



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 28, 2022 – 04:23 PM EDT

PDB ID : 7US5
Title : X-ray crystal structure of GDP-D-glycero-D-manno-heptose 4,6-Dehydratase from *Campylobacter jejuni*
Authors : Thoden, J.B.; Xiang, D.F.; Raushel, F.M.; Holden, H.M.
Deposited on : 2022-04-23
Resolution : 2.10 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	:	2.29
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)	:	2.29

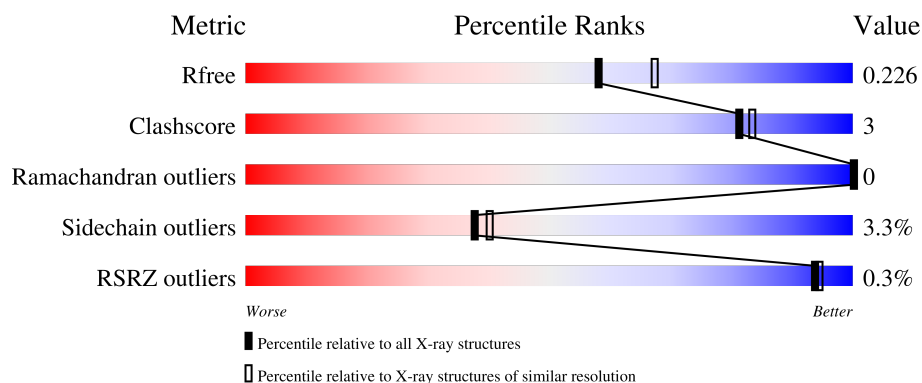
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION





The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	365	 87% 7% • 5%
1	B	365	 85% 8% 6%
1	C	365	 84% 9% • 6%
1	D	365	 87% 5% • 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12341 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 GDP-D-GLYCERO-D-MANNO-HEPTOSE 4,6-DEHYDRATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	8	0
			2819	1794	480	531	14			
1	B	342	Total	C	N	O	S	0	5	0
			2760	1754	471	522	13			
1	C	342	Total	C	N	O	S	0	1	0
			2753	1749	472	520	12			
1	D	343	Total	C	N	O	S	0	1	0
			2758	1752	473	521	12			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q5M6Q7
A	-18	GLY	-	expression tag	UNP Q5M6Q7
A	-17	SER	-	expression tag	UNP Q5M6Q7
A	-16	SER	-	expression tag	UNP Q5M6Q7
A	-15	HIS	-	expression tag	UNP Q5M6Q7
A	-14	HIS	-	expression tag	UNP Q5M6Q7
A	-13	HIS	-	expression tag	UNP Q5M6Q7
A	-12	HIS	-	expression tag	UNP Q5M6Q7
A	-11	HIS	-	expression tag	UNP Q5M6Q7
A	-10	HIS	-	expression tag	UNP Q5M6Q7
A	-9	SER	-	expression tag	UNP Q5M6Q7
A	-8	SER	-	expression tag	UNP Q5M6Q7
A	-7	GLY	-	expression tag	UNP Q5M6Q7
A	-6	LEU	-	expression tag	UNP Q5M6Q7
A	-5	VAL	-	expression tag	UNP Q5M6Q7
A	-4	PRO	-	expression tag	UNP Q5M6Q7
A	-3	ARG	-	expression tag	UNP Q5M6Q7
A	-2	GLY	-	expression tag	UNP Q5M6Q7
A	-1	SER	-	expression tag	UNP Q5M6Q7
A	0	HIS	-	expression tag	UNP Q5M6Q7
A	1	MET	-	expression tag	UNP Q5M6Q7

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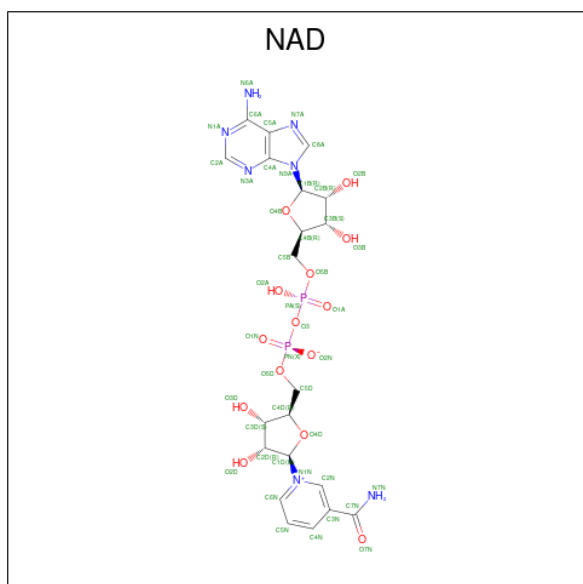
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP Q5M6Q7
B	-18	GLY	-	expression tag	UNP Q5M6Q7
B	-17	SER	-	expression tag	UNP Q5M6Q7
B	-16	SER	-	expression tag	UNP Q5M6Q7
B	-15	HIS	-	expression tag	UNP Q5M6Q7
B	-14	HIS	-	expression tag	UNP Q5M6Q7
B	-13	HIS	-	expression tag	UNP Q5M6Q7
B	-12	HIS	-	expression tag	UNP Q5M6Q7
B	-11	HIS	-	expression tag	UNP Q5M6Q7
B	-10	HIS	-	expression tag	UNP Q5M6Q7
B	-9	SER	-	expression tag	UNP Q5M6Q7
B	-8	SER	-	expression tag	UNP Q5M6Q7
B	-7	GLY	-	expression tag	UNP Q5M6Q7
B	-6	LEU	-	expression tag	UNP Q5M6Q7
B	-5	VAL	-	expression tag	UNP Q5M6Q7
B	-4	PRO	-	expression tag	UNP Q5M6Q7
B	-3	ARG	-	expression tag	UNP Q5M6Q7
B	-2	GLY	-	expression tag	UNP Q5M6Q7
B	-1	SER	-	expression tag	UNP Q5M6Q7
B	0	HIS	-	expression tag	UNP Q5M6Q7
B	1	MET	-	expression tag	UNP Q5M6Q7
C	-19	MET	-	expression tag	UNP Q5M6Q7
C	-18	GLY	-	expression tag	UNP Q5M6Q7
C	-17	SER	-	expression tag	UNP Q5M6Q7
C	-16	SER	-	expression tag	UNP Q5M6Q7
C	-15	HIS	-	expression tag	UNP Q5M6Q7
C	-14	HIS	-	expression tag	UNP Q5M6Q7
C	-13	HIS	-	expression tag	UNP Q5M6Q7
C	-12	HIS	-	expression tag	UNP Q5M6Q7
C	-11	HIS	-	expression tag	UNP Q5M6Q7
C	-10	HIS	-	expression tag	UNP Q5M6Q7
C	-9	SER	-	expression tag	UNP Q5M6Q7
C	-8	SER	-	expression tag	UNP Q5M6Q7
C	-7	GLY	-	expression tag	UNP Q5M6Q7
C	-6	LEU	-	expression tag	UNP Q5M6Q7
C	-5	VAL	-	expression tag	UNP Q5M6Q7
C	-4	PRO	-	expression tag	UNP Q5M6Q7
C	-3	ARG	-	expression tag	UNP Q5M6Q7
C	-2	GLY	-	expression tag	UNP Q5M6Q7
C	-1	SER	-	expression tag	UNP Q5M6Q7
C	0	HIS	-	expression tag	UNP Q5M6Q7
C	1	MET	-	expression tag	UNP Q5M6Q7

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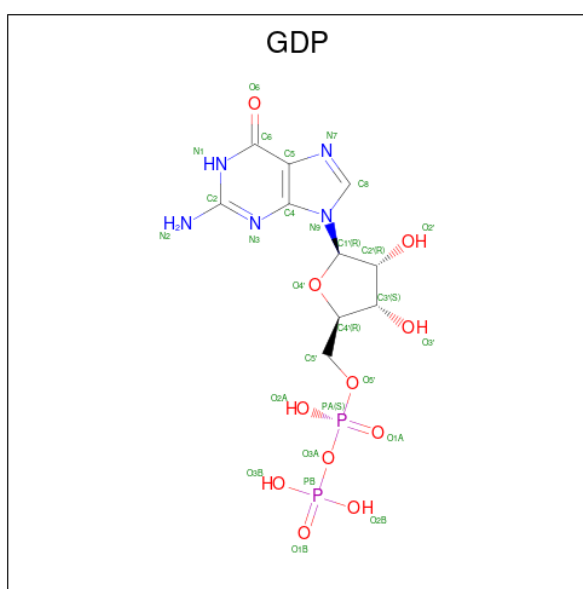
Chain	Residue	Modelled	Actual	Comment	Reference
D	-19	MET	-	expression tag	UNP Q5M6Q7
D	-18	GLY	-	expression tag	UNP Q5M6Q7
D	-17	SER	-	expression tag	UNP Q5M6Q7
D	-16	SER	-	expression tag	UNP Q5M6Q7
D	-15	HIS	-	expression tag	UNP Q5M6Q7
D	-14	HIS	-	expression tag	UNP Q5M6Q7
D	-13	HIS	-	expression tag	UNP Q5M6Q7
D	-12	HIS	-	expression tag	UNP Q5M6Q7
D	-11	HIS	-	expression tag	UNP Q5M6Q7
D	-10	HIS	-	expression tag	UNP Q5M6Q7
D	-9	SER	-	expression tag	UNP Q5M6Q7
D	-8	SER	-	expression tag	UNP Q5M6Q7
D	-7	GLY	-	expression tag	UNP Q5M6Q7
D	-6	LEU	-	expression tag	UNP Q5M6Q7
D	-5	VAL	-	expression tag	UNP Q5M6Q7
D	-4	PRO	-	expression tag	UNP Q5M6Q7
D	-3	ARG	-	expression tag	UNP Q5M6Q7
D	-2	GLY	-	expression tag	UNP Q5M6Q7
D	-1	SER	-	expression tag	UNP Q5M6Q7
D	0	HIS	-	expression tag	UNP Q5M6Q7
D	1	MET	-	expression tag	UNP Q5M6Q7

