wwPDB X-ray Structure Validation Summary Report (i)

Jun 18, 2024 – 01:28 AM EDT

PDB ID	:	2XAL
Title	:	Lead derivative of Inositol 1,3,4,5,6-pentakisphosphate 2-kinase from A. thaliana in complex with ADP and IP6.
Authors	:	Gonzalez, B.; Banos-Sanz, J.I.; Villate, M.; Brearley, C.A.; Sanz-Aparicio, J.
Deposited on	:	2010-03-31
Resolution	:	3.20 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

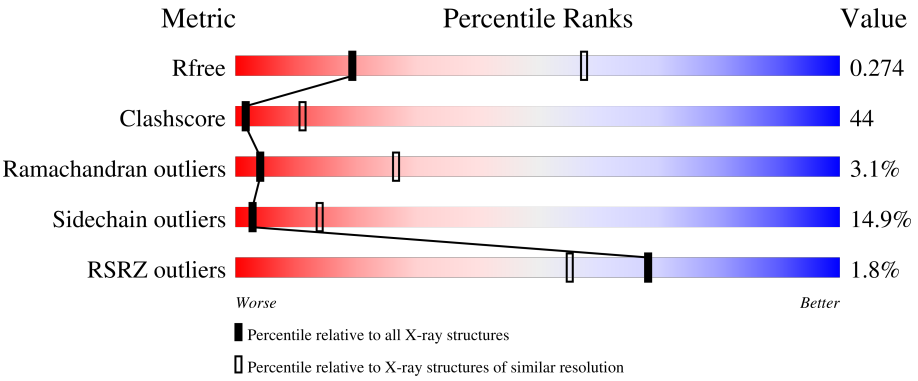
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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

Mol	Chain	Length	Quality of chain
1	A	451	2% 42% 40% 10% 7%
1	B	451	2% 39% 45% 10% • 6%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6851 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.

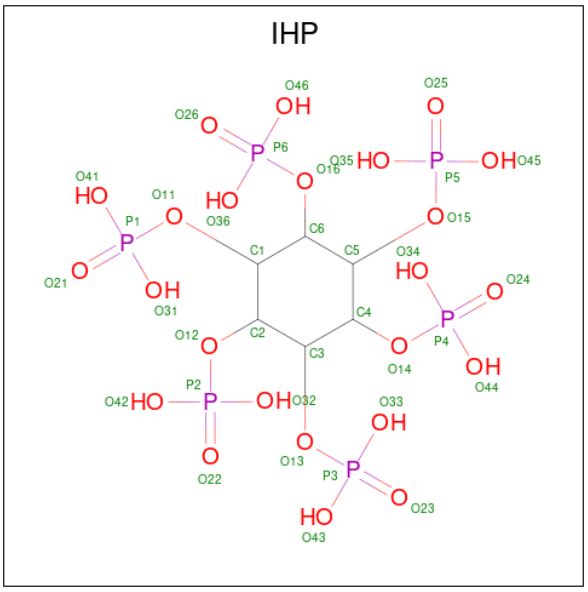
- Molecule 1 is a protein called INOSITOL-PENTAKISPHOSPHATE 2-KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	420	Total	C	N	O	S	0	0	0
			3338	2120	565	640	13			
1	B	425	Total	C	N	O	S	0	0	0
			3381	2148	574	645	14			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	SER	ALA	conflict	UNP Q93YN9
A	90	GLN	LYS	conflict	UNP Q93YN9
A	157	THR	SER	conflict	UNP Q93YN9
A	204	ILE	ASN	conflict	UNP Q93YN9
A	224	ARG	SER	conflict	UNP Q93YN9
A	321	CYS	SER	conflict	UNP Q93YN9
A	325	ILE	LEU	conflict	UNP Q93YN9
A	337	ARG	LYS	conflict	UNP Q93YN9
B	54	SER	ALA	conflict	UNP Q93YN9
B	90	GLN	LYS	conflict	UNP Q93YN9
B	157	THR	SER	conflict	UNP Q93YN9
B	204	ILE	ASN	conflict	UNP Q93YN9
B	224	ARG	SER	conflict	UNP Q93YN9
B	321	CYS	SER	conflict	UNP Q93YN9
B	325	ILE	LEU	conflict	UNP Q93YN9
B	337	ARG	LYS	conflict	UNP Q93YN9

- Molecule 2 is INOSITOL HEXAKISPHOSPHATE (three-letter code: IHP) (formula: $C_6H_{18}O_{24}P_6$).

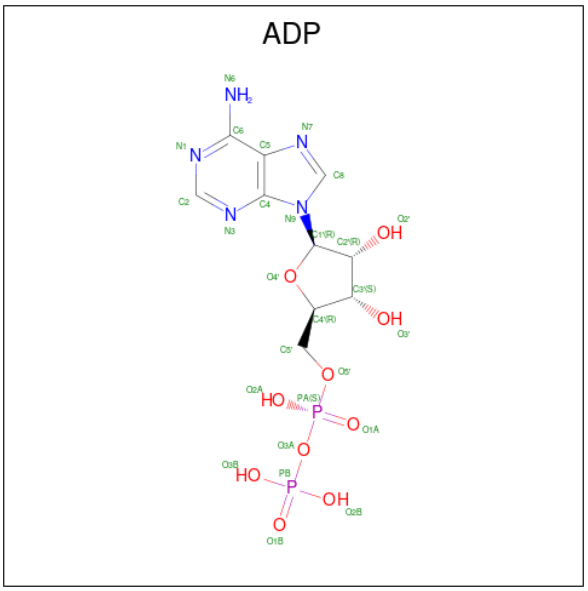


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O P 36 6 24 6	0	0
2	B	1	Total C O P 36 6 24 6	0	0

