



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2025 – 04:51 pm BST

PDB ID : 9GTG / pdb_00009gtg
Title : RIPK1 in complex with AZ"902
Authors : Petersen, J.
Deposited on : 2024-09-17
Resolution : 2.25 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	:	1.8.4, 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	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.44

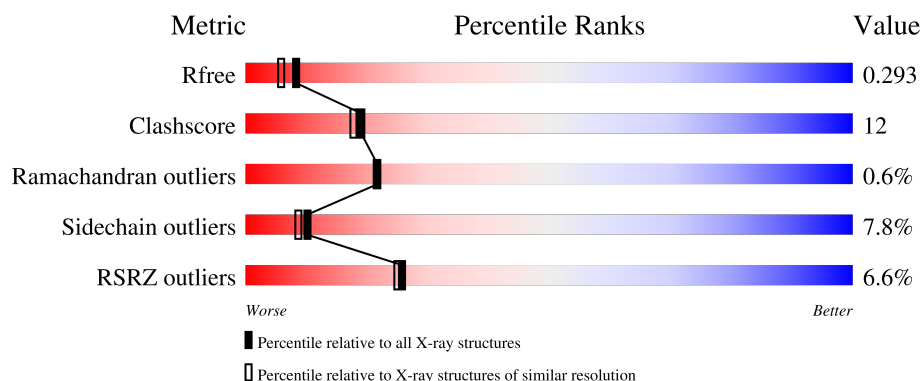
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


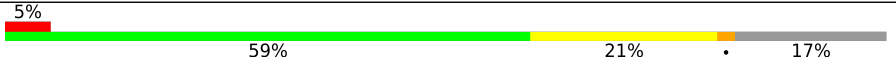
The reported resolution of this entry is 2.25 Å.

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	1763 (2.26-2.26)
Clashscore	180529	1919 (2.26-2.26)
Ramachandran outliers	177936	1884 (2.26-2.26)
Sidechain outliers	177891	1885 (2.26-2.26)
RSRZ outliers	164620	1763 (2.26-2.26)

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	313	
1	B	313	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4225 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 Receptor-interacting serine/threonine-protein kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	259	Total	C	N	O	S	0	0	0
			2054	1322	340	376	16			
1	B	259	Total	C	N	O	S	0	0	0
			2059	1324	342	377	16			

There are 46 discrepancies between the modelled and reference sequences:

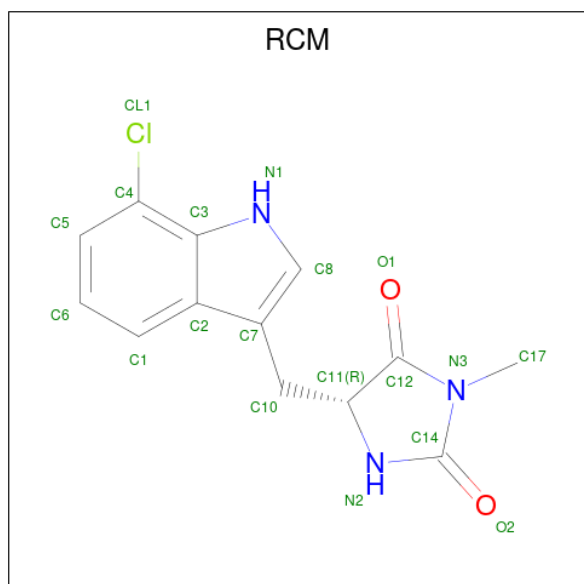
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	initiating methionine	UNP Q13546
A	-17	GLY	-	expression tag	UNP Q13546
A	-16	HIS	-	expression tag	UNP Q13546
A	-15	HIS	-	expression tag	UNP Q13546
A	-14	HIS	-	expression tag	UNP Q13546
A	-13	HIS	-	expression tag	UNP Q13546
A	-12	HIS	-	expression tag	UNP Q13546
A	-11	HIS	-	expression tag	UNP Q13546
A	-10	GLY	-	expression tag	UNP Q13546
A	-9	GLY	-	expression tag	UNP Q13546
A	-8	GLY	-	expression tag	UNP Q13546
A	-7	GLU	-	expression tag	UNP Q13546
A	-6	ASN	-	expression tag	UNP Q13546
A	-5	LEU	-	expression tag	UNP Q13546
A	-4	TYR	-	expression tag	UNP Q13546
A	-3	PHE	-	expression tag	UNP Q13546
A	-2	GLN	-	expression tag	UNP Q13546
A	-1	GLY	-	expression tag	UNP Q13546
A	0	SER	-	expression tag	UNP Q13546
A	34	ALA	CYS	conflict	UNP Q13546
A	127	ALA	CYS	conflict	UNP Q13546
A	233	ALA	CYS	conflict	UNP Q13546
A	240	ALA	CYS	conflict	UNP Q13546
B	-18	MET	-	initiating methionine	UNP Q13546
B	-17	GLY	-	expression tag	UNP Q13546

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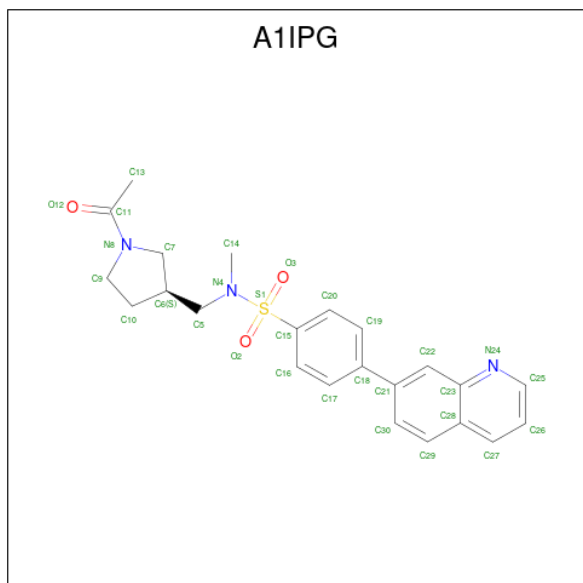
Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	expression tag	UNP Q13546
B	-15	HIS	-	expression tag	UNP Q13546
B	-14	HIS	-	expression tag	UNP Q13546
B	-13	HIS	-	expression tag	UNP Q13546
B	-12	HIS	-	expression tag	UNP Q13546
B	-11	HIS	-	expression tag	UNP Q13546
B	-10	GLY	-	expression tag	UNP Q13546
B	-9	GLY	-	expression tag	UNP Q13546
B	-8	GLY	-	expression tag	UNP Q13546
B	-7	GLU	-	expression tag	UNP Q13546
B	-6	ASN	-	expression tag	UNP Q13546
B	-5	LEU	-	expression tag	UNP Q13546
B	-4	TYR	-	expression tag	UNP Q13546
B	-3	PHE	-	expression tag	UNP Q13546
B	-2	GLN	-	expression tag	UNP Q13546
B	-1	GLY	-	expression tag	UNP Q13546
B	0	SER	-	expression tag	UNP Q13546
B	34	ALA	CYS	conflict	UNP Q13546
B	127	ALA	CYS	conflict	UNP Q13546
B	233	ALA	CYS	conflict	UNP Q13546
B	240	ALA	CYS	conflict	UNP Q13546

