



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:36 PM UTC

PDB ID : 3PEF / pdb_00003pef
Title : Crystal structure of gamma-hydroxybutyrate dehydrogenase from *Geobacter metallireducens* in complex with NADP+
Authors : Zhang, Y.; Garavito, R.M.
Deposited on : 2010-10-26
Resolution : 2.07 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

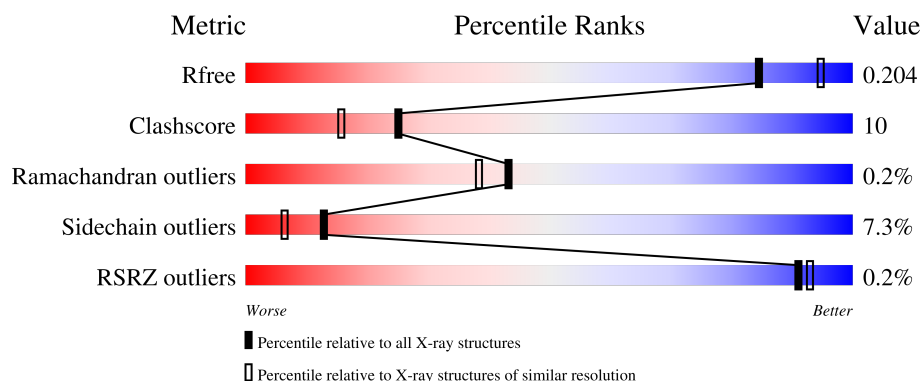
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	287	 84% 14% .
1	B	287	 79% 17% .
1	C	287	 80% 16% .
1	D	287	 83% 15% .
1	E	287	 87% 11% .

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Mol	Chain	Length	Quality of chain
1	F	287	 76%20% . .
1	G	287	 79%18% .
1	H	287	 84%14% .

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	288	-	-	X	-
3	GOL	A	289	-	-	X	-
3	GOL	C	288	-	-	X	-
3	GOL	E	289	-	-	X	-
4	PEG	A	291	-	-	X	-
4	PEG	D	288	-	-	X	-
4	PEG	E	290	-	-	X	-
4	PEG	G	288	-	-	X	-
4	PEG	H	288	-	-	X	-
5	EDO	A	292	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18166 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 6-phosphogluconate dehydrogenase, NAD-binding.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	1	0
			2095	1323	363	389	20			
1	B	287	Total	C	N	O	S	0	2	0
			2095	1324	360	389	22			
1	C	287	Total	C	N	O	S	0	0	0
			2087	1318	360	389	20			
1	D	286	Total	C	N	O	S	0	2	0
			2089	1320	359	390	20			
1	E	286	Total	C	N	O	S	0	2	0
			2092	1322	358	392	20			
1	F	285	Total	C	N	O	S	0	0	0
			2070	1309	355	386	20			
1	G	287	Total	C	N	O	S	0	0	0
			2087	1318	360	389	20			
1	H	286	Total	C	N	O	S	0	1	0
			2087	1319	359	389	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	MET	engineered mutation	UNP Q39R98
A	285	TYR	ILE	engineered mutation	UNP Q39R98
B	1	SER	MET	engineered mutation	UNP Q39R98
B	285	TYR	ILE	engineered mutation	UNP Q39R98
C	1	SER	MET	engineered mutation	UNP Q39R98
C	285	TYR	ILE	engineered mutation	UNP Q39R98
D	1	SER	MET	engineered mutation	UNP Q39R98
D	285	TYR	ILE	engineered mutation	UNP Q39R98
E	1	SER	MET	engineered mutation	UNP Q39R98
E	285	TYR	ILE	engineered mutation	UNP Q39R98
F	1	SER	MET	engineered mutation	UNP Q39R98
F	285	TYR	ILE	engineered mutation	UNP Q39R98
G	1	SER	MET	engineered mutation	UNP Q39R98

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Chain	Residue	Modelled	Actual	Comment	Reference
G	285	TYR	ILE	engineered mutation	UNP Q39R98
H	1	SER	MET	engineered mutation	UNP Q39R98
H	285	TYR	ILE	engineered mutation	UNP Q39R98

- # NAP

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



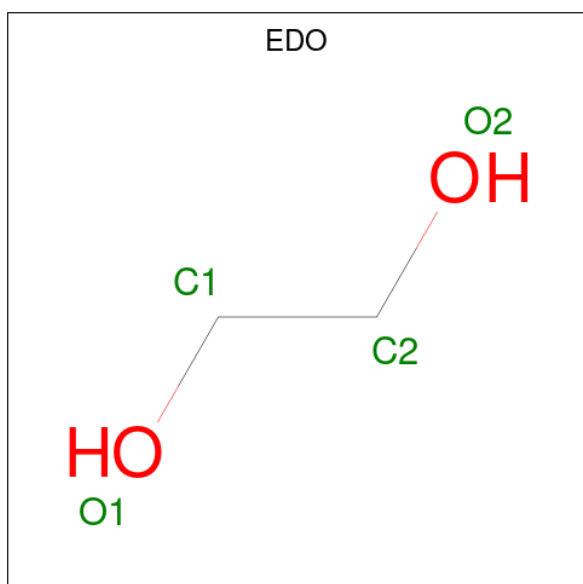
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	D	1	Total	C	O	0	0
			7	4	3		
4	E	1	Total	C	O	0	0
			7	4	3		
4	G	1	Total	C	O	0	0
			7	4	3		
4	H	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

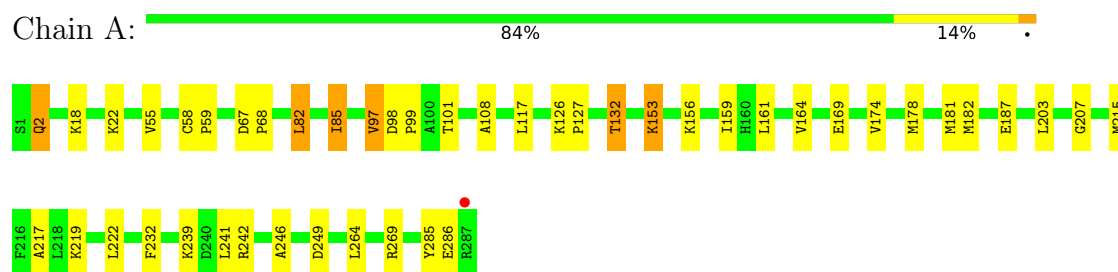
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	172	Total	O	0	0
			172	172		
6	B	126	Total	O	0	0
			126	126		
6	C	88	Total	O	0	0
			88	88		
6	D	159	Total	O	0	0
			159	159		
6	E	165	Total	O	0	0
			165	165		
6	F	72	Total	O	0	0
			72	72		
6	G	96	Total	O	0	0
			96	96		
6	H	121	Total	O	0	0
			121	121		

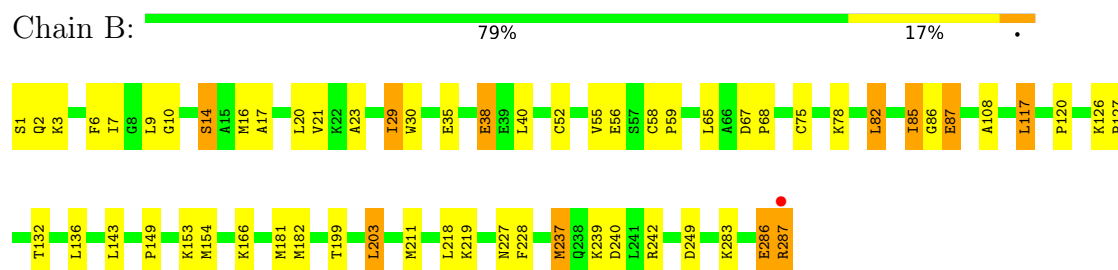
3 Residue-property plots [i](#)

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.

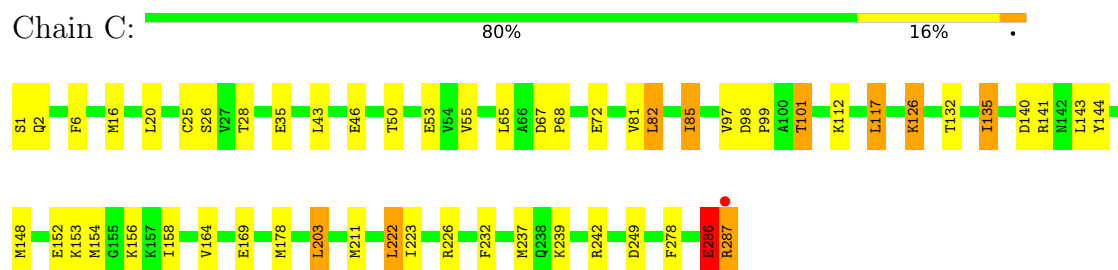
- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding



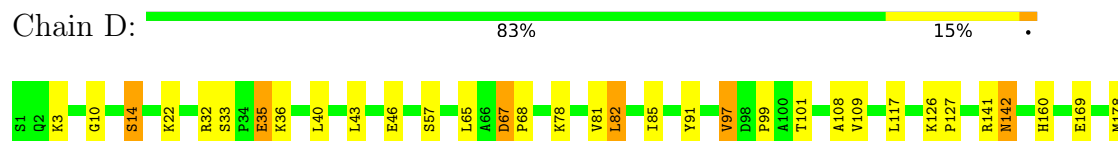
- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding



- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding



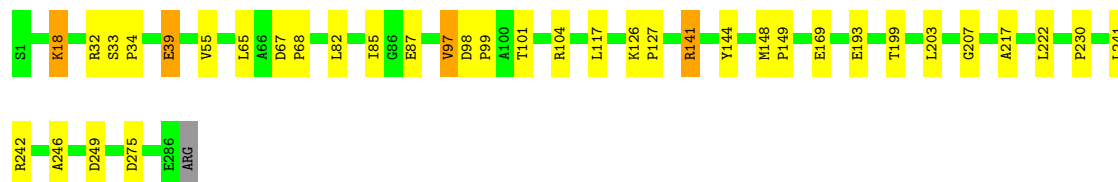
- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding





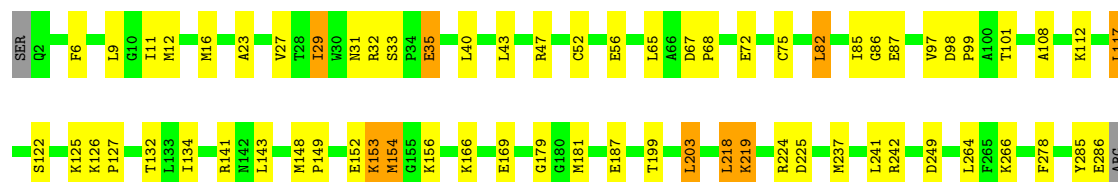
- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding

Chain E: 87% 11% .



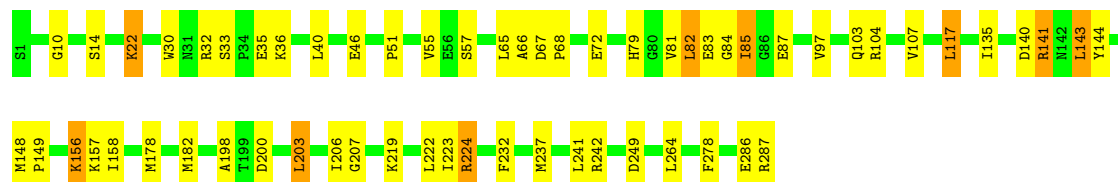
- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding

Chain F: 76% 20% . .



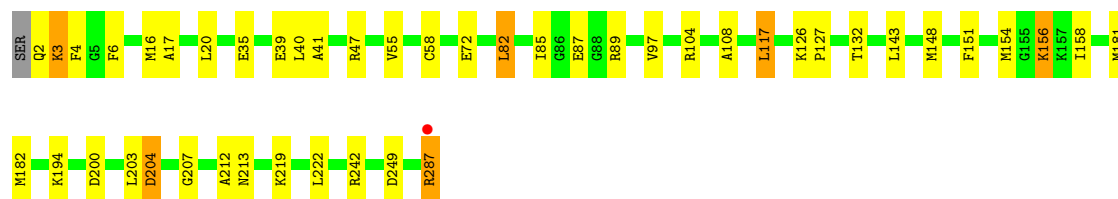
- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding

Chain G: 79% 18% .



- Molecule 1: 6-phosphogluconate dehydrogenase, NAD-binding

Chain H: 84% 14% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.97Å 79.14Å 95.47Å 82.15° 88.80° 87.66°	Depositor
Resolution (Å)	43.16 – 2.07 43.16 – 2.07	Depositor EDS
% Data completeness (in resolution range)	91.9 (43.16-2.07) 91.9 (43.16-2.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.07Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.156 , 0.209 0.154 , 0.204	Depositor DCC
R_{free} test set	3751 reflections (2.80%)	wwPDB-VP
Wilson B-factor (Å ²)	30.7	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.068 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18166	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CSO, NAP, EDO, PEG

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	0.55	1/2123 (0.0%)	0.84	3/2852 (0.1%)
1	B	0.53	0/2126	0.80	0/2856
1	C	0.55	1/2112 (0.0%)	0.80	1/2838 (0.0%)
1	D	0.50	0/2120	0.82	7/2849 (0.2%)
1	E	0.53	0/2117	0.84	5/2846 (0.2%)
1	F	0.46	0/2095	0.78	1/2816 (0.0%)
1	G	0.51	2/2112 (0.1%)	0.81	1/2838 (0.0%)
1	H	0.45	0/2115	0.82	3/2842 (0.1%)
All	All	0.51	4/16920 (0.0%)	0.81	21/22737 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	222	LEU	C-N	-7.46	1.24	1.33
1	G	223	ILE	C-N	-6.02	1.26	1.33
1	A	222	LEU	C-N	5.20	1.40	1.33
1	C	222	LEU	C-O	-5.12	1.18	1.24

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	222	LEU	O-C-N	-9.80	111.74	122.12
1	H	222	LEU	CA-C-N	7.50	130.27	120.60
1	H	222	LEU	C-N-CA	7.50	130.27	120.60
1	C	286	GLU	N-CA-C	6.96	120.96	109.96
1	E	222	LEU	CA-C-N	6.59	128.86	120.56

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2095	0	2130	47	0
1	B	2095	0	2131	45	0
1	C	2087	0	2117	61	0
1	D	2089	0	2121	30	0
1	E	2092	0	2117	30	0
1	F	2070	0	2096	46	0
1	G	2087	0	2117	40	0
1	H	2087	0	2115	40	0
2	A	48	0	25	0	0
2	B	48	0	25	0	0
2	C	48	0	25	4	0
2	D	48	0	25	1	0
2	E	48	0	25	0	0
2	F	48	0	25	1	0
2	G	48	0	25	2	0
2	H	48	0	25	0	0
3	A	18	0	24	16	0
3	B	6	0	8	0	0
3	C	6	0	8	9	0
3	E	12	0	16	5	0
4	A	7	0	10	5	0
4	D	7	0	10	5	0
4	E	7	0	10	6	0
4	G	7	0	10	4	0
4	H	7	0	10	10	0
5	A	4	0	6	4	0
6	A	172	0	0	4	0
6	B	126	0	0	1	0
6	C	88	0	0	4	0
6	D	159	0	0	1	0
6	E	165	0	0	1	0
6	F	72	0	0	2	0
6	G	96	0	0	3	0
6	H	121	0	0	0	0
All	All	18166	0	17256	334	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 10.

The worst 5 of 334 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:287:ARG:HH11	1:C:287:ARG:CG	1.64	1.11
1:C:287:ARG:HH11	1:C:287:ARG:HG3	1.17	1.09
1:G:178:MET:HE3	1:G:237:MET:HE1	1.42	1.02
1:G:237:MET:HE3	1:G:278:PHE:CD2	1.96	0.99
1:F:16:MET:HB3	1:F:154:MET:HE2	1.43	0.99

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	285/287 (99%)	277 (97%)	7 (2%)	1 (0%)	30	23
1	B	286/287 (100%)	277 (97%)	8 (3%)	1 (0%)	36	30
1	C	284/287 (99%)	274 (96%)	8 (3%)	2 (1%)	18	10
1	D	285/287 (99%)	278 (98%)	7 (2%)	0	100	100
1	E	285/287 (99%)	277 (97%)	8 (3%)	0	100	100
1	F	282/287 (98%)	272 (96%)	10 (4%)	0	100	100
1	G	284/287 (99%)	272 (96%)	11 (4%)	1 (0%)	30	23
1	H	284/287 (99%)	274 (96%)	10 (4%)	0	100	100
All	All	2275/2296 (99%)	2201 (97%)	69 (3%)	5 (0%)	43	38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	286	GLU
1	C	2	GLN

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Mol	Chain	Res	Type
1	A	2	GLN
1	C	140	ASP
1	G	140	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	206/205 (100%)	194 (94%)	12 (6%)	18	11
1	B	207/205 (101%)	191 (92%)	16 (8%)	12	5
1	C	205/205 (100%)	189 (92%)	16 (8%)	11	5
1	D	206/205 (100%)	193 (94%)	13 (6%)	16	9
1	E	206/205 (100%)	193 (94%)	13 (6%)	16	9
1	F	203/205 (99%)	184 (91%)	19 (9%)	8	3
1	G	205/205 (100%)	187 (91%)	18 (9%)	9	4
1	H	205/205 (100%)	191 (93%)	14 (7%)	14	8
All	All	1643/1640 (100%)	1522 (93%)	121 (7%)	13	6

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	18	LYS
1	H	39[B]	GLU
1	F	35	GLU
1	H	39[A]	GLU
1	H	203	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	2	GLN
1	G	79	HIS

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Mol	Chain	Res	Type
1	G	142	ASN
1	C	2	GLN
1	B	2	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSO	A	52	1	3,6,7	0.61	0	1,6,8	0.40	0
1	CSO	D	52	1	3,6,7	0.71	0	1,6,8	0.56	0
1	CSO	G	52	1	3,6,7	0.74	0	1,6,8	0.46	0
1	CSO	F	52	1	3,6,7	0.68	0	1,6,8	0.02	0
1	CSO	B	52	1	3,6,7	0.65	0	1,6,8	0.45	0
1	CSO	C	52	1	3,6,7	0.72	0	1,6,8	0.14	0
1	CSO	E	52	1	3,6,7	0.71	0	1,6,8	0.24	0
1	CSO	H	52	1	3,6,7	0.67	0	1,6,8	0.33	0

