

Full wwPDB X-ray Structure Validation Report (i)

Aug 16, 2023 – 03:54 AM EDT

PDB ID : 1Z5M

Title: Crystal Structure Of N1-[3-[[5-bromo-2-[[3-[(1-pyrrolidinylcarbonyl)amino

[phenyl]amino]-4-pyrimidinyl]amino[propyl]-2,2-dimethylpropanediamide

Complexed with Human PDK1

Authors: Whitlow, M.; Adler, M.

Deposited on : 2005-03-18

Resolution : 2.17 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: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.35

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)

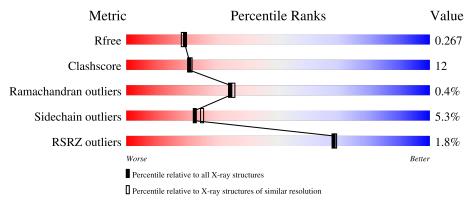
Validation Pipeline (wwPDB-VP) : 2.35

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 2.17 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	Similar resolution $(\# \text{Entries, resolution range}(\text{\AA}))$
R_{free}	130704	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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		
			2%		
1	A	286	70%	24%	• •



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 2388 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.

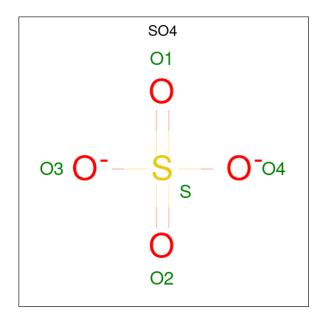
• Molecule 1 is a protein called 3-phosphoinositide dependent protein kinase-1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	A	276	Total 2255	C 1468	N 370	O 409	P 1	S 7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Α	241	SEP	SER	modified residue	UNP O15530

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



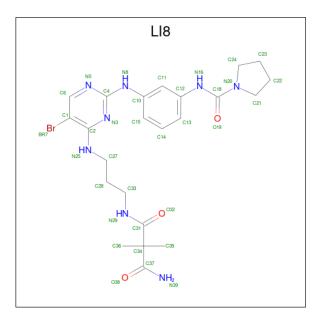
Mol	Chain	Residues	Ato	ms		ZeroOcc	AltConf
2	A	1	Total 5	O 4	S 1	0	0

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



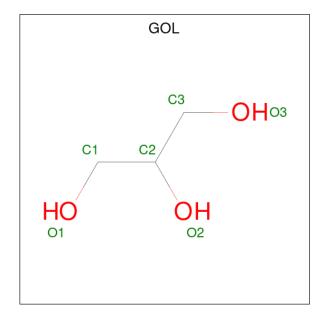
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

• Molecule 4 is N-(3-{[5-BROMO-2-({3-[(PYRROLIDIN-1-YLCARBONYL)AMINO]PHE NYL}AMINO)PYRIMIDIN-4-YL]AMINO}PROPYL)-2,2-DIMETHYLMALONAMIDE (three-letter code: LI8) (formula: $C_{23}H_{31}BrN_8O_3$).



4 A 1 Total Br C N O 0 0	0

• Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0
5	A	1	Total C O 6 3 3	0	0

• Molecule 6 is water.

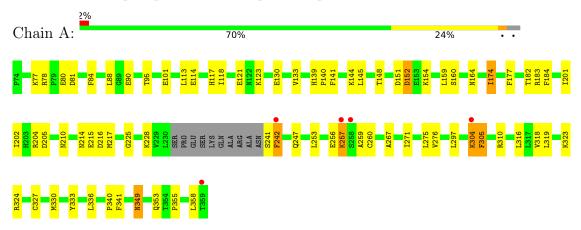
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	74	Total O 74 74	0	0



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: 3-phosphoinositide dependent protein kinase-1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	124.61Å 124.61Å 46.97Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	8.00 - 2.17	Depositor
Resolution (A)	19.66 - 2.17	EDS
% Data completeness	96.4 (8.00-2.17)	Depositor
(in resolution range)	95.2 (19.66-2.17)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) > 1$	3.34 (at 2.17Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
D.D.	0.212 , 0.269	Depositor
R, R_{free}	0.211 , 0.267	DCC
R_{free} test set	902 reflections (4.18%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 68.1	EDS
L-test for twinning ²	$< L > = 0.42, < L^2> = 0.24$	Xtriage
Estimated twinning fraction	0.077 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2388	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: LI8, SO4, GOL, SEP, CL

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).

