



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:00 PM UTC

PDB ID : 5Y5U / pdb_00005y5u
Title : Crystal structures of spleen tyrosine kinase in complex with a novel inhibitor
Authors : Lee, S.J.; Lee, B.I.
Deposited on : 2017-08-09
Resolution : 2.14 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

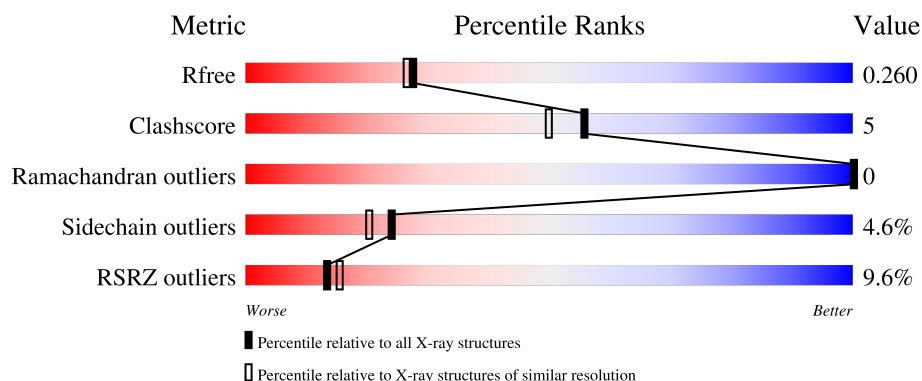
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	293	
1	B	293	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4373 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 Tyrosine-protein kinase SYK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	266	Total	C	N	O	S	0	0	0
			2166	1393	364	390	19			
1	B	257	Total	C	N	O	S	0	0	0
			2082	1336	351	376	19			

There are 26 discrepancies between the modelled and reference sequences:

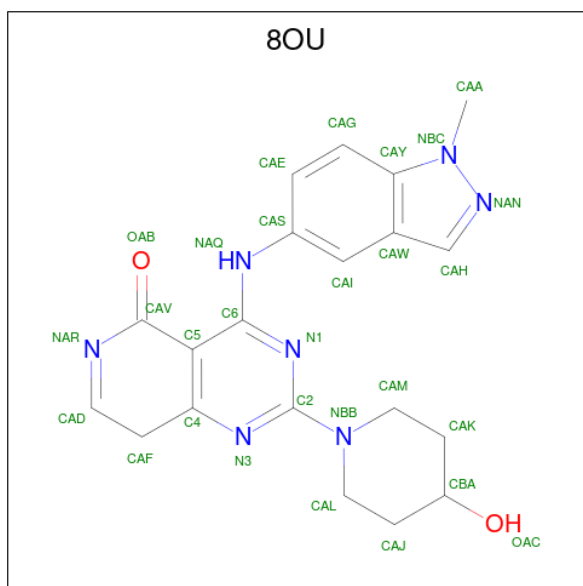
Chain	Residue	Modelled	Actual	Comment	Reference
A	353	MET	-	expression tag	UNP P43405
A	354	ALA	-	expression tag	UNP P43405
A	355	LEU	-	expression tag	UNP P43405
A	636	LEU	-	expression tag	UNP P43405
A	637	GLU	-	expression tag	UNP P43405
A	638	HIS	-	expression tag	UNP P43405
A	639	HIS	-	expression tag	UNP P43405
A	640	HIS	-	expression tag	UNP P43405
A	641	HIS	-	expression tag	UNP P43405
A	642	HIS	-	expression tag	UNP P43405
A	643	HIS	-	expression tag	UNP P43405
A	644	HIS	-	expression tag	UNP P43405
A	645	HIS	-	expression tag	UNP P43405
B	353	MET	-	expression tag	UNP P43405
B	354	ALA	-	expression tag	UNP P43405
B	355	LEU	-	expression tag	UNP P43405
B	636	LEU	-	expression tag	UNP P43405
B	637	GLU	-	expression tag	UNP P43405
B	638	HIS	-	expression tag	UNP P43405
B	639	HIS	-	expression tag	UNP P43405
B	640	HIS	-	expression tag	UNP P43405
B	641	HIS	-	expression tag	UNP P43405
B	642	HIS	-	expression tag	UNP P43405
B	643	HIS	-	expression tag	UNP P43405
B	644	HIS	-	expression tag	UNP P43405

