1	G	298	GLU	3.3
1	H	88	ASP	3.3
1	B	29	HIS	3.3
1	H	97	LEU	3.3
1	B	304	GLU	3.3
1	D	313	VAL	3.2
1	C	98	SER	3.2
1	C	97	LEU	3.2
1	H	265	LEU	3.2
1	H	296	ILE	3.2
1	B	309	VAL	3.2
1	B	315	PRO	3.2
1	G	289	PRO	3.2
1	E	84	VAL	3.2
1	F	302	ARG	3.2
1	D	83	LEU	3.2
1	H	301	ARG	3.2
1	B	305	ALA	3.2
1	G	86	ARG	3.2
1	D	190	ALA	3.1
1	H	90	PRO	3.1
1	D	68	PRO	3.1
1	D	295	GLN	3.1
1	E	301	ARG	3.1
1	D	302	ARG	3.1
1	G	188	LEU	3.0
1	D	146	VAL	3.0
1	F	191	LEU	3.0
1	H	102	MET	3.0
1	F	301	ARG	3.0
1	H	80	VAL	3.0
1	E	307	GLU	3.0
1	F	169	VAL	3.0
1	D	307	GLU	3.0
1	D	184	CYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	34	VAL	2.9
1	H	307	GLU	2.9
1	D	160	LEU	2.9
1	F	28	ALA	2.9
1	D	55	LEU	2.9
1	F	141	ALA	2.9
1	D	169	VAL	2.9
1	G	273	ALA	2.9
1	F	182	VAL	2.8
1	F	307	GLU	2.8
1	D	50	GLU	2.8
1	F	299	ASN	2.8
1	D	65	ALA	2.8
1	F	68	PRO	2.8
1	E	31	GLY	2.8
1	H	178	ALA	2.8
1	G	296	ILE	2.8
1	D	246	ALA	2.8
1	G	311	ASN	2.8
1	D	133	TRP	2.8
1	D	49	GLU	2.8
1	C	6	SER	2.7
1	H	95	THR	2.7
1	F	311	ASN	2.7
1	G	292	ALA	2.7
1	B	70	LEU	2.7
1	D	33	ASP	2.7
1	D	206	PRO	2.7
1	H	313	VAL	2.7
1	F	298	GLU	2.7
1	H	302	ARG	2.7
1	D	229	PHE	2.7
1	F	133	TRP	2.7
1	F	176	PRO	2.7
1	H	269	SER	2.7
1	F	175	THR	2.7
1	G	192	PRO	2.6
1	H	144	ILE	2.6
1	E	297	VAL	2.6
1	D	27	ALA	2.6
1	E	306	GLY	2.6
1	D	52	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	67	PHE	2.6
1	F	229	PHE	2.6
1	B	5	ALA	2.6
1	H	86	ARG	2.6
1	D	216	ASN	2.6
1	C	99	ASP	2.5
1	F	304	GLU	2.5
1	F	183	SER	2.5
1	F	208	THR	2.5
1	C	100	PRO	2.5
1	D	294	PRO	2.5
1	D	28	ALA	2.5
1	D	32	LEU	2.5
1	G	304	GLU	2.5
1	G	99	ASP	2.5
1	D	311	ASN	2.5
1	G	84	VAL	2.5
1	D	132	ARG	2.4
1	B	308	PRO	2.4
1	E	288	ILE	2.4
1	J	5	ALA	2.4
1	D	315	PRO	2.4
1	F	217	ALA	2.4
1	G	82	ALA	2.4
1	G	306	GLY	2.4
1	B	313	VAL	2.4
1	G	319	TYR	2.4
1	F	71	LYS	2.4
1	E	64	PHE	2.4
1	F	174	ARG	2.3
1	B	87	ASP	2.3
1	F	147	GLY	2.3
1	D	272	TRP	2.3
1	D	98	SER	2.3
1	F	73	VAL	2.3
1	F	248	ARG	2.3
1	D	30	PRO	2.3
1	F	100	PRO	2.3
1	D	9	LEU	2.3
1	F	245	ALA	2.3
1	H	271	LEU	2.3
1	D	215	MET	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	80	VAL	2.3
1	F	9	LEU	2.3
1	H	314	ASP	2.3
1	G	316	ARG	2.3
1	G	178	ALA	2.3
1	D	191	LEU	2.3
1	D	271	LEU	2.3
1	F	89	LEU	2.3
1	F	207	LEU	2.3
1	F	29	HIS	2.3
1	F	185	PHE	2.3
1	B	98	SER	2.3
1	D	26	GLN	2.3
1	D	22	LYS	2.2
1	F	213	GLY	2.2
1	D	168	ASP	2.2
1	G	299	ASN	2.2
1	B	138	PRO	2.2
1	F	30	PRO	2.2
1	B	94	VAL	2.2
1	D	63	PHE	2.2
1	H	91	ASP	2.2
1	E	93	PRO	2.2
1	B	297	VAL	2.2
1	D	25	LEU	2.2
1	F	48	PRO	2.2
1	B	300	ILE	2.2
1	F	198	SER	2.2
1	B	299	ASN	2.1
1	D	73	VAL	2.1
1	H	85	ALA	2.1
1	G	290	ARG	2.1
1	G	153	ASP	2.1
1	F	293	ALA	2.1
1	G	314	ASP	2.1
1	I	315	PRO	2.1
1	F	156	ALA	2.1
1	F	319	TYR	2.1
1	H	294	PRO	2.1
1	E	53	TYR	2.1
1	F	98	SER	2.1
1	H	179	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	51	VAL	2.1
1	F	318	GLY	2.1
1	E	304	GLU	2.0
1	H	153	ASP	2.0
1	E	83	LEU	2.0
1	E	100	PRO	2.0
1	B	301	ARG	2.0
1	H	137	HIS	2.0
1	F	144	ILE	2.0
1	F	10	VAL	2.0
1	G	144	ILE	2.0
1	F	226	GLY	2.0
1	G	79	GLY	2.0
1	D	219	ARG	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.

