



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 07:49 am BST

PDB ID : 3JQ6
Title : Crystal structure of pteridine reductase 1 (PTR1) from Trypanosoma brucei in ternary complex with cofactor (NADP+) and inhibitor 6,7-bis(1-methylethyl)pteridine-2,4-diamine (DX1)
Authors : Tulloch, L.B.; Hunter, W.N.
Deposited on : 2009-09-06
Resolution : 1.80 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

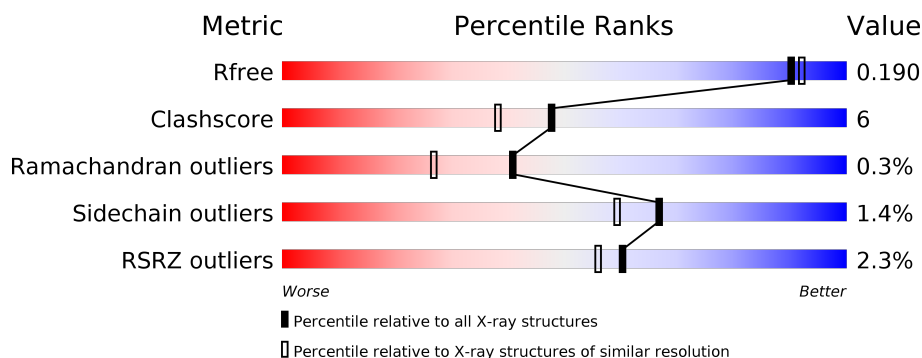
1 Overall quality at a glance

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 $\leq 5\%$. 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	288	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>8%</div> <div>14%</div> </div> </div>
1	B	288	<div> <div>3%</div> <div> <div></div> <div>76%</div> <div>9%</div> <div>14%</div> </div> </div>
1	C	288	<div> <div>0%</div> <div> <div></div> <div>77%</div> <div>9%</div> <div>14%</div> </div> </div>
1	D	288	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>8%</div> <div>14%</div> </div> </div>

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	DX1	A	270	-	-	X	-
4	DTT	A	271	X	-	-	-
4	DTT	B	271	X	-	-	-
4	DTT	C	271	X	-	-	-
4	DTT	D	271	X	-	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9046 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	249	Total	C	N	O	S	0	24	0
			1994	1258	346	377	13			
1	B	247	Total	C	N	O	S	0	18	0
			1924	1212	332	369	11			
1	C	248	Total	C	N	O	S	0	15	0
			1890	1195	331	352	12			
1	D	249	Total	C	N	O	S	0	18	0
			1919	1216	331	360	12			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q581W1
A	-18	GLY	-	EXPRESSION TAG	UNP Q581W1
A	-17	SER	-	EXPRESSION TAG	UNP Q581W1
A	-16	SER	-	EXPRESSION TAG	UNP Q581W1
A	-15	HIS	-	EXPRESSION TAG	UNP Q581W1
A	-14	HIS	-	EXPRESSION TAG	UNP Q581W1
A	-13	HIS	-	EXPRESSION TAG	UNP Q581W1
A	-12	HIS	-	EXPRESSION TAG	UNP Q581W1
A	-11	HIS	-	EXPRESSION TAG	UNP Q581W1
A	-10	HIS	-	EXPRESSION TAG	UNP Q581W1
A	-9	SER	-	EXPRESSION TAG	UNP Q581W1
A	-8	SER	-	EXPRESSION TAG	UNP Q581W1
A	-7	GLY	-	EXPRESSION TAG	UNP Q581W1
A	-6	LEU	-	EXPRESSION TAG	UNP Q581W1
A	-5	VAL	-	EXPRESSION TAG	UNP Q581W1
A	-4	PRO	-	EXPRESSION TAG	UNP Q581W1
A	-3	ARG	-	EXPRESSION TAG	UNP Q581W1
A	-2	GLY	-	EXPRESSION TAG	UNP Q581W1
A	-1	SER	-	EXPRESSION TAG	UNP Q581W1
A	0	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-19	MET	-	EXPRESSION TAG	UNP Q581W1

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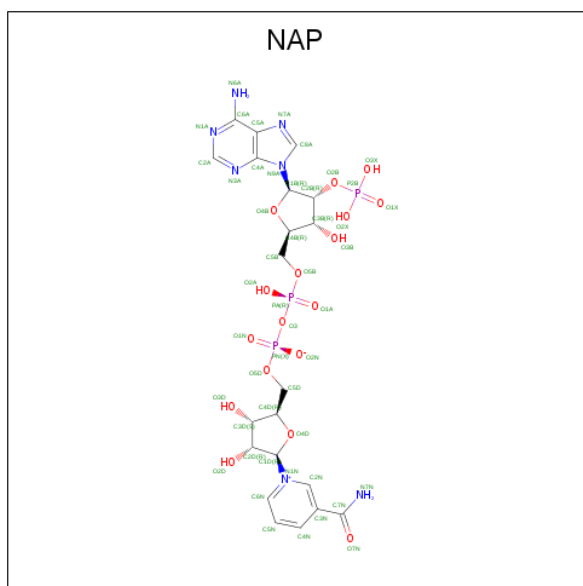
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q581W1
B	-17	SER	-	EXPRESSION TAG	UNP Q581W1
B	-16	SER	-	EXPRESSION TAG	UNP Q581W1
B	-15	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-14	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-13	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-12	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-11	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-10	HIS	-	EXPRESSION TAG	UNP Q581W1
B	-9	SER	-	EXPRESSION TAG	UNP Q581W1
B	-8	SER	-	EXPRESSION TAG	UNP Q581W1
B	-7	GLY	-	EXPRESSION TAG	UNP Q581W1
B	-6	LEU	-	EXPRESSION TAG	UNP Q581W1
B	-5	VAL	-	EXPRESSION TAG	UNP Q581W1
B	-4	PRO	-	EXPRESSION TAG	UNP Q581W1
B	-3	ARG	-	EXPRESSION TAG	UNP Q581W1
B	-2	GLY	-	EXPRESSION TAG	UNP Q581W1
B	-1	SER	-	EXPRESSION TAG	UNP Q581W1
B	0	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-19	MET	-	EXPRESSION TAG	UNP Q581W1
C	-18	GLY	-	EXPRESSION TAG	UNP Q581W1
C	-17	SER	-	EXPRESSION TAG	UNP Q581W1
C	-16	SER	-	EXPRESSION TAG	UNP Q581W1
C	-15	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-14	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-13	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-12	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-11	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-10	HIS	-	EXPRESSION TAG	UNP Q581W1
C	-9	SER	-	EXPRESSION TAG	UNP Q581W1
C	-8	SER	-	EXPRESSION TAG	UNP Q581W1
C	-7	GLY	-	EXPRESSION TAG	UNP Q581W1
C	-6	LEU	-	EXPRESSION TAG	UNP Q581W1
C	-5	VAL	-	EXPRESSION TAG	UNP Q581W1
C	-4	PRO	-	EXPRESSION TAG	UNP Q581W1
C	-3	ARG	-	EXPRESSION TAG	UNP Q581W1
C	-2	GLY	-	EXPRESSION TAG	UNP Q581W1
C	-1	SER	-	EXPRESSION TAG	UNP Q581W1
C	0	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-19	MET	-	EXPRESSION TAG	UNP Q581W1
D	-18	GLY	-	EXPRESSION TAG	UNP Q581W1
D	-17	SER	-	EXPRESSION TAG	UNP Q581W1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP Q581W1
D	-15	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-14	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-13	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-12	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-11	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-10	HIS	-	EXPRESSION TAG	UNP Q581W1
D	-9	SER	-	EXPRESSION TAG	UNP Q581W1
D	-8	SER	-	EXPRESSION TAG	UNP Q581W1
D	-7	GLY	-	EXPRESSION TAG	UNP Q581W1
D	-6	LEU	-	EXPRESSION TAG	UNP Q581W1
D	-5	VAL	-	EXPRESSION TAG	UNP Q581W1
D	-4	PRO	-	EXPRESSION TAG	UNP Q581W1
D	-3	ARG	-	EXPRESSION TAG	UNP Q581W1
D	-2	GLY	-	EXPRESSION TAG	UNP Q581W1
D	-1	SER	-	EXPRESSION TAG	UNP Q581W1
D	0	HIS	-	EXPRESSION TAG	UNP Q581W1

