wwPDB X-ray Structure Validation Summary Report (i)

Oct 12, 2021 – 10:31 AM EDT

PDB ID	:	1ZBH
Title	:	3'-end specific recognition of histone mRNA stem-loop by 3'-exonuclease
Authors	:	Cheng, Y.; Patel, D.J.
Deposited on	:	2005-04-08
Resolution	:	3.00 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 following versions of software and data (see references (i)) were used in the production of this report:

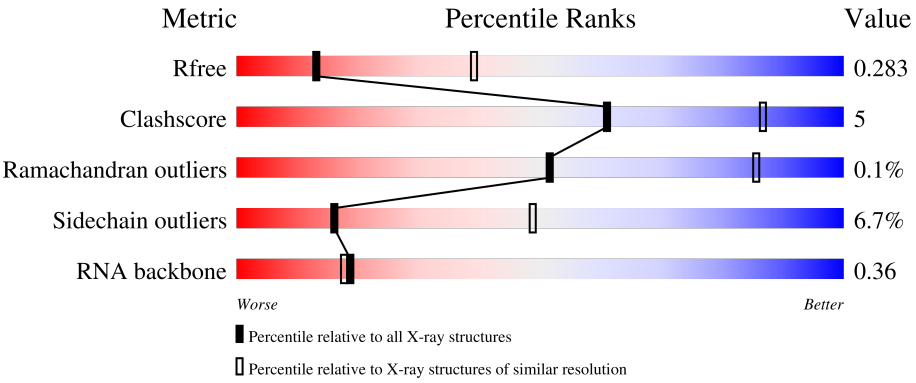
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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%

Mol	Chain	Length	Quality of chain
1	E	20	35% 40% 5% 20%
1	F	20	35% 30% 15% 20%
2	A	299	82% 13% • •
2	B	299	64% 10% • 25%
2	C	299	67% 7% • 25%
2	D	299	79% 15% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9138 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 RNA chain called 5'-R(*CP*CP*GP*GP*CP*UP*CP*UP*UP*UP*UP*CP *AP*GP*AP*GP*CP*CP*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	16	Total	C	N	O	P	0	0	0
			333	150	55	113	15			
1	E	16	Total	C	N	O	P	0	0	0
			333	150	55	113	15			

- Molecule 2 is a protein called 3'-5' exonuclease ERI1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	289	Total	C	N	O	S	0	0	0
			2354	1503	395	439	17			
2	B	225	Total	C	N	O	S	0	0	0
			1823	1164	302	343	14			
2	C	225	Total	C	N	O	S	0	0	0
			1823	1164	302	343	14			
2	D	289	Total	C	N	O	S	0	0	0
			2354	1503	395	439	17			

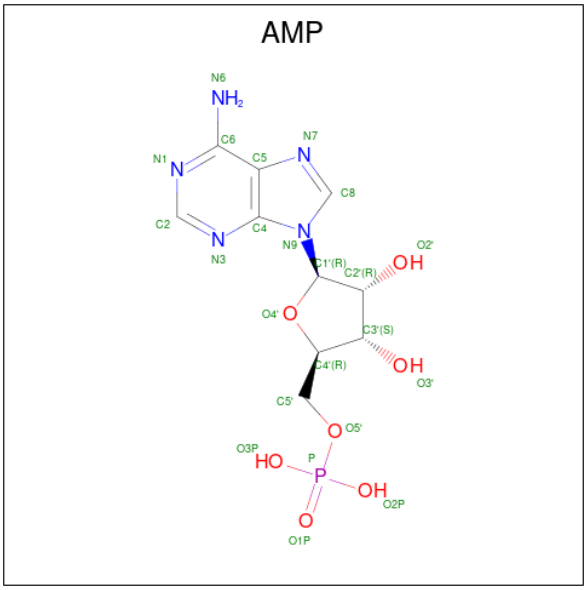
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	213	LEU	TRP	engineered mutation	UNP Q8IV48
A	293	ASN	HIS	engineered mutation	UNP Q8IV48
B	213	LEU	TRP	engineered mutation	UNP Q8IV48
B	293	ASN	HIS	engineered mutation	UNP Q8IV48
C	213	LEU	TRP	engineered mutation	UNP Q8IV48
C	293	ASN	HIS	engineered mutation	UNP Q8IV48
D	213	LEU	TRP	engineered mutation	UNP Q8IV48
D	293	ASN	HIS	engineered mutation	UNP Q8IV48

