Full wwPDB X-ray Structure Validation Report ⓘ

Jun 21, 2023 – 12:13 PM JST

PDB ID	:	8I1O
Title	:	Crystal structure of APSK2 domain from human PAPSS2 in complex with exogenous APS and ADP
Authors	:	Zhang, L.; Song, W.Y.; Zhang, L.
Deposited on	:	2023-01-13
Resolution	:	2.40 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*
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:

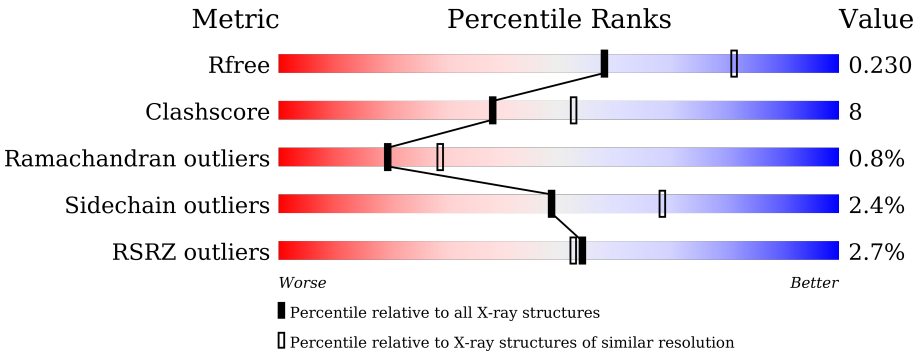
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.33
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 >=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	203	77% 17%
1	B	203	84% 12%
1	C	203	75% 19%
1	D	203	7% 77% 19%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ADX	A	302	X	-	-	-
3	ADX	B	302	X	-	-	-
3	ADX	C	302	X	-	-	-
3	ADX	D	302	X	-	-	-

2 Entry composition

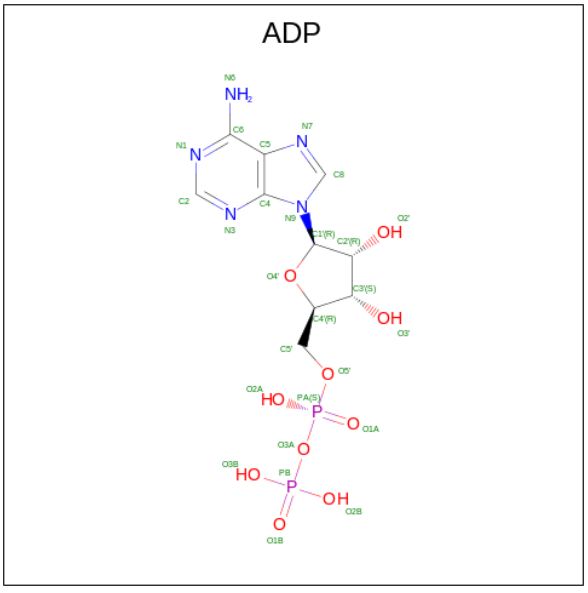
There are 4 unique types of molecules in this entry. The entry contains 6456 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	0	0	0
			1520	954	274	287	5			
1	B	195	Total	C	N	O	S	0	0	0
			1520	954	274	287	5			
1	C	196	Total	C	N	O	S	0	0	0
			1529	960	277	287	5			
1	D	195	Total	C	N	O	S	0	0	0
			1519	954	274	286	5			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

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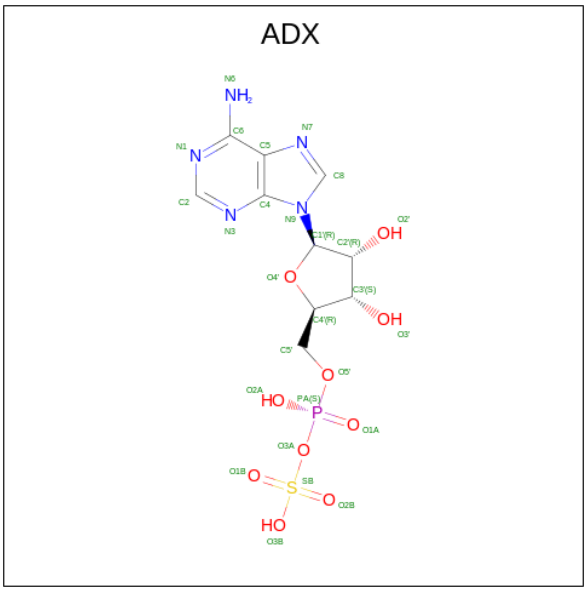
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is ADENOSINE-5'-PHOSPHOSULFATE (three-letter code: ADX) (formula: $C_{10}H_{14}N_5O_{10}PS$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			27	10	5	10	1	1		
3	B	1	Total	C	N	O	P	S	0	0
			27	10	5	10	1	1		
3	C	1	Total	C	N	O	P	S	0	0
			27	10	5	10	1	1		
3	D	1	Total	C	N	O	P	S	0	0
			27	10	5	10	1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	50	Total	O	0	0
			50	50		
4	B	42	Total	O	0	0
			42	42		

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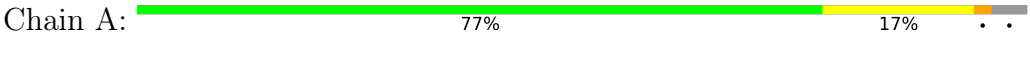
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	39	Total O 39 39	0	0
4	D	21	Total O 21 21	0	0

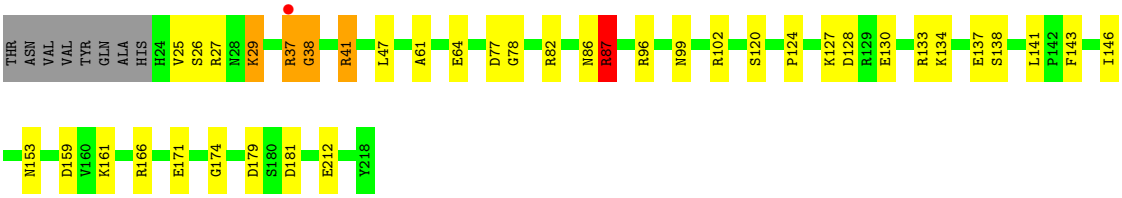
3 Residue-property plots (i)

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: Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2

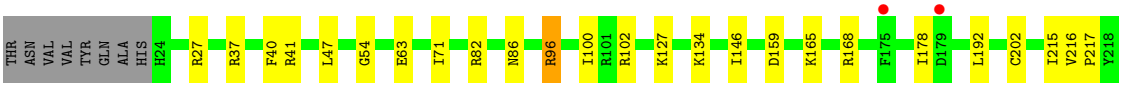
Chain A:





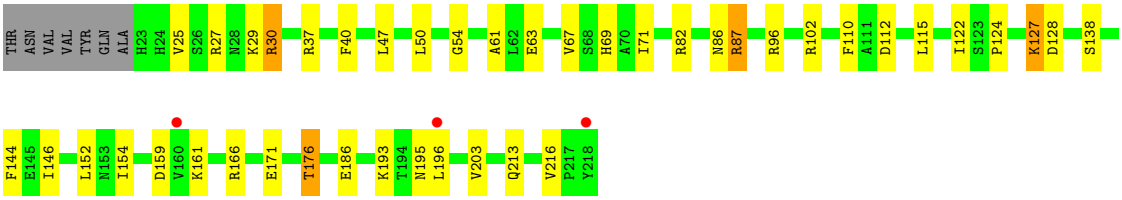
• Molecule 1: Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2

Chain B:



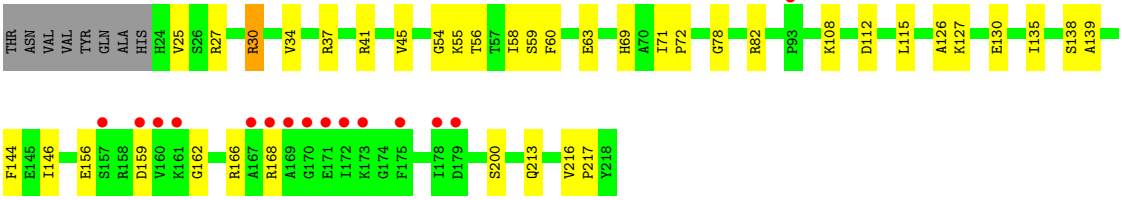
• Molecule 1: Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2

Chain C:



• Molecule 1: Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	64.72Å 53.03Å 130.64Å 90.00° 102.44° 90.00°	Depositor
Resolution (Å)	48.97 – 2.40 48.97 – 2.40	Depositor EDS
% Data completeness (in resolution range)	78.8 (48.97-2.40) 78.8 (48.97-2.40)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	10.07 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.20	Depositor
R, R_{free}	0.192 , 0.230 0.192 , 0.230	Depositor DCC
R_{free} test set	1385 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	37.0	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 37.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6456	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% 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: ADP, ADX

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	0.59	0/1549	0.91	5/2091 (0.2%)
1	B	0.64	0/1549	0.88	3/2091 (0.1%)
1	C	0.60	0/1559	0.83	0/2106
1	D	0.59	0/1548	0.83	0/2091
All	All	0.61	0/6205	0.86	8/8379 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	96	ARG	NE-CZ-NH2	-9.45	115.58	120.30
1	A	87	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	A	87	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	B	96	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	A	181	ASP	CB-CG-OD1	6.18	123.86	118.30
1	B	96	ARG	CD-NE-CZ	5.95	131.93	123.60
1	A	29	LYS	CD-CE-NZ	5.85	125.16	111.70
1	A	181	ASP	CB-CG-OD2	-5.08	113.73	118.30

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	1520	0	1507	25	0
1	B	1520	0	1507	17	0
1	C	1529	0	1514	30	1
1	D	1519	0	1507	25	0
2	A	27	0	12	0	0
2	B	27	0	12	1	0
2	C	27	0	12	1	0
2	D	27	0	12	1	0
3	A	27	0	10	1	0
3	B	27	0	10	3	0
3	C	27	0	10	4	0
3	D	27	0	10	0	0
4	A	50	0	0	2	0
4	B	42	0	0	0	0
4	C	39	0	0	2	0
4	D	21	0	0	0	0
All	All	6456	0	6123	94	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.

