



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:37 PM UTC

PDB ID : 6VNC / pdb_00006vnc
Title : JAK2 JH1 in complex with BL2-096
Authors : Davis, R.R.; Schonbrunn, E.
Deposited on : 2020-01-29
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

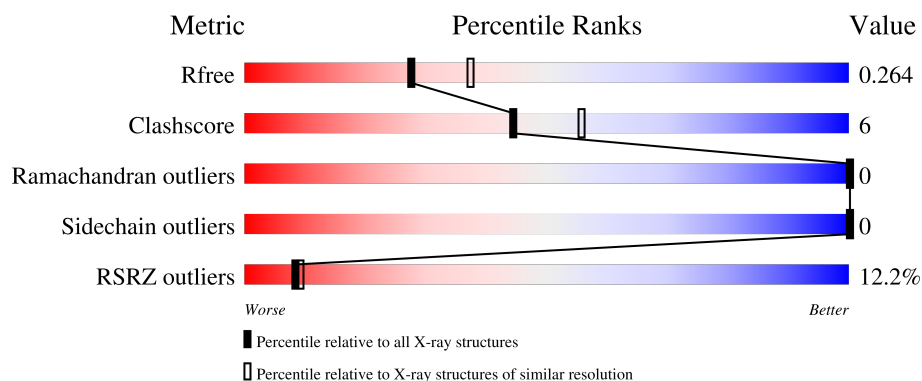
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	308	11% 83% 14% .
1	B	308	12% 78% 15% 6%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4971 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tyrosine-protein kinase JAK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	289	Total	C	N	O	P	S	0	0	0
			2395	1521	417	442	1	14			
1	A	297	Total	C	N	O	P	S	0	0	0
			2461	1565	426	455	1	14			

There are 30 discrepancies between the modelled and reference sequences:

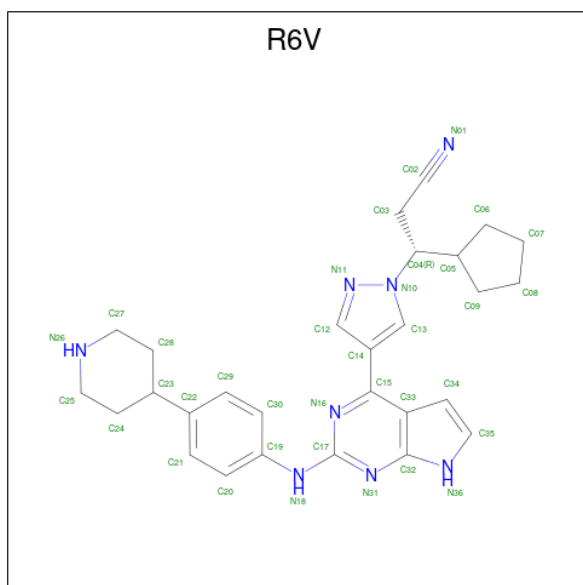
Chain	Residue	Modelled	Actual	Comment	Reference
B	825	HIS	-	expression tag	UNP O60674
B	826	HIS	-	expression tag	UNP O60674
B	827	HIS	-	expression tag	UNP O60674
B	828	HIS	-	expression tag	UNP O60674
B	829	HIS	-	expression tag	UNP O60674
B	830	HIS	-	expression tag	UNP O60674
B	831	HIS	-	expression tag	UNP O60674
B	832	HIS	-	expression tag	UNP O60674
B	833	GLU	-	expression tag	UNP O60674
B	834	ASN	-	expression tag	UNP O60674
B	835	LEU	-	expression tag	UNP O60674
B	836	TYR	-	expression tag	UNP O60674
B	837	PHE	-	expression tag	UNP O60674
B	838	GLN	-	expression tag	UNP O60674
B	839	GLY	-	expression tag	UNP O60674
A	825	HIS	-	expression tag	UNP O60674
A	826	HIS	-	expression tag	UNP O60674
A	827	HIS	-	expression tag	UNP O60674
A	828	HIS	-	expression tag	UNP O60674
A	829	HIS	-	expression tag	UNP O60674
A	830	HIS	-	expression tag	UNP O60674
A	831	HIS	-	expression tag	UNP O60674
A	832	HIS	-	expression tag	UNP O60674
A	833	GLU	-	expression tag	UNP O60674
A	834	ASN	-	expression tag	UNP O60674

