



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 08:15 PM UTC

PDB ID : 5CB5 / pdb_00005cb5
Title : Structural Insights into the Mechanism of Escherichia coli Ymdb
Authors : Zhang, W.; Wang, C.; Song, Y.; Shao, C.; Zhang, X.; Zang, J.
Deposited on : 2015-06-30
Resolution : 2.80 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (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

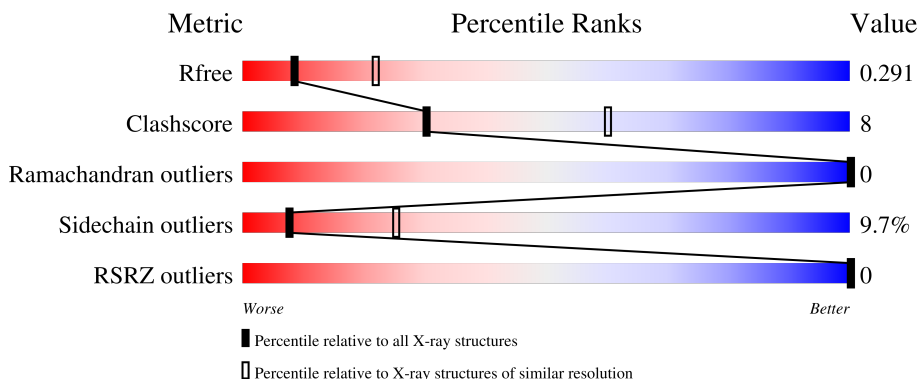
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 $\leq 5\%$. 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	183	
1	B	183	
1	C	183	
1	D	183	
1	E	183	

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Mol	Chain	Length	Quality of chain
1	F	183	
1	G	183	
1	H	183	
1	I	183	
1	J	183	
1	K	183	
1	L	183	
1	M	183	
1	N	183	
1	O	183	
1	P	183	
1	Q	183	
1	R	183	

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
3	SO4	C	202	-	-	X	-
3	SO4	D	202	-	-	X	-
3	SO4	J	202	-	-	X	-
3	SO4	K	202	-	-	X	-
3	SO4	M	202	-	-	X	-
3	SO4	O	202	-	-	X	-
3	SO4	Q	403	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 23896 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 O-acetyl-ADP-ribose deacetylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	R	173	1281	810	229	238	4	0	0	0
1	A	173	1259	798	222	235	4	0	0	0
1	B	172	1280	809	228	239	4	0	0	0
1	C	173	1283	811	226	242	4	0	0	0
1	D	170	1236	781	220	231	4	0	0	0
1	E	173	1293	816	230	243	4	0	0	0
1	F	173	1283	810	226	243	4	0	0	0
1	G	173	1280	810	226	240	4	0	0	0
1	H	173	1293	816	230	243	4	0	0	0
1	I	173	1272	805	226	237	4	0	0	0
1	J	172	1280	808	228	240	4	0	0	0
1	K	172	1256	796	219	237	4	0	0	0
1	L	172	1259	797	222	236	4	0	0	0
1	M	173	1279	809	226	240	4	0	0	0
1	N	173	1255	794	221	236	4	0	0	0
1	O	171	1271	803	226	238	4	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	173	Total	C	N	O	S	0	0	0
			1277	807	227	239	4			
1	Q	173	Total	C	N	O	S	0	0	0
			1289	814	229	242	4			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	-5	HIS	-	expression tag	UNP P0A8D6
R	-4	HIS	-	expression tag	UNP P0A8D6
R	-3	HIS	-	expression tag	UNP P0A8D6
R	-2	HIS	-	expression tag	UNP P0A8D6
R	-1	HIS	-	expression tag	UNP P0A8D6
R	0	HIS	-	expression tag	UNP P0A8D6
R	25	ALA	ASN	engineered mutation	UNP P0A8D6
R	35	ALA	ASP	engineered mutation	UNP P0A8D6
A	-5	HIS	-	expression tag	UNP P0A8D6
A	-4	HIS	-	expression tag	UNP P0A8D6
A	-3	HIS	-	expression tag	UNP P0A8D6
A	-2	HIS	-	expression tag	UNP P0A8D6
A	-1	HIS	-	expression tag	UNP P0A8D6
A	0	HIS	-	expression tag	UNP P0A8D6
A	25	ALA	ASN	engineered mutation	UNP P0A8D6
A	35	ALA	ASP	engineered mutation	UNP P0A8D6
B	-5	HIS	-	expression tag	UNP P0A8D6
B	-4	HIS	-	expression tag	UNP P0A8D6
B	-3	HIS	-	expression tag	UNP P0A8D6
B	-2	HIS	-	expression tag	UNP P0A8D6
B	-1	HIS	-	expression tag	UNP P0A8D6
B	0	HIS	-	expression tag	UNP P0A8D6
B	25	ALA	ASN	engineered mutation	UNP P0A8D6
B	35	ALA	ASP	engineered mutation	UNP P0A8D6
C	-5	HIS	-	expression tag	UNP P0A8D6
C	-4	HIS	-	expression tag	UNP P0A8D6
C	-3	HIS	-	expression tag	UNP P0A8D6
C	-2	HIS	-	expression tag	UNP P0A8D6
C	-1	HIS	-	expression tag	UNP P0A8D6
C	0	HIS	-	expression tag	UNP P0A8D6
C	25	ALA	ASN	engineered mutation	UNP P0A8D6
C	35	ALA	ASP	engineered mutation	UNP P0A8D6
D	-5	HIS	-	expression tag	UNP P0A8D6
D	-4	HIS	-	expression tag	UNP P0A8D6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	HIS	-	expression tag	UNP P0A8D6
D	-2	HIS	-	expression tag	UNP P0A8D6
D	-1	HIS	-	expression tag	UNP P0A8D6
D	0	HIS	-	expression tag	UNP P0A8D6
D	25	ALA	ASN	engineered mutation	UNP P0A8D6
D	35	ALA	ASP	engineered mutation	UNP P0A8D6
E	-5	HIS	-	expression tag	UNP P0A8D6
E	-4	HIS	-	expression tag	UNP P0A8D6
E	-3	HIS	-	expression tag	UNP P0A8D6
E	-2	HIS	-	expression tag	UNP P0A8D6
E	-1	HIS	-	expression tag	UNP P0A8D6
E	0	HIS	-	expression tag	UNP P0A8D6
E	25	ALA	ASN	engineered mutation	UNP P0A8D6
E	35	ALA	ASP	engineered mutation	UNP P0A8D6
F	-5	HIS	-	expression tag	UNP P0A8D6
F	-4	HIS	-	expression tag	UNP P0A8D6
F	-3	HIS	-	expression tag	UNP P0A8D6
F	-2	HIS	-	expression tag	UNP P0A8D6
F	-1	HIS	-	expression tag	UNP P0A8D6
F	0	HIS	-	expression tag	UNP P0A8D6
F	25	ALA	ASN	engineered mutation	UNP P0A8D6
F	35	ALA	ASP	engineered mutation	UNP P0A8D6
G	-5	HIS	-	expression tag	UNP P0A8D6
G	-4	HIS	-	expression tag	UNP P0A8D6
G	-3	HIS	-	expression tag	UNP P0A8D6
G	-2	HIS	-	expression tag	UNP P0A8D6
G	-1	HIS	-	expression tag	UNP P0A8D6
G	0	HIS	-	expression tag	UNP P0A8D6
G	25	ALA	ASN	engineered mutation	UNP P0A8D6
G	35	ALA	ASP	engineered mutation	UNP P0A8D6
H	-5	HIS	-	expression tag	UNP P0A8D6
H	-4	HIS	-	expression tag	UNP P0A8D6
H	-3	HIS	-	expression tag	UNP P0A8D6
H	-2	HIS	-	expression tag	UNP P0A8D6
H	-1	HIS	-	expression tag	UNP P0A8D6
H	0	HIS	-	expression tag	UNP P0A8D6
H	25	ALA	ASN	engineered mutation	UNP P0A8D6
H	35	ALA	ASP	engineered mutation	UNP P0A8D6
I	-5	HIS	-	expression tag	UNP P0A8D6
I	-4	HIS	-	expression tag	UNP P0A8D6
I	-3	HIS	-	expression tag	UNP P0A8D6
I	-2	HIS	-	expression tag	UNP P0A8D6

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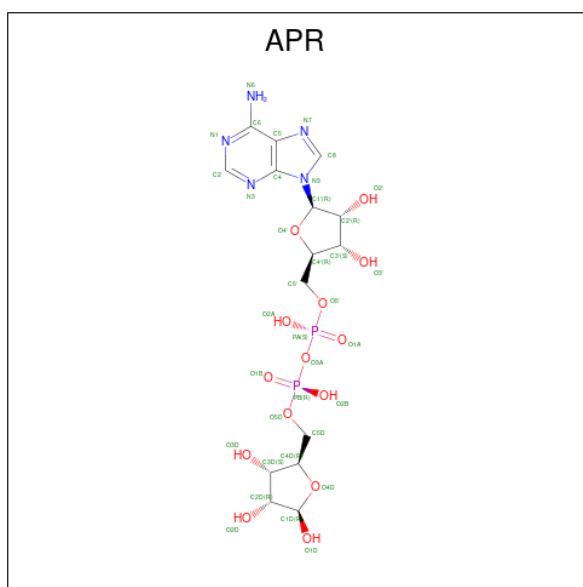
Chain	Residue	Modelled	Actual	Comment	Reference
I	-1	HIS	-	expression tag	UNP P0A8D6
I	0	HIS	-	expression tag	UNP P0A8D6
I	25	ALA	ASN	engineered mutation	UNP P0A8D6
I	35	ALA	ASP	engineered mutation	UNP P0A8D6
J	-5	HIS	-	expression tag	UNP P0A8D6
J	-4	HIS	-	expression tag	UNP P0A8D6
J	-3	HIS	-	expression tag	UNP P0A8D6
J	-2	HIS	-	expression tag	UNP P0A8D6
J	-1	HIS	-	expression tag	UNP P0A8D6
J	0	HIS	-	expression tag	UNP P0A8D6
J	25	ALA	ASN	engineered mutation	UNP P0A8D6
J	35	ALA	ASP	engineered mutation	UNP P0A8D6
K	-5	HIS	-	expression tag	UNP P0A8D6
K	-4	HIS	-	expression tag	UNP P0A8D6
K	-3	HIS	-	expression tag	UNP P0A8D6
K	-2	HIS	-	expression tag	UNP P0A8D6
K	-1	HIS	-	expression tag	UNP P0A8D6
K	0	HIS	-	expression tag	UNP P0A8D6
K	25	ALA	ASN	engineered mutation	UNP P0A8D6
K	35	ALA	ASP	engineered mutation	UNP P0A8D6
L	-5	HIS	-	expression tag	UNP P0A8D6
L	-4	HIS	-	expression tag	UNP P0A8D6
L	-3	HIS	-	expression tag	UNP P0A8D6
L	-2	HIS	-	expression tag	UNP P0A8D6
L	-1	HIS	-	expression tag	UNP P0A8D6
L	0	HIS	-	expression tag	UNP P0A8D6
L	25	ALA	ASN	engineered mutation	UNP P0A8D6
L	35	ALA	ASP	engineered mutation	UNP P0A8D6
M	-5	HIS	-	expression tag	UNP P0A8D6
M	-4	HIS	-	expression tag	UNP P0A8D6
M	-3	HIS	-	expression tag	UNP P0A8D6
M	-2	HIS	-	expression tag	UNP P0A8D6
M	-1	HIS	-	expression tag	UNP P0A8D6
M	0	HIS	-	expression tag	UNP P0A8D6
M	25	ALA	ASN	engineered mutation	UNP P0A8D6
M	35	ALA	ASP	engineered mutation	UNP P0A8D6
N	-5	HIS	-	expression tag	UNP P0A8D6
N	-4	HIS	-	expression tag	UNP P0A8D6
N	-3	HIS	-	expression tag	UNP P0A8D6
N	-2	HIS	-	expression tag	UNP P0A8D6
N	-1	HIS	-	expression tag	UNP P0A8D6
N	0	HIS	-	expression tag	UNP P0A8D6

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Chain	Residue	Modelled	Actual	Comment	Reference
N	25	ALA	ASN	engineered mutation	UNP P0A8D6
N	35	ALA	ASP	engineered mutation	UNP P0A8D6
O	-5	HIS	-	expression tag	UNP P0A8D6
O	-4	HIS	-	expression tag	UNP P0A8D6
O	-3	HIS	-	expression tag	UNP P0A8D6
O	-2	HIS	-	expression tag	UNP P0A8D6
O	-1	HIS	-	expression tag	UNP P0A8D6
O	0	HIS	-	expression tag	UNP P0A8D6
O	25	ALA	ASN	engineered mutation	UNP P0A8D6
O	35	ALA	ASP	engineered mutation	UNP P0A8D6
P	-5	HIS	-	expression tag	UNP P0A8D6
P	-4	HIS	-	expression tag	UNP P0A8D6
P	-3	HIS	-	expression tag	UNP P0A8D6
P	-2	HIS	-	expression tag	UNP P0A8D6
P	-1	HIS	-	expression tag	UNP P0A8D6
P	0	HIS	-	expression tag	UNP P0A8D6
P	25	ALA	ASN	engineered mutation	UNP P0A8D6
P	35	ALA	ASP	engineered mutation	UNP P0A8D6
Q	-5	HIS	-	expression tag	UNP P0A8D6
Q	-4	HIS	-	expression tag	UNP P0A8D6
Q	-3	HIS	-	expression tag	UNP P0A8D6
Q	-2	HIS	-	expression tag	UNP P0A8D6
Q	-1	HIS	-	expression tag	UNP P0A8D6
Q	0	HIS	-	expression tag	UNP P0A8D6
Q	25	ALA	ASN	engineered mutation	UNP P0A8D6
Q	35	ALA	ASP	engineered mutation	UNP P0A8D6

- Molecule 2 is ADENOSINE-5-DIPHOSPHORIBOSE (CCD ID: APR) (formula: C₁₅H₂₃N₅O₁₄P₂).



