



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:14 PM UTC

PDB ID : 5HZK / pdb_00005hzk
Title : Crystal structure of photoinhibitable Intersectin1 containing wildtype LOV2 domain in complex with Cdc42
Authors : Tarnawski, M.; Dagliyan, O.; Chu, P.H.; Shirvanyants, D.; Dokholyan, N.V.; Hahn, K.M.; Schlichting, I.
Deposited on : 2016-02-02
Resolution : 3.30 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)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

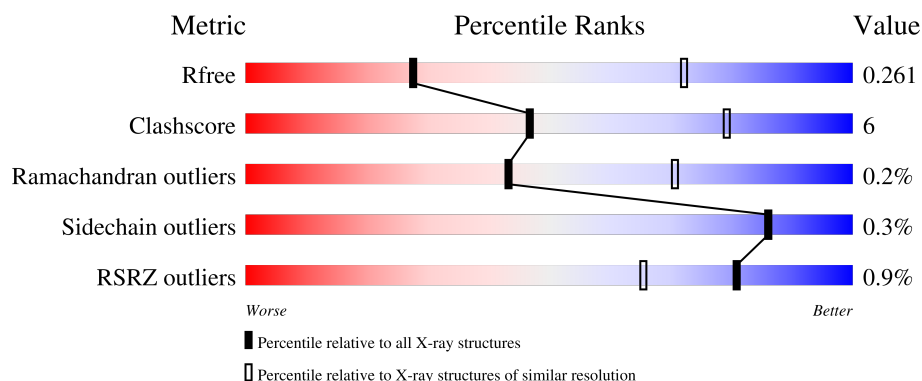
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	190	2% 78% 14% 7%
1	C	190	82% 11% 7%
2	B	502	% 77% 14% 8%
2	D	502	81% 13% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10477 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 Cell division control protein 42 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	176	Total	C	N	O	S	0	0	0
			1373	883	220	264	6			
1	C	176	Total	C	N	O	S	0	0	0
			1373	883	220	264	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P60953
A	0	ALA	-	expression tag	UNP P60953
A	188	SER	CYS	engineered mutation	UNP P60953
C	-1	GLY	-	expression tag	UNP P60953
C	0	ALA	-	expression tag	UNP P60953
C	188	SER	CYS	engineered mutation	UNP P60953

- Molecule 2 is a protein called Intersectin-1,NPH1-1,Intersectin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	460	Total	C	N	O	S	0	0	0
			3763	2397	654	692	20			
2	D	471	Total	C	N	O	S	0	0	0
			3850	2453	669	708	20			

There are 16 discrepancies between the modelled and reference sequences:

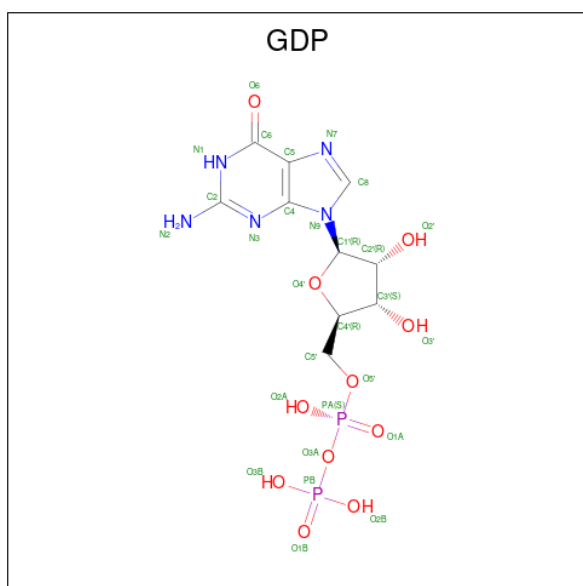
Chain	Residue	Modelled	Actual	Comment	Reference
B	1724	LEU	-	expression tag	UNP Q15811
B	1725	GLU	-	expression tag	UNP Q15811
B	1726	HIS	-	expression tag	UNP Q15811
B	1727	HIS	-	expression tag	UNP Q15811
B	1728	HIS	-	expression tag	UNP Q15811
B	1729	HIS	-	expression tag	UNP Q15811

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1730	HIS	-	expression tag	UNP Q15811
B	1731	HIS	-	expression tag	UNP Q15811
D	1724	LEU	-	expression tag	UNP Q15811
D	1725	GLU	-	expression tag	UNP Q15811
D	1726	HIS	-	expression tag	UNP Q15811
D	1727	HIS	-	expression tag	UNP Q15811
D	1728	HIS	-	expression tag	UNP Q15811
D	1729	HIS	-	expression tag	UNP Q15811
D	1730	HIS	-	expression tag	UNP Q15811
D	1731	HIS	-	expression tag	UNP Q15811

