



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:14 PM UTC

PDB ID : 5UK8 / pdb_00005uk8
Title : The co-structure of (R)-4-(6-(1-(cyclopropylsulfonyl)cyclopropyl)-2-(1H-indol-4-yl)pyrimidin-4-yl)-3-methylmorpholine and a rationally designed PI3K-alpha mutant that mimics ATR
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Deposited on : 2017-01-20
Resolution : 2.50 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

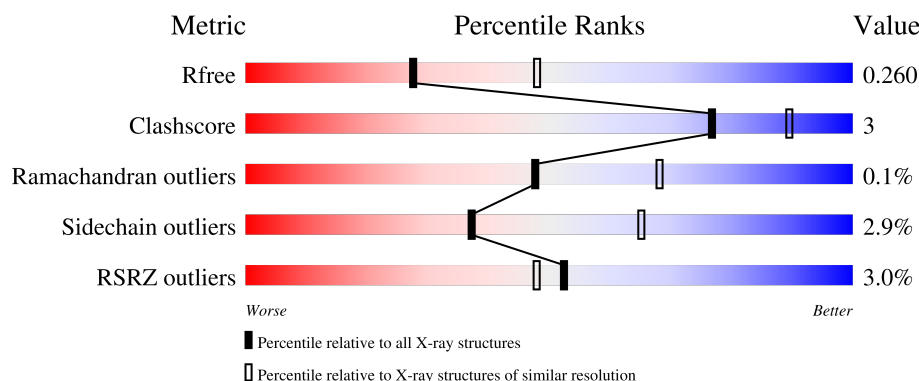
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	1074	
2	B	293	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10364 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 Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1008	Total	C	N	O	S	0	3	0
			8154	5215	1393	1479	67			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	LYS	MET	engineered mutation	UNP P42336
A	233	LYS	LEU	engineered mutation	UNP P42336
A	770	GLU	ARG	engineered mutation	UNP P42336
A	780	LYS	TRP	engineered mutation	UNP P42336
A	798	ILE	GLU	engineered mutation	UNP P42336
A	800	MET	ILE	engineered mutation	UNP P42336
A	850	TRP	VAL	engineered mutation	UNP P42336
A	930	VAL	PHE	engineered mutation	UNP P42336
A	1069	HIS	-	expression tag	UNP P42336
A	1070	HIS	-	expression tag	UNP P42336
A	1071	HIS	-	expression tag	UNP P42336
A	1072	HIS	-	expression tag	UNP P42336
A	1073	HIS	-	expression tag	UNP P42336
A	1074	HIS	-	expression tag	UNP P42336

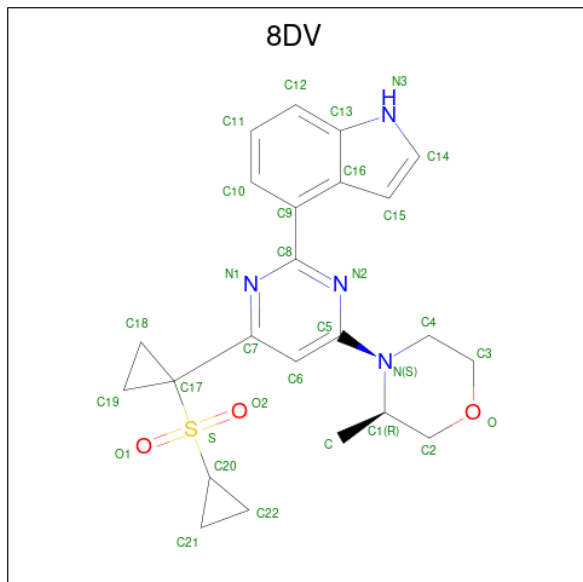
- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	244	Total	C	N	O	S	0	0	0
			1994	1242	360	387	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	306	TYR	THR	engineered mutation	UNP P27986

- Molecule 3 is (R)-4-(6-(1-(cyclopropylsulfonyl)cyclopropyl)-2-(1H-indol-4-yl)pyrimidin-4-yl)-3-methylmorpholine (CCD ID: 8DV) (formula: $C_{23}H_{26}N_4O_3S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			31	23	4	3	1		