All (94) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:ARG:NH2	1:C:176:THR:HG22	1.98	0.79
1:A:26:SER:OG	1:A:29:LYS:HG2	1.83	0.78
1:C:37:ARG:NH1	1:C:69:HIS:O	2.17	0.78
1:A:27:ARG:NH1	1:A:141:LEU:HD21	1.99	0.77
1:A:166:ARG:NH1	1:A:171:GLU:OE1	2.24	0.70
1:A:174:GLY:N	1:A:179:ASP:OD1	2.25	0.70
1:A:127:LYS:HE2	1:A:128:ASP:OD1	1.93	0.69
1:D:27:ARG:NH2	1:D:139:ALA:O	2.26	0.67
1:A:212:GLU:OE1	4:A:401:HOH:O	2.14	0.66
1:C:71:ILE:HD13	1:C:216:VAL:HG22	1.78	0.65
1:B:96:ARG:NH1	3:B:302:ADX:O2B	2.31	0.64
1:A:38:GLY:O	1:A:41:ARG:NH2	2.33	0.62
1:B:37:ARG:O	1:B:41:ARG:NH1	2.32	0.62
1:D:45:VAL:HG13	1:D:146:ILE:CD1	2.30	0.62
1:C:27:ARG:HD2	1:C:40:PHE:CZ	2.35	0.61
1:B:37:ARG:NH2	1:B:217:PRO:HG2	2.17	0.60
1:D:162:GLY:O	1:D:166:ARG:HG3	2.00	0.60
1:D:37:ARG:NH2	1:D:69:HIS:O	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:ARG:NH2	3:B:302:ADX:N1	2.51	0.57
1:B:96:ARG:HH22	3:B:302:ADX:C2	2.18	0.57
1:C:50:LEU:HD13	1:C:152:LEU:HD23	1.85	0.57
1:D:126:ALA:O	1:D:130:GLU:HG3	2.04	0.57
1:C:63:GLU:HG2	1:D:25:VAL:HG13	1.87	0.56
1:D:126:ALA:HB3	1:D:127:LYS:NZ	2.20	0.56
1:D:37:ARG:NH1	1:D:217:PRO:HG2	2.21	0.56
1:A:37:ARG:HD2	1:A:37:ARG:H	1.69	0.56
1:C:47:LEU:HD23	1:C:146:ILE:HB	1.88	0.55
1:C:176:THR:CG2	3:C:302:ADX:H2	2.36	0.55
1:A:130:GLU:O	1:A:134:LYS:HG3	2.06	0.55
1:A:137:GLU:OE2	4:A:402:HOH:O	2.18	0.54
1:D:25:VAL:O	1:D:30:ARG:NH2	2.41	0.54
1:B:168:ARG:CZ	1:B:178:ILE:HD12	2.38	0.53
1:C:67:VAL:HG21	1:D:25:VAL:HG21	1.89	0.53
1:C:110:PHE:HD2	1:C:115:LEU:HD12	1.74	0.53
1:C:27:ARG:HA	1:C:30:ARG:HG3	1.91	0.53
1:A:47:LEU:HD23	1:A:146:ILE:HB	1.91	0.52
1:D:30:ARG:O	1:D:34:VAL:HG23	2.09	0.52
1:D:126:ALA:HB3	1:D:127:LYS:HZ3	1.75	0.52
1:D:45:VAL:HG13	1:D:146:ILE:HD12	1.93	0.51
1:C:176:THR:HG23	3:C:302:ADX:H2	1.93	0.51
1:C:166:ARG:HG2	1:C:171:GLU:HB2	1.93	0.51
1:C:25:VAL:HG13	1:C:29:LYS:HD3	1.92	0.51
1:B:71:ILE:HD13	1:B:216:VAL:HG22	1.94	0.50
1:C:87:ARG:NH2	4:C:401:HOH:O	2.30	0.50
1:C:176:THR:HB	4:C:405:HOH:O	2.12	0.49
1:D:156:GLU:OE2	1:D:168:ARG:HD2	2.13	0.49
1:D:78:GLY:O	1:D:82:ARG:HB2	2.13	0.48
1:B:47:LEU:HD23	1:B:146:ILE:HB	1.95	0.48
1:C:86:ASN:OD1	1:C:102:ARG:HD2	2.14	0.48
1:D:71:ILE:HD13	1:D:216:VAL:HG22	1.95	0.47
1:B:41:ARG:HD3	1:B:215:ILE:O	2.14	0.47
1:B:27:ARG:HG3	1:B:40:PHE:CE1	2.50	0.47
1:C:144:PHE:CE1	1:C:213:GLN:HG3	2.50	0.47
1:A:61:ALA:HA	1:A:64:GLU:HG2	1.96	0.47
1:D:27:ARG:HD2	1:D:112:ASP:OD1	2.15	0.47
1:A:133:ARG:HB2	1:A:143:PHE:CD1	2.50	0.47
1:A:127:LYS:HG3	1:A:128:ASP:N	2.29	0.46
1:D:59:SER:O	1:D:63:GLU:HG2	2.16	0.45
1:A:161:LYS:HE2	3:A:302:ADX:O3'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:56:THR:HG23	2:D:301:ADP:O1B	2.17	0.45
1:C:154:ILE:HG21	1:C:195:ASN:OD1	2.16	0.45
1:A:37:ARG:HD2	1:A:37:ARG:N	2.31	0.45
1:D:72:PRO:HB2	1:D:115:LEU:HD22	1.99	0.45
1:A:86:ASN:OD1	1:A:102:ARG:HD2	2.15	0.45
1:C:186:GLU:HA	1:C:186:GLU:OE2	2.17	0.45
1:C:54:GLY:HA2	2:C:301:ADP:H5'1	1.99	0.45
1:C:127:LYS:HG2	1:C:128:ASP:N	2.31	0.45
1:A:82:ARG:O	1:A:87:ARG:HA	2.18	0.44
1:A:82:ARG:HH21	1:A:99:ASN:ND2	2.15	0.44
1:B:134:LYS:HD2	1:B:134:LYS:HA	1.87	0.44
1:C:122:ILE:CD1	3:C:302:ADX:H5'	2.47	0.44
1:C:193:LYS:HD3	1:C:196:LEU:HD12	1.99	0.44
1:C:82:ARG:O	1:C:87:ARG:HA	2.17	0.44
1:C:27:ARG:HD3	1:C:112:ASP:OD1	2.17	0.44
1:C:124:PRO:HD3	3:C:302:ADX:O1B	2.17	0.44
1:A:78:GLY:O	1:A:82:ARG:HB2	2.18	0.43
1:D:54:GLY:O	1:D:58:ILE:HG12	2.18	0.43
1:A:77:ASP:HB3	1:A:120:SER:OG	2.18	0.43
1:C:25:VAL:CG1	1:C:29:LYS:HB3	2.48	0.43
1:D:60:PHE:HA	1:D:63:GLU:HG2	2.01	0.43
1:D:108:LYS:HD2	1:D:135:ILE:HG22	2.01	0.43
1:D:55:LYS:HB2	1:D:55:LYS:HE2	1.79	0.42
1:D:144:PHE:CE1	1:D:213:GLN:HG3	2.54	0.42
1:B:86:ASN:OD1	1:B:102:ARG:HD2	2.20	0.42
1:B:100:ILE:HD13	1:B:100:ILE:HA	1.85	0.42
1:B:192:LEU:HD13	1:B:202:CYS:HB3	2.02	0.42
1:B:41:ARG:CD	1:B:215:ILE:O	2.68	0.42
1:A:82:ARG:HD3	1:A:82:ARG:HA	1.66	0.41
1:C:61:ALA:HB3	1:C:203:VAL:HG21	2.03	0.41
1:B:54:GLY:HA2	2:B:301:ADP:H5'1	2.02	0.41
1:A:25:VAL:HG22	1:B:63:GLU:OE1	2.21	0.41
1:A:96:ARG:HD3	1:A:124:PRO:HG3	2.02	0.40
1:C:96:ARG:HH21	1:C:176:THR:HG22	1.85	0.40
1:A:161:LYS:HB2	1:A:161:LYS:HZ3	1.87	0.40

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:C:29:LYS:NZ	1:C:138:SER:OG[2_444]	2.17	0.03

