



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 08:30 PM UTC

PDB ID : 7Z9T / pdb_00007z9t
Title : Crystal structure of p38alpha C162S in complex with ATPgS and CAS
2094667-81-7 (in catalytic site, Y35 out), P 1 21 1
Authors : Baginski, B.; Pous, J.; Gonzalez, L.; Macias, M.J.; Nebreda, A.R.
Deposited on : 2022-03-21
Resolution : 2.60 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 Phenix2.0
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

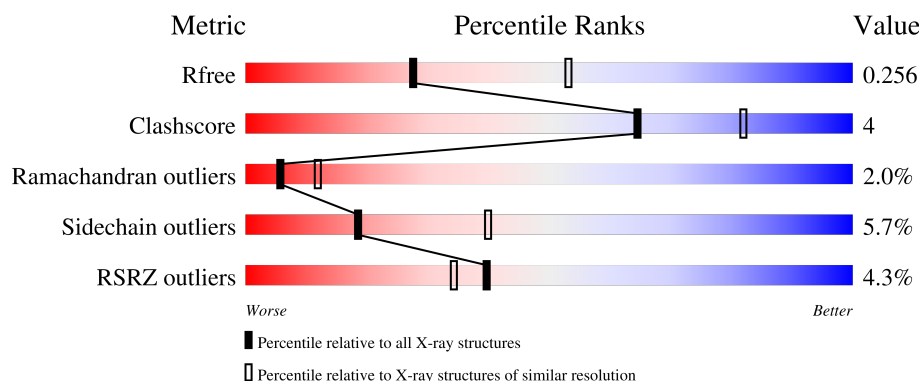
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	359	5% 84% 11% ..
1	BBB	359	3% 83% 13% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5835 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.

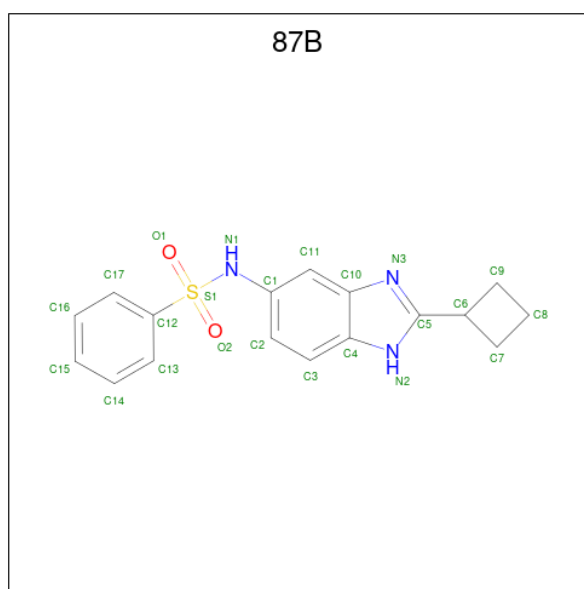
- Molecule 1 is a protein called Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	349	Total	C	N	O	S	115	0	0
			2816	1803	483	518	12			
1	BBB	350	Total	C	N	O	S	96	0	0
			2825	1808	484	521	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	162	SER	CYS	conflict	UNP P47811
BBB	162	SER	CYS	conflict	UNP P47811

- Molecule 2 is N-(2-cyclobutyl-1H-1,3-benzodiazol-5-yl)benzenesulfonamide (CCD ID: 87B) (formula: C₁₇H₁₇N₃O₂S) (labeled as "Ligand of Interest" by depositor).



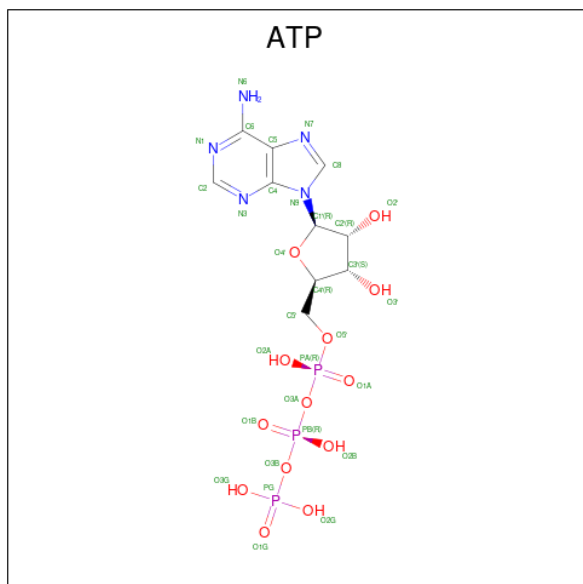
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	S	0	0
			23	17	3	2	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	BBB	1	Total	C	N	O	S	23	0
			23	17	3	2	1		

