



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 28, 2026 – 04:02 AM UTC

PDB ID : 9R1W / pdb_00009r1w
Title : PLK1 SURFACE ENTROPY REDUCTION (SER) MUTANT IN COMPLEX
WITH THIAZOLIDINONE INHIBITOR COMPOUND 1
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Deposited on : 2025-04-28
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

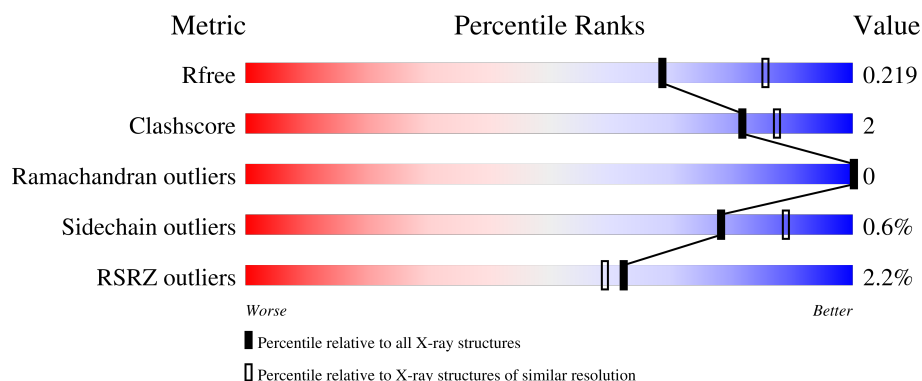
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	AAA	325	 2% 85% 6% 9%
1	BBB	325	 2% 84% 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5177 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.

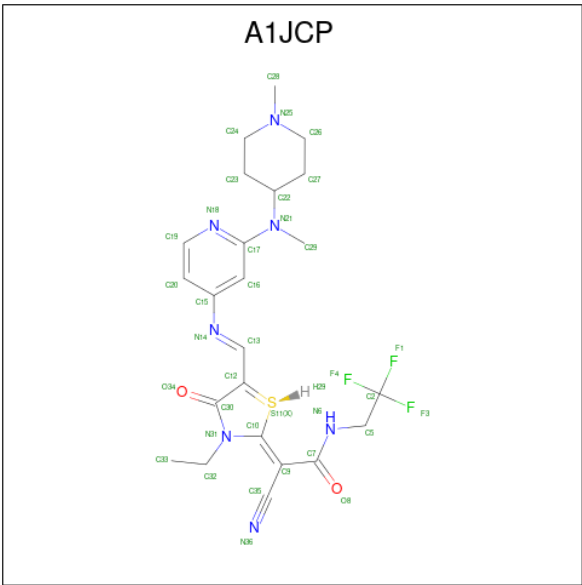
- Molecule 1 is a protein called Serine/threonine-protein kinase PLK1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	297	Total	C	N	O	S	0	14	0
			2474	1588	432	440	14			
1	BBB	288	Total	C	N	O	S	0	10	0
			2385	1533	418	421	13			

There are 8 discrepancies between the modelled and reference sequences:

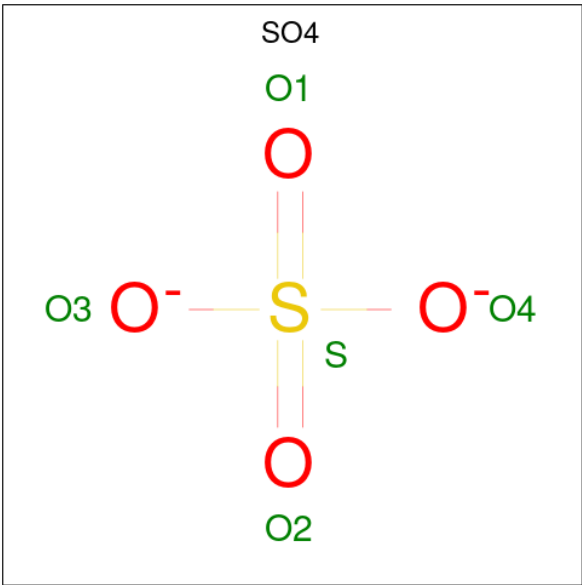
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	16	GLY	-	expression tag	UNP P53350
AAA	17	SER	-	expression tag	UNP P53350
AAA	225	ASP	LYS	engineered mutation	UNP P53350
AAA	226	ALA	LYS	engineered mutation	UNP P53350
BBB	16	GLY	-	expression tag	UNP P53350
BBB	17	SER	-	expression tag	UNP P53350
BBB	225	ASP	LYS	engineered mutation	UNP P53350
BBB	226	ALA	LYS	engineered mutation	UNP P53350

