wwPDB X-ray Structure Validation Summary Report (i)

Jan 4, 2024 – 04:59 pm GMT

PDB ID	:	5L42
Title	:	Leishmania major Pteridine reductase 1 (PTR1) in complex with compound 3
Authors	:	Dello Iacono, L.; Di Pisa, F.; Pozzi, C.; Landi, G.; Mangani, S.
Deposited on	:	2016-05-24
Resolution	:	2.10 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:

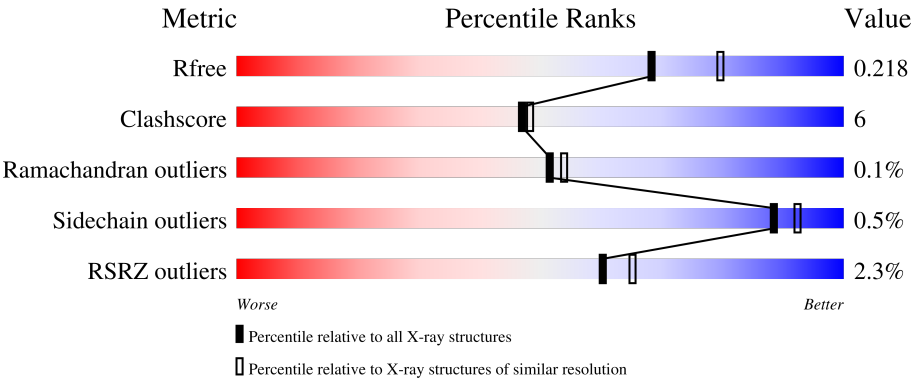
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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	81% 10% • 8%
1	B	288	81% 10% • 8%
1	C	288	3% 82% 7% 11%
1	D	288	2% 82% 6% 12%

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	ACT	A	306	-	-	X	-
5	ACT	B	306	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 9009 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

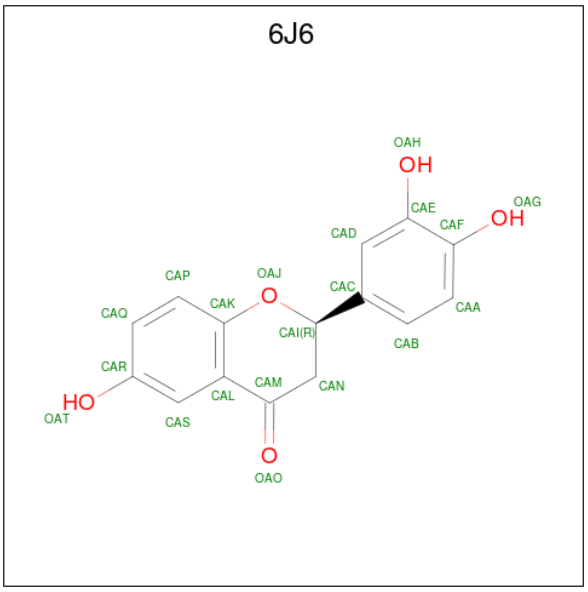
- Molecule 1 is a protein called Pteridine reductase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	9	0
			1982	1259	348	365	10			
1	B	266	Total	C	N	O	S	0	7	0
			2002	1270	350	373	9			
1	C	257	Total	C	N	O	S	0	8	0
			1928	1220	346	353	9			
1	D	254	Total	C	N	O	S	0	7	0
			1903	1208	336	350	9			

There are 4 discrepancies between the modelled and reference sequences:

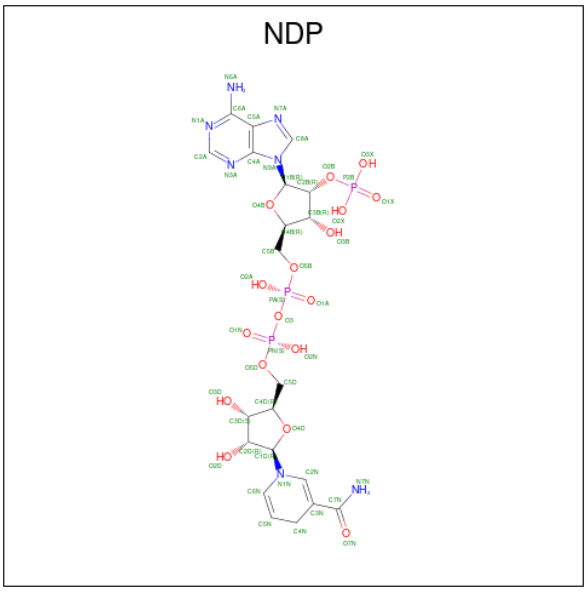
Chain	Residue	Modelled	Actual	Comment	Reference
A	162	VAL	PHE	engineered mutation	UNP Q01782
B	162	VAL	PHE	engineered mutation	UNP Q01782
C	162	VAL	PHE	engineered mutation	UNP Q01782
D	162	VAL	PHE	engineered mutation	UNP Q01782

- Molecule 2 is (2 {R})-2-[3,4-bis(oxidanyl)phenyl]-6-oxidanyl-2,3-dihydrochromen-4-one (three-letter code: 6J6) (formula: $C_{15}H_{12}O_5$).



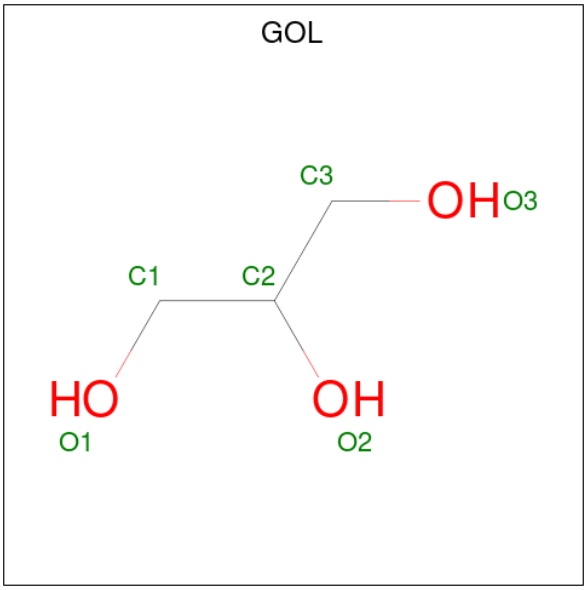
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 20 15 5	0	0
2	B	1	Total C O 20 15 5	0	0
2	C	1	Total C O 20 15 5	0	0
2	D	1	Total C O 20 15 5	0	0

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



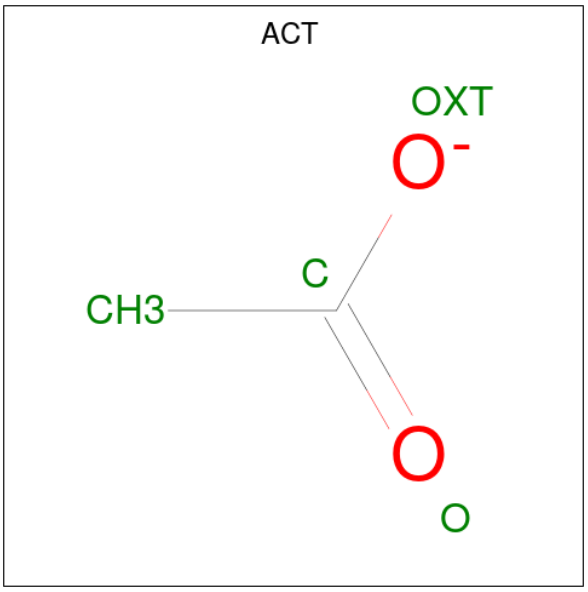
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



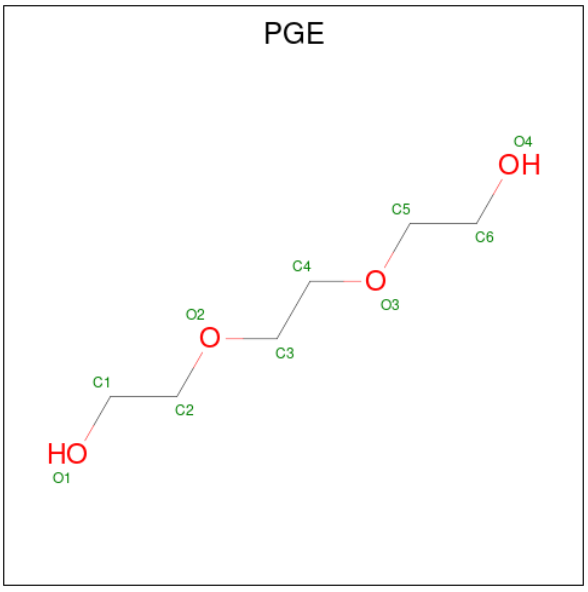
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O		0	0
			6	3	3			
4	A	1	Total	C	O		0	0
			6	3	3			
4	B	1	Total	C	O		0	0
			6	3	3			
4	B	1	Total	C	O		0	0
			6	3	3			
4	B	1	Total	C	O		0	0
			6	3	3			
4	C	1	Total	C	O		0	0
			6	3	3			

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



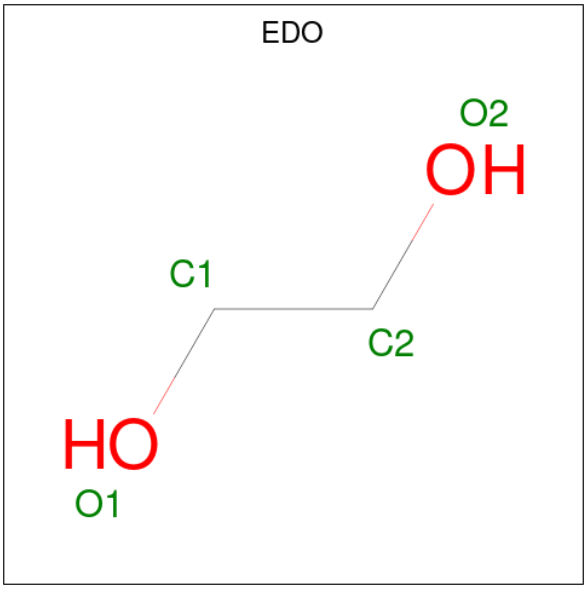
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 10 6 4	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 8 is water.