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	BBB	1	Total	C	N	O	P	31	0
			31	10	5	13	3		

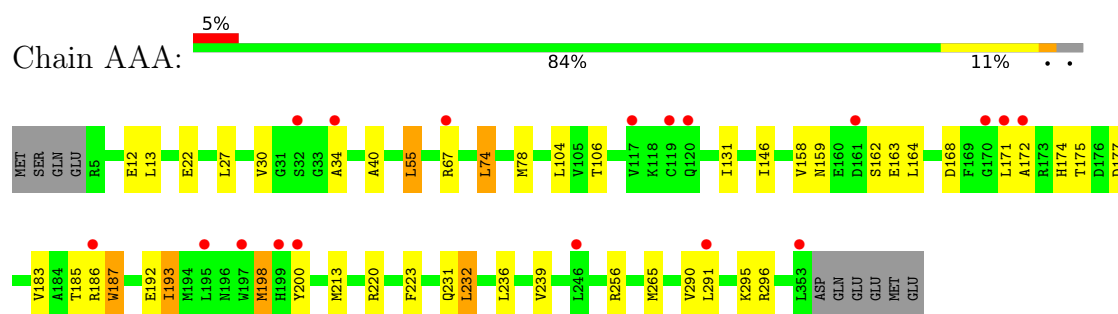
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	49	Total	O	0	0
			49	49		
4	BBB	68	Total	O	0	0
			68	68		

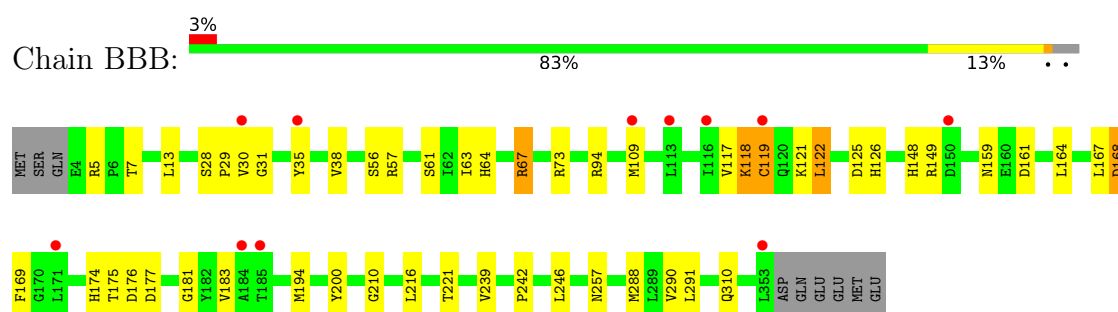
3 Residue-property plots [i](#)

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: Mitogen-activated protein kinase 14



- Molecule 1: Mitogen-activated protein kinase 14



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.14Å 68.07Å 79.98Å 90.00° 94.78° 90.00°	Depositor
Resolution (Å)	79.70 – 2.60 79.70 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.9 (79.70-2.60) 98.9 (79.70-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.34 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
R, R_{free}	0.199 , 0.254 0.201 , 0.256	Depositor DCC
R_{free} test set	1103 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	46.9	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.3	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	0.94	EDS
Total number of atoms	5835	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.32% 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: ATP, 87B

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	0.48	2/2883 (0.1%)	0.83	0/3915
1	BBB	0.47	0/2892	0.83	0/3927
All	All	0.47	2/5775 (0.0%)	0.83	0/7842

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	172	ALA	C-N	-7.06	1.24	1.33
1	AAA	34	ALA	C-N	-5.16	1.26	1.33

