wwPDB X-ray Structure Validation Summary Report (i)

May 30, 2020 – 03:35 am BST

PDB ID	:	4CLE
Title	:	Crystal structure of pteridine reductase 1 (PTR1) from Trypanosoma brucei in ternary complex with cofactor and inhibitor
Authors	:	Barrack, K.L.; Hunter, W.N.
Deposited on	:	2014-01-14
Resolution	:	1.80 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

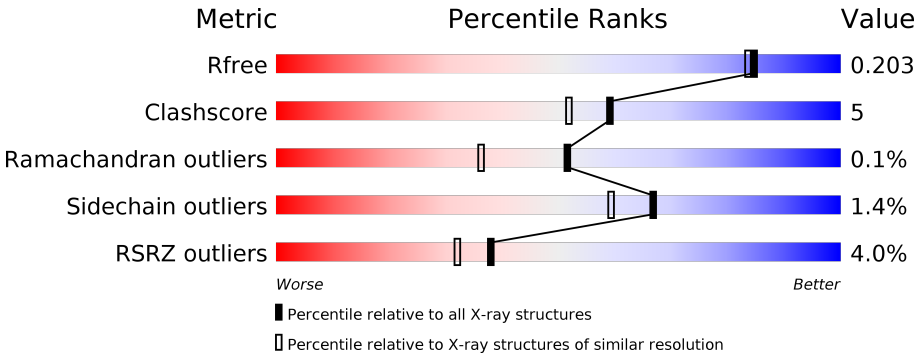
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 <=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	288	5% 77% 9% • 13%
1	B	288	3% 80% 7% 13%
1	C	288	5% 79% 8% 13%
1	D	288	% 78% 8% • 13%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	JR2	A	1271	-	-	X	-
3	JR2	D	1271	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8818 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 PTERIDINE REDUCTASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	7	0
			1921	1208	338	364	11			
1	B	250	Total	C	N	O	S	0	3	0
			1880	1181	330	358	11			
1	C	251	Total	C	N	O	S	0	6	0
			1909	1199	336	362	12			
1	D	250	Total	C	N	O	S	0	4	0
			1887	1184	333	358	12			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP O76290
A	-18	GLY	-	expression tag	UNP O76290
A	-17	SER	-	expression tag	UNP O76290
A	-16	SER	-	expression tag	UNP O76290
A	-15	HIS	-	expression tag	UNP O76290
A	-14	HIS	-	expression tag	UNP O76290
A	-13	HIS	-	expression tag	UNP O76290
A	-12	HIS	-	expression tag	UNP O76290
A	-11	HIS	-	expression tag	UNP O76290
A	-10	HIS	-	expression tag	UNP O76290
A	-9	SER	-	expression tag	UNP O76290
A	-8	SER	-	expression tag	UNP O76290
A	-7	GLY	-	expression tag	UNP O76290
A	-6	LEU	-	expression tag	UNP O76290
A	-5	VAL	-	expression tag	UNP O76290
A	-4	PRO	-	expression tag	UNP O76290
A	-3	ARG	-	expression tag	UNP O76290
A	-2	GLY	-	expression tag	UNP O76290
A	-1	SER	-	expression tag	UNP O76290
A	0	HIS	-	expression tag	UNP O76290
B	-19	MET	-	expression tag	UNP O76290

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP O76290
B	-17	SER	-	expression tag	UNP O76290
B	-16	SER	-	expression tag	UNP O76290
B	-15	HIS	-	expression tag	UNP O76290
B	-14	HIS	-	expression tag	UNP O76290
B	-13	HIS	-	expression tag	UNP O76290
B	-12	HIS	-	expression tag	UNP O76290
B	-11	HIS	-	expression tag	UNP O76290
B	-10	HIS	-	expression tag	UNP O76290
B	-9	SER	-	expression tag	UNP O76290
B	-8	SER	-	expression tag	UNP O76290
B	-7	GLY	-	expression tag	UNP O76290
B	-6	LEU	-	expression tag	UNP O76290
B	-5	VAL	-	expression tag	UNP O76290
B	-4	PRO	-	expression tag	UNP O76290
B	-3	ARG	-	expression tag	UNP O76290
B	-2	GLY	-	expression tag	UNP O76290
B	-1	SER	-	expression tag	UNP O76290
B	0	HIS	-	expression tag	UNP O76290
C	-19	MET	-	expression tag	UNP O76290
C	-18	GLY	-	expression tag	UNP O76290
C	-17	SER	-	expression tag	UNP O76290
C	-16	SER	-	expression tag	UNP O76290
C	-15	HIS	-	expression tag	UNP O76290
C	-14	HIS	-	expression tag	UNP O76290
C	-13	HIS	-	expression tag	UNP O76290
C	-12	HIS	-	expression tag	UNP O76290
C	-11	HIS	-	expression tag	UNP O76290
C	-10	HIS	-	expression tag	UNP O76290
C	-9	SER	-	expression tag	UNP O76290
C	-8	SER	-	expression tag	UNP O76290
C	-7	GLY	-	expression tag	UNP O76290
C	-6	LEU	-	expression tag	UNP O76290
C	-5	VAL	-	expression tag	UNP O76290
C	-4	PRO	-	expression tag	UNP O76290
C	-3	ARG	-	expression tag	UNP O76290
C	-2	GLY	-	expression tag	UNP O76290
C	-1	SER	-	expression tag	UNP O76290
C	0	HIS	-	expression tag	UNP O76290
D	-19	MET	-	expression tag	UNP O76290
D	-18	GLY	-	expression tag	UNP O76290
D	-17	SER	-	expression tag	UNP O76290

