



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 01:05 pm BST

PDB ID : 4Y8D
Title : Crystal structure of Cyclin-G associated kinase (GAK) complexed with selective 12i inhibitor
Authors : Chaikuad, A.; Heroven, C.; Nowak, R.; De Jonghe, S.; von Delft, F.; Arrow-smith, C.H.; Edwards, A.M.; Bountra, C.; Knapp, S.; Structural Genomics Consortium (SGC)
Deposited on : 2015-02-16
Resolution : 2.10 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

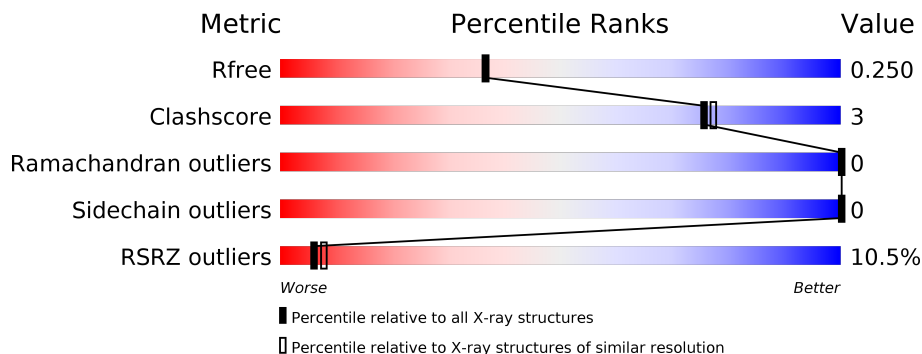
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 on 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	340	
1	B	340	
2	C	140	
2	D	140	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6441 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 Cyclin-G-associated kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	262	2083	1324	370	377	12	0	4	0
1	B	262	2095	1331	371	381	12	0	6	0

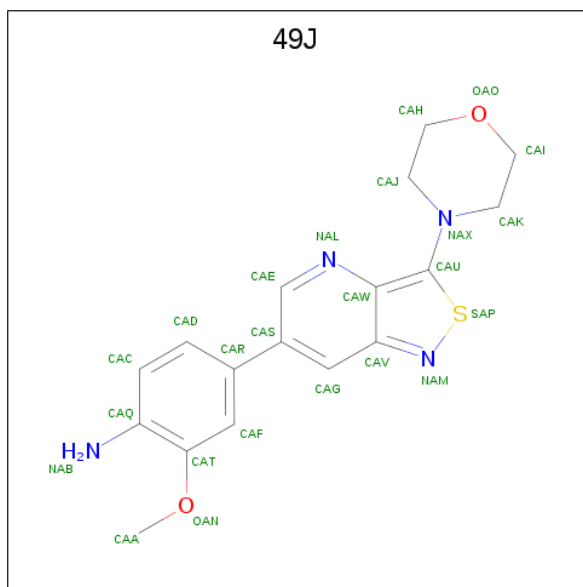
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	SER	-	expression tag	UNP O14976
A	13	MET	-	expression tag	UNP O14976
B	12	SER	-	expression tag	UNP O14976
B	13	MET	-	expression tag	UNP O14976

- Molecule 2 is a protein called nanobody.

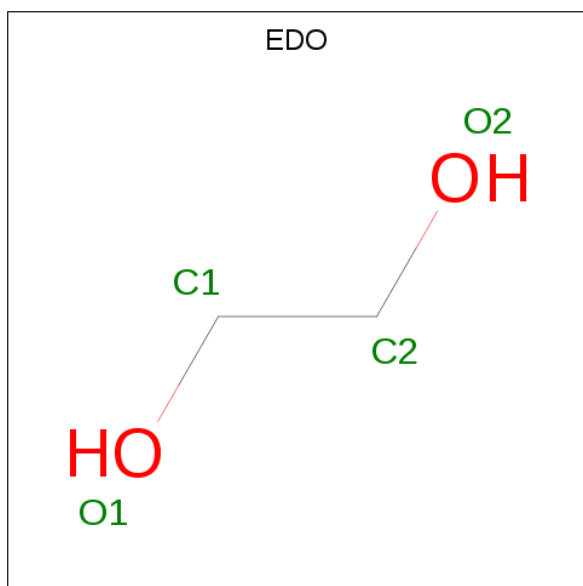
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	120	894	546	160	182	6	0	0	0
2	D	121	903	552	163	182	6	0	1	0

