



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:41 PM UTC

PDB ID : 3TTF / pdb_00003ttf
Title : Crystal structure of E. coli HypF with AMP and carbamoyl phosphate
Authors : Petkun, S.; Shi, R.; Li, Y.; Cygler, M.
Deposited on : 2011-09-14
Resolution : 1.92 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

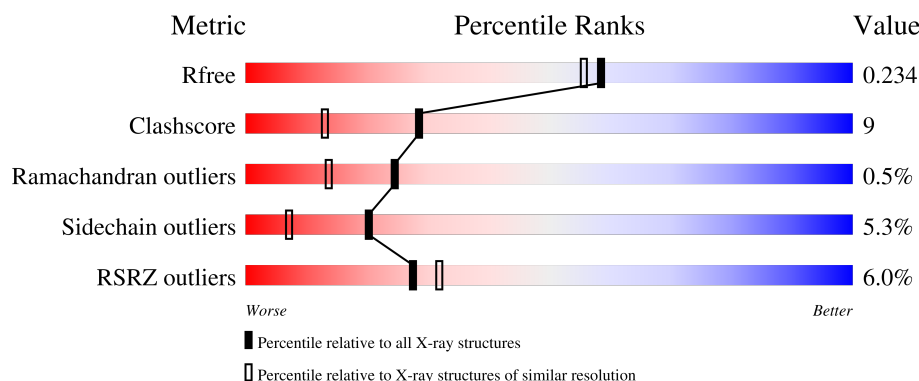
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.92 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1188 (1.92-1.92)
Clashscore	190562	1209 (1.92-1.92)
Ramachandran outliers	187476	1195 (1.92-1.92)
Sidechain outliers	187428	1195 (1.92-1.92)
RSRZ outliers	180081	1188 (1.92-1.92)

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

Mol	Chain	Length	Quality of chain
1	A	657	6% 80% 17% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5380 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 Transcriptional regulatory protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	646	Total	C	N	O	S	0	1	0
			4930	3114	886	893	37			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	GLY	-	expression tag	UNP Q7ABC4
A	91	SER	-	expression tag	UNP Q7ABC4
A	571	ALA	GLN	conflict	UNP Q7ABC4
A	572	ALA	GLN	conflict	UNP Q7ABC4
A	573	ALA	GLN	conflict	UNP Q7ABC4

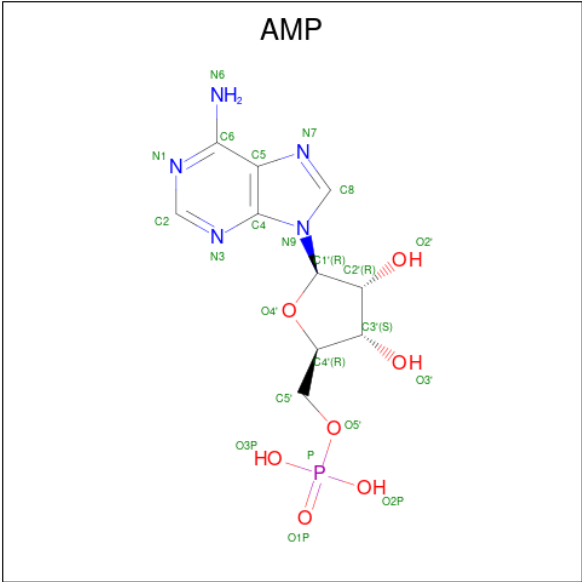
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Zn	0	0
			3	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	423	Total	O	0	0
			423	423		

- Molecule 1: Transcriptional regulatory protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	46.36Å 75.63Å 200.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.33 – 1.92 100.33 – 1.92	Depositor EDS
% Data completeness (in resolution range)	90.5 (100.33-1.92) 90.5 (100.33-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 1.92Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.177 , 0.225 0.185 , 0.234	Depositor DCC
R_{free} test set	2532 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.662	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5380	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, AMP, ZN

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	0.92	0/5055	0.99	6/6902 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	558	VAL	N-CA-C	6.70	114.78	108.15
1	A	707	ARG	NE-CZ-NH2	-5.80	113.98	119.20
1	A	577	VAL	N-CA-C	-5.66	104.99	110.42
1	A	278	VAL	N-CA-CB	-5.59	102.29	111.45
1	A	278	VAL	CG1-CB-CG2	5.39	122.65	110.80
1	A	466	MET	N-CA-C	5.01	118.55	112.23

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4930	0	4842	86	0
2	A	3	0	0	0	0
3	A	1	0	0	0	0
4	A	23	0	12	2	0
5	A	423	0	0	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5380	0	4854	86	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 9.

