



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 18, 2024 – 04:10 AM EDT

PDB ID : 5RAD
Title : PanDDA analysis group deposition – Crystal Structure of JMJD1B in complex with FM001568a
Authors : Snee, M.; Nowak, R.; Johansson, C.; Burgess-Brown, N.A.; Arrowsmith, C.H.; Bountra, C.; Edwards, A.M.; Oppermann, U.
Deposited on : 2020-03-16
Resolution : 1.90 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	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
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)	:	2.37.1

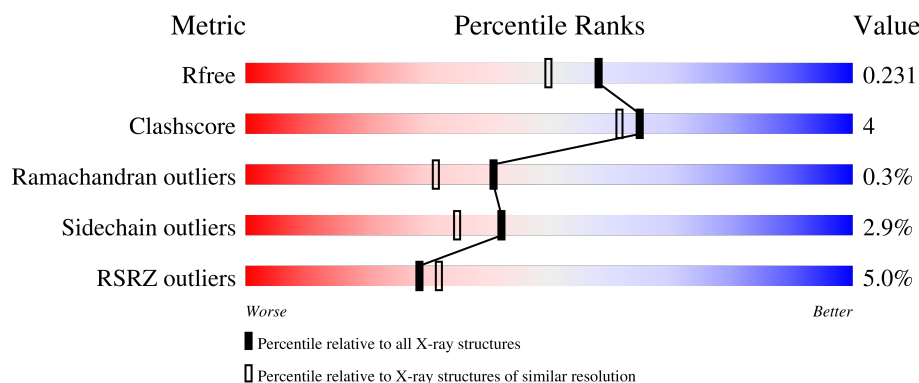
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	372	
1	B	372	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	AYJ	A	1801	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6283 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 Lysine-specific demethylase 3B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	5	0
			2768	1752	483	516	17			
1	B	344	Total	C	N	O	S	0	2	0
			2798	1774	492	517	15			

There are 50 discrepancies between the modelled and reference sequences:

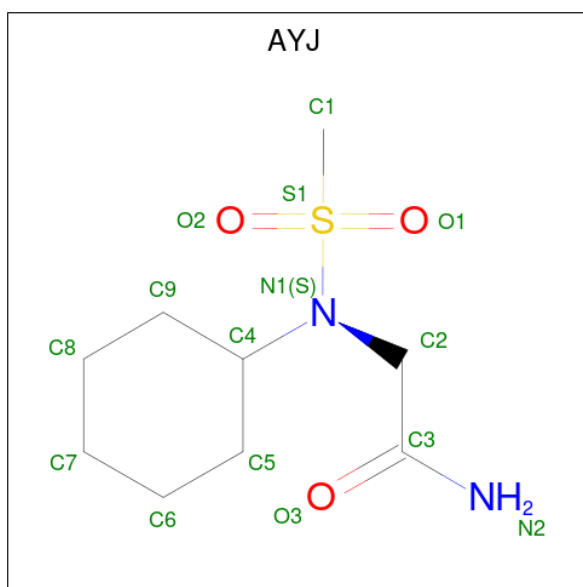
Chain	Residue	Modelled	Actual	Comment	Reference
A	1357	MET	-	initiating methionine	UNP Q7LBC6
A	1358	HIS	-	expression tag	UNP Q7LBC6
A	1359	HIS	-	expression tag	UNP Q7LBC6
A	1360	HIS	-	expression tag	UNP Q7LBC6
A	1361	HIS	-	expression tag	UNP Q7LBC6
A	1362	HIS	-	expression tag	UNP Q7LBC6
A	1363	HIS	-	expression tag	UNP Q7LBC6
A	1364	SER	-	expression tag	UNP Q7LBC6
A	1365	SER	-	expression tag	UNP Q7LBC6
A	1366	GLY	-	expression tag	UNP Q7LBC6
A	1367	VAL	-	expression tag	UNP Q7LBC6
A	1368	ASP	-	expression tag	UNP Q7LBC6
A	1369	LEU	-	expression tag	UNP Q7LBC6
A	1370	GLY	-	expression tag	UNP Q7LBC6
A	1371	THR	-	expression tag	UNP Q7LBC6
A	1372	GLU	-	expression tag	UNP Q7LBC6
A	1373	ASN	-	expression tag	UNP Q7LBC6
A	1374	LEU	-	expression tag	UNP Q7LBC6
A	1375	TYR	-	expression tag	UNP Q7LBC6
A	1376	PHE	-	expression tag	UNP Q7LBC6
A	1377	GLN	-	expression tag	UNP Q7LBC6
A	1378	SER	-	expression tag	UNP Q7LBC6
A	1379	MET	-	expression tag	UNP Q7LBC6
A	1601	GLU	GLN	conflict	UNP Q7LBC6
A	1606	HIS	GLY	conflict	UNP Q7LBC6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	1357	MET	-	initiating methionine	UNP Q7LBC6
B	1358	HIS	-	expression tag	UNP Q7LBC6
B	1359	HIS	-	expression tag	UNP Q7LBC6
B	1360	HIS	-	expression tag	UNP Q7LBC6
B	1361	HIS	-	expression tag	UNP Q7LBC6
B	1362	HIS	-	expression tag	UNP Q7LBC6
B	1363	HIS	-	expression tag	UNP Q7LBC6
B	1364	SER	-	expression tag	UNP Q7LBC6
B	1365	SER	-	expression tag	UNP Q7LBC6
B	1366	GLY	-	expression tag	UNP Q7LBC6
B	1367	VAL	-	expression tag	UNP Q7LBC6
B	1368	ASP	-	expression tag	UNP Q7LBC6
B	1369	LEU	-	expression tag	UNP Q7LBC6
B	1370	GLY	-	expression tag	UNP Q7LBC6
B	1371	THR	-	expression tag	UNP Q7LBC6
B	1372	GLU	-	expression tag	UNP Q7LBC6
B	1373	ASN	-	expression tag	UNP Q7LBC6
B	1374	LEU	-	expression tag	UNP Q7LBC6
B	1375	TYR	-	expression tag	UNP Q7LBC6
B	1376	PHE	-	expression tag	UNP Q7LBC6
B	1377	GLN	-	expression tag	UNP Q7LBC6
B	1378	SER	-	expression tag	UNP Q7LBC6
B	1379	MET	-	expression tag	UNP Q7LBC6
B	1601	GLU	GLN	conflict	UNP Q7LBC6
B	1606	HIS	GLY	conflict	UNP Q7LBC6