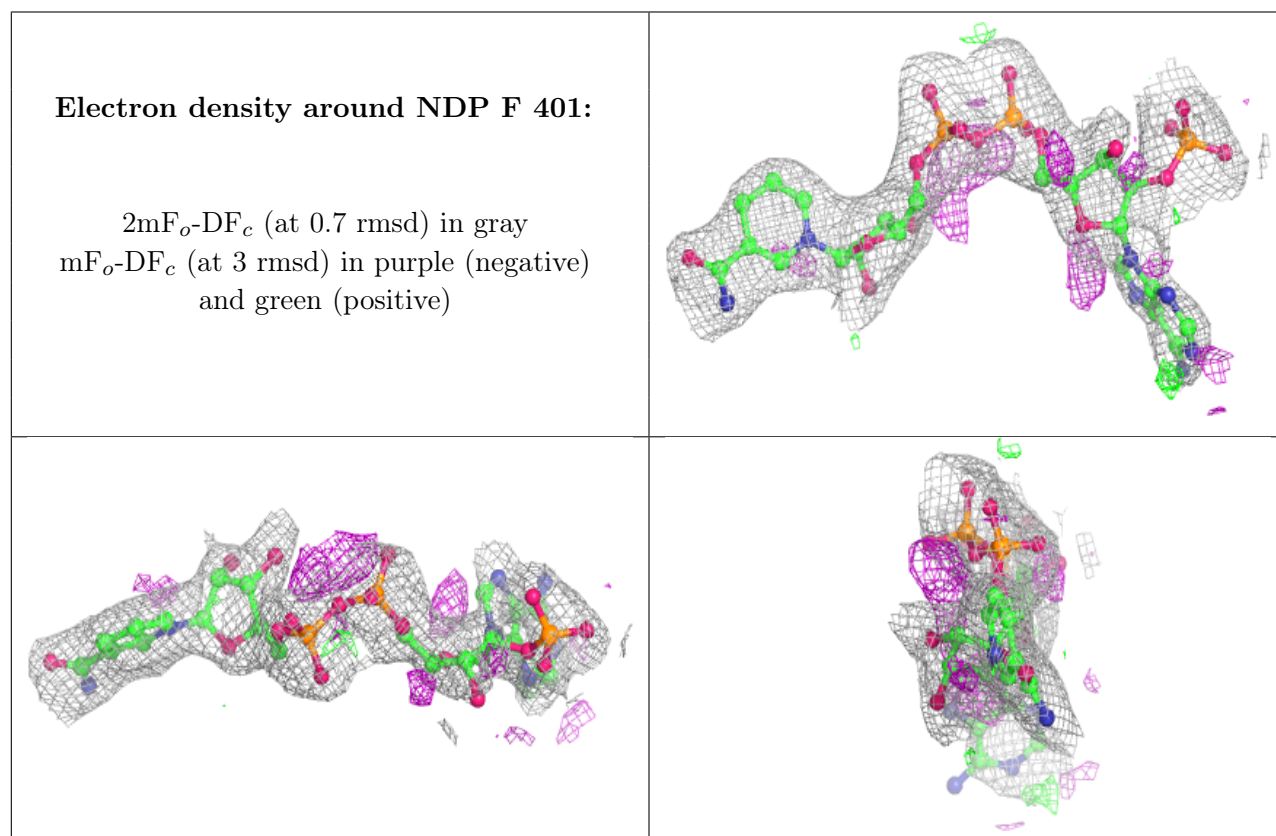
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MES	B	402	12/12	0.82	0.23	61,89,100,111	0
3	MES	F	402	12/12	0.86	0.20	54,97,113,113	0
2	NDP	F	401	48/48	0.87	0.18	40,79,107,120	0
3	MES	C	402	12/12	0.87	0.18	43,59,72,73	0
3	MES	D	402	12/12	0.87	0.15	61,93,109,135	0
3	MES	A	403	12/12	0.87	0.20	43,73,96,108	0
2	NDP	D	401	48/48	0.88	0.15	48,84,121,139	0
3	MES	E	402	12/12	0.92	0.17	53,72,91,99	0
2	NDP	H	401	48/48	0.92	0.13	44,72,92,105	0

