



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 20, 2023 – 11:14 AM EDT

PDB ID : 5HVK  
Title : Crystal structure of LIMK1 mutant D460N in complex with full-length cofilin-1  
Authors : Hamill, S.; Boggon, T.J.  
Deposited on : 2016-01-28  
Resolution : 3.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 2.35.1  
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) : 2.35.1

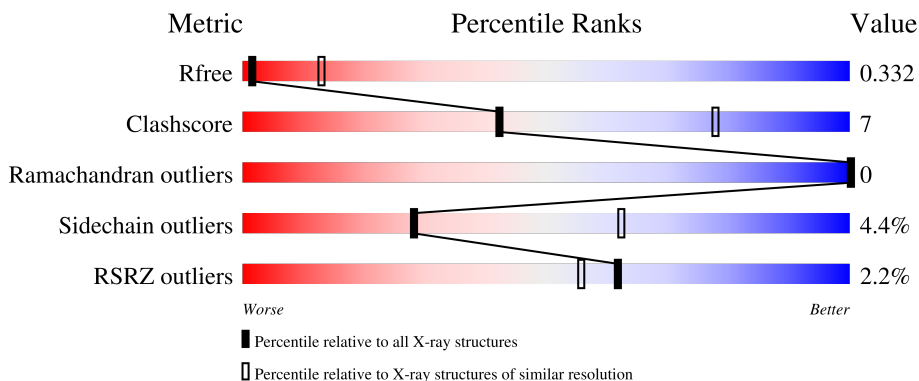
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	315	 3% 80% 14% • 5%
1	C	315	 2% 77% 13% • 7%
2	B	165	 % 71% 24% 5%
3	D	165	 3% 68% 30% ••

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:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
5	MG	C	702	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 7446 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 LIM domain kinase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	298	2427	1546	436	424	1	20	0	0	0
1	C	292	2387	1524	427	416	1	19	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	324	GLY	-	expression tag	UNP P53667
A	325	ALA	-	expression tag	UNP P53667
A	326	MET	-	expression tag	UNP P53667
A	327	GLY	-	expression tag	UNP P53667
A	328	SER	-	expression tag	UNP P53667
A	460	ASN	ASP	engineered mutation	UNP P53667
C	324	GLY	-	expression tag	UNP P53667
C	325	ALA	-	expression tag	UNP P53667
C	326	MET	-	expression tag	UNP P53667
C	327	GLY	-	expression tag	UNP P53667
C	328	SER	-	expression tag	UNP P53667
C	460	ASN	ASP	engineered mutation	UNP P53667

- Molecule 2 is a protein called Cofilin-1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
2	B	165	1292	822	210	252	1	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	69	THR	ALA	engineered mutation	UNP P23528

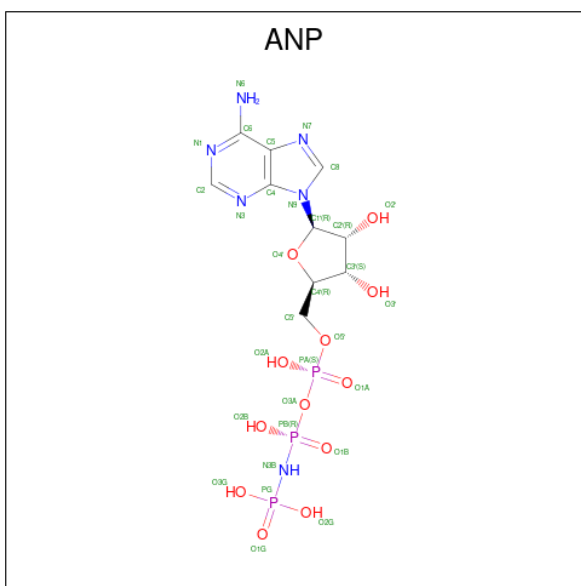
- Molecule 3 is a protein called Cofilin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	D	164	1280	816	209	248	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	69	THR	ALA	engineered mutation	UNP P23528

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	27	10	6	9	2	0	0
4	C	1	31	10	6	12	3	0	0