- Molecule 3 is 2-methoxy-4-[3-(morpholin-4-yl)[1,2]thiazolo[4,3-b]pyridin-6-yl]aniline (three-letter code: 49J) (formula: C₁₇H₁₈N₄O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			24	17	4	2	1		
3	B	1	Total	C	N	O	S	0	0
			24	17	4	2	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	1
			8	4	4		

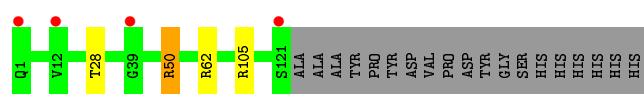
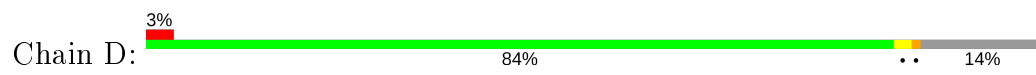
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	110	Total	O	0	0
			110	110		
5	C	96	Total	O	0	0
			96	96		
5	B	98	Total	O	0	0
			98	98		
5	D	90	Total	O	0	0
			90	90		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	37.71Å 68.70Å 89.87Å 109.70° 95.08° 99.04°	Depositor
Resolution (Å)	43.58 – 2.10 42.58 – 2.10	Depositor EDS
% Data completeness (in resolution range)	94.7 (43.58-2.10) 94.7 (42.58-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.10Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.192 , 0.232 0.217 , 0.250	Depositor DCC
R_{free} test set	2310 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtrriage
Anisotropy	0.253	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6441	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, 49J

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	0.58	0/2133	0.70	3/2881 (0.1%)
1	B	0.58	0/2151	0.70	3/2905 (0.1%)
2	C	0.80	0/907	0.83	1/1226 (0.1%)
2	D	0.78	0/919	0.85	1/1242 (0.1%)
All	All	0.65	0/6110	0.74	8/8254 (0.1%)

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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	50	ARG	NE-CZ-NH1	6.79	123.70	120.30
1	B	293	ARG	NE-CZ-NH1	-6.47	117.06	120.30
1	B	293	ARG	NE-CZ-NH2	6.36	123.48	120.30
1	A	293	ARG	NE-CZ-NH1	-5.60	117.50	120.30
1	A	293	ARG	NE-CZ-NH2	5.29	122.95	120.30
1	A	157	ARG	NE-CZ-NH2	-5.15	117.72	120.30
1	B	157	ARG	NE-CZ-NH2	-5.12	117.74	120.30
2	C	50	ARG	NE-CZ-NH1	5.01	122.81	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	236	SER	Peptide
1	B	236	SER	Peptide

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	2083	0	2097	15	0
1	B	2095	0	2112	11	0
2	C	894	0	858	5	0
2	D	903	0	867	6	0
3	A	24	0	18	1	0
3	B	24	0	18	1	0
4	B	4	0	6	0	0
4	C	12	0	18	0	0
4	D	8	0	12	0	0
5	A	110	0	0	4	0
5	B	98	0	0	1	0
5	C	96	0	0	3	0
5	D	90	0	0	4	0
All	All	6441	0	6006	36	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 3.

