



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:20 PM UTC

PDB ID : 7B7Z / pdb_00007b7z
Title : DeAMPylation complex of monomeric FICD and AMPylated BiP (state 1)
Authors : Perera, L.A.; Ron, D.
Deposited on : 2020-12-12
Resolution : 1.70 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

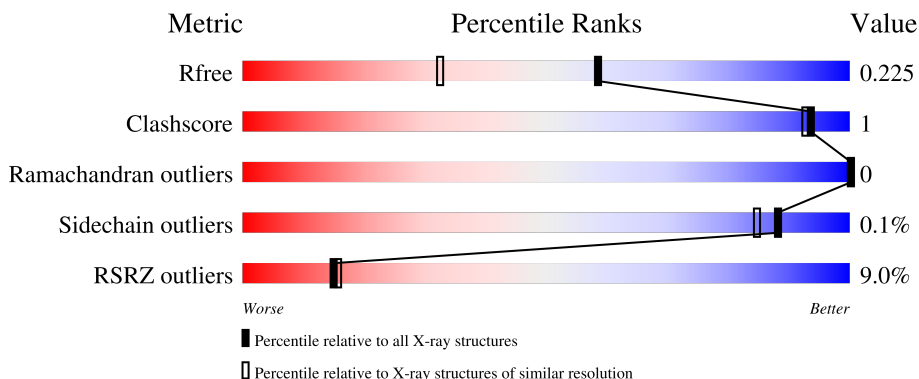
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. 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	B	523	9% 96% .
2	A	343	8% 97% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7868 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 Endoplasmic reticulum chaperone BiP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	522	Total	C	N	O	S	0	11	0
			4044	2547	687	800	10			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	27	SER	-	expression tag	UNP G3I8R9
B	229	ALA	THR	engineered mutation	UNP G3I8R9
B	461	PHE	VAL	engineered mutation	UNP G3I8R9

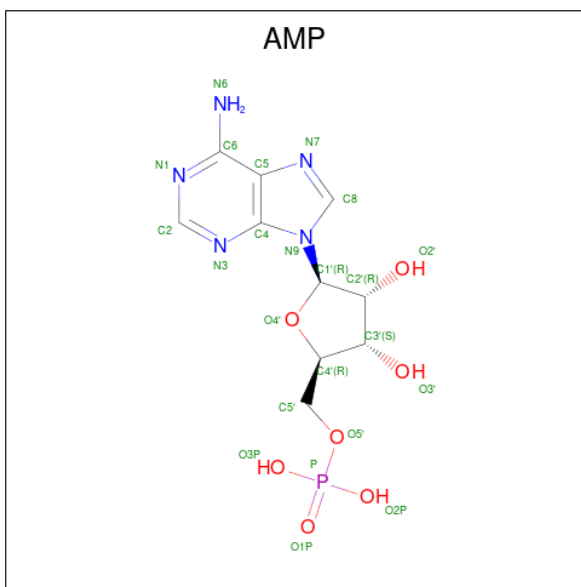
- Molecule 2 is a protein called Protein adenylyltransferase FICD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	340	Total	C	N	O	S	0	13	0
			2829	1793	496	527	13			

There are 3 discrepancies between the modelled and reference sequences:

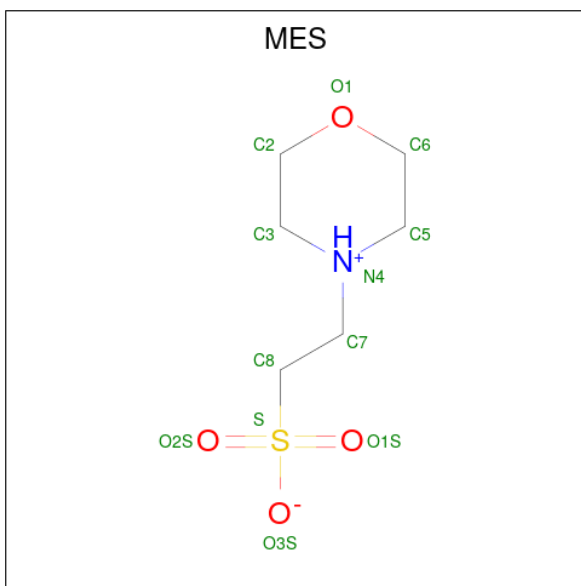
Chain	Residue	Modelled	Actual	Comment	Reference
A	103	SER	-	expression tag	UNP Q9BVA6
A	258	ASP	LEU	engineered mutation	UNP Q9BVA6
A	363	ALA	HIS	engineered mutation	UNP Q9BVA6