- Molecule 2 is (2 {Z})-2-cyano-2-[3-ethyl-5-[({E})-[2-[methyl-(1-methylpiperidin-4-yl)amino]pyridin-4-yl]iminomethyl]-4-oxidanylidene-1,3-thiazol-2-ylidene]- {N}-[2,2,2-tris(fluoranyl)ethyl]ethanamide (CCD ID: A1JCP) (formula: C₂₃H₂₈F₃N₇O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	AAA	1	Total	C	F	N	O	S	0	0
			36	23	3	7	2	1		
2	BBB	1	Total	C	F	N	O	S	0	0
			36	23	3	7	2	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total	O	S	0	0
			5	4	1		
3	AAA	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total	O	S	0	0
			5	4	1		
3	AAA	1	Total	O	S	0	0
			5	4	1		
3	BBB	1	Total	O	S	0	0
			5	4	1		
3	BBB	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	AAA	1	Total	C	O	0	0
			6	3	3		
4	AAA	1	Total	C	O	0	0
			6	3	3		
4	AAA	1	Total	C	O	0	0
			6	3	3		
4	BBB	1	Total	C	O	0	0
			6	3	3		
4	BBB	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	1	Total 1	Cl 1	0	0

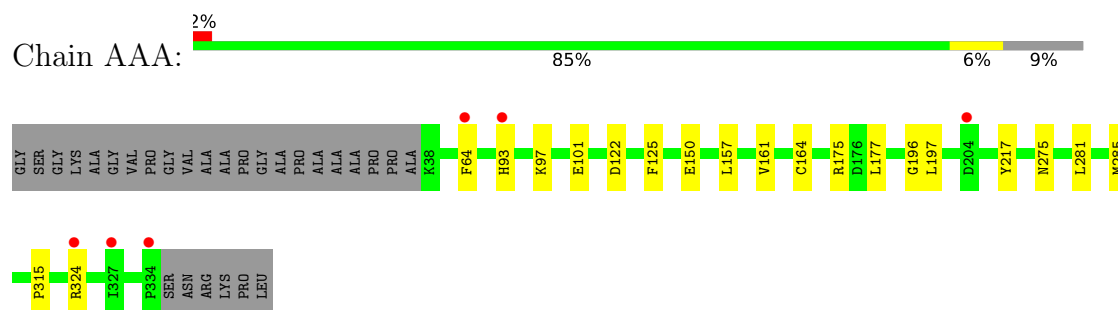
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	AAA	108	Total 108	O 108	0	0
6	BBB	77	Total 77	O 77	0	0

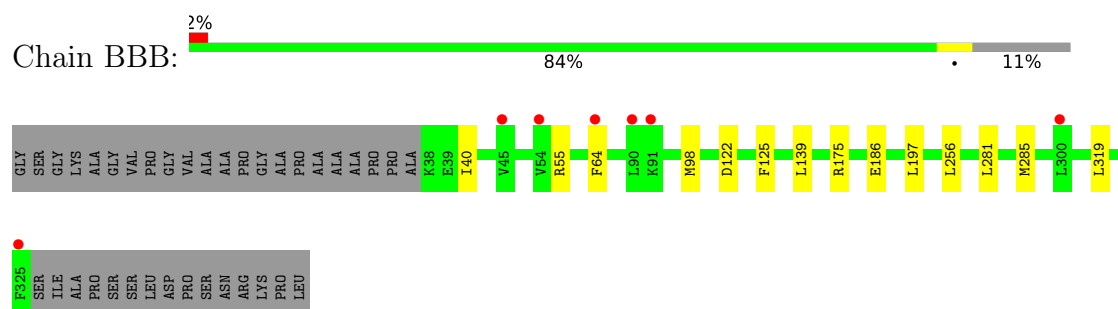
3 Residue-property plots [i](#)

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: Serine/threonine-protein kinase PLK1