All (36) 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)
2:D:105:ARG:NH2	5:D:341:HOH:O	2.24	0.69
2:D:62[A]:ARG:NH1	5:D:301:HOH:O	2.27	0.67
1:A:37:GLU:N	5:A:559:HOH:O	2.29	0.64
3:A:401:49J:NAL	3:A:401:49J:H7	2.12	0.64
1:A:297:GLN:HG3	5:A:501:HOH:O	1.98	0.63
1:B:261:HIS:CD2	1:B:262:PRO:HD2	2.39	0.57
2:C:105:ARG:NH2	5:C:350:HOH:O	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:HIS:CD2	1:A:262:PRO:HD2	2.40	0.56
1:A:236:SER:HA	5:A:555:HOH:O	2.06	0.55
1:B:40:LEU:HD13	1:B:57:ALA:HB1	1.91	0.52
1:A:40:LEU:HD13	1:A:57:ALA:HB1	1.92	0.52
2:D:28:THR:O	2:D:50:ARG:HD2	2.12	0.50
1:B:297:GLN:HG3	5:B:501:HOH:O	2.12	0.49
1:A:241:GLY:HA2	1:B:76:GLU:CD	2.34	0.48
1:A:62:SER:OG	1:A:64:ARG:NH2	2.47	0.48
2:C:28:THR:O	2:C:50:ARG:HD2	2.14	0.47
2:D:62[A]:ARG:CZ	5:D:301:HOH:O	2.63	0.45
1:B:261:HIS:CG	1:B:262:PRO:HD2	2.52	0.45
1:A:261:HIS:CG	1:A:262:PRO:HD2	2.52	0.45
1:A:100[B]:GLN:NE2	5:A:554:HOH:O	2.34	0.44
1:A:241:GLY:HA2	1:B:76:GLU:HG3	1.99	0.44
1:A:40:LEU:HB3	1:A:59:ASP:HA	2.00	0.43
1:A:89:MET:SD	1:A:99:VAL:HG23	2.59	0.43
1:A:76:GLU:CD	1:B:241:GLY:HA2	2.40	0.43
2:C:42:ARG:NH2	5:C:393:HOH:O	2.43	0.42
2:C:42:ARG:NH1	5:C:387:HOH:O	2.53	0.42
3:B:401:49J:CAK	3:B:401:49J:NAL	2.83	0.42
1:B:40:LEU:HB3	1:B:59:ASP:HA	2.01	0.42
1:B:89:MET:SD	1:B:99:VAL:HG23	2.60	0.42
1:A:72:LEU:CD2	1:A:118:GLU:HG2	2.50	0.42
2:D:62[A]:ARG:NH2	5:D:301:HOH:O	2.53	0.42
1:A:110:GLU:H	1:A:110:GLU:CD	2.23	0.42
2:D:62[B]:ARG:HG3	2:D:62[B]:ARG:HH21	1.84	0.42
1:B:110:GLU:H	1:B:110:GLU:CD	2.23	0.41
2:C:84:LYS:HB2	2:C:85:PRO:HD2	2.01	0.41
1:B:72:LEU:CD2	1:B:118:GLU:HG2	2.50	0.41

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	260/340 (76%)	251 (96%)	9 (4%)	0	100	100
1	B	262/340 (77%)	249 (95%)	13 (5%)	0	100	100
2	C	118/140 (84%)	117 (99%)	1 (1%)	0	100	100
2	D	120/140 (86%)	120 (100%)	0	0	100	100
All	All	760/960 (79%)	737 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	227/294 (77%)	227 (100%)	0	100	100
1	B	230/294 (78%)	230 (100%)	0	100	100
2	C	94/110 (86%)	94 (100%)	0	100	100
2	D	94/110 (86%)	94 (100%)	0	100	100
All	All	645/808 (80%)	645 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [i](#)

8 ligands are modelled in this entry.

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	EDO	C	201	-	3,3,3	0.41	0	2,2,2	0.45	0
4	EDO	D	202	-	3,3,3	0.63	0	2,2,2	0.16	0
4	EDO	C	202[B]	-	3,3,3	0.63	0	2,2,2	0.10	0
4	EDO	C	202[A]	-	3,3,3	0.75	0	2,2,2	0.22	0
3	49J	B	401	-	24,27,27	2.19	7 (29%)	29,38,38	2.51	12 (41%)
4	EDO	D	201	-	3,3,3	0.51	0	2,2,2	0.74	0
4	EDO	B	402	-	3,3,3	0.42	0	2,2,2	0.23	0
3	49J	A	401	-	24,27,27	2.07	8 (33%)	29,38,38	2.67	12 (41%)

