



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 02:58 pm BST

PDB ID : 4I5E
Title : Crystal structure of Ralstonia sp. alcohol dehydrogenase in complex with NADP+
Authors : Jarasch, A.; Lerchner, A.; Meining, W.; Schiefner, A.; Skerra, A.
Deposited on : 2012-11-28
Resolution : 2.80 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 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 : 2.11
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) : 2.11

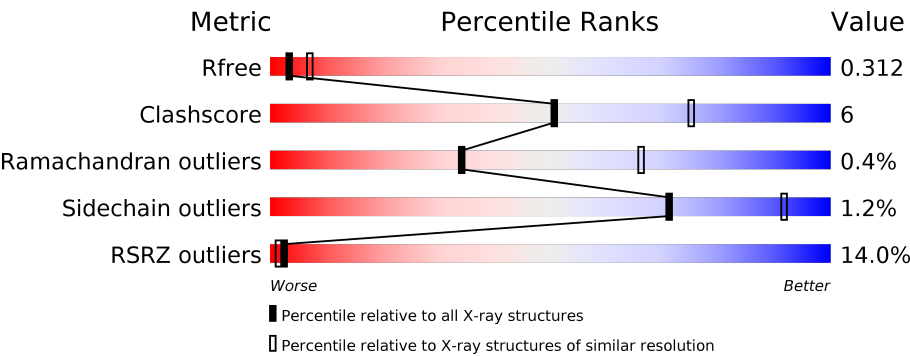
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 on 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	262	<div><div>10%</div><div><div></div><div>83%</div><div>10%</div><div>• 5%</div></div></div>
1	B	262	<div><div>19%</div><div><div></div><div>83%</div><div>11%</div><div>• 5%</div></div></div>
1	C	262	<div><div>16%</div><div><div></div><div>83%</div><div>11%</div><div>• 5%</div></div></div>
1	D	262	<div><div>11%</div><div><div></div><div>84%</div><div>11%</div><div>• 5%</div></div></div>
1	E	262	<div><div>11%</div><div><div></div><div>84%</div><div>10%</div><div>• 5%</div></div></div>
1	F	262	<div><div>11%</div><div><div></div><div>83%</div><div>11%</div><div>• 5%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	G	262	<div><div></div><div>18%</div><div></div><div>83%</div><div></div><div>12%</div><div>5%</div></div>
1	H	262	<div><div></div><div>10%</div><div></div><div>84%</div><div></div><div>11%</div><div>5%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15560 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 Alcohol dehydrogenase/short-chain dehydrogenase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	B	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	C	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	D	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	E	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	F	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	G	249	Total	C	N	O	0	0	0
			1882	1181	336	365			
1	H	249	Total	C	N	O	0	0	0
			1882	1181	336	365			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-12	MET	-	EXPRESSION TAG	UNP C0IR58
A	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
A	-10	SER	-	EXPRESSION TAG	UNP C0IR58
A	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
A	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
A	-7	SER	-	EXPRESSION TAG	UNP C0IR58
A	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
A	0	GLY	-	EXPRESSION TAG	UNP C0IR58

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	EXPRESSION TAG	UNP C0IR58
B	-12	MET	-	EXPRESSION TAG	UNP C0IR58
B	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
B	-10	SER	-	EXPRESSION TAG	UNP C0IR58
B	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
B	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
B	-7	SER	-	EXPRESSION TAG	UNP C0IR58
B	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
B	0	GLY	-	EXPRESSION TAG	UNP C0IR58
B	1	ALA	-	EXPRESSION TAG	UNP C0IR58
C	-12	MET	-	EXPRESSION TAG	UNP C0IR58
C	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
C	-10	SER	-	EXPRESSION TAG	UNP C0IR58
C	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
C	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
C	-7	SER	-	EXPRESSION TAG	UNP C0IR58
C	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
C	0	GLY	-	EXPRESSION TAG	UNP C0IR58
C	1	ALA	-	EXPRESSION TAG	UNP C0IR58
D	-12	MET	-	EXPRESSION TAG	UNP C0IR58
D	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
D	-10	SER	-	EXPRESSION TAG	UNP C0IR58
D	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
D	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
D	-7	SER	-	EXPRESSION TAG	UNP C0IR58
D	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
D	0	GLY	-	EXPRESSION TAG	UNP C0IR58

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1	ALA	-	EXPRESSION TAG	UNP C0IR58
E	-12	MET	-	EXPRESSION TAG	UNP C0IR58
E	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
E	-10	SER	-	EXPRESSION TAG	UNP C0IR58
E	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
E	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
E	-7	SER	-	EXPRESSION TAG	UNP C0IR58
E	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
E	0	GLY	-	EXPRESSION TAG	UNP C0IR58
E	1	ALA	-	EXPRESSION TAG	UNP C0IR58
F	-12	MET	-	EXPRESSION TAG	UNP C0IR58
F	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
F	-10	SER	-	EXPRESSION TAG	UNP C0IR58
F	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
F	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
F	-7	SER	-	EXPRESSION TAG	UNP C0IR58
F	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
F	0	GLY	-	EXPRESSION TAG	UNP C0IR58
F	1	ALA	-	EXPRESSION TAG	UNP C0IR58
G	-12	MET	-	EXPRESSION TAG	UNP C0IR58
G	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
G	-10	SER	-	EXPRESSION TAG	UNP C0IR58
G	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
G	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
G	-7	SER	-	EXPRESSION TAG	UNP C0IR58
G	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
G	0	GLY	-	EXPRESSION TAG	UNP C0IR58

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1	ALA	-	EXPRESSION TAG	UNP C0IR58
H	-12	MET	-	EXPRESSION TAG	UNP C0IR58
H	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
H	-10	SER	-	EXPRESSION TAG	UNP C0IR58
H	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
H	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
H	-7	SER	-	EXPRESSION TAG	UNP C0IR58
H	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
H	0	GLY	-	EXPRESSION TAG	UNP C0IR58
H	1	ALA	-	EXPRESSION TAG	UNP C0IR58

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- The chemical structure of Naproxen sodium (NAP) is shown. It consists of a naproxen moiety (a 2-(6-ethoxycarbonyl-2-naphthyl)propanoic acid derivative) and a sodium ion (Na⁺) associated with the carboxylate group. The structure is labeled with various atoms and groups, including the naphthalene ring, the propionic acid side chain, and the sodium ion.

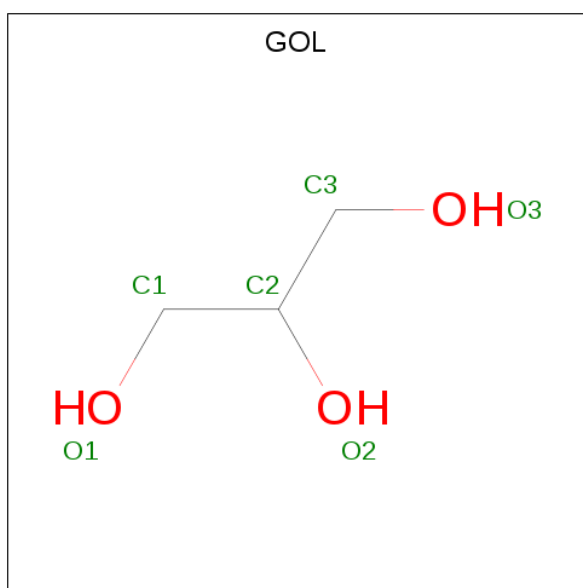
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	C	1	Total 48	C 21	N 7	O 17	P 3	0	0



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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		

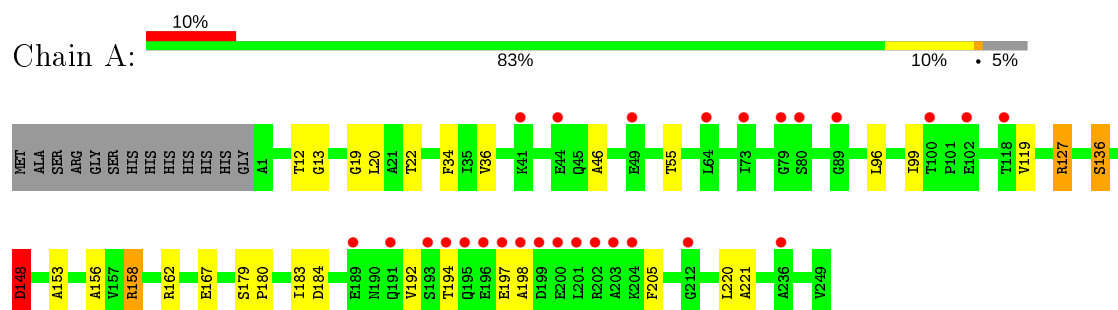
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	14	Total 14	O 14	0	0
4	B	15	Total 15	O 15	0	0
4	C	10	Total 10	O 10	0	0
4	D	11	Total 11	O 11	0	0
4	E	12	Total 12	O 12	0	0
4	F	16	Total 16	O 16	0	0
4	G	8	Total 8	O 8	0	0
4	H	10	Total 10	O 10	0	0

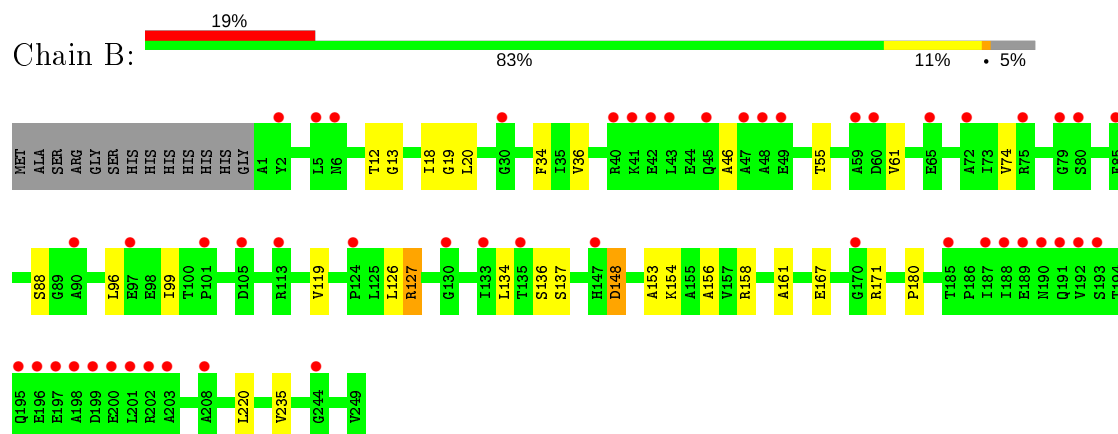
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

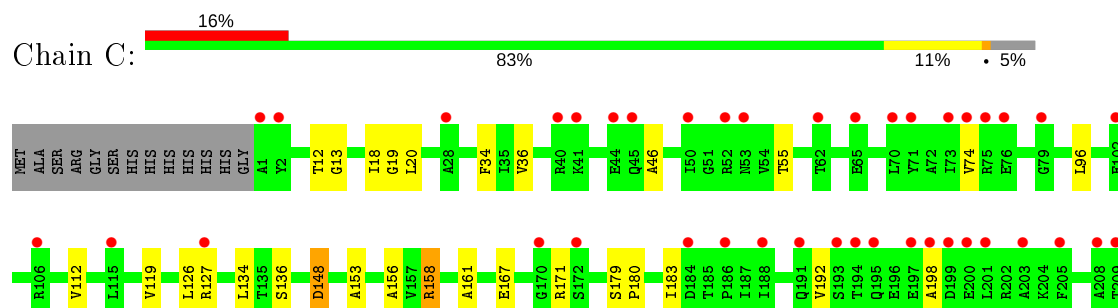
- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase

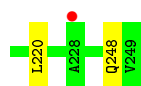


- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase

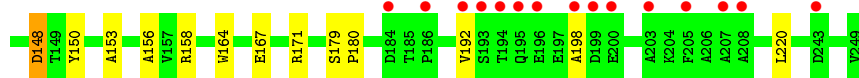
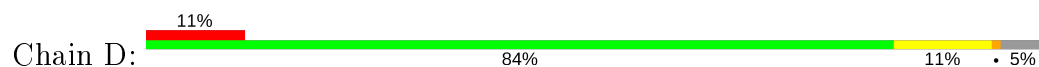


- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase

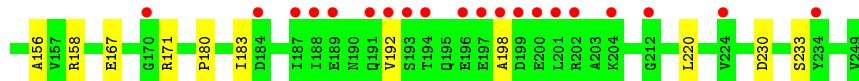
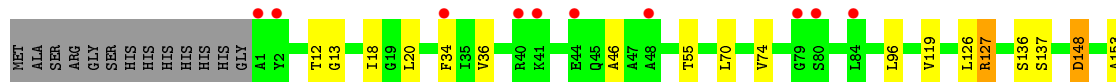
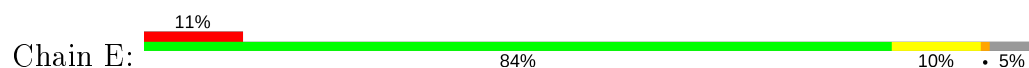




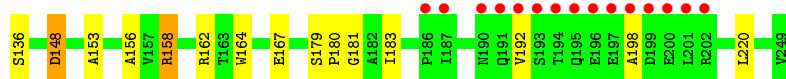
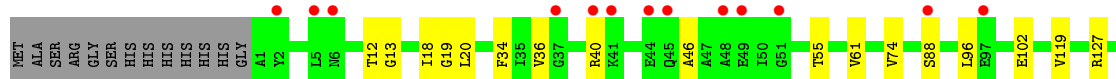
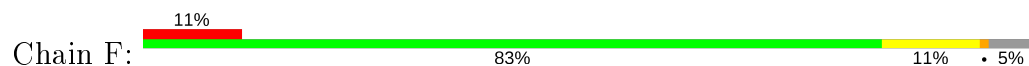
- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