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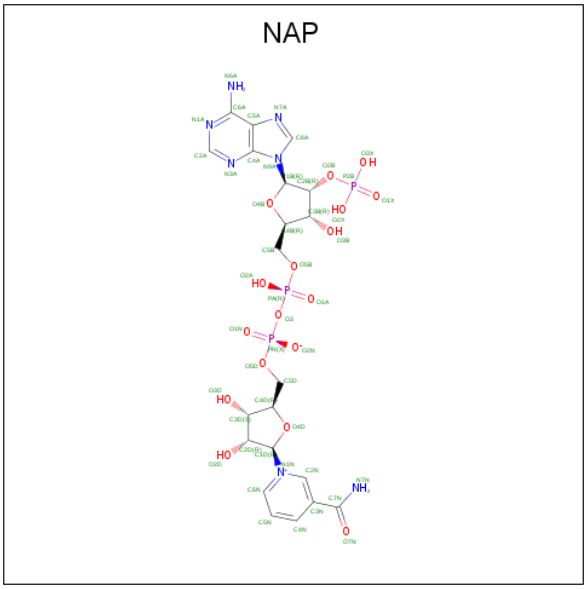
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP O76290
D	-15	HIS	-	expression tag	UNP O76290
D	-14	HIS	-	expression tag	UNP O76290
D	-13	HIS	-	expression tag	UNP O76290
D	-12	HIS	-	expression tag	UNP O76290
D	-11	HIS	-	expression tag	UNP O76290
D	-10	HIS	-	expression tag	UNP O76290
D	-9	SER	-	expression tag	UNP O76290
D	-8	SER	-	expression tag	UNP O76290
D	-7	GLY	-	expression tag	UNP O76290
D	-6	LEU	-	expression tag	UNP O76290
D	-5	VAL	-	expression tag	UNP O76290
D	-4	PRO	-	expression tag	UNP O76290
D	-3	ARG	-	expression tag	UNP O76290
D	-2	GLY	-	expression tag	UNP O76290
D	-1	SER	-	expression tag	UNP O76290
D	0	HIS	-	expression tag	UNP O76290

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



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

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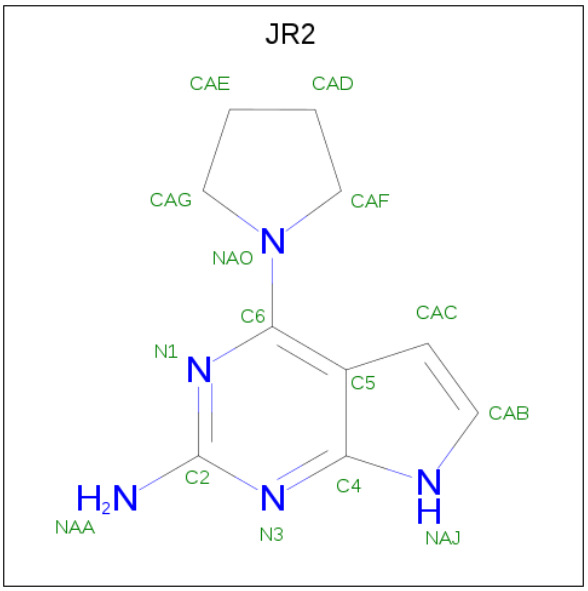
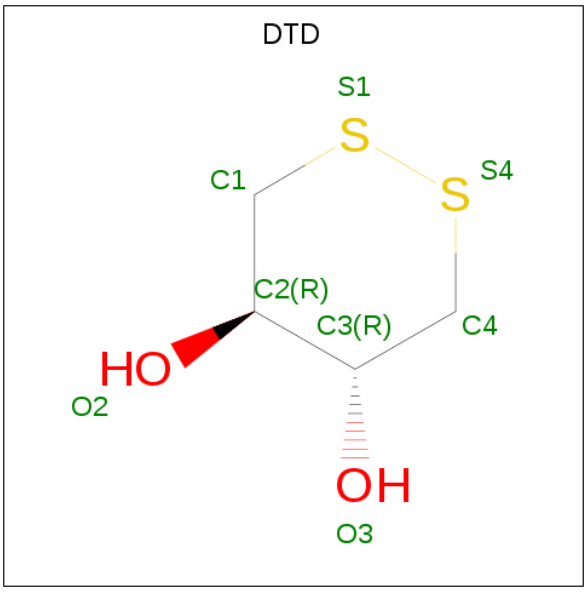
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C N O P 48 21 7 17 3	0	0
2	D	1	Total C N O P 48 21 7 17 3	0	0

- Molecule 3 is 4-(pyrrolidin-1-yl)-7H-pyrrolo[2,3-d]pyrimidin-2-amine (three-letter code: JR2) (formula: $C_{10}H_{13}N_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 15 10 5	0	0
3	A	1	Total C N 15 10 5	0	0
3	B	1	Total C N 15 10 5	0	0
3	C	1	Total C N 15 10 5	0	0
3	D	1	Total C N 15 10 5	0	0
3	D	1	Total C N 15 10 5	0	0

- Molecule 4 is DITHIANE DIOL (three-letter code: DTD) (formula: $C_4H_8O_2S_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O S 8 4 2 2	0	0
4	C	1	Total C O S 8 4 2 2	0	0

- Molecule 5 is water.

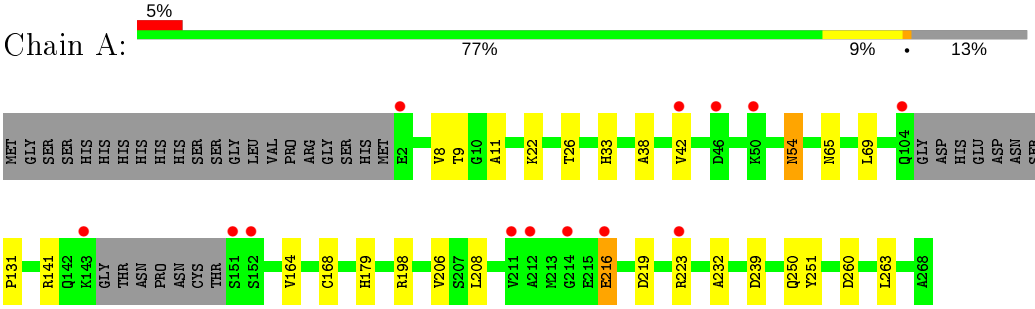
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	267	Total O 267 267	0	0
5	B	236	Total O 236 236	0	0
5	C	216	Total O 216 216	0	0
5	D	204	Total O 204 204	0	0

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.