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

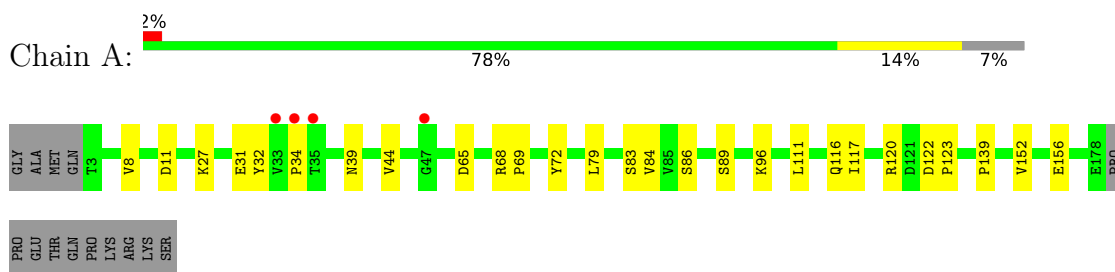
- Molecule 4 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



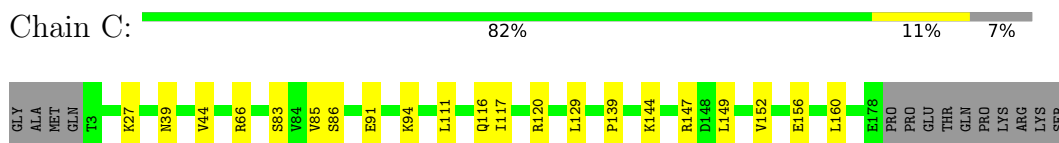
3 Residue-property plots

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.

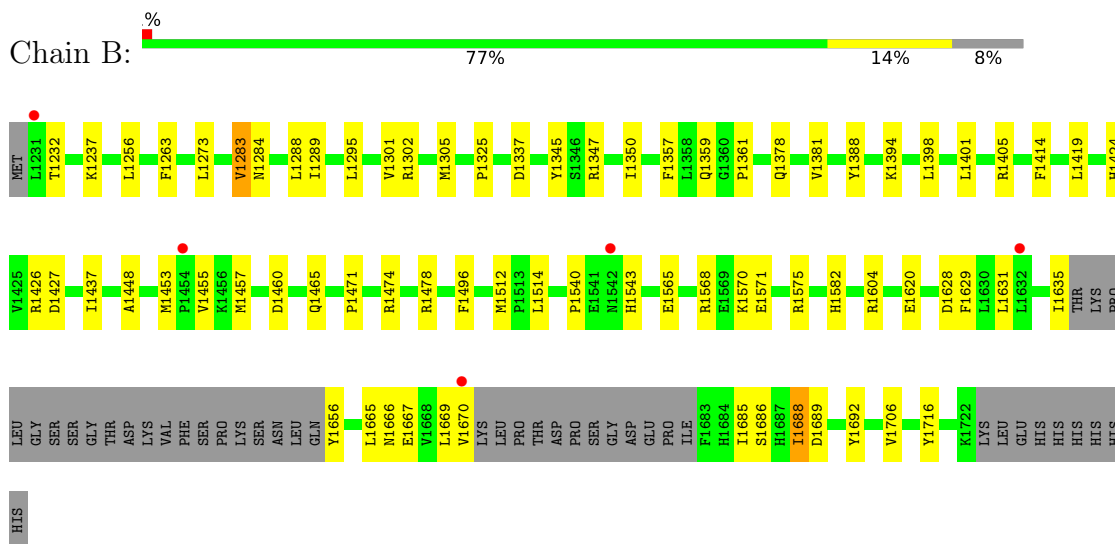
- Molecule 1: Cell division control protein 42 homolog



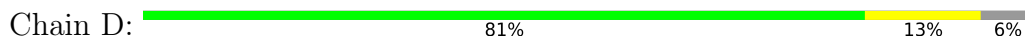
- Molecule 1: Cell division control protein 42 homolog



