wwPDB X-ray Structure Validation Summary Report (i)

Mar 8, 2026 – 04:43 PM UTC

PDB ID	:	5JDC / pdb_00005jdc
Title	:	Trypanosoma brucei PTR1 in complex with inhibitor NP-13 (Hesperetin)
Authors	:	Mangani, S.; Pozzi, C.; Di Pisa, F.; Landi, G.; Dello Iacono, L.
Deposited on	:	2016-04-16
Resolution	:	1.78 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

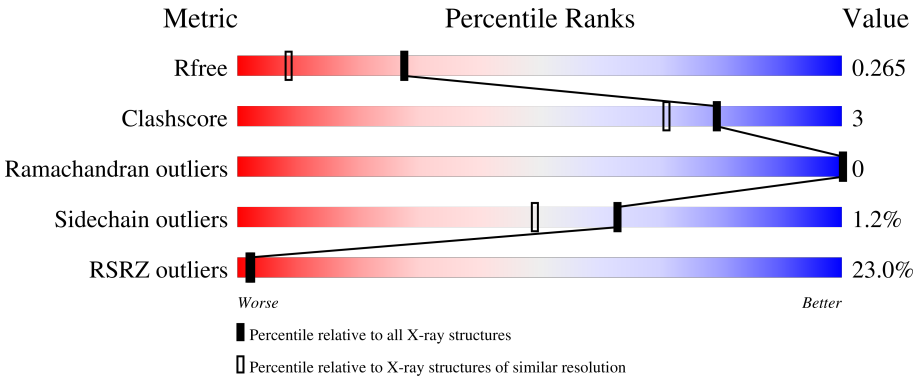
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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}	180053	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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 >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	288	21% 80% 6% 14%
1	B	288	10% 80% 5% 15%
1	D	288	25% 78% 8% 14%
2	C	288	22% 74% 9% 17%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7836 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	249	Total	C	N	O	S	0	0	0
			1845	1161	326	347	11			
1	B	246	Total	C	N	O	S	0	3	0
			1838	1156	320	350	12			
1	D	248	Total	C	N	O	S	0	2	0
			1831	1152	325	343	11			

There are 60 discrepancies between the modelled and reference sequences:

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

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Chain	Residue	Modelled	Actual	Comment	Reference
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
D	-19	MET	-	initiating methionine	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

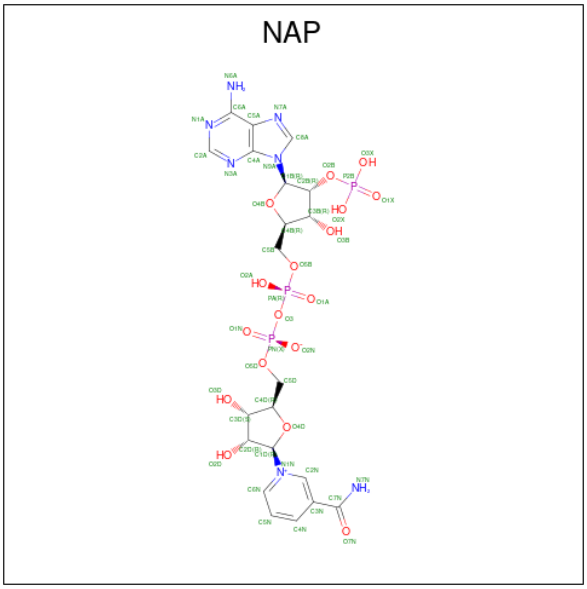
- Molecule 2 is a protein called Pteridine reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	239	Total	C	N	O	S	0	0	0
			1771	1114	313	334	10			

There are 20 discrepancies between the modelled and reference sequences:

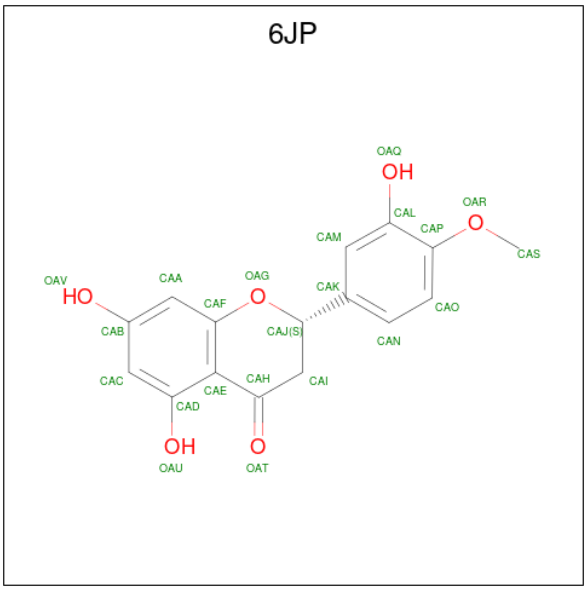
Chain	Residue	Modelled	Actual	Comment	Reference
C	-19	MET	-	initiating methionine	UNP O76290
C	-18	GLY	-	expression tag	UNP O76290
C	-17	SER	-	expression tag	UNP O76290
C	-16	SER	-	expression tag	UNP O76290
C	-15	HIS	-	expression tag	UNP O76290
C	-14	HIS	-	expression tag	UNP O76290
C	-13	HIS	-	expression 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 (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



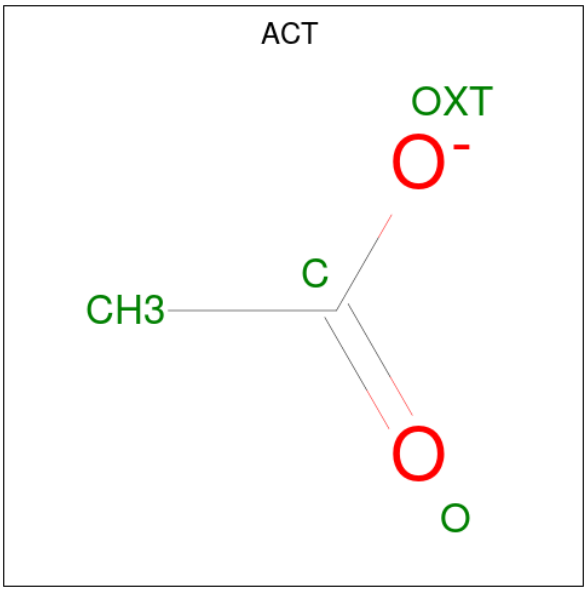
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 48 21 7 17 3	0	0
3	B	1	Total C N O P 48 21 7 17 3	0	0
3	C	1	Total C N O P 48 21 7 17 3	0	0
3	D	1	Total C N O P 48 21 7 17 3	0	0

- Molecule 4 is (2S)-5,7-dihydroxy-2-(3-hydroxy-4-methoxyphenyl)-2,3-dihydro-4H-1-benzopyran-4-one (CCD ID: 6JP) (formula: $C_{16}H_{14}O_6$).



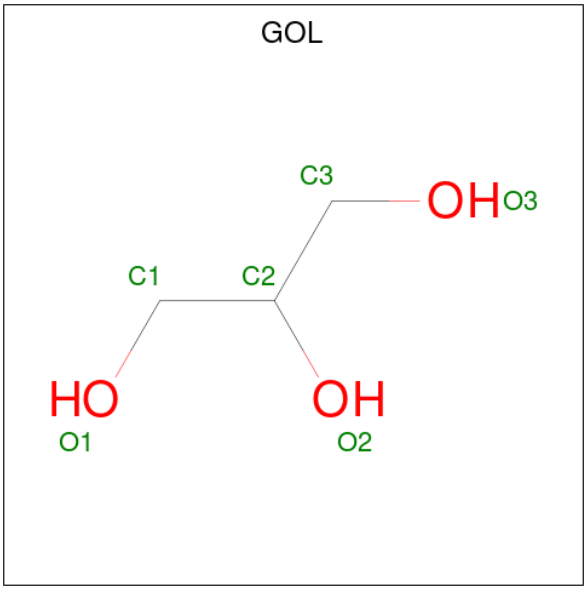
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 22 16 6	0	0
4	B	1	Total C O 22 16 6	0	0
4	C	1	Total C O 22 16 6	0	0
4	D	1	Total C O 22 16 6	0	0

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is water.