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Mg 2 2	0	0
3	B	2	Total Mg 2 2	0	0
3	C	2	Total Mg 2 2	0	0
3	D	2	Total Mg 2 2	0	0

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O P 23 10 5 7 1	0	0
4	B	1	Total C N O P 23 10 5 7 1	0	0
4	C	1	Total C N O P 23 10 5 7 1	0	0
4	D	1	Total C N O P 23 10 5 7 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	F	1	Total O 1 1	0	0
5	A	8	Total O 8 8	0	0

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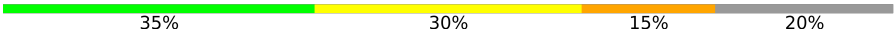
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	5	Total O 5 5	0	0
5	C	2	Total O 2 2	0	0
5	D	2	Total O 2 2	0	0

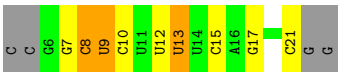
3 Residue-property plots (i)

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. 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. 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: 5'-R(*CP*CP*GP*GP*CP*UP*CP*UP*UP*UP*UP*CP*AP*GP*AP*GP*CP*CP*GP*G)-3'

Chain F:



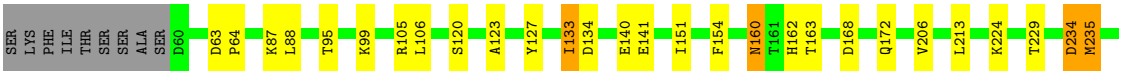


• Molecule 1: 5'-R(*CP*CP*GP*GP*CP*UP*CP*UP*UP*UP*UP*CP*AP*GP*AP*GP*CP*CP*GP*G)-3'

Chain E:

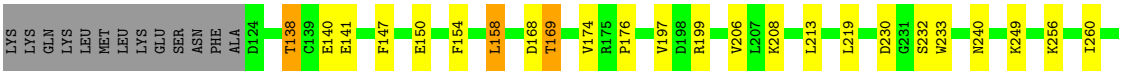
• Molecule 2: 3'-5' exonuclease ERI1

Chain A:



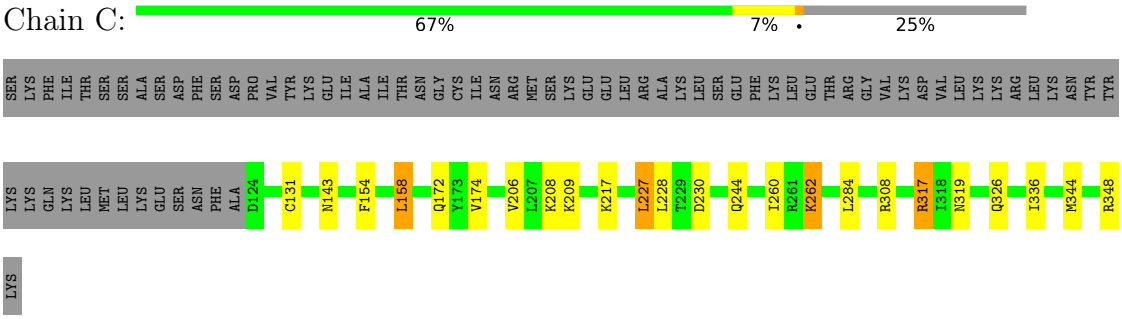
• Molecule 2: 3'-5' exonuclease ERI1

Chain B:



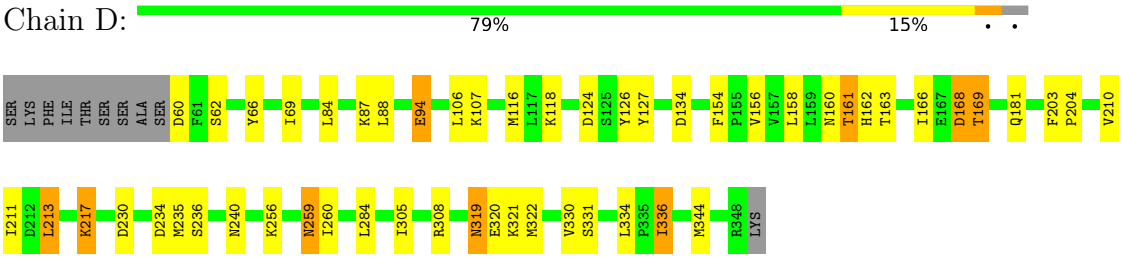
• Molecule 2: 3'-5' exonuclease ERI1

Chain C:



• Molecule 2: 3'-5' exonuclease ERI1

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	50.39Å 195.15Å 87.97Å 90.00° 92.13° 90.00°	Depositor
Resolution (Å)	19.92 – 3.00 19.91 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.8 (19.92-3.00) 95.7 (19.91-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.36 (at 2.98Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.209 , 0.260 0.264 , 0.283	Depositor DCC
R_{free} test set	3372 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å^2)	41.9	Xtriage
Anisotropy	0.419	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 5.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.056 for h,-k,-l	Xtriage
F_o,F_c correlation	0.84	EDS
Total number of atoms	9138	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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: MG, AMP

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	E	0.66	0/370	1.27	3/574 (0.5%)
1	F	0.65	0/370	1.32	3/574 (0.5%)
2	A	0.33	0/2402	0.49	0/3235
2	B	0.33	0/1864	0.49	0/2521
2	C	0.33	0/1864	0.48	0/2521
2	D	0.35	0/2402	0.49	0/3235
All	All	0.37	0/9272	0.61	6/12660 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	7	G	O3'-P-O5'	-11.54	82.08	104.00
1	E	7	G	O3'-P-O5'	-11.16	82.80	104.00
1	F	7	G	OP1-P-O3'	-9.85	83.52	105.20
1	E	7	G	OP1-P-O3'	-8.45	86.60	105.20
1	E	7	G	OP2-P-O3'	-8.43	86.65	105.20

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	E	333	0	173	0	0
1	F	333	0	173	3	0
2	A	2354	0	2381	21	0
2	B	1823	0	1817	13	0
2	C	1823	0	1817	17	0
2	D	2354	0	2381	31	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	23	0	12	0	0
4	B	23	0	12	0	0
4	C	23	0	12	0	0
4	D	23	0	12	0	0
5	A	8	0	0	0	0
5	B	5	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
5	F	1	0	0	0	0
All	All	9138	0	8790	81	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 5.

The worst 5 of 81 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:C:317:ARG:HH11	2:C:317:ARG:HG3	1.18	1.03
2:D:259:ASN:H	2:D:319:ASN:HD21	1.13	0.93
2:D:127:TYR:O	2:D:161:THR:HG21	1.82	0.80
2:D:160:ASN:ND2	2:D:163:THR:H	1.81	0.78
2:C:317:ARG:HG3	2:C:317:ARG:NH1	1.97	0.72

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	A	287/299 (96%)	276 (96%)	10 (4%)	1 (0%)	41 76
2	B	223/299 (75%)	218 (98%)	5 (2%)	0	100 100
2	C	223/299 (75%)	217 (97%)	6 (3%)	0	100 100
2	D	287/299 (96%)	277 (96%)	10 (4%)	0	100 100
All	All	1020/1196 (85%)	988 (97%)	31 (3%)	1 (0%)	51 85

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	99	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
2	A	267/276 (97%)	247 (92%)	20 (8%)	13 43
2	B	208/276 (75%)	191 (92%)	17 (8%)	11 39
2	C	208/276 (75%)	201 (97%)	7 (3%)	37 72
2	D	267/276 (97%)	247 (92%)	20 (8%)	13 43
All	All	950/1104 (86%)	886 (93%)	64 (7%)	16 49

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	217	LYS
2	D	240	ASN
2	B	168	ASP
2	B	158	LEU
2	D	256	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20

such sidechains are listed below:

Mol	Chain	Res	Type
2	D	172	GLN
2	D	259	ASN
2	D	326	GLN
2	D	319	ASN
2	B	311	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	15/20 (75%)	8 (53%)	1 (6%)
1	F	15/20 (75%)	6 (40%)	0
All	All	30/40 (75%)	14 (46%)	1 (3%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	F	8	C
1	F	9	U
1	F	12	U
1	F	13	U
1	F	15	C

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	14	U

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 12 ligands modelled in this entry, 8 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	$\#\|Z\| > 2$
4	AMP	B	2002	3	22,25,25	1.03	1 (4%)	25,38,38	1.31	3 (12%)
4	AMP	D	4002	3	22,25,25	1.07	2 (9%)	25,38,38	1.27	3 (12%)
4	AMP	A	1002	3	22,25,25	1.07	2 (9%)	25,38,38	1.29	3 (12%)
4	AMP	C	3002	3	22,25,25	1.02	1 (4%)	25,38,38	1.26	2 (8%)