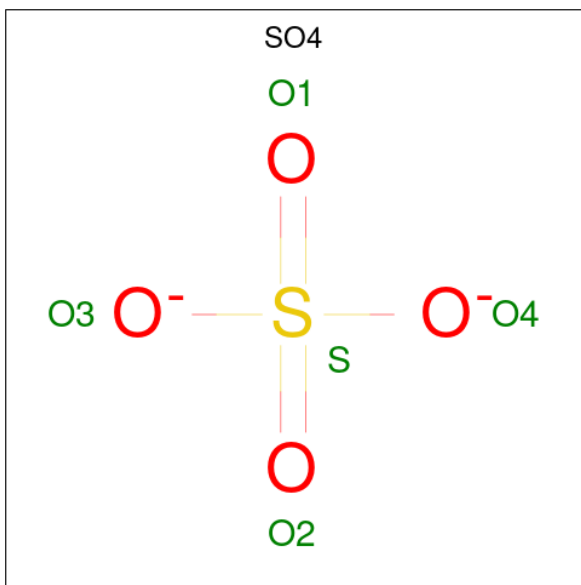
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	R	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	A	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	B	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	C	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	D	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	E	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	G	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	H	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	I	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	J	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	K	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	L	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	N	1	Total	C	N	O	P	0	0
			36	15	5	14	2		
2	O	1	Total	C	N	O	P	0	0
			36	15	5	14	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	P	1	Total 36	C 15	N 5	O 14	P 2	0	0
2	Q	1	Total 36	C 15	N 5	O 14	P 2	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



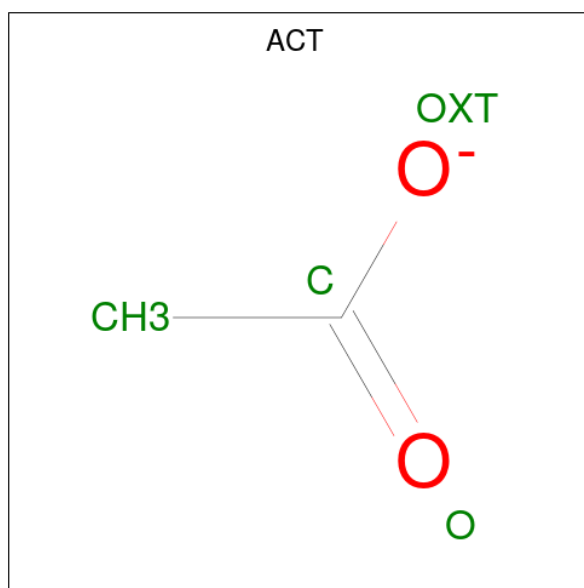
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	R	1	Total 5	O 4	S 1	0	0
3	A	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0
3	C	1	Total 5	O 4	S 1	0	0
3	D	1	Total 5	O 4	S 1	0	0
3	E	1	Total 5	O 4	S 1	0	0
3	F	1	Total 5	O 4	S 1	0	0
3	G	1	Total 5	O 4	S 1	0	0
3	H	1	Total 5	O 4	S 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	M	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	O	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	Q	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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


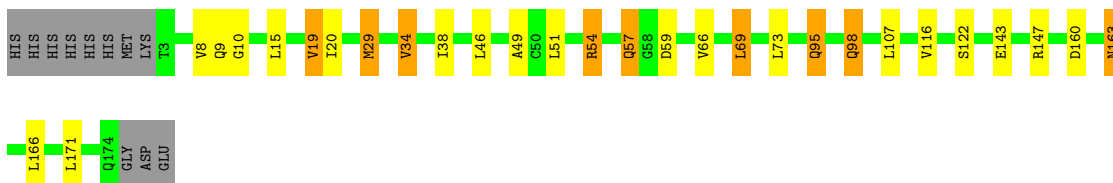
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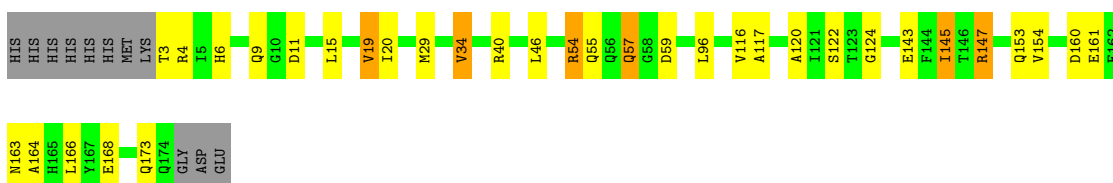
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	E	11	Total O 11 11	0	0
6	F	10	Total O 10 10	0	0
6	G	8	Total O 8 8	0	0
6	H	12	Total O 12 12	0	0
6	I	12	Total O 12 12	0	0
6	J	12	Total O 12 12	0	0
6	K	11	Total O 11 11	0	0
6	L	11	Total O 11 11	0	0
6	M	15	Total O 15 15	0	0
6	N	12	Total O 12 12	0	0
6	O	11	Total O 11 11	0	0
6	P	14	Total O 14 14	0	0
6	Q	9	Total O 9 9	0	0

ASP
GLU


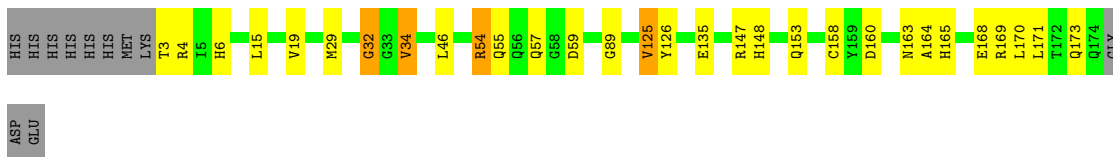
- Molecule 1: O-acetyl-ADP-ribose deacetylase

Chain J:  78% 11% 5% 6%


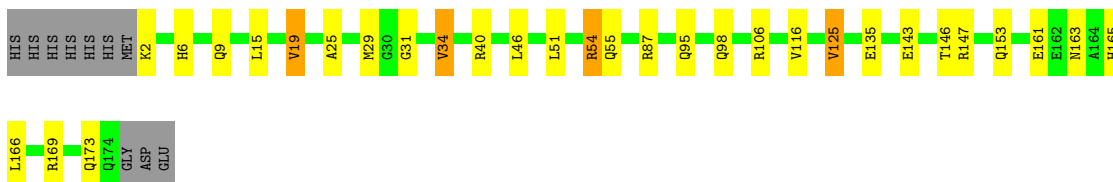
- Molecule 1: O-acetyl-ADP-ribose deacetylase

Chain K:  75% 15% 6%


- Molecule 1: O-acetyl-ADP-ribose deacetylase

Chain L:  78% 14% 6%ASP
GLU


- Molecule 1: O-acetyl-ADP-ribose deacetylase

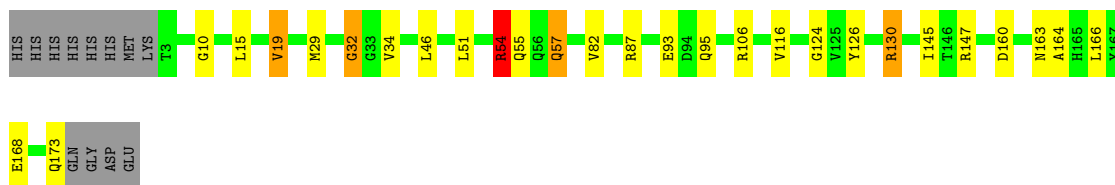
Chain M:  78% 15% 5%

- Molecule 1: O-acetyl-ADP-ribose deacetylase


Chain N:  80% 9% 5% 5%

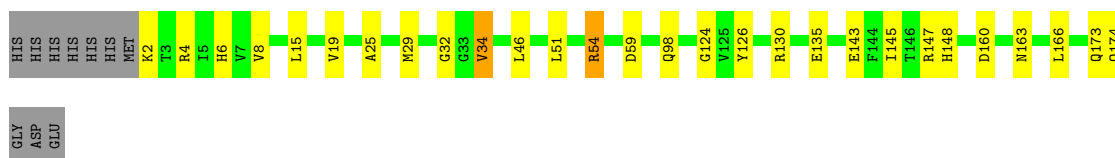
- Molecule 1: O-acetyl-ADP-ribose deacetylase

Chain O:  78% 13% 7%




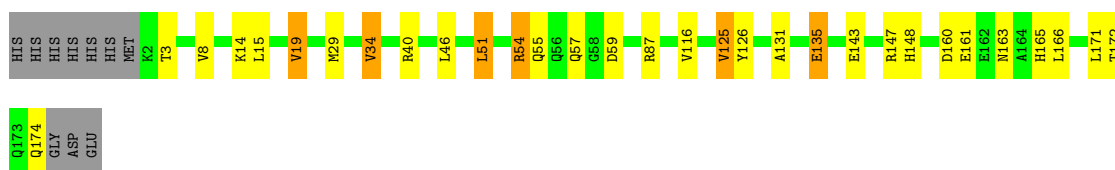
- Molecule 1: O-acetyl-ADP-ribose deacetylase

Chain P:  79% 14% 5%



- Molecule 1: O-acetyl-ADP-ribose deacetylase

Chain Q:  78% 14% 5%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	289.14Å 289.14Å 114.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.72 – 2.80 38.72 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.8 (38.72-2.80) 98.9 (38.72-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.262 , 0.290 0.262 , 0.291	Depositor DCC
R_{free} test set	6667 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	37.0	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 9.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.408 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	23896	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 19.99 % 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 9.5839e-03.*

¹Intensities estimated from amplitudes.

²Theoretical 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: APR, ZOD, ACT, 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	1.13	1/1284 (0.1%)	1.29	4/1757 (0.2%)
1	B	1.14	3/1305 (0.2%)	1.29	4/1782 (0.2%)
1	C	1.13	1/1308 (0.1%)	1.25	4/1787 (0.2%)
1	D	1.20	3/1261 (0.2%)	1.30	4/1727 (0.2%)
1	E	1.10	0/1318	1.27	4/1799 (0.2%)
1	F	1.11	0/1308	1.27	3/1788 (0.2%)
1	G	1.11	0/1305	1.23	1/1783 (0.1%)
1	H	1.12	0/1318	1.23	2/1799 (0.1%)
1	I	1.08	0/1296	1.25	3/1771 (0.2%)
1	J	1.12	0/1305	1.24	4/1783 (0.2%)
1	K	1.14	1/1280 (0.1%)	1.25	0/1752
1	L	1.11	0/1284	1.24	3/1758 (0.2%)
1	M	1.12	0/1304	1.25	2/1782 (0.1%)
1	N	1.12	0/1279	1.28	2/1751 (0.1%)
1	O	1.10	1/1296 (0.1%)	1.27	5/1771 (0.3%)
1	P	1.09	0/1302	1.22	3/1780 (0.2%)
1	Q	1.12	0/1314	1.25	2/1794 (0.1%)
1	R	1.13	0/1306	1.24	3/1784 (0.2%)
All	All	1.12	10/23373 (0.0%)	1.26	53/31948 (0.2%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	87	ARG	CA-C	7.09	1.56	1.52
1	B	90	GLU	N-CA	6.08	1.53	1.46
1	D	170	LEU	CA-C	5.91	1.60	1.52
1	A	122	SER	N-CA	5.74	1.53	1.46
1	B	161	GLU	CA-CB	5.57	1.62	1.53

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	87	ARG	N-CA-C	-14.68	86.76	109.96
1	H	29	MET	N-CA-C	-10.04	93.98	109.95
1	A	88	GLY	N-CA-C	-9.59	100.59	112.68
1	B	29	MET	N-CA-C	8.68	123.17	112.59
1	E	88	GLY	N-CA-C	-8.06	100.17	112.51

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	1259	0	1237	28	0
1	B	1280	0	1278	29	0
1	C	1283	0	1273	23	0
1	D	1236	0	1204	34	1
1	E	1293	0	1290	16	0
1	F	1283	0	1268	52	0
1	G	1280	0	1267	13	0
1	H	1293	0	1290	16	0
1	I	1272	0	1265	21	0
1	J	1280	0	1273	21	0
1	K	1256	0	1238	24	0
1	L	1259	0	1237	27	0
1	M	1279	0	1269	21	0
1	N	1255	0	1228	30	0
1	O	1271	0	1265	17	0
1	P	1277	0	1263	20	0
1	Q	1289	0	1284	24	0
1	R	1281	0	1276	17	0
2	A	36	0	21	1	0
2	B	36	0	21	2	0
2	C	36	0	21	2	0
2	D	36	0	21	4	0
2	E	36	0	21	1	0
2	G	36	0	21	1	0
2	H	36	0	21	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	36	0	21	0	0
2	J	36	0	21	1	0
2	K	36	0	21	4	0
2	L	36	0	21	4	0
2	N	36	0	21	1	0
2	O	36	0	21	3	0
2	P	36	0	21	3	0
2	Q	36	0	21	3	0
2	R	36	0	21	1	0
3	A	5	0	0	1	0
3	B	5	0	0	1	0
3	C	5	0	0	2	0
3	D	5	0	0	3	0
3	E	5	0	0	1	0
3	F	5	0	0	0	0
3	G	5	0	0	0	0
3	H	5	0	0	1	0
3	I	5	0	0	0	0
3	J	5	0	0	3	0
3	K	5	0	0	2	0
3	L	5	0	0	1	0
3	M	5	0	0	3	0
3	N	5	0	0	0	0
3	O	5	0	0	3	0
3	P	5	0	0	1	0
3	Q	5	0	0	3	0
3	R	5	0	0	1	0
4	C	4	0	3	0	0
4	J	4	0	3	0	0
4	Q	4	0	3	0	0
5	F	39	0	23	4	0
5	M	39	0	23	6	0
6	A	11	0	0	0	0
6	B	16	0	0	1	0
6	C	10	0	0	0	0
6	D	12	0	0	0	0
6	E	11	0	0	1	0
6	F	10	0	0	0	0
6	G	8	0	0	0	0
6	H	12	0	0	1	0
6	I	12	0	0	0	0
6	J	12	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	K	11	0	0	0	0
6	L	11	0	0	2	0
6	M	15	0	0	0	0
6	N	12	0	0	1	0
6	O	11	0	0	0	0
6	P	14	0	0	2	0
6	Q	9	0	0	1	0
6	R	17	0	0	2	0
All	All	23896	0	23096	394	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 8.

