



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2022 – 02:08 PM JST

PDB ID : 7VTO
Title : The crystal structure of PAK1 with the inhibitor GW8510
Authors : Zhu, S.J.
Deposited on : 2021-10-30
Resolution : 2.59 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
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) : 2.31.2

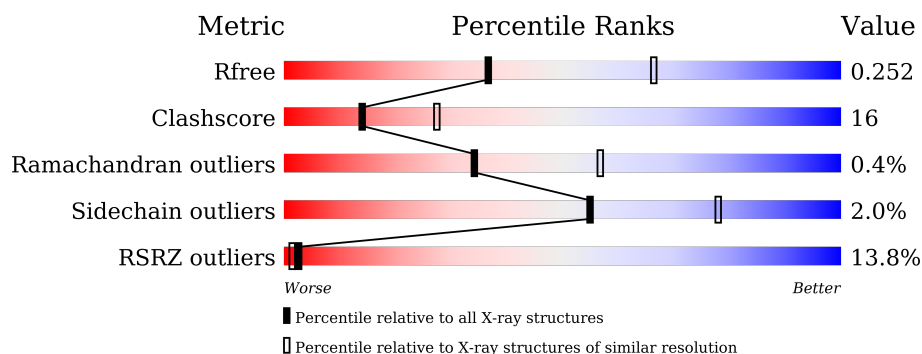
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.59 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (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	A	301	
1	B	301	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4264 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.

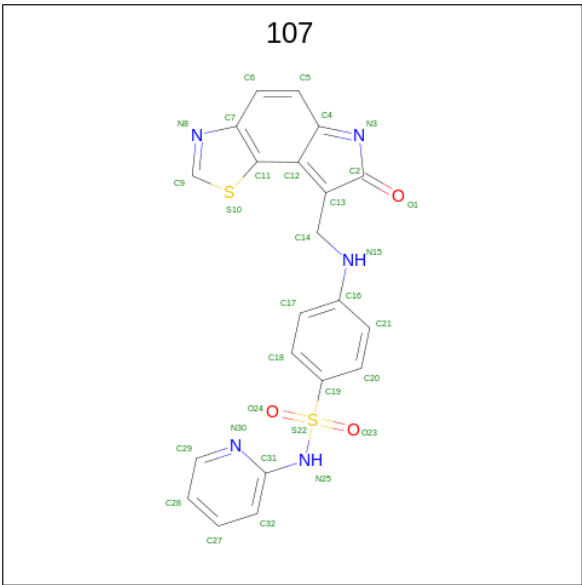
- Molecule 1 is a protein called Serine/threonine-protein kinase PAK 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	P	S	0	1	0
			2041	1294	345	386	1	15			
1	B	278	Total	C	N	O	P	S	0	0	0
			2151	1362	360	413	1	15			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	expression tag	UNP Q13153
A	389	ASN	ASP	conflict	UNP Q13153
A	546	GLY	-	expression tag	UNP Q13153
A	547	ASN	-	expression tag	UNP Q13153
A	548	SER	-	expression tag	UNP Q13153
B	248	GLY	-	expression tag	UNP Q13153
B	389	ASN	ASP	conflict	UNP Q13153
B	546	GLY	-	expression tag	UNP Q13153
B	547	ASN	-	expression tag	UNP Q13153
B	548	SER	-	expression tag	UNP Q13153

- Molecule 2 is 4-[(7-OXO-7H-THIAZOLO[5,4-E]INDOL-8-YLMETHYL)-AMINO]-N-PYRIDIN-2-YL-BENZENESULFONAMIDE (three-letter code: 107) (formula: C₂₁H₁₅N₅O₃S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			31	21	5	3	2		
2	B	1	Total	C	N	O	S	0	0
			31	21	5	3	2		

