wwPDB X-ray Structure Validation Summary Report (i)

Oct 29, 2024 – 01:45 pm GMT

PDB ID	:	9FIT
Title	:	Structure-guided discovery of selective USP7 inhibitors with in vivo activity
Authors	:	Baker, L.M.; Murray, J.; Hubbard, R.E.; Whitehead, N.
Deposited on	:	2024-05-29
Resolution	:	2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

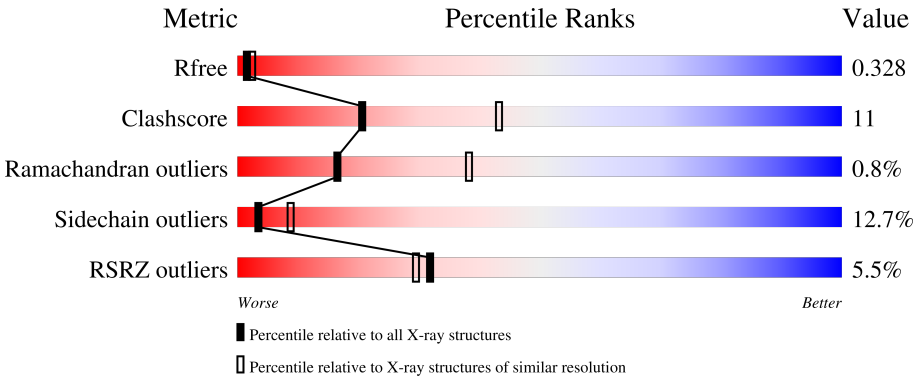
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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	355	4% 64% 24% • • 8%
1	B	355	6% 63% 25% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10730 atoms, of which 5280 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.

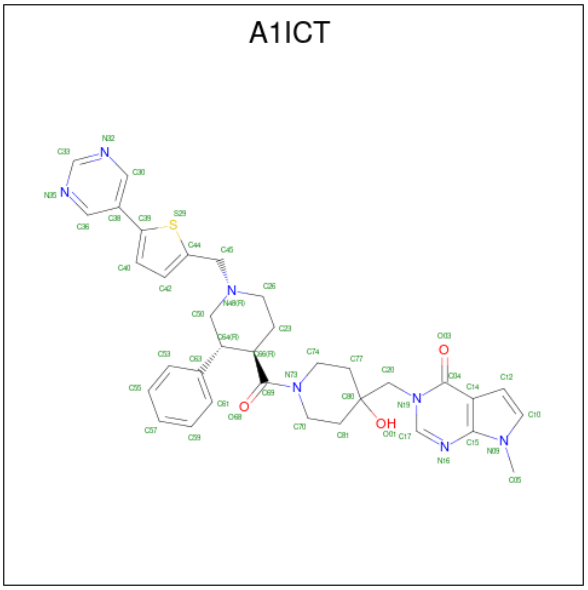
- Molecule 1 is a protein called Ubiquitin carboxyl-terminal hydrolase 7.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	327	Total	C	H	N	O	S	73	0	0
			5240	1670	2602	447	505	16			
1	B	326	Total	C	H	N	O	S	72	0	0
			5237	1672	2602	443	505	15			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	GLY	-	expression tag	UNP Q93009
A	409	ALA	PHE	engineered mutation	UNP Q93009
B	206	GLY	-	expression tag	UNP Q93009
B	409	ALA	PHE	engineered mutation	UNP Q93009

- Molecule 2 is 7-methyl-3-[[4-oxidanyl-1-[(3 {R},4 {R})-3-phenyl-1-[(5-pyrimidin-5-ylthiophen-2-yl)methyl]piperidin-4-yl]carbonyl-piperidin-4-yl]methyl]pyrrolo[2,3-d]pyrimidin-4-one (three-letter code: A1ICT) (formula: $C_{34}H_{37}N_7O_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	S	4	0
			83	34	38	7	3	1		
2	B	1	Total	C	H	N	O	S	4	0
			83	34	38	7	3	1		

- Molecule 3 is water.