- Molecule 3 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

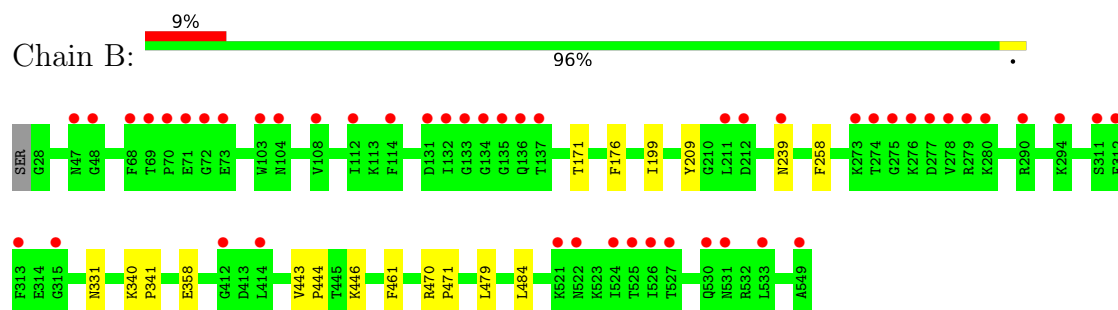
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	522	Total 522	O 522	0	0
6	A	438	Total 438	O 438	0	0

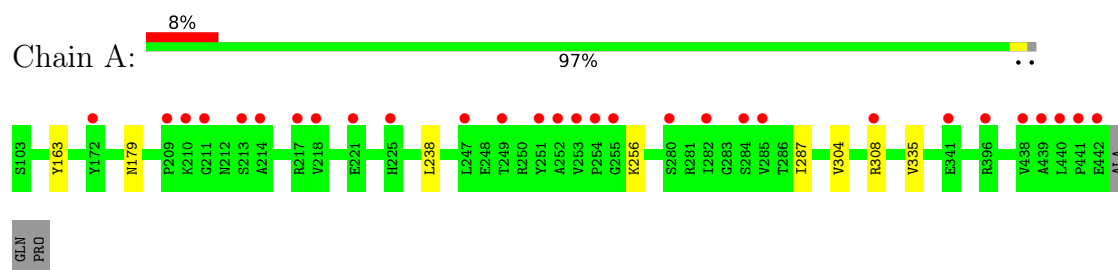
3 Residue-property plots [i](#)

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: Endoplasmic reticulum chaperone BiP



- Molecule 2: Protein adenylyltransferase FICD



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.37Å 104.08Å 105.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.25 – 1.70 74.14 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (74.25-1.70) 99.7 (74.14-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.195 , 0.221 0.202 , 0.225	Depositor DCC
R_{free} test set	5973 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	23.7	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.008 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7868	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 4.10% 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

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.98	0/4106	1.32	0/5566
2	A	0.97	0/2886	1.42	0/3910
All	All	0.98	0/6992	1.37	0/9476

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	B	4044	0	3984	14	0
2	A	2829	0	2796	5	0
3	B	22	0	12	0	0
4	B	12	0	13	0	0
5	A	1	0	0	0	0
6	A	438	0	0	0	0
6	B	522	0	0	1	0
All	All	7868	0	6805	19	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 1.

