



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2021 – 04:49 PM EDT

PDB ID : 1FDU  
Title : HUMAN 17-BETA-HYDROXYSTEROID-DEHYDROGENASE TYPE 1  
MUTANT H221L COMPLEXED WITH ESTRADIOL AND NADP+  
Authors : Mazza, C.; Breton, R.; Housset, D.; Fontecilla-Camps, J.-C.  
Deposited on : 1998-01-14  
Resolution : 2.70 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
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) : 2.23.2

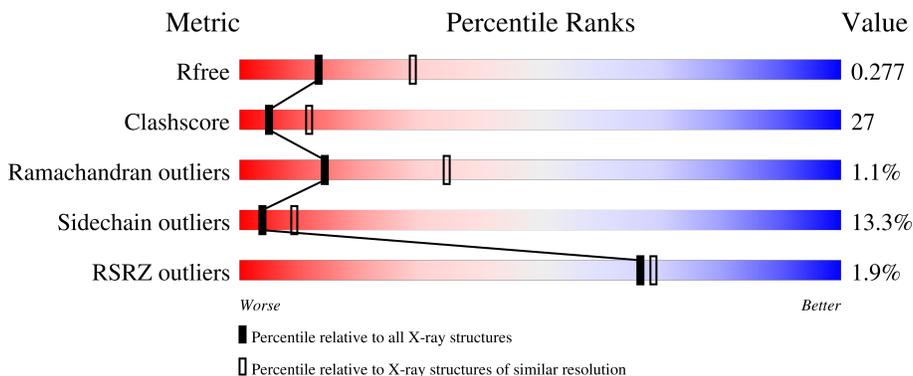
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	327	 2% 39% 39% 7% • 14%
1	B	327	 % 39% 37% 8% • 14%
1	C	327	 % 41% 33% 11% • 13%
1	D	327	 2% 46% 32% 6% • 14%

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
2	SO4	C	403	-	-	X	-
2	SO4	D	402	-	-	X	-
3	EST	A	351	-	-	X	-

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9114 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 17-BETA-HYDROXYSTEROID DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	281	2148	1366	380	390	12	0	0	0
1	B	280	2144	1364	379	389	12	0	0	0
1	C	285	2179	1384	384	399	12	0	0	0
1	D	281	2153	1369	380	392	12	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

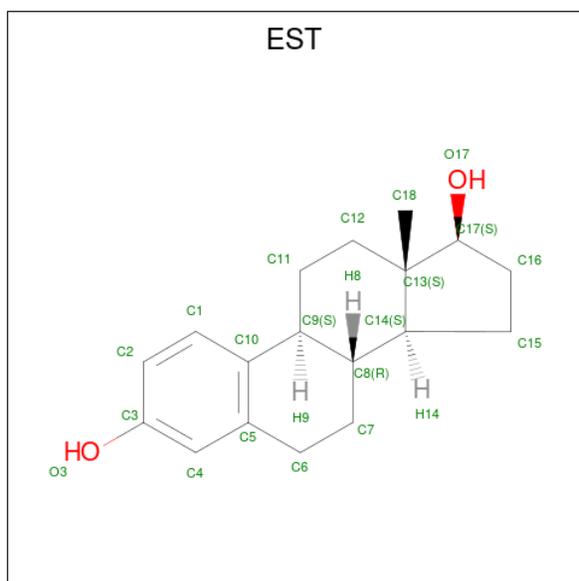
Chain	Residue	Modelled	Actual	Comment	Reference
A	221	LEU	HIS	engineered mutation	UNP P14061
A	301	ARG	ALA	conflict	UNP P14061
B	221	LEU	HIS	engineered mutation	UNP P14061
B	301	ARG	ALA	conflict	UNP P14061
C	221	LEU	HIS	engineered mutation	UNP P14061
C	301	ARG	ALA	conflict	UNP P14061
D	221	LEU	HIS	engineered mutation	UNP P14061
D	301	ARG	ALA	conflict	UNP P14061

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is ESTRADIOL (three-letter code: EST) (formula: C<sub>18</sub>H<sub>24</sub>O<sub>2</sub>).





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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	B	53	Total 53	O 53	0	0
5	C	48	Total 48	O 48	0	0
5	D	46	Total 46	O 46	0	0





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	115.80Å 78.78Å 121.19Å 90.00° 92.91° 90.00°	Depositor
Resolution (Å)	10.00 – 2.70 24.09 – 2.71	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.70) 89.6 (24.09-2.71)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.33 (at 2.71Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.220 , 0.295 0.212 , 0.277	Depositor DCC
$R_{free}$ test set	2691 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.0	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 75.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.011 for h,-k,-l 0.109 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	9114	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: EST, NAP, SO4

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	0.78	0/2186	1.64	31/2963 (1.0%)
1	B	0.74	0/2182	1.66	34/2958 (1.1%)
1	C	0.79	0/2219	1.74	41/3010 (1.4%)
1	D	0.77	0/2191	1.64	28/2970 (0.9%)
All	All	0.77	0/8778	1.67	134/11901 (1.1%)

There are no bond length outliers.

The worst 5 of 134 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	37	ARG	NE-CZ-NH1	-15.57	112.52	120.30
1	B	214	ARG	NE-CZ-NH2	-14.44	113.08	120.30
1	C	37	ARG	NE-CZ-NH1	-13.82	113.39	120.30
1	D	67	ARG	NE-CZ-NH1	13.09	126.84	120.30
1	D	214	ARG	NE-CZ-NH2	-12.99	113.80	120.30

There are no chirality outliers.

There are no planarity outliers.

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

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2148	0	2200	126	0
1	B	2144	0	2197	117	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2179	0	2225	132	0
1	D	2153	0	2203	121	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	2	0
2	D	5	0	0	2	0
3	A	20	0	24	10	0
3	B	20	0	24	6	0
3	C	20	0	23	3	0
3	D	20	0	23	6	0
4	A	48	0	25	6	0
4	B	48	0	25	5	0
4	C	48	0	25	5	0
4	D	48	0	25	5	0
5	A	51	0	0	9	0
5	B	53	0	0	3	0
5	C	48	0	0	2	0
5	D	46	0	0	3	0
All	All	9114	0	9019	483	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 27.