- Molecule 2 is 2-[cyclohexyl(methylsulfonyl)amino]ethanamide (three-letter code: AYJ) (formula: C₉H₁₈N₂O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	9	2	3	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Cl	0	0
			4	4		
3	B	1	Total	Cl	0	0
			1	1		

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mn	0	0
			1	1		
4	B	1	Total	Mn	0	0
			1	1		

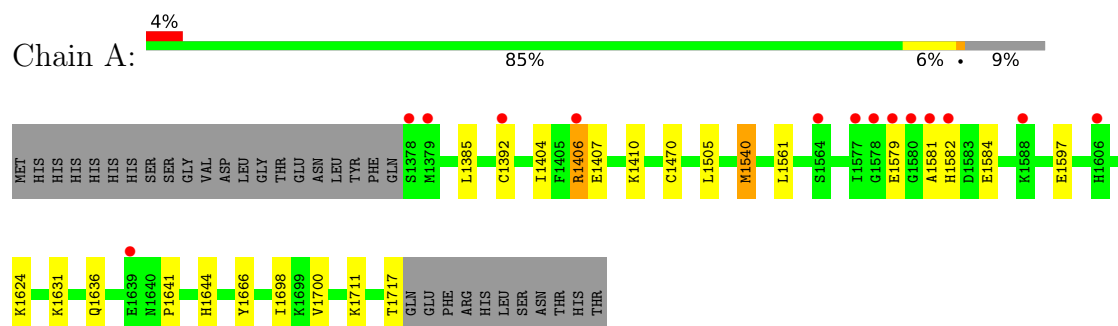
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	379	Total	O	0	0
			379	379		
5	B	316	Total	O	0	0
			316	316		