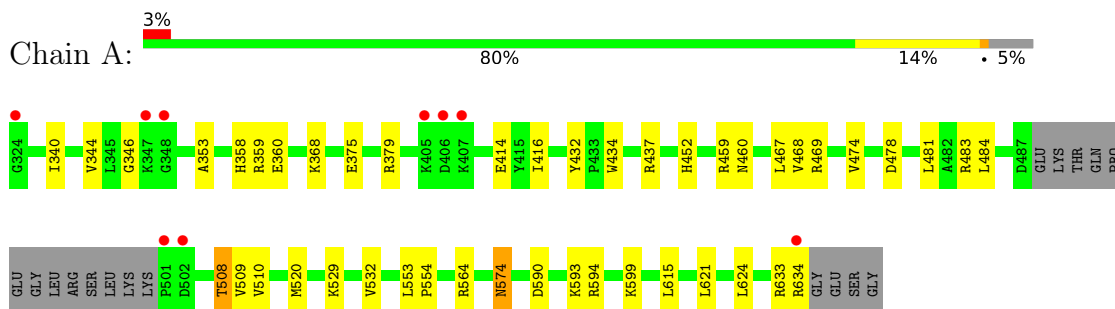
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0
5	C	1	Total Mg 1 1	0	0

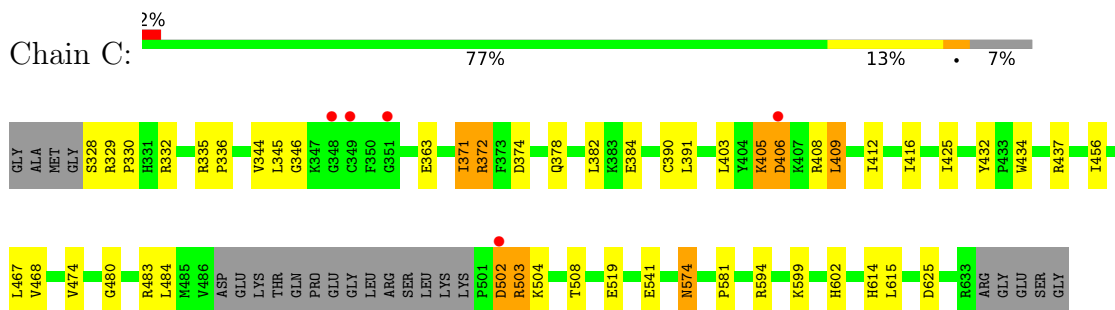
### 3 Residue-property plots

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.

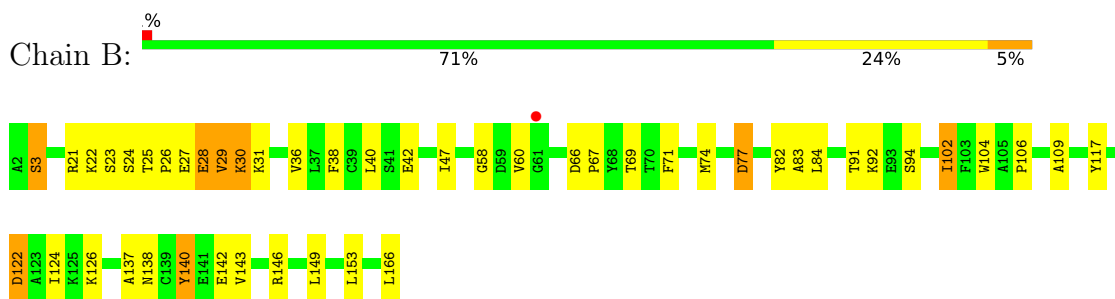
- Molecule 1: LIM domain kinase 1



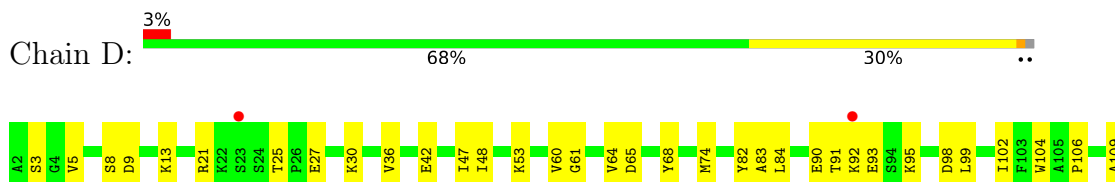
- Molecule 1: LIM domain kinase 1



- Molecule 2: Cofilin-1



- Molecule 3: Cofilin-1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.12Å 102.28Å 141.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.11 – 3.50 48.11 – 3.47	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.11-3.50) 84.6 (48.11-3.47)	Depositor EDS
$R_{merge}$	0.54	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.98 (at 3.48Å)	Xtrriage
Refinement program	PHENIX dev_1819	Depositor
R, $R_{free}$	0.273 , 0.310 0.287 , 0.332	Depositor DCC
$R_{free}$ test set	797 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.9	Xtrriage
Anisotropy	0.956	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 36.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.83	EDS
Total number of atoms	7446	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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 49.43 % 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 7.4693e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: ANP, TPO, SEP, MG

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	0.22	0/2475	0.41	0/3335
1	C	0.22	0/2435	0.44	1/3283 (0.0%)
2	B	0.24	0/1300	0.48	0/1742
3	D	0.22	0/1299	0.45	0/1742
All	All	0.22	0/7509	0.44	1/10102 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	409	LEU	CA-CB-CG	5.22	127.32	115.30

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	2427	0	2425	25	0
1	C	2387	0	2389	23	0
2	B	1292	0	1332	27	0
3	D	1280	0	1323	27	0
4	A	27	0	11	1	0
4	C	31	0	13	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	0	0
5	C	1	0	0	0	0
All	All	7446	0	7493	103	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 7.