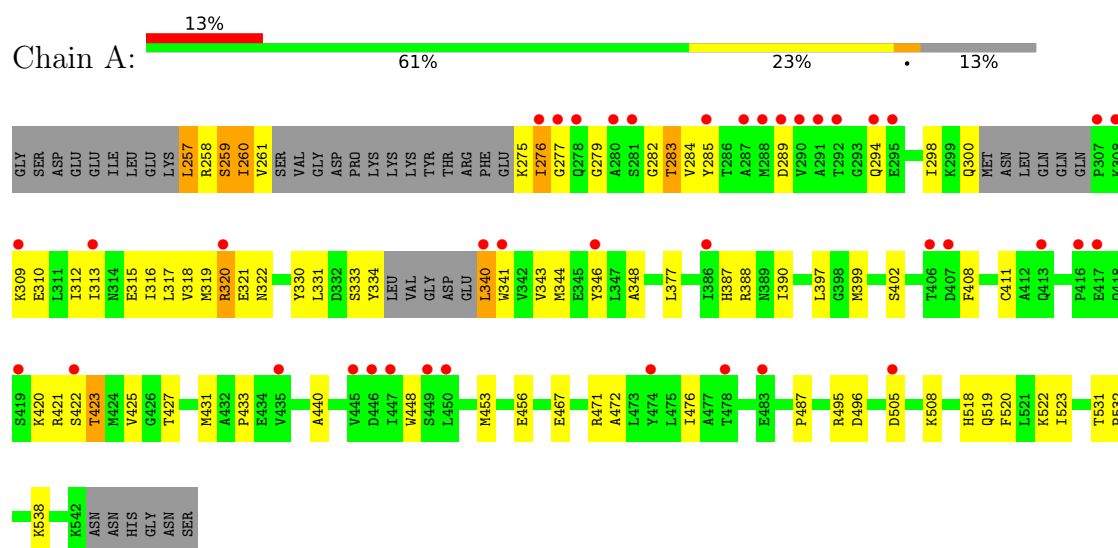
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	O	0	0
			4	4		
3	B	6	Total	O	0	0
			6	6		

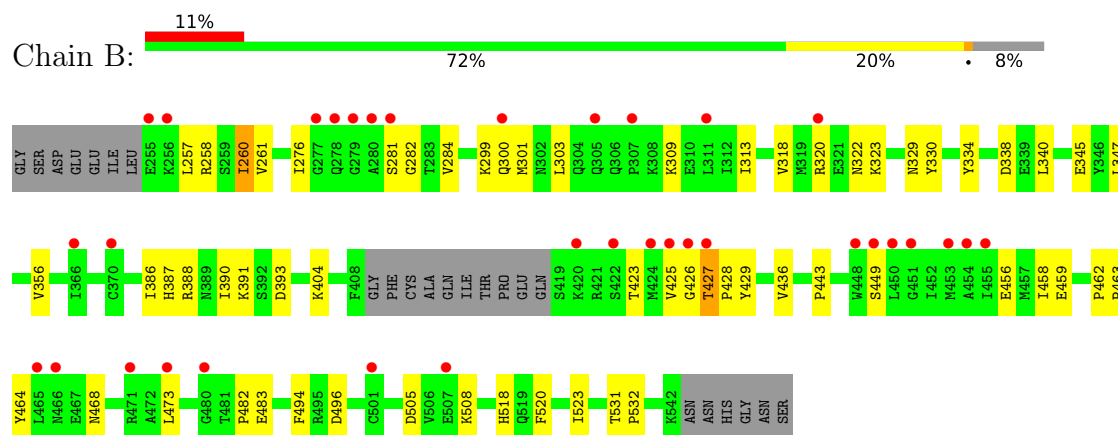
3 Residue-property plots [i](#)

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 PAK 1



• Molecule 1: Serine/threonine-protein kinase PAK 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.53Å 81.81Å 66.27Å 90.00° 106.07° 90.00°	Depositor
Resolution (Å)	24.75 – 2.59 24.75 – 2.59	Depositor EDS
% Data completeness (in resolution range)	99.2 (24.75-2.59) 99.1 (24.75-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.60Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.235 , 0.252 0.235 , 0.252	Depositor DCC
R_{free} test set	938 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	65.9	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4264	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 5.45% 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: TPO, 107

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	0.44	0/2060	0.57	0/2782
1	B	0.49	0/2172	0.60	0/2936
All	All	0.46	0/4232	0.59	0/5718

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	A	2041	0	2076	84	0
1	B	2151	0	2175	52	0
2	A	31	0	15	5	0
2	B	31	0	15	3	0
3	A	4	0	0	0	0
3	B	6	0	0	0	0
All	All	4264	0	4281	134	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 16.