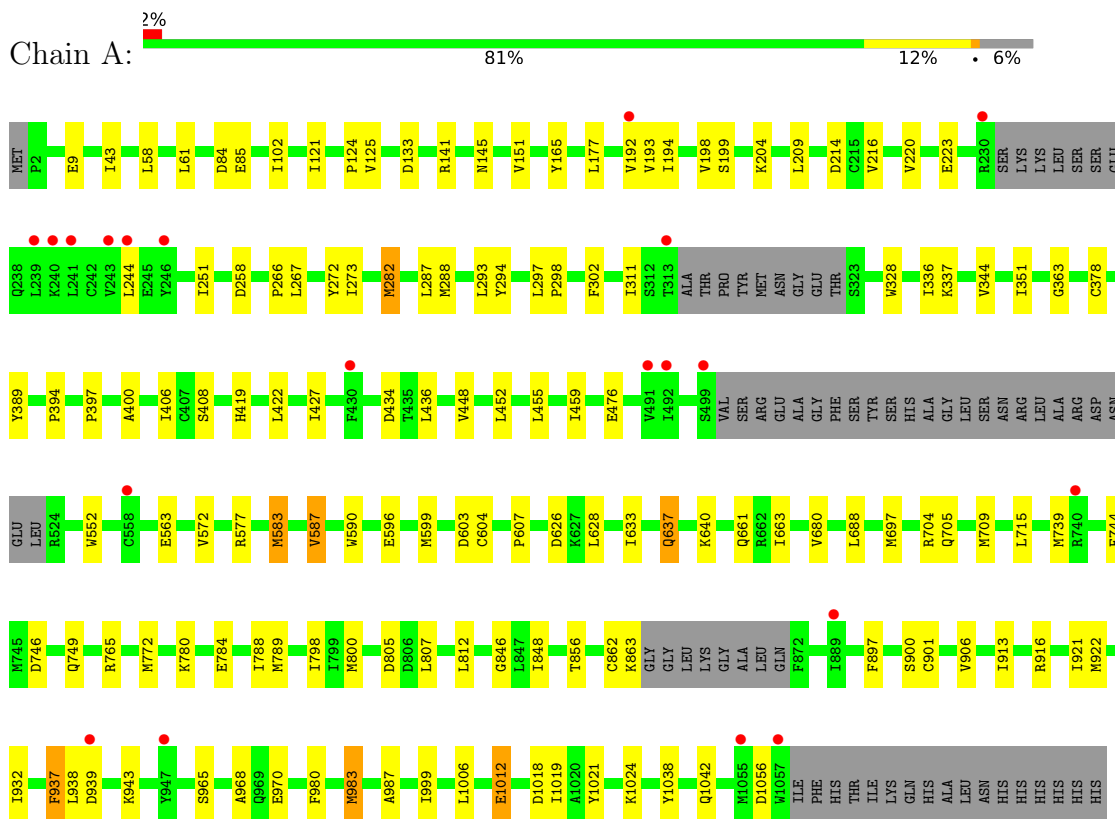
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	160	Total	O	0	0
			160	160		
4	B	25	Total	O	0	0
			25	25		

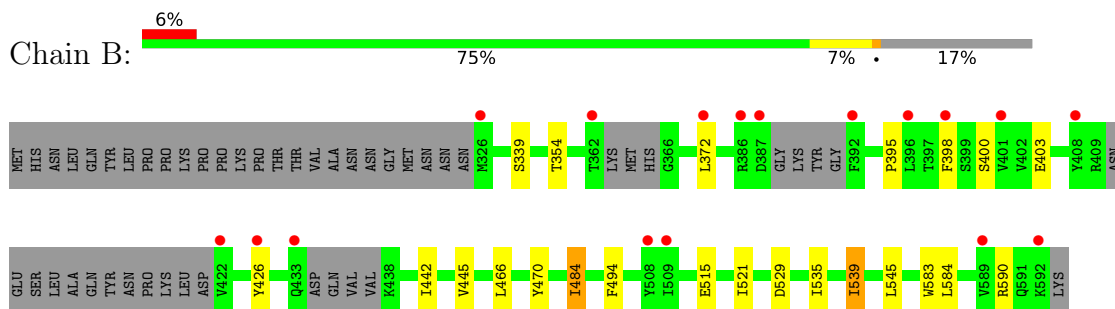
3 Residue-property plots

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: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform



- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.03Å 107.10Å 134.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.52 – 2.50 48.52 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.52-2.50) 99.6 (48.52-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 2.51Å)	Xtriage
Refinement program	REFMAC, BUSTER	Depositor
R, R_{free}	0.198 , 0.240 0.214 , 0.260	Depositor DCC
R_{free} test set	2657 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	56.3	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10364	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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: 8DV

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	0.85	2/8339 (0.0%)	1.33	37/11291 (0.3%)
2	B	0.82	0/2022	1.48	11/2713 (0.4%)
All	All	0.84	2/10361 (0.0%)	1.36	48/14004 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	633	ILE	CG1-CD1	5.44	1.73	1.51
1	A	216	VAL	CA-C	5.37	1.58	1.52

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	258	ASP	CA-CB-CG	6.94	119.54	112.60
1	A	603	ASP	CA-CB-CG	6.85	119.45	112.60
1	A	937	PHE	CA-CB-CG	6.42	120.22	113.80
1	A	133	ASP	CA-CB-CG	6.31	118.91	112.60
1	A	983	MET	CA-C-N	6.31	128.64	120.44
1	A	983	MET	C-N-CA	6.31	128.64	120.44
1	A	939	ASP	CA-CB-CG	6.18	118.78	112.60
2	B	339	SER	CA-C-N	6.00	128.60	120.38
2	B	339	SER	C-N-CA	6.00	128.60	120.38
1	A	970	GLU	CA-C-N	5.83	128.10	120.28
1	A	970	GLU	C-N-CA	5.83	128.10	120.28
1	A	84	ASP	CA-CB-CG	5.66	118.26	112.60
1	A	145	ASN	CA-C-N	5.65	127.68	120.56
1	A	145	ASN	C-N-CA	5.65	127.68	120.56
1	A	9	GLU	CB-CG-CD	5.65	122.20	112.60
1	A	124	PRO	CA-C-N	5.64	128.48	120.53
1	A	124	PRO	C-N-CA	5.64	128.48	120.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	223	GLU	CB-CG-CD	5.60	122.12	112.60
1	A	626	ASP	CA-CB-CG	5.37	117.97	112.60
2	B	529	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	746	ASP	CA-CB-CG	5.36	117.96	112.60
1	A	805	ASP	CA-CB-CG	5.29	117.89	112.60
1	A	587	VAL	CA-C-N	5.26	127.59	120.38
1	A	587	VAL	C-N-CA	5.26	127.59	120.38
2	B	583	TRP	CA-C-N	5.23	127.72	120.29
2	B	583	TRP	C-N-CA	5.23	127.72	120.29
2	B	529	ASP	CA-C-N	5.19	127.24	120.28
2	B	529	ASP	C-N-CA	5.19	127.24	120.28
1	A	900	SER	CA-C-N	5.19	127.66	120.29
1	A	900	SER	C-N-CA	5.19	127.66	120.29
2	B	398	PHE	CA-C-N	5.18	127.17	120.44
2	B	398	PHE	C-N-CA	5.18	127.17	120.44
1	A	1056	ASP	N-CA-C	-5.16	108.25	114.75
1	A	198	VAL	CA-C-N	5.16	128.49	120.60
1	A	198	VAL	C-N-CA	5.16	128.49	120.60
1	A	125	VAL	CA-C-N	5.14	127.88	120.38
1	A	125	VAL	C-N-CA	5.14	127.88	120.38
1	A	577	ARG	CA-C-N	5.12	127.41	120.44
1	A	577	ARG	C-N-CA	5.12	127.41	120.44
1	A	378	CYS	CA-C-N	5.11	128.78	120.60
1	A	378	CYS	C-N-CA	5.11	128.78	120.60
1	A	272	TYR	CA-C-N	5.07	127.05	120.56
1	A	272	TYR	C-N-CA	5.07	127.05	120.56
2	B	470	TYR	CA-C-N	5.06	127.48	120.29
2	B	470	TYR	C-N-CA	5.06	127.48	120.29
1	A	812	LEU	CA-C-N	5.02	126.97	120.44
1	A	812	LEU	C-N-CA	5.02	126.97	120.44
1	A	244	LEU	N-CA-C	-5.01	106.85	113.17