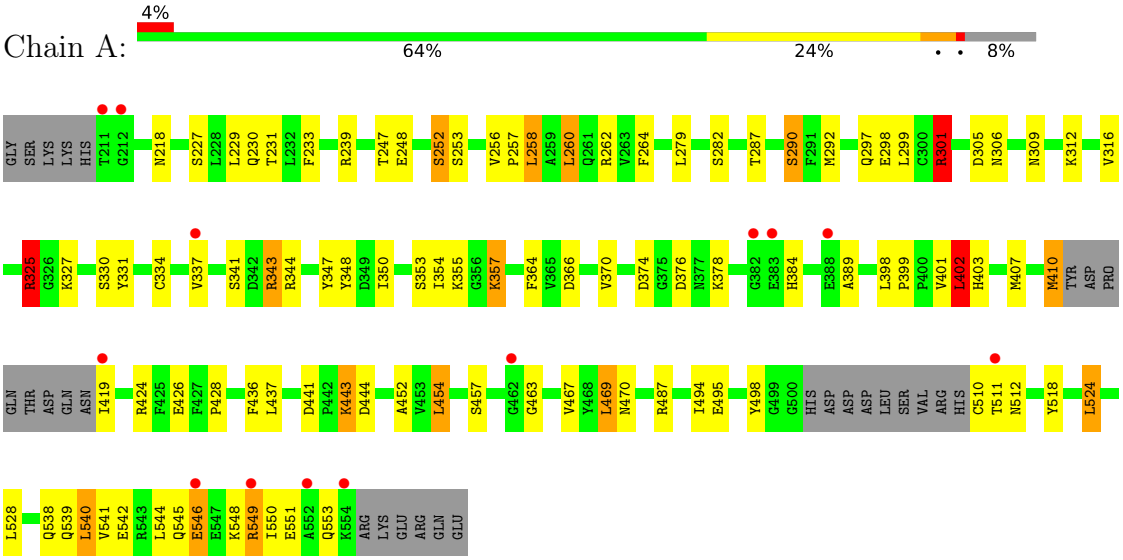
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total	O	0	0
			45	45		
3	B	42	Total	O	0	0
			42	42		

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.

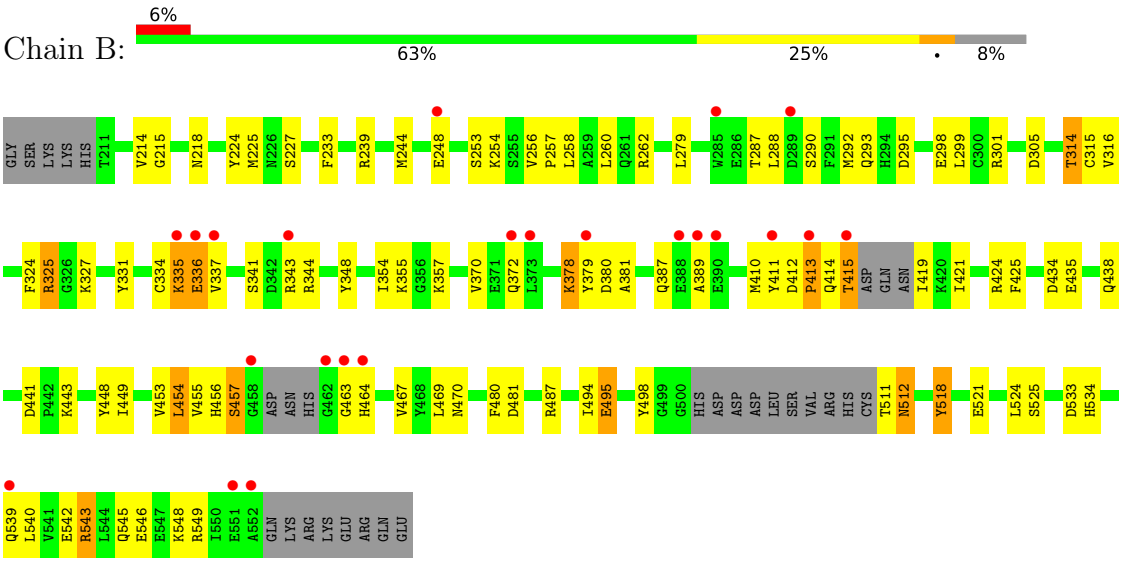
• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 7