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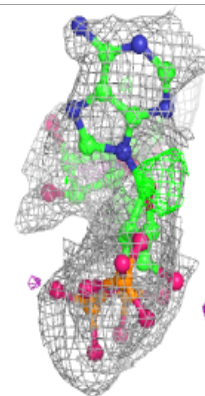
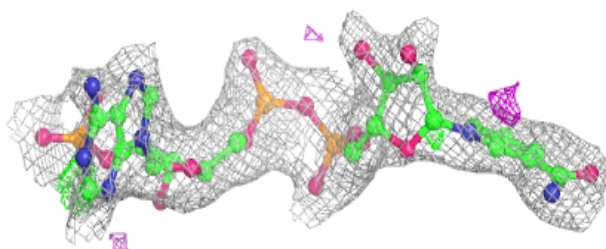
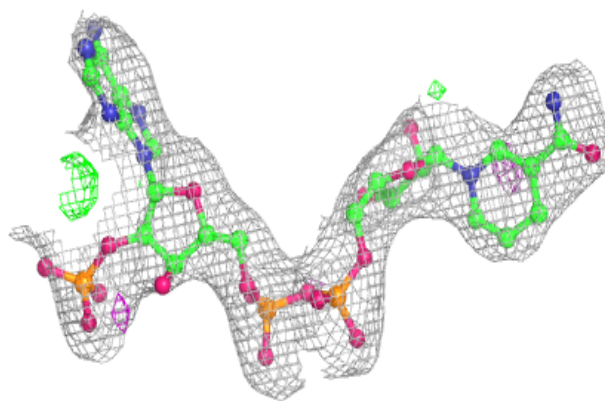
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NDP	G	401	48/48	0.93	0.14	44,63,90,101	0
2	NDP	B	401	48/48	0.94	0.11	29,39,49,55	0
3	MES	J	402	12/12	0.94	0.13	28,43,55,62	0
3	MES	I	402	12/12	0.95	0.14	33,51,60,69	0
3	MES	A	402	12/12	0.95	0.14	32,43,64,65	0
2	NDP	A	401	48/48	0.97	0.10	20,27,35,44	0
2	NDP	I	401	48/48	0.97	0.11	19,26,32,36	0
2	NDP	J	401	48/48	0.97	0.11	17,27,37,40	0
2	NDP	E	401	48/48	0.97	0.08	27,36,43,47	0
2	NDP	C	401	48/48	0.98	0.11	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.