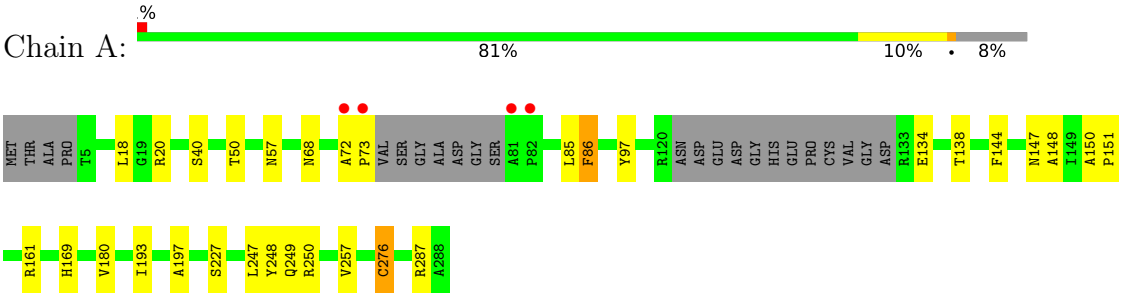
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	218	Total O 218 218	0	0
8	B	195	Total O 195 195	0	0
8	C	228	Total O 228 228	0	0
8	D	199	Total O 199 199	0	0

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.

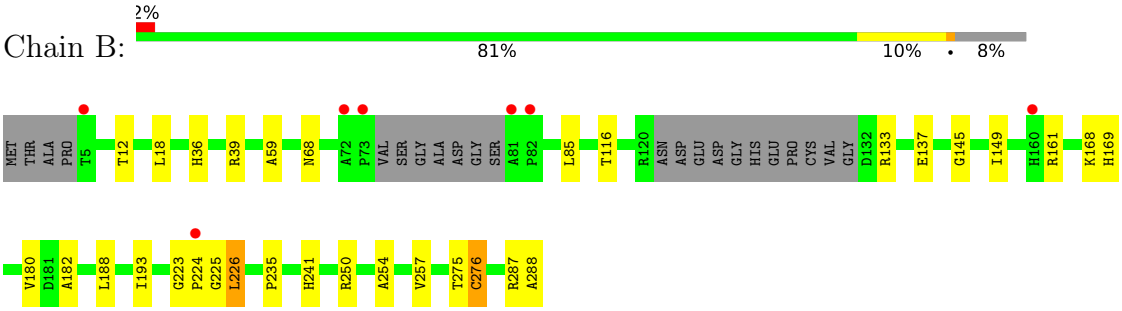
• Molecule 1: Pteridine reductase 1

Chain A:



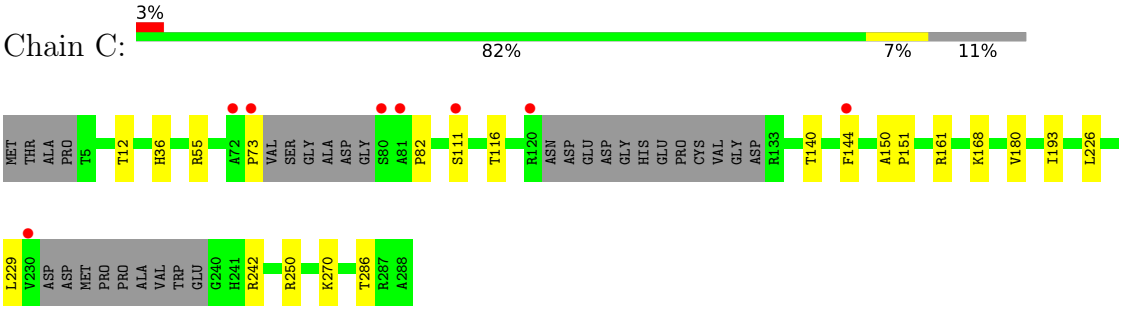
• Molecule 1: Pteridine reductase 1

Chain B:



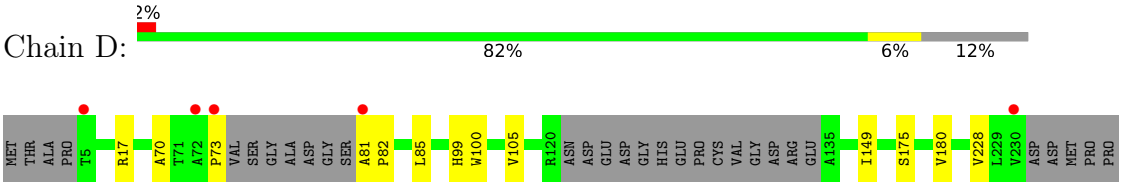
• Molecule 1: Pteridine reductase 1

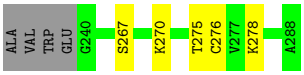
Chain C:



• Molecule 1: Pteridine reductase 1

Chain D:




ALA
VAL
TRP
GLU
G240
S267
K270
T275
C276
V277
K278
A288

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	94.70Å 104.19Å 137.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.35 – 2.10 45.64 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.35-2.10) 99.2 (45.64-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.65 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.165 , 0.214 0.173 , 0.218	Depositor DCC
R_{free} test set	3968 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	20.2	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 55.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	9009	wwPDB-VP
Average B, all atoms (Å^2)	23.0	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 24.60 % 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 3.7144e-03. 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NDP, PGE, EDO, CSX, GOL, ACT, 6J6

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	0.93	0/2041	0.89	0/2784
1	B	0.91	0/2054	0.89	0/2801
1	C	0.87	0/1979	0.85	0/2691
1	D	0.93	0/1951	0.86	0/2656
All	All	0.91	0/8025	0.87	0/10932

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	1982	0	2000	26	0
1	B	2002	0	2023	36	0
1	C	1928	0	1956	21	0
1	D	1903	0	1936	19	0
2	A	20	0	0	0	0
2	B	20	0	0	2	0
2	C	20	0	0	4	0
2	D	20	0	0	1	0
3	A	48	0	26	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	48	0	26	3	0
3	C	48	0	26	2	0
3	D	48	0	26	0	0
4	A	12	0	16	3	0
4	B	18	0	24	3	0
4	C	6	0	8	0	0
5	A	12	0	9	4	0
5	B	4	0	3	2	0
6	A	10	0	14	5	0
7	A	8	0	12	1	0
7	C	4	0	6	1	0
7	D	8	0	12	3	0
8	A	218	0	0	1	1
8	B	195	0	0	3	0
8	C	228	0	0	2	0
8	D	199	0	0	3	1
All	All	9009	0	8123	101	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 101 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ARG:HH22	5:A:306:ACT:H1	1.05	1.11
1:A:20:ARG:HH22	5:A:306:ACT:CH3	1.76	0.96
1:A:20:ARG:NH2	5:A:306:ACT:H1	1.85	0.89
1:C:55[B]:ARG:HD2	8:C:555:HOH:O	1.80	0.81
1:B:180:VAL:HG21	1:B:276:CSX:HG	1.45	0.81

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:401:HOH:O	8:D:563:HOH:O[2_554]	2.12	0.08

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	267/288 (93%)	252 (94%)	15 (6%)	0	100	100
1	B	266/288 (92%)	252 (95%)	14 (5%)	0	100	100
1	C	256/288 (89%)	244 (95%)	11 (4%)	1 (0%)	34	32
1	D	252/288 (88%)	242 (96%)	10 (4%)	0	100	100
All	All	1041/1152 (90%)	990 (95%)	50 (5%)	1 (0%)	51	54

