



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2025 – 06:50 PM EDT

PDB ID : 3BMN  
Title : Structure of Pteridine Reductase 1 (PTR1) from Trypanosoma brucei in ternary complex with cofactor (NADP+) and inhibitor (Compound AX3)  
Authors : Martini, V.P.; Iulek, J.; Tulloch, L.B.; Hunter, W.N.  
Deposited on : 2007-12-13  
Resolution : 1.98 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

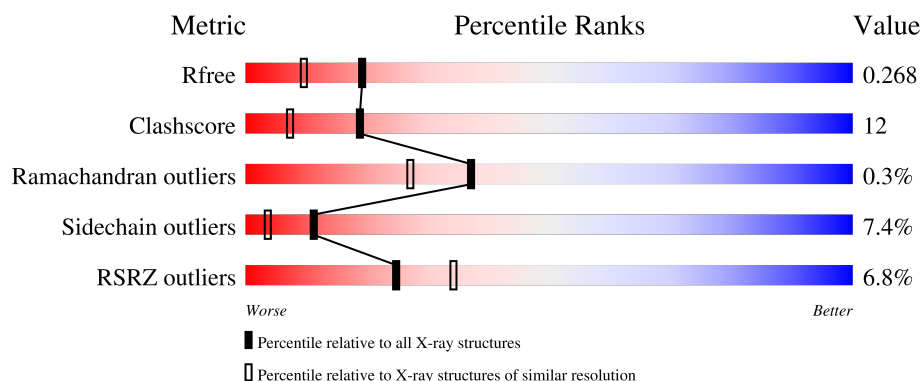
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.98 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))
$R_{free}$	164625	1356 (1.98-1.98)
Clashscore	180529	1437 (1.98-1.98)
Ramachandran outliers	177936	1426 (1.98-1.98)
Sidechain outliers	177891	1426 (1.98-1.98)
RSRZ outliers	164620	1356 (1.98-1.98)

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>5%</div> <div>66%</div> <div>18%</div> <div>13%</div> </div>
2	B	288	<div> <div>8%</div> <div>67%</div> <div>17%</div> <div>12%</div> </div>
2	C	288	<div> <div>5%</div> <div>67%</div> <div>19%</div> <div>13%</div> </div>
2	D	288	<div> <div>6%</div> <div>68%</div> <div>17%</div> <div>12%</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
5	GOL	A	273[B]	-	-	X	-
6	EDO	D	273	-	-	X	-

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 8465 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	251	Total	C	N	O	S	0	8	0
			1907	1205	333	358	11			

There are 20 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

- Molecule 2 is a protein called Pteridine reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	252	Total	C	N	O	S	0	5	0
			1904	1201	334	357	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	251	Total	C	N	O	S	0	6	0
			1895	1193	331	358	13			
2	D	253	Total	C	N	O	S	0	7	0
			1921	1210	338	362	11			

There are 60 discrepancies between the modelled and reference sequences:

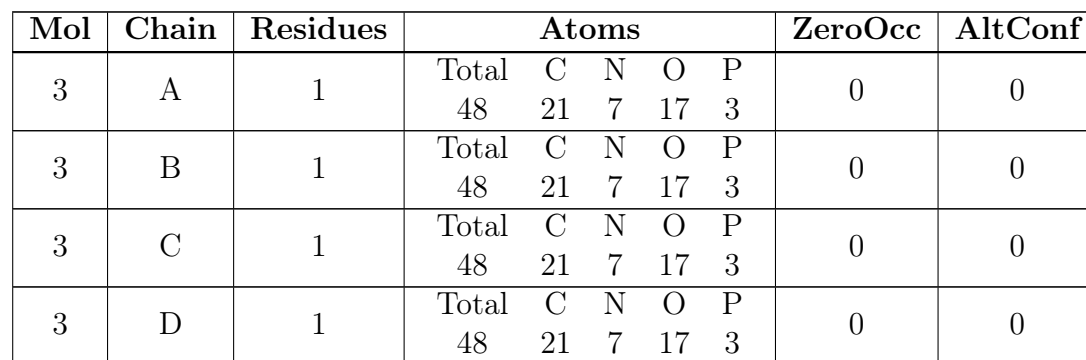
Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	expression tag	UNP O76290
B	-18	GLY	-	expression tag	UNP O76290
B	-17	SER	-	expression tag	UNP O76290
B	-16	SER	-	expression tag	UNP O76290
B	-15	HIS	-	expression tag	UNP O76290
B	-14	HIS	-	expression tag	UNP O76290
B	-13	HIS	-	expression tag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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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

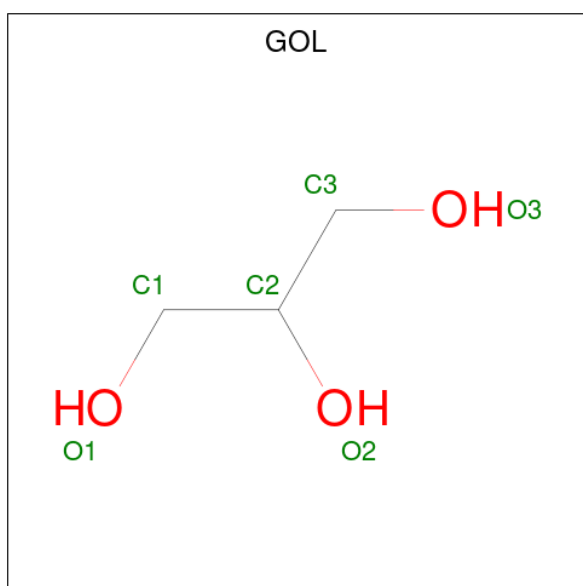
- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



- AX3
- 
- Chemical structure of AX3 (2,4,6-triaminopyrimidin-5-(1H-cyclopropyl)amine). The structure shows a pyrimidine ring with amino groups at positions 2, 4, and 6. A cyclopropylmethyl group is attached to the nitrogen at position 5. Labels in green indicate atom types: NAA for amino nitrogens, NAF for ring nitrogens, CAI for ring carbons, CAJ for the cyclopropylmethyl chain carbons, CAD for cyclopropyl ring carbons, and CAC for the cyclopropyl ring carbons. Labels in blue indicate atom types: H<sub>2</sub>N for amino groups and NH for the ring nitrogen.