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

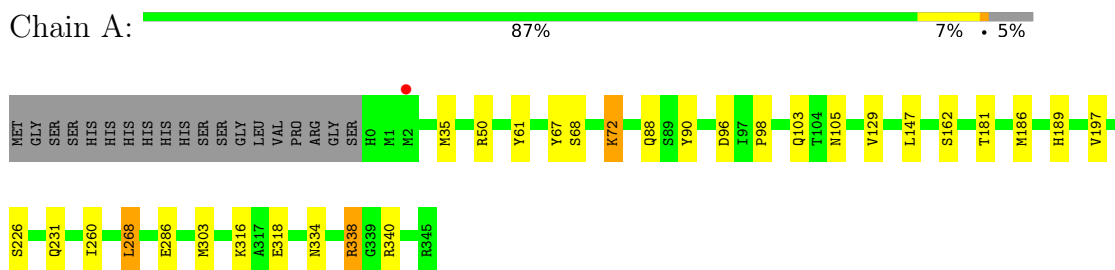
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	286	Total	O	0	1
			287	287		
5	B	231	Total	O	0	0
			231	231		
5	C	210	Total	O	0	1
			211	211		
5	D	210	Total	O	0	0
			210	210		

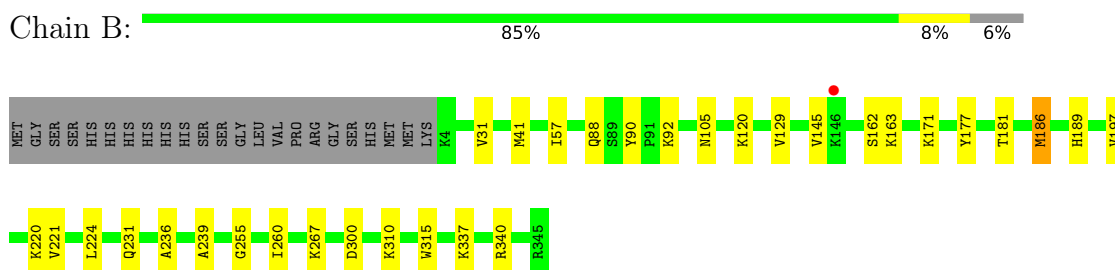
3 Residue-property plots

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

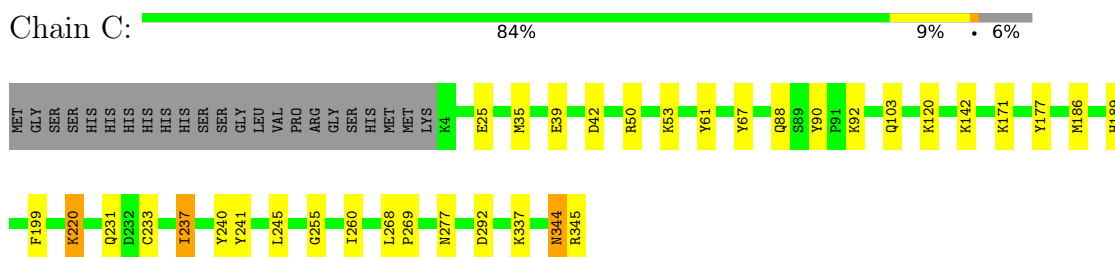
• Molecule 1: GDP-D-GLYCERO-D-MANNO-HEPTOSE 4,6-DEHYDRATASE



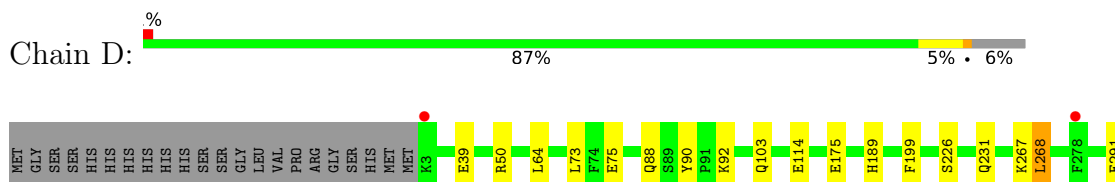
• Molecule 1: GDP-D-GLYCERO-D-MANNO-HEPTOSE 4,6-DEHYDRATASE

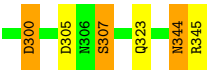


• Molecule 1: GDP-D-GLYCERO-D-MANNO-HEPTOSE 4,6-DEHYDRATASE



• Molecule 1: GDP-D-GLYCERO-D-MANNO-HEPTOSE 4,6-DEHYDRATASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	112.67Å 182.95Å 75.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.97 – 2.10 36.94 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (36.97-2.10) 99.5 (36.94-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.46 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.169 , 0.221 0.175 , 0.226	Depositor DCC
R_{free} test set	4572 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12341	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, NAD, GDP

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	0.69	0/2899	0.83	0/3909
1	B	0.70	0/2830	0.85	1/3819 (0.0%)
1	C	0.70	0/2812	0.83	0/3794
1	D	0.70	2/2817 (0.1%)	0.84	1/3801 (0.0%)
All	All	0.70	2/11358 (0.0%)	0.84	2/15323 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	114	GLU	CD-OE1	-5.32	1.19	1.25
1	D	175	GLU	CD-OE1	5.06	1.31	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	300	ASP	CB-CA-C	-7.46	95.47	110.40
1	B	41	MET	CA-CB-CG	-5.43	104.07	113.30