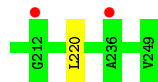
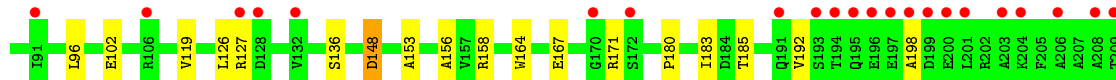
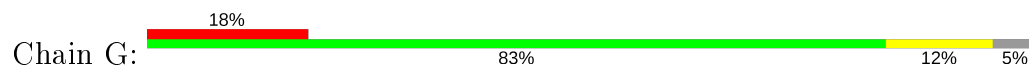
- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



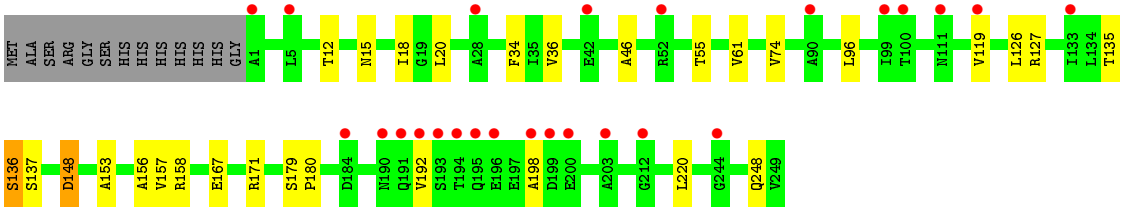
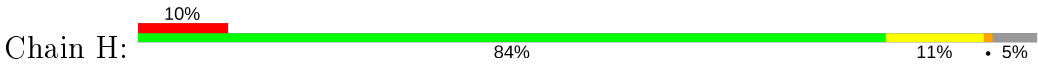
- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



● Molecule 1: Alclohol dehydrogenase/short-chain dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.34Å 74.55Å 132.69Å 80.98° 85.99° 64.60°	Depositor
Resolution (Å)	29.60 – 2.80 29.56 – 2.80	Depositor EDS
% Data completeness (in resolution range)	93.7 (29.60-2.80) 93.8 (29.56-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.80Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.261 , 0.305 0.268 , 0.312	Depositor DCC
R_{free} test set	2942 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.266	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	15560	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.28 % 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 4.8141e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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, NAP

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	4/1905 (0.2%)	0.96	7/2581 (0.3%)
1	B	0.54	0/1905	0.69	3/2581 (0.1%)
1	C	0.49	1/1905 (0.1%)	0.63	0/2581
1	D	0.51	2/1905 (0.1%)	0.64	1/2581 (0.0%)
1	E	0.57	2/1905 (0.1%)	0.95	4/2581 (0.2%)
1	F	0.56	2/1905 (0.1%)	0.67	1/2581 (0.0%)
1	G	0.52	2/1905 (0.1%)	0.64	1/2581 (0.0%)
1	H	0.53	1/1905 (0.1%)	0.65	1/2581 (0.0%)
All	All	0.55	14/15240 (0.1%)	0.74	18/20648 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	127	ARG	CZ-NH1	-13.63	1.15	1.33
1	G	127	ARG	CZ-NH1	-8.06	1.22	1.33
1	H	127	ARG	CZ-NH1	-7.58	1.23	1.33
1	E	127	ARG	CZ-NH1	-7.57	1.23	1.33
1	F	127	ARG	CZ-NH1	-7.29	1.23	1.33
1	A	148	ASP	CG-OD1	-7.11	1.09	1.25
1	C	127	ARG	CZ-NH1	-6.69	1.24	1.33
1	D	127	ARG	CZ-NH1	-6.63	1.24	1.33
1	E	127	ARG	CD-NE	-6.37	1.35	1.46
1	A	127	ARG	CZ-NH2	-6.24	1.25	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	164	TRP	CD2-CE2	5.80	1.48	1.41
1	A	148	ASP	CG-OD2	-5.79	1.12	1.25
1	F	164	TRP	CD2-CE2	5.34	1.47	1.41
1	G	164	TRP	CD2-CE2	5.33	1.47	1.41

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	127	ARG	NE-CZ-NH2	23.25	131.93	120.30
1	E	127	ARG	NE-CZ-NH1	-23.18	108.71	120.30
1	A	127	ARG	NE-CZ-NH2	22.71	131.66	120.30
1	A	148	ASP	CB-CG-OD2	15.64	132.37	118.30
1	E	127	ARG	CD-NE-CZ	12.53	141.14	123.60
1	A	148	ASP	OD1-CG-OD2	-12.15	100.21	123.30
1	A	127	ARG	NH1-CZ-NH2	-10.29	108.08	119.40
1	A	148	ASP	CB-CG-OD1	10.12	127.41	118.30
1	B	127	ARG	NE-CZ-NH1	7.60	124.10	120.30
1	B	127	ARG	NE-CZ-NH2	7.43	124.02	120.30
1	H	127	ARG	NE-CZ-NH1	7.24	123.92	120.30
1	G	127	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	B	127	ARG	NH1-CZ-NH2	-6.99	111.71	119.40
1	A	127	ARG	CG-CD-NE	6.87	126.22	111.80
1	F	127	ARG	NE-CZ-NH1	6.69	123.64	120.30
1	A	158	ARG	NE-CZ-NH1	6.53	123.56	120.30
1	D	127	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	E	127	ARG	NH1-CZ-NH2	-6.26	112.52	119.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	127	ARG	Sidechain

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	1882	0	1922	21	0
1	B	1882	0	1922	25	0
1	C	1882	0	1922	23	0
1	D	1882	0	1922	22	0
1	E	1882	0	1922	22	0
1	F	1882	0	1922	27	2
1	G	1882	0	1922	23	2
1	H	1882	0	1922	25	0
2	A	48	0	25	1	0
2	B	48	0	25	5	0
2	C	48	0	25	1	0
2	D	48	0	25	4	0
2	E	48	0	25	4	0
2	F	48	0	25	7	0
2	G	48	0	25	6	0
2	H	48	0	25	6	0
3	A	6	0	8	1	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	E	6	0	8	0	0
4	A	14	0	0	0	0
4	B	15	0	0	0	0
4	C	10	0	0	0	0
4	D	11	0	0	2	0
4	E	12	0	0	1	0
4	F	16	0	0	0	0
4	G	8	0	0	0	0
4	H	10	0	0	1	0
All	All	15560	0	15608	173	2

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 6.

