



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:35 AM UTC

PDB ID : 9S2V / pdb_00009s2v
Title : NSP14 IN COMPLEX WITH LIGAND TDI-014925-CL-2 (compound 58)
Authors : Steinbacher, S.; Huggins, D.J.
Deposited on : 2025-07-22
Resolution : 2.38 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

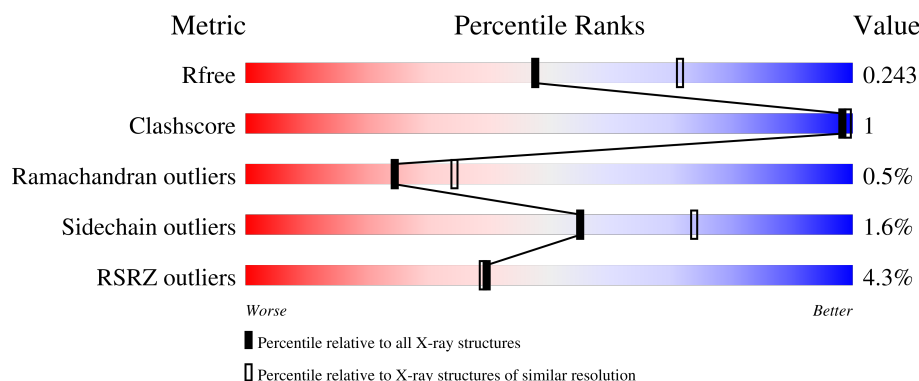
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	528	3% 80% 16%
1	B	528	4% 80% 18%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7391 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 Guanine-N7 methyltransferase nsp14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	24	0	0
			3561	2293	604	631	33			
1	B	433	Total	C	N	O	S	21	0	0
			3482	2242	593	614	33			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P0DTD1
A	90	ALA	ASP	engineered mutation	UNP P0DTD1
A	92	ALA	GLU	engineered mutation	UNP P0DTD1
B	0	SER	-	expression tag	UNP P0DTD1
B	90	ALA	ASP	engineered mutation	UNP P0DTD1
B	92	ALA	GLU	engineered mutation	UNP P0DTD1

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

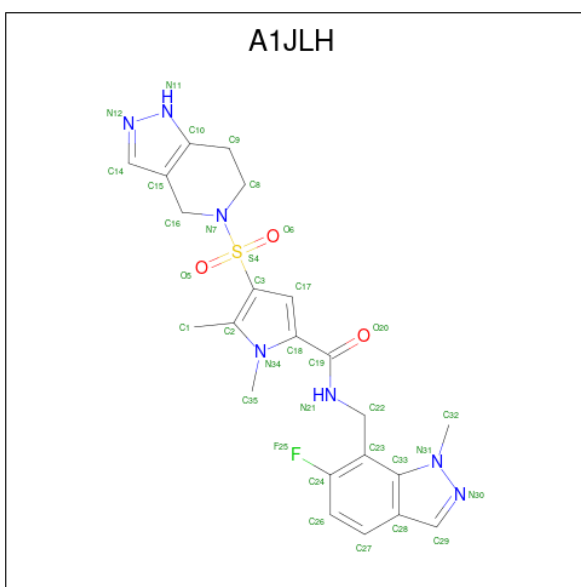
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Zn	0	0
			3	3		
2	B	3	Total	Zn	0	0
			3	3		

- Molecule 3 is S-ADENOSYL-L-HOMOCYSTEINE (CCD ID: SAH) (formula: C₁₄H₂₀N₆O₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			26	14	6	5	1		
3	B	1	Total	C	N	O	S	0	0
			26	14	6	5	1		

- Molecule 4 is {N}-[(6-fluoranyl-1-methyl-indazol-7-yl)methyl]-1,5-dimethyl-4-(1,4,6,7-tetrahydropyrazolo[4,3-c]pyridin-5-ylsulfonyl)pyrrole-2-carboxamide (CCD ID: A1JLH) (formula: C₂₂H₂₄FN₇O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	F	N	O	S	0	0
			34	22	1	7	3	1		

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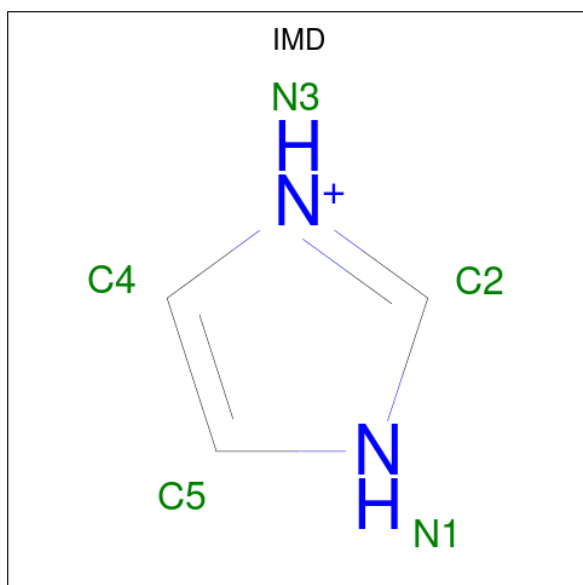
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	F	N	O	S	
			34	22	1	7	3	1	
								0	0

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Cl		
			3	3	0	0
5	B	2	Total	Cl		
			2	2	0	0

- Molecule 6 is IMIDAZOLE (CCD ID: IMD) (formula: C₃H₅N₂).