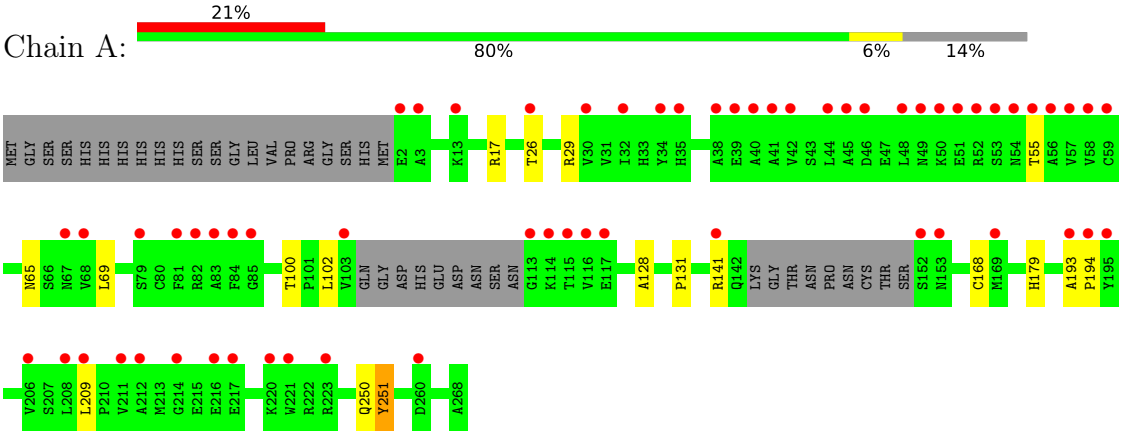
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	66	Total O 66 66	0	0
7	B	86	Total O 86 86	0	0
7	C	54	Total O 54 54	0	0
7	D	51	Total O 51 51	0	0

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.

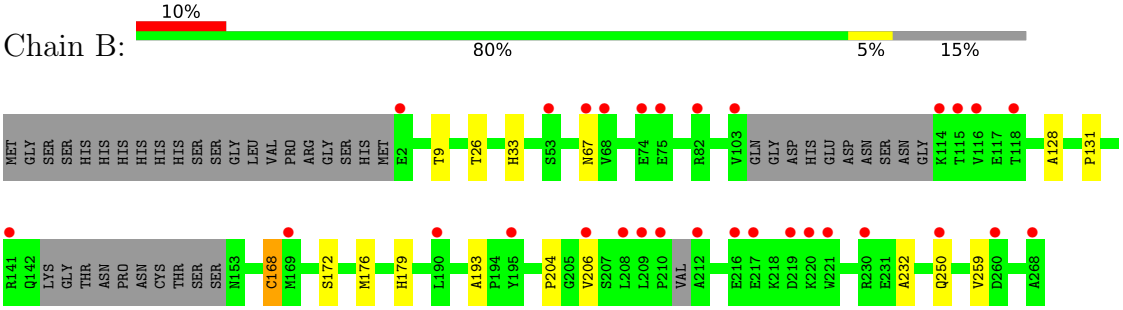
• Molecule 1: Pteridine reductase

Chain A:



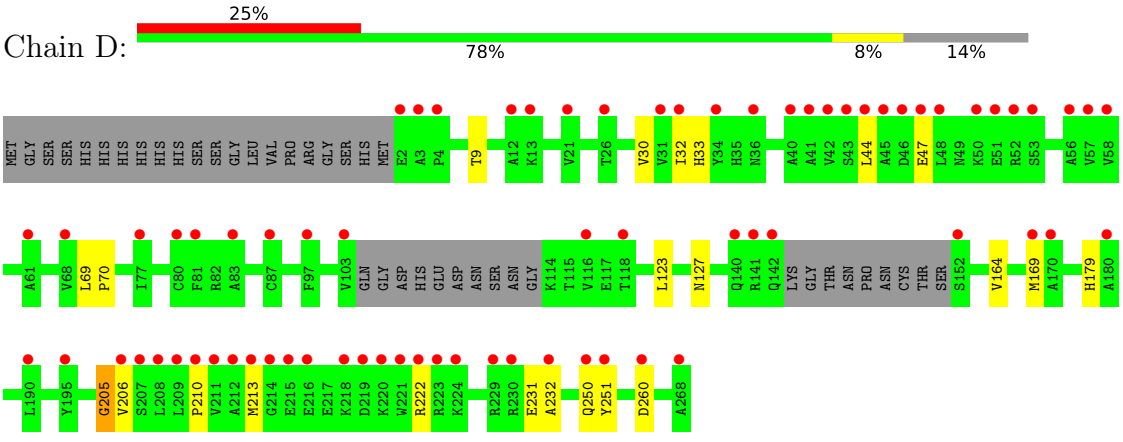
• Molecule 1: Pteridine reductase

Chain B:



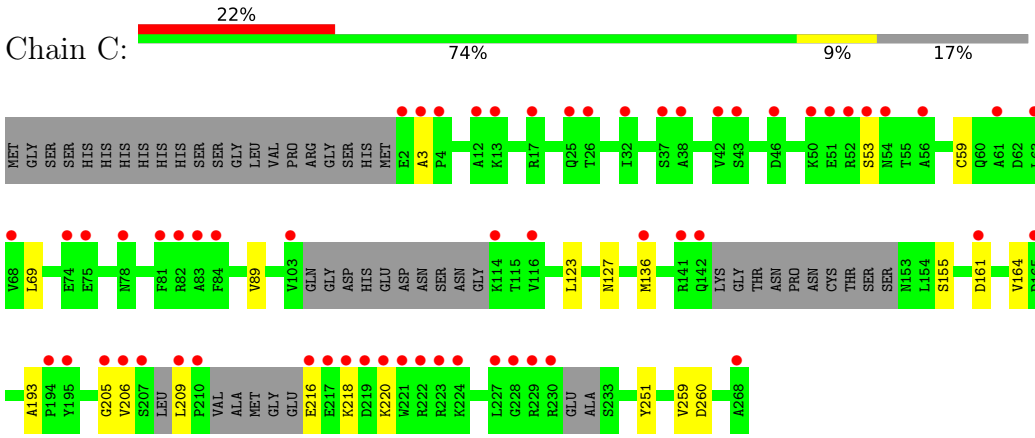
• Molecule 1: Pteridine reductase

Chain D:



• Molecule 2: Pteridine reductase

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	74.84Å 90.04Å 82.94Å 90.00° 115.78° 90.00°	Depositor
Resolution (Å)	53.68 – 1.78 53.68 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.1 (53.68-1.78) 99.1 (53.68-1.78)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.45 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.208 , 0.241 (Not available) , 0.265	Depositor DCC
R_{free} test set	4615 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å^2)	14.5	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 33.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.008 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	7836	wwPDB-VP
Average B, all atoms (Å^2)	21.0	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 38.38 % 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 3.7194e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: OCS, 6JP, GOL, NAP, CSX, 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	1.18	1/1864 (0.1%)	1.10	2/2528 (0.1%)
1	B	1.35	3/1855 (0.2%)	1.11	4/2516 (0.2%)
1	D	1.19	1/1856 (0.1%)	1.13	5/2520 (0.2%)
2	C	1.22	2/1777 (0.1%)	1.11	4/2408 (0.2%)
All	All	1.24	7/7352 (0.1%)	1.11	15/9972 (0.2%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	259	VAL	C-N	22.85	1.64	1.33
1	B	193	ALA	C-O	-6.00	1.19	1.24
1	B	204	PRO	CA-C	-5.78	1.45	1.52
1	D	205	GLY	C-N	-5.61	1.26	1.33
2	C	193	ALA	C-O	-5.48	1.19	1.24

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	206	VAL	CA-C-O	8.90	129.91	120.48
2	C	259	VAL	O-C-N	6.42	130.60	122.57
2	C	205	GLY	N-CA-C	-6.35	104.43	110.21
1	D	251	TYR	CA-C-O	6.28	126.59	119.18
1	D	205	GLY	O-C-N	-6.13	114.73	122.70

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	1845	0	1867	13	0
1	B	1838	0	1846	9	0
1	D	1831	0	1846	11	0
2	C	1771	0	1776	10	0
3	A	48	0	25	0	0
3	B	48	0	25	0	0
3	C	48	0	25	0	0
3	D	48	0	25	1	0
4	A	22	0	0	1	0
4	B	22	0	0	3	0
4	C	22	0	0	0	0
4	D	22	0	0	0	0
5	A	4	0	3	1	0
5	C	4	0	3	0	0
6	C	6	0	8	0	0
7	A	66	0	0	1	0
7	B	86	0	0	1	0
7	C	54	0	0	0	0
7	D	51	0	0	0	0
All	All	7836	0	7449	40	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 3.