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	180	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	206/222 (93%)	205 (100%)	1 (0%)	88	92
1	B	209/222 (94%)	207 (99%)	2 (1%)	76	82
1	C	199/222 (90%)	198 (100%)	1 (0%)	88	92
1	D	198/222 (89%)	198 (100%)	0	100	100
All	All	812/888 (91%)	808 (100%)	4 (0%)	88	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	86	PHE
1	B	226	LEU
1	B	235	PRO
1	C	168	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	160	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	276	1	3,6,7	0.81	0	1,6,8	1.76	0
1	CSX	C	276	1	3,6,7	0.82	0	1,6,8	1.98	0
1	CSX	B	276	1	3,6,7	0.42	0	1,6,8	4.04	1 (100%)
1	CSX	A	276	1	3,6,7	0.44	0	1,6,8	4.08	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	276	1	-	0/1/5/7	-
1	CSX	C	276	1	-	0/1/5/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSX	B	276	1	-	0/1/5/7	-
1	CSX	A	276	1	-	0/1/5/7	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	276	CSX	CA-CB-SG	-4.08	104.45	113.36
1	B	276	CSX	CA-CB-SG	-4.04	104.53	113.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	276	CSX	3	0
1	B	276	CSX	2	0
1	A	276	CSX	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

24 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	$\#\|Z\| > 2$
5	ACT	B	306	-	3,3,3	0.77	0	3,3,3	1.16	0
3	NDP	A	302	-	45,52,52	1.11	3 (6%)	53,80,80	1.62	11 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	6J6	A	301	-	22,22,22	2.34	5 (22%)	32,32,32	1.77	7 (21%)
7	EDO	C	304	-	3,3,3	0.47	0	2,2,2	0.39	0
7	EDO	A	309	-	3,3,3	0.27	0	2,2,2	0.35	0
3	NDP	C	302	-	45,52,52	1.08	4 (8%)	53,80,80	1.34	7 (13%)
2	6J6	C	301	-	22,22,22	2.43	6 (27%)	32,32,32	2.10	11 (34%)
4	GOL	A	303	-	5,5,5	0.73	0	5,5,5	1.11	0
7	EDO	D	304	-	3,3,3	0.46	0	2,2,2	0.34	0
4	GOL	B	305	-	5,5,5	0.53	0	5,5,5	0.64	0
4	GOL	C	303	-	5,5,5	0.64	0	5,5,5	0.44	0
6	PGE	A	308	-	9,9,9	0.74	0	8,8,8	0.92	0
3	NDP	D	302	-	45,52,52	1.16	5 (11%)	53,80,80	1.45	7 (13%)
4	GOL	A	304	-	5,5,5	0.62	0	5,5,5	1.14	0
2	6J6	D	301	-	22,22,22	1.81	4 (18%)	32,32,32	1.69	6 (18%)
5	ACT	A	305	-	3,3,3	0.89	0	3,3,3	0.49	0
5	ACT	A	306	-	3,3,3	1.07	0	3,3,3	0.75	0
3	NDP	B	302	-	45,52,52	1.24	5 (11%)	53,80,80	1.51	7 (13%)
2	6J6	B	301	-	22,22,22	2.35	6 (27%)	32,32,32	1.84	10 (31%)
7	EDO	A	310	-	3,3,3	0.57	0	2,2,2	0.41	0
5	ACT	A	307	-	3,3,3	0.69	0	3,3,3	1.00	0
4	GOL	B	304	-	5,5,5	0.30	0	5,5,5	0.66	0
7	EDO	D	303	-	3,3,3	0.45	0	2,2,2	0.45	0
4	GOL	B	303	-	5,5,5	0.54	0	5,5,5	1.33	1 (20%)

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	NDP	A	302	-	-	1/30/77/77	0/5/5/5
2	6J6	A	301	-	-	0/4/16/16	0/3/3/3
7	EDO	C	304	-	-	1/1/1/1	-
7	EDO	A	309	-	-	1/1/1/1	-
3	NDP	C	302	-	-	1/30/77/77	0/5/5/5
2	6J6	C	301	-	-	0/4/16/16	0/3/3/3
4	GOL	A	303	-	-	4/4/4/4	-
7	EDO	D	304	-	-	1/1/1/1	-
4	GOL	B	305	-	-	2/4/4/4	-
4	GOL	C	303	-	-	1/4/4/4	-
6	PGE	A	308	-	-	4/7/7/7	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NDP	D	302	-	-	2/30/77/77	0/5/5/5
4	GOL	A	304	-	-	4/4/4/4	-
2	6J6	D	301	-	-	0/4/16/16	0/3/3/3
3	NDP	B	302	-	-	5/30/77/77	0/5/5/5
2	6J6	B	301	-	-	0/4/16/16	0/3/3/3
7	EDO	A	310	-	-	1/1/1/1	-
4	GOL	B	304	-	-	2/4/4/4	-
7	EDO	D	303	-	-	1/1/1/1	-
4	GOL	B	303	-	-	2/4/4/4	-

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	6J6	CAC-CAI	-7.28	1.39	1.51
2	B	301	6J6	CAC-CAI	-6.95	1.39	1.51
2	C	301	6J6	CAC-CAI	-6.47	1.40	1.51
2	D	301	6J6	CAC-CAI	-5.64	1.41	1.51
2	C	301	6J6	OAJ-CAK	-5.18	1.30	1.38

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	301	6J6	CAK-CAL-CAM	-5.14	116.90	119.85
3	A	302	NDP	N3A-C2A-N1A	-4.85	121.09	128.68
2	D	301	6J6	OAJ-CAK-CAL	-4.78	116.61	122.09
3	B	302	NDP	N3A-C2A-N1A	-4.75	121.26	128.68
2	A	301	6J6	CAK-OAJ-CAI	4.50	123.07	115.50

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	NDP	C5B-O5B-PA-O3
4	A	303	GOL	O1-C1-C2-C3
4	A	303	GOL	C1-C2-C3-O3
4	A	304	GOL	C1-C2-C3-O3
4	B	304	GOL	O1-C1-C2-C3

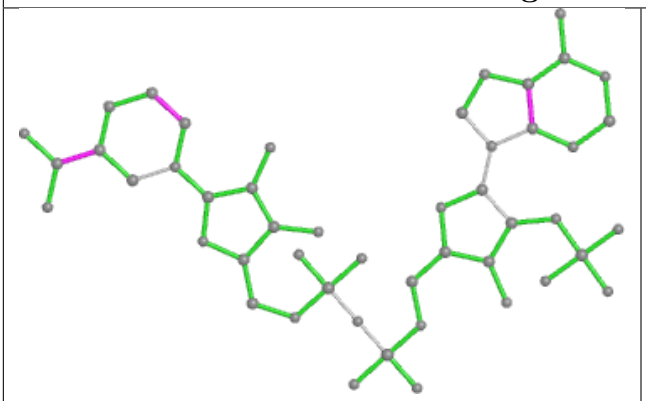
There are no ring outliers.

17 monomers are involved in 34 short contacts:

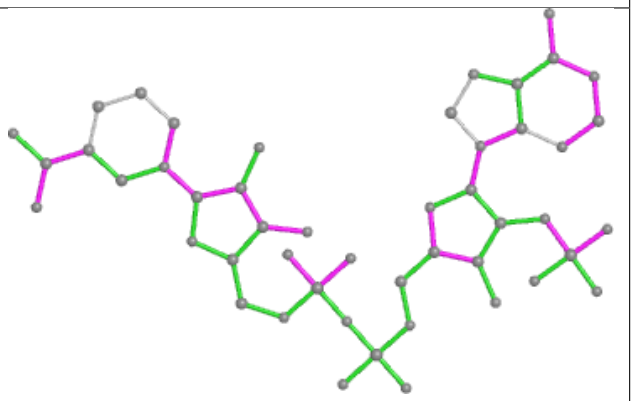
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	306	ACT	2	0
3	A	302	NDP	1	0
7	C	304	EDO	1	0
3	C	302	NDP	2	0
2	C	301	6J6	4	0
4	A	303	GOL	1	0
7	D	304	EDO	2	0
4	B	305	GOL	2	0
6	A	308	PGE	5	0
4	A	304	GOL	2	0
2	D	301	6J6	1	0
5	A	306	ACT	4	0
3	B	302	NDP	3	0
2	B	301	6J6	2	0
7	A	310	EDO	1	0
4	B	304	GOL	1	0
7	D	303	EDO	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 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.