All (86) 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:297:VAL:HB	5:A:1067:HOH:O	0.97	1.13
1:A:683:GLN:HG3	5:A:790:HOH:O	1.44	1.13
1:A:517:CYS:HB2	5:A:886:HOH:O	0.89	1.05
1:A:506:MET:HE3	5:A:953:HOH:O	1.78	0.82
1:A:475:HIS:HE1	5:A:1069:HOH:O	1.68	0.75
1:A:521:ASN:HD22	1:A:523:ARG:H	1.34	0.74
1:A:152:VAL:HG12	1:A:153:MET:HE3	1.70	0.74
1:A:402:LYS:NZ	1:A:615:GLU:OE1	2.22	0.70
1:A:683:GLN:OE1	1:A:687:ARG:NH2	2.25	0.70
1:A:158:LEU:HD21	1:A:179:VAL:HG13	1.73	0.70
1:A:517:CYS:SG	5:A:790:HOH:O	2.49	0.69
1:A:153:MET:HE2	1:A:153:MET:HA	1.74	0.69
1:A:406:CYS:SG	1:A:413:VAL:CG2	2.80	0.69
1:A:634:HIS:HD2	1:A:636:VAL:H	1.39	0.68
1:A:475:HIS:CE1	5:A:1069:HOH:O	2.42	0.68
1:A:351:HIS:HD2	1:A:353:ARG:H	1.42	0.65
1:A:506:MET:CE	5:A:953:HOH:O	2.39	0.63
1:A:308:HIS:HD2	5:A:961:HOH:O	1.82	0.62
1:A:153:MET:HE3	1:A:353:ARG:HG3	1.82	0.61
1:A:178:PRO:HD2	5:A:977:HOH:O	2.00	0.61
1:A:521:ASN:ND2	1:A:523:ARG:H	1.99	0.59
1:A:148:ARG:NH1	1:A:177:GLN:O	2.36	0.58
1:A:302:PRO:HG3	1:A:311:LEU:HG	1.85	0.58
1:A:358:ARG:HD2	1:A:430:GLN:NE2	2.19	0.58
1:A:169:PRO:HA	1:A:174:PHE:CD1	2.39	0.58
1:A:492:ASP:HB3	5:A:939:HOH:O	2.04	0.57
1:A:504:ILE:HD13	5:A:807:HOH:O	2.04	0.57
1:A:102:ILE:HG12	1:A:441:ILE:HD13	1.88	0.56
1:A:153:MET:CE	1:A:353:ARG:HG3	2.37	0.55
1:A:122:ARG:NH2	1:A:162:CYS:SG	2.75	0.55
1:A:501:LEU:HB3	1:A:698:VAL:HB	1.88	0.55
1:A:308:HIS:HE1	5:A:87:HOH:O	1.90	0.55
1:A:280:LYS:HE3	1:A:294:LEU:O	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:521:ASN:ND2	1:A:524:GLU:H	2.05	0.54
1:A:325:LEU:HD23	1:A:328:LYS:HD2	1.90	0.53
1:A:670:ASP:OD1	1:A:707:ARG:HD3	2.08	0.53
1:A:159:CYS:HB3	1:A:184:CYS:HB3	1.91	0.53
1:A:369:GLU:OE1	1:A:705:ARG:NH2	2.43	0.52
1:A:396:CYS:HB2	1:A:406:CYS:HB3	1.92	0.51
1:A:179:VAL:HG22	1:A:180:ALA:H	1.73	0.51
1:A:166:TYR:CE1	1:A:175:HIS:HA	2.46	0.51
1:A:169:PRO:HA	1:A:174:PHE:HD1	1.75	0.51
1:A:153:MET:HG3	1:A:178:PRO:HA	1.92	0.50
1:A:173:ARG:HD3	1:A:179:VAL:HG23	1.92	0.50
1:A:638:MET:HG2	1:A:650:PHE:HB2	1.92	0.49
1:A:306:LEU:HD11	1:A:349:LEU:HD21	1.95	0.48
1:A:181:CYS:SG	1:A:183:GLU:HB2	2.54	0.48
1:A:147:ASP:CG	1:A:149:PRO:HD2	2.39	0.48
1:A:499:LEU:HG	1:A:501:LEU:HD13	1.97	0.47
1:A:698:VAL:HG22	4:A:747:AMP:N3	2.30	0.47
1:A:503:GLY:C	1:A:504:ILE:HD12	2.40	0.47
1:A:535:ALA:O	1:A:537:PRO:HD3	2.14	0.46
1:A:406:CYS:SG	1:A:413:VAL:HG21	2.54	0.46
1:A:393:PRO:HB2	1:A:446:PRO:HA	1.98	0.46
1:A:336:GLN:NE2	1:A:336:GLN:HA	2.29	0.46
1:A:670:ASP:OD1	1:A:707:ARG:CD	2.62	0.46
1:A:316:CYS:HB2	1:A:317:PRO:HD2	1.98	0.45
1:A:193:HIS:HE1	5:A:945:HOH:O	1.99	0.45
1:A:308:HIS:O	1:A:312:GLN:HG3	2.16	0.45
1:A:634:HIS:HE1	1:A:670:ASP:OD2	1.99	0.45
1:A:369:GLU:OE2	1:A:700:HIS:HD2	2.00	0.45
1:A:283:VAL:HG12	1:A:286:LEU:HG	1.99	0.44
1:A:190:TRP:CZ2	1:A:209:GLN:HG3	2.53	0.44
1:A:253:MET:HE1	1:A:307:GLN:CD	2.42	0.43
1:A:181:CYS:HB2	1:A:182:PRO:CD	2.49	0.43
1:A:521:ASN:HD22	1:A:521:ASN:C	2.26	0.43
1:A:402:LYS:NZ	5:A:905:HOH:O	2.50	0.43
1:A:406:CYS:HB2	1:A:731:SER:HB2	2.01	0.43
1:A:501:LEU:HD12	1:A:515:GLY:HA2	2.00	0.43
1:A:179:VAL:HG22	1:A:180:ALA:N	2.33	0.43
1:A:426:GLY:N	5:A:1072:HOH:O	2.49	0.42
1:A:424:ASP:O	1:A:427:ILE:HG22	2.18	0.42
1:A:457:TYR:HB2	1:A:460:CYS:SG	2.59	0.42
1:A:502:ASP:HA	1:A:698:VAL:HG23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:623:GLU:OE1	4:A:747:AMP:N6	2.49	0.42
1:A:634:HIS:CD2	1:A:636:VAL:H	2.28	0.42
1:A:335:GLU:H	1:A:335:GLU:CD	2.28	0.41
1:A:148:ARG:O	1:A:154:ALA:HB2	2.20	0.41
1:A:179:VAL:O	1:A:180:ALA:HB3	2.20	0.41
1:A:426:GLY:CA	5:A:1072:HOH:O	2.69	0.41
1:A:369:GLU:CD	1:A:705:ARG:NH2	2.79	0.41
1:A:721:GLN:HB2	5:A:1035:HOH:O	2.21	0.41
1:A:219:LYS:NZ	1:A:334:ASN:HD21	2.17	0.41
1:A:148:ARG:HB3	1:A:149:PRO:HD3	2.03	0.40
1:A:192:SER:O	1:A:193:HIS:C	2.64	0.40
1:A:428:GLN:NE2	5:A:1074:HOH:O	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	645/657 (98%)	616 (96%)	26 (4%)	3 (0%)	24	14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	179	VAL
1	A	514	GLY
1	A	178	PRO