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
1	CSO	A	52	1	-	1/1/5/7	-
1	CSO	D	52	1	-	1/1/5/7	-
1	CSO	G	52	1	-	1/1/5/7	-
1	CSO	F	52	1	-	0/1/5/7	-
1	CSO	B	52	1	-	1/1/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSO	C	52	1	-	1/1/5/7	-
1	CSO	E	52	1	-	1/1/5/7	-
1	CSO	H	52	1	-	1/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	G	52	CSO	N-CA-CB-SG
1	A	52	CSO	N-CA-CB-SG
1	B	52	CSO	N-CA-CB-SG
1	C	52	CSO	N-CA-CB-SG
1	D	52	CSO	N-CA-CB-SG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	F	52	CSO	2	0
1	B	52	CSO	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

21 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAP	A	301	-	50,52,52	1.57	6 (12%)	71,80,80	1.66	12 (16%)
3	GOL	C	288	-	5,5,5	0.36	0	5,5,5	1.02	0
4	PEG	H	288	-	6,6,6	0.70	0	5,5,5	0.60	0
2	NAP	G	301	-	50,52,52	1.60	4 (8%)	71,80,80	1.53	10 (14%)
4	PEG	E	290	-	6,6,6	0.75	0	5,5,5	0.51	0
2	NAP	E	301	-	50,52,52	1.66	5 (10%)	71,80,80	1.53	12 (16%)
3	GOL	E	288	-	5,5,5	0.45	0	5,5,5	0.14	0
4	PEG	A	291	-	6,6,6	0.75	0	5,5,5	0.50	0
2	NAP	D	301	-	50,52,52	1.60	6 (12%)	71,80,80	1.66	14 (19%)
2	NAP	B	301	-	50,52,52	1.60	6 (12%)	71,80,80	1.51	11 (15%)
4	PEG	D	288	-	6,6,6	0.75	0	5,5,5	0.42	0
3	GOL	A	289	-	5,5,5	0.40	0	5,5,5	0.63	0
3	GOL	B	288	-	5,5,5	0.37	0	5,5,5	0.31	0
4	PEG	G	288	-	6,6,6	0.77	0	5,5,5	0.41	0
5	EDO	A	292	-	3,3,3	0.41	0	2,2,2	0.46	0
2	NAP	F	301	-	50,52,52	1.63	5 (10%)	71,80,80	1.60	10 (14%)
3	GOL	E	289	-	5,5,5	0.38	0	5,5,5	0.59	0
3	GOL	A	290	-	5,5,5	0.35	0	5,5,5	0.63	0
2	NAP	C	301	-	50,52,52	1.62	4 (8%)	71,80,80	1.57	11 (15%)
3	GOL	A	288	-	5,5,5	0.36	0	5,5,5	1.32	0
2	NAP	H	301	-	50,52,52	1.61	4 (8%)	71,80,80	1.59	11 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAP	A	301	-	-	13/35/67/67	0/5/5/5
3	GOL	C	288	-	-	2/4/4/4	-
4	PEG	H	288	-	-	1/4/4/4	-
2	NAP	G	301	-	-	11/35/67/67	0/5/5/5
4	PEG	E	290	-	-	0/4/4/4	-
2	NAP	E	301	-	-	13/35/67/67	0/5/5/5
3	GOL	E	288	-	-	2/4/4/4	-
4	PEG	A	291	-	-	1/4/4/4	-
2	NAP	D	301	-	-	7/35/67/67	0/5/5/5
2	NAP	B	301	-	-	8/35/67/67	0/5/5/5
4	PEG	D	288	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	289	-	-	1/4/4/4	-
3	GOL	B	288	-	-	2/4/4/4	-
4	PEG	G	288	-	-	4/4/4/4	-
5	EDO	A	292	-	-	0/1/1/1	-
2	NAP	F	301	-	-	9/35/67/67	0/5/5/5
3	GOL	E	289	-	-	1/4/4/4	-
3	GOL	A	290	-	-	2/4/4/4	-
2	NAP	C	301	-	-	13/35/67/67	0/5/5/5
3	GOL	A	288	-	-	2/4/4/4	-
2	NAP	H	301	-	-	9/35/67/67	0/5/5/5

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	NAP	O7N-C7N	9.10	1.41	1.24
2	F	301	NAP	O7N-C7N	8.92	1.40	1.24
2	B	301	NAP	O7N-C7N	8.85	1.40	1.24
2	G	301	NAP	O7N-C7N	8.80	1.40	1.24
2	H	301	NAP	O7N-C7N	8.79	1.40	1.24

The worst 5 of 91 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	NAP	N3A-C2A-N1A	-6.07	119.40	128.58
2	H	301	NAP	N3A-C2A-N1A	-6.01	119.48	128.58
2	C	301	NAP	N3A-C2A-N1A	-5.88	119.68	128.58
2	B	301	NAP	N3A-C2A-N1A	-5.55	120.17	128.58
2	G	301	NAP	N3A-C2A-N1A	-5.55	120.17	128.58

There are no chirality outliers.

5 of 104 torsion outliers are listed below:

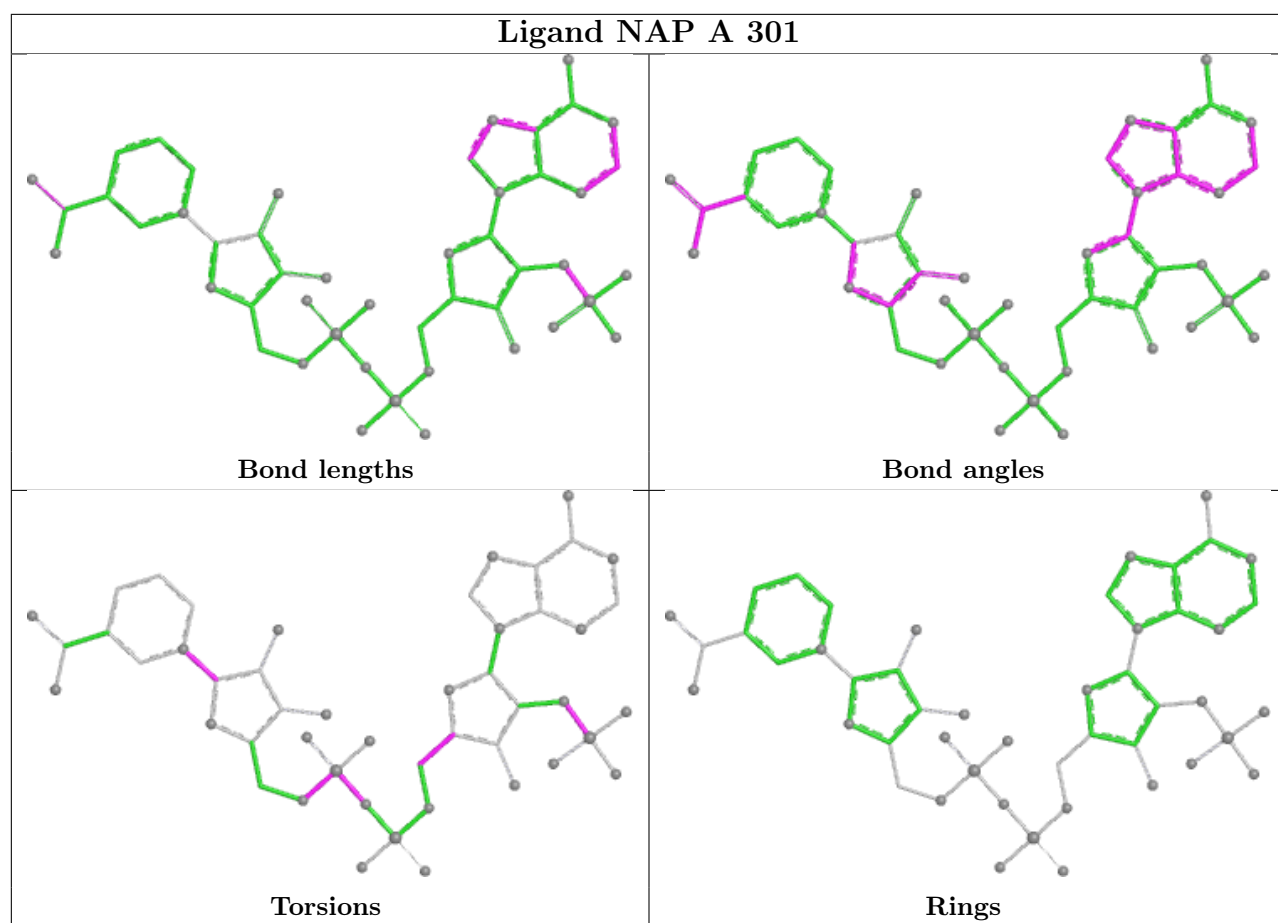
Mol	Chain	Res	Type	Atoms
2	A	301	NAP	C5D-O5D-PN-O3
2	A	301	NAP	C5D-O5D-PN-O1N
2	A	301	NAP	C5D-O5D-PN-O2N
2	A	301	NAP	O4D-C1D-N1N-C2N
2	A	301	NAP	O4D-C1D-N1N-C6N