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



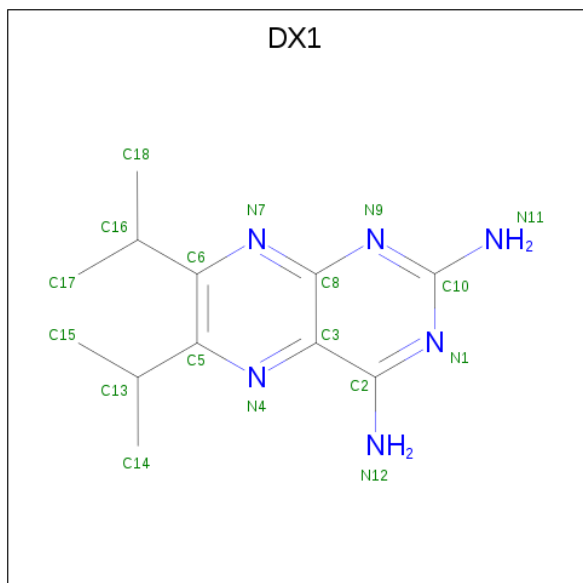
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

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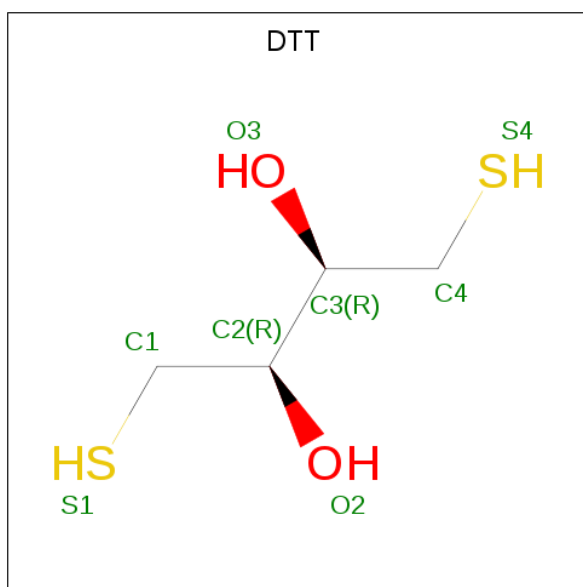
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 3 is 6,7-bis(1-methylethyl)pteridine-2,4-diamine (three-letter code: DX1) (formula: $C_{12}H_{18}N_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			18	12	6		
3	B	1	Total	C	N	0	0
			18	12	6		
3	C	1	Total	C	N	0	0
			18	12	6		
3	D	1	Total	C	N	0	0
			18	12	6		

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula: $C_4H_{10}O_2S_2$).



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

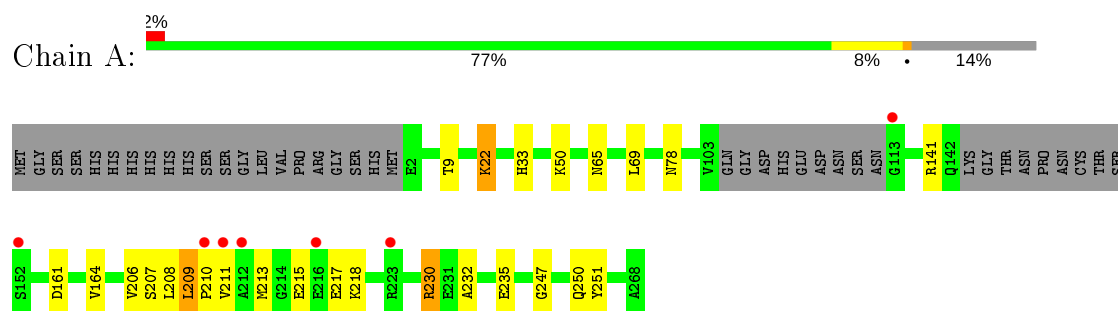
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	258	Total	O	0	0
			258	258		
5	B	247	Total	O	0	0
			247	247		
5	C	273	Total	O	0	0
			273	273		
5	D	245	Total	O	0	0
			245	245		

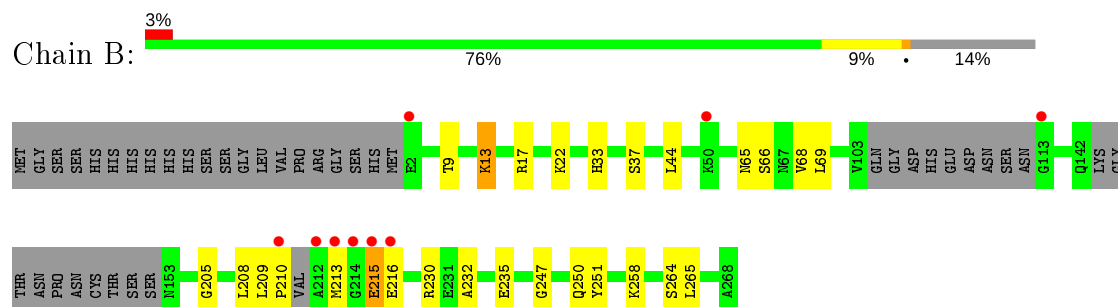
3 Residue-property plots

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.

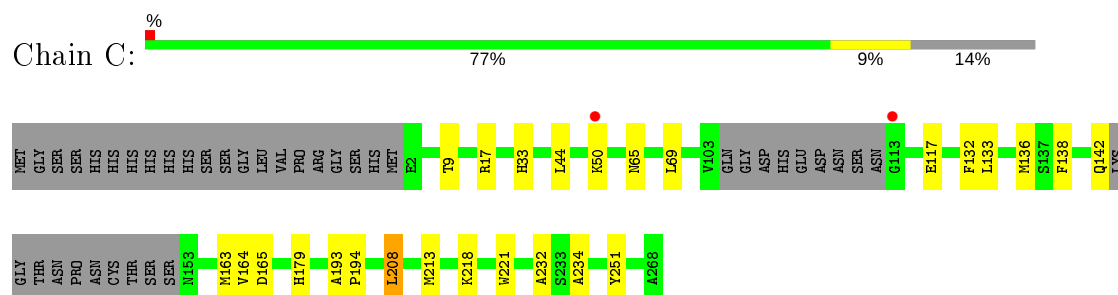
- Molecule 1: Pteridine reductase 1



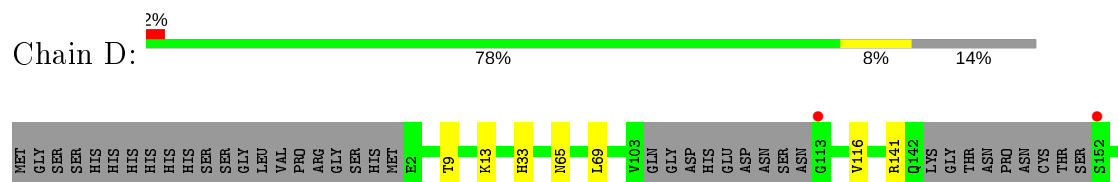
- Molecule 1: Pteridine reductase 1

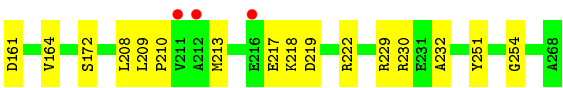


- Molecule 1: Pteridine reductase 1



- Molecule 1: Pteridine reductase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.14Å 89.47Å 84.34Å 90.00° 115.48° 90.00°	Depositor
Resolution (Å)	30.66 – 1.80 30.65 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.66-1.80) 99.9 (30.65-1.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 1.80Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.150 , 0.190 0.150 , 0.190	Depositor DCC
R_{free} test set	4650 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	15.6	Xtriage
Anisotropy	1.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9046	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 23.83 % 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 4.3196e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, DX1, DTT