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	508/513 (99%)	481 (95%)	27 (5%)	20 7

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	GLN
1	A	102	ILE
1	A	152	VAL
1	A	188	LEU
1	A	216	VAL
1	A	239	LEU
1	A	267	LEU
1	A	277	LEU
1	A	278	VAL
1	A	294	LEU
1	A	301	LEU
1	A	336	GLN
1	A	379	PRO
1	A	397	LEU
1	A	401	LEU
1	A	419	LEU
1	A	472	THR
1	A	501	LEU
1	A	504	ILE
1	A	521	ASN
1	A	531	LEU
1	A	566	GLU
1	A	583	GLU
1	A	640	ARG
1	A	704	LEU
1	A	718	LEU
1	A	723	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	HIS
1	A	204	GLN

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Mol	Chain	Res	Type
1	A	295	ASN
1	A	308	HIS
1	A	324	ASN
1	A	334	ASN
1	A	351	HIS
1	A	430	GLN
1	A	451	HIS
1	A	521	ASN
1	A	587	ASN
1	A	634	HIS
1	A	663	GLN
1	A	700	HIS
1	A	721	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	A	747	2	25,25,25	1.61	4 (16%)	37,38,38	2.08	8 (21%)

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	A	747	2	-	0/10/26/26	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	747	AMP	C5-C4	5.21	1.48	1.39
4	A	747	AMP	C5-C6	3.24	1.50	1.41
4	A	747	AMP	C8-N7	2.86	1.37	1.31
4	A	747	AMP	O4'-C1'	2.00	1.46	1.42

