



Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2025 – 04:36 PM JST

PDB ID : 9LIO / pdb_00009lio
Title : Human cGAS catalytic domain bound with XL-3123
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Deposited on : 2025-01-14
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 Phenix2.0rc1
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

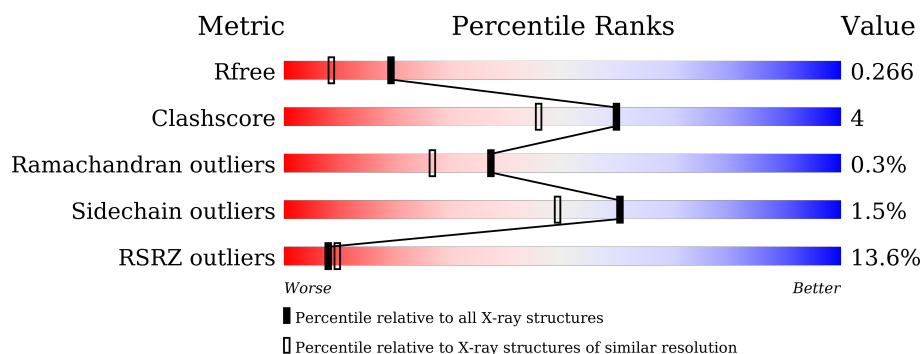
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	164625	1028 (1.92-1.92)
Clashscore	180529	1100 (1.92-1.92)
Ramachandran outliers	177936	1087 (1.92-1.92)
Sidechain outliers	177891	1087 (1.92-1.92)
RSRZ outliers	164620	1028 (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	366	<div> <div>12%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>6%</div> </div> </div>
1	B	366	<div> <div>14%</div> <div> <div></div> <div>83%</div> <div>10%</div> <div>7%</div> </div> </div>

2 Entry composition [i](#)

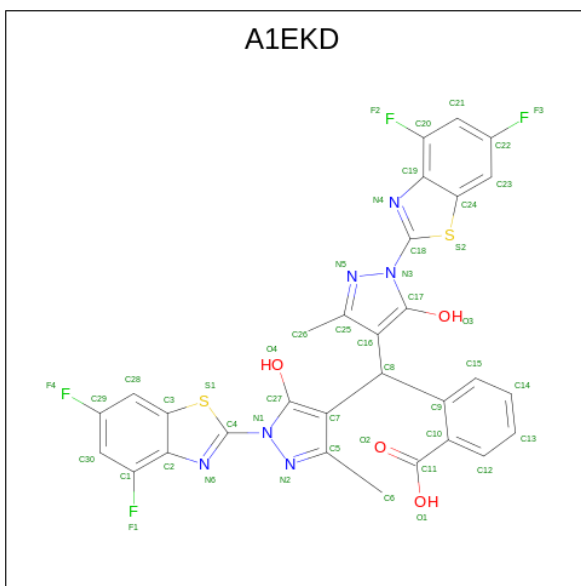
There are 4 unique types of molecules in this entry. The entry contains 5771 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	344	Total	C	N	O	S	0	0	0
			2756	1768	467	506	15			
1	B	339	Total	C	N	O	S	0	0	0
			2752	1768	468	501	15			

- Molecule 2 is 2-[bis[1-[4,6-bis(fluoranyl)-1,3-benzothiazol-2-yl]-3-methyl-5-oxidanyl-pyrazol-4-yl]methyl]benzoic acid (CCD ID: A1EKD) (formula: C₃₀H₁₈F₄N₆O₄S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0
			46	30	4	6	4	2	
2	B	1	Total	C	F	N	O	S	0
			46	30	4	6	4	2	