The worst 5 of 394 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:F:9:GLN:OE1	1:F:161:GLU:CG	1.68	1.40
1:N:84:PRO:HB3	1:N:96:LEU:CD1	1.60	1.32
1:M:31:GLY:HA3	5:M:201:ZOD:O03	1.16	1.27
1:A:88:GLY:O	1:A:93:GLU:OE1	1.58	1.20
1:F:31:GLY:HA3	5:F:201:ZOD:O03	1.04	1.20

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)
1:D:29:MET:CE	1:D:29:MET:CE[6_554]	2.16	0.04

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	171/183 (93%)	166 (97%)	5 (3%)	0	100	100
1	B	170/183 (93%)	166 (98%)	4 (2%)	0	100	100
1	C	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
1	D	168/183 (92%)	162 (96%)	6 (4%)	0	100	100
1	E	171/183 (93%)	167 (98%)	4 (2%)	0	100	100
1	F	171/183 (93%)	165 (96%)	6 (4%)	0	100	100
1	G	171/183 (93%)	166 (97%)	5 (3%)	0	100	100
1	H	171/183 (93%)	167 (98%)	4 (2%)	0	100	100
1	I	171/183 (93%)	165 (96%)	6 (4%)	0	100	100
1	J	170/183 (93%)	165 (97%)	5 (3%)	0	100	100
1	K	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
1	L	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
1	M	171/183 (93%)	167 (98%)	4 (2%)	0	100	100
1	N	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
1	O	169/183 (92%)	166 (98%)	3 (2%)	0	100	100
1	P	171/183 (93%)	167 (98%)	4 (2%)	0	100	100
1	Q	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
1	R	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
All	All	3069/3294 (93%)	2997 (98%)	72 (2%)	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	124/141 (88%)	113 (91%)	11 (9%)	9	29
1	B	130/141 (92%)	114 (88%)	16 (12%)	4	16
1	C	130/141 (92%)	115 (88%)	15 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	121/141 (86%)	106 (88%)	15 (12%)	4	16
1	E	132/141 (94%)	122 (92%)	10 (8%)	12	36
1	F	130/141 (92%)	115 (88%)	15 (12%)	5	18
1	G	128/141 (91%)	116 (91%)	12 (9%)	8	27
1	H	132/141 (94%)	117 (89%)	15 (11%)	5	19
1	I	127/141 (90%)	119 (94%)	8 (6%)	16	45
1	J	130/141 (92%)	117 (90%)	13 (10%)	7	24
1	K	125/141 (89%)	111 (89%)	14 (11%)	6	19
1	L	125/141 (89%)	119 (95%)	6 (5%)	23	56
1	M	129/141 (92%)	114 (88%)	15 (12%)	5	18
1	N	123/141 (87%)	109 (89%)	14 (11%)	5	19
1	O	129/141 (92%)	118 (92%)	11 (8%)	10	31
1	P	128/141 (91%)	118 (92%)	10 (8%)	11	35
1	Q	131/141 (93%)	119 (91%)	12 (9%)	8	27
1	R	129/141 (92%)	118 (92%)	11 (8%)	10	31
All	All	2303/2538 (91%)	2080 (90%)	223 (10%)	8	25

5 of 223 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	161	GLU
1	Q	125	VAL
1	K	19	VAL
1	Q	55	GLN
1	O	166	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	95	GLN
1	L	92	ASN
1	J	103	ASN
1	K	95	GLN
1	M	39	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

39 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	APR	N	201	-	39,39,39	1.54	6 (15%)	56,60,60	1.82	14 (25%)
2	APR	Q	402	-	39,39,39	1.55	7 (17%)	56,60,60	1.67	15 (26%)
2	APR	G	201	-	39,39,39	1.52	7 (17%)	56,60,60	1.86	16 (28%)
4	ACT	J	203	-	3,3,3	1.18	0	3,3,3	0.47	0
3	SO4	C	202	-	4,4,4	0.63	0	6,6,6	0.99	0
2	APR	K	201	-	39,39,39	1.48	5 (12%)	56,60,60	1.95	19 (33%)
2	APR	I	201	-	39,39,39	1.50	8 (20%)	56,60,60	2.03	11 (19%)
3	SO4	E	202	-	4,4,4	0.42	0	6,6,6	0.71	0
3	SO4	L	202	-	4,4,4	0.68	0	6,6,6	0.62	0
3	SO4	O	202	-	4,4,4	0.63	0	6,6,6	0.86	0
3	SO4	Q	403	-	4,4,4	0.39	0	6,6,6	0.74	0
2	APR	R	201	-	39,39,39	1.31	4 (10%)	56,60,60	1.79	14 (25%)
3	SO4	P	202	-	4,4,4	0.51	0	6,6,6	0.38	0
3	SO4	F	202	-	4,4,4	0.59	0	6,6,6	0.38	0
3	SO4	A	202	-	4,4,4	0.58	0	6,6,6	0.43	0
4	ACT	Q	401	-	3,3,3	0.60	0	3,3,3	1.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	M	202	-	4,4,4	0.54	0	6,6,6	0.35	0
3	SO4	H	202	-	4,4,4	0.37	0	6,6,6	0.97	0
2	APR	E	201	-	39,39,39	1.30	6 (15%)	56,60,60	2.06	19 (33%)
3	SO4	J	202	-	4,4,4	0.54	0	6,6,6	0.70	0
2	APR	D	201	-	39,39,39	1.97	10 (25%)	56,60,60	2.09	20 (35%)
3	SO4	N	202	-	4,4,4	0.45	0	6,6,6	0.98	0
2	APR	C	201	-	39,39,39	1.33	5 (12%)	56,60,60	1.87	14 (25%)
3	SO4	G	202	-	4,4,4	0.72	0	6,6,6	0.54	0
2	APR	O	201	-	39,39,39	1.40	5 (12%)	56,60,60	1.58	12 (21%)
2	APR	B	201	-	39,39,39	1.51	7 (17%)	56,60,60	1.56	14 (25%)
3	SO4	K	202	-	4,4,4	0.46	0	6,6,6	0.37	0
3	SO4	I	202	-	4,4,4	0.51	0	6,6,6	0.54	0
3	SO4	D	202	-	4,4,4	0.45	0	6,6,6	0.53	0
4	ACT	C	203	-	3,3,3	0.84	0	3,3,3	1.20	0
3	SO4	B	202	-	4,4,4	0.54	0	6,6,6	0.39	0
5	ZOD	M	201	-	42,42,42	1.57	7 (16%)	58,64,64	1.86	18 (31%)
3	SO4	R	202	-	4,4,4	0.32	0	6,6,6	0.76	0
2	APR	J	201	-	39,39,39	1.34	5 (12%)	56,60,60	1.92	15 (26%)
2	APR	P	201	-	39,39,39	1.46	3 (7%)	56,60,60	1.96	15 (26%)
2	APR	L	201	-	39,39,39	1.96	6 (15%)	56,60,60	2.03	17 (30%)
5	ZOD	F	201	-	42,42,42	1.47	8 (19%)	58,64,64	1.97	17 (29%)
2	APR	H	201	-	39,39,39	1.47	6 (15%)	56,60,60	1.88	16 (28%)
2	APR	A	201	-	39,39,39	1.67	5 (12%)	56,60,60	1.75	10 (17%)

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
2	APR	N	201	-	-	6/22/54/54	0/4/4/4
2	APR	C	201	-	-	3/22/54/54	0/4/4/4
2	APR	Q	402	-	-	6/22/54/54	0/4/4/4
2	APR	G	201	-	-	10/22/54/54	0/4/4/4
2	APR	R	201	-	-	11/22/54/54	0/4/4/4
5	ZOD	M	201	-	-	8/26/58/58	0/4/4/4
2	APR	A	201	-	-	7/22/54/54	0/4/4/4
2	APR	O	201	-	-	8/22/54/54	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	APR	J	201	-	-	6/22/54/54	0/4/4/4
2	APR	P	201	-	-	11/22/54/54	0/4/4/4
2	APR	L	201	-	-	1/22/54/54	0/4/4/4
2	APR	B	201	-	-	4/22/54/54	0/4/4/4
2	APR	K	201	-	-	7/22/54/54	0/4/4/4
5	ZOD	F	201	-	-	12/26/58/58	0/4/4/4
2	APR	I	201	-	-	11/22/54/54	0/4/4/4
2	APR	H	201	-	-	9/22/54/54	0/4/4/4
2	APR	E	201	-	-	7/22/54/54	0/4/4/4
2	APR	D	201	-	-	10/22/54/54	0/4/4/4

The worst 5 of 110 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	L	201	APR	PA-O3A	6.98	1.67	1.59
2	A	201	APR	C5-C4	5.62	1.49	1.39
2	B	201	APR	C5-C4	5.43	1.48	1.39
2	P	201	APR	C5-C4	5.37	1.48	1.39
2	L	201	APR	C5-C4	5.31	1.48	1.39

The worst 5 of 276 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	201	APR	C5-C4-N3	-5.68	118.89	126.72
2	I	201	APR	C4-C5-N7	-5.67	104.10	110.58
2	N	201	APR	C5-C4-N3	-5.36	119.34	126.72
2	G	201	APR	C4-N9-C8	5.20	111.19	105.74
2	C	201	APR	C5-C4-N3	-5.18	119.59	126.72

There are no chirality outliers.

5 of 137 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	R	201	APR	C5D-O5D-PB-O1B
2	D	201	APR	C5'-O5'-PA-O1A
2	D	201	APR	C5'-O5'-PA-O2A
2	D	201	APR	C5D-O5D-PB-O1B
2	G	201	APR	C5D-O5D-PB-O1B

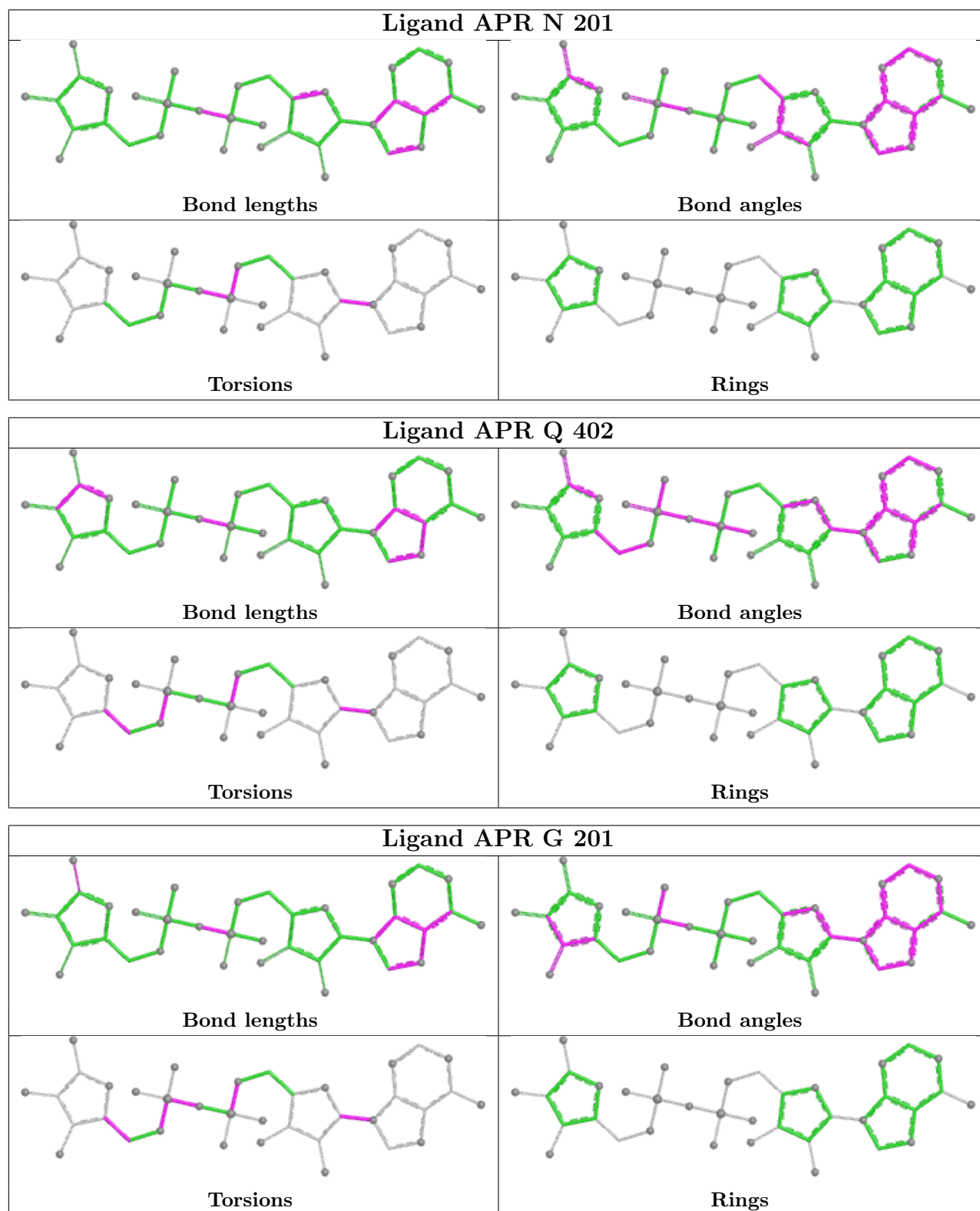
There are no ring outliers.