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Chain	Residue	Modelled	Actual	Comment	Reference
A	835	LEU	-	expression tag	UNP O60674
A	836	TYR	-	expression tag	UNP O60674
A	837	PHE	-	expression tag	UNP O60674
A	838	GLN	-	expression tag	UNP O60674
A	839	GLY	-	expression tag	UNP O60674

- Molecule 2 is (3R)-3-cyclopentyl-3-[4-(2-{[4-(piperidin-4-yl)phenyl]amino}-7H-pyrrolo[2,3-d]pyrimidin-4-yl)-1H-pyrazol-1-yl]propanenitrile (CCD ID: R6V) (formula: C₂₈H₃₂N₈) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	N	0	0
			36	28	8		
2	A	1	Total	C	N	0	0
			36	28	8		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	25	Total	O	0	0
			25	25		
3	A	18	Total	O	0	0
			18	18		

- Molecule 1: Tyrosine-protein kinase JAK2



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	112.68Å 112.68Å 70.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.95 – 2.30 43.95 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.7 (43.95-2.30) 99.7 (43.95-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.14-3260_3260	Depositor
R, R_{free}	0.226 , 0.269 0.224 , 0.264	Depositor DCC
R_{free} test set	937 reflections (2.39%)	wwPDB-VP
Wilson B-factor (Å ²)	54.5	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.042 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4971	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: R6V, PTR

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	0.27	0/2498	0.51	0/3362
1	B	0.32	0/2429	0.70	9/3267 (0.3%)
All	All	0.29	0/4927	0.61	9/6629 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	947	ARG	CB-CG-CD	-9.29	89.93	111.30
1	B	1015	GLU	CA-CB-CG	-7.36	99.38	114.10
1	B	859	ASN	CA-C-N	-5.91	112.42	122.11
1	B	859	ASN	C-N-CA	-5.91	112.42	122.11
1	B	846	GLU	CA-C-N	5.86	129.62	120.82
1	B	846	GLU	C-N-CA	5.86	129.62	120.82
1	B	1073	MET	CA-CB-CG	-5.11	103.88	114.10
1	B	1014	GLY	CA-C-N	-5.02	114.07	123.05
1	B	1014	GLY	C-N-CA	-5.02	114.07	123.05

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	860	PHE	Sidechain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2461	0	2436	28	0
1	B	2395	0	2377	30	2
2	A	36	0	0	0	0
2	B	36	0	0	2	0
3	A	18	0	0	1	0
3	B	25	0	0	4	0
All	All	4971	0	4813	58	2

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 6.

