Full wwPDB X-ray Structure Validation Report (i)

Jun 24, 2024 – 02:59 AM EDT

PDB ID	:	6QGG
Title	:	Structure of human Bcl-2 in complex with analogue of ABT-737
Authors	:	Dokurno, P.; Murray, J.; Davidson, J.; Chen, I.; Davis, B.; Graham, C.J.; Harris, R.; Jordan, A.M.; Matassova, N.; Pedder, C.; Ray, S.; Roughley, S.; Smith, J.; Walmsley, C.; Wang, Y.; Whitehead, N.; Williamson, D.S.; Casara, P.; Le Diguarher, T.; Hickman, J.; Stark, J.; Kotschy, A.; Geneste, O.; Hubbard, R.E.
Deposited on	:	2019-01-11
Resolution	:	1.50 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:

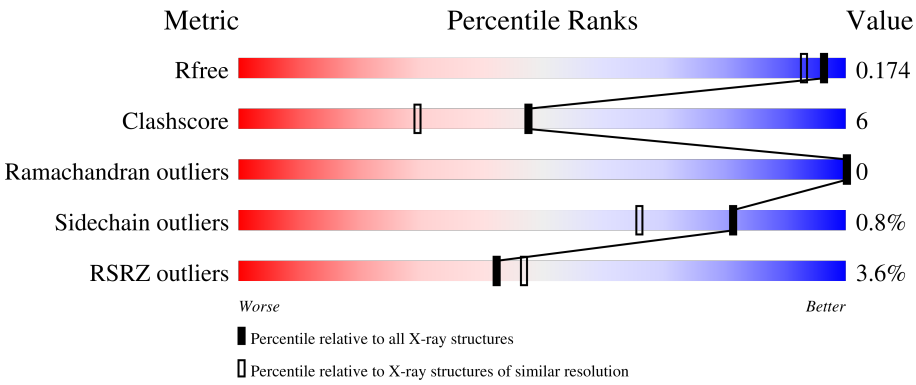
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)

1 Overall quality at a glance (i)

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

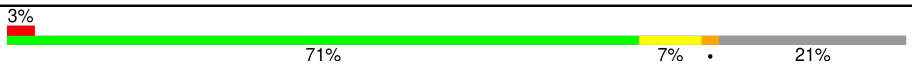
The reported resolution of this entry is 1.50 Å.

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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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	177	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1330 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 Apoptosis regulator Bcl-2,Bcl-2-like protein 1,Apoptosis regulator Bcl-2,Bcl-2-like protein 1.

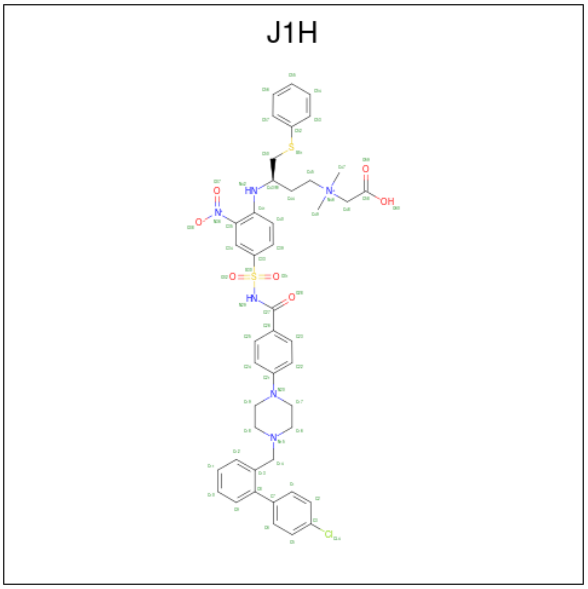
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	140	1150	731	197	216	6	0	3	0