- Molecule 3 is LEAD (II) ION (three-letter code: PB) (formula: Pb).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Pb 2 2	0	0
3	B	2	Total Pb 2 2	0	0

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

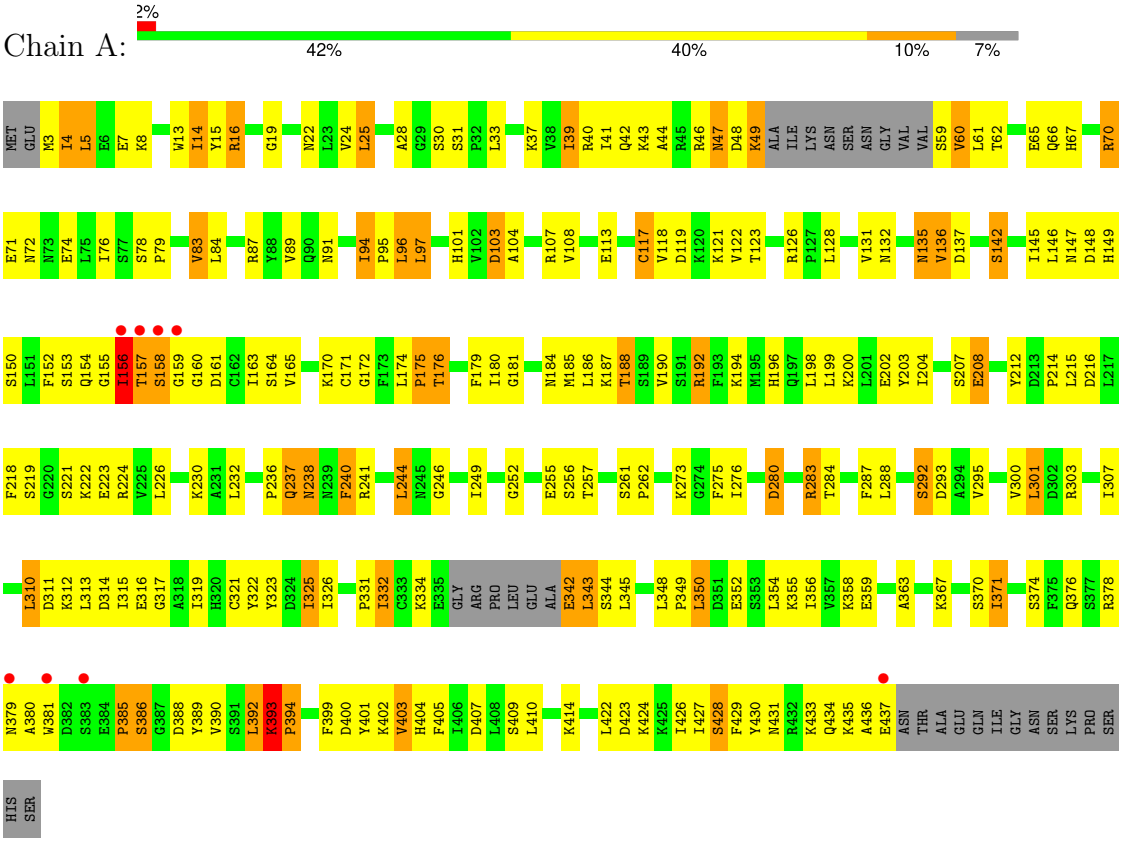
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		
5	B	1	Total	Zn	0	0
			1	1		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

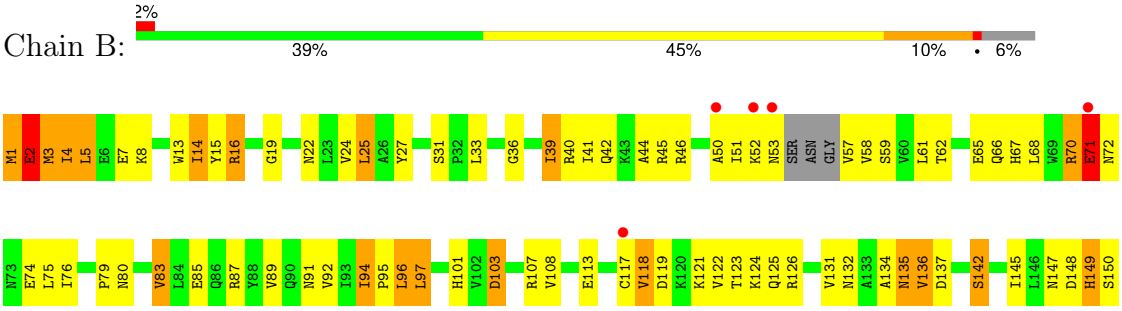
• Molecule 1: INOSITOL-PENTAKISPHOSPHATE 2-KINASE