All (58) 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:B:883:LYS:NZ	3:B:1303:HOH:O	1.94	1.00
1:B:1036:ASP:OD1	3:B:1301:HOH:O	1.88	0.89
1:B:907:HIS:O	3:B:1302:HOH:O	1.93	0.83
1:B:868:TYR:O	1:B:876:GLY:HA3	1.92	0.70
1:B:846:GLU:OE1	1:B:926:LYS:NZ	2.22	0.67
1:B:845:GLU:OE1	1:B:847:ARG:NH2	2.28	0.66
1:A:868:TYR:O	1:A:876:GLY:HA3	1.96	0.65
1:A:962:LYS:NZ	3:A:1302:HOH:O	1.95	0.64
1:A:930:GLU:OE2	1:A:991:LYS:NZ	2.32	0.63
1:B:971:ARG:NH2	1:B:1002:PRO:O	2.33	0.61
1:A:853:GLN:HG2	1:A:865:MET:HE2	1.80	0.61
1:A:918:TYR:HD2	1:A:925:LEU:HD13	1.64	0.60
1:A:1104:GLU:HG2	1:A:1114:PRO:HD3	1.85	0.59
1:B:932:LEU:HD12	1:B:983:LEU:HB2	1.85	0.58
2:B:1201:R6V:C30	2:B:1201:R6V:N16	2.66	0.58
1:B:919:SER:O	1:B:923:ARG:N	2.34	0.57
1:A:971:ARG:NH2	1:A:1002:PRO:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1080:GLU:HA	1:A:1083:LYS:HG2	1.87	0.55
1:B:1062:MET:HA	1:B:1065:ILE:HG12	1.90	0.54
1:A:861:GLY:C	1:A:885:GLN:OE1	2.52	0.53
1:B:853:GLN:HG2	1:B:865:MET:HE2	1.91	0.52
1:B:989:ARG:NH1	3:B:1306:HOH:O	2.42	0.52
1:A:932:LEU:HD21	1:A:991:LYS:HD2	1.93	0.51
1:B:1104:GLU:OE1	1:B:1122:ARG:NH1	2.33	0.50
1:A:855:LEU:HD11	1:A:865:MET:HB2	1.94	0.50
1:B:857:LYS:HD3	1:B:862:SER:HB3	1.93	0.50
1:A:976:ASP:HB2	1:A:997:LEU:HD12	1.94	0.49
1:A:925:LEU:HD12	1:A:926:LYS:H	1.78	0.49
1:A:945:LYS:HG3	1:A:946:GLU:OE2	2.12	0.48
1:A:1088:LEU:O	1:A:1099:TYR:OH	2.30	0.48
1:A:942:GLN:HG3	1:A:943:LYS:HD3	1.97	0.47
1:B:884:LEU:HD23	1:B:884:LEU:HA	1.45	0.47
1:A:862:SER:N	1:A:885:GLN:OE1	2.48	0.47
1:A:1087:ARG:HE	1:A:1106:TRP:HB3	1.80	0.47
1:B:935:GLY:HA2	2:B:1201:R6V:C30	2.44	0.46
1:A:873:ASP:N	1:A:873:ASP:OD1	2.49	0.46
1:A:946:GLU:OE2	1:A:946:GLU:N	2.49	0.46
1:B:1045:TYR:O	1:B:1049:THR:HG23	2.16	0.45
1:B:888:THR:O	1:B:892:LEU:HB2	2.16	0.45
1:B:1053:LYS:H	1:B:1053:LYS:HG3	1.54	0.45
1:A:932:LEU:HD22	1:A:983:LEU:HB2	1.99	0.44
1:B:860:PHE:HD2	1:B:884:LEU:CD2	2.31	0.44
1:A:945:LYS:CG	1:A:946:GLU:OE2	2.66	0.44
1:A:1065:ILE:O	1:A:1069:LYS:HE3	2.17	0.44
1:B:918:TYR:C	1:B:918:TYR:CD1	2.96	0.43
1:A:918:TYR:HB3	1:A:925:LEU:HA	2.00	0.43
1:B:861:GLY:HA3	1:B:883:LYS:O	2.17	0.43
1:B:873:ASP:OD1	1:B:873:ASP:N	2.51	0.43
1:B:965:GLU:O	1:B:969:THR:HG23	2.19	0.43
1:A:1070:GLN:HG2	1:A:1071:GLY:H	1.82	0.43
1:B:892:LEU:O	1:B:896:GLU:HG3	2.19	0.42
1:B:1045:TYR:OH	1:B:1060:GLU:HG3	2.20	0.42
1:A:1061:PHE:HA	1:A:1064:MET:HE3	2.00	0.42
1:B:929:MET:HE3	1:B:929:MET:HB2	1.96	0.41
1:A:838:GLN:OE1	1:A:838:GLN:HA	2.20	0.41
1:B:920:ALA:N	1:B:921:GLY:HA3	2.34	0.41
1:B:1117:ARG:HB3	1:A:886:HIS:ND1	2.36	0.41
1:B:867:ARG:NH1	1:B:876:GLY:O	2.54	0.40

All (2) 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)
1:B:883:LYS:NZ	1:B:1007:PTR:O3P[2_654]	1.28	0.92
1:B:883:LYS:CE	1:B:1007:PTR:O3P[2_654]	2.02	0.18