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	EDO	C	201	-	-	1/1/1/1	-
4	EDO	D	202	-	-	1/1/1/1	-
4	EDO	C	202[B]	-	-	0/1/1/1	-
4	EDO	C	202[A]	-	-	1/1/1/1	-
3	49J	B	401	-	-	0/6/18/18	0/4/4/4
4	EDO	D	201	-	-	1/1/1/1	-
4	EDO	B	402	-	-	1/1/1/1	-
3	49J	A	401	-	-	0/6/18/18	0/4/4/4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	49J	CAE-NAL	6.18	1.41	1.31
3	B	401	49J	CAG-CAV	-5.23	1.33	1.41
3	A	401	49J	CAG-CAV	-4.94	1.34	1.41
3	A	401	49J	CAE-NAL	4.31	1.38	1.31
3	A	401	49J	CAU-CAW	-3.73	1.33	1.42
3	A	401	49J	CAR-CAS	-3.57	1.40	1.49
3	B	401	49J	CAU-CAW	-3.55	1.33	1.42
3	B	401	49J	CAR-CAS	-2.67	1.42	1.49
3	A	401	49J	CAJ-CAH	-2.51	1.40	1.50
3	B	401	49J	CAQ-CAT	-2.48	1.37	1.40
3	B	401	49J	CAJ-NAX	2.39	1.50	1.46
3	A	401	49J	CAK-NAX	2.20	1.50	1.46
3	A	401	49J	CAW-CAV	-2.19	1.35	1.42
3	A	401	49J	CAW-NAL	-2.18	1.34	1.37
3	B	401	49J	CAW-CAV	-2.00	1.36	1.42

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	49J	CAS-CAE-NAL	-7.45	118.65	125.55
3	B	401	49J	CAS-CAE-NAL	-6.47	119.56	125.55
3	A	401	49J	CAE-NAL-CAW	5.37	122.14	116.78
3	B	401	49J	CAT-CAQ-NAB	-5.33	114.89	119.46
3	A	401	49J	CAV-CAW-NAL	-4.52	119.63	125.00
3	B	401	49J	CAV-CAW-NAL	-4.15	120.07	125.00
3	A	401	49J	OAO-CAH-CAJ	-3.88	103.25	111.80
3	A	401	49J	CAC-CAQ-CAT	3.85	121.58	118.25
3	A	401	49J	CAK-NAX-CAJ	3.79	119.89	111.52
3	B	401	49J	OAO-CAI-CAK	-3.72	103.60	111.80
3	B	401	49J	CAC-CAQ-CAT	3.61	121.37	118.25
3	A	401	49J	CAJ-NAX-CAU	-3.49	116.90	121.29
3	B	401	49J	CAE-NAL-CAW	3.27	120.05	116.78
3	A	401	49J	CAH-CAJ-NAX	-3.10	104.30	110.02
3	B	401	49J	CAK-NAX-CAJ	2.82	117.75	111.52
3	B	401	49J	CAF-CAT-CAQ	-2.73	119.16	120.92
3	A	401	49J	CAF-CAT-CAQ	-2.61	119.23	120.92
3	B	401	49J	CAH-CAJ-NAX	-2.55	105.31	110.02
3	A	401	49J	OAN-CAT-CAQ	2.40	115.64	114.05
3	A	401	49J	CAT-CAQ-NAB	-2.31	117.48	119.46
3	B	401	49J	OAN-CAT-CAF	2.29	128.06	124.12
3	B	401	49J	CAG-CAV-NAM	-2.26	125.42	130.35
3	B	401	49J	CAI-OAO-CAH	2.04	116.71	109.89
3	A	401	49J	CAD-CAC-CAQ	-2.03	119.27	121.42

There are no chirality outliers.