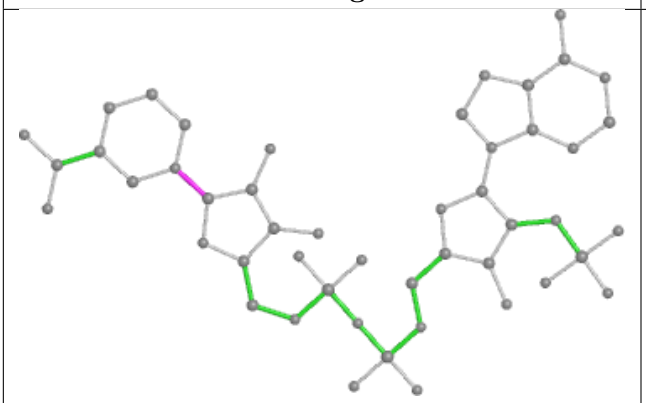
Ligand NDP A 302



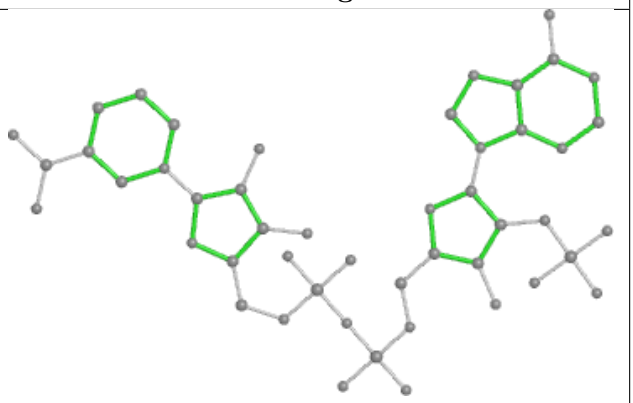
Bond lengths



Bond angles

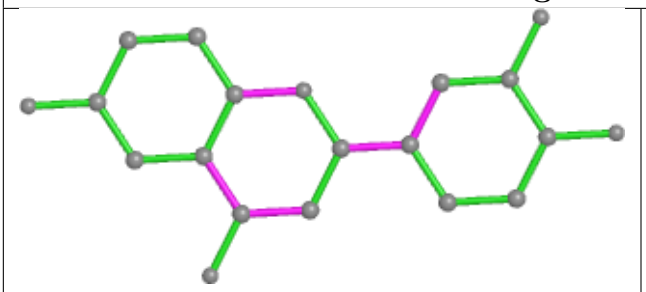


Torsions

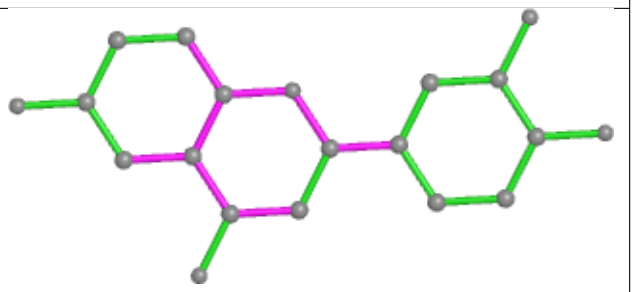


Rings

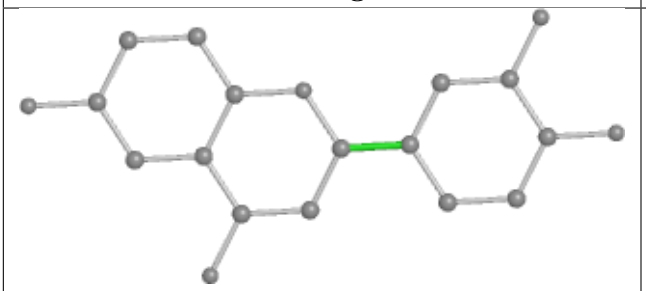
Ligand 6J6 A 301



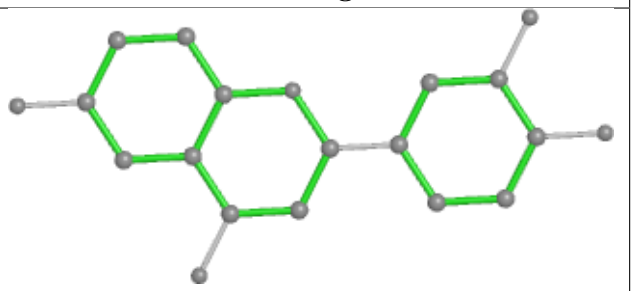
Bond lengths



Bond angles

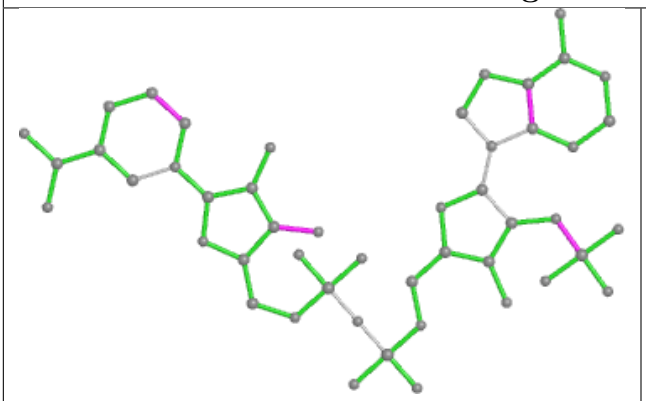


Torsions

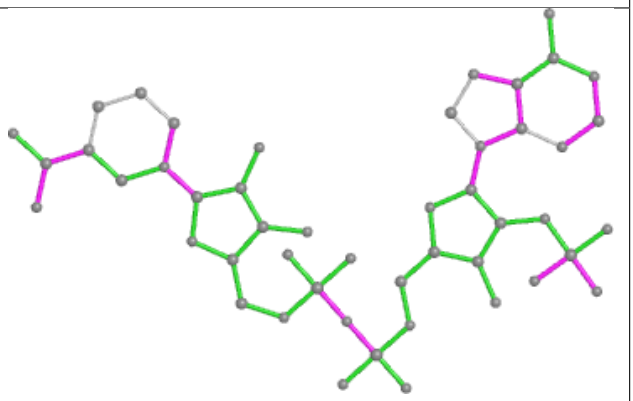


Rings

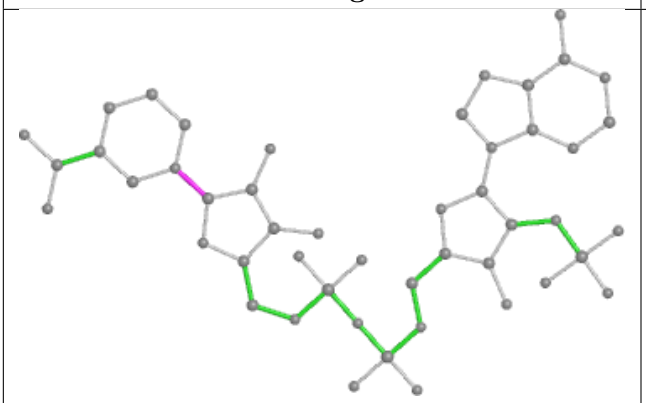
Ligand NDP C 302



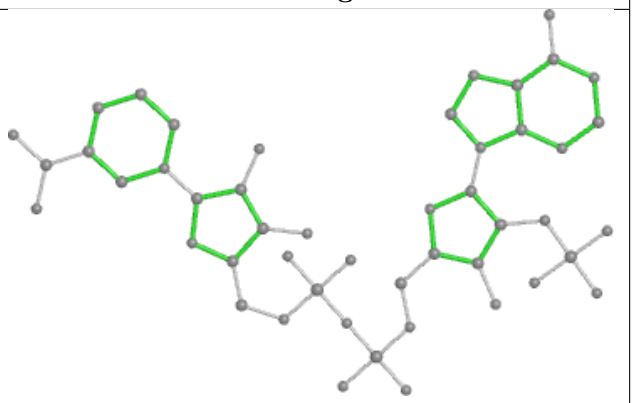
Bond lengths



Bond angles

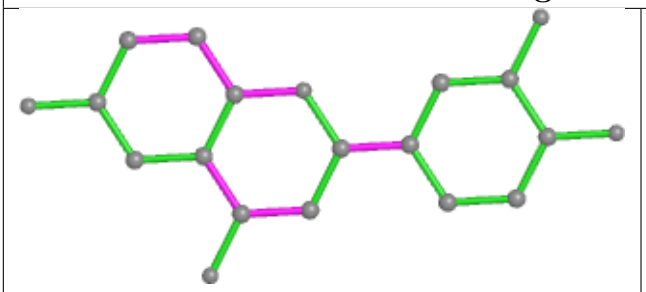


Torsions

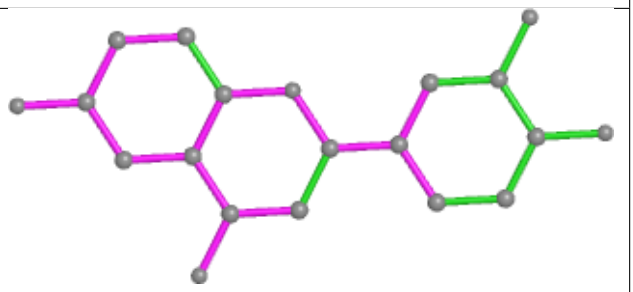


Rings

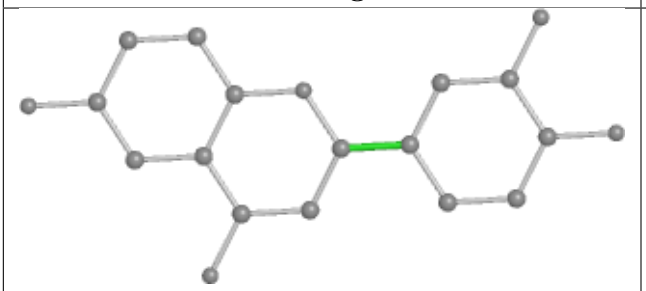
Ligand 6J6 C 301



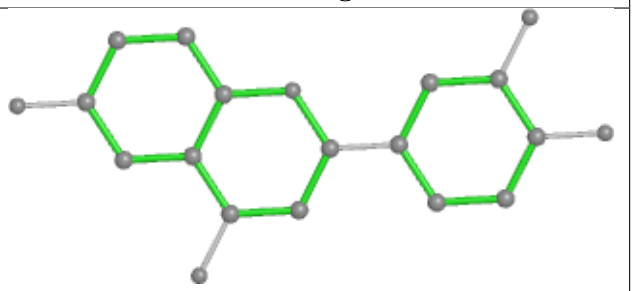
Bond lengths



Bond angles

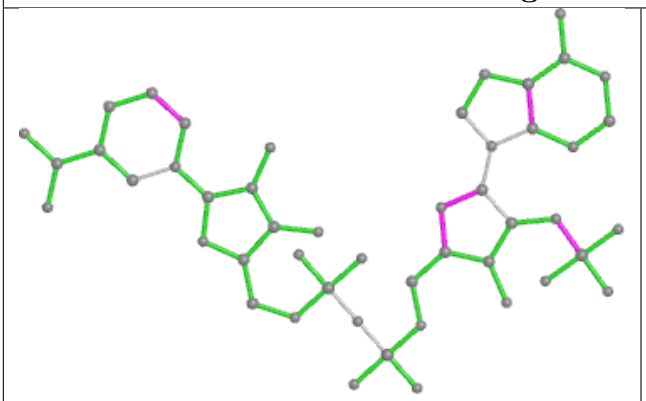


Torsions

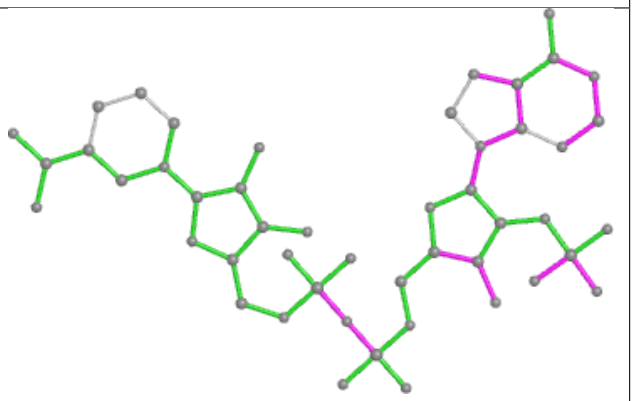


Rings

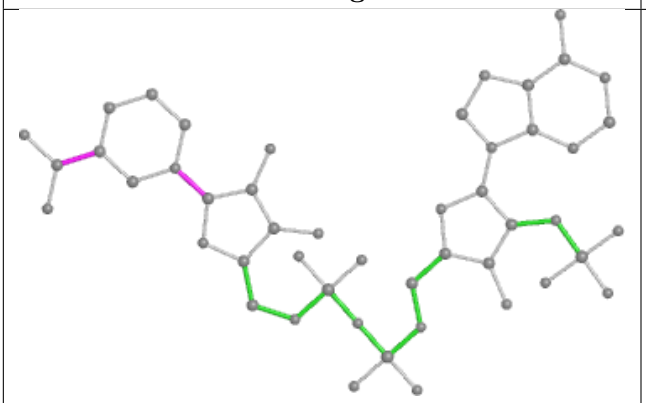
Ligand NDP D 302



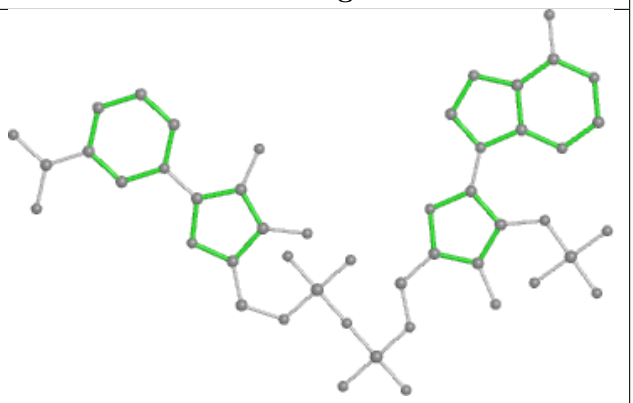
Bond lengths



Bond angles

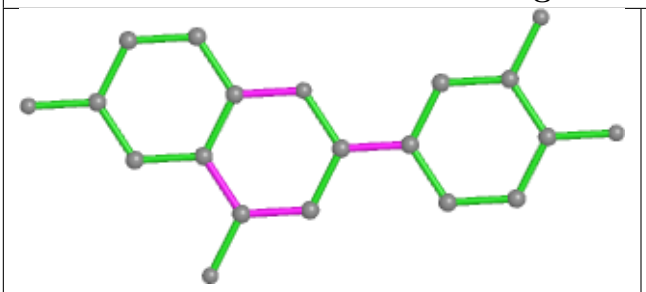


Torsions

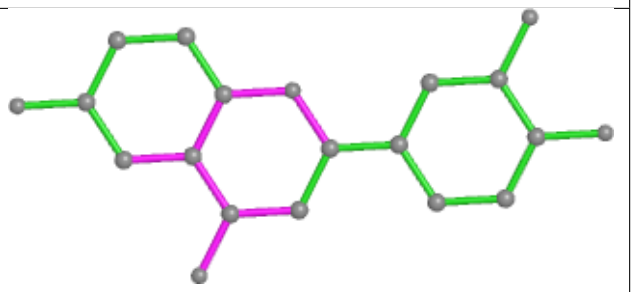


Rings

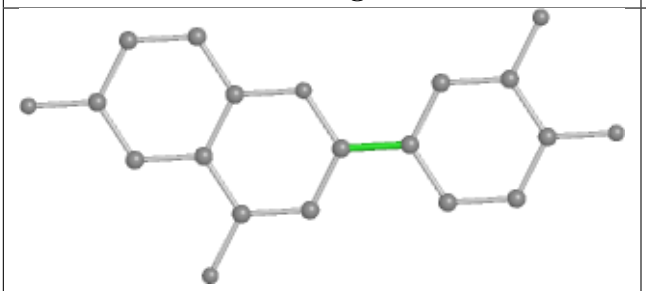
Ligand 6J6 D 301



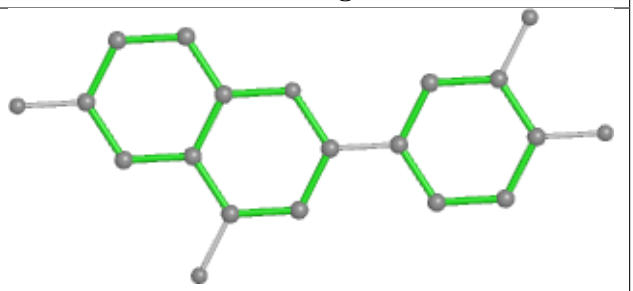
Bond lengths



Bond angles