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	initiating methionine	UNP P10415
A	8	SER	-	expression tag	UNP P10415
A	9	GLN	-	expression tag	UNP P10415
A	20	SER	HIS	engineered mutation	UNP P10415
A	95	GLN	LEU	engineered mutation	UNP P10415
A	106	LEU	ARG	engineered mutation	UNP P10415
A	124	GLY	PHE	engineered mutation	UNP P10415
A	127	TYR	ARG	engineered mutation	UNP P10415
A	128	ALA	GLY	engineered mutation	UNP P10415
A	129	SER	ARG	engineered mutation	UNP P10415
A	168	VAL	PRO	engineered mutation	UNP P10415
A	175	ALA	LEU	engineered mutation	UNP P10415
A	178	ALA	THR	engineered mutation	UNP P10415
A	179	THR	GLU	engineered mutation	UNP P10415
A	183	ASP	ARG	engineered mutation	UNP P10415
A	218	LEU	-	expression tag	UNP Q07817
A	219	GLU	-	expression tag	UNP Q07817
A	220	HIS	-	expression tag	UNP Q07817
A	221	HIS	-	expression tag	UNP Q07817
A	222	HIS	-	expression tag	UNP Q07817
A	223	HIS	-	expression tag	UNP Q07817
A	224	HIS	-	expression tag	UNP Q07817
A	225	HIS	-	expression tag	UNP Q07817

- Molecule 2 is [(3 {R})-3-[[4-[[4-[4-[[2-(4-chlorophenyl)phenyl]methyl]piperazin-1-yl]phenyl]carbonylsulfamoyl]-2-nitro-phenyl]amino]-4-phenylsulfanyl-butyl]-(2-hydroxy-2-oxoethyl)-

dimethyl-azanium (three-letter code: J1H) (formula: $C_{44}H_{48}ClN_6O_7S_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Cl	N	O	S		
2	A	1	60	44	1	6	7	2	0	0

- Molecule 3 is water.

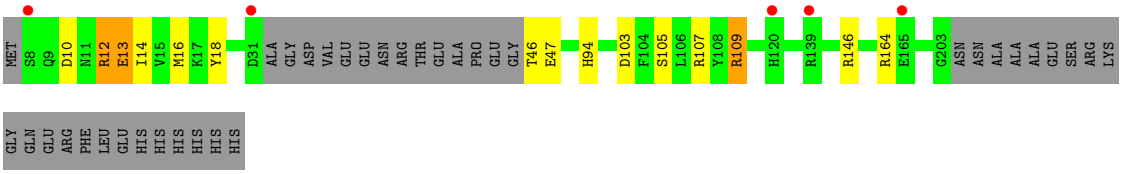
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	120	120	120	0	0

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: Apoptosis regulator Bcl-2,Bcl-2-like protein 1,Apoptosis regulator Bcl-2,Bcl-2-like protein 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	55.28Å 55.28Å 58.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.50 14.83 – 1.50	Depositor EDS
% Data completeness (in resolution range)	94.6 (15.00-1.50) 94.7 (14.83-1.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.32 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.151 , 0.173 0.152 , 0.174	Depositor DCC
R_{free} test set	1217 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å^2)	13.3	Xtriage
Anisotropy	0.015	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.47 , 60.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	1330	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: J1H

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	0.87	0/1187	1.08	4/1607 (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

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	18	TYR	CB-CG-CD1	10.96	127.57	121.00
1	A	18	TYR	CB-CG-CD2	-10.37	114.78	121.00
1	A	109	ARG	NE-CZ-NH2	6.14	123.37	120.30
1	A	18	TYR	CG-CD2-CE2	5.40	125.62	121.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	12	ARG	Sidechain
1	A	146	ARG	Sidechain
1	A	164	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	1150	0	1079	14	0
2	A	60	0	0	1	0
3	A	120	0	0	6	2
All	All	1330	0	1079	14	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 (14) 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:105[B]:SER:OG	3:A:501:HOH:O	1.72	1.02
1:A:103:ASP:HB3	3:A:505:HOH:O	1.83	0.78
1:A:109:ARG:NH2	3:A:502:HOH:O	2.18	0.77
1:A:14:ILE:HD11	1:A:47:GLU:HG3	1.80	0.63
1:A:103:ASP:CB	3:A:505:HOH:O	2.45	0.60
1:A:13:GLU:OE2	1:A:46:THR:HB	2.03	0.59
1:A:103:ASP:CG	3:A:505:HOH:O	2.44	0.56
1:A:13:GLU:OE1	1:A:94:HIS:CE1	2.60	0.55
1:A:107:ARG:HG3	3:A:563:HOH:O	2.05	0.55
1:A:13:GLU:OE1	1:A:94:HIS:HE1	1.95	0.50
1:A:10:ASP:CG	1:A:46:THR:HA	2.37	0.44
1:A:12:ARG:O	1:A:16:MET:HG2	2.18	0.43
1:A:103:ASP:OD2	2:A:401:J1H:C47	2.68	0.42
1:A:107:ARG:HH11	1:A:107:ARG:HD3	1.66	0.41

