



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 24, 2025 – 10:16 PM JST

PDB ID : 9KXB / pdb_00009kxb
Title : Crystal structure of S. aureus tryptophanyl-tRNA synthetase complexed with 3-methylchuangxinmycin
Authors : Ren, Y.; Qiao, H.; Wang, S.; Liu, W.; Fang, P.
Deposited on : 2024-12-06
Resolution : 2.21 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 Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.45.1

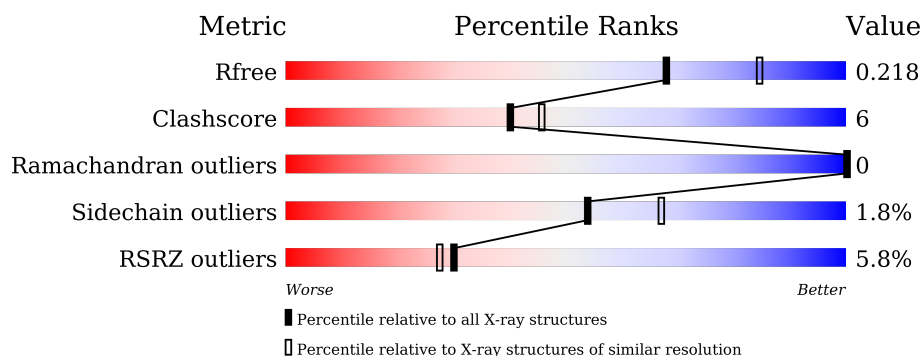
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.21 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}	164625	7167 (2.24-2.20)
Clashscore	180529	8096 (2.24-2.20)
Ramachandran outliers	177936	8010 (2.24-2.20)
Sidechain outliers	177891	8011 (2.24-2.20)
RSRZ outliers	164620	7166 (2.24-2.20)

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	335	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>• •</div> </div> </div>
1	B	335	<div> <div>12%</div> <div> <div></div> <div>81%</div> <div>13%</div> <div>• •</div> </div> </div>
1	C	335	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>• 5%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7847 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.

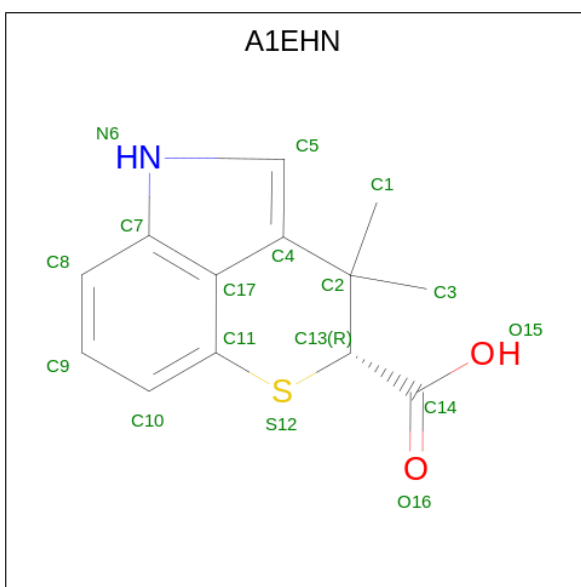
- Molecule 1 is a protein called Tryptophan-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2527	1605	429	480	13			
1	B	320	Total	C	N	O	S	0	0	0
			2491	1583	425	470	13			
1	C	319	Total	C	N	O	S	0	0	0
			2496	1585	422	476	13			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	330	HIS	-	expression tag	UNP W8U075
A	331	HIS	-	expression tag	UNP W8U075
A	332	HIS	-	expression tag	UNP W8U075
A	333	HIS	-	expression tag	UNP W8U075
A	334	HIS	-	expression tag	UNP W8U075
A	335	HIS	-	expression tag	UNP W8U075
B	330	HIS	-	expression tag	UNP W8U075
B	331	HIS	-	expression tag	UNP W8U075
B	332	HIS	-	expression tag	UNP W8U075
B	333	HIS	-	expression tag	UNP W8U075
B	334	HIS	-	expression tag	UNP W8U075
B	335	HIS	-	expression tag	UNP W8U075
C	330	HIS	-	expression tag	UNP W8U075
C	331	HIS	-	expression tag	UNP W8U075
C	332	HIS	-	expression tag	UNP W8U075
C	333	HIS	-	expression tag	UNP W8U075
C	334	HIS	-	expression tag	UNP W8U075
C	335	HIS	-	expression tag	UNP W8U075

