



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 12:00 am BST

PDB ID : 5XZG
Title : Mouse cGAS bound to the inhibitor RU521
Authors : Vincent, J.; Adura, C.; Gao, P.; Luz, A.; Lama, L.; Asano, Y.; Okamoto, R.;
Imaeda, T.; Aida, J.; Rothamel, K.; Gogakos, T.; Steinberg, J.; Reasoner, S.;
Aso, K.; Tuschl, T.; Patel, D.J.; Glickman, J.F.; Ascano, M.
Deposited on : 2017-07-12
Resolution : 1.83 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 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 : 2.11
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) : 2.11

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3738 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 Cyclic GMP-AMP synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	357	2937	1889	497	538	13	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	146	SER	-	expression tag	UNP Q8C6L5

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*AP*AP*TP*TP*GP*CP*CP*GP*AP*AP*GP*AP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	E	15	308	147	63	84	14	0	0	0

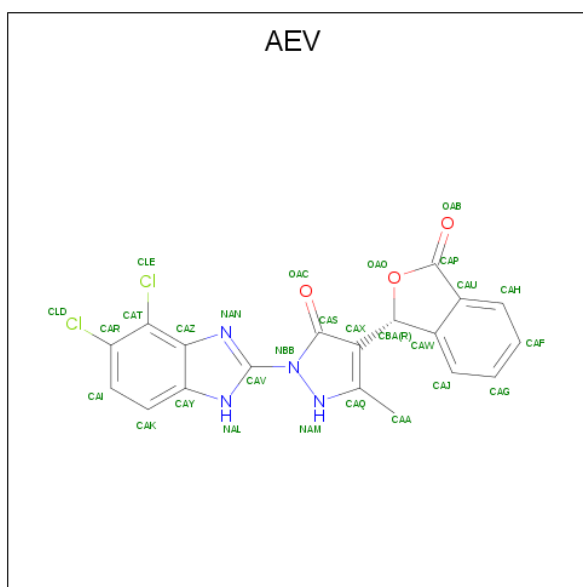
- Molecule 3 is a DNA chain called DNA (5'-D(P*CP*GP*TP*CP*TP*TP*CP*GP*GP*CP*AP*AP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	F	14	284	136	47	87	14	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 2-(4,5-dichloro-1H-benzimidazol-2-yl)-5-methyl-4-[(1R)-3-oxo-1,3-dihydro-2-benzofuran-1-yl]-1,2-dihydro-3H-pyrazol-3-one (three-letter code: AEV) (formula: C₁₉H₁₂Cl₂N₄O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	Cl	N			O
5	A	1	28	19	2	4	3	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	145	Total	O	0	0
			145	145		
6	E	23	Total	O	0	0
			23	23		
6	F	12	Total	O	0	0
			12	12		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	85.56Å 98.43Å 130.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.22 – 1.83 49.21 – 1.83	Depositor EDS
% Data completeness (in resolution range)	92.3 (49.22-1.83) 83.4 (49.21-1.83)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.88 (at 1.83Å)	Xtrriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.194 , 0.232 0.196 , 0.229	Depositor DCC
R_{free} test set	2282 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtrriage
Anisotropy	0.252	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3738	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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: ZN, AEV

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	0.43	0/3001	0.54	0/4031
2	E	1.16	4/347 (1.2%)	0.82	0/534
3	F	1.18	5/316 (1.6%)	0.92	0/485
All	All	0.63	9/3664 (0.2%)	0.62	0/5050

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	10	DA	O3'-P	-6.21	1.53	1.61
2	E	11	DA	O3'-P	-6.03	1.53	1.61
2	E	7	DC	O3'-P	-5.98	1.53	1.61
3	F	9	DT	O3'-P	-5.71	1.54	1.61
3	F	8	DT	O3'-P	-5.71	1.54	1.61
3	F	11	DG	O3'-P	-5.71	1.54	1.61
2	E	9	DG	O3'-P	-5.67	1.54	1.61
3	F	10	DC	O3'-P	-5.37	1.54	1.61
3	F	12	DG	O3'-P	-5.29	1.54	1.61

There are no bond angle outliers.

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	2937	0	2967	35	0
2	E	308	0	169	5	0
3	F	284	0	160	4	0
4	A	1	0	0	0	0
5	A	28	0	0	5	0
6	A	145	0	0	1	0
6	E	23	0	0	0	0
6	F	12	0	0	0	0
All	All	3738	0	3296	40	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 6.