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	AAA	2816	0	2805	22	0
1	BBB	2825	0	2811	20	0
2	AAA	23	0	0	1	0
2	BBB	23	0	0	0	0
3	BBB	31	0	12	0	0
4	AAA	49	0	0	1	0
4	BBB	68	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5835	0	5628	42	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 (42) 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:290:VAL:O	1:AAA:296:ARG:NH1	2.26	0.68
1:BBB:159:ASN:HB3	1:BBB:161:ASP:H	1.64	0.63
1:BBB:117:VAL:HG21	1:BBB:216:LEU:HD22	1.82	0.62
1:AAA:158:VAL:HG13	1:AAA:162:SER:HA	1.82	0.60
1:AAA:186:ARG:O	1:AAA:187:TRP:HB2	2.00	0.60
1:BBB:239:VAL:HG21	1:BBB:291:LEU:HD13	1.82	0.60
1:AAA:192:GLU:OE2	1:AAA:296:ARG:NH2	2.35	0.59
1:AAA:12:GLU:OE1	4:AAA:501:HOH:O	2.17	0.57
1:BBB:121:LYS:O	1:BBB:122:LEU:O	2.24	0.55
1:BBB:164:LEU:C	1:BBB:164:LEU:HD23	2.33	0.53
1:BBB:73:ARG:HD2	4:BBB:508:HOH:O	2.10	0.52
1:AAA:223:PHE:O	1:AAA:231:GLN:NE2	2.42	0.52
1:AAA:74:LEU:HD21	1:AAA:146:ILE:HD13	1.94	0.50
1:BBB:239:VAL:HG21	1:BBB:291:LEU:CD1	2.42	0.49
1:BBB:64:HIS:O	1:BBB:67:ARG:HG3	2.13	0.49
1:BBB:29:PRO:O	1:BBB:31:GLY:N	2.45	0.49
1:AAA:158:VAL:HG12	1:AAA:159:ASN:O	2.13	0.49
1:AAA:30:VAL:O	1:AAA:30:VAL:HG13	2.13	0.49
1:BBB:61:SER:OG	1:BBB:63:ILE:HG22	2.14	0.48
1:BBB:119:CYS:O	1:BBB:119:CYS:SG	2.71	0.48
1:BBB:167:LEU:O	1:BBB:168:ASP:C	2.56	0.47
1:AAA:239:VAL:HG11	1:AAA:291:LEU:HD13	1.97	0.47
1:BBB:121:LYS:O	1:BBB:216:LEU:O	2.32	0.46
1:AAA:106:THR:HG23	2:AAA:401:87B:C15	2.46	0.46
1:AAA:232:LEU:HD22	1:AAA:236:LEU:CD1	2.45	0.46
1:BBB:210:GLY:HA2	1:BBB:288:MET:HE3	1.97	0.46
1:BBB:148:HIS:O	1:BBB:149:ARG:HB2	2.15	0.45
1:AAA:55:LEU:HD21	1:AAA:104:LEU:HD11	1.99	0.45
1:AAA:74:LEU:O	1:AAA:78:MET:HG2	2.17	0.45
1:BBB:57:ARG:HH21	1:BBB:57:ARG:HG3	1.82	0.44
1:AAA:159:ASN:HD22	1:AAA:163:GLU:HB2	1.82	0.44
1:BBB:118:LYS:H	1:BBB:118:LYS:HG2	1.62	0.44
1:AAA:27:LEU:HA	1:AAA:40:ALA:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:131:ILE:HG13	1:AAA:213:MET:HG3	2.01	0.43
1:BBB:242:PRO:HB3	1:BBB:246:LEU:HD23	2.00	0.42
1:AAA:232:LEU:HD23	1:AAA:232:LEU:HA	1.95	0.42
1:BBB:56:SER:O	1:BBB:57:ARG:C	2.63	0.41
1:BBB:5:ARG:NH1	4:BBB:506:HOH:O	2.43	0.41
1:AAA:164:LEU:C	1:AAA:164:LEU:HD23	2.46	0.41
1:AAA:193:ILE:C	1:AAA:193:ILE:HD12	2.46	0.41
1:AAA:186:ARG:O	1:AAA:187:TRP:CB	2.66	0.40
1:AAA:192:GLU:HB2	1:AAA:198:MET:HE3	2.04	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	AAA	347/359 (97%)	326 (94%)	15 (4%)	6 (2%)	7	15
1	BBB	348/359 (97%)	321 (92%)	19 (6%)	8 (2%)	5	9
All	All	695/718 (97%)	647 (93%)	34 (5%)	14 (2%)	6	12

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	175	THR
1	AAA	185	THR
1	BBB	122	LEU
1	BBB	175	THR
1	AAA	168	ASP
1	AAA	174	HIS
1	AAA	187	TRP
1	BBB	30	VAL
1	BBB	168	ASP