All (19) 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:B:171:THR:HG22	1:B:199[A]:ILE:HG23	1.62	0.81
1:B:209:TYR:OH	1:B:358:GLU:HG3	2.06	0.56
1:B:461:PHE:HB2	1:B:484:LEU:HB3	1.89	0.54
1:B:171:THR:HG22	1:B:199[A]:ILE:CG2	2.36	0.51
2:A:304:VAL:O	2:A:308[B]:ARG:HD2	2.11	0.50
1:B:446:LYS:NZ	6:B:706:HOH:O	2.48	0.46
1:B:171:THR:HA	1:B:199[A]:ILE:O	2.16	0.45
1:B:239[B]:ASN:CG	1:B:239[B]:ASN:O	2.58	0.45
1:B:340:LYS:HB2	1:B:341:PRO:HD3	1.99	0.44
2:A:238:LEU:HD21	2:A:256:LYS:HG2	1.98	0.44
1:B:171:THR:HA	1:B:199[B]:ILE:O	2.18	0.44
1:B:443:VAL:HA	1:B:444:PRO:C	2.43	0.44
2:A:163:TYR:CE2	2:A:179:ASN:HB3	2.54	0.43
1:B:484:LEU:C	1:B:484:LEU:HD23	2.44	0.42
2:A:304:VAL:O	2:A:308[B]:ARG:NH1	2.52	0.42
1:B:479:LEU:C	1:B:479:LEU:HD23	2.44	0.42
2:A:287:ILE:HG13	2:A:335[B]:VAL:HG21	2.02	0.42
1:B:258:PHE:HA	1:B:331:ASN:OD1	2.20	0.42
1:B:470:ARG:HA	1:B:471:PRO:HD3	1.96	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	B	531/523 (102%)	520 (98%)	11 (2%)	0	100	100
2	A	352/343 (103%)	349 (99%)	3 (1%)	0	100	100
All	All	883/866 (102%)	869 (98%)	14 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	B	430/443 (97%)	429 (100%)	1 (0%)	87	84
2	A	304/301 (101%)	304 (100%)	0	100	100
All	All	734/744 (99%)	733 (100%)	1 (0%)	88	85

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	176	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	110	GLN
1	B	265	HIS
1	B	343	GLN
1	B	409	GLN
1	B	457	ASN
2	A	226	HIS
2	A	245	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	MES	B	601	-	12,12,12	0.70	0	15,16,16	0.29	0
3	AMP	B	600	5,1	21,24,25	0.20	0	30,35,38	0.38	0

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	MES	B	601	-	-	3/6/14/14	0/1/1/1
3	AMP	B	600	5,1	-	0/7/25/26	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

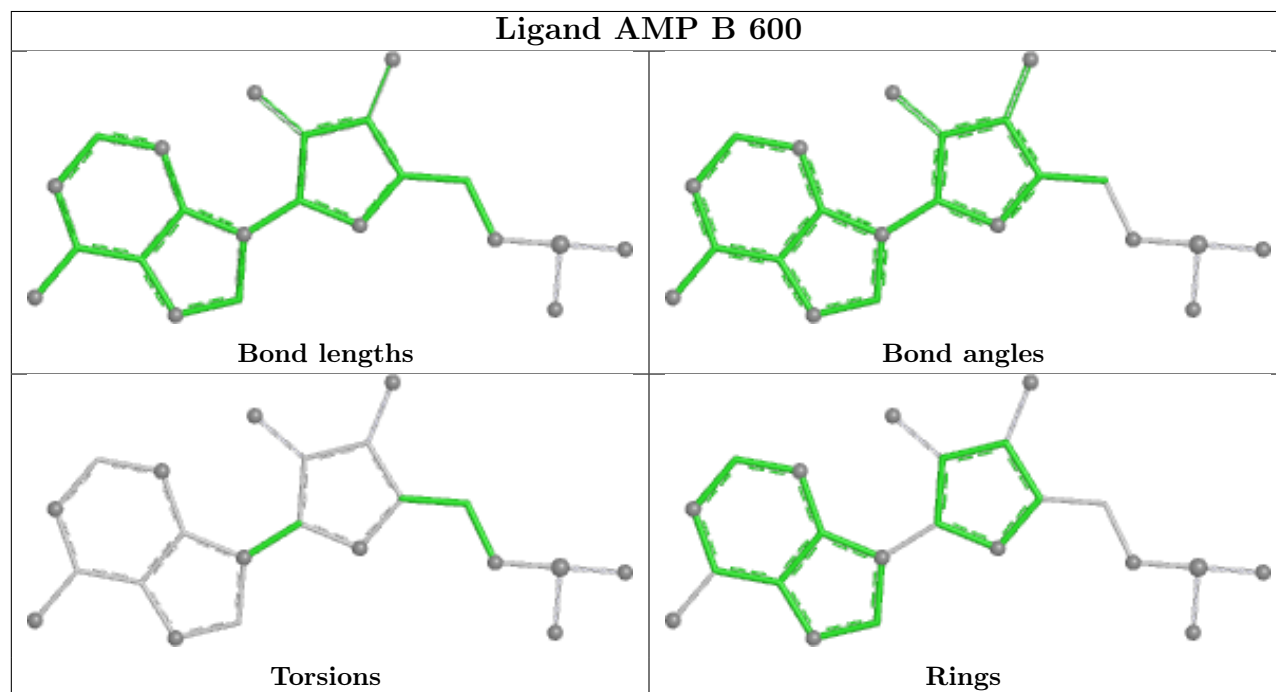
Mol	Chain	Res	Type	Atoms
4	B	601	MES	C7-C8-S-O3S
4	B	601	MES	C7-C8-S-O1S
4	B	601	MES	C7-C8-S-O2S