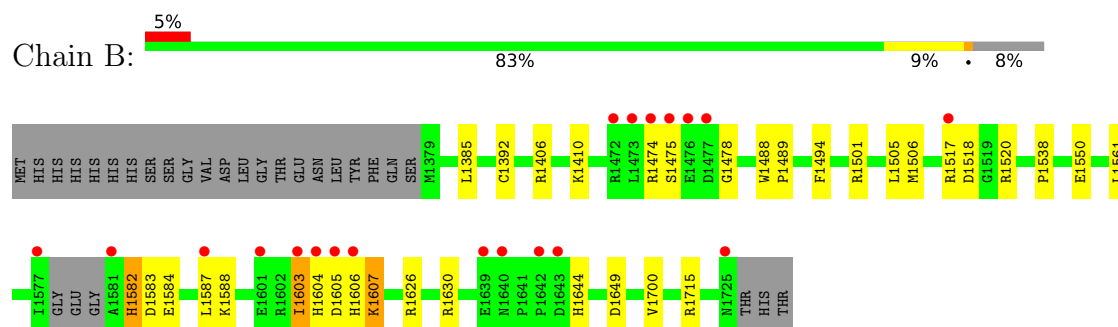
3 Residue-property plots [i](#)

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: Lysine-specific demethylase 3B



• Molecule 1: Lysine-specific demethylase 3B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.69Å 93.68Å 93.32Å 90.00° 107.81° 90.00°	Depositor
Resolution (Å)	54.99 – 1.90 54.93 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.0 (54.99-1.90) 99.1 (54.93-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.180 , 0.219 0.194 , 0.231	Depositor DCC
R_{free} test set	3669 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 45.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6283	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% 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: CL, MN, AYJ

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	0.78	0/2841	0.84	0/3854
1	B	0.75	0/2872	0.81	0/3895
All	All	0.76	0/5713	0.82	0/7749

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	2768	0	2650	18	0
1	B	2798	0	2685	27	0
2	A	15	0	0	0	0
3	A	4	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	379	0	0	11	0
5	B	316	0	0	8	0
All	All	6283	0	5335	45	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 (45) 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:A:1624:LYS:NZ	5:A:1901:HOH:O	1.96	0.88
1:B:1474:ARG:HD2	1:B:1478:GLY:O	1.75	0.86
1:A:1406[A]:ARG:NH1	5:A:1902:HOH:O	2.11	0.84
1:A:1406[A]:ARG:NH2	5:A:1905:HOH:O	2.20	0.72
1:A:1385:LEU:HD12	1:A:1392[B]:CYS:SG	2.33	0.68
1:A:1631:LYS:HE2	1:A:1666:TYR:OH	1.95	0.67
1:B:1406:ARG:CB	5:B:2154:HOH:O	2.43	0.67
1:A:1582:HIS:O	1:A:1582:HIS:CG	2.48	0.66
1:A:1470:CYS:O	5:A:1903:HOH:O	2.13	0.66
1:B:1518:ASP:HB3	5:B:2130:HOH:O	1.97	0.64
1:B:1517[B]:ARG:CG	1:B:1517[B]:ARG:HH11	2.11	0.63
1:A:1407:GLU:HG2	5:A:2229:HOH:O	1.98	0.63
1:B:1550:GLU:HG3	5:B:2089:HOH:O	1.99	0.61
1:B:1517[B]:ARG:HH11	1:B:1517[B]:ARG:HG3	1.67	0.60
1:B:1517[B]:ARG:HG3	1:B:1517[B]:ARG:NH1	2.19	0.58
1:B:1505:LEU:HD22	1:B:1700:VAL:HG11	1.88	0.56
1:B:1506:MET:CE	1:B:1538:PRO:HG3	2.35	0.55
1:B:1410:LYS:HE2	5:B:2177:HOH:O	2.08	0.54
1:A:1597:GLU:OE1	5:A:1904:HOH:O	2.19	0.52
1:A:1385:LEU:CD1	1:A:1392[B]:CYS:SG	3.00	0.50
1:A:1641:PRO:HD2	5:A:1906:HOH:O	2.13	0.48
1:B:1715:ARG:HG3	5:B:2132:HOH:O	2.12	0.48
1:B:1626:ARG:O	1:B:1630:ARG:HG3	2.13	0.47
1:A:1505:LEU:HD22	1:A:1700:VAL:HG11	1.97	0.46
1:A:1711:LYS:CB	5:A:2100:HOH:O	2.63	0.46
1:B:1488:TRP:HA	1:B:1489:PRO:C	2.34	0.46
1:B:1587:LEU:HD13	1:B:1603:ILE:HD11	1.97	0.46
1:B:1385:LEU:HD12	1:B:1392:CYS:SG	2.56	0.46
1:B:1582:HIS:C	1:B:1584:GLU:H	2.19	0.46
1:B:1506:MET:HE3	1:B:1538:PRO:HD3	1.97	0.45
1:B:1644:HIS:NE2	1:B:1649:ASP:OD2	2.49	0.45
1:B:1506:MET:HE2	1:B:1538:PRO:HG3	1.99	0.45
1:A:1561:LEU:C	1:A:1561:LEU:HD12	2.37	0.44
1:B:1715:ARG:HD3	5:B:2183:HOH:O	2.17	0.44
1:B:1520:ARG:NE	5:B:1914:HOH:O	2.51	0.44
1:B:1410:LYS:CE	5:B:2177:HOH:O	2.66	0.43
1:A:1410:LYS:NZ	5:A:1902:HOH:O	2.52	0.43
1:B:1517[B]:ARG:HH11	1:B:1517[B]:ARG:HB2	1.84	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1644:HIS:CE1	1:B:1649:ASP:OD2	2.72	0.42
1:A:1582:HIS:CE1	5:A:2019:HOH:O	2.73	0.42
1:A:1540:MET:HE2	1:A:1698:ILE:CG2	2.49	0.42
1:B:1607:LYS:HZ2	1:B:1607:LYS:HA	1.85	0.41
1:A:1636:GLN:NE2	5:A:1907:HOH:O	2.25	0.41
1:B:1517[B]:ARG:HH11	1:B:1517[B]:ARG:CB	2.33	0.41
1:B:1561:LEU:HD12	1:B:1561:LEU:C	2.41	0.41