All (134) 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:281:SER:O	1:B:301:MET:HG3	1.25	1.29
1:A:277:GLY:HA3	1:A:283:THR:HG22	1.42	0.99
1:B:260:ILE:HD12	1:B:260:ILE:H	1.25	0.98
1:B:429:TYR:CD1	1:B:462:PRO:CB	2.50	0.94
1:B:347:LEU:O	2:B:601:107:H17	1.70	0.91
1:B:429:TYR:CD1	1:B:462:PRO:HB2	2.07	0.90
1:B:426:GLY:O	1:B:427:THR:OG1	1.90	0.88
1:B:429:TYR:CE1	1:B:462:PRO:HB3	2.11	0.85
1:A:276:ILE:HD12	2:A:601:107:C17	2.08	0.83
1:B:436:VAL:HG13	1:B:473:LEU:HD12	1.65	0.78
1:A:315:GLU:O	1:A:319:MET:HG3	1.85	0.75
1:A:257:LEU:HD13	1:A:258:ARG:H	1.50	0.74
1:B:284:VAL:HG22	1:B:299:LYS:HG3	1.69	0.73
1:B:257:LEU:O	1:B:260:ILE:HD12	1.89	0.72
1:A:317:LEU:O	1:A:321:GLU:HG2	1.93	0.69
1:B:356:VAL:HG11	1:B:456:GLU:HG2	1.74	0.69
1:B:429:TYR:CE1	1:B:462:PRO:CB	2.73	0.68
1:A:420:LYS:O	1:A:421:ARG:HG2	1.93	0.68
1:A:330:TYR:HA	1:A:344:MET:HG2	1.74	0.67
1:A:505:ASP:HB3	1:A:508:LYS:HB2	1.76	0.67
1:A:300:GLN:HG3	1:A:341:TRP:NE1	2.11	0.66
1:A:309:LYS:HA	1:A:312:ILE:HD12	1.78	0.66
1:A:258:ARG:O	1:A:261:VAL:HG23	1.96	0.66
1:A:276:ILE:CD1	2:A:601:107:C17	2.74	0.64
1:A:275:LYS:HB2	1:A:285:TYR:CD2	2.32	0.64
1:B:260:ILE:HD12	1:B:260:ILE:N	2.07	0.64
1:B:318:VAL:O	1:B:322:ASN:ND2	2.26	0.63
1:A:277:GLY:CA	1:A:283:THR:HG22	2.24	0.63
1:A:316:ILE:O	1:A:320:ARG:CG	2.46	0.63
1:A:340:LEU:O	1:A:341:TRP:HD1	1.81	0.63
1:A:312:ILE:HD13	1:A:340:LEU:HD12	1.82	0.62
1:A:276:ILE:HG13	1:A:276:ILE:O	1.99	0.62
1:A:298:ILE:HG12	1:A:343:VAL:HG22	1.81	0.61
1:B:483:GLU:HA	1:B:483:GLU:OE1	1.98	0.61
1:A:316:ILE:O	1:A:320:ARG:HG2	2.01	0.61
1:A:388:ARG:CZ	1:A:425:VAL:HG11	2.31	0.61
1:A:312:ILE:HG21	1:A:340:LEU:HD11	1.82	0.60
1:A:260:ILE:O	1:A:260:ILE:HG23	2.00	0.60
1:A:423:TPO:HG21	1:A:423:TPO:O3P	2.01	0.60
1:B:391:LYS:HG3	1:B:393:ASP:OD1	2.01	0.60
1:B:303:LEU:HD23	1:B:338:ASP:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:ARG:HA	1:B:261:VAL:HG22	1.84	0.59
1:B:426:GLY:C	1:B:427:THR:HG1	1.99	0.58
1:A:420:LYS:HG2	1:A:440:ALA:HB1	1.84	0.58
1:A:257:LEU:CD1	1:A:258:ARG:H	2.16	0.58
1:B:347:LEU:HD11	1:B:404:LYS:HD2	1.86	0.58
1:A:258:ARG:HB3	1:A:258:ARG:NH2	2.19	0.57
1:A:399:MET:HE1	1:A:538:LYS:HE3	1.86	0.57
1:B:260:ILE:H	1:B:260:ILE:CD1	2.04	0.57
1:A:472:ALA:O	1:A:476:ILE:HG13	2.04	0.57
1:B:458:ILE:HG21	1:B:494:PHE:HE2	1.70	0.56
1:B:505:ASP:OD2	1:B:508:LYS:NZ	2.26	0.56
1:A:257:LEU:HD13	1:A:258:ARG:N	2.18	0.55
1:A:496:ASP:OD2	1:A:518:HIS:NE2	2.33	0.55
1:A:423:TPO:HG23	1:B:468:ASN:HD21	1.70	0.55
1:B:429:TYR:CD1	1:B:462:PRO:HB3	2.32	0.55
1:A:257:LEU:N	1:A:259:SER:HG	2.05	0.55
1:B:427:THR:N	1:B:428:PRO:CD	2.71	0.54
1:A:316:ILE:O	1:A:320:ARG:HG3	2.08	0.54
1:B:282:GLY:HA3	1:B:300:GLN:O	2.07	0.54
1:B:260:ILE:HG22	1:B:320:ARG:HH11	1.72	0.54
1:A:312:ILE:HD13	1:A:340:LEU:CD1	2.37	0.54
1:A:340:LEU:C	1:A:341:TRP:HD1	2.12	0.53
1:B:260:ILE:CG2	1:B:320:ARG:HH11	2.20	0.53
1:A:312:ILE:O	1:A:316:ILE:HD12	2.09	0.53
1:A:408:PHE:HB3	1:A:411:CYS:SG	2.49	0.53
1:A:279:GLY:O	1:A:282:GLY:O	2.28	0.52