Mal	Chain	Boı	nd lengths	Bond	angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5
1	A	0.63	1/2300 (0.0%)	0.78	0/3101

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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\textup{\AA})$	$\operatorname{Ideal}(\text{\AA})$
1	A	141	PHE	CE1-CZ	5.07	1.47	1.37

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	333	TYR	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	2255	0	2274	57	0
2	A	5	0	0	0	0
3	A	1	0	0	0	0
4	A	35	0	31	3	0
5	A	18	0	24	5	0
6	A	74	0	0	1	0
All	All	2388	0	2329	57	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 12.

All (57) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
1 4 059 1 DIJ 11011	1 4 050 41 4 1100	distance (Å)	overlap (Å)
1:A:253:LEU:HD11	1:A:259:ALA:HB2	1.52	0.89
1:A:297:LEU:HB2	1:A:319:LEU:HD11	1.61	0.83
1:A:130:GLU:HB2	1:A:225:GLY:HA2	1.63	0.79
1:A:78:ARG:HH12	1:A:80:GLU:HB2	1.47	0.79
1:A:349:ASN:HD22	1:A:349:ASN:H	1.33	0.75
1:A:78:ARG:NH1	1:A:78:ARG:HB2	2.04	0.73
1:A:349:ASN:HD22	1:A:349:ASN:N	1.89	0.70
1:A:160:SER:O	4:A:501:LI8:H6	1.92	0.70
1:A:78:ARG:NH1	1:A:80:GLU:HB2	2.08	0.68
1:A:78:ARG:HB2	1:A:78:ARG:HH11	1.60	0.67
1:A:267:ALA:O	1:A:271:ILE:HG13	1.96	0.65
1:A:305:PHE:HD1	1:A:310:ARG:HB2	1.63	0.63
1:A:253:LEU:HD11	1:A:259:ALA:CB	2.26	0.62
1:A:174:ILE:HD11	1:A:177:PHE:CD1	2.35	0.61
1:A:159:LEU:HD12	4:A:501:LI8:BR7	2.55	0.61
1:A:304:LYS:NZ	1:A:304:LYS:HB3	2.16	0.61
1:A:225:GLY:HA3	5:A:607:GOL:H12	1.85	0.58
1:A:304:LYS:HB3	1:A:304:LYS:HZ3	1.68	0.56
1:A:88:LEU:O	4:A:501:LI8:H211	2.05	0.56
1:A:349:ASN:ND2	1:A:353:GLN:HE21	2.05	0.55
1:A:205:ASP:O	1:A:210:ASN:ND2	2.40	0.54
1:A:117:HIS:O	1:A:121:GLU:HB2	2.08	0.53
1:A:78:ARG:HH11	1:A:78:ARG:CB	2.21	0.53
1:A:349:ASN:N	1:A:349:ASN:ND2	2.56	0.52
1:A:349:ASN:H	1:A:349:ASN:ND2	2.06	0.51
1:A:202:ILE:HD12	1:A:228:LYS:HD3	1.94	0.50
1:A:84:PHE:H	5:A:602:GOL:H12	1.77	0.49
1:A:90:GLU:HG2	1:A:95:THR:HG23	1.95	0.49