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	2819	0	2821	13	0
1	B	2760	0	2746	17	0
1	C	2753	0	2732	18	0
1	D	2758	0	2734	13	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
3	A	28	0	12	0	0
3	B	28	0	12	0	0
3	C	28	0	12	0	0
3	D	28	0	12	0	0
4	A	4	0	6	0	0
4	B	4	0	6	0	0
4	C	12	0	18	3	0
4	D	4	0	6	0	0
5	A	287	0	0	0	0
5	B	231	0	0	1	0
5	C	211	0	0	3	0
5	D	210	0	0	2	0
All	All	12341	0	11221	59	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (59) 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:103[B]:GLN:NE2	5:D:501:HOH:O	1.76	1.16
1:A:226:SER:HB3	1:A:268:LEU:HD22	1.62	0.82
1:C:344:ASN:HD22	1:C:344:ASN:C	1.91	0.74
1:D:344:ASN:C	1:D:344:ASN:HD22	1.91	0.72
1:D:226:SER:HB3	1:D:268:LEU:HD22	1.74	0.68
4:C:405:EDO:H11	1:D:39:GLU:HA	1.79	0.64
1:D:344:ASN:HD22	1:D:345:ARG:N	2.00	0.59
1:A:340:ARG:HH21	1:B:340:ARG:HH21	1.50	0.58
1:D:305:ASP:OD1	1:D:307:SER:OG	2.23	0.56
1:C:103[A]:GLN:OE1	5:C:501:HOH:O	2.18	0.55
1:C:344:ASN:HD22	1:C:345:ARG:N	2.05	0.55
1:B:186:MET:HE3	1:B:236:ALA:HB1	1.90	0.54
1:C:90:TYR:CZ	1:C:92:LYS:HB3	2.43	0.54
1:C:344:ASN:C	1:C:344:ASN:ND2	2.61	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:GLU:HA	4:C:405:EDO:H22	1.90	0.53
1:C:220:LYS:HD3	5:C:682:HOH:O	2.07	0.52
1:A:129:VAL:O	1:A:181:THR:HA	2.10	0.52
1:A:189:HIS:HA	1:A:231:GLN:O	2.10	0.52
1:B:189:HIS:HA	1:B:231:GLN:O	2.10	0.52
1:D:344:ASN:C	1:D:344:ASN:ND2	2.62	0.51
1:B:186:MET:CE	1:B:236:ALA:HB1	2.41	0.51
1:A:103[A]:GLN:HE21	1:D:103[A]:GLN:HE22	1.59	0.51
1:A:35:MET:O	1:A:61:TYR:HA	2.11	0.50
1:B:129:VAL:O	1:B:181:THR:HA	2.12	0.49
1:D:189:HIS:HA	1:D:231:GLN:O	2.14	0.48
1:B:310:LYS:NZ	5:B:506:HOH:O	2.47	0.47
1:D:226:SER:HA	1:D:300:ASP:O	2.15	0.47
1:A:90:TYR:CZ	1:A:197:VAL:HB	2.49	0.47
1:A:186:MET:SD	1:A:260:ILE:HB	2.55	0.47
1:A:334[B]:ASN:HD21	1:A:338:ARG:NH1	2.11	0.47
1:B:186:MET:SD	1:B:236:ALA:HB1	2.55	0.47
1:B:186:MET:HG2	1:B:260:ILE:HB	1.97	0.47
1:B:221:VAL:HG21	1:B:224:LEU:HD21	1.96	0.46
1:B:105:ASN:HB2	1:B:162:SER:HB2	1.97	0.46
1:C:35:MET:O	1:C:61:TYR:HA	2.16	0.46
1:B:90:TYR:CZ	1:B:197:VAL:HB	2.51	0.45
1:B:120:LYS:HE2	1:B:177:TYR:O	2.17	0.45
1:B:31:VAL:O	1:B:57:ILE:HA	2.16	0.45
1:A:68:SER:O	1:A:72:LYS:HD3	2.16	0.45
1:C:186:MET:HG3	1:C:240:TYR:OH	2.16	0.44
1:A:67:TYR:CD2	1:C:67:TYR:CD2	3.06	0.44
1:C:199:PHE:CZ	1:C:268:LEU:HB3	2.52	0.44
1:D:199:PHE:CE2	1:D:268:LEU:HG	2.53	0.44
1:C:186:MET:SD	1:C:260:ILE:HB	2.57	0.43
1:D:90:TYR:CZ	1:D:92:LYS:HB3	2.54	0.43
1:C:189:HIS:HA	1:C:231:GLN:O	2.19	0.43
1:C:268:LEU:N	1:C:269:PRO:CD	2.81	0.43
1:A:105:ASN:HB2	1:A:162:SER:HB2	2.00	0.42
1:C:171:LYS:HG2	1:C:255:GLY:O	2.19	0.42
1:B:163:LYS:HD2	1:B:163:LYS:HA	1.83	0.42
1:B:171:LYS:HE3	1:B:255:GLY:O	2.19	0.42
1:D:75:GLU:OE2	5:D:502:HOH:O	2.21	0.42
4:C:405:EDO:H21	5:C:654:HOH:O	2.18	0.42
1:A:96:ASP:C	1:A:98:PRO:HD3	2.40	0.41
1:B:239:ALA:HB2	1:B:315:TRP:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:LYS:HE2	1:C:177:TYR:O	2.19	0.41
1:C:241:TYR:CZ	1:C:245:LEU:HD11	2.55	0.41
1:C:233:CYS:O	1:C:237:ILE:HD12	2.20	0.41
1:B:90:TYR:CZ	1:B:92:LYS:HB3	2.56	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	352/365 (96%)	342 (97%)	10 (3%)	0	100	100
1	B	345/365 (94%)	337 (98%)	8 (2%)	0	100	100
1	C	341/365 (93%)	336 (98%)	5 (2%)	0	100	100
1	D	342/365 (94%)	335 (98%)	7 (2%)	0	100	100
All	All	1380/1460 (94%)	1350 (98%)	30 (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	310/319 (97%)	299 (96%)	11 (4%)	36	38
1	B	302/319 (95%)	295 (98%)	7 (2%)	50	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	300/319 (94%)	288 (96%)	12 (4%)	31	32
1	D	300/319 (94%)	290 (97%)	10 (3%)	38	40
All	All	1212/1276 (95%)	1172 (97%)	40 (3%)	38	40

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	ARG
1	A	72	LYS
1	A	88	GLN
1	A	147	LEU
1	A	268	LEU
1	A	286[A]	GLU
1	A	286[B]	GLU
1	A	303	MET
1	A	316	LYS
1	A	318	GLU
1	A	338	ARG
1	B	88	GLN
1	B	145	VAL
1	B	186	MET
1	B	220	LYS
1	B	267	LYS
1	B	300	ASP
1	B	337	LYS
1	C	25	GLU
1	C	42	ASP
1	C	50	ARG
1	C	53	LYS
1	C	88	GLN
1	C	142	LYS
1	C	220	LYS
1	C	237	ILE
1	C	277	ASN
1	C	292	ASP
1	C	337	LYS
1	C	344	ASN
1	D	50	ARG
1	D	64	LEU
1	D	73	LEU
1	D	88	GLN

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Mol	Chain	Res	Type
1	D	267	LYS
1	D	268	LEU
1	D	291	GLU
1	D	307	SER
1	D	323	GLN
1	D	344	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	259	ASN
1	B	277	ASN
1	C	259	ASN
1	C	344	ASN
1	D	259	ASN
1	D	302	GLN
1	D	323	GLN
1	D	344	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

14 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
4	EDO	C	404	-	3,3,3	0.12	0	2,2,2	0.25	0
3	GDP	D	402	-	24,30,30	0.83	1 (4%)	30,47,47	1.69	4 (13%)
4	EDO	C	403	-	3,3,3	0.39	0	2,2,2	0.29	0
3	GDP	A	402	-	24,30,30	1.00	1 (4%)	30,47,47	1.43	6 (20%)
4	EDO	C	405	-	3,3,3	0.62	0	2,2,2	0.79	0
4	EDO	B	403	-	3,3,3	0.14	0	2,2,2	0.23	0
3	GDP	C	402	-	24,30,30	0.92	1 (4%)	30,47,47	1.32	5 (16%)
4	EDO	D	403	-	3,3,3	0.15	0	2,2,2	0.36	0
2	NAD	A	401	-	42,48,48	0.71	2 (4%)	50,73,73	0.81	2 (4%)
2	NAD	C	401	-	42,48,48	0.58	0	50,73,73	0.85	2 (4%)
4	EDO	A	403	-	3,3,3	0.11	0	2,2,2	0.70	0
2	NAD	D	401	-	42,48,48	0.67	1 (2%)	50,73,73	0.86	2 (4%)
2	NAD	B	401	-	42,48,48	0.72	1 (2%)	50,73,73	0.83	4 (8%)
3	GDP	B	402	-	24,30,30	0.89	0	30,47,47	1.43	6 (20%)

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
4	EDO	C	404	-	-	0/1/1/1	-
3	GDP	D	402	-	-	4/12/32/32	0/3/3/3
4	EDO	C	403	-	-	0/1/1/1	-
3	GDP	A	402	-	-	3/12/32/32	0/3/3/3
4	EDO	C	405	-	-	1/1/1/1	-
4	EDO	B	403	-	-	0/1/1/1	-
3	GDP	C	402	-	-	4/12/32/32	0/3/3/3
4	EDO	D	403	-	-	0/1/1/1	-
2	NAD	A	401	-	-	3/26/62/62	0/5/5/5
2	NAD	C	401	-	-	3/26/62/62	0/5/5/5
4	EDO	A	403	-	-	1/1/1/1	-
2	NAD	D	401	-	-	5/26/62/62	0/5/5/5
2	NAD	B	401	-	-	5/26/62/62	0/5/5/5
3	GDP	B	402	-	-	4/12/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	NAD	C2N-N1N	3.19	1.38	1.35
3	A	402	GDP	O4'-C1'	2.46	1.44	1.41
2	A	401	NAD	C2N-N1N	2.44	1.37	1.35
2	D	401	NAD	C2N-N1N	2.38	1.37	1.35
3	C	402	GDP	C6-N1	-2.36	1.34	1.37
3	D	402	GDP	C5-C4	2.10	1.48	1.43
2	A	401	NAD	C8A-N7A	-2.09	1.31	1.34

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	402	GDP	O6-C6-N1	4.64	126.13	120.65
3	D	402	GDP	O6-C6-C5	-4.18	116.20	124.37
3	B	402	GDP	O6-C6-C5	-3.64	117.26	124.37
3	B	402	GDP	O6-C6-N1	3.58	124.88	120.65
3	C	402	GDP	O3B-PB-O2B	3.01	119.13	107.64
3	C	402	GDP	O2B-PB-O3A	-2.86	95.03	104.64
3	A	402	GDP	O6-C6-C5	-2.79	118.93	124.37
3	A	402	GDP	C2-N1-C6	-2.75	120.03	125.10
3	A	402	GDP	C5-C6-N1	2.72	118.75	113.95
2	D	401	NAD	C5A-C6A-N6A	2.71	124.47	120.35
3	B	402	GDP	O3B-PB-O1B	2.62	120.95	110.68
2	D	401	NAD	C6N-N1N-C2N	-2.57	119.63	121.97
2	C	401	NAD	C5A-C6A-N6A	2.49	124.14	120.35
3	D	402	GDP	O3A-PB-O1B	-2.36	98.07	111.19
2	C	401	NAD	C6N-N1N-C2N	-2.27	119.91	121.97
2	B	401	NAD	C6N-N1N-C2N	-2.23	119.94	121.97
3	C	402	GDP	C8-N7-C5	2.20	107.19	102.99
2	B	401	NAD	O2A-PA-O1A	2.19	123.07	112.24
2	A	401	NAD	C6N-N1N-C2N	-2.18	119.98	121.97
3	B	402	GDP	C5-C6-N1	2.17	117.79	113.95
3	A	402	GDP	O3B-PB-O2B	2.16	115.89	107.64
3	A	402	GDP	O2A-PA-O1A	2.16	122.90	112.24
2	B	401	NAD	PN-O3-PA	-2.11	125.58	132.83
3	C	402	GDP	C5-C6-N1	2.09	117.64	113.95
3	D	402	GDP	C5-C6-N1	2.08	117.63	113.95
3	C	402	GDP	O6-C6-C5	-2.08	120.31	124.37
3	B	402	GDP	C8-N7-C5	2.04	106.88	102.99
3	A	402	GDP	O3A-PB-O1B	-2.04	99.89	111.19
2	B	401	NAD	C5A-C6A-N6A	2.02	123.43	120.35
3	B	402	GDP	O3B-PB-O2B	2.01	115.33	107.64
2	A	401	NAD	O2A-PA-O1A	2.01	122.16	112.24

There are no chirality outliers.

