



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:19 AM UTC

PDB ID : 9NCV / pdb_00009ncv
Title : Crystal Structure of WDR5 in complex with Triazole-Based Inhibitors
Authors : Goins, C.M.; Stauffer, S.R.
Deposited on : 2025-02-17
Resolution : 1.58 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

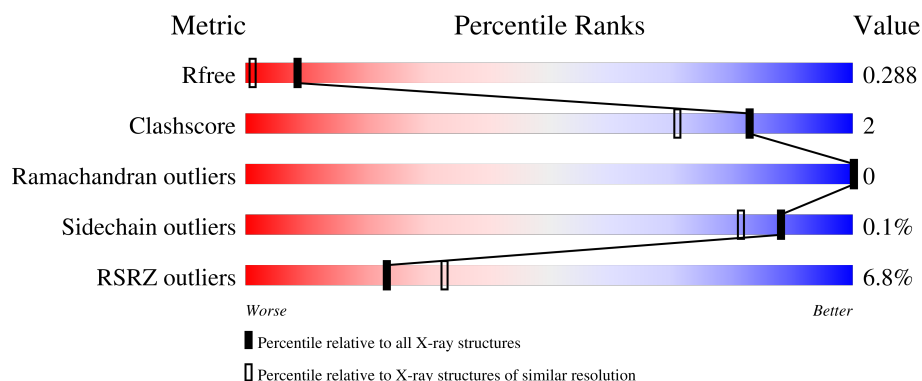
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	424	 5% 66% 30%
1	B	424	 7% 65% 5% 30%
1	C	424	 3% 65% 30%
1	D	424	 4% 65% 5% 30%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10456 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 WD repeat-containing protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	1	0
			2261	1441	374	435	11			
1	B	296	Total	C	N	O	S	0	2	0
			2268	1446	374	437	11			
1	C	296	Total	C	N	O	S	0	2	0
			2271	1449	374	437	11			
1	D	296	Total	C	N	O	S	0	2	0
			2267	1445	375	436	11			

