



# Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2025 – 04:34 PM JST

PDB ID : 9J2X / pdb\_00009j2x  
Title : Human cGAS catalytic domain bound with RU.521  
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Deposited on : 2024-08-07  
Resolution : 2.29 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

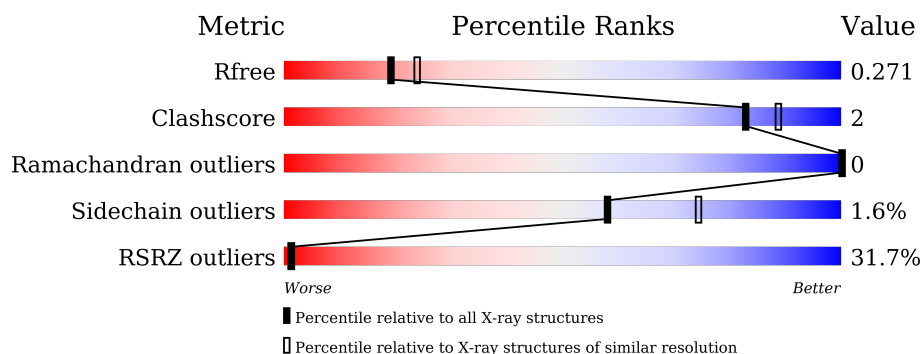
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.29 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))
$R_{free}$	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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  $\geq 3$ , 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	366	<div> <div>28%</div> <div>86%</div> <div>7%</div> <div>7%</div> </div>
1	B	366	<div> <div>28%</div> <div>74%</div> <div>9%</div> <div>17%</div> </div>

## 2 Entry composition [i](#)

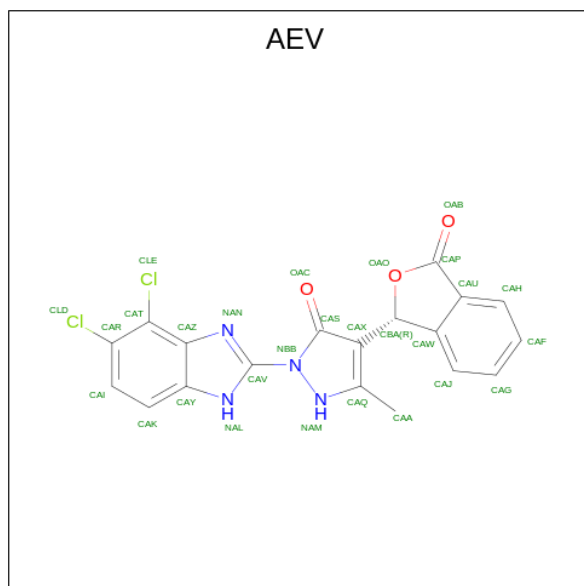
There are 5 unique types of molecules in this entry. The entry contains 5062 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
1	A	340	Total	C	N	O	S	0	0	0
			2634	1688	447	485	14			
1	B	303	Total	C	N	O	S	0	0	0
			2279	1453	396	419	11			

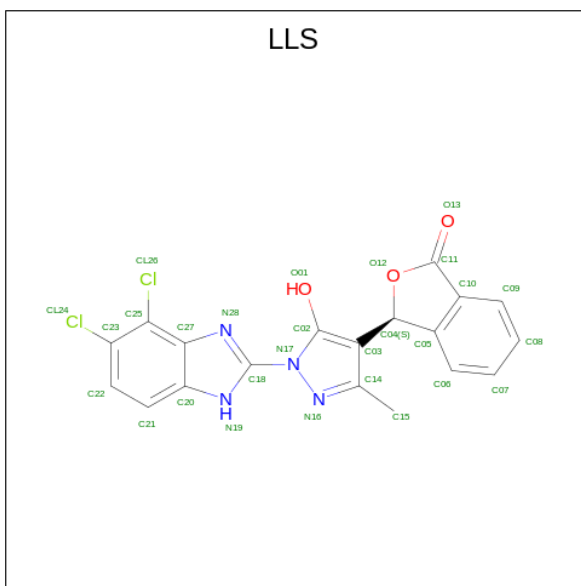
- Molecule 2 is 2-(4,5-dichloro-1H-benzimidazol-2-yl)-5-methyl-4-[(1R)-3-oxo-1,3-dihydro-2-benzofuran-1-yl]-1,2-dihydro-3H-pyrazol-3-one (CCD ID: AEV) (formula: C<sub>19</sub>H<sub>12</sub>Cl<sub>2</sub>N<sub>4</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is (3 {S})-3-[1-[4,5-bis(chloranyl)-1 {H}-benzimidazol-2-yl]-3-methyl-5-oxidanyl-pyrazol-4-yl]-3 {H}-2-benzofuran-1-one (CCD ID: LLS) (formula: C<sub>19</sub>H<sub>12</sub>Cl<sub>2</sub>N<sub>4</sub>O<sub>3</sub>) (labeled

as "Ligand of Interest" by depositor).