All (33) torsion outliers are listed below:

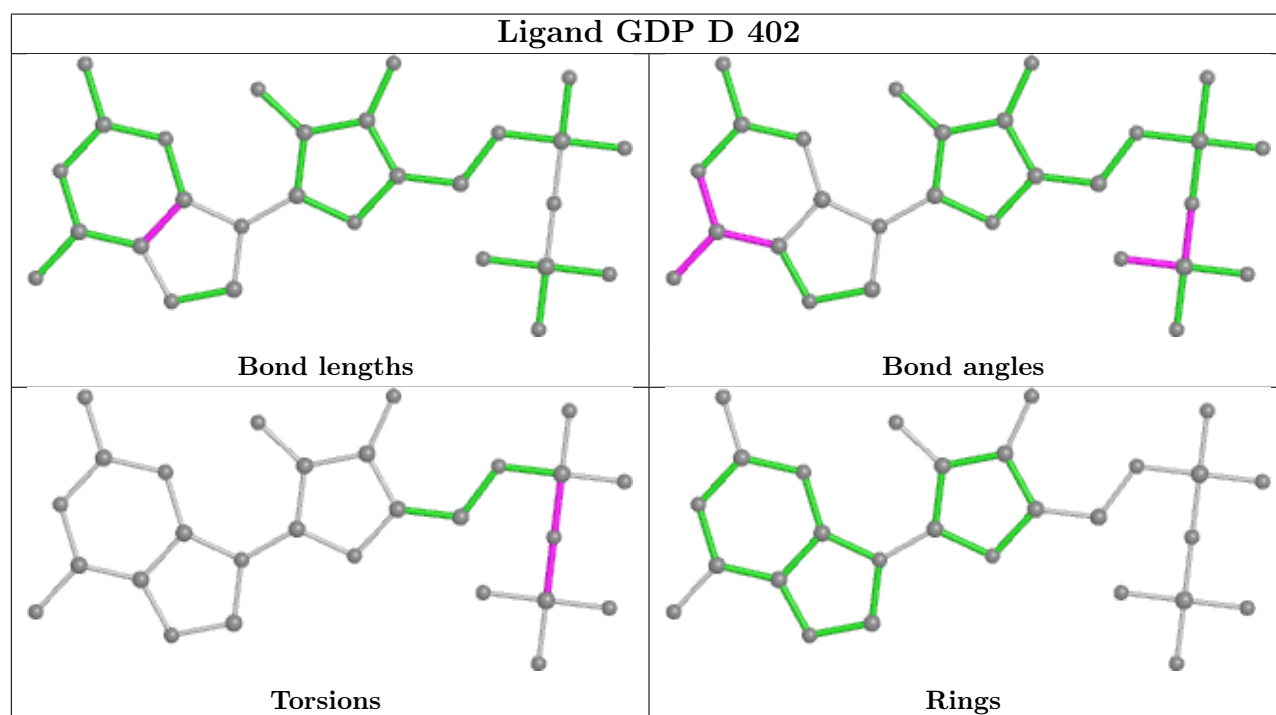
Mol	Chain	Res	Type	Atoms
2	B	401	NAD	C5B-O5B-PA-O1A
2	D	401	NAD	C5D-O5D-PN-O2N
3	A	402	GDP	PA-O3A-PB-O3B
3	A	402	GDP	PB-O3A-PA-O5'
3	B	402	GDP	PA-O3A-PB-O3B
3	B	402	GDP	PB-O3A-PA-O5'
3	C	402	GDP	PA-O3A-PB-O2B
3	C	402	GDP	PA-O3A-PB-O3B
3	D	402	GDP	PA-O3A-PB-O3B
3	D	402	GDP	PB-O3A-PA-O5'
4	C	405	EDO	O1-C1-C2-O2
3	C	402	GDP	PB-O3A-PA-O5'
2	B	401	NAD	C5B-O5B-PA-O3
2	D	401	NAD	C5D-O5D-PN-O3
4	A	403	EDO	O1-C1-C2-O2
2	B	401	NAD	O4B-C4B-C5B-O5B
2	A	401	NAD	O4B-C4B-C5B-O5B
2	A	401	NAD	PN-O3-PA-O1A
2	D	401	NAD	PN-O3-PA-O2A
3	B	402	GDP	PA-O3A-PB-O1B
3	C	402	GDP	PA-O3A-PB-O1B
3	D	402	GDP	PA-O3A-PB-O1B
3	A	402	GDP	PA-O3A-PB-O2B
3	B	402	GDP	PA-O3A-PB-O2B
3	D	402	GDP	PA-O3A-PB-O2B
2	B	401	NAD	C5D-O5D-PN-O3
2	C	401	NAD	C5D-O5D-PN-O3
2	C	401	NAD	O4B-C4B-C5B-O5B
2	A	401	NAD	PN-O3-PA-O2A
2	B	401	NAD	C5D-O5D-PN-O1N
2	C	401	NAD	C5D-O5D-PN-O1N
2	D	401	NAD	C5D-O5D-PN-O1N
2	D	401	NAD	O4B-C4B-C5B-O5B

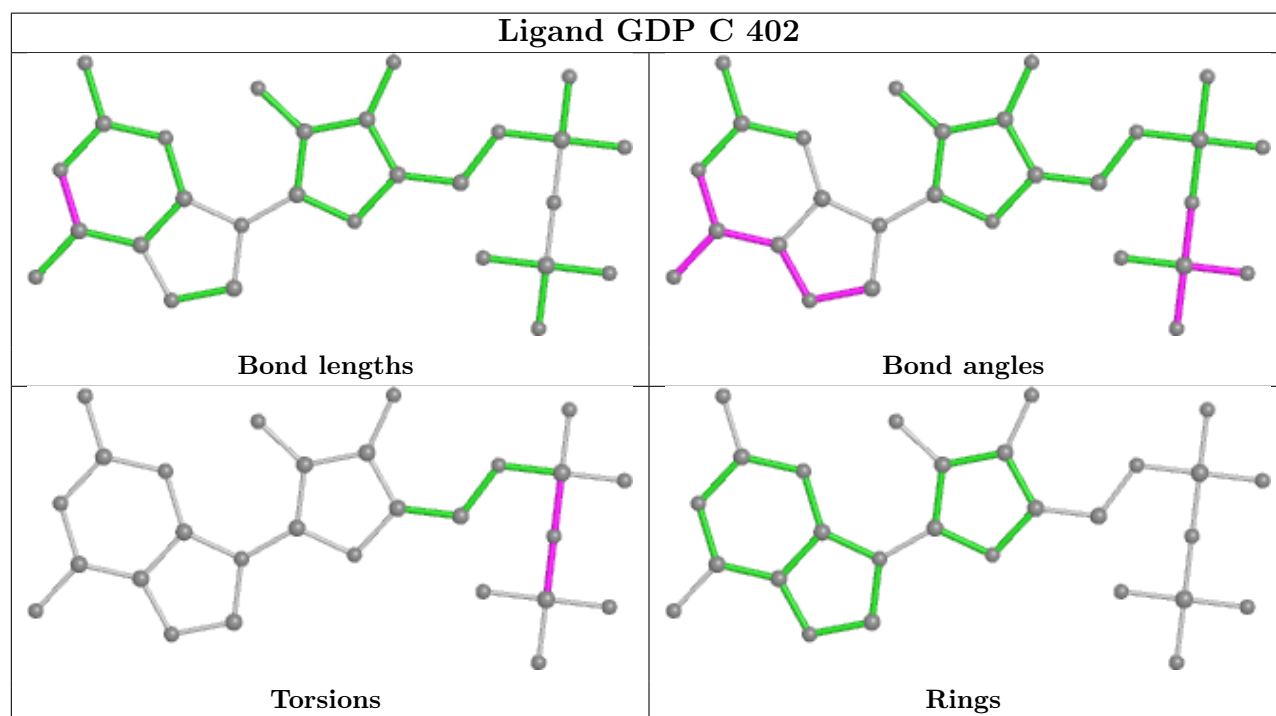
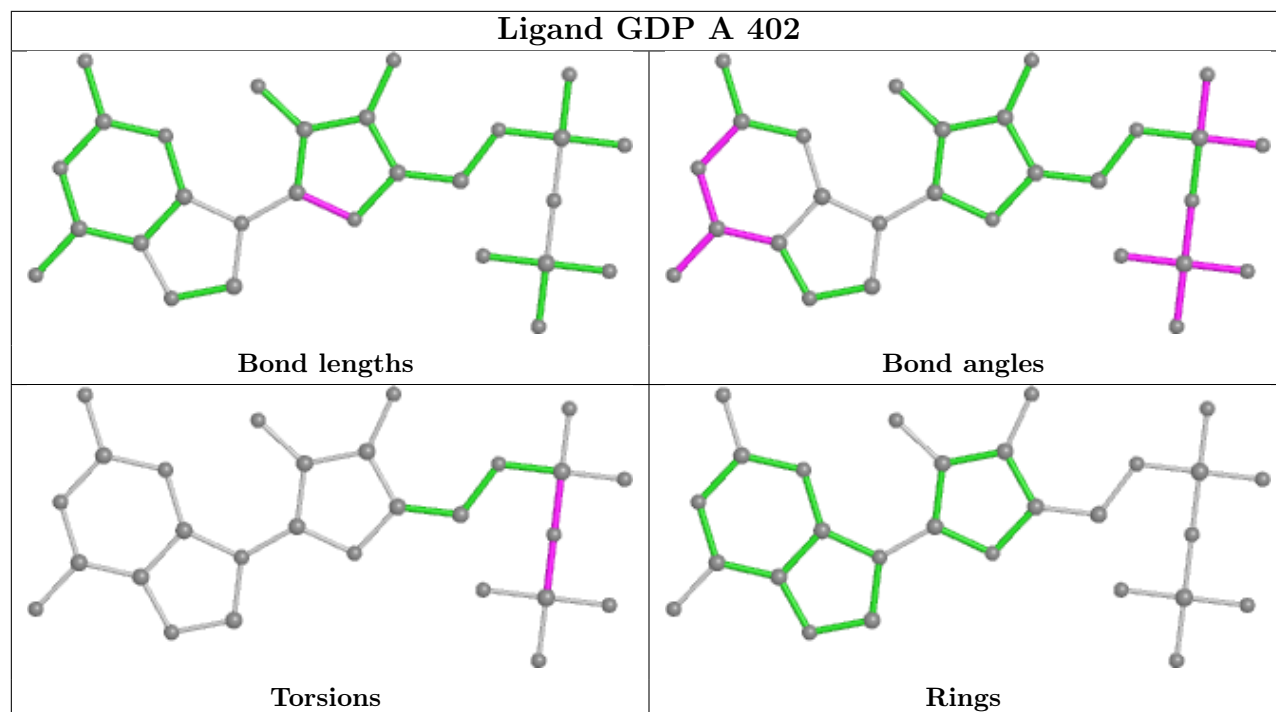
There are no ring outliers.

