



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2025 – 08:09 AM EDT

PDB ID : 9NCW / pdb\_00009ncw  
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](mailto: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>.

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

MolProbity : 4-5-2 with Phenix2.0rc1  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

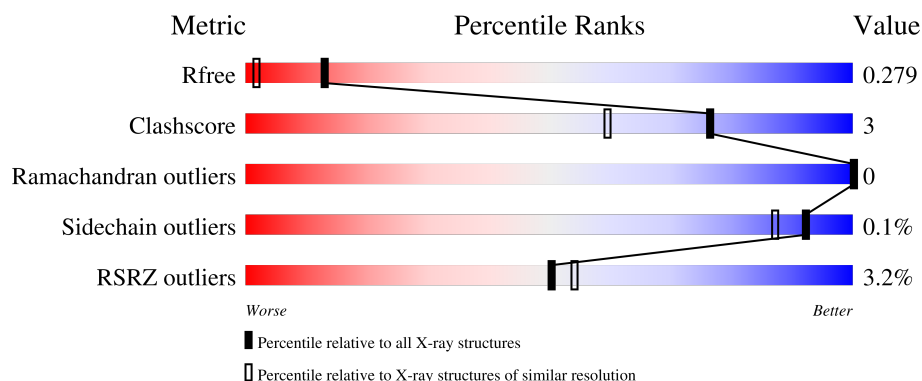
# 1 Overall quality at a glance

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))
$R_{free}$	164625	7165 (1.60-1.56)
Clashscore	180529	1026 (1.58-1.58)
Ramachandran outliers	177936	1005 (1.58-1.58)
Sidechain outliers	177891	1004 (1.58-1.58)
RSRZ outliers	164620	7163 (1.60-1.56)

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  $\geq 3$ , 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	
1	B	424	
1	C	424	
1	D	424	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10305 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
			2263	1444	372	436	11			
1	B	296	Total	C	N	O	S	0	1	0
			2271	1449	375	436	11			
1	C	296	Total	C	N	O	S	0	1	0
			2271	1449	375	436	11			
1	D	296	Total	C	N	O	S	0	1	0
			2269	1448	374	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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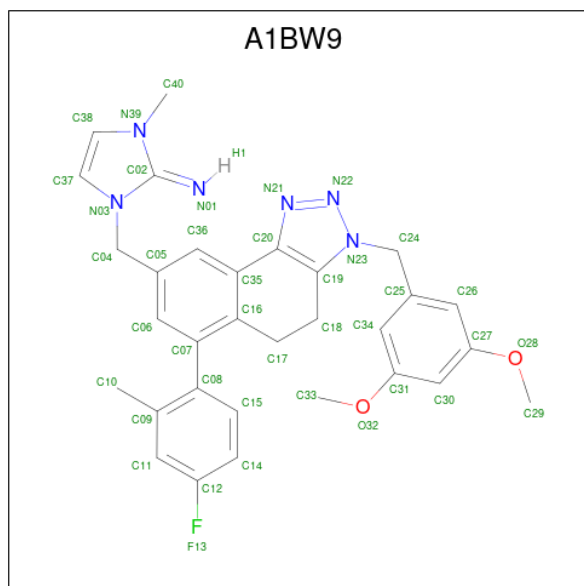
Chain	Residue	Modelled	Actual	Comment	Reference
D	-23	LYS	-	expression tag	UNP P61964
D	-22	ARG	-	expression tag	UNP P61964
D	-21	GLN	-	expression tag	UNP P61964
D	-20	GLY	-	expression tag	UNP P61964
D	-19	LYS	-	expression tag	UNP P61964
D	-18	GLU	-	expression tag	UNP P61964
D	-17	MET	-	expression tag	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 1-{[(6P)-3-[(3,5-dimethoxyphenyl)methyl]-6-(4-fluoro-2-methylphenyl)-4,5-dihydro-3H-naphtho[1,2-d][1,2,3]triazol-8-yl)methyl]-3-methyl-1,3-dihydro-2H-imidazol-2-imine (CCD ID: A1BW9) (formula: C<sub>31</sub>H<sub>31</sub>FN<sub>6</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			40	31	1	6	2		
2	B	1	Total	C	F	N	O	0	0
			40	31	1	6	2		