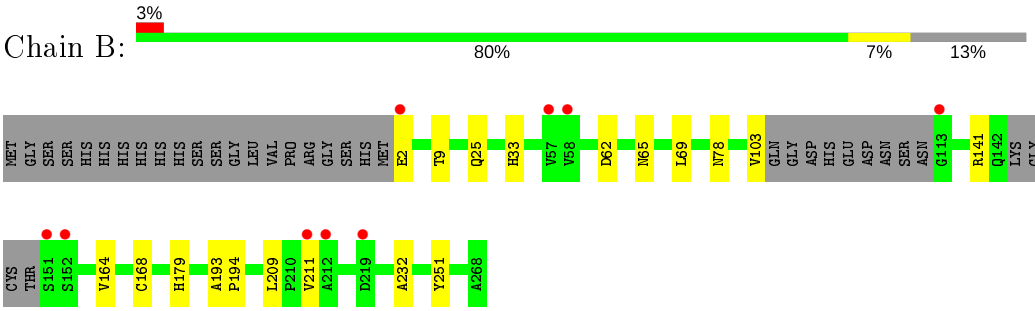
- Molecule 1: PTERIDINE REDUCTASE 1

Chain A:



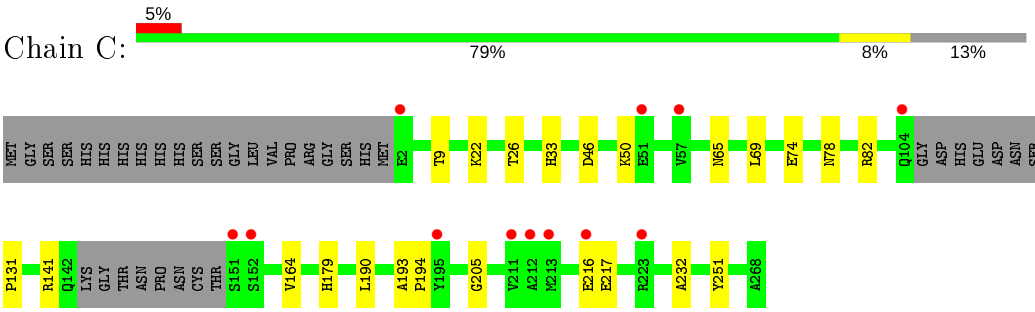
- Molecule 1: PTERIDINE REDUCTASE 1

Chain B:



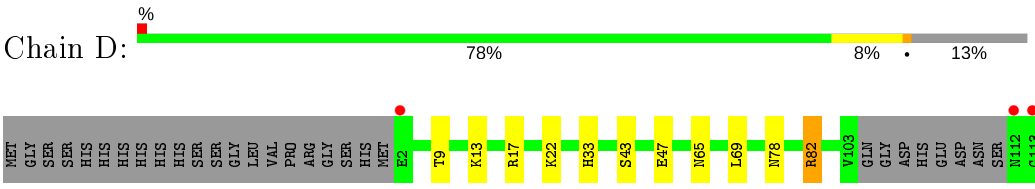
- Molecule 1: PTERIDINE REDUCTASE 1

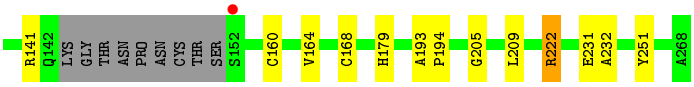
Chain C:



- Molecule 1: PTERIDINE REDUCTASE 1

Chain D:




R141
Q142
LYS
GLY
THR
ASN
PRO
ASN
CYS
THR
SER
S152
C160
V164
C168
H179
A193
P194
G205
L209
R222
E231
A232
Y251
A268

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	74.10Å 88.49Å 84.24Å 90.00° 115.25° 90.00°	Depositor
Resolution (Å)	38.26 – 1.80 23.32 – 1.80	Depositor EDS
% Data completeness (in resolution range)	96.0 (38.26-1.80) 96.1 (23.32-1.80)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.09 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.152 , 0.193 0.165 , 0.203	Depositor DCC
R_{free} test set	4422 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	20.2	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 47.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	8818	wwPDB-VP
Average B, all atoms (Å^2)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.30% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NAP, JR2, DTD

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	0.65	0/1951	0.78	2/2646 (0.1%)
1	B	0.69	0/1910	0.78	1/2591 (0.0%)
1	C	0.68	0/1942	0.76	0/2632
1	D	0.65	0/1920	0.81	5/2604 (0.2%)
All	All	0.67	0/7723	0.78	8/10473 (0.1%)

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	82	ARG	NE-CZ-NH2	-9.58	115.51	120.30
1	D	82	ARG	NE-CZ-NH1	8.30	124.45	120.30
1	D	222	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	A	198	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	A	260	ASP	CB-CG-OD1	6.10	123.79	118.30

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	1921	0	1952	18	0
1	B	1880	0	1902	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1909	0	1937	15	1
1	D	1887	0	1909	20	1
2	A	48	0	25	0	0
2	B	48	0	25	0	0
2	C	48	0	25	1	0
2	D	48	0	25	0	0
3	A	30	0	26	8	0
3	B	15	0	13	0	0
3	C	15	0	13	0	0
3	D	30	0	26	9	0
4	B	8	0	8	2	0
4	C	8	0	8	0	0
5	A	267	0	0	2	1
5	B	236	0	0	4	1
5	C	216	0	0	0	0
5	D	204	0	0	6	0
All	All	8818	0	7894	74	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 5.

The worst 5 of 74 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)
3:A:1271:JR2:HAC	5:A:2196:HOH:O	1.71	0.91
1:D:222:ARG:HD2	5:D:2173:HOH:O	1.70	0.91
1:D:78[A]:ASN:OD1	1:D:141:ARG:NH1	2.04	0.90
1:A:206[B]:VAL:HG23	3:A:1271:JR2:HAG	1.66	0.74
3:D:1271:JR2:HAC	3:D:1271:JR2:CAG	2.20	0.72

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)
5:A:2012:HOH:O	5:B:2196:HOH:O[2_555]	2.09	0.11
1:C:216:GLU:OE1	1:D:47:GLU:OE2[2_646]	2.19	0.01

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	253/288 (88%)	245 (97%)	7 (3%)	1 (0%)	34 21
1	B	247/288 (86%)	238 (96%)	9 (4%)	0	100 100
1	C	251/288 (87%)	241 (96%)	10 (4%)	0	100 100
1	D	248/288 (86%)	241 (97%)	7 (3%)	0	100 100
All	All	999/1152 (87%)	965 (97%)	33 (3%)	1 (0%)	51 36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	LEU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	206/231 (89%)	201 (98%)	5 (2%)	49 36
1	B	201/231 (87%)	199 (99%)	2 (1%)	76 71
1	C	205/231 (89%)	202 (98%)	3 (2%)	65 56
1	D	202/231 (87%)	201 (100%)	1 (0%)	88 87
All	All	814/924 (88%)	803 (99%)	11 (1%)	67 59

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	250	GLN
1	B	2	GLU
1	C	74	GLU
1	A	216	GLU
1	C	22	LYS

