



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 9, 2021 – 04:02 PM EDT

PDB ID : 6W3E  
Title : Structure of phosphorylated IRE1 in complex with G-0701  
Authors : Ferri, E.; Wang, W.; Joachim, R.; Mortara, K.  
Deposited on : 2020-03-09  
Resolution : 2.74 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.20  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.20

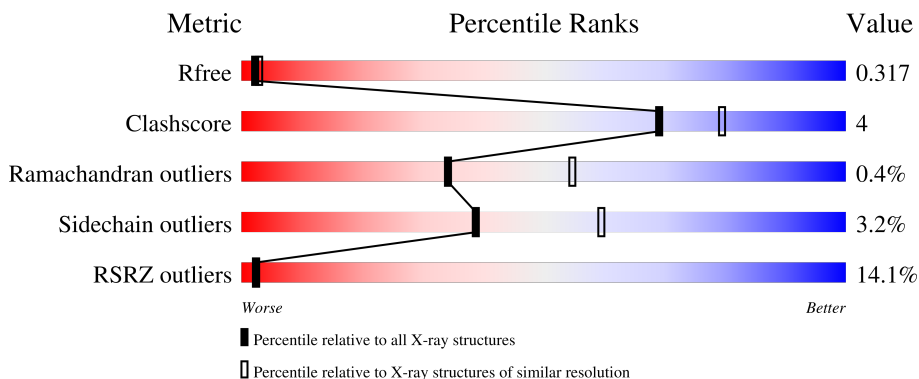
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.74 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))
$R_{free}$	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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	431	 10% 78% 7% 15%
1	B	431	 14% 77% 13% • 10%

## 2 Entry composition [i](#)

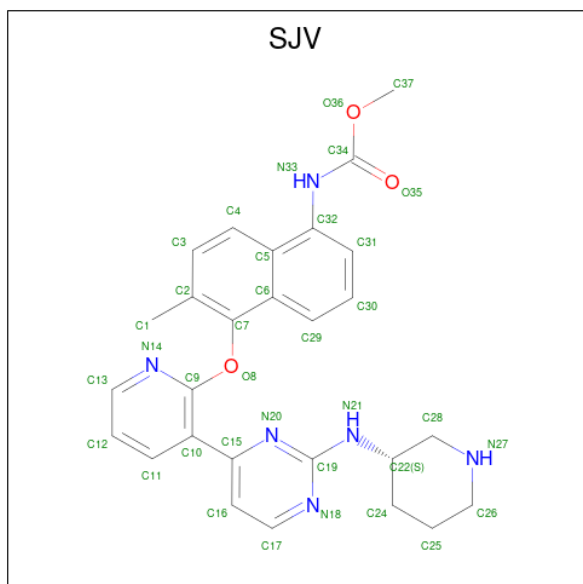
There are 2 unique types of molecules in this entry. The entry contains 11782 atoms, of which 5751 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase/endoribonuclease IRE1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	366	Total	C	H	N	O	S	0	0	0
			5686	1853	2793	504	519	17			
1	B	389	Total	C	H	N	O	P	0	0	0
			6022	1952	2956	538	556	2			

- Molecule 2 is methyl {N}-[6-methyl-5-[3-[2-[[3 {S}]-piperidin-3-yl]amino]pyrimidin-4-yl]pyridin-2-yl]oxy-naphthalen-1-yl]carbamate (three-letter code: SJV) (formula: C<sub>27</sub>H<sub>28</sub>N<sub>6</sub>O<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).