- Molecule 2 is (5R)-5-[(7-chloro-1H-indol-3-yl)methyl]-3-methylimidazolidine-2,4-dione (CCD ID: RCM) (formula: C₁₃H₁₂ClN₃O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			19	13	1	3	2		
2	B	1	Total	C	Cl	N	O	0	0
			19	13	1	3	2		

- Molecule 3 is {N}-[[[(3 {S})-1-ethanoylpyrrolidin-3-yl]methyl]- {N}-methyl-4-quinolin-7-yl-benzenesulfonamide (CCD ID: A1IPG) (formula: C₂₃H₂₅N₃O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			30	23	3	3	1		
3	B	1	Total	C	N	O	S	0	0
			30	23	3	3	1		

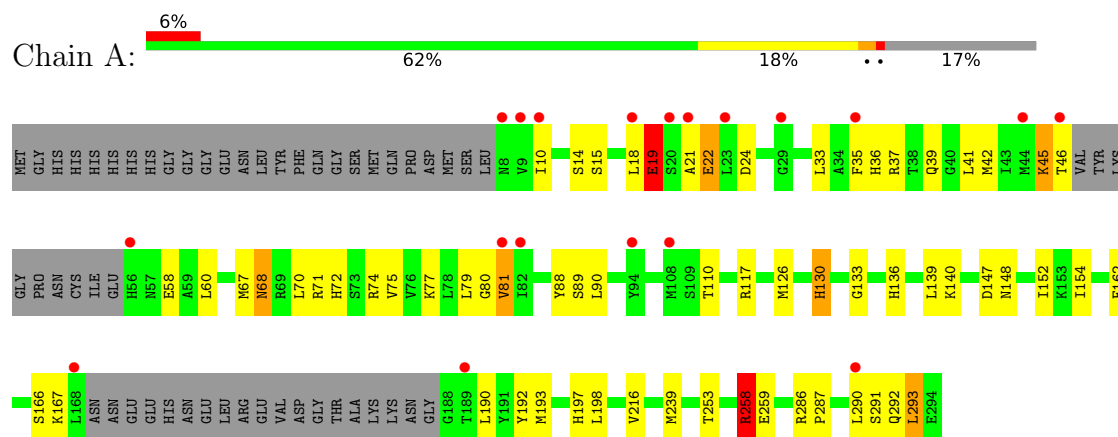
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	7	Total	O	0	0
			7	7		
4	B	7	Total	O	0	0
			7	7		

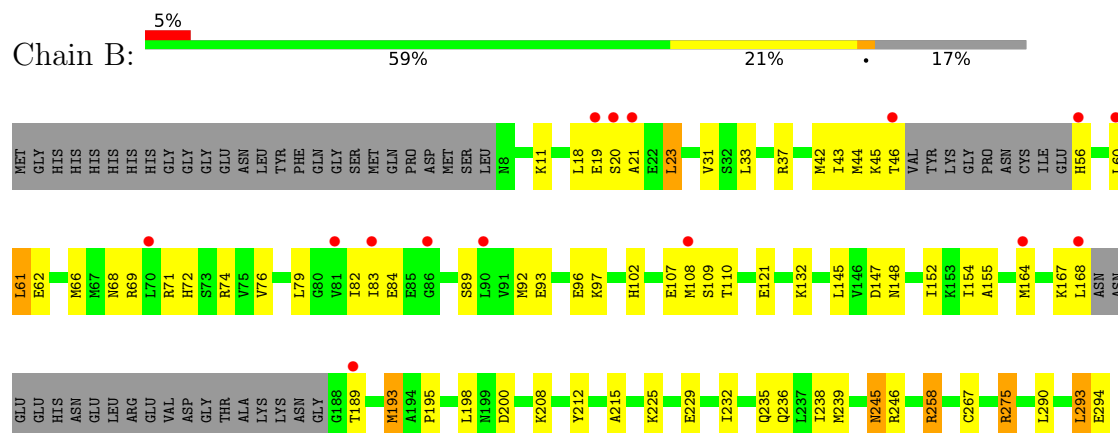
3 Residue-property plots [i](#)

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: Receptor-interacting serine/threonine-protein kinase 1



- Molecule 1: Receptor-interacting serine/threonine-protein kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	47.08Å 96.49Å 129.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.27 – 2.25 77.27 – 2.25	Depositor EDS
% Data completeness (in resolution range)	85.6 (77.27-2.25) 85.7 (77.27-2.25)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.25Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.217 , 0.295 0.227 , 0.293	Depositor DCC
R_{free} test set	1362 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	65.3	Xtriage
Anisotropy	0.104	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 45.3	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	0.95	EDS
Total number of atoms	4225	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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: A1IPG, RCM