- Molecule 2: Intersectin-1,NPH1-1,Intersectin-1



- Molecule 2: Intersectin-1,NPH1-1,Intersectin-1



LYS	MET	F1496	L1231
LEU	L1256	R1502	L1288
PRO	L1273	THR	I1289
ASP	V1283	M1505	M1290
PRO	N1284	PRO	L1295
SER	E1287	M1512	R1302
GLY	I1289	P1513	R1326
ASP	M1290	I1531	R1353
GLU	L1295	PRO	V1583
PRO	R1302	I1535	Q1584
ILE	R1326	P1540	C1585
F1683	R1353	H1543	E1586
H1684	Q1359	E1565	R1604
I1685	G1360	R1668	K1605
S1686	P1361	N1572	N1618
Y1692	E1380	V1583	K1619
R1695	L1398	Q1584	E1620
V1706	Q1412	C1585	D1628
S1713	L1419	E1586	F1629
Y1716	L1424	R1604	I1635
K1723	V1425	K1605	T1636
LEU	R1426	N1618	LYS
GLU	D1427	K1619	PRO
HIS	K1438	E1620	LEU
HIS	V1455	D1628	GLY
HIS	K1456	F1629	SER
HIS	M1457	I1635	SER
HIS	D1460	T1636	GLY
HIS	Q1465	LYS	THR
HIS	R1474	ASP	LYS
HIS	R1478	LYS	V1647
HIS		V1656	
HIS		Y1659	
HIS		M1666	
HIS		L1669	
HIS		V1670	

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	112.37Å 119.08Å 131.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.38 – 3.30 47.38 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.38-3.30) 99.9 (47.38-3.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.207 , 0.257 0.214 , 0.261	Depositor DCC
R_{free} test set	1355 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	86.3	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 71.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10477	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

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: GDP, FMN

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	0.29	0/1403	0.73	0/1911
1	C	0.29	0/1403	0.74	0/1911
2	B	0.28	0/3832	0.69	1/5162 (0.0%)
2	D	0.27	0/3921	0.69	1/5282 (0.0%)
All	All	0.28	0/10559	0.70	2/14266 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1427	ASP	CB-CA-C	-5.65	109.54	117.23
2	B	1427	ASP	CB-CA-C	-5.65	109.55	117.23

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	1373	0	1385	16	0
1	C	1373	0	1385	13	0
2	B	3763	0	3831	55	0
2	D	3850	0	3924	41	0
3	A	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	28	0	12	1	0
4	B	31	0	19	1	0
4	D	31	0	19	1	0
All	All	10477	0	10587	119	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 6.

The worst 5 of 119 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:1302:ARG:NH1	2:D:1460:ASP:OD2	1.82	1.11
2:D:1474:ARG:HG3	2:D:1478:ARG:HE	1.49	0.77
2:D:1540:PRO:HG2	2:D:1543:HIS:HB2	1.69	0.74
2:D:1604:ARG:NH1	2:D:1628:ASP:OD2	2.21	0.73
2:B:1478:ARG:HH11	2:B:1570:LYS:NZ	1.86	0.72

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	174/190 (92%)	170 (98%)	4 (2%)	0	100	100
1	C	174/190 (92%)	170 (98%)	4 (2%)	0	100	100
2	B	454/502 (90%)	434 (96%)	18 (4%)	2 (0%)	30	60
2	D	465/502 (93%)	446 (96%)	18 (4%)	1 (0%)	43	71
All	All	1267/1384 (92%)	1220 (96%)	44 (4%)	3 (0%)	43	71

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	1283	VAL
2	B	1688	ILE
2	D	1283	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	156/168 (93%)	154 (99%)	2 (1%)	61	74
1	C	156/168 (93%)	154 (99%)	2 (1%)	61	74
2	B	419/458 (92%)	419 (100%)	0	100	100
2	D	430/458 (94%)	430 (100%)	0	100	100
All	All	1161/1252 (93%)	1157 (100%)	4 (0%)	86	86

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

Mol	Chain	Res	Type
1	A	27	LYS
1	A	44	VAL
1	C	27	LYS
1	C	44	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	1548	HIS
2	D	1687	HIS
2	B	1546	HIS
2	B	1548	HIS
1	C	61	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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](#)

4 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GDP	C	201	-	29,30,30	1.16	2 (6%)	45,47,47	1.78	7 (15%)
3	GDP	A	200	-	29,30,30	1.16	3 (10%)	45,47,47	1.76	7 (15%)
4	FMN	D	1801	-	33,33,33	1.05	2 (6%)	48,50,50	1.21	7 (14%)
4	FMN	B	1801	-	33,33,33	1.04	2 (6%)	48,50,50	1.21	7 (14%)

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	GDP	C	201	-	-	5/16/32/32	0/3/3/3
3	GDP	A	200	-	-	5/16/32/32	0/3/3/3
4	FMN	D	1801	-	-	0/18/18/18	0/3/3/3
4	FMN	B	1801	-	-	0/18/18/18	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1801	FMN	C4A-N5	3.59	1.38	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1801	FMN	C4A-N5	3.58	1.38	1.30
3	A	200	GDP	C5-C4	3.18	1.47	1.38
3	C	201	GDP	C5-C4	3.17	1.47	1.38
4	D	1801	FMN	C10-N1	2.56	1.38	1.33

