



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 10:54 AM UTC

PDB ID : 4ZY6 / pdb_00004zy6
Title : Crystal structure of P21-activated kinase 1 in complex with an inhibitor compound 29
Authors : Rouge, L.; Wang, W.
Deposited on : 2015-05-21
Resolution : 2.15 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

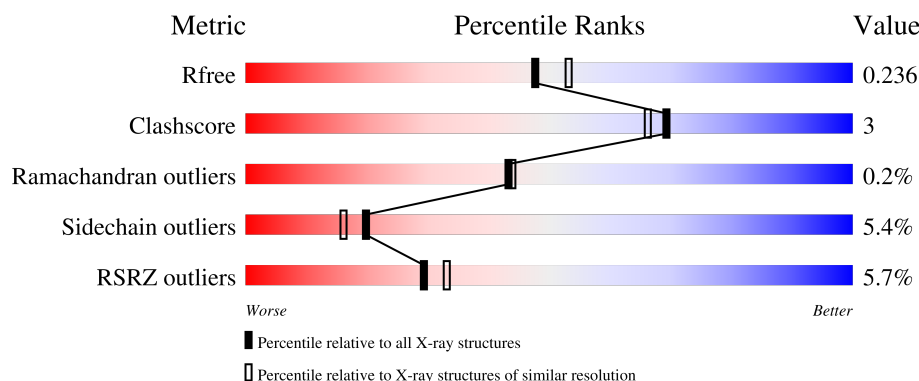
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	7% 84% 10% 6%
1	B	301	4% 79% 12% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4707 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.

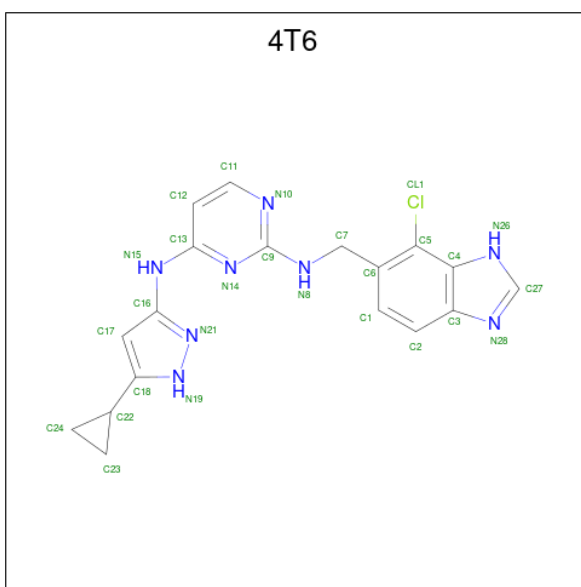
- Molecule 1 is a protein called Serine/threonine-protein kinase PAK 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	1	0
			2229	1419	374	421	15			
1	B	280	Total	C	N	O	S	0	0	0
			2175	1384	364	412	15			

There are 10 discrepancies between the modelled and reference sequences:

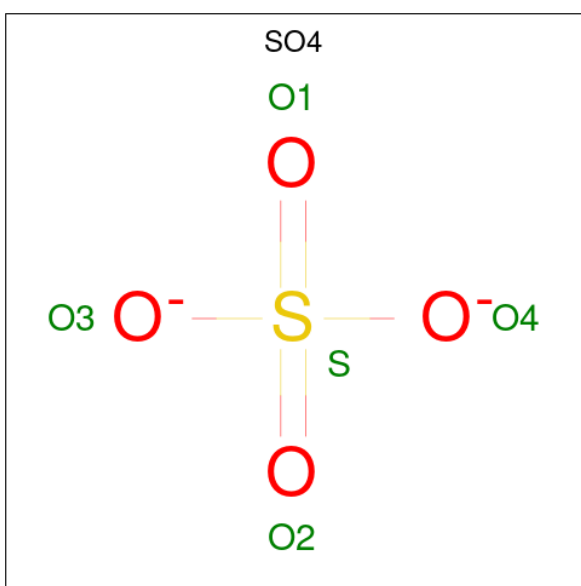
Chain	Residue	Modelled	Actual	Comment	Reference
A	248	GLY	-	expression tag	UNP Q13153
A	389	ASN	ASP	engineered mutation	UNP Q13153
A	546	GLY	-	expression tag	UNP Q13153
A	547	ASN	-	expression tag	UNP Q13153
A	548	SER	-	expression tag	UNP Q13153
B	248	GLY	-	expression tag	UNP Q13153
B	389	ASN	ASP	engineered mutation	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 N 2 -[(7-chloro-1H-benzimidazol-6-yl)methyl]-N 4 -(5-cyclopropyl-1H-pyrazol-3-yl)pyrimidine-2,4-diamine (CCD ID: 4T6) (formula: C₁₈H₁₇ClN₈).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 27	C 18	Cl 1	N 8	0	0
2	B	1	Total 27	C 18	Cl 1	N 8	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