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	0.66	3/2095 (0.1%)	1.03	0/2821
1	B	0.65	1/2099 (0.0%)	1.04	3/2824 (0.1%)
All	All	0.65	4/4194 (0.1%)	1.03	3/5645 (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	3
1	B	0	4
All	All	0	7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	197	HIS	CE1-NE2	6.33	1.38	1.32
1	A	130	HIS	CE1-NE2	5.82	1.38	1.32
1	A	136	HIS	CE1-NE2	5.63	1.38	1.32
1	B	102	HIS	CE1-NE2	5.26	1.37	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	110	THR	CB-CA-C	7.13	118.08	109.31
1	B	147	ASP	CA-CB-CG	6.70	119.30	112.60
1	B	232	ILE	N-CA-C	-5.52	107.43	111.90

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	117	ARG	Sidechain
1	A	19	GLU	Peptide
1	A	258	ARG	Sidechain
1	B	258	ARG	Sidechain
1	B	275	ARG	Sidechain
1	B	37	ARG	Sidechain
1	B	71	ARG	Sidechain

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	2054	0	2069	43	2
1	B	2059	0	2079	54	2
2	A	19	0	12	2	0
2	B	19	0	12	1	0
3	A	30	0	0	0	0
3	B	30	0	0	1	0
4	A	7	0	0	0	0
4	B	7	0	0	1	0
All	All	4225	0	4172	97	2

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 12.

All (97) 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:19:GLU:OE2	1:B:21:ALA:CB	1.85	1.23
1:B:19:GLU:OE2	1:B:21:ALA:HB2	1.05	1.22
1:B:19:GLU:HG3	1:B:20:SER:O	1.41	1.19
1:B:19:GLU:HG3	1:B:20:SER:C	1.69	1.16
1:B:19:GLU:CG	1:B:20:SER:C	2.19	1.15
1:A:193:MET:HE3	1:A:198:LEU:HD23	1.42	1.01
1:B:19:GLU:CG	1:B:20:SER:O	2.09	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:SER:O	1:A:37:ARG:NH1	1.98	0.97
1:A:42:MET:HE2	1:A:79:LEU:HD13	1.56	0.88
1:B:167:LYS:O	1:B:168:LEU:HG	1.74	0.86
1:B:167:LYS:O	1:B:168:LEU:CG	2.27	0.82
1:B:19:GLU:HG2	1:B:20:SER:C	2.07	0.79
1:A:33:LEU:HD11	1:A:41:LEU:HD22	1.65	0.77
1:B:19:GLU:HG3	1:B:20:SER:CA	2.17	0.74
1:B:107:GLU:O	1:B:109:SER:N	2.21	0.73
1:B:19:GLU:CD	1:B:20:SER:O	2.34	0.70
1:B:19:GLU:OE2	1:B:20:SER:O	2.10	0.70
1:B:19:GLU:HG3	1:B:20:SER:N	2.09	0.67
1:B:19:GLU:CG	1:B:20:SER:CA	2.73	0.66
1:B:46:THR:HA	1:B:89:SER:OG	1.96	0.66
1:A:36:HIS:ND1	1:A:39:GLN:HB2	2.12	0.65
1:A:72:HIS:HD2	1:A:74:ARG:H	1.46	0.63
1:B:11:LYS:HE2	1:B:61:LEU:HD11	1.81	0.63
1:A:18:LEU:O	1:A:19:GLU:HB2	2.00	0.60
1:A:193:MET:CE	1:A:198:LEU:HD23	2.27	0.59
1:B:82:ILE:HB	1:B:89:SER:HB2	1.85	0.59
1:B:167:LYS:O	1:B:168:LEU:CB	2.51	0.57
1:A:152:ILE:C	1:A:152:ILE:HD12	2.30	0.57
1:B:42:MET:HE2	1:B:79:LEU:HD13	1.86	0.57
1:A:46:THR:HG22	1:A:89:SER:OG	2.07	0.55
1:A:46:THR:HA	1:A:89:SER:OG	2.08	0.54
1:A:18:LEU:O	1:A:19:GLU:CB	2.56	0.53
1:A:72:HIS:CD2	1:A:74:ARG:H	2.26	0.53
1:A:190:LEU:HD22	1:A:193:MET:HE2	1.90	0.53
1:A:190:LEU:HD22	1:A:193:MET:CE	2.39	0.53
1:B:18:LEU:O	1:B:19:GLU:C	2.53	0.52
1:B:74:ARG:NH1	4:B:401:HOH:O	2.37	0.52
1:B:97:LYS:HE2	1:B:148:ASN:HA	1.92	0.51
1:B:19:GLU:OE2	1:B:21:ALA:CA	2.55	0.51
1:A:67:MET:HE2	2:A:301:RCM:C8	2.41	0.51
1:A:193:MET:HE3	1:A:198:LEU:CD2	2.30	0.51
1:A:126:MET:SD	1:A:154:ILE:HD13	2.51	0.50
1:B:56:HIS:HB2	1:B:60:LEU:HD13	1.93	0.50
1:B:19:GLU:CD	1:B:20:SER:C	2.78	0.49
1:A:36:HIS:ND1	1:A:39:GLN:N	2.61	0.49
1:A:139:LEU:O	1:A:140:LYS:HB3	2.13	0.48
1:B:293:LEU:O	1:B:294:GLU:CB	2.61	0.48
1:A:130:HIS:O	1:A:133:GLY:N	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:LYS:O	1:B:168:LEU:CD1	2.61	0.48
1:B:19:GLU:OE2	1:B:20:SER:C	2.56	0.48
1:B:19:GLU:HG2	1:B:20:SER:CA	2.43	0.47
1:B:66:MET:SD	1:B:69:ARG:NH1	2.88	0.47
1:A:147:ASP:OD1	1:A:147:ASP:C	2.57	0.47
1:B:167:LYS:O	1:B:168:LEU:HD12	2.15	0.46
1:B:11:LYS:CE	1:B:61:LEU:HD11	2.43	0.46
1:B:193:MET:HE2	1:B:198:LEU:HD23	1.97	0.46
1:A:68:ASN:HD21	1:A:71:ARG:HH21	1.63	0.46
1:A:258:ARG:HG3	1:A:259:GLU:OE2	2.16	0.46
1:B:215:ALA:HB2	1:B:267:CYS:HB2	1.97	0.46
1:A:45:LYS:O	1:A:89:SER:HA	2.16	0.46
1:A:67:MET:CE	1:A:70:LEU:HD11	2.46	0.45
1:B:74:ARG:HD2	1:B:121:GLU:HB3	1.98	0.45
1:B:198:LEU:HB3	1:B:238:ILE:HG23	1.98	0.45
1:A:290:LEU:HD12	1:A:291:SER:N	2.31	0.45
1:A:292:GLN:O	1:A:293:LEU:HD12	2.16	0.45
1:B:208:LYS:NZ	1:B:275:ARG:O	2.39	0.45
1:A:67:MET:HG3	1:A:162:PHE:CE1	2.52	0.45
1:B:235:GLN:O	1:B:236:GLN:C	2.59	0.44
1:B:154:ILE:O	2:B:302:RCM:H11	2.17	0.44
1:B:152:ILE:C	1:B:152:ILE:HD12	2.44	0.43
1:B:33:LEU:HD12	1:B:42:MET:O	2.19	0.43
1:B:145:LEU:HD13	3:B:301:A1IPG:C25	2.49	0.42
1:B:167:LYS:C	1:B:168:LEU:HG	2.43	0.42
1:A:67:MET:HE3	1:A:70:LEU:CD1	2.49	0.42
1:A:286:ARG:N	1:A:287:PRO:HD2	2.35	0.42
1:A:258:ARG:HB2	1:A:258:ARG:CZ	2.49	0.42
1:B:23:LEU:HD23	1:B:23:LEU:HA	1.90	0.42
1:B:195:PRO:HD3	1:B:212:TYR:CE2	2.55	0.42
1:B:83:ILE:C	1:B:84:GLU:HG3	2.44	0.42
1:A:21:ALA:O	1:A:22:GLU:C	2.62	0.42
1:B:19:GLU:CG	1:B:20:SER:N	2.80	0.42
1:A:10:ILE:O	1:A:80:GLY:HA3	2.20	0.41
1:A:81:VAL:HG12	1:A:90:LEU:HD23	2.03	0.41
1:B:245:ASN:O	1:B:246:ARG:HD3	2.20	0.41
1:A:290:LEU:HD12	1:A:290:LEU:C	2.45	0.41
1:B:76:VAL:HG21	1:B:155:ALA:HB2	2.02	0.41
1:B:225:LYS:NZ	1:B:229:GLU:OE2	2.28	0.41
1:A:81:VAL:CG1	1:A:90:LEU:HD23	2.50	0.41
1:A:42:MET:HG2	1:A:79:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:MET:HE3	1:A:70:LEU:HD11	2.02	0.40
1:A:192:TYR:CE1	1:A:216:VAL:HG12	2.56	0.40
1:B:72:HIS:CD2	1:B:74:ARG:H	2.40	0.40
1:A:46:THR:C	1:A:88:TYR:O	2.63	0.40
1:A:166:SER:O	1:A:167:LYS:C	2.64	0.40
1:B:212:TYR:CD1	1:B:212:TYR:C	2.99	0.40
1:A:75:VAL:HG13	2:A:301:RCM:C6	2.51	0.40
1:B:46:THR:HG22	1:B:89:SER:OG	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:PHE:CE2	1:B:19:GLU:OE1[3_645]	1.59	0.61
1:A:35:PHE:CD2	1:B:19:GLU:OE1[3_645]	2.19	0.01