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Chain	Residue	Modelled	Actual	Comment	Reference
B	645	HIS	-	expression tag	UNP P43405

- Molecule 2 is 4-[(1-methylindazol-5-yl)amino]-2-(4-oxidanylpiperidin-1-yl)-8H-pyrido[4,3-d]pyrimidin-5-one (CCD ID: 8OU) (formula: C₂₀H₂₁N₇O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			29	20	7	2		
2	B	1	Total	C	N	O	0	0
			29	20	7	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	42	Total	O	0	0
			42	42		
3	B	25	Total	O	0	0
			25	25		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	40.16Å 42.01Å 87.66Å 79.83° 90.78° 79.60°	Depositor
Resolution (Å)	30.00 – 2.14 30.00 – 2.14	Depositor EDS
% Data completeness (in resolution range)	94.0 (30.00-2.14) 94.4 (30.00-2.14)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.238 , 0.260 0.244 , 0.260	Depositor DCC
R_{free} test set	1451 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 29.1	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	0.93	EDS
Total number of atoms	4373	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.87% 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: 8OU

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	1.00	9/2216 (0.4%)	1.00	5/2985 (0.2%)
1	B	0.82	4/2126 (0.2%)	0.96	4/2859 (0.1%)
All	All	0.91	13/4342 (0.3%)	0.98	9/5844 (0.2%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	607	LEU	C-O	-7.45	1.15	1.24
1	A	492	HIS	CD2-NE2	-7.34	1.29	1.37
1	A	492	HIS	CG-ND1	-6.07	1.31	1.38
1	A	491	VAL	C-O	-5.93	1.17	1.24
1	A	616	ARG	C-O	-5.67	1.16	1.24
1	A	613	VAL	C-O	-5.65	1.17	1.24
1	B	597	CYS	C-O	-5.49	1.17	1.24
1	A	434	ARG	C-O	-5.38	1.17	1.23
1	A	534	TRP	NE1-CE2	-5.17	1.31	1.37
1	B	511	SER	C-O	-5.15	1.17	1.23
1	A	609	TRP	NE1-CE2	-5.11	1.31	1.37
1	B	429	ASN	C-O	-5.03	1.18	1.24
1	B	468	ASP	CA-C	-5.02	1.46	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	512	ASP	N-CA-C	12.55	125.59	110.91
1	A	412	ALA	N-CA-C	8.80	120.96	111.36
1	A	613	VAL	CB-CA-C	-6.06	103.96	112.14
1	A	374	ASP	N-CA-C	5.88	120.61	113.38
1	A	492	HIS	N-CA-C	5.52	117.10	111.14
1	B	468	ASP	N-CA-C	-5.52	105.16	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	442	GLU	N-CA-C	-5.39	106.87	113.50
1	A	414	LYS	N-CA-C	-5.18	105.63	111.28
1	B	512	ASP	CB-CA-C	-5.18	103.20	112.27

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	2166	0	2161	22	0
1	B	2082	0	2088	17	0
2	A	29	0	0	2	0
2	B	29	0	0	1	0
3	A	42	0	0	1	0
3	B	25	0	0	1	0
All	All	4373	0	4249	40	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 5.