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	AMP	B	2002	3	-	2/6/26/26	0/3/3/3
4	AMP	D	4002	3	-	1/6/26/26	0/3/3/3
4	AMP	A	1002	3	-	2/6/26/26	0/3/3/3
4	AMP	C	3002	3	-	1/6/26/26	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	4002	AMP	C5-C4	2.68	1.48	1.40
4	A	1002	AMP	C5-C4	2.61	1.47	1.40
4	B	2002	AMP	C5-C4	2.50	1.47	1.40
4	C	3002	AMP	C5-C4	2.50	1.47	1.40
4	A	1002	AMP	C2-N3	2.15	1.35	1.32

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	2002	AMP	N3-C2-N1	-3.52	123.17	128.68
4	A	1002	AMP	N3-C2-N1	-3.46	123.28	128.68
4	C	3002	AMP	N3-C2-N1	-3.44	123.30	128.68
4	D	4002	AMP	N3-C2-N1	-3.36	123.42	128.68
4	B	2002	AMP	C4-C5-N7	-2.61	106.68	109.40

There are no chirality outliers.

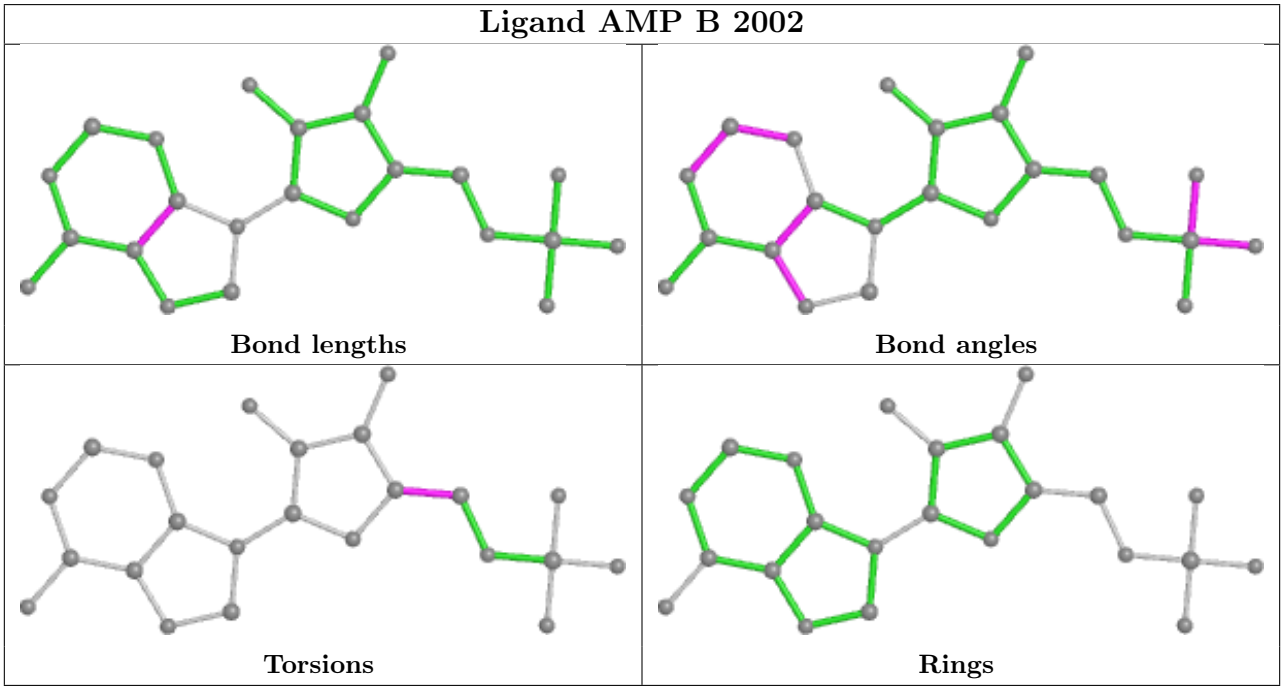
5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1002	AMP	O4'-C4'-C5'-O5'
4	A	1002	AMP	C3'-C4'-C5'-O5'
4	B	2002	AMP	O4'-C4'-C5'-O5'
4	B	2002	AMP	C3'-C4'-C5'-O5'
4	D	4002	AMP	O4'-C4'-C5'-O5'

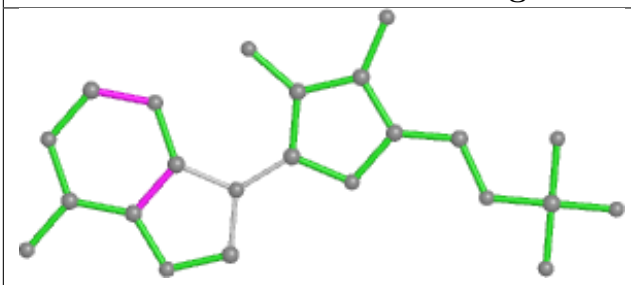
There are no ring outliers.

