Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 11:40 am BST

PDB ID	:	5DEW
Title	:	Crystal structure of PAK1 in complex with an inhibitor compound 5
Authors	:	Oh, A.; Tam, C.; Wang, W.
Deposited on	:	2015-08-26
Resolution	:	1.90 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

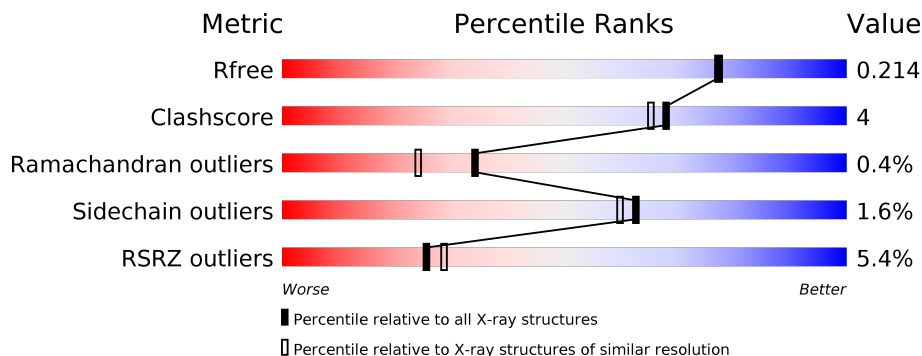|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	Percentile Ranks	Value
Rfree		0.214
Clashscore		4
Ramachandran outliers		0.4%
Sidechain outliers		1.6%
RSRZ outliers		5.4%

Worse ← → *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	297	2% / 92% / 7% ·
1	B	297	8% / 81% / 12% · 5%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5019 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	295	Total	C	N	O	S	0	0	0
			2312	1464	388	444	16			
1	B	281	Total	C	N	O	S	0	0	0
			2182	1388	365	414	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	389	ASN	ASP	engineered mutation	UNP Q13153
A	423	GLU	THR	engineered mutation	UNP Q13153
B	389	ASN	ASP	engineered mutation	UNP Q13153
B	423	GLU	THR	engineered mutation	UNP Q13153

- Molecule 2 is 8-[(trans-4-aminocyclohexyl)methyl]-6-[2-chloro-4-(6-methylpyrazin-2-yl)p henyl]-2-(ethylamino)pyrido[2,3-d]pyrimidin-7(8H)-one (three-letter code: 59N) (formula: $C_{27}H_{30}ClN_7O$).

59N
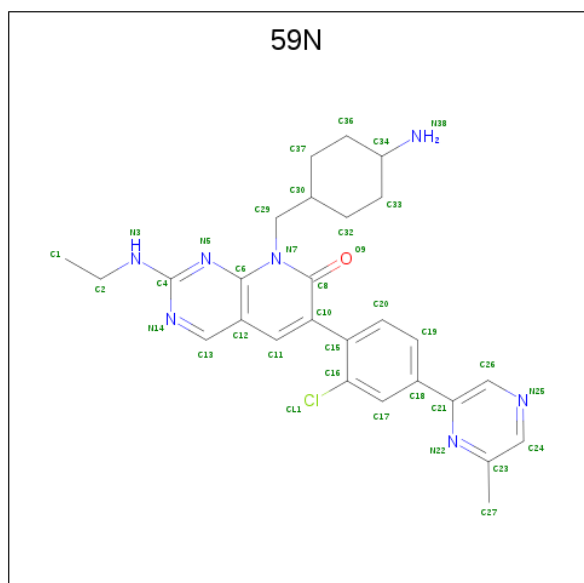
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 36	C 27	Cl 1	N 7	O 1	0	0
2	B	1	Total 36	C 27	Cl 1	N 7	O 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	245	Total 245	O 245	0	0
3	B	208	Total 208	O 208	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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.
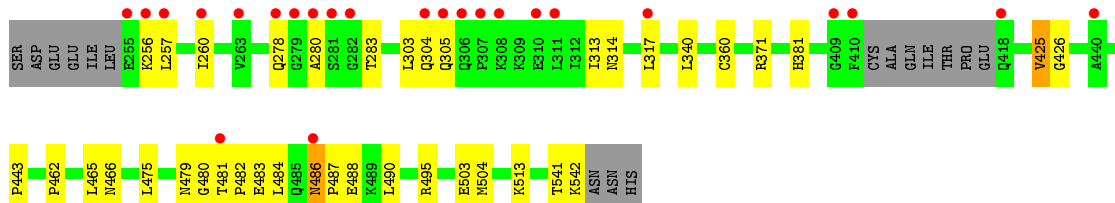
- Molecule 1: Serine/threonine-protein kinase PAK 1