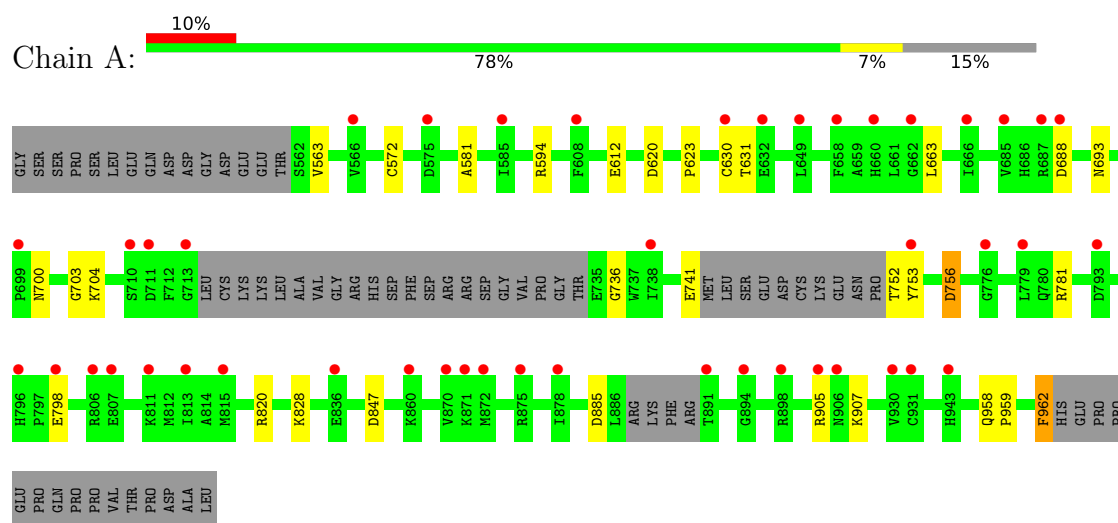


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			37	27	1	6	3		
2	B	1	Total	C	H	N	O	0	0
			37	27	1	6	3		

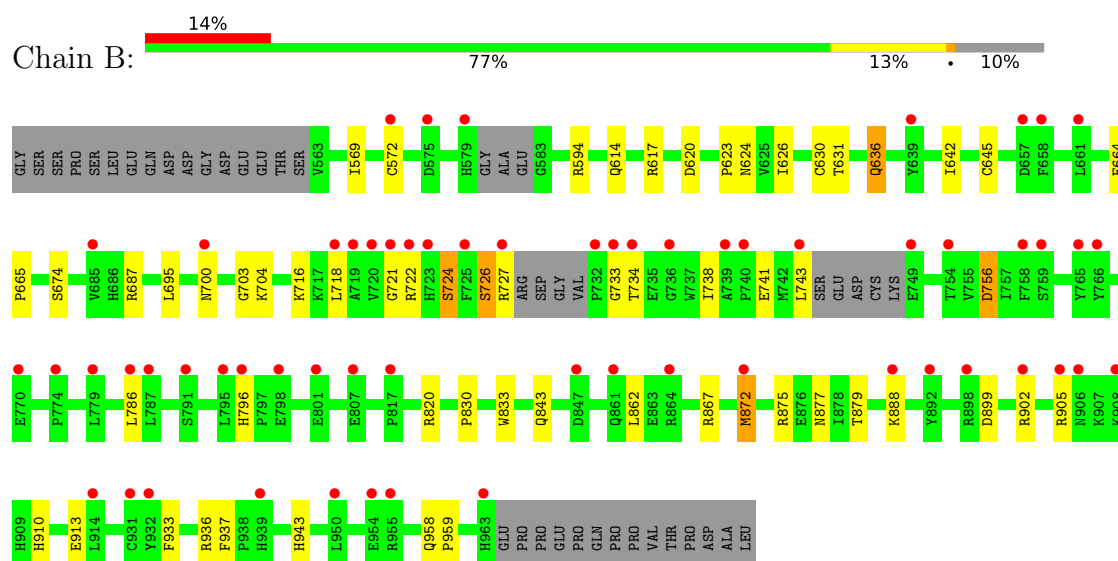
### 3 Residue-property plots

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: Serine/threonine-protein kinase/endoribonuclease IRE1



- Molecule 1: Serine/threonine-protein kinase/endoribonuclease IRE1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.67Å 139.24Å 63.95Å 90.00° 114.90° 90.00°	Depositor
Resolution (Å)	55.94 – 2.74 55.94 – 2.74	Depositor EDS
% Data completeness (in resolution range)	67.4 (55.94-2.74) 67.4 (55.94-2.74)	Depositor EDS
$R_{merge}$	0.18	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.25 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, $R_{free}$	0.262 , 0.317 0.263 , 0.317	Depositor DCC
$R_{free}$ test set	1742 reflections (10.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.8	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 75.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.044 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.83	EDS
Total number of atoms	11782	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

<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

### 5.1 Standard geometry

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

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	0.23	0/2964	0.43	0/4013
1	B	0.23	0/3116	0.43	0/4213
All	All	0.23	0/6080	0.43	0/8226

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

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	2893	2793	2797	17	0
1	B	3066	2956	2956	30	0
2	A	36	1	0	0	0
2	B	36	1	0	1	0
All	All	6031	5751	5753	43	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 4.