The worst 5 of 483 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:C:193:MET:HA	1:C:196:VAL:HG23	1.38	1.01
1:D:174:LEU:HB3	1:D:175:PRO:HD3	1.41	0.99
1:D:174:LEU:HB3	1:D:175:PRO:CD	1.95	0.97
1:C:100:GLU:HA	1:D:123:GLN:HG2	1.45	0.96
1:A:264:ARG:HA	1:A:267:LEU:HD12	1.51	0.93

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	277/327 (85%)	245 (88%)	31 (11%)	1 (0%)	34	60
1	B	276/327 (84%)	246 (89%)	25 (9%)	5 (2%)	8	21
1	C	283/327 (86%)	253 (89%)	25 (9%)	5 (2%)	8	21
1	D	277/327 (85%)	250 (90%)	26 (9%)	1 (0%)	34	60
All	All	1113/1308 (85%)	994 (89%)	107 (10%)	12 (1%)	14	34

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	197	LEU
1	C	199	SER
1	C	271	SER
1	D	174	LEU
1	C	270	PRO

### 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	231/258 (90%)	205 (89%)	26 (11%)	6	13
1	B	231/258 (90%)	196 (85%)	35 (15%)	3	7
1	C	235/258 (91%)	199 (85%)	36 (15%)	2	7
1	D	232/258 (90%)	205 (88%)	27 (12%)	5	12
All	All	929/1032 (90%)	805 (87%)	124 (13%)	4	9

5 of 124 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	257	GLU
1	D	174	LEU
1	C	123	GLN

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Mol	Chain	Res	Type
1	D	153	ASP
1	D	260	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	224	GLN
1	D	231	GLN
1	B	280	HIS
1	B	274	ASN
1	D	274	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	A	401	-	4,4,4	0.74	0	6,6,6	0.91	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAP	B	364	-	45,52,52	1.73	6 (13%)	56,80,80	1.75	13 (23%)
3	EST	C	353	-	23,23,23	0.79	0	36,36,36	1.83	9 (25%)
2	SO4	D	402	-	4,4,4	0.59	0	6,6,6	0.73	0
3	EST	D	352	-	23,23,23	1.13	1 (4%)	36,36,36	2.28	13 (36%)
4	NAP	C	363	-	45,52,52	1.99	8 (17%)	56,80,80	1.63	8 (14%)
2	SO4	C	403	-	4,4,4	0.61	0	6,6,6	0.68	0
4	NAP	D	362	-	45,52,52	1.74	6 (13%)	56,80,80	1.70	8 (14%)
3	EST	B	354	-	23,23,23	1.10	1 (4%)	36,36,36	2.55	11 (30%)
2	SO4	B	400	-	4,4,4	0.72	0	6,6,6	0.65	0
3	EST	A	351	-	23,23,23	0.81	1 (4%)	36,36,36	2.37	14 (38%)
4	NAP	A	361	-	45,52,52	1.99	9 (20%)	56,80,80	1.55	7 (12%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAP	B	364	-	-	4/31/67/67	0/5/5/5
3	EST	C	353	-	-	-	0/4/4/4
4	NAP	D	362	-	-	7/31/67/67	0/5/5/5
4	NAP	C	363	-	-	10/31/67/67	0/5/5/5
3	EST	D	352	-	-	-	0/4/4/4
3	EST	B	354	-	-	-	0/4/4/4
3	EST	A	351	-	-	-	0/4/4/4
4	NAP	A	361	-	-	12/31/67/67	0/5/5/5

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	361	NAP	P2B-O2B	-9.35	1.41	1.59
4	C	363	NAP	P2B-O2B	-8.90	1.42	1.59
4	D	362	NAP	P2B-O2B	-7.57	1.45	1.59
4	B	364	NAP	P2B-O2B	-7.32	1.45	1.59
4	C	363	NAP	C2N-N1N	5.52	1.41	1.35

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	354	EST	C7-C8-C14	8.31	126.28	112.08
3	B	354	EST	C11-C12-C13	5.71	122.57	112.78
4	D	362	NAP	O7N-C7N-C3N	5.66	126.41	119.63
4	B	364	NAP	N3A-C2A-N1A	-5.61	119.91	128.68
3	D	352	EST	C15-C14-C8	5.43	128.03	119.08