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 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	B	522/523 (99%)	0.53	49 (9%) 14 14	10, 30, 55, 72	11 (2%)
2	A	340/343 (99%)	0.46	29 (8%) 16 17	9, 27, 47, 60	13 (3%)
All	All	862/866 (99%)	0.50	78 (9%) 15 16	9, 28, 52, 72	24 (2%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	282	ILE	5.1
2	A	211	GLY	4.5
1	B	104	ASN	4.4
1	B	103	TRP	4.1
1	B	135	GLY	4.0
1	B	530	GLN	3.9
2	A	438	VAL	3.9
1	B	412	GLY	3.7
2	A	252	ALA	3.7
1	B	274	THR	3.5
1	B	132	ILE	3.5
2	A	440	LEU	3.5
1	B	70	PRO	3.4
2	A	442	GLU	3.3
1	B	549	ALA	3.2
1	B	134	GLY	3.2
2	A	251	TYR	3.1
2	A	396[A]	ARG	3.1
1	B	280	LYS	3.0
1	B	315	GLY	3.0
1	B	524	ILE	2.9
1	B	239[A]	ASN	2.9
1	B	48	GLY	2.9
2	A	253	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
2	A	439	ALA	2.9
1	B	311	SER	2.8
2	A	254	PRO	2.8
1	B	313	PHE	2.7
1	B	522	ASN	2.7
1	B	533	LEU	2.7
1	B	312	PHE	2.7
1	B	212	ASP	2.7
1	B	73	GLU	2.7
1	B	112	ILE	2.6
1	B	275	GLY	2.6
1	B	136	GLN	2.6
1	B	526	ILE	2.6
2	A	221	GLU	2.6
1	B	137	THR	2.5
1	B	527	THR	2.5
1	B	72	GLY	2.5
2	A	255	GLY	2.5
2	A	341	GLU	2.5
1	B	114	PHE	2.5
2	A	218	VAL	2.5
1	B	47	ASN	2.5
1	B	68	PHE	2.5
2	A	247	LEU	2.5
1	B	133	GLY	2.4
2	A	441	PRO	2.4
1	B	531	ASN	2.4
2	A	308[A]	ARG	2.4
1	B	414	LEU	2.4
1	B	273	LYS	2.4
2	A	213	SER	2.4
1	B	525	THR	2.3
2	A	214	ALA	2.3
1	B	108	VAL	2.3
1	B	279	ARG	2.3
2	A	217	ARG	2.3
1	B	276	LYS	2.2
1	B	277	ASP	2.2
2	A	172	TYR	2.2
1	B	290	ARG	2.2
1	B	294	LYS	2.2
2	A	210	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	71	GLU	2.1
1	B	211	LEU	2.1
1	B	278	VAL	2.1
1	B	131	ASP	2.1
1	B	69	THR	2.1
1	B	521	LYS	2.1
2	A	284	SER	2.0
2	A	225	HIS	2.0
2	A	249	THR	2.0
2	A	209	PRO	2.0
2	A	280	SER	2.0
2	A	285	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](#)