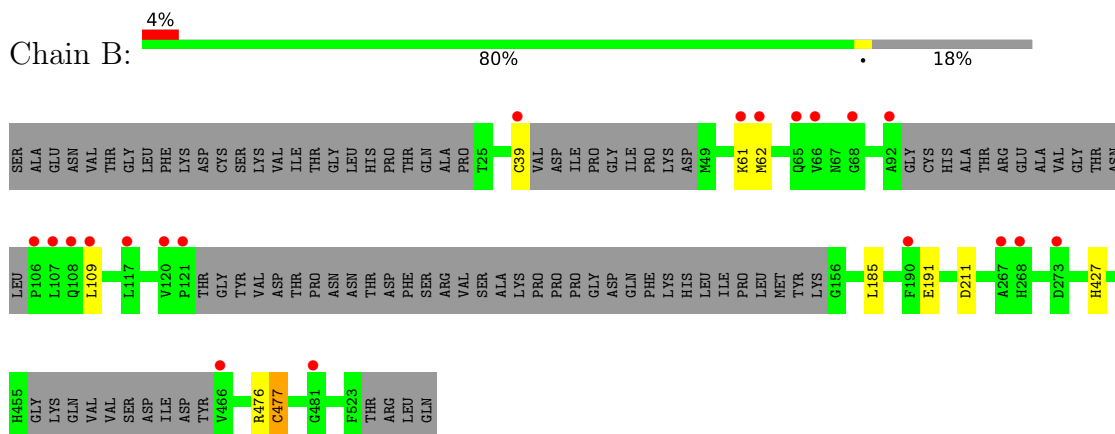


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N		
			5	3	2	0	0
6	B	1	Total	C	N		
			5	3	2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	119	Total	O		
			119	119	0	0
7	B	88	Total	O		
			88	88	0	0

- Molecule 1: Guanine-N7 methyltransferase nsp14



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	67.46Å 100.96Å 90.43Å 90.00° 108.33° 90.00°	Depositor
Resolution (Å)	64.12 – 2.38 64.12 – 2.38	Depositor EDS
% Data completeness (in resolution range)	98.2 (64.12-2.38) 98.3 (64.12-2.38)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.193 , 0.245 0.195 , 0.243	Depositor DCC
R_{free} test set	1125 reflections (2.37%)	wwPDB-VP
Wilson B-factor (Å ²)	58.4	Xtriage
Anisotropy	0.397	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7391	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: CL, ZN, SAH, A1JLH, IMD

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	1.02	2/3661 (0.1%)	1.40	1/4971 (0.0%)
1	B	1.02	0/3580	1.39	1/4857 (0.0%)
All	All	1.02	2/7241 (0.0%)	1.39	2/9828 (0.0%)

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
1	B	0	2
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210	CYS	CB-SG	-5.42	1.63	1.81
1	A	42	ILE	N-CA	5.12	1.50	1.46

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	CYS	CB-CA-C	-9.08	92.04	111.11
1	B	427	HIS	CA-CB-CG	-5.46	108.34	113.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	45	ILE	Peptide
1	B	185	LEU	Peptide
1	B	476	ARG	Peptide

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	3561	0	3455	8	0
1	B	3482	0	3369	0	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	26	0	19	0	0
3	B	26	0	19	0	0
4	A	34	0	0	0	0
4	B	34	0	0	0	0
5	A	3	0	0	0	0
5	B	2	0	0	0	0
6	A	5	0	5	0	0
6	B	5	0	5	0	0
7	A	119	0	0	0	0
7	B	88	0	0	0	0
All	All	7391	0	6872	8	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 1.

All (8) 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:45:ILE:HG22	1:A:46:PRO:HD3	1.83	0.60
1:A:442:LEU:HD12	1:A:443:PRO:HD2	1.94	0.49
1:A:200:LYS:NZ	1:A:224:TYR:OH	2.47	0.47
1:A:210:CYS:SG	1:A:229:HIS:CE1	3.08	0.46
1:A:329:LEU:HD22	1:A:348:TRP:CE2	2.53	0.43
1:A:257:HIS:CE1	1:A:264:HIS:HB2	2.55	0.42
1:A:184:VAL:HG12	1:A:277:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:MET:HE2	1:A:71:ASN:HA	2.03	0.41

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	437/528 (83%)	419 (96%)	16 (4%)	2 (0%)	24	34
1	B	423/528 (80%)	406 (96%)	15 (4%)	2 (0%)	24	34
All	All	860/1056 (81%)	825 (96%)	31 (4%)	4 (0%)	24	34

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	ILE
1	B	477	CYS
1	B	61	LYS
1	A	480	GLY

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	388/461 (84%)	382 (98%)	6 (2%)	57	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	379/461 (82%)	373 (98%)	6 (2%)	55 74
All	All	767/922 (83%)	755 (98%)	12 (2%)	55 74

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	GLU
1	A	191	GLU
1	A	301	ASP
1	A	357	SER
1	A	452	CYS
1	A	453	GLU
1	B	39	CYS
1	B	62	MET
1	B	109	LEU
1	B	191	GLU
1	B	211	ASP
1	B	477	CYS