All (173) 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:E:183:ILE:HB	2:E:301:NAP:N7N	1.90	0.86
1:E:183:ILE:HB	2:E:301:NAP:H72N	1.41	0.83
1:G:183:ILE:HB	2:G:301:NAP:N7N	2.01	0.75
1:B:34:PHE:CD1	1:B:55:THR:HB	2.26	0.71
1:E:34:PHE:CD1	1:E:55:THR:HB	2.29	0.67
1:A:194:THR:OG1	1:A:197:GLU:HG3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:119:VAL:HG12	1:H:96:LEU:HD21	1.77	0.67
1:F:34:PHE:CD1	1:F:55:THR:HB	2.31	0.66
1:H:34:PHE:CD1	1:H:55:THR:HB	2.30	0.66
1:G:34:PHE:CD1	1:G:55:THR:HB	2.31	0.65
1:D:34:PHE:CD1	1:D:55:THR:HB	2.32	0.65
1:C:34:PHE:CD1	1:C:55:THR:HB	2.32	0.64
1:B:34:PHE:HD1	1:B:55:THR:HB	1.63	0.63
1:A:205:PHE:CZ	3:A:302:GOL:H11	2.35	0.61
1:E:34:PHE:HD1	1:E:55:THR:HB	1.66	0.61
1:A:119:VAL:HG12	1:B:96:LEU:HD21	1.83	0.60
1:D:133:ILE:HG13	4:D:411:HOH:O	2.02	0.60
1:G:34:PHE:HD1	1:G:55:THR:HB	1.67	0.59
1:F:34:PHE:HD1	1:F:55:THR:HB	1.67	0.59
1:A:34:PHE:CD1	1:A:55:THR:HB	2.39	0.58
1:H:15:ASN:OD1	2:H:301:NAP:O3B	2.21	0.58
1:A:180:PRO:HB3	1:A:220:LEU:CD1	2.33	0.58
1:C:183:ILE:HB	2:C:301:NAP:N7N	2.19	0.58
1:C:34:PHE:HD1	1:C:55:THR:HB	1.69	0.58
1:E:180:PRO:HB3	1:E:220:LEU:HD13	1.85	0.58
1:H:34:PHE:HD1	1:H:55:THR:HB	1.68	0.58
1:B:153:ALA:O	1:B:156:ALA:HB3	2.03	0.57
1:H:18:ILE:HD12	2:H:301:NAP:H51N	1.87	0.57
1:A:96:LEU:HD21	1:B:119:VAL:HG12	1.85	0.57
1:G:153:ALA:O	1:G:156:ALA:HB3	2.05	0.57
1:D:137:SER:HB2	2:D:301:NAP:H6N	1.88	0.56
1:E:180:PRO:HB3	1:E:220:LEU:CD1	2.35	0.56
1:F:61:VAL:HG22	2:F:301:NAP:N1A	2.20	0.56
1:D:34:PHE:HD1	1:D:55:THR:HB	1.70	0.56
1:A:183:ILE:HB	2:A:301:NAP:N7N	2.21	0.55
1:F:18:ILE:HD13	1:F:220:LEU:HD22	1.86	0.55
1:A:180:PRO:HB3	1:A:220:LEU:HD13	1.87	0.55
1:H:18:ILE:HD13	1:H:220:LEU:HD22	1.88	0.55
1:F:183:ILE:HB	2:F:301:NAP:N7N	2.22	0.54
1:G:180:PRO:HB3	1:G:220:LEU:HD13	1.89	0.54
1:H:180:PRO:HB3	1:H:220:LEU:HD13	1.90	0.54
1:B:137:SER:HB2	2:B:301:NAP:H6N	1.90	0.54
1:C:18:ILE:HD13	1:C:220:LEU:HD22	1.90	0.54
1:H:137:SER:HB2	2:H:301:NAP:H6N	1.88	0.54
1:G:180:PRO:HB3	1:G:220:LEU:CD1	2.37	0.54
1:D:180:PRO:HB3	1:D:220:LEU:CD1	2.38	0.53
1:D:18:ILE:HD13	1:D:220:LEU:HD22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:153:ALA:O	1:F:156:ALA:HB3	2.09	0.53
2:G:301:NAP:H52N	2:G:301:NAP:H52A	1.91	0.53
1:B:18:ILE:HD13	1:B:220:LEU:HD22	1.89	0.53
1:F:61:VAL:HG22	2:F:301:NAP:C6A	2.38	0.53
1:H:180:PRO:HB3	1:H:220:LEU:CD1	2.39	0.53
1:C:180:PRO:HB3	1:C:220:LEU:CD1	2.39	0.52
1:F:180:PRO:HB3	1:F:220:LEU:HD13	1.91	0.52
1:H:137:SER:OG	2:H:301:NAP:H5N	2.09	0.52
1:E:96:LEU:HD21	1:F:119:VAL:HG12	1.91	0.52
1:G:18:ILE:HD13	1:G:220:LEU:HD22	1.91	0.52
1:E:13:GLY:HA2	2:E:301:NAP:H1B	1.92	0.51
1:H:153:ALA:O	1:H:156:ALA:HB3	2.11	0.51
1:E:18:ILE:HD13	1:E:220:LEU:HD22	1.91	0.51
1:F:180:PRO:HB3	1:F:220:LEU:CD1	2.41	0.51
1:A:13:GLY:O	1:A:19:GLY:HA3	2.11	0.51
1:D:153:ALA:O	1:D:156:ALA:HB3	2.11	0.51
1:D:180:PRO:HB3	1:D:220:LEU:HD13	1.92	0.50
1:C:180:PRO:HB3	1:C:220:LEU:HD13	1.92	0.50
1:B:180:PRO:HB3	1:B:220:LEU:CD1	2.42	0.50
1:A:148:ASP:OD2	1:B:167:GLU:OE2	2.30	0.49
1:G:185:THR:OG1	2:G:301:NAP:O2N	2.22	0.49
1:C:153:ALA:O	1:C:156:ALA:HB3	2.12	0.49
1:G:18:ILE:HD11	2:G:301:NAP:H71N	1.78	0.49
1:B:34:PHE:CE2	1:B:74:VAL:HG13	2.47	0.48
1:E:119:VAL:HG12	1:F:96:LEU:HD21	1.95	0.48
1:E:20:LEU:HD13	1:E:46:ALA:HB1	1.96	0.48
1:D:137:SER:OG	2:D:301:NAP:H5N	2.13	0.48
1:B:154:LYS:HE3	2:B:301:NAP:O2D	2.13	0.48
1:C:12:THR:HA	1:C:36:VAL:HB	1.95	0.48
1:C:34:PHE:CE2	1:C:74:VAL:HG13	2.49	0.48
1:D:20:LEU:HD13	1:D:46:ALA:HB1	1.97	0.47
1:H:12:THR:HA	1:H:36:VAL:HB	1.97	0.47
2:D:301:NAP:H1B	2:D:301:NAP:O3X	2.15	0.47
1:E:34:PHE:CE2	1:E:74:VAL:HG13	2.49	0.47
1:H:34:PHE:CE2	1:H:74:VAL:HG13	2.50	0.47
1:G:12:THR:HA	1:G:36:VAL:HB	1.97	0.47
1:E:153:ALA:O	1:E:156:ALA:HB3	2.15	0.47
1:A:167:GLU:OE2	1:B:148:ASP:OD1	2.33	0.47
1:B:180:PRO:HB3	1:B:220:LEU:HD13	1.96	0.47
1:D:12:THR:HA	1:D:36:VAL:HB	1.97	0.46
1:F:12:THR:HA	1:F:36:VAL:HB	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:ILE:HD11	1:A:148:ASP:HB2	1.98	0.46
1:D:34:PHE:CE2	1:D:74:VAL:HG13	2.50	0.46
1:A:192:VAL:HG21	1:A:198:ALA:HB2	1.97	0.46
1:B:34:PHE:HE2	1:B:74:VAL:HG13	1.80	0.46
1:B:20:LEU:HD13	1:B:46:ALA:HB1	1.98	0.46
1:G:34:PHE:CE2	1:G:74:VAL:HG13	2.50	0.46
1:A:34:PHE:HD1	1:A:55:THR:HB	1.81	0.46
1:D:13:GLY:O	1:D:19:GLY:HA3	2.16	0.46
1:B:12:THR:HA	1:B:36:VAL:HB	1.98	0.46
1:C:34:PHE:HE2	1:C:74:VAL:HG13	1.80	0.46
1:H:34:PHE:HE2	1:H:74:VAL:HG13	1.81	0.46
1:H:61:VAL:HG22	2:H:301:NAP:N1A	2.31	0.46
1:B:134:LEU:HD12	1:B:161:ALA:HB2	1.98	0.46
1:D:150:TYR:OH	2:D:301:NAP:C6N	2.64	0.46
1:F:34:PHE:CE2	1:F:74:VAL:HG13	2.50	0.46
1:G:34:PHE:HE2	1:G:74:VAL:HG13	1.80	0.46
1:E:12:THR:HA	1:E:36:VAL:HB	1.98	0.45
1:C:126:LEU:O	1:C:171:ARG:NH2	2.49	0.45
1:E:192:VAL:HG21	1:E:198:ALA:HB2	1.99	0.45
1:F:88:SER:HB2	2:F:301:NAP:C4A	2.45	0.45
1:B:126:LEU:O	1:B:171:ARG:NH2	2.49	0.45
1:D:34:PHE:HE2	1:D:74:VAL:HG13	1.82	0.45
1:E:34:PHE:HE2	1:E:74:VAL:HG13	1.80	0.45
1:E:167:GLU:OE2	1:F:148:ASP:OD1	2.35	0.45
1:G:183:ILE:HB	2:G:301:NAP:H72N	1.76	0.45
1:H:135:THR:HG21	2:H:301:NAP:H4D	1.98	0.45
1:H:192:VAL:HG21	1:H:198:ALA:HB2	1.99	0.45
1:B:13:GLY:O	1:B:19:GLY:HA3	2.17	0.45
1:C:136:SER:HB3	1:C:179:SER:OG	2.16	0.45
1:G:192:VAL:HG21	1:G:198:ALA:HB2	1.99	0.45
1:E:230:ASP:O	1:E:233:SER:HB3	2.18	0.44
1:G:20:LEU:HD13	1:G:46:ALA:HB1	1.97	0.44
1:G:96:LEU:HD21	1:H:119:VAL:HG12	1.99	0.44
1:A:153:ALA:O	1:A:156:ALA:HB3	2.17	0.44
1:C:148:ASP:OD1	1:D:167:GLU:OE2	2.34	0.44
1:C:96:LEU:HD21	1:D:119:VAL:HG12	1.98	0.44
1:F:61:VAL:HG13	2:F:301:NAP:C2A	2.47	0.44
1:A:20:LEU:HD13	1:A:46:ALA:HB1	2.00	0.44
1:C:20:LEU:HD13	1:C:46:ALA:HB1	1.99	0.44
1:H:157:VAL:HG21	4:H:409:HOH:O	2.17	0.44
1:C:192:VAL:HG21	1:C:198:ALA:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:167:GLU:OE2	1:H:148:ASP:OD1	2.36	0.44
1:H:20:LEU:HD13	1:H:46:ALA:HB1	1.99	0.44
1:C:134:LEU:HD12	1:C:161:ALA:HB2	2.00	0.44
1:F:20:LEU:HD13	1:F:46:ALA:HB1	1.99	0.44
1:D:192:VAL:HG21	1:D:198:ALA:HB2	1.99	0.44
1:F:34:PHE:HE2	1:F:74:VAL:HG13	1.82	0.44
1:A:162:ARG:HD3	1:C:248:GLN:O	2.18	0.44
1:F:162:ARG:HD3	1:H:248:GLN:O	2.18	0.43
1:F:192:VAL:HG21	1:F:198:ALA:HB2	1.99	0.43
1:F:180:PRO:HG2	2:F:301:NAP:C6N	2.48	0.43
1:E:148:ASP:OD1	1:F:167:GLU:OE2	2.35	0.43
1:B:235:VAL:HA	4:D:403:HOH:O	2.19	0.43
1:E:70:LEU:O	1:E:74:VAL:HG23	2.18	0.43
1:A:180:PRO:HB3	1:A:220:LEU:HD11	2.01	0.43
1:B:61:VAL:HG22	2:B:301:NAP:C6A	2.49	0.43
1:E:126:LEU:O	1:E:171:ARG:NH2	2.51	0.43
1:G:38:ARG:H	2:G:301:NAP:P2B	2.42	0.43
1:D:136:SER:HB3	1:D:179:SER:OG	2.20	0.42
1:G:13:GLY:O	1:G:19:GLY:HA3	2.19	0.42
1:A:12:THR:HA	1:A:36:VAL:HB	2.01	0.42
1:H:126:LEU:O	1:H:171:ARG:NH2	2.52	0.42
1:A:22:THR:HA	1:A:221:ALA:HB1	2.01	0.42
1:H:136:SER:HB3	1:H:179:SER:OG	2.19	0.42
1:C:167:GLU:OE2	1:D:148:ASP:OD1	2.37	0.42
1:E:137:SER:OG	2:E:301:NAP:H5N	2.20	0.42
1:G:126:LEU:O	1:G:171:ARG:NH2	2.52	0.42
1:F:136:SER:HB3	1:F:179:SER:OG	2.19	0.42
1:F:13:GLY:O	1:F:19:GLY:HA3	2.20	0.42
1:C:119:VAL:HG12	1:D:96:LEU:HD21	2.01	0.42
1:F:181:GLY:O	2:F:301:NAP:H4N	2.19	0.41
1:C:112:VAL:HG23	1:C:153:ALA:HB1	2.02	0.41
1:G:148:ASP:OD1	1:H:167:GLU:OE2	2.39	0.41
1:B:18:ILE:CG2	1:B:220:LEU:HD23	2.51	0.41
2:B:301:NAP:O2N	2:B:301:NAP:H2N	2.21	0.41
1:B:34:PHE:CE1	1:B:55:THR:HB	2.54	0.41
1:C:158:ARG:HD3	1:C:158:ARG:C	2.40	0.41
4:E:411:HOH:O	1:F:162:ARG:HD2	2.20	0.41
1:C:13:GLY:O	1:C:19:GLY:HA3	2.21	0.41
1:A:136:SER:HB3	1:A:179:SER:OG	2.21	0.41
1:B:99:ILE:HD11	1:B:148:ASP:HB2	2.03	0.41
1:F:158:ARG:C	1:F:158:ARG:HD3	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:70:LEU:O	1:G:74:VAL:HG23	2.21	0.41
1:D:126:LEU:O	1:D:171:ARG:NH2	2.54	0.40
1:B:88:SER:HB2	2:B:301:NAP:C4A	2.52	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:40:ARG:NH2	1:G:102:GLU:OE2[1_655]	1.91	0.29
1:F:102:GLU:OE2	1:G:40:ARG:NH2[1_655]	2.13	0.07

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	247/262 (94%)	235 (95%)	10 (4%)	2 (1%)	19	49
1	B	247/262 (94%)	240 (97%)	6 (2%)	1 (0%)	34	66
1	C	247/262 (94%)	238 (96%)	9 (4%)	0	100	100
1	D	247/262 (94%)	238 (96%)	8 (3%)	1 (0%)	34	66
1	E	247/262 (94%)	240 (97%)	6 (2%)	1 (0%)	34	66
1	F	247/262 (94%)	238 (96%)	9 (4%)	0	100	100
1	G	247/262 (94%)	239 (97%)	7 (3%)	1 (0%)	34	66
1	H	247/262 (94%)	240 (97%)	6 (2%)	1 (0%)	34	66
All	All	1976/2096 (94%)	1908 (97%)	61 (3%)	7 (0%)	34	66

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	136	SER

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Mol	Chain	Res	Type
1	A	136	SER
1	G	136	SER
1	H	136	SER
1	A	184	ASP
1	D	136	SER
1	E	136	SER

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	194/204 (95%)	191 (98%)	3 (2%)	65	89
1	B	194/204 (95%)	191 (98%)	3 (2%)	65	89
1	C	194/204 (95%)	192 (99%)	2 (1%)	76	93
1	D	194/204 (95%)	192 (99%)	2 (1%)	76	93
1	E	194/204 (95%)	192 (99%)	2 (1%)	76	93
1	F	194/204 (95%)	192 (99%)	2 (1%)	76	93
1	G	194/204 (95%)	192 (99%)	2 (1%)	76	93
1	H	194/204 (95%)	192 (99%)	2 (1%)	76	93
All	All	1552/1632 (95%)	1534 (99%)	18 (1%)	71	92

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	ARG
1	A	148	ASP
1	A	158	ARG
1	B	127	ARG
1	B	148	ASP
1	B	158	ARG
1	C	148	ASP
1	C	158	ARG
1	D	148	ASP

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Mol	Chain	Res	Type
1	D	158	ARG
1	E	148	ASP
1	E	158	ARG
1	F	148	ASP
1	F	158	ARG
1	G	148	ASP
1	G	158	ARG
1	H	148	ASP
1	H	158	ARG

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

Mol	Chain	Res	Type
1	B	87	ASN
1	D	87	ASN
1	E	87	ASN
1	F	87	ASN
1	G	87	ASN
1	H	87	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 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	GOL	C	302	-	5,5,5	0.29	0	5,5,5	0.35	0
2	NAP	B	301	-	45,52,52	1.15	4 (8%)	56,80,80	1.66	14 (25%)
3	GOL	E	302	-	5,5,5	0.61	0	5,5,5	0.57	0
2	NAP	D	301	-	45,52,52	1.12	4 (8%)	56,80,80	1.55	11 (19%)
2	NAP	F	301	-	45,52,52	1.18	5 (11%)	56,80,80	1.59	11 (19%)
2	NAP	C	301	-	45,52,52	0.89	1 (2%)	56,80,80	1.48	8 (14%)
2	NAP	G	301	-	45,52,52	0.86	2 (4%)	56,80,80	1.45	8 (14%)
3	GOL	B	302	-	5,5,5	0.36	0	5,5,5	0.37	0
2	NAP	A	301	-	45,52,52	0.97	3 (6%)	56,80,80	1.29	5 (8%)
2	NAP	H	301	-	45,52,52	0.94	2 (4%)	56,80,80	1.28	7 (12%)
2	NAP	E	301	-	45,52,52	1.11	4 (8%)	56,80,80	1.57	9 (16%)
3	GOL	A	302	-	5,5,5	0.41	0	5,5,5	0.30	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
3	GOL	C	302	-	-	4/4/4/4	-
2	NAP	B	301	-	-	7/31/67/67	0/5/5/5
3	GOL	E	302	-	-	2/4/4/4	-
2	NAP	D	301	-	-	9/31/67/67	0/5/5/5
2	NAP	F	301	-	-	6/31/67/67	0/5/5/5
2	NAP	C	301	-	-	6/31/67/67	0/5/5/5
2	NAP	G	301	-	-	10/31/67/67	0/5/5/5
3	GOL	B	302	-	-	4/4/4/4	-
2	NAP	A	301	-	-	7/31/67/67	0/5/5/5
2	NAP	H	301	-	-	10/31/67/67	0/5/5/5
2	NAP	E	301	-	-	9/31/67/67	0/5/5/5
3	GOL	A	302	-	-	4/4/4/4	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	NAP	C5A-C4A	3.58	1.50	1.40
2	D	301	NAP	O4B-C1B	3.47	1.45	1.41
2	E	301	NAP	C2A-N3A	3.24	1.37	1.32
2	F	301	NAP	O4D-C1D	3.21	1.45	1.41
2	F	301	NAP	O4B-C1B	2.92	1.45	1.41
2	F	301	NAP	C5A-C4A	2.92	1.48	1.40
2	D	301	NAP	C5A-C4A	2.87	1.48	1.40
2	E	301	NAP	C5A-C4A	2.77	1.48	1.40
2	D	301	NAP	O4D-C1D	2.73	1.44	1.41
2	B	301	NAP	C2A-N3A	2.70	1.36	1.32
2	H	301	NAP	O4D-C1D	2.65	1.44	1.41
2	G	301	NAP	C5A-C4A	2.63	1.47	1.40
2	A	301	NAP	C5A-C4A	2.59	1.47	1.40
2	F	301	NAP	C8A-N7A	2.56	1.39	1.34
2	C	301	NAP	C5A-C4A	2.53	1.47	1.40
2	A	301	NAP	C2A-N3A	2.50	1.36	1.32
2	B	301	NAP	C8A-N7A	2.45	1.39	1.34
2	H	301	NAP	C5A-C4A	2.38	1.47	1.40
2	B	301	NAP	O4B-C1B	2.25	1.44	1.41
2	F	301	NAP	C2A-N3A	2.21	1.35	1.32
2	G	301	NAP	O4D-C1D	2.21	1.44	1.41
2	D	301	NAP	C2A-N3A	2.17	1.35	1.32
2	E	301	NAP	C2D-C1D	2.14	1.57	1.53
2	A	301	NAP	O4D-C1D	2.10	1.44	1.41
2	E	301	NAP	P2B-O2B	2.05	1.63	1.59