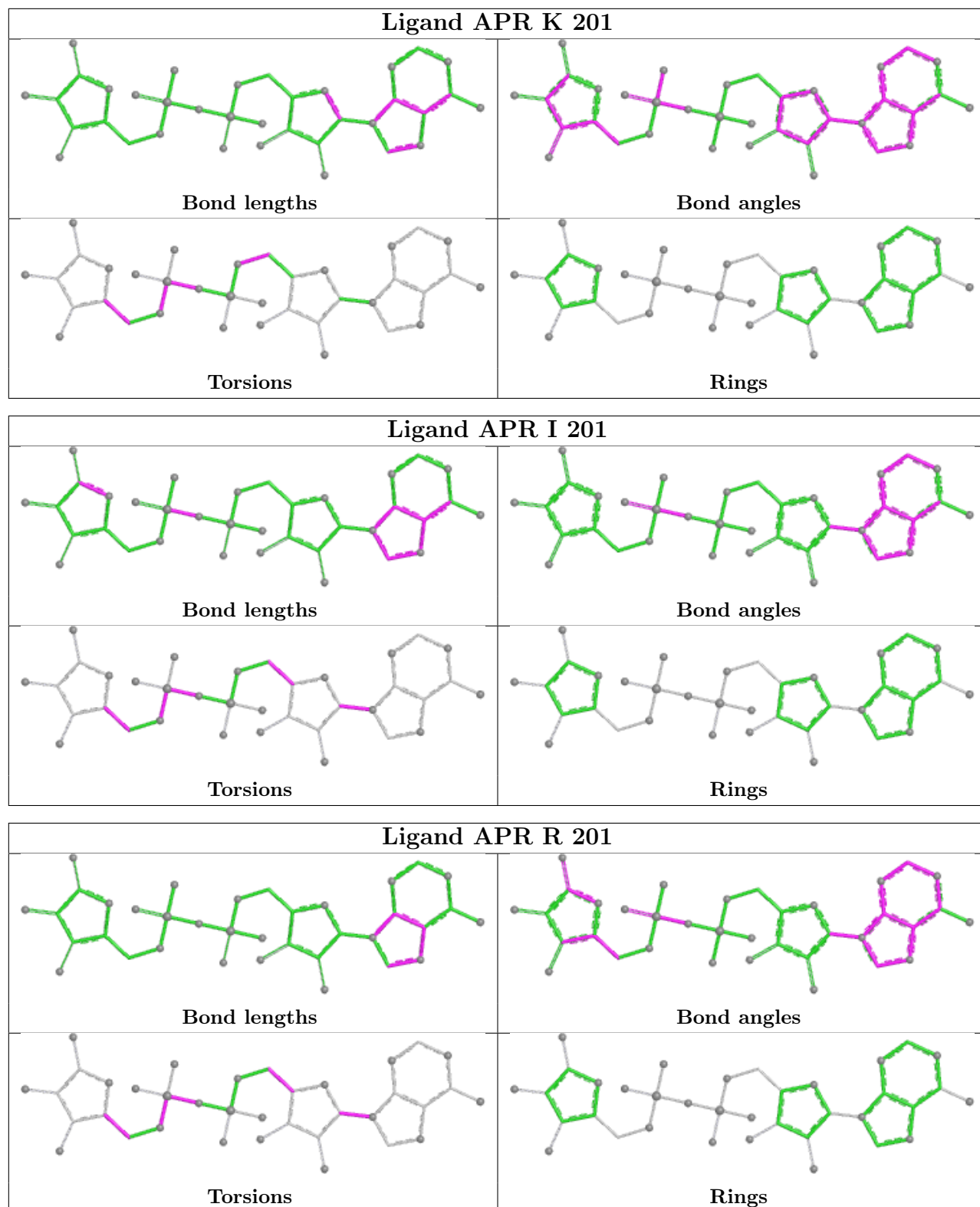
31 monomers are involved in 69 short contacts:

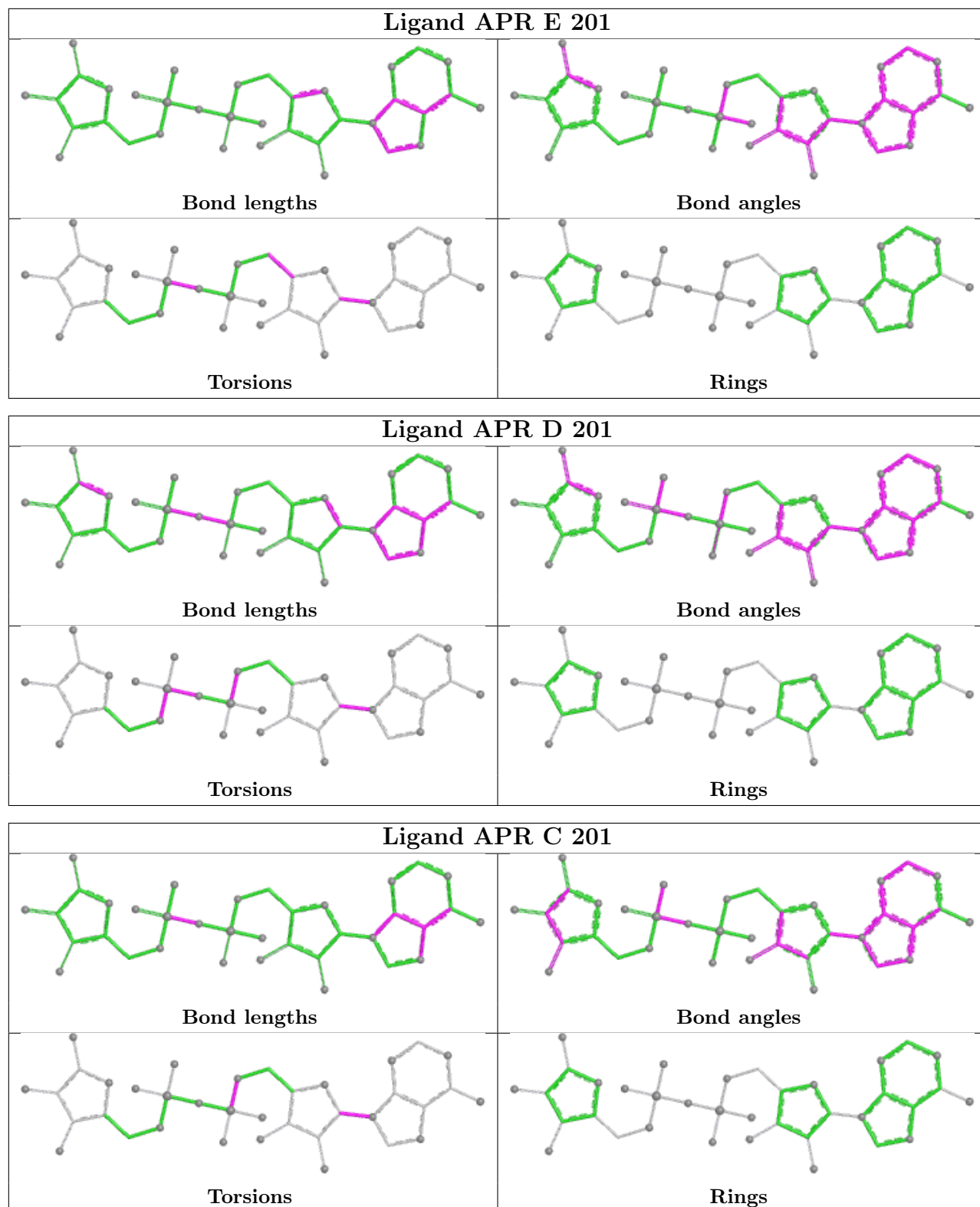
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	N	201	APR	1	0
2	Q	402	APR	3	0
2	G	201	APR	1	0
3	C	202	SO4	2	0
2	K	201	APR	4	0
3	E	202	SO4	1	0
3	L	202	SO4	1	0
3	O	202	SO4	3	0
3	Q	403	SO4	3	0
2	R	201	APR	1	0
3	P	202	SO4	1	0
3	A	202	SO4	1	0
3	M	202	SO4	3	0
3	H	202	SO4	1	0
2	E	201	APR	1	0
3	J	202	SO4	3	0
2	D	201	APR	4	0
2	C	201	APR	2	0
2	O	201	APR	3	0
2	B	201	APR	2	0
3	K	202	SO4	2	0
3	D	202	SO4	3	0
3	B	202	SO4	1	0
5	M	201	ZOD	6	0
3	R	202	SO4	1	0
2	J	201	APR	1	0
2	P	201	APR	3	0
2	L	201	APR	4	0
5	F	201	ZOD	4	0
2	H	201	APR	2	0
2	A	201	APR	1	0

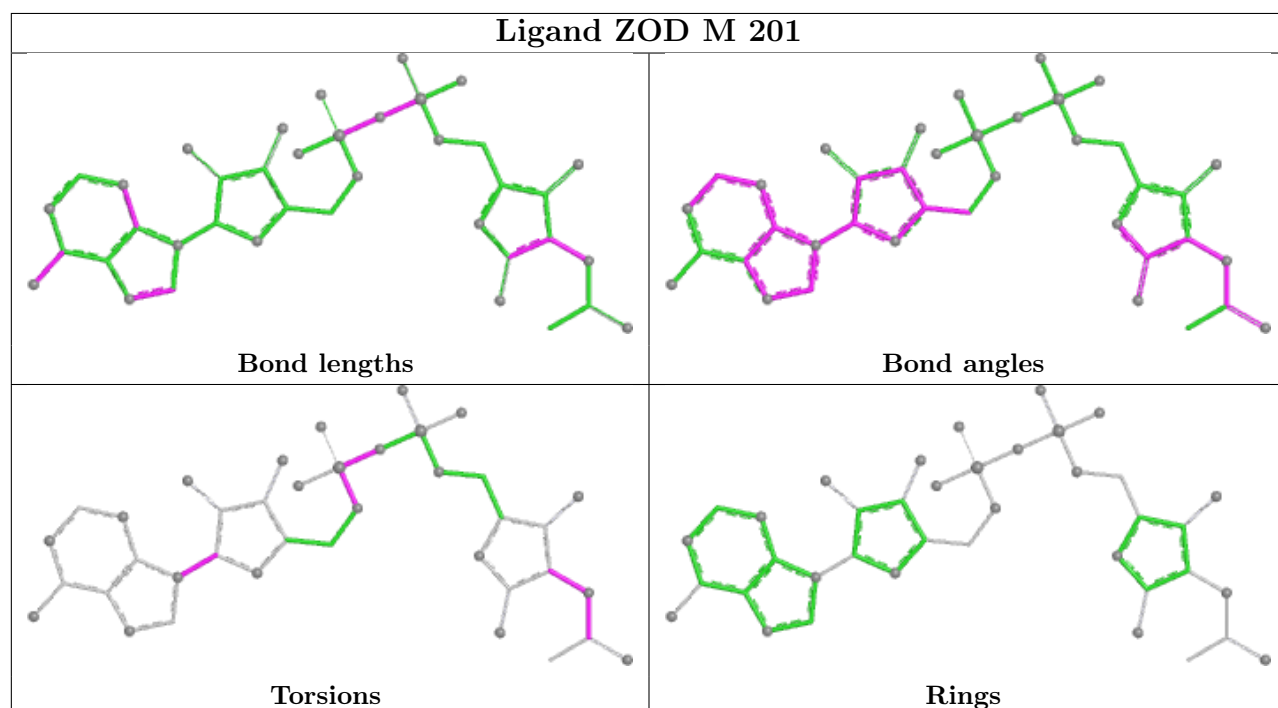
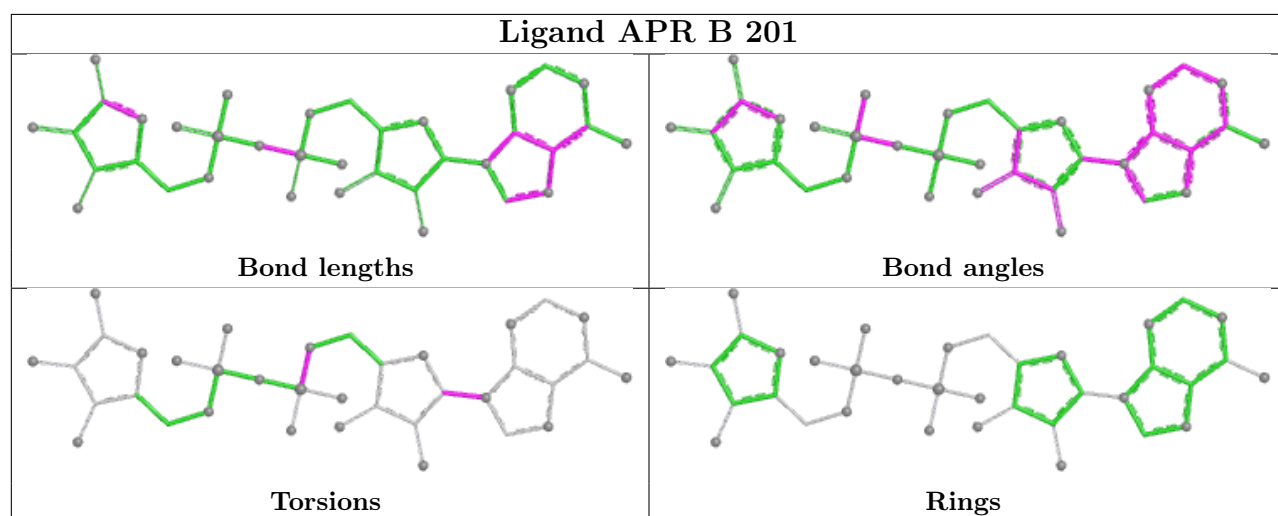
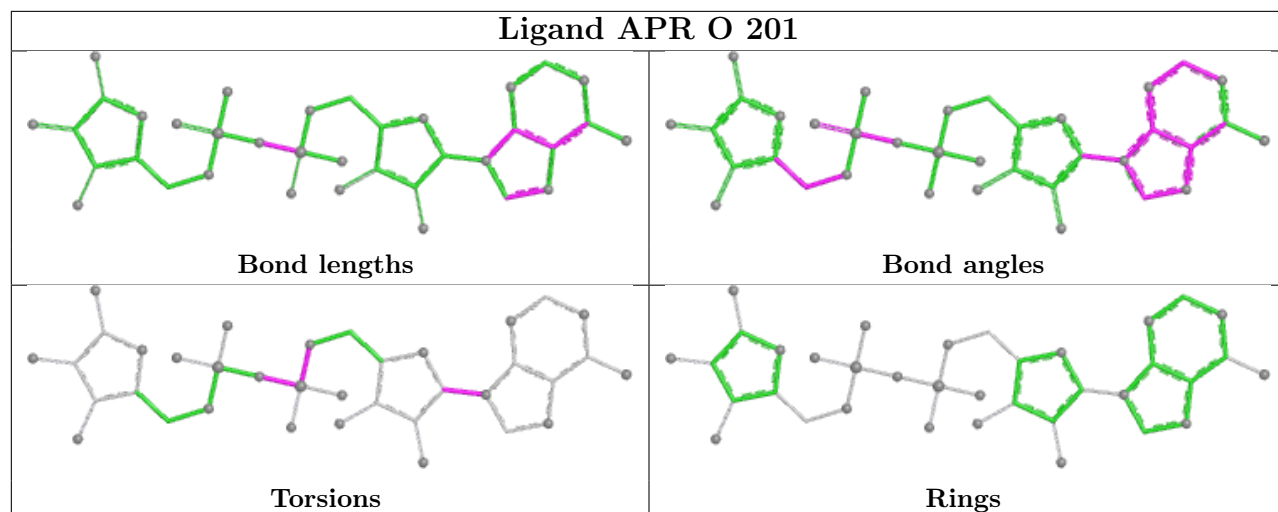
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