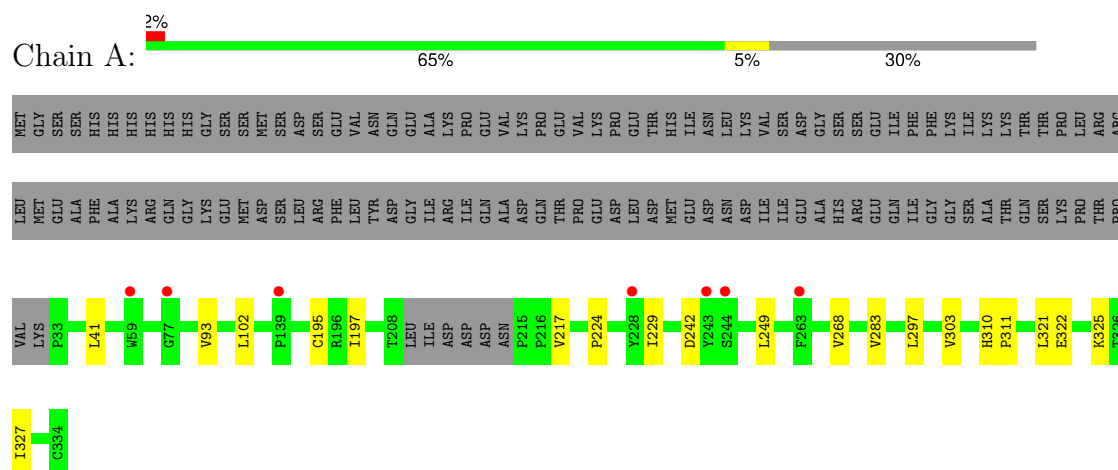
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	264	Total	O	0	0
			264	264		
3	B	277	Total	O	0	0
			277	277		
3	C	304	Total	O	0	0
			304	304		
3	D	306	Total	O	0	0
			306	306		

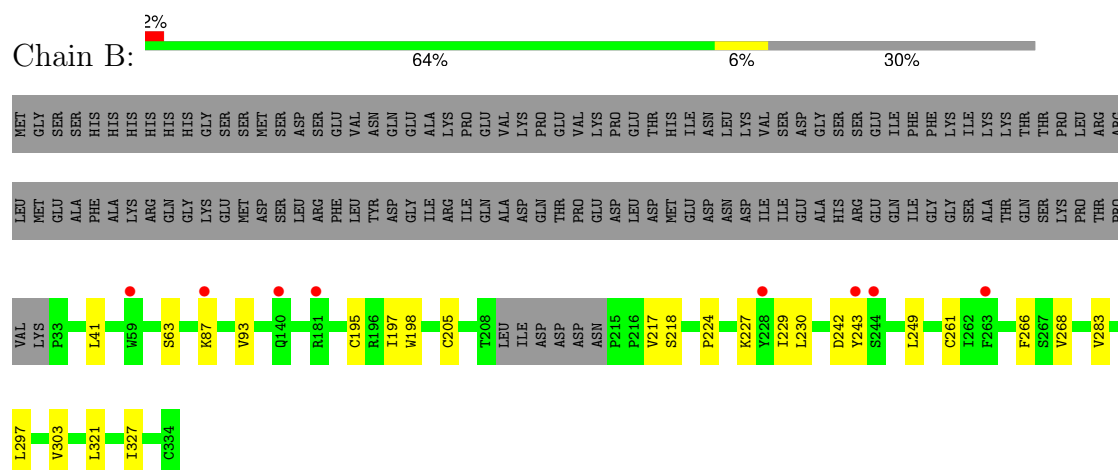
### 3 Residue-property plots

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.

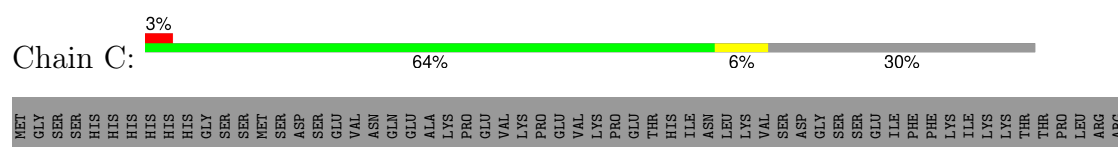
#### • Molecule 1: WD repeat-containing protein 5