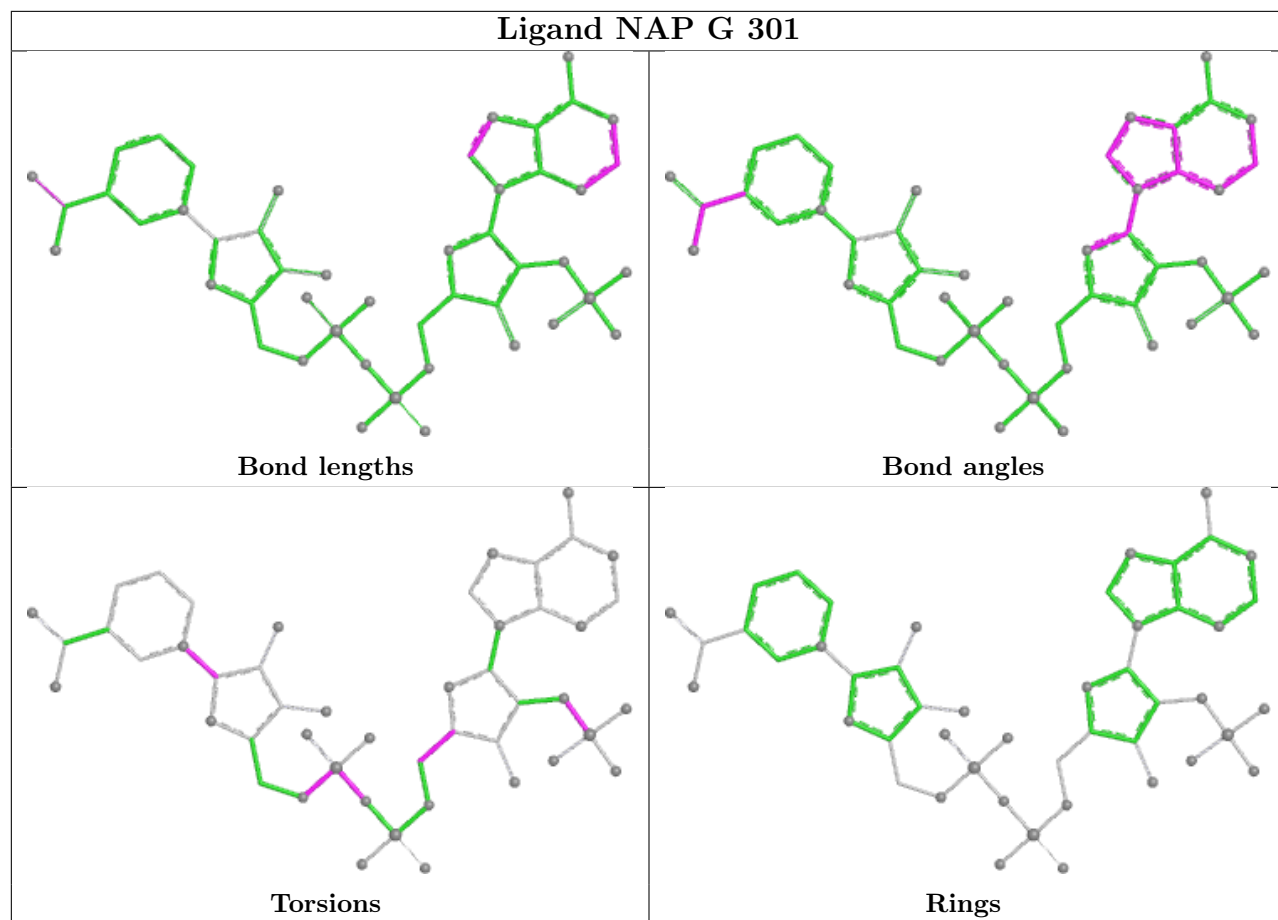
There are no ring outliers.

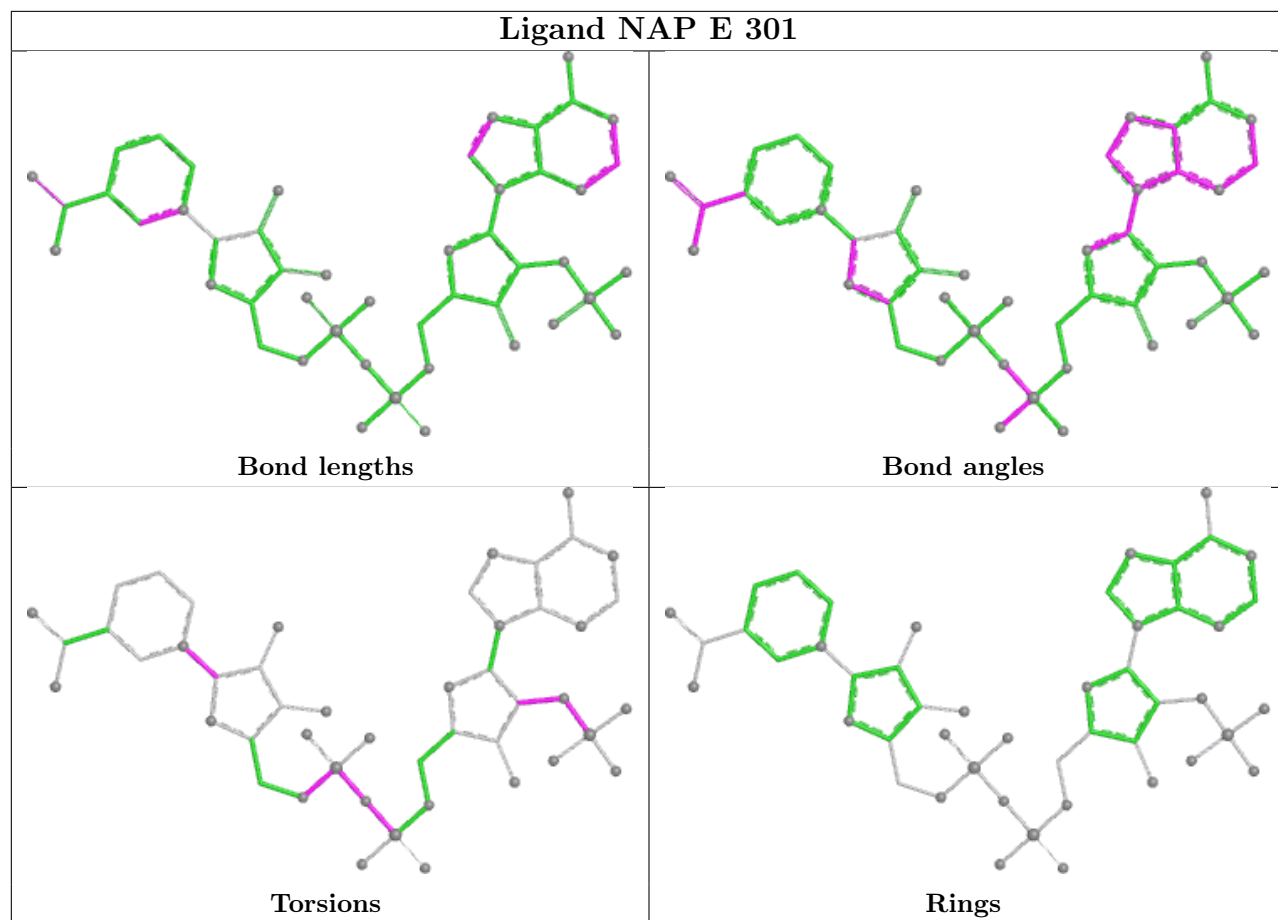
16 monomers are involved in 68 short contacts:

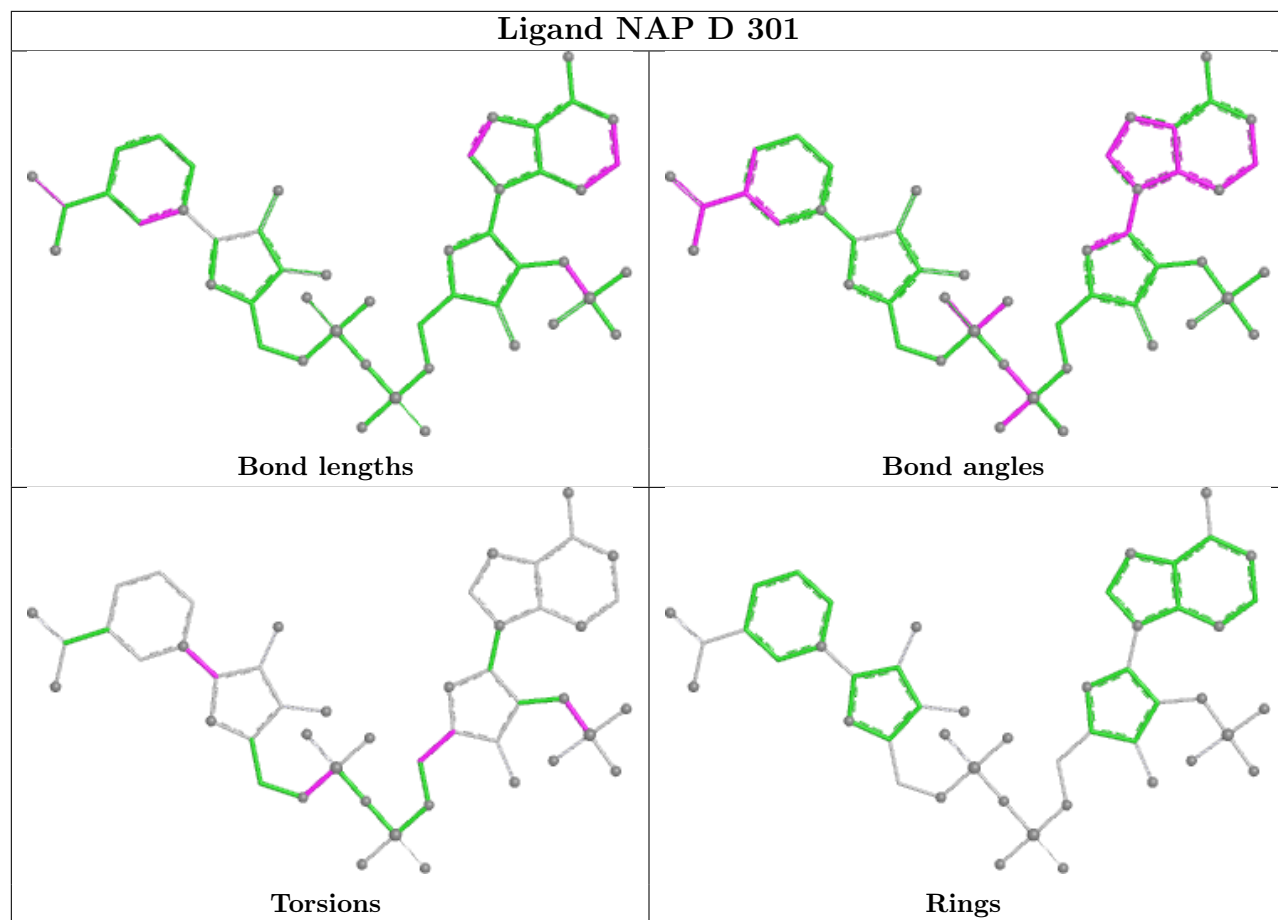
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	288	GOL	9	0
4	H	288	PEG	10	0
2	G	301	NAP	2	0
4	E	290	PEG	6	0
3	E	288	GOL	1	0
4	A	291	PEG	5	0
2	D	301	NAP	1	0
4	D	288	PEG	5	0
3	A	289	GOL	8	0
4	G	288	PEG	4	0
5	A	292	EDO	4	0
2	F	301	NAP	1	0
3	E	289	GOL	4	0
3	A	290	GOL	3	0
2	C	301	NAP	4	0
3	A	288	GOL	5	0

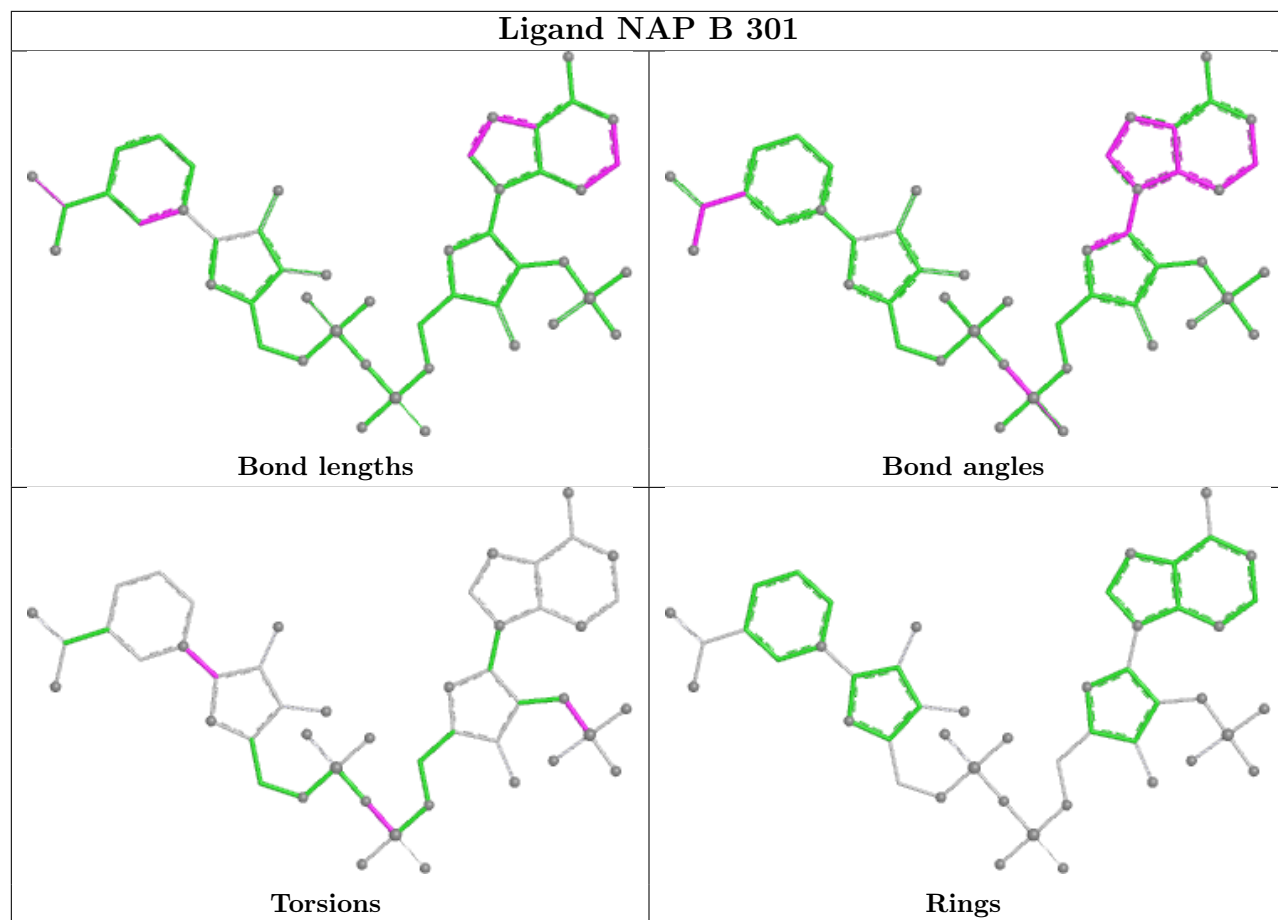
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