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	26	HIS
1	A	67	ASN
1	A	256	ASN
1	B	245	GLN
1	B	283	HIS
1	B	386	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 11 are monoatomic - leaving 6 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SAH	A	604	-	27,28,28	0.54	1 (3%)	36,40,40	0.64	1 (2%)
6	IMD	A	609	-	5,5,5	0.26	0	5,5,5	0.64	0
4	A1JLH	A	605	-	35,38,38	2.09	9 (25%)	47,58,58	2.57	16 (34%)
4	A1JLH	B	605	-	35,38,38	2.14	8 (22%)	47,58,58	2.57	17 (36%)
3	SAH	B	604	-	27,28,28	0.50	0	36,40,40	0.56	1 (2%)
6	IMD	B	608	-	5,5,5	0.19	0	5,5,5	0.59	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
3	SAH	A	604	-	-	4/15/31/31	0/3/3/3
6	IMD	A	609	-	-	-	0/1/1/1
4	A1JLH	A	605	-	-	3/19/30/30	0/5/5/5
4	A1JLH	B	605	-	-	3/19/30/30	0/5/5/5
3	SAH	B	604	-	-	2/15/31/31	0/3/3/3
6	IMD	B	608	-	-	-	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	605	A1JLH	N31-N30	7.68	1.41	1.37
4	A	605	A1JLH	N31-N30	6.44	1.40	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	605	A1JLH	C10-N11	-5.15	1.30	1.35
4	A	605	A1JLH	C10-N11	-4.92	1.30	1.35
4	A	605	A1JLH	C14-C15	-4.54	1.35	1.40
4	B	605	A1JLH	C14-C15	-4.33	1.35	1.40
4	A	605	A1JLH	C28-C29	3.60	1.46	1.42
4	A	605	A1JLH	N11-N12	3.43	1.43	1.36
4	B	605	A1JLH	C29-N30	-3.22	1.28	1.32
4	B	605	A1JLH	C28-C29	3.10	1.45	1.42
4	B	605	A1JLH	N11-N12	2.96	1.42	1.36
4	A	605	A1JLH	C14-N12	2.63	1.38	1.33
4	A	605	A1JLH	C9-C10	-2.40	1.46	1.49
4	A	605	A1JLH	C33-N31	2.35	1.38	1.37
3	A	604	SAH	OXT-C	-2.31	1.23	1.30
4	B	605	A1JLH	C14-N12	2.13	1.37	1.33
4	B	605	A1JLH	C10-C15	2.11	1.40	1.37
4	A	605	A1JLH	C10-C15	2.01	1.40	1.37

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	605	A1JLH	C9-C8-N7	7.95	116.66	109.21
4	B	605	A1JLH	C9-C8-N7	7.15	115.91	109.21
4	B	605	A1JLH	C29-N30-N31	6.17	110.73	106.36
4	A	605	A1JLH	C15-C14-N12	-5.84	106.33	111.45
4	B	605	A1JLH	C28-C29-N30	-5.55	107.86	112.05
4	A	605	A1JLH	C28-C29-N30	-4.79	108.43	112.05
4	A	605	A1JLH	C1-C2-C3	-4.76	125.46	132.34
4	B	605	A1JLH	C15-C14-N12	-4.72	107.32	111.45
4	A	605	A1JLH	C29-N30-N31	4.60	109.62	106.36
4	A	605	A1JLH	C16-N7-C8	4.60	120.10	113.34
4	A	605	A1JLH	C1-C2-N34	4.57	126.43	122.18
4	B	605	A1JLH	C1-C2-C3	-4.47	125.89	132.34
4	B	605	A1JLH	C16-N7-C8	4.18	119.50	113.34
4	A	605	A1JLH	C19-C18-N34	4.03	127.96	122.81
4	B	605	A1JLH	C33-N31-N30	-4.01	108.98	110.95
4	A	605	A1JLH	C10-N11-N12	-3.82	105.76	111.02
4	B	605	A1JLH	C9-C10-C15	-3.46	122.99	125.65
4	B	605	A1JLH	C1-C2-N34	3.46	125.39	122.18
4	B	605	A1JLH	C10-N11-N12	-3.27	106.51	111.02
4	B	605	A1JLH	C19-C18-N34	3.24	126.94	122.81
3	A	604	SAH	OXT-C-O	-3.23	116.76	124.08
4	A	605	A1JLH	F25-C24-C23	3.12	121.53	117.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	605	A1JLH	C23-C22-N21	-2.68	105.75	111.26
4	A	605	A1JLH	C14-N12-N11	2.52	108.97	105.19
4	B	605	A1JLH	F25-C24-C23	2.47	120.73	117.64
4	A	605	A1JLH	C9-C10-C15	-2.44	123.78	125.65
4	B	605	A1JLH	C26-C27-C28	-2.41	118.48	121.74
4	A	605	A1JLH	C33-N31-N30	-2.24	109.85	110.95
4	B	605	A1JLH	C28-C33-C23	-2.18	118.38	122.47
3	B	604	SAH	OXT-C-O	-2.16	119.17	124.08
4	A	605	A1JLH	O6-S4-O5	2.14	122.76	119.69
4	A	605	A1JLH	C23-C22-N21	-2.14	106.87	111.26
4	A	605	A1JLH	C28-C33-C23	-2.11	118.51	122.47
4	B	605	A1JLH	C14-N12-N11	2.11	108.35	105.19
4	B	605	A1JLH	C35-N34-C2	2.07	128.09	124.17

There are no chirality outliers.