All (103) 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:B:23:SER:HB3	2:B:28:GLU:HB3	1.69	0.73
1:C:328:SER:O	1:C:329:ARG:NE	2.25	0.70
3:D:83:ALA:HB3	3:D:102:ILE:HB	1.73	0.70
1:C:378:GLN:HG3	1:C:382:LEU:HD13	1.76	0.66
3:D:64:VAL:H	3:D:65:ASP:HA	1.61	0.65
2:B:77:ASP:OD1	2:B:77:ASP:N	2.31	0.64
2:B:83:ALA:HB3	2:B:102:ILE:HB	1.81	0.62
1:A:459:ARG:NH2	1:A:481:LEU:O	2.32	0.62
1:C:468:VAL:HG22	1:C:474:VAL:HG22	1.82	0.62
1:C:432:TYR:HB3	1:C:437:ARG:HH21	1.66	0.60
1:C:502:ASP:N	1:C:503:ARG:HA	2.16	0.60
1:A:564:ARG:HH12	1:A:633:ARG:HB2	1.67	0.59
1:A:432:TYR:HB3	1:A:437:ARG:HH21	1.68	0.58
1:C:332:ARG:NH1	1:C:363:GLU:OE1	2.37	0.57
2:B:36:VAL:HG12	2:B:84:LEU:HB2	1.87	0.57
3:D:104:TRP:HA	3:D:137:ALA:HB3	1.87	0.57
1:A:414:GLU:OE2	1:A:469:ARG:NH2	2.37	0.56
2:B:146:ARG:HD2	2:B:166:LEU:HD21	1.87	0.56
4:C:701:ANP:O2G	4:C:701:ANP:O2B	2.24	0.56
1:C:416:ILE:HG21	1:C:467:LEU:HB3	1.88	0.55
1:A:460:ASN:ND2	1:A:478:ASP:OD2	2.40	0.55
2:B:26:PRO:HA	2:B:29:VAL:HG23	1.90	0.54
4:C:701:ANP:O1B	3:D:3:SER:OG	2.26	0.54
3:D:151:GLU:HA	3:D:155:GLY:HA3	1.90	0.53
3:D:82:TYR:OH	3:D:117:TYR:O	2.23	0.53
1:C:456:ILE:HG12	1:C:484:LEU:HG	1.90	0.52
2:B:106:PRO:HG2	2:B:109:ALA:HB2	1.91	0.52
1:C:371:ILE:HD12	1:C:372:ARG:HB2	1.92	0.51
3:D:99:LEU:HD23	3:D:131:ILE:HD11	1.93	0.51
1:C:425:ILE:HD13	1:C:541:GLU:HB3	1.93	0.51
1:C:344:VAL:HG12	1:C:346:GLY:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:104:TRP:HA	2:B:137:ALA:HB3	1.93	0.50
2:B:91:THR:HG23	2:B:94:SER:HB2	1.94	0.50
1:C:434:TRP:HE1	1:C:574:ASN:HB2	1.76	0.50
1:C:406:ASP:OD1	1:C:406:ASP:N	2.42	0.49
1:A:481:LEU:HD22	1:A:510:VAL:HG11	1.94	0.49
3:D:68:TYR:CD2	3:D:146:ARG:HG2	2.48	0.48
1:A:532:VAL:HG11	1:A:594:ARG:HB3	1.94	0.48
1:A:340:ILE:HD11	1:A:359:ARG:HE	1.79	0.48
1:A:509:VAL:HG13	1:A:520:MET:HG2	1.94	0.48
1:A:375:GLU:O	1:A:379:ARG:HG3	2.13	0.48
1:A:615:LEU:HD12	1:A:615:LEU:H	1.79	0.47
2:B:82:TYR:OH	2:B:117:TYR:O	2.30	0.47
1:A:590:ASP:HB3	1:A:593:LYS:HE2	1.95	0.47
2:B:30:LYS:HG2	2:B:58:GLY:HA3	1.97	0.47
3:D:53:LYS:HD2	3:D:74:MET:HG3	1.96	0.47
1:A:358:HIS:HE1	1:A:360:GLU:HB3	1.79	0.47
1:A:621:LEU:HD23	1:A:624:LEU:HD12	1.97	0.47
2:B:71:PHE:HA	2:B:74:MET:HE2	1.96	0.47
1:A:468:VAL:HG22	1:A:474:VAL:HG22	1.97	0.47
3:D:47:ILE:HD12	3:D:124:ILE:HG21	1.97	0.47
3:D:36:VAL:HG12	3:D:84:LEU:HB2	1.97	0.46
3:D:140:TYR:HA	3:D:143:VAL:HG12	1.97	0.46
4:A:1001:ANP:O1B	4:A:1001:ANP:O1A	2.32	0.46
2:B:40:LEU:HB3	2:B:47:ILE:HG12	1.97	0.46
2:B:42:GLU:OE2	2:B:42:GLU:N	2.43	0.46
3:D:27:GLU:O	3:D:30:LYS:HG2	2.15	0.46