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	8154	0	8047	52	0
2	B	1994	0	1891	7	0
3	A	31	0	0	0	0
4	A	160	0	0	1	0
4	B	25	0	0	0	0
All	All	10364	0	9938	59	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 (59) 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:772:MET:HE1	1:A:780:LYS:HB2	1.56	0.87
1:A:298:PRO:HG2	1:A:697:MET:HG2	1.81	0.63
2:B:494:PHE:HB3	2:B:535:ILE:HG12	1.82	0.62
1:A:897:PHE:O	1:A:901:CYS:HB2	2.00	0.61
1:A:408:SER:HB3	1:A:422:LEU:HD21	1.87	0.56
1:A:194:ILE:HD11	1:A:220:VAL:HG12	1.89	0.55
1:A:596:GLU:HA	1:A:599:MET:HE2	1.89	0.55
1:A:220:VAL:HG21	1:A:267:LEU:HD13	1.89	0.54
1:A:267:LEU:HG	1:A:273:ILE:HG13	1.90	0.54
1:A:328:TRP:HA	1:A:394:PRO:HB3	1.90	0.53
1:A:916:ARG:HB3	1:A:921:ILE:HD11	1.90	0.53
2:B:484:ILE:HG13	2:B:545:LEU:HD23	1.91	0.52
1:A:788:ILE:HG23	1:A:789:MET:HG3	1.92	0.52
1:A:194:ILE:HD12	1:A:209:LEU:HD22	1.91	0.52
1:A:363:GLY:N	1:A:607:PRO:HG3	2.25	0.52
1:A:344:VAL:HG11	1:A:406:ILE:HG21	1.93	0.51
1:A:572:VAL:HG21	1:A:583:MET:HG2	1.93	0.51
1:A:965:SER:HB3	1:A:968:ALA:HB3	1.92	0.50
1:A:336:ILE:HD12	1:A:389:TYR:CE2	2.47	0.50
1:A:204:LYS:HD3	1:A:789:MET:HE3	1.92	0.49
1:A:151:VAL:HG21	1:A:302:PHE:HB2	1.95	0.48
1:A:552:TRP:HZ3	1:A:583:MET:HE2	1.78	0.48
1:A:739:MET:HG2	1:A:744:PHE:CE1	2.48	0.48
2:B:400:SER:HB2	2:B:403:GLU:OE1	2.13	0.48
2:B:445:VAL:HG13	2:B:584:LEU:HD13	1.95	0.47
1:A:294:TYR:HA	1:A:297:LEU:HD12	1.95	0.47
1:A:765[A]:ARG:HE	1:A:784:GLU:HG2	1.79	0.47
1:A:906:VAL:HG21	1:A:987:ALA:HB3	1.97	0.46
1:A:640:LYS:HE2	1:A:680:VAL:HG11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1006:LEU:HD21	1:A:1019:ILE:HD11	1.96	0.46
2:B:442:ILE:HA	2:B:445:VAL:HG12	1.97	0.46
1:A:214:ASP:HA	1:A:266:PRO:HB3	1.97	0.45
1:A:1012:GLU:O	1:A:1018:ASP:HB3	2.16	0.45
1:A:121:ILE:HG12	1:A:688:LEU:HB3	1.98	0.45
1:A:58:LEU:HB3	1:A:61:LEU:HD12	1.99	0.45
1:A:800:MET:CE	1:A:848:ILE:HD12	2.47	0.44
1:A:448:VAL:HG13	1:A:452:LEU:HD23	1.99	0.44
1:A:739:MET:HA	1:A:744:PHE:CD1	2.53	0.43
1:A:637:GLN:HG3	4:A:1221:HOH:O	2.19	0.43
1:A:937:PHE:CD1	1:A:938:LEU:HG	2.53	0.43
1:A:165:TYR:O	1:A:661:GLN:HB2	2.19	0.43
1:A:980:PHE:HA	1:A:983:MET:HE3	2.01	0.43
1:A:419:HIS:HB3	1:A:455:LEU:HD11	2.01	0.43
1:A:628:LEU:HD23	1:A:663:ILE:HD13	2.00	0.43
1:A:705:GLN:O	1:A:709:MET:HG2	2.18	0.42
1:A:587:VAL:HA	1:A:590:TRP:HB2	2.00	0.42
1:A:1021:TYR:HA	1:A:1024:LYS:HE3	2.00	0.42
1:A:397:PRO:HD2	1:A:400:ALA:HB2	2.02	0.42
1:A:807:LEU:HD12	1:A:846:GLY:HA3	2.01	0.42
1:A:856:THR:HG22	1:A:922:MET:HG2	2.02	0.41
2:B:354:THR:HA	2:B:426:TYR:O	2.20	0.41
1:A:193:VAL:HG23	1:A:282:MET:HG2	2.02	0.41
2:B:535:ILE:HG22	2:B:539:ILE:HD12	2.03	0.41
1:A:288:MET:HE2	1:A:293:LEU:HB2	2.03	0.41
1:A:704:ARG:NH1	1:A:749:GLN:O	2.54	0.41
1:A:1038:TYR:O	1:A:1042:GLN:HG2	2.21	0.41
1:A:337:LYS:HB3	1:A:476:GLU:HB3	2.02	0.40
1:A:43:ILE:HG13	1:A:85:GLU:O	2.21	0.40
1:A:459:ILE:HD12	1:A:604:CYS:SG	2.60	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	1001/1074 (93%)	957 (96%)	44 (4%)	0	100	100
2	B	234/293 (80%)	223 (95%)	10 (4%)	1 (0%)	30	49
All	All	1235/1367 (90%)	1180 (96%)	54 (4%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	395	PRO