There are 444 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-89	MET	-	initiating methionine	UNP P61964
A	-88	GLY	-	expression tag	UNP P61964
A	-87	SER	-	expression tag	UNP P61964
A	-86	SER	-	expression tag	UNP P61964
A	-85	HIS	-	expression tag	UNP P61964
A	-84	HIS	-	expression tag	UNP P61964
A	-83	HIS	-	expression tag	UNP P61964
A	-82	HIS	-	expression tag	UNP P61964
A	-81	HIS	-	expression tag	UNP P61964
A	-80	HIS	-	expression tag	UNP P61964
A	-79	GLY	-	expression tag	UNP P61964
A	-78	SER	-	expression tag	UNP P61964
A	-77	SER	-	expression tag	UNP P61964
A	-76	MET	-	expression tag	UNP P61964
A	-75	SER	-	expression tag	UNP P61964
A	-74	ASP	-	expression tag	UNP P61964
A	-73	SER	-	expression tag	UNP P61964
A	-72	GLU	-	expression tag	UNP P61964
A	-71	VAL	-	expression tag	UNP P61964
A	-70	ASN	-	expression tag	UNP P61964
A	-69	GLN	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-68	GLU	-	expression tag	UNP P61964
A	-67	ALA	-	expression tag	UNP P61964
A	-66	LYS	-	expression tag	UNP P61964
A	-65	PRO	-	expression tag	UNP P61964
A	-64	GLU	-	expression tag	UNP P61964
A	-63	VAL	-	expression tag	UNP P61964
A	-62	LYS	-	expression tag	UNP P61964
A	-61	PRO	-	expression tag	UNP P61964
A	-60	GLU	-	expression tag	UNP P61964
A	-59	VAL	-	expression tag	UNP P61964
A	-58	LYS	-	expression tag	UNP P61964
A	-57	PRO	-	expression tag	UNP P61964
A	-56	GLU	-	expression tag	UNP P61964
A	-55	THR	-	expression tag	UNP P61964
A	-54	HIS	-	expression tag	UNP P61964
A	-53	ILE	-	expression tag	UNP P61964
A	-52	ASN	-	expression tag	UNP P61964
A	-51	LEU	-	expression tag	UNP P61964
A	-50	LYS	-	expression tag	UNP P61964
A	-49	VAL	-	expression tag	UNP P61964
A	-48	SER	-	expression tag	UNP P61964
A	-47	ASP	-	expression tag	UNP P61964
A	-46	GLY	-	expression tag	UNP P61964
A	-45	SER	-	expression tag	UNP P61964
A	-44	SER	-	expression tag	UNP P61964
A	-43	GLU	-	expression tag	UNP P61964
A	-42	ILE	-	expression tag	UNP P61964
A	-41	PHE	-	expression tag	UNP P61964
A	-40	PHE	-	expression tag	UNP P61964
A	-39	LYS	-	expression tag	UNP P61964
A	-38	ILE	-	expression tag	UNP P61964
A	-37	LYS	-	expression tag	UNP P61964
A	-36	LYS	-	expression tag	UNP P61964
A	-35	THR	-	expression tag	UNP P61964
A	-34	THR	-	expression tag	UNP P61964
A	-33	PRO	-	expression tag	UNP P61964
A	-32	LEU	-	expression tag	UNP P61964
A	-31	ARG	-	expression tag	UNP P61964
A	-30	ARG	-	expression tag	UNP P61964
A	-29	LEU	-	expression tag	UNP P61964
A	-28	MET	-	expression tag	UNP P61964
A	-27	GLU	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	ALA	-	expression tag	UNP P61964
A	-25	PHE	-	expression tag	UNP P61964
A	-24	ALA	-	expression tag	UNP P61964
A	-23	LYS	-	expression tag	UNP P61964
A	-22	ARG	-	expression tag	UNP P61964
A	-21	GLN	-	expression tag	UNP P61964
A	-20	GLY	-	expression tag	UNP P61964
A	-19	LYS	-	expression tag	UNP P61964
A	-18	GLU	-	expression tag	UNP P61964
A	-17	MET	-	expression tag	UNP P61964
A	-16	ASP	-	expression tag	UNP P61964
A	-15	SER	-	expression tag	UNP P61964
A	-14	LEU	-	expression tag	UNP P61964
A	-13	ARG	-	expression tag	UNP P61964
A	-12	PHE	-	expression tag	UNP P61964
A	-11	LEU	-	expression tag	UNP P61964
A	-10	TYR	-	expression tag	UNP P61964
A	-9	ASP	-	expression tag	UNP P61964
A	-8	GLY	-	expression tag	UNP P61964
A	-7	ILE	-	expression tag	UNP P61964
A	-6	ARG	-	expression tag	UNP P61964
A	-5	ILE	-	expression tag	UNP P61964
A	-4	GLN	-	expression tag	UNP P61964
A	-3	ALA	-	expression tag	UNP P61964
A	-2	ASP	-	expression tag	UNP P61964
A	-1	GLN	-	expression tag	UNP P61964
A	0	THR	-	expression tag	UNP P61964
A	1	PRO	-	expression tag	UNP P61964
A	2	GLU	-	expression tag	UNP P61964
A	3	ASP	-	expression tag	UNP P61964
A	4	LEU	-	expression tag	UNP P61964
A	5	ASP	-	expression tag	UNP P61964
A	6	MET	-	expression tag	UNP P61964
A	7	GLU	-	expression tag	UNP P61964
A	8	ASP	-	expression tag	UNP P61964
A	9	ASN	-	expression tag	UNP P61964
A	10	ASP	-	expression tag	UNP P61964
A	11	ILE	-	expression tag	UNP P61964
A	12	ILE	-	expression tag	UNP P61964
A	13	GLU	-	expression tag	UNP P61964
A	14	ALA	-	expression tag	UNP P61964
A	15	HIS	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ARG	-	expression tag	UNP P61964
A	17	GLU	-	expression tag	UNP P61964
A	18	GLN	-	expression tag	UNP P61964
A	19	ILE	-	expression tag	UNP P61964
A	20	GLY	-	expression tag	UNP P61964
A	21	GLY	-	expression tag	UNP P61964
B	-89	MET	-	initiating methionine	UNP P61964
B	-88	GLY	-	expression tag	UNP P61964
B	-87	SER	-	expression tag	UNP P61964
B	-86	SER	-	expression tag	UNP P61964
B	-85	HIS	-	expression tag	UNP P61964
B	-84	HIS	-	expression tag	UNP P61964
B	-83	HIS	-	expression tag	UNP P61964
B	-82	HIS	-	expression tag	UNP P61964
B	-81	HIS	-	expression tag	UNP P61964
B	-80	HIS	-	expression tag	UNP P61964
B	-79	GLY	-	expression tag	UNP P61964
B	-78	SER	-	expression tag	UNP P61964
B	-77	SER	-	expression tag	UNP P61964
B	-76	MET	-	expression tag	UNP P61964
B	-75	SER	-	expression tag	UNP P61964
B	-74	ASP	-	expression tag	UNP P61964
B	-73	SER	-	expression tag	UNP P61964
B	-72	GLU	-	expression tag	UNP P61964
B	-71	VAL	-	expression tag	UNP P61964
B	-70	ASN	-	expression tag	UNP P61964
B	-69	GLN	-	expression tag	UNP P61964
B	-68	GLU	-	expression tag	UNP P61964
B	-67	ALA	-	expression tag	UNP P61964
B	-66	LYS	-	expression tag	UNP P61964
B	-65	PRO	-	expression tag	UNP P61964
B	-64	GLU	-	expression tag	UNP P61964
B	-63	VAL	-	expression tag	UNP P61964
B	-62	LYS	-	expression tag	UNP P61964
B	-61	PRO	-	expression tag	UNP P61964
B	-60	GLU	-	expression tag	UNP P61964
B	-59	VAL	-	expression tag	UNP P61964
B	-58	LYS	-	expression tag	UNP P61964
B	-57	PRO	-	expression tag	UNP P61964
B	-56	GLU	-	expression tag	UNP P61964
B	-55	THR	-	expression tag	UNP P61964
B	-54	HIS	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-53	ILE	-	expression tag	UNP P61964
B	-52	ASN	-	expression tag	UNP P61964
B	-51	LEU	-	expression tag	UNP P61964
B	-50	LYS	-	expression tag	UNP P61964
B	-49	VAL	-	expression tag	UNP P61964
B	-48	SER	-	expression tag	UNP P61964
B	-47	ASP	-	expression tag	UNP P61964
B	-46	GLY	-	expression tag	UNP P61964
B	-45	SER	-	expression tag	UNP P61964
B	-44	SER	-	expression tag	UNP P61964
B	-43	GLU	-	expression tag	UNP P61964
B	-42	ILE	-	expression tag	UNP P61964
B	-41	PHE	-	expression tag	UNP P61964
B	-40	PHE	-	expression tag	UNP P61964
B	-39	LYS	-	expression tag	UNP P61964
B	-38	ILE	-	expression tag	UNP P61964
B	-37	LYS	-	expression tag	UNP P61964
B	-36	LYS	-	expression tag	UNP P61964
B	-35	THR	-	expression tag	UNP P61964
B	-34	THR	-	expression tag	UNP P61964
B	-33	PRO	-	expression tag	UNP P61964
B	-32	LEU	-	expression tag	UNP P61964
B	-31	ARG	-	expression tag	UNP P61964
B	-30	ARG	-	expression tag	UNP P61964
B	-29	LEU	-	expression tag	UNP P61964
B	-28	MET	-	expression tag	UNP P61964
B	-27	GLU	-	expression tag	UNP P61964
B	-26	ALA	-	expression tag	UNP P61964
B	-25	PHE	-	expression tag	UNP P61964
B	-24	ALA	-	expression tag	UNP P61964
B	-23	LYS	-	expression tag	UNP P61964
B	-22	ARG	-	expression tag	UNP P61964
B	-21	GLN	-	expression tag	UNP P61964
B	-20	GLY	-	expression tag	UNP P61964
B	-19	LYS	-	expression tag	UNP P61964
B	-18	GLU	-	expression tag	UNP P61964
B	-17	MET	-	expression tag	UNP P61964
B	-16	ASP	-	expression tag	UNP P61964
B	-15	SER	-	expression tag	UNP P61964
B	-14	LEU	-	expression tag	UNP P61964
B	-13	ARG	-	expression tag	UNP P61964
B	-12	PHE	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	LEU	-	expression tag	UNP P61964
B	-10	TYR	-	expression tag	UNP P61964
B	-9	ASP	-	expression tag	UNP P61964
B	-8	GLY	-	expression tag	UNP P61964
B	-7	ILE	-	expression tag	UNP P61964
B	-6	ARG	-	expression tag	UNP P61964
B	-5	ILE	-	expression tag	UNP P61964
B	-4	GLN	-	expression tag	UNP P61964
B	-3	ALA	-	expression tag	UNP P61964
B	-2	ASP	-	expression tag	UNP P61964
B	-1	GLN	-	expression tag	UNP P61964
B	0	THR	-	expression tag	UNP P61964
B	1	PRO	-	expression tag	UNP P61964
B	2	GLU	-	expression tag	UNP P61964
B	3	ASP	-	expression tag	UNP P61964
B	4	LEU	-	expression tag	UNP P61964
B	5	ASP	-	expression tag	UNP P61964
B	6	MET	-	expression tag	UNP P61964
B	7	GLU	-	expression tag	UNP P61964
B	8	ASP	-	expression tag	UNP P61964
B	9	ASN	-	expression tag	UNP P61964
B	10	ASP	-	expression tag	UNP P61964
B	11	ILE	-	expression tag	UNP P61964
B	12	ILE	-	expression tag	UNP P61964
B	13	GLU	-	expression tag	UNP P61964
B	14	ALA	-	expression tag	UNP P61964
B	15	HIS	-	expression tag	UNP P61964
B	16	ARG	-	expression tag	UNP P61964
B	17	GLU	-	expression tag	UNP P61964
B	18	GLN	-	expression tag	UNP P61964
B	19	ILE	-	expression tag	UNP P61964
B	20	GLY	-	expression tag	UNP P61964
B	21	GLY	-	expression tag	UNP P61964
C	-89	MET	-	initiating methionine	UNP P61964
C	-88	GLY	-	expression tag	UNP P61964
C	-87	SER	-	expression tag	UNP P61964
C	-86	SER	-	expression tag	UNP P61964
C	-85	HIS	-	expression tag	UNP P61964
C	-84	HIS	-	expression tag	UNP P61964
C	-83	HIS	-	expression tag	UNP P61964
C	-82	HIS	-	expression tag	UNP P61964
C	-81	HIS	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-80	HIS	-	expression tag	UNP P61964
C	-79	GLY	-	expression tag	UNP P61964
C	-78	SER	-	expression tag	UNP P61964
C	-77	SER	-	expression tag	UNP P61964
C	-76	MET	-	expression tag	UNP P61964
C	-75	SER	-	expression tag	UNP P61964
C	-74	ASP	-	expression tag	UNP P61964
C	-73	SER	-	expression tag	UNP P61964
C	-72	GLU	-	expression tag	UNP P61964
C	-71	VAL	-	expression tag	UNP P61964
C	-70	ASN	-	expression tag	UNP P61964
C	-69	GLN	-	expression tag	UNP P61964
C	-68	GLU	-	expression tag	UNP P61964
C	-67	ALA	-	expression tag	UNP P61964
C	-66	LYS	-	expression tag	UNP P61964
C	-65	PRO	-	expression tag	UNP P61964
C	-64	GLU	-	expression tag	UNP P61964
C	-63	VAL	-	expression tag	UNP P61964
C	-62	LYS	-	expression tag	UNP P61964
C	-61	PRO	-	expression tag	UNP P61964
C	-60	GLU	-	expression tag	UNP P61964
C	-59	VAL	-	expression tag	UNP P61964
C	-58	LYS	-	expression tag	UNP P61964
C	-57	PRO	-	expression tag	UNP P61964
C	-56	GLU	-	expression tag	UNP P61964
C	-55	THR	-	expression tag	UNP P61964
C	-54	HIS	-	expression tag	UNP P61964
C	-53	ILE	-	expression tag	UNP P61964
C	-52	ASN	-	expression tag	UNP P61964
C	-51	LEU	-	expression tag	UNP P61964
C	-50	LYS	-	expression tag	UNP P61964
C	-49	VAL	-	expression tag	UNP P61964
C	-48	SER	-	expression tag	UNP P61964
C	-47	ASP	-	expression tag	UNP P61964
C	-46	GLY	-	expression tag	UNP P61964
C	-45	SER	-	expression tag	UNP P61964
C	-44	SER	-	expression tag	UNP P61964
C	-43	GLU	-	expression tag	UNP P61964
C	-42	ILE	-	expression tag	UNP P61964
C	-41	PHE	-	expression tag	UNP P61964
C	-40	PHE	-	expression tag	UNP P61964
C	-39	LYS	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-38	ILE	-	expression tag	UNP P61964
C	-37	LYS	-	expression tag	UNP P61964
C	-36	LYS	-	expression tag	UNP P61964
C	-35	THR	-	expression tag	UNP P61964
C	-34	THR	-	expression tag	UNP P61964
C	-33	PRO	-	expression tag	UNP P61964
C	-32	LEU	-	expression tag	UNP P61964
C	-31	ARG	-	expression tag	UNP P61964
C	-30	ARG	-	expression tag	UNP P61964
C	-29	LEU	-	expression tag	UNP P61964
C	-28	MET	-	expression tag	UNP P61964
C	-27	GLU	-	expression tag	UNP P61964
C	-26	ALA	-	expression tag	UNP P61964
C	-25	PHE	-	expression tag	UNP P61964
C	-24	ALA	-	expression tag	UNP P61964
C	-23	LYS	-	expression tag	UNP P61964
C	-22	ARG	-	expression tag	UNP P61964
C	-21	GLN	-	expression tag	UNP P61964
C	-20	GLY	-	expression tag	UNP P61964
C	-19	LYS	-	expression tag	UNP P61964
C	-18	GLU	-	expression tag	UNP P61964
C	-17	MET	-	expression tag	UNP P61964
C	-16	ASP	-	expression tag	UNP P61964
C	-15	SER	-	expression tag	UNP P61964
C	-14	LEU	-	expression tag	UNP P61964
C	-13	ARG	-	expression tag	UNP P61964
C	-12	PHE	-	expression tag	UNP P61964
C	-11	LEU	-	expression tag	UNP P61964
C	-10	TYR	-	expression tag	UNP P61964
C	-9	ASP	-	expression tag	UNP P61964
C	-8	GLY	-	expression tag	UNP P61964
C	-7	ILE	-	expression tag	UNP P61964
C	-6	ARG	-	expression tag	UNP P61964
C	-5	ILE	-	expression tag	UNP P61964
C	-4	GLN	-	expression tag	UNP P61964
C	-3	ALA	-	expression tag	UNP P61964
C	-2	ASP	-	expression tag	UNP P61964
C	-1	GLN	-	expression tag	UNP P61964
C	0	THR	-	expression tag	UNP P61964
C	1	PRO	-	expression tag	UNP P61964
C	2	GLU	-	expression tag	UNP P61964
C	3	ASP	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4	LEU	-	expression tag	UNP P61964
C	5	ASP	-	expression tag	UNP P61964
C	6	MET	-	expression tag	UNP P61964
C	7	GLU	-	expression tag	UNP P61964
C	8	ASP	-	expression tag	UNP P61964
C	9	ASN	-	expression tag	UNP P61964
C	10	ASP	-	expression tag	UNP P61964
C	11	ILE	-	expression tag	UNP P61964
C	12	ILE	-	expression tag	UNP P61964
C	13	GLU	-	expression tag	UNP P61964
C	14	ALA	-	expression tag	UNP P61964
C	15	HIS	-	expression tag	UNP P61964
C	16	ARG	-	expression tag	UNP P61964
C	17	GLU	-	expression tag	UNP P61964
C	18	GLN	-	expression tag	UNP P61964
C	19	ILE	-	expression tag	UNP P61964
C	20	GLY	-	expression tag	UNP P61964
C	21	GLY	-	expression tag	UNP P61964
D	-89	MET	-	initiating methionine	UNP P61964
D	-88	GLY	-	expression tag	UNP P61964
D	-87	SER	-	expression tag	UNP P61964
D	-86	SER	-	expression tag	UNP P61964
D	-85	HIS	-	expression tag	UNP P61964
D	-84	HIS	-	expression tag	UNP P61964
D	-83	HIS	-	expression tag	UNP P61964
D	-82	HIS	-	expression tag	UNP P61964
D	-81	HIS	-	expression tag	UNP P61964
D	-80	HIS	-	expression tag	UNP P61964
D	-79	GLY	-	expression tag	UNP P61964
D	-78	SER	-	expression tag	UNP P61964
D	-77	SER	-	expression tag	UNP P61964
D	-76	MET	-	expression tag	UNP P61964
D	-75	SER	-	expression tag	UNP P61964
D	-74	ASP	-	expression tag	UNP P61964
D	-73	SER	-	expression tag	UNP P61964
D	-72	GLU	-	expression tag	UNP P61964
D	-71	VAL	-	expression tag	UNP P61964
D	-70	ASN	-	expression tag	UNP P61964
D	-69	GLN	-	expression tag	UNP P61964
D	-68	GLU	-	expression tag	UNP P61964
D	-67	ALA	-	expression tag	UNP P61964
D	-66	LYS	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-65	PRO	-	expression tag	UNP P61964
D	-64	GLU	-	expression tag	UNP P61964
D	-63	VAL	-	expression tag	UNP P61964
D	-62	LYS	-	expression tag	UNP P61964
D	-61	PRO	-	expression tag	UNP P61964
D	-60	GLU	-	expression tag	UNP P61964
D	-59	VAL	-	expression tag	UNP P61964
D	-58	LYS	-	expression tag	UNP P61964
D	-57	PRO	-	expression tag	UNP P61964
D	-56	GLU	-	expression tag	UNP P61964
D	-55	THR	-	expression tag	UNP P61964
D	-54	HIS	-	expression tag	UNP P61964
D	-53	ILE	-	expression tag	UNP P61964
D	-52	ASN	-	expression tag	UNP P61964
D	-51	LEU	-	expression tag	UNP P61964
D	-50	LYS	-	expression tag	UNP P61964
D	-49	VAL	-	expression tag	UNP P61964
D	-48	SER	-	expression tag	UNP P61964
D	-47	ASP	-	expression tag	UNP P61964
D	-46	GLY	-	expression tag	UNP P61964
D	-45	SER	-	expression tag	UNP P61964
D	-44	SER	-	expression tag	UNP P61964
D	-43	GLU	-	expression tag	UNP P61964
D	-42	ILE	-	expression tag	UNP P61964
D	-41	PHE	-	expression tag	UNP P61964
D	-40	PHE	-	expression tag	UNP P61964
D	-39	LYS	-	expression tag	UNP P61964
D	-38	ILE	-	expression tag	UNP P61964
D	-37	LYS	-	expression tag	UNP P61964
D	-36	LYS	-	expression tag	UNP P61964
D	-35	THR	-	expression tag	UNP P61964
D	-34	THR	-	expression tag	UNP P61964
D	-33	PRO	-	expression tag	UNP P61964
D	-32	LEU	-	expression tag	UNP P61964
D	-31	ARG	-	expression tag	UNP P61964
D	-30	ARG	-	expression tag	UNP P61964
D	-29	LEU	-	expression tag	UNP P61964
D	-28	MET	-	expression tag	UNP P61964
D	-27	GLU	-	expression tag	UNP P61964
D	-26	ALA	-	expression tag	UNP P61964
D	-25	PHE	-	expression tag	UNP P61964
D	-24	ALA	-	expression tag	UNP P61964