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

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	62.56Å　　81.05Å　　66.50Å 90.00°　　106.39°　　90.00°	Depositor
Resolution (Å)	48.23　–　1.90 48.23　–　1.89	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.23-1.90) 99.2 (48.23-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.43 (at 1.88Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.175　,　0.215 0.176　,　0.214	Depositor DCC
R_{free} test set	2592 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	24.7	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.7	EDS
L-test for twinning[2]	$<|L|> = 0.49$, $<L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5019	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.66% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ 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: 59N

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	0.38	0/2350	0.56	0/3178
1	B	0.36	0/2218	0.54	2/2999 (0.1%)
All	All	0.37	0/4568	0.55	2/6177 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	486	ASN	C-N-CD	-7.40	104.31	120.60
1	B	486	ASN	C-N-CA	5.32	144.35	122.00

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	2312	0	2345	14	0
1	B	2182	0	2209	21	0
2	A	36	0	0	0	0
2	B	36	0	0	0	0
3	A	245	0	0	4	0
3	B	208	0	0	3	0
All	All	5019	0	4554	35	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 (35) 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:A:415:THR:HG23	1:A:418:GLN:H	1.50	0.74
1:B:513:LYS:NZ	3:B:704:HOH:O	2.28	0.66
1:A:407:ASP:OD1	3:A:701:HOH:O	2.15	0.65
1:A:275:LYS:HE3	1:A:278:GLN:HB2	1.79	0.63
1:B:371:ARG:NH1	3:B:706:HOH:O	2.35	0.59
1:B:503:GLU:OE1	3:B:701:HOH:O	2.17	0.59
1:B:484:LEU:HB3	1:B:487:PRO:HB3	1.84	0.59
1:B:260:ILE:HD11	1:B:313:ILE:HG23	1.89	0.54
1:B:257:LEU:HD11	1:B:340:LEU:HD13	1.89	0.54
1:B:256:LYS:HG3	1:B:313:ILE:HG21	1.89	0.54
1:A:418:GLN:O	3:A:702:HOH:O	2.19	0.54
1:A:336:VAL:O	1:A:339:GLU:HG2	2.09	0.53
1:A:315:GLU:O	1:A:319:MET:HG2	2.12	0.50
1:B:488:GLU:CD	1:B:488:GLU:H	2.16	0.49
1:A:519:GLN:HA	1:A:522:LYS:HE2	1.96	0.47
1:B:425:VAL:HG23	1:B:426:GLY:H	1.80	0.47
1:B:541:THR:O	1:B:542:LYS:HD2	2.16	0.45
1:A:328:VAL:HG21	1:A:396:LEU:HD12	1.98	0.45
1:B:483:GLU:H	1:B:483:GLU:CD	2.20	0.44
1:B:480:GLY:HA2	1:B:481:THR:C	2.38	0.44
1:B:314:ASN:HA	1:B:317:LEU:HD12	2.00	0.43
1:B:304:GLN:HA	1:B:305:GLN:HA	1.63	0.43
1:A:320:ARG:HD3	1:A:330:TYR:CZ	2.54	0.43
1:B:475:LEU:O	1:B:479:ASN:HB2	2.19	0.43
1:B:490:LEU:HB2	1:B:495:ARG:HG3	2.01	0.42
1:A:496:ASP:O	1:A:500:ARG:HG3	2.19	0.42
1:B:462:PRO:HG2	1:B:465:LEU:HD13	2.02	0.42
1:A:303:LEU:HD23	1:A:303:LEU:HA	1.83	0.41
1:B:481:THR:HA	1:B:482:PRO:HD3	1.70	0.41
1:B:303:LEU:O	1:B:305:GLN:HA	2.20	0.41
1:B:278:GLN:HB3	1:B:283:THR:HA	2.01	0.41
1:A:354:ASP:OD1	3:A:703:HOH:O	2.22	0.41
1:B:381:HIS:CG	1:B:443:PRO:HB3	2.56	0.40
1:A:418:GLN:HG3	3:A:702:HOH:O	2.21	0.40
1:A:336:VAL:HG13	1:A:339:GLU:HG3	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	A	293/297 (99%)	291 (99%)	2 (1%)	0	100	100
1	B	277/297 (93%)	264 (95%)	11 (4%)	2 (1%)	22	12
All	All	570/594 (96%)	555 (97%)	13 (2%)	2 (0%)	34	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	486	ASN
1	B	280	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	256/258 (99%)	252 (98%)	4 (2%)	62	60
1	B	238/258 (92%)	234 (98%)	4 (2%)	60	57
All	All	494/516 (96%)	486 (98%)	8 (2%)	62	60