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	897/980 (92%)	872 (97%)	25 (3%)	38	66
2	B	206/272 (76%)	199 (97%)	7 (3%)	32	60
All	All	1103/1252 (88%)	1071 (97%)	32 (3%)	37	65

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	ILE
1	A	141	ARG
1	A	177	LEU
1	A	192	VAL
1	A	199	SER
1	A	251	ILE
1	A	282	MET
1	A	287	LEU
1	A	311	ILE
1	A	351	ILE
1	A	427	ILE
1	A	434	ASP

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Mol	Chain	Res	Type
1	A	436	LEU
1	A	563	GLU
1	A	583	MET
1	A	637	GLN
1	A	715	LEU
1	A	798	ILE
1	A	862	CYS
1	A	863	LYS
1	A	913	ILE
1	A	932	ILE
1	A	943	LYS
1	A	999	ILE
1	A	1012	GLU
2	B	372	LEU
2	B	466	LEU
2	B	484	ILE
2	B	515	GLU
2	B	521	ILE
2	B	539	ILE
2	B	590	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	219	GLN
1	A	296	GLN
1	A	384	ASN
1	A	530	GLN
1	A	630	GLN
1	A	661	GLN
1	A	714	ASN
1	A	855	HIS
2	B	406	ASN
2	B	499	GLN
2	B	501	GLN

5.3.3 RNA ⓘ

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](#)

1 ligand is 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	8DV	A	1101	-	31,36,36	0.55	0	37,56,56	0.80	2 (5%)

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	8DV	A	1101	-	-	2/23/46/46	0/6/6/6

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	8DV	C5-N2-C8	2.60	118.36	116.00
3	A	1101	8DV	C5-C6-C7	-2.42	115.01	117.73

There are no chirality outliers.