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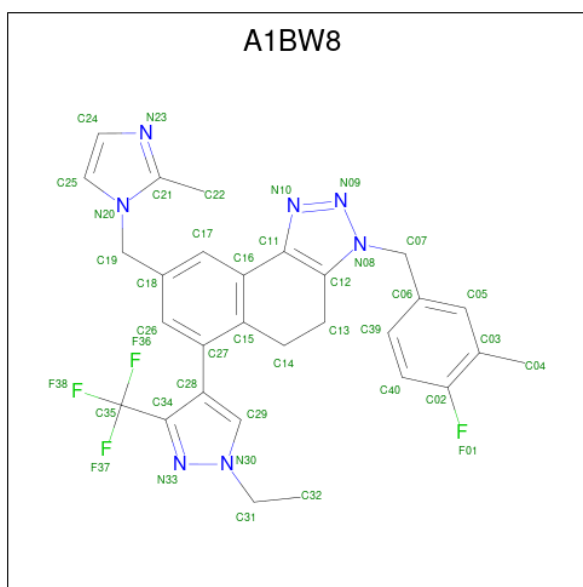
Chain	Residue	Modelled	Actual	Comment	Reference
D	-23	LYS	-	expression tag	UNP P61964
D	-22	ARG	-	expression tag	UNP P61964
D	-21	GLN	-	expression tag	UNP P61964
D	-20	GLY	-	expression tag	UNP P61964
D	-19	LYS	-	expression tag	UNP P61964
D	-18	GLU	-	expression tag	UNP P61964
D	-17	MET	-	expression tag	UNP P61964
D	-16	ASP	-	expression tag	UNP P61964
D	-15	SER	-	expression tag	UNP P61964
D	-14	LEU	-	expression tag	UNP P61964
D	-13	ARG	-	expression tag	UNP P61964
D	-12	PHE	-	expression tag	UNP P61964
D	-11	LEU	-	expression tag	UNP P61964
D	-10	TYR	-	expression tag	UNP P61964
D	-9	ASP	-	expression tag	UNP P61964
D	-8	GLY	-	expression tag	UNP P61964
D	-7	ILE	-	expression tag	UNP P61964
D	-6	ARG	-	expression tag	UNP P61964
D	-5	ILE	-	expression tag	UNP P61964
D	-4	GLN	-	expression tag	UNP P61964
D	-3	ALA	-	expression tag	UNP P61964
D	-2	ASP	-	expression tag	UNP P61964
D	-1	GLN	-	expression tag	UNP P61964
D	0	THR	-	expression tag	UNP P61964
D	1	PRO	-	expression tag	UNP P61964
D	2	GLU	-	expression tag	UNP P61964
D	3	ASP	-	expression tag	UNP P61964
D	4	LEU	-	expression tag	UNP P61964
D	5	ASP	-	expression tag	UNP P61964
D	6	MET	-	expression tag	UNP P61964
D	7	GLU	-	expression tag	UNP P61964
D	8	ASP	-	expression tag	UNP P61964
D	9	ASN	-	expression tag	UNP P61964
D	10	ASP	-	expression tag	UNP P61964
D	11	ILE	-	expression tag	UNP P61964
D	12	ILE	-	expression tag	UNP P61964
D	13	GLU	-	expression tag	UNP P61964
D	14	ALA	-	expression tag	UNP P61964
D	15	HIS	-	expression tag	UNP P61964
D	16	ARG	-	expression tag	UNP P61964
D	17	GLU	-	expression tag	UNP P61964
D	18	GLN	-	expression tag	UNP P61964

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Chain	Residue	Modelled	Actual	Comment	Reference
D	19	ILE	-	expression tag	UNP P61964
D	20	GLY	-	expression tag	UNP P61964
D	21	GLY	-	expression tag	UNP P61964

- Molecule 2 is (6P)-6-[1-ethyl-3-(trifluoromethyl)-1H-pyrazol-4-yl]-3-[(4-fluoro-3-methylphenyl)methyl]-8-[(2-methyl-1H-imidazol-1-yl)methyl]-4,5-dihydro-3H-naphtho[1,2-d][1,2,3]triazole (CCD ID: A1BW8) (formula: C₂₉H₂₇F₄N₇) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	F	N	0	0
			40	29	4	7		
2	B	1	Total	C	F	N	0	0
			40	29	4	7		
2	C	1	Total	C	F	N	0	0
			40	29	4	7		
2	D	1	Total	C	F	N	0	0
			40	29	4	7		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	304	Total	O	0	0
			304	304		
3	B	307	Total	O	0	0
			307	307		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	303	Total 303	O 303	0	0
3	D	315	Total 315	O 315	0	0

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.