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	0.52	0/2052	0.58	0/2781
1	B	0.49	0/1974	0.60	0/2674
1	C	0.51	0/1941	0.59	0/2631
1	D	0.49	0/1985	0.58	0/2689
All	All	0.50	0/7952	0.59	0/10775

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1994	0	2045	44	0
1	B	1924	0	1954	22	0
1	C	1890	0	1947	20	0
1	D	1919	0	1987	17	0
2	A	48	0	25	0	0
2	B	48	0	25	1	0
2	C	48	0	25	0	0
2	D	48	0	25	0	0
3	A	18	0	18	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	18	0	18	1	0
3	C	18	0	18	0	0
3	D	18	0	18	3	0
4	A	8	0	9	0	0
4	B	8	0	9	0	0
4	C	8	0	9	2	0
4	D	8	0	9	0	0
5	A	258	0	0	5	0
5	B	247	0	0	8	1
5	C	273	0	0	6	1
5	D	245	0	0	5	0
All	All	9046	0	8141	99	1

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 (99) 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:A:210[B]:PRO:HG3	1:A:213[B]:MET:SD	1.39	1.56
1:A:209[B]:LEU:HB3	1:A:210[B]:PRO:CD	1.39	1.45
1:A:210[B]:PRO:CG	1:A:213[B]:MET:SD	2.29	1.20
1:A:209[B]:LEU:HB3	1:A:210[B]:PRO:HD3	1.19	1.11
1:A:209[B]:LEU:HB3	1:A:210[B]:PRO:HD2	1.25	1.11
1:A:209[B]:LEU:CB	1:A:210[B]:PRO:CD	2.27	1.09
1:A:209[B]:LEU:CB	1:A:210[B]:PRO:HD3	1.78	1.08
1:A:22:LYS:HE3	1:A:235:GLU:HG3	1.49	0.93
1:A:209[B]:LEU:HA	3:A:270:DX1:H17	1.55	0.87
1:C:136[B]:MET:HE1	1:D:116:VAL:HG21	1.60	0.82
1:C:165:ASP:OD1	5:C:714:HOH:O	2.00	0.80
1:A:209[B]:LEU:HD12	1:A:213[B]:MET:SD	2.24	0.78
1:D:210:PRO:HD3	3:D:270:DX1:H17	1.67	0.77
1:A:209[B]:LEU:HA	3:A:270:DX1:C17	2.20	0.72
1:A:209[B]:LEU:HD12	1:A:210[B]:PRO:HD3	1.72	0.72
1:A:209[B]:LEU:CD1	1:A:210[B]:PRO:HD3	2.20	0.71
1:A:213[B]:MET:HG3	1:A:217[B]:GLU:OE2	1.90	0.70
1:B:235[A]:GLU:OE2	5:B:407:HOH:O	2.08	0.70
1:C:179:HIS:HE1	5:C:714:HOH:O	1.73	0.69
1:A:215[B]:GLU:HA	1:A:218:LYS:HD3	1.72	0.69
1:A:209[B]:LEU:CG	1:A:210[B]:PRO:HD3	2.23	0.69
1:B:13[A]:LYS:HE2	1:B:37:SER:OG	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209[B]:LEU:CA	3:A:270:DX1:H17	2.22	0.69
1:A:250[A]:GLN:HG2	5:C:487:HOH:O	1.93	0.67
1:B:210:PRO:HG2	1:B:213:MET:H	1.60	0.66
3:B:270:DX1:H15B	5:B:457:HOH:O	1.96	0.65
1:B:215:GLU:O	5:B:493:HOH:O	2.14	0.65
1:D:141:ARG:HG2	5:D:602:HOH:O	1.97	0.64
3:D:270:DX1:H15B	5:D:569:HOH:O	1.98	0.64
1:A:206[A]:VAL:HG12	3:A:270:DX1:H15	1.79	0.64
1:A:210[B]:PRO:HA	3:A:270:DX1:H18	1.80	0.62
1:A:210[B]:PRO:CA	3:A:270:DX1:H18	2.29	0.62
1:A:215[B]:GLU:HG2	1:A:218:LYS:NZ	2.15	0.62
3:A:270:DX1:H15B	5:A:488:HOH:O	2.02	0.59
1:B:17:ARG:HD3	5:B:402:HOH:O	2.03	0.58
1:C:221:TRP:HZ2	4:C:271:DTT:H12	1.68	0.58
1:A:209[B]:LEU:C	3:A:270:DX1:H17	2.24	0.57
1:A:207[B]:SER:O	1:A:208[B]:LEU:C	2.43	0.56
1:A:250[A]:GLN:OE1	5:A:274:HOH:O	2.17	0.56
1:C:138:PHE:O	1:C:142:GLN:HG2	2.06	0.56
1:D:13:LYS:HD3	5:D:590:HOH:O	2.06	0.55
1:A:213[A]:MET:SD	1:A:218:LYS:HG3	2.48	0.54
1:A:161:ASP:HB3	1:A:164:VAL:HG13	1.91	0.53
5:A:520:HOH:O	1:C:194:PRO:HG3	2.09	0.53
1:B:9:THR:HA	1:B:33:HIS:HB3	1.91	0.53
1:A:22:LYS:CE	1:A:235:GLU:HG3	2.33	0.52
1:B:232:ALA:HB2	1:D:251:TYR:CE2	2.45	0.51
1:D:217[A]:GLU:HG2	5:D:676:HOH:O	2.11	0.51
1:D:222:ARG:HG2	1:D:230:ARG:HA	1.93	0.51
1:A:9:THR:HA	1:A:33:HIS:HB3	1.93	0.51
1:C:163:MET:HG3	5:C:629:HOH:O	2.10	0.51
1:B:210:PRO:HD3	5:B:458:HOH:O	2.10	0.51
1:B:17:ARG:HG3	1:B:44:LEU:HD22	1.92	0.51
1:A:65:ASN:HA	1:A:69:LEU:HD22	1.93	0.50
1:A:215[B]:GLU:HG2	1:A:218:LYS:HZ2	1.77	0.50
1:A:213[B]:MET:CG	1:A:217[B]:GLU:OE2	2.60	0.50
1:A:230:ARG:HD3	5:A:307:HOH:O	2.11	0.50
1:A:209[B]:LEU:HG	1:A:218:LYS:HG2	1.94	0.49
1:B:247:GLY:O	1:B:250:GLN:HG2	2.13	0.49
1:B:22:LYS:HZ2	1:B:235[B]:GLU:HG3	1.77	0.49
1:D:210:PRO:CD	3:D:270:DX1:H17	2.41	0.49
1:D:9:THR:HA	1:D:33:HIS:HB3	1.95	0.48
1:C:142:GLN:C	5:C:604:HOH:O	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:65:ASN:HA	1:D:69:LEU:HD22	1.97	0.47
1:A:232:ALA:HB2	1:C:251:TYR:CE2	2.49	0.47
1:B:205:GLY:O	2:B:269:NAP:H4N	2.15	0.47
1:A:247:GLY:O	1:A:250[B]:GLN:HG2	2.15	0.47
1:D:213:MET:HA	5:D:668:HOH:O	2.16	0.45
1:A:78[A]:ASN:OD1	1:A:141[A]:ARG:NH2	2.37	0.45
1:C:9:THR:HA	1:C:33:HIS:HB3	1.99	0.45
1:B:65:ASN:HA	1:B:69:LEU:HD22	1.98	0.45
1:B:215:GLU:HB2	5:B:512:HOH:O	2.17	0.44
1:C:208:LEU:HD22	1:C:234:ALA:HB2	1.99	0.44
1:C:117:GLU:HG3	5:C:654:HOH:O	2.17	0.44
1:A:50:LYS:HB3	1:A:50:LYS:HE2	1.93	0.44
1:B:22:LYS:NZ	1:B:235[B]:GLU:HG3	2.33	0.43
1:B:66:SER:OG	1:B:68[B]:VAL:HG12	2.18	0.43
1:C:65:ASN:HA	1:C:69:LEU:HD22	1.99	0.43
1:A:22:LYS:HE3	1:A:235:GLU:CG	2.35	0.43
1:C:213:MET:O	1:C:218:LYS:HE3	2.18	0.43
1:B:251:TYR:CE2	1:D:232:ALA:HB2	2.53	0.43
1:D:213:MET:HB3	1:D:218:LYS:HE3	2.01	0.42
1:B:210:PRO:CD	5:B:458:HOH:O	2.66	0.42
1:C:133:LEU:HD23	1:C:136[B]:MET:CE	2.49	0.42
1:C:193:ALA:N	1:C:194:PRO:CD	2.83	0.42
1:A:215[B]:GLU:HG2	1:A:218:LYS:HZ3	1.84	0.42
1:B:210:PRO:HD2	1:B:213:MET:HB3	2.02	0.41
1:C:221:TRP:CZ2	4:C:271:DTT:H12	2.52	0.41
1:A:210[B]:PRO:CD	1:A:213[B]:MET:SD	3.05	0.41
1:A:251:TYR:CE2	1:C:232:ALA:HB2	2.55	0.40
1:D:161:ASP:HB3	1:D:164:VAL:HG13	2.02	0.40
1:D:219:ASP:HA	1:D:222:ARG:HB2	2.03	0.40
1:B:209:LEU:N	5:B:521:HOH:O	2.51	0.40
1:C:17[B]:ARG:HH11	1:C:44:LEU:HB2	1.86	0.40
1:B:258[B]:LYS:HD2	1:B:264:SER:OG	2.21	0.40
1:C:132:PHE:HE1	1:D:172[A]:SER:HG	1.68	0.40
1:A:211[B]:VAL:HA	5:A:519:HOH:O	2.21	0.40
1:A:215[B]:GLU:O	1:A:218:LYS:HB2	2.21	0.40
1:B:265:LEU:HD11	1:D:254:GLY:HA3	2.03	0.40