1:A:289:ASP:N	1:A:294:GLN:O	2.37	0.52
1:A:538:LYS:NZ	2:A:601:107:O24	2.41	0.52
1:B:427:THR:N	1:B:428:PRO:HD3	2.25	0.52
1:A:453:MET:O	1:A:456:GLU:HB2	2.09	0.52
1:A:257:LEU:CD1	1:A:258:ARG:N	2.72	0.52
1:A:318:VAL:O	1:A:322:ASN:ND2	2.37	0.51
1:A:427:THR:O	1:A:431:MET:HG3	2.11	0.51
1:B:329:ASN:ND2	1:B:345:GLU:OE2	2.44	0.51
1:A:423:TPO:HG23	1:B:468:ASN:ND2	2.26	0.51
1:A:257:LEU:HD13	1:A:258:ARG:HG3	1.93	0.50
1:A:258:ARG:NH2	1:A:258:ARG:CB	2.75	0.50
1:A:333:SER:C	1:A:334:TYR:CD1	2.86	0.50
1:A:331:LEU:HB2	1:A:343:VAL:O	2.12	0.49
1:A:277:GLY:N	1:A:284:VAL:O	2.46	0.49
1:A:487:PRO:HB2	1:A:495:ARG:HE	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:520:PHE:O	1:A:523:ILE:HG12	2.13	0.48
1:A:258:ARG:HB3	1:A:258:ARG:CZ	2.43	0.48
1:A:275:LYS:HB2	1:A:285:TYR:CE2	2.48	0.48
1:B:463:PRO:HB2	1:B:482:PRO:HG3	1.96	0.48
1:B:464:TYR:CZ	1:B:482:PRO:HD3	2.49	0.47
1:A:276:ILE:HD12	2:A:601:107:C18	2.44	0.47
1:A:377:LEU:HD21	1:A:390:ILE:HD11	1.97	0.47
1:B:520:PHE:O	1:B:523:ILE:HG12	2.14	0.47
1:A:313:ILE:O	1:A:317:LEU:HD23	2.15	0.47
1:A:408:PHE:HD2	1:A:411:CYS:SG	2.38	0.47
1:B:260:ILE:CG2	1:B:320:ARG:NH1	2.78	0.47
1:A:260:ILE:C	1:A:261:VAL:HG23	2.35	0.47
1:B:429:TYR:HD1	1:B:462:PRO:HB2	1.69	0.46
1:B:260:ILE:HG23	1:B:320:ARG:NH1	2.30	0.46
1:B:387:HIS:O	1:B:388:ARG:HB2	2.15	0.46
1:A:421:ARG:HD2	1:A:423:TPO:O2P	2.16	0.46
1:B:496:ASP:OD2	1:B:518:HIS:NE2	2.48	0.46
1:A:300:GLN:CG	1:A:341:TRP:NE1	2.80	0.45
1:A:408:PHE:HB3	1:A:411:CYS:HG	1.81	0.45
1:A:309:LYS:O	1:A:312:ILE:HB	2.17	0.45
1:A:467:GLU:OE1	1:A:471:ARG:HG2	2.16	0.44
1:B:334:TYR:O	1:B:340:LEU:HD12	2.18	0.44
1:A:276:ILE:HA	2:A:601:107:C28	2.47	0.44
1:A:309:LYS:HD3	1:A:312:ILE:HD12	1.99	0.44
1:A:531:THR:OG1	1:A:532:PRO:HD3	2.17	0.44
1:A:260:ILE:C	1:A:261:VAL:CG2	2.86	0.44
1:B:429:TYR:CD1	1:B:462:PRO:CG	3.00	0.44
1:B:458:ILE:HG13	1:B:459:GLU:HG2	1.98	0.44
1:B:458:ILE:HG13	1:B:459:GLU:CG	2.48	0.44
1:B:463:PRO:O	1:B:464:TYR:HB2	2.18	0.44
1:B:386:ILE:HD12	1:B:443:PRO:HA	1.98	0.43
1:B:309:LYS:O	1:B:313:ILE:HG12	2.18	0.43
1:A:397:LEU:HA	1:A:402:SER:O	2.18	0.43
1:B:323:LYS:NZ	1:B:330:TYR:O	2.51	0.43
1:A:346:TYR:CE2	1:A:348:ALA:HB2	2.54	0.43
1:A:258:ARG:CB	1:A:258:ARG:HH21	2.33	0.42
1:B:390:ILE:HB	1:B:449:SER:HB2	2.01	0.42
1:A:387:HIS:O	1:A:388:ARG:HB2	2.19	0.42
1:A:257:LEU:N	1:A:257:LEU:HD12	2.35	0.42
1:A:289:ASP:HB3	1:A:294:GLN:N	2.35	0.42
1:B:531:THR:OG1	1:B:532:PRO:HD3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:LYS:HE2	1:A:285:TYR:CE2	2.56	0.41
1:A:260:ILE:CD1	1:A:320:ARG:HD3	2.50	0.41
1:A:260:ILE:HD11	1:A:320:ARG:HD3	2.03	0.41
1:A:312:ILE:CG2	1:A:340:LEU:HD11	2.50	0.41
1:B:347:LEU:O	2:B:601:107:C17	2.56	0.41
1:A:519:GLN:O	1:A:522:LYS:HB2	2.20	0.41
1:A:433:PRO:HD3	1:A:448:TRP:CE2	2.56	0.41
1:A:318:VAL:HG11	1:A:411:CYS:SG	2.61	0.40
1:A:340:LEU:C	1:A:341:TRP:CD1	2.94	0.40
1:A:310:GLU:H	1:A:310:GLU:CD	2.23	0.40
1:B:276:ILE:HD12	2:B:601:107:H141	2.03	0.40