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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 8 4 4	0	1
5	B	1	Total C O 8 4 4	0	1
5	C	1	Total C O 8 4 4	0	1
5	D	1	Total C O 6 3 3	0	0

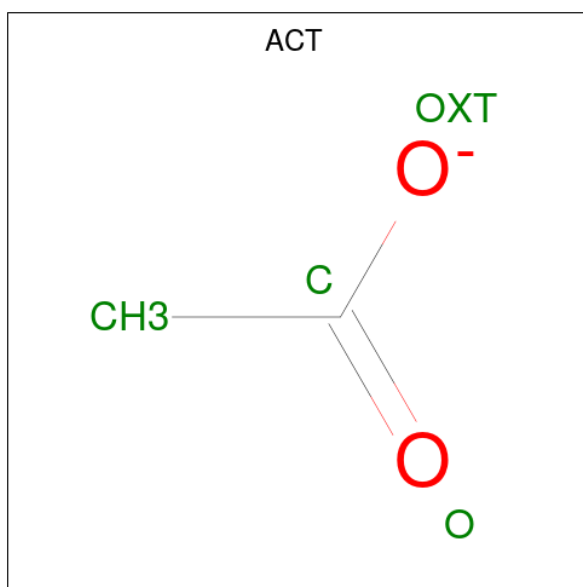
- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula:  $C_2H_6O_2$ ).





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

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	D	1	Total	C	O	0	0
			4	2	2		

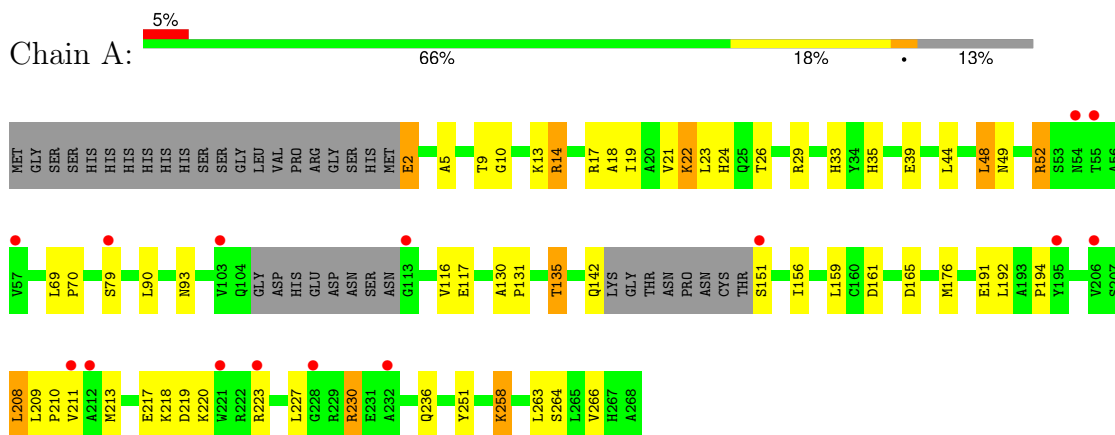
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	108	Total 108	O 108	0	0
8	B	153	Total 153	O 153	0	0
8	C	144	Total 144	O 144	0	0
8	D	135	Total 135	O 135	0	0

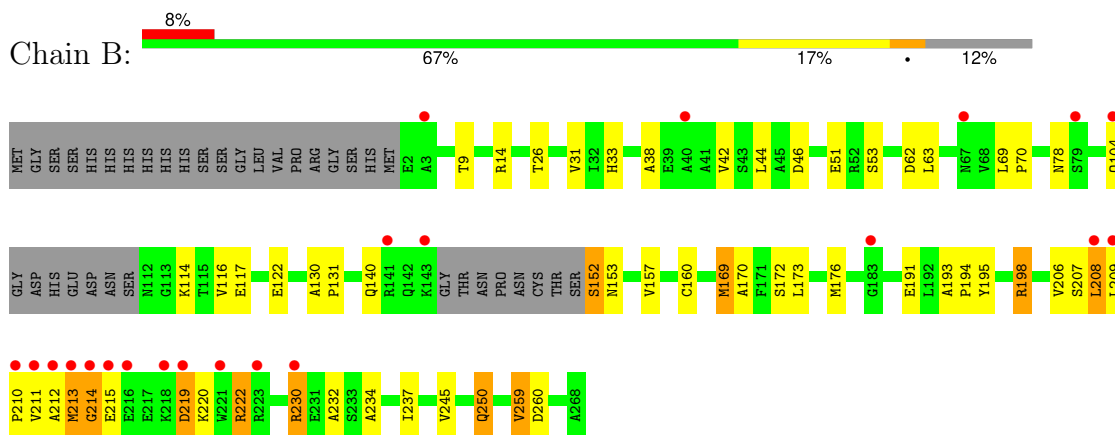
### 3 Residue-property plots [i](#)

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.