All (1) 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:B:435:HOH:O	5:C:683:HOH:O[1_655]	2.13	0.07

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	264/288 (92%)	249 (94%)	13 (5%)	2 (1%)	19	7
1	B	253/288 (88%)	245 (97%)	7 (3%)	1 (0%)	34	21
1	C	251/288 (87%)	242 (96%)	8 (3%)	1 (0%)	34	21
1	D	256/288 (89%)	248 (97%)	8 (3%)	0	100	100
All	All	1024/1152 (89%)	984 (96%)	36 (4%)	4 (0%)	41	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209[A]	LEU
1	A	209[B]	LEU
1	B	208	LEU
1	C	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	217/231 (94%)	215 (99%)	2 (1%)	78	75
1	B	209/231 (90%)	204 (98%)	5 (2%)	49	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	204/231 (88%)	202 (99%)	2 (1%)	76	71
1	D	210/231 (91%)	207 (99%)	3 (1%)	67	59
All	All	840/924 (91%)	828 (99%)	12 (1%)	67	59

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LYS
1	A	230	ARG
1	B	13[A]	LYS
1	B	215	GLU
1	B	216[A]	GLU
1	B	216[B]	GLU
1	B	230	ARG
1	C	50	LYS
1	C	164	VAL
1	D	208	LEU
1	D	209	LEU
1	D	229	ARG

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

Mol	Chain	Res	Type
1	A	25	GLN
1	A	166	GLN
1	B	65	ASN
1	B	67	ASN
1	B	166	GLN
1	C	67	ASN
1	C	250	GLN
1	D	166	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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
4	DTT	A	271	-	7,7,7	0.51	0	4,8,8	0.52	0
4	DTT	B	271	-	7,7,7	0.42	0	4,8,8	0.62	0
4	DTT	C	271	-	7,7,7	0.37	0	4,8,8	0.77	0
2	NAP	A	269	-	45,52,52	1.64	4 (8%)	56,80,80	1.17	4 (7%)
2	NAP	B	269	-	45,52,52	1.69	3 (6%)	56,80,80	1.14	3 (5%)
3	DX1	A	270	-	19,19,19	1.24	2 (10%)	24,28,28	2.25	8 (33%)
3	DX1	C	270	-	19,19,19	1.20	2 (10%)	24,28,28	2.05	6 (25%)
2	NAP	C	269	-	45,52,52	1.64	4 (8%)	56,80,80	1.26	4 (7%)
3	DX1	B	270	-	19,19,19	1.21	2 (10%)	24,28,28	2.19	6 (25%)
3	DX1	D	270	-	19,19,19	1.33	2 (10%)	24,28,28	2.26	8 (33%)
4	DTT	D	271	-	7,7,7	0.40	0	4,8,8	1.21	0
2	NAP	D	269	-	45,52,52	1.57	4 (8%)	56,80,80	1.38	5 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	DTT	A	271	-	1/1/2/2	4/8/8/8	-
4	DTT	B	271	-	1/1/2/2	2/8/8/8	-
4	DTT	C	271	-	1/1/2/2	3/8/8/8	-
2	NAP	A	269	-	-	0/31/67/67	0/5/5/5
2	NAP	B	269	-	-	0/31/67/67	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DX1	A	270	-	-	0/8/8/8	0/2/2/2
3	DX1	C	270	-	-	0/8/8/8	0/2/2/2
2	NAP	C	269	-	-	0/31/67/67	0/5/5/5
3	DX1	B	270	-	-	0/8/8/8	0/2/2/2
3	DX1	D	270	-	-	0/8/8/8	0/2/2/2
4	DTT	D	271	-	1/1/2/2	6/8/8/8	-
2	NAP	D	269	-	-	0/31/67/67	0/5/5/5