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

Mol	Chain	Res	Type
1	B	179	HIS
1	C	36	ASN
1	C	179	HIS
1	D	179	HIS

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	JR2	D	1270	-	15,17,17	0.79	0	16,24,24	2.07	3 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	JR2	B	1270	-	15,17,17	0.93	1 (6%)	16,24,24	2.18	3 (18%)
4	DTD	B	1271	-	6,8,8	0.75	0	6,10,10	1.59	1 (16%)
2	NAP	C	1269	-	45,52,52	0.78	1 (2%)	56,80,80	1.11	5 (8%)
3	JR2	A	1271	-	15,17,17	1.24	1 (6%)	16,24,24	2.18	6 (37%)
3	JR2	A	1270	-	15,17,17	1.11	1 (6%)	16,24,24	1.81	4 (25%)
3	JR2	D	1271	-	15,17,17	1.21	2 (13%)	16,24,24	1.95	4 (25%)
2	NAP	D	1269	-	45,52,52	0.97	2 (4%)	56,80,80	1.30	6 (10%)
4	DTD	C	1271	-	6,8,8	0.68	0	6,10,10	2.69	3 (50%)
2	NAP	B	1269	-	45,52,52	1.10	3 (6%)	56,80,80	1.09	4 (7%)
2	NAP	A	1269	-	45,52,52	1.03	1 (2%)	56,80,80	1.28	5 (8%)
3	JR2	C	1270	-	15,17,17	1.16	1 (6%)	16,24,24	1.67	3 (18%)

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	JR2	D	1270	-	-	0/4/11/11	0/3/3/3
3	JR2	B	1270	-	-	0/4/11/11	0/3/3/3
4	DTD	B	1271	-	-	-	0/0/1/1
2	NAP	C	1269	-	-	2/31/67/67	0/5/5/5
3	JR2	A	1271	-	-	0/4/11/11	0/3/3/3
3	JR2	A	1270	-	-	0/4/11/11	0/3/3/3
3	JR2	D	1271	-	-	0/4/11/11	0/3/3/3
2	NAP	D	1269	-	-	2/31/67/67	0/5/5/5
4	DTD	C	1271	-	-	-	0/0/1/1
2	NAP	B	1269	-	-	1/31/67/67	0/5/5/5
2	NAP	A	1269	-	-	3/31/67/67	0/5/5/5
3	JR2	C	1270	-	-	0/4/11/11	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1269	NAP	P2B-O2B	3.76	1.66	1.59
3	A	1271	JR2	C6-N1	3.73	1.37	1.32
2	B	1269	NAP	P2B-O2B	3.22	1.65	1.59
2	B	1269	NAP	C3N-C7N	3.15	1.55	1.50
2	D	1269	NAP	P2B-O2B	3.07	1.65	1.59

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	1271	JR2	N3-C2-N1	-5.41	120.00	127.22
3	D	1270	JR2	C2-N3-C4	5.26	121.37	115.36
3	B	1270	JR2	C2-N3-C4	5.18	121.28	115.36
3	B	1270	JR2	N3-C2-N1	-4.83	120.78	127.22
3	A	1271	JR2	N3-C2-N1	-4.67	120.99	127.22

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1269	NAP	C5B-O5B-PA-O1A
2	D	1269	NAP	C5B-O5B-PA-O1A
2	A	1269	NAP	C5B-O5B-PA-O1A
2	A	1269	NAP	C5B-O5B-PA-O3
2	B	1269	NAP	C3B-C2B-O2B-P2B

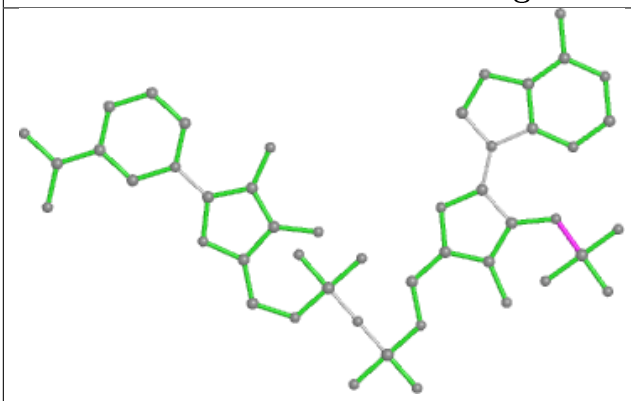
There are no ring outliers.

6 monomers are involved in 20 short contacts:

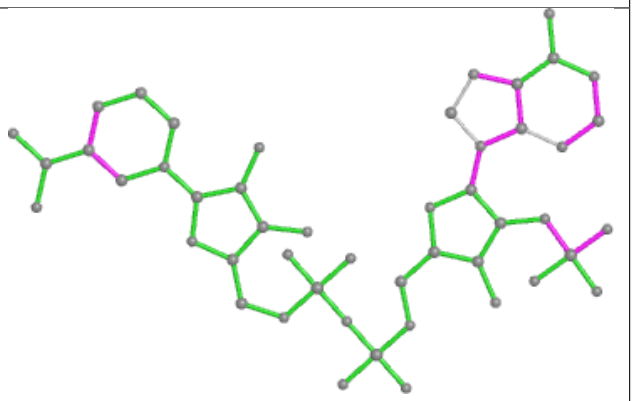
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1270	JR2	3	0
4	B	1271	DTD	2	0
2	C	1269	NAP	1	0
3	A	1271	JR2	7	0
3	A	1270	JR2	1	0
3	D	1271	JR2	7	0

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 then 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.