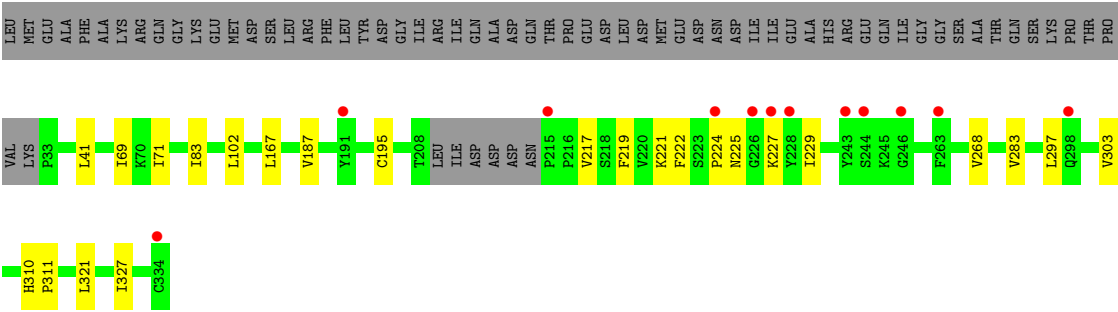
#### • Molecule 1: WD repeat-containing protein 5



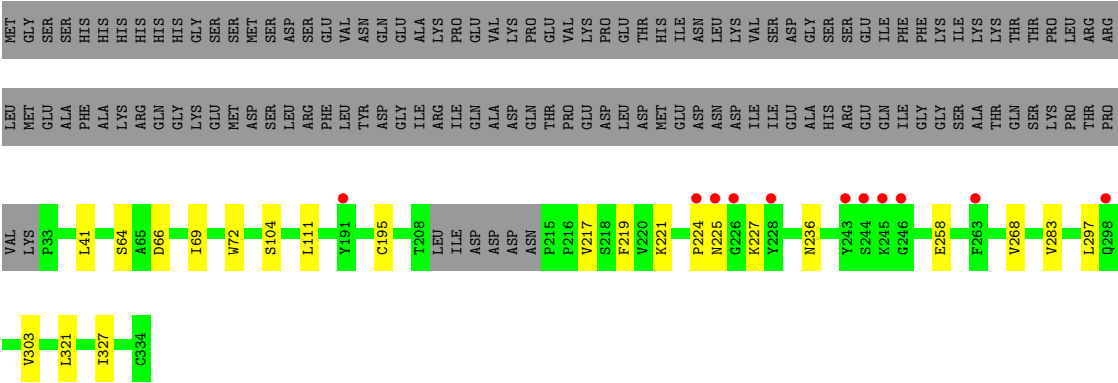
#### • Molecule 1: WD repeat-containing protein 5







● Molecule 1: WD repeat-containing protein 5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.53Å 68.70Å 93.02Å 91.29° 103.26° 90.38°	Depositor
Resolution (Å)	38.23 – 1.58 38.23 – 1.58	Depositor EDS
% Data completeness (in resolution range)	95.0 (38.23-1.58) 95.5 (38.23-1.58)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 1.58Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, $R_{free}$	0.249 , 0.275 0.253 , 0.279	Depositor DCC
$R_{free}$ test set	7080 reflections (4.65%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	13.0	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 47.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l 0.005 for -h,k,-l 0.000 for -h,-k,h+l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10305	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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 89.03 % 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 3.9680e-08. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: A1BW9