All (43) 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:700:ASN:OD1	1:B:704:LYS:N	2.18	0.76
1:B:724:SEP:O1P	1:B:724:SEP:N	2.24	0.70
1:B:741:GLU:OE1	1:B:820:ARG:NH1	2.32	0.62
1:B:899:ASP:OD1	1:B:902:ARG:NH2	2.34	0.59
1:B:910:HIS:ND1	1:B:913:GLU:OE1	2.34	0.59
1:B:933:PHE:O	1:B:937:PHE:N	2.36	0.59
1:A:700:ASN:OD1	1:A:703:GLY:N	2.38	0.56
1:A:752:THR:OG1	1:A:753:TYR:N	2.37	0.56
1:B:630:CYS:SG	1:B:631:THR:N	2.78	0.56
1:A:700:ASN:OD1	1:A:704:LYS:N	2.38	0.56
1:B:624:ASN:OD1	1:B:674:SER:OG	2.24	0.55
1:B:626:ILE:HD11	1:B:642:ILE:CG2	2.37	0.54
1:A:741:GLU:OE2	1:A:820:ARG:NH1	2.41	0.54
1:B:756:ASP:N	1:B:756:ASP:OD1	2.41	0.53
1:A:623:PRO:HG3	1:B:623:PRO:HG3	1.91	0.53
1:A:847:ASP:OD2	1:A:905:ARG:NH1	2.42	0.52
1:A:630:CYS:SG	1:A:631:THR:N	2.82	0.52
1:B:877:ASN:O	1:B:936:ARG:NH1	2.42	0.52
1:B:733:GLY:O	1:B:734:THR:OG1	2.26	0.51
1:A:756:ASP:N	1:A:756:ASP:OD1	2.45	0.50
1:B:645:CYS:O	2:B:1001:SJV:N21	2.44	0.49
1:A:594:ARG:NH1	1:B:620:ASP:OD1	2.46	0.49
1:B:636:GLN:OE1	1:B:636:GLN:N	2.47	0.48
1:A:688:ASP:O	1:A:693:ASN:ND2	2.46	0.47
1:B:626:ILE:HD12	1:B:695:LEU:HD12	1.98	0.46
1:A:905:ARG:HH22	1:B:905:ARG:HH22	1.63	0.46
1:A:828:LYS:HD2	1:A:962:PHE:HB3	1.98	0.45
1:A:798:GLU:N	1:A:798:GLU:OE1	2.51	0.44
1:A:620:ASP:OD2	1:B:594:ARG:NH1	2.48	0.44
1:A:885:ASP:OD1	1:A:907:LYS:NZ	2.50	0.44
1:B:830:PRO:HA	1:B:833:TRP:CG	2.51	0.44
1:B:862:LEU:O	1:B:943:HIS:NE2	2.46	0.44
1:B:626:ILE:HD12	1:B:695:LEU:CD1	2.48	0.43
1:B:614:GLN:OE1	1:B:617:ARG:NH2	2.44	0.43
1:A:736:GLY:HA2	1:A:781:ARG:HB3	2.00	0.43
1:A:958:GLN:N	1:A:959:PRO:HD2	2.34	0.43
1:B:626:ILE:HD11	1:B:642:ILE:HG21	2.00	0.43
1:B:664:GLU:N	1:B:665:PRO:CD	2.83	0.41
1:B:867:ARG:O	1:B:872:MET:N	2.45	0.41
1:B:700:ASN:OD1	1:B:703:GLY:N	2.53	0.41
1:B:726:SEP:OG	1:B:727:ARG:N	2.54	0.41
1:B:743:LEU:HB3	1:B:786:LEU:HD21	2.03	0.41

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:958:GLN:N	1:B:959:PRO:HD2	2.36	0.40

There are no symmetry-related clashes.