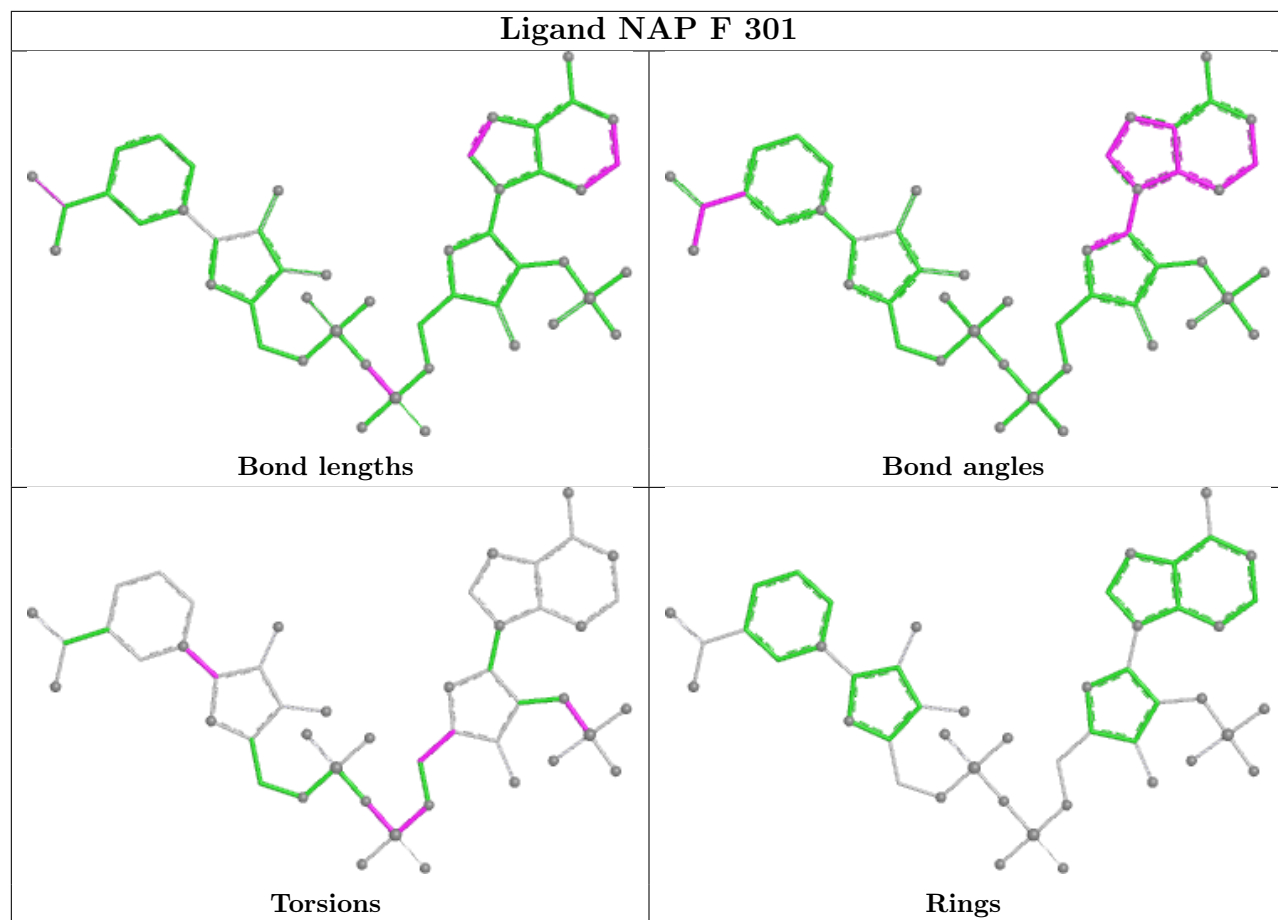


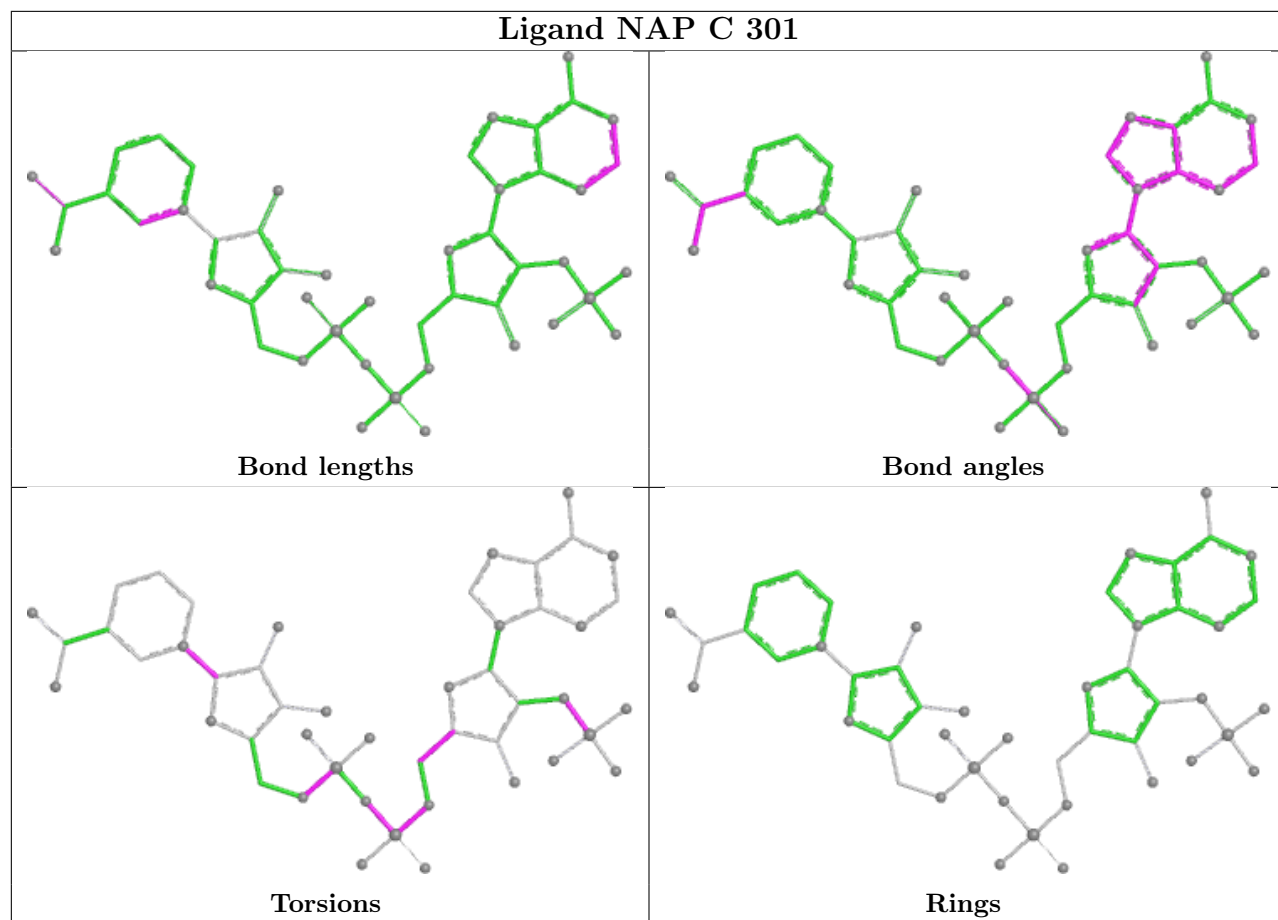


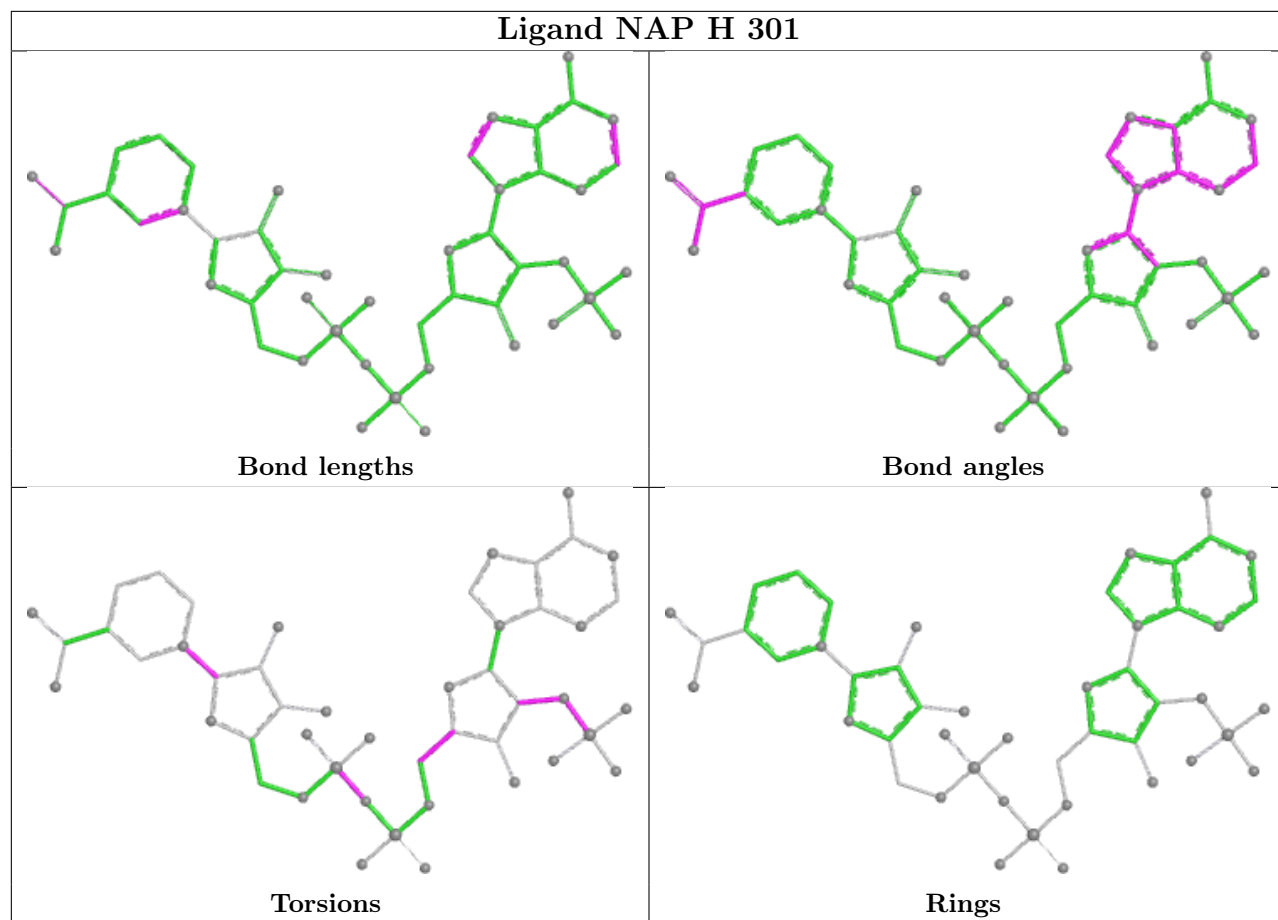












5.7 Other polymers [i](#)

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	286/287 (99%)	-0.71	1 (0%) 90 92	18, 27, 45, 79	1 (0%)
1	B	286/287 (99%)	-0.43	1 (0%) 90 92	15, 38, 64, 99	2 (0%)
1	C	286/287 (99%)	-0.39	1 (0%) 90 92	20, 38, 69, 104	0
1	D	285/287 (99%)	-0.60	0 100 100	16, 31, 51, 80	2 (0%)
1	E	285/287 (99%)	-0.67	0 100 100	14, 29, 45, 81	2 (0%)
1	F	284/287 (98%)	-0.17	0 100 100	25, 45, 81, 111	0
1	G	286/287 (99%)	-0.29	0 100 100	19, 40, 76, 101	0
1	H	285/287 (99%)	-0.41	1 (0%) 88 90	21, 38, 60, 79	1 (0%)
All	All	2283/2296 (99%)	-0.46	4 (0%) 91 93	14, 34, 67, 111	8 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	287	ARG	3.7
1	B	287	ARG	3.4
1	A	287	ARG	3.3
1	H	287	ARG	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	CSO	B	52	7/8	0.88	0.09	41,46,70,87	0
1	CSO	F	52	7/8	0.88	0.08	65,67,74,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	CSO	G	52	7/8	0.89	0.10	61,63,89,102	0
1	CSO	D	52	7/8	0.92	0.07	32,35,53,72	0
1	CSO	H	52	7/8	0.92	0.10	47,52,64,89	0
1	CSO	A	52	7/8	0.94	0.08	22,26,45,73	0
1	CSO	C	52	7/8	0.94	0.08	51,55,67,87	0
1	CSO	E	52	7/8	0.95	0.08	25,29,42,81	0