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	747	AMP	C5-C4-N3	-6.57	117.67	126.72
4	A	747	AMP	N3-C4-N9	4.40	134.65	127.17
4	A	747	AMP	C4-C5-N7	-4.37	105.58	110.58
4	A	747	AMP	C2-N3-C4	4.17	122.02	111.83
4	A	747	AMP	N3-C2-N1	-3.64	123.08	128.58
4	A	747	AMP	C5-N7-C8	3.07	108.28	103.45
4	A	747	AMP	O4'-C1'-N9	2.98	113.82	108.09
4	A	747	AMP	C6-C5-N7	2.55	137.00	132.09

There are no chirality outliers.

There are no torsion outliers.

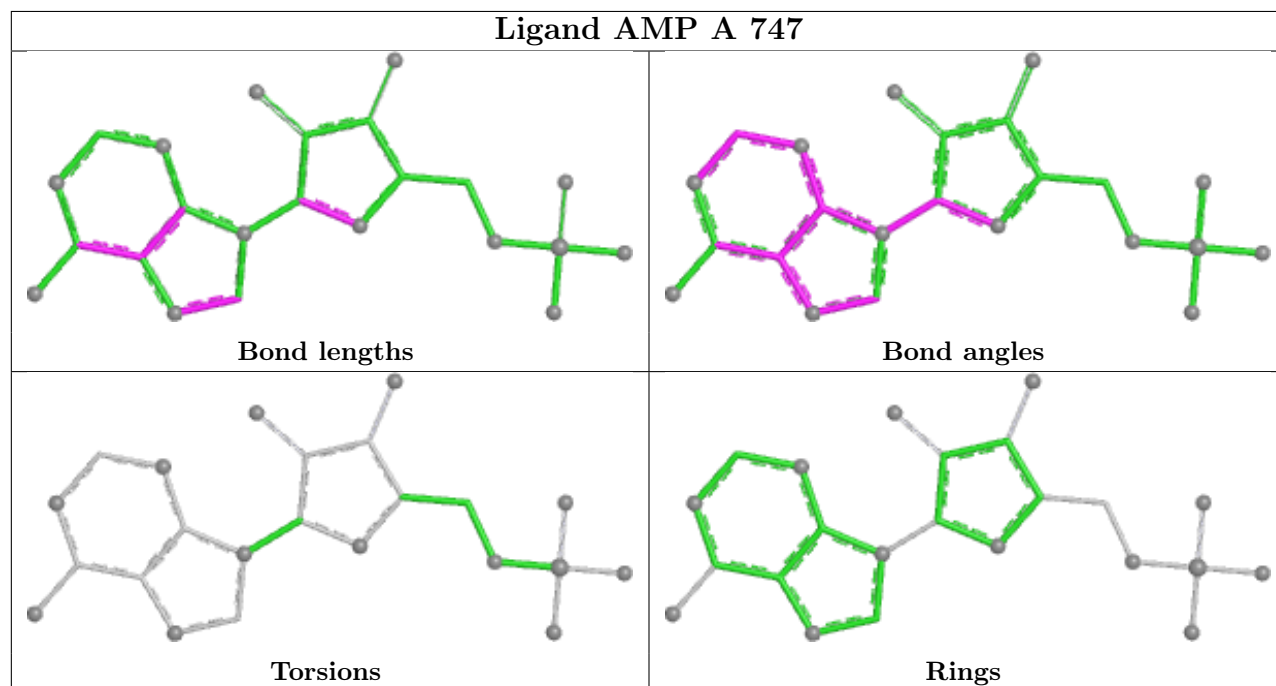
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	747	AMP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	646/657 (98%)	0.22	39 (6%)	27 32	12, 26, 60, 89	1 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	149	PRO	7.2
1	A	170	LEU	5.6
1	A	146	TYR	5.4
1	A	174	PHE	5.3
1	A	178	PRO	4.8
1	A	150	PHE	4.6
1	A	145	PRO	4.4
1	A	144	MET	4.0
1	A	179	VAL	3.8
1	A	176	ALA	3.8
1	A	147	ASP	3.6
1	A	169	PRO	3.6
1	A	181	CYS	3.5
1	A	161	ALA	3.3
1	A	158	LEU	3.0
1	A	166	TYR	2.9
1	A	120	GLY	2.9
1	A	194	GLY	2.8
1	A	160	PRO	2.8
1	A	180	ALA	2.7
1	A	156	PHE	2.7
1	A	175	HIS	2.6
1	A	148	ARG	2.6
1	A	234	ASN	2.6
1	A	124	TYR	2.5
1	A	159	CYS	2.4
1	A	325	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	171	ASP	2.3
1	A	177	GLN	2.3
1	A	167	ARG	2.2
1	A	172	ARG	2.2
1	A	173	ARG	2.2
1	A	182	PRO	2.1
1	A	102	ILE	2.1
1	A	183	GLU	2.1
1	A	462	TRP	2.1
1	A	101	GLN	2.1
1	A	572	ALA	2.1
1	A	152	VAL	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](#)