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

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	21	Total	O	0	0
			21	21		
5	B	14	Total	O	0	0
			14	14		



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	222.65Å 48.39Å 86.88Å 90.00° 112.58° 90.00°	Depositor
Resolution (Å)	43.44 – 2.29 43.44 – 2.29	Depositor EDS
% Data completeness (in resolution range)	83.8 (43.44-2.29) 84.0 (43.44-2.29)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.17 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.254 , 0.271 0.254 , 0.271	Depositor DCC
$R_{free}$ test set	2074 reflections (5.30%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	28.9	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.022 for -h-2*1,-k,l	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	5062	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: AEV, LLS, 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	0.90	0/2682	1.17	16/3618 (0.4%)
1	B	0.88	0/2313	1.20	14/3108 (0.5%)
All	All	0.89	0/4995	1.19	30/6726 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

There are no bond length outliers.

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	222	ALA	CA-C-N	6.62	126.25	119.56
1	B	222	ALA	C-N-CA	6.62	126.25	119.56
1	A	449	ASN	CA-C-N	6.53	126.67	119.87
1	A	449	ASN	C-N-CA	6.53	126.67	119.87
1	B	449	ASN	CA-C-N	6.24	125.86	119.56
1	B	449	ASN	C-N-CA	6.24	125.86	119.56
1	A	265	PHE	CA-CB-CG	6.05	119.85	113.80
1	A	390	HIS	CA-C-N	-5.95	116.27	122.69
1	A	390	HIS	C-N-CA	-5.95	116.27	122.69
1	A	222	ALA	CA-C-N	5.95	125.62	119.56
1	A	222	ALA	C-N-CA	5.95	125.62	119.56
1	B	330	TRP	CA-C-N	5.83	125.84	119.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	330	TRP	C-N-CA	5.83	125.84	119.89
1	A	344	LEU	CA-C-N	5.73	132.48	121.54
1	A	344	LEU	C-N-CA	5.73	132.48	121.54
1	A	392	LYS	N-CA-C	-5.62	105.23	111.36
1	B	424	PHE	N-CA-CB	-5.62	102.03	110.91
1	B	390	HIS	CA-C-N	-5.59	116.66	122.69
1	B	390	HIS	C-N-CA	-5.59	116.66	122.69
1	A	330	TRP	CA-C-N	5.56	125.51	119.78
1	A	330	TRP	C-N-CA	5.56	125.51	119.78
1	A	424	PHE	N-CA-CB	-5.50	102.14	111.17
1	A	234	VAL	CA-C-N	5.38	124.84	119.24
1	A	234	VAL	C-N-CA	5.38	124.84	119.24
1	B	514	ASN	CA-CB-CG	-5.30	107.30	112.60
1	A	389	ASN	CB-CA-C	5.29	119.61	111.95
1	B	360	VAL	N-CA-CB	-5.24	106.00	111.61
1	B	344	LEU	CA-C-N	5.22	131.51	121.54
1	B	344	LEU	C-N-CA	5.22	131.51	121.54
1	B	516	PHE	N-CA-CB	-5.06	101.36	110.37

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	423	ARG	Sidechain
1	A	476	ARG	Sidechain
1	B	349	ARG	Sidechain
1	B	406	ARG	Sidechain

## 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	2634	0	2498	12	0
1	B	2279	0	2066	10	0
2	A	28	0	0	0	0
2	B	28	0	0	0	0
3	A	28	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	28	0	0	2	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	21	0	0	0	0
5	B	14	0	0	0	0
All	All	5062	0	4564	22	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 2.

All (22) 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:485:ILE:HD12	3:B:601:LLS:CL24	2.00	0.97
1:A:485:ILE:CD1	3:A:602:LLS:CL24	2.52	0.95
1:A:485:ILE:HD13	3:A:602:LLS:CL24	2.05	0.93
1:A:288:ILE:HD11	1:A:298:MET:HB2	1.74	0.68
1:A:209:LEU:HD22	1:A:231:LYS:HD3	1.82	0.62
1:A:281:ARG:O	1:A:298:MET:HE1	2.00	0.60
1:A:298:MET:HE2	1:A:308:VAL:CG2	2.40	0.52
1:B:307:ALA:O	1:B:308:VAL:C	2.53	0.51
1:A:298:MET:HE2	1:A:308:VAL:HG22	1.94	0.50
1:A:485:ILE:HD12	3:A:602:LLS:CL24	2.43	0.50
1:B:186:VAL:HA	1:B:189:VAL:N	2.30	0.47
1:A:377:LEU:O	3:A:602:LLS:CL26	2.69	0.47
1:B:419:GLN:HB3	1:B:518:VAL:HG22	1.95	0.47
1:A:288:ILE:CD1	1:A:298:MET:HB2	2.44	0.44
1:B:245:THR:C	1:B:247:ALA:H	2.25	0.43
1:B:208:LEU:HD23	1:B:208:LEU:HA	1.77	0.43
1:A:227:ASP:OD2	3:A:602:LLS:C07	2.66	0.43
1:B:377:LEU:O	3:B:601:LLS:CL26	2.74	0.43
1:A:442:PHE:O	1:A:445:VAL:HG22	2.20	0.41
1:B:240:GLU:O	1:B:250:PHE:N	2.38	0.41
1:B:201:SER:O	1:B:202:ALA:C	2.62	0.41
1:B:190:VAL:O	1:B:191:ASP:C	2.64	0.41