3:D:120:SER:HA	3:D:123:ALA:HB3	1.97	0.46
1:C:615:LEU:H	1:C:615:LEU:HD12	1.80	0.46
1:C:502:ASP:HB2	1:C:504:LYS:N	2.31	0.45
1:C:519:GLU:OE2	1:C:594:ARG:NH1	2.49	0.45
3:D:154:GLY:HA3	3:D:155:GLY:HA2	1.77	0.45
3:D:91:THR:OG1	3:D:92:LYS:N	2.49	0.45
3:D:160:SER:HA	3:D:165:PRO:HA	1.98	0.45
2:B:149:LEU:O	2:B:153:LEU:HG	2.16	0.44
3:D:9:ASP:OD1	3:D:9:ASP:N	2.45	0.44
3:D:90:GLU:HG2	3:D:95:LYS:HG3	1.99	0.44
2:B:138:ASN:N	2:B:142:GLU:OE1	2.49	0.44
1:A:459:ARG:NH1	1:A:508:TPO:O	2.47	0.44
1:A:481:LEU:HD21	2:B:3:SEP:O2P	2.18	0.44
1:A:529:LYS:HB3	1:A:594:ARG:HD2	1.99	0.44
2:B:22:LYS:HD3	2:B:22:LYS:HA	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:ALA:HB2	1:A:368:LYS:HD2	2.00	0.43
3:D:60:VAL:HA	3:D:61:GLY:HA2	1.71	0.43
2:B:24:SER:O	2:B:25:THR:OG1	2.30	0.43
2:B:60:VAL:HG13	2:B:67:PRO:HG3	2.00	0.43
2:B:66:ASP:OD2	2:B:69:THR:HG23	2.19	0.43
1:C:384:GLU:HB2	1:C:480:GLY:HA2	2.01	0.43
3:D:121:LYS:HG2	3:D:125:LYS:NZ	2.34	0.43
1:A:483:ARG:HD2	1:A:484:LEU:H	1.84	0.43
1:C:502:ASP:N	1:C:502:ASP:OD1	2.51	0.43
3:D:42:GLU:OE1	3:D:42:GLU:N	2.48	0.43
2:B:140:TYR:HA	2:B:143:VAL:HG12	2.01	0.42
1:C:329:ARG:HB3	1:C:330:PRO:HD2	2.00	0.42
3:D:64:VAL:N	3:D:65:ASP:HA	2.27	0.42
1:A:529:LYS:HD2	1:A:594:ARG:HB2	2.02	0.42
3:D:8:SER:HB2	3:D:48:ILE:HG22	2.00	0.42
1:A:434:TRP:HE1	1:A:574:ASN:HB3	1.84	0.42
2:B:27:GLU:O	2:B:31:LYS:HG2	2.20	0.42
3:D:161:LEU:HG	3:D:162:GLU:HG2	2.02	0.42
3:D:5:VAL:HG21	3:D:120:SER:OG	2.21	0.41
1:A:416:ILE:HG21	1:A:467:LEU:HB3	2.03	0.41
1:C:403:LEU:HB2	1:C:412:ILE:HD11	2.02	0.41
2:B:38:PHE:HB2	2:B:82:TYR:HB2	2.02	0.41
1:A:553:LEU:HD12	1:A:554:PRO:HD2	2.02	0.41
1:A:344:VAL:HG12	1:A:346:GLY:H	1.85	0.40
2:B:25:THR:O	2:B:29:VAL:HG22	2.21	0.40
1:C:405:LYS:O	1:C:408:ARG:N	2.46	0.40
2:B:91:THR:OG1	2:B:92:LYS:N	2.53	0.40
3:D:106:PRO:HG2	3:D:109:ALA:HB2	2.03	0.40
2:B:122:ASP:O	2:B:126:LYS:HB2	2.21	0.40
1:C:335:ARG:HD2	1:C:336:PRO:HD2	2.03	0.40
1:C:581:PRO:HG2	1:C:625:ASP:HA	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	293/315 (93%)	277 (94%)	16 (6%)	0	100	100
1	C	287/315 (91%)	274 (96%)	13 (4%)	0	100	100
2	B	162/165 (98%)	153 (94%)	9 (6%)	0	100	100
3	D	162/165 (98%)	154 (95%)	8 (5%)	0	100	100
All	All	904/960 (94%)	858 (95%)	46 (5%)	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	265/279 (95%)	261 (98%)	4 (2%)	65	84
1	C	262/279 (94%)	246 (94%)	16 (6%)	18	51
2	B	143/143 (100%)	134 (94%)	9 (6%)	18	51
3	D	143/144 (99%)	136 (95%)	7 (5%)	25	59
All	All	813/845 (96%)	777 (96%)	36 (4%)	28	62