There are no symmetry-related clashes.

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	254/301 (84%)	247 (97%)	6 (2%)	1 (0%)	34	57
1	B	273/301 (91%)	269 (98%)	3 (1%)	1 (0%)	34	57
All	All	527/602 (88%)	516 (98%)	9 (2%)	2 (0%)	34	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	427	THR
1	A	259	SER

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	222/259 (86%)	215 (97%)	7 (3%)	39	65
1	B	234/259 (90%)	232 (99%)	2 (1%)	78	91
All	All	456/518 (88%)	447 (98%)	9 (2%)	55	78

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

Mol	Chain	Res	Type
1	A	257	LEU
1	A	260	ILE
1	A	276	ILE
1	A	283	THR
1	A	320	ARG
1	A	340	LEU
1	A	422	SER
1	B	260	ILE
1	B	425	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	306	GLN
1	B	468	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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$
1	TPO	B	423	1	8,10,11	0.82	0	10,14,16	1.40	2 (20%)
1	TPO	A	423	1	8,10,11	1.00	0	10,14,16	1.28	1 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	B	423	1	-	1/9/11/13	-
1	TPO	A	423	1	-	4/9/11/13	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	423	TPO	CG2-CB-CA	-2.63	107.97	113.16
1	B	423	TPO	O-C-CA	-2.42	118.42	124.78
1	A	423	TPO	CG2-CB-CA	-2.26	108.70	113.16

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	423	TPO	N-CA-CB-CG2
1	A	423	TPO	N-CA-CB-OG1
1	A	423	TPO	C-CA-CB-CG2
1	B	423	TPO	O-C-CA-CB
1	A	423	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	423	TPO	4	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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$
2	107	A	601	-	28,35,35	2.11	8 (28%)	37,51,51	3.34	13 (35%)
2	107	B	601	-	28,35,35	2.07	6 (21%)	37,51,51	3.08	11 (29%)

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	107	A	601	-	-	2/15/28/28	0/5/5/5
2	107	B	601	-	-	3/15/28/28	0/5/5/5

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	107	C2-N3	-5.62	1.27	1.37
2	A	601	107	S22-N25	4.95	1.71	1.63
2	A	601	107	C2-N3	-4.94	1.29	1.37
2	B	601	107	C2-C13	-4.34	1.37	1.49
2	A	601	107	C2-C13	-4.19	1.37	1.49
2	B	601	107	S22-N25	4.13	1.70	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	107	O1-C2	-3.84	1.17	1.23
2	A	601	107	C19-S22	3.84	1.82	1.76
2	B	601	107	C19-S22	3.45	1.81	1.76
2	A	601	107	O1-C2	-3.25	1.18	1.23
2	A	601	107	O24-S22	2.66	1.46	1.43
2	A	601	107	C16-N15	2.39	1.45	1.38
2	A	601	107	O23-S22	2.36	1.46	1.43
2	B	601	107	C16-N15	2.29	1.45	1.38

