



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2025 – 08:19 PM EDT

PDB ID : 3BMQ  
Title : Structure of Pteridine Reductase 1 (PTR1) from Trypanosoma brucei in ternary complex with cofactor (NADP+) and inhibitor (Compound AX5)  
Authors : Martini, V.P.; Iulek, J.; Hunter, W.N.  
Deposited on : 2007-12-13  
Resolution : 1.70 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

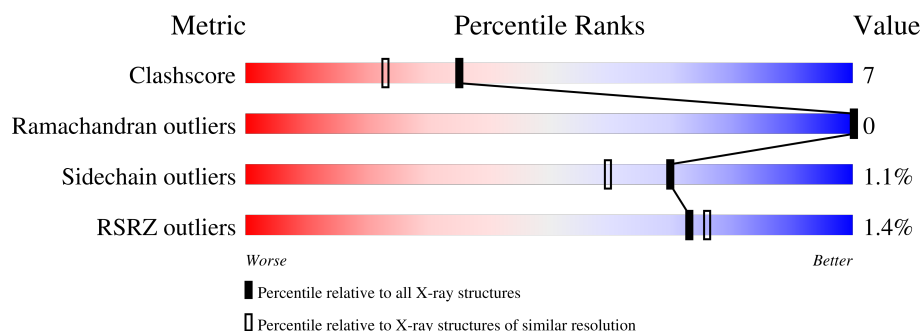
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
Clashscore	180529	5671 (1.70-1.70)
Ramachandran outliers	177936	5594 (1.70-1.70)
Sidechain outliers	177891	5594 (1.70-1.70)
RSRZ outliers	164620	5159 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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>77%</div> <div>10%</div> <div>12%</div> </div>
1	D	288	<div> <div>77%</div> <div>11%</div> <div>12%</div> </div>
2	B	288	<div> <div>79%</div> <div>8%</div> <div>12%</div> </div>
2	C	288	<div> <div>77%</div> <div>9%</div> <div>13%</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	CSX	D	168	-	-	X	-
5	DTT	D	271	X	-	X	-
7	GOL	B	272	-	-	X	-
7	GOL	C	272	-	-	X	-
7	GOL	C	273	-	-	X	-

## 2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 9392 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	10	0
			1929	1220	335	362	12			
1	D	253	Total	C	N	O	S	0	14	0
			1961	1240	342	368	11			

There are 40 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
D	-19	MET	-	expression tag	UNP O76290
D	-18	GLY	-	expression tag	UNP O76290
D	-17	SER	-	expression tag	UNP O76290
D	-16	SER	-	expression tag	UNP O76290
D	-15	HIS	-	expression tag	UNP O76290

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Chain	Residue	Modelled	Actual	Comment	Reference
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 a protein called Pteridine reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	252	Total	C	N	O	S	0	11	0
			1930	1221	337	361	11			
2	C	251	Total	C	N	O	S	0	9	0
			1913	1205	336	361	11			

There are 40 discrepancies between the modelled and reference sequences:

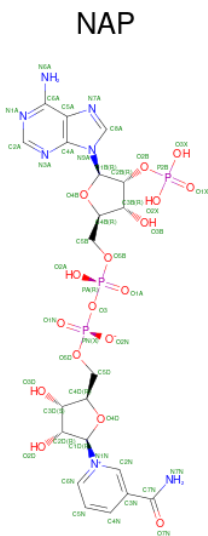
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP O76290
B	-18	GLY	-	expression tag	UNP O76290
B	-17	SER	-	expression tag	UNP O76290
B	-16	SER	-	expression tag	UNP O76290
B	-15	HIS	-	expression tag	UNP O76290
B	-14	HIS	-	expression tag	UNP O76290
B	-13	HIS	-	expression tag	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

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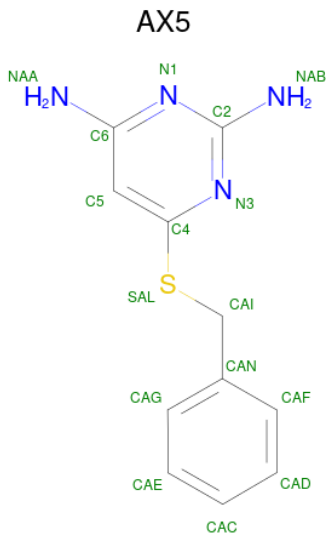
Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	PRO	-	expression tag	UNP O76290
B	-3	ARG	-	expression tag	UNP O76290
B	-2	GLY	-	expression tag	UNP O76290
B	-1	SER	-	expression tag	UNP O76290
B	0	HIS	-	expression tag	UNP O76290
C	-19	MET	-	expression tag	UNP O76290
C	-18	GLY	-	expression tag	UNP 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

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



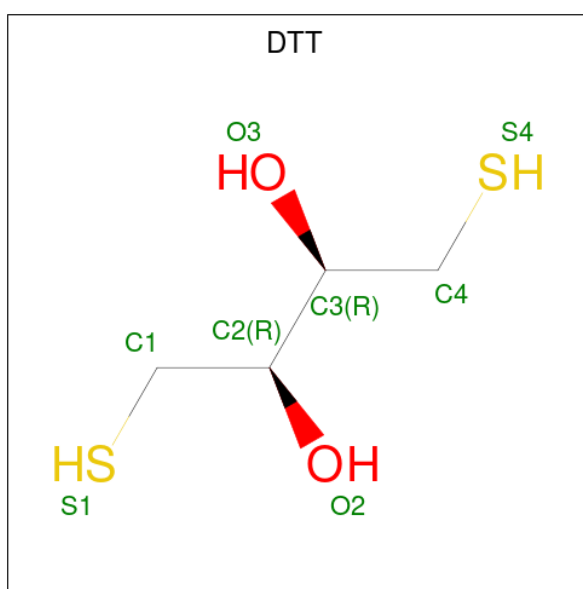
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	C	1	Total 48	C 21	N 7	O 17	P 3	0	0
3	D	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 4 is 6-(benzylsulfanyl)pyrimidine-2,4-diamine (three-letter code: AX5) (formula:  $\text{C}_{11}\text{H}_{12}\text{N}_4\text{S}$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	S	0	0
			16	11	4	1		
4	B	1	Total	C	N	S	0	0
			16	11	4	1		
4	C	1	Total	C	N	S	0	0
			16	11	4	1		
4	D	1	Total	C	N	S	0	0
			16	11	4	1		

