



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 10:50 am BST

PDB ID : 4BFR
Title : Discovery and Optimization of Pyrimidone Indoline Amide PI3Kbeta Inhibitors for the Treatment of Phosphatase and TENsin homologue (PTEN)-Deficient Cancers
Authors : Certal, V.; Carry, J.C.; Halley, F.; Virone-Oddos, A.; Thompson, F.; Filoche-Romme, B.; El-Ahmad, Y.; Karlsson, A.; Charrier, V.; Delorme, C.; Rak, A.; Abecassis, P.Y.; Amara, C.; Vincent, L.; Bonnevaux, H.; Nicolas, J.P.; Mathieu, M.; Bertrand, T.; Marquette, J.P.; Michot, N.; Benard, T.; Perrin, M.A.; Perron, S.; Monget, S.; Gruss-Leleu, F.; Doerflinger, G.; Guizani, H.; Brollo, M.; Delbarre, L.; Bertin, L.; Richepin, P.; Loyau, V.; Garcia-Echeverria, C.; Lengauer, C.; Schio, L.
Deposited on : 2013-03-22
Resolution : 2.80 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 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 : 2.11
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)

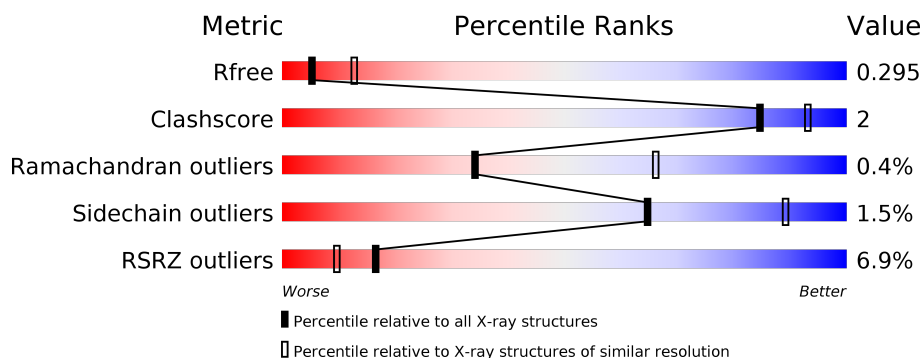
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 on 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	952	 8% 82% 7% 10%
1	B	952	 4% 81% 7% 12%

Ideal geometry (proteins) : Engh & Huber (2001)
 Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.11

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13777 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.

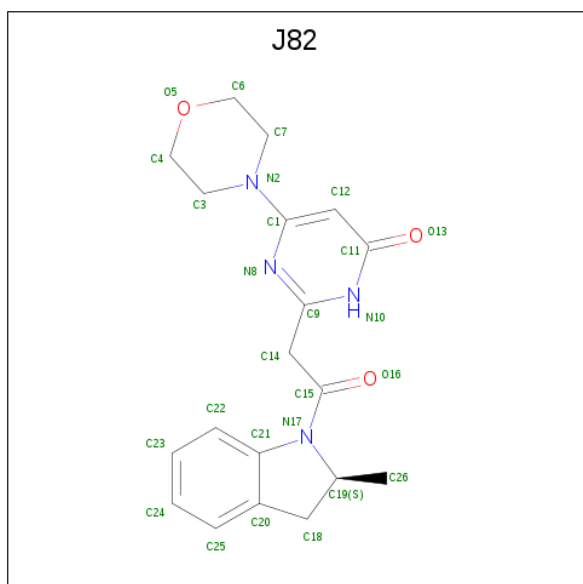
- Molecule 1 is a protein called PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE 3-KINASE CATALYTIC S SUBUNIT BETA ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	855	Total	C	N	O	S	0	0	0
			6902	4436	1165	1259	42			
1	B	836	Total	C	N	O	S	0	0	0
			6743	4339	1138	1225	41			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	113	GLY	-	expression tag	UNP Q8BTI9
B	113	GLY	-	expression tag	UNP Q8BTI9