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

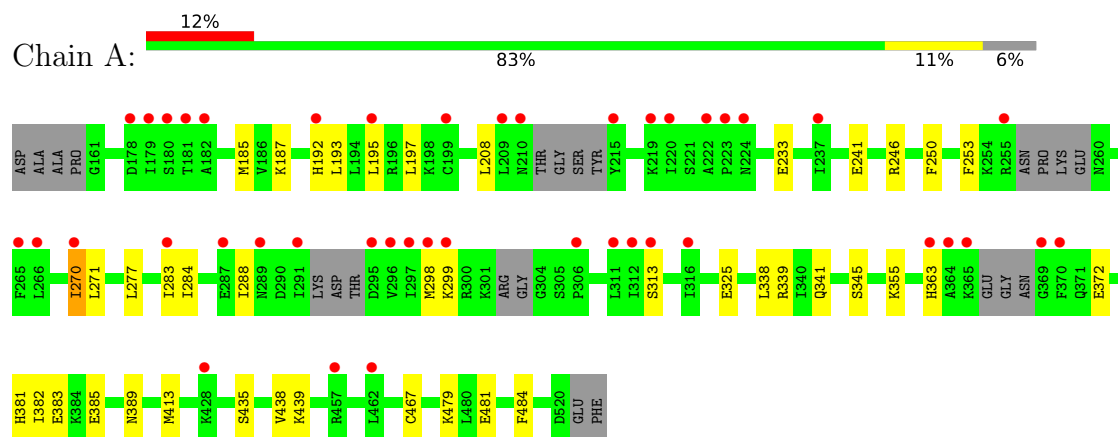
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	89	Total 89	O 89	0	0
4	B	80	Total 80	O 80	0	0

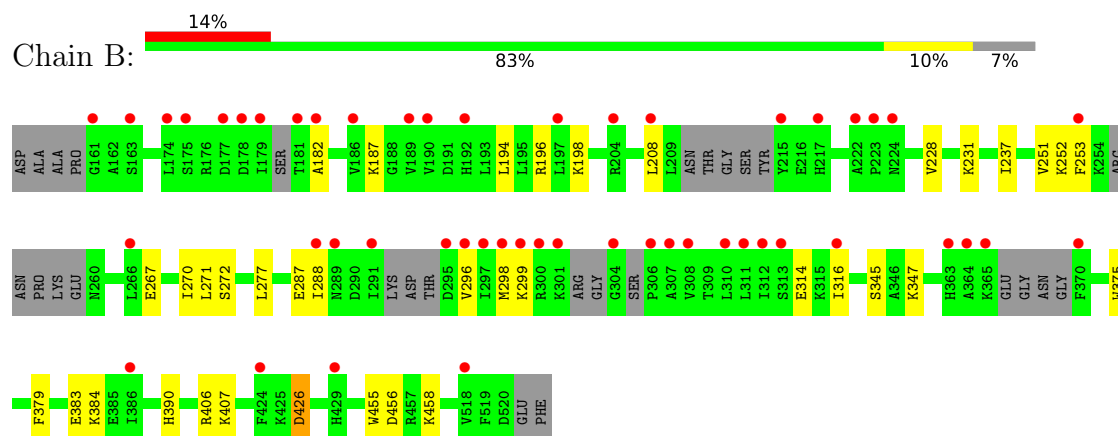
3 Residue-property plots

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: Cyclic GMP-AMP synthase



• Molecule 1: Cyclic GMP-AMP synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	210.48Å 45.95Å 86.38Å 90.00° 112.68° 90.00°	Depositor
Resolution (Å)	78.12 – 1.92 78.12 – 1.92	Depositor EDS
% Data completeness (in resolution range)	99.6 (78.12-1.92) 99.6 (78.12-1.92)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 1.92Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.224 , 0.268 0.224 , 0.266	Depositor DCC
R_{free} test set	2949 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	34.0	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.008 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5771	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.86% 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: ZN, A1EKD

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	0.40	0/2807	0.56	0/3770
1	B	0.40	0/2801	0.59	0/3754
All	All	0.40	0/5608	0.58	0/7524

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	A	2756	0	2723	26	0
1	B	2752	0	2755	21	0
2	A	46	0	0	2	0
2	B	46	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	89	0	0	1	0
4	B	80	0	0	0	0
All	All	5771	0	5478	47	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 4.