All (40) 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)
2:B:701:8OU:CAE	2:B:701:8OU:N1	2.48	0.75
1:B:429:ASN:HB3	1:B:432:ILE:HG12	1.67	0.74
1:A:450:MET:HE1	2:A:701:8OU:CAE	2.19	0.72
1:A:433:VAL:HG21	1:A:511:SER:HB3	1.76	0.67
1:A:482:MET:HE2	1:A:495:LEU:HD22	1.81	0.63
1:A:559:GLY:HA2	1:A:562:MET:HE3	1.81	0.63
1:A:601:MET:HE3	1:A:629:TYR:CD2	2.37	0.60
1:B:469:LYS:HB3	3:B:822:HOH:O	2.05	0.57
1:A:558:PHE:CD2	1:A:562:MET:HE2	2.44	0.53
1:B:601:MET:HE1	1:B:626:LEU:HD23	1.89	0.53
1:B:527:LYS:HE2	1:B:548:LYS:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:440:GLU:OE1	1:B:444:TRP:CH2	2.63	0.52
1:B:428:ASP:OD1	1:B:428:ASP:C	2.53	0.51
1:B:601:MET:HE3	1:B:629:TYR:CD2	2.47	0.50
1:A:404:LEU:HD11	1:A:413:LEU:HB3	1.93	0.49
1:A:530:THR:HG23	1:A:531:HIS:N	2.27	0.49
1:B:429:ASN:HB3	1:B:432:ILE:CG1	2.42	0.48
1:A:601:MET:HE2	1:A:601:MET:HA	1.97	0.47
1:B:460:LEU:CD2	1:B:466:VAL:HG11	2.45	0.47
1:A:446:LEU:HG	1:A:448:MET:HE2	1.98	0.45
1:B:537:LYS:HE3	1:B:572:PRO:O	2.16	0.45
1:B:512:ASP:C	1:B:512:ASP:OD2	2.58	0.45
1:A:517:LYS:HE3	1:A:526:TYR:CZ	2.51	0.45
1:B:382:PHE:CZ	1:B:416:GLU:HG3	2.53	0.44
1:A:491:VAL:HG12	1:A:493:ARG:HG3	1.99	0.44
1:A:464:ARG:NE	3:A:802:HOH:O	2.51	0.43
1:A:450:MET:HE3	2:A:701:8OU:OAB	2.18	0.43
1:B:513:PHE:CD1	1:B:513:PHE:N	2.87	0.43
1:A:440:GLU:HB3	1:A:444:TRP:CZ3	2.54	0.42
1:A:365:LEU:HG	1:A:390:TYR:CZ	2.55	0.42
1:B:363:VAL:HG11	1:B:425:GLN:NE2	2.35	0.42
1:A:433:VAL:CG2	1:A:511:SER:HB3	2.48	0.42
1:B:443:SER:OG	1:B:444:TRP:N	2.52	0.41
1:A:450:MET:HE2	1:A:452:GLU:HA	2.02	0.41
1:A:370:LEU:HD21	1:A:372:LEU:HD21	2.02	0.41
1:B:443:SER:OG	1:B:444:TRP:O	2.38	0.41
1:A:413:LEU:O	1:A:414:LYS:C	2.64	0.41
1:B:464:ARG:N	1:B:464:ARG:HD2	2.36	0.40
1:A:450:MET:HE3	1:A:451:ALA:N	2.37	0.40
1:A:414:LYS:O	1:A:418:LEU:HD22	2.22	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	262/293 (89%)	254 (97%)	8 (3%)	0	100	100
1	B	251/293 (86%)	241 (96%)	10 (4%)	0	100	100
All	All	513/586 (88%)	495 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	231/256 (90%)	219 (95%)	12 (5%)	21	16
1	B	223/256 (87%)	214 (96%)	9 (4%)	28	25
All	All	454/512 (89%)	433 (95%)	21 (5%)	24	20

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	365	LEU
1	A	384	THR
1	A	414	LYS
1	A	418	LEU
1	A	438	ILE
1	A	440	GLU
1	A	443	SER
1	A	469	LYS
1	A	530	THR
1	A	531	HIS
1	A	586	GLU
1	A	614	GLU
1	B	403	ILE
1	B	405	LYS
1	B	413	LEU
1	B	427	LEU
1	B	443	SER
1	B	524	ASN

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Mol	Chain	Res	Type
1	B	527	LYS
1	B	598	PRO
1	B	625	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	463	ASN
1	A	465	HIS
1	A	499	ASN
1	A	570	GLN
1	B	391	GLN
1	B	505	GLN
1	B	615	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](#)

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	8OU	A	701	-	31,33,33	5.40	13 (41%)	40,48,48	5.42	21 (52%)
2	8OU	B	701	-	31,33,33	5.17	11 (35%)	40,48,48	3.21	19 (47%)