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	301	NAP	N3A-C2A-N1A	-4.04	122.36	128.68
2	H	301	NAP	N3A-C2A-N1A	-3.95	122.50	128.68
2	B	301	NAP	O4D-C1D-C2D	-3.95	101.16	106.93
2	F	301	NAP	N3A-C2A-N1A	-3.86	122.64	128.68
2	D	301	NAP	C6N-N1N-C2N	-3.79	118.52	121.97
2	B	301	NAP	N3A-C2A-N1A	-3.68	122.93	128.68
2	A	301	NAP	N3A-C2A-N1A	-3.64	122.98	128.68
2	F	301	NAP	O2D-C2D-C1D	3.63	124.26	110.85
2	E	301	NAP	C3D-C2D-C1D	3.60	106.39	100.98
2	B	301	NAP	PN-O3-PA	-3.57	120.58	132.83
2	F	301	NAP	C4A-C5A-N7A	-3.56	105.69	109.40
2	C	301	NAP	N3A-C2A-N1A	-3.53	123.16	128.68
2	E	301	NAP	C6N-N1N-C2N	-3.53	118.76	121.97
2	E	301	NAP	PN-O3-PA	-3.53	120.72	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	301	NAP	C1B-N9A-C4A	-3.49	120.51	126.64
2	A	301	NAP	C4A-C5A-N7A	-3.35	105.90	109.40
2	E	301	NAP	N3A-C2A-N1A	-3.28	123.56	128.68
2	D	301	NAP	C4A-C5A-N7A	-3.23	106.03	109.40
2	B	301	NAP	C6N-N1N-C2N	-3.20	119.06	121.97
2	C	301	NAP	C6N-N1N-C2N	-3.17	119.08	121.97
2	D	301	NAP	N3A-C2A-N1A	-3.17	123.72	128.68
2	C	301	NAP	C4A-C5A-N7A	-3.12	106.14	109.40
2	G	301	NAP	C2N-C3N-C4N	3.10	121.77	118.26
2	D	301	NAP	O2B-C2B-C1B	3.09	121.23	110.10
2	H	301	NAP	C4A-C5A-N7A	-3.03	106.24	109.40
2	B	301	NAP	C4A-C5A-N7A	-2.95	106.33	109.40
2	E	301	NAP	O4D-C4D-C3D	2.90	110.85	105.11
2	B	301	NAP	C1B-N9A-C4A	-2.87	121.59	126.64
2	C	301	NAP	C2N-C3N-C4N	2.85	121.49	118.26
2	G	301	NAP	C4A-C5A-N7A	-2.79	106.49	109.40
2	D	301	NAP	O2B-P2B-O1X	-2.76	98.75	109.39
2	F	301	NAP	C5D-C4D-C3D	-2.75	104.86	115.18
2	C	301	NAP	C1B-N9A-C4A	-2.72	121.87	126.64
2	G	301	NAP	C6N-N1N-C2N	-2.67	119.54	121.97
2	D	301	NAP	O4B-C1B-C2B	-2.67	101.96	106.59
2	F	301	NAP	O3X-P2B-O2X	2.61	117.60	107.64
2	B	301	NAP	C3D-C2D-C1D	2.58	104.86	100.98
2	F	301	NAP	O4D-C1D-C2D	-2.56	103.18	106.93
2	G	301	NAP	C2A-N1A-C6A	2.55	123.11	118.75
2	D	301	NAP	C3D-C2D-C1D	2.51	104.76	100.98
2	B	301	NAP	C2A-N1A-C6A	2.50	123.03	118.75
2	D	301	NAP	C5B-C4B-C3B	-2.49	105.84	115.18
2	H	301	NAP	PN-O3-PA	-2.48	124.33	132.83
2	A	301	NAP	C3D-C2D-C1D	2.48	104.71	100.98
2	A	301	NAP	C6N-N1N-C2N	-2.46	119.73	121.97
2	C	301	NAP	O3X-P2B-O2X	2.42	116.88	107.64
2	E	301	NAP	N6A-C6A-N1A	2.40	123.55	118.57
2	H	301	NAP	C6N-N1N-C2N	-2.39	119.79	121.97
2	H	301	NAP	O2A-PA-O1A	2.39	124.05	112.24
2	B	301	NAP	O5B-C5B-C4B	2.37	117.16	108.99
2	B	301	NAP	O2X-P2B-O1X	2.36	119.91	110.68
2	B	301	NAP	C5N-C6N-N1N	2.30	123.71	120.40
2	F	301	NAP	O4D-C4D-C5D	2.28	116.88	109.37
2	C	301	NAP	PN-O3-PA	-2.27	125.05	132.83
2	F	301	NAP	O2N-PN-O5D	2.24	118.15	107.75
2	F	301	NAP	C5A-C6A-N6A	2.21	123.72	120.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	NAP	C5N-C6N-N1N	2.18	123.53	120.40
2	C	301	NAP	C5N-C6N-N1N	2.18	123.52	120.40
2	D	301	NAP	C5N-C6N-N1N	2.17	123.52	120.40
2	F	301	NAP	PN-O3-PA	-2.17	125.38	132.83
2	H	301	NAP	C2A-N1A-C6A	2.16	122.45	118.75
2	D	301	NAP	O4B-C4B-C3B	-2.16	100.84	105.11
2	E	301	NAP	C2N-C3N-C4N	2.15	120.69	118.26
2	H	301	NAP	C1B-N9A-C4A	-2.13	122.90	126.64
2	B	301	NAP	O5D-C5D-C4D	-2.07	101.85	108.99
2	A	301	NAP	C1B-N9A-C4A	-2.07	123.00	126.64
2	E	301	NAP	O5B-C5B-C4B	-2.07	101.88	108.99
2	G	301	NAP	O2A-PA-O1A	2.04	122.33	112.24
2	G	301	NAP	O4B-C1B-C2B	-2.03	103.07	106.59
2	G	301	NAP	O3X-P2B-O2X	2.02	115.35	107.64
2	D	301	NAP	O3X-P2B-O2X	2.01	115.34	107.64
2	B	301	NAP	O2N-PN-O1N	2.01	122.17	112.24
2	B	301	NAP	O5B-PA-O1A	2.01	116.90	109.07

There are no chirality outliers.

All (78) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	302	GOL	O1-C1-C2-C3
2	B	301	NAP	C5D-O5D-PN-O3
2	B	301	NAP	C5D-O5D-PN-O1N
2	B	301	NAP	C5D-O5D-PN-O2N
2	B	301	NAP	O4D-C4D-C5D-O5D
2	B	301	NAP	C3D-C4D-C5D-O5D
3	E	302	GOL	O1-C1-C2-C3
2	D	301	NAP	C5B-O5B-PA-O3
2	D	301	NAP	C1B-C2B-O2B-P2B
2	D	301	NAP	C2B-O2B-P2B-O1X
2	D	301	NAP	C5D-O5D-PN-O3
2	D	301	NAP	C5D-O5D-PN-O2N
2	F	301	NAP	C2B-O2B-P2B-O1X
2	F	301	NAP	C5D-O5D-PN-O3
2	F	301	NAP	C5D-O5D-PN-O2N
2	C	301	NAP	C2B-O2B-P2B-O3X
2	C	301	NAP	C5D-O5D-PN-O1N
2	C	301	NAP	C5D-O5D-PN-O2N
2	G	301	NAP	C2B-O2B-P2B-O3X
3	B	302	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	B	302	GOL	C1-C2-C3-O3
3	B	302	GOL	O2-C2-C3-O3
2	A	301	NAP	PN-O3-PA-O5B
2	A	301	NAP	C2B-O2B-P2B-O1X
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	H	301	NAP	C5B-O5B-PA-O1A
2	H	301	NAP	C5B-O5B-PA-O2A
2	H	301	NAP	C2B-O2B-P2B-O1X
2	E	301	NAP	C5B-O5B-PA-O3
2	E	301	NAP	C2B-O2B-P2B-O1X
2	E	301	NAP	C5D-O5D-PN-O3
2	E	301	NAP	C5D-O5D-PN-O2N
3	A	302	GOL	O1-C1-C2-C3
2	D	301	NAP	O4B-C4B-C5B-O5B
2	D	301	NAP	C3B-C4B-C5B-O5B
2	G	301	NAP	O4B-C4B-C5B-O5B
2	E	301	NAP	O4B-C4B-C5B-O5B
2	D	301	NAP	C4B-C5B-O5B-PA
3	C	302	GOL	O2-C2-C3-O3
3	A	302	GOL	O1-C1-C2-O2
3	C	302	GOL	C1-C2-C3-O3
3	A	302	GOL	C1-C2-C3-O3
3	C	302	GOL	O1-C1-C2-O2
3	E	302	GOL	O1-C1-C2-O2
3	B	302	GOL	O1-C1-C2-O2
2	H	301	NAP	O4D-C4D-C5D-O5D
2	G	301	NAP	C3B-C4B-C5B-O5B
3	A	302	GOL	O2-C2-C3-O3
2	G	301	NAP	C2N-C3N-C7N-O7N
2	F	301	NAP	PN-O3-PA-O5B
2	C	301	NAP	C2B-O2B-P2B-O1X
2	G	301	NAP	C2B-O2B-P2B-O1X
2	G	301	NAP	C4N-C3N-C7N-O7N
2	B	301	NAP	C2B-O2B-P2B-O2X
2	H	301	NAP	C5B-O5B-PA-O3
2	H	301	NAP	C2B-O2B-P2B-O3X
2	E	301	NAP	C2B-O2B-P2B-O3X
2	H	301	NAP	C3D-C4D-C5D-O5D
2	D	301	NAP	C5B-O5B-PA-O2A
2	E	301	NAP	C5B-O5B-PA-O1A

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Mol	Chain	Res	Type	Atoms
2	E	301	NAP	C5B-O5B-PA-O2A
2	G	301	NAP	O4D-C4D-C5D-O5D
2	G	301	NAP	C4N-C3N-C7N-N7N
2	G	301	NAP	C2N-C3N-C7N-N7N
2	A	301	NAP	O4B-C4B-C5B-O5B
2	H	301	NAP	PN-O3-PA-O2A
2	H	301	NAP	PN-O3-PA-O5B
2	F	301	NAP	C4D-C5D-O5D-PN
2	C	301	NAP	C5D-O5D-PN-O3
2	A	301	NAP	C2B-O2B-P2B-O2X
2	E	301	NAP	PA-O3-PN-O2N
2	B	301	NAP	O4B-C4B-C5B-O5B
2	F	301	NAP	O4B-C4B-C5B-O5B
2	C	301	NAP	O4B-C4B-C5B-O5B
2	G	301	NAP	C3D-C4D-C5D-O5D
2	H	301	NAP	O4B-C4B-C5B-O5B

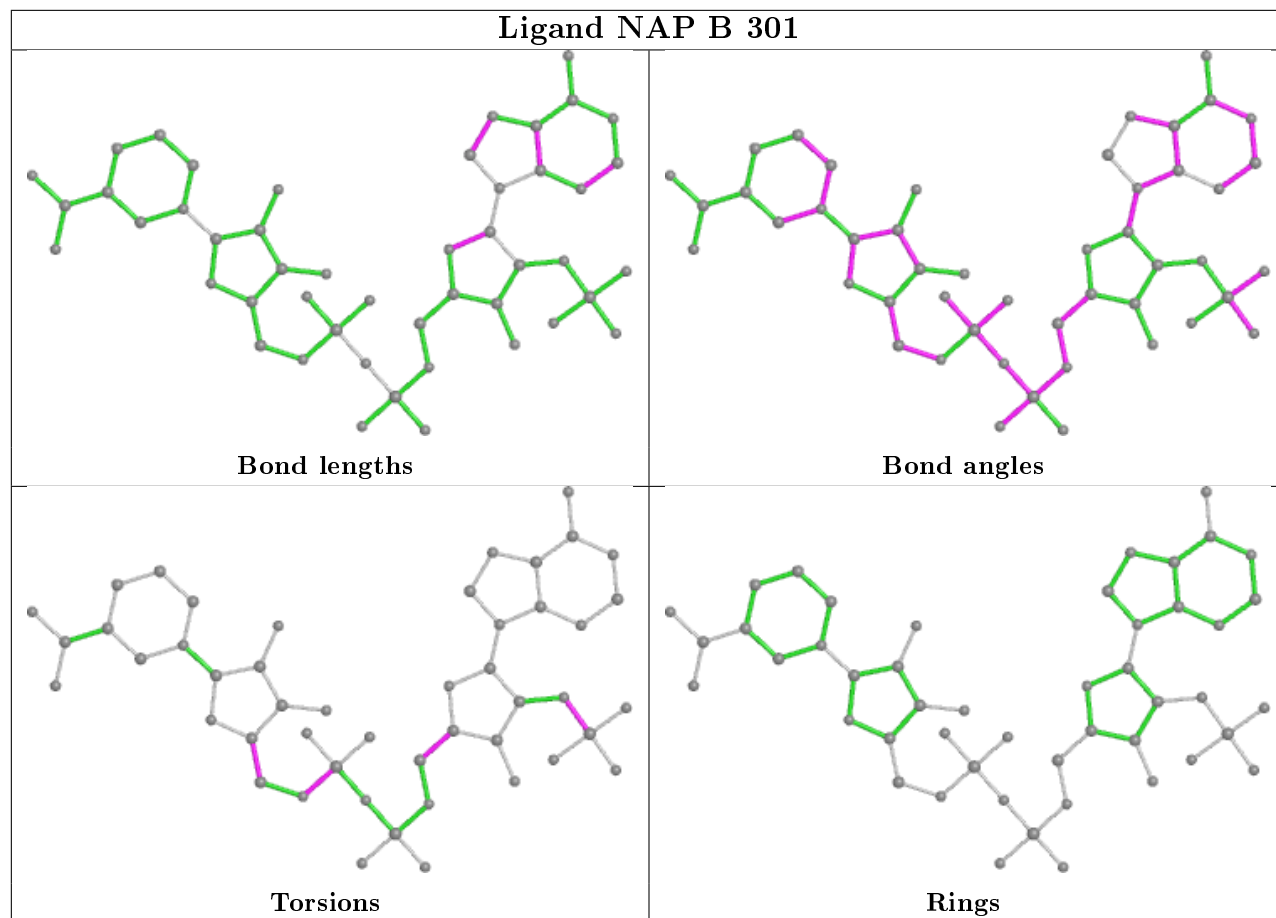
There are no ring outliers.