All (12) torsion outliers are listed below:

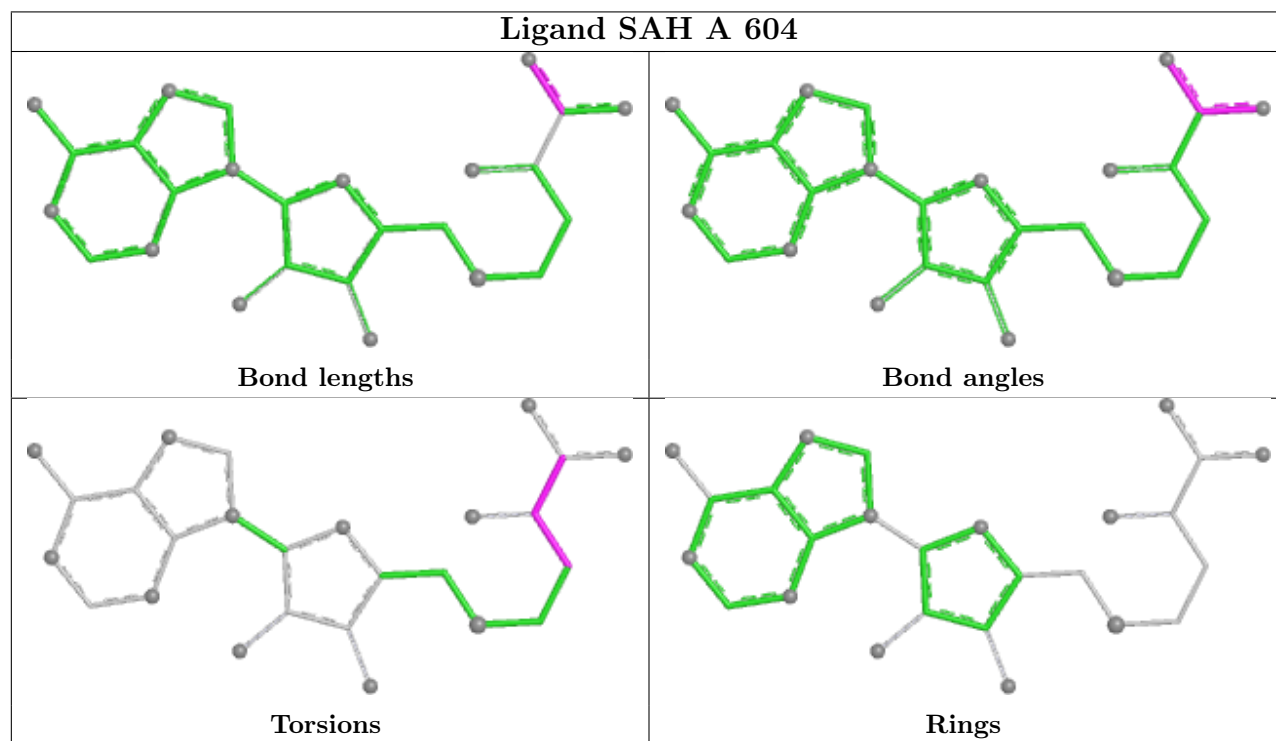
Mol	Chain	Res	Type	Atoms
3	A	604	SAH	N-CA-CB-CG
3	A	604	SAH	C-CA-CB-CG
3	B	604	SAH	N-CA-CB-CG
3	B	604	SAH	C-CA-CB-CG
4	A	605	A1JLH	C8-N7-S4-O6
4	B	605	A1JLH	C8-N7-S4-O6
4	A	605	A1JLH	C8-N7-S4-O5
4	B	605	A1JLH	C8-N7-S4-O5
4	A	605	A1JLH	C8-N7-S4-C3
3	A	604	SAH	O-C-CA-CB
3	A	604	SAH	OXT-C-CA-CB
4	B	605	A1JLH	C8-N7-S4-C3

There are no ring outliers.