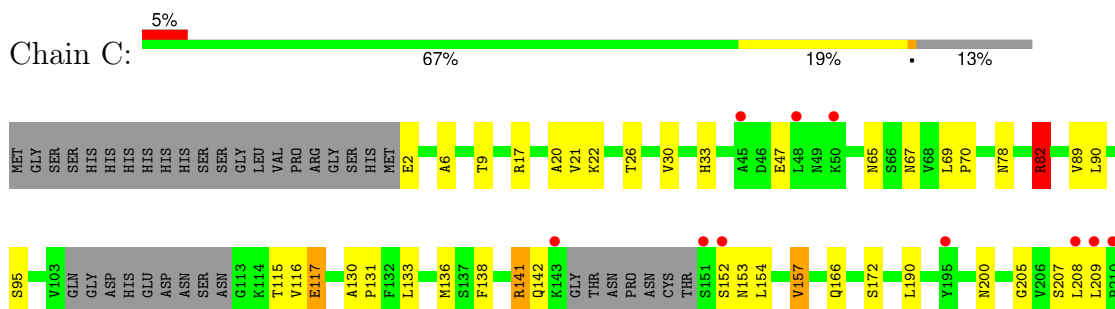
- Molecule 1: Pteridine reductase

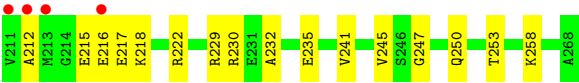


- Molecule 2: Pteridine reductase

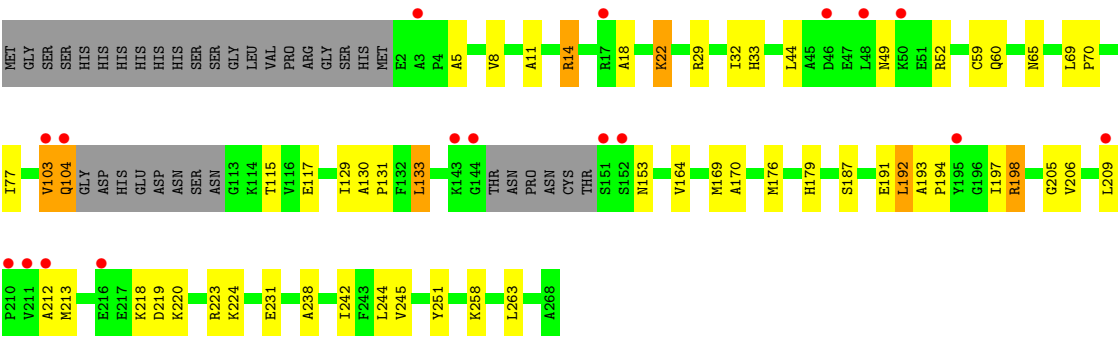


- Molecule 2: Pteridine reductase





● Molecule 2: Pteridine reductase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.84Å 87.50Å 84.23Å 90.00° 116.08° 90.00°	Depositor
Resolution (Å)	75.59 – 1.98 75.59 – 1.98	Depositor EDS
% Data completeness (in resolution range)	96.0 (75.59-1.98) 96.0 (75.59-1.98)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.63 (at 1.98Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.206 , 0.267 0.213 , 0.268	Depositor DCC
$R_{free}$ test set	3210 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtriage
Anisotropy	1.020	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 56.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8465	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	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 26.51 % 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 2.5983e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: NAP, CSX, EDO, AX3, GOL, ACT

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	0.33	0/1950	0.98	7/2644 (0.3%)
2	B	0.36	0/1946	0.97	6/2639 (0.2%)
2	C	0.34	0/1940	0.93	3/2630 (0.1%)
2	D	0.38	0/1969	0.93	4/2666 (0.2%)
All	All	0.35	0/7805	0.95	20/10579 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1

There are no bond length outliers.

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	ASP	CB-CG-OD1	-10.73	108.64	118.30
2	D	198	ARG	NE-CZ-NH2	-9.79	115.41	120.30
1	A	14	ARG	NE-CZ-NH2	-9.71	115.44	120.30
2	D	198	ARG	NE-CZ-NH1	8.40	124.50	120.30
1	A	52	ARG	NE-CZ-NH1	6.96	123.78	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	212	ALA	Peptide

## 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	1907	0	1964	58	0
2	B	1904	0	1950	39	0
2	C	1895	0	1935	37	0
2	D	1921	0	1971	64	0
3	A	48	0	25	5	0
3	B	48	0	25	0	0
3	C	48	0	25	2	0
3	D	48	0	25	1	0
4	A	12	0	10	2	0
4	B	12	0	10	2	0
4	C	12	0	10	1	0
4	D	12	0	10	0	0
5	A	20	0	24	4	0
5	B	8	0	8	0	0
5	C	8	0	8	0	0
5	D	6	0	8	0	0
6	C	4	0	6	0	0
6	D	8	0	12	11	0
7	D	4	0	3	0	0
8	A	108	0	0	6	0
8	B	153	0	0	10	0
8	C	144	0	0	10	0
8	D	135	0	0	10	0
All	All	8465	0	8029	187	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 187 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)
2:D:103:VAL:HG13	2:D:104:GLN:N	1.87	0.90
8:B:325:HOH:O	2:D:103:VAL:HG12	1.75	0.87
1:A:131:PRO:O	1:A:135:THR:HG23	1.75	0.85
2:D:77:ILE:HG12	8:D:365:HOH:O	1.75	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:GLN:HE21	2:B:250[B]:GLN:HG3	1.43	0.83

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	252/288 (88%)	241 (96%)	11 (4%)	0	100	100
2	B	251/288 (87%)	235 (94%)	14 (6%)	2 (1%)	16	7
2	C	251/288 (87%)	240 (96%)	11 (4%)	0	100	100
2	D	254/288 (88%)	242 (95%)	11 (4%)	1 (0%)	30	20
All	All	1008/1152 (88%)	958 (95%)	47 (5%)	3 (0%)	37	27

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	213	MET
2	B	214	GLY
2	D	103	VAL

### 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	206/230 (90%)	191 (93%)	15 (7%)	11	4
2	B	205/231 (89%)	182 (89%)	23 (11%)	5	1
2	C	205/231 (89%)	184 (90%)	21 (10%)	6	1
2	D	207/231 (90%)	200 (97%)	7 (3%)	32	21
All	All	823/923 (89%)	757 (92%)	66 (8%)	11	2

5 of 66 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	230	ARG
2	D	22[A]	LYS
2	D	231	GLU
2	B	104	GLN
2	B	78	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	65	ASN
2	D	54	ASN
2	B	140	GLN
2	B	112	ASN
2	C	250	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	A	168	1	3,6,7	0.62	0	1,6,8	0.81	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSX	A	168	1	-	0/2/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