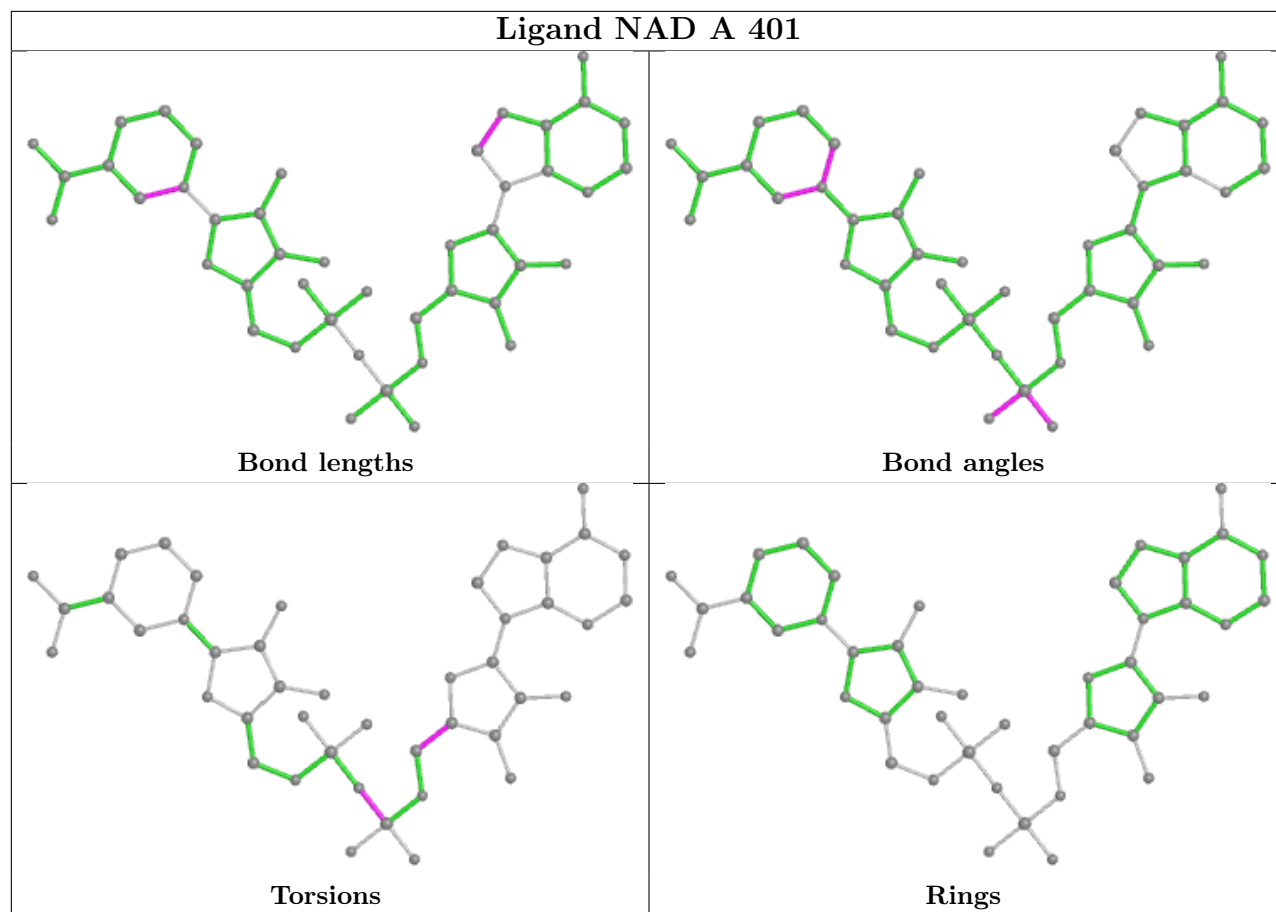
1 monomer is involved in 3 short contacts:

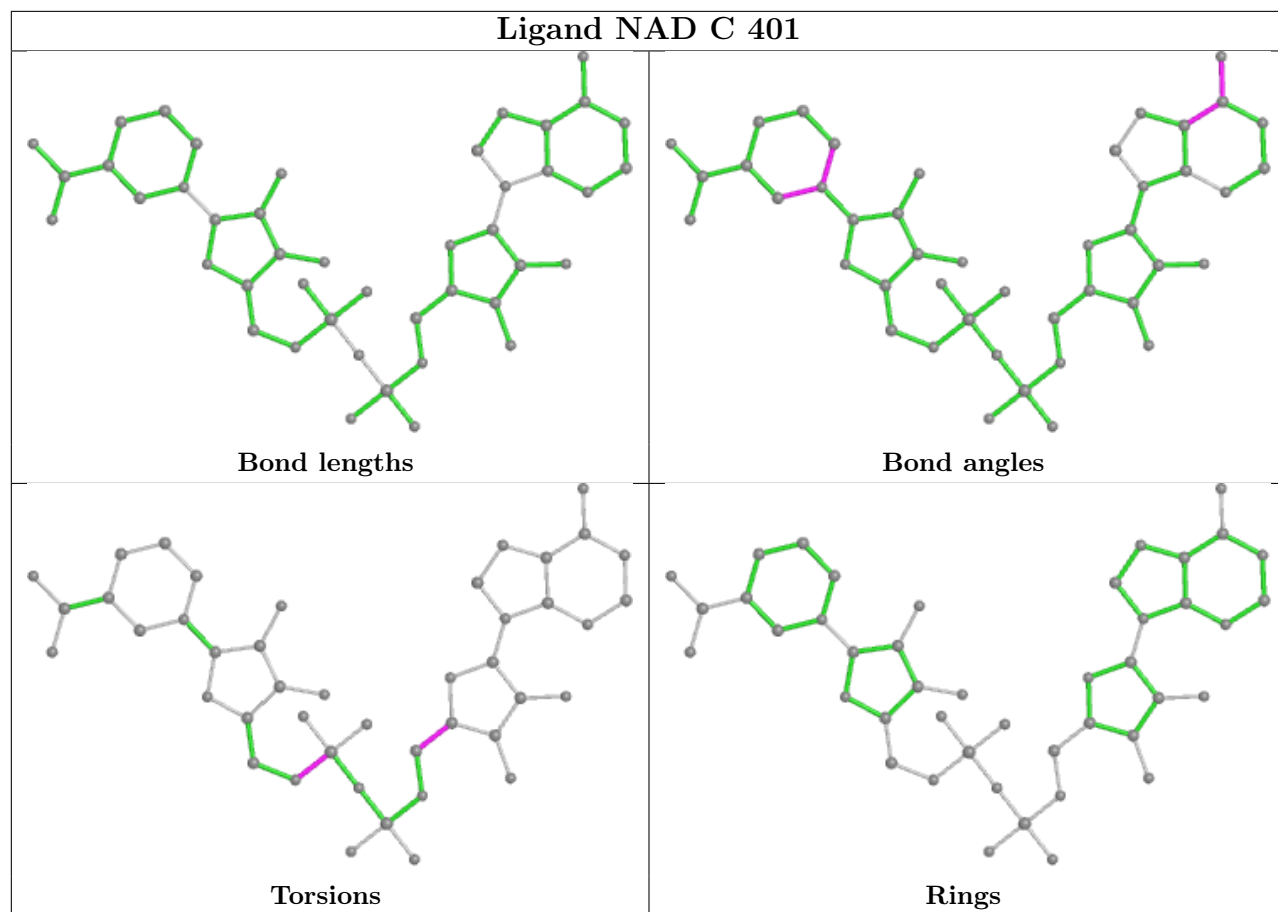
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	405	EDO	3	0