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	294/308 (96%)	290 (99%)	4 (1%)	0	100	100
1	B	286/308 (93%)	282 (99%)	4 (1%)	0	100	100
All	All	580/616 (94%)	572 (99%)	8 (1%)	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	270/280 (96%)	270 (100%)	0	100	100
1	B	263/280 (94%)	263 (100%)	0	100	100
All	All	533/560 (95%)	533 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	1067	ASN
1	B	1125	GLN
1	A	944	HIS
1	A	955	GLN
1	A	1003	GLN
1	A	1077	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	PTR	B	1007	1	15,16,17	1.99	4 (26%)	17,22,24	1.00	1 (5%)
1	PTR	A	1007	1	15,16,17	1.33	1 (6%)	17,22,24	0.59	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PTR	B	1007	1	-	0/10/11/13	0/1/1/1
1	PTR	A	1007	1	-	1/10/11/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1007	PTR	P-O1P	4.51	1.64	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1007	PTR	OH-CZ	-4.33	1.30	1.40
1	B	1007	PTR	P-OH	3.95	1.67	1.59
1	B	1007	PTR	OH-CZ	-3.77	1.32	1.40
1	B	1007	PTR	P-O3P	-2.26	1.46	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1007	PTR	O3P-P-O2P	2.52	117.24	107.80
1	A	1007	PTR	O2P-P-OH	2.00	111.23	105.32

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1007	PTR	CZ-OH-P-O1P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1007	PTR	0	2

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	R6V	A	1201	-	40,41,41	2.19	9 (22%)	45,57,57	2.44	13 (28%)
2	R6V	B	1201	-	40,41,41	2.43	9 (22%)	45,57,57	3.04	17 (37%)

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	R6V	A	1201	-	-	3/22/38/38	0/6/6/6
2	R6V	B	1201	-	-	1/22/38/38	0/6/6/6

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	R6V	C17-N18	7.06	1.51	1.36
2	B	1201	R6V	C09-C05	-6.70	1.37	1.53
2	A	1201	R6V	C09-C05	-6.49	1.37	1.53
2	B	1201	R6V	C15-C14	5.37	1.53	1.48
2	A	1201	R6V	C15-C14	5.19	1.53	1.48
2	B	1201	R6V	C06-C05	5.13	1.66	1.53
2	A	1201	R6V	C06-C05	4.90	1.66	1.53
2	A	1201	R6V	C17-N18	4.66	1.46	1.36
2	B	1201	R6V	C19-N18	4.07	1.49	1.40
2	A	1201	R6V	C07-C06	-3.67	1.36	1.51
2	B	1201	R6V	C07-C06	-3.65	1.37	1.51
2	B	1201	R6V	C03-C02	3.46	1.53	1.46
2	B	1201	R6V	C33-C32	-3.23	1.37	1.41
2	A	1201	R6V	C03-C02	3.03	1.52	1.46
2	A	1201	R6V	C35-N36	-2.76	1.33	1.38
2	A	1201	R6V	C19-N18	2.65	1.46	1.40
2	B	1201	R6V	C35-N36	-2.59	1.33	1.38
2	A	1201	R6V	C33-C32	-2.40	1.38	1.41