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	193/203 (95%)	184 (95%)	6 (3%)	3 (2%)	9 13
1	B	193/203 (95%)	187 (97%)	5 (3%)	1 (0%)	29 41
1	C	194/203 (96%)	186 (96%)	7 (4%)	1 (0%)	29 41
1	D	193/203 (95%)	188 (97%)	4 (2%)	1 (0%)	29 41
All	All	773/812 (95%)	745 (96%)	22 (3%)	6 (1%)	19 29

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	37	ARG
1	A	38	GLY
1	A	159	ASP
1	C	159	ASP
1	B	159	ASP
1	D	159	ASP

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	164/171 (96%)	160 (98%)	4 (2%)	49 68
1	B	164/171 (96%)	161 (98%)	3 (2%)	59 76
1	C	165/171 (96%)	160 (97%)	5 (3%)	41 61
1	D	164/171 (96%)	160 (98%)	4 (2%)	49 68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	657/684 (96%)	641 (98%)	16 (2%)	49 68

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ARG
1	A	87	ARG
1	A	138	SER
1	A	153	ASN
1	B	82	ARG
1	B	127	LYS
1	B	165	LYS
1	C	30	ARG
1	C	87	ARG
1	C	127	LYS
1	C	161	LYS
1	C	176	THR
1	D	30	ARG
1	D	41	ARG
1	D	138	SER
1	D	200	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	B	32	GLN
1	D	32	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	ADX	B	302	-	25,29,29	3.56	10 (40%)	26,45,45	3.41	13 (50%)
3	ADX	C	302	-	25,29,29	3.39	8 (32%)	26,45,45	2.84	10 (38%)
2	ADP	D	301	-	24,29,29	0.91	1 (4%)	29,45,45	1.36	5 (17%)
2	ADP	B	301	-	24,29,29	0.94	1 (4%)	29,45,45	1.30	4 (13%)
2	ADP	A	301	-	24,29,29	1.03	2 (8%)	29,45,45	1.33	3 (10%)
3	ADX	A	302	-	25,29,29	3.77	9 (36%)	26,45,45	2.35	8 (30%)
3	ADX	D	302	-	25,29,29	3.46	10 (40%)	26,45,45	2.92	9 (34%)
2	ADP	C	301	-	24,29,29	0.92	1 (4%)	29,45,45	1.47	6 (20%)

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	ADX	B	302	-	2/2/6/6	3/6/32/32	0/3/3/3
3	ADX	C	302	-	2/2/6/6	2/6/32/32	0/3/3/3
2	ADP	B	301	-	-	3/12/32/32	0/3/3/3
2	ADP	D	301	-	-	1/12/32/32	0/3/3/3
2	ADP	A	301	-	-	4/12/32/32	0/3/3/3
3	ADX	A	302	-	2/2/6/6	0/6/32/32	0/3/3/3
2	ADP	C	301	-	-	2/12/32/32	0/3/3/3
3	ADX	D	302	-	2/2/6/6	3/6/32/32	0/3/3/3

All (42) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	302	ADX	C2'-C1'	-13.13	1.33	1.53
3	A	302	ADX	C2'-C1'	-12.58	1.34	1.53
3	D	302	ADX	C2'-C1'	-12.55	1.34	1.53
3	C	302	ADX	C2'-C1'	-12.34	1.35	1.53
3	A	302	ADX	PA-O3A	8.64	1.66	1.59
3	D	302	ADX	PA-O3A	6.18	1.64	1.59
3	B	302	ADX	PA-O3A	6.17	1.64	1.59
3	A	302	ADX	C2'-C3'	-5.94	1.37	1.53
3	C	302	ADX	C2'-C3'	-5.75	1.37	1.53
3	C	302	ADX	C2-N3	5.21	1.40	1.32
3	A	302	ADX	C2-N3	5.14	1.40	1.32
3	D	302	ADX	C2-N3	5.03	1.40	1.32
3	B	302	ADX	C2'-C3'	-4.61	1.40	1.53
3	C	302	ADX	PA-O3A	4.41	1.62	1.59
3	B	302	ADX	C2-N3	4.29	1.39	1.32
3	D	302	ADX	C2'-C3'	-4.16	1.42	1.53
3	A	302	ADX	O4'-C1'	-3.93	1.35	1.41
3	C	302	ADX	O2'-C2'	-3.75	1.34	1.43
3	D	302	ADX	O4'-C1'	-3.74	1.35	1.41
3	B	302	ADX	O2'-C2'	-3.41	1.34	1.43
3	B	302	ADX	O4'-C1'	-3.25	1.36	1.41
3	A	302	ADX	O2'-C2'	-3.18	1.35	1.43
3	A	302	ADX	C2-N1	3.10	1.39	1.33
3	D	302	ADX	C2-N1	3.06	1.39	1.33
3	C	302	ADX	C2-N1	3.01	1.39	1.33
3	B	302	ADX	O4'-C4'	-2.99	1.38	1.45
3	B	302	ADX	C2-N1	2.98	1.39	1.33
3	D	302	ADX	O2'-C2'	-2.96	1.36	1.43
3	C	302	ADX	O4'-C1'	-2.84	1.37	1.41
3	D	302	ADX	C5-C4	-2.65	1.33	1.40
3	B	302	ADX	C5-C4	-2.41	1.34	1.40
2	A	301	ADP	C5-C4	2.35	1.47	1.40
3	A	302	ADX	C5-C4	-2.34	1.34	1.40
3	B	302	ADX	O1B-SB	2.32	1.55	1.45
2	B	301	ADP	C5-C4	2.31	1.47	1.40
2	D	301	ADP	C5-C4	2.24	1.46	1.40
2	C	301	ADP	C5-C4	2.21	1.46	1.40
3	D	302	ADX	C6-C5	-2.18	1.35	1.43
2	A	301	ADP	O4'-C1'	2.17	1.44	1.41
3	C	302	ADX	C5-C4	-2.15	1.35	1.40
3	D	302	ADX	O1B-SB	2.09	1.54	1.45
3	A	302	ADX	C6-C5	-2.01	1.35	1.43

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	302	ADX	N3-C2-N1	-7.32	117.23	128.68
3	B	302	ADX	O5'-PA-O3A	-7.29	81.69	102.98
3	B	302	ADX	C1'-N9-C4	-7.26	113.88	126.64
3	B	302	ADX	N3-C2-N1	-6.64	118.30	128.68
3	A	302	ADX	N3-C2-N1	-6.50	118.52	128.68
3	C	302	ADX	C1'-N9-C4	-6.46	115.28	126.64
3	C	302	ADX	N3-C2-N1	-6.22	118.95	128.68
3	C	302	ADX	C3'-C2'-C1'	5.96	109.95	100.98
3	B	302	ADX	O5'-PA-O1A	-5.69	86.82	109.07
3	D	302	ADX	C1'-N9-C4	-5.37	117.20	126.64
3	A	302	ADX	O2'-C2'-C1'	5.36	130.66	110.85
3	D	302	ADX	O2'-C2'-C3'	5.28	128.90	111.82
3	C	302	ADX	O2'-C2'-C1'	5.23	130.16	110.85
3	D	302	ADX	O2'-C2'-C1'	4.89	128.92	110.85
3	B	302	ADX	O2'-C2'-C3'	4.77	127.25	111.82
3	D	302	ADX	C2'-C3'-C4'	-4.73	93.45	102.64
3	B	302	ADX	O2'-C2'-C1'	4.68	128.15	110.85
3	C	302	ADX	O4'-C1'-C2'	4.45	113.43	106.93
3	D	302	ADX	O4'-C1'-C2'	4.32	113.24	106.93
3	D	302	ADX	O4'-C4'-C3'	-4.29	96.63	105.11
3	A	302	ADX	O4'-C1'-C2'	4.23	113.11	106.93
3	B	302	ADX	O4'-C1'-C2'	4.21	113.07	106.93
3	A	302	ADX	C3'-C2'-C1'	4.07	107.11	100.98
2	A	301	ADP	N3-C2-N1	-4.00	122.42	128.68
2	D	301	ADP	N3-C2-N1	-3.77	122.78	128.68
3	C	302	ADX	C4-C5-N7	-3.75	105.49	109.40
3	B	302	ADX	O2A-PA-O5'	-3.61	90.96	107.75
3	B	302	ADX	C4-C5-N7	-3.61	105.64	109.40
2	C	301	ADP	N3-C2-N1	-3.31	123.50	128.68
3	A	302	ADX	O2'-C2'-C3'	3.14	121.98	111.82
2	C	301	ADP	PA-O3A-PB	-3.09	122.23	132.83
3	D	302	ADX	C5-C6-N6	-3.06	115.70	120.35
3	B	302	ADX	O4'-C4'-C5'	-2.99	99.52	109.37
3	A	302	ADX	C4-C5-N7	-2.96	106.32	109.40
2	B	301	ADP	N3-C2-N1	-2.94	124.08	128.68
2	C	301	ADP	C3'-C2'-C1'	2.64	104.95	100.98
2	B	301	ADP	C4-C5-N7	-2.50	106.80	109.40
3	C	302	ADX	O2'-C2'-C3'	2.48	119.83	111.82
2	B	301	ADP	O4'-C1'-C2'	-2.46	103.33	106.93
3	B	302	ADX	C3'-C2'-C1'	2.37	104.55	100.98
2	C	301	ADP	O4'-C1'-C2'	-2.37	103.46	106.93
2	C	301	ADP	O3B-PB-O2B	2.36	116.64	107.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	301	ADP	O3B-PB-O2B	2.35	116.60	107.64
2	A	301	ADP	C4-C5-N7	-2.34	106.96	109.40
3	B	302	ADX	O2A-PA-O1A	2.32	123.69	112.24
3	B	302	ADX	O4'-C4'-C3'	-2.30	100.56	105.11
2	D	301	ADP	N6-C6-N1	2.26	123.27	118.57
2	D	301	ADP	C5'-C4'-C3'	-2.26	106.72	115.18
2	D	301	ADP	C2-N1-C6	2.23	122.57	118.75
3	C	302	ADX	O5'-PA-O1A	2.21	117.70	109.07
3	A	302	ADX	O3'-C3'-C2'	-2.21	104.69	111.82
3	C	302	ADX	O2A-PA-O5'	-2.18	97.61	107.75
2	A	301	ADP	C2-N1-C6	2.17	122.47	118.75
3	A	302	ADX	O4'-C4'-C3'	-2.16	100.84	105.11
3	C	302	ADX	PA-O5'-C5'	-2.06	109.61	121.68
2	C	301	ADP	O3A-PB-O1B	-2.03	99.93	111.19
2	B	301	ADP	PA-O3A-PB	-2.01	125.93	132.83
3	D	302	ADX	O5'-C5'-C4'	-2.00	102.10	108.99