The worst 5 of 40 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:B:168[A]:CSX:HG	4:B:302:6JP:CAS	1.81	0.94
2:C:161:ASP:HB3	2:C:164:VAL:HG13	1.76	0.67
1:A:141:ARG:HG2	7:A:465:HOH:O	1.95	0.66
1:A:193:ALA:HB3	1:A:194:PRO:HD3	1.82	0.60
1:A:251:TYR:CE2	1:B:232:ALA:HB2	2.37	0.59

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	242/288 (84%)	234 (97%)	8 (3%)	0	100	100
1	B	239/288 (83%)	233 (98%)	6 (2%)	0	100	100
1	D	243/288 (84%)	234 (96%)	9 (4%)	0	100	100
2	C	225/288 (78%)	218 (97%)	7 (3%)	0	100	100
All	All	949/1152 (82%)	919 (97%)	30 (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	193/230 (84%)	191 (99%)	2 (1%)	68	55
1	B	192/230 (84%)	191 (100%)	1 (0%)	81	73
1	D	191/230 (83%)	189 (99%)	2 (1%)	68	55
2	C	184/229 (80%)	180 (98%)	4 (2%)	45	26
All	All	760/919 (83%)	751 (99%)	9 (1%)	63	49

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	47	GLU
1	D	169	MET
2	C	53	SER

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Mol	Chain	Res	Type
2	C	166	GLN
2	C	216	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	54	ASN
2	C	92	ASN
1	D	179	HIS
1	D	92	ASN
1	D	140	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

6 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	B	168[B]	1	3,6,7	1.38	0	1,6,8	3.37	1 (100%)
2	CSX	C	168	2	3,6,7	0.48	0	1,6,8	1.16	0
1	CSX	A	168	1	3,6,7	0.54	0	1,6,8	1.10	0
1	CSX	B	168[A]	1	3,6,7	0.87	0	1,6,8	0.17	0
2	OCS	C	59	2	6,8,9	2.45	2 (33%)	7,11,13	1.71	2 (28%)
1	CSX	D	168	1	3,6,7	0.58	0	1,6,8	1.06	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	B	168[B]	1	-	2/2/5/7	-
2	CSX	C	168	2	-	0/2/5/7	-
1	CSX	A	168	1	-	0/2/5/7	-
1	CSX	B	168[A]	1	-	0/2/5/7	-
2	OCS	C	59	2	-	1/4/7/9	-
1	CSX	D	168	1	-	0/2/5/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	59	OCS	OD3-SG	5.00	1.59	1.45
2	C	59	OCS	CB-CA	-2.97	1.51	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	168[B]	CSX	CA-CB-SG	3.37	121.10	113.17
2	C	59	OCS	OD3-SG-CB	3.09	111.38	106.76
2	C	59	OCS	CA-CB-SG	-2.20	110.34	113.61

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	168[B]	CSX	N-CA-CB-SG
1	B	168[B]	CSX	C-CA-CB-SG
2	C	59	OCS	N-CA-CB-SG

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	168	CSX	1	0
1	B	168[A]	CSX	2	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

11 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	A	301	-	50,52,52	1.41	9 (18%)	71,80,80	1.64	14 (19%)
4	6JP	D	302	-	24,24,24	1.99	6 (25%)	35,35,35	1.53	6 (17%)
5	ACT	C	303	-	3,3,3	0.89	0	3,3,3	0.28	0
3	NAP	C	301	-	50,52,52	1.59	7 (14%)	71,80,80	1.73	17 (23%)
4	6JP	C	302	-	24,24,24	1.69	3 (12%)	35,35,35	1.73	7 (20%)
5	ACT	A	303	-	3,3,3	1.28	0	3,3,3	1.10	0
3	NAP	D	301	-	50,52,52	1.56	9 (18%)	71,80,80	1.87	18 (25%)
4	6JP	A	302	-	24,24,24	1.86	3 (12%)	35,35,35	1.65	6 (17%)
3	NAP	B	301	-	50,52,52	1.53	7 (14%)	71,80,80	1.92	18 (25%)
4	6JP	B	302	-	24,24,24	1.87	6 (25%)	35,35,35	2.18	9 (25%)
6	GOL	C	304	-	5,5,5	0.78	0	5,5,5	0.80	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAP	A	301	-	-	0/35/67/67	0/5/5/5
4	6JP	D	302	-	-	2/6/18/18	0/3/3/3
3	NAP	C	301	-	-	1/35/67/67	0/5/5/5
4	6JP	C	302	-	-	2/6/18/18	0/3/3/3
3	NAP	D	301	-	-	2/35/67/67	0/5/5/5
4	6JP	A	302	-	-	2/6/18/18	0/3/3/3
3	NAP	B	301	-	-	0/35/67/67	0/5/5/5
4	6JP	B	302	-	-	3/6/18/18	0/3/3/3
6	GOL	C	304	-	-	0/4/4/4	-

The worst 5 of 50 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	302	6JP	CAK-CAJ	-5.54	1.42	1.51
3	C	301	NAP	C5A-C4A	5.28	1.48	1.39
4	D	302	6JP	CAI-CAH	-4.93	1.41	1.50
3	C	301	NAP	PN-O3	4.93	1.64	1.59
4	B	302	6JP	CAI-CAH	-4.78	1.41	1.50

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	302	6JP	OAR-CAP-CAL	6.16	123.78	114.55
4	C	302	6JP	CAS-OAR-CAP	5.68	125.84	117.51
3	D	301	NAP	C4A-N9A-C8A	5.17	111.16	105.74
3	B	301	NAP	C3N-C7N-N7N	5.00	123.89	117.74
4	B	302	6JP	CAS-OAR-CAP	4.68	124.38	117.51

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	302	6JP	CAO-CAP-OAR-CAS
4	B	302	6JP	CAL-CAP-OAR-CAS
3	D	301	NAP	C5B-O5B-PA-O1A
3	C	301	NAP	C2B-O2B-P2B-O2X
4	C	302	6JP	CAI-CAJ-CAK-CAN

There are no ring outliers.