- Molecule 2 is 2-[2-(2-METHYL-2,3-DIHYDRO-INDOL-1-YL)-2-OXO-ETHYL]-6-MORPHOLIN-4-YL-3H-PYRIMIDIN-4-ONE (three-letter code: J82) (formula: C₁₉H₂₂N₄O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	19	4	3		
2	B	1	Total	C	N	O	0	0
			26	19	4	3		

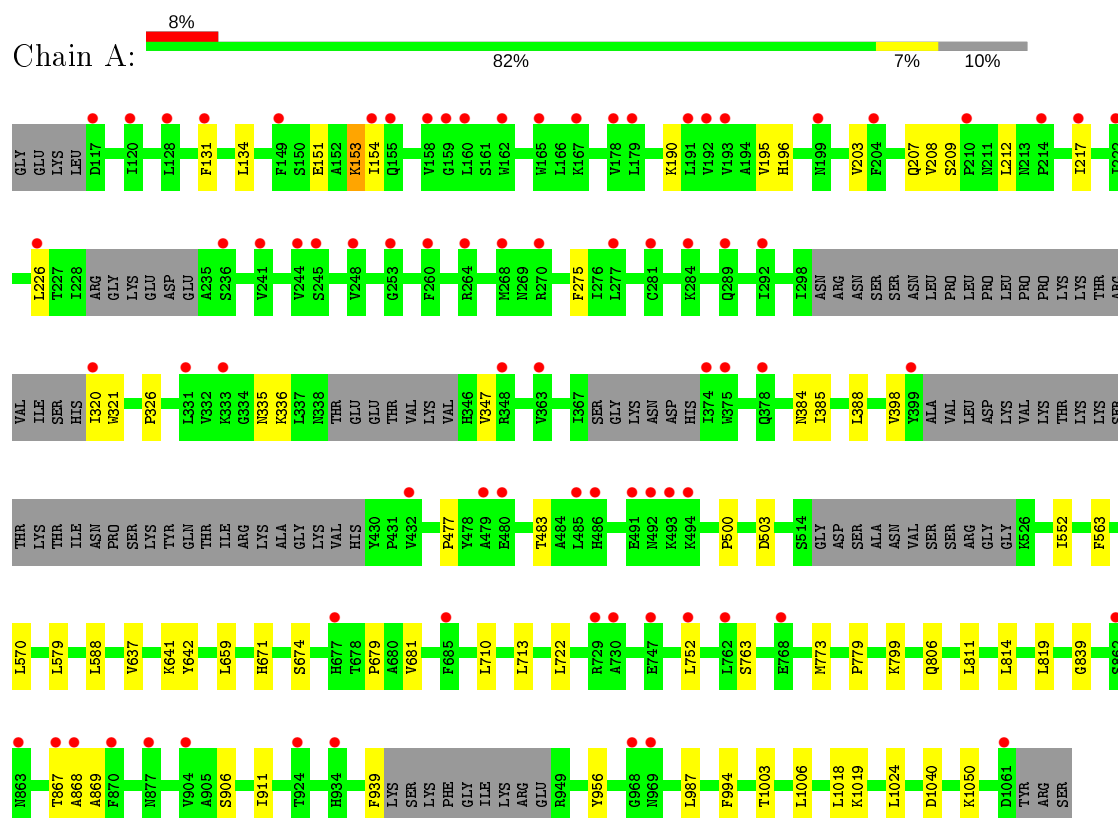
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	33	Total	O	0	0
			33	33		
3	B	47	Total	O	0	0
			47	47		

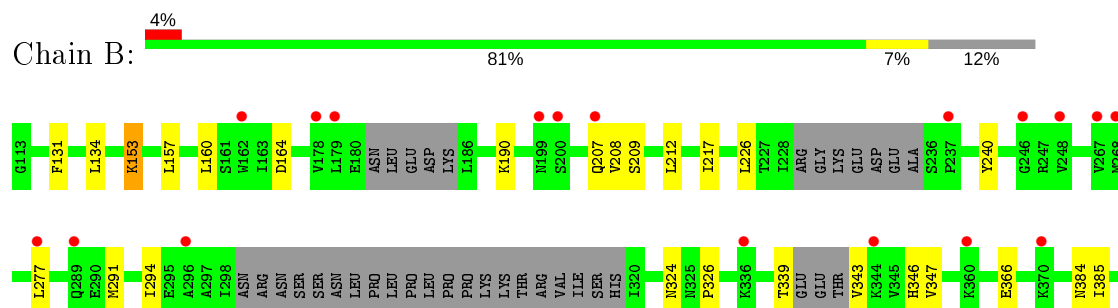
3 Residue-property plots [i](#)