- Chain A:
-
- 5%
- 66%
- 30%
- Met Gly Ser His His His His His Gly Ser Met Met Asp Ser Glu Val Asn Gln Glu Lys Pro Glu Val Lys Pro Glu Val Lys Thr His Ile Asn Leu Lys Val Ser Asp Gly Ser Ser Ser Ser Ile Phe Phe Lys Ile Lys Lys Thr Thr Pro Leu Arg
- Leu Met Glu Ala Phe Ala Lys Gln Gly Lys Glu Met Asp Ser Leu Arg Phe Leu Tyr Asp Gly Ile Arg Ile Gln Ala Asp Thr Pro Glu Asp Leu Asp Met Glu Ile Ile Glu Ala His Arg Glu Ile Ser Ala Thr Gln Val P33 T40 L41 W59 S63 V83 S117 F149 D150 V158 Y191 L194 C195 T208 ILE ASP ASP ASP P215 P216 V217 S218 G226 K227 Y228 T233 W241 D242 Y243 S244 C248 L249 C261 I262 F263 V283 L297 C298
- V303 A308 P311 L321 E322 I327 W330 C334

- Chain B:
-
- | Category | Percentage |
|-----------|------------|
| Green | 7% |
| Yellow | 65% |
| Grey | 5% |
| Dark Grey | 30% |

- Chain C:**
-
- 3% 65% 30%
- MET GLY SER SER HIS HIS HIS HIS GLY GLY SER MET MET SER ASP SER GLU VAL ASN ALA PRO VAL GLU LYS VAL LYS THR THR ILE LEU LYS VAL SER ASP GLY SER SER SER LEU PHE PHE ILE LYS LYS THR THR PRO LEU ARG

LEU	MET	GLU	ALA	ALA	ALA	LYS	ARG	GLN	GLY	LYS	GLU	MET	ASP	SER	SER	LEU	ARG	PHE	V103	LEU	TYR	ASP	GLN	ILE	ARG	ILE	GLN	ASP	GLN	THR	PRO	GLU	ASP	LEU	ASP	MET	GLU	ASP	ASN	ASN	ASN	ILE	ILE	GLU	ALA	HIS	ARG	GLU	GLN	ILE	GLY	GLY	SER	THR	GLN	SER	LYS	PRO	THR	PRO
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VAL	LYS	P33	L41	F63	K67	L68	I69	I83	V93	L102	V103	S104	L111	F149	Y191	L194	C195	R196	I197	T208	LEU	ILE	ASP	ASP	ASP	ASP	ASN	P215	P216	V217	S218	K227	Y228	I229	D242	Y243	S244	K245	G246	L249	C261	T269	E322
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I327	C334
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● Molecule 1: WD repeat-containing protein 5



MET	GLY	SER	SER	HIS	HIS	HIS	HIS	HIS	GLN	GLY	SER	SER	MET	MET	SER	ASP	SER	GLU	VAL	ASN	GLN	GLY	PRO	LYS	GLU	VAL	LYS	PRO	GLU	ASP	PRO	GLU	THR	THR	HIS	ILE	ASN	LEU	LYS	VAL	SER	ILE	PHE	PHE	LYS	ILE	LYS	LYS	THR	THR	PRO	LEU	ARG	ARG
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LEU	MET	GLU	ALA	ALA	ALA	LYS	ARG	GLN	GLY	LYS	GLU	MET	ASP	ASP	LEU	ARG	PHE	V103	LEU	TYR	ASP	GLN	ILE	ARG	ILE	GLN	ALA	ASP	GLN	THR	PRO	GLU	ASP	LEU	ILE	ASP	MET	GLU	ASP	ASN	ASN	ASN	ILE	ILE	GLU	ALA	HIS	ARG	GLU	GLN	ILE	GLY	GLY	SER	THR	ALA	GLN	SER	LYS	PRO	THR	PRO
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VAL	LYS	P33	F39	T40	L41	D76	S84	V118	K120	S148	F149	D150	E151	W156	D172	Y191	L194	C195	A201	T208	LEU	ILE	ASP	ASP	ASP	ASN	P215	P216	V217	N225	G226	K227	Y243	S244	K245	G246	C261	V283	E292	L297
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T312	I315	E322	K325	T326	I327	K331	C334
------	------	------	------	------	------	------	------

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	46.77Å 68.83Å 94.38Å 89.40° 76.65° 89.97°	Depositor
Resolution (Å)	45.50 – 1.58 45.50 – 1.58	Depositor EDS
% Data completeness (in resolution range)	95.3 (45.50-1.58) 95.6 (45.50-1.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 1.58Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.253 , 0.287 0.254 , 0.288	Depositor DCC
R_{free} test set	7621 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	13.6	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for h,-k,h-l 0.010 for -h,k,-l 0.000 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10456	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 82.91 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.4772e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: A1BW8

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	0.25	0/2318	0.51	0/3149
1	B	0.25	0/2329	0.51	0/3165
1	C	0.25	0/2332	0.50	0/3168
1	D	0.24	0/2327	0.50	0/3160
All	All	0.25	0/9306	0.50	0/12642

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	2261	0	2193	8	0
1	B	2268	0	2199	12	0
1	C	2271	0	2205	10	0
1	D	2267	0	2207	14	0
2	A	40	0	0	0	0
2	B	40	0	0	1	0
2	C	40	0	0	0	0
2	D	40	0	0	0	0
3	A	304	0	0	1	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	307	0	0	2	0
3	C	303	0	0	1	0
3	D	315	0	0	4	0
All	All	10456	0	8804	44	1

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 2.

All (44) 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:D:225:ASN:O	3:D:501:HOH:O	1.78	1.00
1:A:195[B]:CYS:SG	1:A:217:VAL:HG11	2.38	0.64
1:D:120:LYS:NZ	3:D:503:HOH:O	2.30	0.63
1:C:195[B]:CYS:SG	1:C:217:VAL:HG11	2.39	0.62
1:B:65:ALA:HA	2:B:401:A1BW8:C32	2.34	0.58
1:B:283:VAL:HB	1:B:297:LEU:HB2	1.87	0.57
1:C:229:ILE:HD12	1:C:243:TYR:HB3	1.86	0.57
1:A:322:GLU:OE1	3:A:501:HOH:O	2.17	0.56
1:B:63:SER:HB3	1:B:93:VAL:HG13	1.85	0.56
1:B:312:THR:O	3:B:501:HOH:O	2.18	0.55
1:D:283:VAL:HB	1:D:297:LEU:HB2	1.91	0.53
1:A:41:LEU:HB2	1:A:327:ILE:HB	1.93	0.51
1:A:63:SER:HB3	1:A:93:VAL:HG13	1.93	0.51
1:D:322:GLU:H	1:D:322:GLU:CD	2.20	0.50
1:C:93:VAL:HG22	1:C:102:LEU:HD22	1.93	0.49
1:D:227:LYS:HE2	3:D:501:HOH:O	2.12	0.48
1:B:159:LYS:NZ	3:B:510:HOH:O	2.47	0.47
1:C:242:ASP:HB2	1:C:249:LEU:HD11	1.96	0.46
1:D:41:LEU:HB2	1:D:327:ILE:HB	1.97	0.46
1:D:191:TYR:HA	1:D:216:PRO:HB3	1.96	0.46
1:C:69:ILE:HB	1:C:83:ILE:HB	1.97	0.46
1:B:224:PRO:HG2	1:B:268:VAL:HG11	1.97	0.46
1:D:151:GLU:HG2	1:D:172:ASP:C	2.40	0.46
1:D:39:PHE:CE2	1:D:76:ASP:HA	2.51	0.46
1:B:69:ILE:HD11	1:B:104:SER:HB3	1.99	0.44
1:D:191:TYR:HE2	1:D:261:CYS:SG	2.41	0.44
1:B:310:HIS:CG	1:B:311:PRO:HD2	2.52	0.43
1:C:67:LYS:NZ	3:C:502:HOH:O	2.41	0.43
1:A:303:VAL:HB	1:A:321:LEU:HD12	2.00	0.43
1:C:197:ILE:HD11	1:C:229:ILE:CD1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:315:ILE:HG12	1:D:331:LYS:HG2	2.00	0.43
1:A:283:VAL:HB	1:A:297:LEU:HB2	2.01	0.42
1:C:41:LEU:HB2	1:C:327:ILE:HB	2.02	0.41
1:D:148:SER:HB3	1:D:150:ASP:OD1	2.20	0.41
1:B:41:LEU:HB2	1:B:327:ILE:HB	2.02	0.41
1:C:218:SER:HB2	1:C:261:CYS:HA	2.03	0.41
1:D:195[B]:CYS:SG	1:D:217:VAL:HG11	2.60	0.41
1:D:325:LYS:NZ	3:D:502:HOH:O	2.24	0.41
1:B:198:TRP:CZ3	1:B:205:CYS:HB2	2.56	0.41
1:A:218:SER:HB2	1:A:261:CYS:HA	2.02	0.40
1:A:148:SER:HB3	1:A:150:ASP:OD1	2.22	0.40
1:B:191:TYR:HA	1:B:216:PRO:HB3	2.03	0.40
1:B:303:VAL:HB	1:B:321:LEU:HD12	2.03	0.40
1:C:104:SER:O	1:C:111:LEU:HA	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:758:HOH:O	3:A:790:HOH:O[1_455]	2.17	0.03

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	293/424 (69%)	284 (97%)	9 (3%)	0	100	100
1	B	294/424 (69%)	285 (97%)	9 (3%)	0	100	100
1	C	294/424 (69%)	286 (97%)	8 (3%)	0	100	100
1	D	294/424 (69%)	285 (97%)	9 (3%)	0	100	100
All	All	1175/1696 (69%)	1140 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	249/373 (67%)	249 (100%)	0	100	100
1	B	251/373 (67%)	251 (100%)	0	100	100
1	C	251/373 (67%)	250 (100%)	1 (0%)	84	75
1	D	251/373 (67%)	251 (100%)	0	100	100
All	All	1002/1492 (67%)	1001 (100%)	1 (0%)	88	81

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	227	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	289	GLN
1	B	298	GLN
1	C	257	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](#)

4 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	A1BW8	B	401	-	45,45,45	1.69	10 (22%)	60,68,68	3.31	21 (35%)
2	A1BW8	D	401	-	45,45,45	1.66	9 (20%)	60,68,68	2.71	18 (30%)
2	A1BW8	A	401	-	45,45,45	1.65	9 (20%)	60,68,68	2.51	18 (30%)
2	A1BW8	C	401	-	45,45,45	1.67	9 (20%)	60,68,68	2.60	21 (35%)