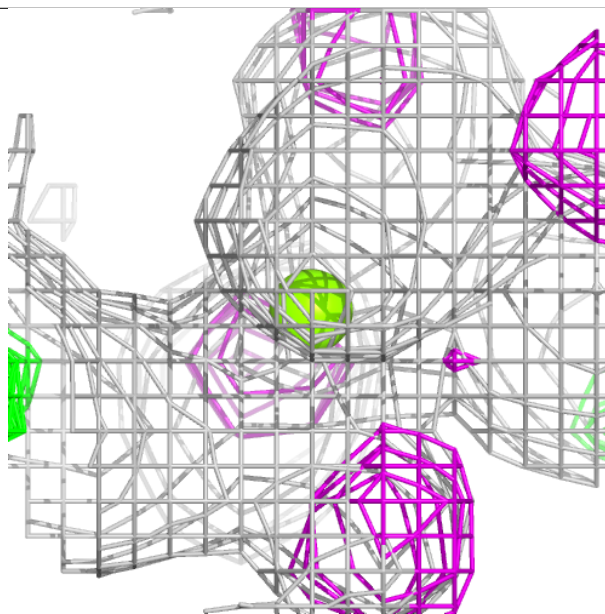
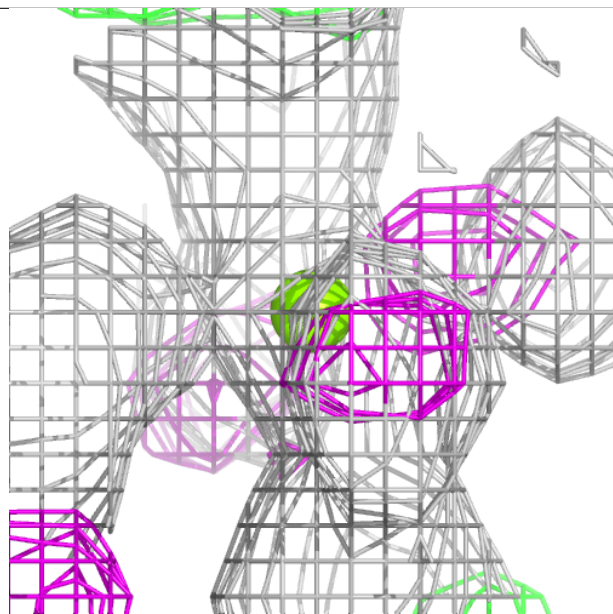
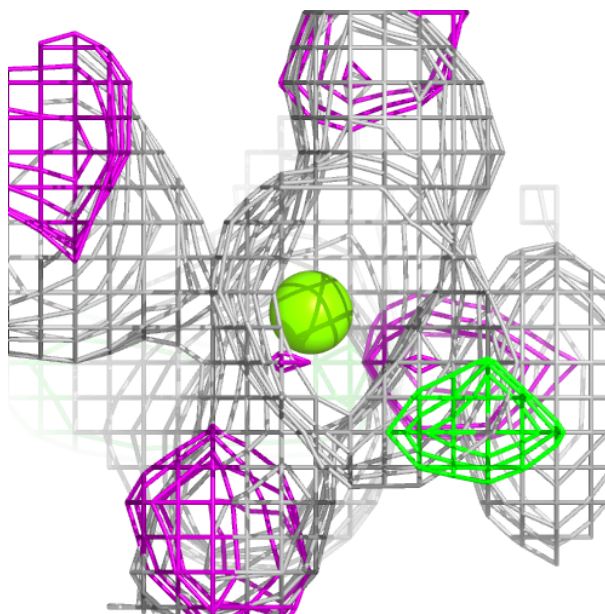
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