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

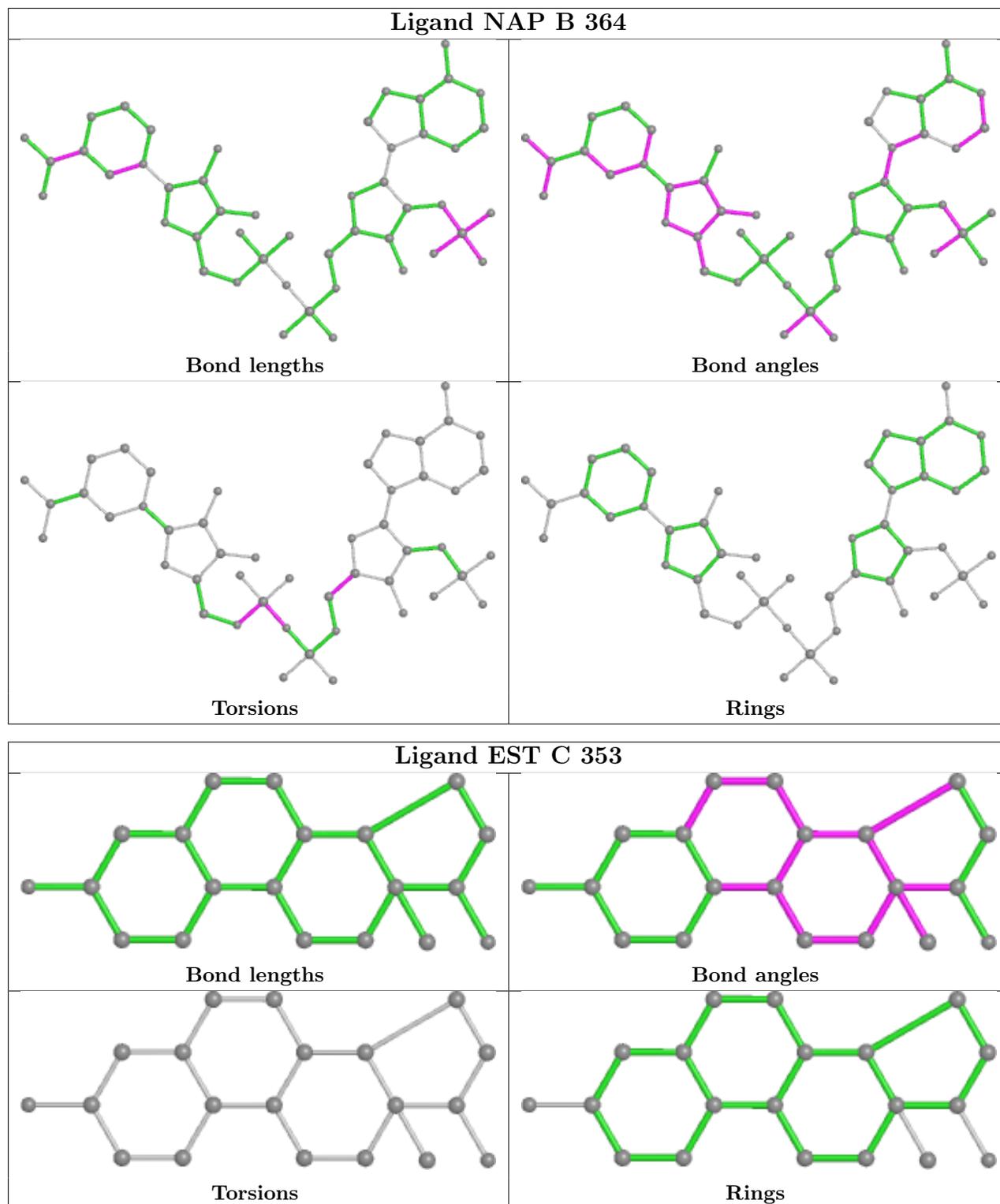
Mol	Chain	Res	Type	Atoms
4	A	361	NAP	C5B-O5B-PA-O1A
4	A	361	NAP	C5B-O5B-PA-O2A
4	A	361	NAP	C5D-O5D-PN-O3
4	A	361	NAP	O4D-C1D-N1N-C2N
4	C	363	NAP	C5B-O5B-PA-O1A

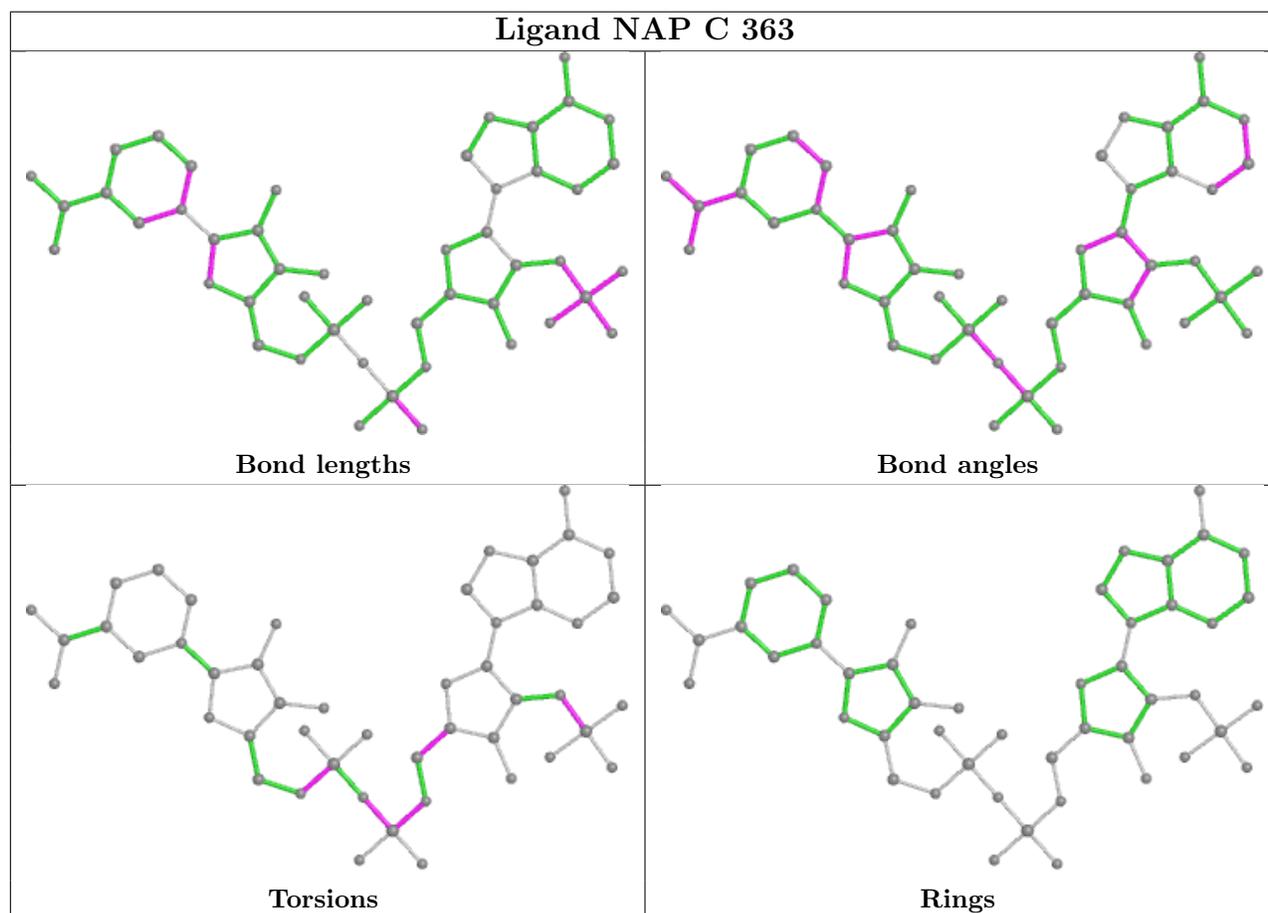
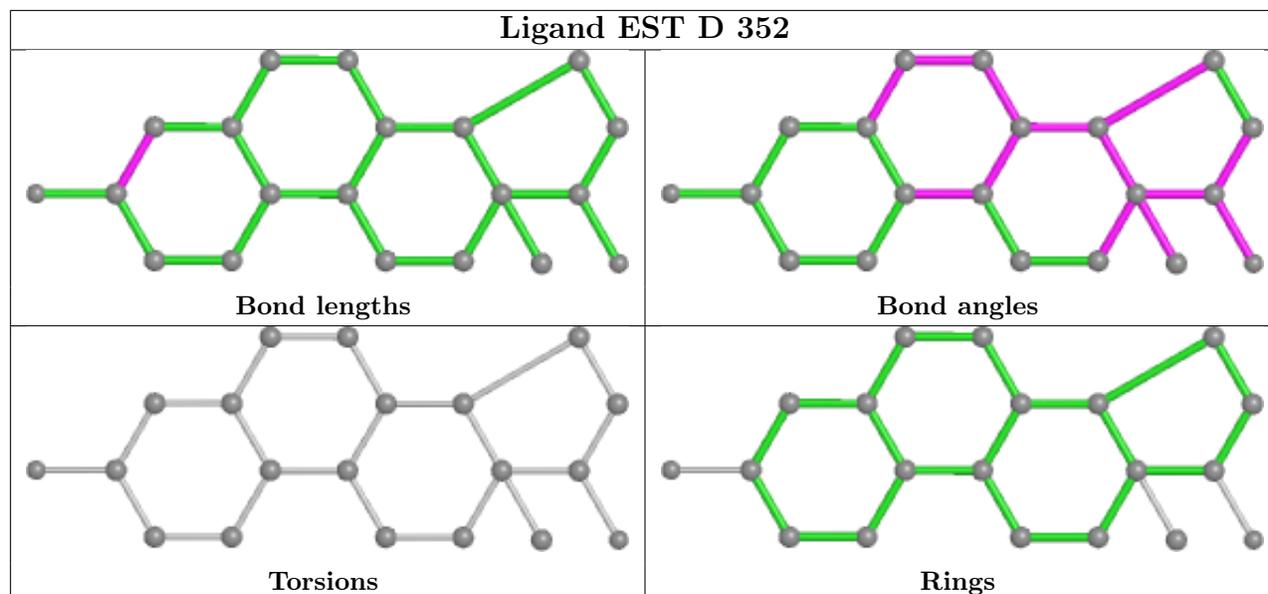
There are no ring outliers.