21 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
7	ACT	D	269	-	3,3,3	0.75	0	3,3,3	1.85	1 (33%)
5	GOL	C	272[B]	-	5,5,5	0.31	0	5,5,5	0.90	0
5	GOL	A	273[B]	-	5,5,5	0.39	0	5,5,5	2.91	2 (40%)
5	GOL	B	271[B]	-	5,5,5	0.30	0	5,5,5	0.93	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAP	D	270	-	46,52,52	1.66	4 (8%)	61,80,80	2.29	15 (24%)
4	AX3	D	271	-	13,13,13	1.03	2 (15%)	18,18,18	2.72	8 (44%)
4	AX3	B	270	-	13,13,13	1.03	0	18,18,18	2.68	10 (55%)
5	GOL	C	272[A]	-	5,5,5	0.33	0	5,5,5	0.55	0
5	GOL	A	271	-	5,5,5	0.39	0	5,5,5	0.57	0
6	EDO	D	273	-	3,3,3	0.36	0	2,2,2	0.69	0
5	GOL	A	273[A]	-	5,5,5	0.38	0	5,5,5	2.80	2 (40%)
5	GOL	B	271[A]	-	5,5,5	0.29	0	5,5,5	0.99	0
3	NAP	B	269	-	46,52,52	1.74	6 (13%)	61,80,80	2.26	10 (16%)
6	EDO	C	271	-	3,3,3	0.45	0	2,2,2	0.23	0
6	EDO	D	272	-	3,3,3	0.47	0	2,2,2	0.42	0
3	NAP	C	269	-	46,52,52	1.69	4 (8%)	61,80,80	2.39	14 (22%)
3	NAP	A	269	-	46,52,52	1.68	3 (6%)	61,80,80	2.51	17 (27%)
5	GOL	A	272	-	5,5,5	0.37	0	5,5,5	0.47	0
4	AX3	A	270	-	13,13,13	1.02	1 (7%)	18,18,18	2.49	8 (44%)
4	AX3	C	270	-	13,13,13	0.94	1 (7%)	18,18,18	3.04	9 (50%)
5	GOL	D	274	-	5,5,5	0.37	0	5,5,5	0.81	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	C	272[B]	-	-	4/4/4/4	-
5	GOL	A	273[B]	-	-	2/4/4/4	-
5	GOL	B	271[B]	-	-	0/4/4/4	-
3	NAP	D	270	-	-	0/31/67/67	0/5/5/5
4	AX3	D	271	-	-	0/4/6/6	0/2/2/2
4	AX3	B	270	-	-	0/4/6/6	0/2/2/2
5	GOL	C	272[A]	-	-	4/4/4/4	-
5	GOL	A	271	-	-	2/4/4/4	-
6	EDO	D	273	-	-	1/1/1/1	-
5	GOL	A	273[A]	-	-	2/4/4/4	-
5	GOL	B	271[A]	-	-	0/4/4/4	-
3	NAP	B	269	-	-	0/31/67/67	0/5/5/5
6	EDO	C	271	-	-	1/1/1/1	-
6	EDO	D	272	-	-	0/1/1/1	-
3	NAP	C	269	-	-	1/31/67/67	0/5/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAP	A	269	-	-	1/31/67/67	0/5/5/5
5	GOL	A	272	-	-	2/4/4/4	-
4	AX3	A	270	-	-	0/4/6/6	0/2/2/2
4	AX3	C	270	-	-	0/4/6/6	0/2/2/2
5	GOL	D	274	-	-	0/4/4/4	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	269	NAP	O7N-C7N	8.98	1.40	1.24
3	C	269	NAP	O7N-C7N	8.80	1.40	1.24
3	B	269	NAP	O7N-C7N	8.74	1.40	1.24
3	D	270	NAP	O7N-C7N	8.59	1.40	1.24
3	D	270	NAP	C2A-N3A	4.09	1.38	1.32

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	269	NAP	O4B-C1B-N9A	9.78	121.71	108.75
3	C	269	NAP	O4B-C1B-N9A	8.97	120.64	108.75
3	D	270	NAP	O4B-C1B-N9A	8.82	120.44	108.75
3	B	269	NAP	C3N-C7N-N7N	8.28	127.94	117.74
3	B	269	NAP	O4B-C1B-N9A	7.97	119.31	108.75

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	269	NAP	C5D-O5D-PN-O2N
5	A	271	GOL	C1-C2-C3-O3
5	A	272	GOL	C1-C2-C3-O3
5	A	273[B]	GOL	O1-C1-C2-C3
5	C	272[A]	GOL	O1-C1-C2-C3

There are no ring outliers.

9 monomers are involved in 26 short contacts:

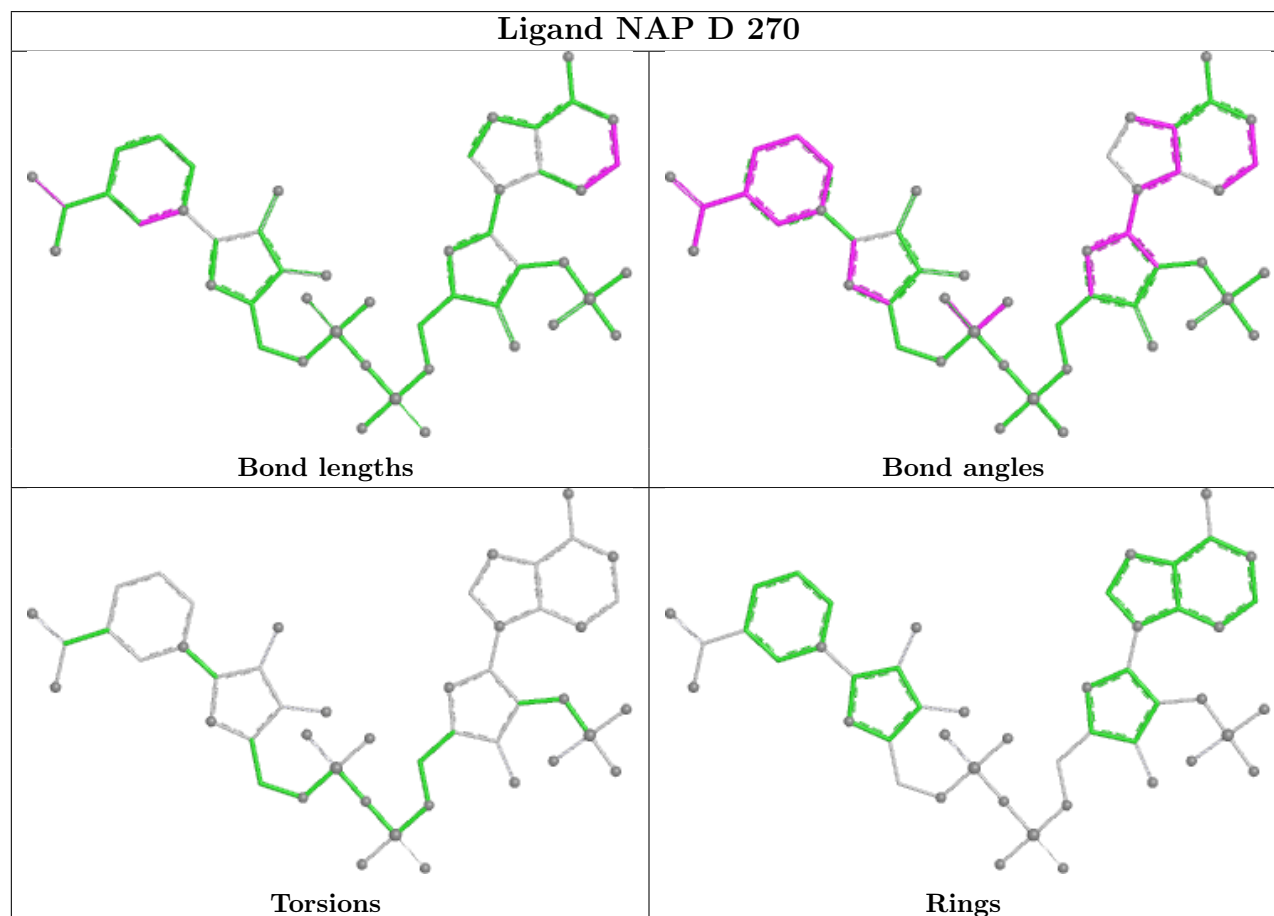
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	273[B]	GOL	4	0
3	D	270	NAP	1	0
4	B	270	AX3	2	0