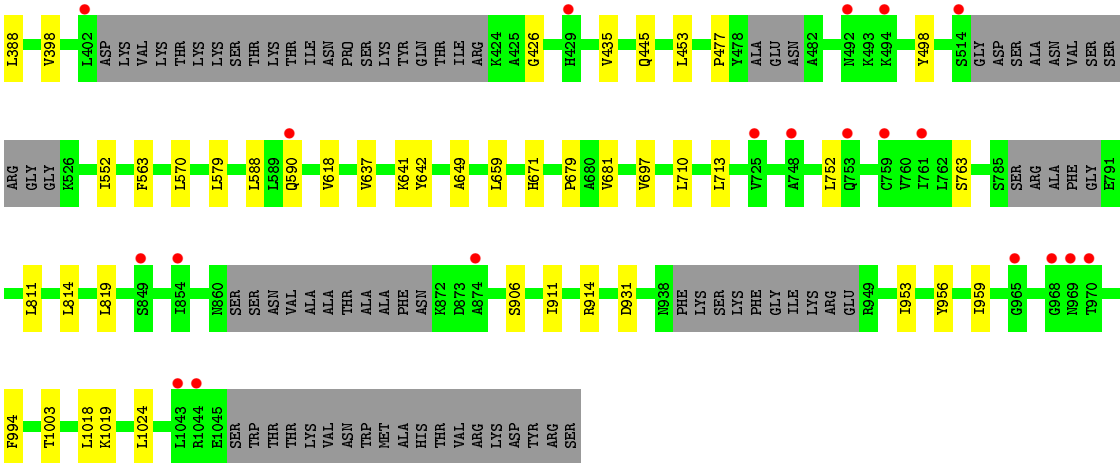
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE 3-KINASE CATALYTIC S SUBUNIT BETA ISOFORM



- Molecule 1: PHOSPHATIDYLINOSITOL 4,5-BISPHOSPHATE 3-KINASE CATALYTIC S SUBUNIT BETA ISOFORM





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	122.31Å 129.03Å 154.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.00 – 2.80 77.45 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (56.00-2.80) 99.7 (77.45-2.80)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.82Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.260 , 0.275 0.280 , 0.295	Depositor DCC
R_{free} test set	3084 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	68.0	Xtriage
Anisotropy	0.278	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	13777	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 3.30% 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: J82

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	0.38	0/7047	0.53	0/9524
1	B	0.38	0/6879	0.52	0/9287
All	All	0.38	0/13926	0.53	0/18811

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	6902	0	6937	31	0
1	B	6743	0	6808	30	0
2	A	26	0	22	1	0
2	B	26	0	22	1	0
3	A	33	0	0	0	0
3	B	47	0	0	0	0
All	All	13777	0	13789	63	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 2.