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A + a ma 1	Atom 2	Interatomic	Clash	
Atom-1	Atom-2	${f distance}({ m \AA})$	overlap (Å)	
1:A:113:LEU:HD21	5:A:607:GOL:O3	2.13	0.48	
1:A:182:THR:HG21	1:A:276:VAL:CG2	2.43	0.48	
1:A:84:PHE:CD1	5:A:606:GOL:H11	2.48	0.48	
1:A:77:LYS:HE3	1:A:101:GLU:OE2	2.13	0.47	
1:A:174:ILE:HD11	1:A:177:PHE:CE1	2.49	0.47	
1:A:297:LEU:HD22	1:A:319:LEU:HD13	1.95	0.47	
1:A:316:LEU:O	1:A:324:ARG:HG2	2.15	0.47	
1:A:184:PHE:CE2	1:A:355:PRO:HB3	2.50	0.46	
1:A:318:VAL:HG11	1:A:323:LYS:HB2	1.97	0.46	
1:A:151:ASP:OD1	1:A:154:LYS:N	2.48	0.46	
1:A:204:ARG:HB3	1:A:242:PHE:HE1	1.81	0.46	
1:A:78:ARG:O	1:A:81:ASP:HB2	2.17	0.45	
1:A:145:LEU:HD11	1:A:148:THR:HG22	1.98	0.45	
1:A:133:VAL:HG13	1:A:201:ILE:HD13	1.97	0.45	
1:A:202:ILE:HD13	1:A:260:CYS:HA	1.99	0.45	
1:A:327:CYS:SG	1:A:330:MET:HG2	2.57	0.44	
1:A:305:PHE:CD1	1:A:310:ARG:HB2	2.49	0.43	
1:A:123:LYS:HA	1:A:123:LYS:HD3	1.86	0.43	
1:A:253:LEU:HD12	1:A:253:LEU:N	2.33	0.42	
1:A:84:PHE:N	5:A:602:GOL:H12	2.33	0.42	
1:A:358:LEU:HD23	1:A:358:LEU:HA	1.79	0.42	
1:A:164:ASN:ND2	1:A:214:ASN:O	2.52	0.42	
1:A:183:ARG:HD3	1:A:341:PHE:O	2.20	0.41	
1:A:139:HIS:CG	1:A:140:PRO:HD2	2.56	0.41	
1:A:152:ASP:HB3	6:A:755:HOH:O	2.20	0.41	
1:A:253:LEU:O	1:A:257:LYS:HA	2.21	0.40	
1:A:297:LEU:HD22	1:A:319:LEU:CD1	2.51	0.40	
1:A:216:ASP:O	1:A:217:MET:HB2	2.21	0.40	
1:A:114:GLU:O	1:A:118:ILE:HG12	2.21	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	272/286 (95%)	254 (93%)	17 (6%)	1 (0%)	34 35	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	257	LYS

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	Analysed Rotameric Outlie		Percentiles
1	A	243/252 (96%)	230 (95%)	13 (5%)	22 25

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	LYS
1	A	152	ASP
1	A	174	ILE
1	A	215	GLU
1	A	242	PHE
1	A	247	GLN
1	A	256	GLU
1	A	275	LEU
1	A	304	LYS
1	A	305	PHE
1	A	336	LEU
1	A	340	PRO
1	A	349	ASN

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	117	HIS
1	A	122	ASN

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Mol	Chain	Res	Type
1	A	274	GLN
1	A	292	GLN
1	A	349	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)

1 non-standard protein/DNA/RNA residue 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).

Mal	Mol Type		Chain Res		Res Link	Tiple	\mathbf{B}_{0}	ond leng	${ m gths}$	В	ond ang	gles
IVIOI	Moi Type	Chain	Link	Counts		RMSZ	# Z > 2	Counts	RMSZ	# Z > 2		
1	SEP	A	241	1	8,9,10	1.60	2 (25%)	8,12,14	2.05	1 (12%)		

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
1	SEP	A	241	1	-	1/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
1	A	241	SEP	P-O3P	-2.73	1.44	1.54
1	A	241	SEP	P-O2P	-2.55	1.45	1.54

All (1) bond angle outliers are listed below:



\mathbf{Mol}	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^o)$
1	A	241	SEP	OG-CB-CA	5.00	113.01	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	241	SEP	CB-OG-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	Вс	Bond lengths			Bond angles		
MIOI	туре				Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2	
5	GOL	A	602	-	5,5,5	0.70	0	5, 5, 5	0.29	0	
4	LI8	A	501	-	36,37,37	1.61	9 (25%)	49,51,51	2.25	12 (24%)	
5	GOL	A	607	-	5,5,5	0.49	0	5,5,5	0.14	0	
5	GOL	A	606	-	5,5,5	0.66	0	5,5,5	0.18	0	
2	SO4	A	600	-	4,4,4	0.22	0	6,6,6	0.13	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
5	GOL	A	606	-	-	1/4/4/4	-
5	GOL	A	607	_	-	2/4/4/4	-
5	GOL	A	602	-	-	2/4/4/4	-
4	LI8	A	501	-	-	6/31/39/39	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	Ideal(Å)
4	A	501	LI8	C2-C1	3.31	1.44	1.40
4	A	501	LI8	O32-C31	3.04	1.28	1.22
4	A	501	LI8	C10-N8	-2.90	1.34	1.40
4	A	501	LI8	C12-N16	-2.90	1.35	1.41
4	A	501	LI8	C11-C10	2.66	1.43	1.39
4	A	501	LI8	C13-C12	2.42	1.43	1.39
4	A	501	LI8	C21-N20	-2.18	1.42	1.47
4	A	501	LI8	C36-C34	2.17	1.58	1.54
4	A	501	LI8	C24-N20	-2.04	1.42	1.47