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	343/372 (92%)	333 (97%)	9 (3%)	1 (0%)	41	31
1	B	342/372 (92%)	328 (96%)	13 (4%)	1 (0%)	41	31
All	All	685/744 (92%)	661 (96%)	22 (3%)	2 (0%)	41	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1581	ALA
1	B	1583	ASP

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	299/331 (90%)	291 (97%)	8 (3%)	44	38
1	B	302/331 (91%)	292 (97%)	10 (3%)	38	29
All	All	601/662 (91%)	583 (97%)	18 (3%)	42	33

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1404	ILE
1	A	1406[A]	ARG
1	A	1406[B]	ARG
1	A	1540	MET
1	A	1579	GLU
1	A	1584	GLU
1	A	1644	HIS
1	A	1717	THR
1	B	1475	SER
1	B	1494	PHE
1	B	1501	ARG
1	B	1582	HIS
1	B	1588	LYS
1	B	1603	ILE
1	B	1604	HIS
1	B	1605	ASP
1	B	1606	HIS
1	B	1607	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	1650	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 7 are monoatomic - leaving 1 for Mogul analysis.

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	AYJ	A	1801	-	14,15,15	1.66	3 (21%)	20,21,21	1.39	4 (20%)

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	AYJ	A	1801	-	-	8/14/22/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1801	AYJ	S1-N1	4.00	1.68	1.62
2	A	1801	AYJ	C1-S1	-3.43	1.67	1.75
2	A	1801	AYJ	C2-C3	2.09	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1801	AYJ	C5-C4-N1	-2.93	108.31	112.42
2	A	1801	AYJ	C2-N1-C4	-2.86	112.60	118.62
2	A	1801	AYJ	C7-C8-C9	-2.25	106.82	111.42
2	A	1801	AYJ	O3-C3-C2	2.23	124.11	120.56

There are no chirality outliers.