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	0.26	0/2321	0.49	0/3155
1	B	0.25	0/2329	0.49	0/3163
1	C	0.25	0/2329	0.51	0/3163
1	D	0.24	0/2327	0.51	0/3161
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	2263	0	2184	11	0
1	B	2271	0	2209	14	0
1	C	2271	0	2209	12	0
1	D	2269	0	2202	13	0
2	A	40	0	0	0	0
2	B	40	0	0	0	0
3	A	264	0	0	0	0
3	B	277	0	0	0	0
3	C	304	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	306	0	0	0	0
All	All	10305	0	8804	50	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 (50) 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:HD22	1:D:227:LYS:HB2	1.55	0.71
1:D:219:PHE:HZ	1:D:221:LYS:HD2	1.64	0.62
1:A:93:VAL:HG22	1:A:102:LEU:HD22	1.82	0.62
1:C:195[B]:CYS:SG	1:C:217:VAL:HG11	2.41	0.60
1:A:283:VAL:HB	1:A:297:LEU:HB2	1.84	0.60
1:A:195[B]:CYS:SG	1:A:217:VAL:HG11	2.41	0.60
1:B:195[B]:CYS:SG	1:B:217:VAL:HG11	2.42	0.59
1:D:195[B]:CYS:SG	1:D:217:VAL:HG11	2.44	0.58
1:D:225:ASN:HB3	1:D:227:LYS:H	1.69	0.57
1:B:41:LEU:HB2	1:B:327:ILE:HB	1.89	0.55
1:B:283:VAL:HB	1:B:297:LEU:HB2	1.90	0.54
1:C:225:ASN:O	1:C:227:LYS:NZ	2.40	0.54
1:D:283:VAL:HB	1:D:297:LEU:HB2	1.90	0.52
1:B:242:ASP:HB2	1:B:249:LEU:HD11	1.90	0.52
1:D:224:PRO:HG2	1:D:268:VAL:HG11	1.93	0.51
1:B:218:SER:HB2	1:B:261:CYS:HA	1.95	0.49
1:C:41:LEU:HB2	1:C:327:ILE:HB	1.94	0.49
1:C:303:VAL:HB	1:C:321:LEU:HD12	1.96	0.48
1:A:197:ILE:HD11	1:A:229:ILE:CD1	2.44	0.48
1:B:197:ILE:HG13	1:B:243:TYR:CE2	2.49	0.48
1:A:224:PRO:HG2	1:A:268:VAL:HG11	1.95	0.48
1:C:224:PRO:HG2	1:C:268:VAL:HG11	1.94	0.47
1:C:219:PHE:HZ	1:C:221:LYS:HD2	1.80	0.46
1:C:283:VAL:HB	1:C:297:LEU:HB2	1.97	0.46
1:A:303:VAL:HB	1:A:321:LEU:HD12	1.98	0.46
1:C:71:ILE:HD11	1:C:102:LEU:HD11	1.98	0.46
1:D:69:ILE:HD11	1:D:104:SER:HB3	1.98	0.45
1:D:303:VAL:HB	1:D:321:LEU:HD12	1.98	0.45
1:A:322:GLU:O	1:A:325:LYS:HE2	2.16	0.45
1:B:224:PRO:HG2	1:B:268:VAL:HG11	1.98	0.44
1:C:187:VAL:HG21	1:C:229:ILE:HD12	1.99	0.44
1:C:222:PHE:CE1	1:C:229:ILE:HD11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:LYS:HB3	1:B:227:LYS:HE3	1.73	0.43
1:D:64:SER:HB3	1:D:66:ASP:OD1	2.18	0.43
1:A:310:HIS:CG	1:A:311:PRO:HD2	2.54	0.43
1:C:69:ILE:HB	1:C:83:ILE:HB	2.00	0.43
1:B:303:VAL:HB	1:B:321:LEU:HD12	2.01	0.43
1:B:63:SER:HB3	1:B:93:VAL:HG13	2.02	0.42
1:B:229:ILE:HD12	1:B:243:TYR:HB2	2.01	0.42
1:C:310:HIS:CG	1:C:311:PRO:HD2	2.55	0.42
1:D:41:LEU:HD23	1:D:72:TRP:CD2	2.54	0.41
1:B:87:LYS:HE2	1:B:87:LYS:HB2	1.74	0.41
1:D:236:ASN:OD1	1:D:258:GLU:HG3	2.19	0.41
1:A:41:LEU:HB2	1:A:327:ILE:HB	2.02	0.41
1:A:197:ILE:HD11	1:A:229:ILE:HD11	2.02	0.41
1:D:41:LEU:HB2	1:D:327:ILE:HB	2.02	0.41
1:D:104:SER:O	1:D:111:LEU:HA	2.21	0.41
1:B:230:LEU:HB2	1:B:266:PHE:CZ	2.56	0.40
1:A:242:ASP:HB2	1:A:249:LEU:HD11	2.02	0.40
1:B:198:TRP:CZ3	1:B:205:CYS:HB2	2.56	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	293/424 (69%)	282 (96%)	11 (4%)	0	100	100
1	B	293/424 (69%)	282 (96%)	11 (4%)	0	100	100
1	C	293/424 (69%)	282 (96%)	11 (4%)	0	100	100
1	D	293/424 (69%)	282 (96%)	11 (4%)	0	100	100
All	All	1172/1696 (69%)	1128 (96%)	44 (4%)	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	248/373 (66%)	248 (100%)	0	100	100
1	B	251/373 (67%)	251 (100%)	0	100	100
1	C	251/373 (67%)	250 (100%)	1 (0%)	89	83
1	D	250/373 (67%)	250 (100%)	0	100	100
All	All	1000/1492 (67%)	999 (100%)	1 (0%)	92	87