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	269	NAP	O7N-C7N	8.67	1.40	1.24
2	C	269	NAP	O7N-C7N	8.46	1.40	1.24
2	A	269	NAP	O7N-C7N	8.18	1.39	1.24
2	D	269	NAP	O7N-C7N	7.77	1.39	1.24
2	A	269	NAP	C2A-N3A	4.25	1.38	1.32
2	B	269	NAP	C2A-N3A	3.87	1.38	1.32
3	D	270	DX1	C5-N4	3.75	1.37	1.31
3	B	270	DX1	C5-N4	3.61	1.37	1.31
3	D	270	DX1	C6-N7	3.58	1.37	1.31
2	D	269	NAP	C2A-N3A	3.57	1.37	1.32
2	C	269	NAP	C2N-N1N	3.26	1.38	1.35
2	C	269	NAP	C2A-N3A	3.20	1.37	1.32
3	C	270	DX1	C6-N7	3.20	1.36	1.31
3	A	270	DX1	C6-N7	3.19	1.36	1.31
3	C	270	DX1	C5-N4	2.90	1.36	1.31
3	A	270	DX1	C5-N4	2.82	1.36	1.31
3	B	270	DX1	C6-N7	2.67	1.35	1.31
2	D	269	NAP	C2A-N1A	2.52	1.38	1.33
2	A	269	NAP	C2A-N1A	2.49	1.38	1.33
2	C	269	NAP	C2A-N1A	2.26	1.38	1.33
2	B	269	NAP	C2A-N1A	2.21	1.38	1.33
2	D	269	NAP	O4B-C1B	-2.09	1.38	1.41
2	A	269	NAP	O4B-C4B	-2.03	1.40	1.45

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	269	NAP	N3A-C2A-N1A	-5.89	119.47	128.68
2	B	269	NAP	N3A-C2A-N1A	-5.57	119.97	128.68
3	B	270	DX1	N9-C10-N1	-5.47	119.93	127.22
2	A	269	NAP	N3A-C2A-N1A	-5.46	120.15	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	269	NAP	N3A-C2A-N1A	-5.40	120.24	128.68
3	D	270	DX1	N9-C10-N1	-5.35	120.09	127.22
3	A	270	DX1	N9-C10-N1	-5.28	120.18	127.22
3	D	270	DX1	C10-N9-C8	4.83	120.88	115.36
3	B	270	DX1	C10-N9-C8	4.78	120.81	115.36
3	C	270	DX1	N9-C10-N1	-4.71	120.94	127.22
3	C	270	DX1	C10-N9-C8	4.63	120.65	115.36
3	A	270	DX1	C6-C5-N4	-4.52	117.61	122.99
3	D	270	DX1	C6-C5-N4	-4.28	117.89	122.99
3	A	270	DX1	C10-N9-C8	4.09	120.03	115.36
2	D	269	NAP	C3N-C7N-N7N	3.83	122.35	117.75
3	C	270	DX1	C6-C5-N4	-3.47	118.86	122.99
3	B	270	DX1	C6-C5-N4	-3.32	119.03	122.99
2	D	269	NAP	O7N-C7N-C3N	-3.27	115.72	119.63
3	A	270	DX1	C13-C5-N4	3.12	120.59	115.92
3	B	270	DX1	C5-C6-N7	-3.10	119.30	122.99
2	B	269	NAP	C1B-N9A-C4A	-3.10	121.20	126.64
3	D	270	DX1	C13-C5-N4	3.06	120.50	115.92
2	A	269	NAP	C1B-N9A-C4A	-2.87	121.60	126.64
2	C	269	NAP	C3N-C7N-N7N	2.82	121.13	117.75
2	C	269	NAP	C1B-N9A-C4A	-2.78	121.75	126.64
3	C	270	DX1	C5-C6-N7	-2.69	119.79	122.99
3	D	270	DX1	N9-C8-N7	2.65	122.25	115.97
2	D	269	NAP	C1B-N9A-C4A	-2.55	122.16	126.64
2	B	269	NAP	C3N-C7N-N7N	2.53	120.78	117.75
3	B	270	DX1	C13-C5-N4	2.47	119.62	115.92
3	A	270	DX1	C5-N4-C3	2.47	121.03	117.24
3	D	270	DX1	C5-N4-C3	2.45	121.00	117.24
3	A	270	DX1	N9-C8-N7	2.40	121.67	115.97
3	C	270	DX1	N9-C8-N7	2.40	121.67	115.97
3	A	270	DX1	C17-C16-C6	-2.31	107.06	110.96
3	C	270	DX1	C5-N4-C3	2.29	120.75	117.24
2	A	269	NAP	C3N-C7N-N7N	2.26	120.46	117.75
3	A	270	DX1	C3-C8-N7	-2.24	118.08	121.71
2	D	269	NAP	C2A-N1A-C6A	2.23	122.56	118.75
3	B	270	DX1	C5-N4-C3	2.20	120.62	117.24
2	C	269	NAP	C5A-C6A-N6A	2.19	123.68	120.35
3	D	270	DX1	C5-C6-N7	-2.19	120.38	122.99
2	A	269	NAP	O2N-PN-O1N	2.11	122.70	112.24
3	D	270	DX1	C3-C8-N7	-2.10	118.30	121.71

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	271	DTT	C3
4	B	271	DTT	C3
4	C	271	DTT	C3
4	D	271	DTT	C3

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	271	DTT	C1-C2-C3-C4
4	A	271	DTT	O3-C3-C4-S4
4	B	271	DTT	C2-C3-C4-S4
4	B	271	DTT	O3-C3-C4-S4
4	C	271	DTT	C1-C2-C3-C4
4	D	271	DTT	C1-C2-C3-O3
4	D	271	DTT	C1-C2-C3-C4
4	D	271	DTT	O2-C2-C3-O3
4	D	271	DTT	O2-C2-C3-C4
4	D	271	DTT	C2-C3-C4-S4
4	D	271	DTT	O3-C3-C4-S4
4	A	271	DTT	O2-C2-C3-C4
4	C	271	DTT	C1-C2-C3-O3
4	A	271	DTT	C2-C3-C4-S4
4	C	271	DTT	O2-C2-C3-O3