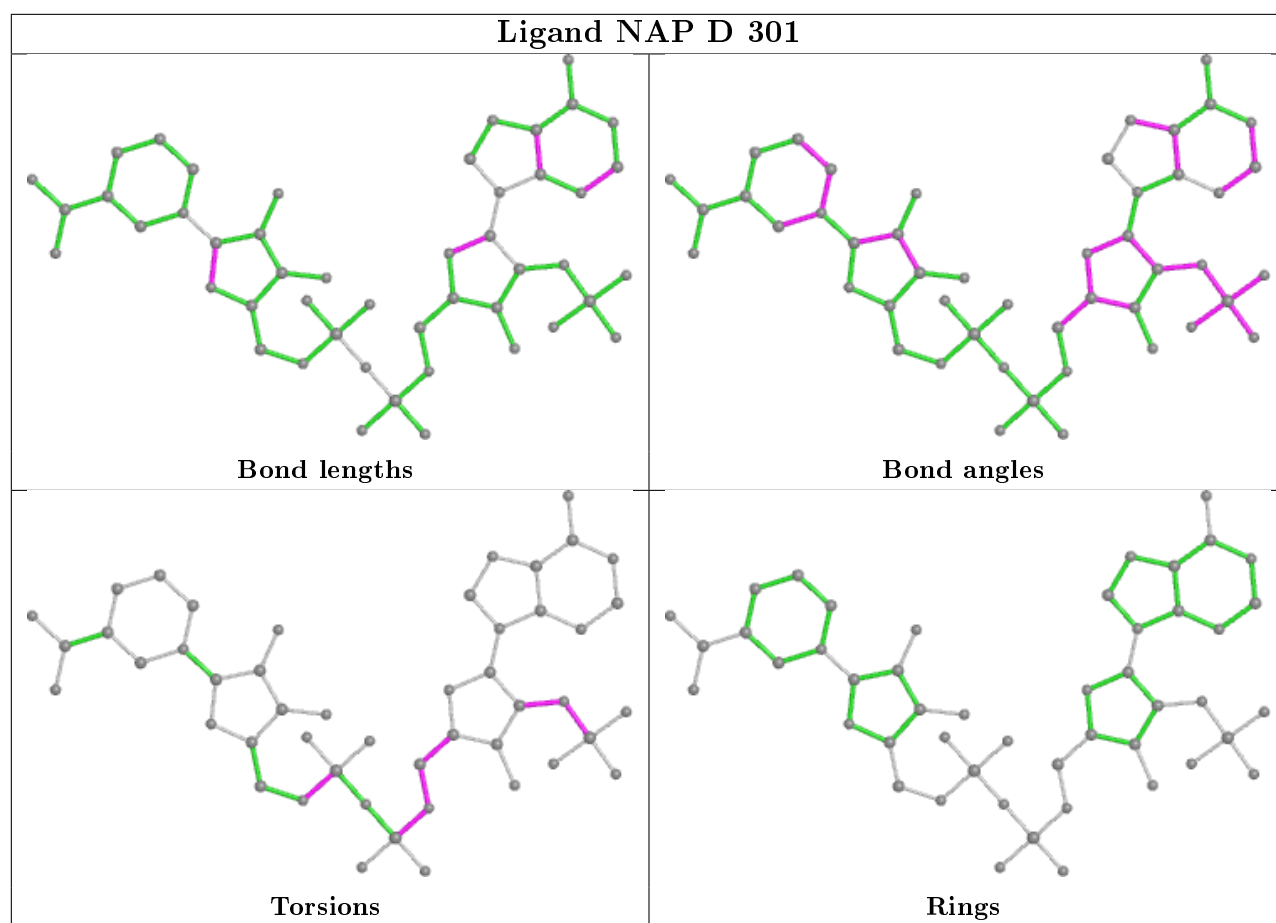
9 monomers are involved in 35 short contacts:

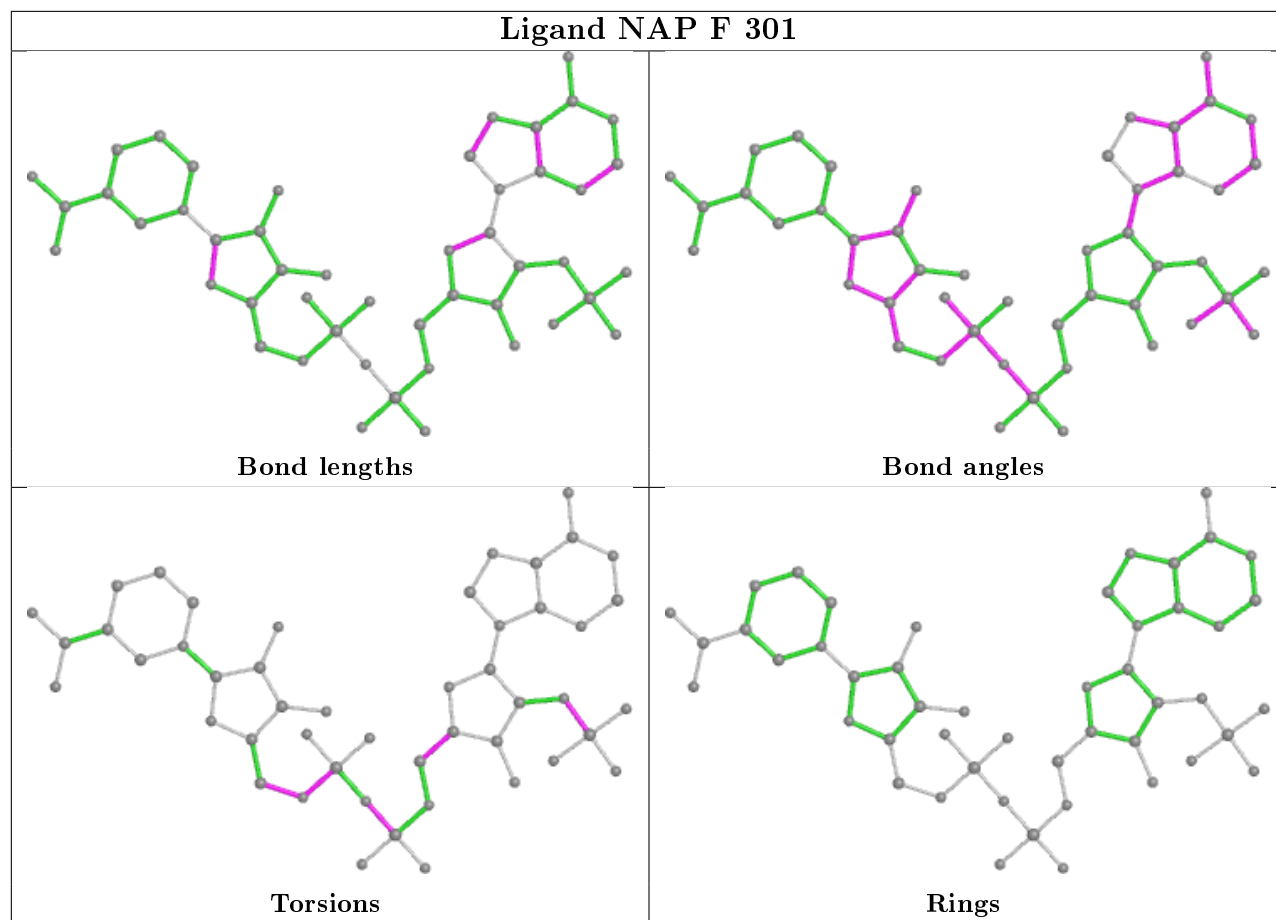
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	NAP	5	0
2	D	301	NAP	4	0
2	F	301	NAP	7	0
2	C	301	NAP	1	0
2	G	301	NAP	6	0
2	A	301	NAP	1	0
2	H	301	NAP	6	0
2	E	301	NAP	4	0
3	A	302	GOL	1	0

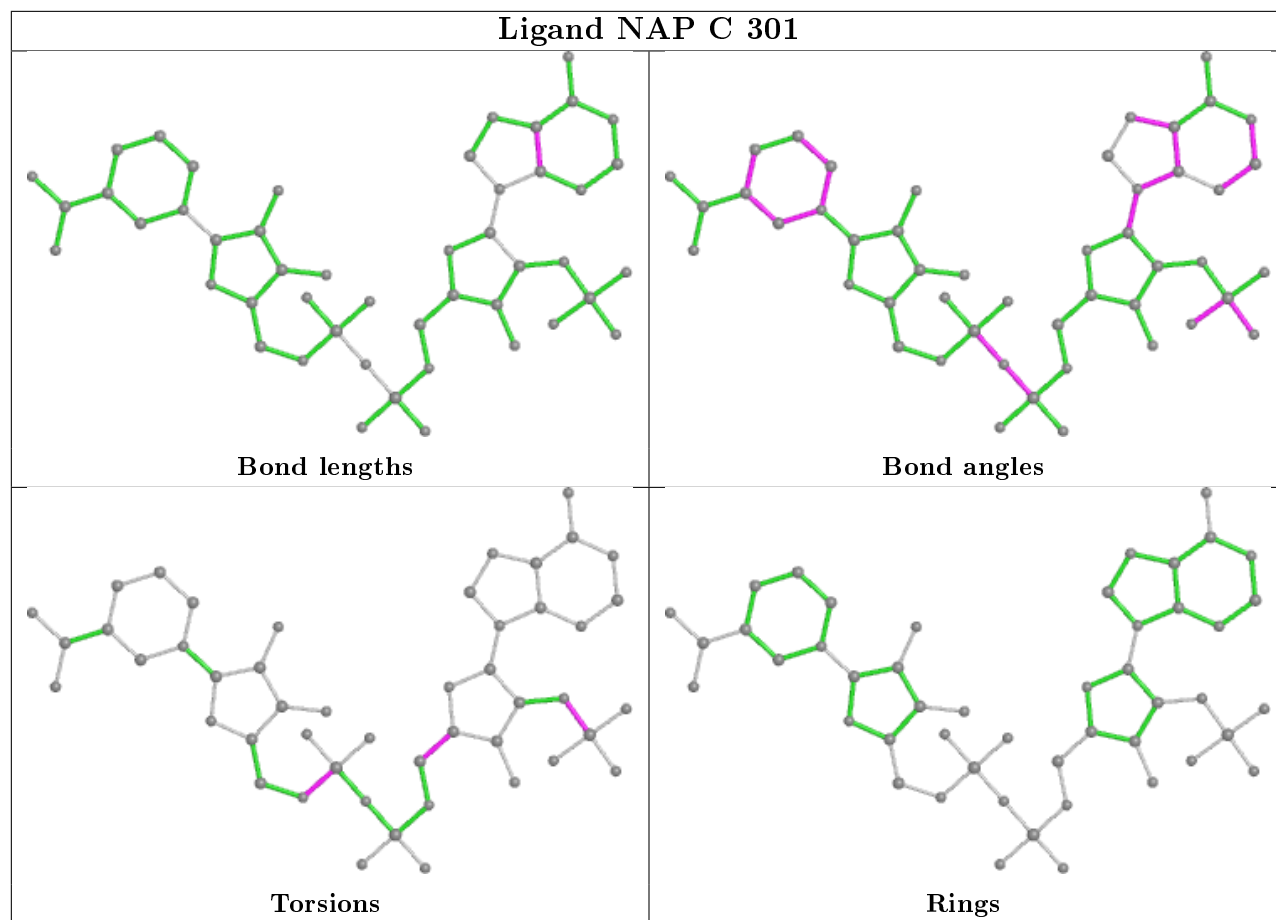
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

