



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2023 – 02:57 PM JST

PDB ID : 8HAQ
Title : The complex of Src with GW8510
Authors : Zhu, S.J.; Bi, S.Z.
Deposited on : 2022-10-26
Resolution : 2.27 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.36
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) : 2.36

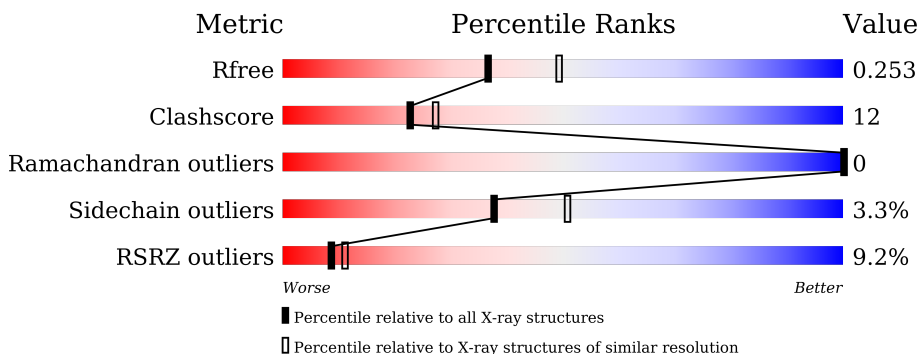
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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 $\leq 5\%$. 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	277	 10% 69% 18% • 11%
1	B	277	 6% 67% 19% • 12%

2 Entry composition i

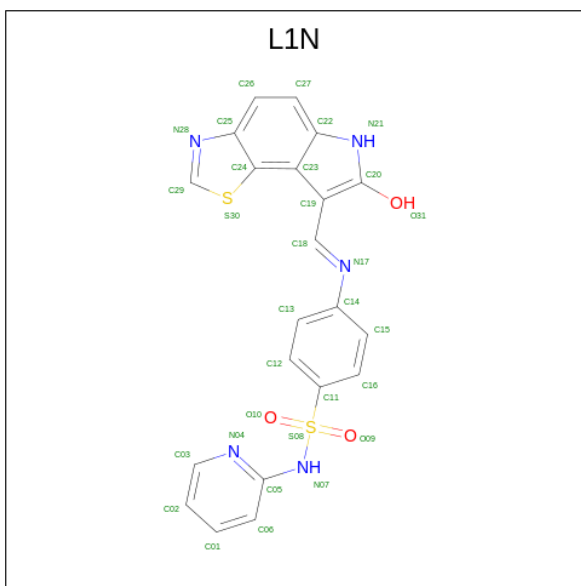
There are 3 unique types of molecules in this entry. The entry contains 4115 atoms, of which 30 are hydrogens and 0 are deuteriums.

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 Isoform 2 of Proto-oncogene tyrosine-protein kinase Src.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	247	Total 1982	1275	331	361	15	0	0	0
1	B	243	Total 1957	1254	329	359	15	0	0	0

- Molecule 2 is 4-[({E})-(7-oxidanyl-6 {H}-pyrrolo[2,3-g][1,3]benzothiazol-8-yl)methylideneamino]- {N}-pyridin-2-yl-benzenesulfonamide (three-letter code: L1N) (formula: C₂₁H₁₅N₅O₃S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			S
2	A	1	Total 46	21	15	5	3	2	0	0
2	B	1	Total 46	21	15	5	3	2	0	0

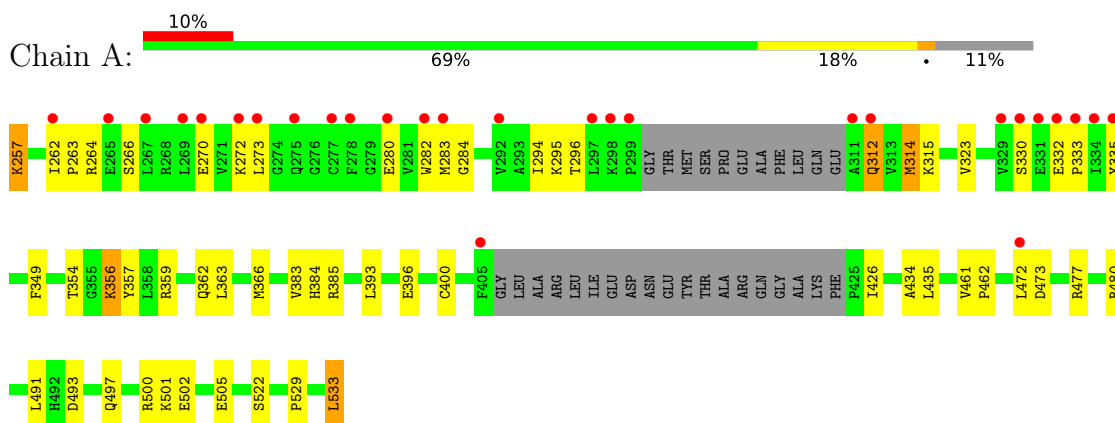
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total 38	O 38	0	0
3	B	46	Total 46	O 46	0	0