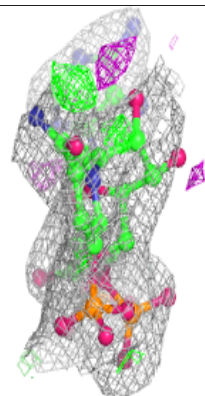
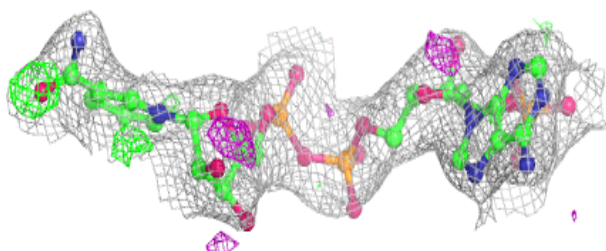
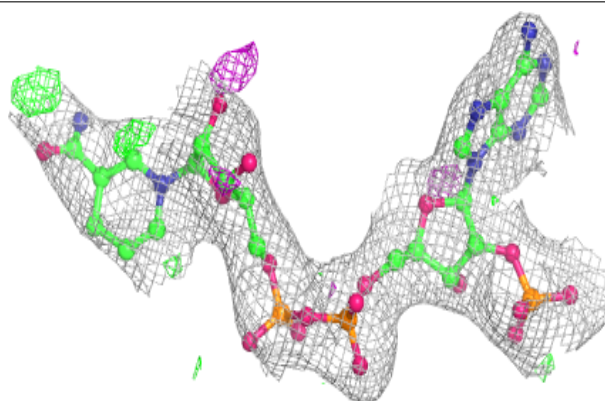


Electron density around NDP D 401:

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

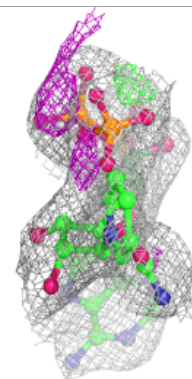
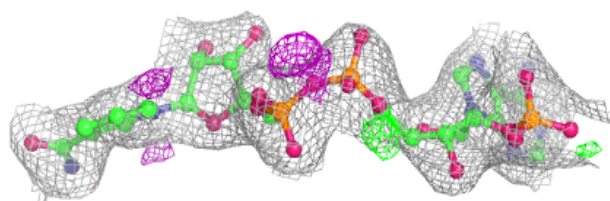
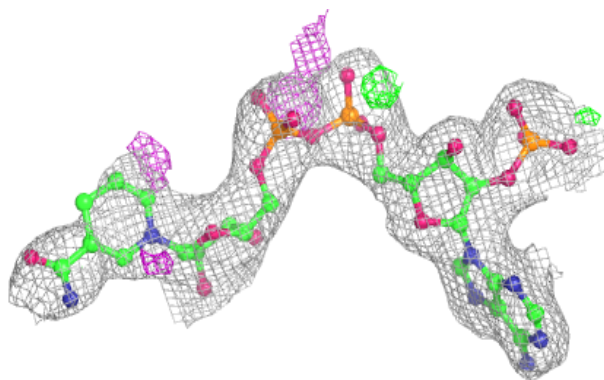
**Electron density around NDP H 401:**