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Mol	Chain	Res	Type
1	BBB	176	ASP
1	BBB	181	GLY
1	AAA	177	ASP
1	BBB	169	PHE
1	BBB	177	ASP

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	AAA	308/318 (97%)	293 (95%)	15 (5%)	22	47
1	BBB	309/318 (97%)	289 (94%)	20 (6%)	15	35
All	All	617/636 (97%)	582 (94%)	35 (6%)	18	40

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	13	LEU
1	AAA	22	GLU
1	AAA	55	LEU
1	AAA	67	ARG
1	AAA	74	LEU
1	AAA	171	LEU
1	AAA	183	VAL
1	AAA	193	ILE
1	AAA	198	MET
1	AAA	200	TYR
1	AAA	220	ARG
1	AAA	232	LEU
1	AAA	256	ARG
1	AAA	265	MET
1	AAA	295	LYS
1	BBB	7	THR
1	BBB	13	LEU
1	BBB	28	SER

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Mol	Chain	Res	Type
1	BBB	35	TYR
1	BBB	38	VAL
1	BBB	67	ARG
1	BBB	94	ARG
1	BBB	109	MET
1	BBB	118	LYS
1	BBB	119	CYS
1	BBB	125	ASP
1	BBB	126	HIS
1	BBB	174	HIS
1	BBB	183	VAL
1	BBB	194	MET
1	BBB	200	TYR
1	BBB	221	THR
1	BBB	257	ASN
1	BBB	290	VAL
1	BBB	310	GLN

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](#)

3 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
3	ATP	BBB	402	-	32,33,33	0.55	0	48,52,52	0.55	0
2	87B	AAA	401	-	26,26,26	2.70	6 (23%)	34,38,38	2.17	4 (11%)
2	87B	BBB	401	-	26,26,26	2.75	6 (23%)	34,38,38	1.84	3 (8%)

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
3	ATP	BBB	402	-	-	8/22/38/38	0/3/3/3
2	87B	AAA	401	-	-	6/11/21/21	0/4/4/4
2	87B	BBB	401	-	-	6/11/21/21	0/4/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	401	87B	C12-S1	-10.56	1.60	1.76
2	AAA	401	87B	C12-S1	-10.41	1.60	1.76
2	BBB	401	87B	C1-N1	-5.23	1.35	1.43
2	AAA	401	87B	O2-S1	4.64	1.48	1.43
2	AAA	401	87B	O1-S1	4.54	1.48	1.43
2	BBB	401	87B	O2-S1	4.20	1.48	1.43
2	BBB	401	87B	O1-S1	4.15	1.48	1.43
2	AAA	401	87B	C1-N1	-4.14	1.36	1.43
2	AAA	401	87B	C10-N3	-2.47	1.34	1.39
2	BBB	401	87B	C10-N3	-2.37	1.35	1.39
2	AAA	401	87B	C5-N3	2.23	1.35	1.32
2	BBB	401	87B	C5-N3	2.13	1.35	1.32

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	401	87B	O2-S1-O1	-8.80	108.83	119.52
2	BBB	401	87B	O2-S1-O1	-8.39	109.33	119.52
2	AAA	401	87B	C12-S1-N1	6.02	114.35	106.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	BBB	401	87B	C12-S1-N1	3.66	111.42	106.88
2	AAA	401	87B	C1-C11-C10	2.56	120.64	118.32
2	AAA	401	87B	C13-C12-S1	2.04	122.00	119.76
2	BBB	401	87B	C8-C7-C6	2.03	90.22	88.48

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	BBB	402	ATP	C5'-O5'-PA-O3A
2	AAA	401	87B	C13-C12-S1-N1
2	AAA	401	87B	C17-C12-S1-N1
2	BBB	401	87B	C17-C12-S1-O2
2	BBB	401	87B	C13-C12-S1-O2
2	BBB	401	87B	C17-C12-S1-N1
2	BBB	401	87B	C13-C12-S1-N1
2	AAA	401	87B	C17-C12-S1-O1
2	AAA	401	87B	C13-C12-S1-O1
3	BBB	402	ATP	PG-O3B-PB-O1B
3	BBB	402	ATP	PA-O3A-PB-O1B
3	BBB	402	ATP	C5'-O5'-PA-O1A
2	AAA	401	87B	C2-C1-N1-S1
2	AAA	401	87B	C11-C1-N1-S1
2	BBB	401	87B	C11-C1-N1-S1
2	BBB	401	87B	C2-C1-N1-S1
3	BBB	402	ATP	C3'-C4'-C5'-O5'
3	BBB	402	ATP	PG-O3B-PB-O2B
3	BBB	402	ATP	PA-O3A-PB-O2B
3	BBB	402	ATP	O4'-C4'-C5'-O5'