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	326/366 (89%)	317 (97%)	9 (3%)	0	100	100
1	B	271/366 (74%)	261 (96%)	10 (4%)	0	100	100
All	All	597/732 (82%)	578 (97%)	19 (3%)	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	A	270/336 (80%)	267 (99%)	3 (1%)	70	83
1	B	219/336 (65%)	214 (98%)	5 (2%)	45	63
All	All	489/672 (73%)	481 (98%)	8 (2%)	58	74

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	209	LEU
1	A	259	GLU
1	A	264	GLN
1	B	213	SER
1	B	231	LYS
1	B	479	LYS
1	B	498	LYS
1	B	515	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	419	GLN
1	A	451	GLN

### 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 6 ligands modelled in this entry, 2 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	$\# Z  > 2$
2	AEV	A	601	3	28,32,32	2.55	8 (28%)	28,49,49	3.51	6 (21%)
3	LLS	A	602	2	27,32,32	2.13	7 (25%)	27,49,49	3.89	7 (25%)
3	LLS	B	601	2	27,32,32	2.00	6 (22%)	27,49,49	3.39	8 (29%)
2	AEV	B	602	3	28,32,32	2.83	8 (28%)	28,49,49	5.91	9 (32%)

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
2	AEV	A	601	3	-	0/3/20/20	0/5/5/5
3	LLS	A	602	2	-	0/0/28/28	0/5/5/5
3	LLS	B	601	2	-	0/0/28/28	0/5/5/5
2	AEV	B	602	3	-	0/3/20/20	0/5/5/5

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	602	AEV	OAC-CAS	8.12	1.40	1.23
2	A	601	AEV	OAC-CAS	7.87	1.39	1.23
3	A	602	LLS	O12-C04	-6.91	1.40	1.46
2	B	602	AEV	OAO-CBA	6.77	1.57	1.46
3	B	601	LLS	O12-C04	-6.07	1.41	1.46
2	B	602	AEV	CAS-NBB	-5.68	1.30	1.39
2	A	601	AEV	CAS-NBB	-5.52	1.31	1.39
2	B	602	AEV	CAJ-CAW	5.40	1.46	1.39
2	A	601	AEV	OAO-CAP	4.27	1.41	1.36
3	A	602	LLS	O12-C11	4.04	1.41	1.36
2	A	601	AEV	CAU-CAW	-3.99	1.33	1.39
3	B	601	LLS	O12-C11	3.96	1.41	1.36
2	A	601	AEV	CAS-CAX	-3.71	1.37	1.46
3	A	602	LLS	C10-C05	-3.59	1.34	1.39
2	B	602	AEV	CAS-CAX	-3.56	1.37	1.46
3	B	601	LLS	C10-C05	-3.47	1.34	1.39
3	A	602	LLS	C03-C04	-3.14	1.49	1.53
3	B	601	LLS	C03-C04	-2.99	1.49	1.53
2	A	601	AEV	OAO-CBA	-2.89	1.41	1.46
2	B	602	AEV	CAU-CAW	2.53	1.42	1.39
3	B	601	LLS	O01-C02	2.51	1.40	1.32
3	A	602	LLS	O01-C02	2.36	1.39	1.32
2	A	601	AEV	CAV-NBB	2.17	1.44	1.40
2	B	602	AEV	CAV-NBB	2.16	1.44	1.40
3	A	602	LLS	C20-C27	-2.16	1.35	1.42
2	A	601	AEV	CAY-CAZ	-2.14	1.35	1.42
2	B	602	AEV	CAY-CAZ	-2.08	1.35	1.42
3	A	602	LLS	N16-N17	-2.03	1.35	1.39
3	B	601	LLS	C23-CL24	2.01	1.78	1.73