## 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	358/431 (83%)	336 (94%)	20 (6%)	2 (1%)	25	44
1	B	379/431 (88%)	352 (93%)	26 (7%)	1 (0%)	41	61
All	All	737/862 (86%)	688 (93%)	46 (6%)	3 (0%)	34	55

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	581	ALA
1	B	721	GLY
1	A	563	VAL

### 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	305/379 (80%)	300 (98%)	5 (2%)	62	78
1	B	319/379 (84%)	304 (95%)	15 (5%)	26	45

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	624/758 (82%)	604 (97%)	20 (3%)	39 59

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	572	CYS
1	A	612	GLU
1	A	663	LEU
1	A	756	ASP
1	A	962	PHE
1	B	569	ILE
1	B	572	CYS
1	B	636	GLN
1	B	687	ARG
1	B	716	LYS
1	B	718	LEU
1	B	722	ARG
1	B	738	ILE
1	B	756	ASP
1	B	796	HIS
1	B	843	GLN
1	B	872	MET
1	B	875	ARG
1	B	879	THR
1	B	888	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	678	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	SEP	B	724	1	8,9,10	1.56	1 (12%)	8,12,14	1.64	2 (25%)
1	SEP	B	726	1	8,9,10	1.56	1 (12%)	8,12,14	1.41	2 (25%)

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	SEP	B	724	1	-	1/5/8/10	-
1	SEP	B	726	1	-	1/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	724	SEP	P-O1P	3.40	1.61	1.50
1	B	726	SEP	P-O1P	3.40	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	724	SEP	OG-CB-CA	3.51	111.56	108.14
1	B	726	SEP	P-OG-CB	-2.58	111.19	118.30
1	B	726	SEP	OG-CB-CA	2.36	110.44	108.14
1	B	724	SEP	P-OG-CB	-2.14	112.40	118.30

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	726	SEP	N-CA-CB-OG
1	B	724	SEP	CA-CB-OG-P

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	724	SEP	1	0
1	B	726	SEP	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides 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	SJV	A	1001	-	39,40,40	0.79	1 (2%)	50,55,55	2.25	13 (26%)
2	SJV	B	1001	-	39,40,40	0.79	1 (2%)	50,55,55	2.36	14 (28%)

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	SJV	A	1001	-	-	0/18/26/26	0/5/5/5
2	SJV	B	1001	-	-	4/18/26/26	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1001	SJV	C19-N21	3.26	1.38	1.34
2	A	1001	SJV	C19-N21	3.09	1.38	1.34

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1001	SJV	O36-C34-N33	7.25	119.40	109.25
2	A	1001	SJV	O36-C34-N33	6.79	118.75	109.25
2	B	1001	SJV	C17-N18-C19	6.18	120.93	115.45
2	A	1001	SJV	C17-N18-C19	6.11	120.87	115.45
2	A	1001	SJV	C15-N20-C19	5.02	120.83	116.69
2	A	1001	SJV	N18-C19-N20	-4.96	121.85	126.55
2	B	1001	SJV	N18-C19-N20	-4.94	121.86	126.55
2	B	1001	SJV	C15-N20-C19	4.87	120.70	116.69
2	B	1001	SJV	C7-O8-C9	4.80	121.80	116.88
2	B	1001	SJV	O8-C9-C10	4.65	121.24	116.61
2	A	1001	SJV	C7-O8-C9	4.32	121.31	116.88
2	B	1001	SJV	O36-C34-O35	-3.91	118.83	124.58
2	A	1001	SJV	C16-C17-N18	-3.86	119.16	123.96
2	B	1001	SJV	C16-C17-N18	-3.86	119.17	123.96
2	A	1001	SJV	O8-C9-C10	3.80	120.39	116.61
2	A	1001	SJV	O36-C34-O35	-3.73	119.09	124.58
2	B	1001	SJV	C16-C15-N20	-2.98	118.11	121.97
2	A	1001	SJV	C16-C15-N20	-2.86	118.26	121.97
2	B	1001	SJV	C2-C7-C6	-2.52	119.25	122.48
2	B	1001	SJV	C13-N14-C9	2.43	122.24	116.43
2	B	1001	SJV	N21-C19-N20	2.37	120.74	117.18
2	A	1001	SJV	C13-N14-C9	2.35	122.05	116.43
2	A	1001	SJV	C19-N21-C22	-2.32	120.39	124.31
2	A	1001	SJV	C2-C7-C6	-2.25	119.59	122.48
2	B	1001	SJV	C17-C16-C15	2.12	119.22	117.22
2	B	1001	SJV	C3-C2-C7	2.09	120.97	117.68
2	A	1001	SJV	C3-C2-C7	2.01	120.84	117.68

There are no chirality outliers.