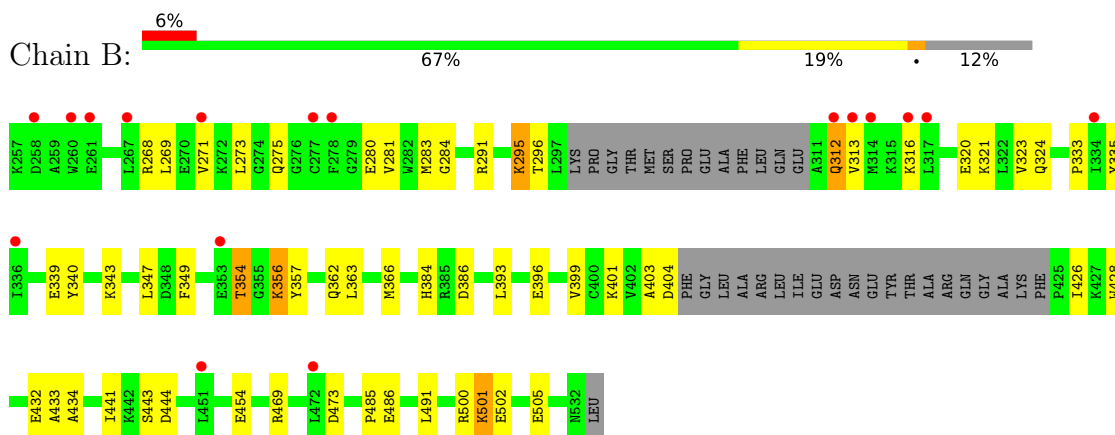
3 Residue-property plots [i](#)

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: Isoform 2 of Proto-oncogene tyrosine-protein kinase Src



- Molecule 1: Isoform 2 of Proto-oncogene tyrosine-protein kinase Src



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	41.83Å 62.58Å 74.26Å 79.30° 87.98° 89.73°	Depositor
Resolution (Å)	32.96 – 2.27 43.22 – 2.27	Depositor EDS
% Data completeness (in resolution range)	97.5 (32.96-2.27) 90.0 (43.22-2.27)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.27Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.207 , 0.250 0.213 , 0.253	Depositor DCC
R_{free} test set	1678 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	34.1	Xtrriage
Anisotropy	0.596	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.042 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4115	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.58% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: L1N

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	0.45	0/2030	0.61	0/2750
1	B	0.45	0/2003	0.62	0/2712
All	All	0.45	0/4033	0.61	0/5462