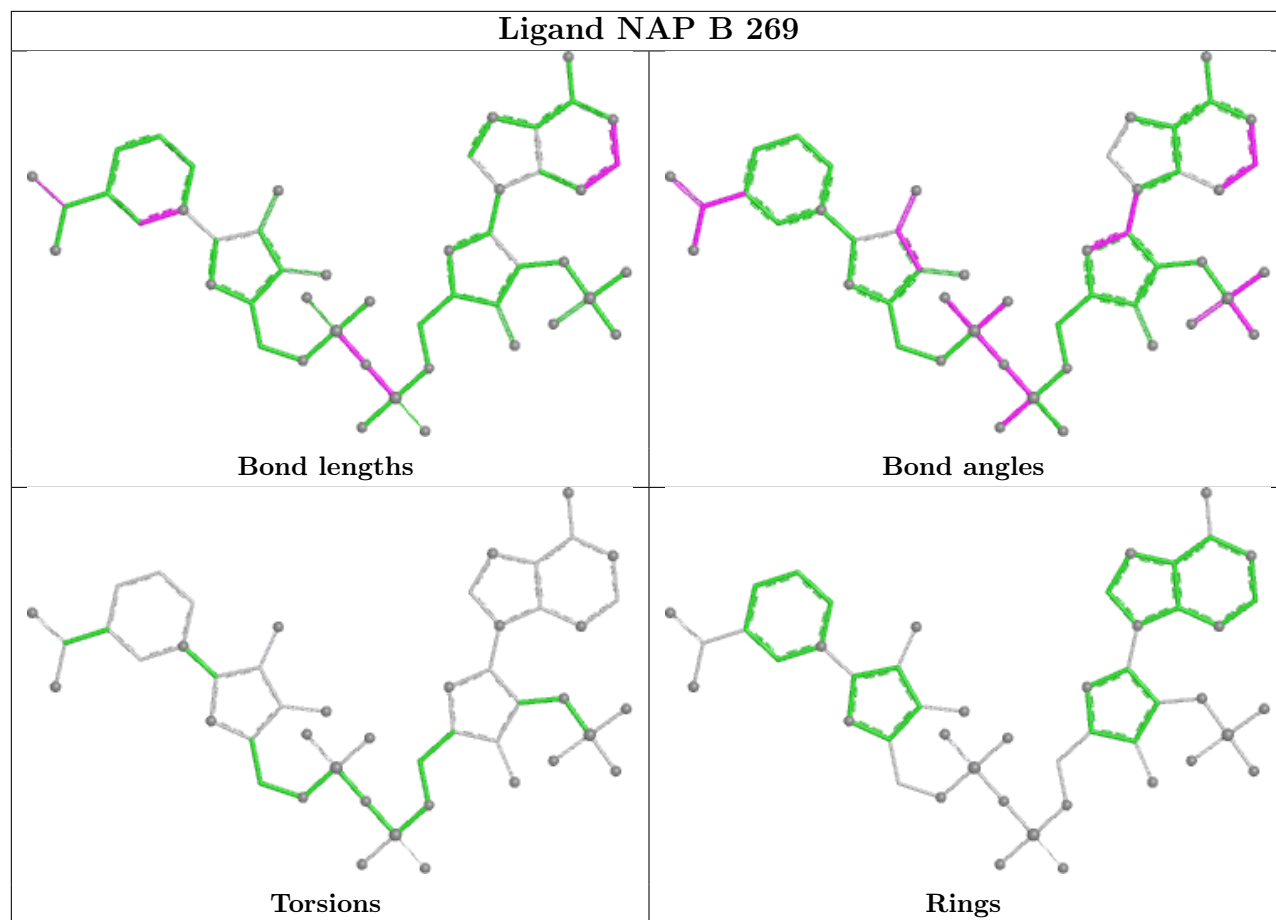
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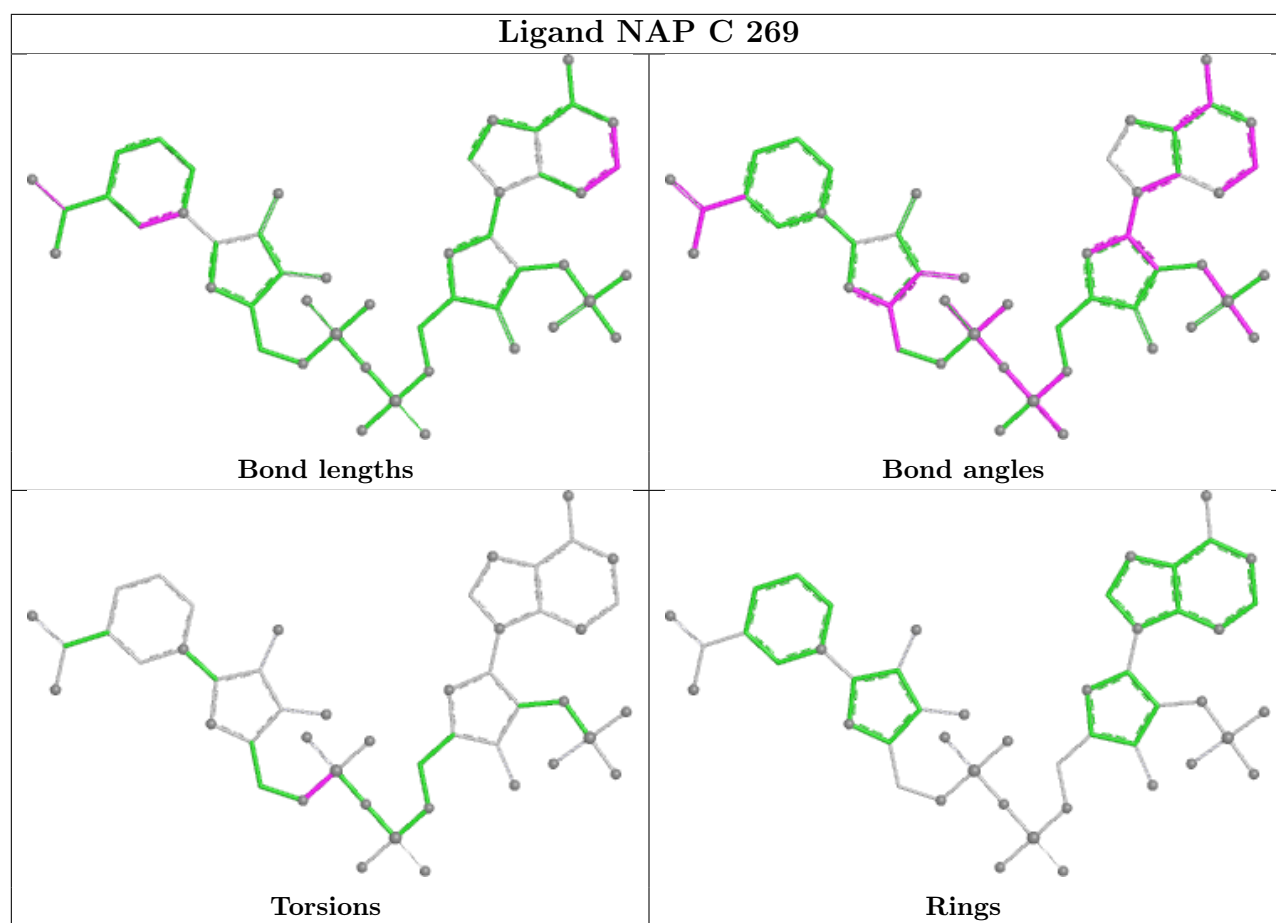
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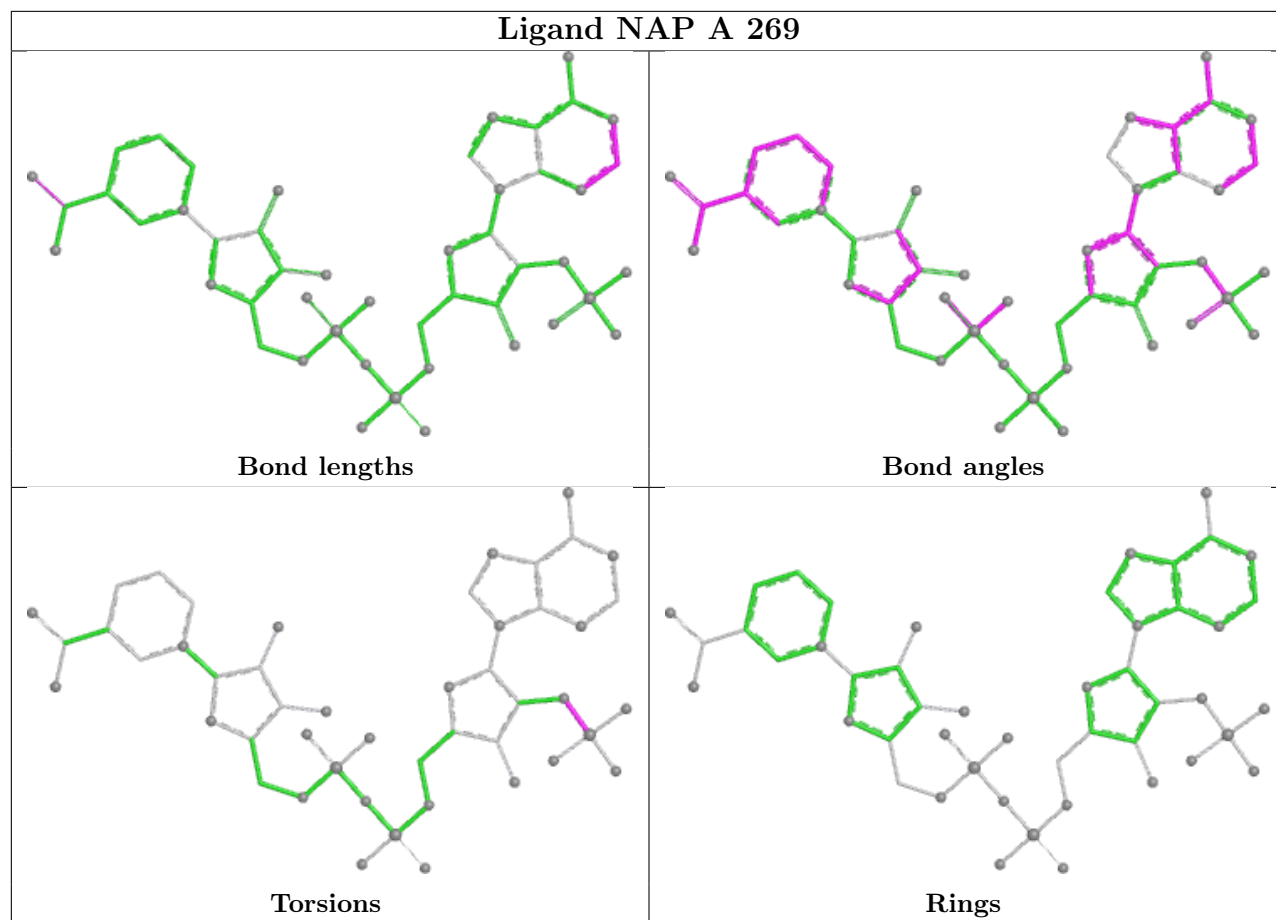
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	273	EDO	10	0
6	D	272	EDO	1	0
3	C	269	NAP	2	0
3	A	269	NAP	5	0
4	A	270	AX3	2	0
4	C	270	AX3	1	0