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	8OU	A	701	-	-	2/8/28/28	0/5/5/5
2	8OU	B	701	-	-	0/8/28/28	0/5/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	8OU	NBC-NAN	-25.11	1.23	1.37
2	A	701	8OU	NBC-NAN	-25.04	1.23	1.37
2	A	701	8OU	CAW-CAH	-8.35	1.32	1.42
2	B	701	8OU	CAW-CAH	-7.77	1.33	1.42
2	A	701	8OU	CAW-CAY	-7.34	1.30	1.41
2	A	701	8OU	CAG-CAY	-5.60	1.30	1.39
2	B	701	8OU	CAG-CAY	-5.53	1.31	1.39
2	A	701	8OU	C5-CAV	-5.34	1.39	1.47
2	B	701	8OU	C5-CAV	-4.92	1.40	1.47
2	A	701	8OU	CAI-CAW	-4.79	1.32	1.40
2	B	701	8OU	CAW-CAY	-4.53	1.34	1.41
2	B	701	8OU	CAA-NBC	3.62	1.51	1.46
2	A	701	8OU	CAS-NAQ	-3.16	1.33	1.40
2	A	701	8OU	CAI-CAS	3.07	1.44	1.39
2	A	701	8OU	CAJ-CAL	-2.98	1.44	1.52
2	B	701	8OU	CAJ-CAL	-2.93	1.44	1.52
2	A	701	8OU	CAJ-CBA	2.38	1.57	1.51
2	B	701	8OU	CAH-NAN	2.29	1.34	1.32
2	B	701	8OU	CAD-NAR	2.28	1.33	1.28
2	A	701	8OU	C6-NAQ	-2.26	1.32	1.36
2	B	701	8OU	CAY-NBC	-2.23	1.32	1.36
2	A	701	8OU	CAA-NBC	2.21	1.49	1.46
2	A	701	8OU	CAL-NBB	2.19	1.50	1.46
2	B	701	8OU	CAI-CAW	-2.12	1.37	1.40

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	8OU	CAE-CAS-CAI	-17.23	98.84	119.66
2	A	701	8OU	CAW-CAI-CAS	11.03	131.04	119.00
2	A	701	8OU	CAI-CAS-NAQ	-10.85	83.38	120.33
2	B	701	8OU	CAW-CAY-NBC	10.59	110.86	106.69
2	A	701	8OU	CAE-CAS-NAQ	10.56	156.36	120.61
2	A	701	8OU	NAQ-C6-N1	-10.05	104.25	119.08
2	A	701	8OU	N3-C2-NBB	8.15	128.72	117.12
2	A	701	8OU	CAG-CAE-CAS	7.71	129.18	120.30
2	A	701	8OU	CAW-CAH-NAN	-6.71	106.99	112.05
2	B	701	8OU	CAA-NBC-NAN	5.94	127.41	120.05
2	B	701	8OU	CAH-NAN-NBC	5.68	110.38	106.36
2	B	701	8OU	CAM-CAK-CBA	-5.58	104.92	111.14
2	A	701	8OU	CAW-CAY-NBC	5.57	108.88	106.69
2	A	701	8OU	CAM-CAK-CBA	-5.35	105.19	111.14
2	A	701	8OU	N3-C2-N1	-5.30	116.86	126.27
2	A	701	8OU	CAS-NAQ-C6	5.22	142.24	129.43
2	B	701	8OU	CAW-CAH-NAN	-4.98	108.29	112.05
2	B	701	8OU	N3-C2-N1	-4.96	117.45	126.27
2	A	701	8OU	CAH-NAN-NBC	4.80	109.76	106.36
2	A	701	8OU	CAG-CAY-CAW	-4.73	115.95	121.78
2	A	701	8OU	CAA-NBC-NAN	4.48	125.61	120.05
2	B	701	8OU	CAE-CAS-CAI	-4.47	114.25	119.66
2	A	701	8OU	C2-N3-C4	4.03	120.61	116.19
2	B	701	8OU	C2-N3-C4	3.85	120.42	116.19
2	B	701	8OU	CAG-CAE-CAS	3.68	124.53	120.30
2	B	701	8OU	CAS-NAQ-C6	-3.59	120.62	129.43
2	B	701	8OU	N3-C2-NBB	3.45	122.03	117.12
2	A	701	8OU	C6-C5-C4	-3.30	113.70	115.97
2	B	701	8OU	C5-C6-N1	-3.28	115.38	122.59
2	B	701	8OU	C6-C5-C4	3.11	118.09	115.97
2	B	701	8OU	NAQ-C6-N1	3.00	123.51	119.08
2	A	701	8OU	CAY-CAW-CAH	2.83	106.09	104.48
2	B	701	8OU	CAA-NBC-CAY	-2.60	125.15	128.36
2	B	701	8OU	CAI-CAW-CAY	2.59	122.18	119.56
2	B	701	8OU	CAG-CAY-NBC	-2.56	128.57	132.00
2	B	701	8OU	CAY-CAW-CAH	-2.53	103.04	104.48
2	B	701	8OU	N1-C2-NBB	2.39	120.52	117.12
2	A	701	8OU	CAG-CAY-NBC	2.36	135.17	132.00
2	A	701	8OU	CAI-CAW-CAH	-2.30	132.10	135.46
2	A	701	8OU	CAI-CAW-CAY	2.22	121.81	119.56