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)
3:A:511:HOH:O	3:A:602:HOH:O[3_555]	1.73	0.47
3:A:528:HOH:O	3:A:602:HOH:O[3_555]	1.85	0.35

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	139/177 (78%)	137 (99%)	2 (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	121/149 (81%)	120 (99%)	1 (1%)	81 66

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

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	$\#\|Z\| > 2$
2	J1H	A	401	-	64,65,65	1.77	19 (29%)	83,92,92	1.24	9 (10%)

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	J1H	A	401	-	-	5/49/61/61	0/6/6/6

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	J1H	O32-S30	4.61	1.48	1.43
2	A	401	J1H	C48-N46	-3.56	1.44	1.51
2	A	401	J1H	O37-N36	3.34	1.28	1.22
2	A	401	J1H	C14-N15	3.31	1.53	1.47
2	A	401	J1H	C43-N42	-3.29	1.39	1.46
2	A	401	J1H	C56-C57	-3.23	1.33	1.38
2	A	401	J1H	C27-N29	-2.97	1.35	1.39
2	A	401	J1H	O28-C27	2.92	1.30	1.23
2	A	401	J1H	O31-S30	2.92	1.46	1.43
2	A	401	J1H	C8-C13	-2.57	1.37	1.40
2	A	401	J1H	C44-C43	2.53	1.58	1.53
2	A	401	J1H	S30-N29	-2.47	1.58	1.64
2	A	401	J1H	C41-N42	2.46	1.43	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	J1H	C9-C8	2.44	1.43	1.40
2	A	401	J1H	C39-C33	2.36	1.42	1.38
2	A	401	J1H	C14-C13	-2.32	1.47	1.51
2	A	401	J1H	C12-C13	2.27	1.43	1.39
2	A	401	J1H	O60-C58	-2.13	1.23	1.30
2	A	401	J1H	O38-N36	-2.09	1.21	1.35

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	401	J1H	C35-C41-N42	-5.05	118.34	123.45
2	A	401	J1H	O32-S30-O31	-3.84	114.85	119.52
2	A	401	J1H	C17-N20-C19	3.12	118.59	111.57
2	A	401	J1H	C9-C8-C7	-3.05	112.64	118.70
2	A	401	J1H	C44-C43-N42	-2.77	105.95	110.49
2	A	401	J1H	C13-C14-N15	-2.43	108.44	112.75
2	A	401	J1H	C7-C8-C13	2.11	127.90	122.73
2	A	401	J1H	O32-S30-N29	2.08	112.71	106.77
2	A	401	J1H	C1-C2-C3	2.04	121.29	119.24

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	J1H	N46-C48-C58-O60
2	A	401	J1H	N46-C48-C58-O59
2	A	401	J1H	C57-C52-S51-C50
2	A	401	J1H	C53-C52-S51-C50
2	A	401	J1H	C8-C13-C14-N15

There are no ring outliers.