No monomer is involved in short contacts.

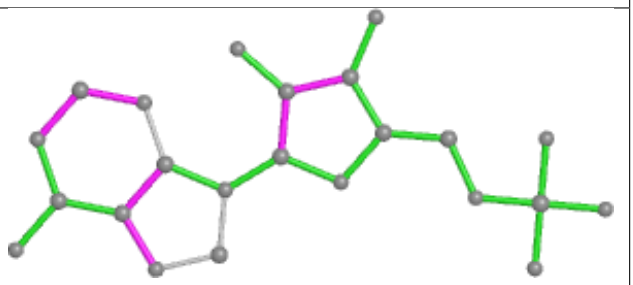
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



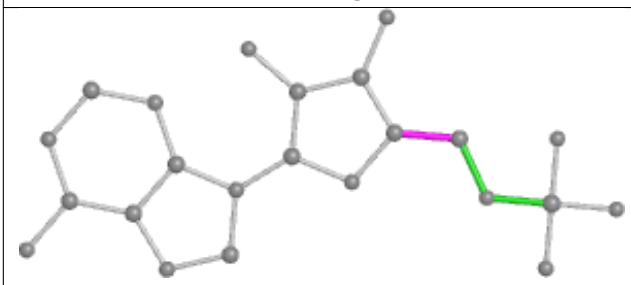
Ligand AMP D 4002



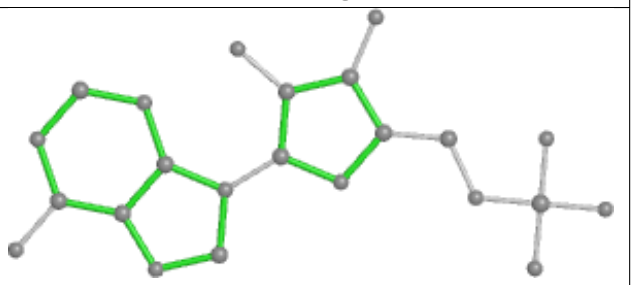
Bond lengths



Bond angles

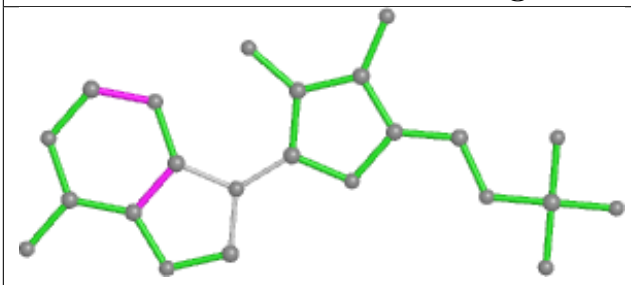


Torsions

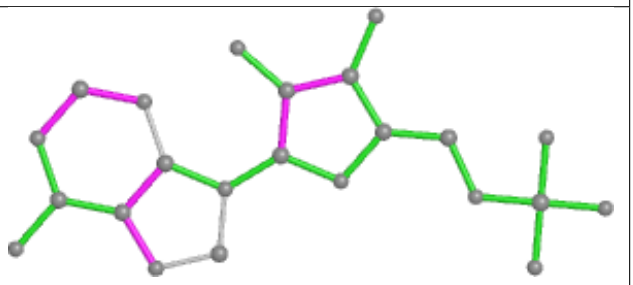


Rings

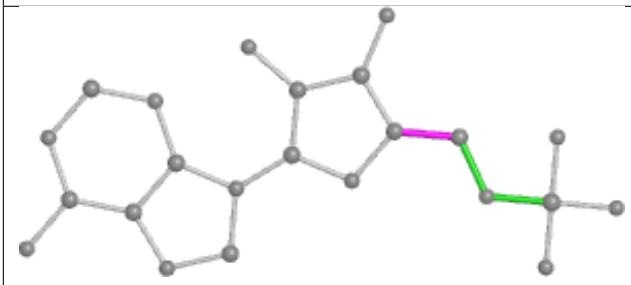
Ligand AMP A 1002



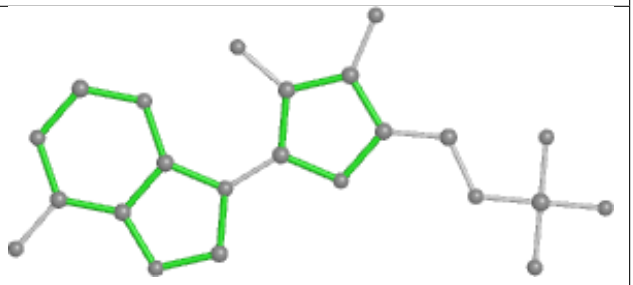
Bond lengths



Bond angles