All (5) torsion outliers are listed below:

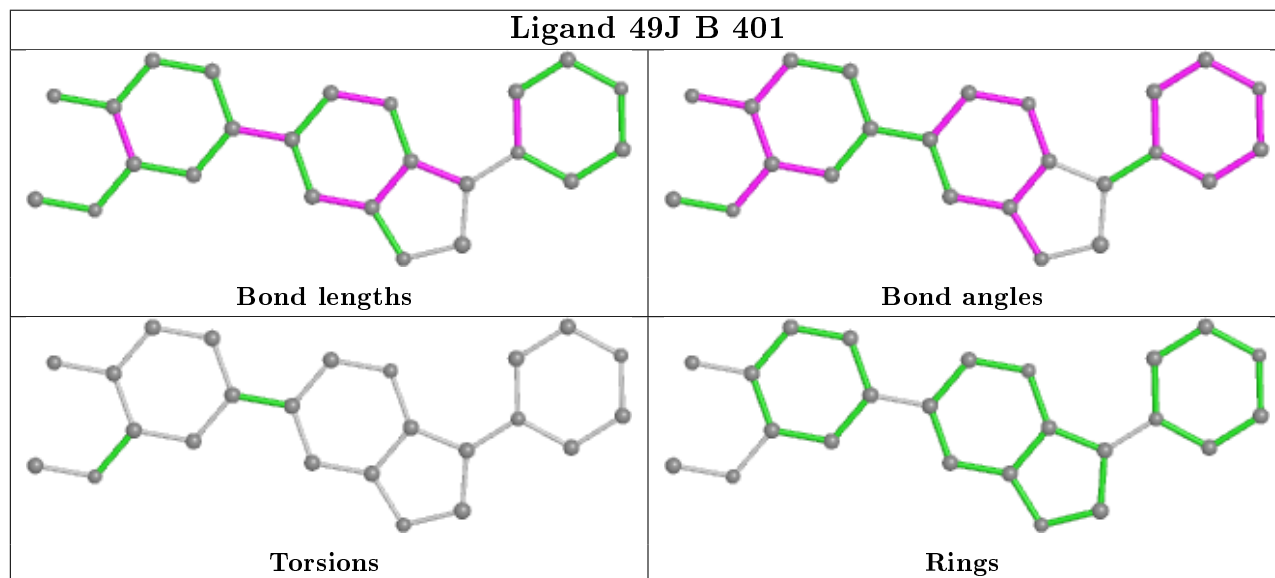
Mol	Chain	Res	Type	Atoms
4	C	201	EDO	O1-C1-C2-O2
4	D	202	EDO	O1-C1-C2-O2
4	D	201	EDO	O1-C1-C2-O2
4	B	402	EDO	O1-C1-C2-O2
4	C	202[A]	EDO	O1-C1-C2-O2