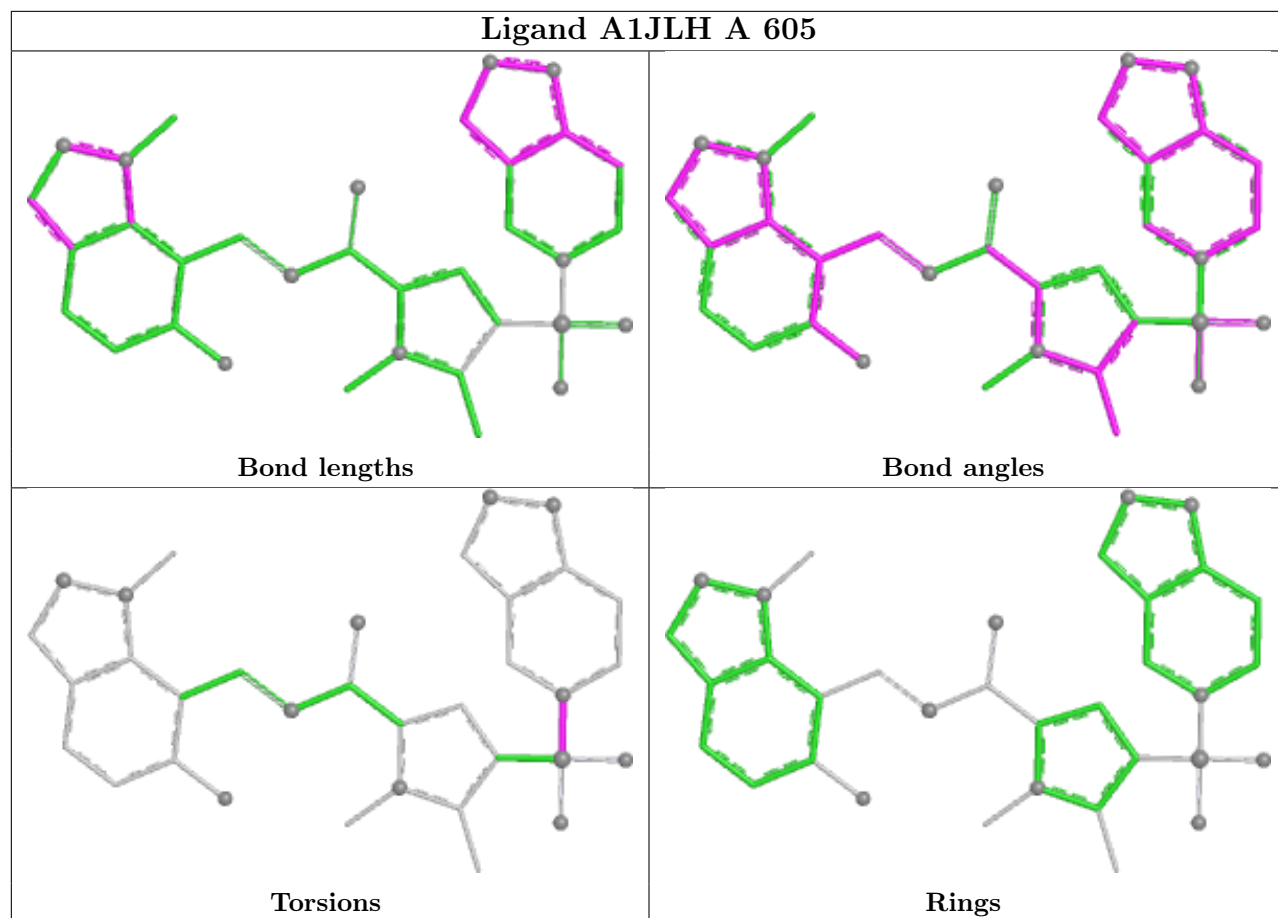
No monomer is involved in short contacts.

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

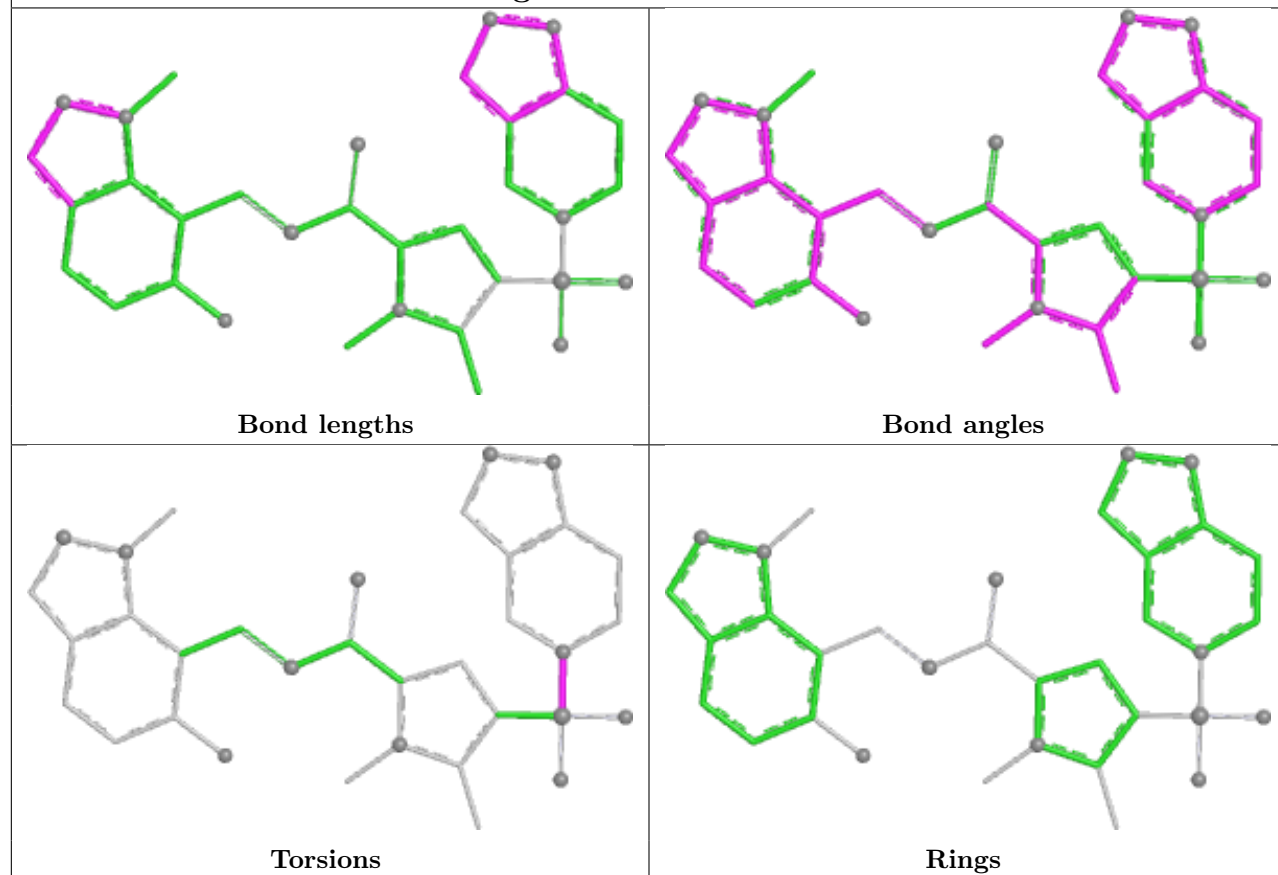
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