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	295	GLU
1	A	332	ASP
1	A	415	THR
1	A	488	GLU

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Mol	Chain	Res	Type
1	B	360	CYS
1	B	425	VAL
1	B	466	ASN
1	B	504	MET

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

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	59N	A	601	-	39,40,40	0.78	2 (5%)	47,57,57	2.39	16 (34%)
2	59N	B	601	-	39,40,40	0.78	2 (5%)	47,57,57	2.15	16 (34%)

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	59N	A	601	-	-	3/15/25/25	0/5/5/5
2	59N	B	601	-	-	1/15/25/25	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	59N	C4-N3	2.71	1.38	1.34
2	B	601	59N	C8-N7	-2.42	1.34	1.38
2	B	601	59N	C4-N3	2.24	1.37	1.34
2	A	601	59N	C8-N7	-2.14	1.35	1.38

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	59N	C10-C8-N7	7.46	121.25	116.15
2	A	601	59N	C10-C8-N7	7.06	120.97	116.15
2	A	601	59N	C2-N3-C4	-5.14	117.51	123.85
2	A	601	59N	C4-N5-C6	4.94	120.89	115.28
2	B	601	59N	C4-N5-C6	4.60	120.50	115.28
2	A	601	59N	C29-N7-C6	4.36	122.31	118.41
2	A	601	59N	C12-C6-N5	-4.03	118.13	123.37
2	A	601	59N	N14-C4-N5	-3.87	122.78	126.52
2	B	601	59N	C37-C36-C34	-3.85	107.12	111.53
2	B	601	59N	N14-C4-N5	-3.85	122.80	126.52
2	A	601	59N	C11-C10-C8	3.76	119.95	117.58
2	B	601	59N	C12-C6-N5	-3.58	118.72	123.37
2	B	601	59N	C17-C16-C15	-3.17	119.65	121.91
2	A	601	59N	C13-N14-C4	3.17	120.58	115.88
2	A	601	59N	C32-C33-C34	-3.14	107.93	111.53
2	B	601	59N	C13-N14-C4	2.97	120.29	115.88
2	A	601	59N	C37-C36-C34	-2.87	108.24	111.53
2	B	601	59N	C11-C10-C8	2.86	119.38	117.58
2	A	601	59N	C12-C13-N14	-2.69	119.02	124.08
2	B	601	59N	C18-C21-N22	2.56	119.66	116.02
2	A	601	59N	C18-C21-N22	2.53	119.62	116.02
2	B	601	59N	C12-C13-N14	-2.49	119.39	124.08
2	B	601	59N	C2-N3-C4	-2.46	120.82	123.85
2	A	601	59N	C10-C11-C12	-2.42	118.05	121.83
2	A	601	59N	C20-C15-C16	2.42	120.31	117.63
2	A	601	59N	C26-N25-C24	2.35	120.68	117.48
2	B	601	59N	C26-N25-C24	2.33	120.65	117.48

Full wwPDB X-ray Structure Validation Report

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	59N	C27-C23-N22	2.24	120.13	116.56
2	B	601	59N	C23-C24-N25	-2.22	119.51	122.42
2	B	601	59N	C36-C34-C33	-2.16	108.05	110.28
2	B	601	59N	C10-C11-C12	-2.14	118.49	121.83
2	A	601	59N	C23-C24-N25	-2.03	119.76	122.42

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	59N	N7-C29-C30-C32
2	A	601	59N	C19-C18-C21-C26
2	A	601	59N	C17-C18-C21-C26
2	A	601	59N	C17-C18-C21-N22

There are no ring outliers.

No monomer is involved in short contacts.