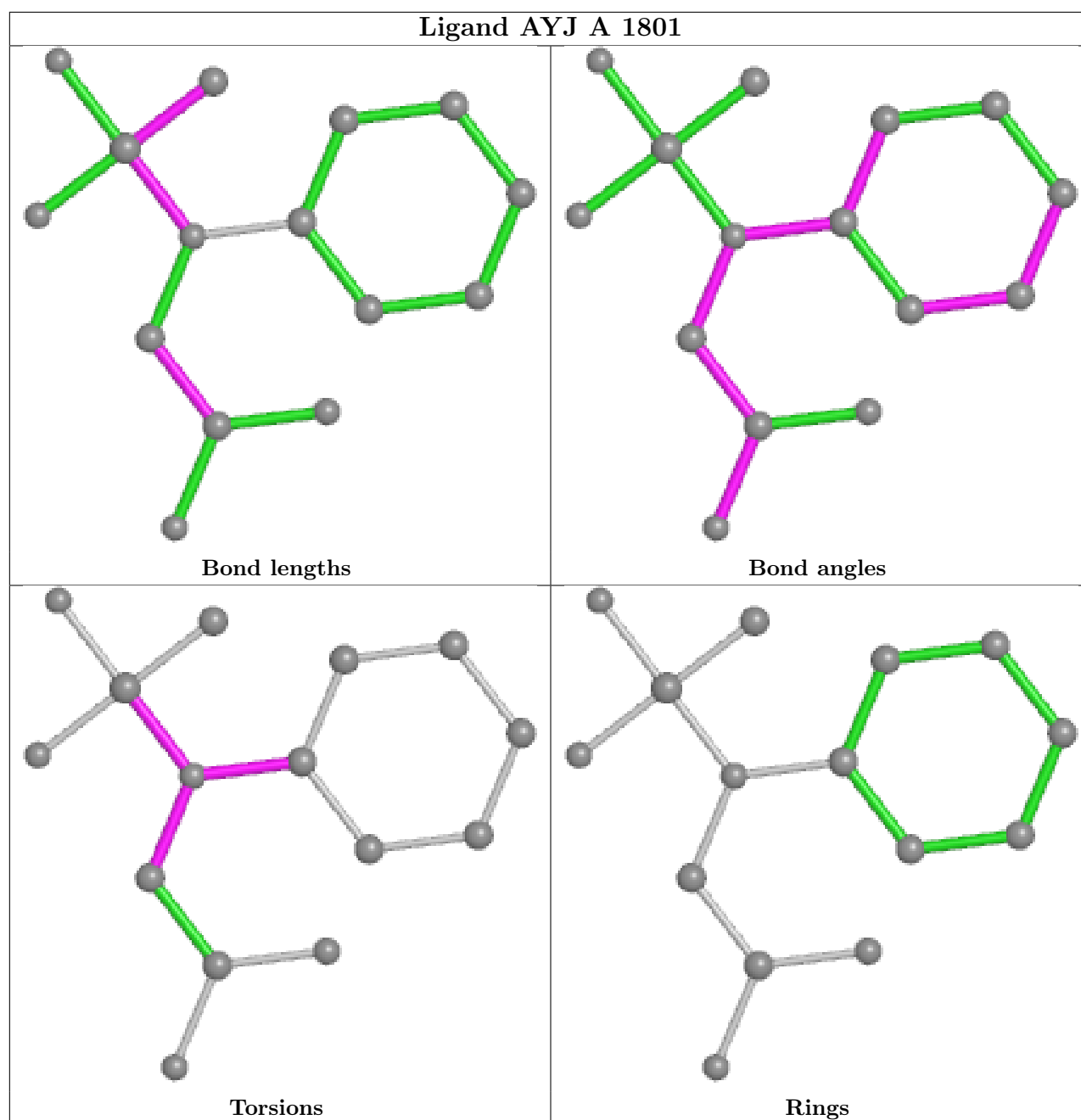
All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1801	AYJ	C9-C4-N1-S1
2	A	1801	AYJ	C9-C4-N1-C2
2	A	1801	AYJ	C4-N1-S1-O2
2	A	1801	AYJ	C2-N1-S1-C1
2	A	1801	AYJ	C2-N1-S1-O2
2	A	1801	AYJ	C3-C2-N1-C4
2	A	1801	AYJ	C4-N1-S1-C1
2	A	1801	AYJ	C5-C4-N1-C2

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, 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	340/372 (91%)	-0.17	14 (4%)	37 40	18, 30, 66, 113	8 (2%)
1	B	344/372 (92%)	0.04	20 (5%)	23 25	20, 34, 67, 130	11 (3%)
All	All	684/744 (91%)	-0.06	34 (4%)	28 32	18, 32, 67, 130	19 (2%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1473	LEU	11.1
1	B	1581	ALA	9.9
1	B	1475	SER	9.2
1	B	1474	ARG	8.3
1	A	1392[A]	CYS	8.2
1	B	1605	ASP	7.2
1	A	1564[A]	SER	7.0
1	A	1406[A]	ARG	6.9
1	A	1581	ALA	6.7
1	B	1477	ASP	6.6
1	B	1517[A]	ARG	6.5
1	B	1476	GLU	6.4
1	B	1577	ILE	6.3
1	B	1472	ARG	6.2
1	A	1379[A]	MET	5.4
1	A	1580	GLY	5.4
1	A	1577	ILE	5.3
1	B	1604	HIS	5.2
1	A	1582	HIS	4.6
1	B	1606	HIS	4.3
1	A	1378	SER	3.8
1	A	1588[A]	LYS	3.7
1	B	1601	GLU	3.4
1	B	1603	ILE	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	1587	LEU	2.9
1	B	1643	ASP	2.7
1	A	1579	GLU	2.7
1	A	1578	GLY	2.7
1	B	1639	GLU	2.7
1	A	1606	HIS	2.6
1	A	1639	GLU	2.5
1	B	1642	PRO	2.4
1	B	1640	ASN	2.4
1	B	1725	ASN	2.3