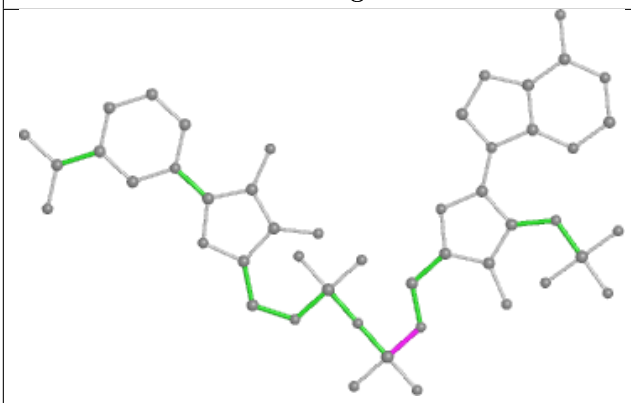
Ligand NAP C 1269



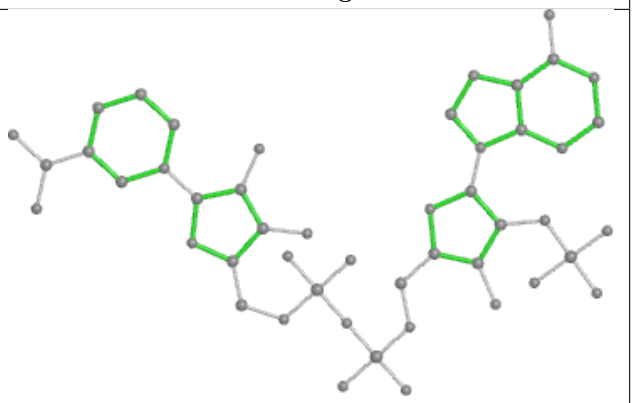
Bond lengths



Bond angles

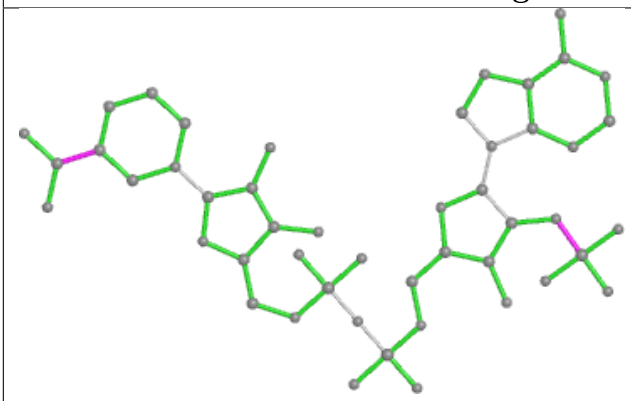


Torsions

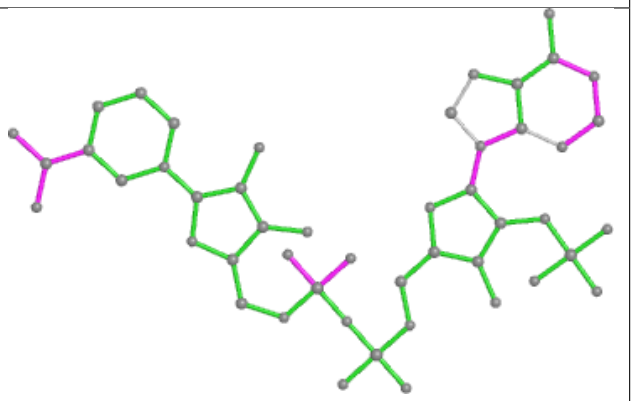


Rings

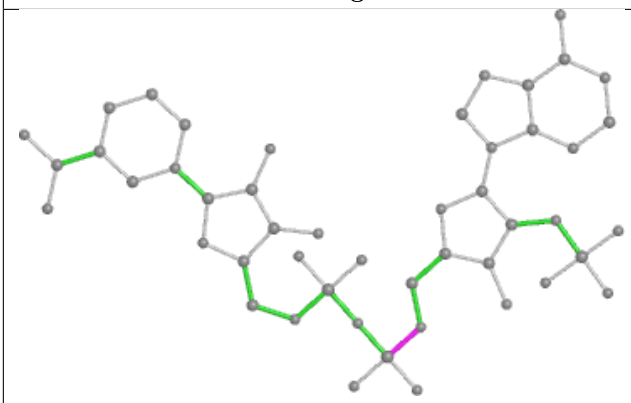
Ligand NAP D 1269



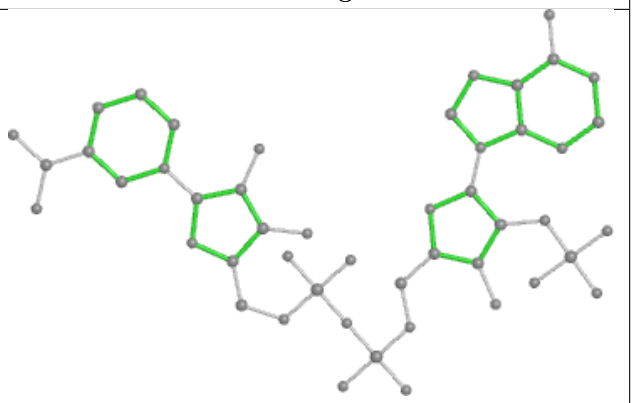
Bond lengths



Bond angles

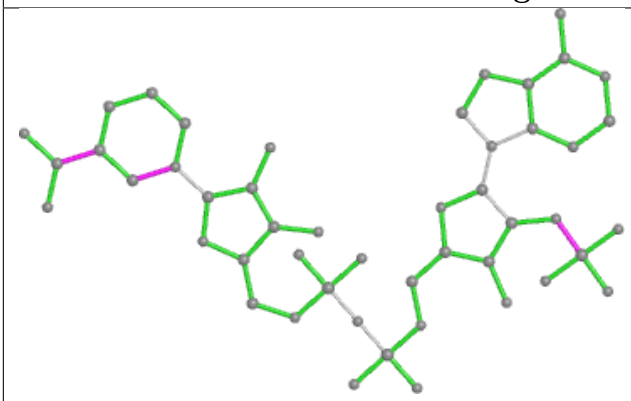


Torsions

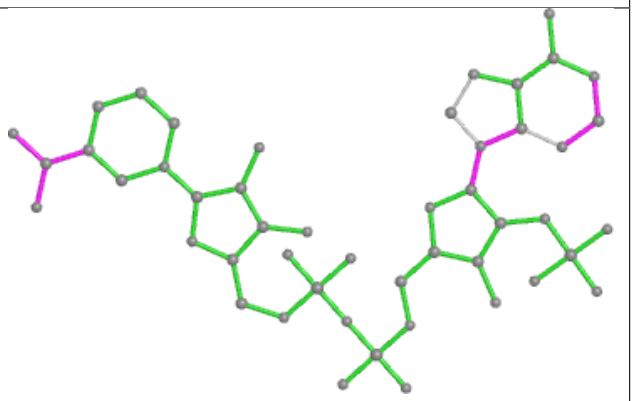


Rings

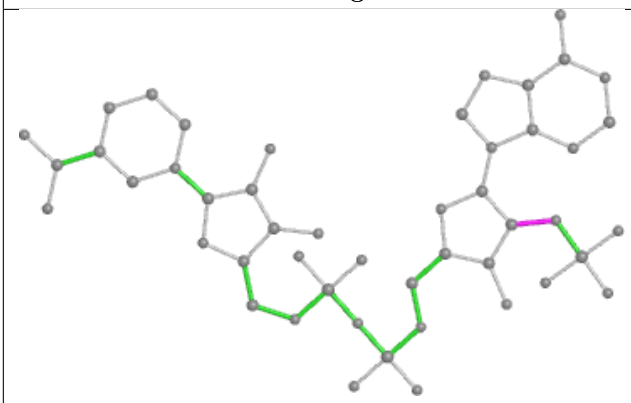
Ligand NAP B 1269



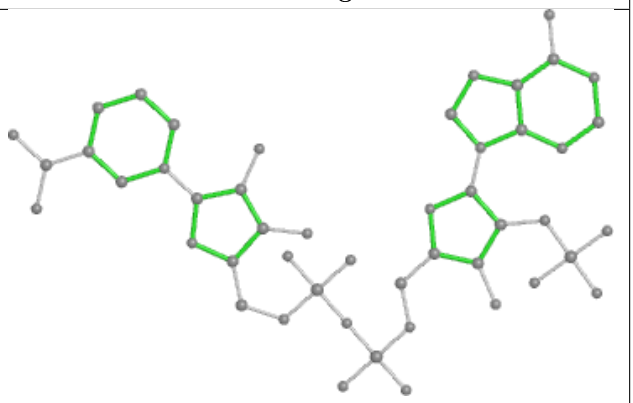