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	A1BW8	B	401	-	-	2/20/29/29	0/6/6/6
2	A1BW8	D	401	-	-	4/20/29/29	0/6/6/6
2	A1BW8	A	401	-	-	5/20/29/29	0/6/6/6
2	A1BW8	C	401	-	-	6/20/29/29	0/6/6/6

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	A1BW8	C13-C12	4.37	1.56	1.49
2	A	401	A1BW8	C13-C12	4.34	1.56	1.49
2	B	401	A1BW8	C13-C12	4.34	1.56	1.49
2	B	401	A1BW8	C16-C15	-4.24	1.32	1.40
2	C	401	A1BW8	C13-C12	4.22	1.56	1.49
2	C	401	A1BW8	C16-C15	-4.03	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	A1BW8	C16-C15	-3.96	1.33	1.40
2	D	401	A1BW8	C27-C28	3.91	1.53	1.49
2	C	401	A1BW8	C27-C28	3.87	1.53	1.49
2	D	401	A1BW8	C16-C15	-3.80	1.33	1.40
2	A	401	A1BW8	C27-C28	3.68	1.53	1.49
2	B	401	A1BW8	N10-N09	3.56	1.37	1.32
2	C	401	A1BW8	N10-N09	3.28	1.37	1.32
2	A	401	A1BW8	N10-N09	3.20	1.37	1.32
2	D	401	A1BW8	N10-N09	3.14	1.37	1.32
2	A	401	A1BW8	C25-N20	-2.95	1.31	1.38
2	C	401	A1BW8	C25-N20	-2.92	1.31	1.38
2	D	401	A1BW8	C25-N20	-2.89	1.31	1.38
2	B	401	A1BW8	C25-N20	-2.88	1.31	1.38
2	C	401	A1BW8	C22-C21	2.88	1.53	1.49
2	B	401	A1BW8	C29-N30	-2.84	1.30	1.34
2	B	401	A1BW8	C17-C16	2.83	1.44	1.39
2	A	401	A1BW8	C24-N23	-2.79	1.32	1.38
2	C	401	A1BW8	C24-N23	-2.72	1.32	1.38
2	A	401	A1BW8	C22-C21	2.65	1.53	1.49
2	B	401	A1BW8	C24-N23	-2.62	1.33	1.38
2	D	401	A1BW8	C22-C21	2.58	1.53	1.49
2	C	401	A1BW8	C17-C16	2.57	1.43	1.39
2	D	401	A1BW8	C24-N23	-2.55	1.33	1.38
2	B	401	A1BW8	C22-C21	2.37	1.52	1.49
2	A	401	A1BW8	C17-C16	2.32	1.43	1.39
2	D	401	A1BW8	C16-C11	-2.24	1.41	1.46
2	C	401	A1BW8	C16-C11	-2.23	1.41	1.46
2	D	401	A1BW8	C17-C16	2.21	1.43	1.39
2	B	401	A1BW8	C16-C11	-2.14	1.41	1.46
2	B	401	A1BW8	C27-C28	2.10	1.51	1.49
2	A	401	A1BW8	C16-C11	-2.05	1.41	1.46

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	A1BW8	C11-C12-N08	9.62	108.17	104.25
2	B	401	A1BW8	C31-N30-N33	9.56	128.74	119.74
2	B	401	A1BW8	C31-N30-C29	-9.24	119.71	128.27
2	D	401	A1BW8	C11-C12-N08	9.15	107.98	104.25
2	C	401	A1BW8	C11-C12-N08	8.96	107.90	104.25
2	A	401	A1BW8	C11-C12-N08	8.80	107.83	104.25
2	B	401	A1BW8	C28-C34-N33	-8.70	107.03	112.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	A1BW8	C28-C34-N33	-8.12	107.39	112.49
2	A	401	A1BW8	C28-C34-N33	-7.66	107.68	112.49
2	B	401	A1BW8	C35-C34-N33	7.08	126.88	118.50
2	C	401	A1BW8	C28-C34-N33	-6.93	108.14	112.49
2	B	401	A1BW8	C29-C28-C34	6.84	108.58	104.07
2	D	401	A1BW8	C07-N08-C12	-6.38	125.05	129.14
2	C	401	A1BW8	C07-N08-C12	-5.94	125.33	129.14
2	D	401	A1BW8	C35-C34-N33	5.83	125.40	118.50
2	D	401	A1BW8	C07-N08-N09	5.39	126.34	119.35
2	D	401	A1BW8	C29-C28-C34	5.26	107.54	104.07
2	C	401	A1BW8	C35-C34-N33	4.99	124.41	118.50
2	C	401	A1BW8	C06-C07-N08	-4.98	105.05	112.76
2	C	401	A1BW8	C07-N08-N09	4.97	125.79	119.35
2	A	401	A1BW8	C35-C34-N33	4.95	124.36	118.50
2	D	401	A1BW8	C06-C07-N08	-4.93	105.13	112.76
2	A	401	A1BW8	C29-C28-C34	4.91	107.31	104.07
2	A	401	A1BW8	C06-C07-N08	-4.83	105.28	112.76
2	C	401	A1BW8	F38-C35-C34	-4.77	105.60	112.39
2	B	401	A1BW8	C07-N08-C12	-4.77	126.08	129.14
2	B	401	A1BW8	C06-C07-N08	-4.67	105.53	112.76
2	B	401	A1BW8	C07-N08-N09	4.63	125.34	119.35
2	B	401	A1BW8	C15-C27-C28	-4.38	117.07	122.35
2	C	401	A1BW8	C29-C28-C34	4.23	106.86	104.07
2	A	401	A1BW8	C07-N08-C12	-4.18	126.46	129.14
2	A	401	A1BW8	C07-N08-N09	4.11	124.67	119.35
2	C	401	A1BW8	C22-C21-N20	3.98	127.61	123.50
2	B	401	A1BW8	C05-C03-C02	3.96	119.73	115.88
2	B	401	A1BW8	C12-N08-N09	-3.75	108.56	111.37
2	D	401	A1BW8	C12-N08-N09	-3.73	108.57	111.37
2	A	401	A1BW8	C22-C21-N20	3.66	127.28	123.50
2	D	401	A1BW8	C05-C03-C02	3.51	119.30	115.88
2	D	401	A1BW8	F38-C35-C34	-3.49	107.42	112.39
2	A	401	A1BW8	C12-N08-N09	-3.37	108.85	111.37
2	C	401	A1BW8	C12-N08-N09	-3.34	108.86	111.37
2	C	401	A1BW8	C05-C03-C02	3.22	119.01	115.88
2	A	401	A1BW8	C05-C03-C02	3.21	119.00	115.88
2	B	401	A1BW8	C18-C19-N20	-3.17	107.93	112.84
2	A	401	A1BW8	C18-C19-N20	-3.03	108.14	112.84
2	B	401	A1BW8	C40-C02-C03	-3.02	119.68	124.46
2	D	401	A1BW8	C31-N30-N33	2.97	122.54	119.74
2	C	401	A1BW8	C25-C24-N23	-2.95	106.88	110.74
2	A	401	A1BW8	C15-C27-C28	-2.84	118.93	122.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	A1BW8	F36-C35-C34	-2.81	108.38	112.39
2	D	401	A1BW8	C24-C25-N20	2.80	109.14	106.22
2	D	401	A1BW8	C25-C24-N23	-2.73	107.16	110.74
2	A	401	A1BW8	F37-C35-C34	-2.73	108.50	112.39
2	B	401	A1BW8	C25-C24-N23	-2.71	107.19	110.74
2	D	401	A1BW8	C18-C19-N20	-2.71	108.65	112.84
2	C	401	A1BW8	C29-N30-N33	-2.70	110.25	113.56
2	C	401	A1BW8	C31-N30-N33	2.66	122.25	119.74
2	A	401	A1BW8	C29-N30-N33	-2.66	110.31	113.56
2	B	401	A1BW8	F38-C35-C34	-2.65	108.62	112.39
2	D	401	A1BW8	C29-N30-N33	-2.61	110.37	113.56
2	D	401	A1BW8	C22-C21-N20	2.59	126.17	123.50
2	A	401	A1BW8	C25-C24-N23	-2.50	107.47	110.74
2	C	401	A1BW8	C24-C25-N20	2.49	108.81	106.22
2	C	401	A1BW8	C40-C02-C03	-2.45	120.59	124.46
2	A	401	A1BW8	C40-C02-C03	-2.45	120.59	124.46
2	B	401	A1BW8	C22-C21-N20	2.43	126.01	123.50
2	D	401	A1BW8	C40-C02-C03	-2.34	120.76	124.46
2	B	401	A1BW8	C04-C03-C02	-2.26	118.98	121.94
2	B	401	A1BW8	C35-C34-C28	-2.19	126.08	129.05
2	B	401	A1BW8	C24-C25-N20	2.18	108.49	106.22
2	C	401	A1BW8	C15-C27-C28	-2.10	119.82	122.35
2	C	401	A1BW8	C24-N23-C21	2.10	108.69	105.86
2	C	401	A1BW8	C16-C11-N10	2.10	132.67	125.23
2	C	401	A1BW8	F01-C02-C03	2.05	120.69	117.66
2	B	401	A1BW8	C27-C26-C18	-2.04	118.21	121.38
2	D	401	A1BW8	C04-C03-C02	-2.03	119.28	121.94
2	C	401	A1BW8	C18-C19-N20	-2.02	109.72	112.84
2	A	401	A1BW8	C24-C25-N20	2.02	108.32	106.22

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	A1BW8	C26-C27-C28-C29
2	A	401	A1BW8	C32-C31-N30-C29
2	B	401	A1BW8	C26-C27-C28-C29
2	C	401	A1BW8	C26-C27-C28-C29
2	D	401	A1BW8	C26-C27-C28-C29
2	A	401	A1BW8	C32-C31-N30-N33
2	A	401	A1BW8	C26-C27-C28-C34
2	B	401	A1BW8	C26-C27-C28-C34