All (47) 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:185:MET:HE3	1:A:185:MET:HA	1.79	0.64
1:B:426:ASP:OD1	1:B:426:ASP:N	2.34	0.61
1:B:288:ILE:HG23	1:B:296:VAL:HG13	1.88	0.56
1:B:456:ASP:OD2	1:B:458:LYS:HE3	2.06	0.56
1:A:284:ILE:O	1:A:288:ILE:HG12	2.07	0.55
1:A:435:SER:OG	2:A:601:A1EKD:N5	2.39	0.55
1:A:192:HIS:HA	1:A:195:LEU:HD12	1.89	0.55
1:B:253:PHE:HZ	1:B:271:LEU:HD22	1.72	0.54
1:B:267:GLU:HG3	1:B:272:SER:HB2	1.89	0.53
1:A:389:ASN:HA	1:B:347:LYS:HZ3	1.74	0.52
1:B:194:LEU:O	1:B:198:LYS:HG3	2.11	0.51
2:A:601:A1EKD:O4	4:A:701:HOH:O	2.19	0.51
1:A:479:LYS:HE2	1:A:481:GLU:HG3	1.91	0.50
1:B:251:VAL:HG23	1:B:375:TRP:CD1	2.46	0.50
1:A:233:GLU:HA	1:A:325:GLU:HB3	1.94	0.50
1:A:413:MET:SD	1:A:467:CYS:HB3	2.52	0.50
2:B:601:A1EKD:S1	2:B:601:A1EKD:O4	2.69	0.50
1:A:193:LEU:O	1:A:197:LEU:HD23	2.14	0.48
1:A:383:GLU:OE1	1:A:439:LYS:NZ	2.47	0.47
1:A:250:PHE:HB3	1:A:270:ILE:HD12	1.97	0.46
1:A:355:LYS:HZ1	1:A:385:GLU:CD	2.22	0.46
1:B:379:PHE:O	1:B:383:GLU:HG3	2.15	0.46
1:A:338:LEU:HD13	1:A:484:PHE:CE1	2.51	0.46
1:B:182:ALA:HB1	1:B:316:ILE:HD13	1.97	0.46
1:B:390:HIS:CE1	1:B:407:LYS:HD2	2.50	0.46
1:B:384:LYS:C	1:B:384:LYS:HD2	2.40	0.46
1:A:250:PHE:HB3	1:A:270:ILE:CD1	2.45	0.45
1:B:253:PHE:CZ	1:B:271:LEU:HD22	2.52	0.45
1:A:339:ARG:HH21	1:A:341:GLN:CD	2.25	0.44
1:A:298:MET:HG2	1:A:299:LYS:N	2.32	0.44
1:A:208:LEU:HA	1:A:208:LEU:HD23	1.74	0.43
1:B:252:LYS:HE2	1:B:270:ILE:HG22	2.01	0.43
1:A:363:HIS:HB3	1:A:372:GLU:OE1	2.18	0.43
1:A:197:LEU:HD13	1:A:283:ILE:HG21	2.00	0.43
1:B:196:ARG:HG2	1:B:287:GLU:OE1	2.18	0.42
1:A:389:ASN:HA	1:B:347:LYS:NZ	2.33	0.42
1:A:413:MET:HB3	1:A:438:VAL:HG13	2.01	0.42
1:B:383:GLU:HG3	1:B:383:GLU:H	1.63	0.41
1:A:241:GLU:OE2	1:A:246:ARG:N	2.51	0.41
1:A:253:PHE:CZ	1:A:271:LEU:HD13	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:LEU:HD23	1:B:208:LEU:HA	1.92	0.41
1:A:277:LEU:HA	1:A:277:LEU:HD23	1.78	0.41
1:A:381:HIS:CE1	1:A:382:ILE:HG12	2.56	0.41
1:B:406:ARG:HG2	1:B:455:TRP:CD2	2.55	0.41
1:B:277:LEU:HD23	1:B:277:LEU:HA	1.85	0.40
1:A:270:ILE:HA	1:A:270:ILE:HD13	1.72	0.40
1:B:298:MET:HG3	1:B:299:LYS:N	2.35	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	332/366 (91%)	324 (98%)	7 (2%)	1 (0%)	37	26
1	B	324/366 (88%)	317 (98%)	6 (2%)	1 (0%)	37	26
All	All	656/732 (90%)	641 (98%)	13 (2%)	2 (0%)	37	26

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	345	SER
1	B	345	SER

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	300/336 (89%)	297 (99%)	3 (1%)	73	67
1	B	304/336 (90%)	298 (98%)	6 (2%)	50	36
All	All	604/672 (90%)	595 (98%)	9 (2%)	60	49

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	187	LYS
1	A	270	ILE
1	A	313	SER
1	B	187	LYS
1	B	228	VAL
1	B	231	LYS
1	B	237	ILE
1	B	314	GLU
1	B	426	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	238	GLN
1	A	351	GLN
1	A	454	GLN
1	B	342	ASN
1	B	351	GLN
1	B	507	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 4 ligands modelled in this entry, 2 are 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
2	A1EKD	A	601	-	38,52,52	0.99	2 (5%)	38,80,80	2.08	5 (13%)
2	A1EKD	B	601	-	38,52,52	0.89	2 (5%)	38,80,80	2.23	4 (10%)