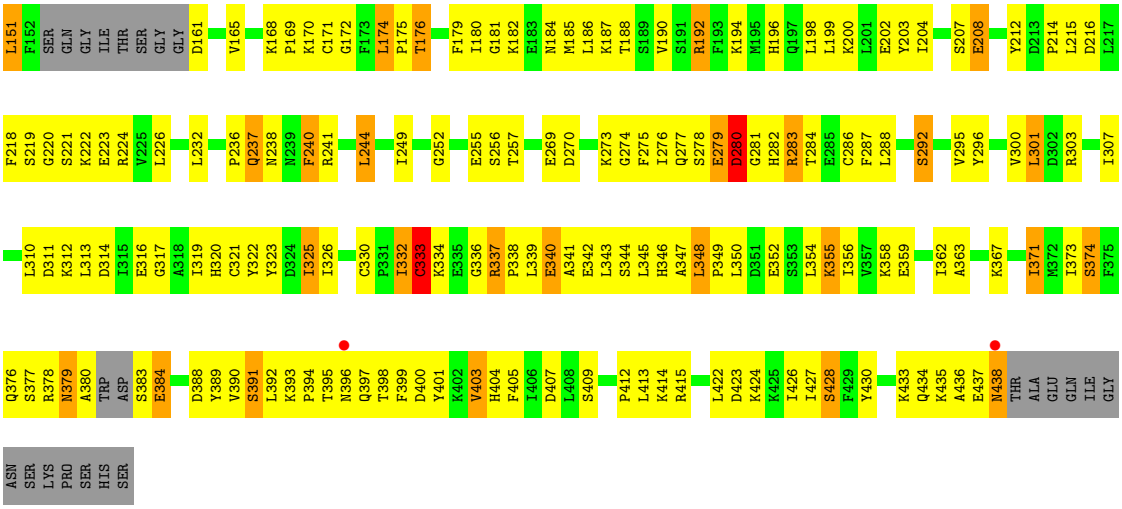
Chain A:



• Molecule 1: INOSITOL-PENTAKISPHOSPHATE 2-KINASE

Chain B:




L151 F152 SER GLN GLY ILE THR SER GLY GLY D161 V165 K168 P169 K170 C171 G172 F173 L174 P175 T176 F179 I180 G181 K182 E183 N184 M185 L186 K187 T188 S189 V190 S191 R192 F193 K194 M195 H196 Q197 L198 L199 K200 L201 E202 Y203 I204 S207 E208 Y212 D213 P214 L215 D216 L217
F218 S219 G220 S221 K222 E223 R224 V225 L226 L232 P236 Q237 N238 N239 F240 R241 L244 I249 G252 E255 S256 T257 E269 D270 K273 G274 F275 I276 Q277 S278 E279 D280 G281 H282 R283 T284 E285 C286 F287 L288 S292 V295 Y296 V300 L301 D302 R303 I307
L310 D311 K312 L313 D314 I315 E316 G317 A318 I319 H320 C321 Y322 Y323 D324 I325 I326 C330 P331 I332 G333 K334 E335 G336 R337 P338 L339 E340 A341 E342 L343 S344 L345 H346 A347 L348 P349 L350 D351 E352 S353 L354 K355 I356 V357 K358 E359 I362 A363 K367 I371 M372 I373 S374 F375
Q376 S377 R378 N379 A380 TRP ASP S383 E384 D388 Y389 V390 S391 L392 K393 P394 T395 N396 Q397 T398 F399 D400 Y401 K402 V403 H404 F405 I406 D407 L408 S409 P412 L413 K414 R415 L422 D423 K424 K425 I426 I427 S428 F429 Y430 K433 Q434 K435 A436 E437 N438 THR ALA GLU GLN ILE GLY
ASN SER LYS PRO SER HIS SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	58.06Å 110.97Å 138.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.71 – 3.20 86.65 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (86.71-3.20) 99.9 (86.65-3.20)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.11 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.210 , 0.268 0.214 , 0.274	Depositor DCC
R_{free} test set	768 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	42.9	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 44.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	6851	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.27% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, IHP, ADP, PB

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	0.56	0/3400	0.66	0/4584
1	B	0.56	0/3441	0.65	0/4637
All	All	0.56	0/6841	0.66	0/9221

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3338	0	3344	263	3
1	B	3381	0	3406	358	4
2	A	36	0	6	1	0
2	B	36	0	6	5	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	27	0	12	4	0
4	B	27	0	12	4	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
All	All	6851	0	6786	604	4

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 44.

The worst 5 of 604 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:ARG:HH12	1:B:182:LYS:CG	1.14	1.58
1:B:52:LYS:HA	1:B:57:VAL:O	1.20	1.38
1:B:280:ASP:HB2	1:B:282:HIS:CD2	1.56	1.38
1:A:46:ARG:NH1	1:B:182:LYS:CG	1.86	1.37
1:A:46:ARG:NH1	1:B:182:LYS:HG3	1.36	1.37

All (4) 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:A:312:LYS:NZ	1:B:202:GLU:CG[1_455]	1.84	0.36
1:B:124:LYS:NZ	1:B:273:LYS:O[4_556]	1.87	0.33
1:A:312:LYS:NZ	1:B:202:GLU:CD[1_455]	2.04	0.16
1:A:381:TRP:CE3	1:B:223:GLU:OE1[3_655]	2.15	0.05

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	414/451 (92%)	366 (88%)	34 (8%)	14 (3%)	3	24
1	B	417/451 (92%)	374 (90%)	31 (7%)	12 (3%)	4	28
All	All	831/902 (92%)	740 (89%)	65 (8%)	26 (3%)	4	26

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	156	ILE

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Mol	Chain	Res	Type
1	A	161	ASP
1	A	343	LEU
1	A	386	SER
1	A	393	LYS

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	374/399 (94%)	322 (86%)	52 (14%)	3 16
1	B	379/399 (95%)	319 (84%)	60 (16%)	2 12
All	All	753/798 (94%)	641 (85%)	112 (15%)	3 14

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	8	LYS
1	B	437	GLU
1	B	97	LEU
1	B	428	SER
1	B	348	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	91	ASN
1	B	282	HIS
1	B	397	GLN
1	B	376	GLN
1	B	196	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 6 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
2	IHP	A	500	3	36,36,36	0.73	0	60,60,60	1.36	10 (16%)
4	ADP	B	600	3	24,29,29	1.03	1 (4%)	29,45,45	1.64	6 (20%)
4	ADP	A	600	3	24,29,29	1.22	2 (8%)	29,45,45	1.43	4 (13%)
2	IHP	B	500	3	36,36,36	0.84	0	60,60,60	1.50	16 (26%)