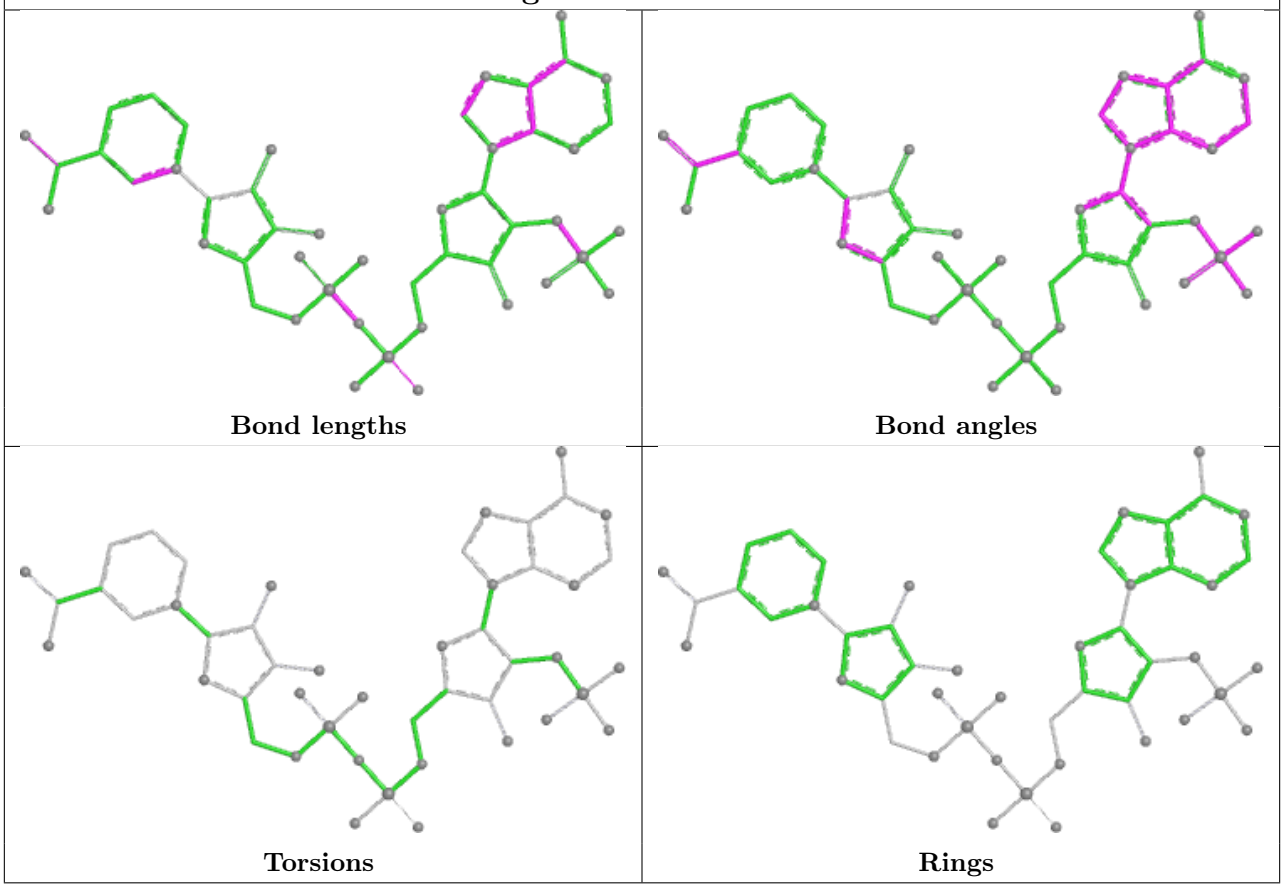
4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	303	ACT	1	0
3	D	301	NAP	1	0
4	A	302	6JP	1	0
4	B	302	6JP	3	0

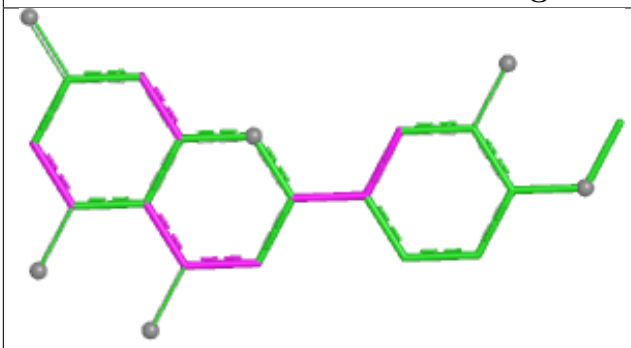
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

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

Ligand NAP A 301



Ligand 6JP D 302



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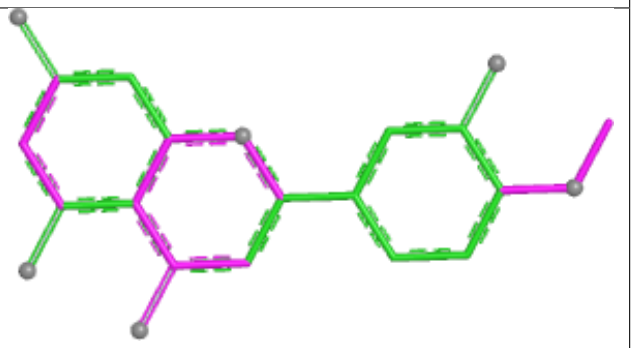
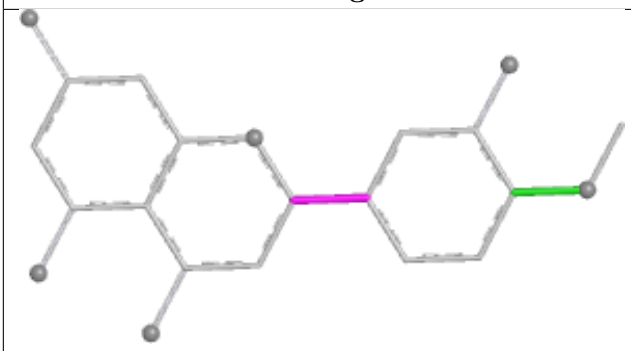


Bond angles



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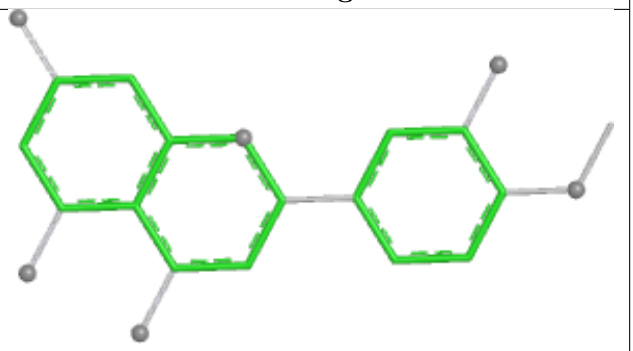
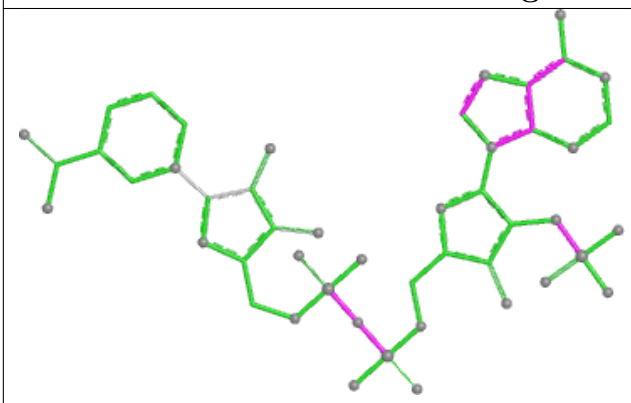


Rings

Ligand NAP C 301



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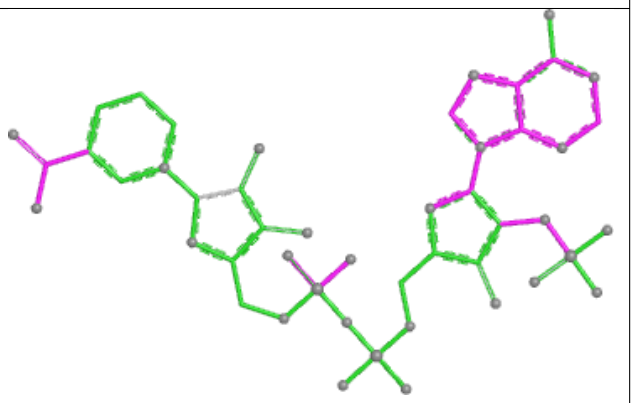

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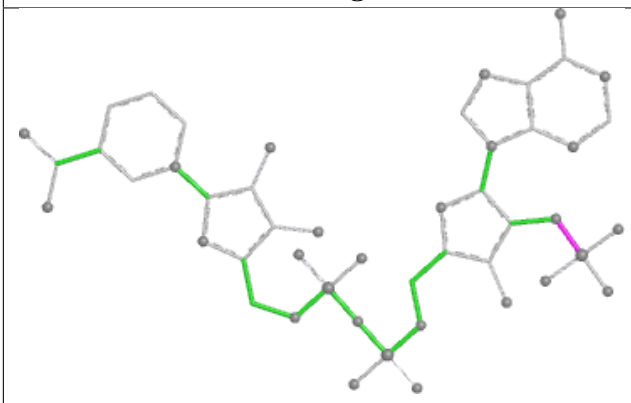