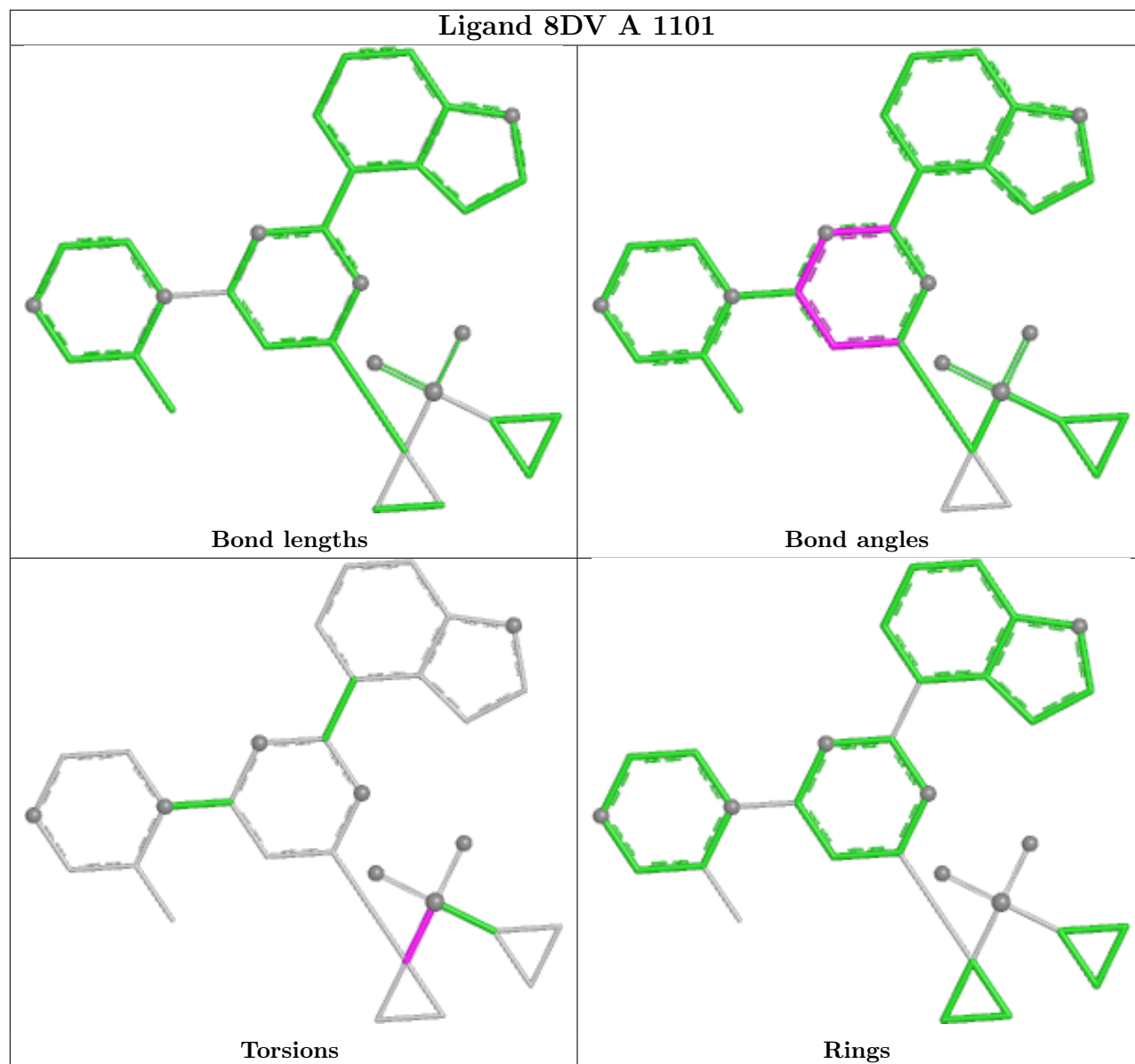
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	8DV	C18-C17-S-O1
3	A	1101	8DV	C18-C17-S-C20