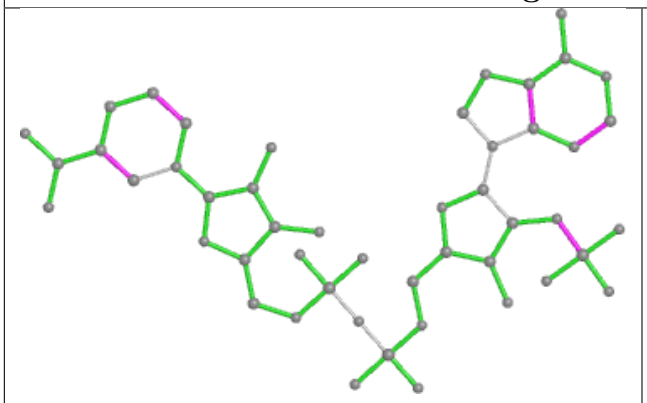


Torsions

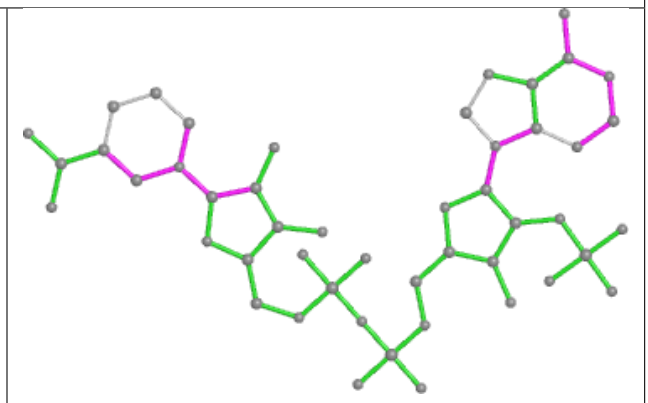


Rings

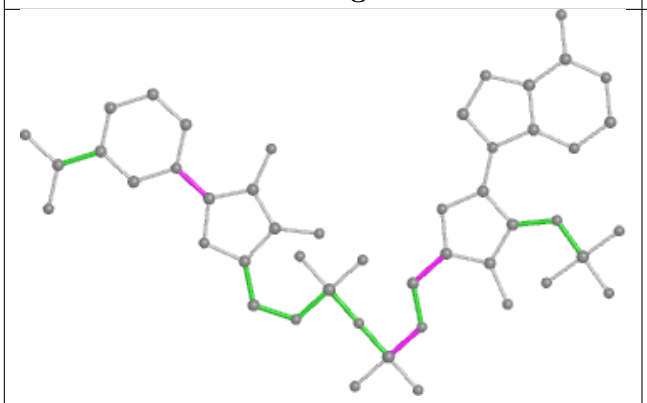
Ligand NDP B 302



Bond lengths



Bond angles



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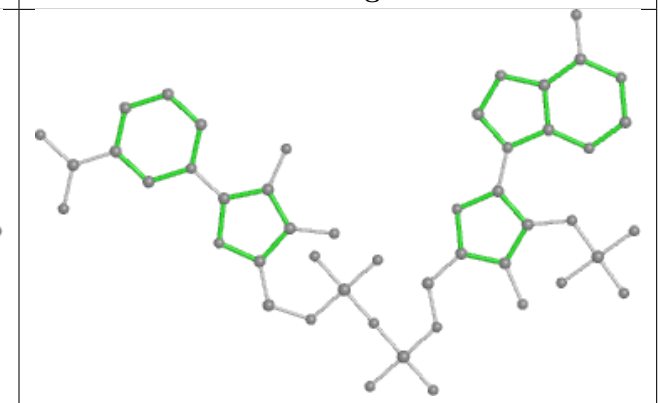
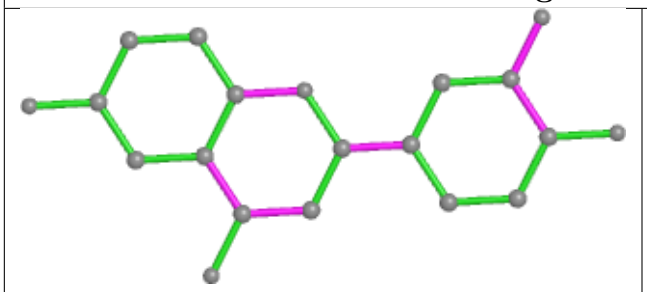
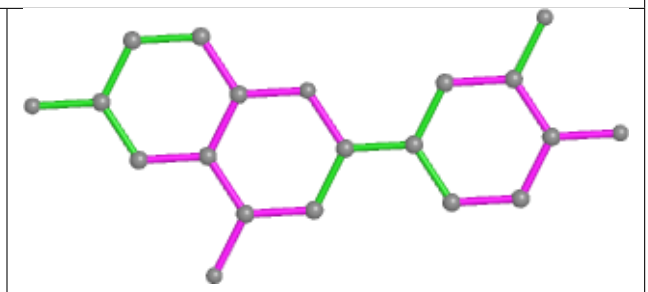


Rings

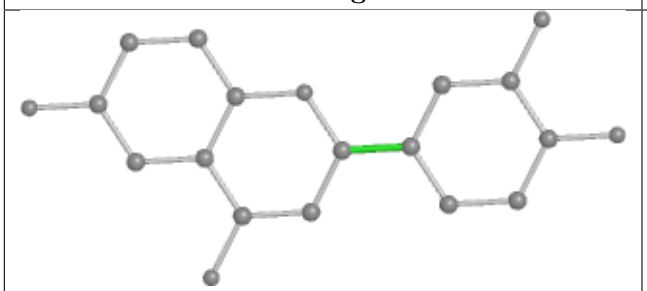
Ligand 6J6 B 301



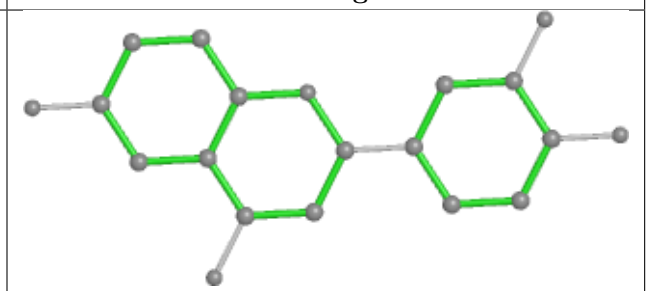
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	264/288 (91%)	-0.48	4 (1%)	73	77	10, 16, 36, 71	1 (0%)
1	B	265/288 (92%)	-0.26	7 (2%)	56	61	11, 21, 42, 76	1 (0%)
1	C	256/288 (88%)	-0.51	8 (3%)	49	55	12, 18, 49, 73	1 (0%)
1	D	253/288 (87%)	-0.50	5 (1%)	65	69	12, 20, 43, 75	1 (0%)
All	All	1038/1152 (90%)	-0.44	24 (2%)	60	65	10, 19, 46, 76	4 (0%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	72	ALA	6.4
1	C	144	PHE	5.4
1	D	230	VAL	4.7
1	B	81	ALA	4.6
1	A	73	PRO	4.5

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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CSX	D	276	7/8	0.61	0.25	25,29,32,32	0
1	CSX	B	276	7/8	0.68	0.25	21,22,23,28	0
1	CSX	A	276	7/8	0.71	0.20	19,20,22,27	0
1	CSX	C	276	7/8	0.93	0.11	21,24,54,59	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

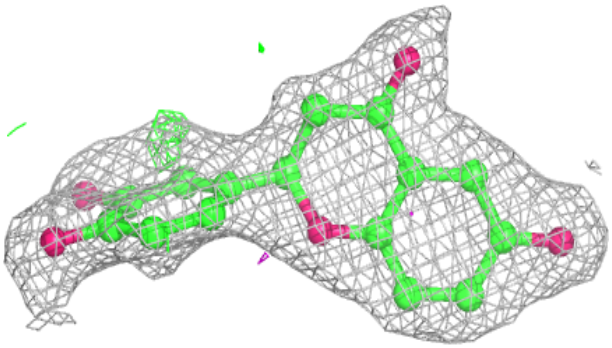
