Full wwPDB X-ray Structure Validation Report (i)

Oct 26, 2026 – 01:22 pm GMT

PDB ID	:	9SYX / pdb_00009syx
Title	:	Crystal structure of PD-2018 bound METTL3-METTL14 complex
Authors	:	Benysek, J.; Boura, E.
Deposited on	:	2025-10-14
Resolution	:	2.14 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 (i) 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 (i)) were used in the production of this report:

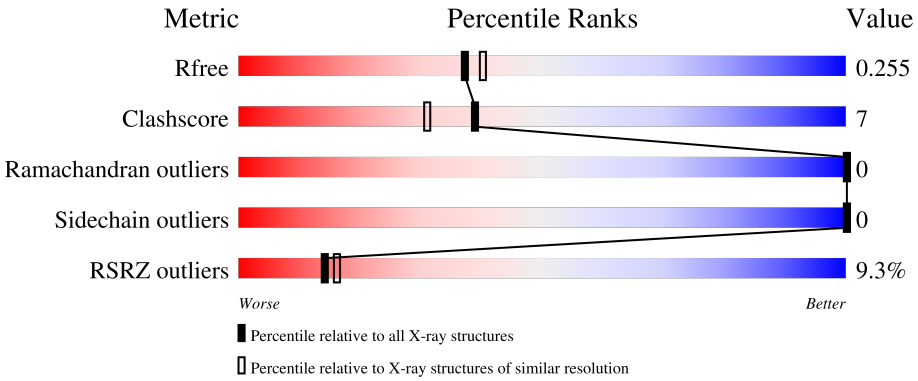
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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 <=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	225	10% 67% 21% 12%
2	B	290	7% 83% 8% 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3778 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 N(6)-adenosine-methyltransferase catalytic subunit METTL3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	1	0
			1563	998	276	279	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	356	MET	-	initiating methionine	UNP Q86U44
A	568	LYS	ARG	engineered mutation	UNP Q86U44

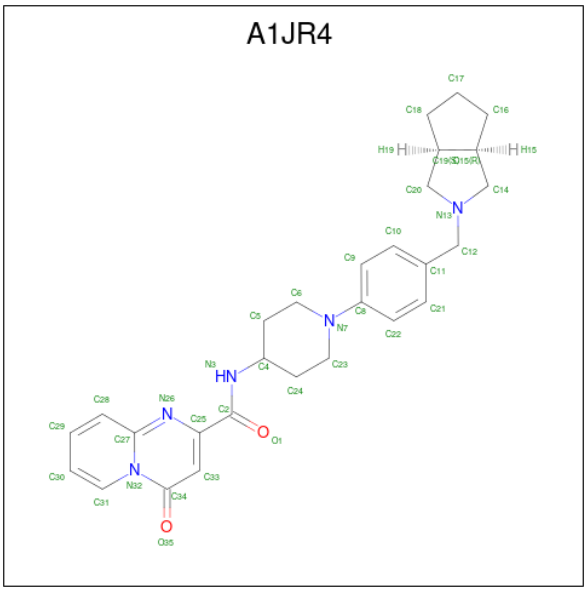
- Molecule 2 is a protein called N(6)-adenosine-methyltransferase non-catalytic subunit METTL14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	265	Total	C	N	O	S	0	3	0
			2138	1365	367	394	12			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	110	MET	-	initiating methionine	UNP Q9HCE5

- Molecule 3 is {N}-[1-[4-[[(3 {a} {S},6 {a} {R})-3,3 {a},4,5,6,6 {a}-hexahydro-1 {H}-cyclopenta[c]pyrrol-2-yl]methyl]phenyl]piperidin-4-yl]-4-oxidanylidene-pyrido[1,2-a]pyrimidine-2-carboxamide (CCD ID: A1JR4) (formula: $C_{28}H_{33}N_5O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 35 28 5 2	0	0

- Molecule 4 is water.