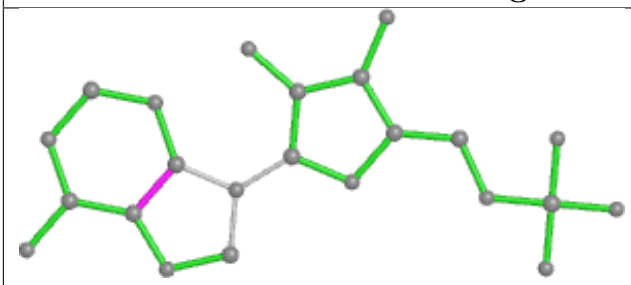


Torsions

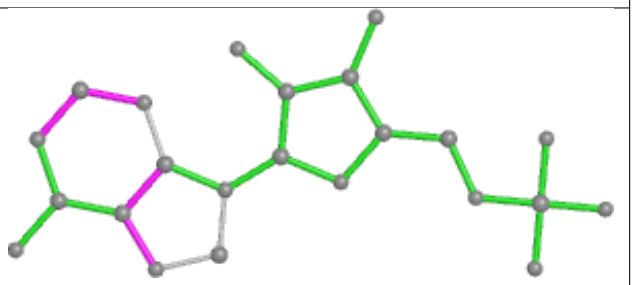


Rings

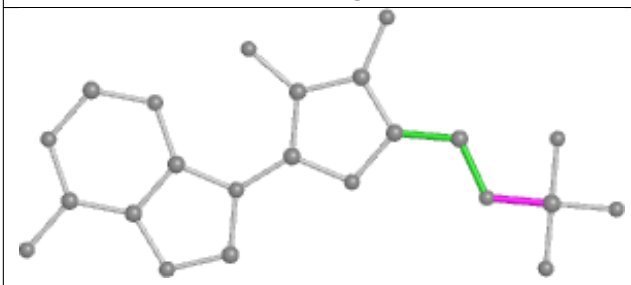
Ligand AMP C 3002



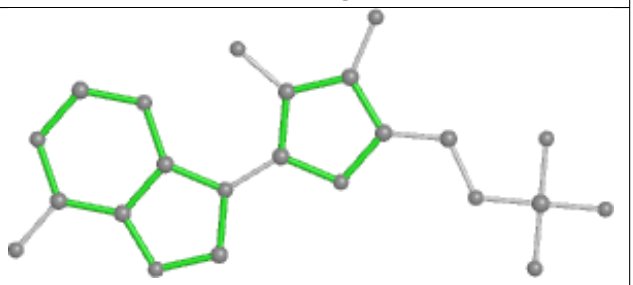
Bond lengths



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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

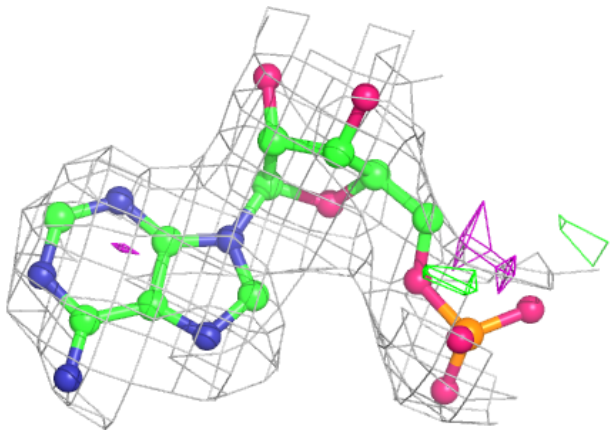
6.4 Ligands

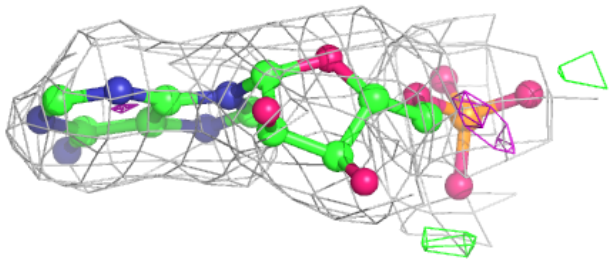
Unable to reproduce the depositors R factor - this section is therefore empty.