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	253/313 (81%)	232 (92%)	20 (8%)	1 (0%)	30	32
1	B	251/313 (80%)	236 (94%)	13 (5%)	2 (1%)	16	14
All	All	504/626 (80%)	468 (93%)	33 (6%)	3 (1%)	22	21

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	B	108	MET
1	B	200	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	A	222/271 (82%)	207 (93%)	15 (7%)	13	11
1	B	224/271 (83%)	204 (91%)	20 (9%)	8	6
All	All	446/542 (82%)	411 (92%)	35 (8%)	10	9

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

Mol	Chain	Res	Type
1	A	14	SER
1	A	22	GLU
1	A	24	ASP
1	A	45	LYS
1	A	58	GLU
1	A	60	LEU
1	A	68	ASN
1	A	77	LYS
1	A	81	VAL
1	A	110	THR
1	A	148	ASN
1	A	239	MET
1	A	253	THR
1	A	258	ARG
1	A	293	LEU
1	B	23	LEU
1	B	31	VAL
1	B	43	ILE
1	B	44	MET
1	B	45	LYS
1	B	61	LEU
1	B	62	GLU
1	B	68	ASN
1	B	92	MET
1	B	93	GLU
1	B	96	GLU
1	B	132	LYS

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Mol	Chain	Res	Type
1	B	164	MET
1	B	189	THR
1	B	193	MET
1	B	239	MET
1	B	245	ASN
1	B	258	ARG
1	B	290	LEU
1	B	293	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	A	68	ASN
1	A	72	HIS
1	A	148	ASN
1	A	245	ASN
1	B	68	ASN
1	B	72	HIS
1	B	102	HIS
1	B	292	GLN

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](#)

4 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	A1IPG	B	301	-	32,33,33	0.86	1 (3%)	42,48,48	2.06	10 (23%)
3	A1IPG	A	302	-	32,33,33	0.67	0	42,48,48	2.19	9 (21%)
2	RCM	A	301	-	19,21,21	1.57	3 (15%)	20,31,31	2.31	6 (30%)
2	RCM	B	302	-	19,21,21	1.28	2 (10%)	20,31,31	2.67	7 (35%)

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	A1IPG	B	301	-	-	6/24/33/33	0/4/4/4
3	A1IPG	A	302	-	-	6/24/33/33	0/4/4/4
2	RCM	A	301	-	-	0/3/20/20	0/3/3/3
2	RCM	B	302	-	-	0/3/20/20	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	RCM	C4-C3	-4.21	1.37	1.42
2	A	301	RCM	C12-N3	-3.60	1.35	1.38
2	B	302	RCM	C14-N3	-3.42	1.32	1.38
3	B	301	A1IPG	C15-S1	2.43	1.79	1.76
2	A	301	RCM	C1-C2	-2.14	1.37	1.42
2	B	302	RCM	C12-N3	-2.03	1.36	1.38