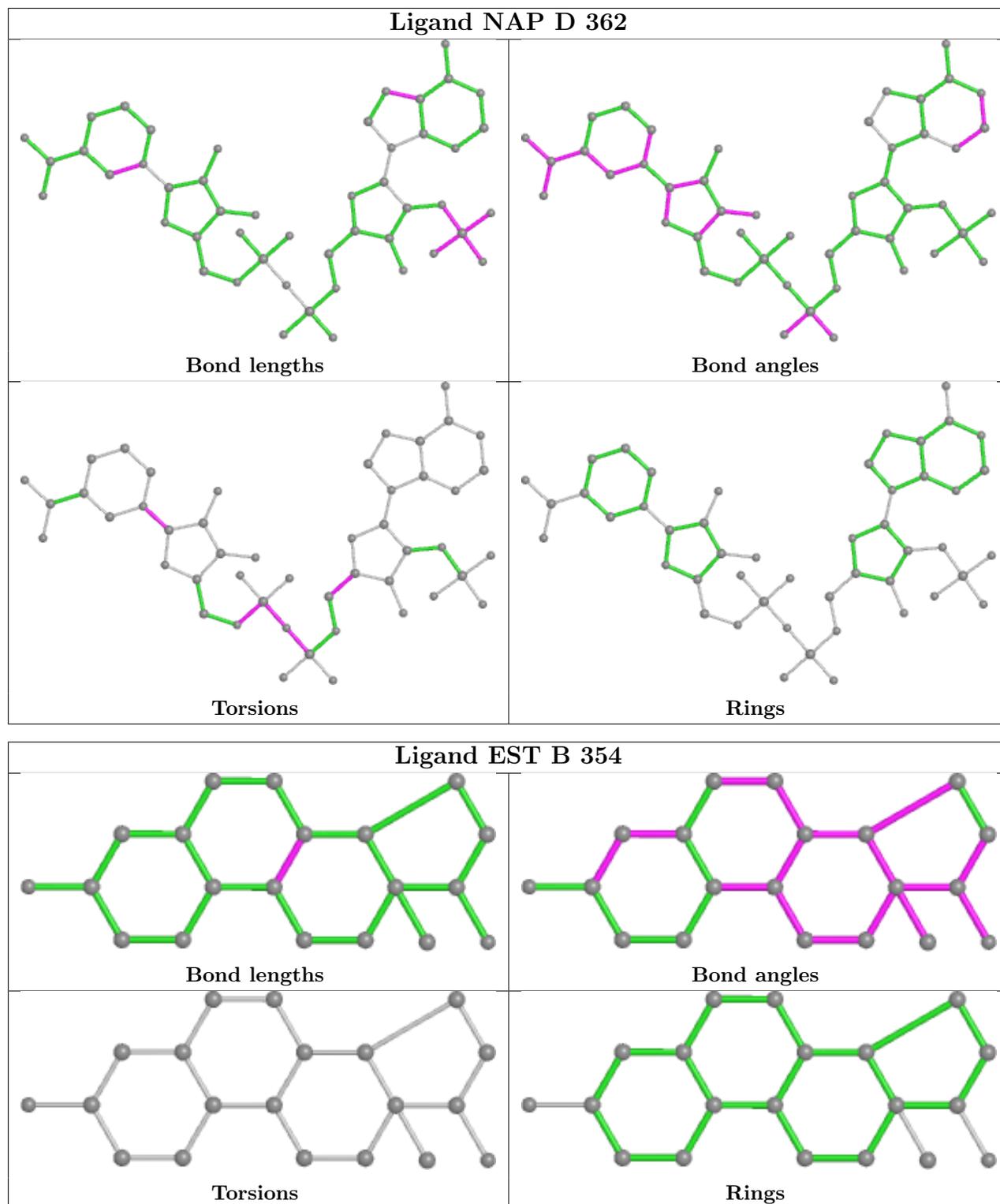
10 monomers are involved in 47 short contacts:

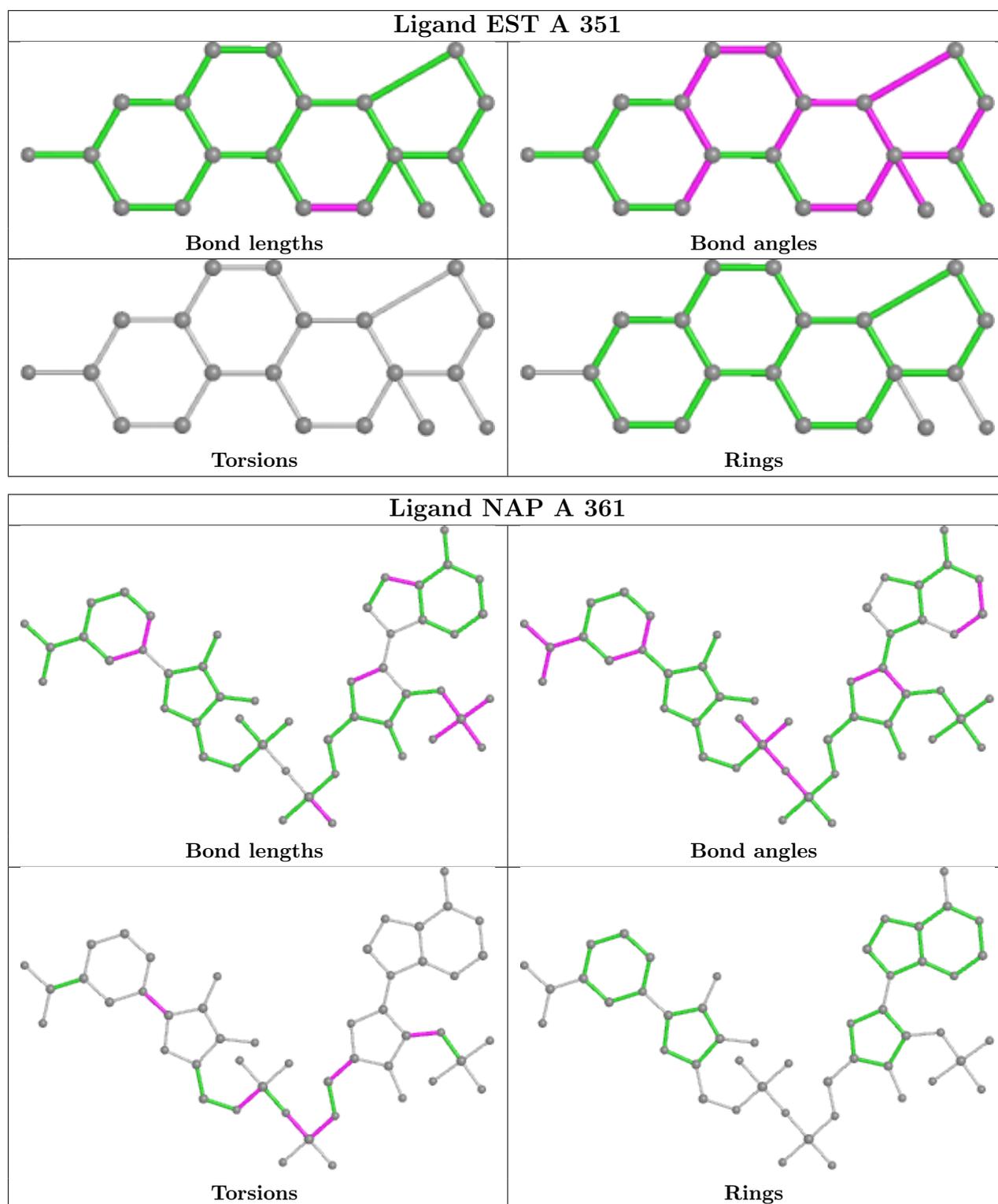
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	364	NAP	5	0
3	C	353	EST	3	0
2	D	402	SO4	2	0
3	D	352	EST	6	0
4	C	363	NAP	5	0
2	C	403	SO4	2	0
4	D	362	NAP	5	0
3	B	354	EST	6	0
3	A	351	EST	10	0
4	A	361	NAP	6	0

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

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	281/327 (85%)	-0.28	7 (2%) 57 59	8, 23, 48, 55	10 (3%)
1	B	280/327 (85%)	-0.35	4 (1%) 75 77	8, 22, 44, 52	13 (4%)
1	C	285/327 (87%)	-0.15	4 (1%) 75 77	8, 23, 49, 56	11 (3%)
1	D	281/327 (85%)	-0.36	6 (2%) 63 65	10, 23, 45, 50	10 (3%)
All	All	1127/1308 (86%)	-0.28	21 (1%) 66 69	8, 23, 47, 56	44 (3%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	197	LEU	5.8
1	A	285	GLY	4.2
1	D	2	ARG	3.8
1	D	1	ALA	3.7
1	B	1	ALA	3.4