All (4) torsion outliers are listed below:

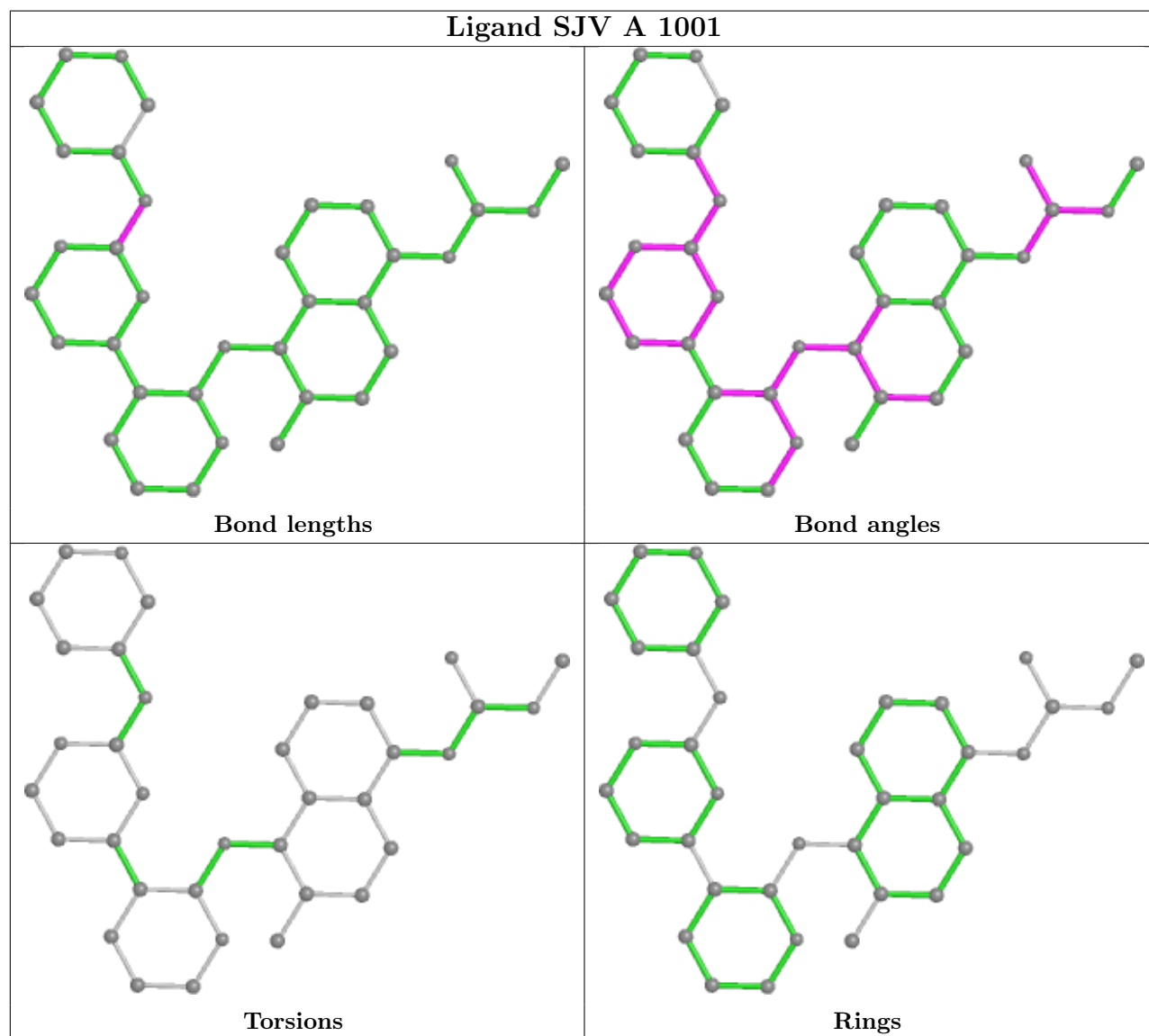
Mol	Chain	Res	Type	Atoms
2	B	1001	SJV	N18-C19-N21-C22
2	B	1001	SJV	N33-C34-O36-C37
2	B	1001	SJV	O35-C34-O36-C37
2	B	1001	SJV	N20-C19-N21-C22