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	AEV	CBA-OAO-CAP	-22.59	100.62	110.78
2	B	602	AEV	CAW-CAU-CAP	-13.65	102.34	108.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	AEV	CBA-OAO-CAP	-13.13	104.88	110.78
2	B	602	AEV	OAO-CAP-CAU	12.11	115.66	108.42
3	A	602	LLS	C04-O12-C11	-10.58	103.34	110.75
3	B	601	LLS	C04-O12-C11	-9.76	103.92	110.75
3	A	602	LLS	O12-C11-O13	9.20	129.04	121.19
3	A	602	LLS	O12-C11-C10	-9.19	102.93	108.42
3	B	601	LLS	O12-C11-O13	8.48	128.43	121.19
2	A	601	AEV	OAO-CAP-OAB	8.28	128.26	121.19
3	B	601	LLS	O12-C11-C10	-7.59	103.88	108.42
3	A	602	LLS	O12-C04-C05	-7.31	99.57	103.49
3	A	602	LLS	C05-C10-C11	-6.54	105.52	108.45
2	B	602	AEV	CAA-CAQ-NAM	5.73	126.54	119.26
3	B	601	LLS	C05-C10-C11	-5.54	105.97	108.45
2	A	601	AEV	CAA-CAQ-NAM	5.34	126.04	119.26
2	B	602	AEV	CAA-CAQ-CAX	-5.32	125.41	131.66
2	A	601	AEV	CAA-CAQ-CAX	-5.03	125.75	131.66
2	B	602	AEV	OAO-CAP-OAB	4.83	125.31	121.19
3	B	601	LLS	O12-C04-C05	-4.75	100.94	103.49
2	A	601	AEV	CAW-CAU-CAP	-3.79	106.76	108.45
2	A	601	AEV	OAO-CAP-CAU	-3.68	106.22	108.42
2	B	602	AEV	CAH-CAU-CAP	3.60	139.83	127.95
2	B	602	AEV	OAB-CAP-CAU	-2.80	118.33	129.07
3	A	602	LLS	C25-C23-CL24	-2.74	117.84	120.54
2	B	602	AEV	CAH-CAU-CAW	-2.74	117.81	121.16
3	B	601	LLS	C25-C23-CL24	-2.45	118.13	120.54
3	B	601	LLS	C27-C25-CL26	2.26	120.54	117.65
3	A	602	LLS	C06-C05-C04	2.16	133.36	128.82
3	B	601	LLS	C06-C05-C04	2.03	133.08	128.82

There are no chirality outliers.

There are no torsion outliers.

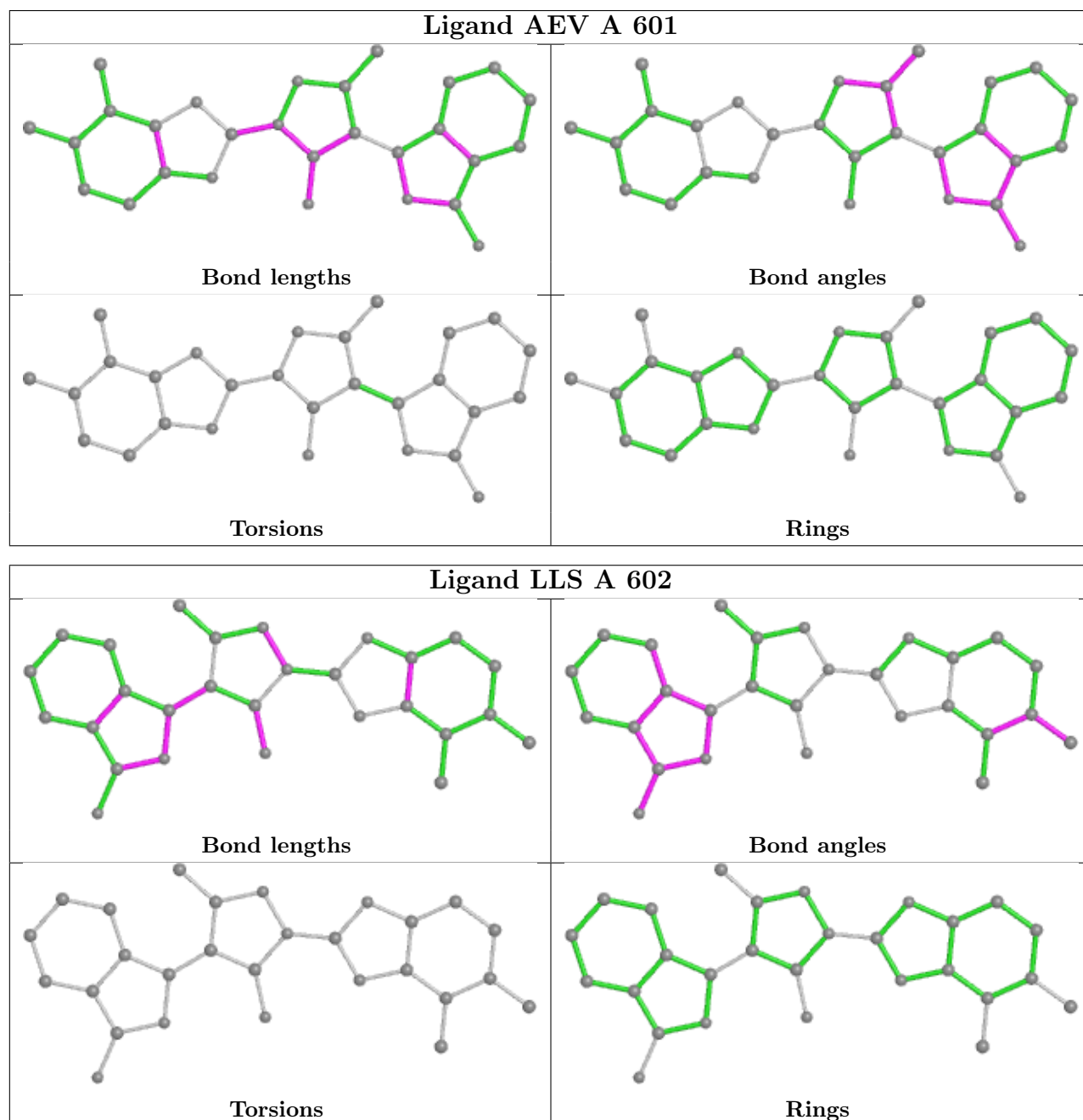
There are no ring outliers.