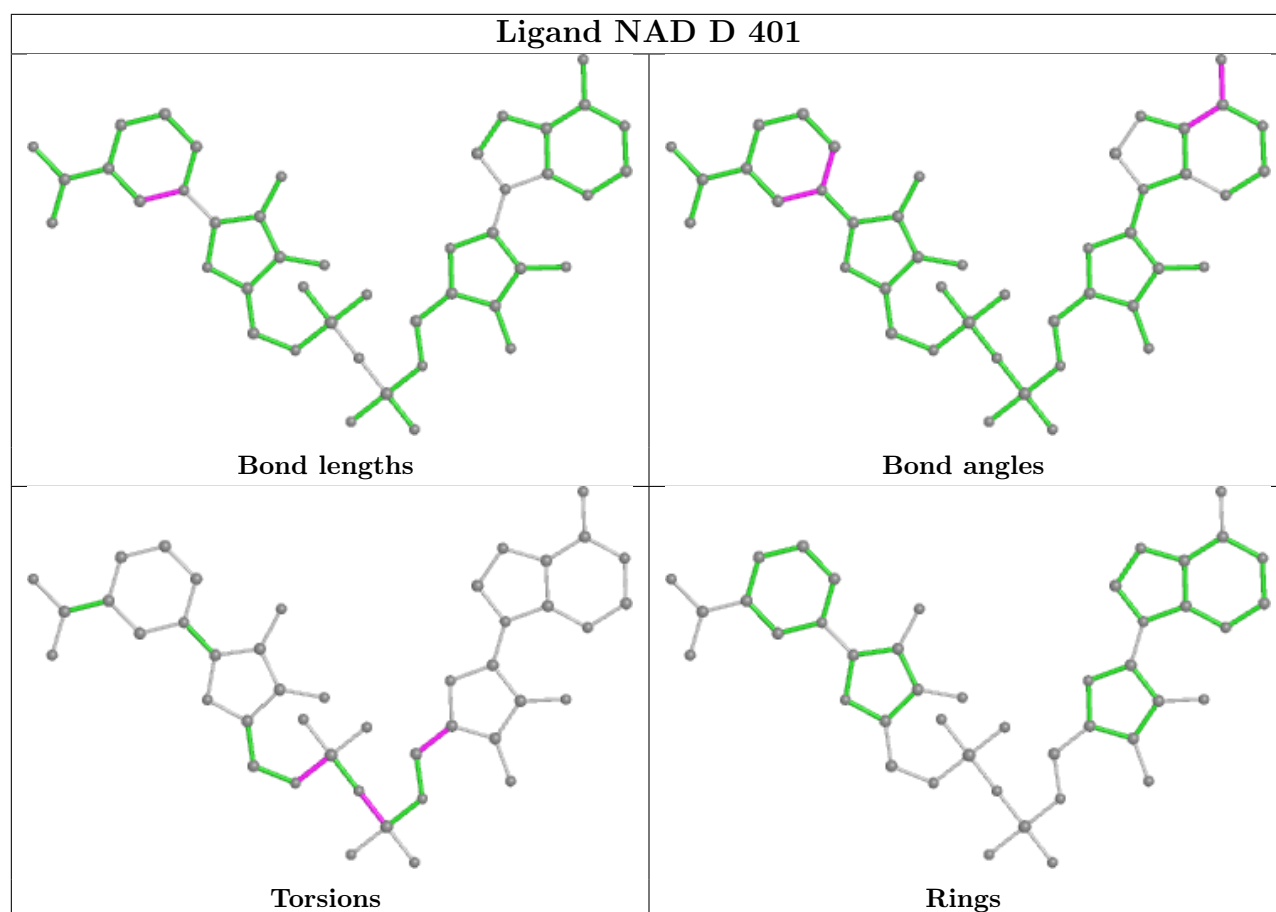
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

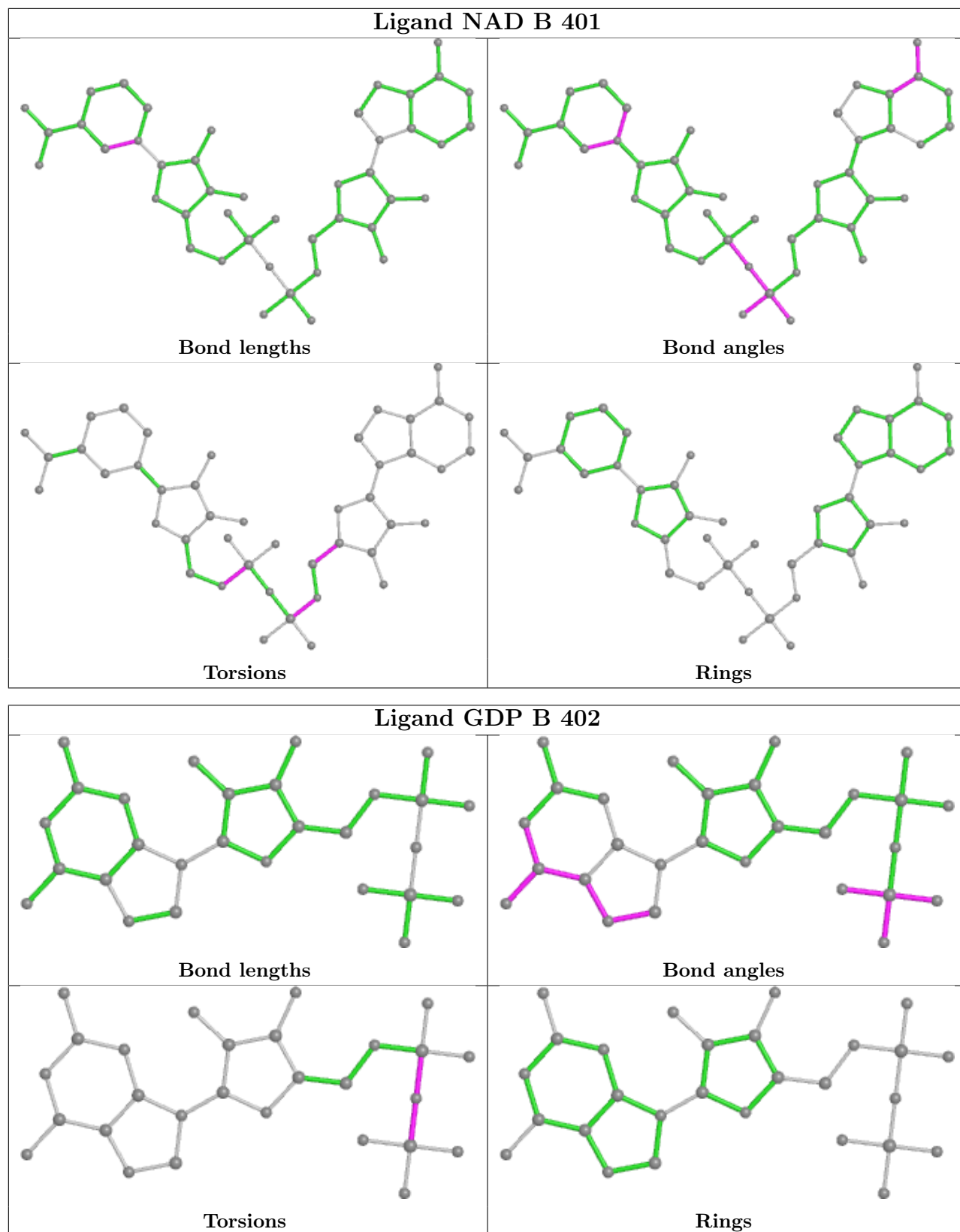












5.7 Other polymers [i](#)

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	346/365 (94%)	-0.57	1 (0%) 94 94	8, 15, 30, 61	0
1	B	342/365 (93%)	-0.38	1 (0%) 94 94	9, 17, 39, 82	0
1	C	342/365 (93%)	-0.40	0 100 100	10, 20, 34, 54	0
1	D	343/365 (93%)	-0.37	2 (0%) 89 91	9, 20, 39, 65	0
All	All	1373/1460 (94%)	-0.43	4 (0%) 94 94	8, 18, 36, 82	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	146	LYS	3.5
1	A	2	MET	3.4
1	D	3	LYS	2.4
1	D	278	PHE	2.1

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](#)