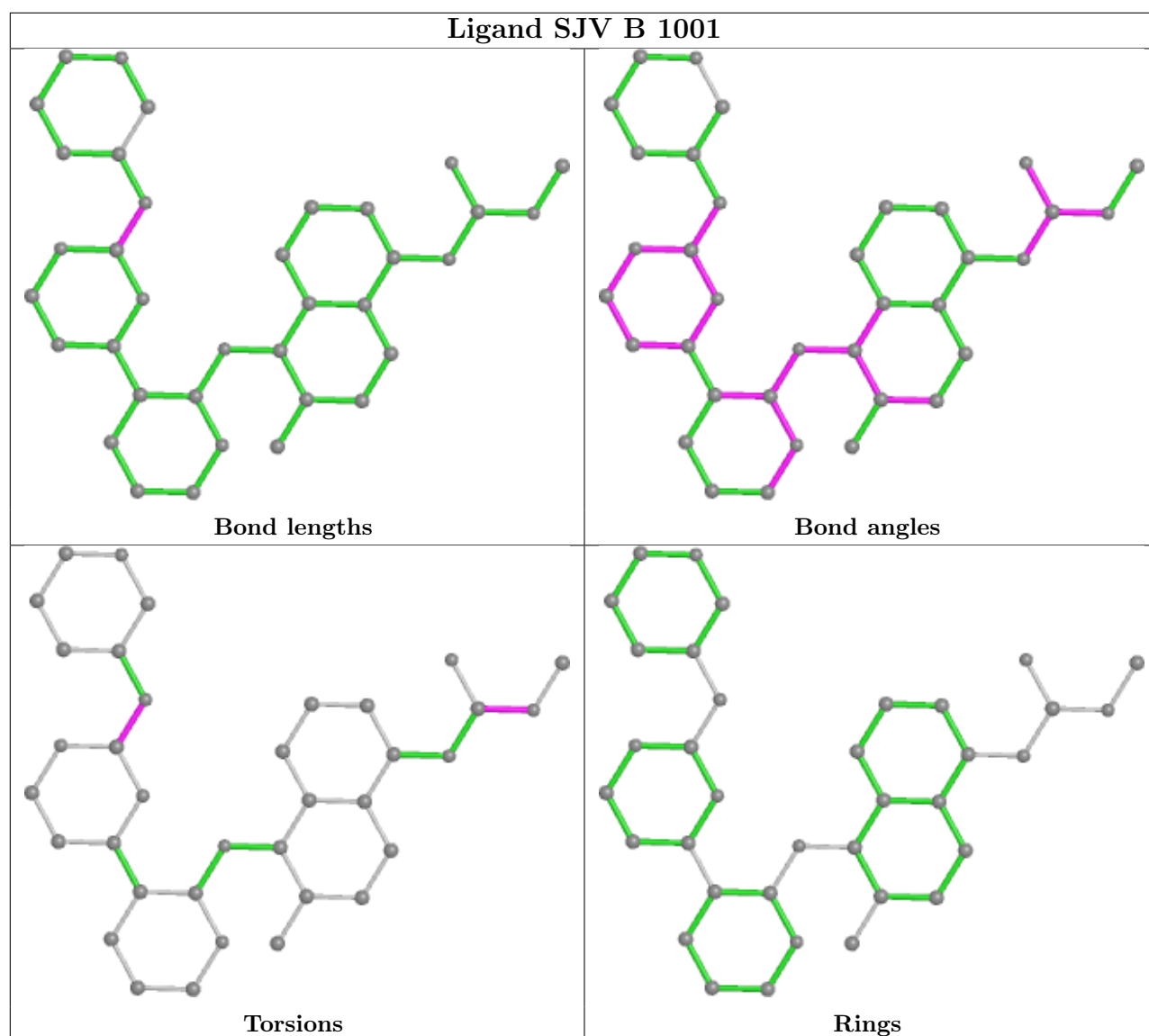
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	SJV	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.