Bond lengths



Bond angles

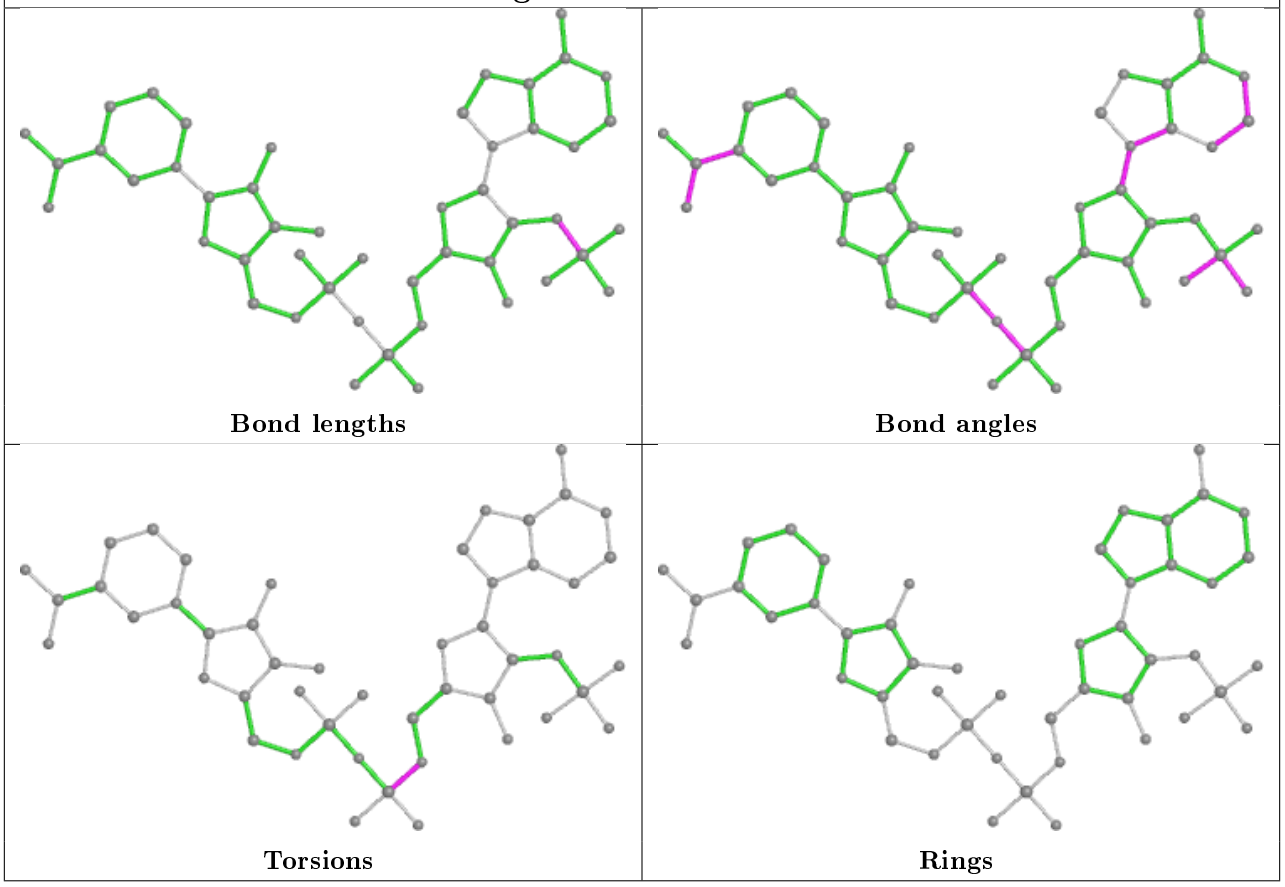


Torsions



Rings

Ligand NAP A 1269



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	252/288 (87%)	-0.03	14 (5%)	24	19	12, 19, 40, 62	0
1	B	250/288 (86%)	-0.11	9 (3%)	42	37	12, 18, 33, 48	0
1	C	251/288 (87%)	-0.08	13 (5%)	27	22	11, 17, 39, 66	0
1	D	250/288 (86%)	-0.14	4 (1%)	72	68	11, 18, 33, 71	0
All	All	1003/1152 (87%)	-0.09	40 (3%)	38	32	11, 18, 37, 71	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	113	GLY	9.6
1	D	112	ASN	6.4
1	B	113	GLY	5.8
1	A	151	SER	5.6
1	C	212	ALA	5.6