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

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

### 6.3 Carbohydrates [i](#)

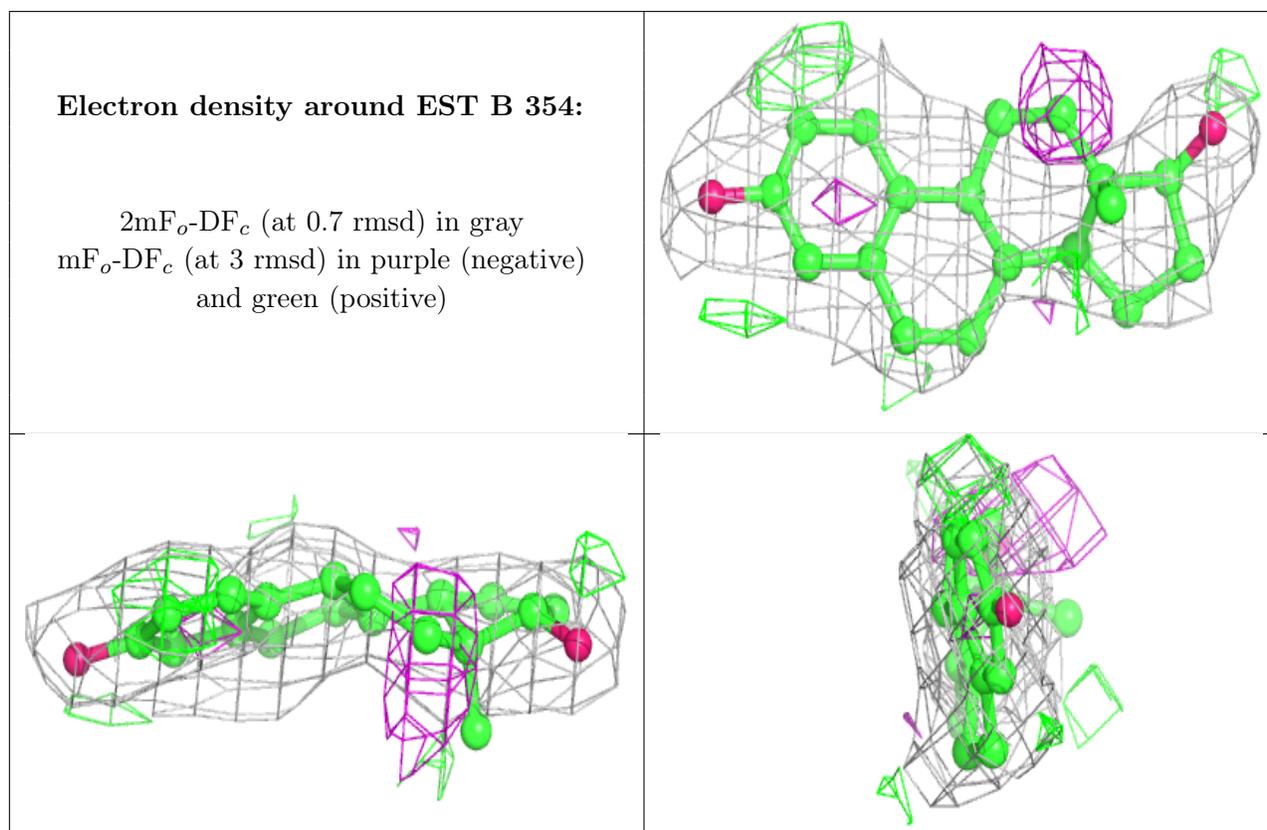
There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

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

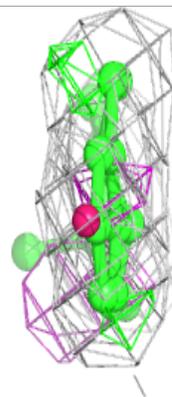
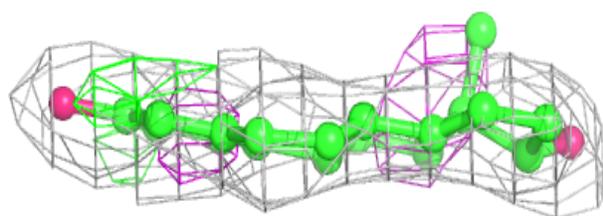
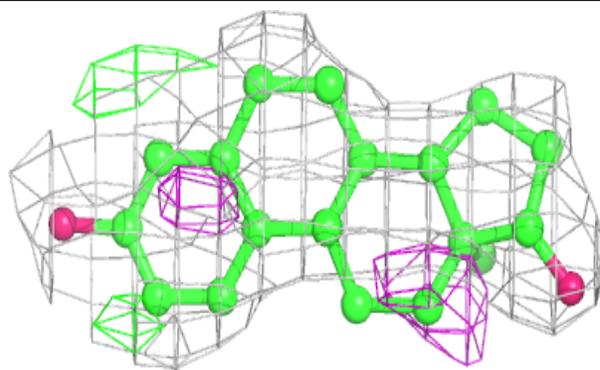
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EST	B	354	20/20	0.73	0.31	56,58,59,59	0
3	EST	D	352	20/20	0.79	0.30	47,50,51,51	0
3	EST	A	351	20/20	0.81	0.30	48,50,51,52	0
3	EST	C	353	20/20	0.83	0.29	61,63,64,64	1
2	SO4	A	401	5/5	0.95	0.18	42,43,43,43	0
2	SO4	C	403	5/5	0.95	0.17	43,43,44,44	0
2	SO4	B	400	5/5	0.97	0.13	46,47,47,47	0
4	NAP	A	361	48/48	0.97	0.12	13,16,19,21	0
4	NAP	B	364	48/48	0.97	0.12	10,17,21,23	0
4	NAP	C	363	48/48	0.97	0.12	13,17,21,23	0
4	NAP	D	362	48/48	0.97	0.12	12,17,21,22	0
2	SO4	D	402	5/5	0.98	0.17	42,43,43,43	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.