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	A1IPG	O3-S1-C15	-8.27	97.58	108.05
2	B	302	RCM	O1-C12-N3	7.04	129.58	123.97
3	B	301	A1IPG	C15-S1-N4	6.04	115.28	107.02
2	A	301	RCM	C11-N2-C14	-5.98	105.73	113.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	RCM	N2-C14-N3	4.82	114.14	107.18
3	B	301	A1IPG	O3-S1-C15	-4.66	102.16	108.05
3	B	301	A1IPG	C21-C22-C23	-4.52	117.49	121.44
2	B	302	RCM	C11-N2-C14	-4.50	107.54	113.02
3	A	302	A1IPG	C21-C22-C23	-4.38	117.60	121.44
3	B	301	A1IPG	C10-C9-N8	4.19	108.23	103.28
2	B	302	RCM	C17-N3-C12	3.97	127.54	123.33
2	B	302	RCM	C3-C4-CL1	3.76	122.42	118.97
2	B	302	RCM	N2-C14-N3	3.70	112.53	107.18
3	A	302	A1IPG	C25-N24-C23	3.59	122.49	116.93
3	A	302	A1IPG	O3-S1-N4	3.50	111.42	107.05
3	A	302	A1IPG	C13-C11-N8	3.48	122.31	118.26
3	B	301	A1IPG	C25-N24-C23	3.44	122.26	116.93
2	A	301	RCM	O1-C12-N3	3.34	126.63	123.97
2	A	301	RCM	O2-C14-N2	-3.34	120.59	126.90
3	B	301	A1IPG	C13-C11-N8	3.29	122.08	118.26
2	B	302	RCM	O2-C14-N3	-3.10	122.68	125.99
3	A	302	A1IPG	C16-C15-S1	-3.09	116.50	119.76
3	A	302	A1IPG	C20-C15-S1	3.07	122.99	119.76
2	A	301	RCM	C17-N3-C14	3.02	127.79	123.82
2	B	302	RCM	C5-C4-C3	-2.75	118.99	121.03
3	B	301	A1IPG	C30-C21-C22	2.63	122.21	118.09
3	A	302	A1IPG	C9-N8-C7	-2.56	104.92	111.55
2	A	301	RCM	C3-C4-CL1	-2.51	116.67	118.97
3	B	301	A1IPG	C6-C7-N8	2.50	109.97	102.04
3	B	301	A1IPG	C30-C29-C28	-2.43	117.06	120.82
3	A	302	A1IPG	C30-C29-C28	-2.19	117.42	120.82
3	B	301	A1IPG	O2-S1-C15	-2.02	105.49	108.05

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	A1IPG	N4-C5-C6-C7
3	A	302	A1IPG	N4-C5-C6-C10
3	B	301	A1IPG	N4-C5-C6-C7
3	B	301	A1IPG	N4-C5-C6-C10
3	A	302	A1IPG	C14-N4-S1-O2
3	A	302	A1IPG	C14-N4-S1-O3
3	A	302	A1IPG	C14-N4-S1-C15
3	B	301	A1IPG	C5-N4-S1-O3
3	B	301	A1IPG	C14-N4-S1-C15

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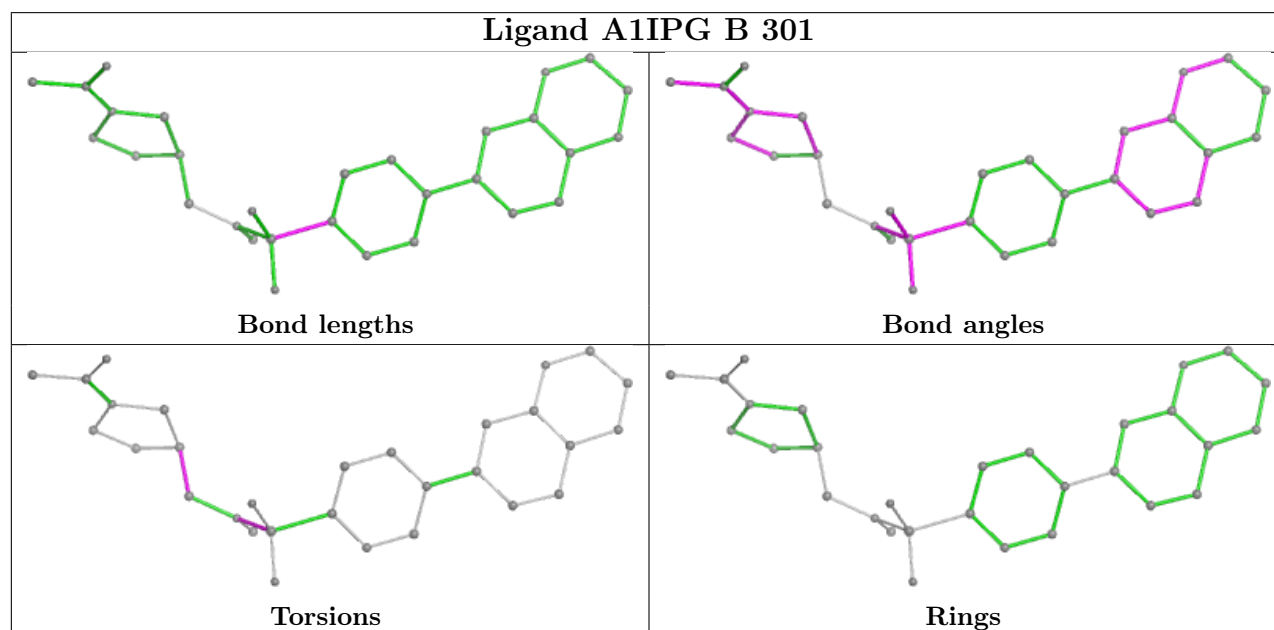
Mol	Chain	Res	Type	Atoms
3	B	301	A1IPG	C5-N4-S1-C15
3	B	301	A1IPG	C14-N4-S1-O3
3	A	302	A1IPG	C6-C5-N4-S1

There are no ring outliers.