All (40) 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:183:GLN:NE2	1:A:190:LYS:O	2.10	0.84
2:E:6:DG:N2	3:F:13:DC:O2	2.14	0.79
1:A:222:ARG:HG2	1:A:240:LYS:HD2	1.68	0.75
1:A:484:LYS:HD2	1:A:484:LYS:H	1.50	0.74
1:A:184:LYS:HD2	1:A:185:ARG:N	2.02	0.74
1:A:419:CYS:SG	5:A:602:AEV:CBA	2.78	0.72
1:A:354:ASP:OD1	1:A:355:GLY:N	2.28	0.67
1:A:176:GLU:N	1:A:176:GLU:OE1	2.29	0.66
1:A:463:GLU:OE1	1:A:483:ARG:HD3	1.98	0.63
1:A:248:LEU:HD22	1:A:262:MET:HE2	1.79	0.63
1:A:185:ARG:O	1:A:187:SER:N	2.30	0.62
1:A:419:CYS:HB3	5:A:602:AEV:CAJ	2.30	0.62
1:A:181:ARG:O	1:A:184:LYS:HB3	2.03	0.59
1:A:463:GLU:HG2	1:A:486:LYS:HE3	1.87	0.56
1:A:182:MET:HG3	1:A:189:PHE:HB2	1.87	0.56
2:E:6:DG:N1	3:F:13:DC:N3	2.42	0.54
1:A:185:ARG:HG3	1:A:186:GLU:H	1.74	0.51
1:A:205:LYS:HE2	1:A:211:GLU:HB2	1.92	0.51
1:A:267:ARG:NH2	6:A:704:HOH:O	2.44	0.51
1:A:257:LEU:HD11	1:A:262:MET:CE	2.41	0.50
1:A:224:GLU:HG3	1:A:240:LYS:HG2	1.93	0.50
1:A:251:PHE:HD2	1:A:262:MET:HE2	1.77	0.49
2:E:15:DG:H1	3:F:4:DC:H42	1.61	0.48
2:E:1:DA:H2''	2:E:2:DA:N7	2.28	0.48
1:A:152:LYS:HA	1:A:152:LYS:HD2	1.48	0.46
1:A:248:LEU:HD13	1:A:262:MET:HE1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:SER:O	1:A:451:LYS:HG3	2.16	0.46
1:A:464:LYS:HE2	1:A:466:ASP:OD1	2.15	0.46
3:F:13:DC:H2"	3:F:14:DA:C8	2.53	0.44
1:A:419:CYS:SG	5:A:602:AEV:CAJ	3.06	0.43
1:A:151:LYS:HD2	1:A:151:LYS:HA	1.60	0.43
1:A:473:PHE:CE2	5:A:602:AEV:CLE	3.09	0.43
1:A:184:LYS:O	1:A:187:SER:HB3	2.18	0.42
1:A:185:ARG:CG	1:A:186:GLU:N	2.83	0.42
1:A:161:ARG:HH12	2:E:12:DG:H21	1.67	0.42
1:A:436:GLN:HB2	1:A:439:GLN:HG3	2.01	0.42
1:A:412:PHE:CE2	1:A:492:LYS:HD2	2.56	0.41
1:A:483:ARG:O	1:A:487:GLU:HG3	2.20	0.41
1:A:430:MET:HG3	1:A:452:LEU:HD13	2.02	0.40
1:A:419:CYS:CB	5:A:602:AEV:CAJ	2.99	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	355/362 (98%)	337 (95%)	13 (4%)	5 (1%)	11 3

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	GLU
1	A	185	ARG
1	A	254	GLY
1	A	241	ARG
1	A	300	ASN

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	327/335 (98%)	321 (98%)	6 (2%)	59 48

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	176	GLU
1	A	185	ARG
1	A	186	GLU
1	A	410	LYS
1	A	479	GLU
1	A	484	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	478	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 carbohydrates in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is 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
5	AEV	A	602	-	26,32,32	3.41	14 (53%)	27,49,49	3.51	6 (22%)

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
5	AEV	A	602	-	-	0/0/20/20	0/5/5/5