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Mol	Chain	Res	Type	Atoms
2	C	401	A1BW8	C26-C27-C28-C34
2	D	401	A1BW8	C26-C27-C28-C34
2	C	401	A1BW8	C18-C19-N20-C21
2	C	401	A1BW8	C32-C31-N30-C29
2	A	401	A1BW8	C18-C19-N20-C21
2	C	401	A1BW8	C15-C27-C28-C29
2	C	401	A1BW8	C32-C31-N30-N33
2	D	401	A1BW8	C15-C27-C28-C29
2	D	401	A1BW8	C32-C31-N30-N33

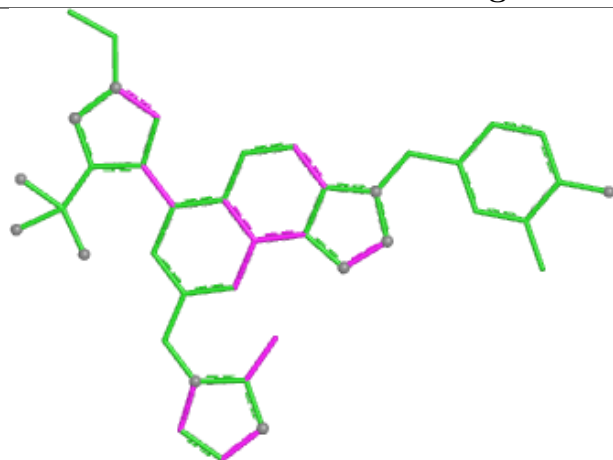
There are no ring outliers.

1 monomer is involved in 1 short contact:

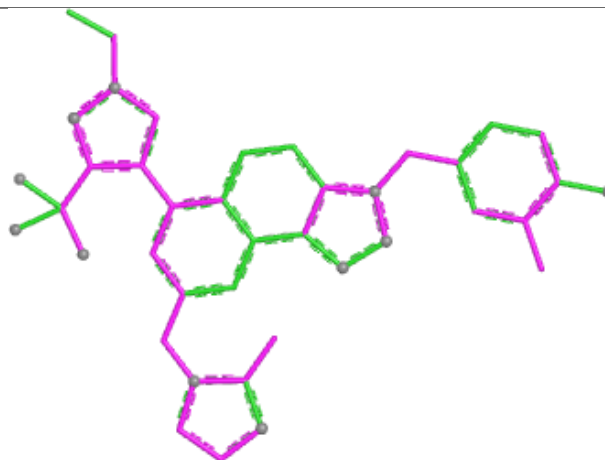
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	A1BW8	1	0

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.