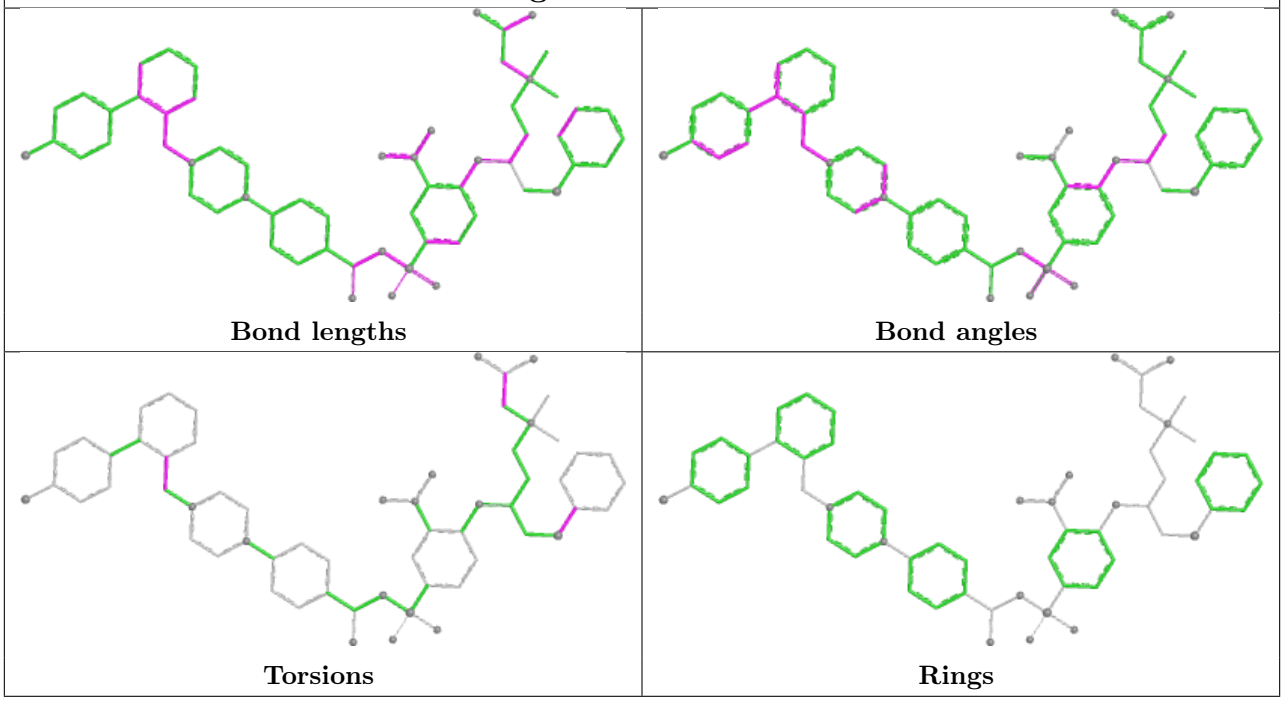
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	J1H	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 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 J1H A 401



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	140/177 (79%)	0.07	5 (3%) 42 47	8, 14, 34, 56	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	8	SER	7.5
1	A	31	ASP	2.9
1	A	139	ARG	2.7
1	A	120	HIS	2.6
1	A	165	GLU	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 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.

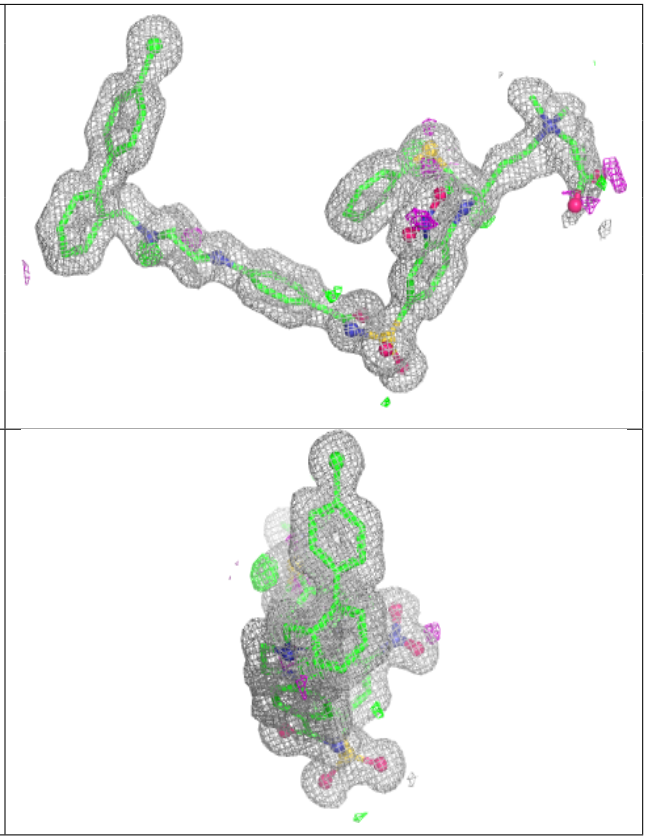
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	J1H	A	401	60/60	0.97	0.08	10,12,31,61	0

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 J1H A 401:

$2mF_o$-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.