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	452	HIS
1	A	574	ASN
1	A	599	LYS
1	A	634	ARG
2	B	21	ARG
2	B	28	GLU
2	B	29	VAL
2	B	30	LYS
2	B	77	ASP
2	B	102	ILE

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Mol	Chain	Res	Type
2	B	122	ASP
2	B	124	ILE
2	B	140	TYR
1	C	345	LEU
1	C	371	ILE
1	C	372	ARG
1	C	374	ASP
1	C	390	CYS
1	C	391	LEU
1	C	405	LYS
1	C	406	ASP
1	C	409	LEU
1	C	483	ARG
1	C	502	ASP
1	C	503	ARG
1	C	574	ASN
1	C	599	LYS
1	C	602	HIS
1	C	614	HIS
3	D	13	LYS
3	D	21	ARG
3	D	25	THR
3	D	93	GLU
3	D	98	ASP
3	D	124	ILE
3	D	140	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	331	HIS
1	C	620	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](#)

3 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SEP	B	3	2	8,9,10	1.52	1 (12%)	8,12,14	1.27	2 (25%)
1	TPO	A	508	1	8,10,11	1.57	1 (12%)	10,14,16	1.76	2 (20%)
1	TPO	C	508	1	8,10,11	1.58	1 (12%)	10,14,16	1.89	1 (10%)

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	SEP	B	3	2	-	4/5/8/10	-
1	TPO	A	508	1	-	3/9/11/13	-
1	TPO	C	508	1	-	1/9/11/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3	SEP	P-O1P	3.37	1.61	1.50
1	C	508	TPO	P-O1P	3.37	1.61	1.50
1	A	508	TPO	P-O1P	3.29	1.61	1.50

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	508	TPO	P-OG1-CB	-5.33	107.10	123.21
1	A	508	TPO	P-OG1-CB	-4.24	110.39	123.21
1	A	508	TPO	CG2-CB-CA	-2.45	108.32	113.16
2	B	3	SEP	P-OG-CB	-2.08	112.58	118.30
2	B	3	SEP	OG-CB-CA	2.01	110.11	108.14

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	508	TPO	N-CA-CB-CG2
1	A	508	TPO	N-CA-CB-OG1
1	A	508	TPO	C-CA-CB-CG2
2	B	3	SEP	N-CA-CB-OG
2	B	3	SEP	CB-OG-P-O1P
2	B	3	SEP	CB-OG-P-O2P
2	B	3	SEP	CB-OG-P-O3P
1	C	508	TPO	C-CA-CB-CG2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	3	SEP	1	0
1	A	508	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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
4	ANP	A	1001	5	24,29,33	1.61	3 (12%)	25,45,52	1.10	2 (8%)
4	ANP	C	701	-	29,33,33	2.18	6 (20%)	31,52,52	1.10	3 (9%)

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	ANP	A	1001	5	-	2/9/32/38	0/3/3/3
4	ANP	C	701	-	-	4/14/38/38	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	701	ANP	PG-O1G	7.82	1.58	1.46
4	A	1001	ANP	PB-O1B	6.35	1.56	1.46
4	C	701	ANP	PB-O1B	6.25	1.56	1.46
4	A	1001	ANP	PB-O2B	-2.58	1.49	1.56
4	C	701	ANP	PB-O2B	-2.55	1.49	1.56
4	C	701	ANP	PG-O3G	-2.52	1.50	1.56
4	C	701	ANP	PG-N3B	2.43	1.69	1.63
4	A	1001	ANP	PB-O3A	-2.35	1.56	1.59
4	C	701	ANP	PB-O3A	-2.30	1.56	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1001	ANP	PB-O3A-PA	-4.09	119.58	132.56
4	C	701	ANP	PB-O3A-PA	-2.83	122.64	132.62
4	A	1001	ANP	C5-C6-N6	2.28	123.81	120.35
4	C	701	ANP	C5-C6-N6	2.27	123.81	120.35
4	C	701	ANP	O1G-PG-N3B	-2.12	108.65	111.77