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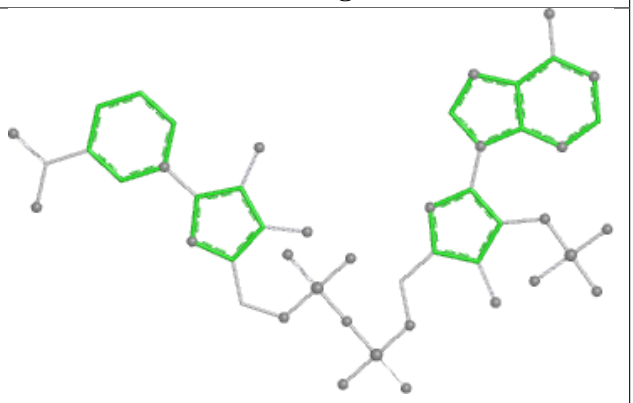
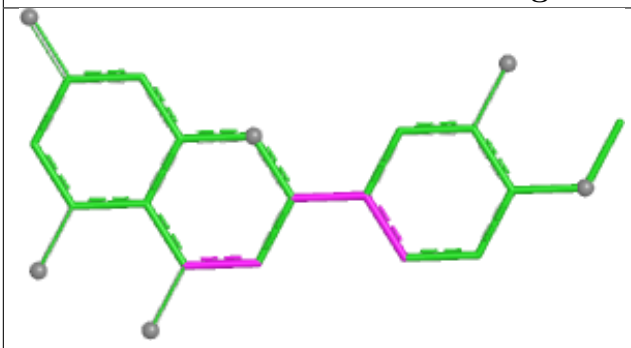
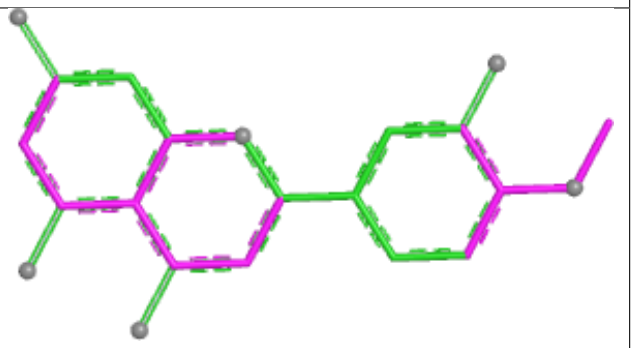