All (63) 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:153:LYS:HD2	1:B:659:LEU:HB3	1.61	0.82
1:A:153:LYS:HD2	1:A:659:LEU:HB3	1.60	0.82
1:A:868:ALA:N	1:A:869:ALA:HA	1.94	0.81
1:A:868:ALA:H	1:A:869:ALA:HA	1.50	0.71
1:B:914:ARG:HB2	1:B:953:ILE:HD13	1.80	0.63
1:B:911:ILE:HG22	1:B:914:ARG:HD3	1.83	0.59
1:B:618:VAL:HG21	1:B:649:ALA:HB1	1.87	0.57
1:A:208:VAL:HG21	1:A:217:ILE:HG12	1.90	0.54
1:A:320:ILE:HG12	1:A:500:PRO:HD3	1.89	0.54
1:B:208:VAL:HG21	1:B:217:ILE:HG12	1.89	0.54
1:B:641:LYS:HG2	1:B:681:VAL:HG11	1.91	0.53
1:A:641:LYS:HG2	1:A:681:VAL:HG11	1.92	0.52
1:B:385:ILE:HA	1:B:388:LEU:HD12	1.91	0.52
1:A:477:PRO:HG2	1:A:679:PRO:HB2	1.92	0.52
1:B:240:TYR:HB3	1:B:277:LEU:HD22	1.92	0.52
1:B:994:PHE:HB3	1:B:1018:LEU:HD21	1.91	0.52
1:A:385:ILE:HA	1:A:388:LEU:HD12	1.91	0.51
1:A:994:PHE:HB3	1:A:1018:LEU:HD21	1.91	0.51
1:B:477:PRO:HG2	1:B:679:PRO:HB2	1.92	0.50
1:B:160:LEU:HG	1:B:164:ASP:HB3	1.94	0.49
1:A:1019:LYS:HA	1:A:1024:LEU:HD12	1.94	0.49
1:B:339:THR:HG23	1:B:343:VAL:HG22	1.95	0.49
1:A:637:VAL:HG11	1:A:671:HIS:HB3	1.96	0.48
1:B:1019:LYS:HA	1:B:1024:LEU:HD12	1.95	0.48
1:B:291:MET:HA	1:B:294:ILE:HD12	1.96	0.47
1:A:151:GLU:HA	1:A:154:ILE:HD12	1.97	0.47
1:A:326:PRO:HA	1:A:384:ASN:HA	1.96	0.47
1:A:196:HIS:HB3	1:A:203:VAL:HG12	1.97	0.46
1:B:346:HIS:HB3	1:B:366:GLU:HG2	1.98	0.46
1:B:956:TYR:HA	1:B:959:ILE:HD12	1.97	0.46
1:A:195:VAL:HG22	1:A:275:PHE:HB2	1.97	0.46
1:B:326:PRO:HA	1:B:384:ASN:HA	1.96	0.46
1:B:294:ILE:HG12	1:B:697:VAL:HB	1.98	0.45
1:A:209:SER:HB3	1:A:212:LEU:HD12	1.99	0.45
2:B:2000:J82:H19	2:B:2000:J82:H142	1.88	0.45
1:A:642:TYR:HB2	1:A:1003:THR:HG21	1.98	0.44
1:A:811:LEU:HA	1:A:814:LEU:HD12	1.98	0.44
1:B:811:LEU:HA	1:B:814:LEU:HD12	1.98	0.44
1:A:336:LYS:HB2	1:A:483:THR:HA	1.99	0.44
1:B:642:TYR:HB2	1:B:1003:THR:HG21	1.98	0.44
1:B:435:VAL:HG21	1:B:453:LEU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:LYS:HD3	1:A:207:GLN:HB3	2.01	0.43
1:B:209:SER:HB3	1:B:212:LEU:HD12	2.00	0.43
1:A:320:ILE:HG23	1:A:321:TRP:H	1.83	0.43
1:B:347:VAL:HG22	1:B:398:VAL:HG22	2.01	0.43
1:B:190:LYS:HD3	1:B:207:GLN:HB3	2.01	0.42
1:B:906:SER:HA	1:B:911:ILE:HD12	2.00	0.42
1:A:806:GLN:HE21	1:A:1006:LEU:HG	1.85	0.42
1:A:347:VAL:HG22	1:A:398:VAL:HG22	2.01	0.42
2:A:2000:J82:H19	2:A:2000:J82:H142	1.90	0.42
1:A:956:TYR:HB3	1:A:1050:LYS:HD2	2.02	0.42
1:A:552:ILE:HG22	1:A:570:LEU:HD12	2.03	0.41
1:A:773:MET:HB3	1:A:779:PRO:HD2	2.03	0.41
1:B:710:LEU:HA	1:B:713:LEU:HD12	2.03	0.41
1:A:906:SER:HA	1:A:911:ILE:HD12	2.02	0.41
1:B:552:ILE:HG22	1:B:570:LEU:HD12	2.03	0.41
1:B:637:VAL:HG11	1:B:671:HIS:HB3	2.03	0.41
1:A:131:PHE:HA	1:A:134:LEU:HD12	2.03	0.40
1:A:710:LEU:HA	1:A:713:LEU:HD12	2.03	0.40
1:A:779:PRO:HB3	1:A:799:LYS:HG2	2.03	0.40
1:A:674:SER:HA	1:A:839:GLY:HA2	2.03	0.40
1:B:131:PHE:HA	1:B:134:LEU:HD12	2.04	0.40
1:B:445:GLN:HA	1:B:498:TYR:HA	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	839/952 (88%)	813 (97%)	23 (3%)	3 (0%)	34	66
1	B	814/952 (86%)	787 (97%)	24 (3%)	3 (0%)	34	66
All	All	1653/1904 (87%)	1600 (97%)	47 (3%)	6 (0%)	34	66