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	107	O24-S22-O23	-14.71	101.47	119.55
2	B	601	107	O24-S22-O23	-12.63	104.02	119.55
2	B	601	107	C9-S10-C11	7.22	98.72	90.88
2	A	601	107	C9-S10-C11	6.87	98.34	90.88
2	A	601	107	C2-N3-C4	6.30	117.60	106.86
2	B	601	107	C2-N3-C4	6.21	117.45	106.86
2	A	601	107	N25-C31-N30	4.92	119.67	114.12
2	B	601	107	C31-N25-S22	-4.31	115.74	124.97
2	B	601	107	C19-S22-N25	4.19	112.11	106.83
2	B	601	107	N25-C31-N30	3.49	118.06	114.12
2	A	601	107	O24-S22-C19	3.09	111.77	107.97
2	A	601	107	C6-C7-N8	-3.04	122.38	130.80
2	A	601	107	C31-N25-S22	-3.01	118.53	124.97
2	B	601	107	C6-C7-N8	-3.00	122.49	130.80
2	A	601	107	C14-N15-C16	-2.79	116.98	122.49
2	B	601	107	O23-S22-C19	2.59	111.16	107.97
2	A	601	107	C29-N30-C31	2.45	120.70	117.22
2	A	601	107	O24-S22-N25	2.27	112.41	106.73
2	A	601	107	C28-C29-N30	-2.26	119.74	123.43
2	B	601	107	C29-N30-C31	2.24	120.39	117.22
2	B	601	107	C7-C11-C12	-2.19	120.28	123.47
2	A	601	107	C7-C11-C12	-2.11	120.40	123.47
2	B	601	107	C28-C29-N30	-2.11	119.98	123.43
2	A	601	107	O23-S22-N25	2.06	111.88	106.73

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	107	C12-C13-C14-N15

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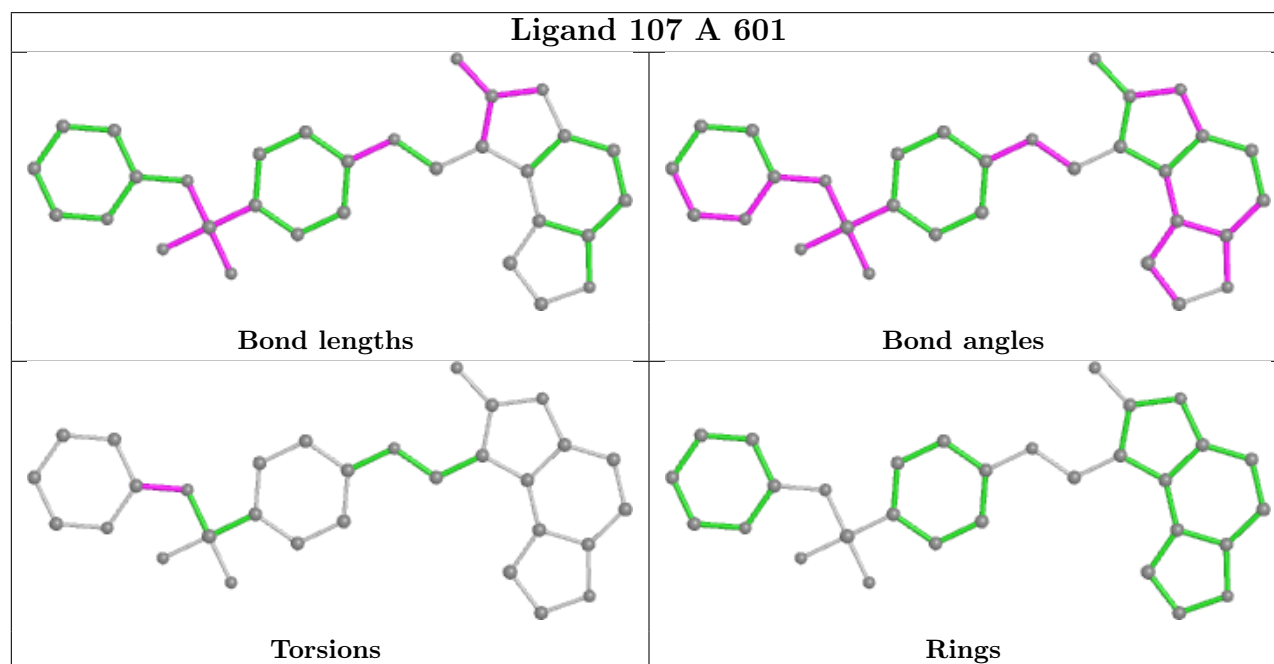
Mol	Chain	Res	Type	Atoms
2	A	601	107	C32-C31-N25-S22
2	A	601	107	N30-C31-N25-S22
2	B	601	107	C20-C19-S22-O23
2	B	601	107	C18-C19-S22-O23