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	201	GDP	C5-C4-N3	-6.15	118.61	128.39
3	A	200	GDP	C5-C4-N3	-6.09	118.69	128.39
3	C	201	GDP	C2-N3-C4	5.07	121.03	112.30
3	A	200	GDP	C2-N3-C4	5.06	121.02	112.30
3	C	201	GDP	N9-C4-N3	4.49	134.94	125.95

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	200	GDP	C5'-O5'-PA-O3A
3	A	200	GDP	C5'-O5'-PA-O1A
3	A	200	GDP	C5'-O5'-PA-O2A
3	A	200	GDP	O4'-C4'-C5'-O5'
3	C	201	GDP	C5'-O5'-PA-O3A

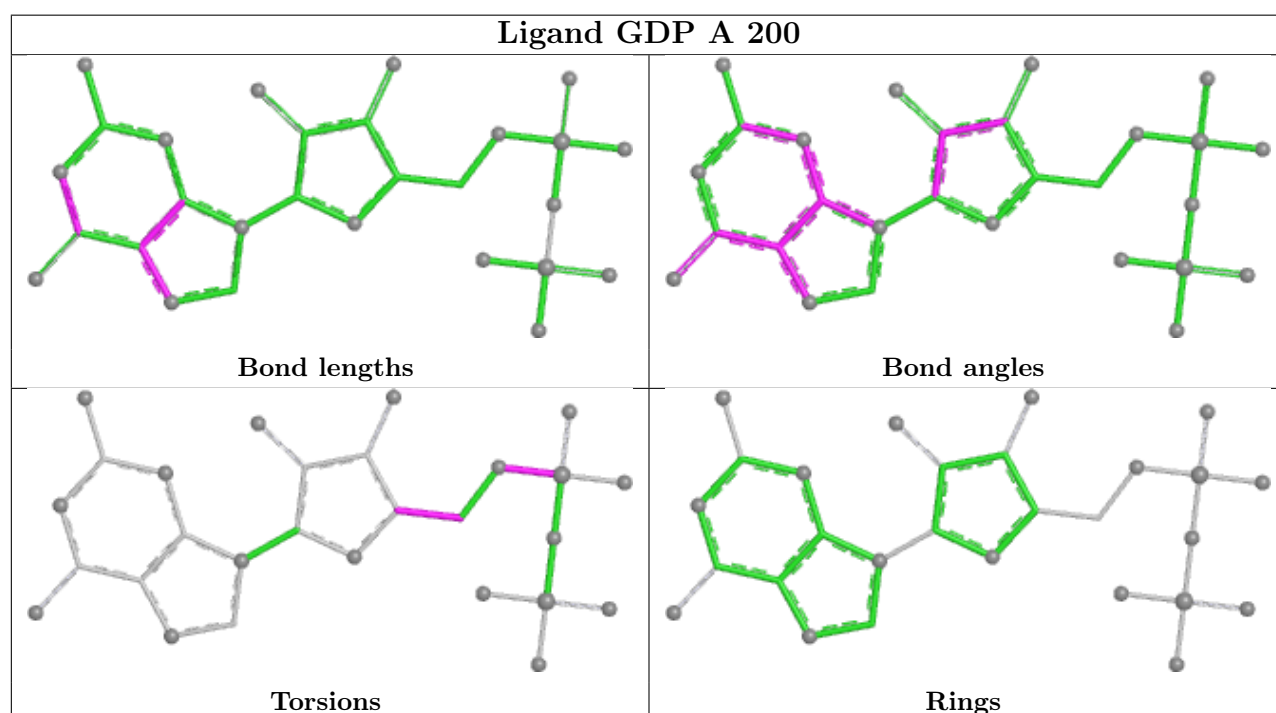
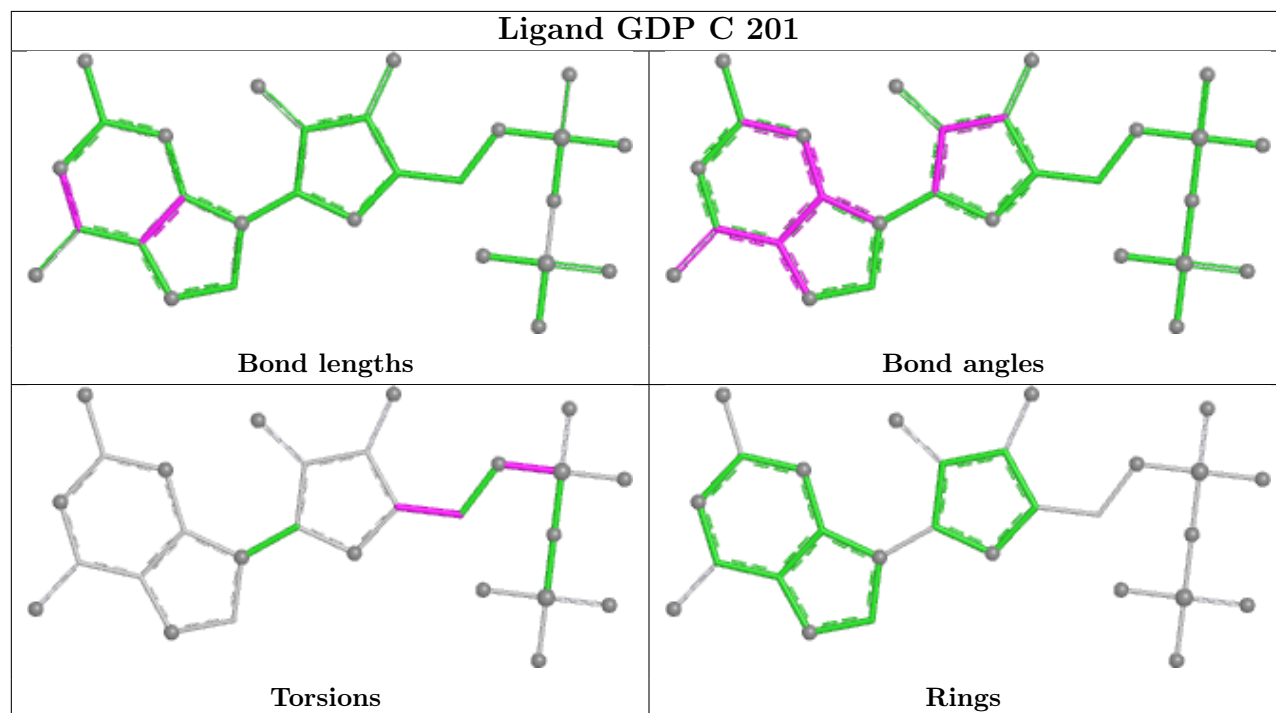
There are no ring outliers.