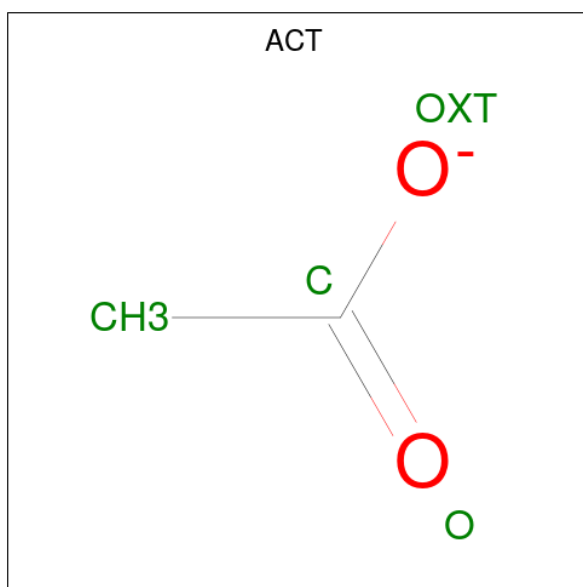
- Molecule 5 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula:  $C_4H_{10}O_2S_2$ ).



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

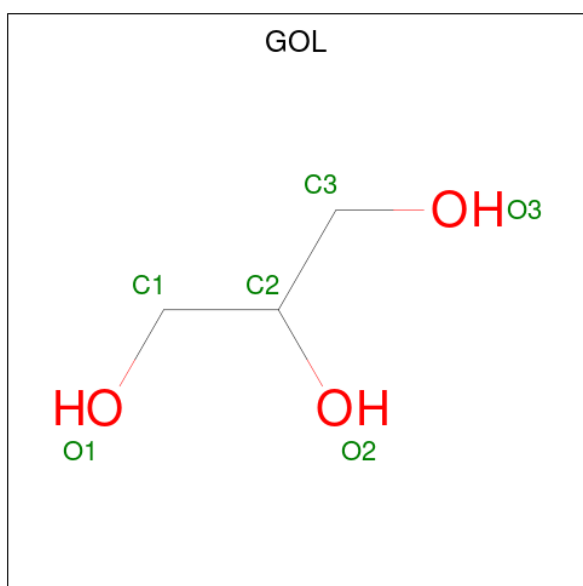
- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).





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

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			6	3	3		

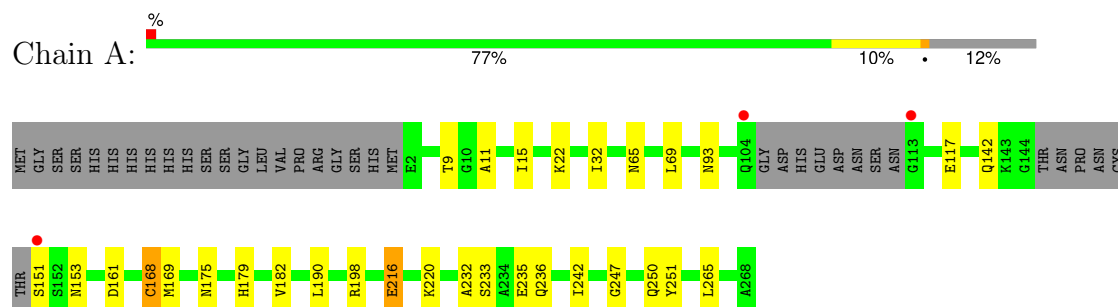
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	350	Total	O	0	0
			350	350		
8	B	382	Total	O	0	0
			382	382		
8	C	319	Total	O	0	0
			319	319		
8	D	310	Total	O	0	2
			310	310		

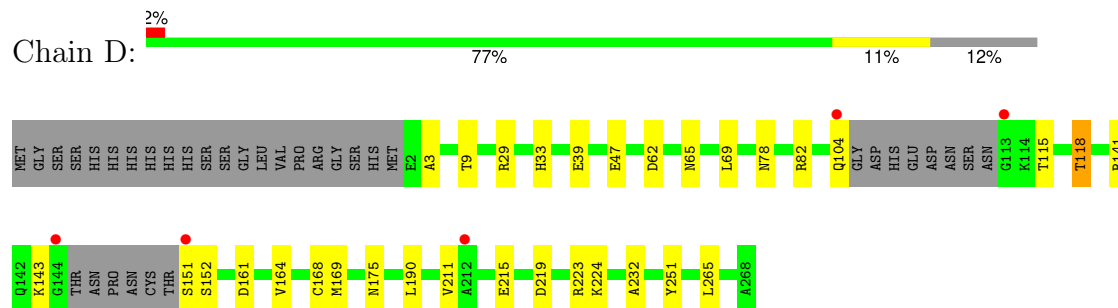
### 3 Residue-property plots [i](#)