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	302	ADX	C1'
3	A	302	ADX	C2'
3	B	302	ADX	C1'
3	B	302	ADX	C2'
3	C	302	ADX	C1'
3	C	302	ADX	C2'
3	D	302	ADX	C1'
3	D	302	ADX	C2'

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	ADX	C5'-O5'-PA-O3A
3	C	302	ADX	O4'-C4'-C5'-O5'
3	C	302	ADX	C3'-C4'-C5'-O5'
3	D	302	ADX	C5'-O5'-PA-O1A
3	D	302	ADX	C5'-O5'-PA-O3A
2	A	301	ADP	O4'-C4'-C5'-O5'
3	B	302	ADX	C3'-C4'-C5'-O5'
2	A	301	ADP	C3'-C4'-C5'-O5'
2	B	301	ADP	PA-O3A-PB-O1B
2	B	301	ADP	PA-O3A-PB-O2B

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Mol	Chain	Res	Type	Atoms
3	B	302	ADX	C5'-O5'-PA-O1A
3	D	302	ADX	C5'-O5'-PA-O2A
2	B	301	ADP	O4'-C4'-C5'-O5'
2	C	301	ADP	PA-O3A-PB-O1B
2	A	301	ADP	PA-O3A-PB-O2B
2	C	301	ADP	O4'-C4'-C5'-O5'
2	D	301	ADP	O4'-C4'-C5'-O5'
2	A	301	ADP	C5'-O5'-PA-O1A

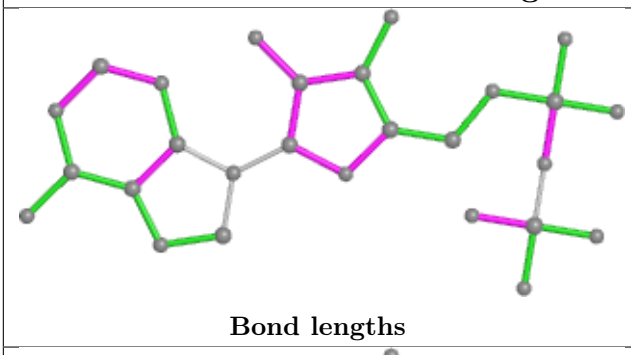
There are no ring outliers.

6 monomers are involved in 11 short contacts:

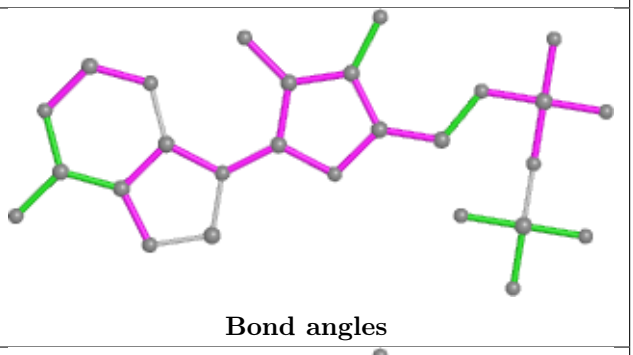
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	302	ADX	3	0
3	C	302	ADX	4	0
2	D	301	ADP	1	0
2	B	301	ADP	1	0
3	A	302	ADX	1	0
2	C	301	ADP	1	0

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 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.

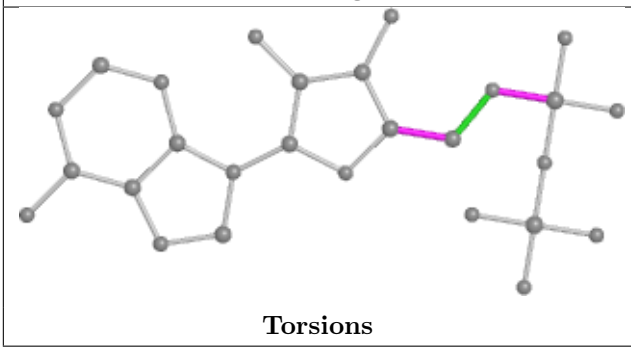
Ligand ADX B 302



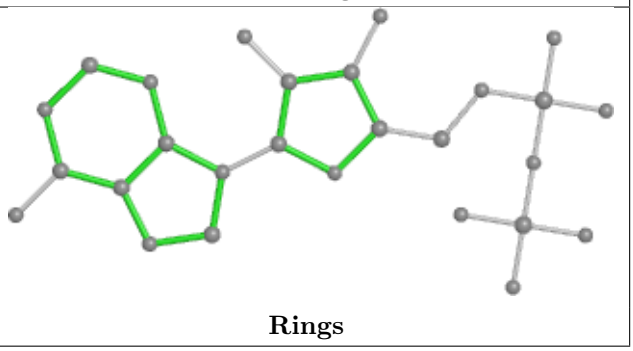
Bond lengths



Bond angles

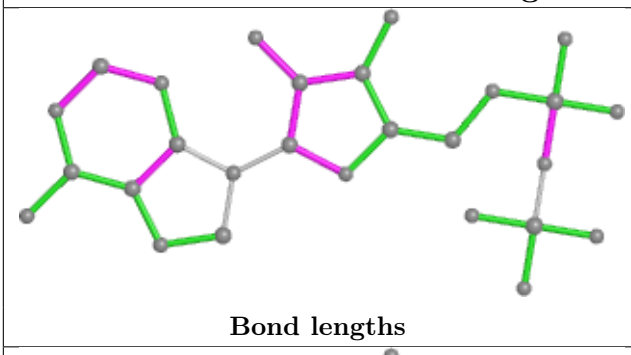


Torsions



Rings

Ligand ADX C 302



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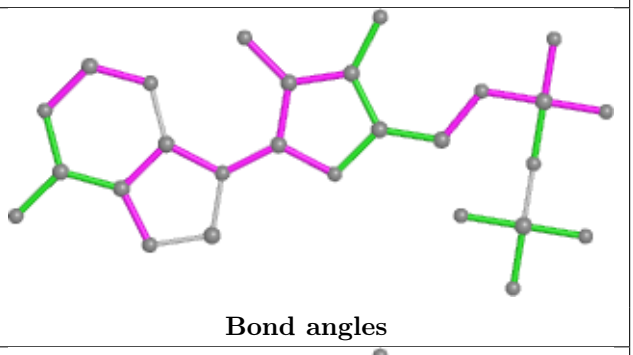
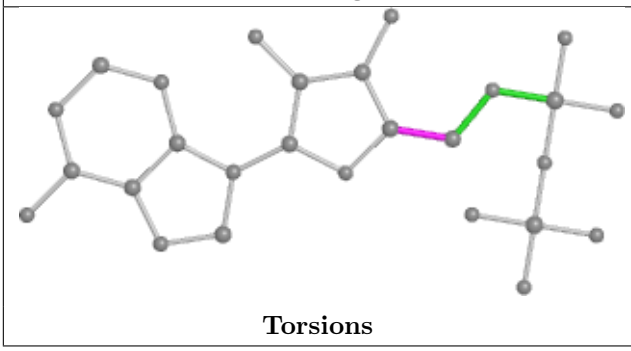