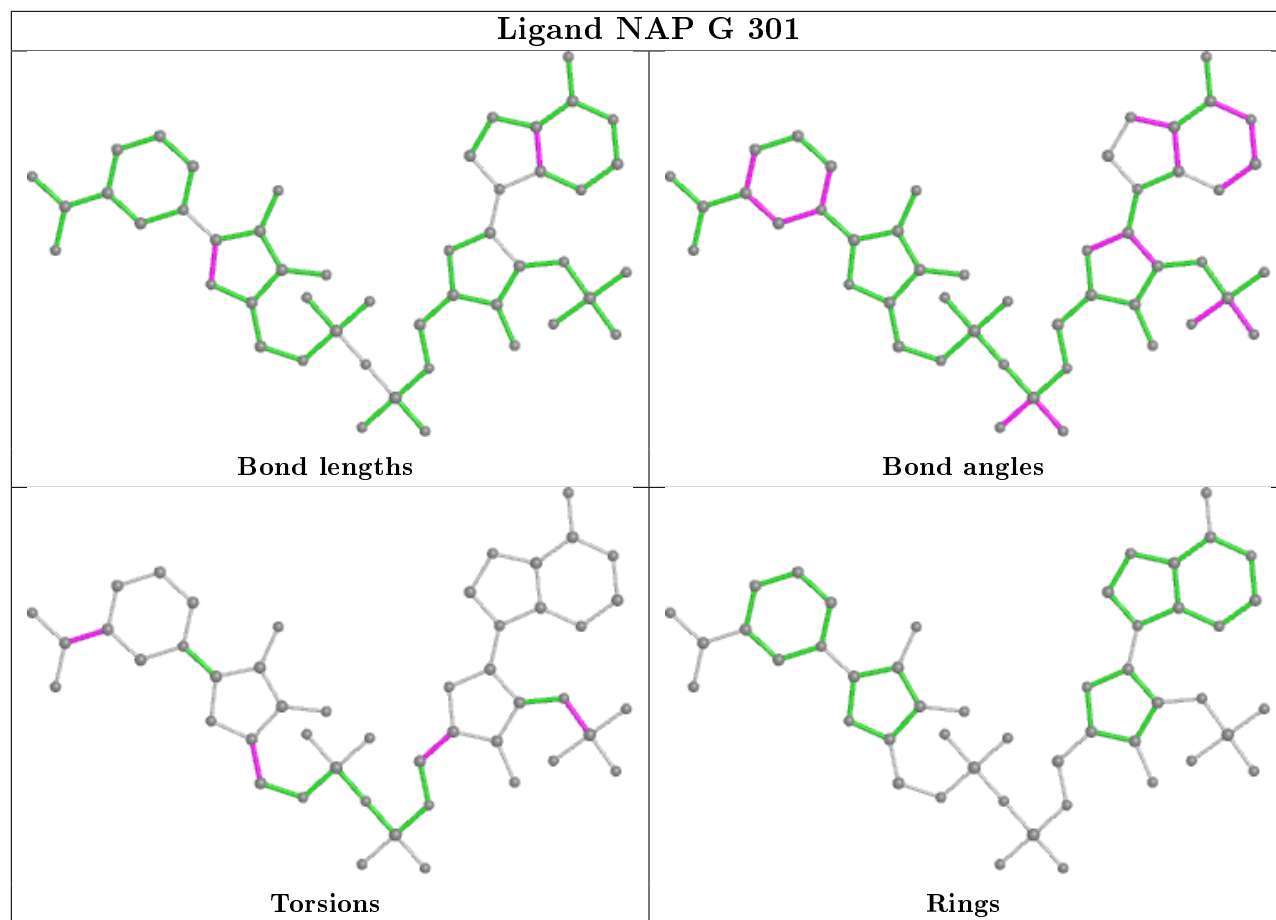
equivalents in the CSD to analyse the geometry.

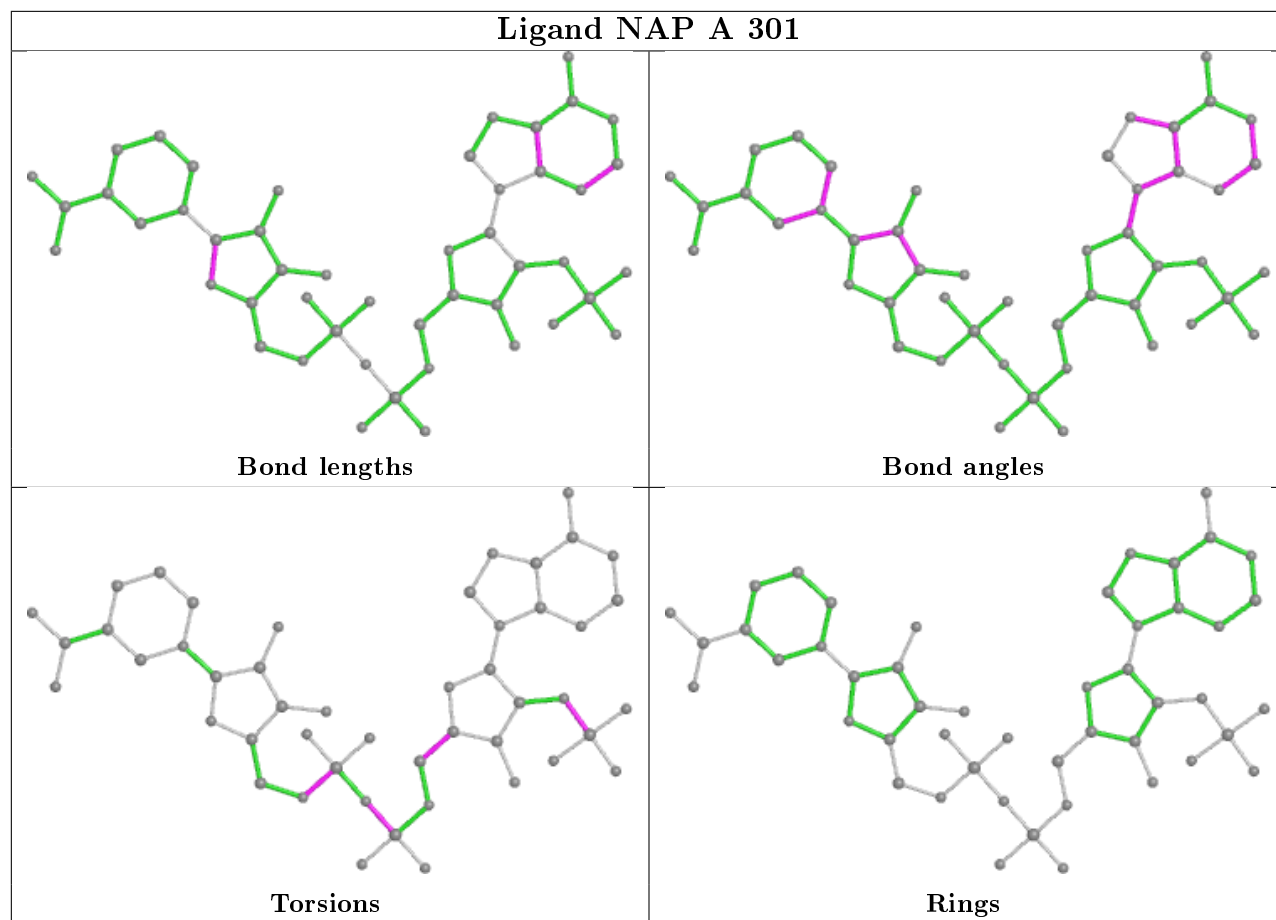


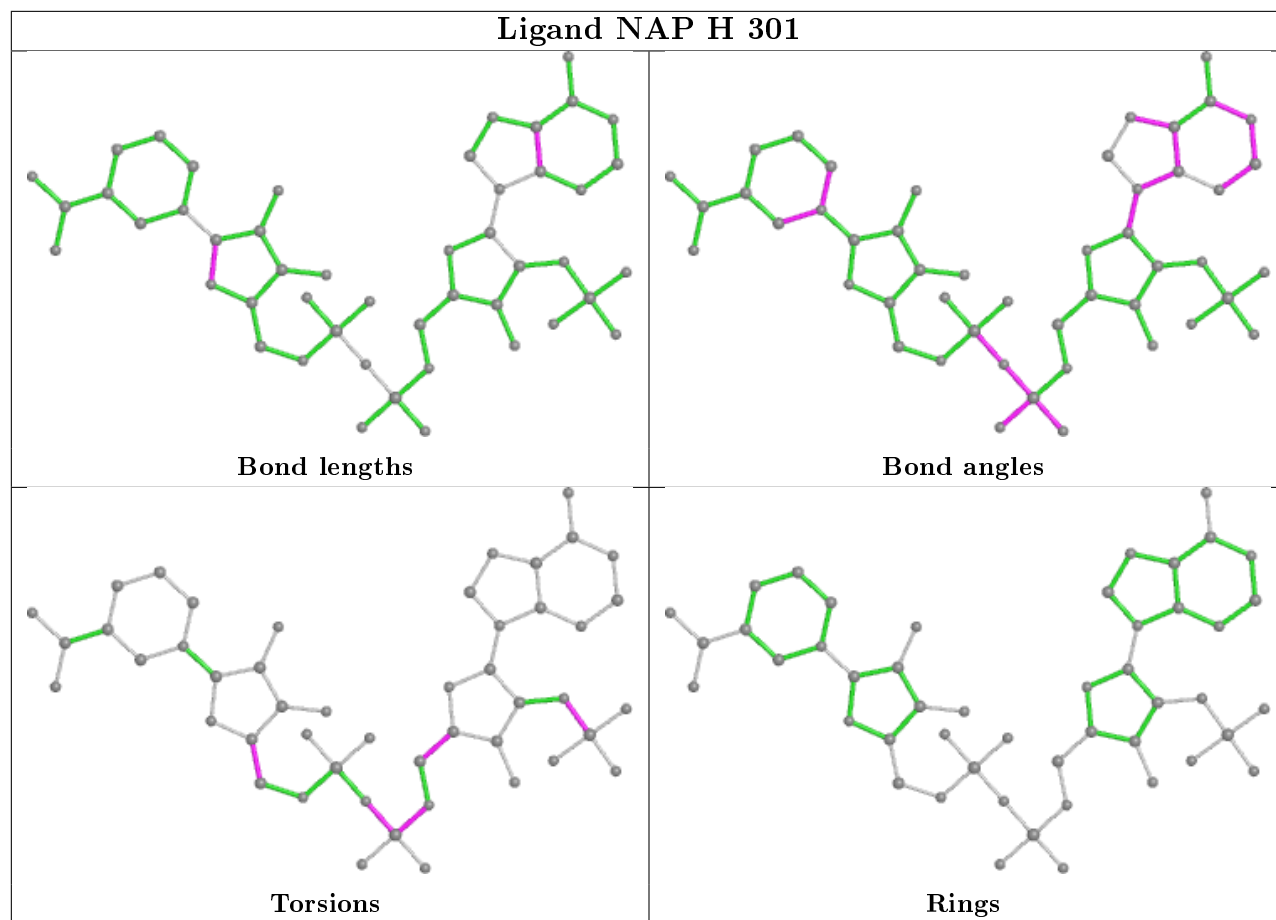


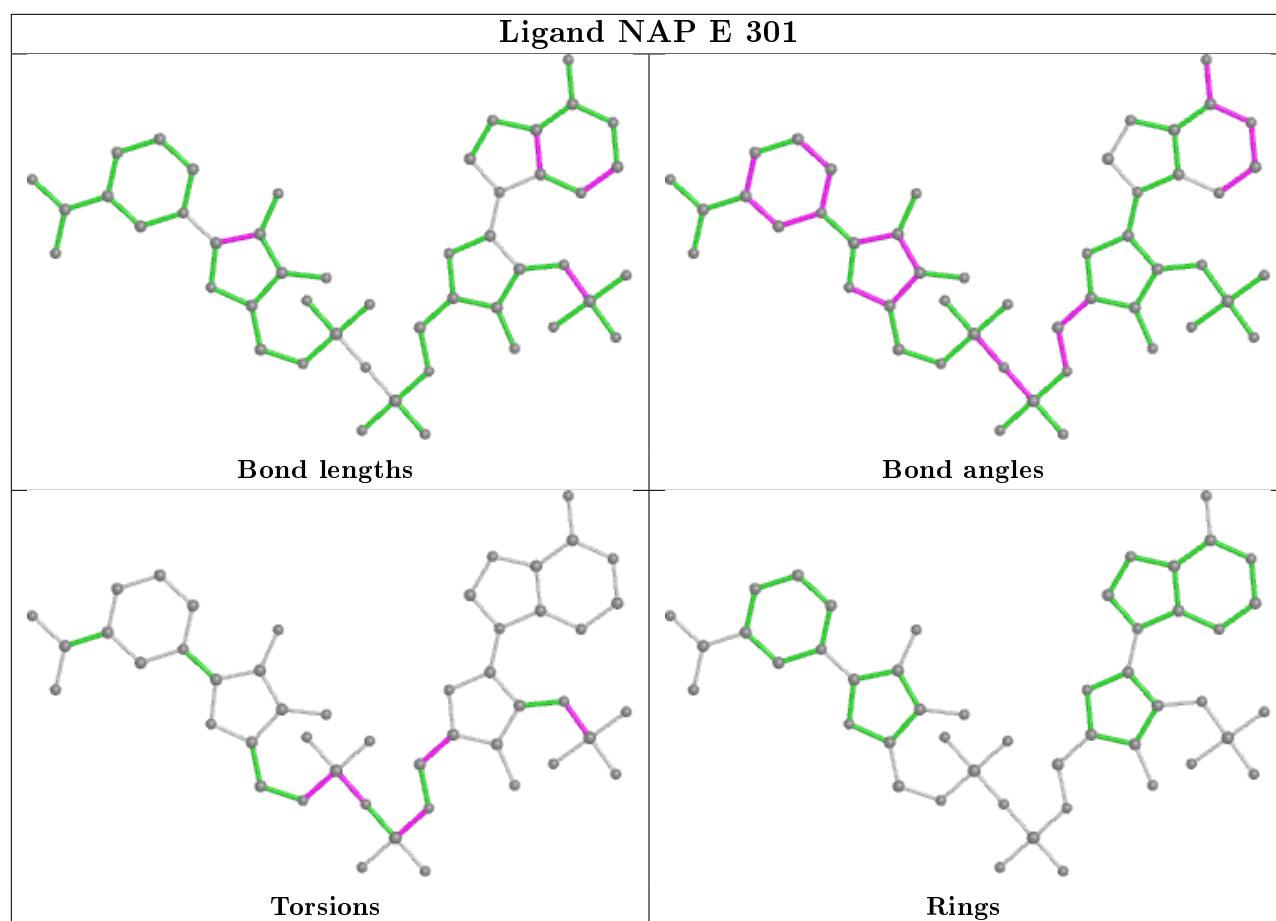












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å²)	Q<0.9	
1	A	249/262 (95%)	0.81	27 (10%)	5	3	25, 53, 104, 145	7 (2%)
1	B	249/262 (95%)	1.08	50 (20%)	1	0	34, 55, 101, 163	11 (4%)
1	C	249/262 (95%)	1.00	42 (16%)	1	1	31, 62, 108, 165	8 (3%)
1	D	249/262 (95%)	0.87	29 (11%)	4	2	31, 54, 98, 151	7 (2%)
1	E	249/262 (95%)	0.84	30 (12%)	4	2	28, 47, 105, 176	7 (2%)
1	F	249/262 (95%)	0.73	28 (11%)	5	3	25, 48, 99, 147	7 (2%)
1	G	249/262 (95%)	1.09	47 (18%)	1	1	25, 58, 109, 139	8 (3%)
1	H	249/262 (95%)	0.72	25 (10%)	7	4	29, 51, 99, 146	6 (2%)
All	All	1992/2096 (95%)	0.89	278 (13%)	2	1	25, 53, 105, 176	61 (3%)