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	8OU	N1-C6-NAQ-CAS
2	A	701	8OU	C5-C6-NAQ-CAS

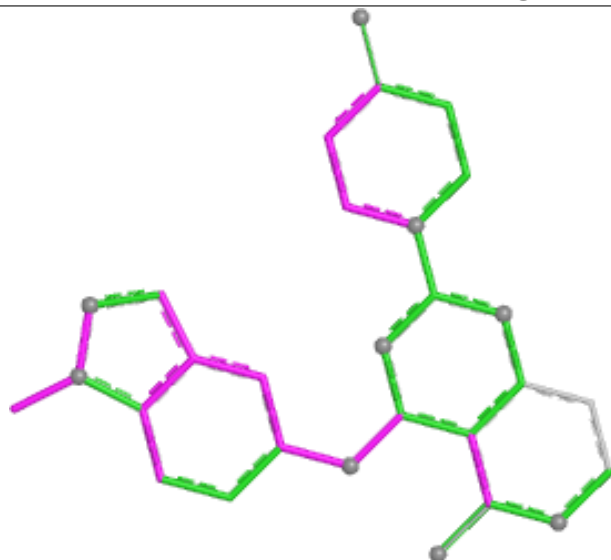
There are no ring outliers.

2 monomers are involved in 3 short contacts:

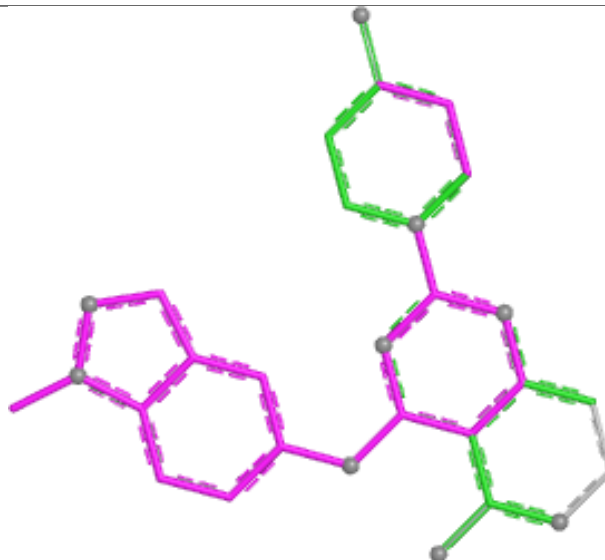
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	8OU	2	0
2	B	701	8OU	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