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	250/288 (86%)	0.78	15 (6%) 29 39	9, 24, 44, 52	8 (3%)
2	B	252/288 (87%)	0.89	22 (8%) 17 25	10, 24, 45, 64	6 (2%)
2	C	251/288 (87%)	0.78	14 (5%) 31 42	11, 24, 43, 57	6 (2%)
2	D	253/288 (87%)	0.84	17 (6%) 25 35	12, 24, 41, 56	7 (2%)
All	All	1006/1152 (87%)	0.82	68 (6%) 25 34	9, 24, 44, 64	27 (2%)

The worst 5 of 68 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	211	VAL	5.7
2	D	211	VAL	5.7
2	D	104	GLN	5.3
2	B	211	VAL	5.2
2	D	212	ALA	4.3

### 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	A	168	7/8	0.87	0.12	21,24,34,35	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

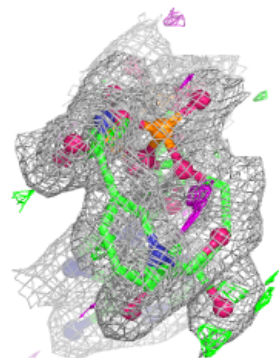
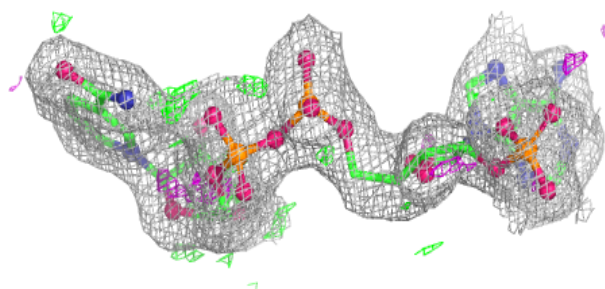
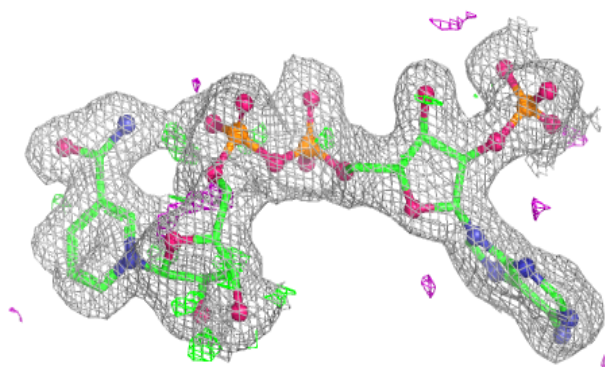
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	GOL	A	273[A]	6/6	0.76	0.22	25,39,41,44	2
5	GOL	A	273[B]	6/6	0.76	0.22	25,34,41,44	2
7	ACT	D	269	4/4	0.76	0.18	35,36,37,38	0
5	GOL	A	272	6/6	0.77	0.17	32,42,45,47	0
5	GOL	A	271	6/6	0.82	0.13	34,42,44,44	0
6	EDO	C	271	4/4	0.83	0.13	39,39,40,42	0
5	GOL	C	272[A]	6/6	0.84	0.14	24,30,33,34	2
5	GOL	C	272[B]	6/6	0.84	0.14	28,32,33,34	2
6	EDO	D	272	4/4	0.85	0.18	24,40,43,47	0
4	AX3	B	270	12/12	0.87	0.12	25,32,39,39	0
4	AX3	D	271	12/12	0.89	0.13	15,20,37,38	0
5	GOL	B	271[A]	6/6	0.89	0.12	12,26,31,33	2
5	GOL	B	271[B]	6/6	0.89	0.12	22,26,31,33	2
4	AX3	A	270	12/12	0.89	0.11	10,22,31,36	0
5	GOL	D	274	6/6	0.90	0.14	20,31,36,37	0
4	AX3	C	270	12/12	0.92	0.09	13,23,34,37	0
3	NAP	B	269	48/48	0.94	0.08	7,21,27,30	0
3	NAP	C	269	48/48	0.94	0.08	8,21,25,31	0
3	NAP	A	269	48/48	0.95	0.08	4,23,31,33	0
6	EDO	D	273	4/4	0.95	0.11	21,23,23,27	0
3	NAP	D	270	48/48	0.95	0.08	2,23,27,31	0