4 monomers are involved in 4 short contacts:

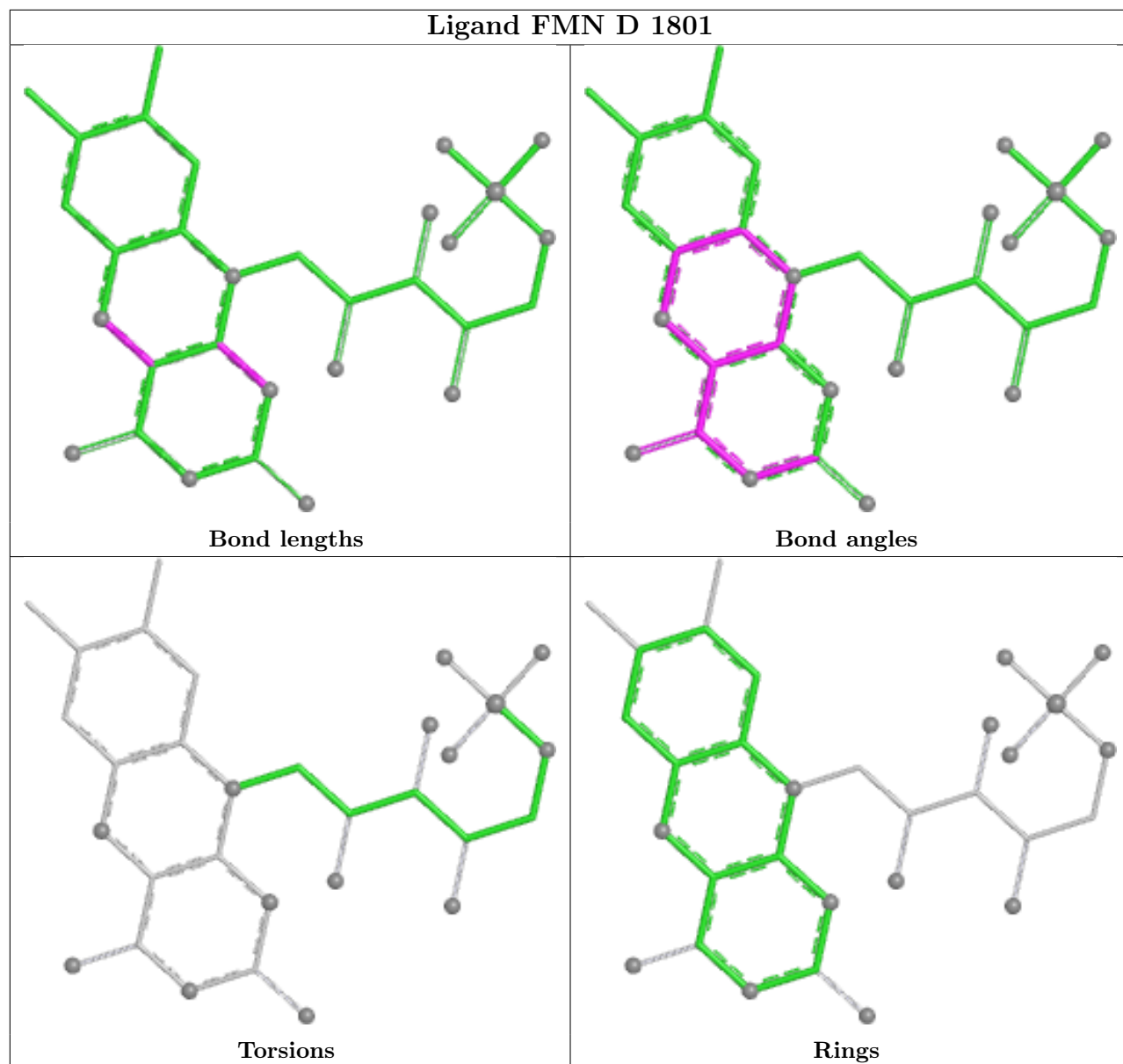
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	201	GDP	1	0
3	A	200	GDP	1	0
4	D	1801	FMN	1	0
4	B	1801	FMN	1	0