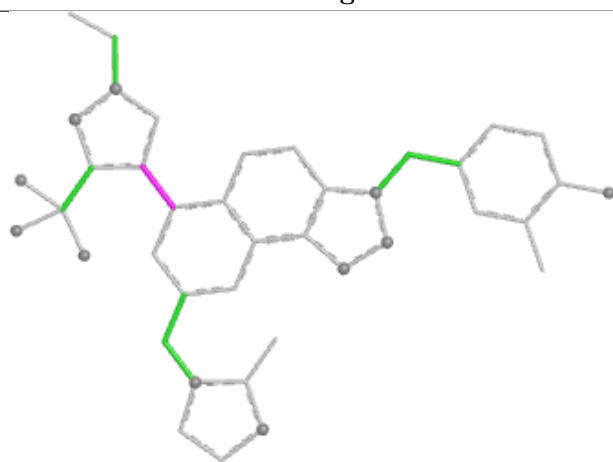
Ligand A1BW8 B 401



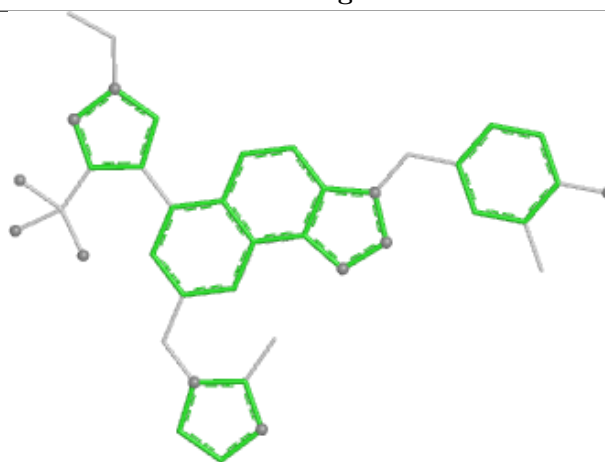
Bond lengths



Bond angles

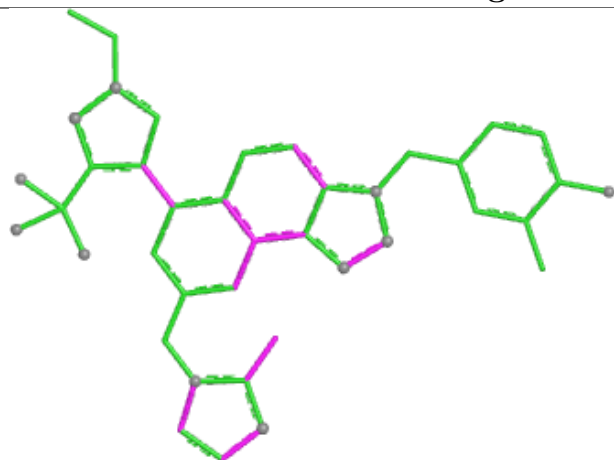


Torsions

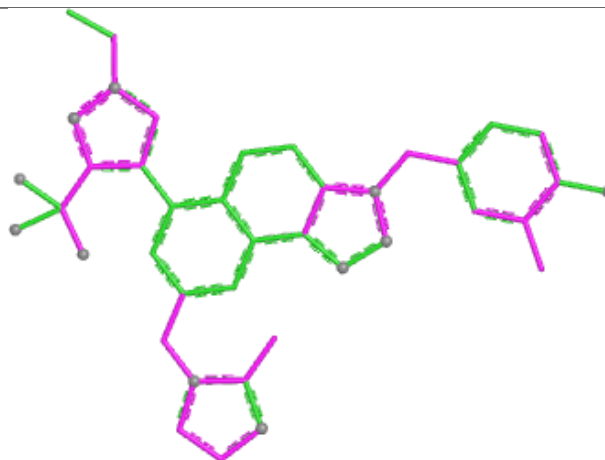


Rings

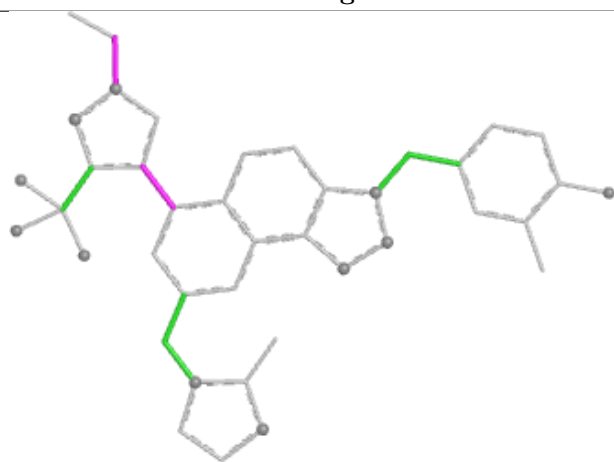
Ligand A1BW8 D 401



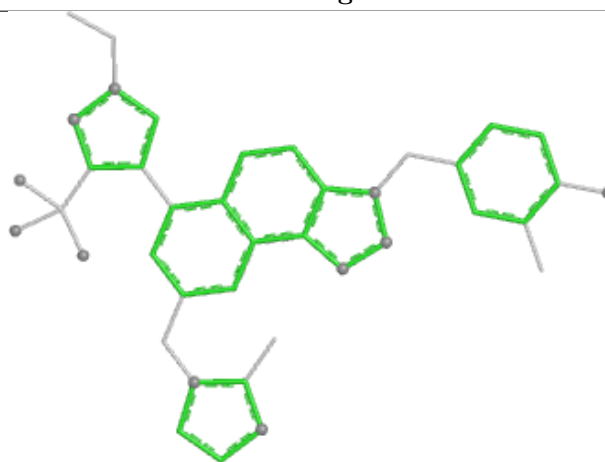
Bond lengths



Bond angles

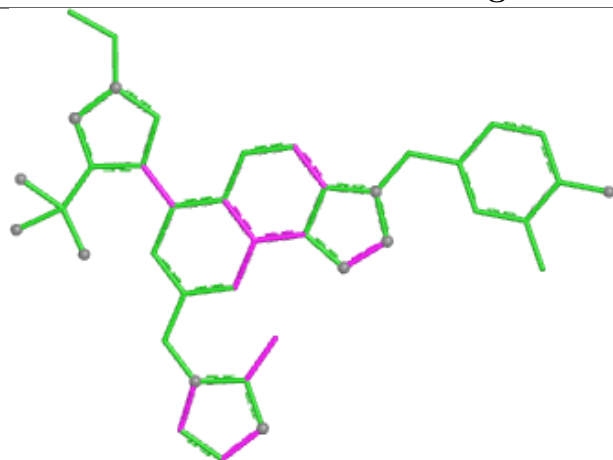


Torsions

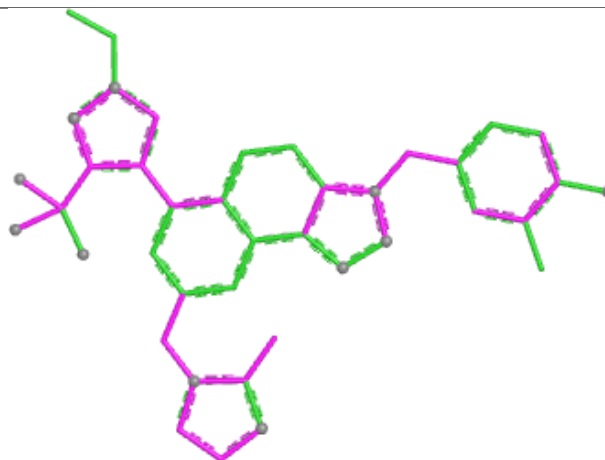


Rings

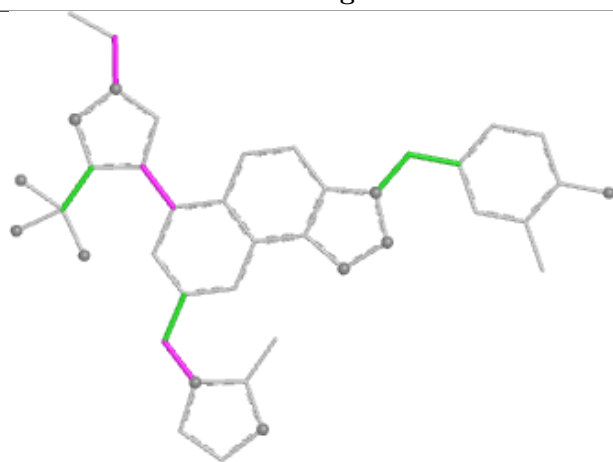
Ligand A1BW8 A 401



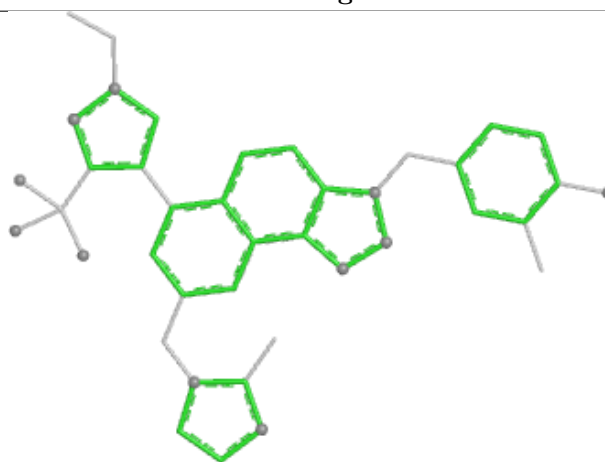
Bond lengths



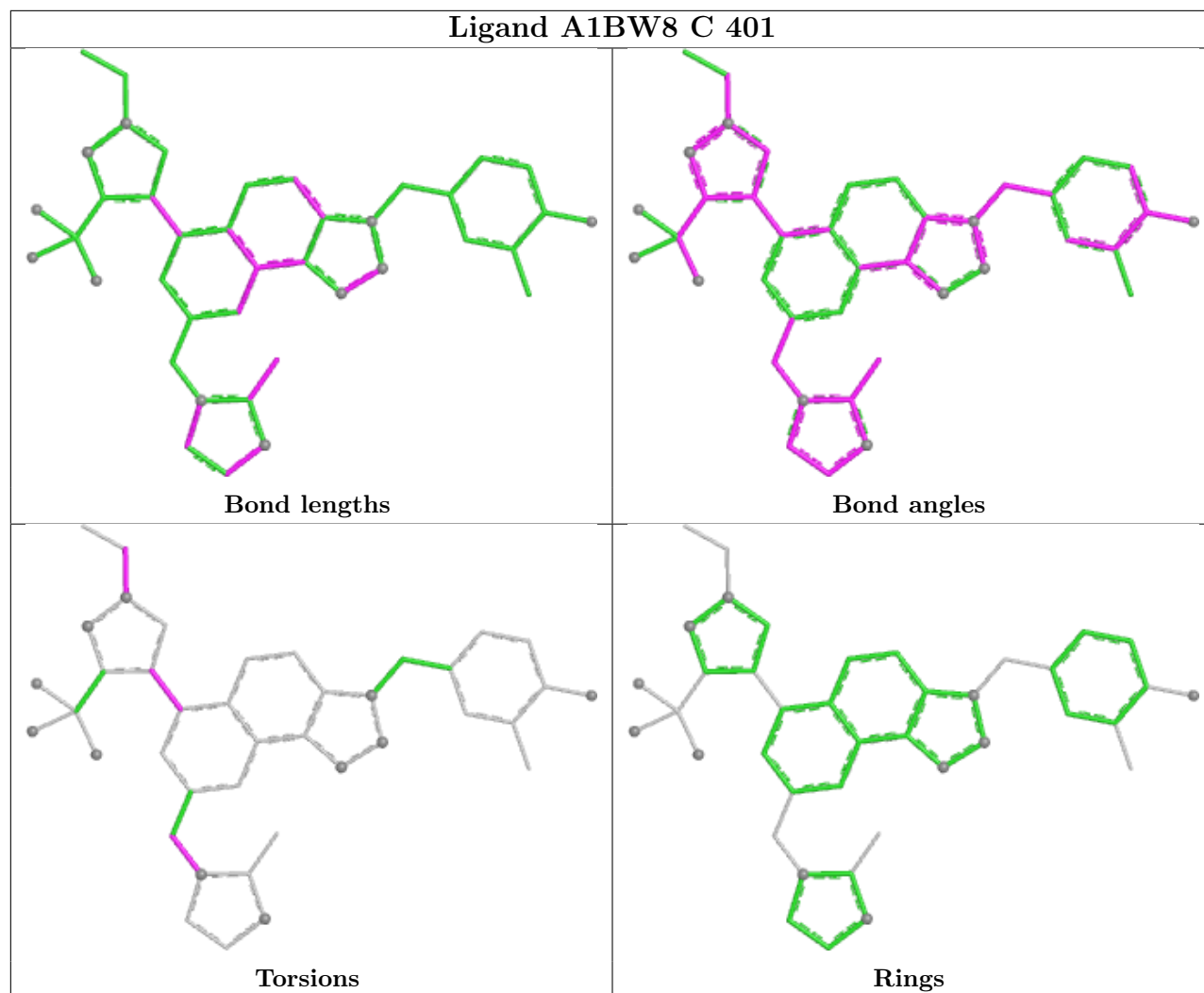
Bond angles



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	296/424 (69%)	0.80	23 (7%)	19 28	9, 14, 24, 31	1 (0%)
1	B	296/424 (69%)	0.86	29 (9%)	13 21	8, 14, 23, 38	2 (0%)
1	C	296/424 (69%)	0.72	14 (4%)	36 48	8, 14, 22, 34	2 (0%)
1	D	296/424 (69%)	0.75	15 (5%)	33 45	8, 14, 21, 32	2 (0%)
All	All	1184/1696 (69%)	0.78	81 (6%)	23 33	8, 14, 23, 38	7 (0%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	243	TYR	6.5
1	C	243	TYR	4.8
1	B	243	TYR	4.4
1	A	215	PRO	4.1
1	C	191	TYR	3.9
1	A	244	SER	3.9
1	B	228	TYR	3.8
1	A	243	TYR	3.7
1	C	215	PRO	3.6
1	B	248	CYS	3.5
1	D	191	TYR	3.5
1	C	246	GLY	3.5
1	B	244	SER	3.4
1	B	215	PRO	3.4
1	B	246	GLY	3.3
1	B	322	GLU	3.3
1	D	84	SER	3.2
1	A	308	ALA	3.1
1	A	249	LEU	3.0
1	B	207	LYS	3.0
1	B	308	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	228	TYR	2.9
1	B	220	VAL	2.9
1	C	322	GLU	2.9
1	B	249	LEU	2.9
1	D	244	SER	2.9
1	C	244	SER	2.8
1	D	208	THR	2.8
1	D	215	PRO	2.8
1	A	191	TYR	2.6
1	D	227	LYS	2.6
1	B	329	LEU	2.6
1	B	197	ILE	2.5
1	B	262	ILE	2.5
1	A	228	TYR	2.5
1	B	185	LEU	2.5
1	A	248	CYS	2.5
1	C	334	CYS	2.5
1	A	298	GLN	2.5
1	A	226	GLY	2.4
1	B	191	TYR	2.4
1	A	263	PHE	2.4
1	B	177	VAL	2.4
1	B	229	ILE	2.4
1	B	242	ASP	2.3
1	C	53	PHE	2.3
1	A	158	VAL	2.3
1	D	292	GLU	2.3
1	C	249	LEU	2.3
1	D	116	VAL	2.3
1	C	197	ILE	2.3
1	B	160	THR	2.2
1	D	201	ALA	2.2
1	C	269	THR	2.2
1	B	225	ASN	2.2
1	A	322	GLU	2.2
1	B	198	TRP	2.2
1	D	334	CYS	2.2
1	A	149	PHE	2.2
1	B	219	PHE	2.2
1	A	93	VAL	2.2
1	A	194	LEU	2.1
1	A	311	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	246	GLY	2.1
1	A	233	THR	2.1
1	B	334	CYS	2.1
1	B	224	PRO	2.1
1	A	40	THR	2.1
1	A	59	TRP	2.1
1	B	75	TYR	2.1
1	A	117	SER	2.1
1	A	330	TRP	2.1
1	B	226	GLY	2.1
1	B	265	ASN	2.1
1	B	323	ASN	2.1
1	C	149	PHE	2.0
1	D	312	THR	2.0
1	C	194	LEU	2.0
1	A	241	TRP	2.0
1	D	156	TRP	2.0
1	D	194	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](#)