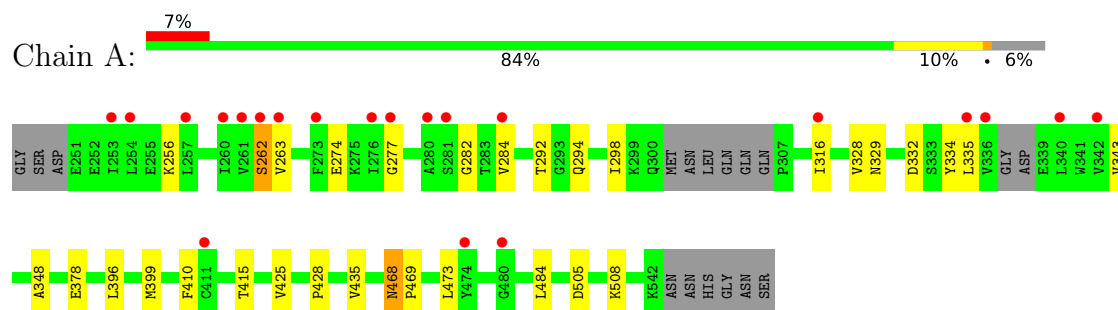
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	105	Total 105	O 105	0	0
4	B	139	Total 139	O 139	0	0

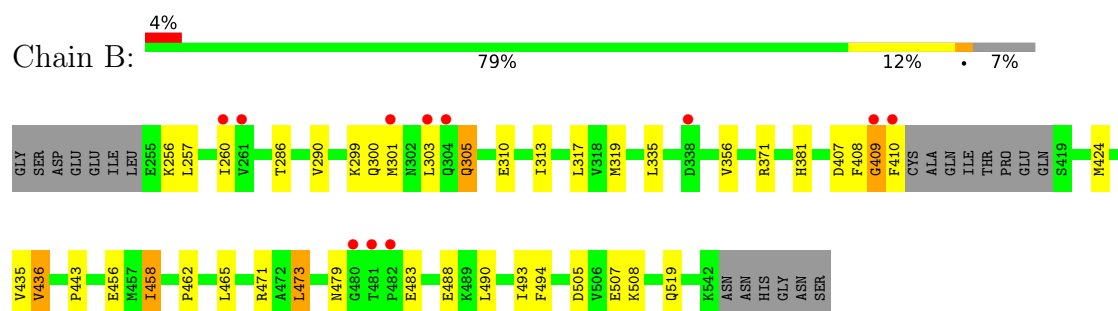
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Serine/threonine-protein kinase 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	62.63Å 82.24Å 66.14Å 90.00° 106.11° 90.00°	Depositor
Resolution (Å)	29.36 – 2.15 29.36 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.36-2.15) 99.2 (29.36-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.16Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.187 , 0.239 0.183 , 0.236	Depositor DCC
R_{free} test set	1754 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4707	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.51% 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: 4T6, SO4