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	IHP	A	500	3	-	7/30/54/54	0/1/1/1
4	ADP	B	600	3	-	4/12/32/32	0/3/3/3
4	ADP	A	600	3	-	0/12/32/32	0/3/3/3
2	IHP	B	500	3	-	10/30/54/54	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	600	ADP	PA-O3A	4.09	1.63	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	600	ADP	PA-O3A	2.90	1.62	1.59
4	A	600	ADP	C1'-N9	-2.01	1.45	1.49

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	600	ADP	O4'-C1'-N9	-4.30	103.05	108.75
4	A	600	ADP	N3-C2-N1	-3.94	123.33	128.67
4	B	600	ADP	N3-C2-N1	-3.47	123.97	128.67
2	B	500	IHP	P2-O12-C2	-3.26	114.73	123.43
4	A	600	ADP	C1'-N9-C4	-2.97	121.43	126.64

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500	IHP	C5-O15-P5-O25
2	A	500	IHP	C3-O13-P3-O23
2	B	500	IHP	C3-O13-P3-O23
4	B	600	ADP	C5'-O5'-PA-O1A
4	B	600	ADP	C5'-O5'-PA-O2A

There are no ring outliers.

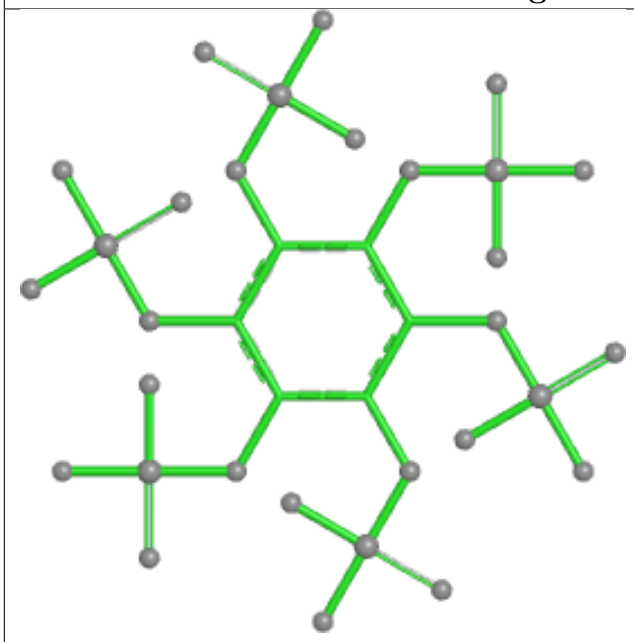
4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	IHP	1	0
4	B	600	ADP	4	0
4	A	600	ADP	4	0
2	B	500	IHP	5	0

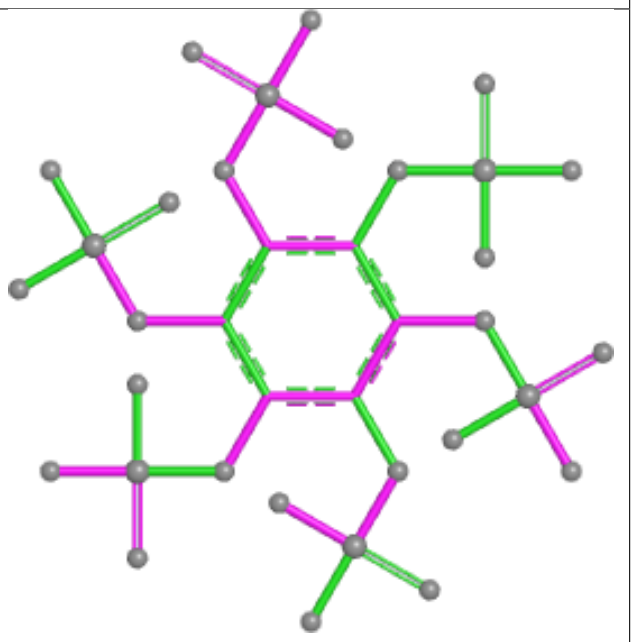
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.