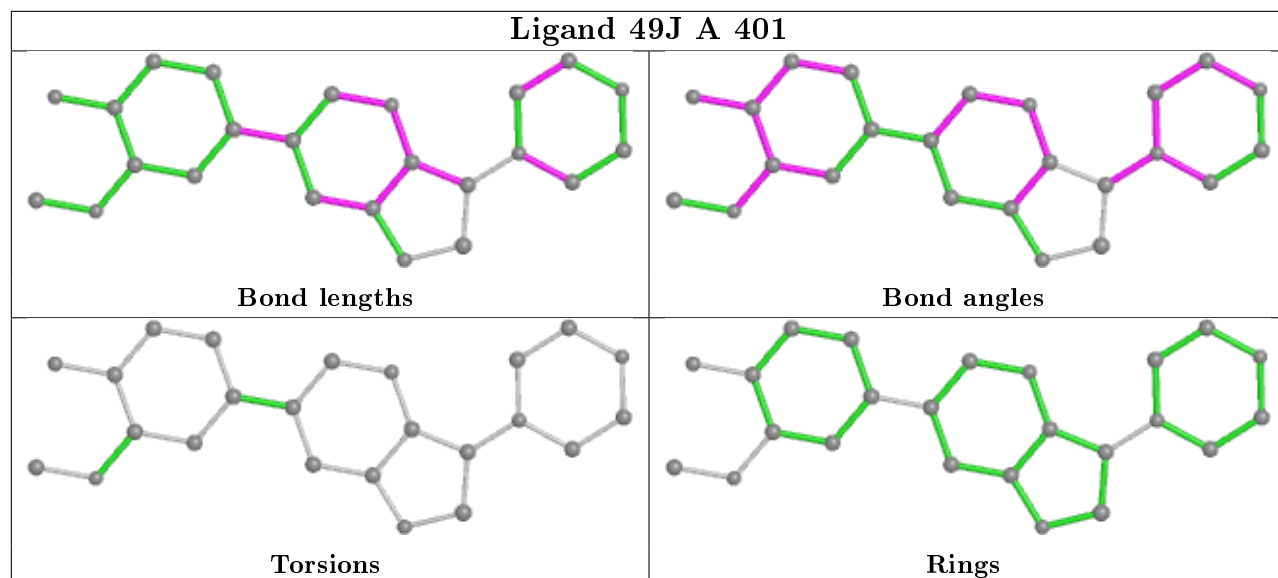
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	49J	1	0
3	A	401	49J	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 [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	262/340 (77%)	0.83	39 (14%) 2 3	32, 74, 155, 170	2 (0%)
1	B	262/340 (77%)	0.74	34 (12%) 3 4	31, 70, 149, 186	1 (0%)
2	C	120/140 (85%)	0.35	3 (2%) 57 62	31, 50, 78, 105	0
2	D	121/140 (86%)	0.38	4 (3%) 46 53	32, 51, 76, 90	1 (0%)
All	All	765/960 (79%)	0.65	80 (10%) 6 8	31, 61, 148, 186	4 (0%)

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	61	GLY	8.3
1	A	50	GLY	7.0
1	A	51	PHE	6.6
1	A	112	SER	5.7
1	B	36	GLY	5.4
1	B	49	GLY	5.2
1	A	107	ILE	5.2
1	B	62	SER	5.1
1	B	64	ARG	5.0
1	A	49	GLY	4.8
1	B	35	LEU	4.7
1	B	60	VAL	4.5
2	D	121	SER	4.4
1	A	141	GLY	4.4
1	B	51	PHE	4.3
1	A	113	ASP	4.0
2	C	1	GLN	3.9
1	A	114	THR	3.8
1	A	108	GLY	3.7
1	B	112	SER	3.7
1	A	61	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	52	ALA	3.6
1	A	263	PHE	3.6
1	A	139	SER	3.5
1	A	236	SER	3.5
1	A	60	VAL	3.5
1	A	135	LYS	3.5
1	A	333	GLU	3.3
1	B	235	TYR	3.3
1	B	107	ILE	3.3
1	B	38	LEU	3.2
1	B	50	GLY	3.2
1	A	47	ALA	3.2
1	A	48	GLU	3.1
1	B	331	LEU	3.0
1	B	263	PHE	2.8
1	B	57	ALA	2.8
1	B	63	GLY	2.7
1	A	37	GLU	2.7
1	B	37	GLU	2.7
1	A	57	ALA	2.7
1	A	235	TYR	2.7
1	A	331	LEU	2.7
1	B	113	ASP	2.6
1	A	38	LEU	2.6
1	A	332	LEU	2.6
1	B	47	ALA	2.6
1	A	201	TYR	2.5
1	A	43	ARG	2.5
1	A	55	TYR	2.4
1	B	43	ARG	2.4
1	A	202	PRO	2.4
1	B	30	GLY	2.4
1	B	201	TYR	2.4
1	B	202	PRO	2.3
1	A	74	ASN	2.3
2	D	1	GLN	2.3
1	B	46	LEU	2.3
2	C	2	VAL	2.3
1	B	137	MET	2.3
1	B	74	ASN	2.3
1	A	118	GLU	2.2
1	A	29	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	277	SER	2.2
1	A	136	LYS	2.2
1	A	75	GLU	2.1
2	D	39	GLY	2.1
1	B	261	HIS	2.1
1	A	200	HIS	2.1
1	A	191	ASP	2.1
2	D	12	VAL	2.1
1	A	277	SER	2.0
1	B	139	SER	2.0
1	B	332	LEU	2.0
1	A	28	PHE	2.0
1	B	140	ARG	2.0
1	A	111	GLU	2.0
1	B	77	GLU	2.0
1	B	333	GLU	2.0
2	C	113	GLN	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 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.