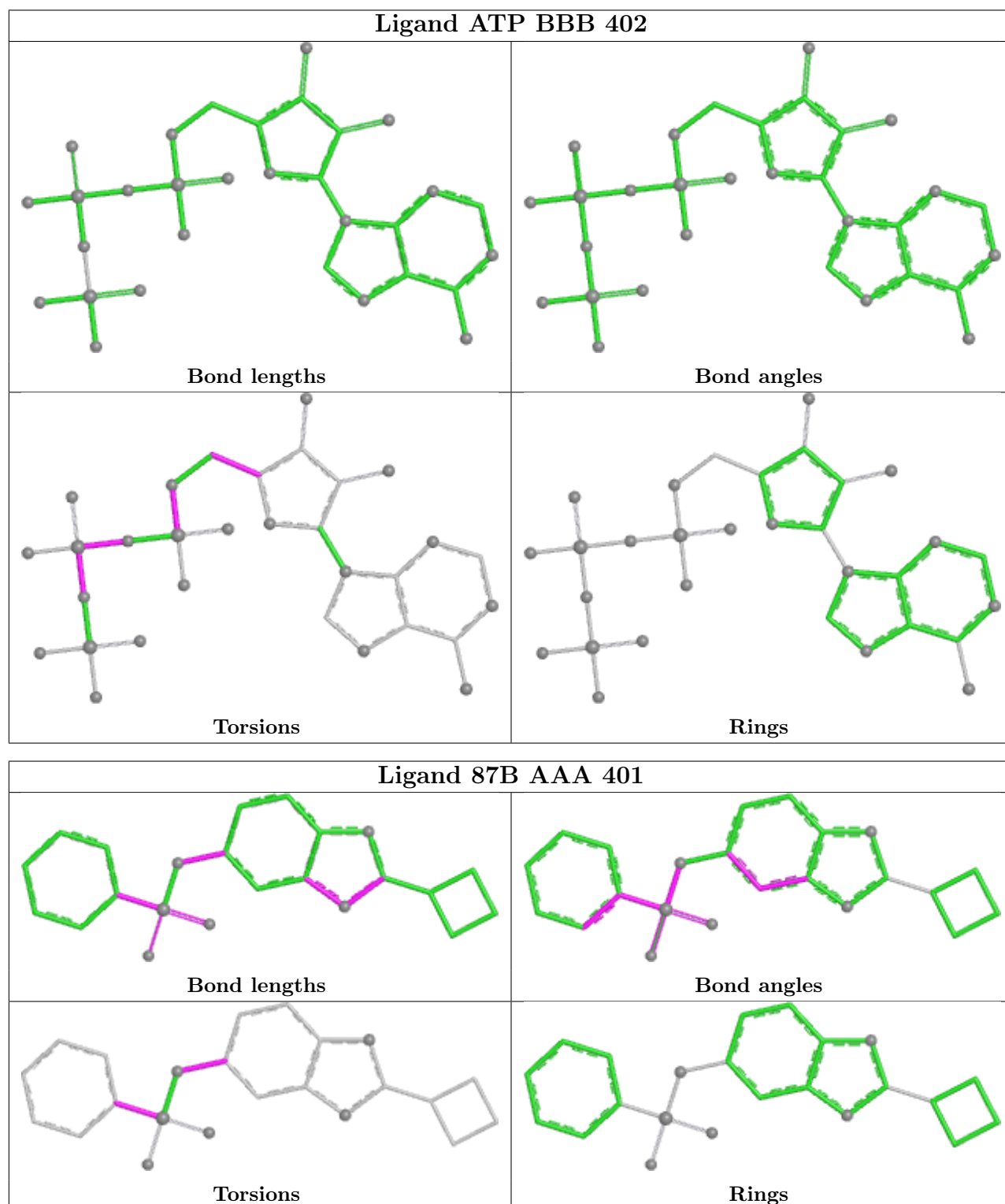
There are no ring outliers.