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	867	THR
1	A	763	SER
1	B	763	SER
1	B	931	ASP
1	A	335	ASN
1	B	426	GLY

5.3.2 Protein sidechains ⓘ

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	763/849 (90%)	751 (98%)	12 (2%)	62	88
1	B	747/849 (88%)	737 (99%)	10 (1%)	69	91
All	All	1510/1698 (89%)	1488 (98%)	22 (2%)	65	89

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	LYS
1	A	226	LEU
1	A	503	ASP
1	A	563	PHE
1	A	579	LEU
1	A	588	LEU
1	A	722	LEU
1	A	752	LEU
1	A	819	LEU
1	A	939	PHE
1	A	987	LEU
1	A	1040	ASP
1	B	153	LYS
1	B	157	LEU
1	B	226	LEU
1	B	324	ASN
1	B	563	PHE

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Mol	Chain	Res	Type
1	B	579	LEU
1	B	588	LEU
1	B	590	GLN
1	B	752	LEU
1	B	819	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	274	HIS
1	A	590	GLN
1	A	671	HIS
1	A	806	GLN
1	A	929	HIS
1	B	590	GLN

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 carbohydrates 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	J82	B	2000	-	28,29,29	1.54	3 (10%)	34,41,41	1.94	6 (17%)
2	J82	A	2000	-	28,29,29	1.58	3 (10%)	34,41,41	1.92	6 (17%)

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	J82	B	2000	-	-	3/10/32/32	0/4/4/4
2	J82	A	2000	-	-	3/10/32/32	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2000	J82	C9-N10	5.27	1.41	1.33
2	B	2000	J82	C9-N10	5.04	1.40	1.33
2	A	2000	J82	C19-N17	4.65	1.53	1.48
2	B	2000	J82	C19-N17	4.59	1.53	1.48
2	A	2000	J82	C11-N10	3.42	1.39	1.33
2	B	2000	J82	C11-N10	3.32	1.38	1.33

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2000	J82	C12-C11-N10	-7.81	114.96	124.08
2	A	2000	J82	C12-C11-N10	-7.79	114.98	124.08
2	B	2000	J82	C11-C12-C1	4.74	122.01	116.19
2	A	2000	J82	C11-C12-C1	4.66	121.91	116.19
2	B	2000	J82	C9-N8-C1	3.11	119.53	116.02
2	A	2000	J82	C9-N8-C1	3.06	119.48	116.02
2	B	2000	J82	C14-C9-N8	2.81	122.06	117.20
2	A	2000	J82	C14-C9-N8	2.69	121.87	117.20
2	A	2000	J82	N10-C9-N8	-2.53	122.72	126.06
2	B	2000	J82	N10-C9-N8	-2.51	122.75	126.06
2	A	2000	J82	C26-C19-C18	-2.36	109.53	114.71
2	B	2000	J82	C26-C19-C18	-2.31	109.64	114.71

There are no chirality outliers.