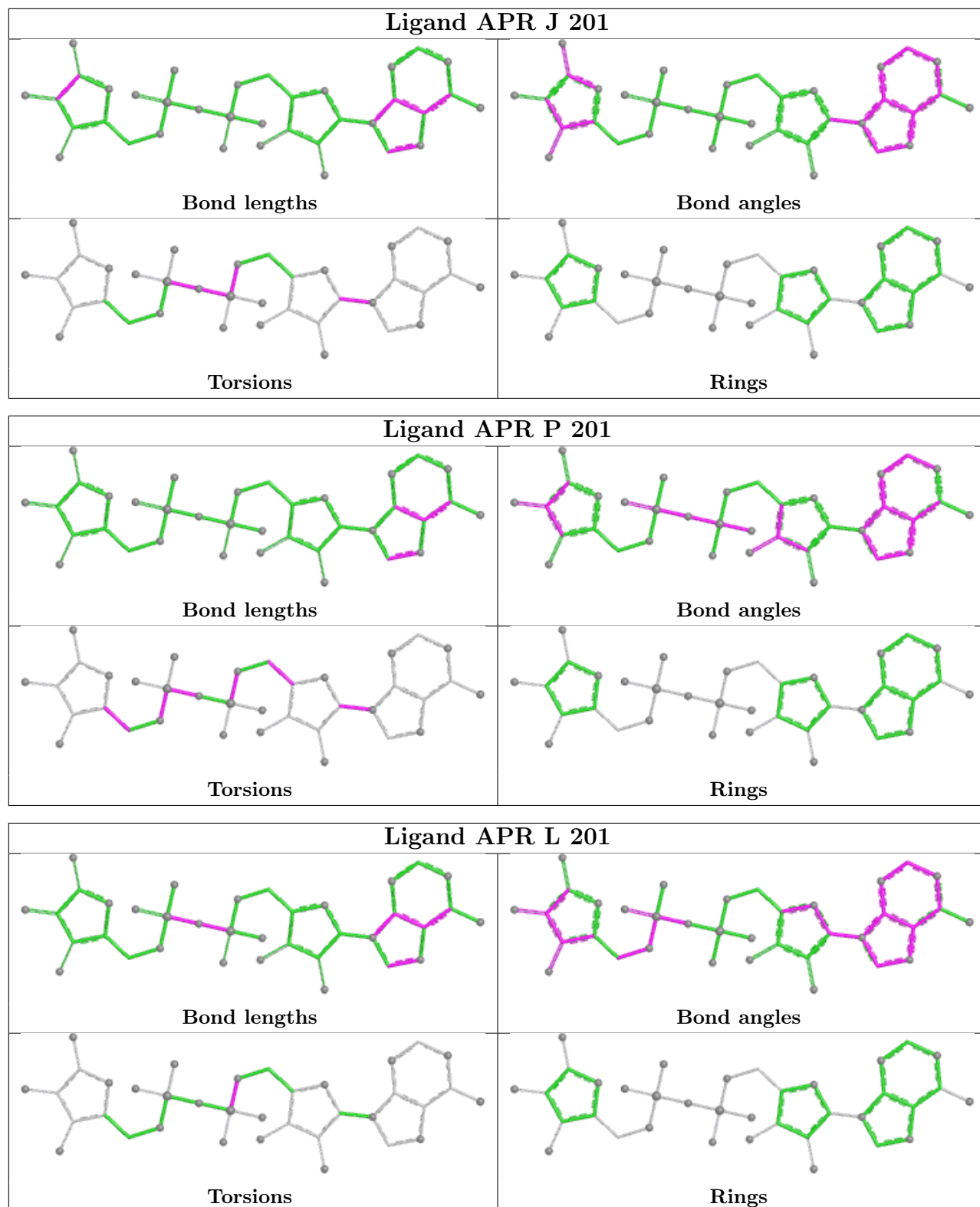
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

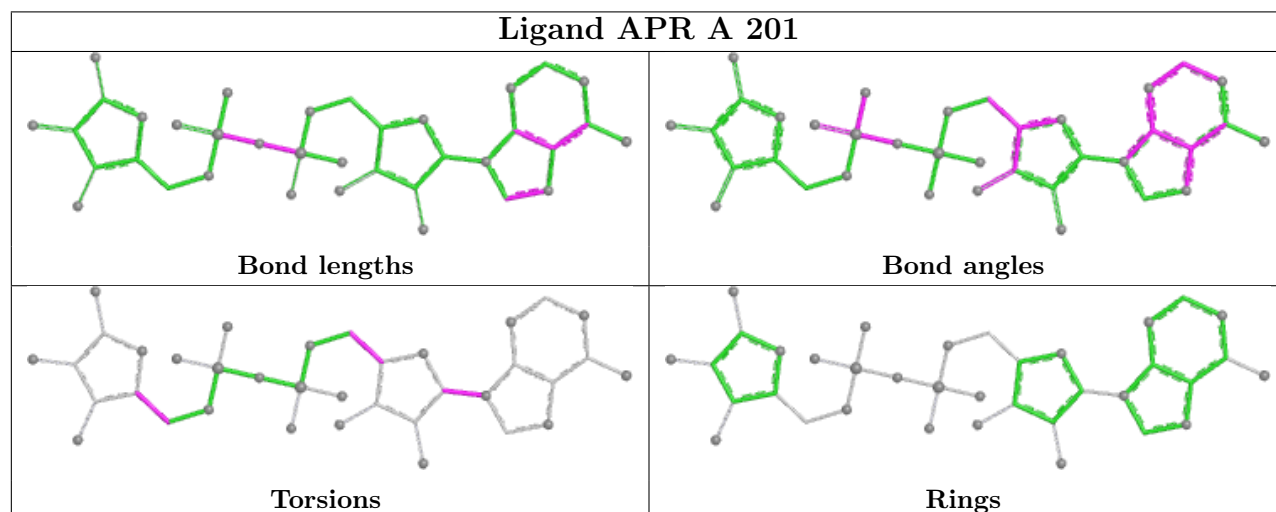
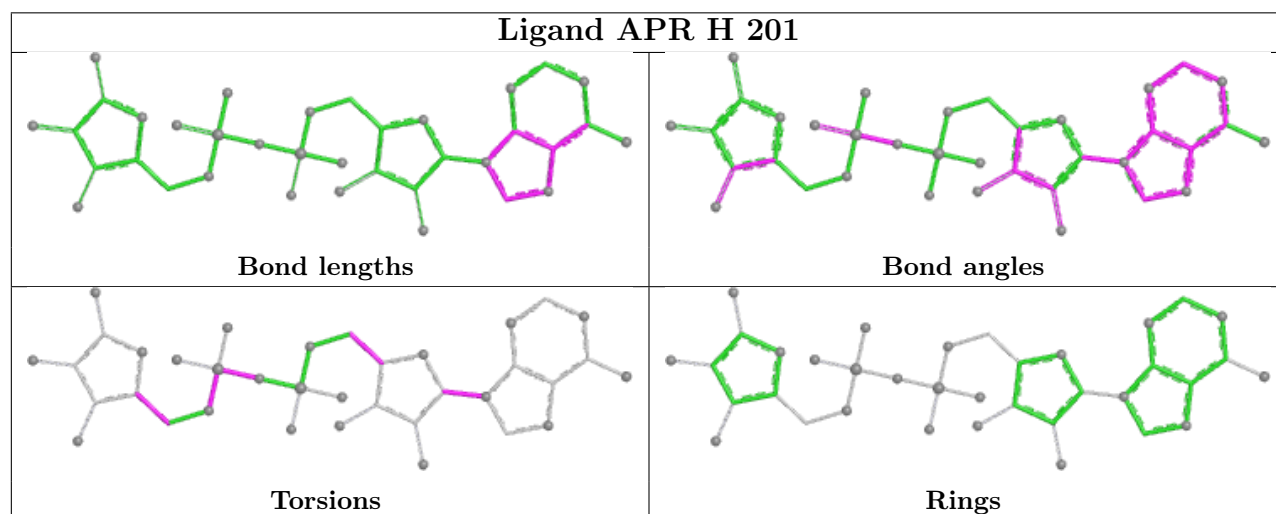
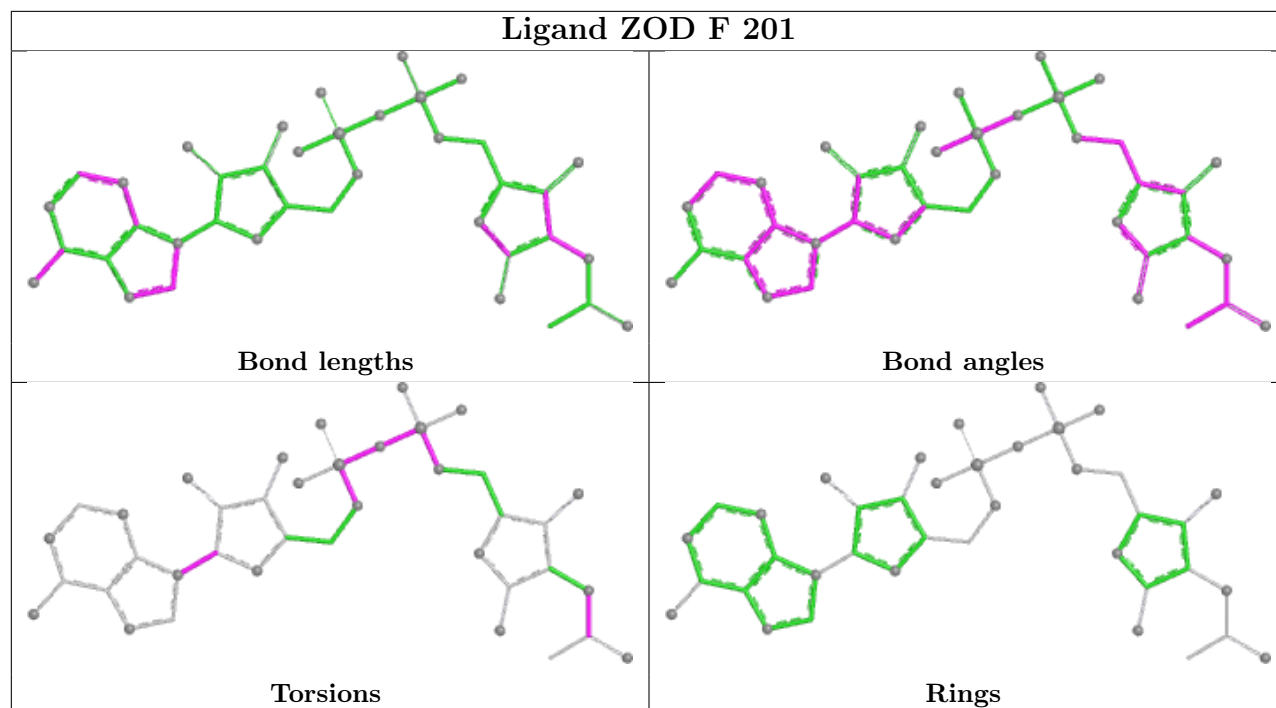












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	173/183 (94%)	-1.62	0 100 100	25, 42, 64, 74	0
1	B	172/183 (93%)	-1.69	0 100 100	19, 34, 53, 71	0
1	C	173/183 (94%)	-1.69	0 100 100	14, 33, 57, 69	0
1	D	170/183 (92%)	-1.60	0 100 100	23, 45, 64, 71	0
1	E	173/183 (94%)	-1.72	0 100 100	15, 29, 53, 68	0
1	F	173/183 (94%)	-1.63	0 100 100	29, 46, 66, 76	0
1	G	173/183 (94%)	-1.62	0 100 100	21, 39, 65, 73	0
1	H	173/183 (94%)	-1.68	0 100 100	15, 29, 54, 61	0
1	I	173/183 (94%)	-1.63	0 100 100	23, 42, 62, 72	0
1	J	172/183 (93%)	-1.66	0 100 100	15, 32, 57, 71	0
1	K	172/183 (93%)	-1.58	0 100 100	23, 42, 68, 82	0
1	L	172/183 (93%)	-1.59	0 100 100	26, 45, 65, 77	0
1	M	173/183 (94%)	-1.62	0 100 100	27, 43, 66, 76	0
1	N	173/183 (94%)	-1.62	0 100 100	18, 41, 68, 78	0
1	O	171/183 (93%)	-1.64	0 100 100	14, 32, 60, 71	0
1	P	173/183 (94%)	-1.62	0 100 100	22, 41, 68, 75	0
1	Q	173/183 (94%)	-1.69	0 100 100	16, 31, 52, 64	0
1	R	173/183 (94%)	-1.63	0 100 100	13, 32, 60, 75	0
All	All	3105/3294 (94%)	-1.64	0 100 100	13, 38, 64, 82	0

There are no RSRZ outliers to report.