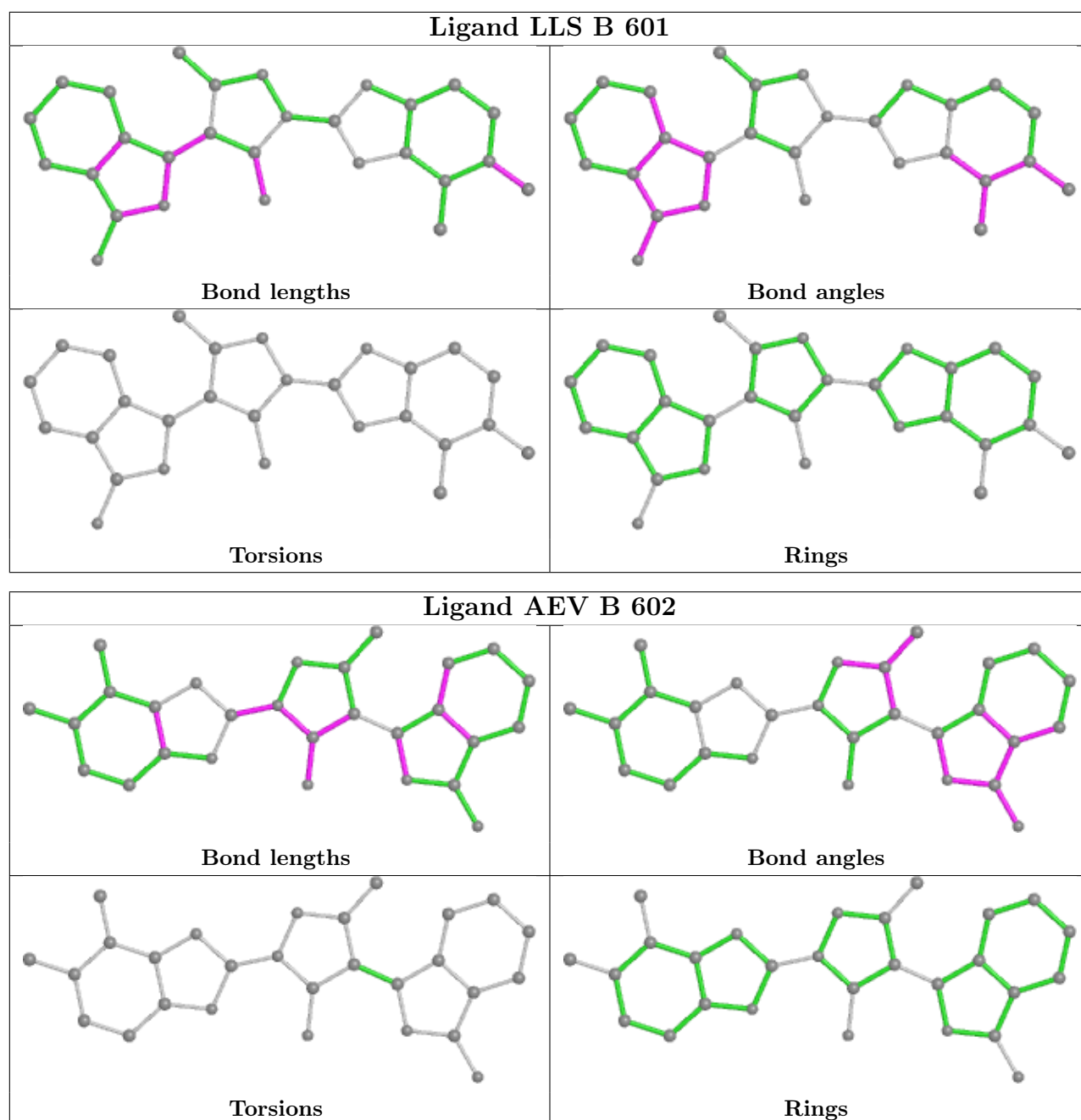
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	LLS	5	0
3	B	601	LLS	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	340/366 (92%)	1.25	103 (30%)  	18, 45, 95, 121	0
1	B	303/366 (82%)	1.49	101 (33%)  	20, 49, 115, 134	0
All	All	643/732 (87%)	1.37	204 (31%)  	18, 47, 103, 134	0