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$\mathbf{Ideal}(^{o})$
4	A	501	LI8	N5-C4-N3	-8.31	118.68	126.55
4	A	501	LI8	C34-C31-N29	5.48	123.44	116.92
4	A	501	LI8	N16-C18-N20	4.43	120.96	115.89
4	A	501	LI8	BR7-C1-C2	4.39	124.54	120.15
4	A	501	LI8	C6-N5-C4	4.36	122.45	115.88
4	A	501	LI8	O38-C37-N39	-4.02	115.13	123.17
4	A	501	LI8	C4-N3-C2	3.02	123.29	116.39
4	A	501	LI8	O32-C31-N29	-2.39	117.84	122.74
4	A	501	LI8	C34-C37-N39	2.36	121.40	116.97
4	A	501	LI8	C1-C6-N5	-2.31	120.25	123.09
4	A	501	LI8	N8-C4-N3	2.17	124.28	116.92
4	A	501	LI8	O19-C18-N20	-2.07	118.88	121.78

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	LI8	O32-C31-C34-C37
5	A	602	GOL	O1-C1-C2-C3
5	A	607	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
5	A	607	GOL	O1-C1-C2-C3
5	A	602	GOL	O1-C1-C2-O2
4	A	501	LI8	O32-C31-C34-C36
4	A	501	LI8	N29-C31-C34-C36
5	A	606	GOL	O1-C1-C2-O2
4	A	501	LI8	C11-C12-N16-C18
4	A	501	LI8	C13-C12-N16-C18
4	A	501	LI8	N29-C31-C34-C37

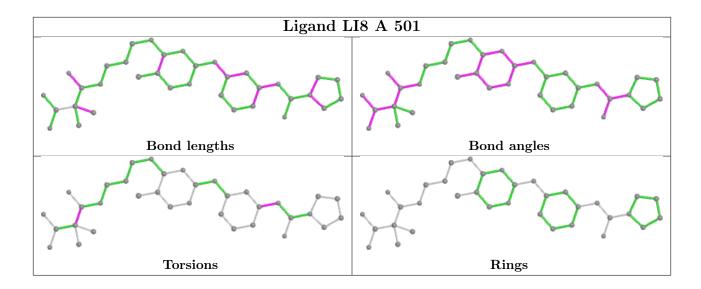
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	602	GOL	2	0
4	A	501	LI8	3	0
5	A	607	GOL	2	0
5	A	606	GOL	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.





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, 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	275/286 (96%)	-0.25	5 (1%)	68	69	9, 22, 46, 68	9 (3%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	242	PHE	3.7
1	A	258	SER	2.5
1	A	359	THR	2.2
1	A	257	LYS	2.1
1	A	304	LYS	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	SEP	A	241	10/11	0.91	0.15	66,68,69,69	1

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

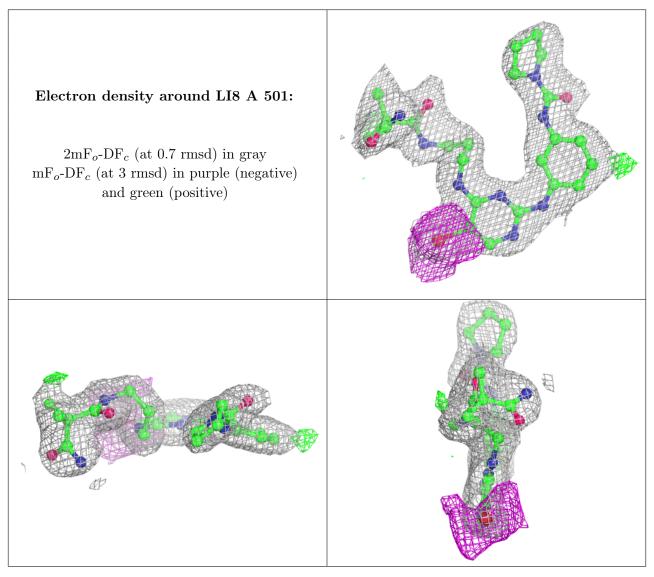
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



median, 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
5	GOL	A	607	6/6	0.77	0.29	54,58,59,59	0
5	GOL	A	606	6/6	0.80	0.17	63,67,67,69	0
5	GOL	A	602	6/6	0.87	0.18	22,31,32,40	0
4	LI8	A	501	35/35	0.88	0.14	18,32,39,75	0
2	SO4	A	600	5/5	0.95	0.14	67,68,69,69	0
3	CL	A	698	1/1	0.98	0.09	26,26,26,26	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.





6.5 Other polymers (i)

There are no such residues in this entry.