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 then 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 59N A 601

Bond lengths

Bond angles

Torsions

Rings

Ligand 59N B 601

Bond lengths

Bond angles

Torsions

Rings
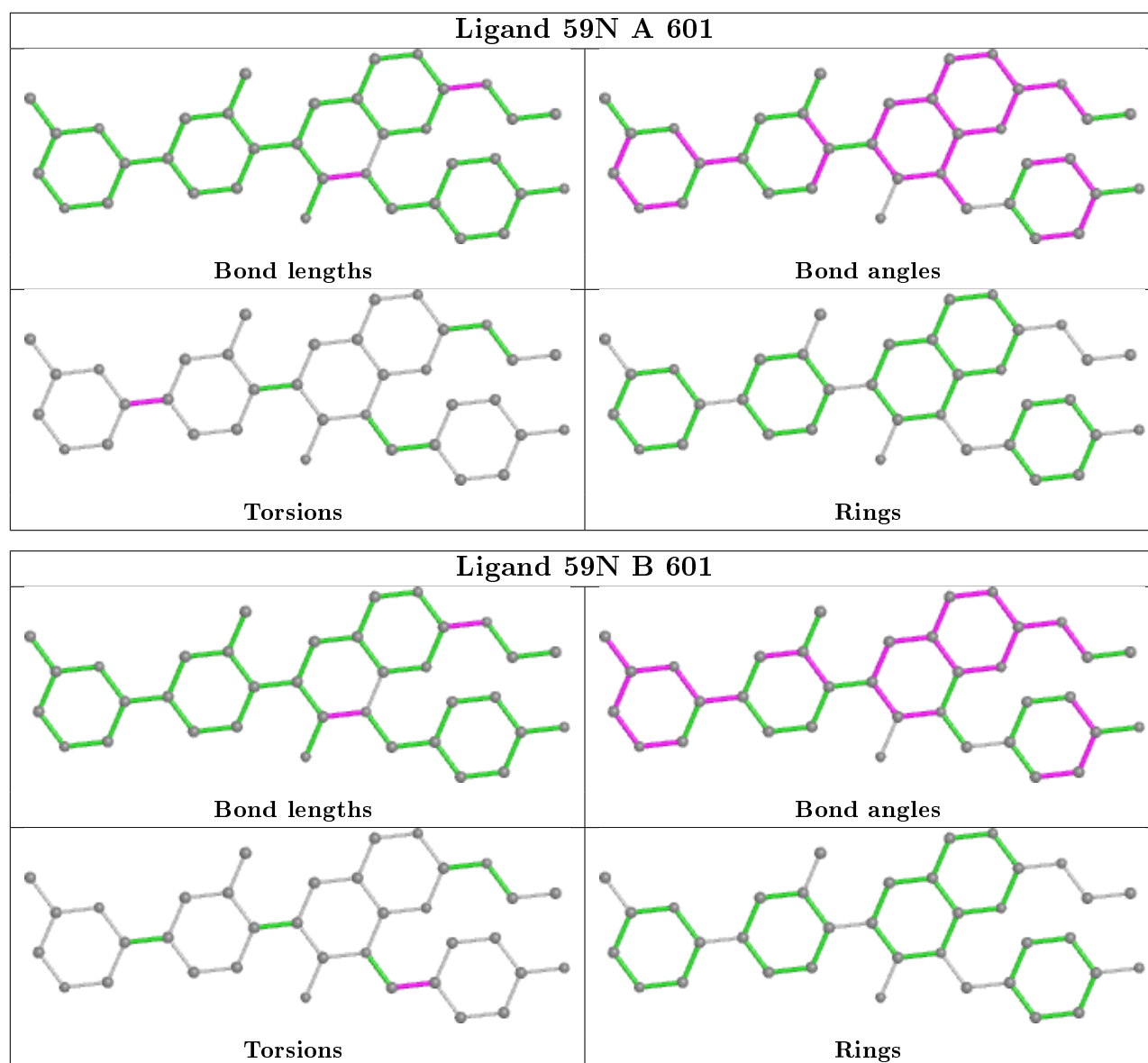
5.7 Other polymers (i)