All (204) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	201	SER	6.1
1	B	265	PHE	5.5
1	B	260	ASN	5.4
1	B	215	TYR	5.3
1	B	287	GLU	5.2
1	B	272	SER	5.2
1	B	203	PHE	5.1
1	B	206	VAL	5.1
1	A	175	SER	5.1
1	B	267	GLU	5.0
1	B	364	ALA	5.0
1	B	183	ALA	4.9
1	B	243	SER	4.8
1	B	235	PRO	4.8
1	B	202	ALA	4.7
1	A	295	ASP	4.7
1	B	300	ARG	4.7
1	B	283	ILE	4.6
1	B	322	LEU	4.6
1	A	288	ILE	4.6
1	B	191	ASP	4.6
1	A	178	ASP	4.5
1	B	280	PHE	4.5
1	B	308	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	308	VAL	4.5
1	B	359	LEU	4.4
1	B	261	PRO	4.4
1	A	199	CYS	4.4
1	B	373	GLU	4.4
1	A	181	THR	4.3
1	B	199	CYS	4.2
1	B	211	THR	4.2
1	A	176	ARG	4.2
1	B	185	MET	4.2
1	B	312	ILE	4.1
1	A	290	ASP	4.1
1	A	202	ALA	4.1
1	B	301	LYS	4.1
1	A	174	LEU	4.0
1	A	322	LEU	4.0
1	A	296	VAL	4.0
1	A	177	ASP	4.0
1	B	313	SER	3.9
1	B	316	ILE	3.9
1	B	244	ASN	3.9
1	B	360	VAL	3.9
1	B	161	GLY	3.9
1	A	277	LEU	3.8
1	B	266	LEU	3.8
1	B	304	GLY	3.8
1	B	189	VAL	3.8
1	A	179	ILE	3.8
1	A	211	THR	3.8
1	A	269	GLU	3.7
1	B	237	ILE	3.7
1	A	283	ILE	3.7
1	B	184	GLY	3.7
1	B	192	HIS	3.7
1	B	197	LEU	3.7
1	A	263	SER	3.7
1	B	252	LYS	3.7
1	B	190	VAL	3.6
1	A	262	LEU	3.6
1	B	270	ILE	3.6
1	B	374	THR	3.6
1	A	316	ILE	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	186	VAL	3.5
1	B	213	SER	3.5
1	A	252	LYS	3.5
1	A	289	ASN	3.5
1	B	249	TYR	3.5
1	B	210	ASN	3.5
1	B	259	GLU	3.5
1	A	365	LYS	3.5
1	B	195	LEU	3.4
1	B	196	ARG	3.4
1	A	166	ARG	3.4
1	A	232	LEU	3.3
1	B	281	ARG	3.3
1	A	260	ASN	3.3
1	B	241	GLU	3.3
1	A	185	MET	3.3
1	B	494	ASN	3.3
1	B	324	LEU	3.3
1	A	214	TYR	3.3
1	B	208	LEU	3.2
1	A	235	PRO	3.2
1	B	250	PHE	3.2
1	A	173	LYS	3.1
1	B	248	TYR	3.1
1	A	195	LEU	3.1
1	A	180	SER	3.1
1	B	226	PHE	3.1
1	A	206	VAL	3.1
1	A	306	PRO	3.1
1	A	297	ILE	3.0
1	B	218	VAL	3.0
1	A	457	ARG	3.0
1	B	220	ILE	3.0
1	B	174	LEU	3.0
1	A	213	SER	3.0
1	A	270	ILE	3.0
1	A	278	SER	3.0
1	B	234	VAL	3.0
1	A	294	THR	2.9
1	B	333	SER	2.9
1	B	520	ASP	2.9
1	A	287	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	286	GLU	2.9
1	A	161	GLY	2.9
1	B	302	ARG	2.9
1	B	380	SER	2.9
1	B	200	ASP	2.9
1	B	318	VAL	2.9
1	B	247	ALA	2.9
1	B	282	LYS	2.9
1	A	215	TYR	2.8
1	A	320	ILE	2.8
1	A	280	PHE	2.8
1	A	271	LEU	2.8
1	A	387	LEU	2.8
1	A	313	SER	2.8
1	A	372	GLU	2.8
1	A	209	LEU	2.8
1	A	264	GLN	2.8
1	B	372	GLU	2.7
1	A	298	MET	2.7
1	A	265	PHE	2.7
1	A	371	GLN	2.7
1	A	203	PHE	2.6
1	A	182	ALA	2.6
1	A	311	LEU	2.6
1	A	521	GLU	2.6
1	B	229	MET	2.6
1	B	515	GLU	2.6
1	A	210	ASN	2.6
1	B	224	ASN	2.6
1	B	166	ARG	2.6
1	B	251	VAL	2.6
1	A	307	ALA	2.6
1	A	237	ILE	2.6
1	A	314	GLU	2.6
1	B	245	THR	2.6
1	A	426	ASP	2.6
1	A	341	GLN	2.5
1	A	196	ARG	2.5
1	A	520	ASP	2.5
1	A	170	GLU	2.5
1	A	268	GLY	2.5
1	B	230	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	208	LEU	2.5
1	A	276	MET	2.4
1	A	184	GLY	2.4
1	B	363	HIS	2.4
1	A	259	GLU	2.4
1	A	284	ILE	2.4
1	B	385	GLU	2.4
1	B	335	GLN	2.4
1	A	267	GLU	2.4
1	A	364	ALA	2.4
1	A	251	VAL	2.4
1	A	186	VAL	2.3
1	B	284	ILE	2.3
1	A	239	LEU	2.3
1	B	238	GLN	2.3
1	A	300	ARG	2.3
1	A	261	PRO	2.3
1	B	309	THR	2.3
1	A	192	HIS	2.3
1	B	163	SER	2.3
1	B	227	ASP	2.3
1	A	250	PHE	2.2
1	A	351	GLN	2.2
1	A	201	SER	2.2
1	A	312	ILE	2.2
1	A	285	LYS	2.2
1	A	286	GLU	2.2
1	A	194	LEU	2.2
1	A	242	TYR	2.2
1	B	232	LEU	2.2
1	B	239	LEU	2.2
1	A	189	VAL	2.2
1	A	479	LYS	2.2
1	B	320	ILE	2.2
1	A	172	LEU	2.2
1	A	310	LEU	2.2
1	B	271	LEU	2.2
1	B	285	LYS	2.2
1	A	245	THR	2.2
1	A	319	ASP	2.2
1	B	212	GLY	2.1
1	A	279	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	205	GLY	2.1
1	B	375	TRP	2.1
1	B	413	MET	2.1
1	B	488	PHE	2.1
1	B	361	PRO	2.1
1	A	317	SER	2.1
1	A	323	ALA	2.1
1	B	378	SER	2.0
1	A	162	ALA	2.0
1	B	228	VAL	2.0
1	A	187	LYS	2.0
1	B	209	LEU	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](#)