All (278) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	191	GLN	9.9
1	G	193	SER	9.6
1	C	191	GLN	9.4
1	E	198	ALA	7.8
1	C	1	ALA	7.4
1	E	193	SER	6.6
1	E	184	ASP	6.3
1	G	198	ALA	6.2
1	H	191	GLN	6.1
1	H	198	ALA	6.1
1	G	197	GLU	6.1
1	D	198	ALA	6.1
1	A	193	SER	6.0
1	C	193	SER	5.8
1	B	198	ALA	5.7
1	A	194	THR	5.7

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Mol	Chain	Res	Type	RSRZ
1	B	202	ARG	5.3
1	F	192	VAL	5.3
1	G	208	ALA	5.3
1	F	193	SER	5.3
1	D	196	GLU	5.3
1	G	2	TYR	5.3
1	B	190	ASN	5.2
1	D	101	PRO	5.1
1	H	199	ASP	5.1
1	F	198	ALA	5.0
1	D	100	THR	4.9
1	A	191	GLN	4.8
1	C	172	SER	4.8
1	H	190	ASN	4.7
1	E	2	TYR	4.7
1	D	200	GLU	4.6
1	C	201	LEU	4.6
1	B	6	ASN	4.5
1	E	80	SER	4.5
1	D	203	ALA	4.4
1	H	196	GLU	4.4
1	D	194	THR	4.4
1	G	194	THR	4.4
1	A	198	ALA	4.3
1	A	202	ARG	4.3
1	C	41	LYS	4.3
1	C	198	ALA	4.3
1	C	195	GLN	4.3
1	F	190	ASN	4.3
1	B	195	GLN	4.2
1	B	188	ILE	4.2
1	C	45	GLN	4.1
1	A	204	LYS	4.0
1	A	200	GLU	4.0
1	B	193	SER	4.0
1	C	170	GLY	4.0
1	D	207	ALA	3.9
1	D	192	VAL	3.9
1	A	197	GLU	3.8
1	G	28	ALA	3.8
1	F	194	THR	3.8
1	C	188	ILE	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	28	ALA	3.8
1	B	187	ILE	3.7
1	E	84	LEU	3.7
1	E	79	GLY	3.7
1	D	184	ASP	3.7
1	B	59	ALA	3.7
1	F	201	LEU	3.7
1	D	195	GLN	3.7
1	B	197	GLU	3.7
1	E	197	GLU	3.6
1	H	90	ALA	3.6
1	B	124	PRO	3.6
1	B	40	ARG	3.6
1	G	195	GLN	3.6
1	C	2	TYR	3.5
1	H	194	THR	3.5
1	C	52	ARG	3.5
1	C	106	ARG	3.5
1	C	53	ASN	3.5
1	E	191	GLN	3.5
1	F	45	GLN	3.5
1	D	1	ALA	3.5
1	G	196	GLU	3.4
1	B	199	ASP	3.4
1	C	73	ILE	3.4
1	G	203	ALA	3.4
1	B	79	GLY	3.4
1	B	200	GLU	3.4
1	G	201	LEU	3.4
1	D	199	ASP	3.4
1	A	236	ALA	3.4
1	G	170	GLY	3.4
1	B	185	THR	3.4
1	A	201	LEU	3.3
1	H	193	SER	3.3
1	C	194	THR	3.3
1	D	52	ARG	3.3
1	B	41	LYS	3.3
1	D	99	ILE	3.3
1	F	196	GLU	3.3
1	G	206	ALA	3.3
1	B	60	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	105	ASP	3.3
1	E	189	GLU	3.2
1	A	100	THR	3.2
1	G	73	ILE	3.2
1	D	105	ASP	3.2
1	H	1	ALA	3.1
1	H	100	THR	3.1
1	F	2	TYR	3.1
1	C	197	GLU	3.1
1	D	51	GLY	3.1
1	B	72	ALA	3.1
1	B	189	GLU	3.1
1	G	83	VAL	3.1
1	E	201	LEU	3.1
1	B	49	GLU	3.0
1	A	89	GLY	3.0
1	B	85	PHE	3.0
1	E	199	ASP	3.0
1	C	44	GLU	3.0
1	F	5	LEU	3.0
1	H	192	VAL	3.0
1	C	65	GLU	3.0
1	B	101	PRO	3.0
1	H	203	ALA	3.0
1	E	212	GLY	3.0
1	F	202	ARG	2.9
1	C	40	ARG	2.9
1	E	192	VAL	2.9
1	D	205	PHE	2.9
1	G	1	ALA	2.9
1	A	195	GLN	2.8
1	F	200	GLU	2.8
1	H	52	ARG	2.8
1	F	191	GLN	2.8
1	A	196	GLU	2.8
1	D	102	GLU	2.8
1	F	49	GLU	2.8
1	G	91	ILE	2.8
1	B	2	TYR	2.8
1	G	20	LEU	2.8
1	B	45	GLN	2.8
1	H	244	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	48	ALA	2.8
1	B	208	ALA	2.8
1	C	115	LEU	2.7
1	G	86	ALA	2.7
1	E	204	LYS	2.7
1	C	102	GLU	2.7
1	D	186	PRO	2.7
1	B	203	ALA	2.7
1	B	244	GLY	2.7
1	H	28	ALA	2.7
1	B	113	ARG	2.7
1	A	64	LEU	2.7
1	F	199	ASP	2.7
1	G	106	ARG	2.7
1	A	102	GLU	2.7
1	A	118	THR	2.6
1	G	61	VAL	2.6
1	D	42	GLU	2.6
1	E	200	GLU	2.6
1	F	187	ILE	2.6
1	C	199	ASP	2.6
1	F	186	PRO	2.6
1	A	73	ILE	2.6
1	H	195	GLN	2.6
1	F	51	GLY	2.6
1	H	212	GLY	2.6
1	C	76	GLU	2.6
1	E	194	THR	2.6
1	B	42	GLU	2.6
1	F	197	GLU	2.6
1	F	41	LYS	2.6
1	G	71	TYR	2.5
1	F	48	ALA	2.5
1	B	170	GLY	2.5
1	C	203	ALA	2.5
1	G	54	VAL	2.5
1	C	184	ASP	2.5
1	A	189	GLU	2.5
1	A	203	ALA	2.5
1	E	48	ALA	2.5
1	C	208	ALA	2.5
1	E	40	ARG	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	202	ARG	2.5
1	G	45	GLN	2.5
1	E	188	ILE	2.5
1	F	195	GLN	2.5
1	C	200	GLU	2.5
1	A	212	GLY	2.5
1	G	212	GLY	2.5
1	D	208	ALA	2.4
1	G	72	ALA	2.4
1	B	80	SER	2.4
1	B	30	GLY	2.4
1	F	40	ARG	2.4
1	C	186	PRO	2.4
1	D	243	ASP	2.4
1	B	97	GLU	2.4
1	B	90	ALA	2.4
1	D	41	LYS	2.4
1	H	99	ILE	2.4
1	A	49	GLU	2.4
1	B	196	GLU	2.3
1	B	191	GLN	2.3
1	G	53	ASN	2.3
1	G	41	LYS	2.3
1	G	40	ARG	2.3
1	A	199	ASP	2.3
1	C	50	ILE	2.3
1	B	130	GLY	2.3
1	G	132	VAL	2.3
1	B	147	HIS	2.3
1	F	44	GLU	2.3
1	G	8	THR	2.3
1	D	193	SER	2.3
1	G	82	ASP	2.3
1	C	71	TYR	2.3
1	B	201	LEU	2.3
1	C	209	THR	2.2
1	G	209	THR	2.2
1	C	75	ARG	2.2
1	A	80	SER	2.2
1	B	133	ILE	2.2
1	H	200	GLU	2.2
1	B	75	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	74	VAL	2.2
1	G	200	GLU	2.2
1	B	43	LEU	2.2
1	B	135	THR	2.2
1	H	119	VAL	2.2
1	A	79	GLY	2.2
1	G	127	ARG	2.2
1	D	95	THR	2.2
1	C	127	ARG	2.2
1	E	41	LYS	2.2
1	F	37	GLY	2.2
1	C	70	LEU	2.2
1	G	60	ASP	2.2
1	A	41	LYS	2.2
1	G	44	GLU	2.2
1	D	104	TYR	2.2
1	G	199	ASP	2.1
1	G	204	LYS	2.1
1	H	42	GLU	2.1
1	E	170	GLY	2.1
1	E	234	TYR	2.1
1	E	1	ALA	2.1
1	B	5	LEU	2.1
1	G	42	GLU	2.1
1	G	88	SER	2.1
1	G	172	SER	2.1
1	H	184	ASP	2.1
1	B	65	GLU	2.1
1	H	133	ILE	2.1
1	F	88	SER	2.1
1	E	196	GLU	2.1
1	E	187	ILE	2.1
1	F	6	ASN	2.1
1	D	103	HIS	2.1
1	C	205	PHE	2.1
1	C	228	ALA	2.1
1	G	39	ARG	2.1
1	H	111	ASN	2.1
1	B	47	ALA	2.1
1	C	79	GLY	2.1
1	A	44	GLU	2.1
1	E	224	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	H	5	LEU	2.0
1	E	44	GLU	2.0
1	G	12	THR	2.0
1	D	63	LYS	2.0
1	F	97	GLU	2.0
1	E	34	PHE	2.0
1	G	128	ASP	2.0
1	G	236	ALA	2.0
1	B	192	VAL	2.0
1	C	62	THR	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 carbohydrates in this entry.

6.4 Ligands [i](#)

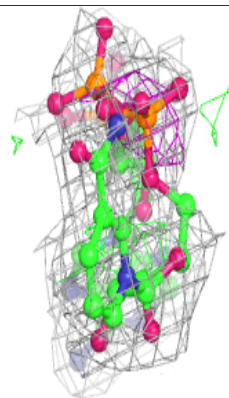
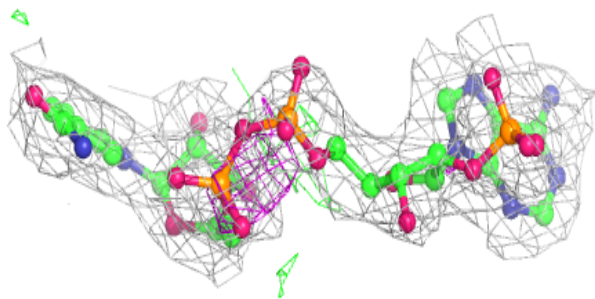
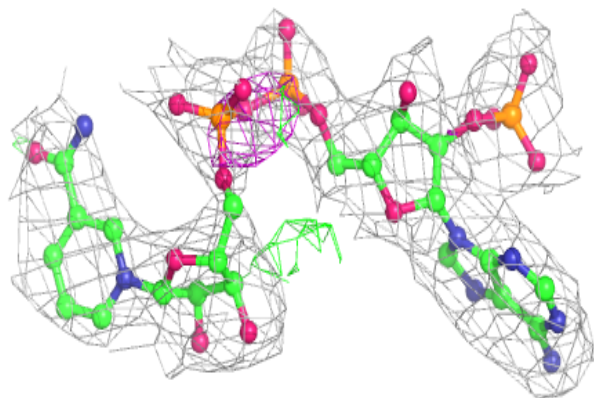
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	GOL	E	302	6/6	0.78	0.34	46,61,72,72	0
3	GOL	A	302	6/6	0.81	0.23	61,61,63,64	0
3	GOL	B	302	6/6	0.82	0.42	68,76,84,96	0
2	NAP	A	301	48/48	0.85	0.23	41,63,74,84	0
2	NAP	G	301	48/48	0.86	0.23	47,66,79,79	0
2	NAP	D	301	48/48	0.88	0.22	54,71,107,132	0
2	NAP	E	301	48/48	0.88	0.21	43,56,66,68	0
2	NAP	C	301	48/48	0.88	0.20	55,69,78,85	0
3	GOL	C	302	6/6	0.89	0.25	63,72,74,78	0
2	NAP	B	301	48/48	0.90	0.20	37,56,76,87	0
2	NAP	F	301	48/48	0.90	0.21	34,48,61,74	0
2	NAP	H	301	48/48	0.91	0.21	47,73,98,109	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.