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

Mol	Chain	Res	Type
1	C	167	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	265	ASN
1	C	289	GLN
1	D	136	ASN
1	D	225	ASN
1	D	289	GLN

### 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	A1BW9	B	401	-	43,45,45	2.60	9 (20%)	55,66,66	1.43	5 (9%)
2	A1BW9	A	401	-	43,45,45	2.57	9 (20%)	55,66,66	1.42	5 (9%)

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	A1BW9	B	401	-	-	3/16/25/25	0/6/6/6
2	A1BW9	A	401	-	-	2/16/25/25	0/6/6/6

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	A1BW9	C02-N03	10.78	1.47	1.38
2	A	401	A1BW9	C02-N03	10.50	1.47	1.38
2	B	401	A1BW9	C38-C37	9.02	1.50	1.34
2	A	401	A1BW9	C38-C37	8.90	1.50	1.34
2	A	401	A1BW9	C35-C16	-3.81	1.35	1.41
2	B	401	A1BW9	C35-C16	-3.74	1.35	1.41
2	A	401	A1BW9	C35-C20	-3.52	1.40	1.47
2	B	401	A1BW9	C35-C20	-3.47	1.40	1.47
2	B	401	A1BW9	C38-N39	3.28	1.44	1.37
2	A	401	A1BW9	C38-N39	2.99	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	A1BW9	C37-N03	2.90	1.44	1.38
2	A	401	A1BW9	C37-N03	2.81	1.44	1.38
2	B	401	A1BW9	C18-C19	2.76	1.56	1.50
2	A	401	A1BW9	C18-C19	2.71	1.56	1.50
2	A	401	A1BW9	C36-C35	2.69	1.44	1.39
2	A	401	A1BW9	C17-C16	2.44	1.55	1.51
2	B	401	A1BW9	C36-C35	2.40	1.43	1.39
2	B	401	A1BW9	C17-C16	2.34	1.55	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	A1BW9	C19-N23-N22	-5.51	108.11	112.85
2	A	401	A1BW9	C19-N23-N22	-5.32	108.28	112.85
2	A	401	A1BW9	C24-N23-N22	3.71	126.13	117.21
2	B	401	A1BW9	C24-N23-N22	3.62	125.92	117.21
2	B	401	A1BW9	F13-C12-C11	3.00	122.54	118.28
2	B	401	A1BW9	N39-C02-N03	2.80	108.93	107.00
2	A	401	A1BW9	F13-C12-C11	2.71	122.13	118.28
2	A	401	A1BW9	N39-C02-N03	2.48	108.71	107.00
2	A	401	A1BW9	C05-C04-N03	-2.38	109.15	112.84
2	B	401	A1BW9	C15-C08-C07	-2.26	114.18	118.74

There are no chirality outliers.

All (5) torsion outliers are listed below:

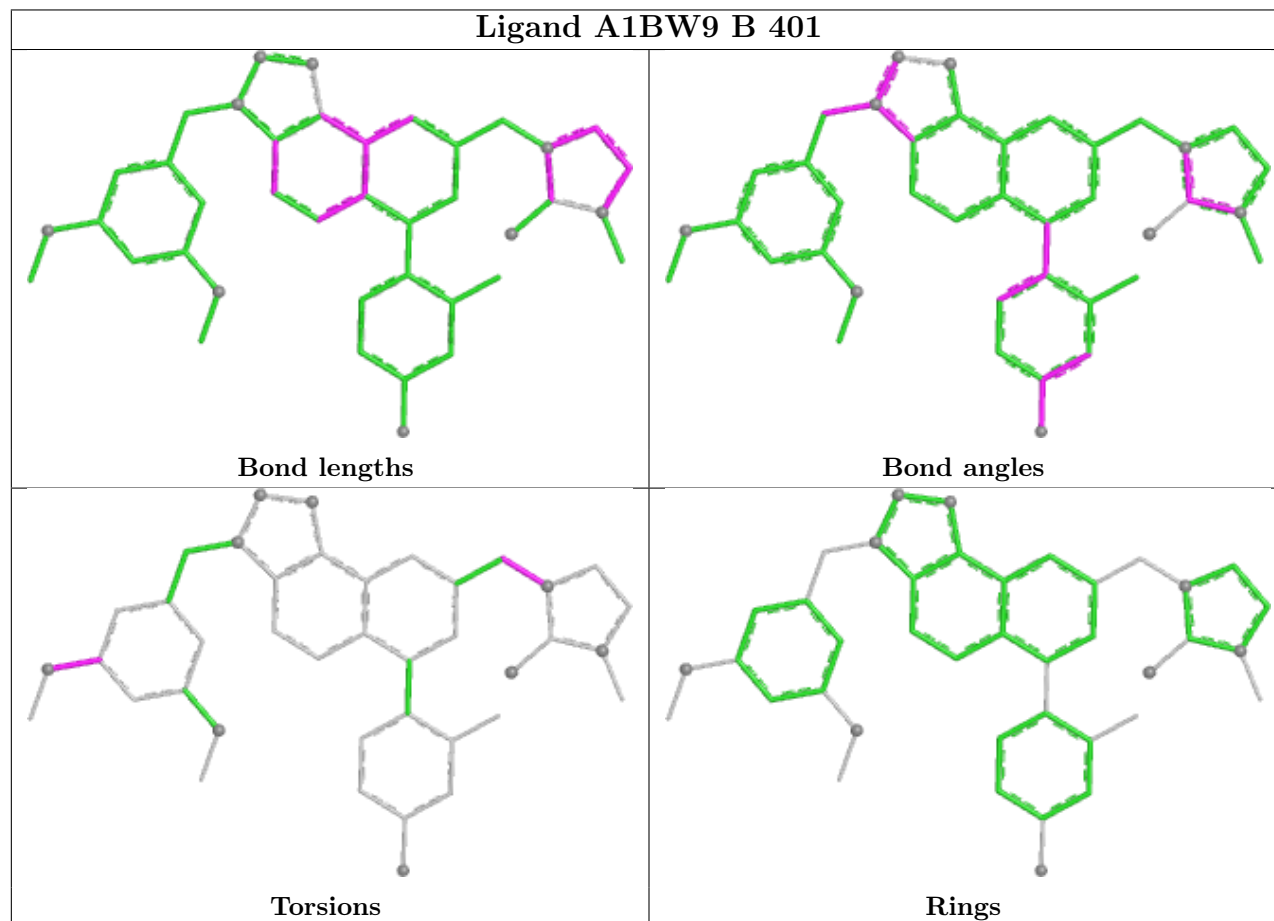
Mol	Chain	Res	Type	Atoms
2	B	401	A1BW9	C30-C31-O32-C33
2	B	401	A1BW9	C34-C31-O32-C33
2	A	401	A1BW9	C30-C31-O32-C33
2	A	401	A1BW9	C34-C31-O32-C33
2	B	401	A1BW9	C05-C04-N03-C02