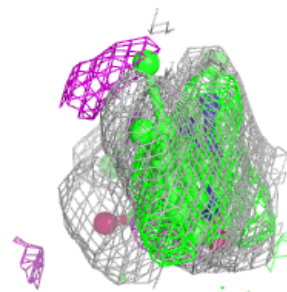
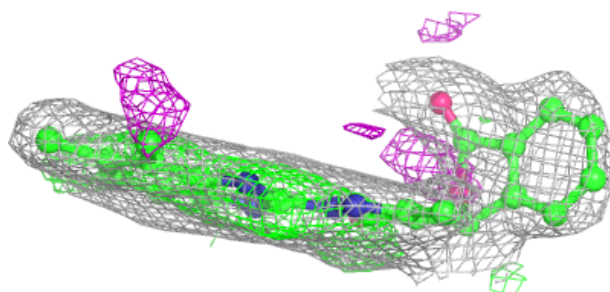
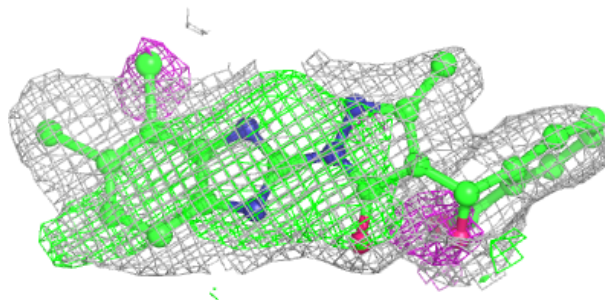
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	LLS	A	602	28/28	0.72	0.30	28,30,39,46	28
2	AEV	B	602	28/28	0.75	0.28	37,44,52,54	28
3	LLS	B	601	28/28	0.75	0.33	42,44,53,55	28
2	AEV	A	601	28/28	0.83	0.22	24,28,38,39	28
4	ZN	B	603	1/1	0.98	0.03	23,23,23,23	0
4	ZN	A	603	1/1	0.99	0.02	24,24,24,24	0