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

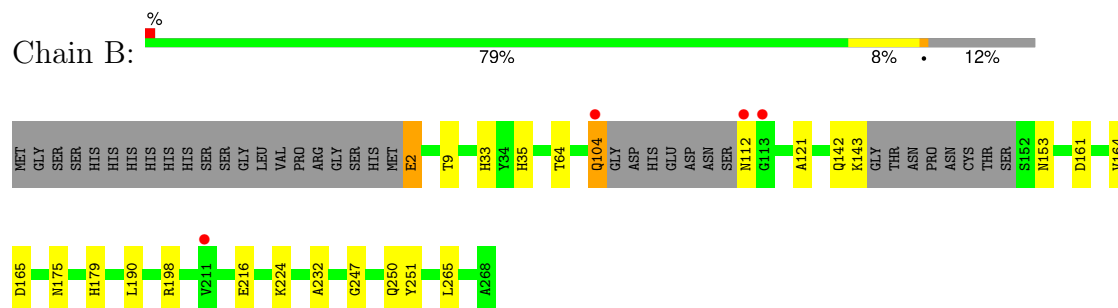
- Molecule 1: Pteridine reductase



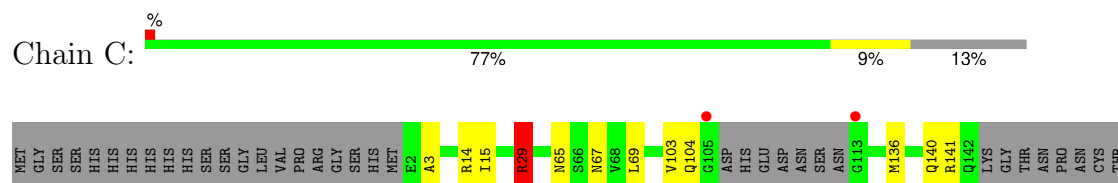
- Molecule 1: Pteridine reductase

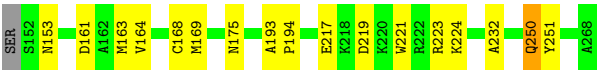


- Molecule 2: Pteridine reductase



- Molecule 2: Pteridine reductase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.72Å 91.16Å 82.83Å 90.00° 115.72° 90.00°	Depositor
Resolution (Å)	74.54 – 1.70 74.54 – 1.70	Depositor EDS
% Data completeness (in resolution range)	85.5 (74.54-1.70) 85.1 (74.54-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.68 (at 1.70Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.131 , 0.178 0.142 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.0	Xtriage
Anisotropy	0.511	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 56.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	9392	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.25% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, DTT, NAP, ACT, CSX, AX5

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	0.89	3/1972 (0.2%)	0.79	2/2670 (0.1%)
1	D	0.84	0/2022	0.83	3/2736 (0.1%)
2	B	0.86	0/1989	0.83	4/2694 (0.1%)
2	C	0.84	0/1967	0.81	3/2665 (0.1%)
All	All	0.86	3/7950 (0.0%)	0.82	12/10765 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	117	GLU	CB-CG	5.82	1.63	1.52
1	A	117	GLU	CG-CD	5.23	1.59	1.51
1	A	182	VAL	CB-CG2	5.00	1.63	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	198	ARG	NE-CZ-NH2	-6.90	116.85	120.30
2	C	14	ARG	NE-CZ-NH2	-6.29	117.15	120.30
1	D	62	ASP	CB-CG-OD1	6.27	123.94	118.30
2	B	198	ARG	NE-CZ-NH1	6.21	123.41	120.30
1	D	82	ARG	NE-CZ-NH1	5.99	123.30	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1929	0	1994	29	0
1	D	1961	0	2033	33	0
2	B	1930	0	1999	25	0
2	C	1913	0	1962	29	0
3	A	48	0	25	1	0
3	B	48	0	25	1	0
3	C	48	0	25	1	0
3	D	48	0	25	1	0
4	A	16	0	12	0	0
4	B	16	0	12	0	0
4	C	16	0	12	0	0
4	D	16	0	12	1	0
5	A	8	0	4	0	0
5	D	8	0	10	7	0
6	B	4	0	3	0	0
6	C	4	0	3	0	0
7	B	6	0	8	6	0
7	C	12	0	16	10	0
8	A	350	0	0	15	3
8	B	382	0	0	16	3
8	C	319	0	0	10	1
8	D	310	0	0	12	1
All	All	9392	0	8180	119	4

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 7.

The worst 5 of 119 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)
8:A:620:HOH:O	1:D:265:LEU:HD23	1.22	1.29
1:A:142:GLN:NE2	8:A:603:HOH:O	1.74	1.16
2:C:140[B]:GLN:NE2	8:C:473:HOH:O	1.88	1.06
1:D:164:VAL:CG2	8:D:893:HOH:O	2.05	1.03
1:D:164:VAL:HG22	8:D:893:HOH:O	1.58	1.01

All (4) 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)
8:C:375:HOH:O	8:D:587:HOH:O[2_556]	1.91	0.29
8:A:401:HOH:O	8:B:703:HOH:O[2_545]	2.09	0.11
8:A:612:HOH:O	8:B:364:HOH:O[2_545]	2.11	0.09
8:A:597:HOH:O	8:B:568:HOH:O[2_545]	2.16	0.04

## 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	254/288 (88%)	245 (96%)	9 (4%)	0	100	100
1	D	260/288 (90%)	251 (96%)	9 (4%)	0	100	100
2	B	256/288 (89%)	248 (97%)	8 (3%)	0	100	100
2	C	254/288 (88%)	246 (97%)	8 (3%)	0	100	100
All	All	1024/1152 (89%)	990 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	208/230 (90%)	206 (99%)	2 (1%)	73	64
1	D	213/230 (93%)	211 (99%)	2 (1%)	75	67
2	B	211/231 (91%)	207 (98%)	4 (2%)	52	37
2	C	207/231 (90%)	204 (99%)	3 (1%)	62	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	839/922 (91%)	828 (99%)	11 (1%)	70	52