All (6) torsion outliers are listed below:

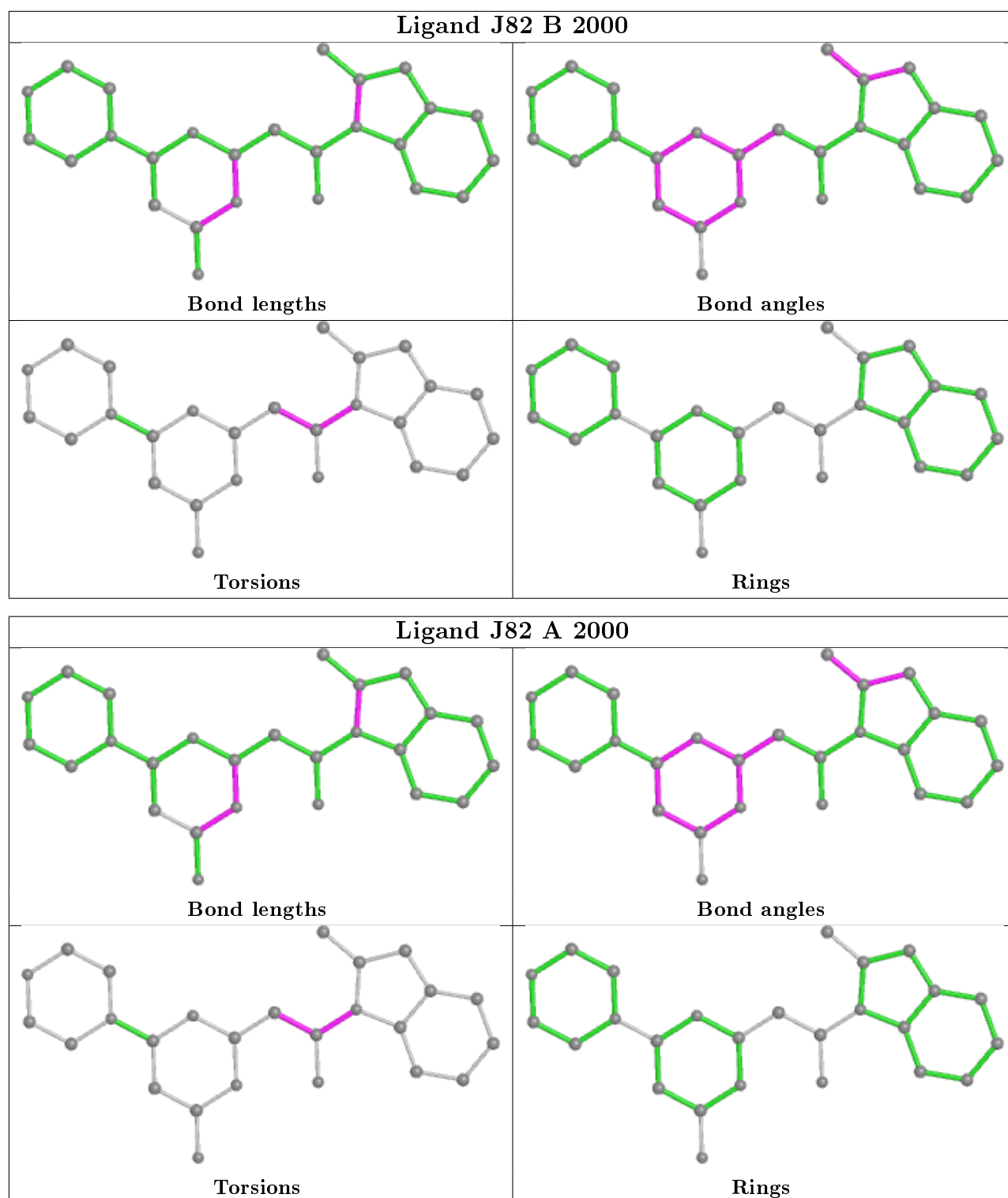
Mol	Chain	Res	Type	Atoms
2	B	2000	J82	C14-C15-N17-C19
2	A	2000	J82	C14-C15-N17-C19
2	B	2000	J82	O16-C15-N17-C19
2	A	2000	J82	O16-C15-N17-C19
2	A	2000	J82	C9-C14-C15-O16
2	B	2000	J82	C9-C14-C15-N17

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2000	J82	1	0
2	A	2000	J82	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 ⓘ