Rings

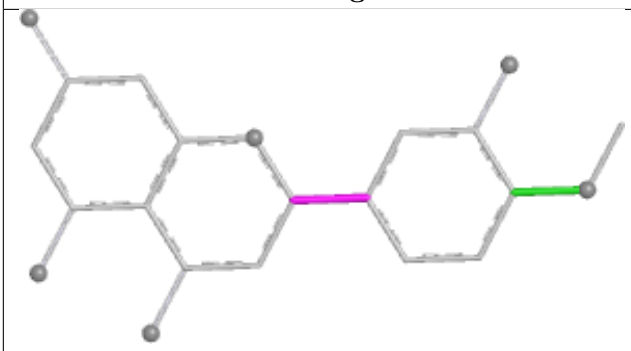
Ligand 6JP C 302



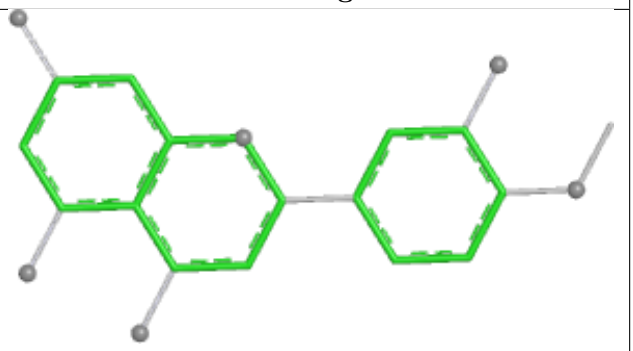
Bond lengths



Bond angles

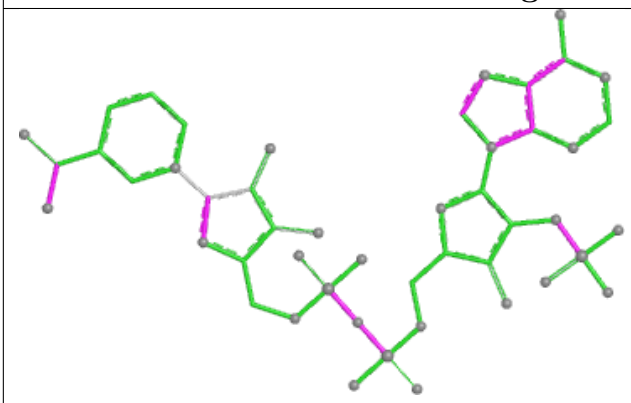


Torsions

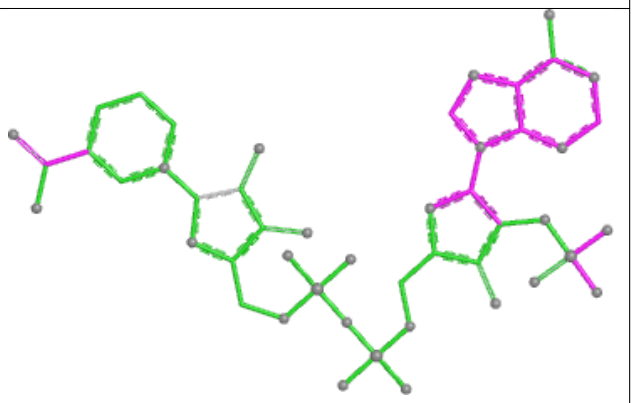


Rings

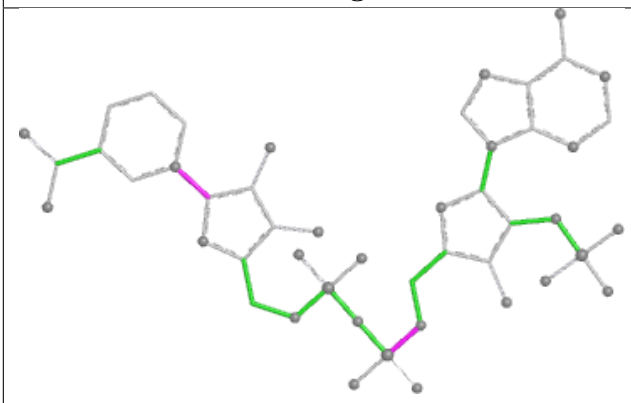
Ligand NAP D 301



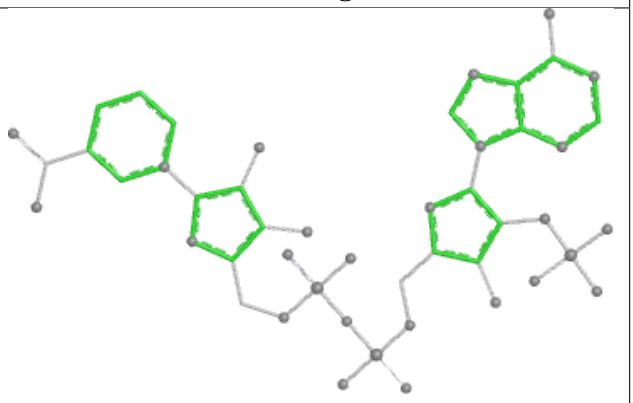
Bond lengths



Bond angles

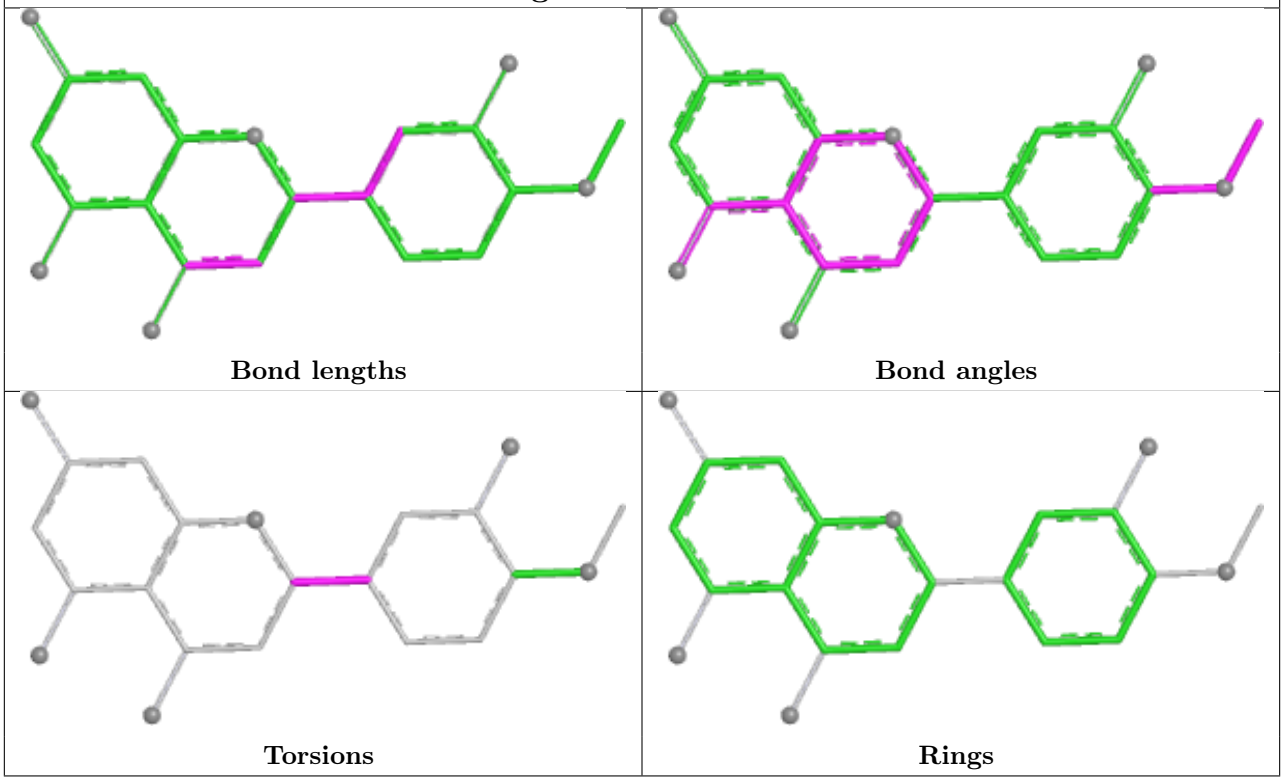


Torsions

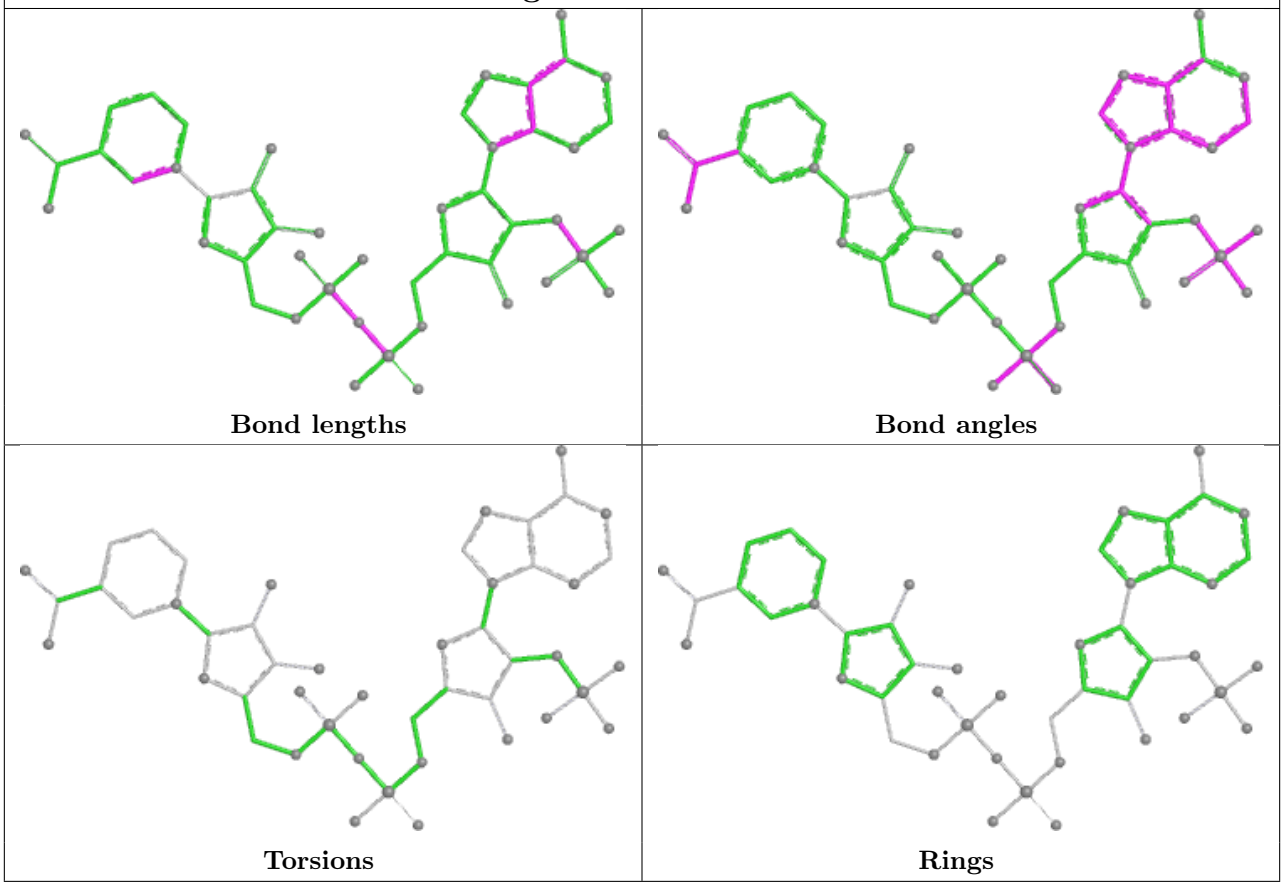


Rings

Ligand 6JP A 302



Ligand NAP B 301



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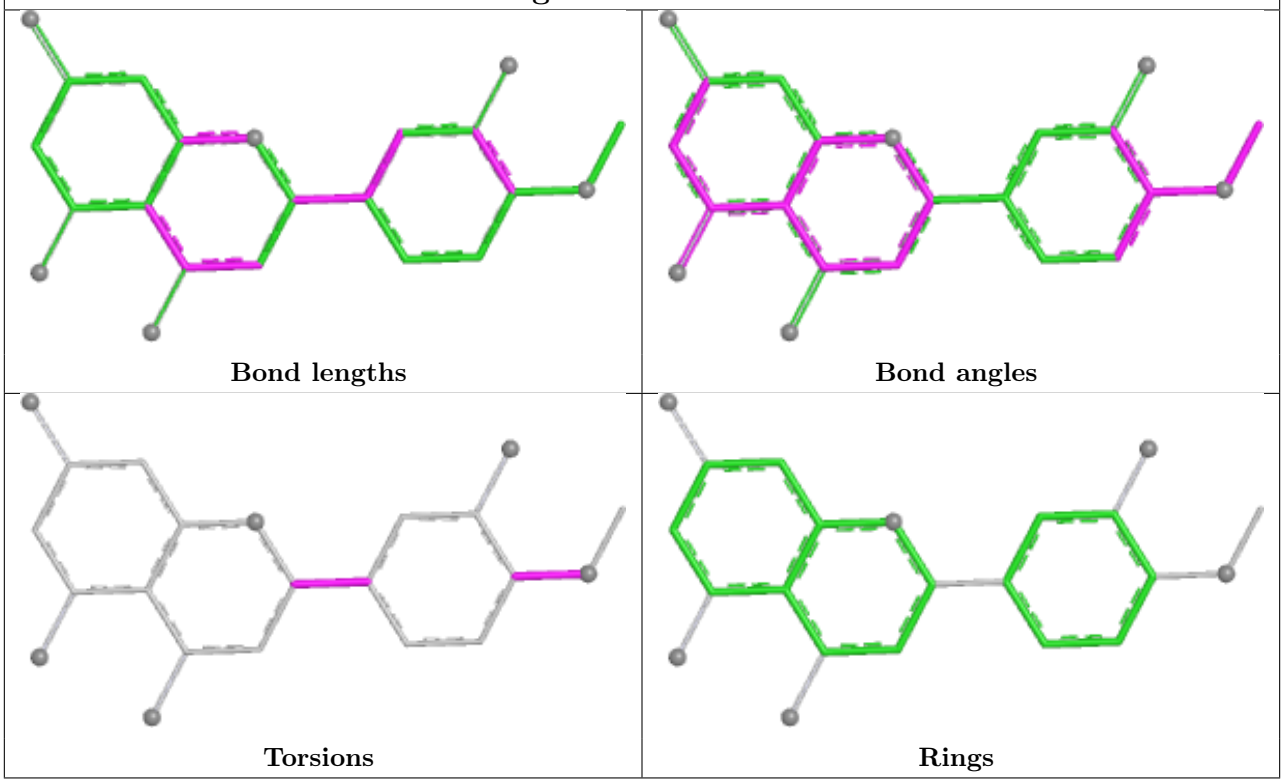