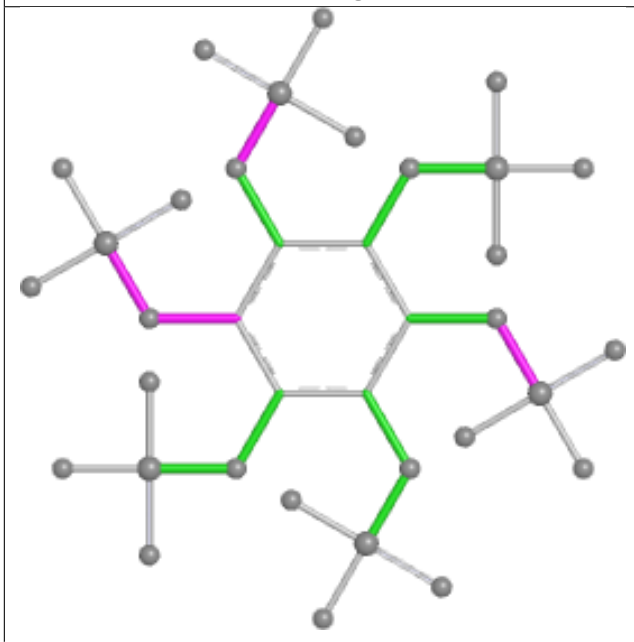
Ligand IHP A 500



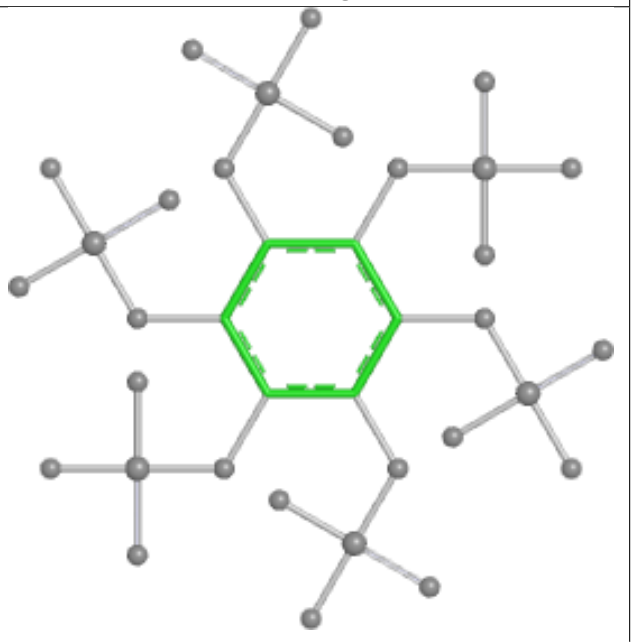
Bond lengths



Bond angles

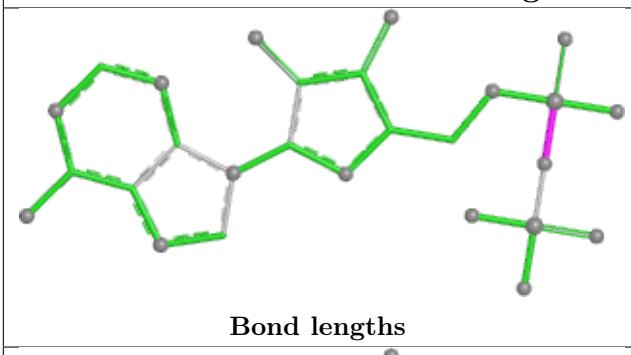


Torsions

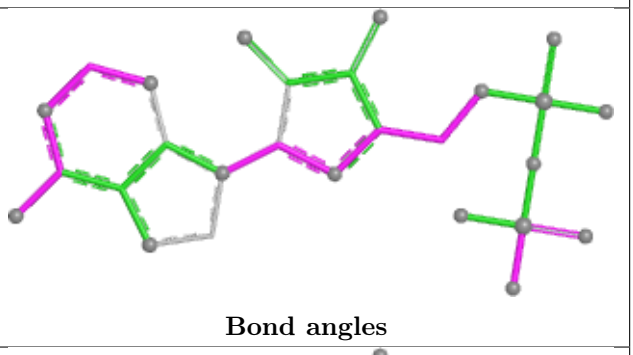


Rings

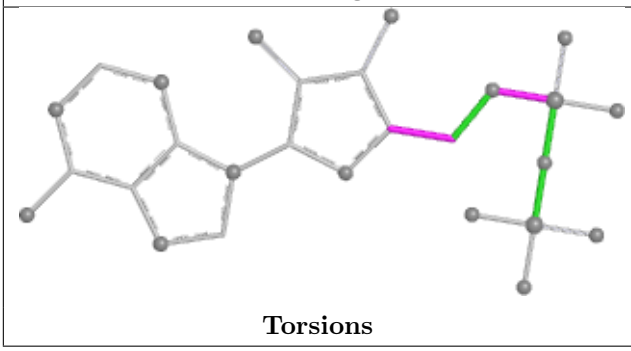
Ligand ADP B 600



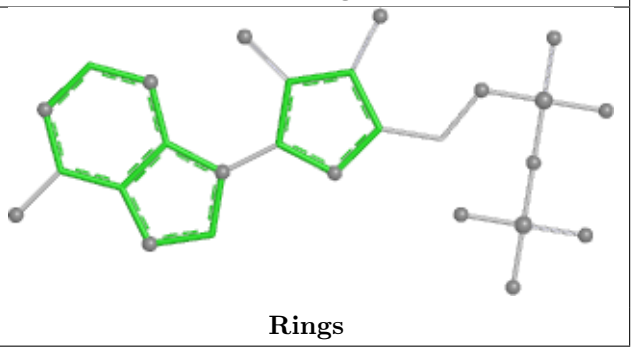
Bond lengths



Bond angles

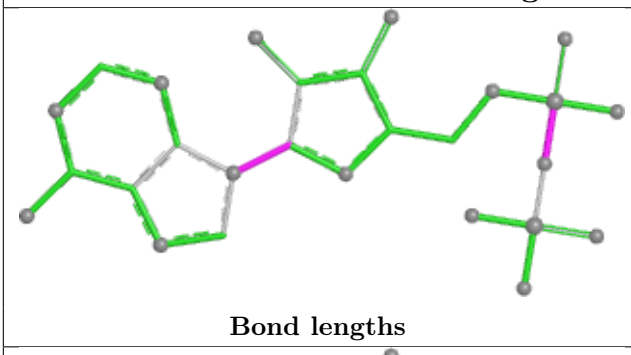


Torsions

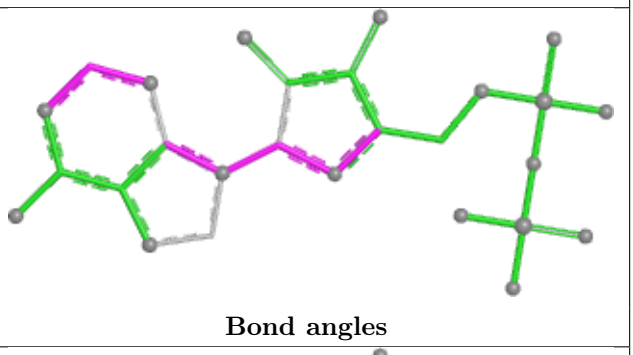


Rings

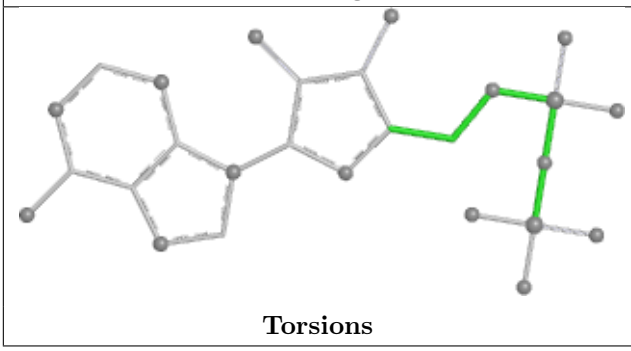
Ligand ADP A 600