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

Mol	Chain	Res	Type
2	C	67	ASN
2	C	250	GLN
1	D	143	LYS
1	D	118	THR
2	B	104[B]	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	250	GLN
1	D	65	ASN
1	A	236	GLN
1	A	250	GLN
2	B	142	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	CSX	D	168	1	3,6,7	0.97	0	1,6,8	1.56	0
1	CSX	A	168[A]	-	3,5,7	0.92	0	1,5,8	0.06	0
1	CSX	A	168[B]	-	3,6,7	1.15	0	1,6,8	2.58	1 (100%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSX	D	168	1	-	0/2/5/7	-
1	CSX	A	168[A]	-	-	0/2/4/7	-
1	CSX	A	168[B]	-	-	0/2/5/7	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	168[B]	CSX	CA-CB-SG	2.58	119.23	113.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	168	CSX	6	0
1	A	168[B]	CSX	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

15 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	NAP	B	270	-	46,52,52	1.46	7 (15%)	61,80,80	1.98	10 (16%)
5	DTT	D	271	-	7,7,7	1.03	0	4,8,8	2.07	1 (25%)
4	AX5	B	271	-	17,17,17	1.06	1 (5%)	20,22,22	2.48	5 (25%)
7	GOL	C	272	-	5,5,5	0.42	0	5,5,5	0.72	0
3	NAP	C	270	-	46,52,52	1.69	7 (15%)	61,80,80	1.73	9 (14%)
3	NAP	A	269	-	46,52,52	1.90	7 (15%)	61,80,80	1.93	10 (16%)
6	ACT	B	269	-	3,3,3	0.77	0	3,3,3	0.82	0
7	GOL	B	272	-	5,5,5	0.48	0	5,5,5	1.07	1 (20%)
7	GOL	C	273	-	5,5,5	0.60	0	5,5,5	0.68	0
3	NAP	D	269	-	46,52,52	1.53	8 (17%)	61,80,80	1.96	12 (19%)
4	AX5	D	270	-	17,17,17	1.72	4 (23%)	20,22,22	2.68	10 (50%)
4	AX5	C	271	-	17,17,17	1.84	3 (17%)	20,22,22	2.81	10 (50%)
4	AX5	A	270	-	17,17,17	1.74	3 (17%)	20,22,22	2.22	7 (35%)
6	ACT	C	269	-	3,3,3	1.00	0	3,3,3	1.68	1 (33%)

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	NAP	B	270	-	-	0/31/67/67	0/5/5/5
5	DTT	D	271	-	1/1/2/2	2/8/8/8	-
4	AX5	B	271	-	-	4/5/5/5	0/2/2/2
7	GOL	C	272	-	-	2/4/4/4	-
3	NAP	C	270	-	-	0/31/67/67	0/5/5/5
3	NAP	A	269	-	-	0/31/67/67	0/5/5/5
7	GOL	B	272	-	-	2/4/4/4	-
7	GOL	C	273	-	-	4/4/4/4	-
3	NAP	D	269	-	-	0/31/67/67	0/5/5/5
4	AX5	D	270	-	-	4/5/5/5	0/2/2/2
4	AX5	C	271	-	-	3/5/5/5	0/2/2/2
4	AX5	A	270	-	-	4/5/5/5	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	270	NAP	O7N-C7N	7.76	1.38	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	269	NAP	O7N-C7N	7.31	1.37	1.24
4	C	271	AX5	C4-N3	5.89	1.39	1.33
3	D	269	NAP	O7N-C7N	5.58	1.34	1.24
3	A	269	NAP	C2N-N1N	5.35	1.40	1.35

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	271	AX5	C2-N3-C4	8.41	121.69	115.50
3	A	269	NAP	N3A-C2A-N1A	-8.05	117.74	128.67
3	D	269	NAP	C4B-O4B-C1B	-7.53	103.03	109.92
3	B	270	NAP	N3A-C2A-N1A	-7.30	118.76	128.67
3	B	270	NAP	C3N-C7N-N7N	6.76	126.07	117.74

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	D	271	DTT	C2

5 of 25 torsion outliers are listed below:

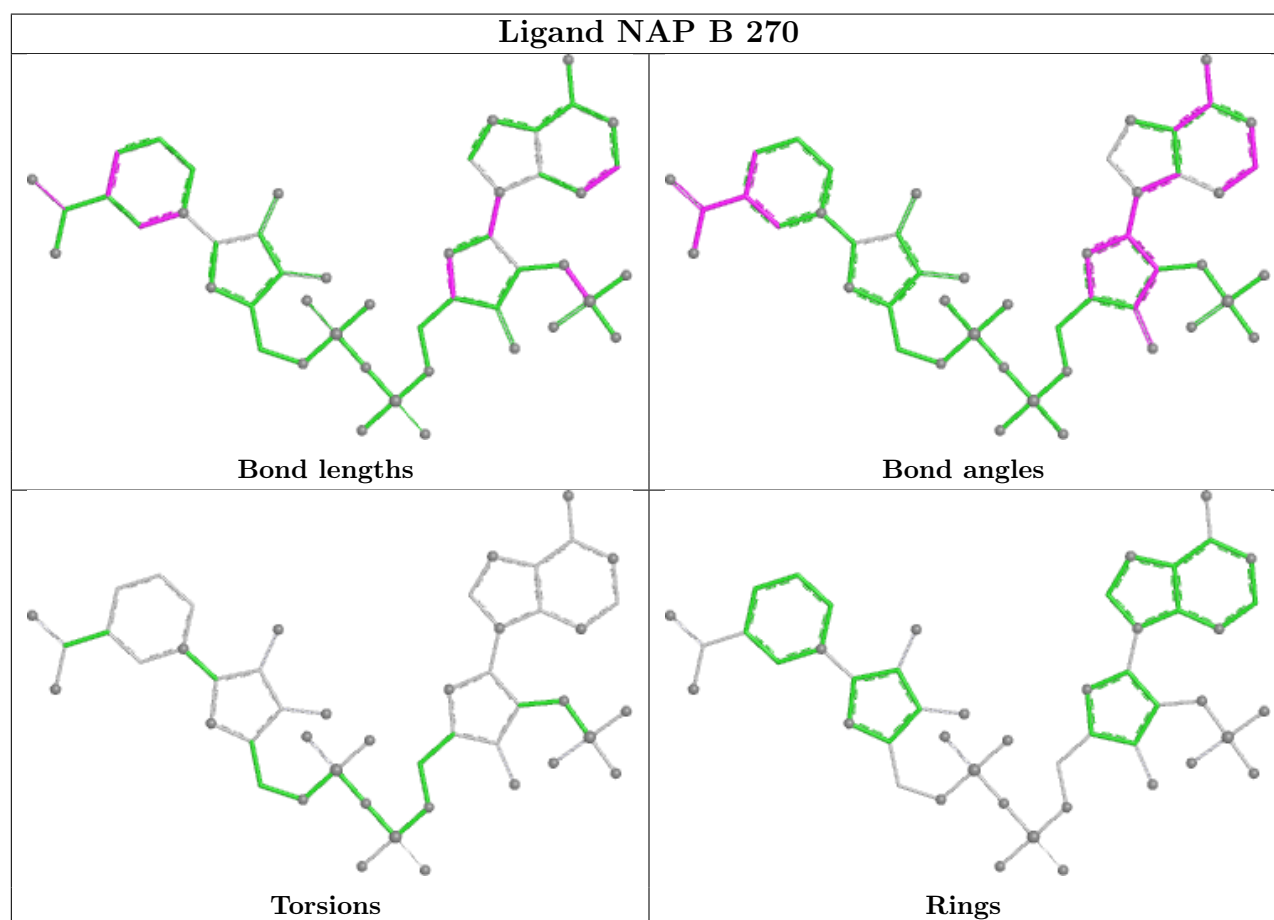
Mol	Chain	Res	Type	Atoms
5	D	271	DTT	C2-C3-C4-S4
7	B	272	GOL	C1-C2-C3-O3
7	C	272	GOL	C1-C2-C3-O3
7	C	273	GOL	O1-C1-C2-C3
7	C	273	GOL	C1-C2-C3-O3

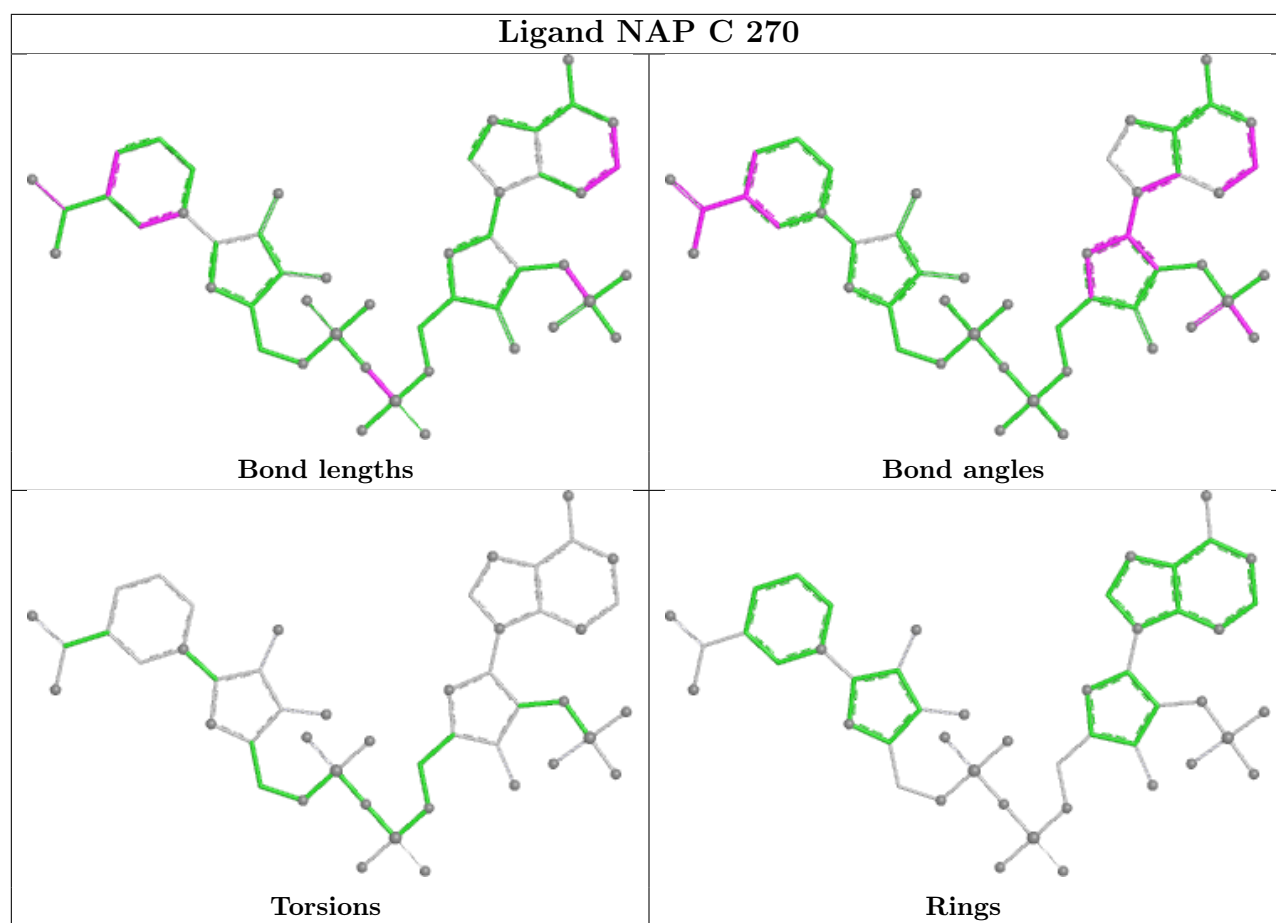
There are no ring outliers.