Bond angles



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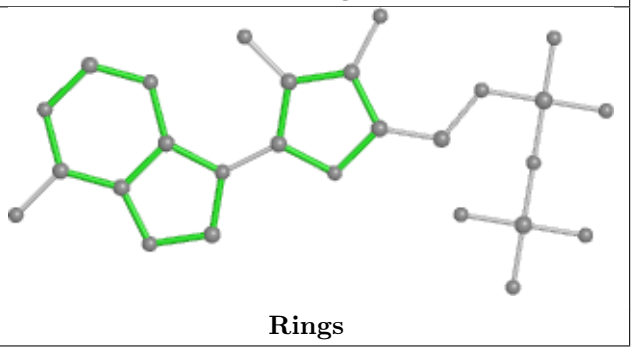
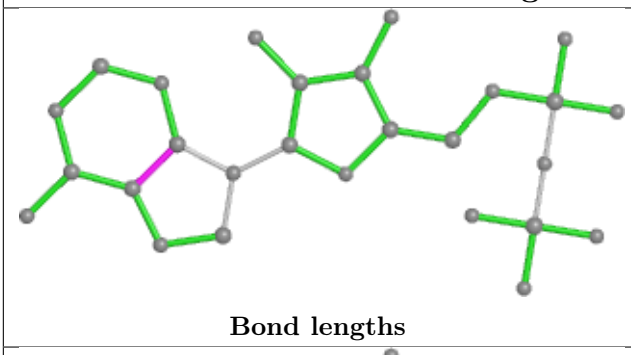
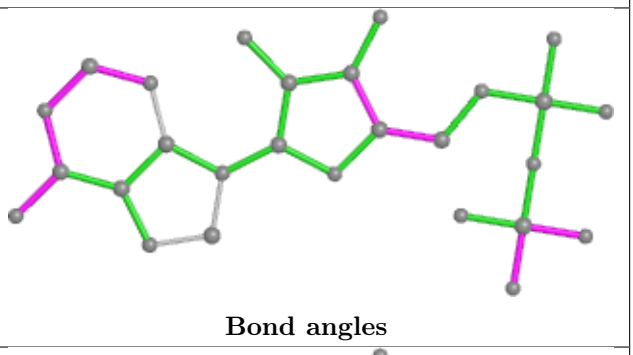