Chain A:



• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 7

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	74.76Å 67.69Å 77.51Å 90.00° 90.54° 90.00°	Depositor
Resolution (Å)	21.66 – 2.70 21.66 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.7 (21.66-2.70) 96.5 (21.66-2.70)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.76 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.273 , 0.328 0.273 , 0.328	Depositor DCC
R_{free} test set	1080 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	10.6	Xtriage
Anisotropy	1.521	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 24.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.014 for h,-k,-l 0.024 for l,-k,h	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	10730	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.17 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.0408e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: A1ICT

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	0.48	0/2690	0.93	5/3626 (0.1%)
1	B	0.46	0/2687	0.94	6/3622 (0.2%)
All	All	0.47	0/5377	0.94	11/7248 (0.2%)

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	A	0	3
1	B	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	543	ARG	NE-CZ-NH2	-9.12	115.74	120.30
1	A	402	LEU	CB-CG-CD2	6.75	122.47	111.00
1	A	325	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	A	410	MET	CG-SD-CE	6.08	109.93	100.20
1	B	244	MET	CG-SD-CE	5.70	109.32	100.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	424	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	510	CYS	Peptide
1	A	549	ARG	Sidechain
1	B	543	ARG	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2638	2602	2587	61	2
1	B	2635	2602	2589	53	2
2	A	45	38	0	1	0
2	B	45	38	0	2	0
3	A	45	0	0	7	0
3	B	42	0	0	9	0
All	All	5450	5280	5176	116	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 11.

The worst 5 of 116 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:297:GLN:O	1:A:301:ARG:HG3	1.56	1.06
1:A:301:ARG:HG2	1:A:301:ARG:HH11	1.27	0.99
1:B:487:ARG:NH2	3:B:701:HOH:O	2.02	0.91
1:A:325:ARG:NH1	1:A:348:TYR:OH	2.05	0.89
1:A:325:ARG:HH11	1:A:325:ARG:HG3	1.35	0.88

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:A:287:THR:O	1:B:288:LEU:CD2[1_554]	1.69	0.51
1:A:287:THR:O	1:B:288:LEU:HD23[1_554]	1.15	0.45

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	321/355 (90%)	290 (90%)	29 (9%)	2 (1%)	22 45
1	B	318/355 (90%)	287 (90%)	28 (9%)	3 (1%)	14 35
All	All	639/710 (90%)	577 (90%)	57 (9%)	5 (1%)	16 38

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	380	ASP
1	B	413	PRO
1	A	306	ASN
1	B	494	ILE
1	A	494	ILE

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	292/320 (91%)	254 (87%)	38 (13%)	3 8
1	B	292/320 (91%)	256 (88%)	36 (12%)	4 9
All	All	584/640 (91%)	510 (87%)	74 (13%)	3 9

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	415	THR

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Mol	Chain	Res	Type
1	B	540	LEU
1	B	434	ASP
1	B	495	GLU
1	A	443	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	422	ASN
1	B	447	ASN
1	B	512	ASN
1	A	512	ASN
1	B	218	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	A1ICT	A	601	-	48,51,51	3.07	19 (39%)	48,74,74	2.98	21 (43%)
2	A1ICT	B	601	-	48,51,51	2.75	21 (43%)	48,74,74	2.51	18 (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	A1ICT	A	601	-	-	0/24/50/50	0/7/7/7
2	A1ICT	B	601	-	-	7/24/50/50	0/7/7/7

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	A1ICT	C14-C04	-9.04	1.29	1.47
2	A	601	A1ICT	C63-C64	-8.39	1.39	1.51
2	B	601	A1ICT	C45-C44	8.08	1.61	1.51
2	B	601	A1ICT	C14-C04	-6.84	1.33	1.47
2	A	601	A1ICT	C14-C15	-6.63	1.31	1.41