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	A1EKD	A	601	-	-	8/16/24/24	0/7/7/7
2	A1EKD	B	601	-	-	7/16/24/24	0/7/7/7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	A1EKD	C1-C2	-3.51	1.38	1.41
2	A	601	A1EKD	C20-C19	-3.23	1.38	1.41
2	B	601	A1EKD	C1-C2	-3.01	1.39	1.41
2	B	601	A1EKD	C20-C19	-2.71	1.39	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	A1EKD	F1-C1-C2	8.65	120.90	117.40
2	B	601	A1EKD	F2-C20-C19	8.31	120.76	117.40
2	A	601	A1EKD	F1-C1-C2	7.39	120.39	117.40
2	A	601	A1EKD	F2-C20-C19	7.19	120.31	117.40
2	B	601	A1EKD	C1-C30-C29	3.03	119.39	116.64
2	B	601	A1EKD	C20-C21-C22	2.92	119.29	116.64
2	A	601	A1EKD	C20-C21-C22	2.89	119.26	116.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	A1EKD	C1-C30-C29	2.80	119.18	116.64
2	A	601	A1EKD	C28-C3-S1	2.33	129.76	125.10

There are no chirality outliers.

All (15) torsion outliers are listed below:

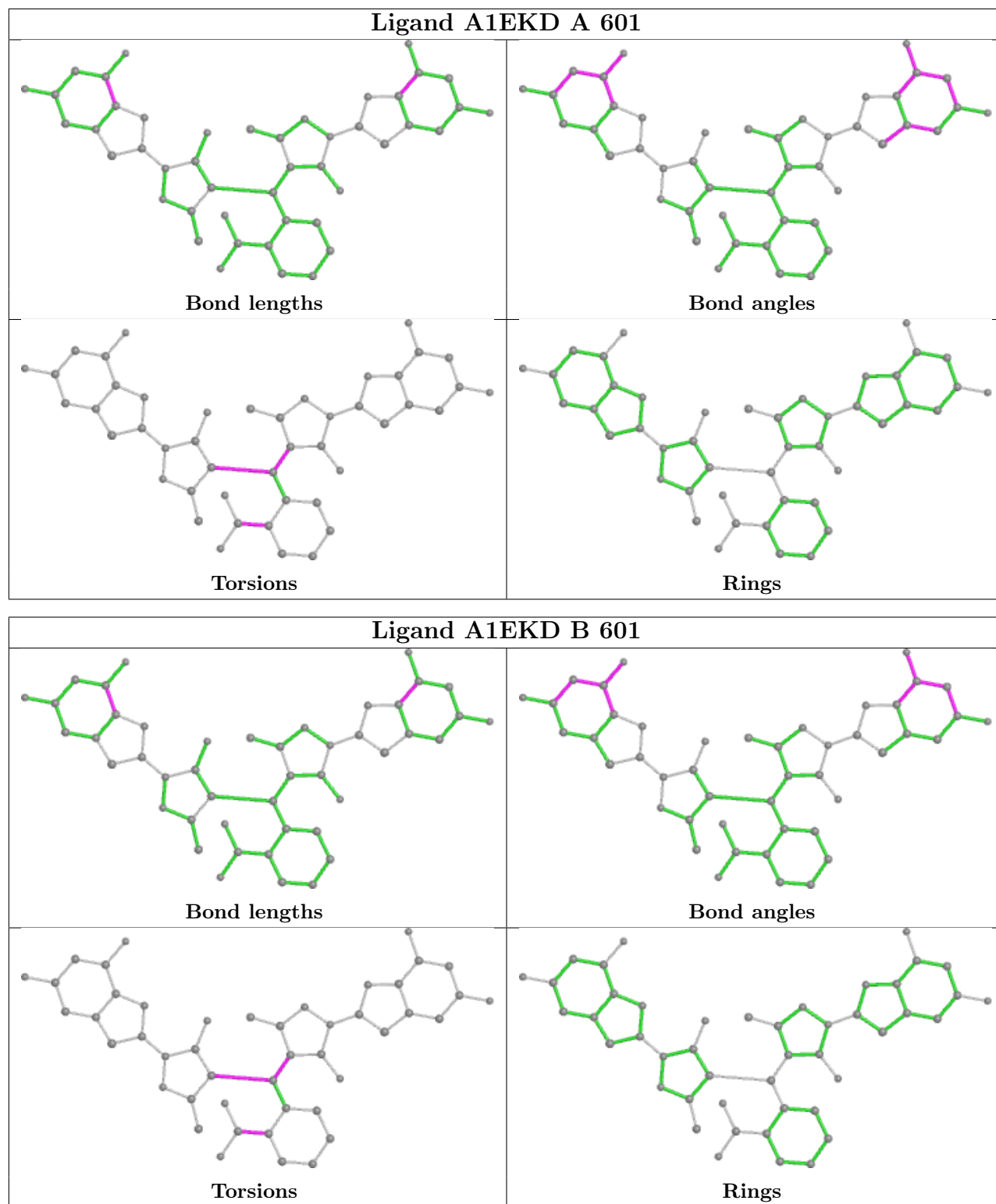
Mol	Chain	Res	Type	Atoms
2	A	601	A1EKD	C5-C7-C8-C9
2	A	601	A1EKD	C25-C16-C8-C7
2	B	601	A1EKD	C5-C7-C8-C9
2	B	601	A1EKD	C25-C16-C8-C7
2	A	601	A1EKD	C12-C10-C11-O2
2	B	601	A1EKD	C12-C10-C11-O2
2	A	601	A1EKD	C12-C10-C11-O1
2	B	601	A1EKD	C12-C10-C11-O1
2	A	601	A1EKD	C9-C10-C11-O1
2	A	601	A1EKD	C9-C10-C11-O2
2	B	601	A1EKD	C9-C10-C11-O2
2	B	601	A1EKD	C9-C10-C11-O1
2	A	601	A1EKD	C25-C16-C8-C9
2	B	601	A1EKD	C25-C16-C8-C9
2	A	601	A1EKD	C27-C7-C8-C9