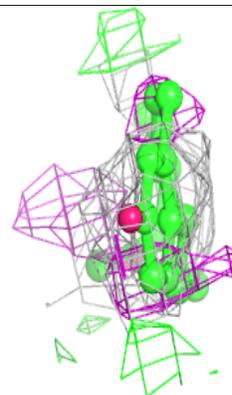
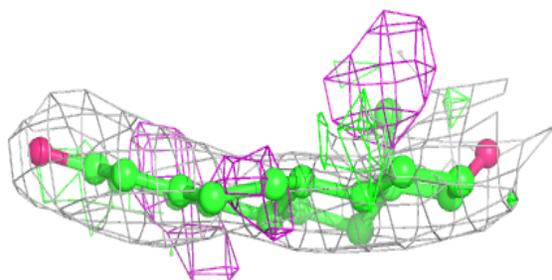
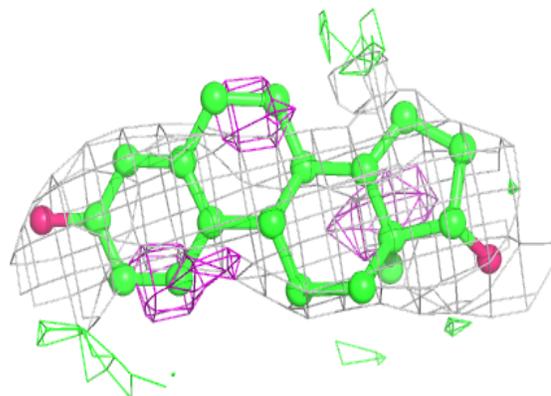


**Electron density around EST D 352:**

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

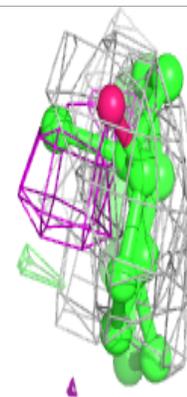
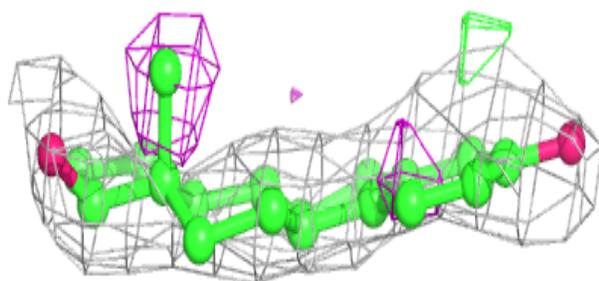
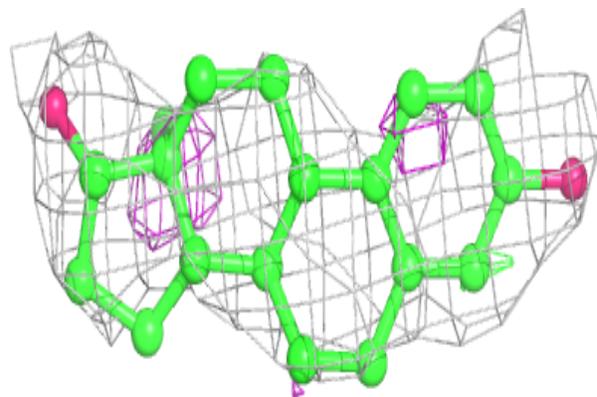
**Electron density around EST A 351:**

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

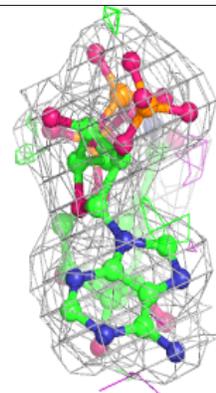
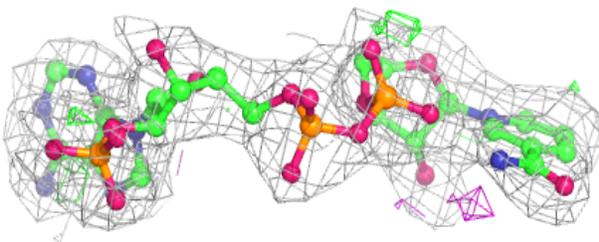
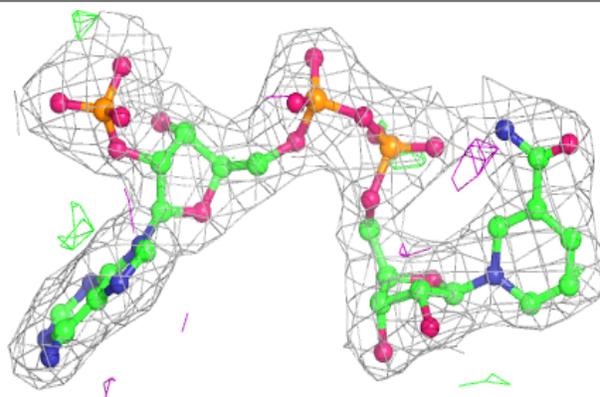


**Electron density around EST C 353:**

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

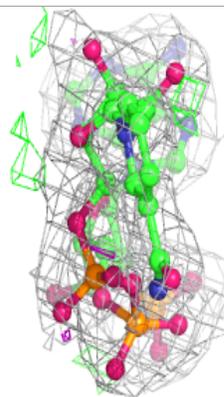
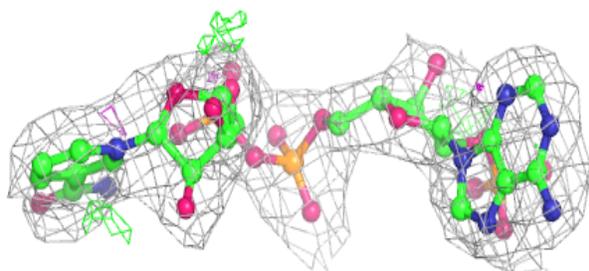
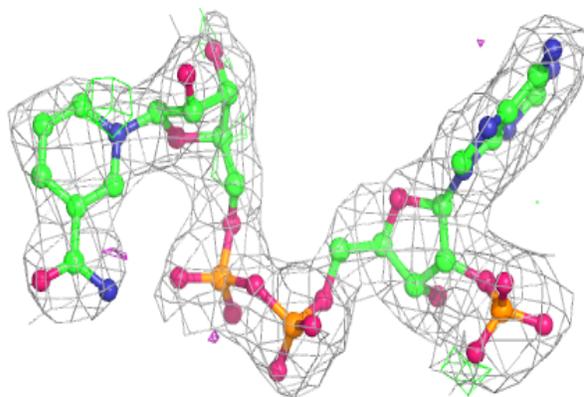
**Electron density around NAP A 361:**