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	A1ICT	C14-C04-N19	11.16	120.31	113.80
2	A	601	A1ICT	N19-C17-N16	-8.76	118.73	126.34
2	B	601	A1ICT	N19-C17-N16	-8.36	119.07	126.34
2	B	601	A1ICT	C61-C63-C53	-4.94	112.13	118.29
2	B	601	A1ICT	C80-C20-N19	-4.81	104.61	114.00

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	A1ICT	C44-C45-N48-C26
2	B	601	A1ICT	C30-C38-C39-S29
2	B	601	A1ICT	C36-C38-C39-S29
2	B	601	A1ICT	C36-C38-C39-C40
2	B	601	A1ICT	C30-C38-C39-C40

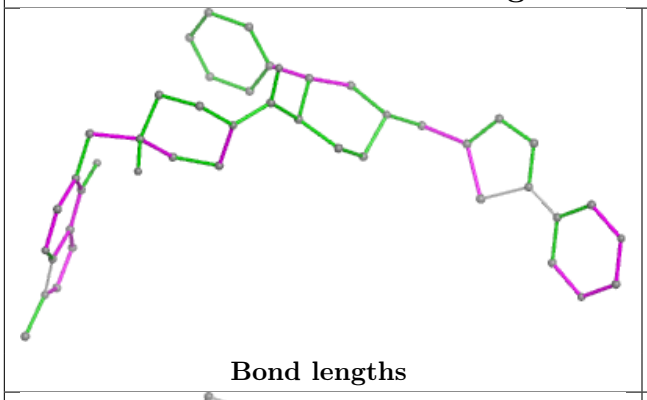
There are no ring outliers.

2 monomers are involved in 3 short contacts:

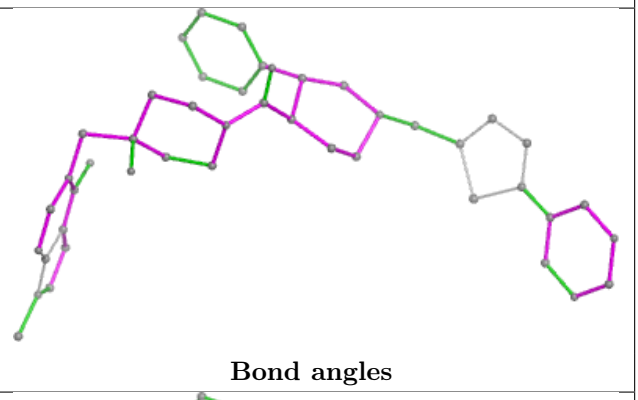
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	A1ICT	1	0
2	B	601	A1ICT	2	0

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 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.