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	R6V	C12-N11-N10	8.79	108.66	104.14
2	A	1201	R6V	C33-C32-N31	-8.68	119.77	127.10
2	B	1201	R6V	C12-N11-N10	8.07	108.29	104.14
2	B	1201	R6V	C14-C15-N16	7.88	123.16	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1201	R6V	C33-C32-N31	-7.83	120.49	127.10
2	B	1201	R6V	N31-C17-N16	-6.15	116.19	126.26
2	B	1201	R6V	C15-N16-C17	5.84	124.54	117.26
2	B	1201	R6V	C19-N18-C17	-4.91	116.15	129.38
2	B	1201	R6V	C32-N36-C35	4.81	110.89	108.11
2	A	1201	R6V	C15-N16-C17	4.04	122.29	117.26
2	B	1201	R6V	C29-C30-C19	3.28	124.08	120.30
2	B	1201	R6V	C30-C29-C22	-3.24	117.95	121.18
2	A	1201	R6V	N31-C17-N16	-3.20	121.01	126.26
2	B	1201	R6V	C28-C23-C22	-3.04	105.47	112.67
2	A	1201	R6V	C32-N36-C35	3.00	109.84	108.11
2	A	1201	R6V	C06-C05-C04	-2.98	107.87	113.06
2	A	1201	R6V	C13-N10-N11	-2.92	110.49	112.45
2	B	1201	R6V	N36-C32-N31	2.84	132.01	127.45
2	B	1201	R6V	C17-N31-C32	2.75	123.11	116.36
2	B	1201	R6V	C13-N10-N11	-2.62	110.69	112.45
2	B	1201	R6V	C04-N10-C13	-2.62	124.52	128.46
2	B	1201	R6V	C34-C35-N36	-2.45	107.42	110.25
2	A	1201	R6V	C14-C15-N16	2.44	117.73	115.30
2	A	1201	R6V	N36-C32-N31	2.41	131.32	127.45
2	B	1201	R6V	C06-C05-C04	-2.39	108.89	113.06
2	A	1201	R6V	C28-C23-C22	-2.18	107.52	112.67
2	A	1201	R6V	C09-C05-C04	-2.09	109.41	113.06
2	B	1201	R6V	N18-C17-N16	2.07	124.00	116.90
2	A	1201	R6V	C32-C33-C34	-2.04	105.39	106.40
2	A	1201	R6V	C34-C35-N36	-2.02	107.92	110.25

There are no chirality outliers.

All (4) torsion outliers are listed below:

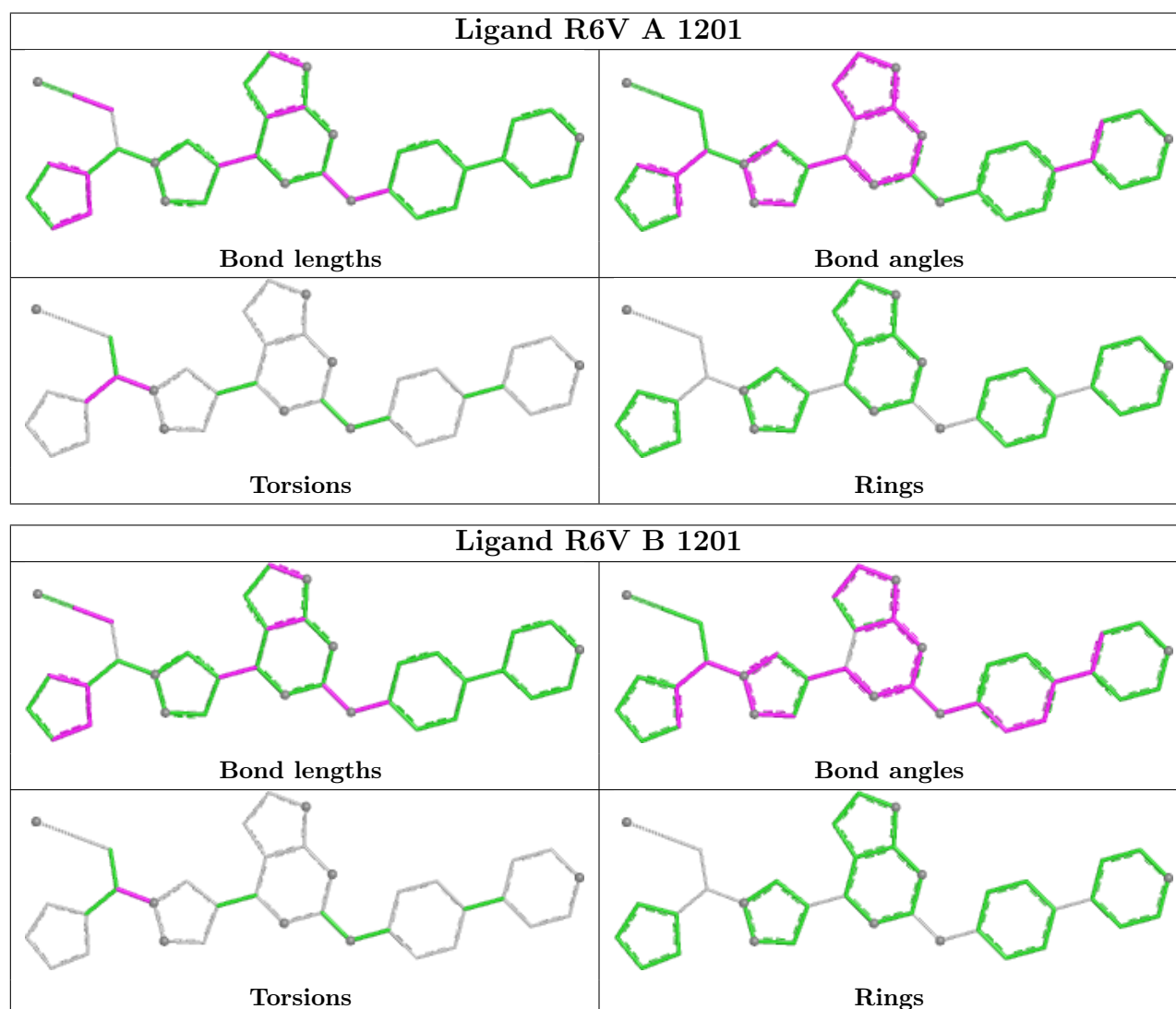
Mol	Chain	Res	Type	Atoms
2	B	1201	R6V	C03-C04-N10-C13
2	A	1201	R6V	C03-C04-N10-C13
2	A	1201	R6V	C03-C04-C05-C06
2	A	1201	R6V	C03-C04-C05-C09