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 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.

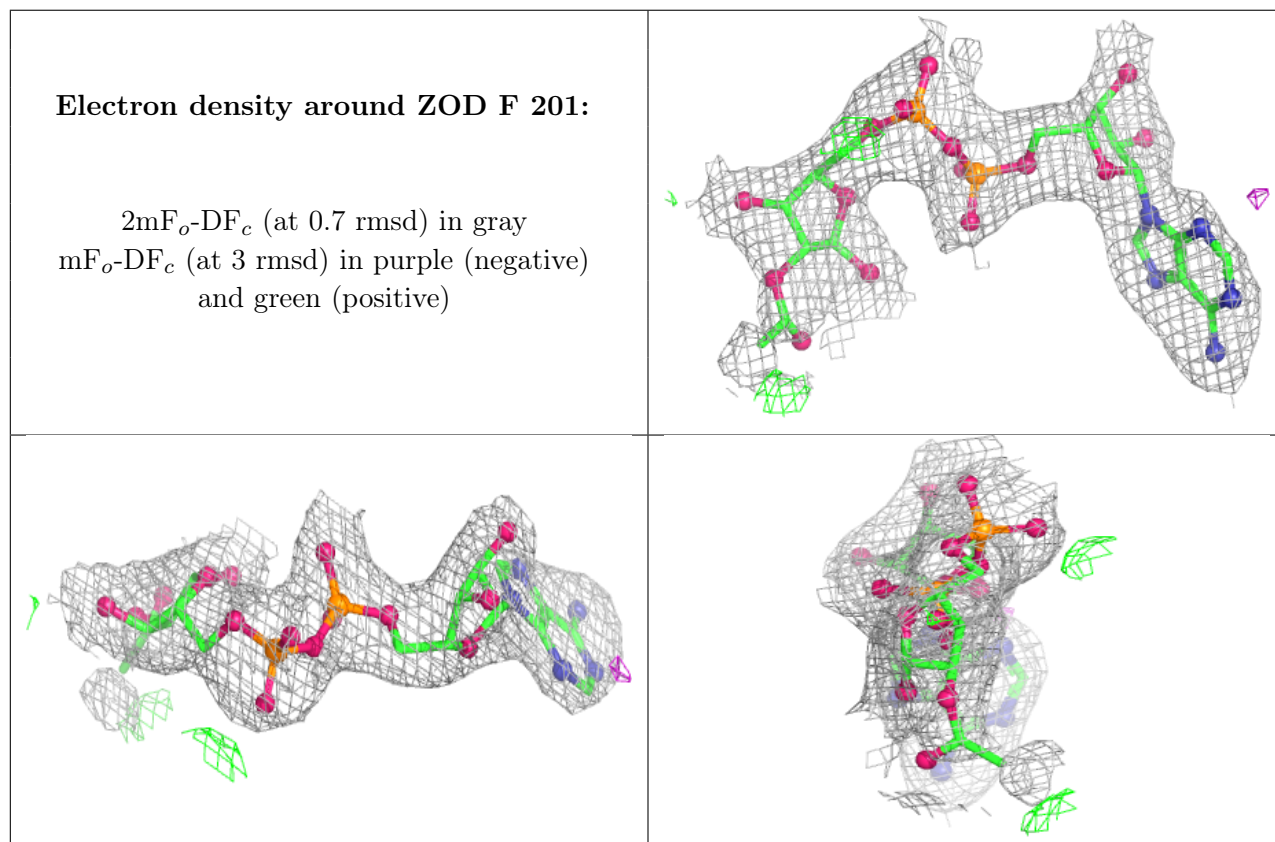
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	ACT	J	203	4/4	0.98	0.07	33,34,34,37	0
3	SO4	M	202	5/5	0.99	0.04	69,74,80,83	0
4	ACT	C	203	4/4	0.99	0.04	37,39,41,44	0
3	SO4	D	202	5/5	0.99	0.09	57,61,62,68	0
4	ACT	Q	401	4/4	0.99	0.05	27,29,29,29	0
5	ZOD	F	201	39/39	0.99	0.03	38,47,56,59	0
2	APR	G	201	36/36	1.00	0.02	24,27,29,32	0
2	APR	H	201	36/36	1.00	0.02	22,24,27,28	0
2	APR	I	201	36/36	1.00	0.02	23,24,26,30	0
2	APR	J	201	36/36	1.00	0.02	23,25,28,32	0
2	APR	K	201	36/36	1.00	0.02	23,26,28,31	0
2	APR	L	201	36/36	1.00	0.02	25,28,32,34	0
2	APR	N	201	36/36	1.00	0.02	24,26,29,29	0
2	APR	O	201	36/36	1.00	0.02	21,24,27,28	0
2	APR	P	201	36/36	1.00	0.02	24,26,29,32	0
2	APR	Q	402	36/36	1.00	0.02	20,24,27,29	0
3	SO4	R	202	5/5	1.00	0.02	25,26,30,33	0
3	SO4	A	202	5/5	1.00	0.03	47,50,56,62	0
3	SO4	B	202	5/5	1.00	0.04	31,32,35,35	0
3	SO4	C	202	5/5	1.00	0.04	25,28,30,30	0
2	APR	R	201	36/36	1.00	0.02	21,24,26,26	0
3	SO4	E	202	5/5	1.00	0.04	25,26,28,29	0
3	SO4	F	202	5/5	1.00	0.04	55,59,62,63	0
3	SO4	G	202	5/5	1.00	0.03	30,34,35,36	0
3	SO4	H	202	5/5	1.00	0.03	27,28,29,30	0
3	SO4	I	202	5/5	1.00	0.03	46,50,56,58	0
3	SO4	J	202	5/5	1.00	0.05	33,35,35,35	0
3	SO4	K	202	5/5	1.00	0.04	66,68,71,74	0
3	SO4	L	202	5/5	1.00	0.04	31,32,34,36	0
2	APR	A	201	36/36	1.00	0.02	22,25,28,28	0
3	SO4	N	202	5/5	1.00	0.02	27,31,33,36	0
3	SO4	O	202	5/5	1.00	0.04	30,31,33,34	0

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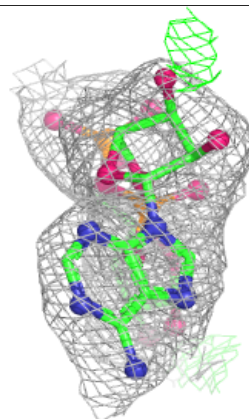
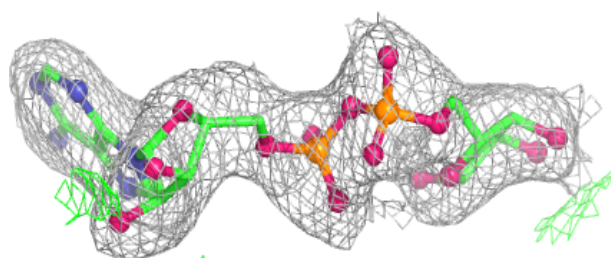
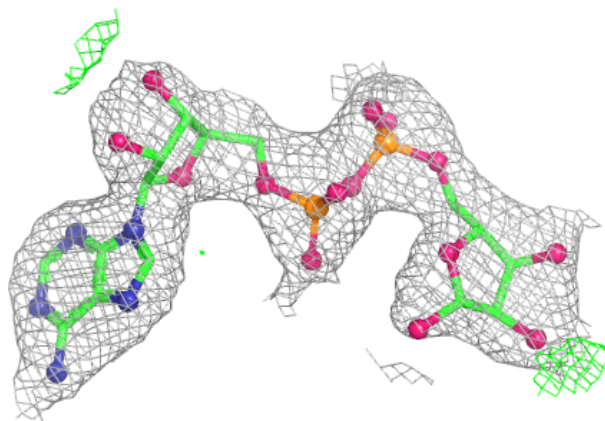
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	P	202	5/5	1.00	0.05	47,47,52,53	0
3	SO4	Q	403	5/5	1.00	0.04	31,32,34,37	0
2	APR	B	201	36/36	1.00	0.02	21,24,26,34	0
2	APR	C	201	36/36	1.00	0.02	20,24,26,32	0
2	APR	D	201	36/36	1.00	0.02	23,24,28,29	0
2	APR	E	201	36/36	1.00	0.02	19,21,25,32	0
5	ZOD	M	201	39/39	1.00	0.03	33,41,51,51	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.

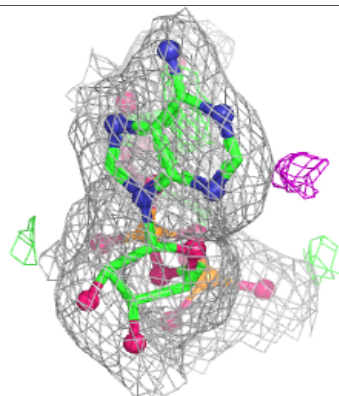
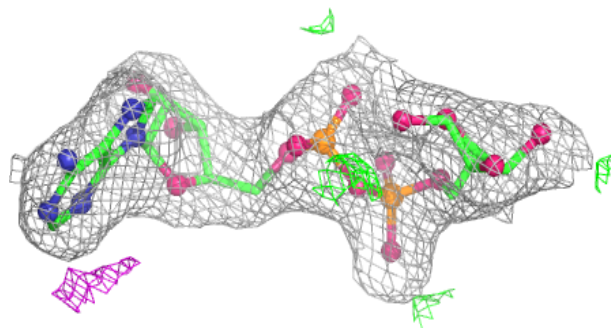
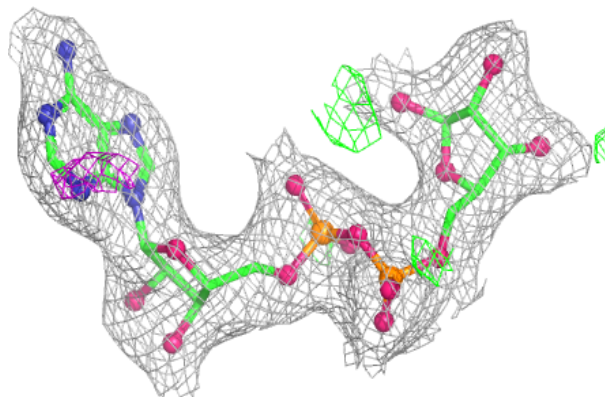


Electron density around APR G 201:

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

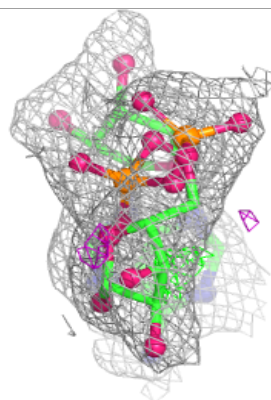
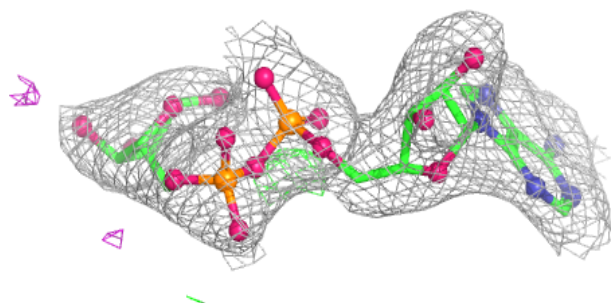
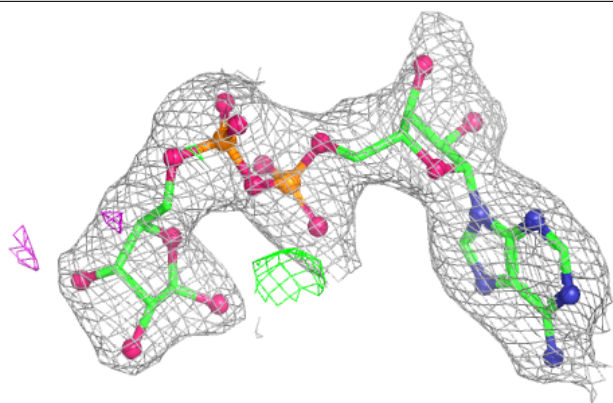
**Electron density around APR H 201:**