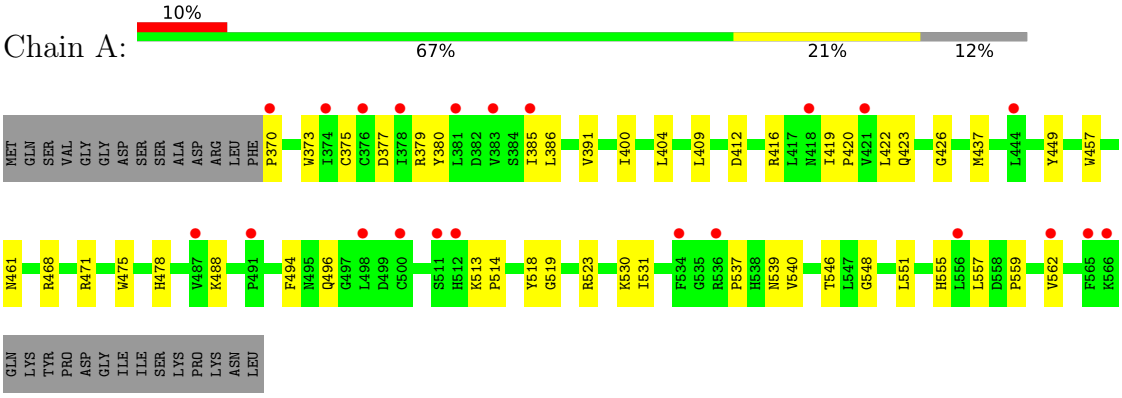
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	10	Total O 10 10	0	0
4	B	32	Total O 32 32	0	0

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.

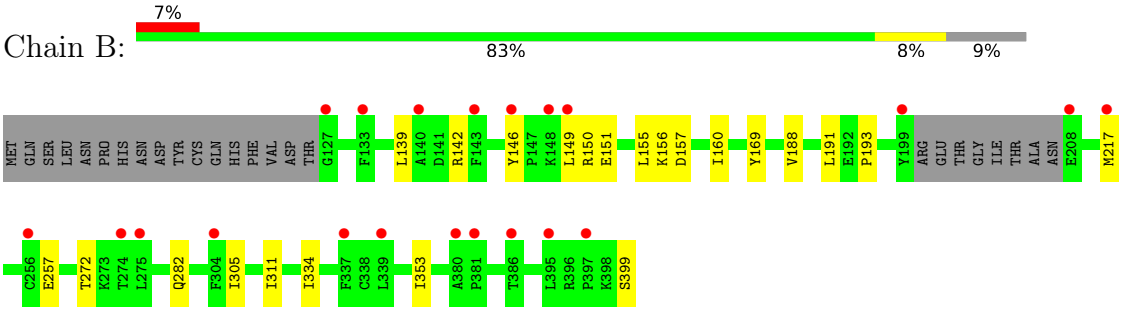
• Molecule 1: N(6)-adenosine-methyltransferase catalytic subunit METTL3

Chain A:



• Molecule 2: N(6)-adenosine-methyltransferase non-catalytic subunit METTL14

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	101.42Å 101.42Å 117.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.91 – 2.14 35.91 – 2.14	Depositor EDS
% Data completeness (in resolution range)	89.6 (35.91-2.14) 89.6 (35.91-2.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.52 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.227 , 0.256 0.227 , 0.255	Depositor DCC
R_{free} test set	1578 reflections (4.59%)	wwPDB-VP
Wilson B-factor (Å^2)	65.0	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 50.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3778	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: A1JR4

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	0.20	0/1606	0.38	0/2188
2	B	0.14	0/2197	0.33	0/2981
All	All	0.17	0/3803	0.35	0/5169

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	1563	0	1519	33	0
2	B	2138	0	2068	21	0
3	A	35	0	0	0	0
4	A	10	0	0	2	0
4	B	32	0	0	0	0
All	All	3778	0	3587	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 7.