Rings

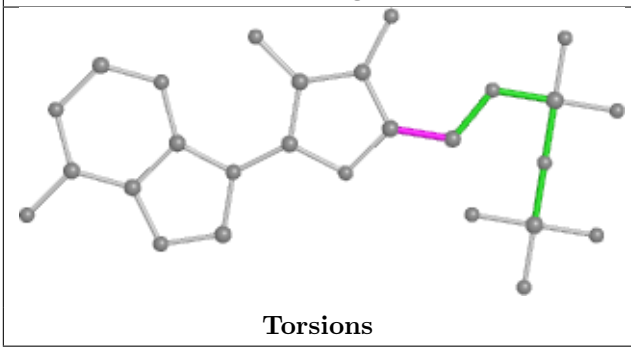
Ligand ADP D 301



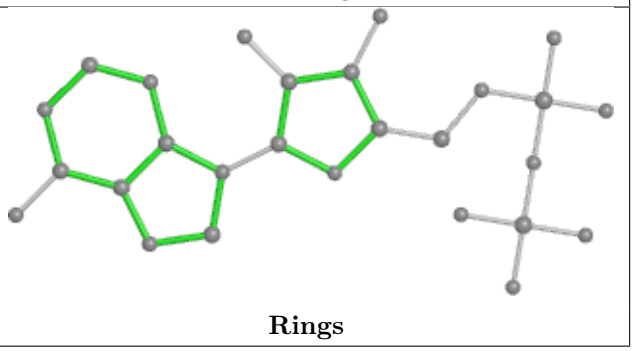
Bond lengths



Bond angles

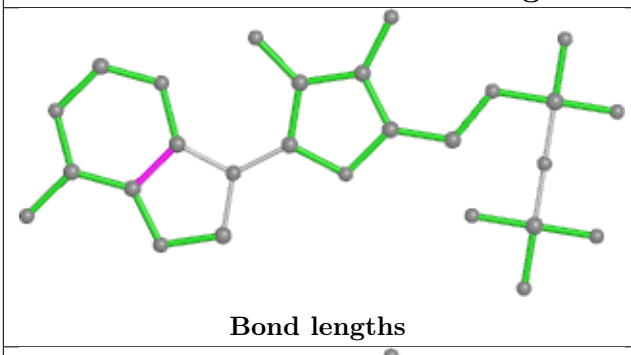


Torsions

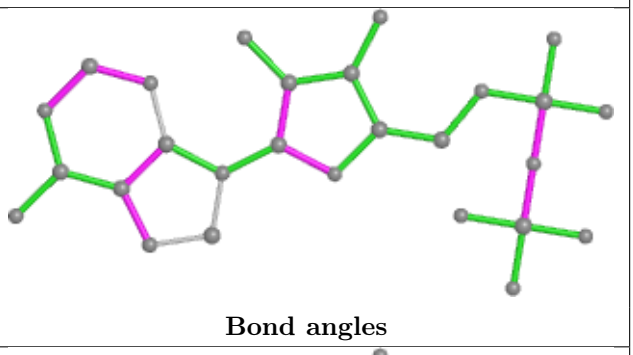


Rings

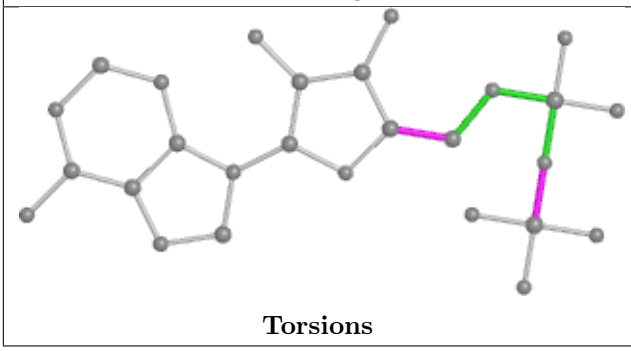
Ligand ADP B 301



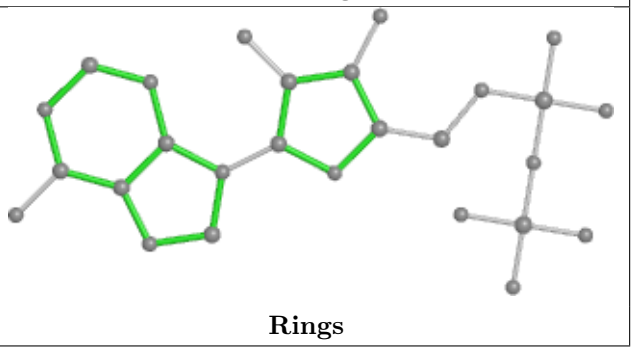
Bond lengths



Bond angles

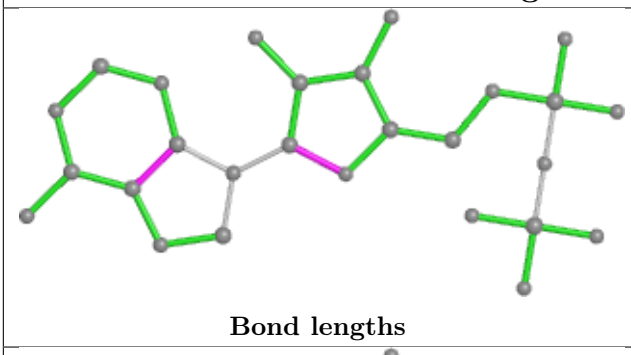


Torsions

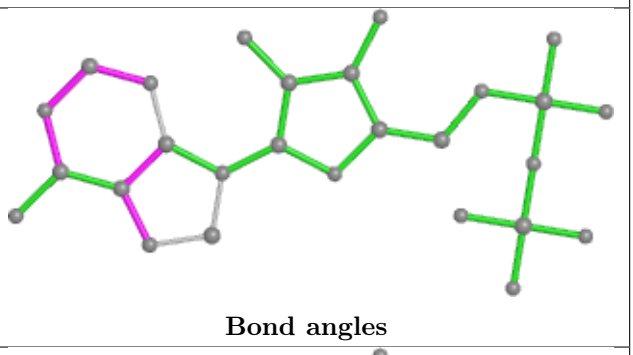


Rings

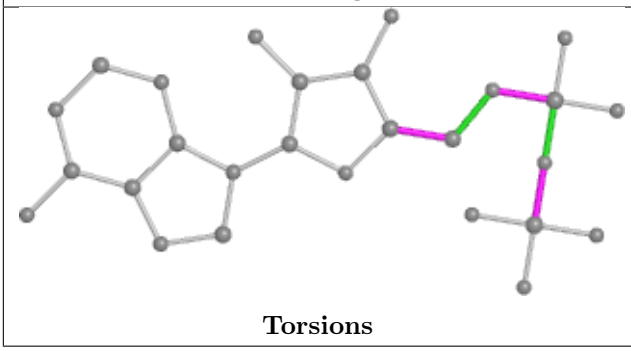
Ligand ADP A 301



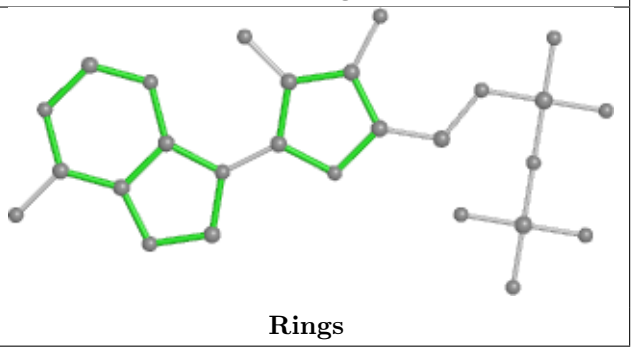
Bond lengths



Bond angles

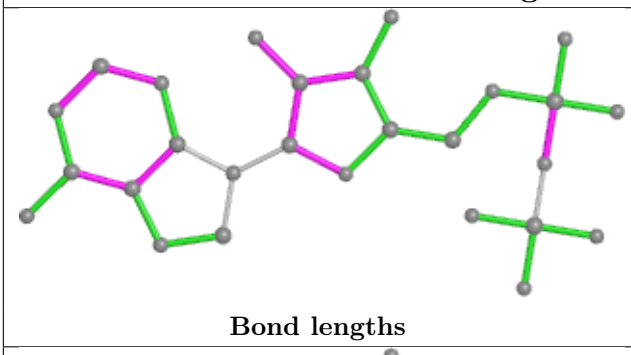


Torsions

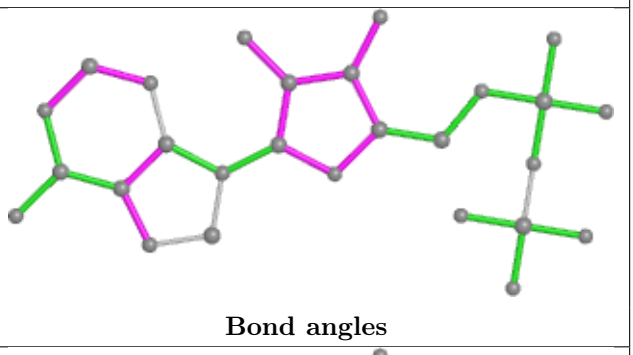


Rings

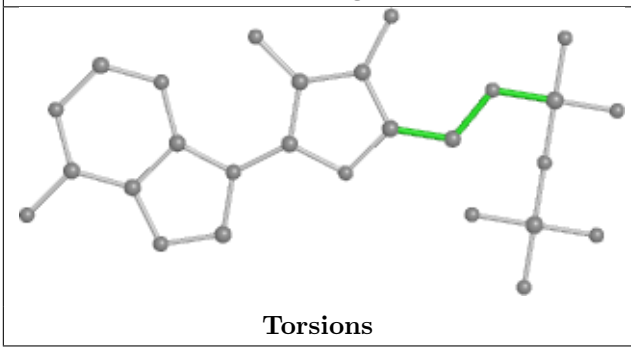
Ligand ADX A 302



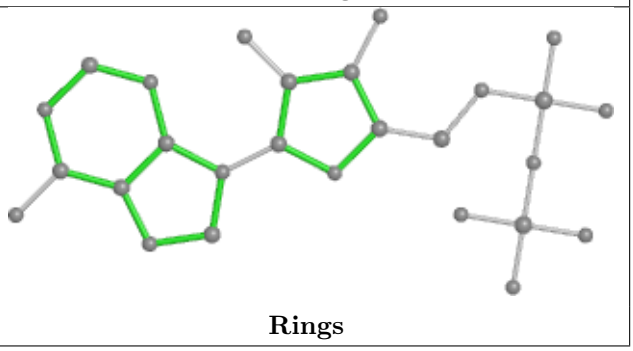
Bond lengths



Bond angles

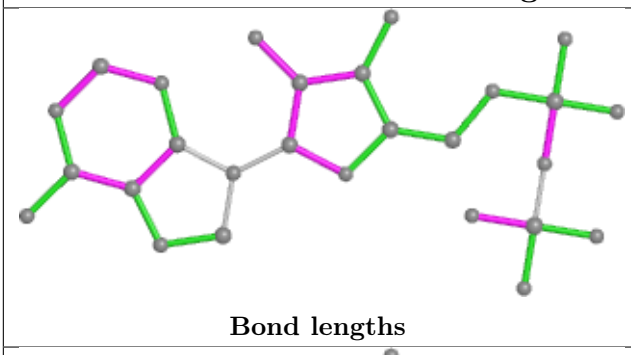


Torsions

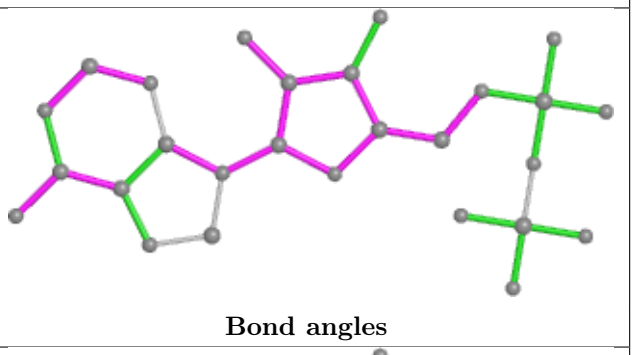


Rings

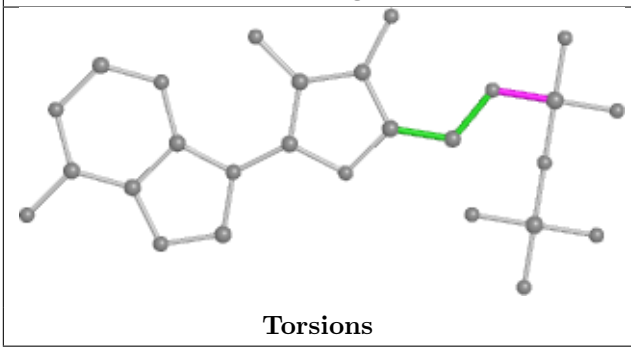
Ligand ADX D 302



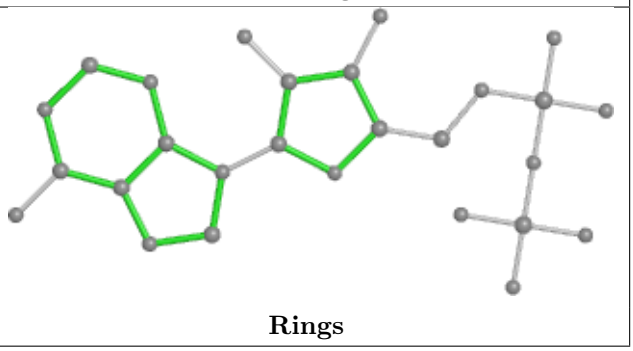
Bond lengths



Bond angles

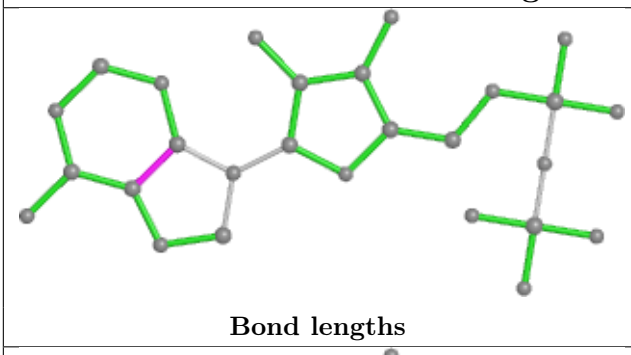


Torsions

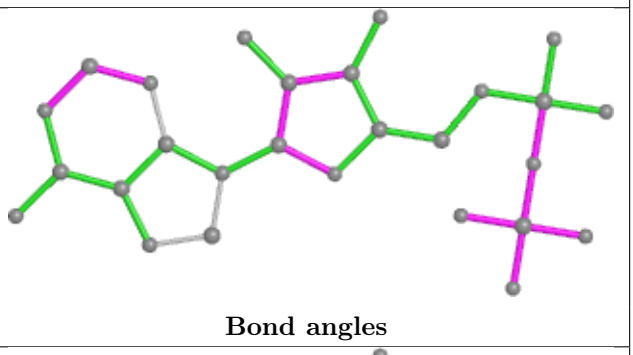


Rings

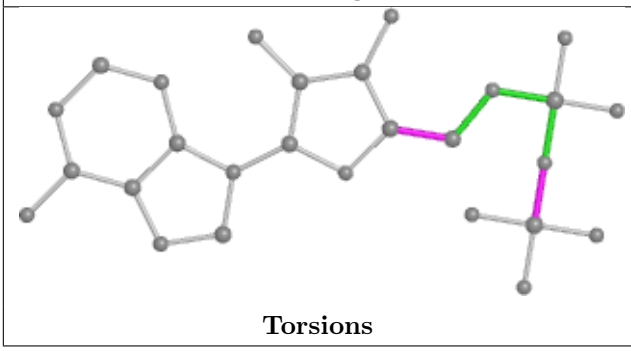
Ligand ADP C 301



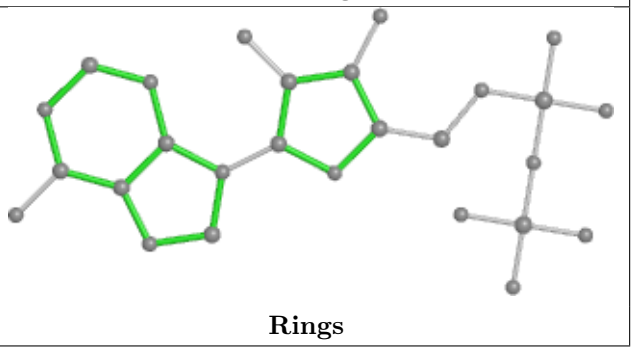
Bond lengths



Bond angles



Torsions



Rings

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	195/203 (96%)	-0.08	1 (0%)	91	89	28, 36, 47, 61	0
1	B	195/203 (96%)	0.05	2 (1%)	82	80	28, 35, 52, 66	0
1	C	196/203 (96%)	-0.06	3 (1%)	73	72	29, 38, 52, 70	0
1	D	195/203 (96%)	0.30	15 (7%)	13	12	29, 38, 61, 80	0
All	All	781/812 (96%)	0.05	21 (2%)	54	52	28, 37, 54, 80	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	169	ALA	4.6
1	D	172	ILE	4.1
1	C	218	TYR	3.7
1	D	171	GLU	3.2
1	D	160	VAL	3.2
1	D	178	ILE	2.8
1	D	93	PRO	2.7
1	B	175	PHE	2.6
1	D	170	GLY	2.6
1	D	157	SER	2.6
1	B	179	ASP	2.6
1	C	160	VAL	2.5
1	D	161	LYS	2.5
1	C	196	LEU	2.5
1	D	159	ASP	2.4
1	D	168	ARG	2.3
1	D	175	PHE	2.3
1	D	179	ASP	2.2
1	A	37	ARG	2.1
1	D	173	LYS	2.1
1	D	167	ALA	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