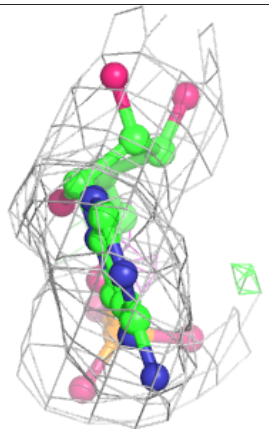
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around AMP A 1002:

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

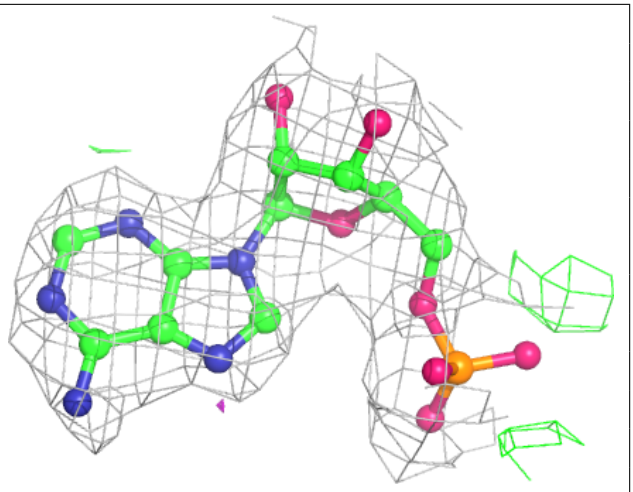


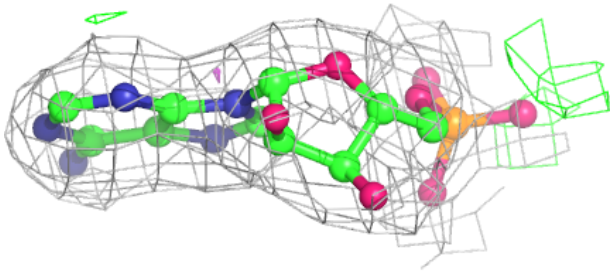


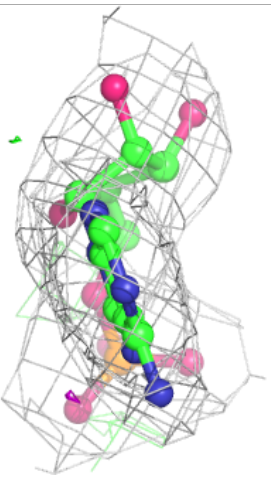


Electron density around AMP B 2002:

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

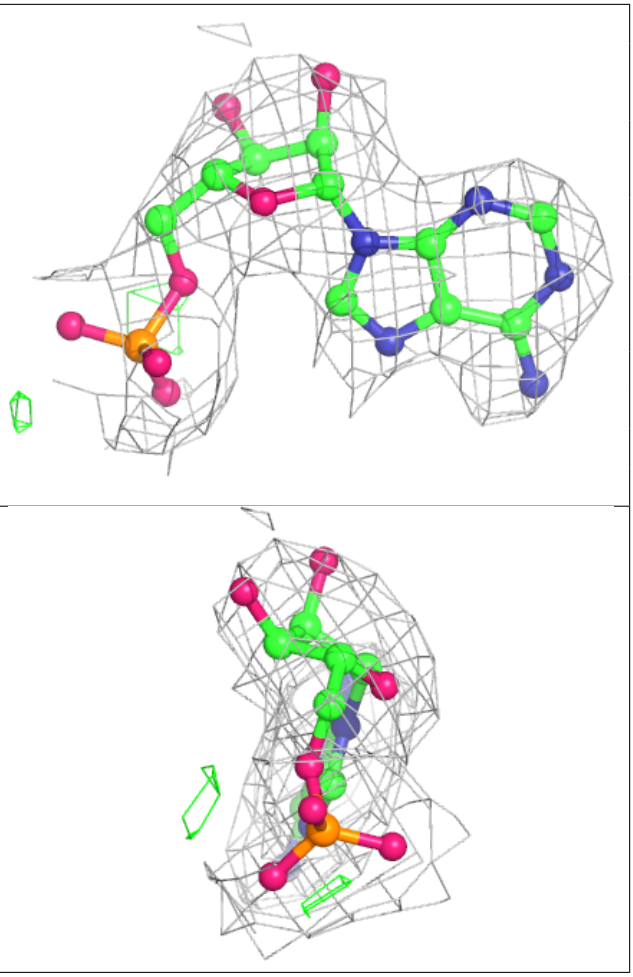






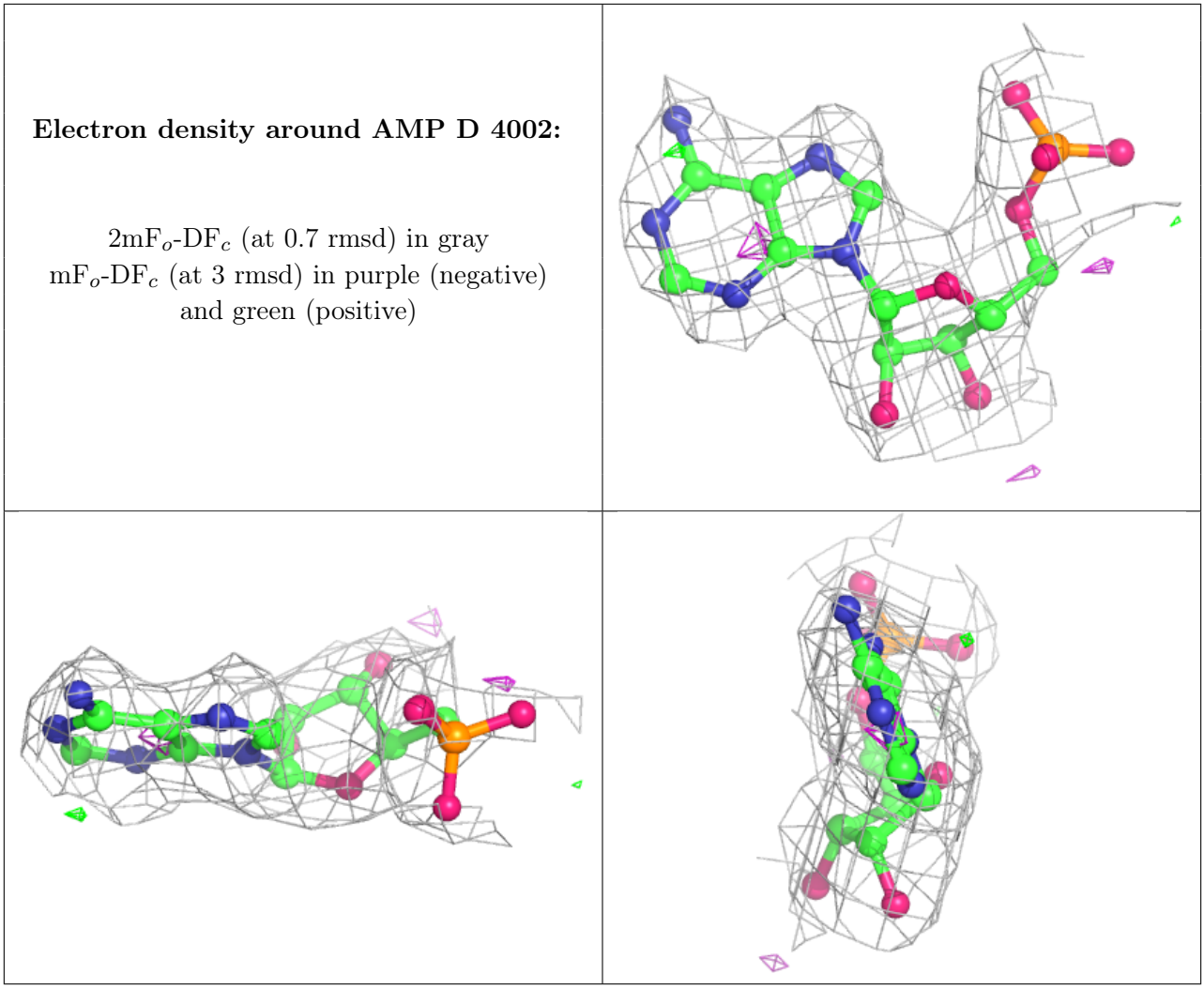
Electron density around AMP C 3002:

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



Electron density around AMP D 4002:

$2mF_o$-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)

Unable to reproduce the depositors R factor - this section is therefore empty.