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	602	AEV	NAM-NBB	-9.61	1.20	1.39
5	A	602	AEV	CAU-CAP	-6.16	1.33	1.47
5	A	602	AEV	CAT-CAZ	-5.52	1.33	1.42
5	A	602	AEV	OAC-CAS	4.82	1.36	1.24
5	A	602	AEV	CAK-CAY	-4.60	1.33	1.41
5	A	602	AEV	CAJ-CAW	-3.87	1.34	1.39
5	A	602	AEV	CAU-CAW	-3.75	1.34	1.39
5	A	602	AEV	CAH-CAU	-3.63	1.34	1.39
5	A	602	AEV	CAV-NBB	-3.39	1.32	1.44
5	A	602	AEV	OAO-CBA	-3.36	1.43	1.46
5	A	602	AEV	CAW-CBA	-3.15	1.43	1.52
5	A	602	AEV	CAS-CAX	-2.47	1.32	1.38
5	A	602	AEV	CAZ-CAY	-2.27	1.35	1.42
5	A	602	AEV	CAA-CAQ	2.06	1.53	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
5	A	602	AEV	CBA-OAO-CAP	-13.04	101.62	110.75
5	A	602	AEV	OAO-CAP-CAU	8.55	113.53	108.42
5	A	602	AEV	CAS-CAX-CBA	-4.40	120.75	127.38
5	A	602	AEV	CAW-CAU-CAP	-4.04	106.65	108.45
5	A	602	AEV	OAO-CAP-OAB	3.56	124.23	121.19
5	A	602	AEV	OAO-CBA-CAW	3.34	105.29	103.49

There are no chirality outliers.

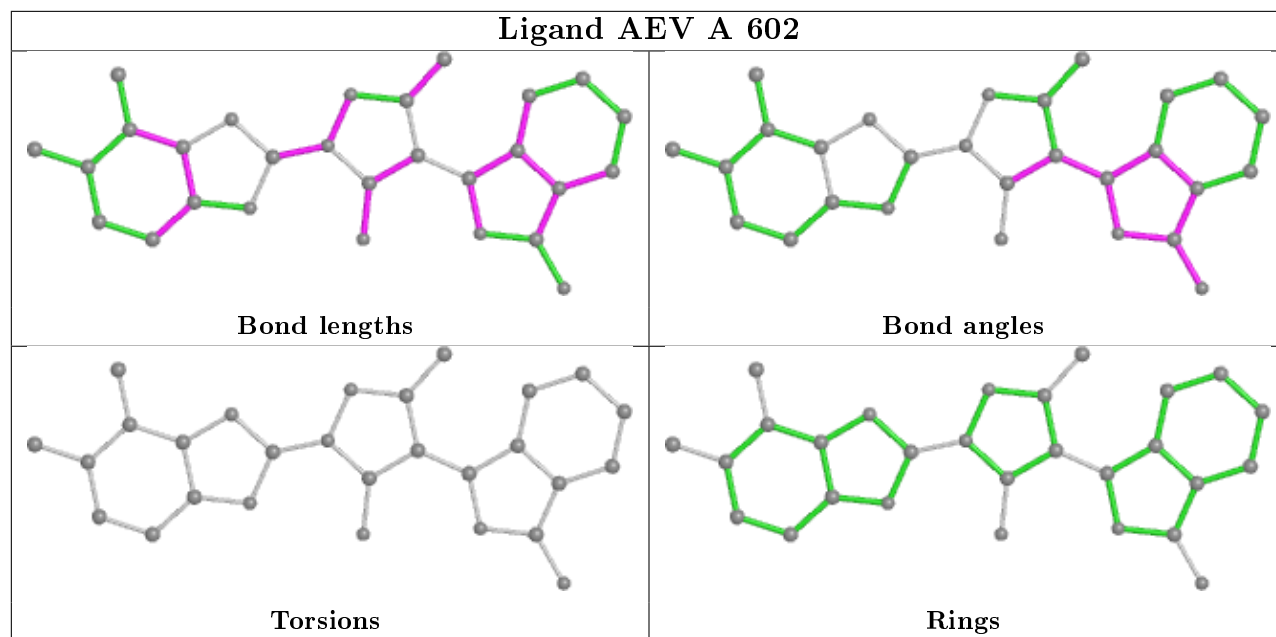
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	602	AEV	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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	357/362 (98%)	0.32	19 (5%) 26 21	30, 49, 92, 145	0
2	E	15/15 (100%)	0.01	1 (6%) 17 14	36, 65, 132, 144	0
3	F	14/14 (100%)	-0.03	0 100 100	41, 71, 139, 140	0
All	All	386/391 (98%)	0.30	20 (5%) 27 22	30, 50, 101, 145	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	ILE	7.4
1	A	247	PRO	7.2
1	A	244	ARG	5.8
1	A	246	ASN	5.4
1	A	243	PRO	5.1
1	A	185	ARG	4.6
1	A	245	GLY	4.4
1	A	222	ARG	3.7
1	A	248	LEU	3.6
1	A	239	PHE	3.4
1	A	186	GLU	3.3
1	A	354	ASP	3.2
1	A	254	GLY	2.8
1	A	250	HIS	2.8
1	A	255	GLU	2.6
1	A	240	LYS	2.4
1	A	221	PRO	2.4
1	A	253	GLU	2.4
1	A	411	GLU	2.3
2	E	1	DA	2.1