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 [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	1982	0	1969	47	0
1	B	1957	0	1944	45	0
2	A	31	15	0	2	0
2	B	31	15	0	1	0
3	A	38	0	0	0	0
3	B	46	0	0	1	0
All	All	4085	30	3913	91	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 (91) 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:366:MET:HG2	1:A:400:CYS:SG	2.11	0.90
1:B:324:GLN:HG2	1:B:339:GLU:OE2	1.78	0.82
1:B:500:ARG:HD2	1:B:505:GLU:CD	2.04	0.78
1:A:312:GLN:HG3	1:A:314:MET:H	1.51	0.75
1:B:281:VAL:HG12	1:B:295:LYS:HG3	1.67	0.75
1:A:270:GLU:HG2	1:A:284:GLY:HA2	1.69	0.74
1:B:396:GLU:O	1:B:399:VAL:HG23	1.88	0.74
1:B:320:GLU:O	1:B:401:LYS:HE2	1.86	0.74
1:A:359:ARG:HH11	1:A:529:PRO:HB2	1.53	0.73
1:A:280:GLU:HG3	1:A:296:THR:OG1	1.88	0.73
1:B:469:ARG:O	1:B:473:ASP:HB2	1.89	0.73
1:A:435:LEU:HD21	1:A:472:LEU:HD21	1.74	0.68
1:A:333:PRO:HB2	1:A:335:TYR:HE1	1.60	0.66
1:B:349:PHE:CE1	1:B:354:THR:HG21	2.31	0.66
1:A:359:ARG:NH1	1:A:529:PRO:HB2	2.11	0.65
1:B:324:GLN:HG3	1:B:339:GLU:HB3	1.78	0.64
1:A:384:HIS:O	1:A:385:ARG:HB2	1.99	0.60
1:A:312:GLN:HG2	1:A:315:LYS:HG3	1.84	0.60
1:A:332:GLU:HA	1:A:333:PRO:C	2.23	0.60
1:B:500:ARG:HD2	1:B:505:GLU:OE2	2.01	0.60
1:B:321:LYS:HA	1:B:401:LYS:HG2	1.85	0.59
1:B:280:GLU:CG	1:B:296:THR:OG1	2.51	0.59
1:A:349:PHE:CE1	1:A:354:THR:HG21	2.38	0.58
1:B:313:VAL:HG13	1:B:316:LYS:HD2	1.85	0.58
1:B:362:GLN:O	1:B:366:MET:HG3	2.04	0.58
1:A:263:PRO:HG2	1:A:266:SER:HB2	1.87	0.57
1:A:500:ARG:NE	1:A:505:GLU:HG2	2.20	0.57
1:A:312:GLN:HG3	1:A:314:MET:N	2.20	0.56
1:B:280:GLU:HG2	1:B:296:THR:OG1	2.04	0.56
1:B:324:GLN:CG	1:B:339:GLU:OE2	2.50	0.55
1:A:323:VAL:HG21	1:A:393:LEU:HD12	1.88	0.55
1:B:485:PRO:O	1:B:486:GLU:HB2	2.05	0.55
1:B:283:MET:HG3	1:B:340:TYR:CE1	2.41	0.55
1:A:359:ARG:HA	1:A:533:LEU:C	2.28	0.55
1:A:272:LYS:HE2	1:A:280:GLU:OE1	2.07	0.54
1:B:501:LYS:HA	1:B:501:LYS:HE2	1.91	0.52
1:A:473:ASP:O	1:A:477:ARG:HG3	2.09	0.52
1:A:396:GLU:OE2	1:A:396:GLU:HA	2.11	0.51
1:B:426:ILE:HD11	1:B:434:ALA:HB1	1.93	0.50
1:A:502:GLU:HA	1:A:502:GLU:OE1	2.11	0.50
1:B:273:LEU:HD11	1:B:283:MET:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:323:VAL:HG21	1:B:393:LEU:HD12	1.94	0.50
1:B:280:GLU:HG3	1:B:296:THR:OG1	2.12	0.49
1:B:356:LYS:HE3	1:B:357:TYR:CZ	2.47	0.49
1:B:441:ILE:O	1:B:444:ASP:HB2	2.13	0.49
1:B:363:LEU:HD23	1:B:366:MET:CE	2.43	0.48
1:B:401:LYS:NZ	3:B:702:HOH:O	2.40	0.48
1:B:428:TRP:HE1	1:B:454:GLU:CD	2.17	0.48
1:B:384:HIS:HD2	1:B:386:ASP:H	1.62	0.48
1:A:294:ILE:HG21	1:A:335:TYR:HD2	1.79	0.47
1:A:522:SER:HB3	1:B:347:LEU:HD21	1.97	0.47
1:B:349:PHE:HE1	1:B:354:THR:HG21	1.78	0.47
1:A:280:GLU:OE1	1:A:282:TRP:NE1	2.45	0.47
1:A:294:ILE:HG21	1:A:335:TYR:CD2	2.50	0.47
1:A:359:ARG:HG2	1:A:533:LEU:C	2.35	0.47
1:A:359:ARG:HH11	1:A:529:PRO:CB	2.23	0.46
1:A:283:MET:HG2	1:A:284:GLY:N	2.30	0.46
1:A:362:GLN:O	1:A:366:MET:HE2	2.15	0.46
1:A:264:ARG:NH1	1:A:333:PRO:HG2	2.31	0.45
1:A:383:VAL:HG12	1:A:385:ARG:HG3	1.98	0.45
1:A:257:LYS:HD2	1:A:330:SER:OG	2.17	0.45
1:A:273:LEU:HD23	2:A:601:L1N:C01	2.47	0.44
1:B:502:GLU:OE1	1:B:505:GLU:OE2	2.36	0.44
1:A:356:LYS:HG3	1:A:357:TYR:CD2	2.52	0.44
1:B:269:LEU:N	1:B:269:LEU:HD12	2.32	0.44
1:A:262:ILE:HB	1:A:263:PRO:HD2	1.99	0.43
1:A:363:LEU:HD23	1:A:366:MET:CE	2.48	0.43
1:A:461:VAL:HG13	1:A:462:PRO:HD2	2.01	0.43
1:A:359:ARG:HA	1:A:533:LEU:O	2.18	0.43
1:A:480:ARG:HH22	1:A:501:LYS:HD3	1.84	0.43
1:B:502:GLU:H	1:B:502:GLU:CD	2.22	0.42
1:B:268:ARG:O	1:B:284:GLY:HA3	2.18	0.42
1:B:384:HIS:CD2	1:B:386:ASP:H	2.38	0.42
1:B:491:LEU:HA	1:B:491:LEU:HD12	1.62	0.42
1:A:426:ILE:HD12	1:A:434:ALA:HB1	2.02	0.42
1:B:363:LEU:HD23	1:B:366:MET:HE3	2.01	0.42
1:B:275:GLN:HG3	1:B:280:GLU:HB3	2.01	0.42
1:A:273:LEU:HD22	2:A:601:L1N:C05	2.49	0.42
1:B:271:VAL:HG11	2:B:601:L1N:C01	2.49	0.42
1:B:393:LEU:HD12	1:B:403:ALA:HB2	2.01	0.42
1:A:257:LYS:HD3	1:A:257:LYS:HA	1.91	0.42
1:A:491:LEU:HD12	1:A:491:LEU:HA	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:501:LYS:HD2	1:A:501:LYS:HA	1.81	0.41
1:B:432:GLU:HG2	1:B:433:ALA:N	2.35	0.41
1:A:493:ASP:O	1:A:497:GLN:HG3	2.20	0.41
1:B:343:LYS:HA	1:B:343:LYS:HD3	1.68	0.41
1:A:533:LEU:HA	1:A:533:LEU:HD13	1.78	0.41
1:B:501:LYS:HE3	1:B:501:LYS:HB2	1.82	0.40
1:A:283:MET:HG2	1:A:284:GLY:H	1.87	0.40
1:B:312:GLN:O	1:B:312:GLN:HG2	2.20	0.40
1:B:333:PRO:HB2	1:B:335:TYR:HE1	1.86	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	241/277 (87%)	238 (99%)	3 (1%)	0	100	100
1	B	237/277 (86%)	231 (98%)	6 (2%)	0	100	100
All	All	478/554 (86%)	469 (98%)	9 (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	213/239 (89%)	207 (97%)	6 (3%)	43 57
1	B	211/239 (88%)	203 (96%)	8 (4%)	33 44
All	All	424/478 (89%)	410 (97%)	14 (3%)	38 51