- Molecule 1: Serine/threonine-protein kinase PLK1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	113.05Å 103.92Å 70.80Å 90.00° 115.44° 90.00°	Depositor
Resolution (Å)	36.90 – 2.20 36.90 – 2.20	Depositor EDS
% Data completeness (in resolution range)	87.3 (36.90-2.20) 87.5 (36.90-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.178 , 0.216 0.182 , 0.219	Depositor DCC
R_{free} test set	1642 reflections (4.36%)	wwPDB-VP
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5177	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% 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: CL, A1JCP, SO4, GOL

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	AAA	0.96	0/2566	1.32	0/3466
1	BBB	0.98	0/2469	1.30	0/3333
All	All	0.97	0/5035	1.31	0/6799

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 [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	AAA	2474	0	2542	13	0
1	BBB	2385	0	2451	9	0
2	AAA	36	0	0	2	0
2	BBB	36	0	0	2	0
3	AAA	20	0	0	0	0
3	BBB	10	0	0	0	0
4	AAA	18	0	24	1	0
4	BBB	12	0	16	2	0
5	AAA	1	0	0	0	0
6	AAA	108	0	0	1	0
6	BBB	77	0	0	0	0
All	All	5177	0	5033	25	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.

The worst 5 of 25 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:AAA:275[B]:ASN:OD1	6:AAA:503:HOH:O	2.05	0.73
1:BBB:186[B]:GLU:OE2	1:BBB:186[B]:GLU:HA	1.96	0.63
1:AAA:175:ARG:HD3	1:AAA:197:LEU:O	2.01	0.60
1:AAA:97:LYS:O	1:AAA:101[B]:GLU:HG3	2.02	0.60
1:BBB:175:ARG:HD3	1:BBB:197:LEU:O	2.03	0.57

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	AAA	309/325 (95%)	298 (96%)	11 (4%)	0	100	100
1	BBB	296/325 (91%)	287 (97%)	9 (3%)	0	100	100
All	All	605/650 (93%)	585 (97%)	20 (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	AAA	280/281 (100%)	278 (99%)	2 (1%)	76	87
1	BBB	268/281 (95%)	267 (100%)	1 (0%)	84	92
All	All	548/562 (98%)	545 (100%)	3 (0%)	78	90

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	64	PHE
1	AAA	93	HIS
1	BBB	64	PHE

Sometimes 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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 1 is monoatomic - leaving 13 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	A1JCP	BBB	401	-	35,38,38	2.13	8 (22%)	38,54,54	1.61	7 (18%)
3	SO4	AAA	402	-	4,4,4	0.34	0	6,6,6	0.08	0
3	SO4	AAA	403	-	4,4,4	0.32	0	6,6,6	0.10	0
4	GOL	AAA	405	-	5,5,5	0.07	0	5,5,5	0.25	0
3	SO4	AAA	407	-	4,4,4	0.34	0	6,6,6	0.09	0
3	SO4	AAA	408	-	4,4,4	0.33	0	6,6,6	0.07	0
4	GOL	AAA	409	-	5,5,5	0.08	0	5,5,5	0.26	0
2	A1JCP	AAA	401	-	35,38,38	1.93	9 (25%)	38,54,54	1.46	7 (18%)
4	GOL	AAA	404	-	5,5,5	0.11	0	5,5,5	0.35	0
4	GOL	BBB	403	-	5,5,5	0.07	0	5,5,5	0.24	0
3	SO4	BBB	402	-	4,4,4	0.34	0	6,6,6	0.09	0
4	GOL	BBB	405	-	5,5,5	0.08	0	5,5,5	0.29	0
3	SO4	BBB	404	-	4,4,4	0.32	0	6,6,6	0.09	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
2	A1JCP	BBB	401	-	-	7/28/57/57	0/3/3/3
4	GOL	AAA	405	-	-	2/4/4/4	-
2	A1JCP	AAA	401	-	-	4/28/57/57	0/3/3/3
4	GOL	AAA	404	-	-	2/4/4/4	-
4	GOL	BBB	403	-	-	2/4/4/4	-
4	GOL	AAA	409	-	-	0/4/4/4	-
4	GOL	BBB	405	-	-	2/4/4/4	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	401	A1JCP	C12-S11	-6.76	1.63	1.74
2	BBB	401	A1JCP	C9-C7	4.83	1.55	1.46
2	AAA	401	A1JCP	C9-C7	4.73	1.55	1.46
2	BBB	401	A1JCP	C13-N14	4.60	1.37	1.28
2	AAA	401	A1JCP	C13-C12	-4.56	1.34	1.47