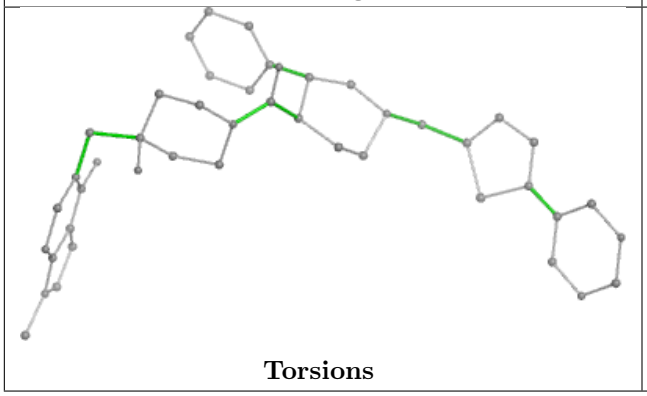
Ligand A1ICT A 601



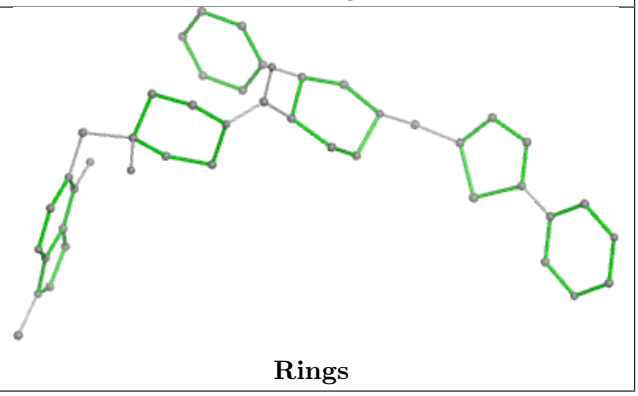
Bond lengths



Bond angles

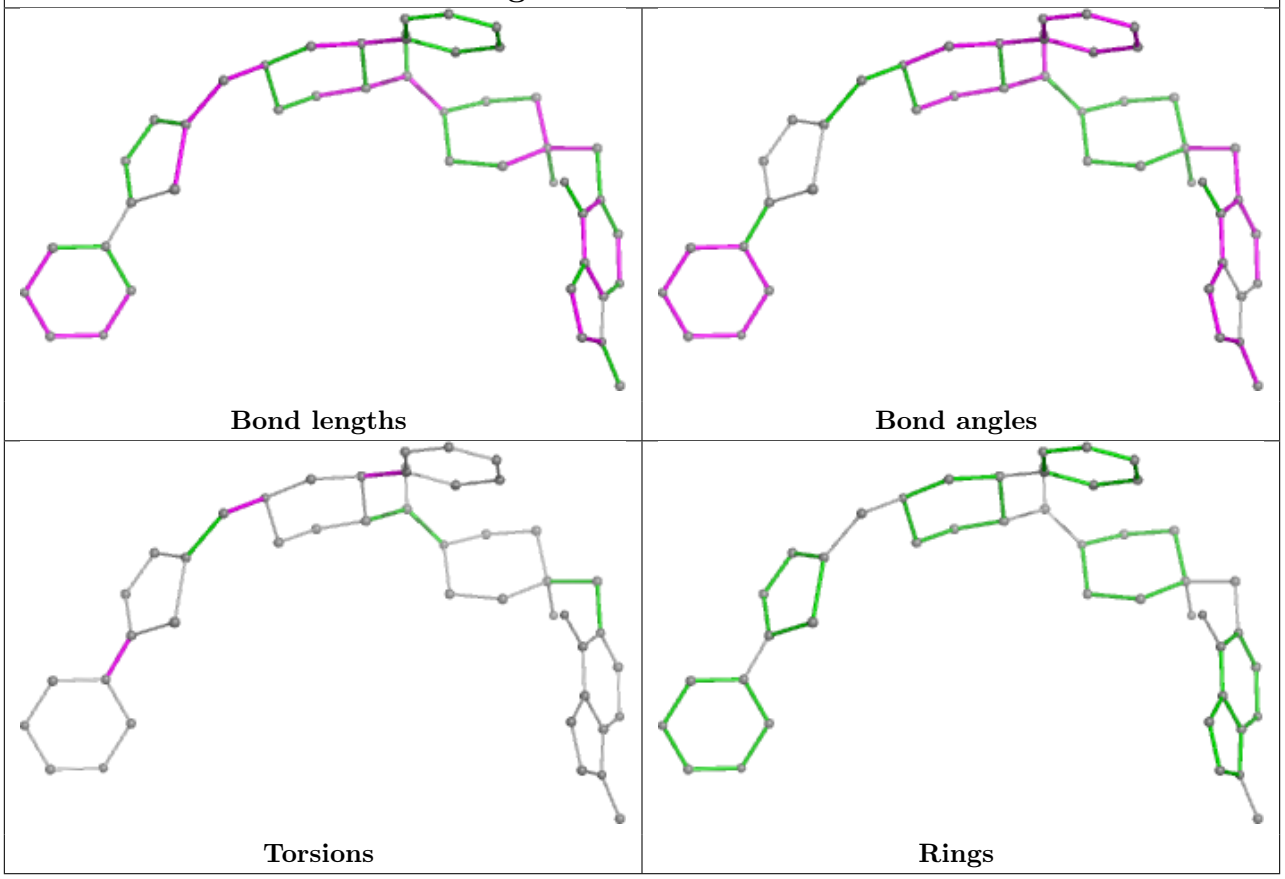


Torsions



Rings

Ligand A1ICT B 601



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^{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	327/355 (92%)	0.43	13 (3%)	43	41	6, 24, 54, 69	0
1	B	326/355 (91%)	0.66	23 (7%)	23	21	7, 30, 68, 106	0
All	All	653/710 (91%)	0.55	36 (5%)	32	29	6, 27, 63, 106	0