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	0.86	0/2265	1.27	11/3060 (0.4%)
1	B	0.87	2/2211 (0.1%)	1.21	7/2990 (0.2%)
All	All	0.87	2/4476 (0.0%)	1.24	18/6050 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	300	GLN	CD-OE1	5.27	1.33	1.23
1	B	305	GLN	CD-OE1	5.10	1.33	1.23

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	TYR	CA-C-N	6.38	133.72	121.54
1	A	334	TYR	C-N-CA	6.38	133.72	121.54
1	A	262	SER	CA-C-N	6.14	132.76	121.70
1	A	262	SER	C-N-CA	6.14	132.76	121.70
1	A	435	VAL	CA-C-N	6.09	128.46	120.60
1	A	435	VAL	C-N-CA	6.09	128.46	120.60
1	A	282	GLY	CA-C-N	5.43	131.48	121.70
1	A	282	GLY	C-N-CA	5.43	131.48	121.70
1	A	468	ASN	CA-CB-CG	5.43	118.03	112.60
1	B	409	GLY	CA-C-N	5.41	131.44	121.70
1	B	409	GLY	C-N-CA	5.41	131.44	121.70
1	B	286	THR	N-CA-C	-5.39	101.50	110.17
1	B	435	VAL	CA-C-N	5.18	127.55	120.46
1	B	435	VAL	C-N-CA	5.18	127.55	120.46
1	A	410	PHE	CA-C-N	5.13	128.00	120.71
1	A	410	PHE	C-N-CA	5.13	128.00	120.71
1	B	505	ASP	CA-C-N	5.11	127.19	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	505	ASP	C-N-CA	5.11	127.19	120.60

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	A	2229	0	2275	12	0
1	B	2175	0	2208	19	0
2	A	27	0	16	1	0
2	B	27	0	16	0	0
3	A	5	0	0	0	0
4	A	105	0	0	1	0
4	B	139	0	0	0	0
All	All	4707	0	4515	31	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 3.

All (31) 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:262:SER:HB3	1:A:263:VAL:HA	1.33	1.04
1:B:409:GLY:HA2	1:B:410:PHE:HB2	1.40	1.04
1:B:408:PHE:N	1:B:409:GLY:HA3	2.06	0.69
1:A:277:GLY:HA3	1:A:284:VAL:H	1.64	0.62
1:B:436:VAL:HG13	1:B:473:LEU:HD13	1.82	0.62
1:A:348:ALA:HB3	1:A:399:MET:HG2	1.84	0.59
1:B:407:ASP:C	1:B:409:GLY:HA3	2.28	0.58
1:A:262:SER:HB3	1:A:263:VAL:CA	2.21	0.56
1:B:409:GLY:HA2	1:B:410:PHE:CB	2.24	0.56
1:B:356:VAL:HG11	1:B:456:GLU:HG2	1.87	0.55
1:B:462:PRO:HG2	1:B:465:LEU:HB2	1.89	0.54
1:B:458:ILE:HG12	1:B:494:PHE:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:424:MET:HE1	1:B:473:LEU:HG	1.90	0.53
1:B:493:ILE:HD11	1:B:519:GLN:HB2	1.95	0.49
1:A:329:ASN:HA	4:A:744:HOH:O	2.12	0.47
1:B:458:ILE:HG12	1:B:494:PHE:HE2	1.78	0.47
1:B:483:GLU:H	1:B:483:GLU:CD	2.24	0.44
1:A:284:VAL:HG21	2:A:601:4T6:CL1	2.55	0.43
1:B:381:HIS:CG	1:B:443:PRO:HB3	2.53	0.43
1:A:505:ASP:HB3	1:A:508:LYS:HB2	2.01	0.43
1:B:371:ARG:HH11	1:B:371:ARG:HG2	1.83	0.43
1:B:408:PHE:N	1:B:409:GLY:CA	2.80	0.43
1:A:292:THR:OG1	1:A:294:GLN:HG2	2.18	0.43
1:B:409:GLY:CA	1:B:410:PHE:HB2	2.29	0.42
1:B:256:LYS:HE3	1:B:317:LEU:HD11	2.01	0.42
1:A:262:SER:CB	1:A:263:VAL:HA	2.24	0.42
1:B:299:LYS:HG2	1:B:301:MET:HE2	2.01	0.42
1:A:428:PRO:HG2	1:A:469:PRO:HB3	2.02	0.41
1:A:298:ILE:HG12	1:A:343:VAL:HG22	2.02	0.41
1:A:328:VAL:HG21	1:A:396:LEU:HD12	2.02	0.41
1:B:257:LEU:HD13	1:B:335:LEU:HD11	2.02	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	279/301 (93%)	264 (95%)	14 (5%)	1 (0%)	30	26
1	B	276/301 (92%)	266 (96%)	10 (4%)	0	100	100
All	All	555/602 (92%)	530 (96%)	24 (4%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	335	LEU