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

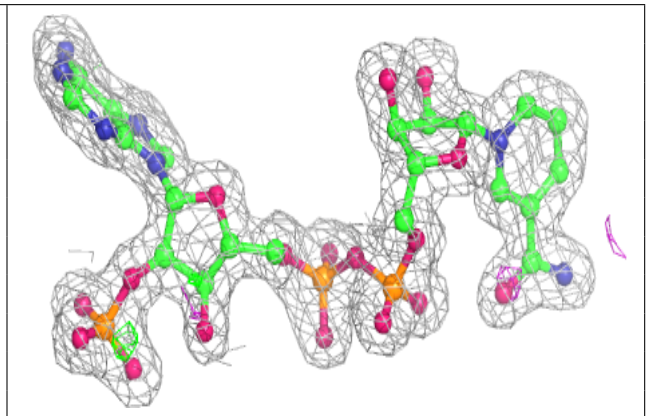
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

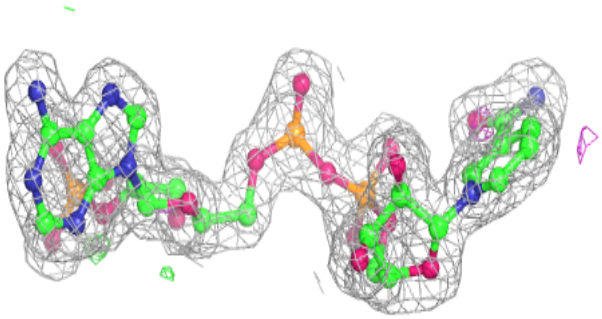
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	JR2	D	1271	15/15	0.63	0.22	37,42,48,50	0
3	JR2	A	1271	15/15	0.73	0.19	39,48,54,58	0
4	DTD	B	1271	8/8	0.78	0.14	55,59,61,71	0
4	DTD	C	1271	8/8	0.83	0.13	41,48,50,53	0
3	JR2	A	1270	15/15	0.94	0.08	14,17,22,22	0
3	JR2	D	1270	15/15	0.95	0.08	14,15,24,26	0
3	JR2	B	1270	15/15	0.96	0.08	13,15,18,19	0
2	NAP	D	1269	48/48	0.97	0.08	12,15,21,25	0
2	NAP	B	1269	48/48	0.97	0.08	12,15,18,19	0
2	NAP	A	1269	48/48	0.97	0.07	12,16,23,28	0
3	JR2	C	1270	15/15	0.97	0.07	15,17,23,24	0
2	NAP	C	1269	48/48	0.98	0.07	11,15,18,20	0

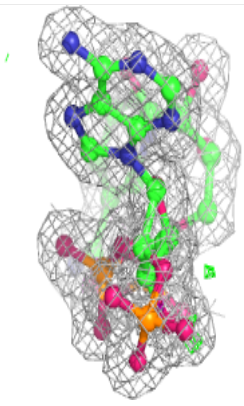
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP D 1269:

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

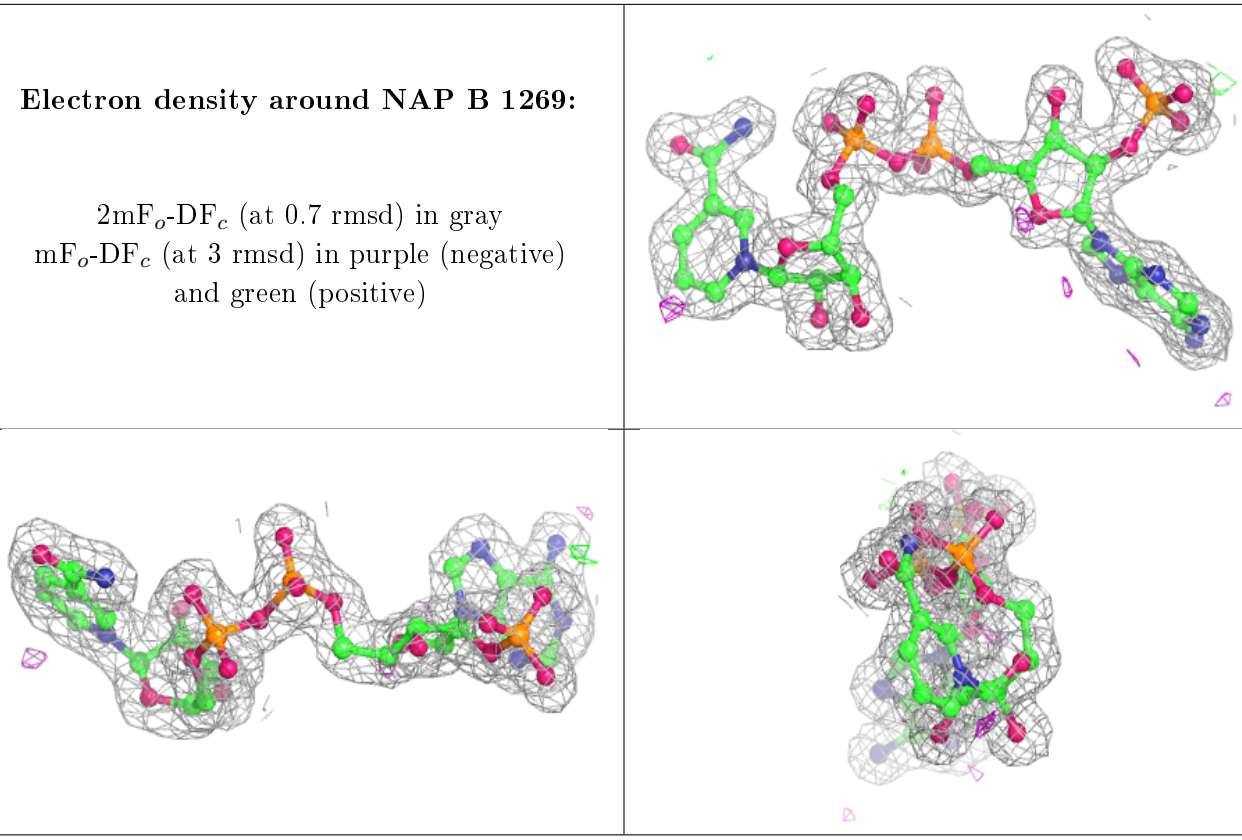






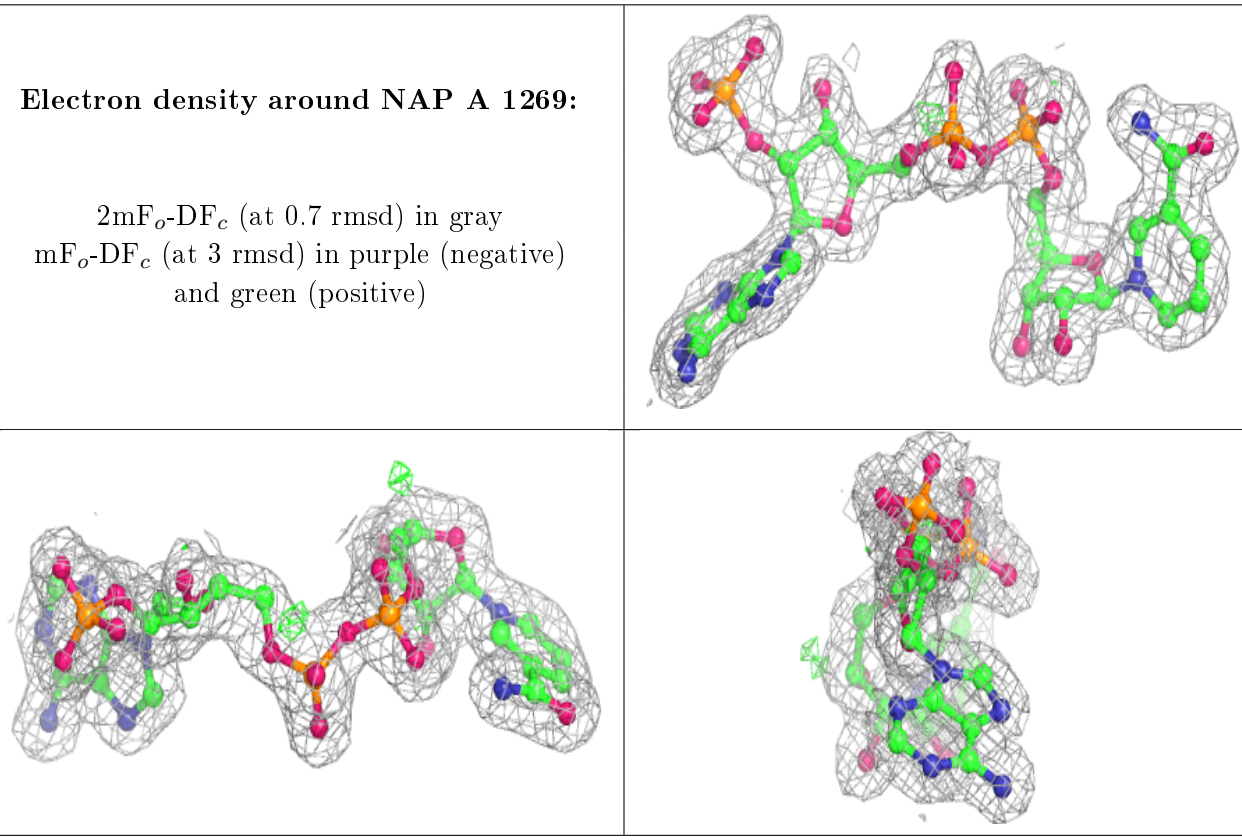
Electron density around NAP B 1269:

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



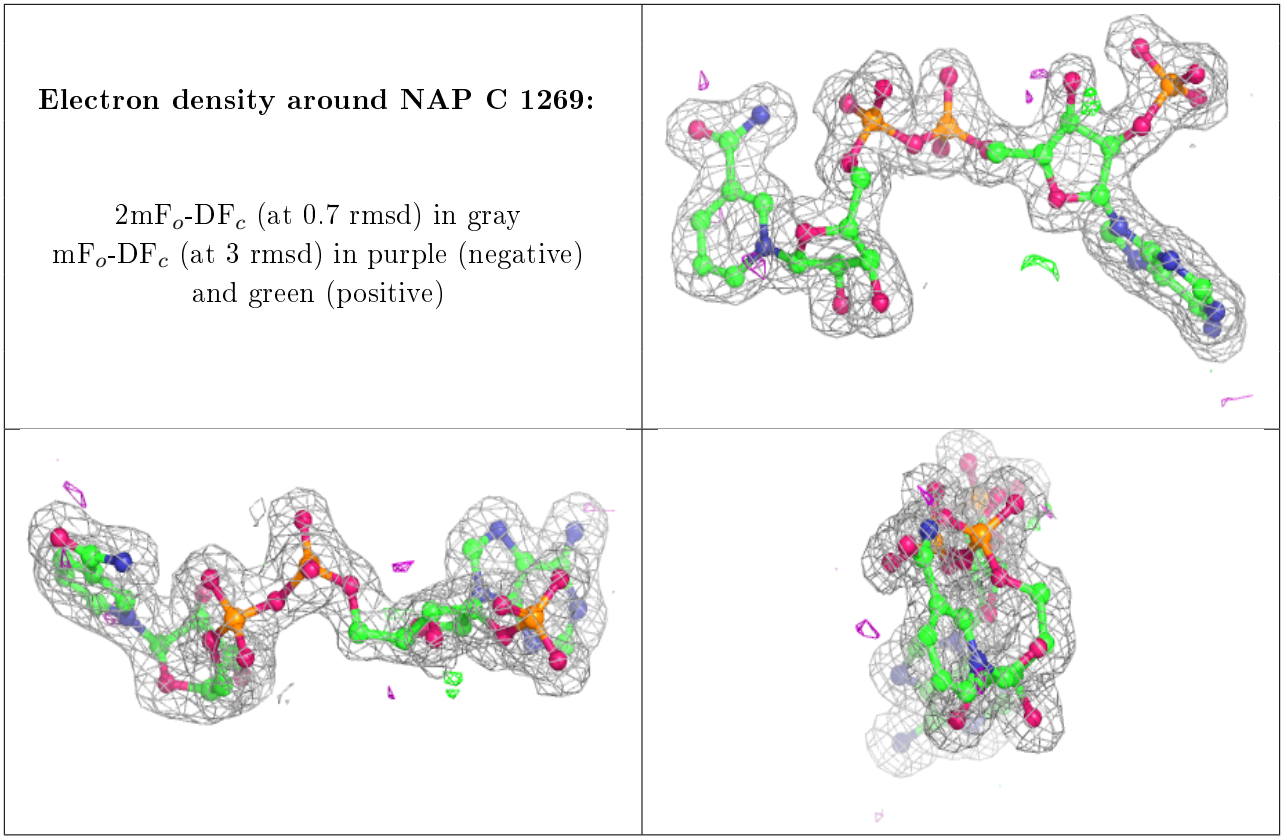
Electron density around NAP A 1269:

$2mF_o$-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 1269:

$2mF_o$-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.