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	ANP	O4'-C4'-C5'-O5'
4	A	1001	ANP	C3'-C4'-C5'-O5'
4	C	701	ANP	PB-N3B-PG-O1G
4	C	701	ANP	PG-N3B-PB-O1B
4	C	701	ANP	C3'-C4'-C5'-O5'
4	C	701	ANP	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 3 short contacts:

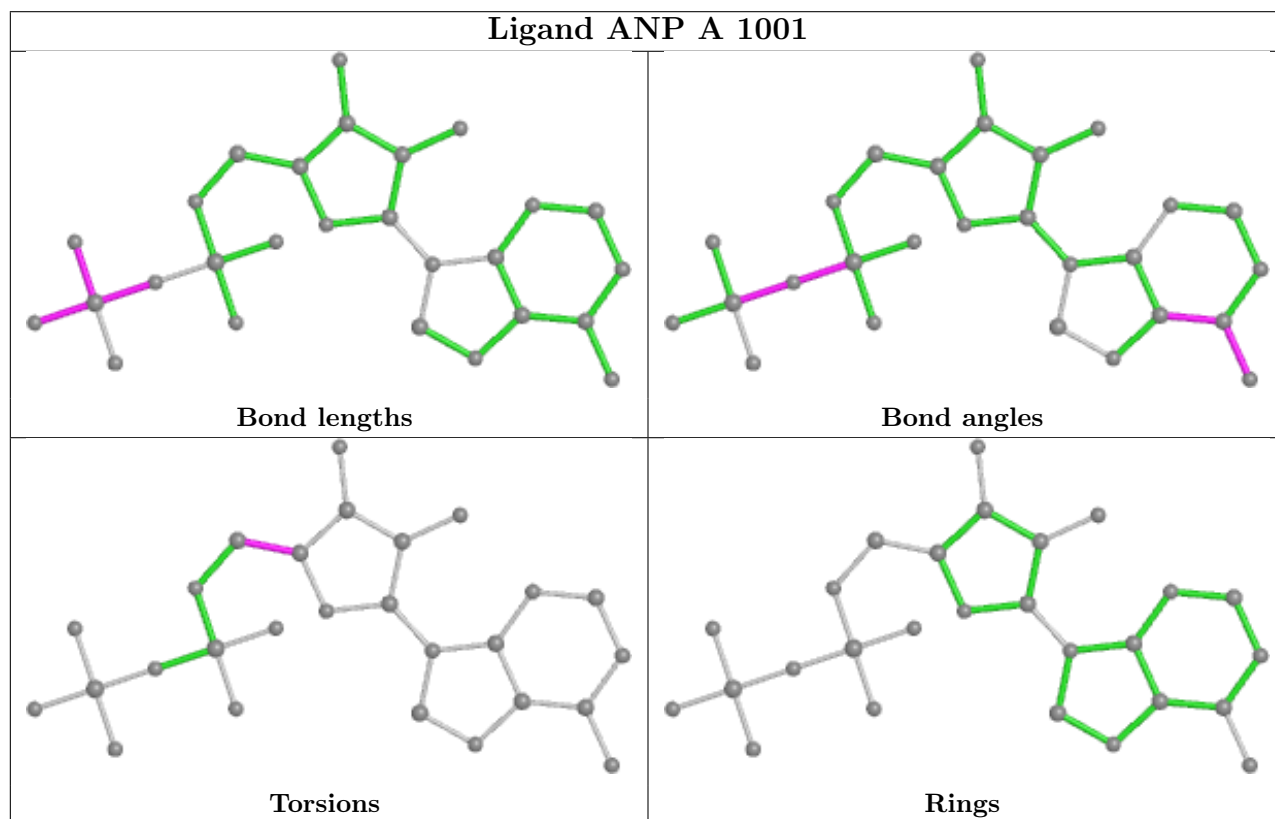
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1001	ANP	1	0