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	257	LYS
1	A	295	LYS
1	A	312	GLN
1	A	314	MET
1	A	356	LYS
1	A	533	LEU
1	B	291	ARG
1	B	295	LYS
1	B	312	GLN
1	B	354	THR
1	B	356	LYS
1	B	404	ASP
1	B	443	SER
1	B	501	LYS

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

Mol	Chain	Res	Type
1	A	324	GLN
1	A	532	ASN
1	B	324	GLN
1	B	384	HIS
1	B	391	ASN
1	B	513	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 [i](#)

There are no monosaccharides 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	L1N	B	601	-	28,35,35	1.61	6 (21%)	36,51,51	3.22	12 (33%)
2	L1N	A	601	-	28,35,35	1.64	6 (21%)	36,51,51	3.25	11 (30%)

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	L1N	B	601	-	-	0/14/16/16	0/5/5/5
2	L1N	A	601	-	-	4/14/16/16	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	L1N	S08-N07	4.52	1.71	1.63
2	B	601	L1N	S08-N07	4.21	1.70	1.63
2	B	601	L1N	C19-C18	3.37	1.52	1.44
2	A	601	L1N	C19-C18	3.30	1.52	1.44
2	A	601	L1N	C11-S08	3.14	1.81	1.76
2	B	601	L1N	C11-S08	2.95	1.81	1.76
2	B	601	L1N	O09-S08	2.35	1.46	1.43
2	B	601	L1N	O10-S08	2.26	1.46	1.43
2	A	601	L1N	O09-S08	2.26	1.46	1.43
2	A	601	L1N	O31-C20	2.22	1.39	1.29
2	A	601	L1N	O10-S08	2.22	1.46	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	L1N	O31-C20	2.08	1.39	1.29