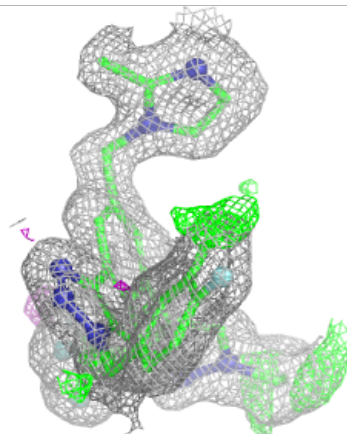
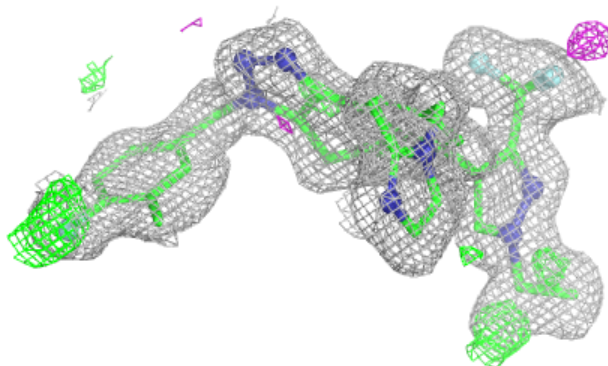
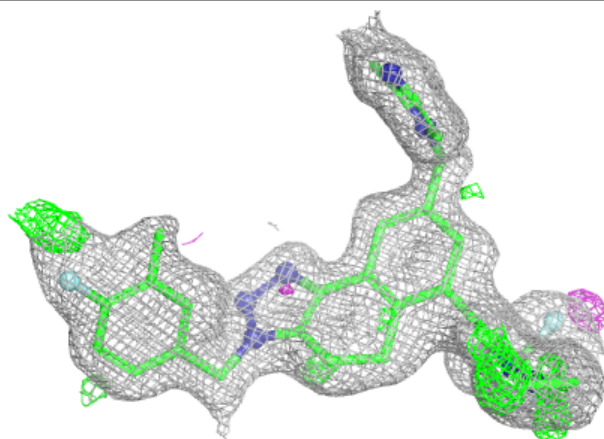
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	A1BW8	B	401	40/40	0.87	0.11	10,15,24,28	0
2	A1BW8	A	401	40/40	0.88	0.11	9,14,23,28	0
2	A1BW8	C	401	40/40	0.90	0.09	11,14,25,27	0
2	A1BW8	D	401	40/40	0.90	0.10	10,14,25,27	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.

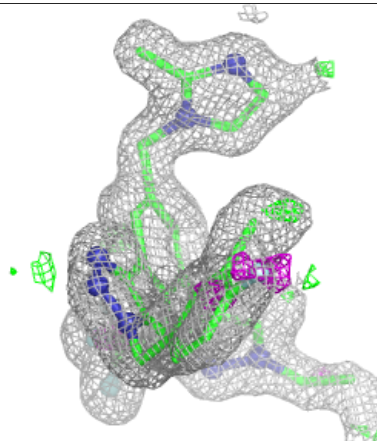
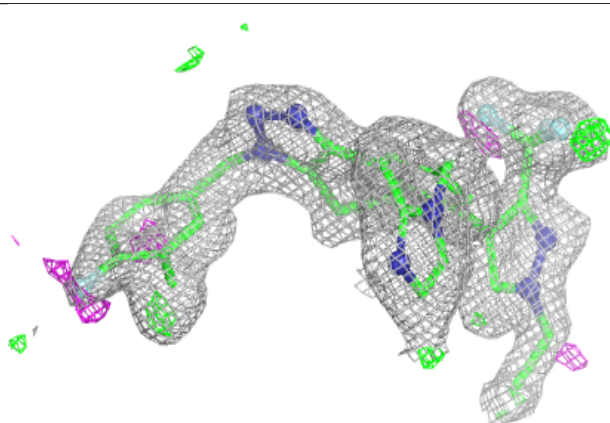
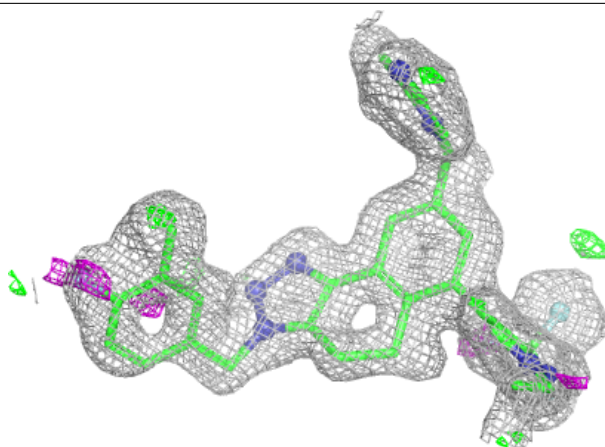
Electron density around A1BW8 B 401:

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



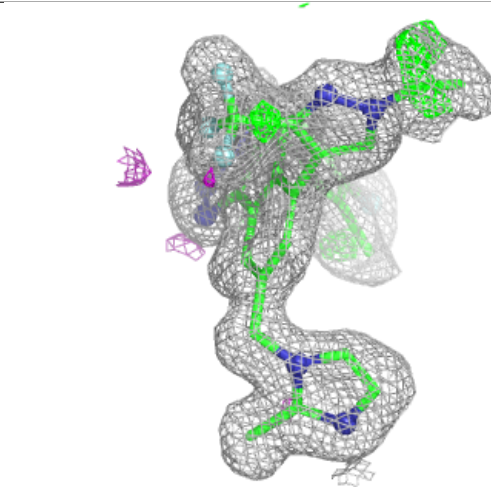
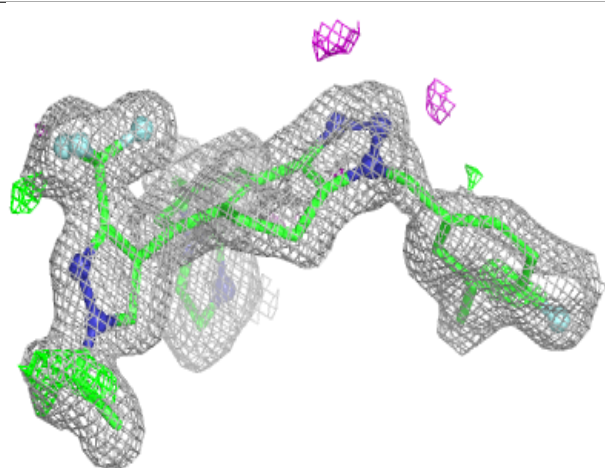
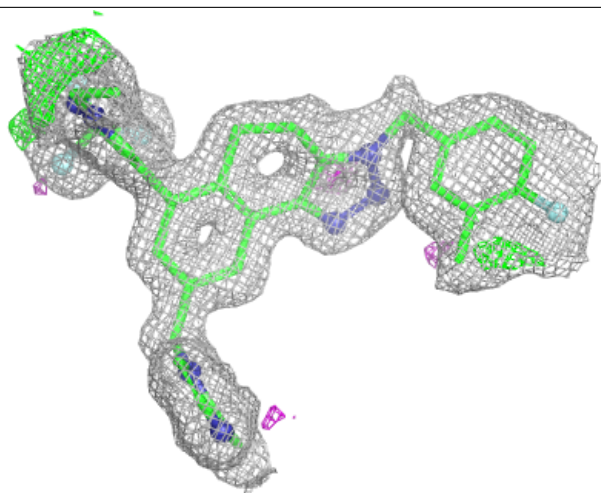
Electron density around A1BW8 A 401:

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



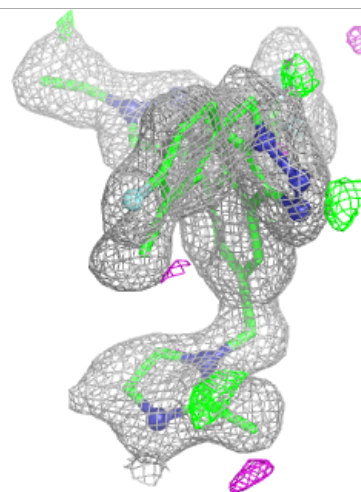
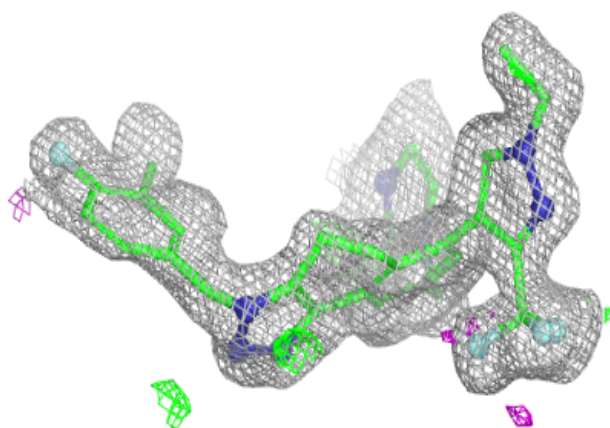
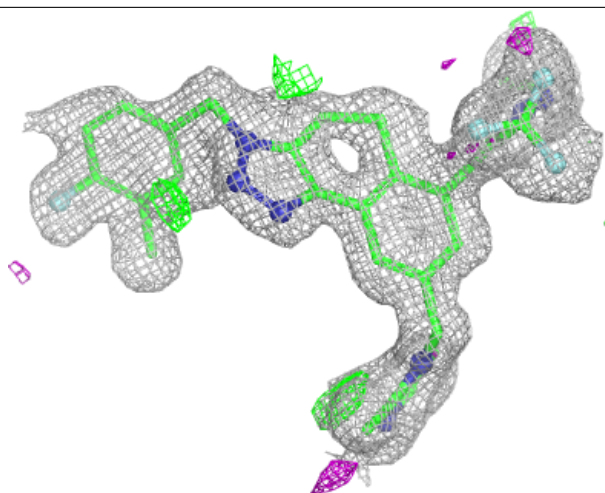
Electron density around A1BW8 C 401:

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



Electron density around A1BW8 D 401:

$2mF_o-DF_c$ (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.