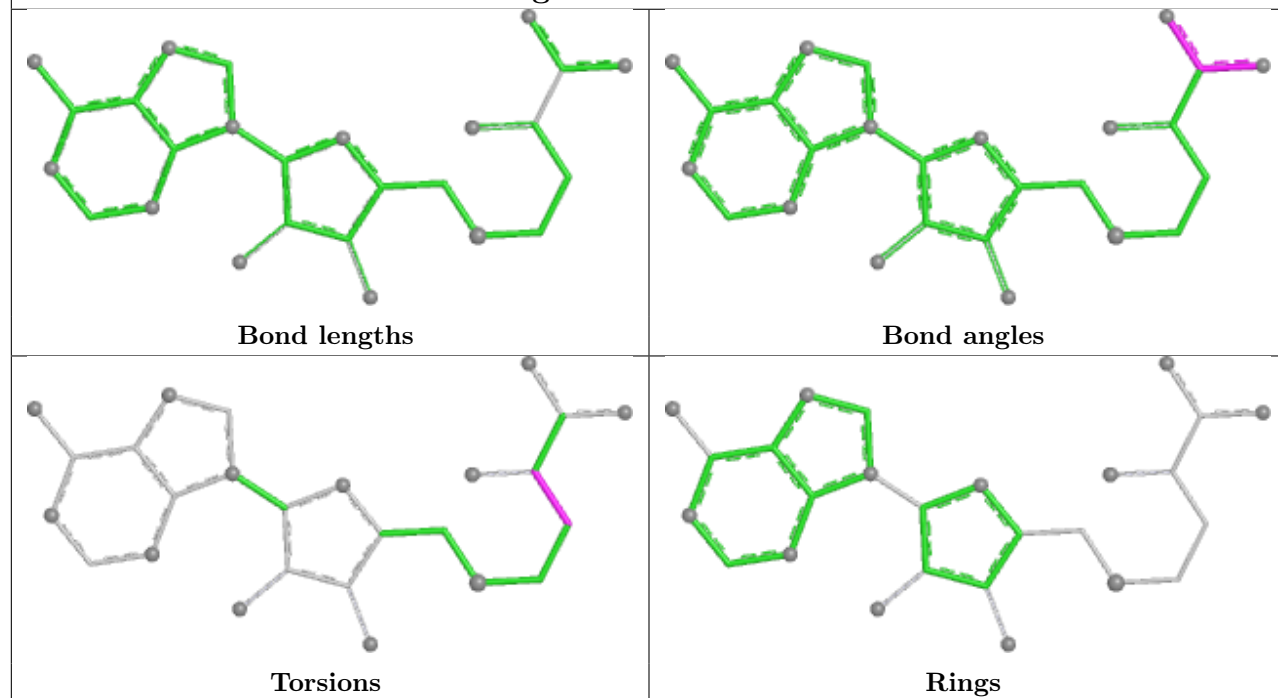
Ligand A1JLH A 605



Ligand A1JLH B 605



Ligand SAH B 604



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	445/528 (84%)	0.25	18 (4%)	42 42	33, 59, 107, 171	10 (2%)
1	B	433/528 (82%)	0.28	20 (4%)	37 37	38, 65, 114, 146	9 (2%)
All	All	878/1056 (83%)	0.27	38 (4%)	40 39	33, 63, 112, 171	19 (2%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	466	VAL	5.3
1	A	45	ILE	5.2
1	B	66	VAL	4.6
1	B	106	PRO	4.3
1	A	466	VAL	4.2
1	B	121	PRO	3.9
1	A	105	LEU	3.9
1	B	92	ALA	3.6
1	A	40	VAL	3.5
1	B	120	VAL	3.4
1	B	65	GLN	3.3
1	B	267	ALA	3.2
1	B	39	CYS	3.2
1	B	108	GLN	3.2
1	A	44	GLY	3.2
1	B	107	LEU	3.1
1	A	41	ASP	3.0
1	A	43	PRO	2.9
1	B	190	PHE	2.8
1	A	48	ASP	2.6
1	B	61	LYS	2.5
1	A	454	SER	2.5
1	A	42	ILE	2.4
1	B	68	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	481	GLY	2.3
1	A	467	PRO	2.3
1	A	64	TYR	2.3
1	A	268	HIS	2.3
1	B	109	LEU	2.2
1	A	46	PRO	2.2
1	A	57	MET	2.2
1	B	117	LEU	2.2
1	A	66	VAL	2.2
1	A	26	HIS	2.2
1	B	268	HIS	2.1
1	B	62	MET	2.1
1	A	58	MET	2.1
1	B	273	ASP	2.1

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 oligosaccharides 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.