The worst 5 of 36 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	415	THR	6.7
1	B	458	GLY	5.3
1	B	336	GLU	5.2
1	B	552	ALA	4.5
1	A	462	GLY	4.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

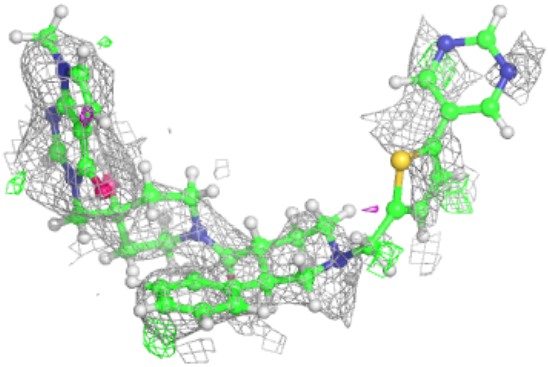
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

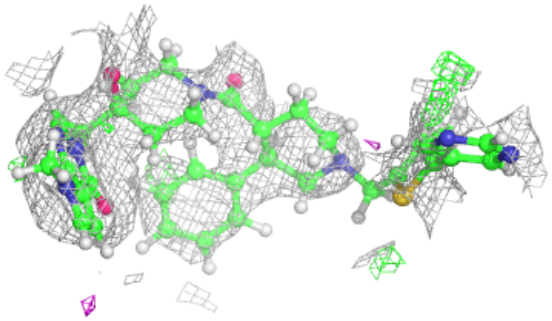
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	A1ICT	B	601	45/45	0.79	0.21	23,46,118,123	4
2	A1ICT	A	601	45/45	0.89	0.12	13,29,45,49	4

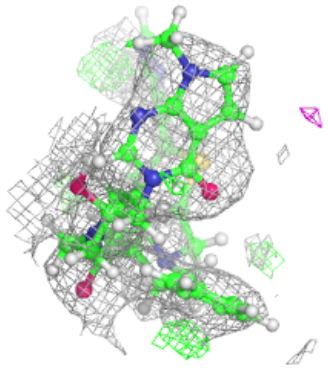
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1ICT B 601:

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

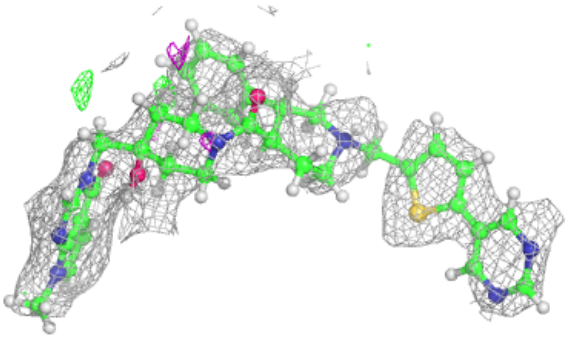


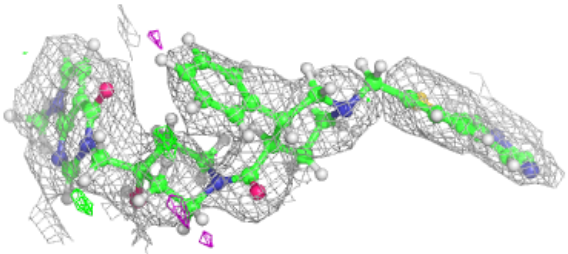


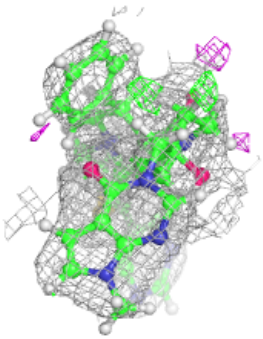


Electron density around A1ICT A 601:

$2mF_o$-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

There are no such residues in this entry.