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:A:494:PHE:HE1	1:A:496:GLN:HB3	1.54	0.72
1:A:513:LYS:NZ	1:A:518:TYR:OH	2.25	0.70
2:B:146:TYR:HB3	2:B:149:LEU:HD13	1.74	0.69
1:A:373:TRP:HB2	1:A:551:LEU:HD13	1.77	0.65
1:A:385:ILE:HG13	1:A:386:LEU:HD23	1.80	0.63
2:B:272:THR:H	2:B:282:GLN:NE2	1.98	0.61
2:B:191:LEU:HD22	2:B:193:PRO:HD3	1.81	0.61
2:B:272:THR:H	2:B:282:GLN:HE22	1.48	0.60
1:A:391:VAL:HB	1:A:530:LYS:HG2	1.84	0.60
1:A:419:ILE:HA	1:A:422:LEU:HD13	1.85	0.59
1:A:494:PHE:CE1	1:A:496:GLN:HB3	2.38	0.58
1:A:555:HIS:CE1	1:A:557:LEU:HD11	2.38	0.58
1:A:513:LYS:NZ	1:A:539:ASN:ND2	2.52	0.57
1:A:559:PRO:HA	1:A:562:VAL:HG12	1.86	0.57
1:A:379:ARG:HD3	1:A:409:LEU:HD21	1.88	0.56
1:A:422:LEU:HD23	1:A:531:ILE:HD13	1.90	0.54
2:B:272:THR:N	2:B:282:GLN:HE22	2.05	0.54
1:A:468:ARG:HG2	2:B:311:ILE:HD13	1.90	0.54
1:A:546:THR:HG22	1:A:551:LEU:HD11	1.92	0.51
1:A:537:PRO:O	1:A:540:VAL:HG22	2.10	0.51
1:A:370:PRO:HB2	1:A:557:LEU:HD23	1.93	0.50
1:A:471:ARG:NH2	2:B:399:SER:HA	2.26	0.50
1:A:419:ILE:N	1:A:420:PRO:HD2	2.27	0.50
2:B:150:ARG:HH11	2:B:150:ARG:HG2	1.77	0.50
2:B:188[B]:VAL:HG21	2:B:334:ILE:HG23	1.95	0.49
2:B:157:ASP:HA	2:B:160:ILE:HD12	1.96	0.48
1:A:513:LYS:HZ1	1:A:539:ASN:ND2	2.11	0.48
1:A:475:TRP:HZ3	2:B:305:ILE:HD13	1.78	0.47
1:A:375:CYS:HA	1:A:548:GLY:O	2.14	0.47
1:A:437:MET:HG2	4:A:702:HOH:O	2.14	0.47
1:A:457:TRP:CE3	1:A:514:PRO:HD3	2.49	0.47
2:B:191:LEU:CD2	2:B:193:PRO:HD3	2.43	0.47
2:B:142:ARG:HE	2:B:142:ARG:HB2	1.38	0.46
1:A:412:ASP:HB3	1:A:416:ARG:NH1	2.31	0.46
1:A:478:HIS:HE1	2:B:257:GLU:OE1	2.01	0.44
2:B:188[B]:VAL:HG21	2:B:334:ILE:CG2	2.48	0.44
1:A:519:GLY:C	1:A:523:ARG:HE	2.26	0.44
1:A:423:GLN:HE21	1:A:426:GLY:HA3	1.82	0.43
1:A:449:TYR:CE2	1:A:488:LYS:HB2	2.53	0.43
1:A:377:ASP:HB3	1:A:380:TYR:HD2	1.83	0.43
2:B:139:LEU:HD23	2:B:139:LEU:HA	1.87	0.43
1:A:461:ASN:HB2	4:A:703:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ILE:HG12	1:A:404:LEU:HD11	2.01	0.42
2:B:169:TYR:HB3	2:B:353:ILE:HD12	2.01	0.42
1:A:379:ARG:HD3	1:A:409:LEU:CD2	2.47	0.42
1:A:513:LYS:HZ2	1:A:539:ASN:ND2	2.16	0.42
2:B:156:LYS:O	2:B:160:ILE:HG13	2.21	0.41
2:B:149:LEU:H	2:B:149:LEU:HD12	1.86	0.41
2:B:217:MET:HB2	2:B:217:MET:HE2	1.82	0.40
2:B:151:GLU:HG3	2:B:155:LEU:HD12	2.02	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	196/225 (87%)	193 (98%)	3 (2%)	0	100	100
2	B	264/290 (91%)	257 (97%)	7 (3%)	0	100	100
All	All	460/515 (89%)	450 (98%)	10 (2%)	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	166/198 (84%)	166 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	228/260 (88%)	228 (100%)	0	100	100
All	All	394/458 (86%)	394 (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 (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	478	HIS
1	A	539	ASN
1	A	550	GLN
2	B	128	HIS
2	B	282	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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is 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	$\#\|Z\|>2$
3	A1JR4	A	601	-	40,40,40	0.24	0	52,57,57	0.56	0

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
3	A1JR4	A	601	-	-	1/16/44/44	0/6/6/6

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

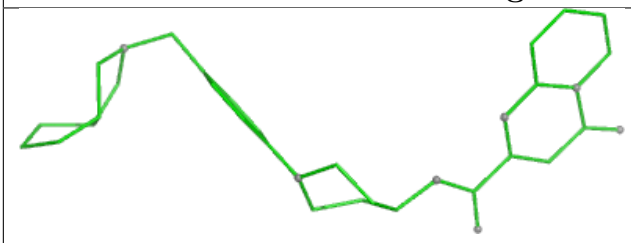
Mol	Chain	Res	Type	Atoms
3	A	601	A1JR4	C22-C8-N7-C23

There are no ring outliers.