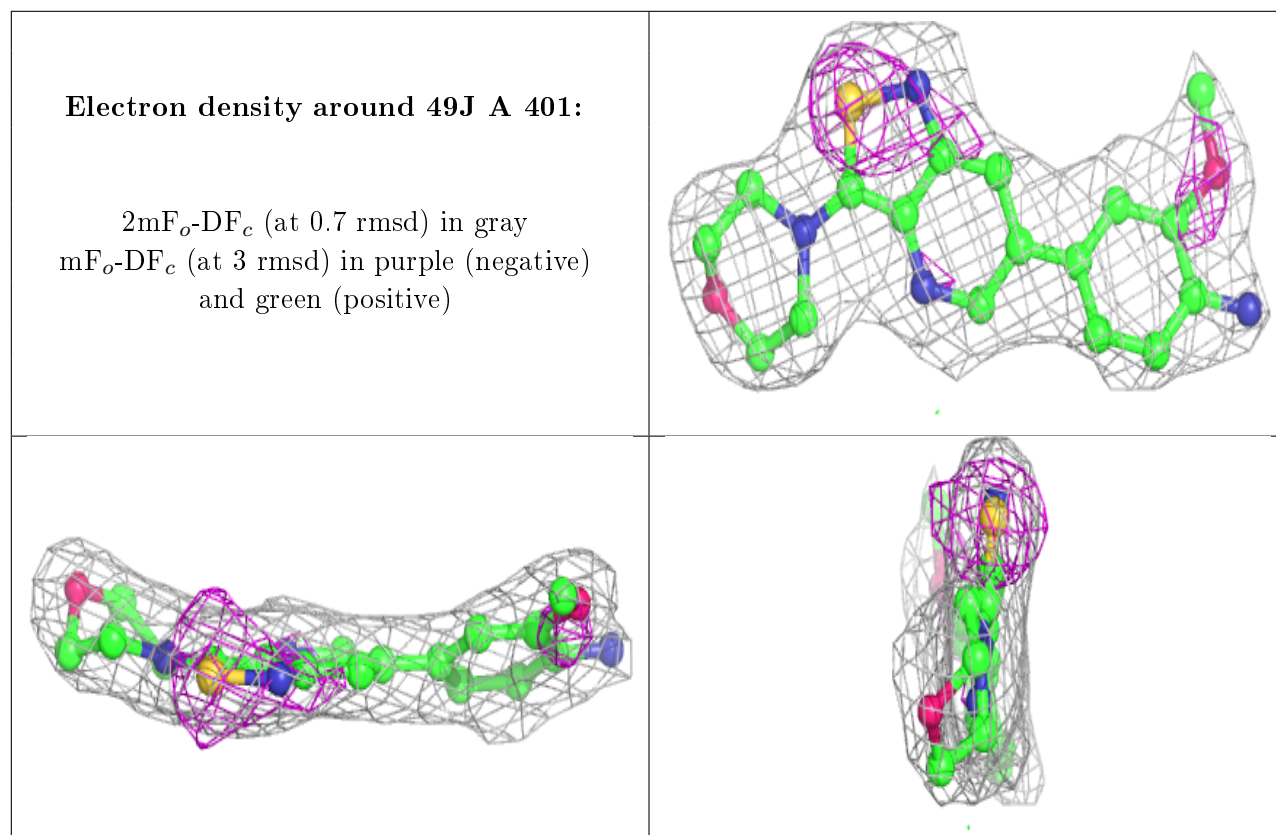
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	EDO	C	201	4/4	0.80	0.25	58,64,64,73	0
4	EDO	B	402	4/4	0.85	0.19	63,64,65,66	0
4	EDO	C	202[A]	4/4	0.86	0.21	39,39,40,41	4
4	EDO	C	202[B]	4/4	0.86	0.21	35,37,39,40	4
3	49J	A	401	24/24	0.92	0.26	38,49,59,60	0
4	EDO	D	201	4/4	0.94	0.15	34,37,40,46	0