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	245/260 (94%)	235 (96%)	10 (4%)	27	26
1	B	238/260 (92%)	222 (93%)	16 (7%)	15	10
All	All	483/520 (93%)	457 (95%)	26 (5%)	20	16

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	256	LYS
1	A	274	GLU
1	A	316	ILE
1	A	332	ASP
1	A	378	GLU
1	A	415	THR
1	A	425	VAL
1	A	468	ASN
1	A	473	LEU
1	A	484	LEU
1	B	260	ILE
1	B	290	VAL
1	B	303	LEU
1	B	305	GLN
1	B	310	GLU
1	B	313	ILE
1	B	319	MET
1	B	436	VAL
1	B	458	ILE
1	B	471	ARG
1	B	473	LEU
1	B	479	ASN
1	B	488	GLU

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Mol	Chain	Res	Type
1	B	490	LEU
1	B	507	GLU
1	B	508	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	314	ASN
1	A	322	ASN
1	A	326	ASN
1	A	375	GLN
1	A	383	ASN
1	A	384	GLN
1	A	517	GLN
1	B	326	ASN

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
2	4T6	B	601	-	31,31,31	1.27	3 (9%)	36,44,44	2.84	13 (36%)
3	SO4	A	602	-	4,4,4	0.27	0	6,6,6	0.14	0
2	4T6	A	601	-	31,31,31	1.15	4 (12%)	36,44,44	2.94	15 (41%)

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	4T6	B	601	-	-	1/13/15/15	0/5/5/5
2	4T6	A	601	-	-	0/13/15/15	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	4T6	C16-N21	-3.11	1.30	1.33
2	A	601	4T6	C9-N8	3.02	1.39	1.34
2	B	601	4T6	C9-N8	2.93	1.39	1.34
2	A	601	4T6	C16-N21	-2.51	1.30	1.33
2	A	601	4T6	C27-N28	2.24	1.36	1.32
2	B	601	4T6	C27-N28	2.04	1.36	1.32
2	A	601	4T6	C27-N26	-2.03	1.30	1.35