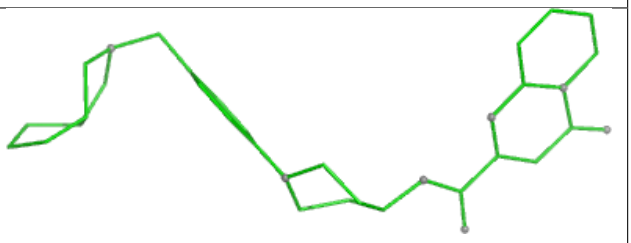
No monomer is involved in short contacts.

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 then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

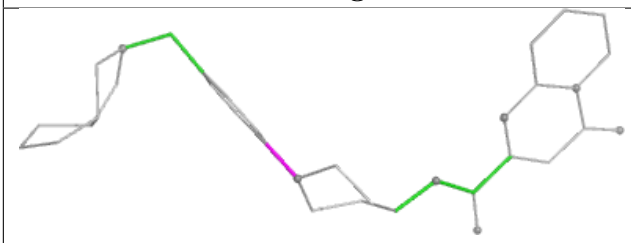
Ligand A1JR4 A 601



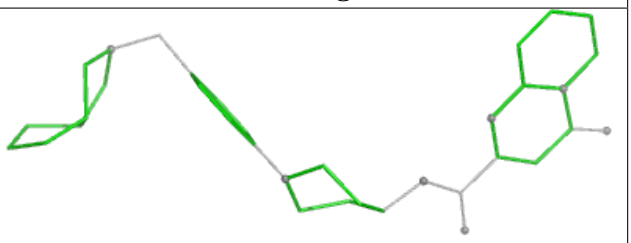
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	197/225 (87%)	0.98	22 (11%) 10 12	44, 83, 118, 128	1 (0%)
2	B	265/290 (91%)	0.59	21 (7%) 18 21	27, 65, 105, 119	3 (1%)
All	All	462/515 (89%)	0.76	43 (9%) 14 16	27, 73, 111, 128	4 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	376	CYS	7.2
2	B	395	LEU	4.8
2	B	208	GLU	4.0
2	B	339	LEU	3.9
1	A	378	ILE	3.9
1	A	383	VAL	3.8
2	B	143	PHE	3.7
2	B	199	TYR	3.7
1	A	556	LEU	3.4
2	B	127	GLY	3.2
1	A	374	ILE	3.2
1	A	370	PRO	3.1
1	A	381	LEU	3.1
1	A	498	LEU	3.0
2	B	274	THR	2.8
2	B	149	LEU	2.8
1	A	512	HIS	2.8
2	B	381	PRO	2.7
1	A	418	ASN	2.7
1	A	444	LEU	2.6
1	A	500	CYS	2.6
1	A	487	VAL	2.5
2	B	146	TYR	2.5
2	B	148	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	337	PHE	2.4
1	A	562	VAL	2.3
1	A	536	ARG	2.3
1	A	534	PHE	2.3
1	A	511	SER	2.3
1	A	421	VAL	2.3
2	B	304	PHE	2.3
2	B	380	ALA	2.2
2	B	275	LEU	2.2
2	B	140	ALA	2.2
1	A	566	LYS	2.2
2	B	397	PRO	2.1
2	B	256	CYS	2.1
1	A	385	ILE	2.1
2	B	133	PHE	2.1
2	B	217	MET	2.0
1	A	491	PRO	2.0
1	A	565	PHE	2.0
2	B	386	THR	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^{th} 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.

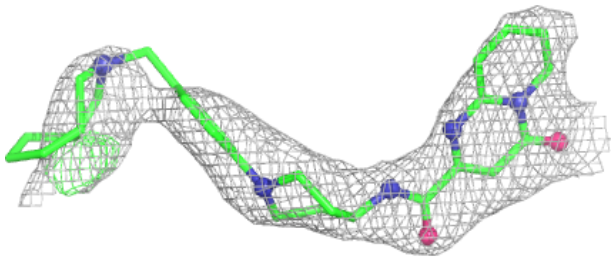
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	A1JR4	A	601	35/35	0.78	0.16	86,102,113,116	0

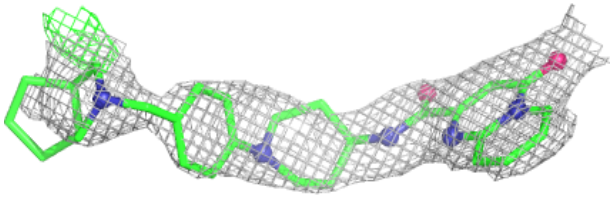
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

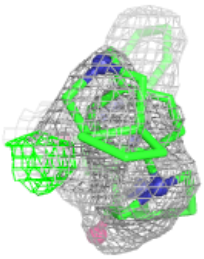
as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around A1JR4 A 601:

$2mF_o$-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.