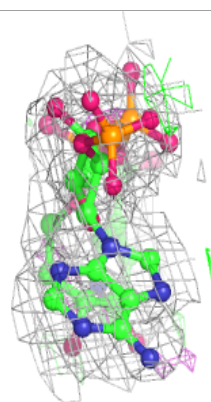
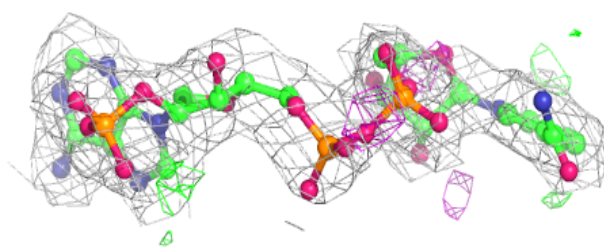
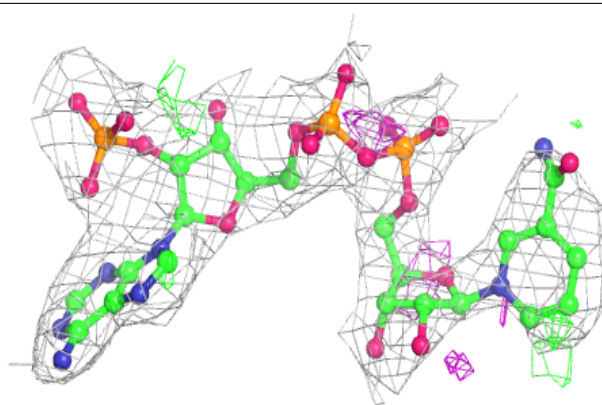
Electron density around NAP A 301:

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

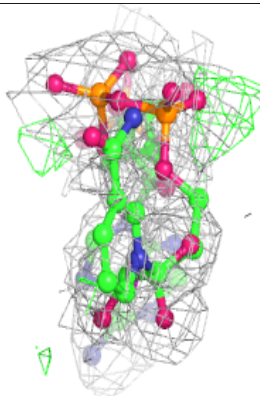
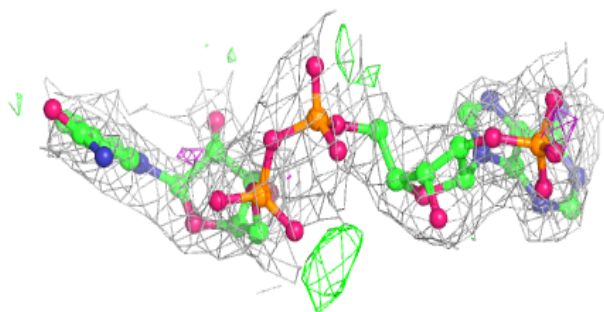
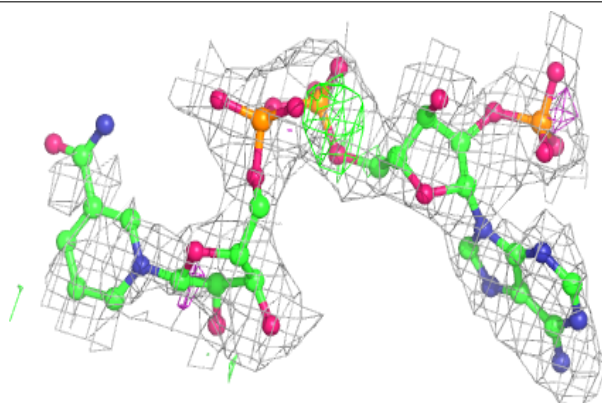


Electron density around NAP G 301:

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

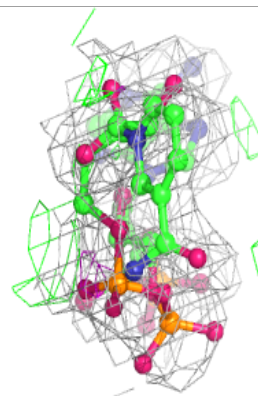
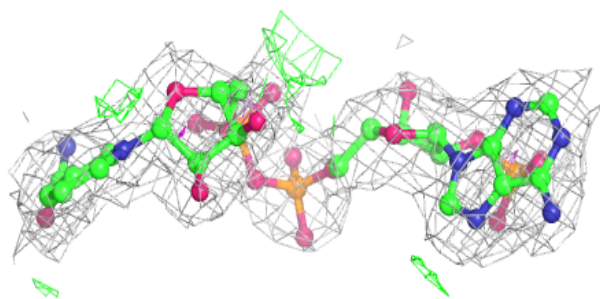
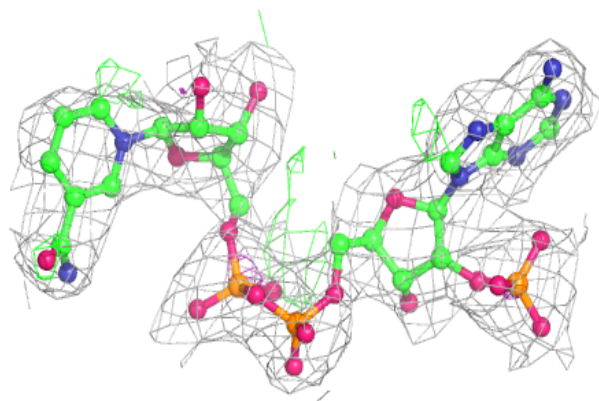
**Electron density around NAP D 301:**

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

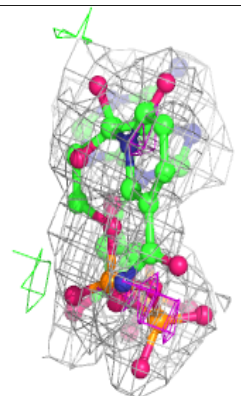
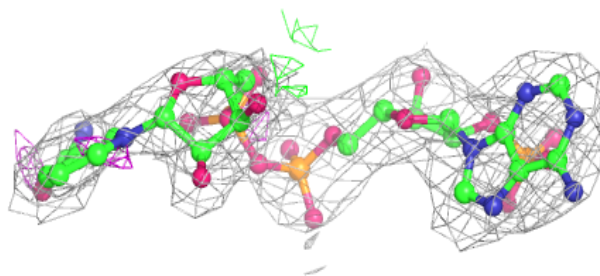
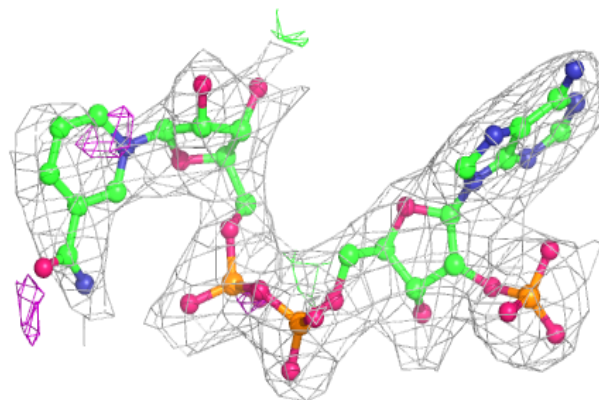


Electron density around NAP E 301:

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

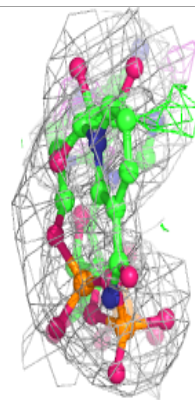
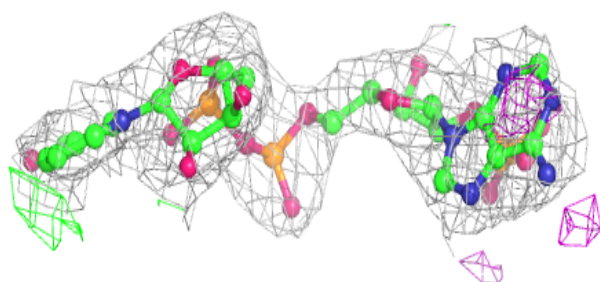
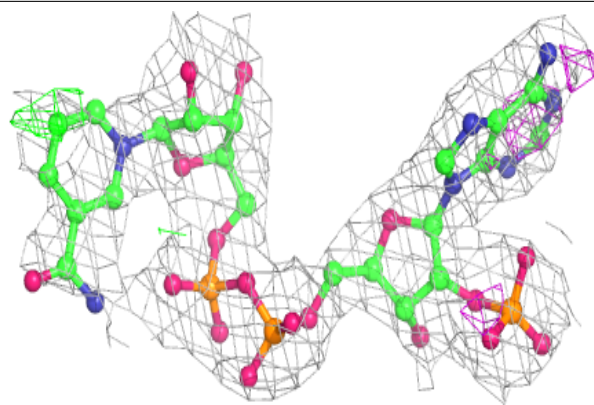
**Electron density around NAP C 301:**

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

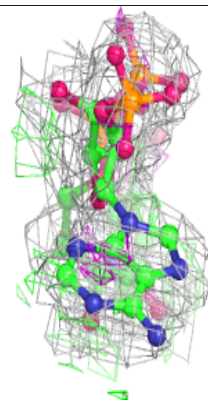
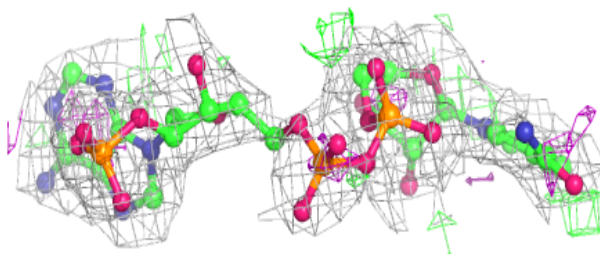
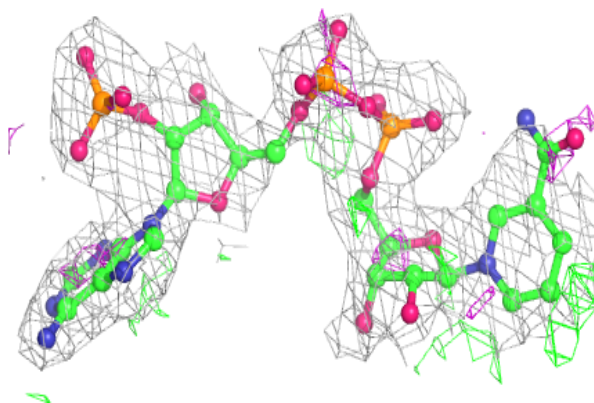


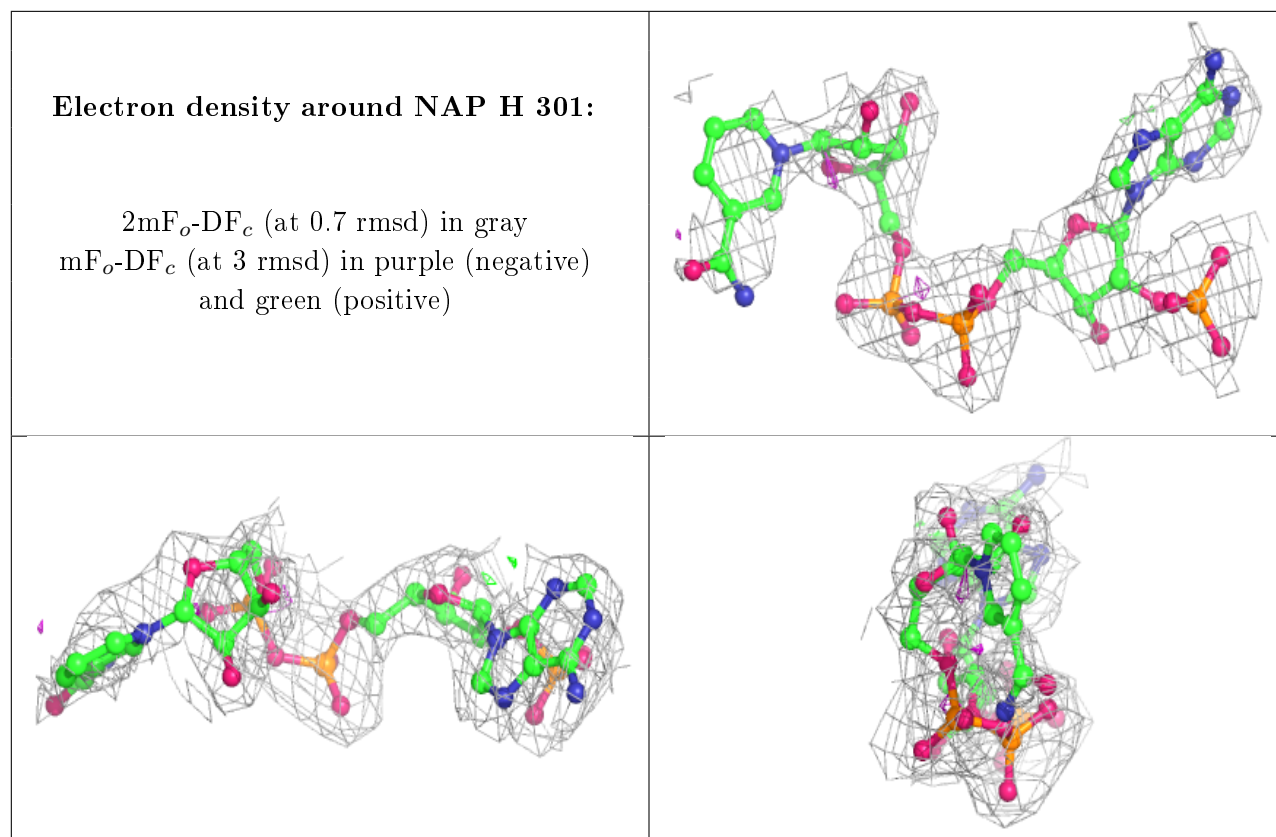
Electron density around NAP B 301:

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

**Electron density around NAP F 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.