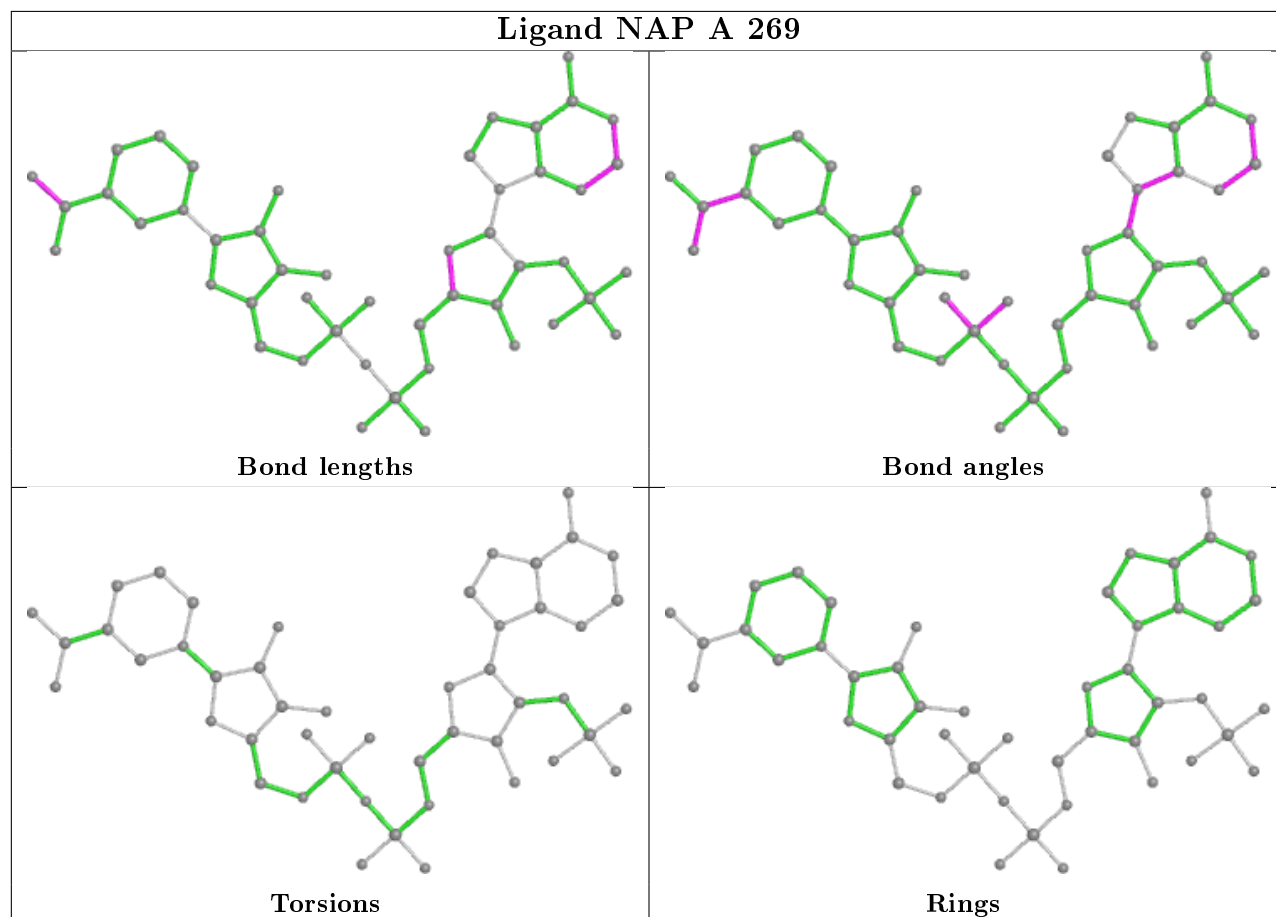
There are no ring outliers.

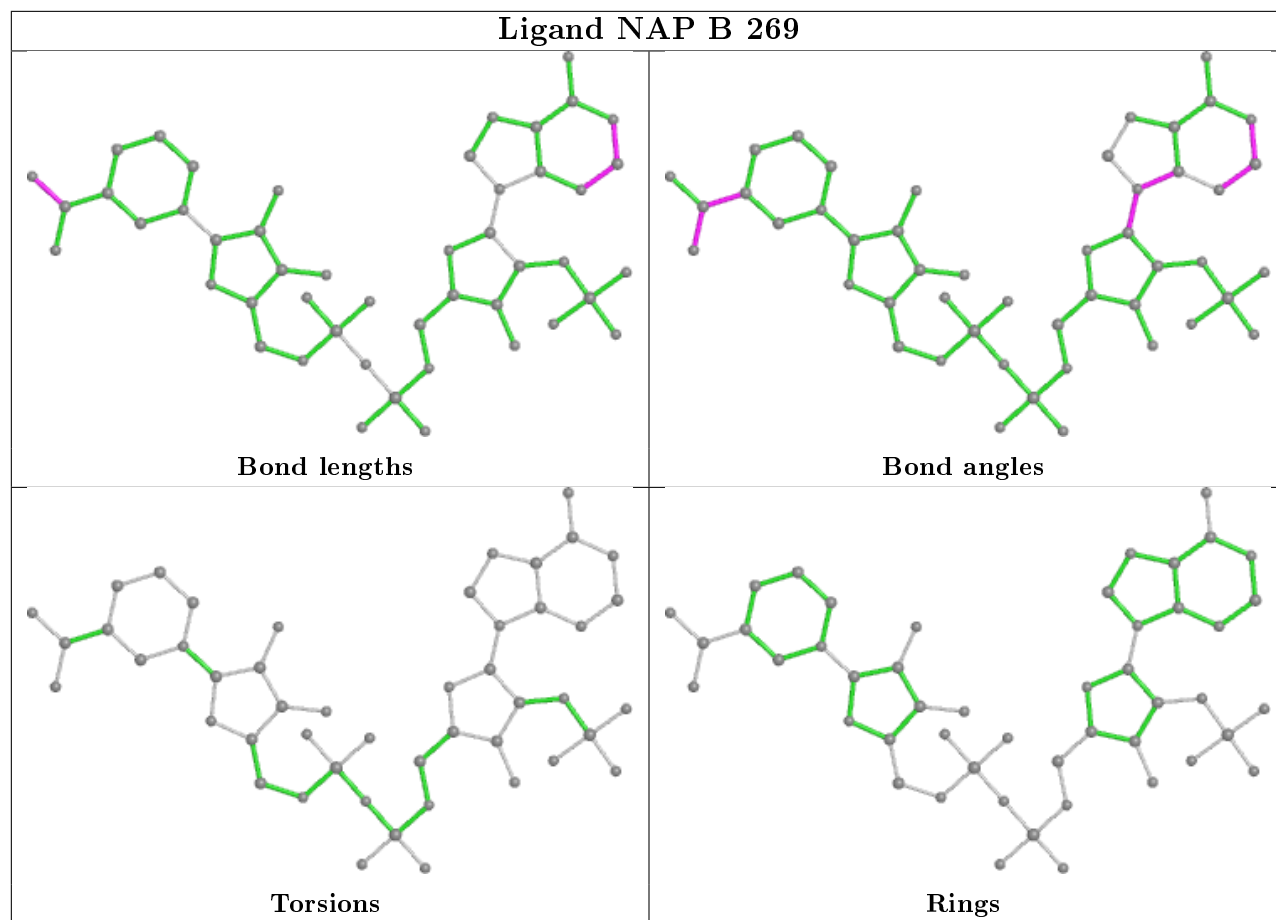
5 monomers are involved in 15 short contacts:

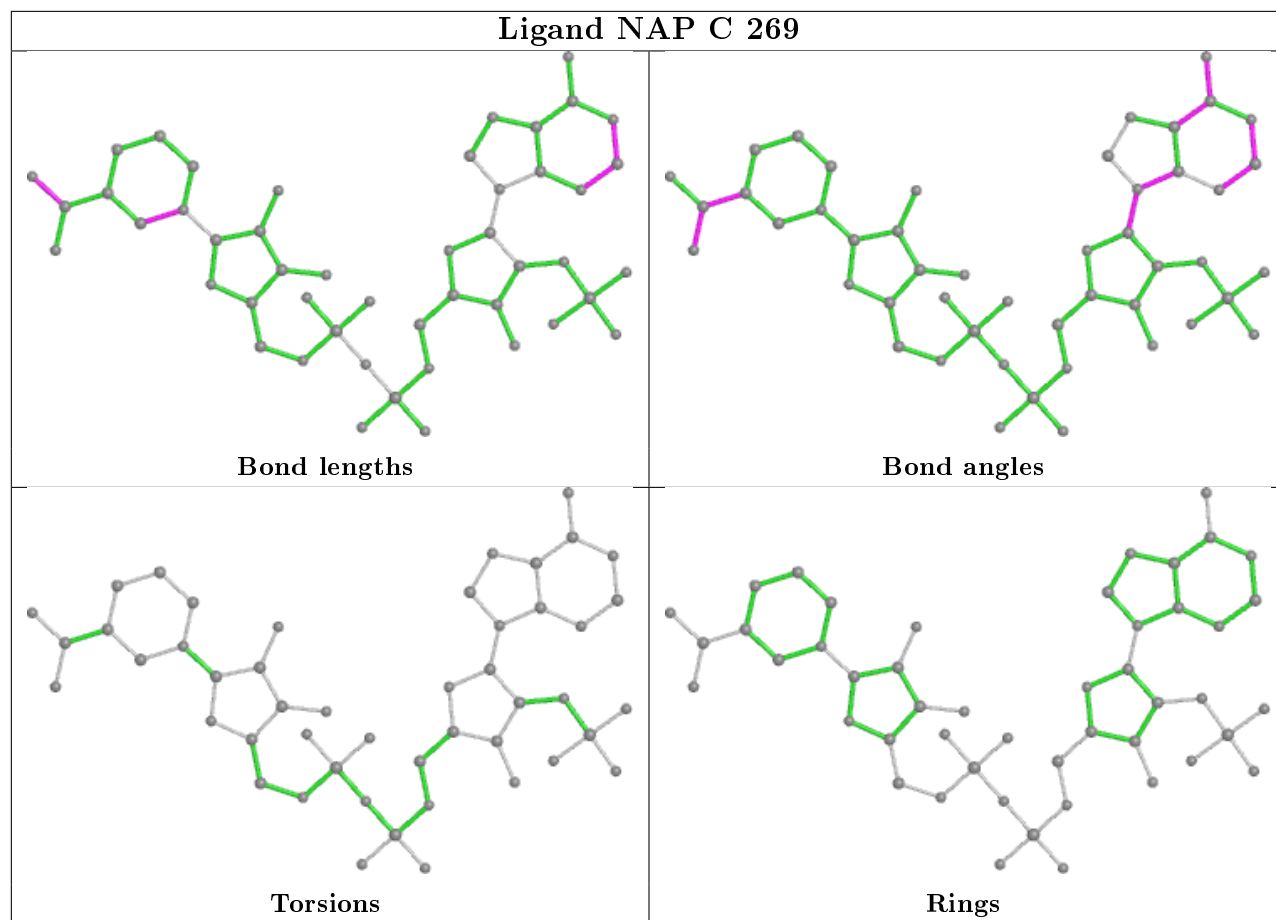
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	271	DTT	2	0
2	B	269	NAP	1	0
3	A	270	DX1	8	0
3	B	270	DX1	1	0
3	D	270	DX1	3	0

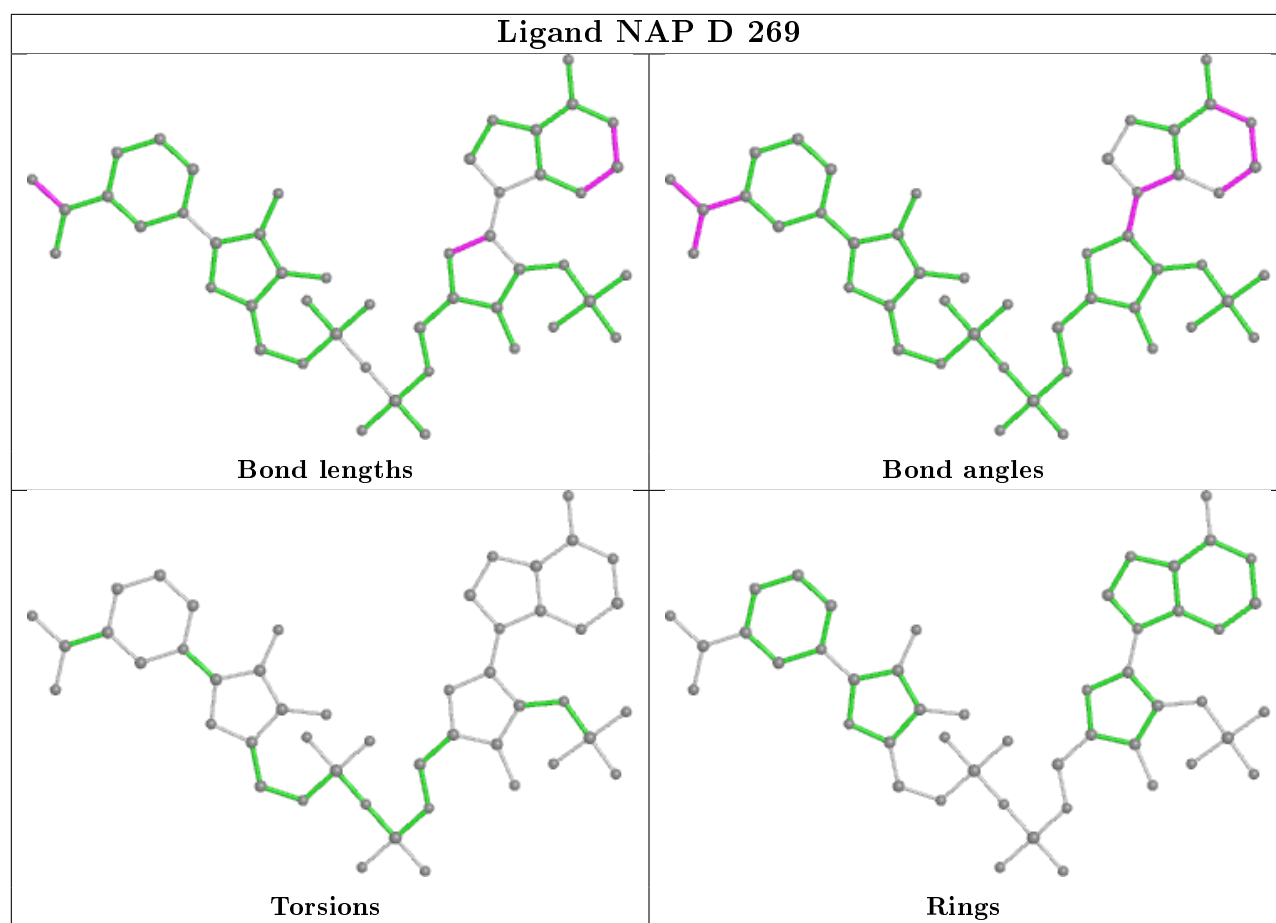
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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(Å ²)	Q<0.9
1	A	249/288 (86%)	-0.24	7 (2%)	53	47	9, 13, 30, 37	3 (1%)
1	B	247/288 (85%)	-0.11	9 (3%)	42	37	10, 14, 29, 43	2 (0%)
1	C	248/288 (86%)	-0.34	2 (0%)	86	84	9, 13, 26, 36	2 (0%)
1	D	249/288 (86%)	-0.30	5 (2%)	65	61	9, 13, 31, 42	1 (0%)
All	All	993/1152 (86%)	-0.25	23 (2%)	60	56	9, 13, 30, 43	8 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	GLY	6.4
1	A	211[A]	VAL	6.2
1	A	210[A]	PRO	4.7
1	D	113	GLY	4.6
1	D	211	VAL	4.5
1	B	113	GLY	4.4
1	C	113	GLY	4.4
1	D	212	ALA	4.2
1	A	216[A]	GLU	3.6
1	A	223	ARG	3.3
1	B	212	ALA	3.2
1	A	152	SER	3.1
1	B	50	LYS	3.1
1	B	216[A]	GLU	3.0
1	D	152	SER	2.9
1	D	216	GLU	2.5
1	B	2	GLU	2.5
1	B	214	GLY	2.5
1	C	50	LYS	2.2
1	B	215	GLU	2.2
1	A	212[A]	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	210	PRO	2.1
1	B	213	MET	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](#)