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BBB	401	A1JCP	C30-N31-C10	-4.65	112.21	116.52
2	BBB	401	A1JCP	C23-C22-N21	-4.13	109.48	111.91
2	AAA	401	A1JCP	C30-N31-C10	-3.79	113.01	116.52
2	AAA	401	A1JCP	C19-N18-C17	3.25	121.54	116.81
2	BBB	401	A1JCP	C19-N18-C17	3.21	121.47	116.81

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	BBB	401	A1JCP	F4-C2-C5-N6
2	BBB	401	A1JCP	C16-C17-N21-C22
2	BBB	401	A1JCP	C16-C17-N21-C29
2	BBB	401	A1JCP	N18-C17-N21-C29
4	AAA	404	GOL	C1-C2-C3-O3

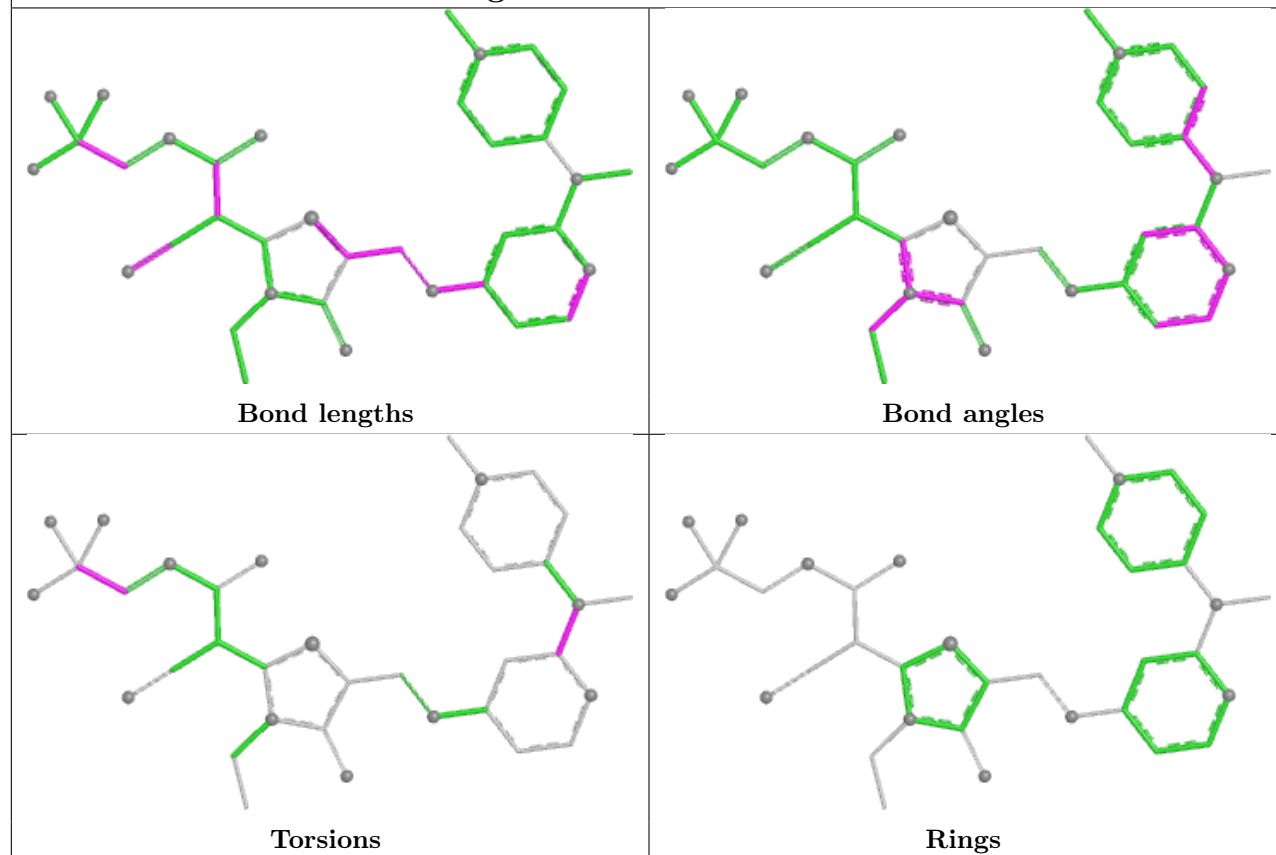
There are no ring outliers.