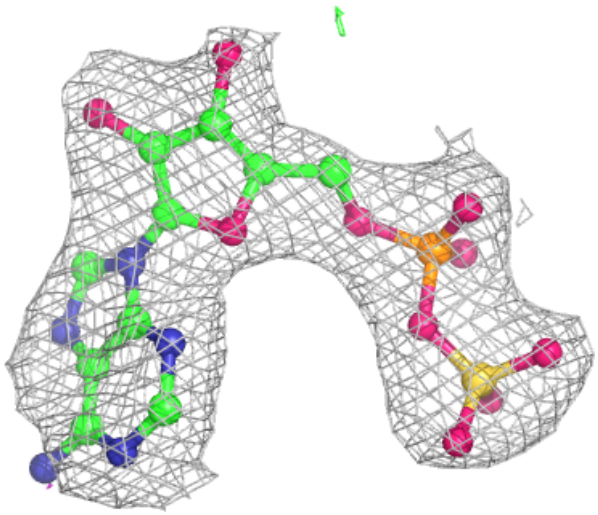
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

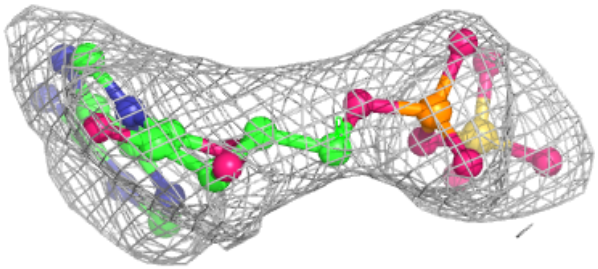
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ADX	D	302	27/27	0.95	0.18	34,53,61,70	0
3	ADX	C	302	27/27	0.96	0.17	31,39,49,54	0
3	ADX	B	302	27/27	0.96	0.17	34,44,53,64	0
3	ADX	A	302	27/27	0.97	0.15	31,44,54,61	0
2	ADP	A	301	27/27	0.98	0.17	27,38,41,44	0
2	ADP	B	301	27/27	0.98	0.13	30,33,36,37	0
2	ADP	C	301	27/27	0.98	0.14	33,38,40,43	0
2	ADP	D	301	27/27	0.98	0.13	33,38,41,45	0

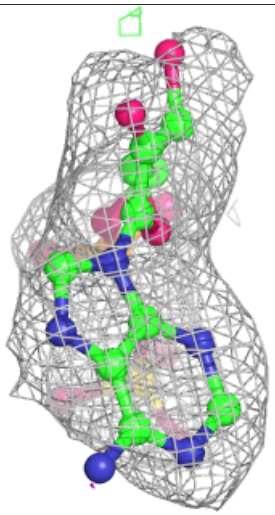
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADX D 302:

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

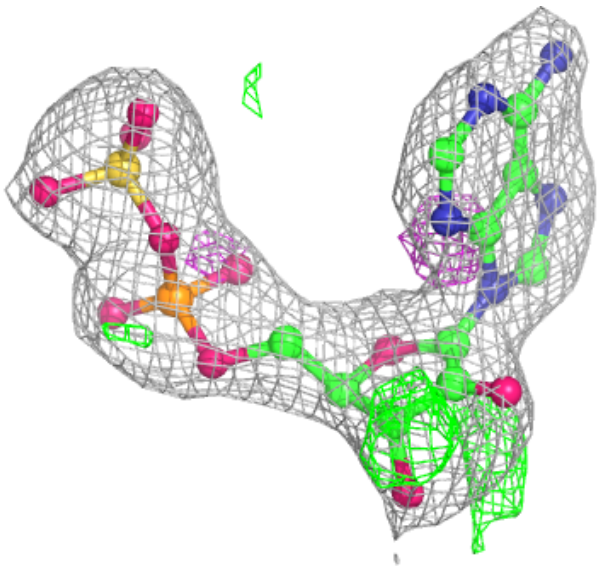


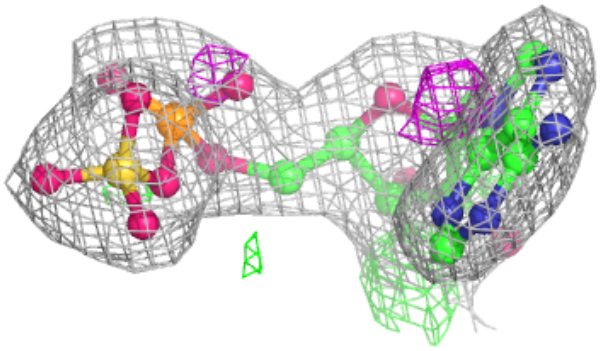


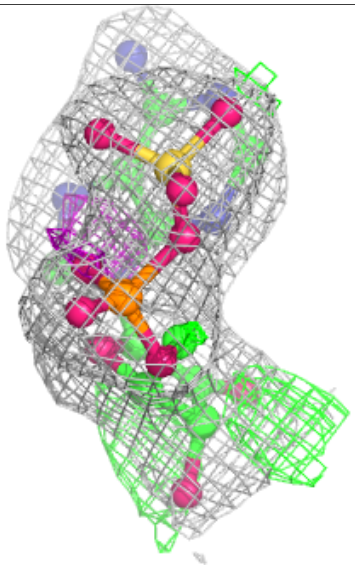


Electron density around ADX C 302:

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

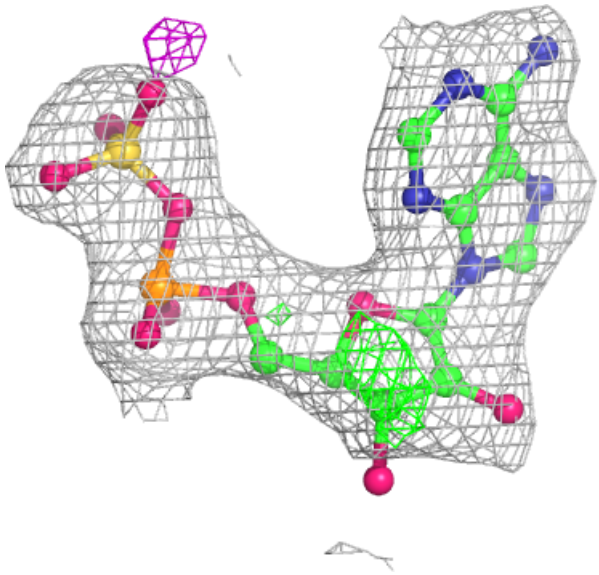


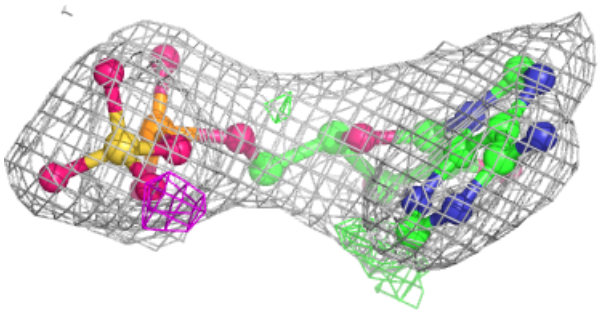


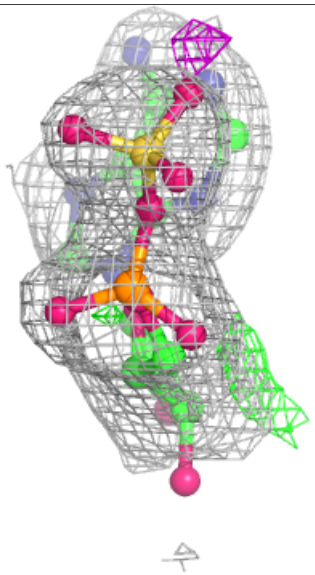


Electron density around ADX B 302:

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

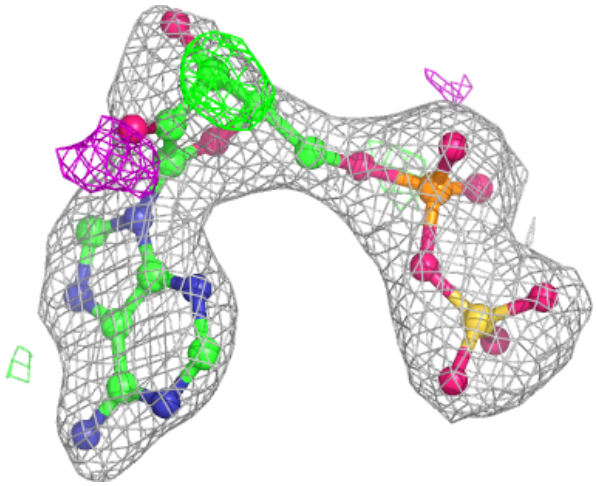


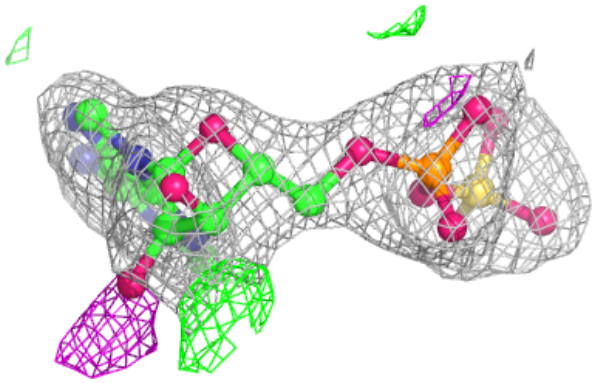


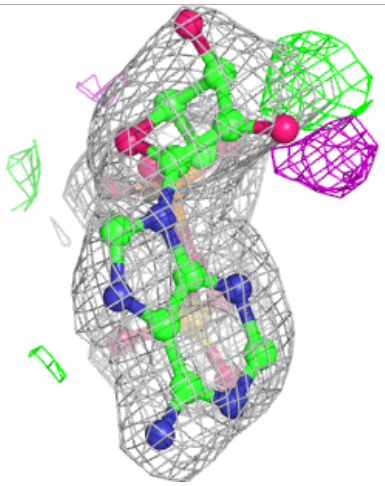


Electron density around ADX A 302:

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

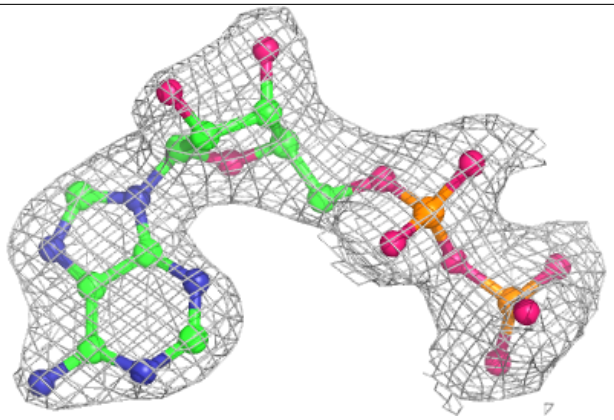


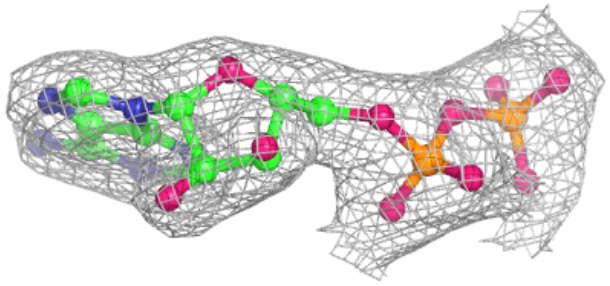


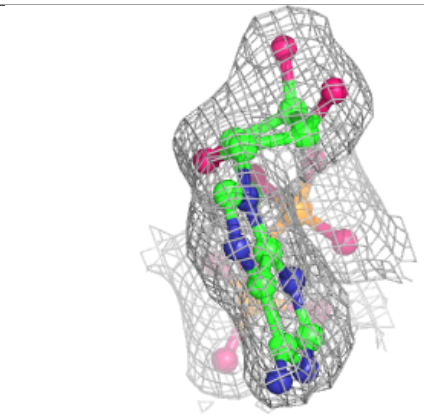


Electron density around ADP A 301:

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

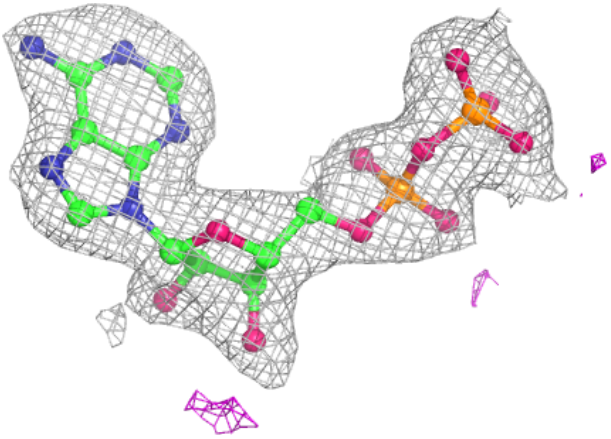


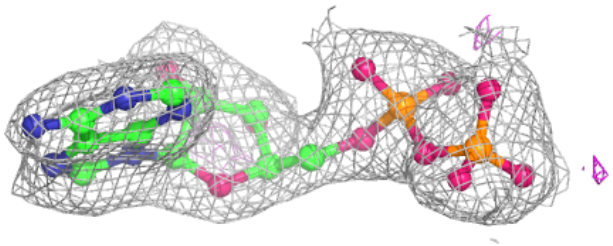


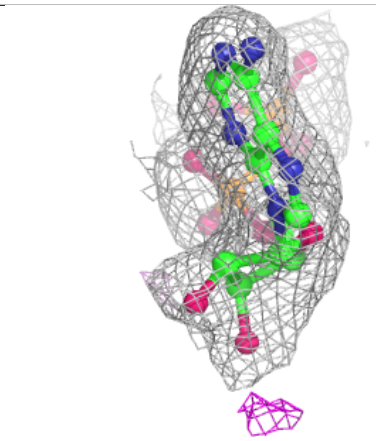


Electron density around ADP B 301:

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

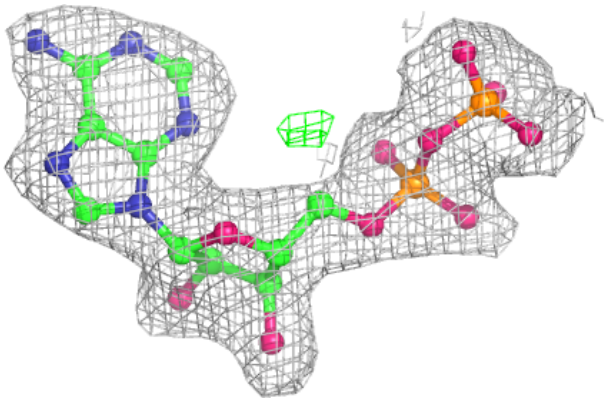


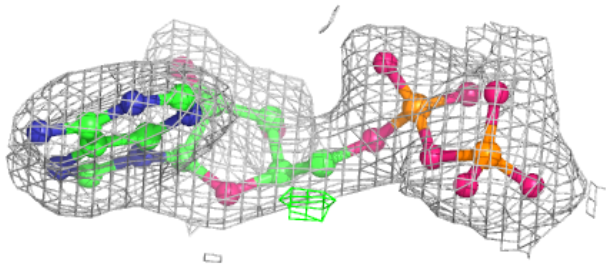


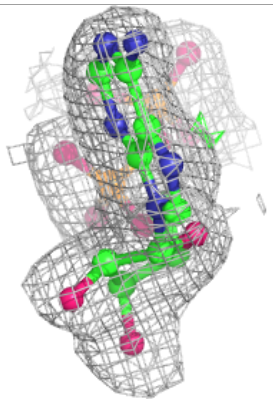


Electron density around ADP C 301:

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

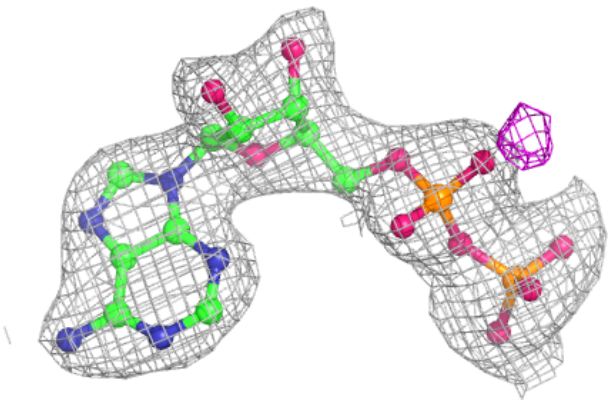


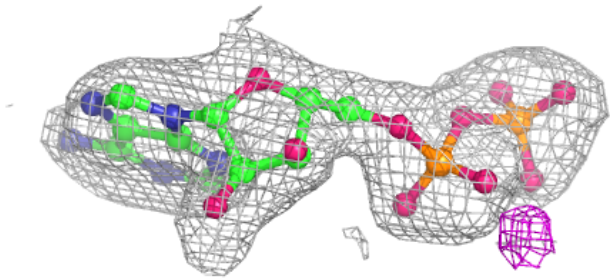


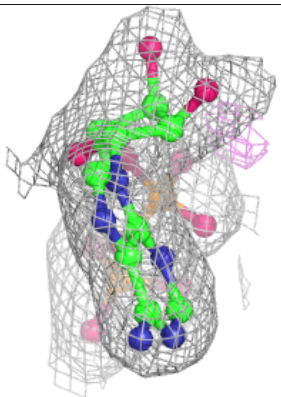


Electron density around ADP D 301:

$2mF_o$-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.