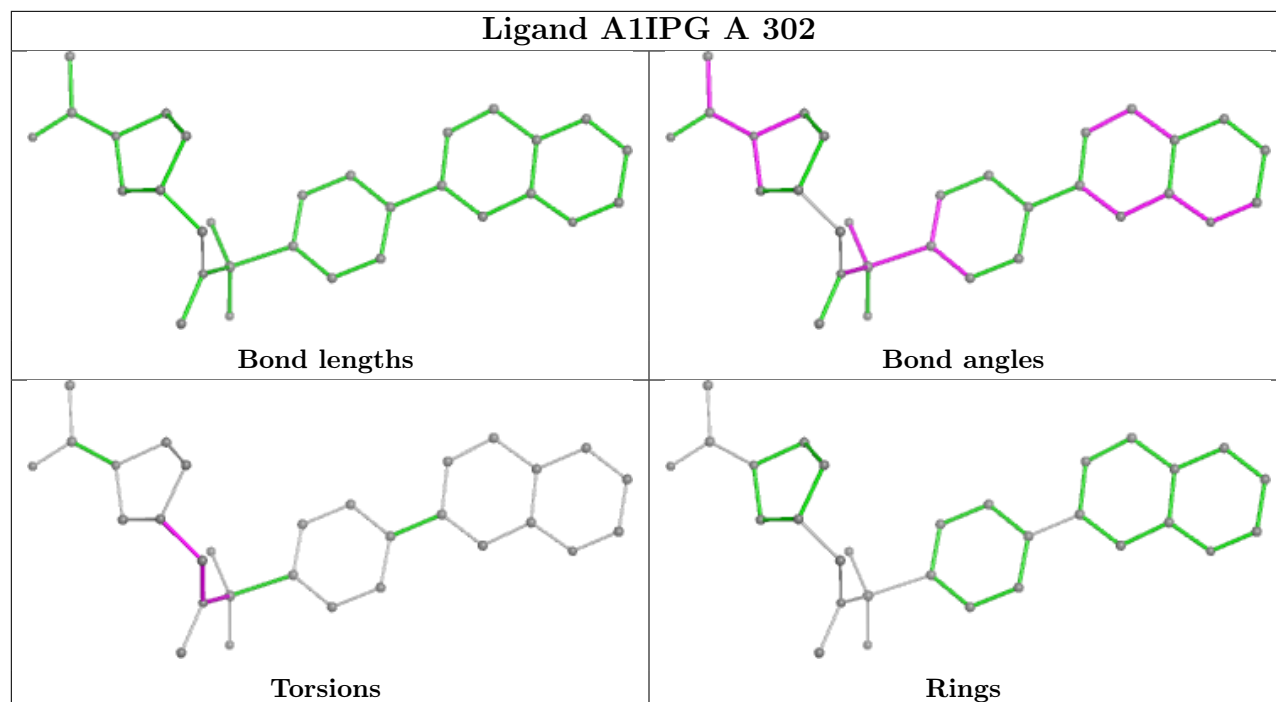
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	A1IPG	1	0
2	A	301	RCM	2	0
2	B	302	RCM	1	0

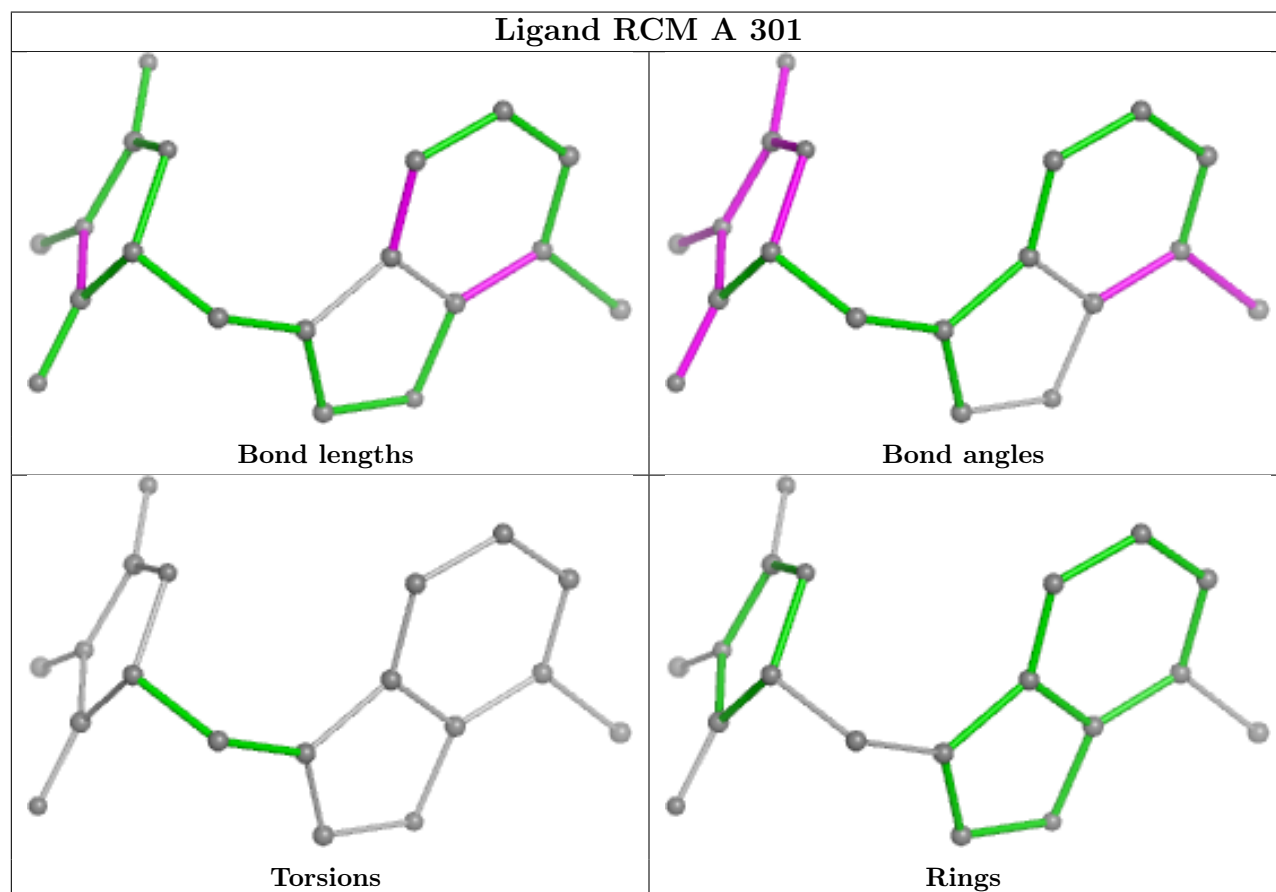
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