6.3 Carbohydrates [i](#)

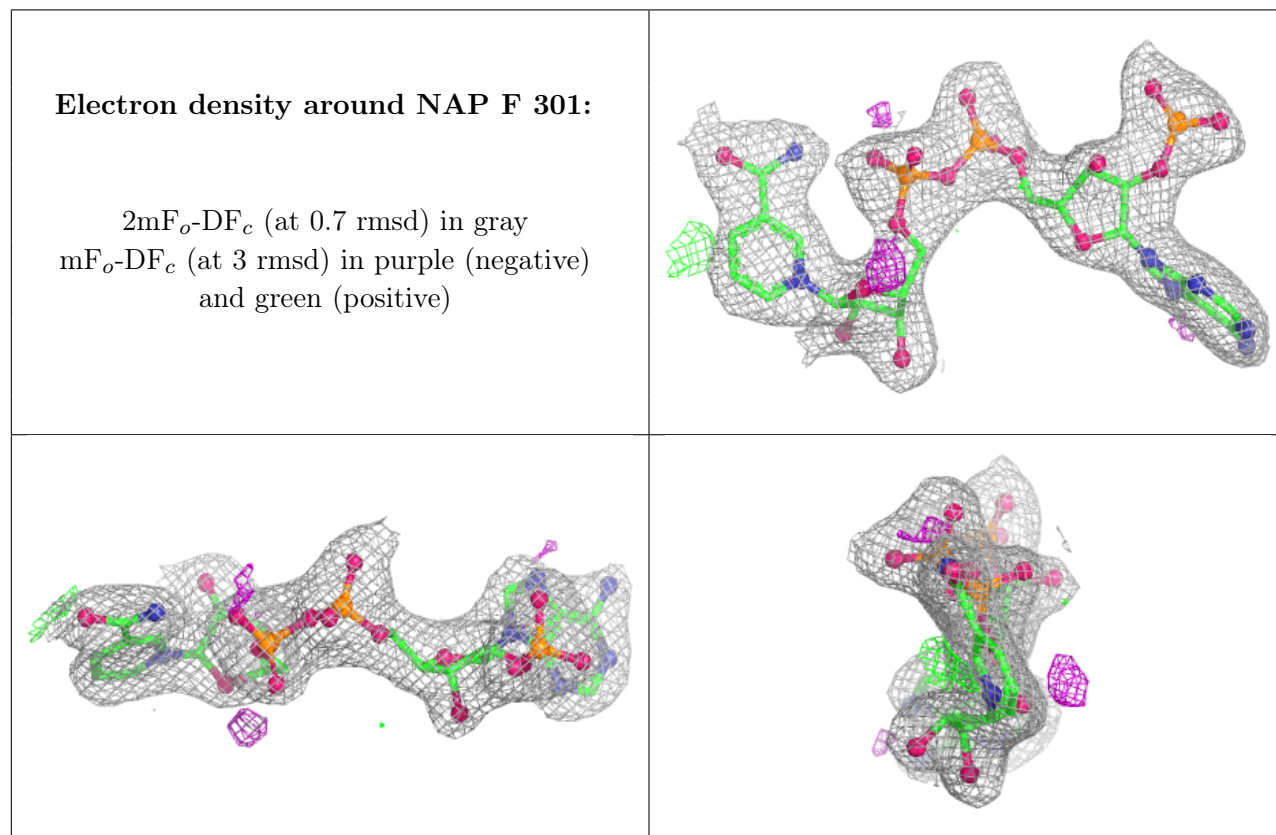
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

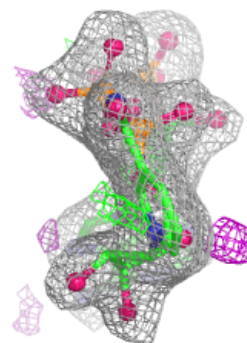
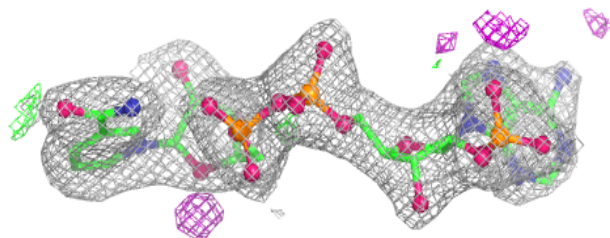
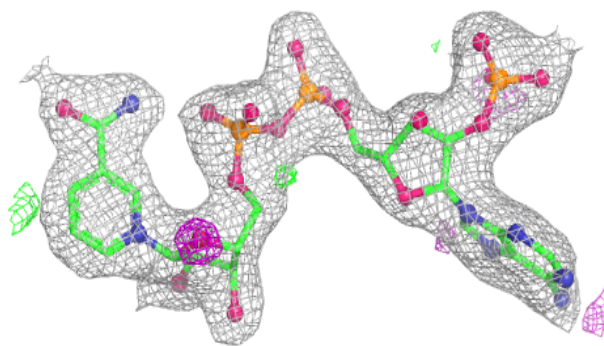
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	A	288	6/6	0.76	0.17	43,47,53,53	0
4	PEG	E	290	7/7	0.79	0.17	31,52,66,68	0
4	PEG	H	288	7/7	0.82	0.14	46,55,67,70	0
4	PEG	G	288	7/7	0.83	0.16	30,36,51,58	0
4	PEG	A	291	7/7	0.83	0.14	35,51,60,66	0
3	GOL	E	288	6/6	0.84	0.14	51,55,61,64	0
3	GOL	B	288	6/6	0.85	0.14	74,75,78,79	0
3	GOL	C	288	6/6	0.86	0.13	41,51,56,57	0
4	PEG	D	288	7/7	0.87	0.11	29,44,49,51	0
3	GOL	A	290	6/6	0.90	0.11	26,43,52,55	0
5	EDO	A	292	4/4	0.91	0.15	44,48,48,49	0
3	GOL	A	289	6/6	0.92	0.09	36,41,48,57	0
3	GOL	E	289	6/6	0.93	0.09	24,39,46,47	0
2	NAP	F	301	48/48	0.96	0.07	30,45,54,58	0
2	NAP	B	301	48/48	0.97	0.06	26,35,53,59	0
2	NAP	G	301	48/48	0.97	0.06	24,39,56,56	0
2	NAP	H	301	48/48	0.97	0.05	22,31,37,41	0
2	NAP	C	301	48/48	0.97	0.06	25,38,45,47	0
2	NAP	D	301	48/48	0.98	0.04	15,26,33,35	0
2	NAP	E	301	48/48	0.98	0.04	17,24,29,32	0
2	NAP	A	301	48/48	0.98	0.04	13,23,27,30	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.

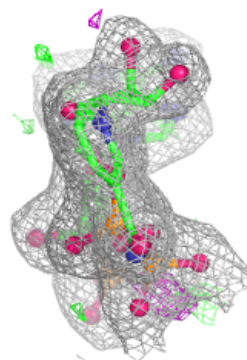
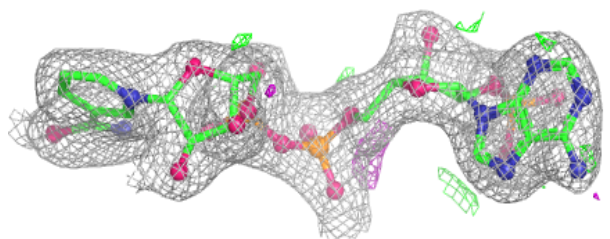
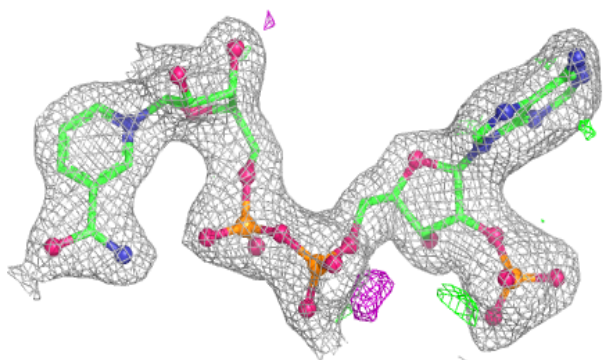


Electron density around NAP B 301:

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

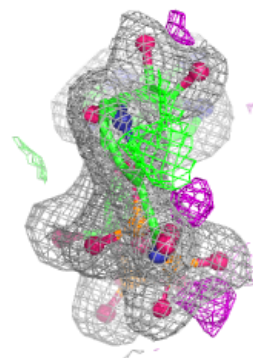
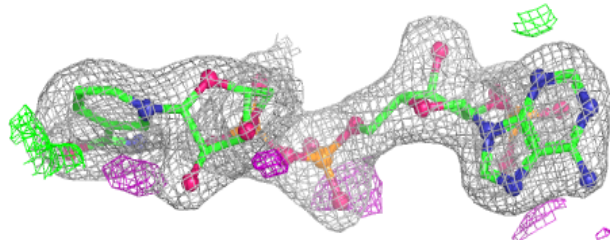
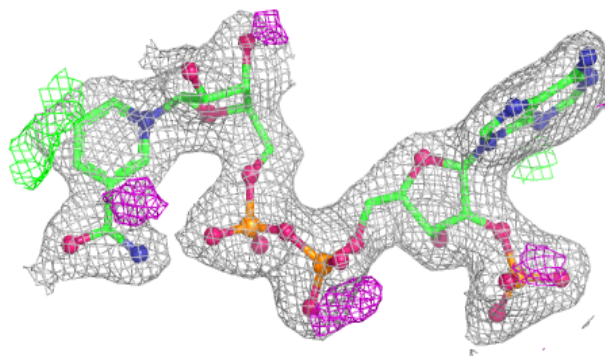
**Electron density around NAP G 301:**

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

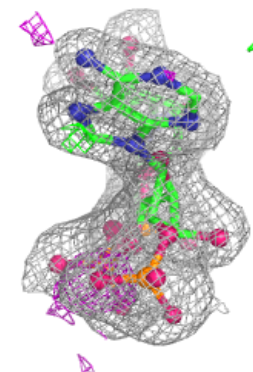
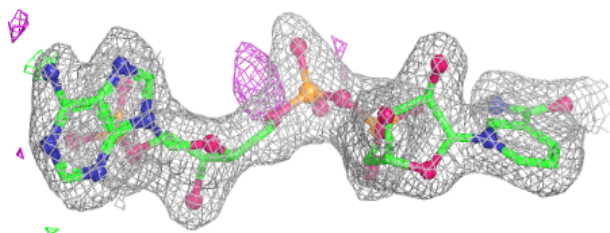
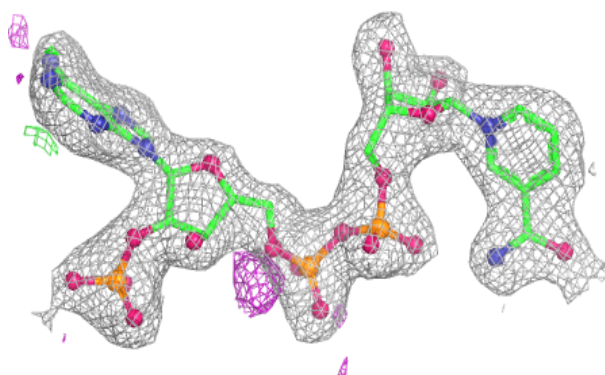


Electron density around NAP H 301:

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

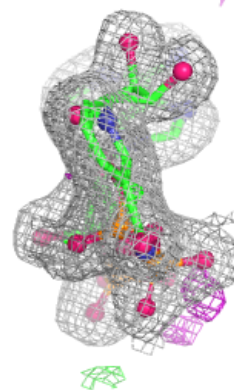
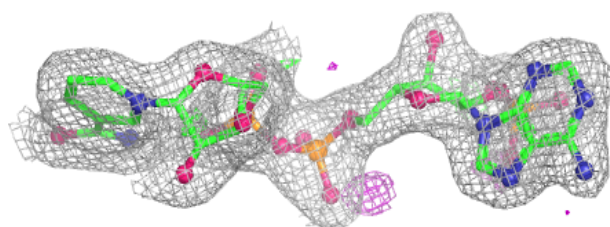
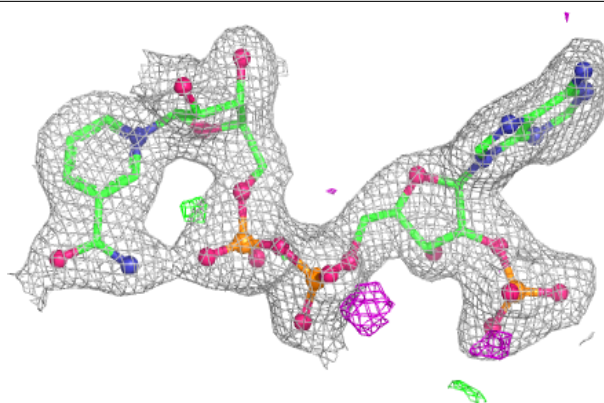
**Electron density around NAP C 301:**

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

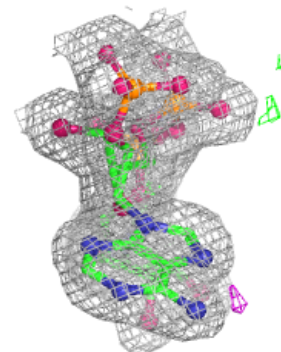
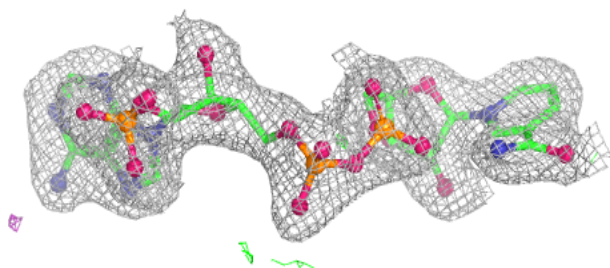
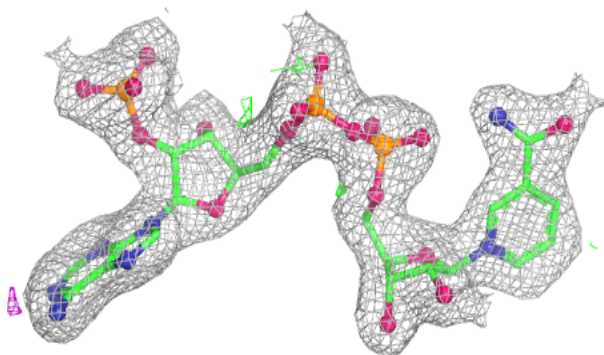


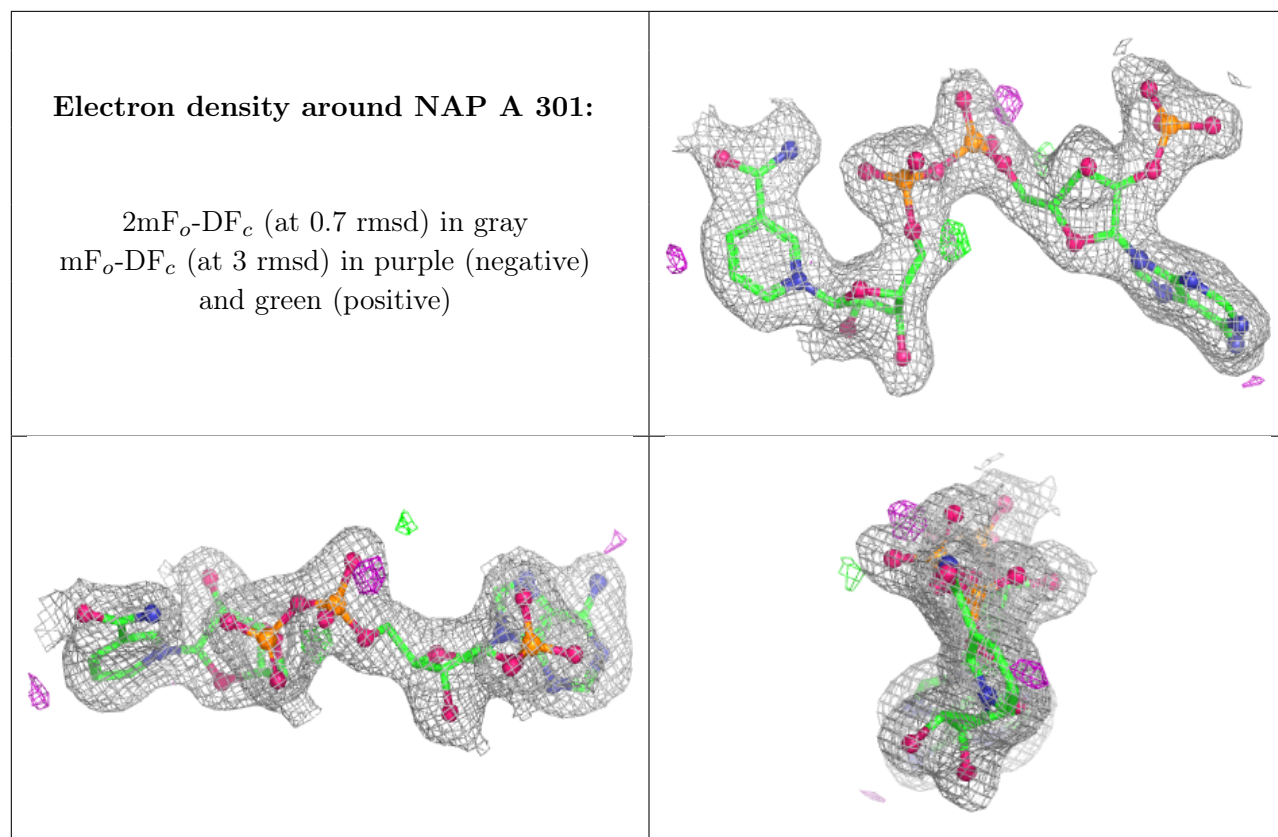
Electron density around NAP D 301:

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

**Electron density around NAP E 301:**

$2mF_o-DF_c$ (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.