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

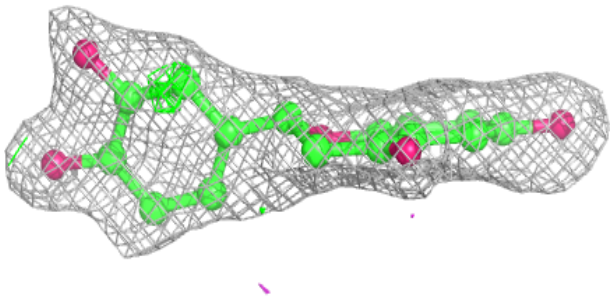
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GOL	C	303	6/6	0.55	0.21	50,55,58,60	0
4	GOL	A	304	6/6	0.72	0.21	38,41,45,45	0
4	GOL	B	305	6/6	0.77	0.18	46,50,53,54	0
7	EDO	A	309	4/4	0.78	0.24	43,45,45,50	0
4	GOL	B	303	6/6	0.79	0.26	41,48,53,62	0
7	EDO	C	304	4/4	0.81	0.21	50,51,51,52	0
7	EDO	D	303	4/4	0.81	0.19	48,48,50,52	0
4	GOL	A	303	6/6	0.82	0.23	40,49,53,54	0
7	EDO	A	310	4/4	0.82	0.20	35,43,44,49	0
6	PGE	A	308	10/10	0.83	0.23	33,43,51,54	0
7	EDO	D	304	4/4	0.83	0.19	37,44,45,54	0
5	ACT	B	306	4/4	0.86	0.15	35,41,45,47	0
5	ACT	A	306	4/4	0.87	0.14	28,31,33,34	0
5	ACT	A	305	4/4	0.87	0.18	51,51,52,55	0
5	ACT	A	307	4/4	0.89	0.21	40,47,49,50	0
4	GOL	B	304	6/6	0.89	0.20	48,50,53,57	0
2	6J6	B	301	20/20	0.90	0.16	14,22,26,28	20
2	6J6	C	301	20/20	0.90	0.13	20,28,41,43	0
2	6J6	A	301	20/20	0.90	0.16	16,19,23,25	20
2	6J6	D	301	20/20	0.92	0.11	26,32,47,48	0
3	NDP	D	302	48/48	0.97	0.07	16,21,24,29	0
3	NDP	C	302	48/48	0.98	0.09	15,18,21,23	0
3	NDP	A	302	48/48	0.98	0.09	13,16,19,20	0
3	NDP	B	302	48/48	0.98	0.09	16,19,23,24	0

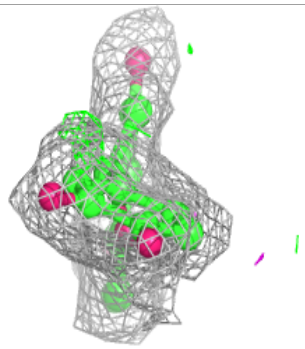
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 6J6 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)