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	L1N	O10-S08-O09	-14.81	101.34	119.55
2	B	601	L1N	O10-S08-O09	-14.63	101.56	119.55
2	A	601	L1N	C29-S30-C24	6.72	98.17	90.88
2	B	601	L1N	C29-S30-C24	6.61	98.06	90.88
2	A	601	L1N	N07-C05-N04	5.49	120.31	114.12
2	B	601	L1N	C19-C18-N17	-5.40	114.99	122.68
2	A	601	L1N	C19-C18-N17	-4.99	115.57	122.68
2	B	601	L1N	N07-C05-N04	4.25	118.91	114.12
2	A	601	L1N	O10-S08-C11	3.06	111.74	107.97
2	B	601	L1N	C05-N07-S08	-3.06	118.42	124.97
2	A	601	L1N	O10-S08-N07	2.73	113.55	106.73
2	B	601	L1N	C03-N04-C05	2.61	120.93	117.22
2	B	601	L1N	C26-C25-N28	-2.61	123.58	130.80
2	B	601	L1N	O09-S08-C11	2.61	111.18	107.97
2	A	601	L1N	C03-N04-C05	2.57	120.87	117.22
2	A	601	L1N	C26-C25-N28	-2.53	123.81	130.80
2	B	601	L1N	O10-S08-C11	2.44	110.98	107.97
2	B	601	L1N	C14-N17-C18	2.44	126.73	120.41
2	A	601	L1N	C25-C24-C23	-2.35	120.05	123.47
2	B	601	L1N	C25-C24-C23	-2.33	120.08	123.47
2	A	601	L1N	O09-S08-C11	2.26	110.75	107.97
2	A	601	L1N	C14-N17-C18	2.15	125.97	120.41
2	B	601	L1N	O10-S08-N07	2.12	112.05	106.73

There are no chirality outliers.

All (4) torsion outliers are listed below:

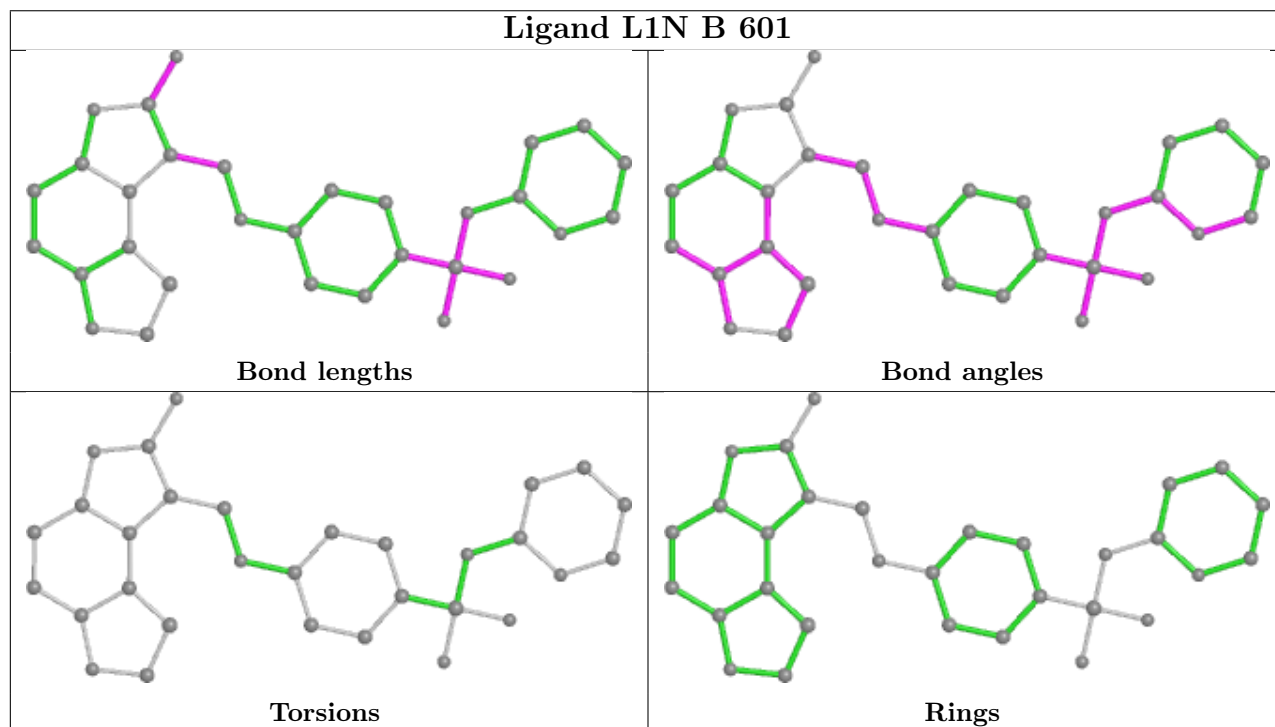
Mol	Chain	Res	Type	Atoms
2	A	601	L1N	C05-N07-S08-O09
2	A	601	L1N	C12-C11-S08-O09
2	A	601	L1N	C16-C11-S08-O09
2	A	601	L1N	C05-N07-S08-C11