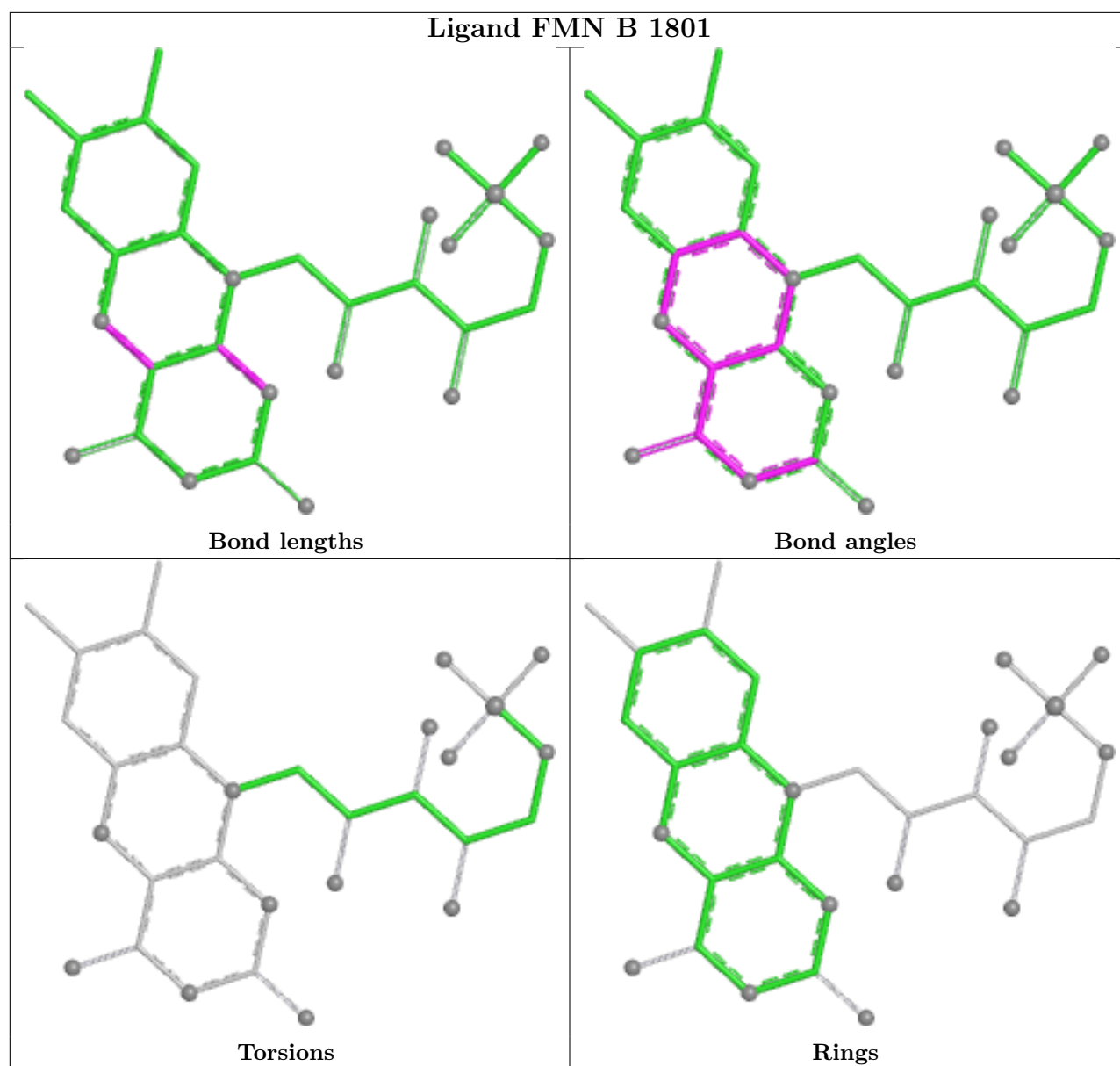
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