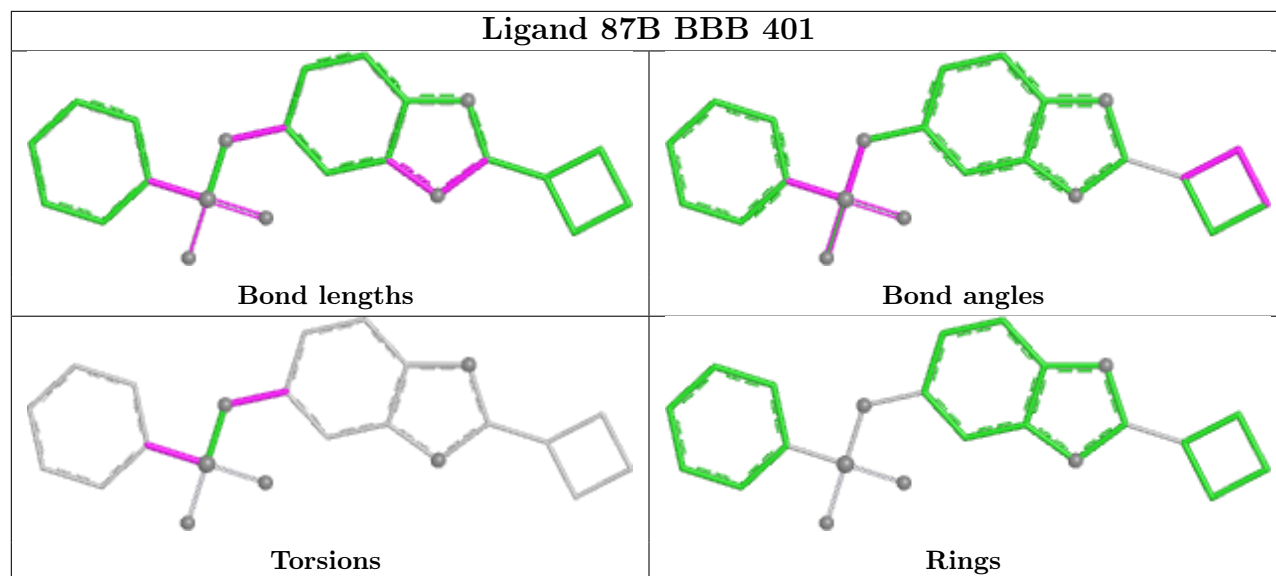
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	401	87B	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	AAA	335/359 (93%)	0.35	18 (5%) 31 26	34, 65, 124, 145	0
1	BBB	338/359 (94%)	0.04	11 (3%) 49 43	23, 47, 97, 128	0
All	All	673/718 (93%)	0.19	29 (4%) 40 34	23, 55, 117, 145	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	119	CYS	5.5
1	AAA	171	LEU	4.8
1	AAA	172	ALA	4.6
1	AAA	197	TRP	4.5
1	AAA	34	ALA	4.0
1	BBB	30	VAL	3.6
1	AAA	186	ARG	2.9
1	AAA	353	LEU	2.8
1	BBB	116	ILE	2.8
1	BBB	185	THR	2.8
1	BBB	113	LEU	2.7
1	BBB	171	LEU	2.7
1	BBB	109	MET	2.7
1	AAA	200	TYR	2.5
1	AAA	170	GLY	2.5
1	AAA	120	GLN	2.5
1	AAA	32	SER	2.5
1	AAA	117	VAL	2.4
1	AAA	195	LEU	2.3
1	BBB	150	ASP	2.3
1	BBB	35	TYR	2.2
1	AAA	119	CYS	2.2
1	BBB	184	ALA	2.2
1	BBB	353	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	AAA	291	LEU	2.2
1	AAA	161	ASP	2.2
1	AAA	246	LEU	2.1
1	AAA	199	HIS	2.1
1	AAA	67	ARG	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