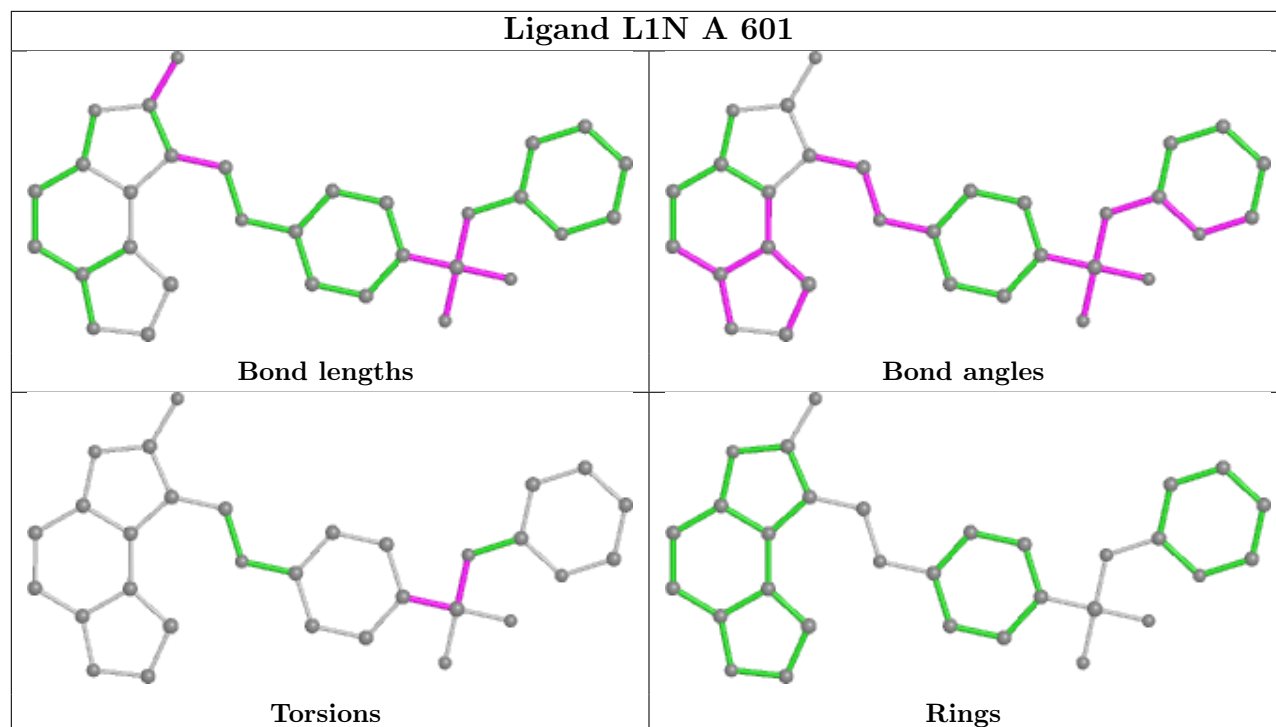
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	L1N	1	0
2	A	601	L1N	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 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 [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, 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	247/277 (89%)	0.75	28 (11%) 5 6	28, 43, 89, 107	0
1	B	243/277 (87%)	0.49	17 (6%) 16 20	28, 43, 80, 97	0
All	All	490/554 (88%)	0.62	45 (9%) 9 11	28, 43, 87, 107	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	332	GLU	6.1
1	A	333	PRO	5.9
1	A	267	LEU	5.6
1	A	269	LEU	5.6
1	A	278	PHE	5.4
1	A	335	TYR	5.4
1	A	283	MET	4.9
1	A	334	ILE	4.6
1	A	298	LYS	4.5
1	A	299	PRO	4.3
1	A	277	CYS	4.3
1	A	275	GLN	4.1
1	A	282	TRP	4.0
1	B	353	GLU	3.8
1	B	278	PHE	3.8
1	A	329	VAL	3.8
1	A	297	LEU	3.6
1	A	262	ILE	3.5
1	B	312	GLN	3.5
1	B	316	LYS	3.4
1	B	314	MET	3.1
1	A	273	LEU	3.1
1	B	334	ILE	2.8
1	B	317	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	405	PHE	2.7
1	A	272	LYS	2.7
1	A	270	GLU	2.7
1	A	331	GLU	2.6
1	A	330	SER	2.6
1	B	277	CYS	2.6
1	B	260	TRP	2.5
1	B	336	ILE	2.5
1	A	472	LEU	2.5
1	A	265	GLU	2.4
1	A	311	ALA	2.3
1	B	258	ASP	2.3
1	B	313	VAL	2.3
1	B	451	LEU	2.2
1	A	312	GLN	2.2
1	A	280	GLU	2.1
1	B	261	GLU	2.1
1	B	472	LEU	2.1
1	B	271	VAL	2.1
1	A	292	VAL	2.1
1	B	267	LEU	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](#)