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, 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	855/952 (89%)	0.86	78 (9%) 9 5	46, 81, 113, 138	0
1	B	836/952 (87%)	0.68	38 (4%) 33 23	49, 70, 95, 138	0
All	All	1691/1904 (88%)	0.77	116 (6%) 16 10	46, 74, 109, 138	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	399	TYR	7.1
1	A	863	ASN	6.5
1	A	117	ASP	5.8
1	A	492	ASN	5.4
1	A	226	LEU	4.7
1	A	162	TRP	4.7
1	B	514	SER	4.4
1	A	160	LEU	4.3
1	A	862	SER	4.2
1	A	494	LYS	4.2
1	A	292	ILE	4.1
1	B	494	LYS	4.0
1	A	968	GLY	4.0
1	B	968	GLY	3.8
1	B	1044	ARG	3.8
1	A	374	ILE	3.7
1	B	199	ASN	3.6
1	A	281	CYS	3.6
1	A	154	ILE	3.6
1	A	289	GLN	3.6
1	B	849	SER	3.5
1	B	402	LEU	3.4
1	A	167	LYS	3.4
1	B	492	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	874	ALA	3.3
1	B	246	GLY	3.2
1	A	969	ASN	3.1
1	A	432	VAL	3.1
1	A	485	LEU	3.1
1	B	725	VAL	3.1
1	A	333	LYS	3.1
1	A	729	ARG	3.1
1	A	868	ALA	3.0
1	B	344	LYS	3.0
1	B	1043	LEU	3.0
1	A	331	LEU	3.0
1	A	479	ALA	3.0
1	A	284	LYS	2.9
1	A	131	PHE	2.9
1	A	210	PRO	2.9
1	A	480	GLU	2.8
1	A	236	SER	2.8
1	B	370	LYS	2.8
1	A	191	LEU	2.8
1	A	867	THR	2.8
1	A	363	VAL	2.8
1	B	179	LEU	2.8
1	A	204	PHE	2.8
1	A	730	ALA	2.8
1	A	685	PHE	2.7
1	A	493	LYS	2.7
1	A	270	ARG	2.6
1	B	429	HIS	2.6
1	B	248	VAL	2.6
1	B	759	CYS	2.6
1	A	214	PRO	2.5
1	A	924	THR	2.5
1	A	747	GLU	2.5
1	B	969	ASN	2.5
1	A	199	ASN	2.5
1	A	165	TRP	2.5
1	B	336	LYS	2.5
1	B	590	GLN	2.5
1	B	268	MET	2.5
1	B	753	GLN	2.4
1	B	296	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	253	GLY	2.4
1	A	192	VAL	2.4
1	A	1061	ASP	2.4
1	A	877	ASN	2.4
1	A	244	VAL	2.4
1	A	128	LEU	2.4
1	B	965	GLY	2.3
1	B	267	VAL	2.3
1	A	491	GLU	2.3
1	B	289	GLN	2.3
1	B	207	GLN	2.3
1	A	277	LEU	2.3
1	A	320	ILE	2.3
1	B	360	LYS	2.3
1	A	762	LEU	2.3
1	A	378	GLN	2.3
1	A	486	HIS	2.3
1	A	348	ARG	2.2
1	A	752	LEU	2.2
1	B	178	VAL	2.2
1	A	677	HIS	2.2
1	A	768	GLU	2.2
1	B	277	LEU	2.2
1	A	155	GLN	2.2
1	A	159	GLY	2.2
1	A	178	VAL	2.2
1	B	970	THR	2.2
1	A	870	PHE	2.2
1	B	237	PRO	2.2
1	A	241	VAL	2.1
1	B	200	SER	2.1
1	A	193	VAL	2.1
1	A	222	ILE	2.1
1	A	375	TRP	2.1
1	B	162	TRP	2.1
1	A	120	ILE	2.1
1	B	761	ILE	2.1
1	A	934	HIS	2.1
1	A	904	VAL	2.1
1	B	854	ILE	2.1
1	A	268	MET	2.1
1	A	260	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	149	PHE	2.0
1	A	179	LEU	2.0
1	B	748	ALA	2.0
1	A	217	ILE	2.0
1	A	245	SER	2.0
1	A	248	VAL	2.0
1	A	158	VAL	2.0
1	A	264	ARG	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 carbohydrates in this entry.