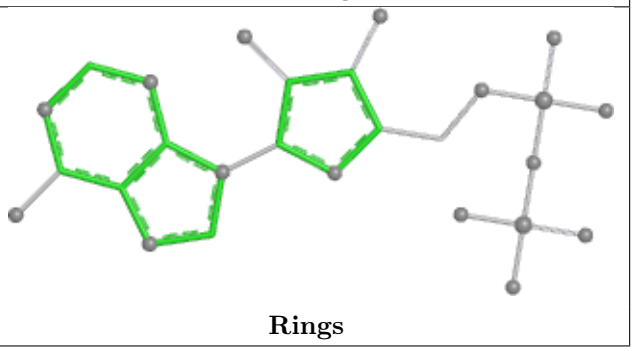
Bond lengths



Bond angles

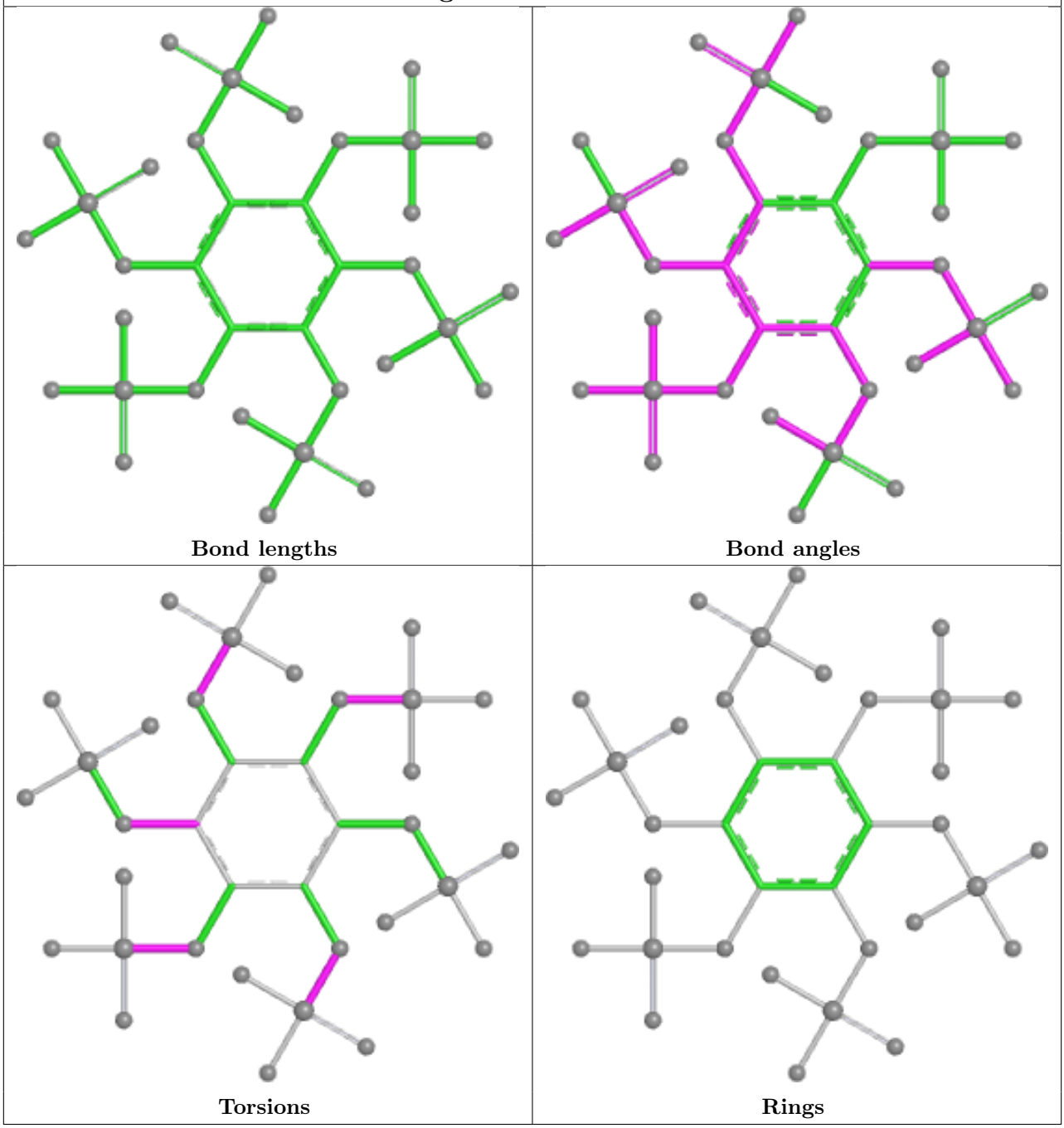


Torsions



Rings

Ligand IHP B 500



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^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	420/451 (93%)	-0.13	8 (1%)	66	53	9, 21, 41, 54	0
1	B	425/451 (94%)	0.02	7 (1%)	72	59	9, 20, 41, 62	0
All	All	845/902 (93%)	-0.05	15 (1%)	68	55	9, 21, 41, 62	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	GLY	3.1
1	A	383	SER	3.0
1	A	437	GLU	2.9
1	A	379	ASN	2.8
1	B	396	ASN	2.5