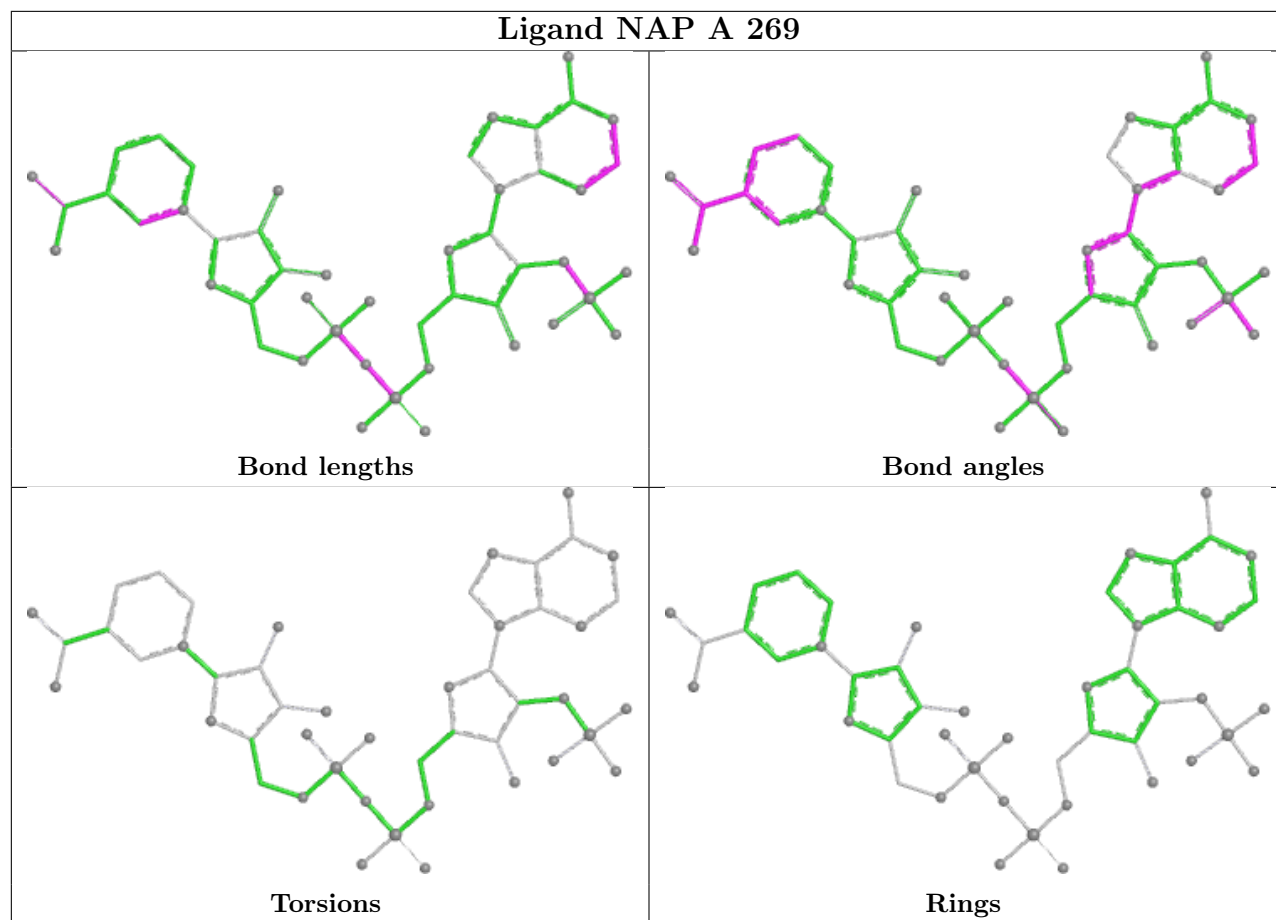
9 monomers are involved in 27 short contacts:

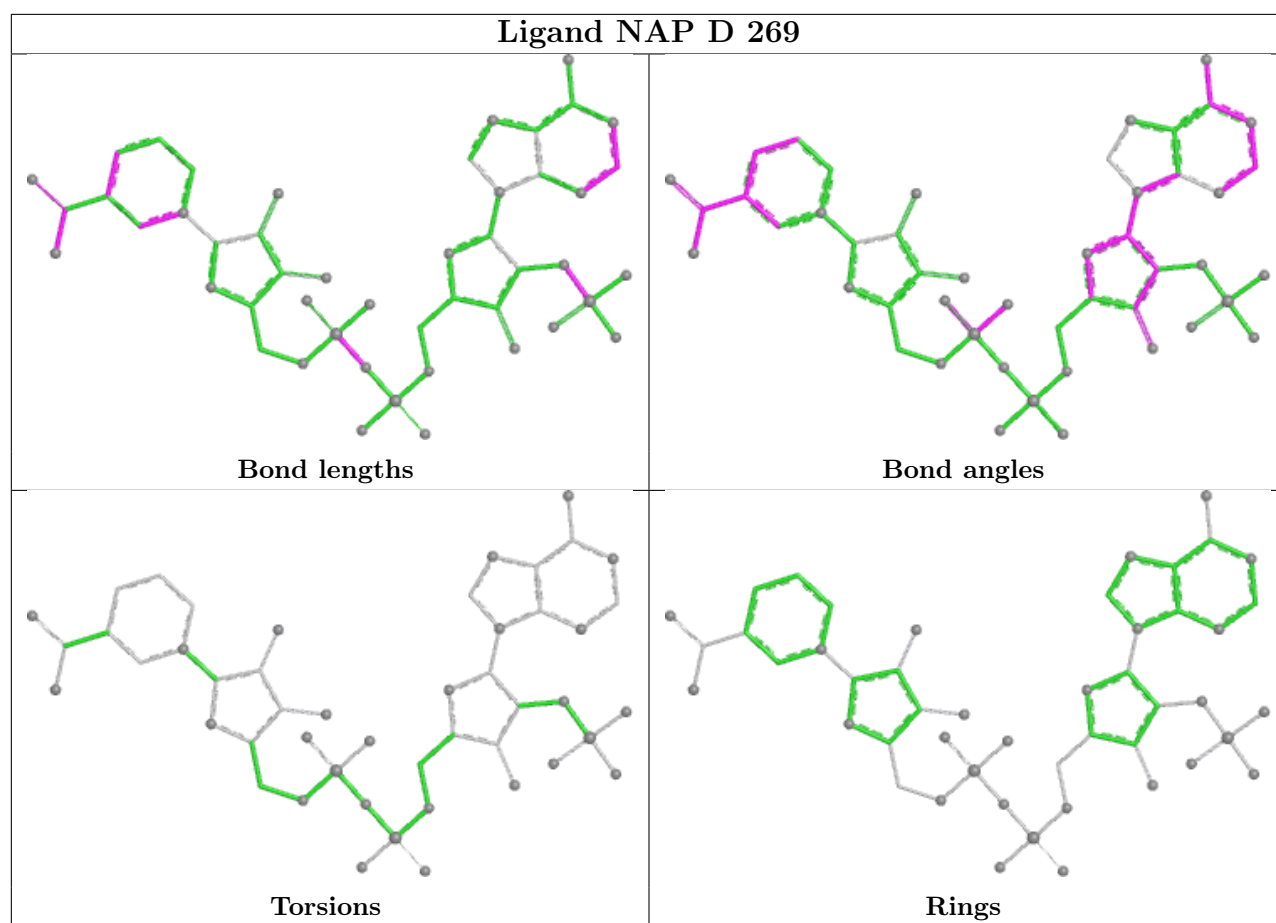
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	270	NAP	1	0
5	D	271	DTT	7	0
7	C	272	GOL	9	0
3	C	270	NAP	1	0
3	A	269	NAP	1	0
7	B	272	GOL	6	0
7	C	273	GOL	5	0
3	D	269	NAP	1	0
4	D	270	AX5	1	0

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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	252/288 (87%)	-0.51	3 (1%) 76 79	4, 9, 19, 37	9 (3%)
1	D	252/288 (87%)	-0.30	5 (1%) 64 68	5, 9, 21, 41	14 (5%)
2	B	252/288 (87%)	-0.53	4 (1%) 70 73	4, 8, 19, 44	11 (4%)
2	C	251/288 (87%)	-0.36	2 (0%) 82 85	4, 9, 20, 32	9 (3%)
All	All	1007/1152 (87%)	-0.42	14 (1%) 73 76	4, 9, 20, 44	43 (4%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	105	GLY	4.9
1	D	104	GLN	4.9
1	D	113	GLY	3.3
1	A	151[A]	SER	3.3
1	D	144	GLY	3.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CSX	D	168	7/8	0.93	0.07	11,15,29,29	0
1	CSX	A	168[B]	7/8	0.95	0.07	11,12,13,18	4
1	CSX	A	168[A]	6/8	0.95	0.07	12,13,14,19	3

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

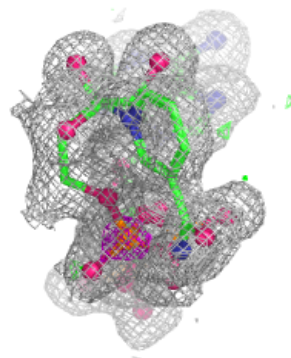
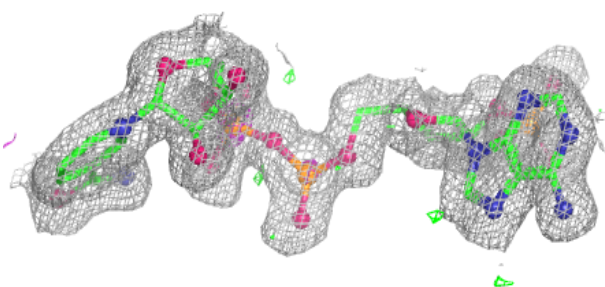
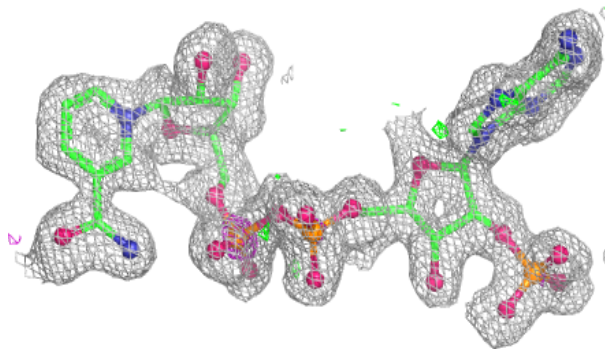
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	DTT	D	271	8/8	0.83	0.12	23,36,38,47	0
5	DTT	A	271[A]	8/8	0.84	0.15	44,49,51,56	0
7	GOL	C	272	6/6	0.87	0.16	39,41,42,44	0
7	GOL	B	272	6/6	0.89	0.13	28,28,31,32	0
7	GOL	C	273	6/6	0.90	0.09	25,30,32,34	0
4	AX5	B	271	16/16	0.95	0.06	6,10,20,20	0
4	AX5	D	270	16/16	0.95	0.07	8,12,25,27	0
6	ACT	C	269	4/4	0.95	0.07	13,16,19,20	0
4	AX5	C	271	16/16	0.96	0.06	7,12,24,25	0
4	AX5	A	270	16/16	0.97	0.05	5,10,19,21	0
3	NAP	D	269	48/48	0.98	0.04	4,7,10,13	0
6	ACT	B	269	4/4	0.98	0.04	10,10,11,12	0
3	NAP	A	269	48/48	0.99	0.04	2,6,9,12	0
3	NAP	B	270	48/48	0.99	0.04	2,6,8,8	0
3	NAP	C	270	48/48	0.99	0.04	4,7,9,11	0