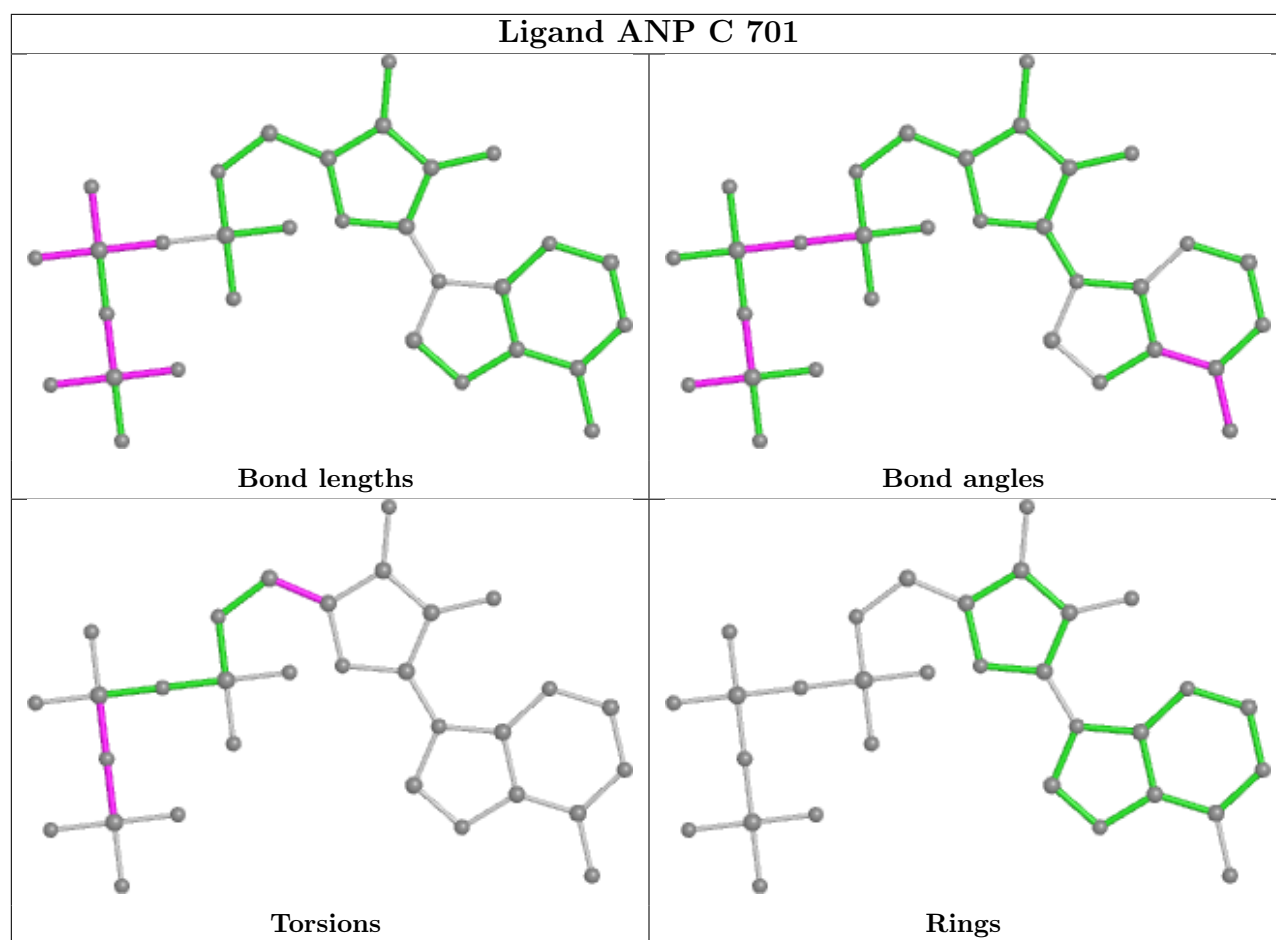
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	701	ANP	2	0

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

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<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	297/315 (94%)	-0.09	9 (3%) 50 44	7, 28, 74, 115	0
1	C	291/315 (92%)	-0.11	5 (1%) 70 64	7, 27, 66, 123	0
2	B	164/165 (99%)	0.22	1 (0%) 89 86	20, 47, 71, 96	0
3	D	164/165 (99%)	0.34	5 (3%) 50 44	28, 55, 81, 93	0
All	All	916/960 (95%)	0.03	20 (2%) 62 56	7, 37, 74, 123	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	348	GLY	5.1
1	A	348	GLY	4.2
1	C	351	GLY	3.6
1	A	406	ASP	3.6
1	C	502	ASP	3.6
1	C	349	CYS	3.4
1	A	634	ARG	3.0
3	D	157	ALA	3.0
3	D	156	SER	2.7
1	A	407	LYS	2.6
3	D	23	SER	2.4
1	A	501	PRO	2.4
1	A	502	ASP	2.4
2	B	61	GLY	2.3
3	D	155	GLY	2.2
1	A	324	GLY	2.2
1	C	406	ASP	2.2
1	A	347	LYS	2.1
1	A	405	LYS	2.1
3	D	92	LYS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
2	SEP	B	3	10/11	0.81	0.39	54,69,104,106	0
1	TPO	A	508	11/12	0.91	0.18	13,16,21,29	0
1	TPO	C	508	11/12	0.94	0.17	17,23,33,39	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