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1201	R6V	2	0

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



5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	296/308 (96%)	1.05	34 (11%)  	49, 67, 102, 131	0
1	B	288/308 (93%)	1.14	37 (12%)  	42, 67, 111, 129	0
All	All	584/616 (94%)	1.09	71 (12%)  	42, 67, 107, 131	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	886	HIS	4.9
1	A	860	PHE	4.6
1	B	860	PHE	4.4
1	B	918	TYR	4.1
1	A	1131	ALA	3.9
1	A	920	ALA	3.7
1	A	1014	GLY	3.5
1	A	993	GLY	3.3
1	B	924	ASN	3.3
1	B	967	LEU	3.3
1	A	902	LEU	3.3
1	A	837	PHE	3.2
1	A	1062	MET	3.2
1	A	995	PHE	3.1
1	B	887	SER	3.0
1	B	1013	PRO	3.0
1	B	1131	ALA	2.9
1	B	858	GLY	2.9
1	A	1071	GLY	2.9
1	A	1097	GLU	2.9
1	A	838	GLN	2.8
1	B	1073	MET	2.7
1	A	905	LEU	2.7
1	B	920	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	976	ASP	2.7
1	B	922	ARG	2.7
1	A	835	LEU	2.7
1	A	1053	LYS	2.7
1	B	1014	GLY	2.6
1	A	918	TYR	2.6
1	A	922	ARG	2.6
1	B	859	ASN	2.6
1	B	1019	PHE	2.6
1	B	1061	PHE	2.5
1	A	839	GLY	2.5
1	B	992	ILE	2.5
1	B	947	ARG	2.4
1	A	877	GLU	2.4
1	B	941	LEU	2.4
1	A	967	LEU	2.4
1	B	994	ASP	2.4
1	A	1073	MET	2.4
1	B	1078	LEU	2.4
1	B	1100	MET	2.4
1	B	1053	LYS	2.4
1	A	888	THR	2.4
1	B	1018	ILE	2.4
1	B	1080	GLU	2.4
1	A	994	ASP	2.3
1	A	1044	LEU	2.3
1	B	857	LYS	2.3
1	B	977	LEU	2.3
1	B	919	SER	2.3
1	A	1040	PHE	2.2
1	A	908	ASP	2.2
1	A	1013	PRO	2.2
1	B	1012	GLU	2.2
1	B	1062	MET	2.2
1	A	841	PRO	2.2
1	B	849	LEU	2.1
1	A	1015	GLU	2.1
1	A	1100	MET	2.1
1	A	844	PHE	2.1
1	A	885	GLN	2.1
1	B	1066	GLY	2.1
1	B	843	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1005	LYS	2.0
1	A	919	SER	2.0
1	B	1063	ARG	2.0
1	B	921	GLY	2.0
1	B	1064	MET	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	PTR	B	1007	16/17	0.90	0.13	56,70,124,125	0
1	PTR	A	1007	16/17	0.91	0.12	55,81,114,119	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