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	A1EKD	2	0
2	B	601	A1EKD	1	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 ⓘ

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	344/366 (93%)	0.78	43 (12%)  	25, 43, 67, 83	0
1	B	339/366 (92%)	0.94	50 (14%)  	25, 46, 72, 82	0
All	All	683/732 (93%)	0.86	93 (13%)  	25, 44, 71, 83	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	296	VAL	5.0
1	B	291	ILE	4.7
1	A	255	ARG	4.5
1	B	178	ASP	4.3
1	B	370	PHE	4.2
1	B	179	ILE	4.1
1	A	295	ASP	3.9
1	B	365	LYS	3.9
1	B	182	ALA	3.9
1	B	296	VAL	3.8
1	A	291	ILE	3.7
1	B	297	ILE	3.5
1	A	181	THR	3.5
1	B	311	LEU	3.4
1	A	297	ILE	3.4
1	A	180	SER	3.3
1	A	365	LYS	3.3
1	B	289	ASN	3.1
1	B	295	ASP	3.1
1	A	298	MET	3.0
1	B	518	VAL	2.9
1	B	363	HIS	2.9
1	A	199	CYS	2.9
1	B	298	MET	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	224	ASN	2.9
1	A	364	ALA	2.9
1	A	195	LEU	2.8
1	B	312	ILE	2.8
1	B	313	SER	2.8
1	A	428	LYS	2.8
1	A	178	ASP	2.8
1	A	311	LEU	2.8
1	B	301	LYS	2.8
1	A	370	PHE	2.7
1	B	215	TYR	2.7
1	B	304	GLY	2.7
1	B	308	VAL	2.6
1	A	179	ILE	2.6
1	A	210	ASN	2.6
1	A	312	ILE	2.5
1	A	215	TYR	2.5
1	A	313	SER	2.5
1	A	457	ARG	2.5
1	B	310	LEU	2.5
1	B	364	ALA	2.5
1	B	253	PHE	2.4
1	B	192	HIS	2.4
1	B	307	ALA	2.4
1	A	265	PHE	2.4
1	A	299	LYS	2.4
1	A	219	LYS	2.3
1	A	363	HIS	2.3
1	A	316	ILE	2.3
1	B	386	ILE	2.3
1	A	182	ALA	2.3
1	A	462	LEU	2.3
1	B	174	LEU	2.3
1	B	181	THR	2.2
1	A	237	ILE	2.2
1	A	223	PRO	2.2
1	B	306	PRO	2.2
1	B	217	HIS	2.2
1	B	177	ASP	2.2
1	B	222	ALA	2.2
1	A	270	ILE	2.2
1	A	287	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	192	HIS	2.2
1	B	189	VAL	2.2
1	A	369	GLY	2.2
1	B	161	GLY	2.2
1	A	209	LEU	2.2
1	A	222	ALA	2.2
1	B	197	LEU	2.2
1	A	224	ASN	2.1
1	B	186	VAL	2.1
1	A	289	ASN	2.1
1	B	300	ARG	2.1
1	B	208	LEU	2.1
1	A	306	PRO	2.1
1	B	223	PRO	2.1
1	A	220	ILE	2.1
1	A	283	ILE	2.1
1	B	190	VAL	2.1
1	B	266	LEU	2.1
1	B	299	LYS	2.1
1	B	429	HIS	2.0
1	A	266	LEU	2.0
1	B	175	SER	2.0
1	B	288	ILE	2.0
1	B	316	ILE	2.0
1	B	163	SER	2.0
1	B	204	ARG	2.0
1	B	424	PHE	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,