5 monomers are involved in 7 short contacts:

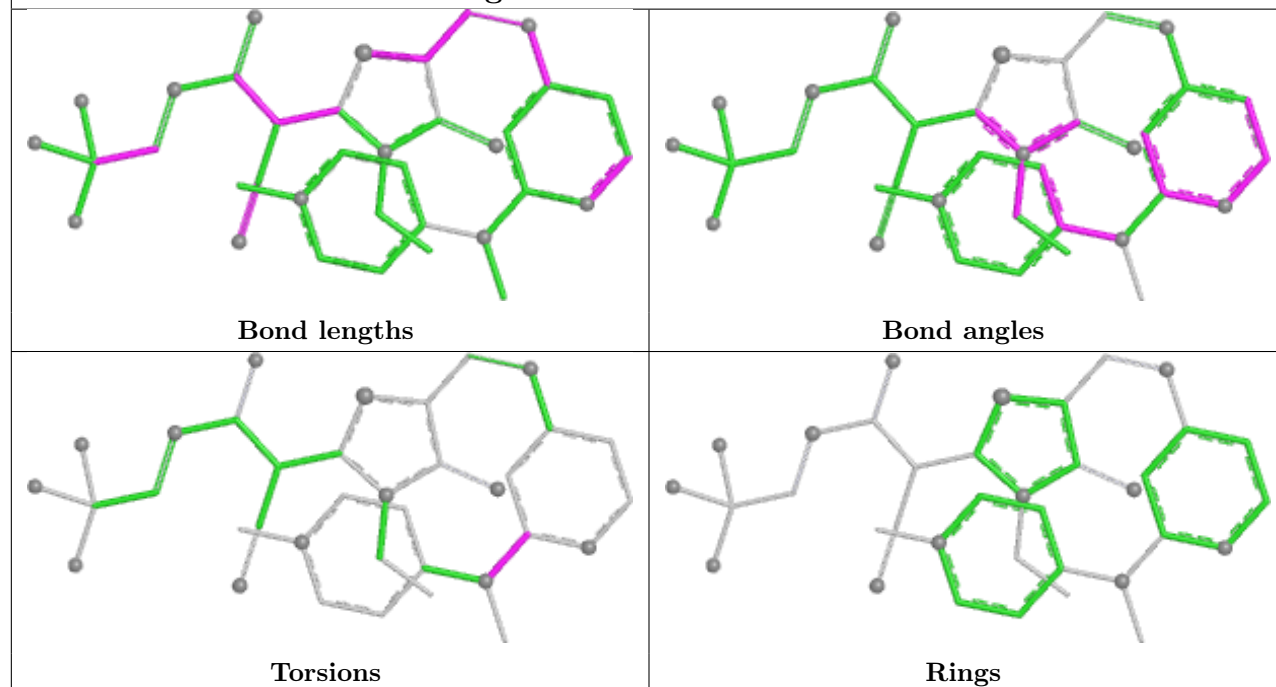
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	BBB	401	A1JCP	2	0
2	AAA	401	A1JCP	2	0
4	AAA	404	GOL	1	0
4	BBB	403	GOL	1	0
4	BBB	405	GOL	1	0

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.

Ligand A1JCP BBB 401



Ligand A1JCP AAA 401



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	AAA	297/325 (91%)	-0.13	6 (2%) 65 62	19, 50, 114, 156	14 (4%)
1	BBB	288/325 (88%)	0.10	7 (2%) 59 56	23, 59, 133, 162	10 (3%)
All	All	585/650 (90%)	-0.02	13 (2%) 62 59	19, 54, 125, 162	24 (4%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	64	PHE	3.6
1	AAA	64	PHE	2.8
1	BBB	300	LEU	2.8
1	AAA	93	HIS	2.6
1	AAA	334	PRO	2.6

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](#)