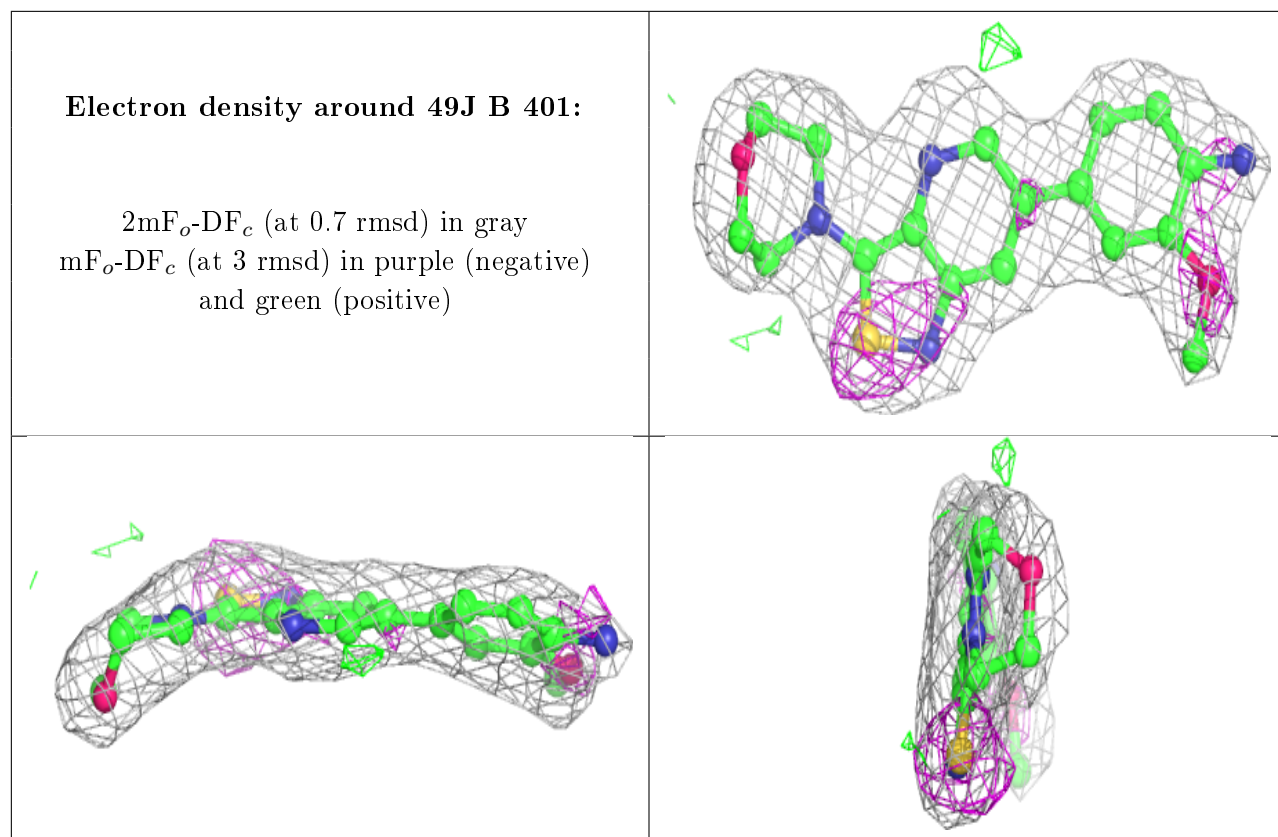
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	D	202	4/4	0.94	0.13	47,50,53,53	0
3	49J	B	401	24/24	0.94	0.22	35,45,49,49	0

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.