Ligand FMN D 1801





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	176/190 (92%)	-0.17	4 (2%) 61 42	47, 78, 143, 191	0
1	C	176/190 (92%)	-0.43	0 100 100	45, 71, 116, 135	0
2	B	460/502 (91%)	-0.07	5 (1%) 78 60	51, 96, 184, 270	0
2	D	471/502 (93%)	-0.05	2 (0%) 88 79	47, 108, 175, 240	0
All	All	1283/1384 (92%)	-0.13	11 (0%) 81 65	45, 94, 171, 270	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	35	THR	4.2
2	B	1231	LEU	2.7
2	B	1670	VAL	2.7
1	A	34	PRO	2.7
2	B	1632	LEU	2.5

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](#)

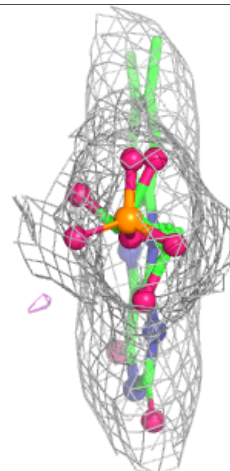
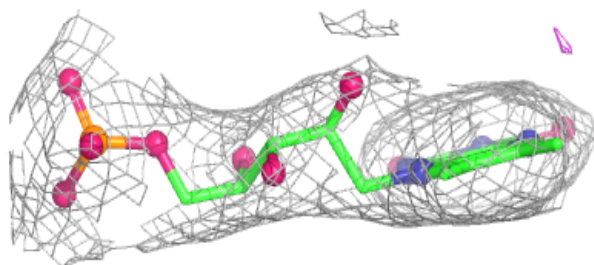
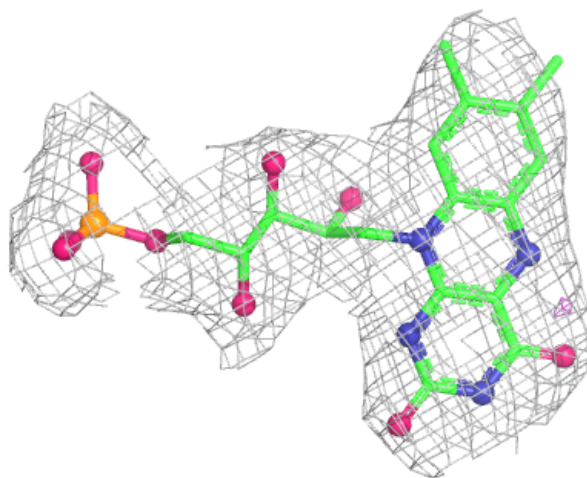
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	FMN	D	1801	31/31	0.93	0.08	58,71,93,94	0
3	GDP	C	201	28/28	0.95	0.07	47,71,84,94	0
4	FMN	B	1801	31/31	0.95	0.08	47,60,77,85	0
3	GDP	A	200	28/28	0.95	0.07	49,63,81,90	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.

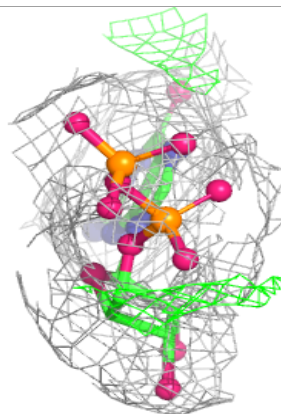
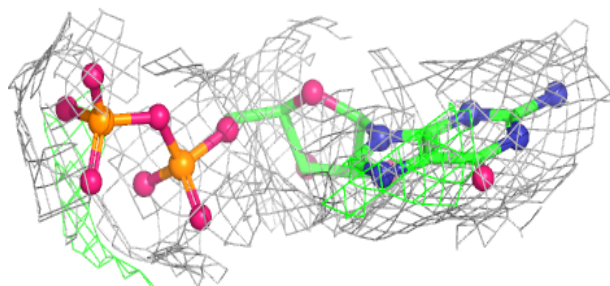
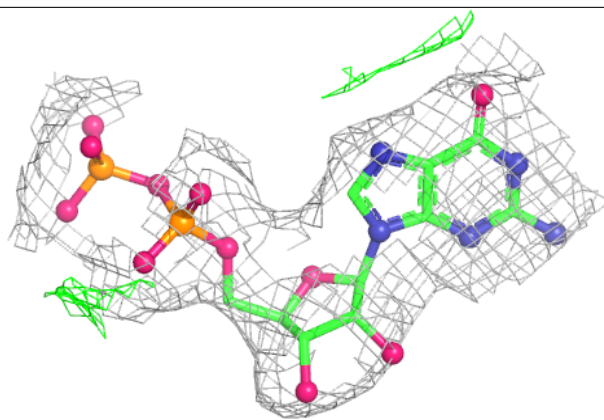
Electron density around FMN D 1801:

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



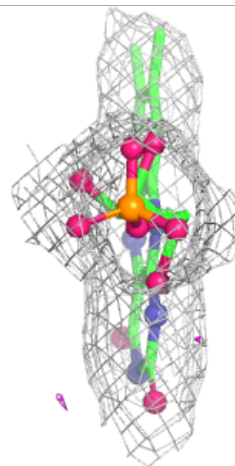
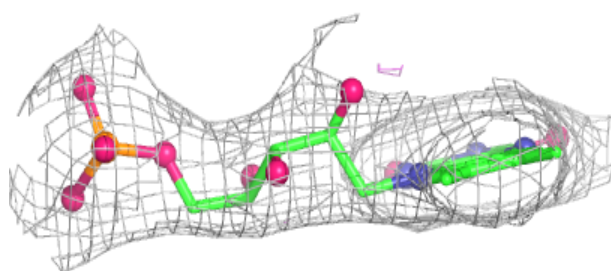
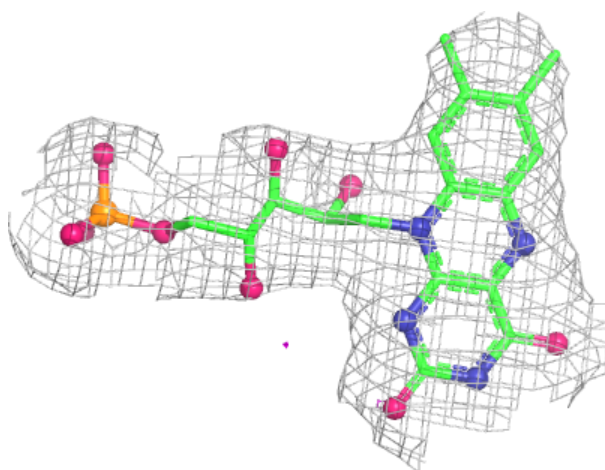
Electron density around GDP C 201:

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



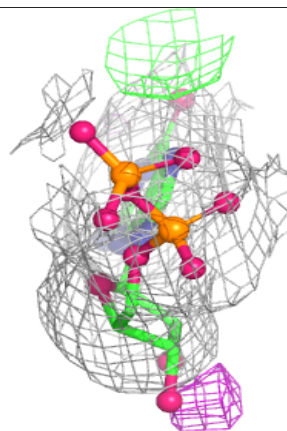
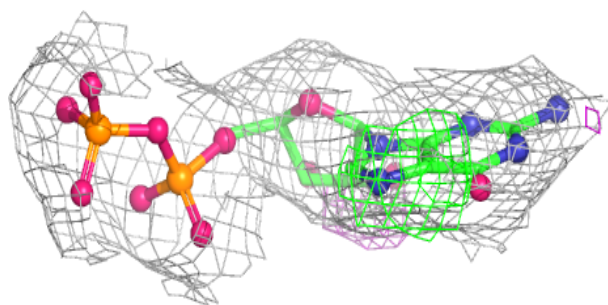
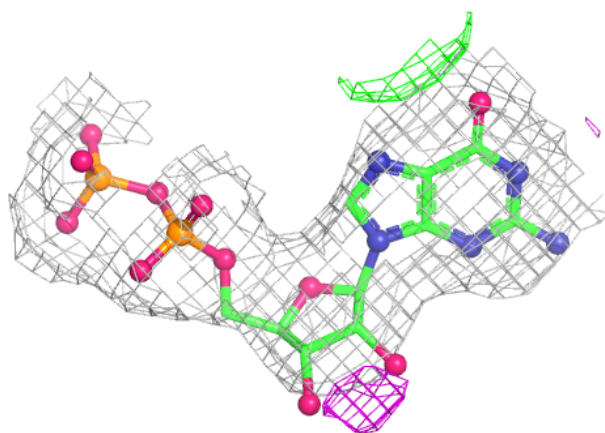
Electron density around FMN B 1801:

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



Electron density around GDP A 200:

$2mF_o - DF_c$ (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.