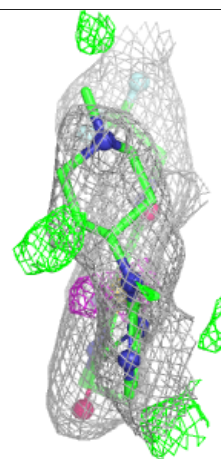
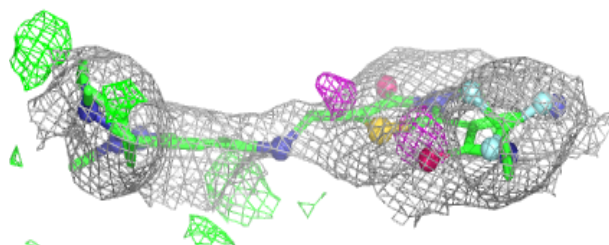
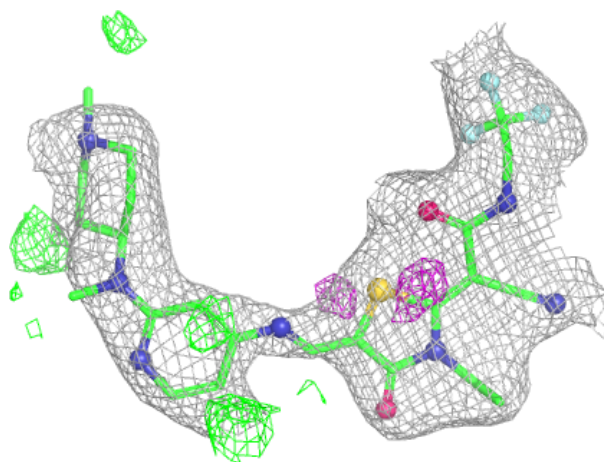
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists 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
3	SO4	AAA	408	5/5	0.67	0.10	104,109,121,142	0
4	GOL	BBB	405	6/6	0.72	0.21	86,88,94,98	0
3	SO4	BBB	404	5/5	0.80	0.09	74,84,95,103	0
2	A1JCP	BBB	401	36/36	0.82	0.15	57,88,120,122	0
4	GOL	AAA	404	6/6	0.83	0.14	43,60,69,81	0
3	SO4	AAA	403	5/5	0.85	0.09	69,72,95,100	0
4	GOL	AAA	409	6/6	0.85	0.10	72,87,88,90	0
3	SO4	AAA	407	5/5	0.85	0.08	87,90,101,103	0
4	GOL	AAA	405	6/6	0.90	0.11	39,64,67,72	0
4	GOL	BBB	403	6/6	0.91	0.10	50,62,63,68	0
2	A1JCP	AAA	401	36/36	0.92	0.12	49,66,124,128	0
3	SO4	AAA	402	5/5	0.93	0.07	61,62,88,90	0
3	SO4	BBB	402	5/5	0.93	0.06	70,76,83,86	0
5	CL	AAA	406	1/1	0.99	0.06	38,38,38,38	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.

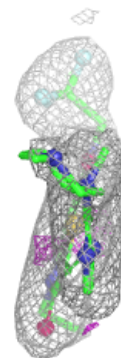
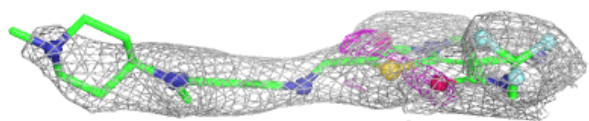
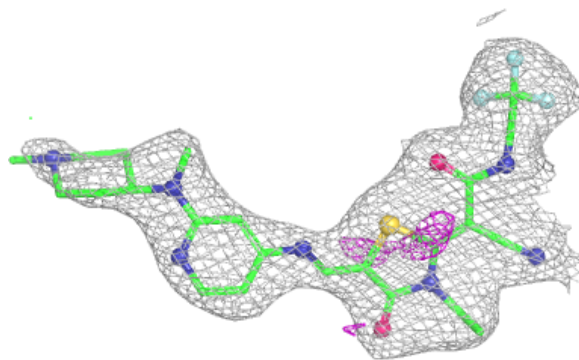
Electron density around A1JCP BBB 401:

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 A1JCP AAA 401:

$2mF_o-DF_c$ (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.