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 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	1008/1074 (93%)	0.27	20 (1%) 65 61	31, 65, 101, 139	3 (0%)
2	B	244/293 (83%)	0.44	17 (6%) 22 20	46, 77, 118, 136	0
All	All	1252/1367 (91%)	0.30	37 (2%) 52 48	31, 67, 110, 139	3 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1057	TRP	4.5
2	B	422	VAL	4.2
1	A	243	VAL	3.7
2	B	592	LYS	3.5
1	A	313	THR	3.3
2	B	387	ASP	3.3
2	B	372	LEU	3.1
2	B	433	GLN	2.9
1	A	499	SER	2.7
1	A	246	TYR	2.7
2	B	408	TYR	2.6
2	B	398	PHE	2.5
2	B	392	PHE	2.5
2	B	508	TYR	2.5
1	A	244	LEU	2.4
1	A	241	LEU	2.4
2	B	326	MET	2.4
1	A	558	CYS	2.3
2	B	426	TYR	2.3
2	B	509	ILE	2.3
1	A	230	ARG	2.3
2	B	362	THR	2.2
1	A	239	LEU	2.2
1	A	1055	MET	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	396	LEU	2.2
2	B	589	VAL	2.2
1	A	939	ASP	2.2
1	A	240	LYS	2.2
1	A	492	ILE	2.1
1	A	889	ILE	2.1
1	A	740[A]	ARG	2.1
2	B	386	ARG	2.1
2	B	401	VAL	2.1
1	A	192	VAL	2.1
1	A	430	PHE	2.1
1	A	947	TYR	2.1
1	A	491	VAL	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](#)

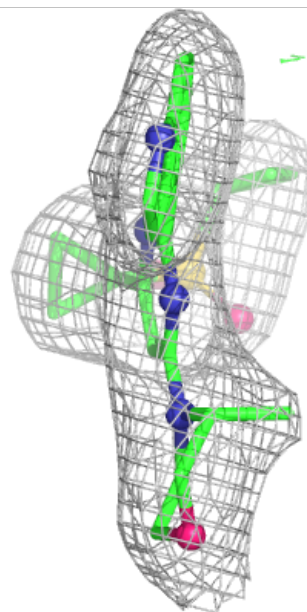
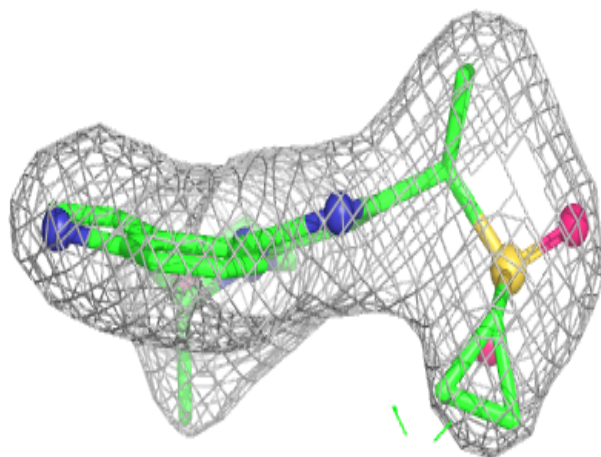
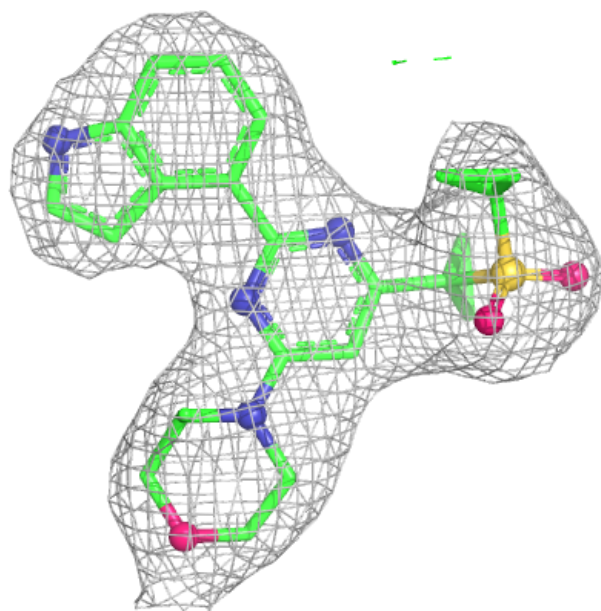
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	8DV	A	1101	31/31	0.95	0.07	44,47,70,74	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 8DV A 1101:

$2mF_o-DF_c$ (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.