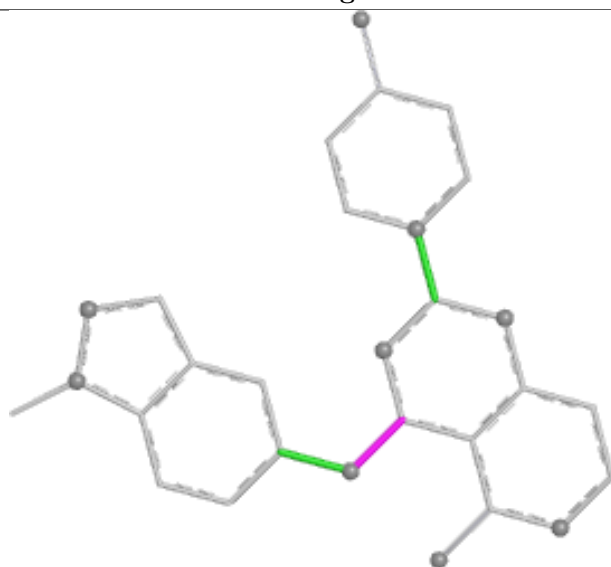
Ligand 8OU A 701



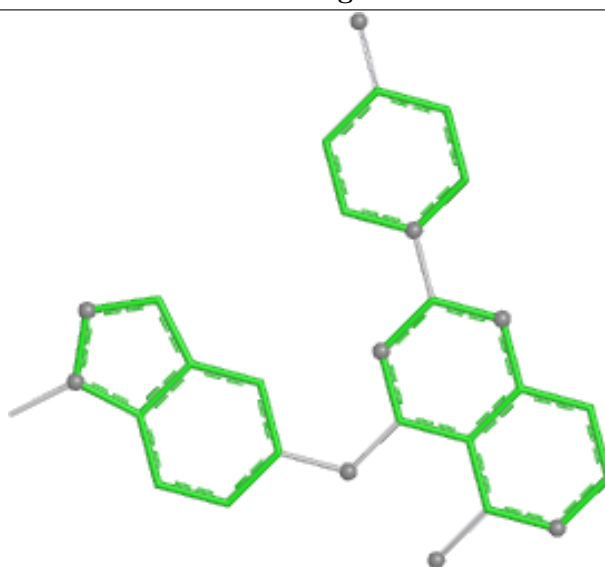
Bond lengths



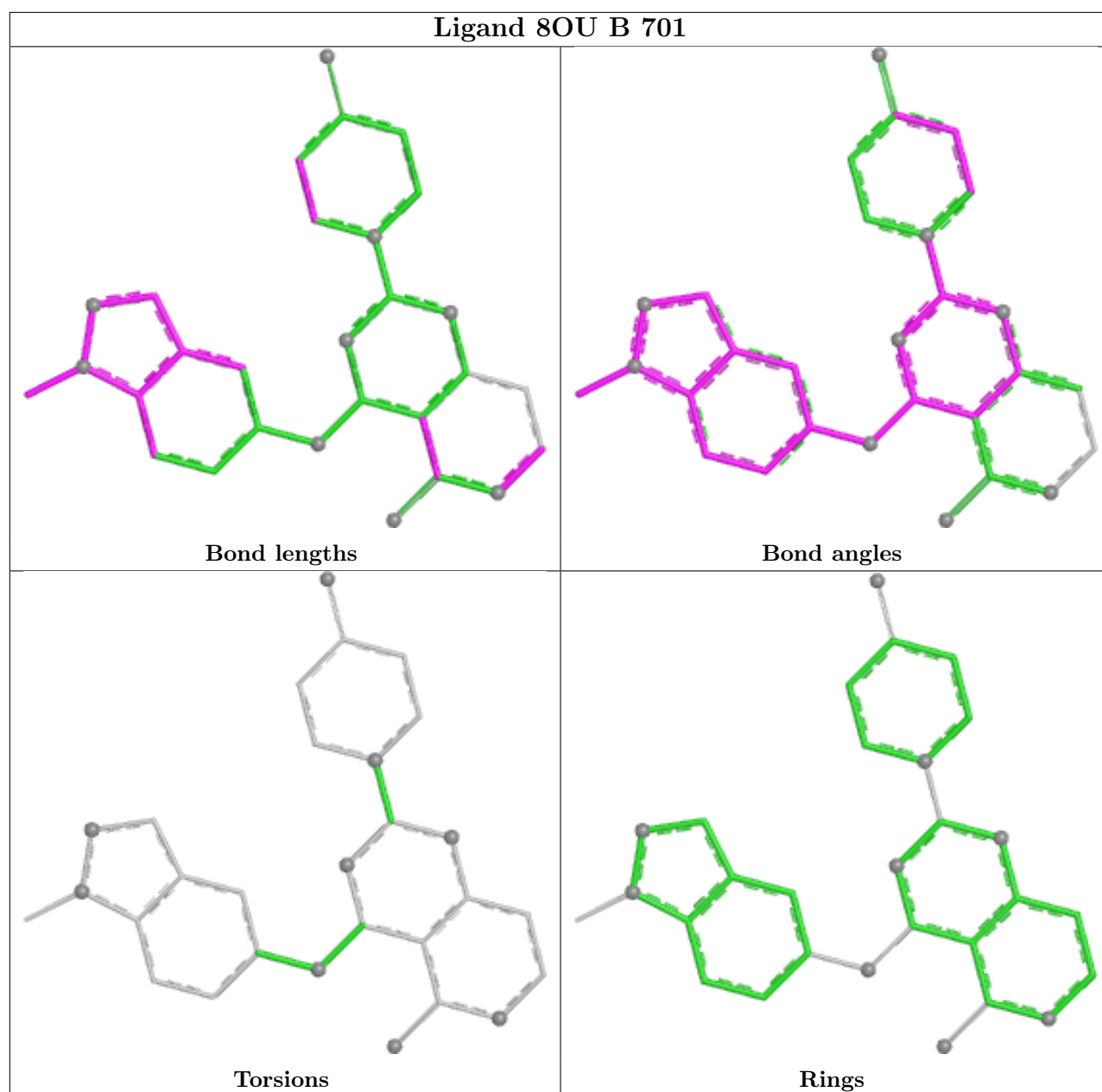
Bond angles



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 ⓘ

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	266/293 (90%)	0.77	24 (9%) 15 17	20, 34, 68, 95	0
1	B	257/293 (87%)	1.04	26 (10%) 12 14	26, 41, 65, 78	0
All	All	523/586 (89%)	0.90	50 (9%) 13 15	20, 38, 65, 95	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	634	VAL	6.9
1	A	404	LEU	5.2
1	A	411	PRO	4.5
1	A	441	ALA	3.9
1	B	363	VAL	3.8
1	A	364	TYR	3.6
1	B	594	PRO	3.3
1	B	404	LEU	3.3
1	B	595	ALA	3.2
1	B	395	VAL	3.1
1	A	413	LEU	3.1
1	A	412	ALA	3.1
1	B	391	GLN	3.1
1	B	467	LYS	3.1
1	B	411	PRO	3.0
1	B	629	TYR	2.9
1	B	383	GLY	2.8
1	B	528	ALA	2.8
1	A	393	LYS	2.8
1	A	382	PHE	2.7
1	A	531	HIS	2.7
1	B	466	VAL	2.7
1	B	472	ILE	2.7
1	B	570	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	394	LYS	2.6
1	A	389	TYR	2.6
1	B	416	GLU	2.6
1	B	593	CYS	2.5
1	B	625	ARG	2.5
1	A	395	VAL	2.5
1	A	442	GLU	2.5
1	A	444	TRP	2.4
1	A	439	CYS	2.4
1	A	416	GLU	2.4
1	A	440	GLU	2.3
1	A	372	LEU	2.3
1	B	406	ASN	2.3
1	B	382	PHE	2.3
1	A	370	LEU	2.3
1	B	475	VAL	2.3
1	A	371	THR	2.3
1	A	375	LYS	2.3
1	A	446	LEU	2.3
1	B	535	PRO	2.2
1	B	461	GLN	2.2
1	B	547	TYR	2.2
1	B	413	LEU	2.1
1	B	491	VAL	2.1
1	A	532	GLY	2.1
1	B	578	GLY	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](#)