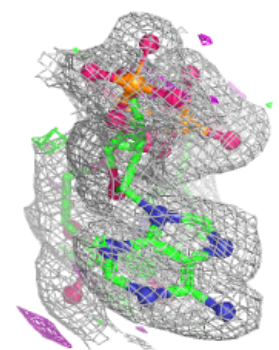
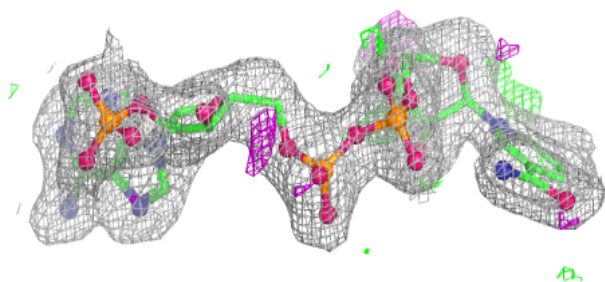
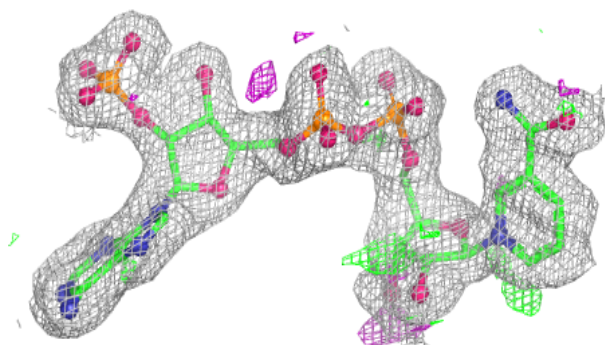
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around NAP B 269:**

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

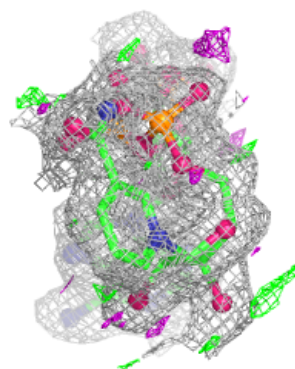
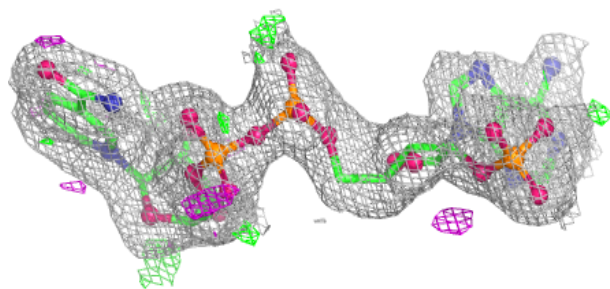
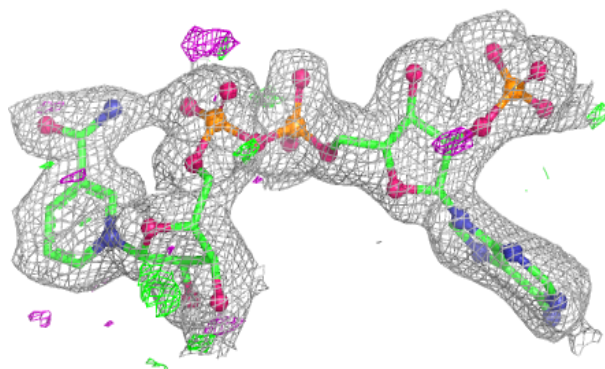
**Electron density around NAP C 269:**

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

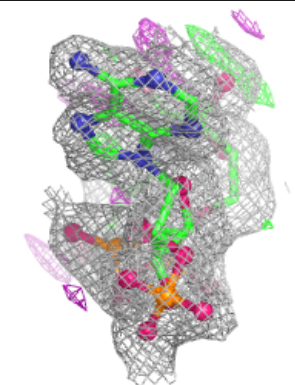
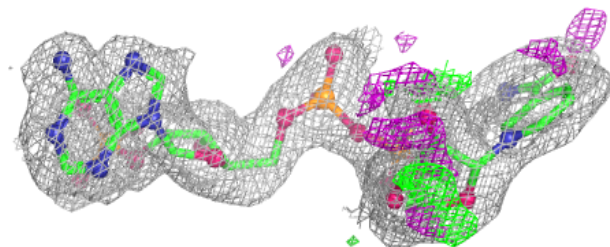
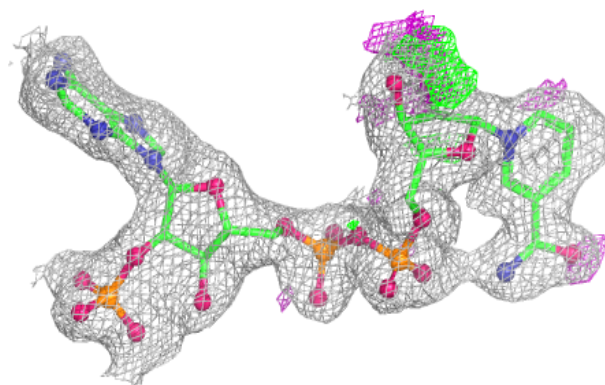


**Electron density around NAP A 269:**

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

**Electron density around NAP D 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.