6.4 Ligands [i](#)

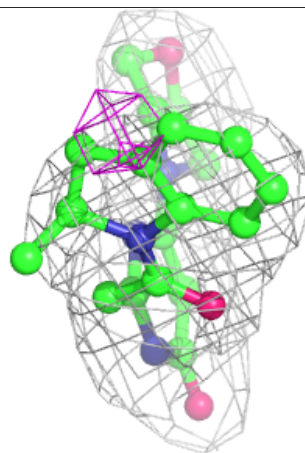
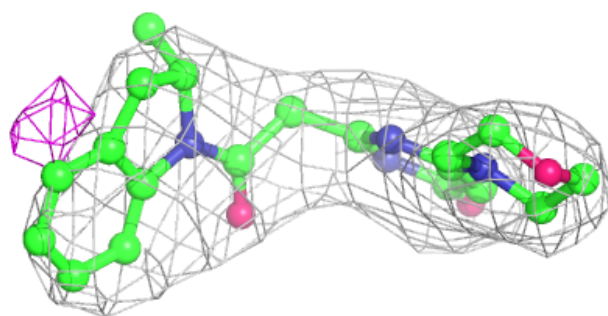
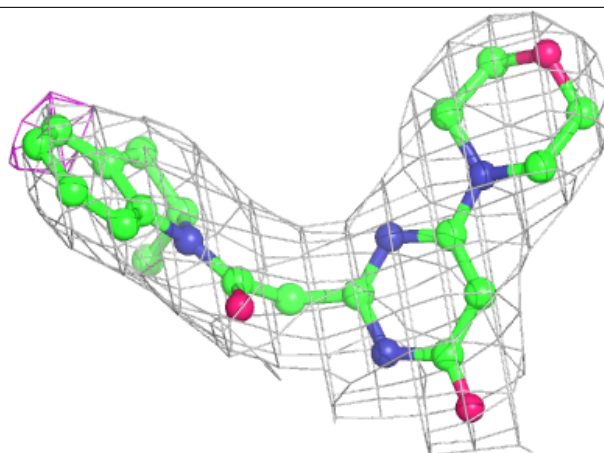
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	J82	B	2000	26/26	0.93	0.24	50,50,51,52	0
2	J82	A	2000	26/26	0.94	0.27	48,49,51,51	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.

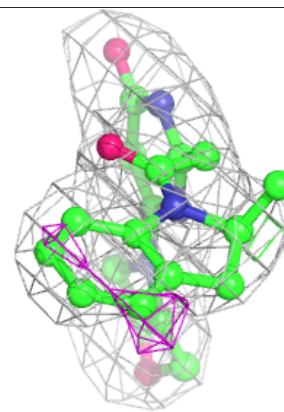
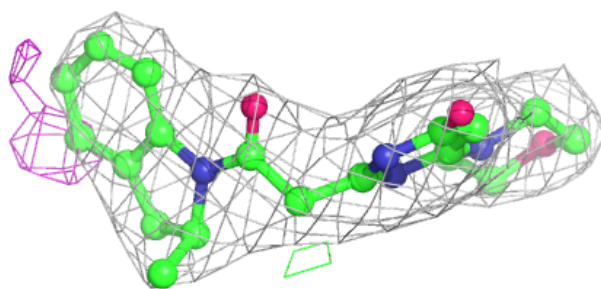
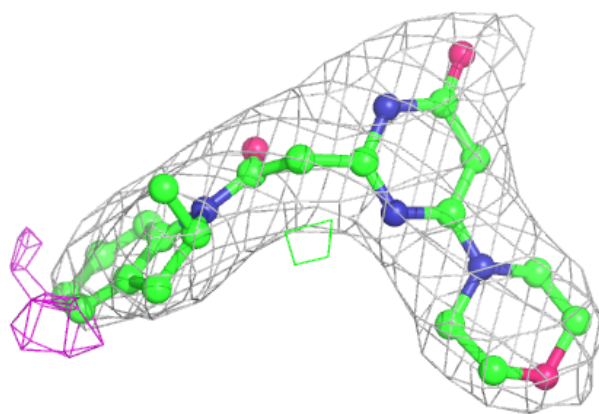
Electron density around J82 B 2000:

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



Electron density around J82 A 2000:

$2mF_o-DF_c$ (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.