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	4T6	C4-C3-N28	-7.44	105.14	110.00
2	B	601	4T6	C11-N10-C9	7.25	121.48	115.42
2	A	601	4T6	C11-N10-C9	7.14	121.39	115.42
2	B	601	4T6	C16-N21-N19	6.44	108.39	103.71
2	A	601	4T6	C16-N21-N19	5.89	108.00	103.71
2	B	601	4T6	C17-C16-N21	-5.87	107.94	112.14
2	B	601	4T6	N10-C9-N14	-5.45	121.16	126.42
2	A	601	4T6	N10-C9-N14	-5.10	121.49	126.42
2	A	601	4T6	C17-C16-N21	-5.01	108.56	112.14
2	B	601	4T6	C4-C3-N28	-5.01	106.73	110.00
2	A	601	4T6	C4-N26-C27	4.53	110.06	106.27
2	B	601	4T6	C12-C11-N10	-4.15	118.88	123.97
2	A	601	4T6	C12-C11-N10	-4.08	118.97	123.97
2	B	601	4T6	C18-C17-C16	3.95	107.55	104.78
2	A	601	4T6	N15-C13-N14	3.67	122.21	113.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	4T6	N15-C13-N14	3.66	122.20	113.33
2	B	601	4T6	C4-N26-C27	3.64	109.32	106.27
2	B	601	4T6	C1-C6-C5	3.41	120.00	117.33
2	A	601	4T6	C18-C17-C16	3.11	106.95	104.78
2	A	601	4T6	N26-C27-N28	-3.01	109.29	113.87
2	A	601	4T6	C2-C3-N28	2.72	134.64	129.62
2	A	601	4T6	C1-C6-C5	2.56	119.34	117.33
2	B	601	4T6	C12-C13-N14	-2.43	119.08	123.15
2	A	601	4T6	C7-C6-C5	-2.16	118.17	121.02
2	B	601	4T6	C7-C6-C5	-2.12	118.22	121.02
2	A	601	4T6	C12-C13-N14	-2.11	119.61	123.15
2	B	601	4T6	C2-C3-N28	2.05	133.41	129.62
2	A	601	4T6	C6-C5-CL1	2.01	121.21	119.16

There are no chirality outliers.

All (1) torsion outliers are listed below:

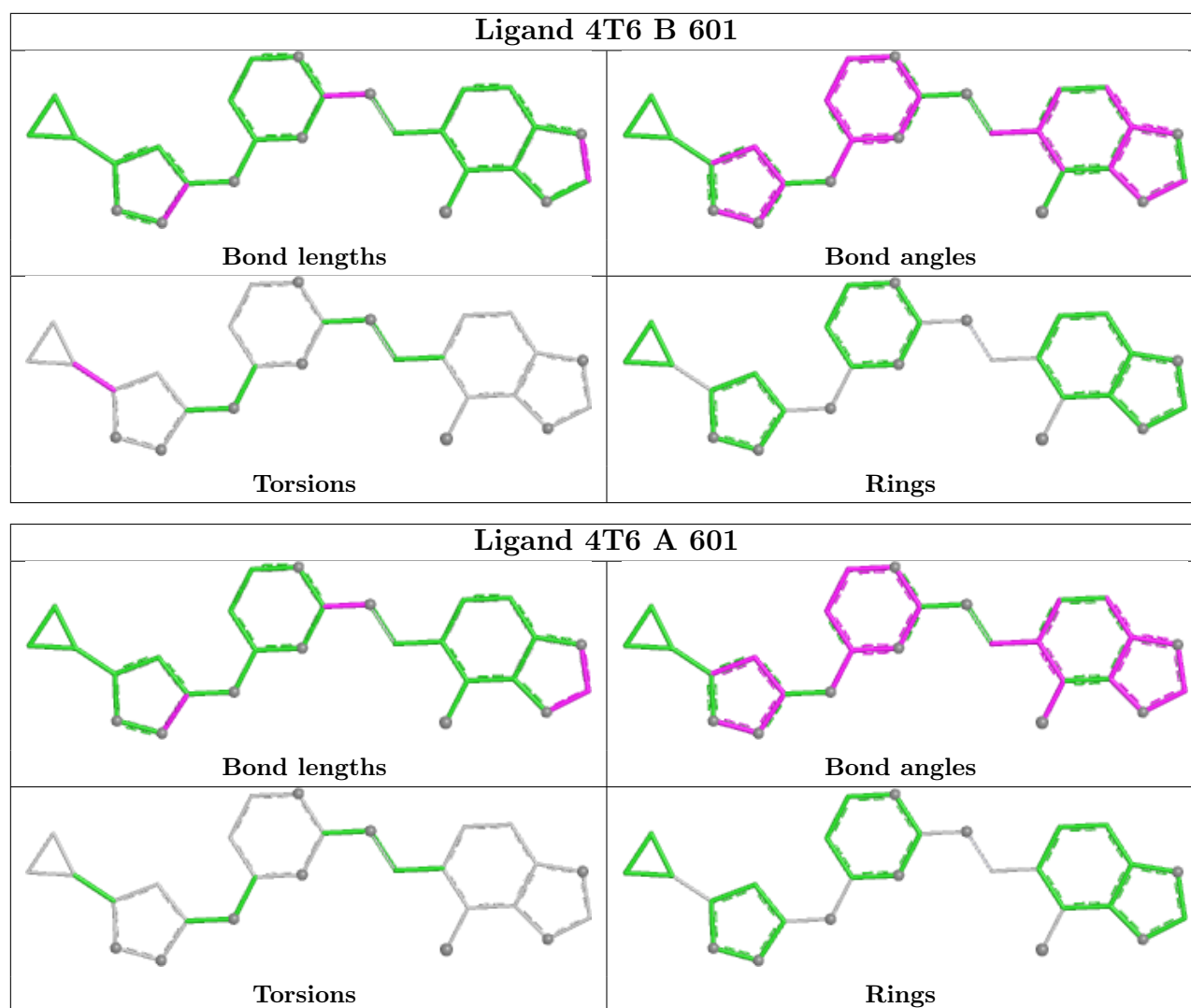
Mol	Chain	Res	Type	Atoms
2	B	601	4T6	C17-C18-C22-C24