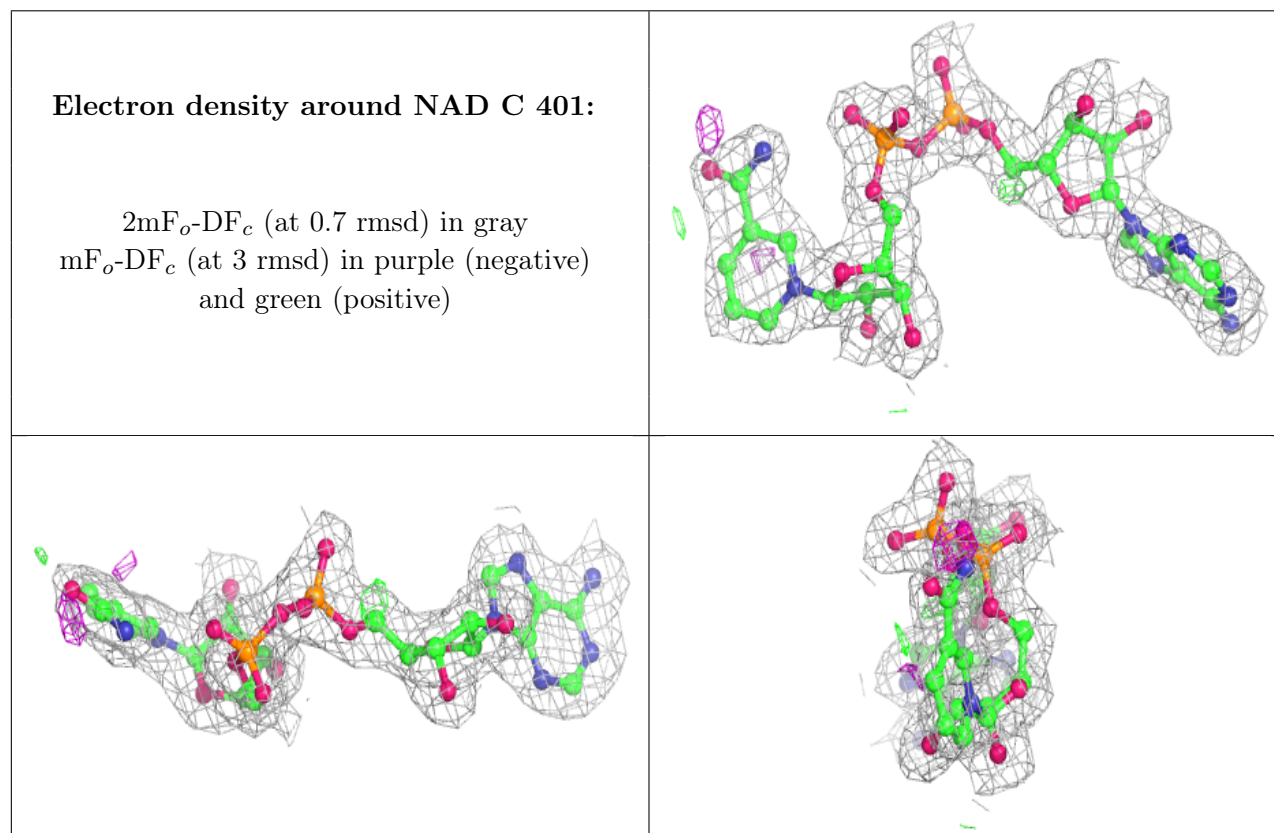
There are no monosaccharides in this entry.

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.

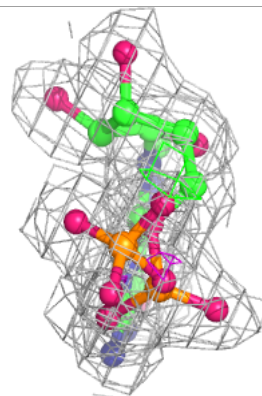
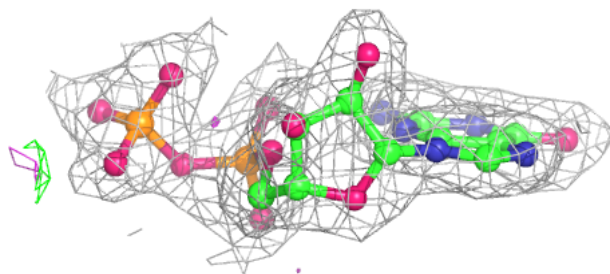
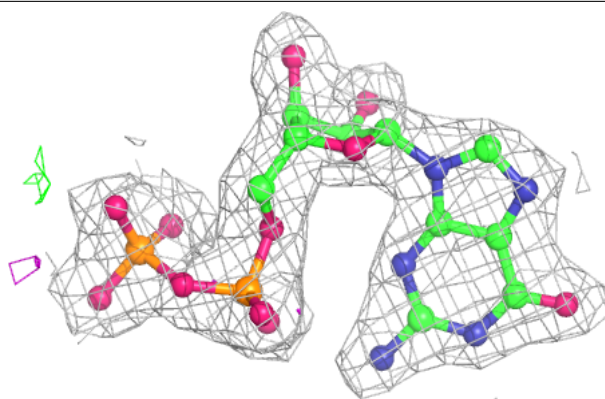
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	C	405	4/4	0.90	0.24	35,35,36,36	0
4	EDO	B	403	4/4	0.93	0.12	24,25,26,27	0
4	EDO	C	403	4/4	0.94	0.12	21,22,24,26	0
4	EDO	C	404	4/4	0.94	0.20	43,45,45,46	0
4	EDO	A	403	4/4	0.94	0.12	24,25,25,26	0
4	EDO	D	403	4/4	0.94	0.09	22,24,24,26	0
2	NAD	C	401	44/44	0.97	0.10	11,14,21,27	0
3	GDP	D	402	28/28	0.97	0.09	14,18,25,26	0
2	NAD	D	401	44/44	0.98	0.10	10,14,18,21	0
3	GDP	A	402	28/28	0.98	0.07	10,11,11,12	0
3	GDP	B	402	28/28	0.98	0.07	15,17,18,19	0
2	NAD	B	401	44/44	0.98	0.09	9,10,20,24	0
2	NAD	A	401	44/44	0.98	0.10	9,10,17,19	0
3	GDP	C	402	28/28	0.99	0.07	11,12,14,15	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.

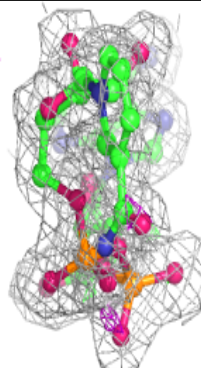
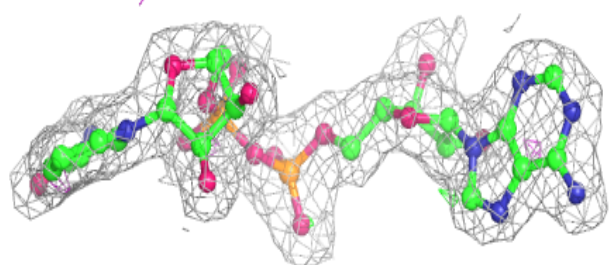
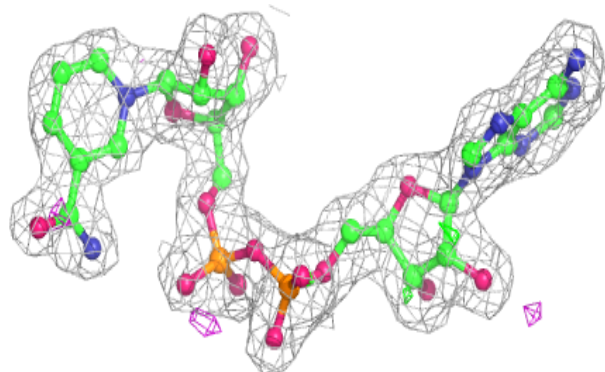


Electron density around GDP D 402:

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

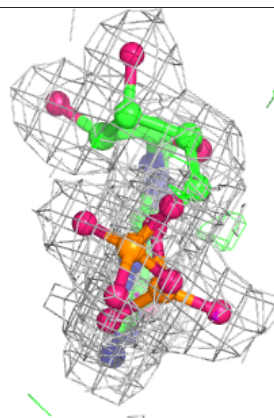
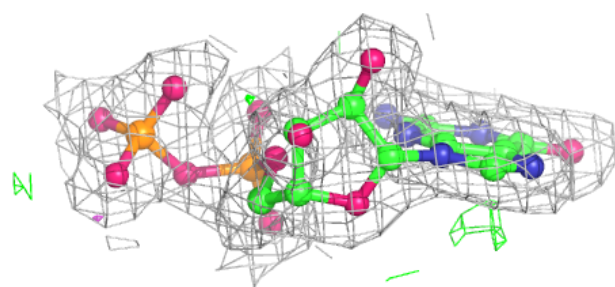
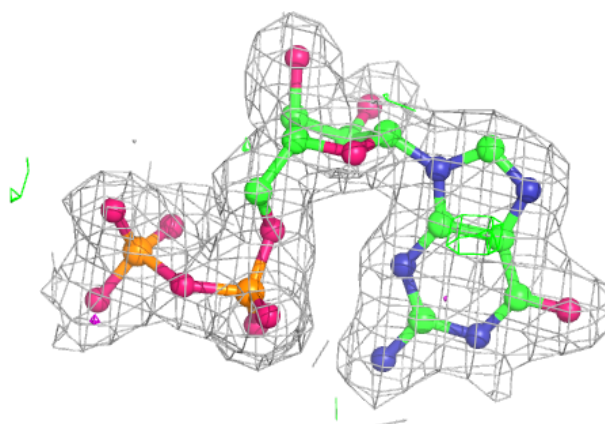
**Electron density around NAD D 401:**