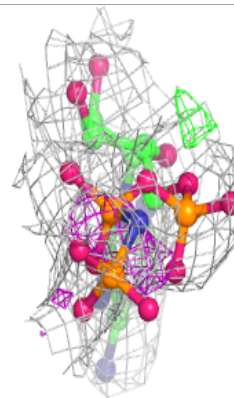
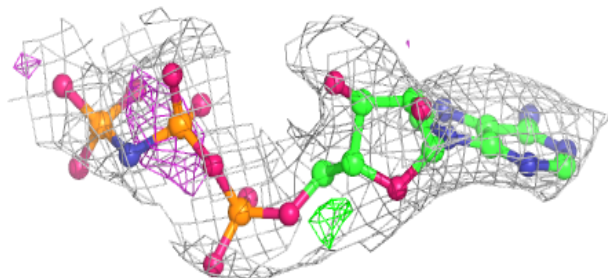
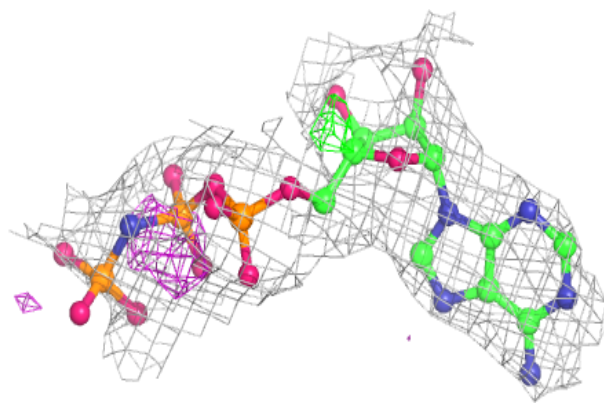
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	MG	C	702	1/1	0.62	0.45	36,36,36,36	0
5	MG	A	1002	1/1	0.64	0.27	19,19,19,19	0
4	ANP	C	701	31/31	0.84	0.27	17,33,93,125	0
4	ANP	A	1001	27/31	0.89	0.24	18,35,70,85	0

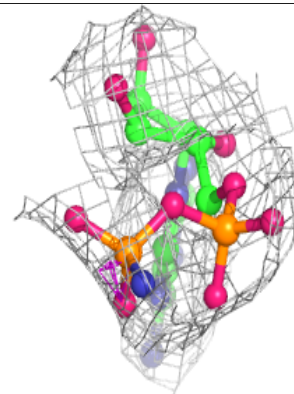
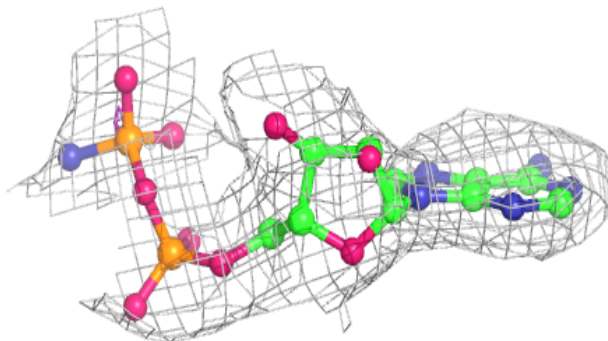
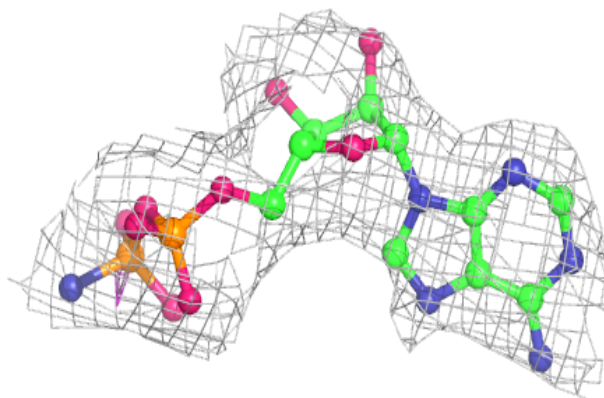
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around ANP C 701:**

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

**Electron density around ANP A 1001:**

$2mF_o-DF_c$  (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.