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	4T6	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	A	284/301 (94%)	0.34	21 (7%) 20 23	21, 58, 117, 164	1 (0%)
1	B	280/301 (93%)	0.07	11 (3%) 43 48	29, 48, 97, 138	0
All	All	564/602 (93%)	0.20	32 (5%) 29 33	21, 53, 113, 164	1 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	410	PHE	5.9
1	A	336	VAL	5.8
1	A	340	LEU	4.2
1	A	276	ILE	4.0
1	A	411	CYS	3.7
1	A	257	LEU	3.6
1	B	409	GLY	3.6
1	A	263	VAL	3.5
1	A	284	VAL	3.3
1	A	280	ALA	3.1
1	A	335	LEU	3.0
1	B	480	GLY	3.0
1	B	481	THR	2.8
1	A	253	ILE	2.8
1	A	277	GLY	2.6
1	A	260	ILE	2.5
1	B	304	GLN	2.4
1	A	262	SER	2.4
1	A	273	PHE	2.4
1	B	482	PRO	2.3
1	B	303	LEU	2.3
1	B	338	ASP	2.3
1	A	261	VAL	2.2
1	B	261	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	316	ILE	2.2
1	B	260	ILE	2.2
1	A	474	TYR	2.2
1	A	281	SER	2.1
1	A	480	GLY	2.1
1	A	342	VAL	2.1
1	B	301	MET	2.0
1	A	254	LEU	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](#)

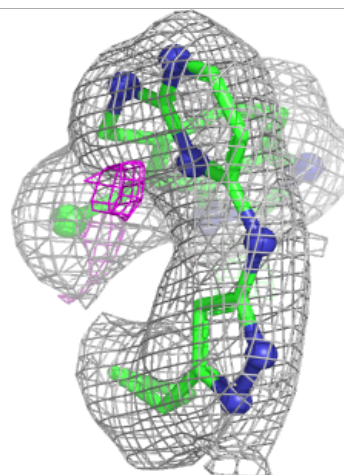
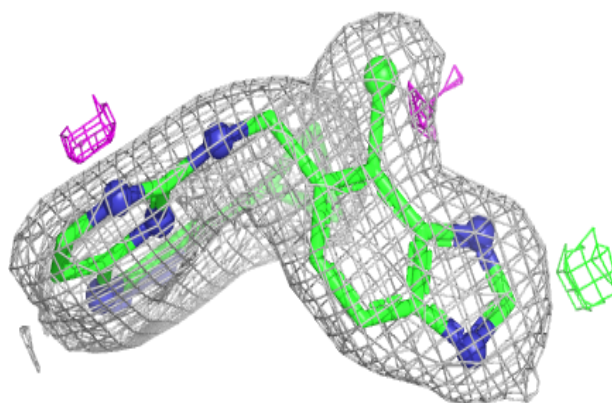
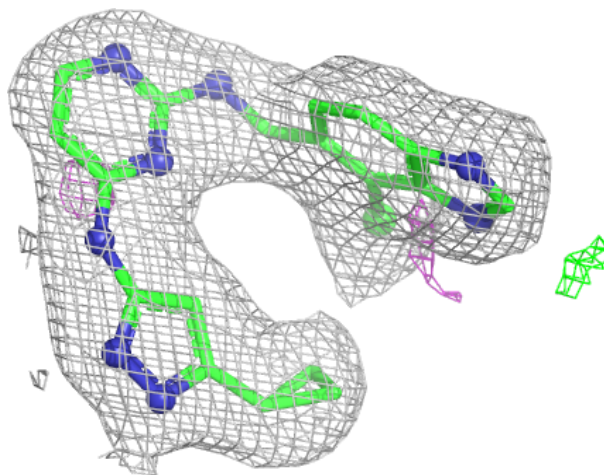
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	SO4	A	602	5/5	0.82	0.11	102,102,103,105	0
2	4T6	B	601	27/27	0.94	0.08	36,46,51,54	0
2	4T6	A	601	27/27	0.95	0.06	39,48,53,55	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.