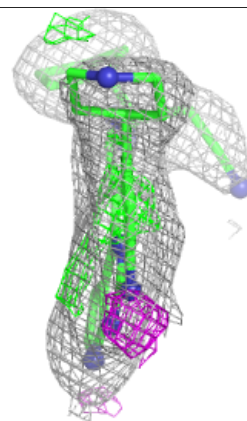
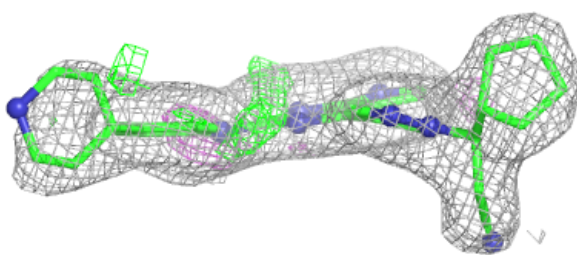
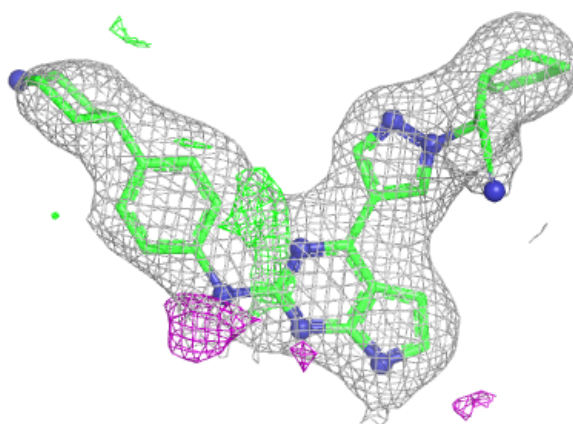
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	R6V	B	1201	36/36	0.93	0.13	39,53,74,94	0
2	R6V	A	1201	36/36	0.96	0.10	47,55,81,99	0

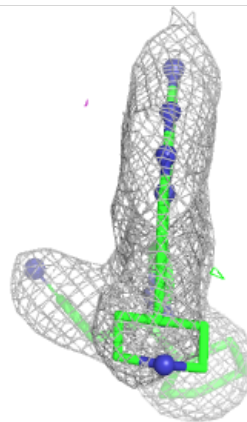
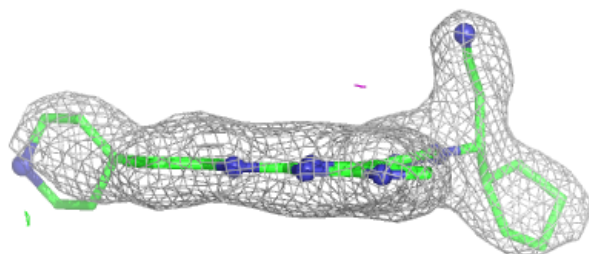
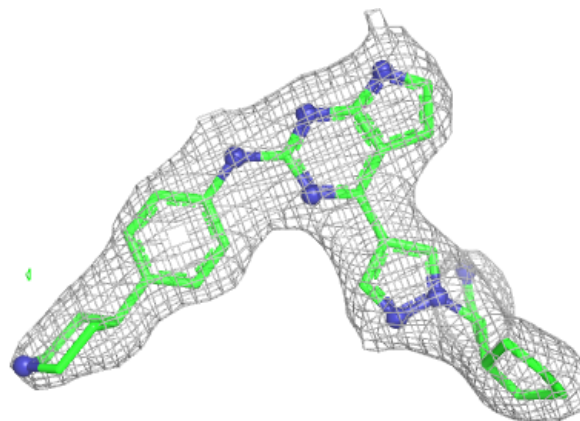
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around R6V B 1201:

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

**Electron density around R6V A 1201:**

$2mF_o-DF_c$ (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.