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

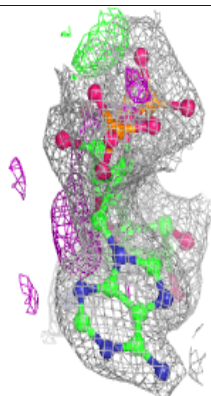
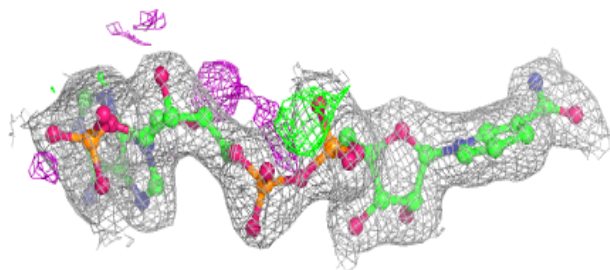
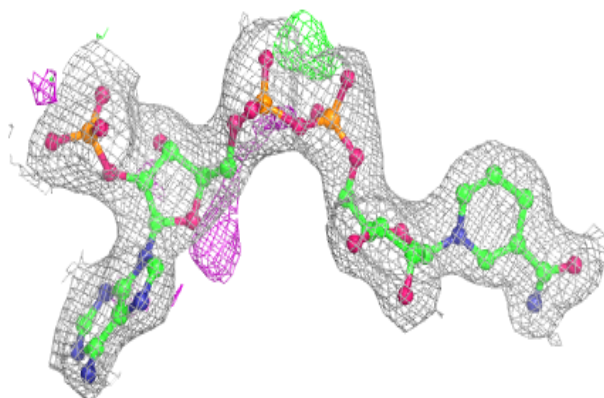


Electron density around NDP G 401:

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

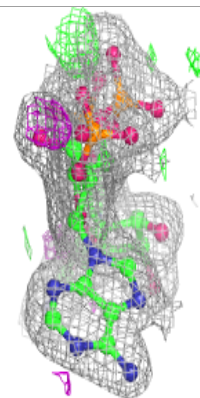
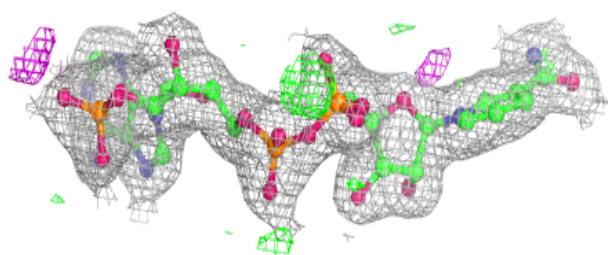
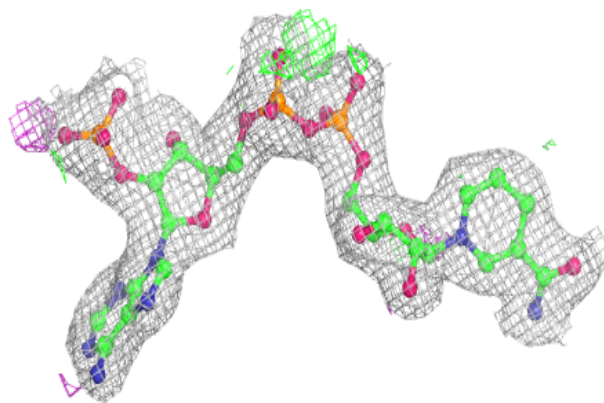
**Electron density around NDP B 401:**