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

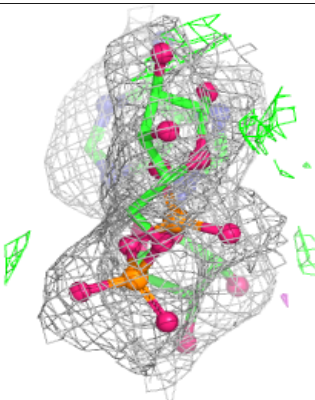
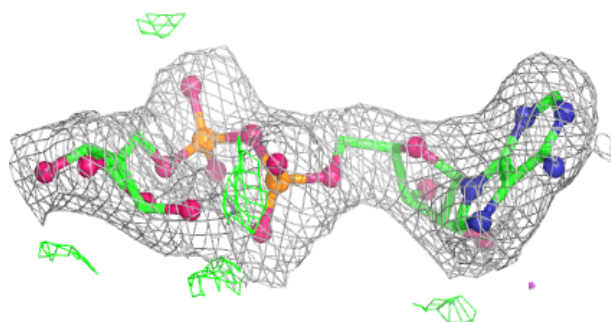
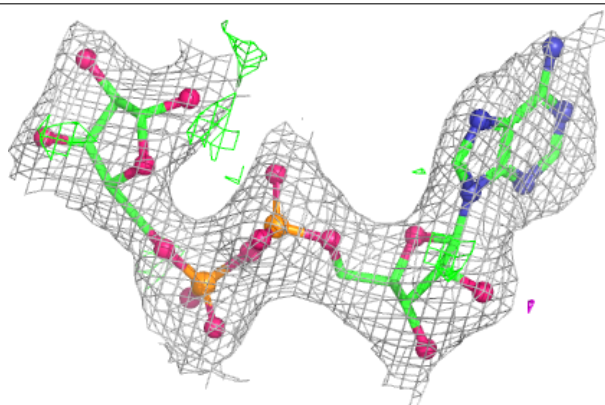


Electron density around APR I 201:

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

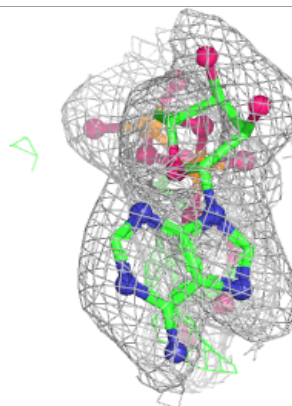
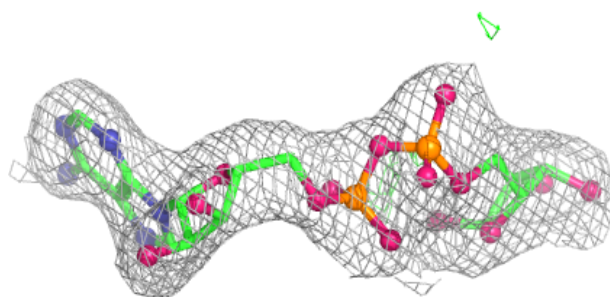
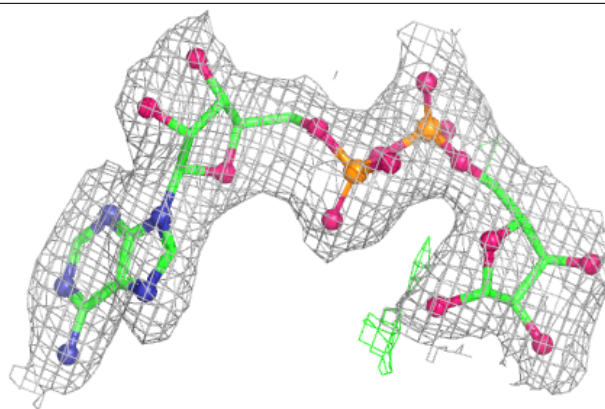
**Electron density around APR J 201:**

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

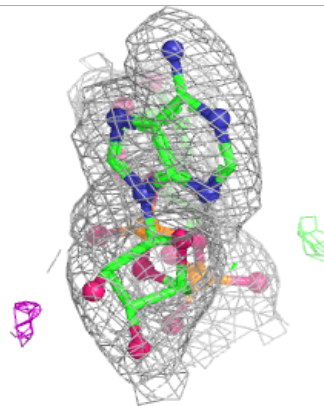
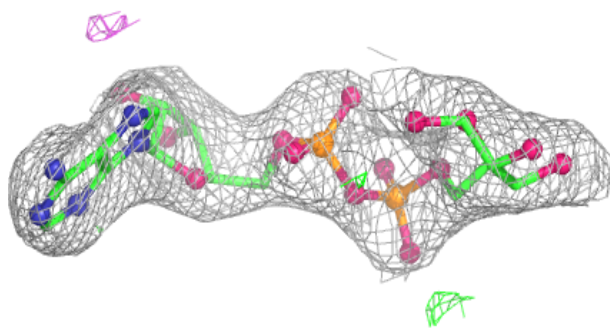
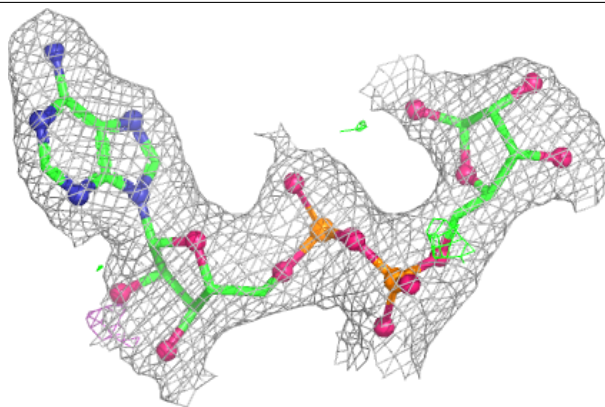


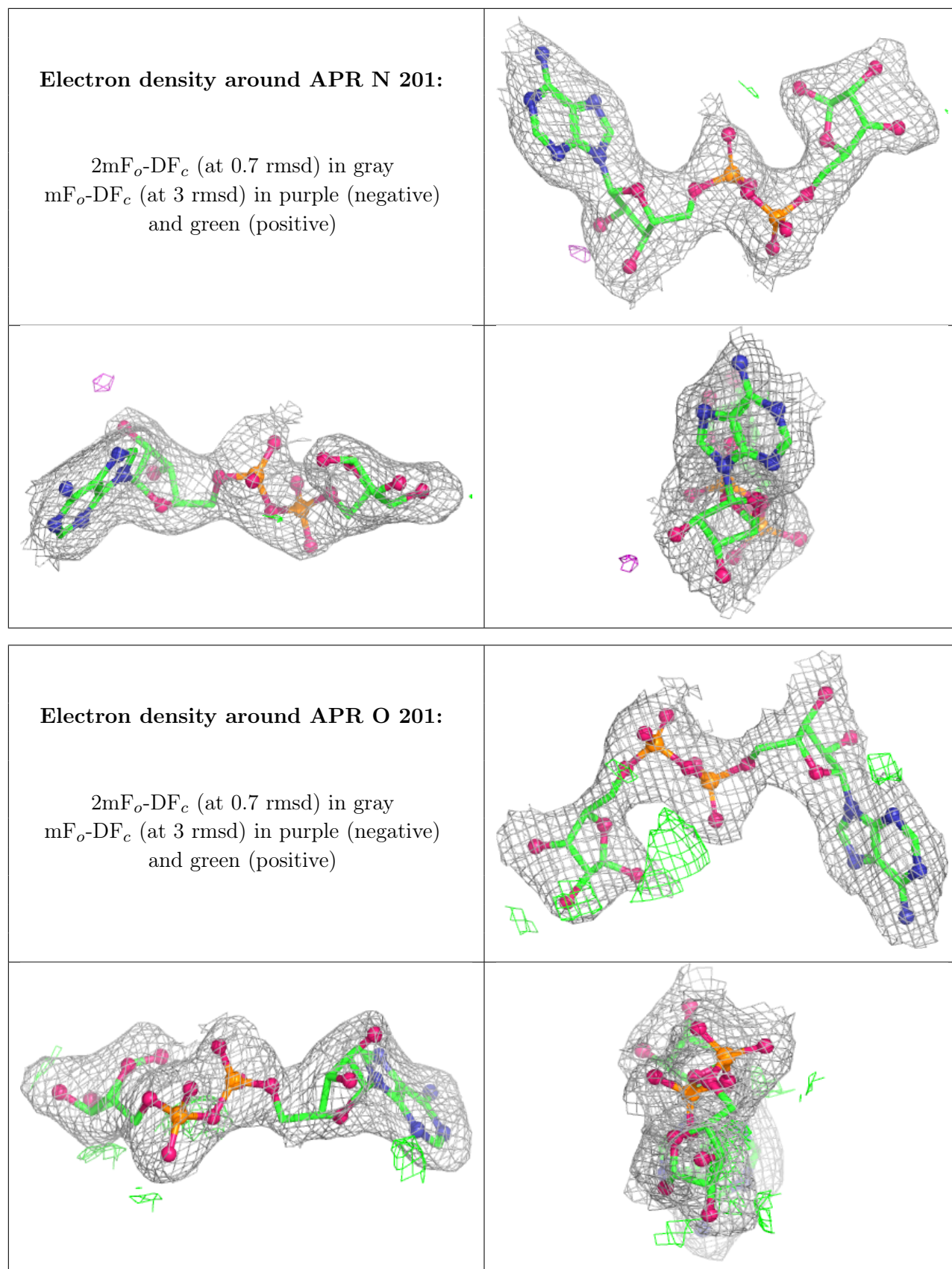
Electron density around APR K 201:

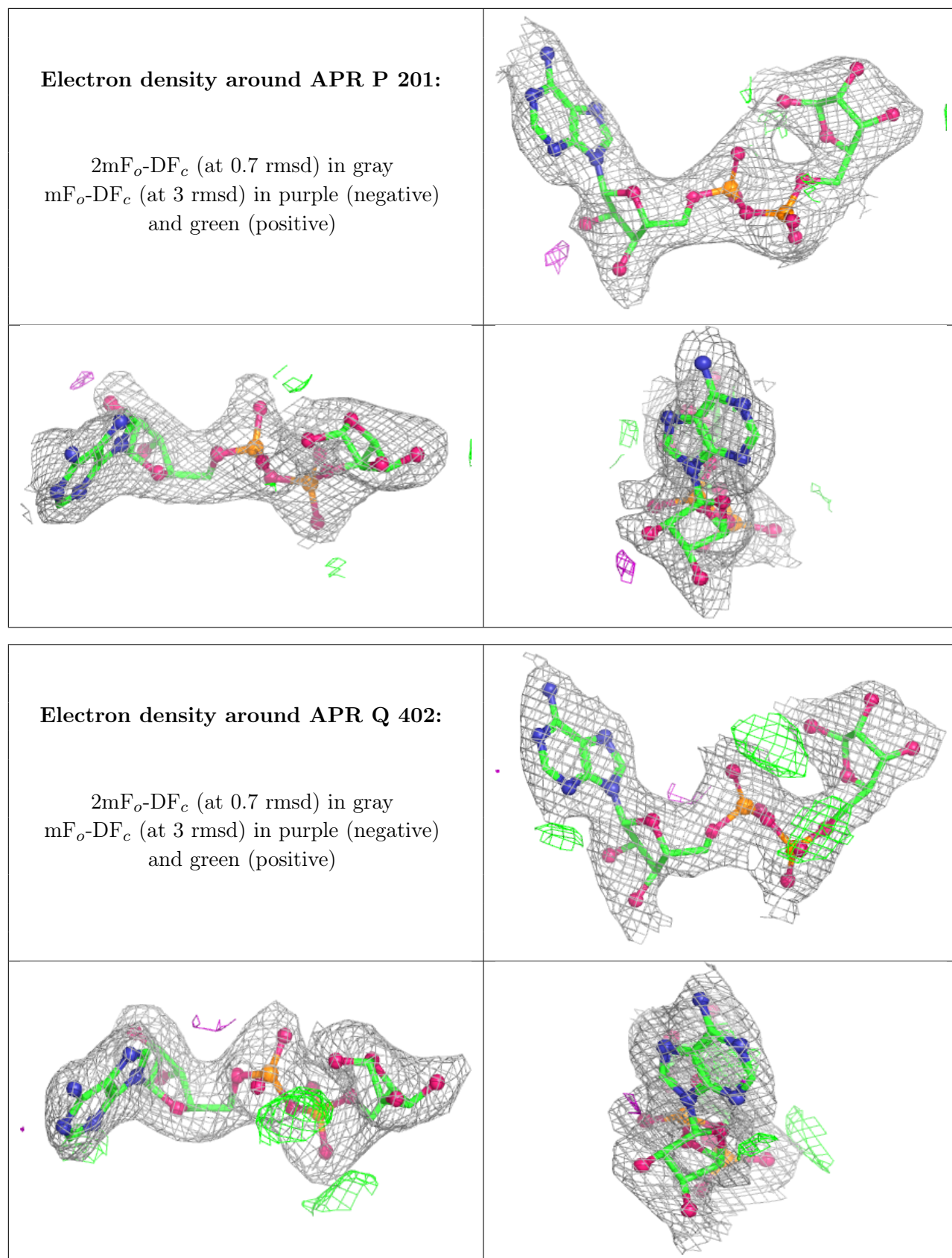
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