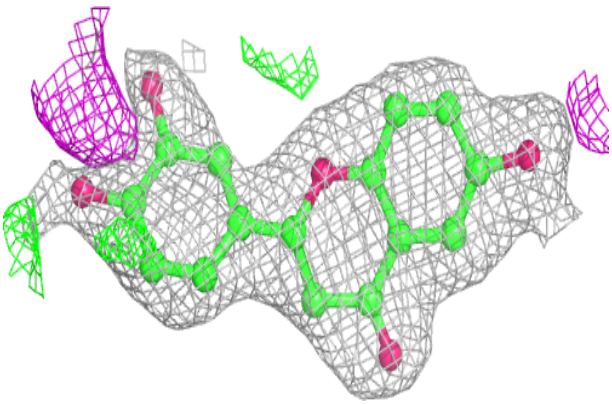


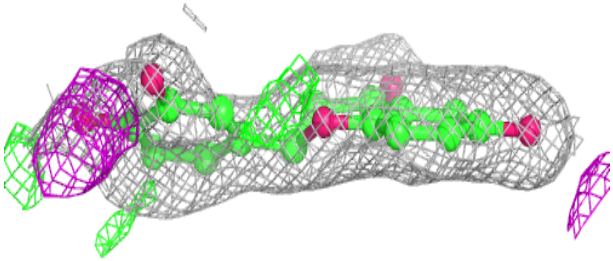


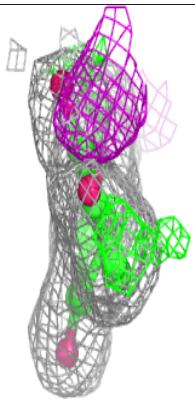


Electron density around 6J6 C 301:

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

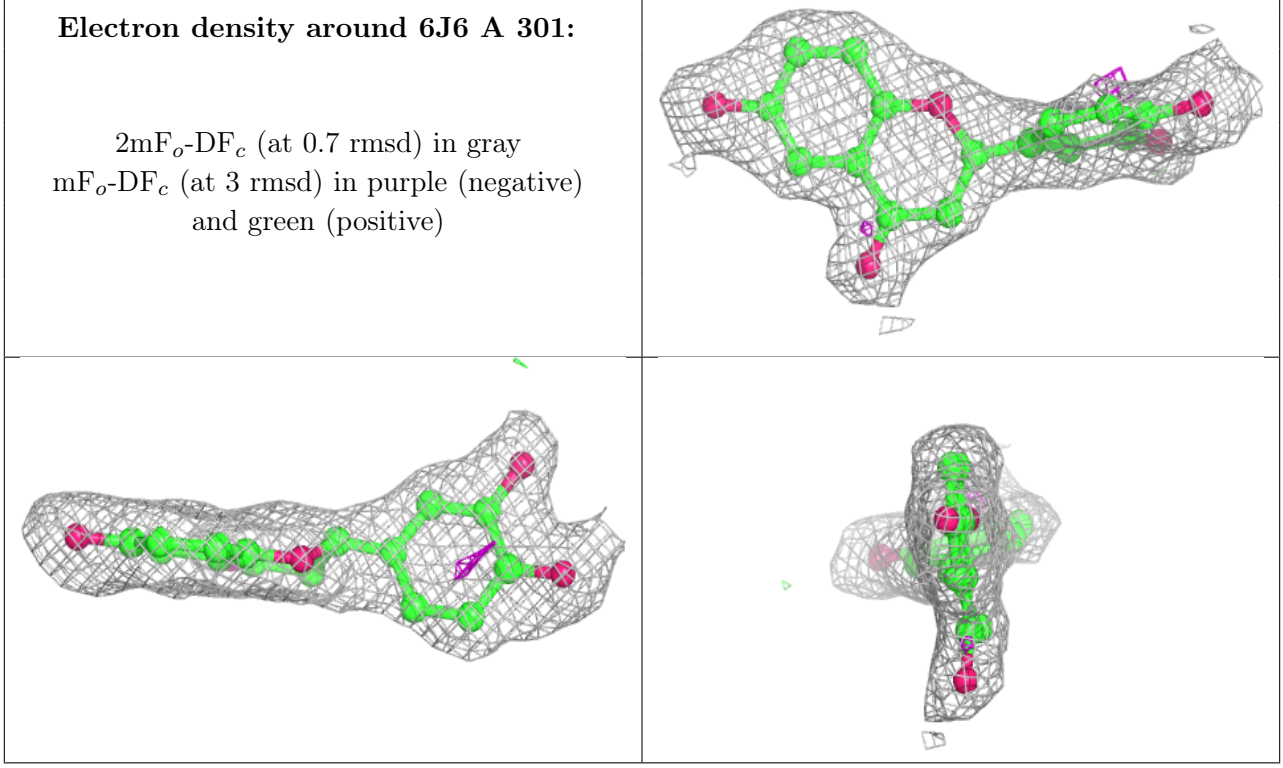






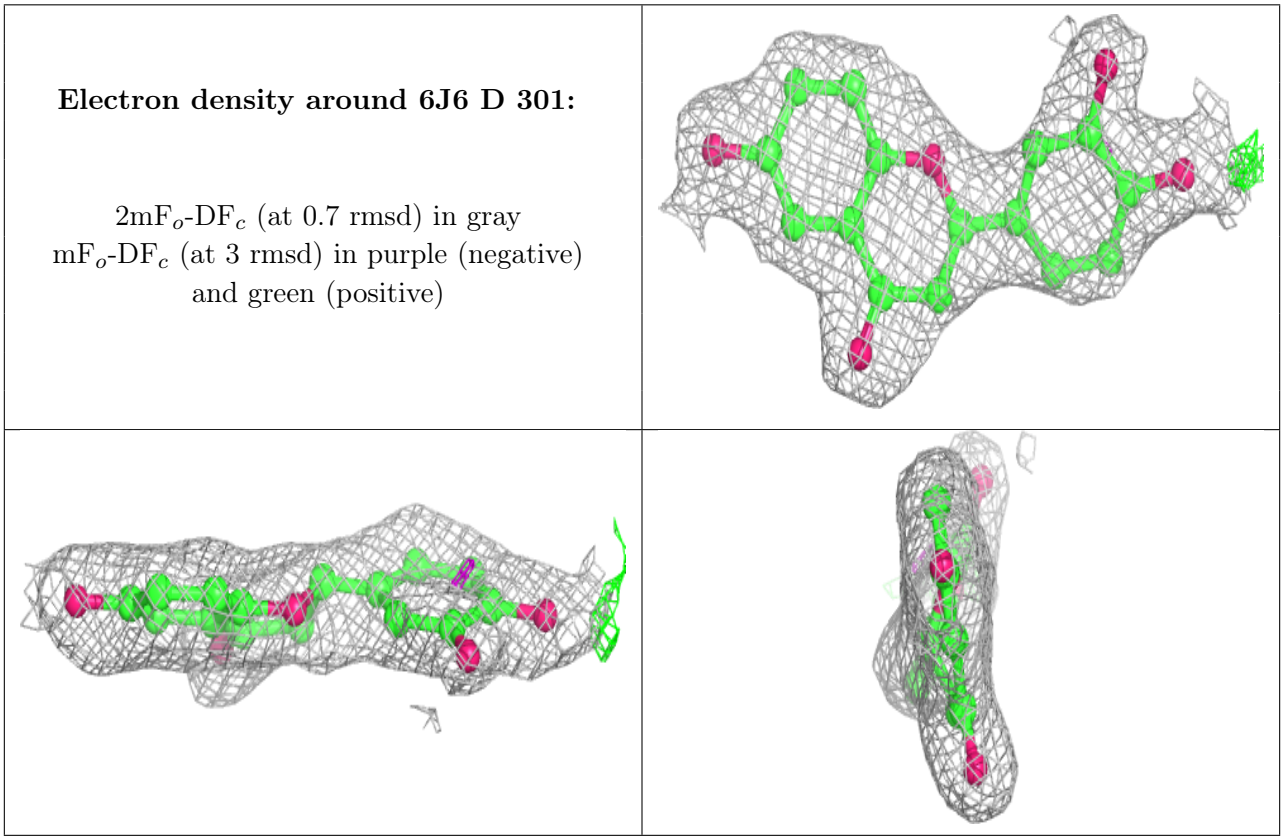
Electron density around 6J6 A 301:

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



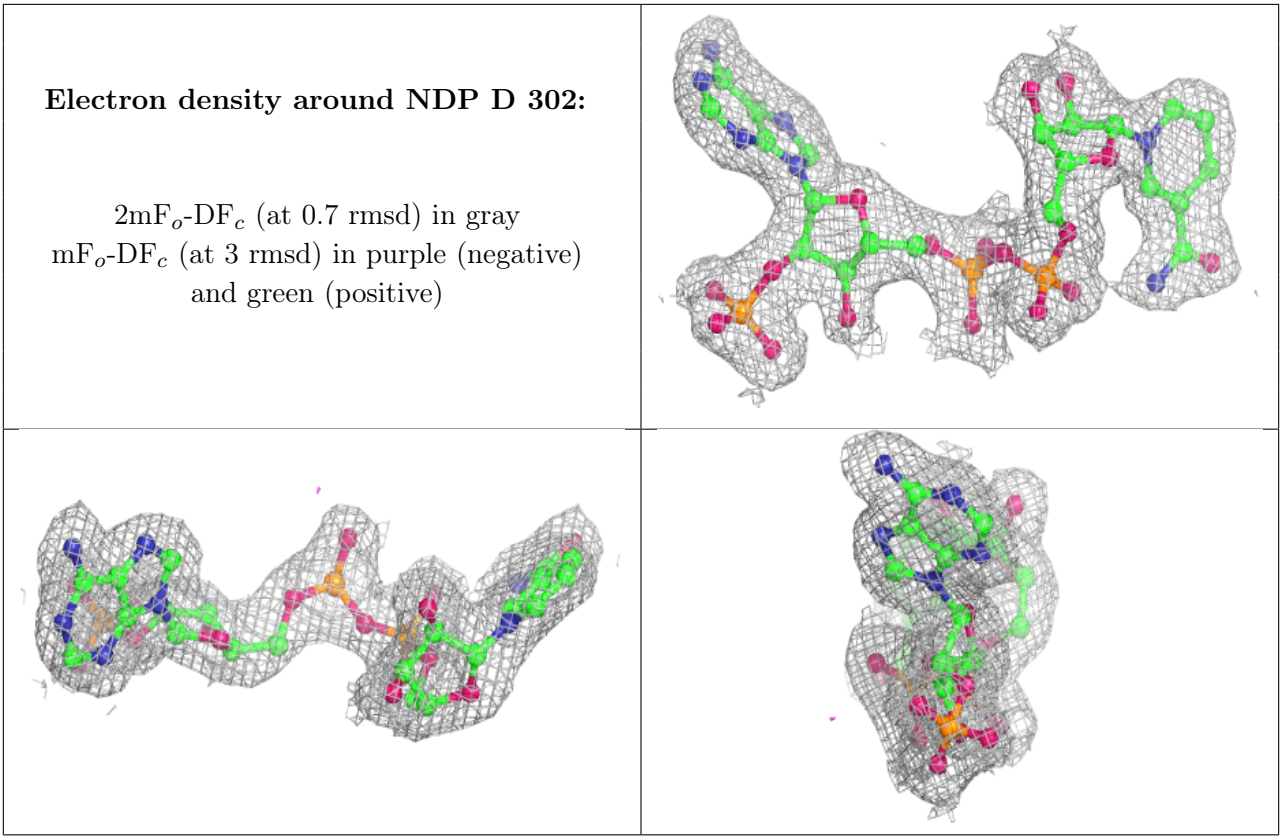
Electron density around 6J6 D 301:

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



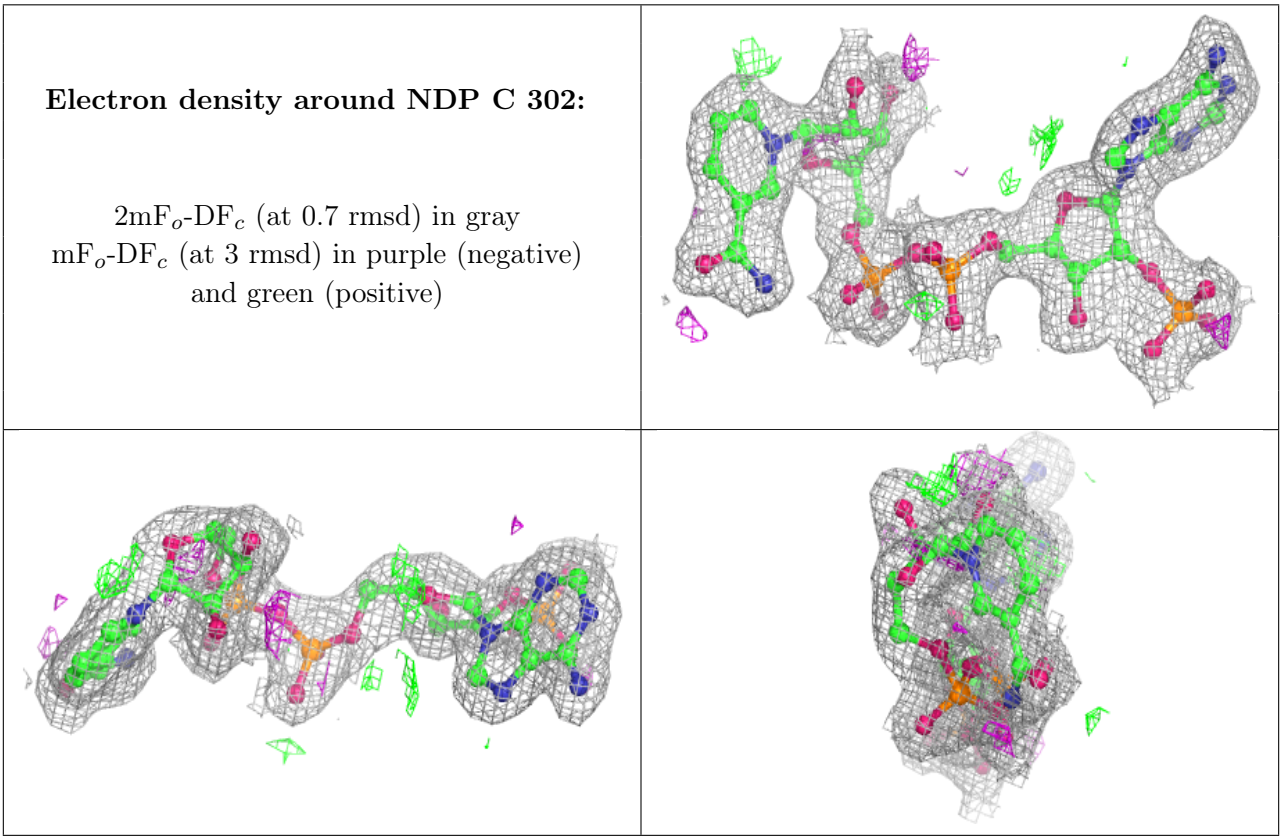
Electron density around NDP D 302:

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



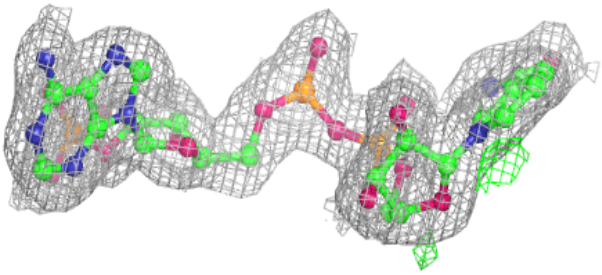
Electron density around NDP C 302:

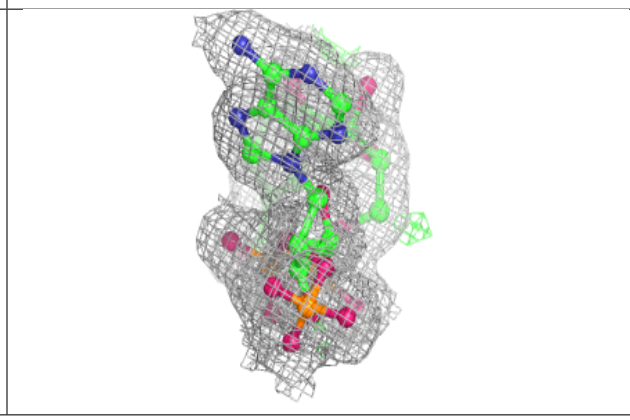
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



Electron density around NDP A 302:

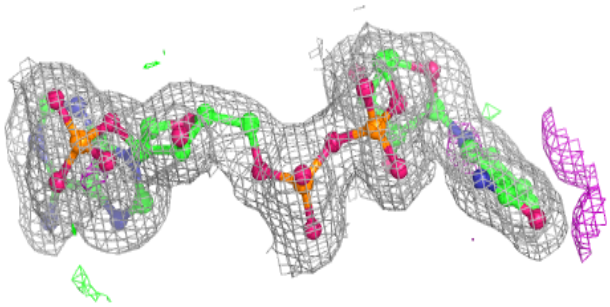
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

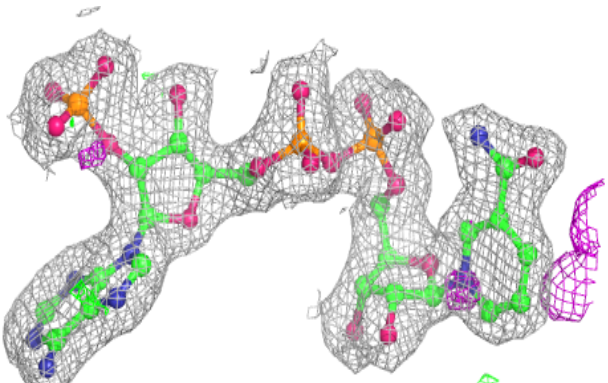




Electron density around NDP B 302:

$2mF_o$-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.