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 monosaccharides in this entry.

6.4 Ligands [i](#)

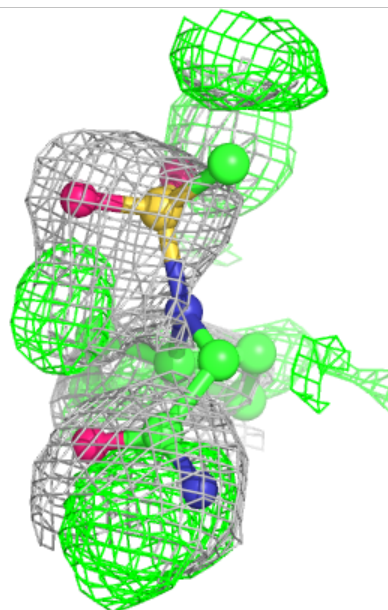
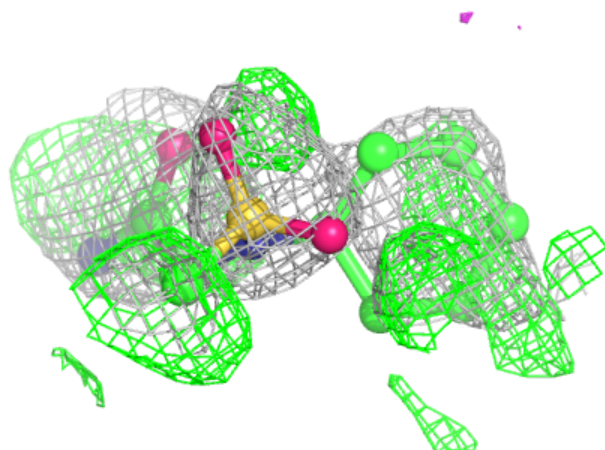
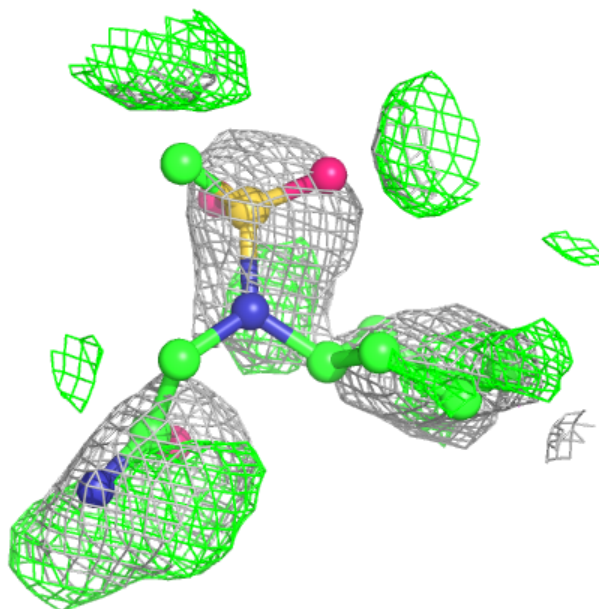
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	AYJ	A	1801	15/15	0.61	0.56	41,45,47,49	15
4	MN	A	1806	1/1	0.84	0.14	56,56,56,56	0
3	CL	A	1805	1/1	0.93	0.10	53,53,53,53	0
4	MN	B	1802	1/1	0.95	0.16	39,39,39,39	0
3	CL	B	1801	1/1	0.97	0.05	43,43,43,43	0
3	CL	A	1804	1/1	0.97	0.04	36,36,36,36	0
3	CL	A	1803	1/1	0.97	0.06	42,42,42,42	0
3	CL	A	1802	1/1	1.00	0.09	25,25,25,25	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 AYJ A 1801:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.