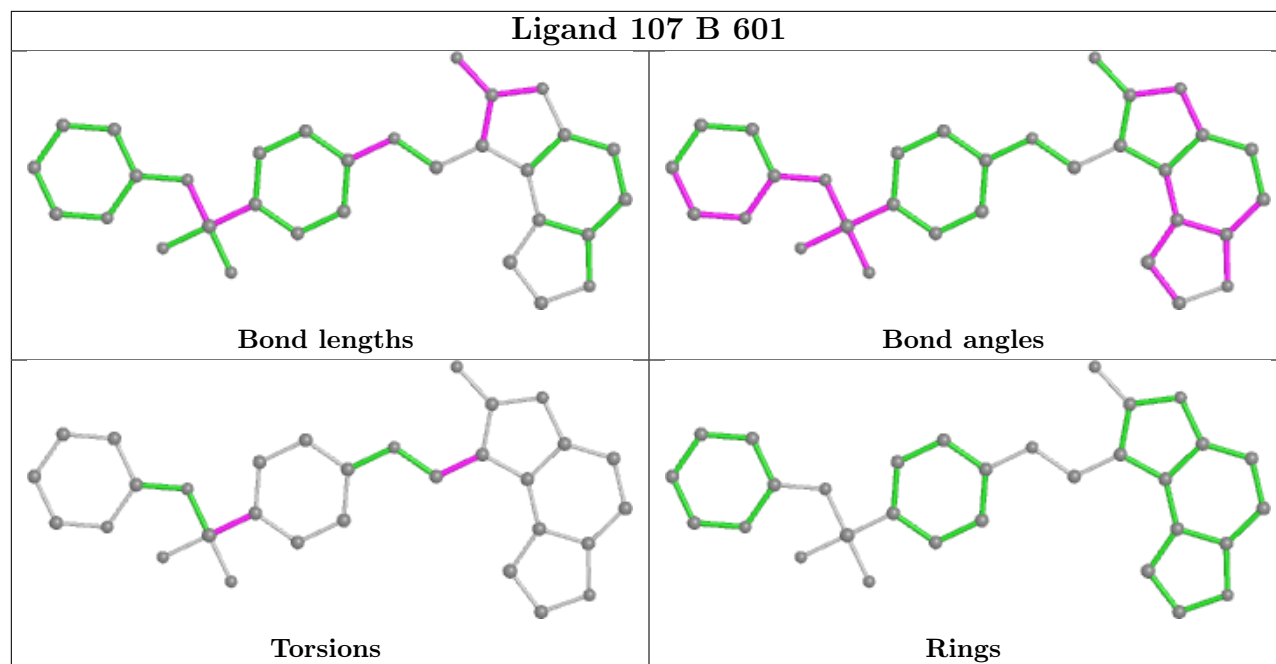
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	107	5	0
2	B	601	107	3	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	261/301 (86%)	0.87	40 (15%) 2 1	44, 71, 115, 130	0
1	B	277/301 (92%)	0.64	34 (12%) 4 2	46, 66, 110, 124	0
All	All	538/602 (89%)	0.75	74 (13%) 2 1	44, 69, 112, 130	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	425	VAL	9.1
1	A	291	ALA	8.6
1	A	292	THR	7.8
1	A	307	PRO	6.0
1	A	308	LYS	5.2
1	A	309	LYS	5.1
1	B	280	ALA	5.0
1	B	255	GLU	4.9
1	A	288	MET	4.7
1	B	278	GLN	4.5
1	B	451	GLY	4.5
1	A	340	LEU	4.2
1	B	307	PRO	4.2
1	A	341	TRP	4.0
1	B	450	LEU	3.9
1	B	480	GLY	3.9
1	B	311	LEU	3.5
1	B	465	LEU	3.5
1	B	507	GLU	3.5
1	B	424	MET	3.5
1	A	294	GLN	3.2
1	A	277	GLY	3.2
1	A	416	PRO	3.0
1	A	419	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	447	ILE	3.0
1	B	281	SER	3.0
1	A	483	GLU	3.0
1	A	474	TYR	2.9
1	A	445	VAL	2.9
1	A	417	GLU	2.9
1	A	285	TYR	2.9
1	B	454	ALA	2.9
1	A	313	ILE	2.8
1	B	453	MET	2.8
1	A	422	SER	2.8
1	A	346	TYR	2.8
1	B	370	CYS	2.8
1	B	471	ARG	2.8
1	B	427	THR	2.7
1	A	290	VAL	2.7
1	A	413	GLN	2.6
1	A	446	ASP	2.6
1	A	450	LEU	2.6
1	B	426	GLY	2.6
1	B	466	ASN	2.6
1	B	501	CYS	2.5
1	B	305	GLN	2.5
1	A	295	GLU	2.5
1	A	320	ARG	2.5
1	A	289	ASP	2.5
1	A	449	SER	2.5
1	B	279	GLY	2.5
1	B	448	TRP	2.5
1	A	281	SER	2.5
1	B	277	GLY	2.4
1	A	407	ASP	2.4
1	B	473	LEU	2.4
1	B	422	SER	2.3
1	B	449	SER	2.3
1	B	420	LYS	2.3
1	A	280	ALA	2.3
1	B	455	ILE	2.2
1	B	256	LYS	2.2
1	A	276	ILE	2.2
1	B	320	ARG	2.2
1	A	278	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	505	ASP	2.1
1	A	406	THR	2.1
1	A	478	THR	2.1
1	A	287	ALA	2.1
1	B	300	GLN	2.1
1	A	386	ILE	2.1
1	B	366	ILE	2.0
1	A	435	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	B	423	11/12	0.75	0.19	94,96,103,107	0
1	TPO	A	423	11/12	0.93	0.12	67,81,88,93	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