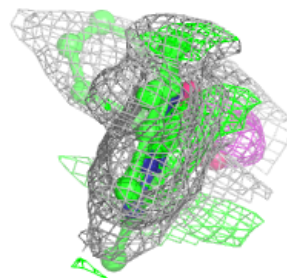
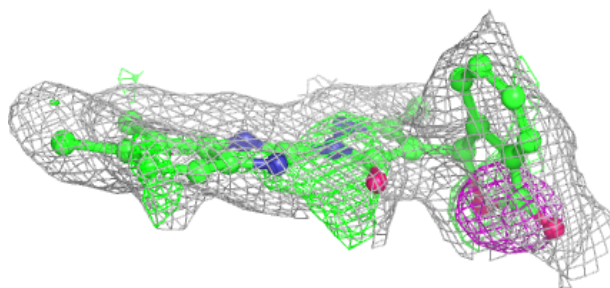
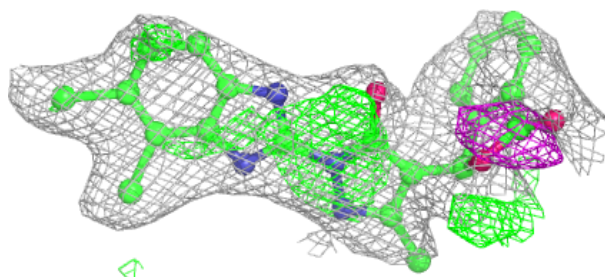
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around LLS A 602:**

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

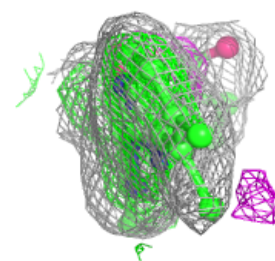
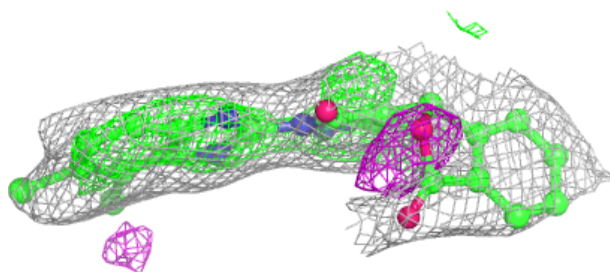
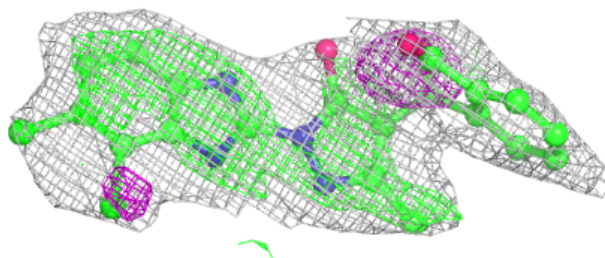
**Electron density around AEV B 602:**

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

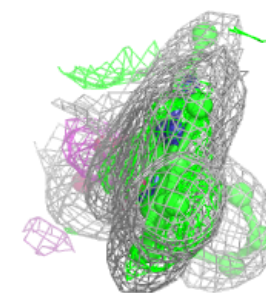
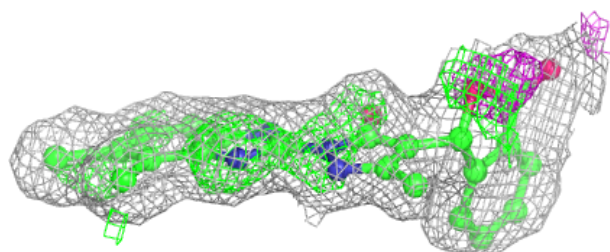
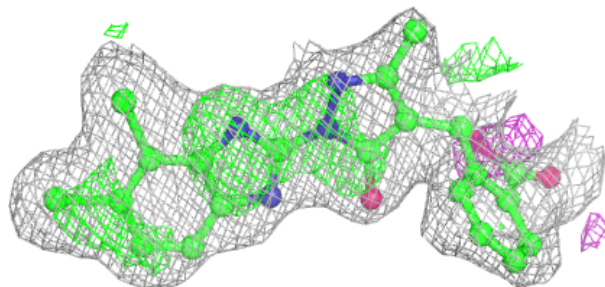


**Electron density around LLS B 601:**

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

**Electron density around AEV A 601:**

$2mF_o-DF_c$  (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.