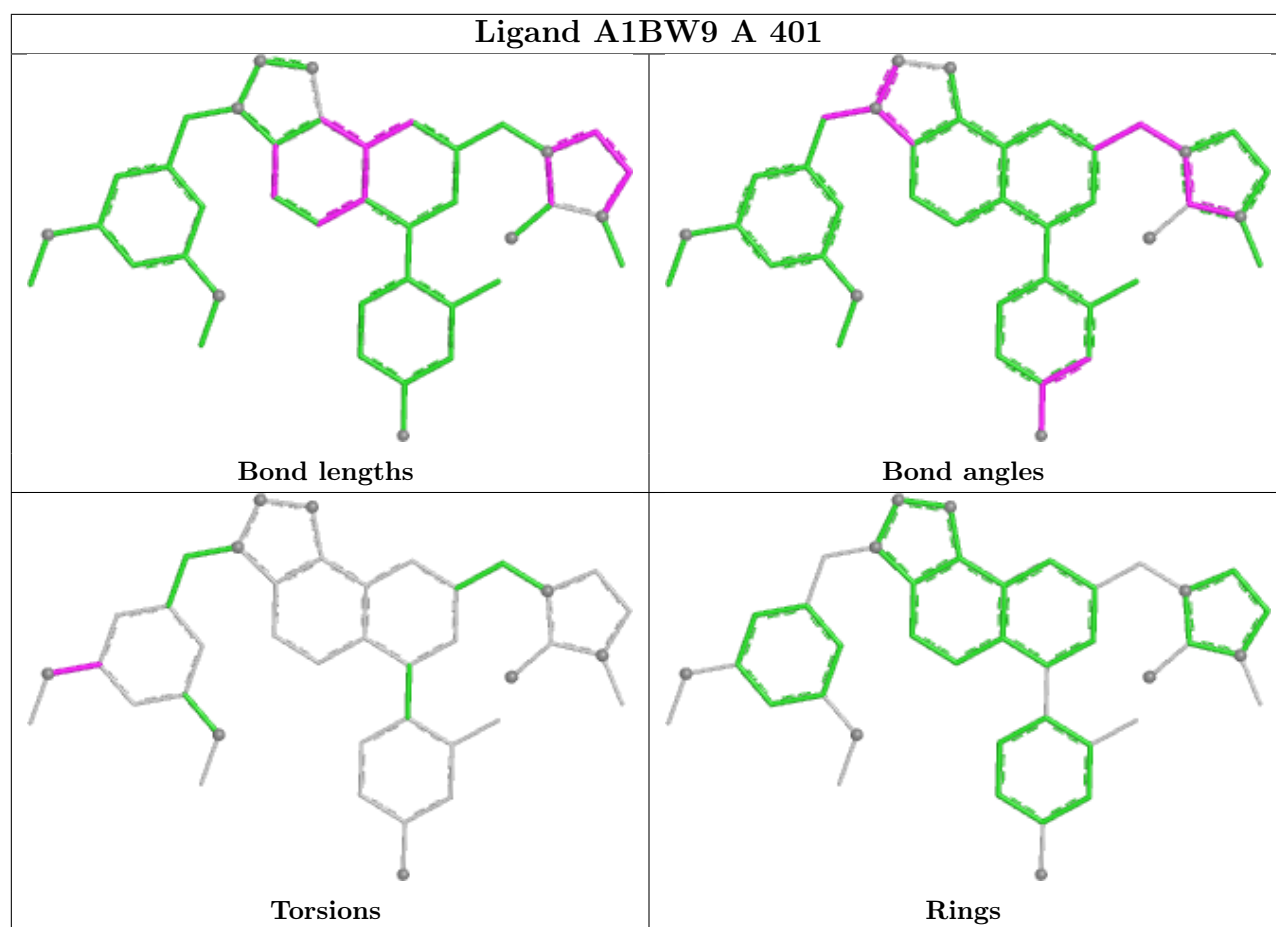
There are no ring outliers.

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	296/424 (69%)	0.27	7 (2%) 59 64	9, 16, 22, 38	1 (0%)
1	B	296/424 (69%)	0.29	8 (2%) 56 60	10, 16, 23, 36	1 (0%)
1	C	296/424 (69%)	0.24	12 (4%) 42 45	9, 14, 24, 41	1 (0%)
1	D	296/424 (69%)	0.23	11 (3%) 45 49	9, 14, 24, 39	1 (0%)
All	All	1184/1696 (69%)	0.26	38 (3%) 50 54	9, 15, 24, 41	4 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	226	GLY	4.9
1	A	243	TYR	4.9
1	D	226	GLY	4.7
1	D	225	ASN	4.2
1	C	263	PHE	4.1
1	C	243	TYR	4.1
1	D	228	TYR	3.8
1	D	243	TYR	3.6
1	C	228	TYR	3.5
1	A	244	SER	3.4
1	C	224	PRO	3.4
1	B	181	ARG	3.3
1	C	246	GLY	3.2
1	D	224	PRO	3.1
1	D	244	SER	3.1
1	C	244	SER	2.9
1	B	243	TYR	2.9
1	D	263	PHE	2.7
1	B	263	PHE	2.7
1	C	227	LYS	2.6
1	C	298	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	263	PHE	2.6
1	A	59	TRP	2.5
1	D	298	GLN	2.5
1	C	334	CYS	2.5
1	D	245	LYS	2.5
1	B	244	SER	2.5
1	B	228	TYR	2.4
1	A	77	GLY	2.3
1	B	87	LYS	2.3
1	D	191	TYR	2.3
1	D	246	GLY	2.3
1	C	191	TYR	2.2
1	A	139	PRO	2.1
1	B	59	TRP	2.1
1	A	228	TYR	2.1
1	B	140	GLN	2.0
1	C	215	PRO	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](#)