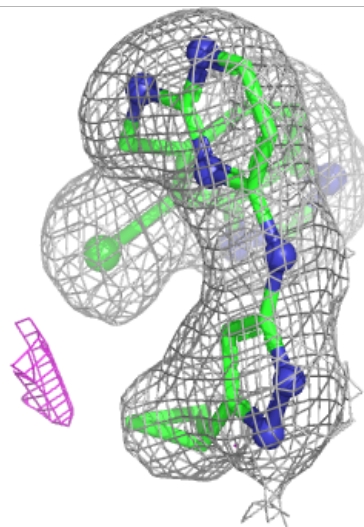
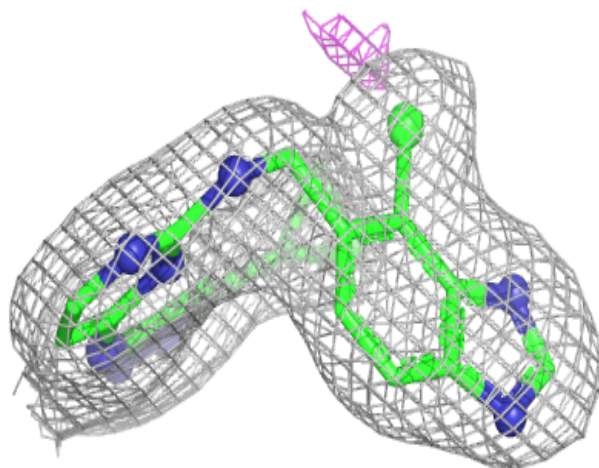
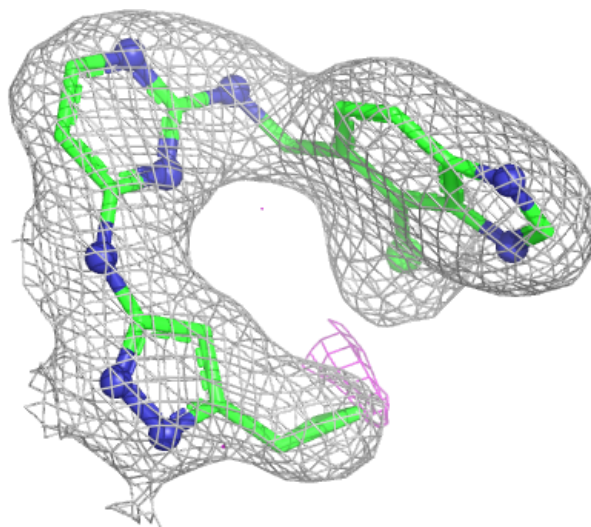
Electron density around 4T6 B 601:

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



Electron density around 4T6 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 ⓘ

There are no such residues in this entry.