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



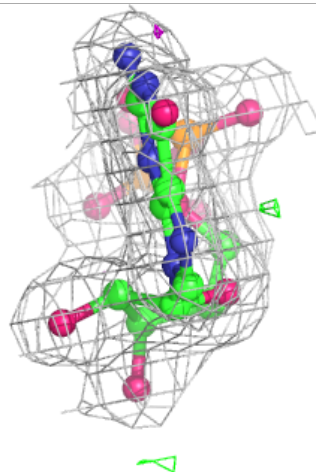
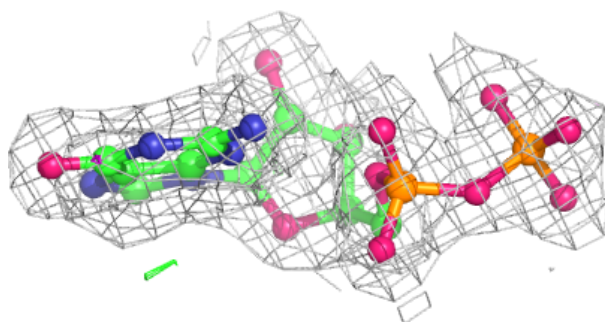
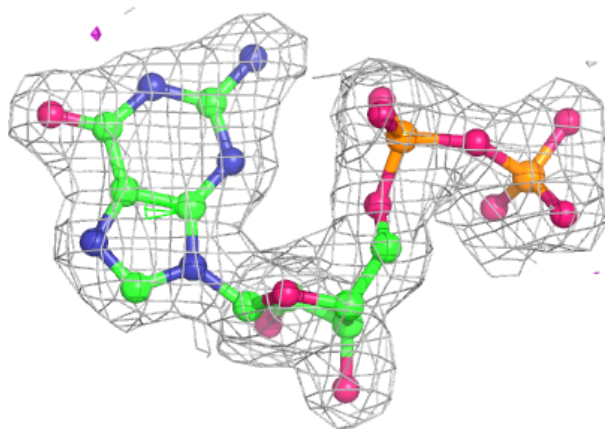
Electron density around GDP A 402:

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



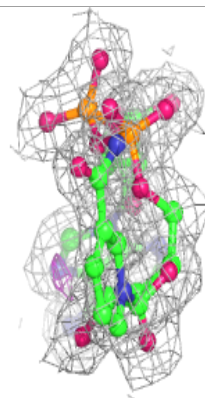
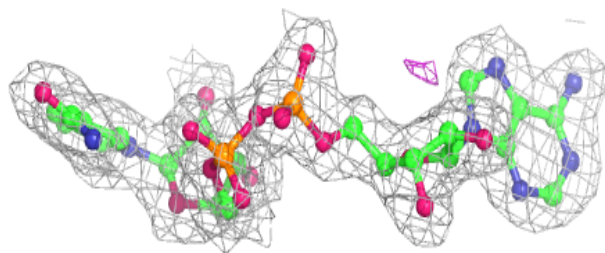
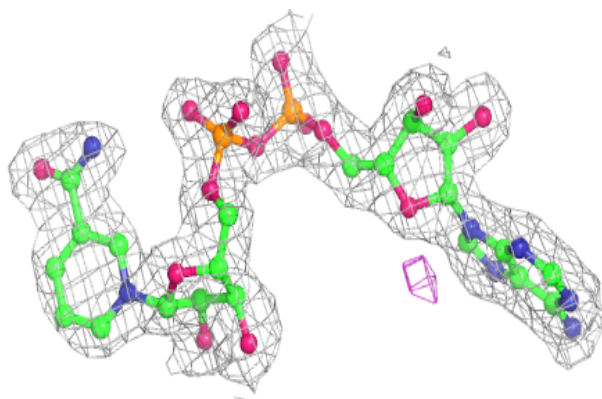
Electron density around GDP B 402:

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

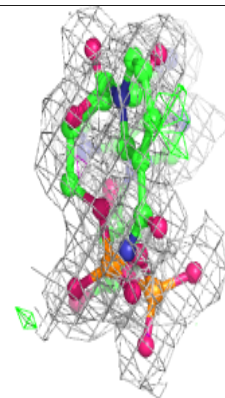
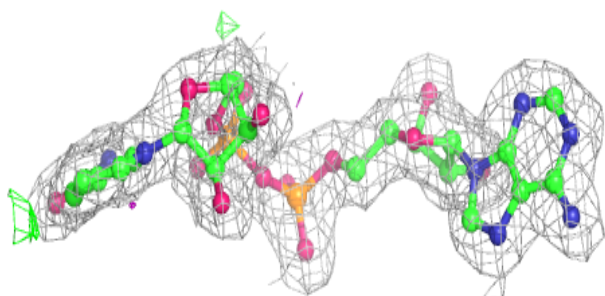
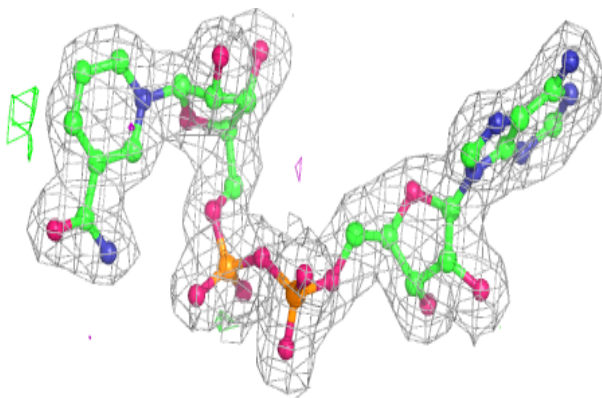


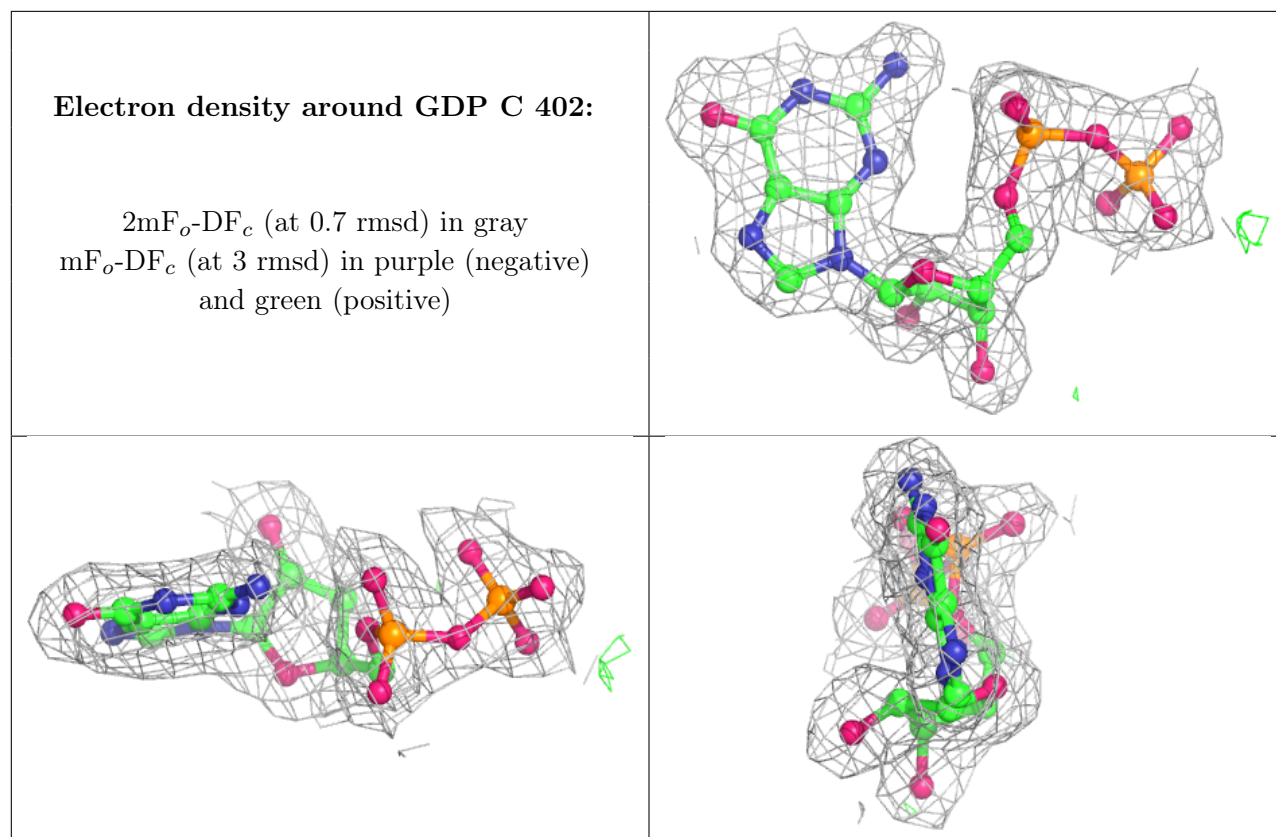
Electron density around NAD B 401:

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

**Electron density around NAD 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.