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

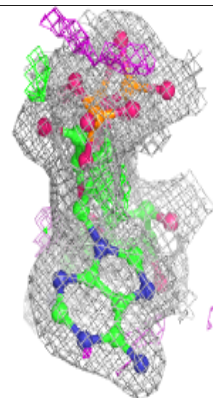
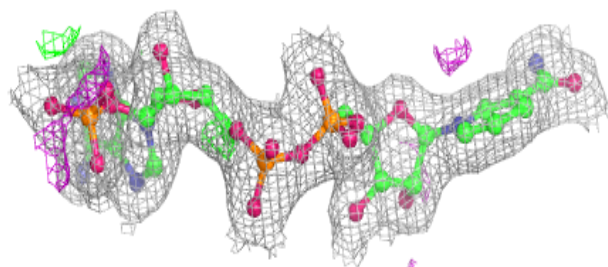
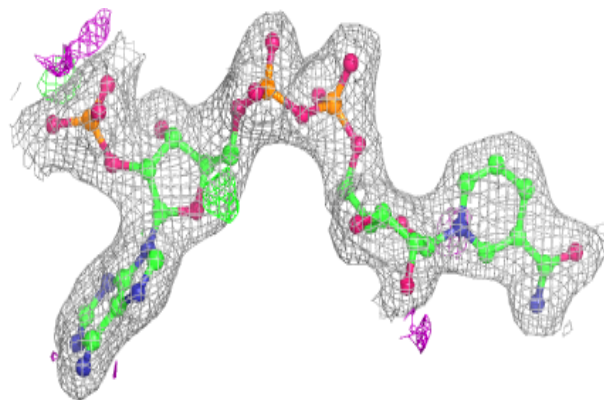


Electron density around NDP A 401:

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

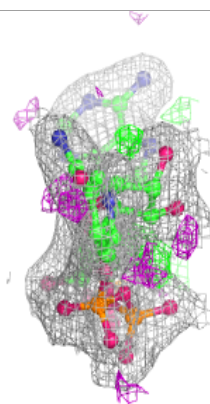
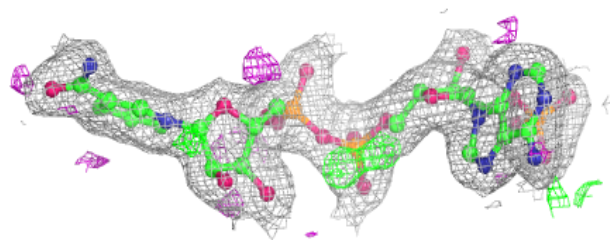
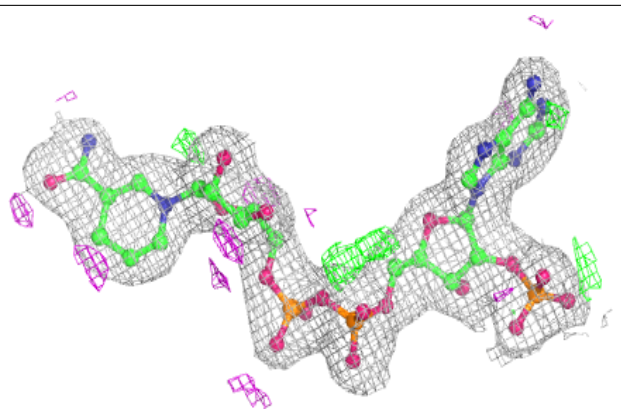
**Electron density around NDP I 401:**

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

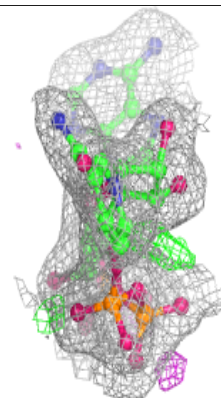
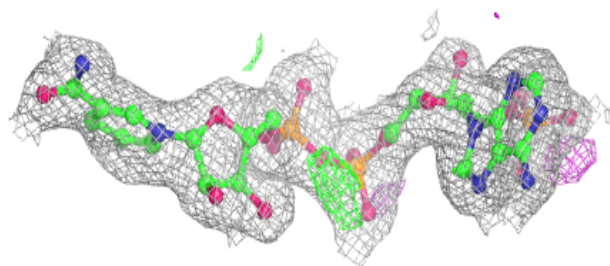
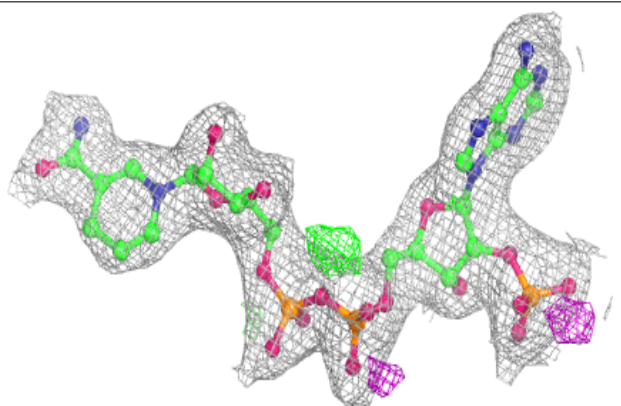