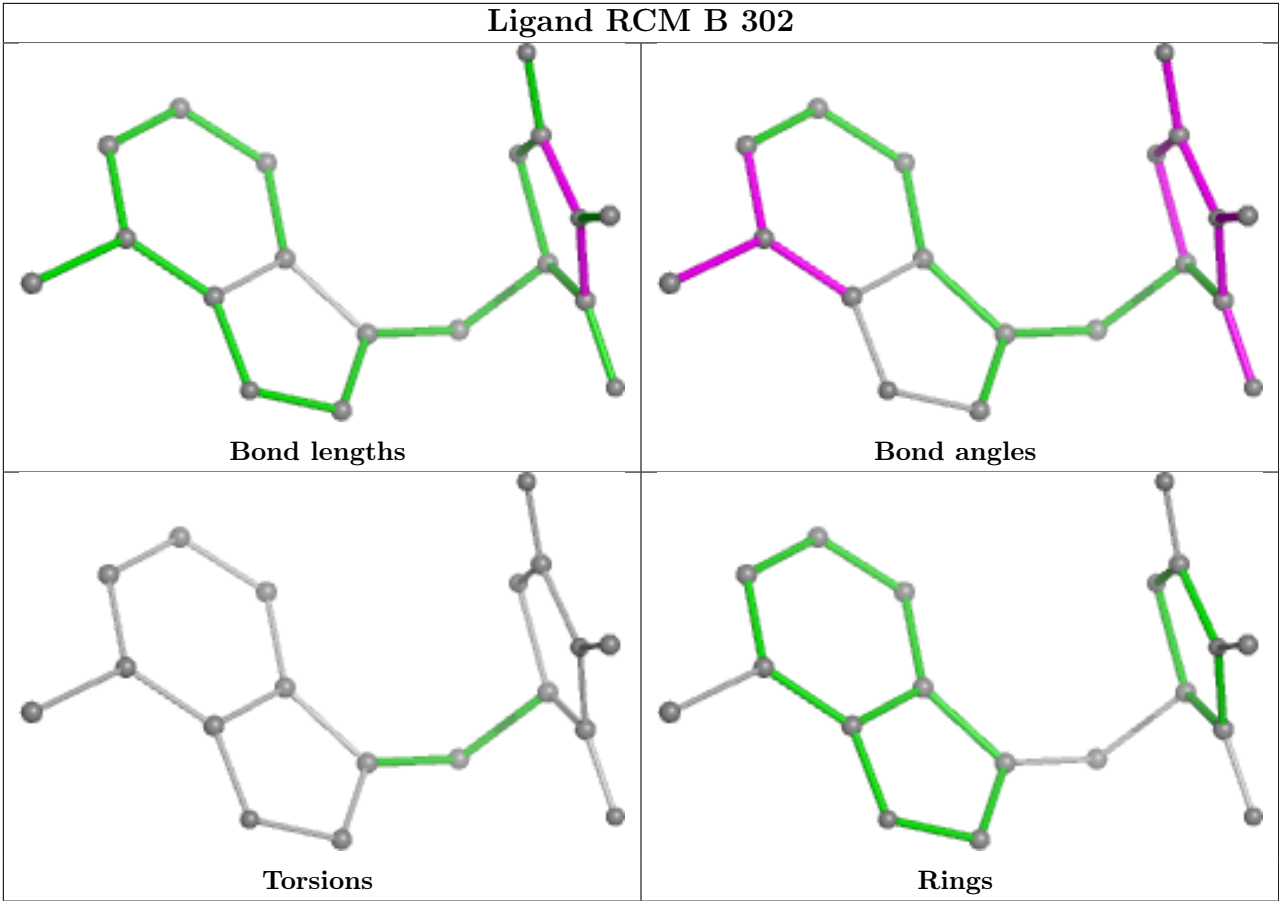


Ligand A1IPG A 302



Ligand RCM A 301





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	19:GLU	C	20:SER	N	3.13

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	259/313 (82%)	0.63	19 (7%) 22 22	40, 68, 121, 159	0
1	B	259/313 (82%)	0.56	15 (5%) 30 29	39, 67, 114, 149	0
All	All	518/626 (82%)	0.59	34 (6%) 26 25	39, 67, 117, 159	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	19	GLU	5.8
1	A	35	PHE	3.8
1	A	20	SER	3.4
1	A	21	ALA	3.3
1	A	290	LEU	3.3
1	A	9	VAL	3.2
1	B	168	LEU	3.2
1	A	56	HIS	2.8
1	B	20	SER	2.8
1	B	108	MET	2.7
1	B	21	ALA	2.7
1	A	168	LEU	2.6
1	B	60	LEU	2.6
1	A	10	ILE	2.6
1	B	70	LEU	2.5
1	A	8	ASN	2.5
1	B	83	ILE	2.4
1	A	44	MET	2.3
1	B	81	VAL	2.3
1	A	189	THR	2.3
1	B	46	THR	2.3
1	B	90	LEU	2.3
1	B	56	HIS	2.3
1	A	23	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	94	TYR	2.2
1	A	46	THR	2.2
1	B	86	GLY	2.2
1	A	82	ILE	2.1
1	A	81	VAL	2.1
1	A	18	LEU	2.1
1	B	189	THR	2.1
1	A	29	GLY	2.0
1	A	108	MET	2.0
1	B	164	MET	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](#)