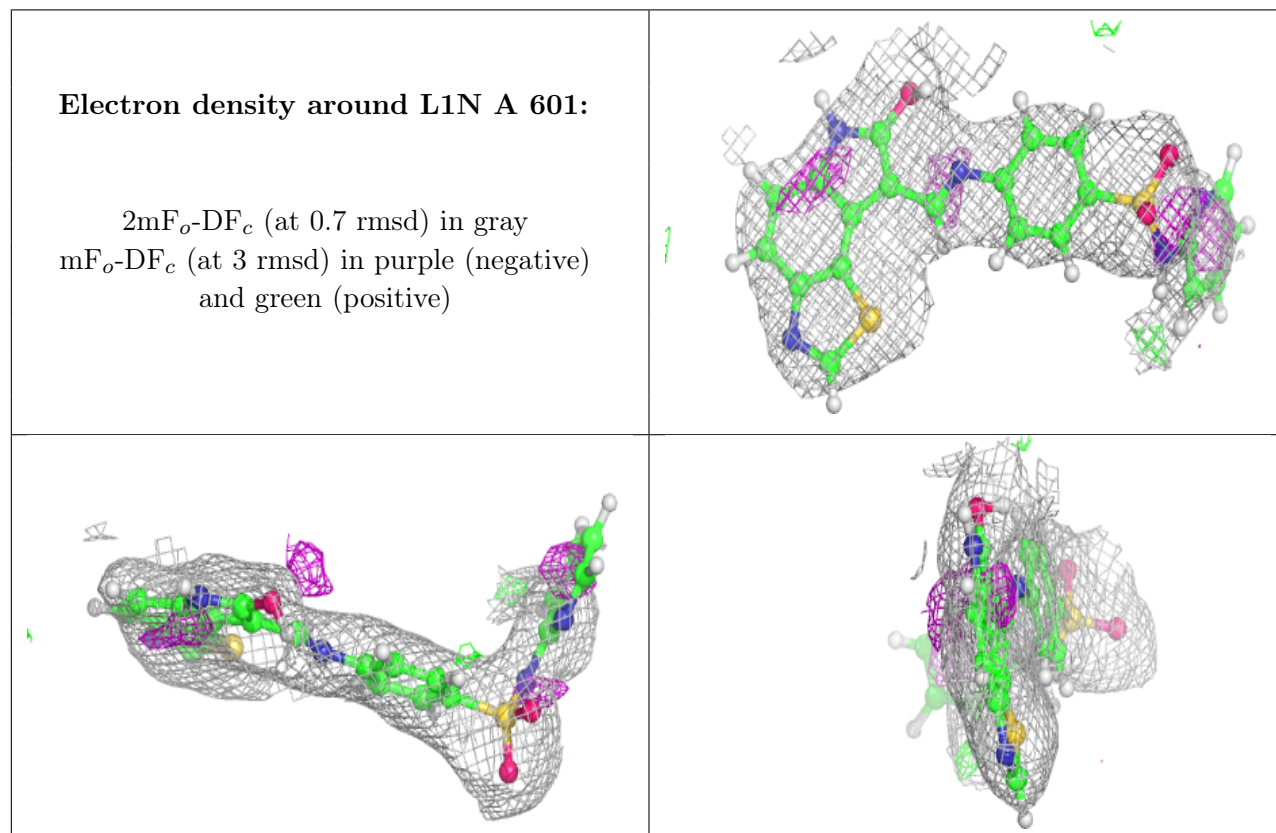
There are no monosaccharides in this entry.