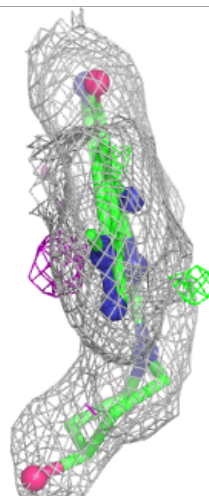
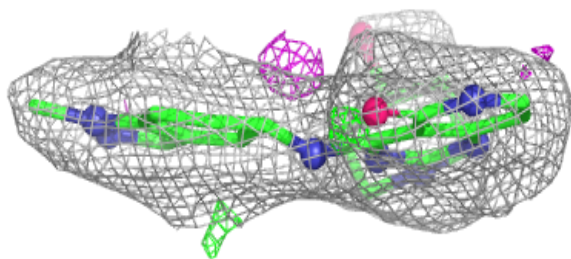
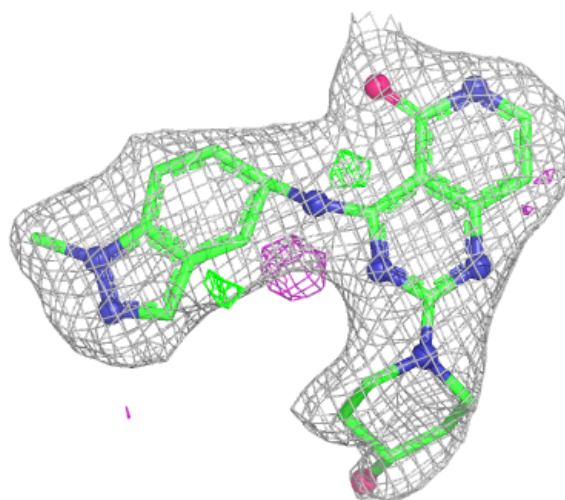
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	8OU	A	701	29/29	0.89	0.10	35,38,44,46	0
2	8OU	B	701	29/29	0.89	0.10	35,39,45,46	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.

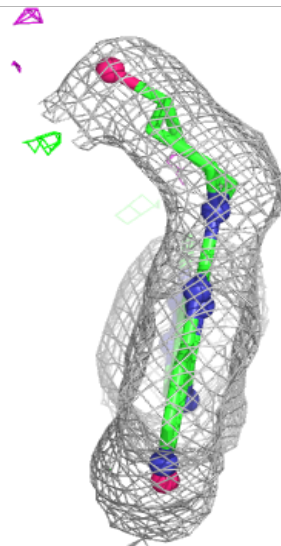
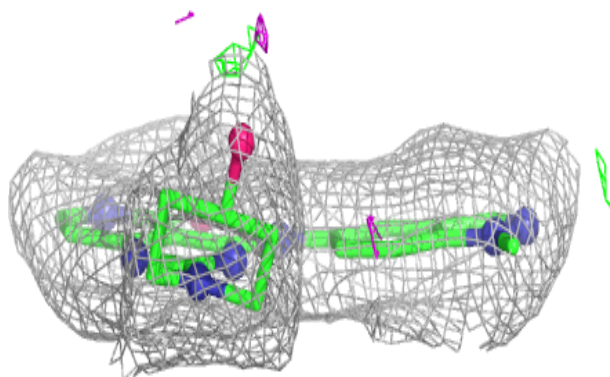
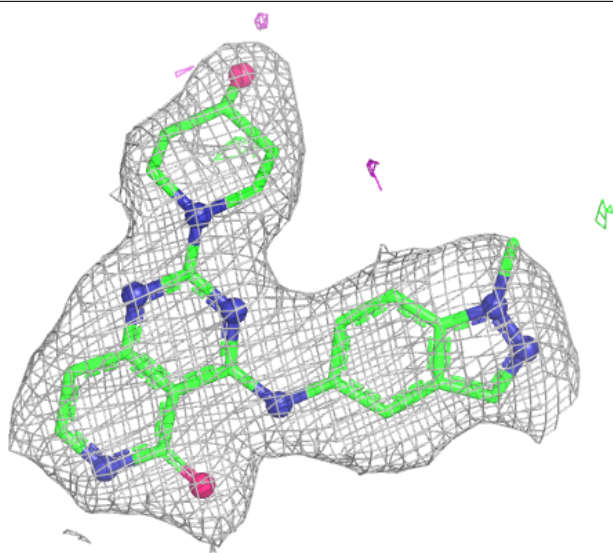
Electron density around 8OU A 701:

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 8OU B 701:

$2mF_o-DF_c$ (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.