## 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	366/431 (84%)	0.94	45 (12%) <b>4</b> <b>4</b>	38, 74, 104, 142	0
1	B	387/431 (89%)	1.11	61 (15%) <b>2</b> <b>1</b>	38, 81, 117, 146	0
All	All	753/862 (87%)	1.03	106 (14%) <b>2</b> <b>2</b>	38, 77, 113, 146	0

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	719	ALA	8.5
1	A	891	THR	6.4
1	B	749	GLU	6.0
1	B	732	PRO	4.5
1	B	722	ARG	4.4
1	B	575	ASP	4.4
1	B	932	TYR	4.3
1	A	872	MET	4.2
1	B	905	ARG	4.2
1	B	723	HIS	4.2
1	B	955	ARG	4.1
1	B	718	LEU	4.0
1	B	963	HIS	4.0
1	A	906	ASN	3.9
1	A	798	GLU	3.7
1	B	954	GLU	3.6
1	B	779	LEU	3.5
1	B	795	LEU	3.5
1	A	713	GLY	3.4
1	B	733	GLY	3.4
1	B	758	PHE	3.4
1	B	725	PHE	3.3
1	A	776	GLY	3.3
1	B	798	GLU	3.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	930	VAL	3.3
1	B	658	PHE	3.3
1	B	734	THR	3.2
1	A	632	GLU	3.2
1	A	793	ASP	3.2
1	B	861	GLN	3.2
1	B	908	LYS	3.1
1	A	807	GLU	3.1
1	A	813	ILE	3.1
1	B	872	MET	3.1
1	A	815	MET	3.1
1	B	736	GLY	3.1
1	B	770	GLU	3.1
1	B	914	LEU	3.0
1	B	774	PRO	3.0
1	A	630	CYS	3.0
1	A	608	PHE	3.0
1	A	931	CYS	3.0
1	B	720	VAL	3.0
1	B	796	HIS	3.0
1	A	660	HIS	2.9
1	A	905	ARG	2.9
1	A	575	ASP	2.9
1	B	864	ARG	2.9
1	A	753	TYR	2.8
1	A	687	ARG	2.8
1	B	727	ARG	2.8
1	A	658	PHE	2.8
1	B	759	SER	2.8
1	B	739	ALA	2.7
1	A	894	GLY	2.7
1	B	787	LEU	2.7
1	A	836	GLU	2.7
1	B	931	CYS	2.7
1	B	801	GLU	2.7
1	A	711	ASP	2.7
1	B	786	LEU	2.6
1	A	871	LYS	2.5
1	B	817	PRO	2.5
1	A	585	ILE	2.5
1	A	806	ARG	2.5
1	A	875	ARG	2.5

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	892	TYR	2.5
1	B	661	LEU	2.4
1	B	700	ASN	2.4
1	A	699	PRO	2.4
1	A	898	ARG	2.4
1	B	888	LYS	2.4
1	B	721	GLY	2.4
1	A	649	LEU	2.4
1	B	766	TYR	2.4
1	B	572	CYS	2.4
1	A	878	ILE	2.3
1	B	685	VAL	2.3
1	B	657	ASP	2.3
1	A	666	ILE	2.3
1	B	791	SER	2.2
1	A	688	ASP	2.2
1	B	898	ARG	2.2
1	A	860	LYS	2.2
1	B	906	ASN	2.2
1	B	639	TYR	2.2
1	A	943	HIS	2.2
1	A	870	VAL	2.2
1	A	662	GLY	2.2
1	A	796	HIS	2.1
1	B	939	HIS	2.1
1	A	811	LYS	2.1
1	A	566	VAL	2.1
1	A	779	LEU	2.1
1	A	685	VAL	2.1
1	B	807	GLU	2.1
1	A	738	ILE	2.1
1	B	765	TYR	2.1
1	A	710	SER	2.1
1	B	902	ARG	2.1
1	B	754	THR	2.0
1	B	950	LEU	2.0
1	B	579	HIS	2.0
1	B	847	ASP	2.0
1	B	740	PRO	2.0
1	B	743	LEU	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, 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
1	SEP	B	726	10/11	0.54	0.33	81,128,158,242	0
1	SEP	B	724	10/11	0.58	0.31	92,143,171,171	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