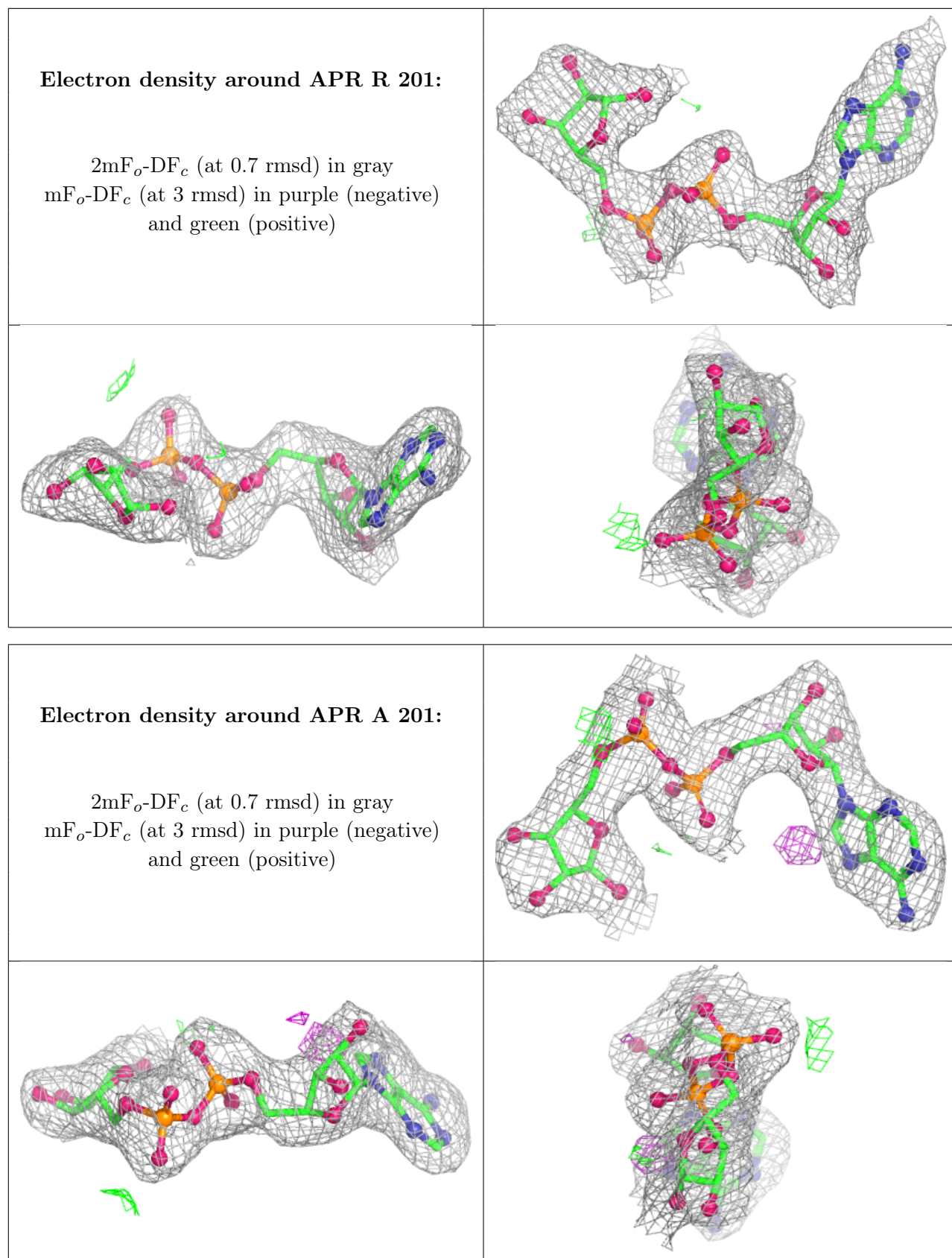
**Electron density around APR L 201:**

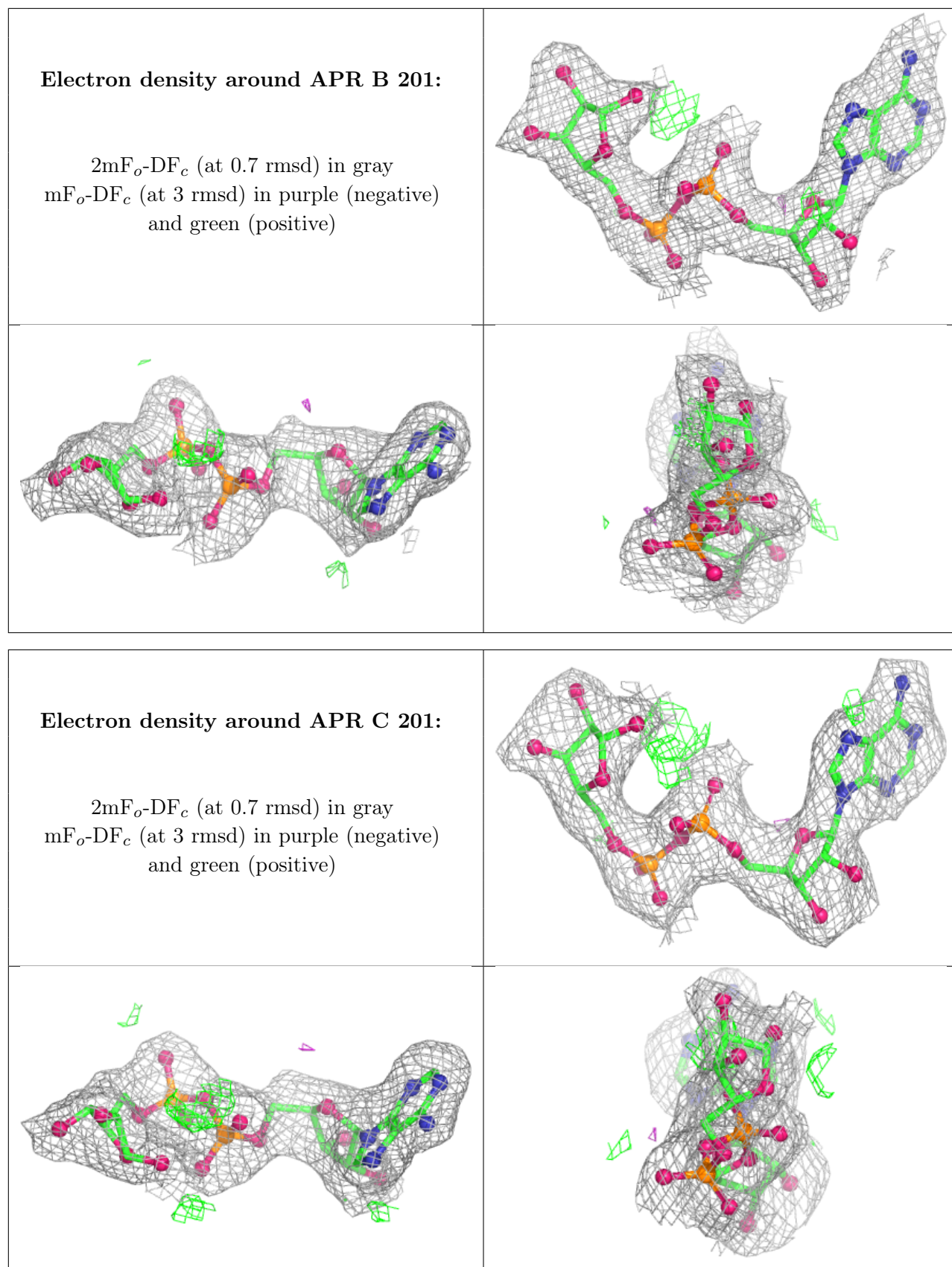
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

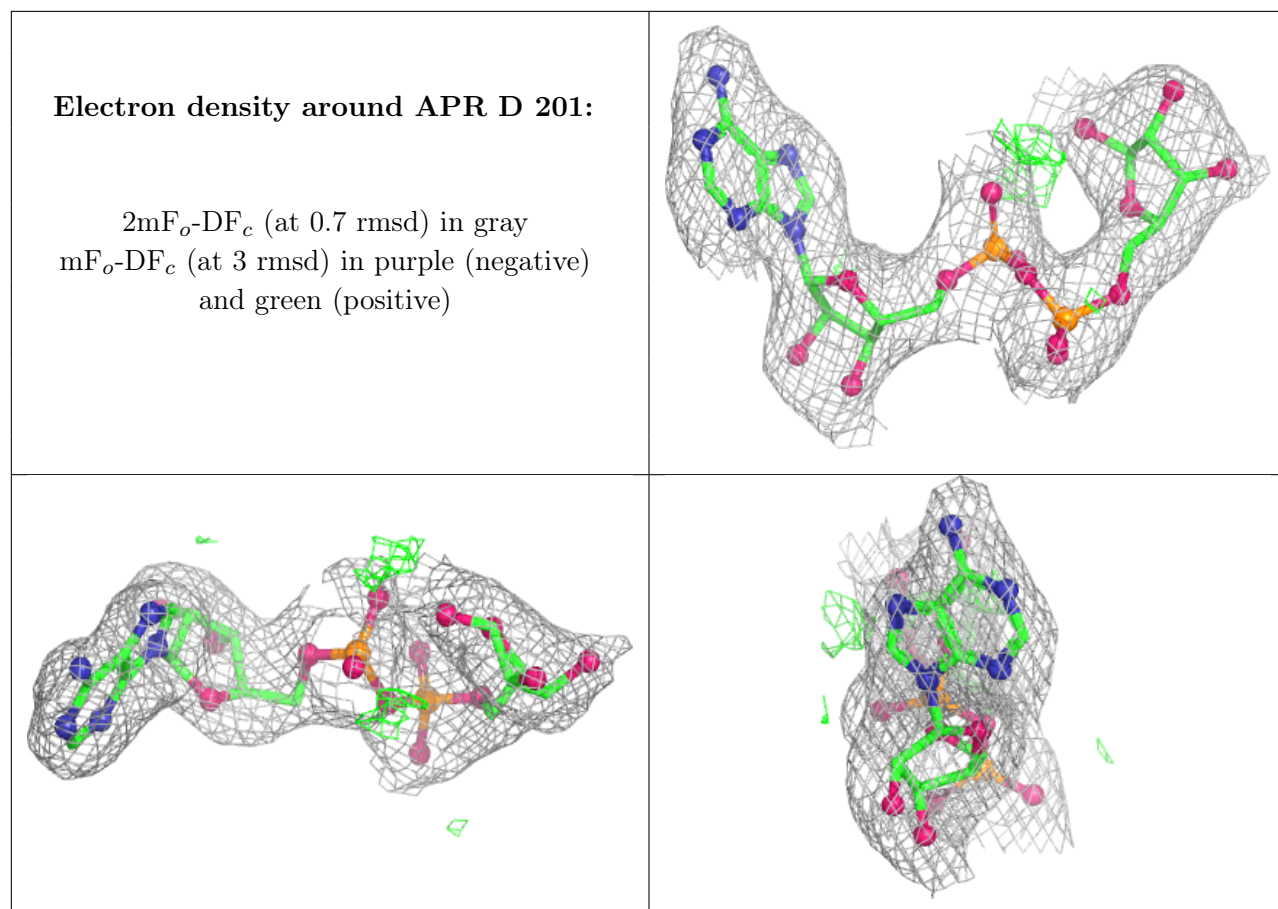






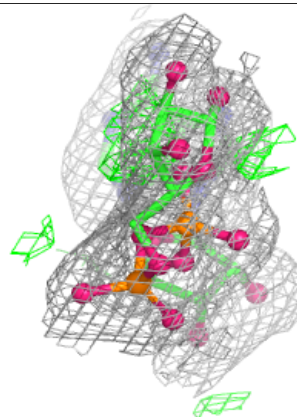
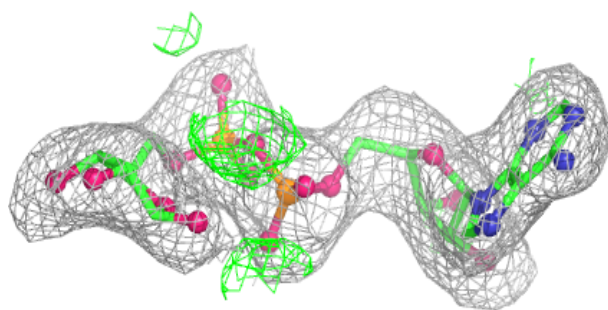
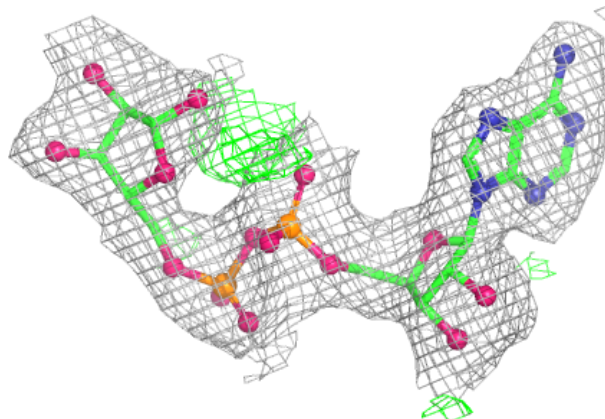




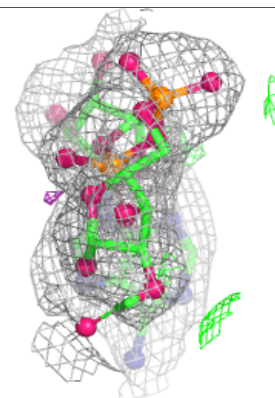
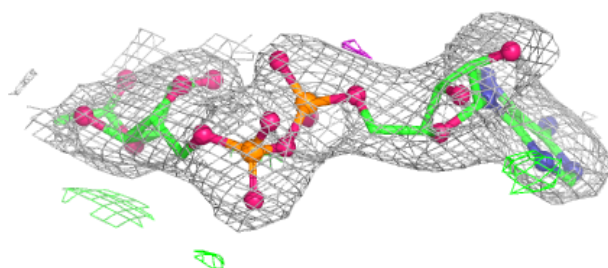
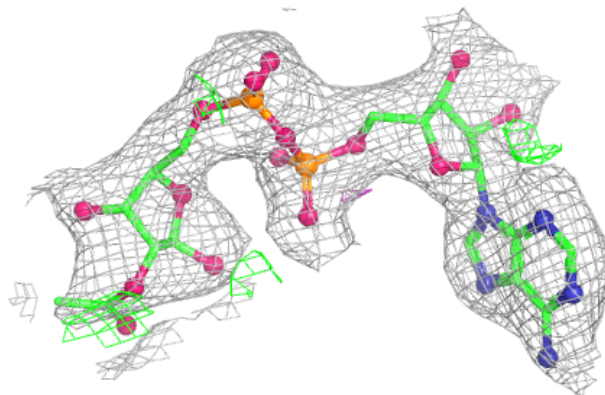


Electron density around APR E 201:

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

**Electron density around ZOD M 201:**

$2mF_o-DF_c$ (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.