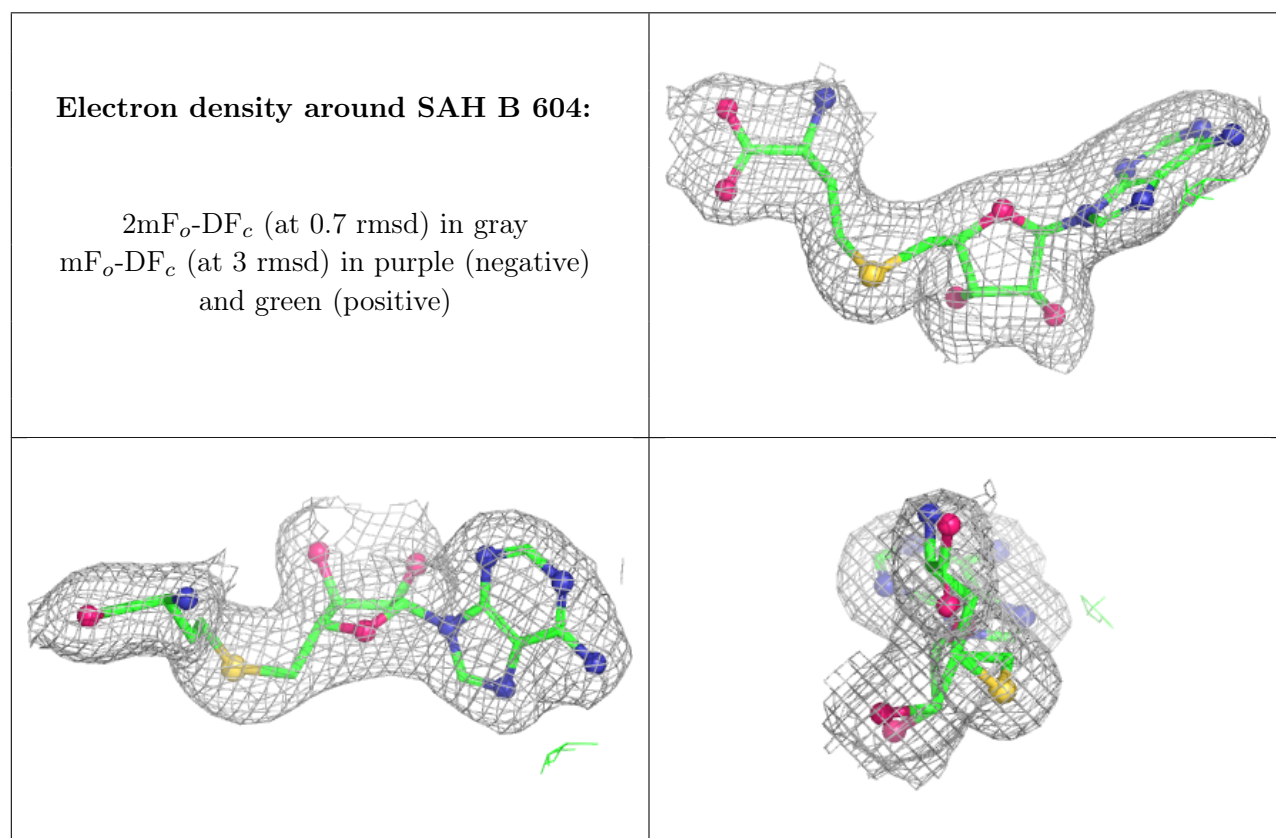
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	CL	A	606	1/1	0.90	0.12	87,87,87,87	0
5	CL	B	607	1/1	0.91	0.16	88,88,88,88	0
6	IMD	A	609	5/5	0.91	0.14	69,77,77,79	0
5	CL	B	606	1/1	0.92	0.13	97,97,97,97	0
5	CL	A	607	1/1	0.93	0.12	80,80,80,80	0
5	CL	A	608	1/1	0.95	0.10	85,85,85,85	0
6	IMD	B	608	5/5	0.95	0.18	57,62,64,67	0
3	SAH	B	604	26/26	0.97	0.06	41,49,52,52	0
3	SAH	A	604	26/26	0.97	0.06	44,49,52,52	0

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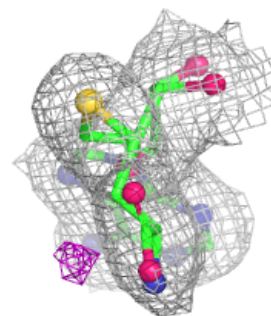
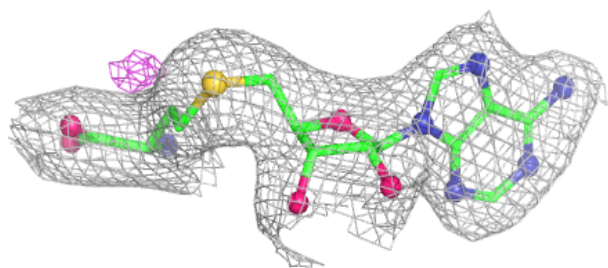
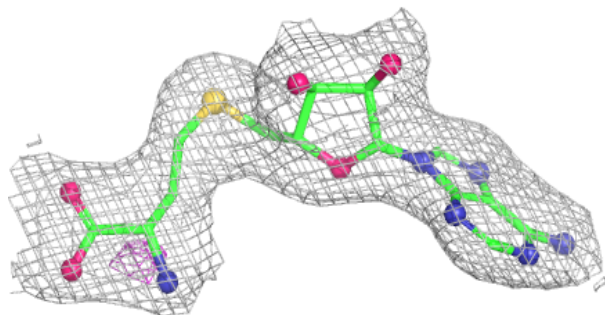
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	A1JLH	B	605	34/34	0.98	0.06	38,46,50,51	0
4	A1JLH	A	605	34/34	0.98	0.06	38,47,53,56	0
2	ZN	B	603	1/1	0.99	0.03	69,69,69,69	0
2	ZN	A	603	1/1	0.99	0.03	77,77,77,77	0
2	ZN	B	601	1/1	0.99	0.03	65,65,65,65	0
2	ZN	B	602	1/1	0.99	0.02	61,61,61,61	0
2	ZN	A	602	1/1	1.00	0.01	51,51,51,51	0
2	ZN	A	601	1/1	1.00	0.02	51,51,51,51	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.