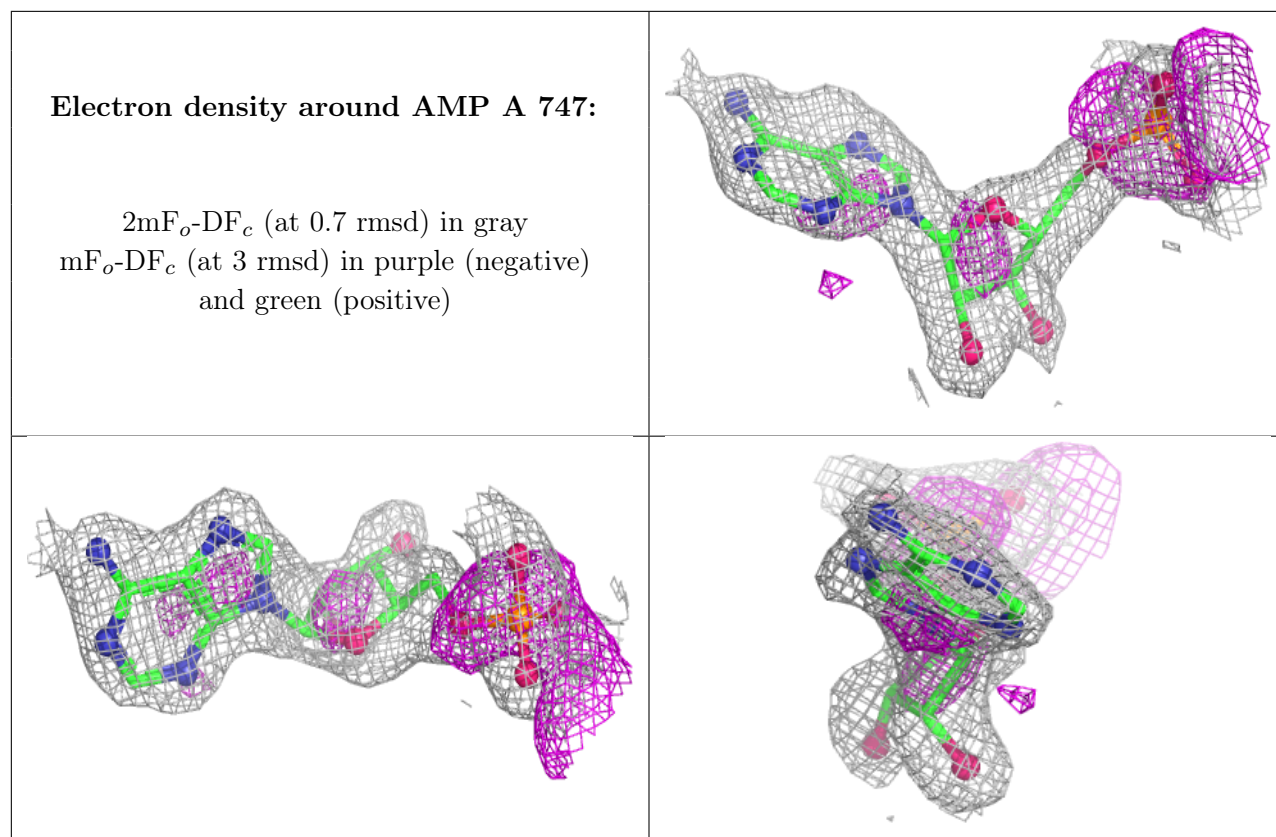
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	AMP	A	747	23/23	0.88	0.12	31,45,46,48	0
2	ZN	A	2	1/1	0.94	0.08	70,70,70,70	0
3	MG	A	4	1/1	0.98	0.06	20,20,20,20	0
2	ZN	A	1	1/1	0.98	0.04	47,47,47,47	0
2	ZN	A	3	1/1	0.99	0.16	39,39,39,39	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.