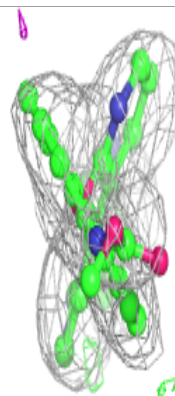
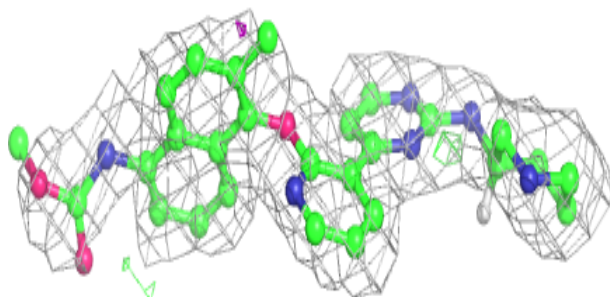
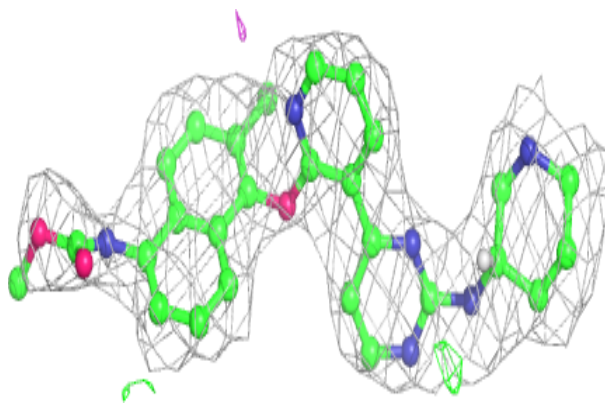
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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	SJV	B	1001	36/36	0.91	0.25	44,58,104,108	0
2	SJV	A	1001	36/36	0.92	0.22	39,51,77,78	0

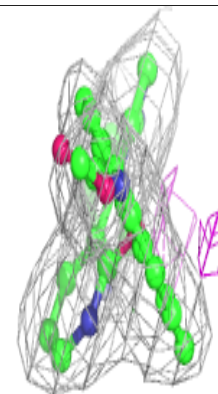
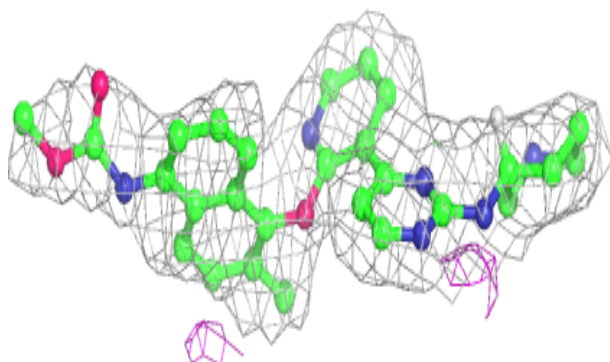
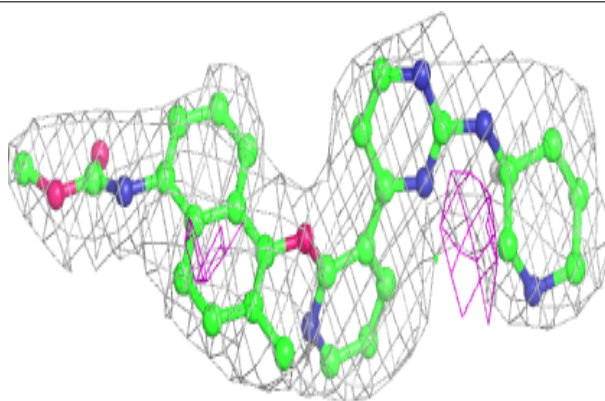
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around SJV B 1001:**

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

**Electron density around SJV A 1001:**

$2mF_o-DF_c$  (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.