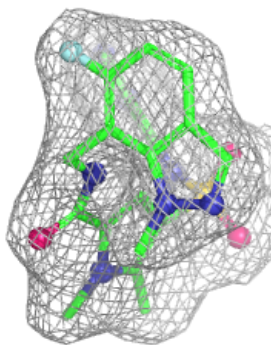
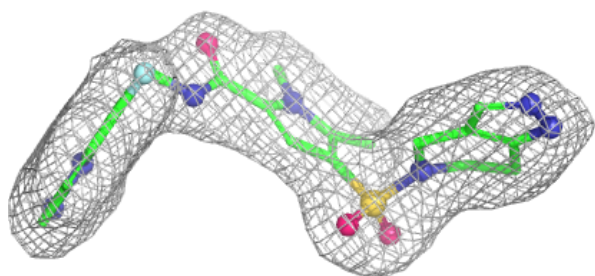
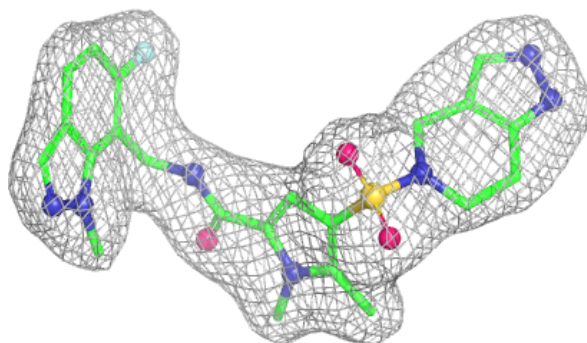


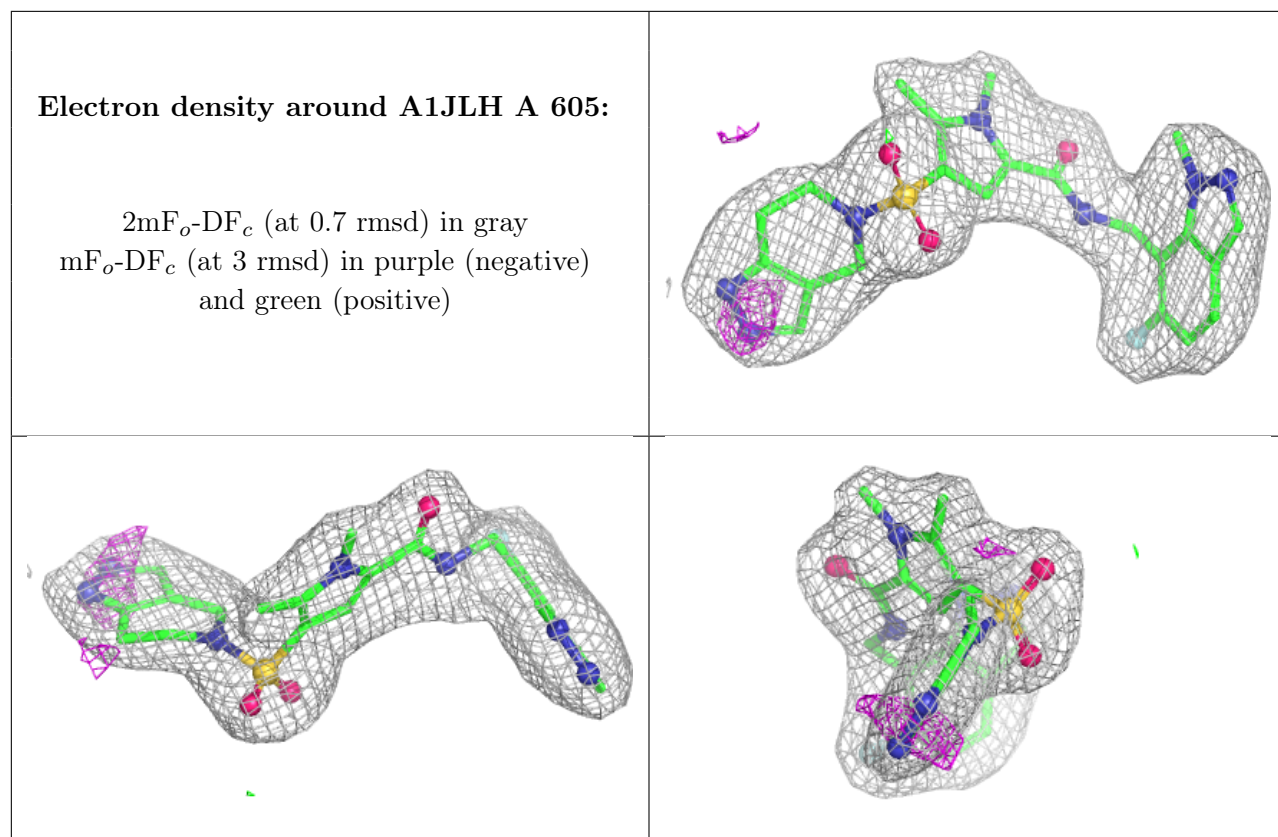
Electron density around SAH A 604:

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

**Electron density around A1JLH B 605:**

$2mF_o-DF_c$ (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.