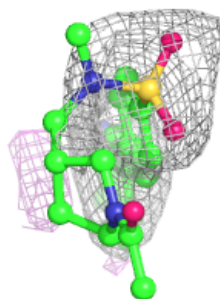
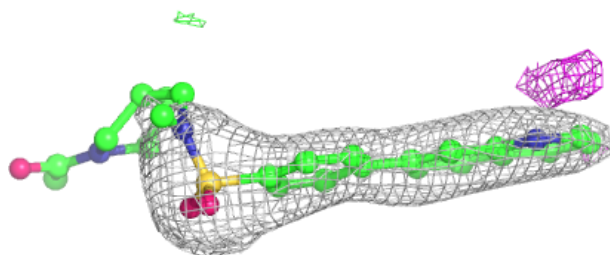
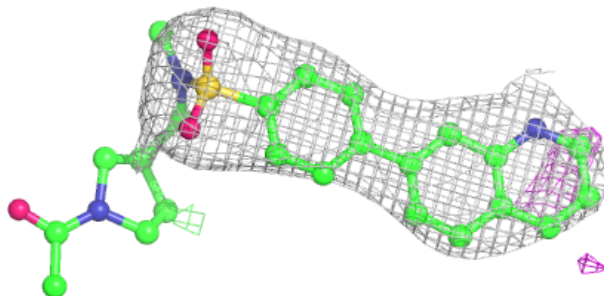
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	A1IPG	A	302	30/30	0.83	0.13	54,82,141,147	0
2	RCM	B	302	19/19	0.89	0.12	55,63,76,82	0
3	A1IPG	B	301	30/30	0.90	0.12	47,59,128,138	0
2	RCM	A	301	19/19	0.94	0.08	49,64,72,81	0

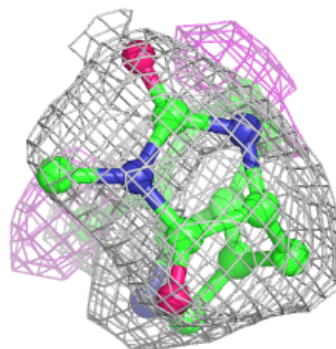
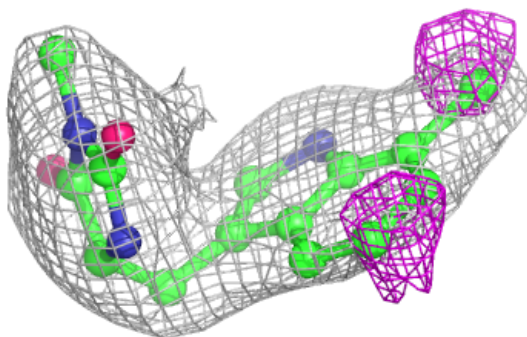
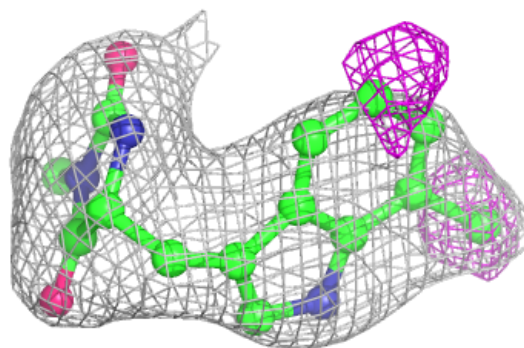
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1IPG A 302:

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

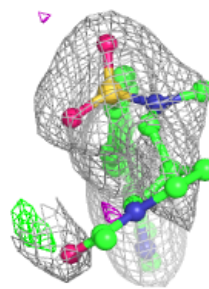
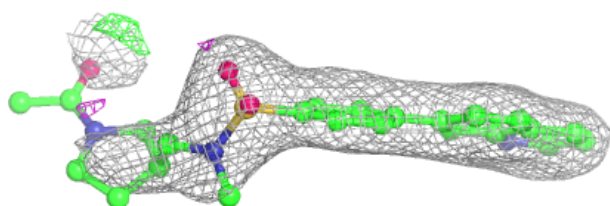
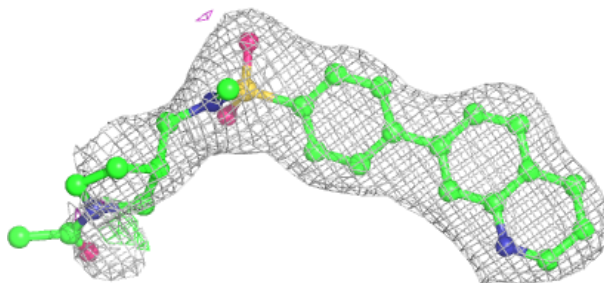
**Electron density around RCM B 302:**

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

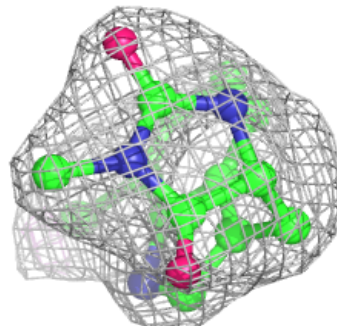
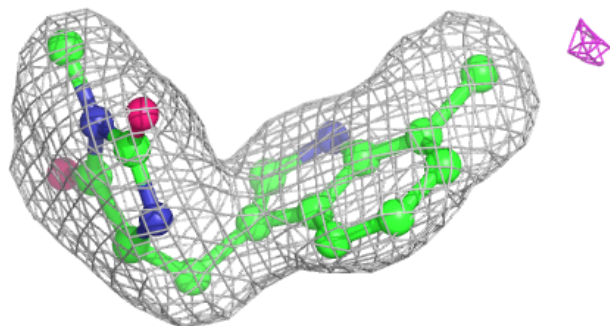
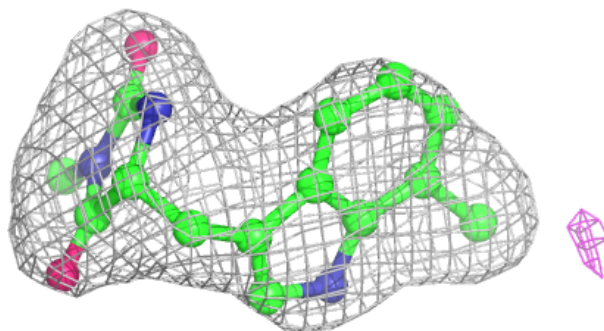


Electron density around A1IPG B 301:

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

**Electron density around RCM A 301:**

$2mF_o-DF_c$ (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.