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

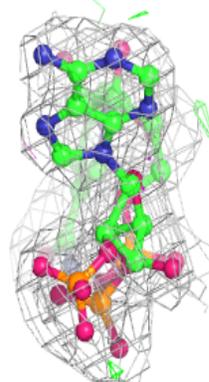
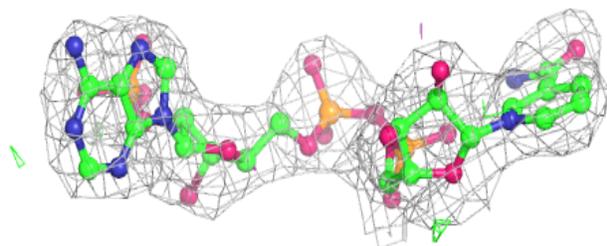
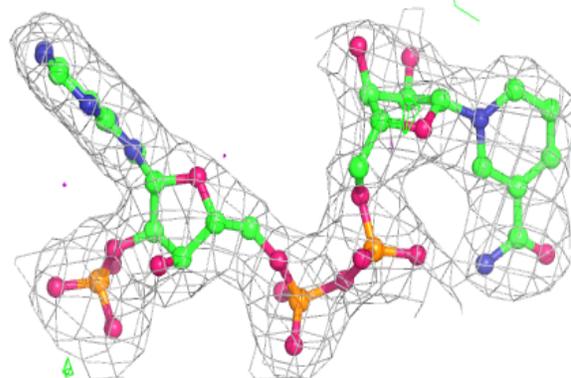


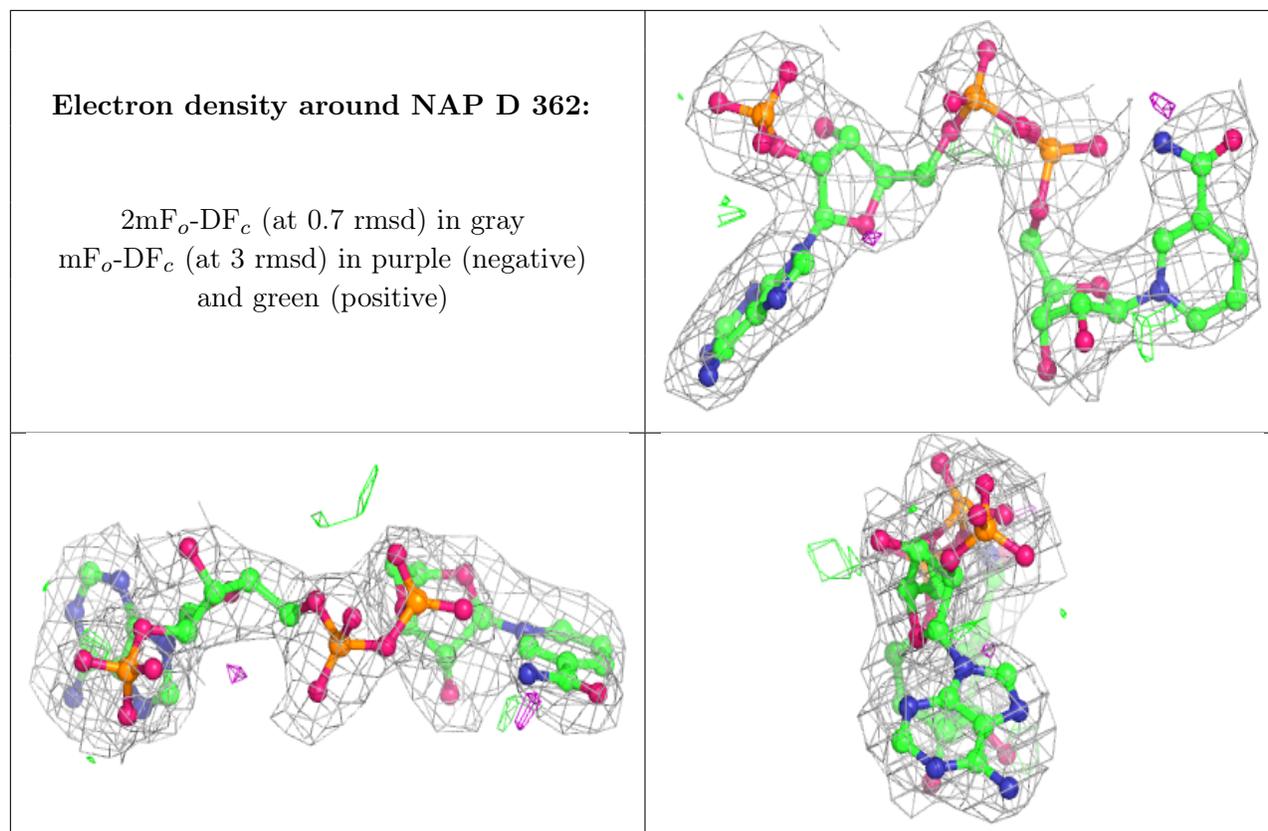
**Electron density around NAP B 364:**

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

**Electron density around NAP C 363:**

$2mF_o-DF_c$  (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.