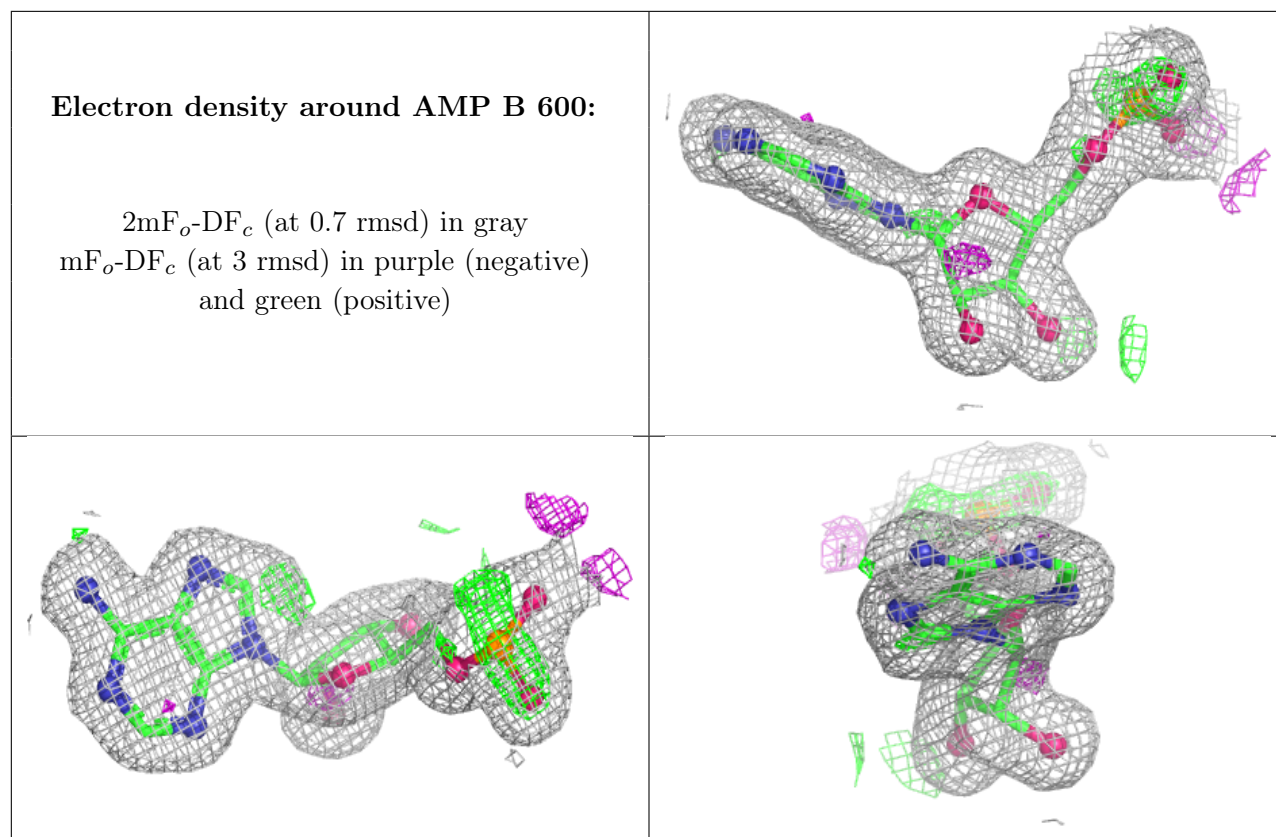
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MES	B	601	12/12	0.87	0.18	36,38,40,41	10
5	MG	A	500	1/1	0.92	0.19	32,32,32,32	1
3	AMP	B	600	22/23	0.96	0.07	21,24,30,32	0

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 MG 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 [i](#)

There are no such residues in this entry.