5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	259:VAL	C	260:ASP	N	1.64

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	248/288 (86%)	1.42	61 (24%)	2	2	10, 19, 38, 51	0
1	B	245/288 (85%)	1.07	30 (12%)	8	9	9, 16, 33, 43	2 (0%)
1	D	247/288 (85%)	1.55	72 (29%)	1	1	9, 19, 40, 55	2 (0%)
2	C	237/288 (82%)	1.54	62 (26%)	1	1	10, 19, 42, 63	0
All	All	977/1152 (84%)	1.39	225 (23%)	2	2	9, 19, 38, 63	4 (0%)

The worst 5 of 225 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	209	LEU	8.7
1	D	211	VAL	8.6
2	C	206	VAL	7.7
2	C	221	TRP	7.3
2	C	220	LYS	6.7

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	CSX	C	168	7/8	0.84	0.14	22,26,41,50	0
1	CSX	A	168	7/8	0.87	0.12	23,28,54,55	0
1	CSX	D	168	7/8	0.87	0.13	23,28,50,54	0
1	CSX	B	168[A]	7/8	0.92	0.12	18,21,22,25	7
1	CSX	B	168[B]	7/8	0.92	0.12	20,23,27,30	7
2	OCS	C	59	9/10	0.93	0.09	16,19,24,24	0

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

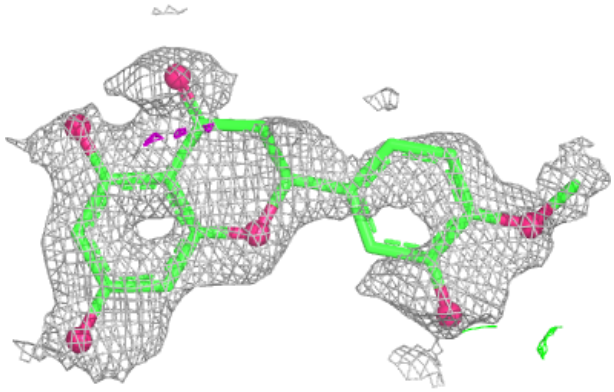
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

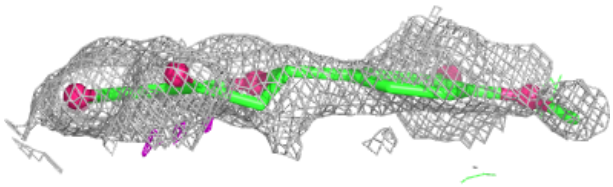
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	6JP	C	302	22/22	0.65	0.24	47,55,64,81	0
4	6JP	D	302	22/22	0.68	0.20	37,44,48,49	0
6	GOL	C	304	6/6	0.72	0.25	29,39,40,44	0
4	6JP	B	302	22/22	0.73	0.22	36,42,58,64	0
4	6JP	A	302	22/22	0.77	0.17	27,35,44,50	0
5	ACT	A	303	4/4	0.81	0.19	22,23,24,34	0
3	NAP	C	301	48/48	0.81	0.15	21,33,45,55	0
5	ACT	C	303	4/4	0.87	0.13	26,27,30,31	0
3	NAP	D	301	48/48	0.88	0.12	17,26,36,41	0
3	NAP	B	301	48/48	0.91	0.10	15,20,31,33	0
3	NAP	A	301	48/48	0.91	0.10	16,21,33,37	0

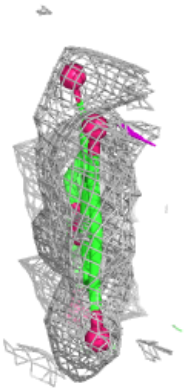
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 6JP C 302:

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

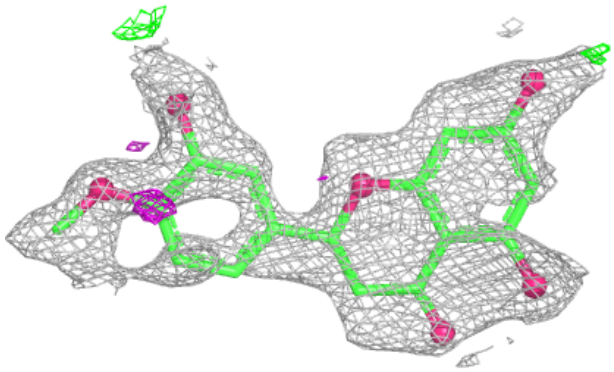


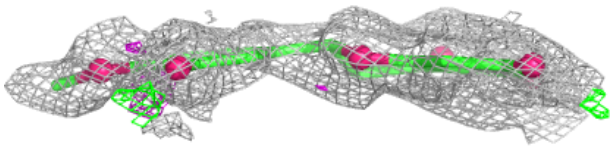


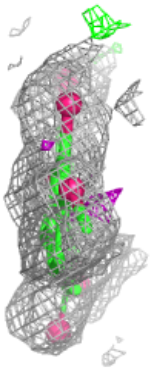


Electron density around 6JP D 302:

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







Electron density around 6JP B 302:

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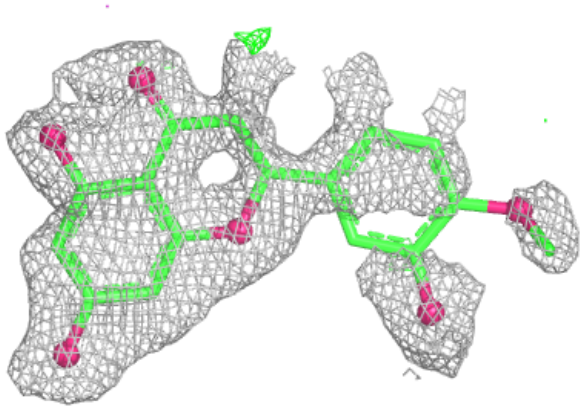
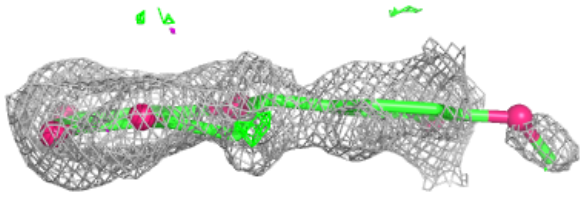
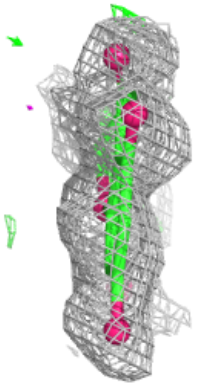
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