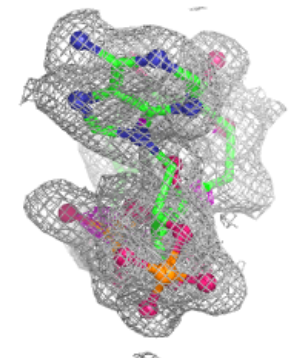
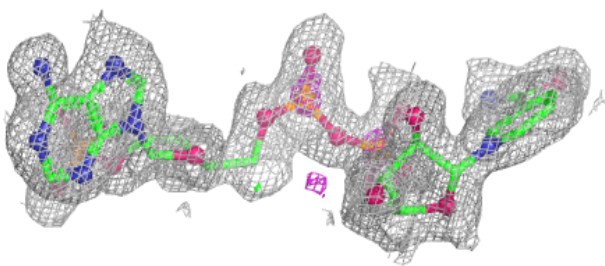
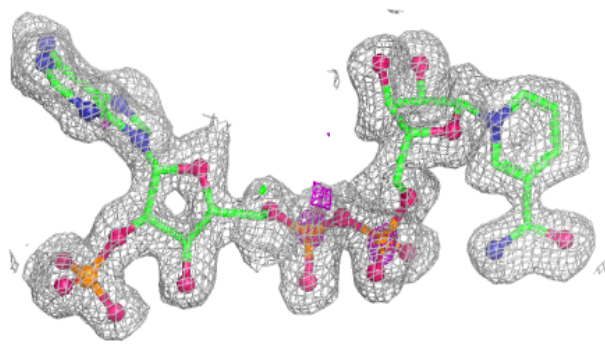
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NAP D 269:**

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

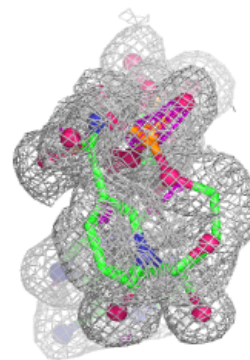
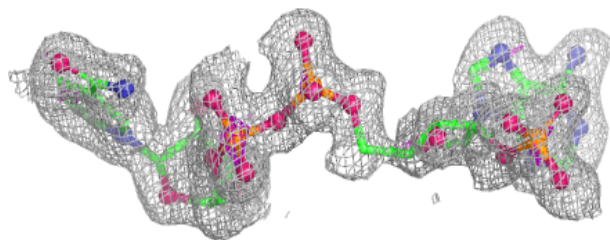
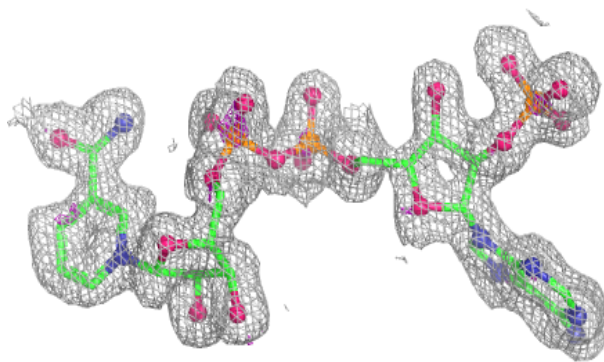
**Electron density around NAP A 269:**

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

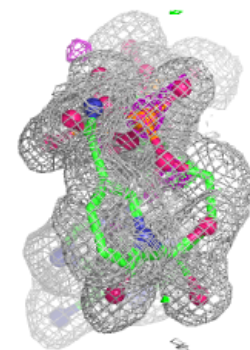
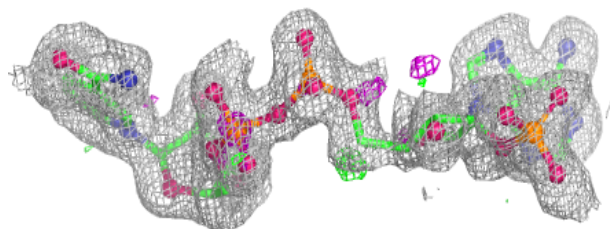
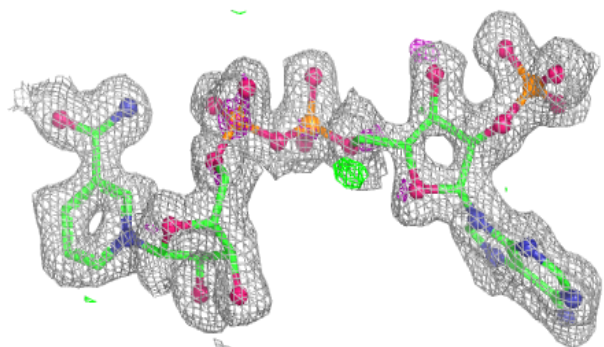


**Electron density around NAP B 270:**

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

**Electron density around NAP C 270:**

$2mF_o-DF_c$  (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.