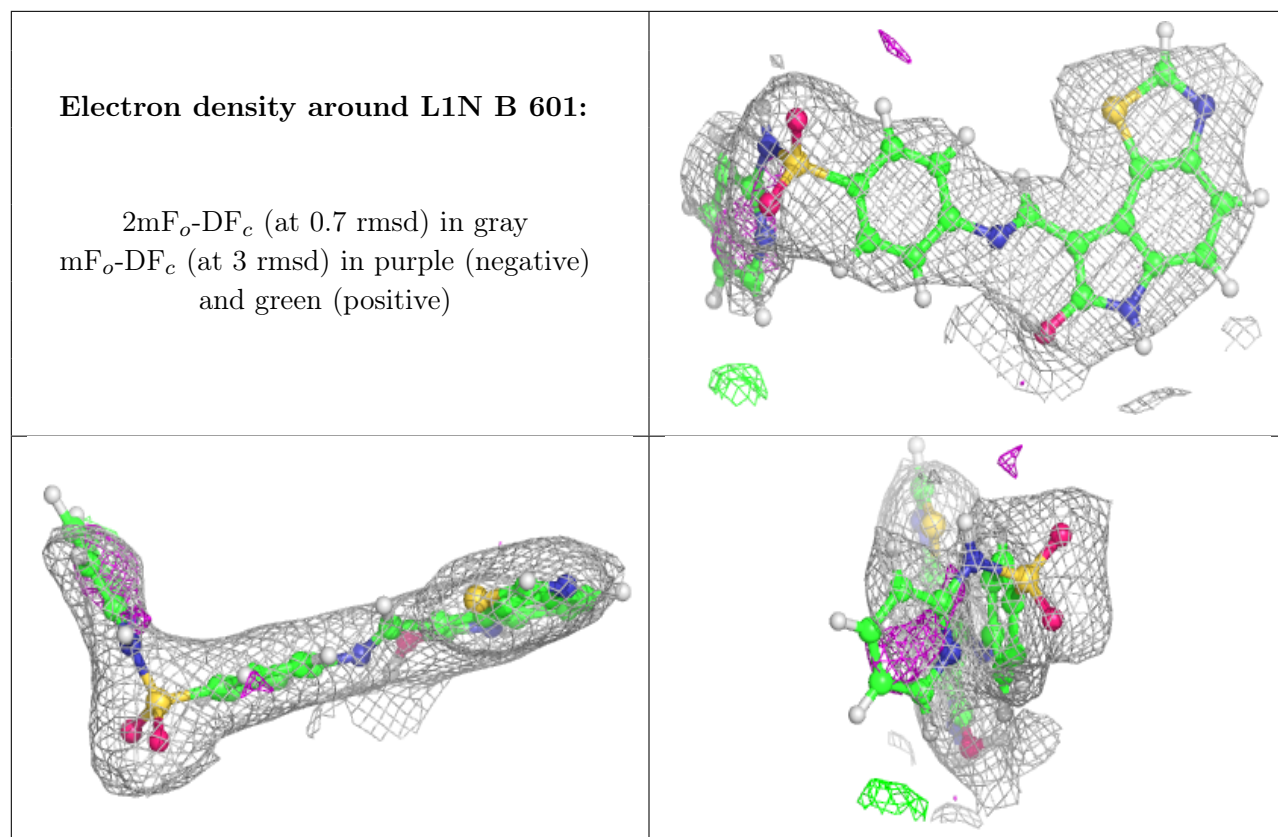
6.4 Ligands [i](#)

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	L1N	A	601	31/31	0.88	0.20	53,70,101,105	0
2	L1N	B	601	31/31	0.91	0.17	46,60,89,93	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.