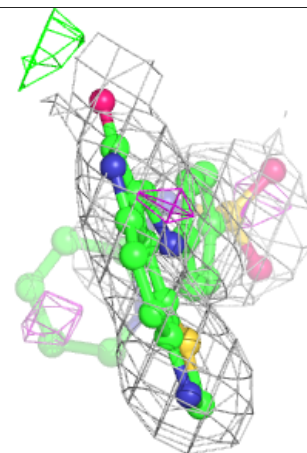
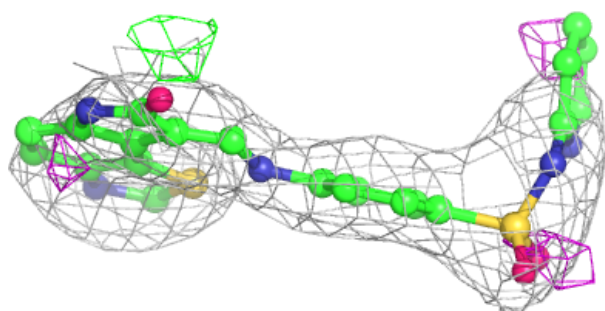
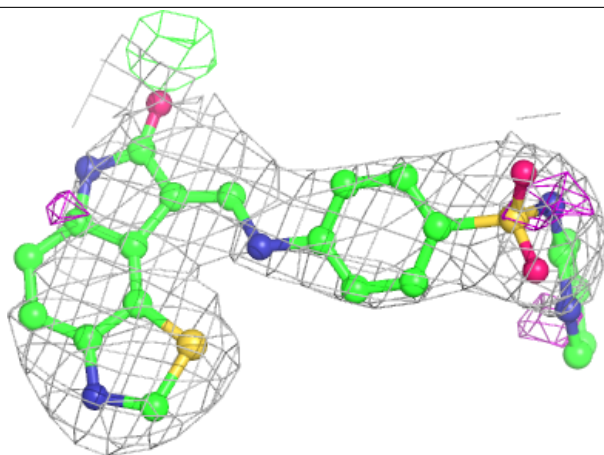
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	107	A	601	31/31	0.75	0.29	81,91,108,116	0
2	107	B	601	31/31	0.94	0.26	68,77,89,90	0

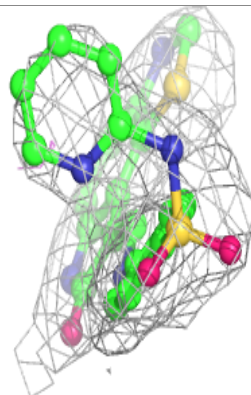
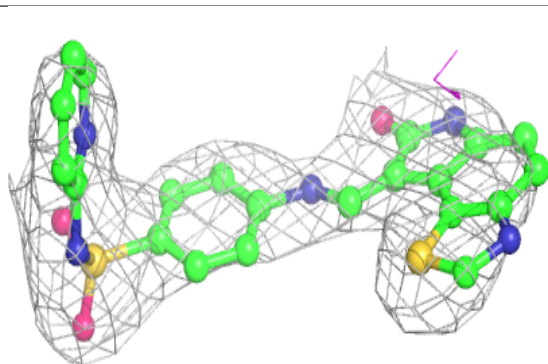
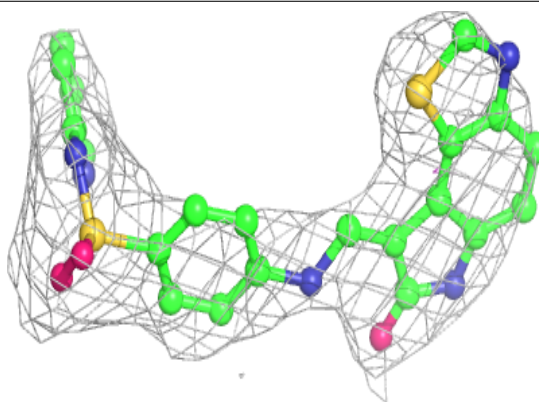
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 107 A 601:

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

**Electron density around 107 B 601:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.