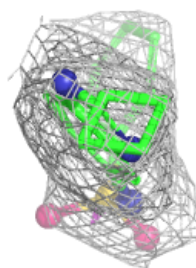
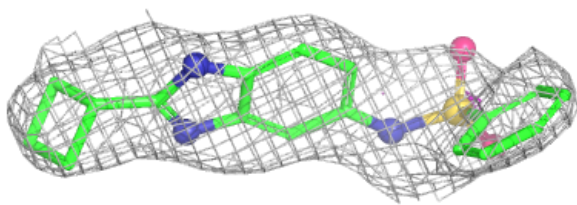
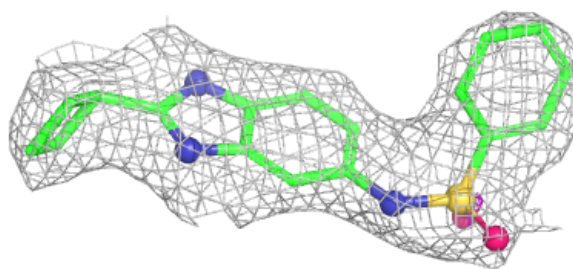
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	87B	AAA	401	23/23	0.89	0.13	73,80,108,110	0
2	87B	BBB	401	23/23	-	-	48,48,48,48	23
3	ATP	BBB	402	31/31	-	-	48,48,48,48	31

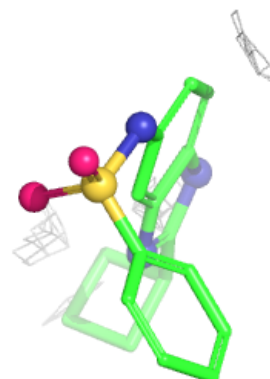
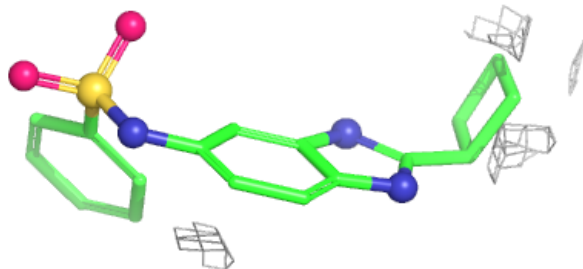
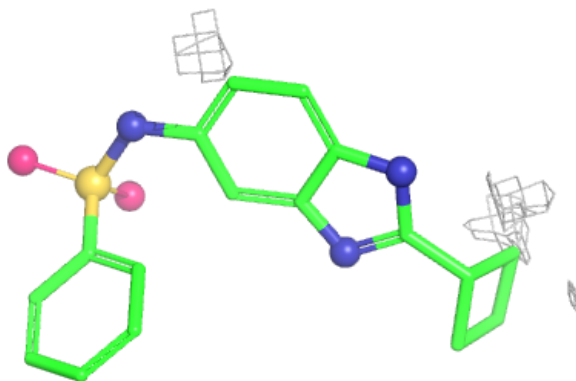
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 87B 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)

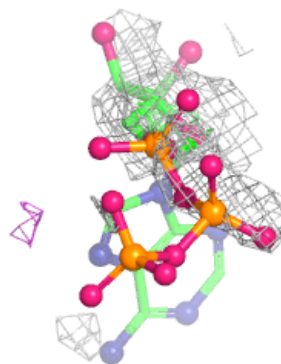
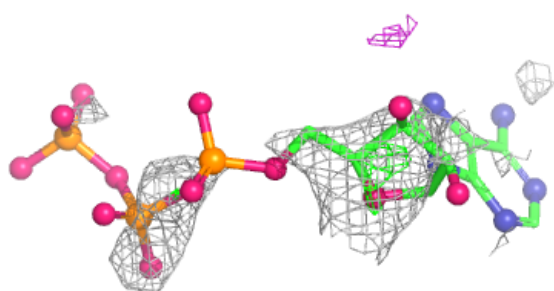
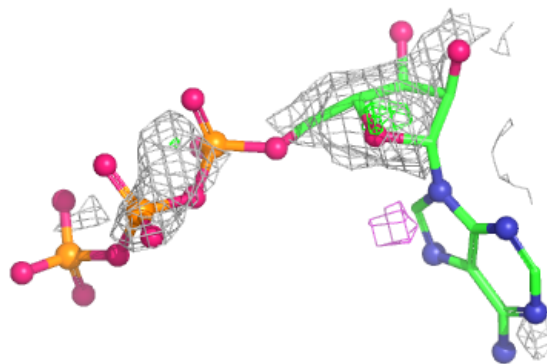
**Electron density around 87B BBB 401:**

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



Electron density around ATP BBB 402:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.