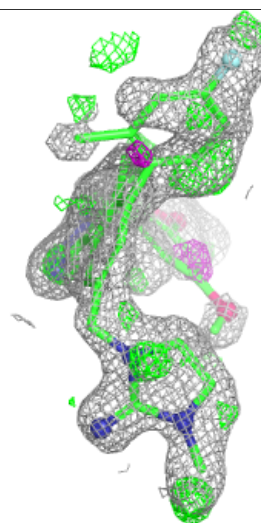
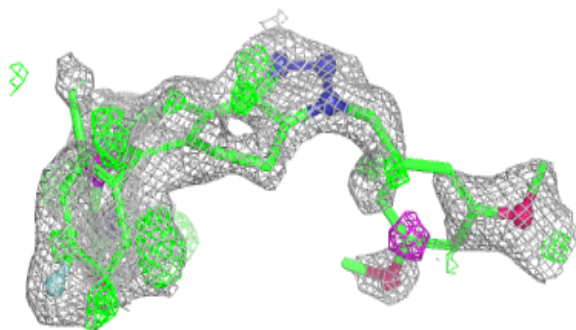
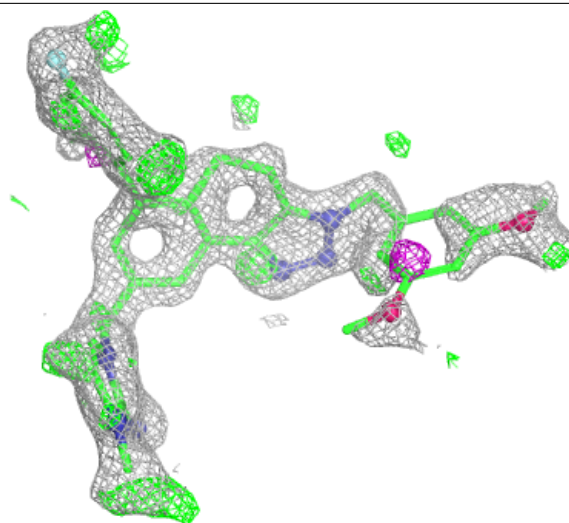
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	A1BW9	A	401	40/40	0.75	0.20	13,18,27,28	40
2	A1BW9	B	401	40/40	0.75	0.19	13,18,26,29	40

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.

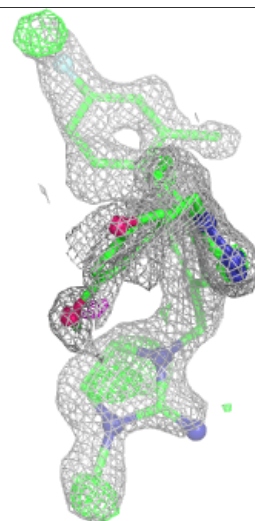
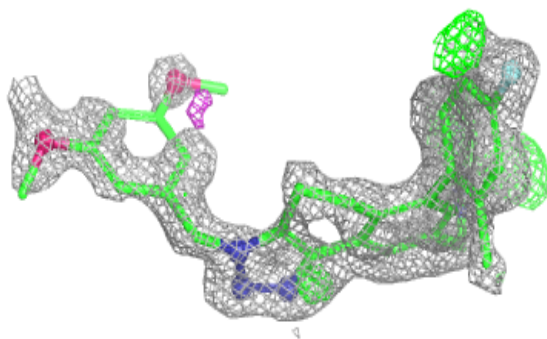
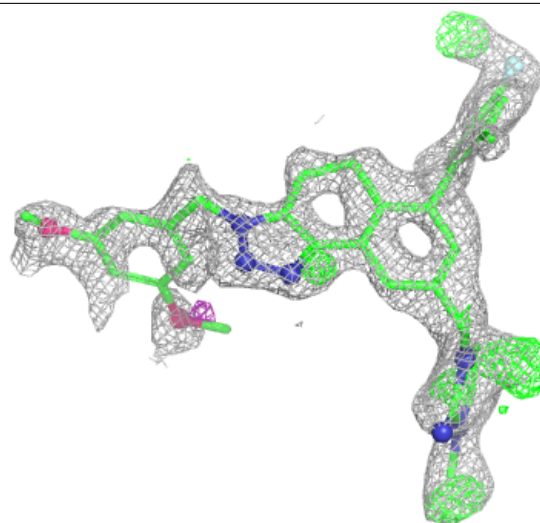
**Electron density around A1BW9 A 401:**

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



**Electron density around A1BW9 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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.