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	A	295/297 (99%)	-0.26	7 (2%)	59	62	16, 30, 60, 115	0
1	B	281/297 (94%)	-0.01	24 (8%)	10	12	15, 31, 88, 138	0
All	All	576/594 (96%)	-0.14	31 (5%)	25	29	15, 30, 79, 138	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	279	GLY	7.1
1	B	307	PRO	6.9
1	B	308	LYS	4.7
1	B	410	PHE	4.0
1	B	409	GLY	3.9
1	B	311	LEU	3.8
1	B	304	GLN	3.6
1	B	281	SER	3.5
1	A	280	ALA	3.4
1	B	257	LEU	3.4
1	B	486	ASN	3.3
1	B	418	GLN	3.3
1	A	416	PRO	3.2
1	B	305	GLN	3.1
1	B	255	GLU	3.0
1	B	306	GLN	2.9
1	A	417	GLU	2.7
1	B	280	ALA	2.6
1	B	256	LYS	2.6
1	A	544	ASN	2.6
1	B	440	ALA	2.6
1	B	317	LEU	2.5
1	B	263	VAL	2.4
1	B	278	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	282	GLY	2.4
1	A	543	ASN	2.3
1	B	310	GLU	2.3
1	B	260	ILE	2.3
1	A	304	GLN	2.3
1	A	415	THR	2.2
1	B	481	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

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

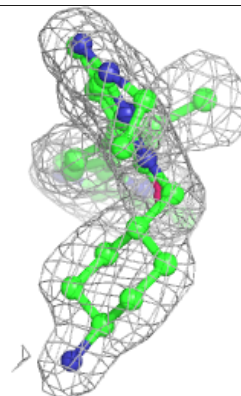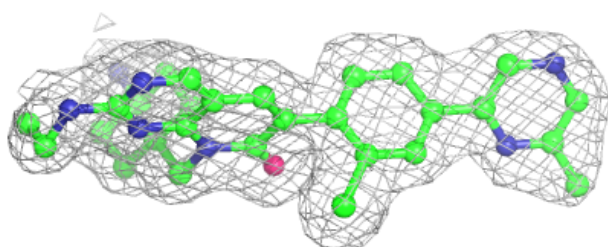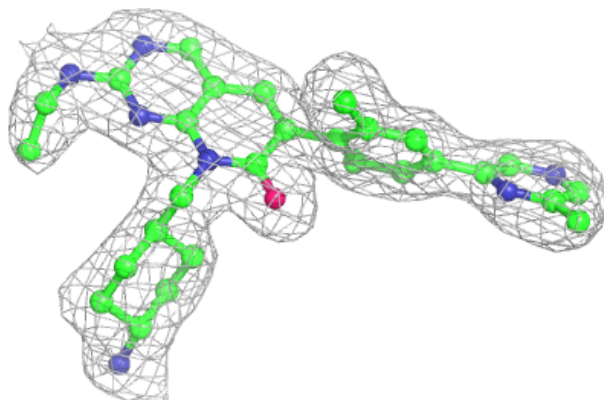| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	59N	B	601	36/36	0.94	0.11	21,30,45,51	0
2	59N	A	601	36/36	0.96	0.08	18,27,39,41	0

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 59N 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)
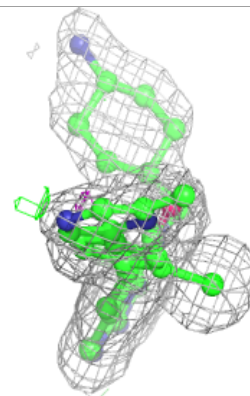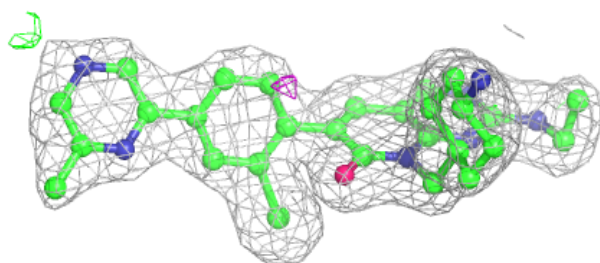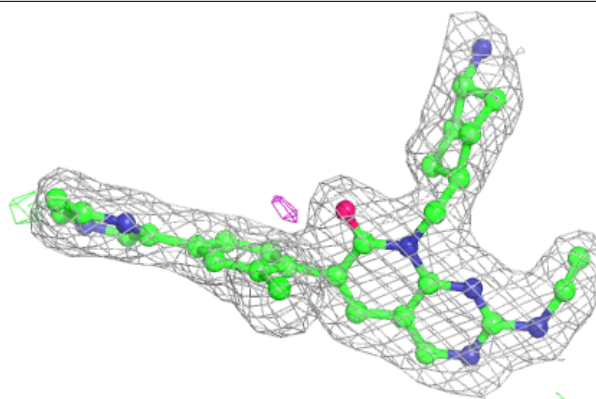
Electron density around 59N A 601:

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

6.5 Other polymers (i)

There are no such residues in this entry.