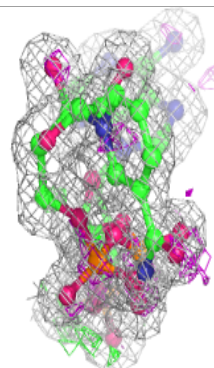
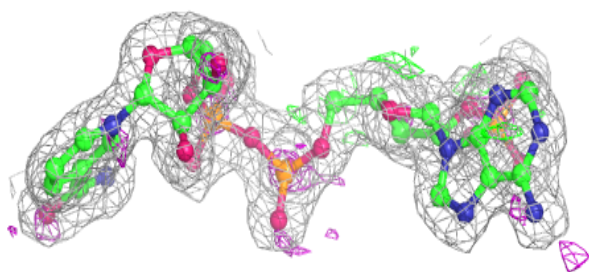
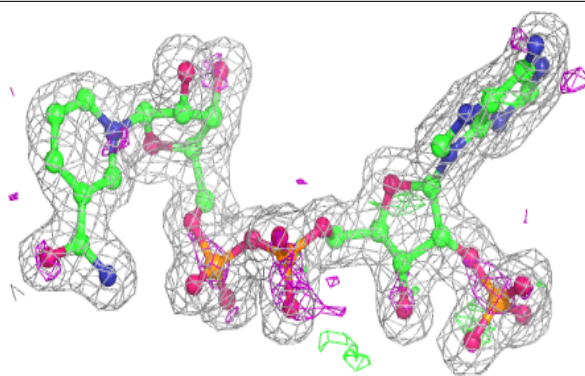
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	DTT	D	271	8/8	0.82	0.22	41,59,64,70	0
3	DX1	B	270	18/18	0.86	0.14	22,29,33,34	0
4	DTT	C	271	8/8	0.89	0.16	43,55,57,65	0
3	DX1	A	270	18/18	0.89	0.17	19,24,32,33	0
3	DX1	D	270	18/18	0.91	0.15	16,25,30,31	0
4	DTT	B	271	8/8	0.91	0.17	37,47,52,59	0
4	DTT	A	271	8/8	0.92	0.25	36,46,50,61	0
3	DX1	C	270	18/18	0.94	0.10	14,22,27,28	0
2	NAP	C	269	48/48	0.97	0.07	9,13,17,18	0
2	NAP	B	269	48/48	0.97	0.07	8,14,17,20	0
2	NAP	A	269	48/48	0.98	0.06	8,12,15,17	0
2	NAP	D	269	48/48	0.98	0.06	7,14,17,20	0

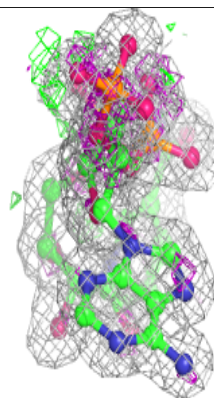
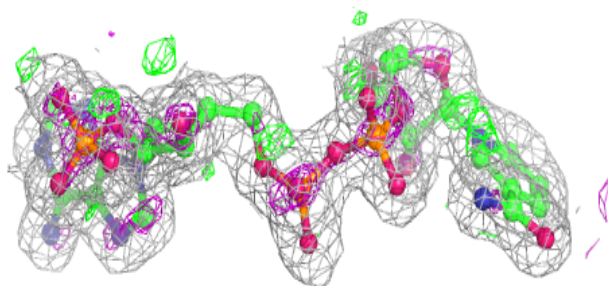
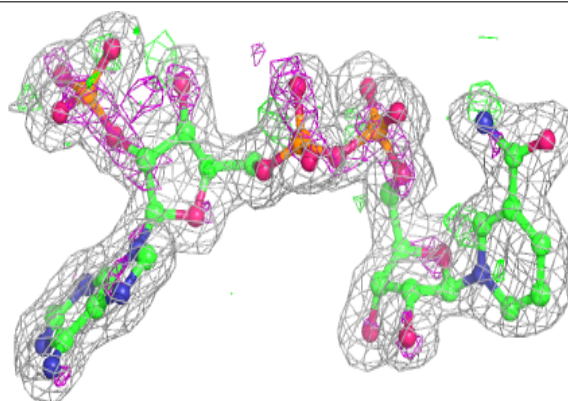
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP C 269:

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

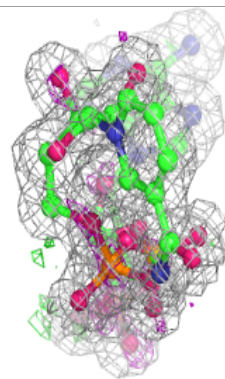
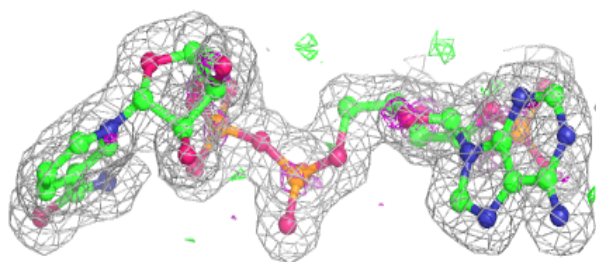
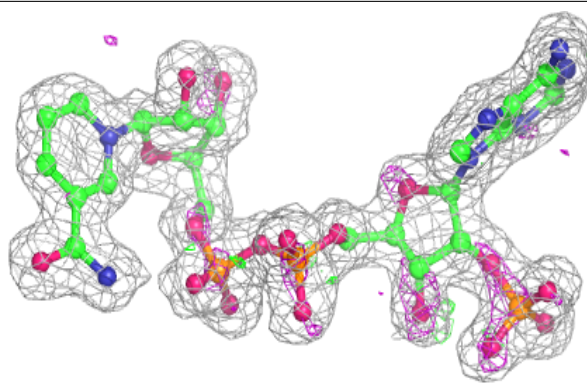
**Electron density around NAP B 269:**

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

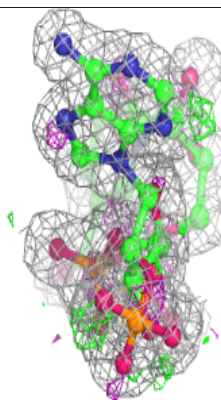
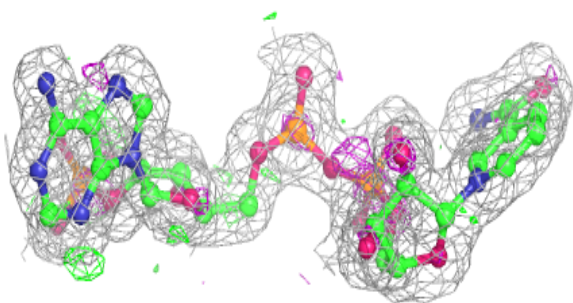
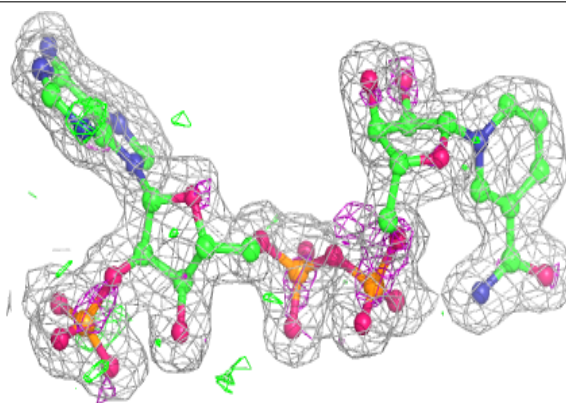


Electron density around NAP A 269:

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

**Electron density around NAP D 269:**

$2mF_o-DF_c$ (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.