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](#)

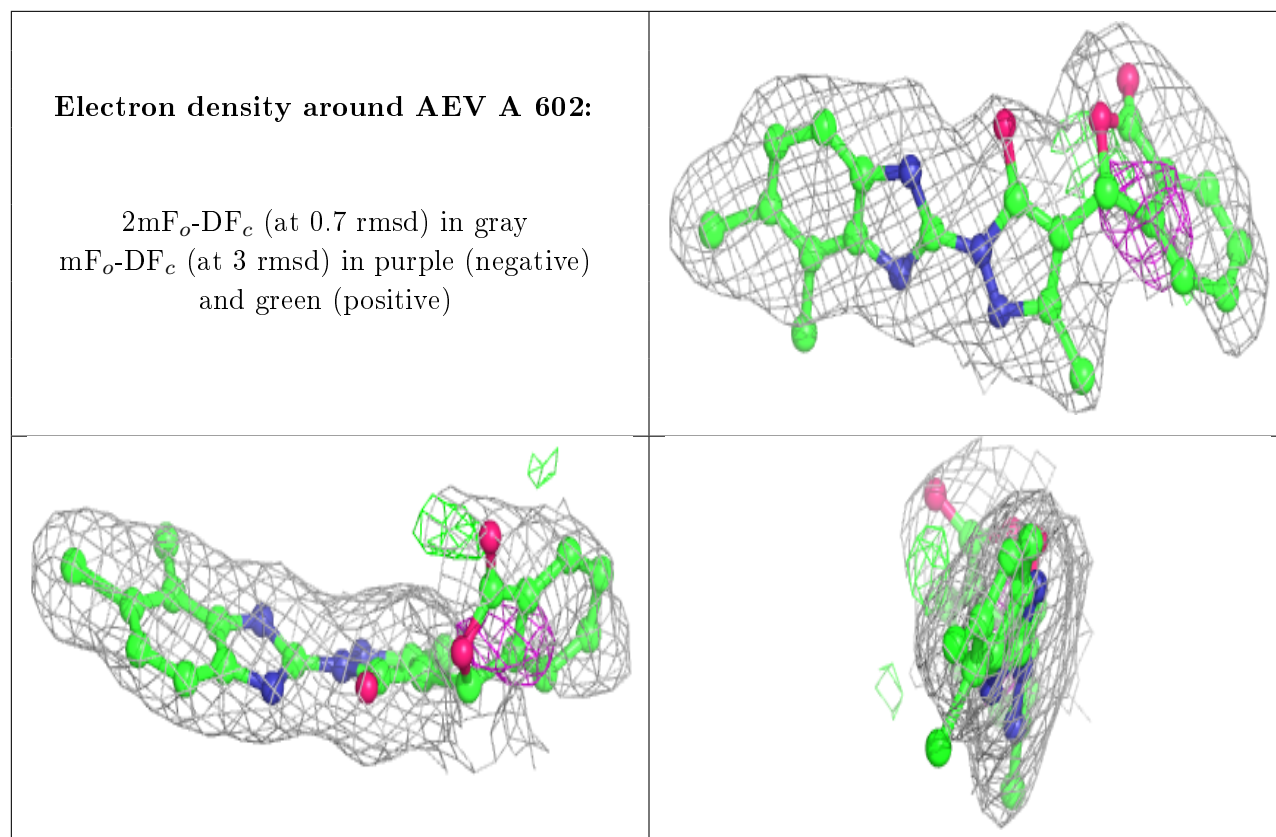
There are no carbohydrates in this entry.

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(\AA^2)	Q<0.9
5	AEV	A	602	28/28	0.88	0.15	58,69,95,217	0
4	ZN	A	601	1/1	0.99	0.11	35,35,35,35	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.