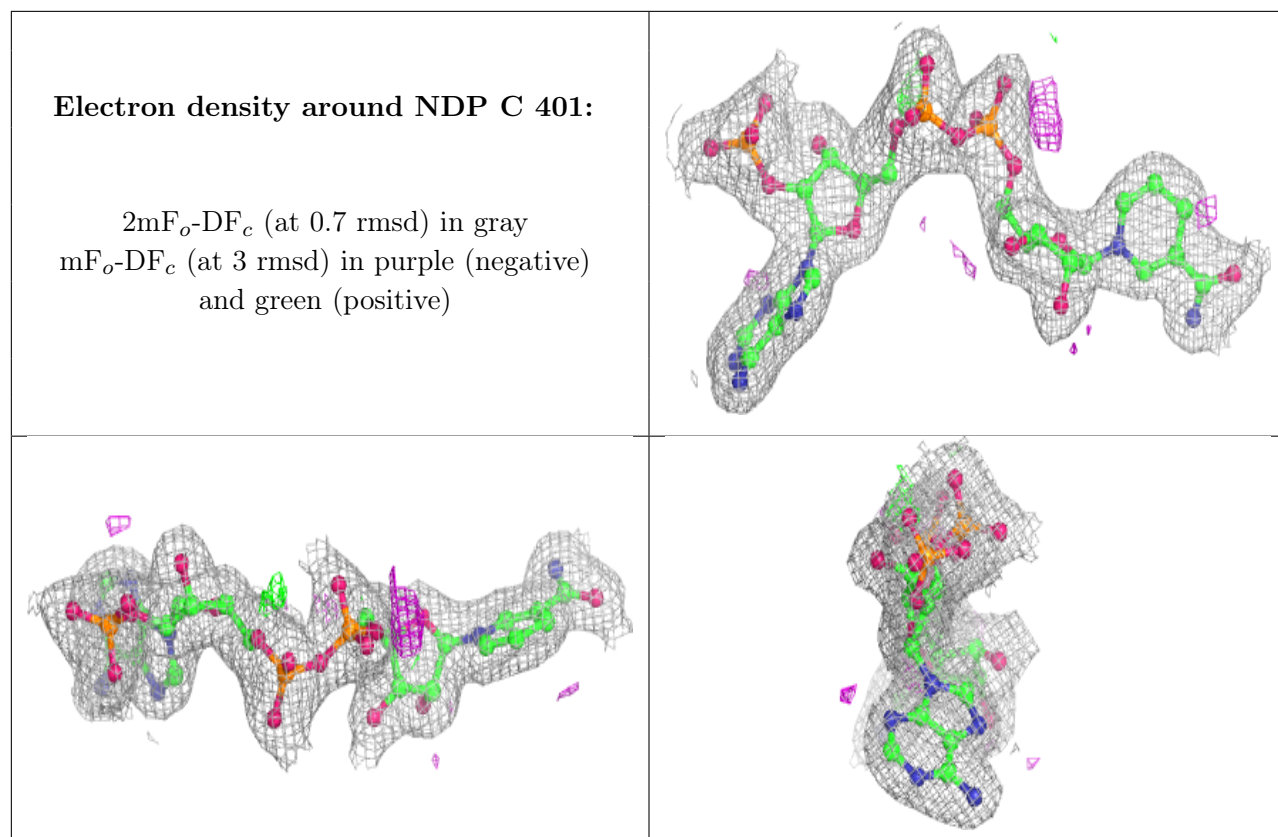
Electron density around NDP J 401:

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

**Electron density around NDP 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.