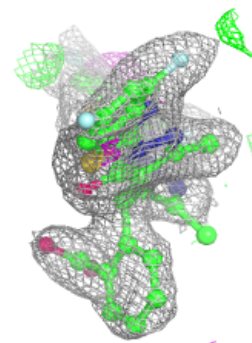
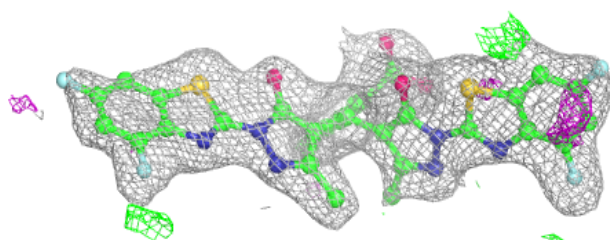
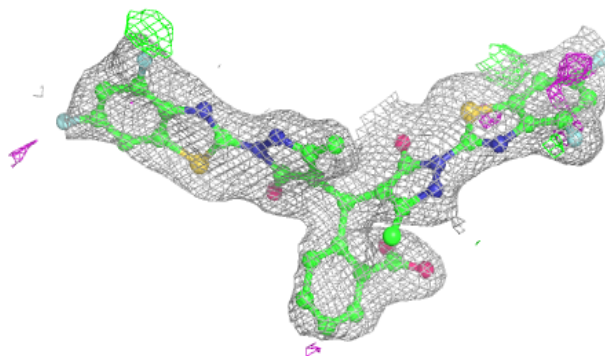
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	A1EKD	B	601	46/46	0.87	0.12	37,50,59,69	0
2	A1EKD	A	601	46/46	0.94	0.09	32,41,51,59	0
3	ZN	A	602	1/1	1.00	0.01	29,29,29,29	0
3	ZN	B	602	1/1	1.00	0.01	29,29,29,29	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.

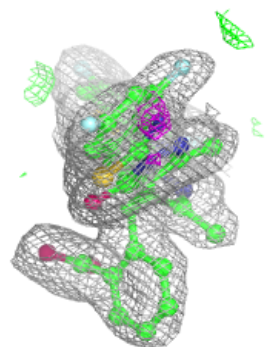
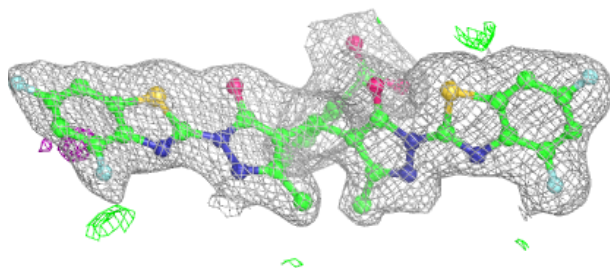
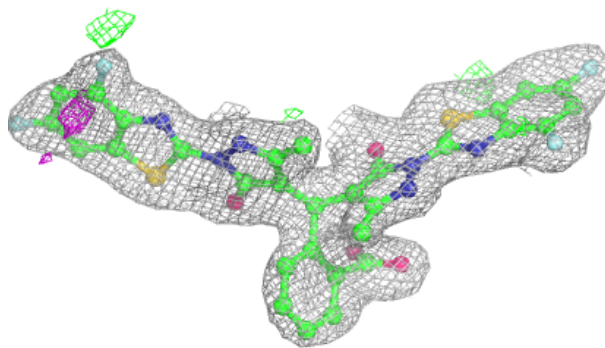
Electron density around A1EKD B 601:

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 A1EKD 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.