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

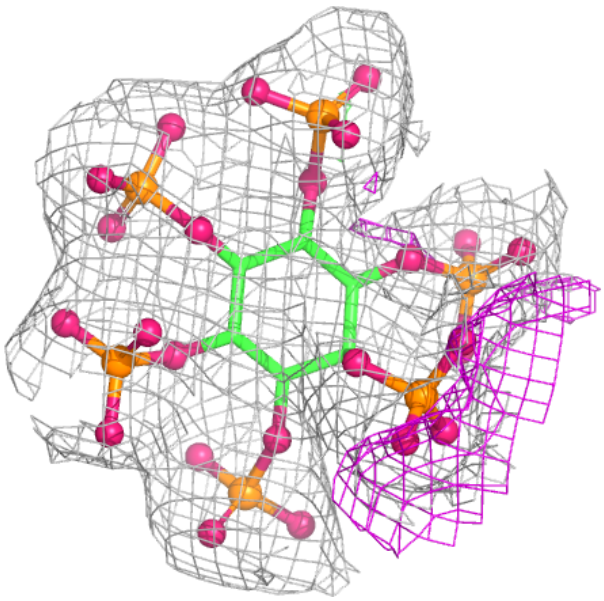
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

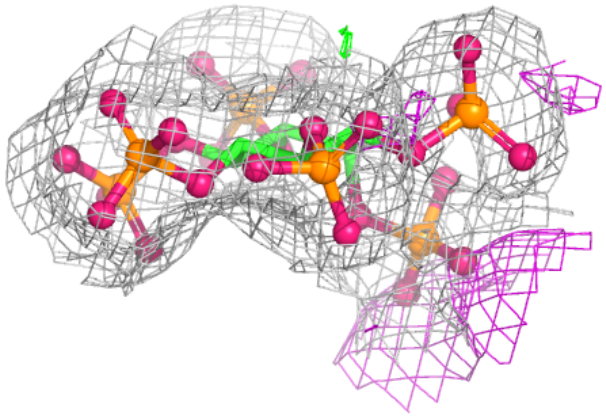
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	IHP	B	500	36/36	0.97	0.11	11,14,18,18	0
4	ADP	B	600	27/27	0.97	0.14	4,8,11,11	0
4	ADP	A	600	27/27	0.98	0.13	9,12,23,24	0
2	IHP	A	500	36/36	0.98	0.11	9,12,22,24	0
5	ZN	A	700	1/1	0.98	0.06	33,33,33,33	0
5	ZN	B	700	1/1	0.98	0.06	56,56,56,56	0
3	PB	A	502	1/1	0.99	0.02	20,20,20,20	0
3	PB	B	503	1/1	0.99	0.03	30,30,30,30	0
3	PB	A	501	1/1	0.99	0.04	27,27,27,27	0
3	PB	B	504	1/1	1.00	0.01	22,22,22,22	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 IHP B 500:

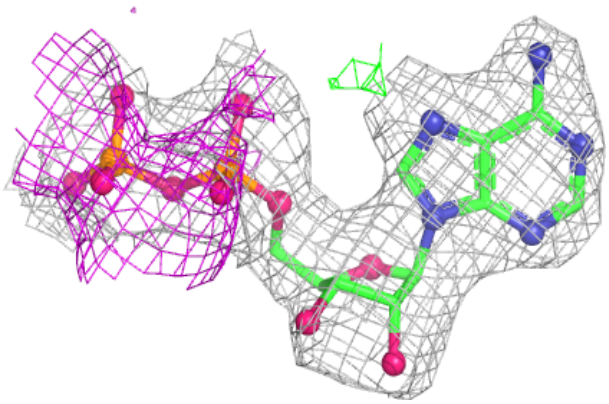
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

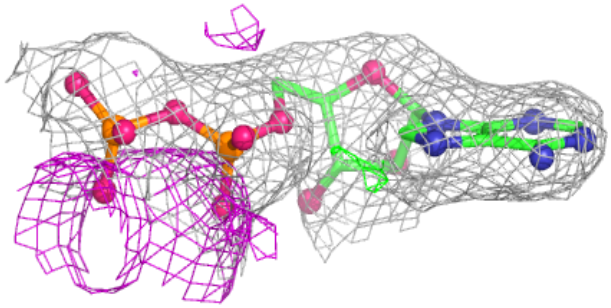


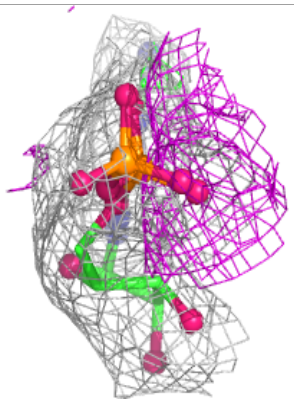


Electron density around ADP B 600:

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

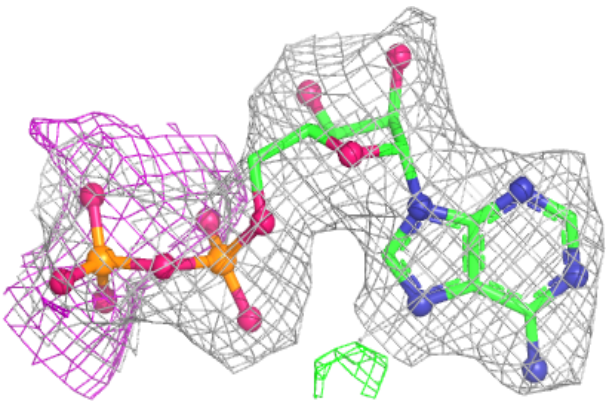


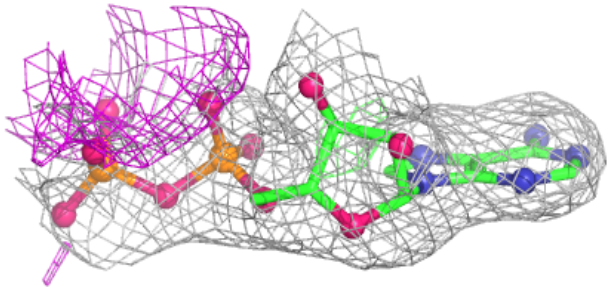


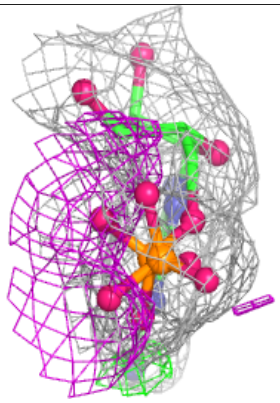


Electron density around ADP A 600:

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

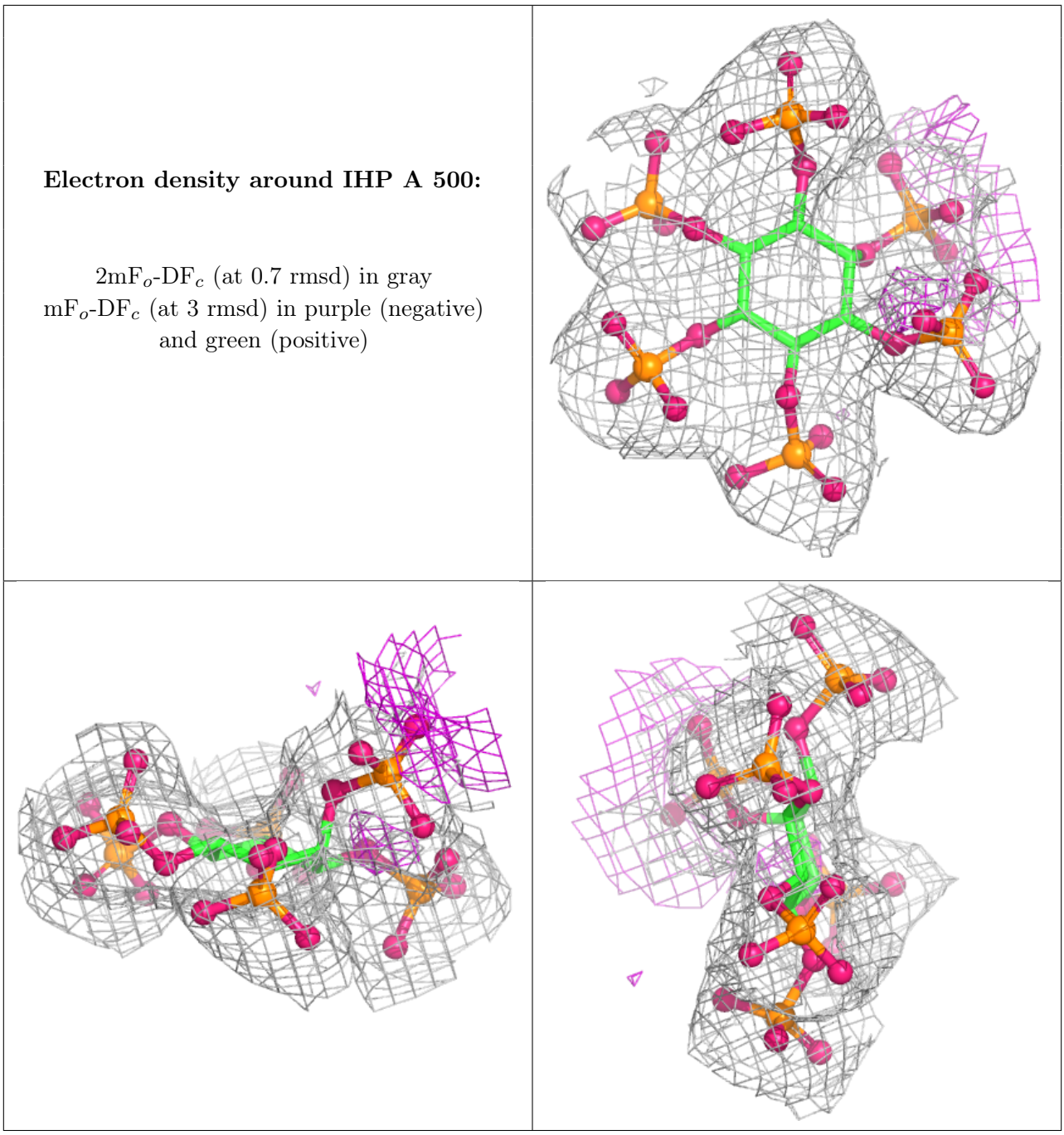






Electron density around IHP A 500:

$2mF_o$-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

There are no such residues in this entry.