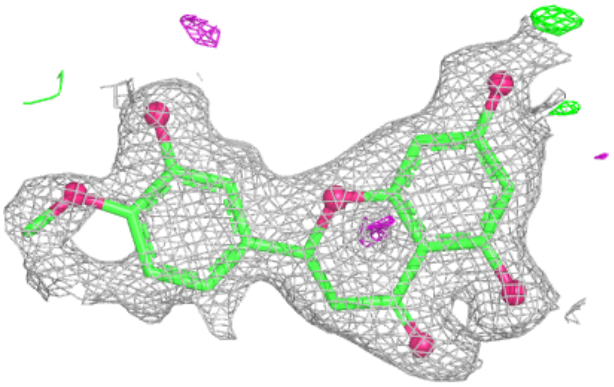


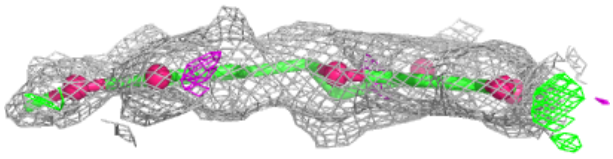


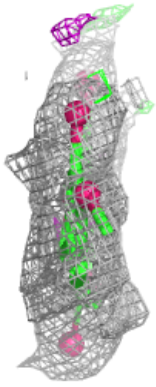


Electron density around 6JP A 302:

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

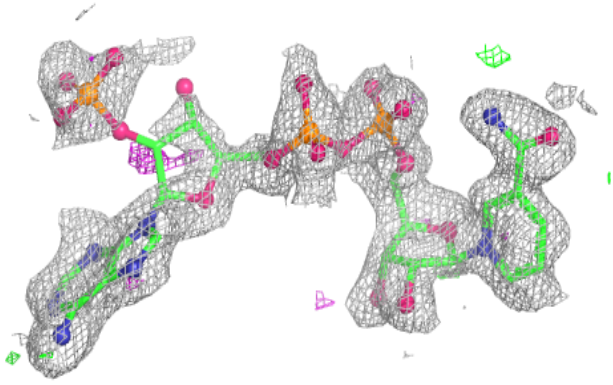


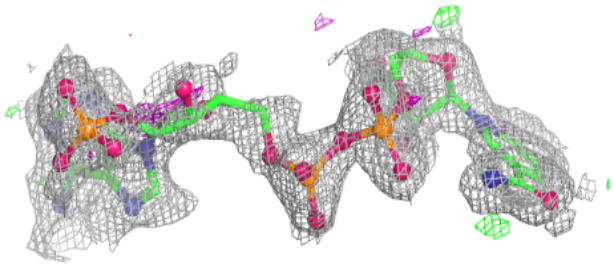


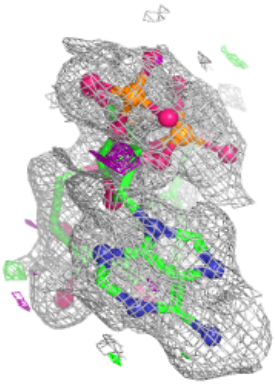


Electron density around NAP C 301:

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

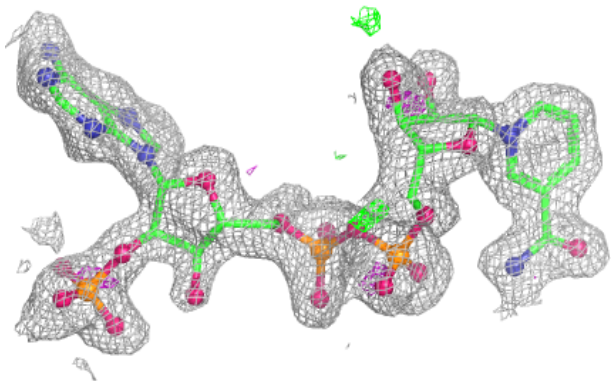


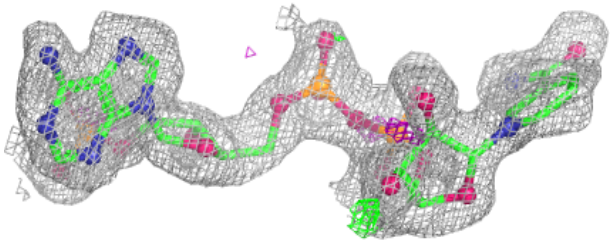


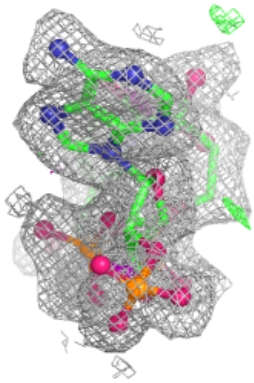


Electron density around NAP D 301:

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

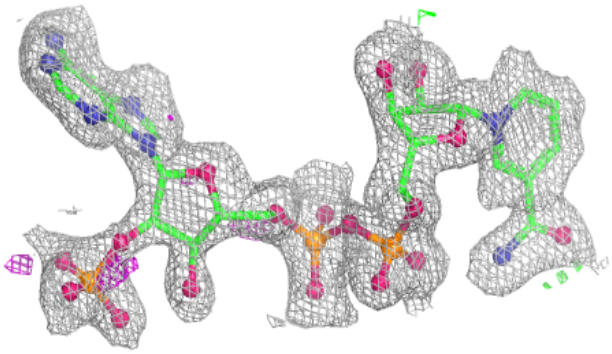


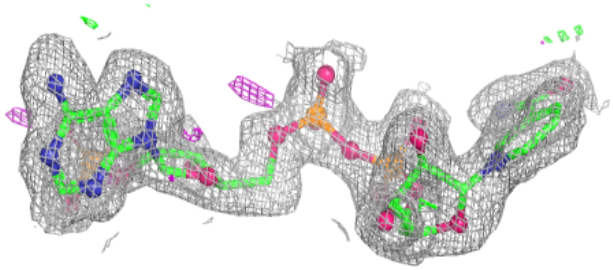


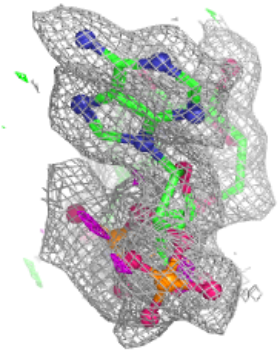


Electron density around NAP B 301:

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

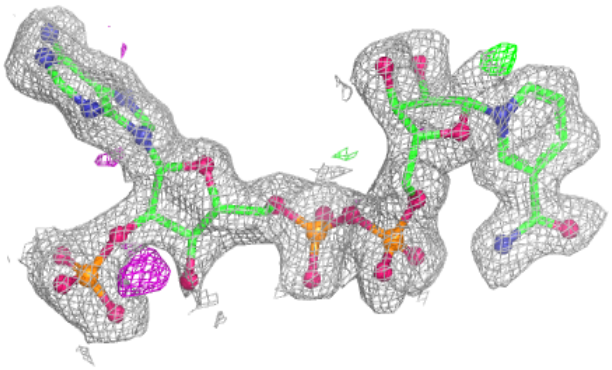


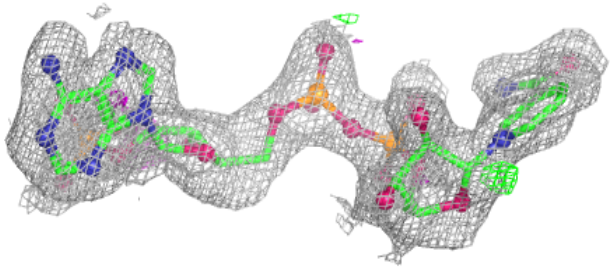


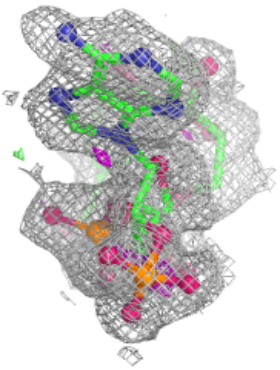


Electron density around NAP A 301:

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







6.5 Other polymers (i)

There are no such residues in this entry.