- Molecule 2 is (6 {R})-5,5-dimethyl-7-thia-2-azatricyclo[6.3.1.0^{4,12}]dodeca-1(12),3,8,10-tetraene-6-carboxylic acid (CCD ID: A1EHN) (formula: C₁₃H₁₃NO₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			17	13	1	2	1		
2	B	1	Total	C	N	O	S	0	0
			17	13	1	2	1		
2	C	1	Total	C	N	O	S	0	0
			17	13	1	2	1		

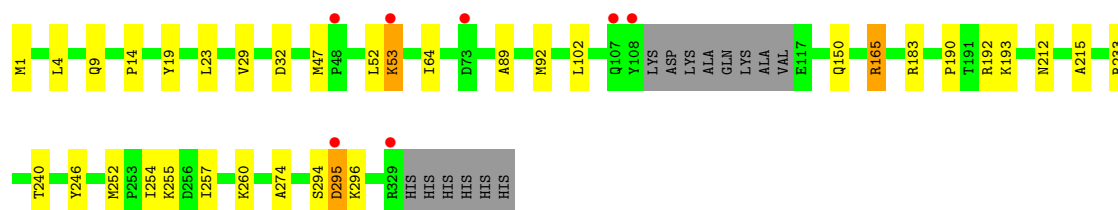
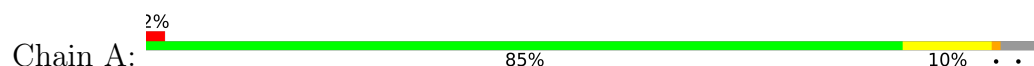
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	132	Total	O	0	0
			132	132		
3	B	65	Total	O	0	0
			65	65		
3	C	85	Total	O	0	0
			85	85		

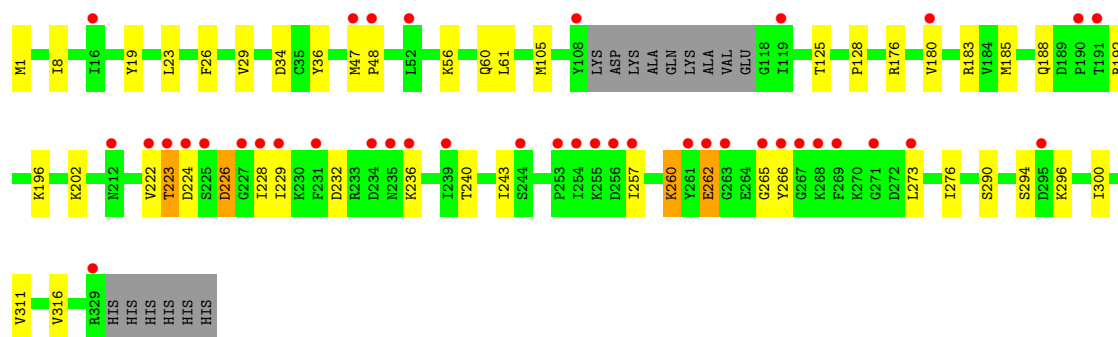
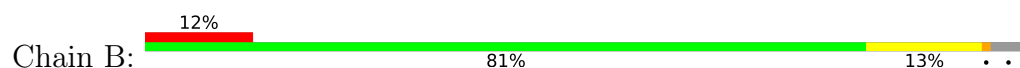
3 Residue-property plots [i](#)

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.

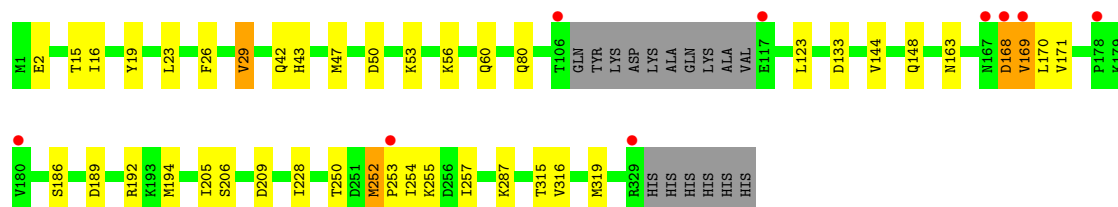
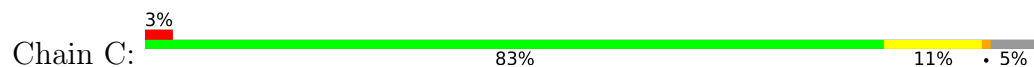
• Molecule 1: Tryptophan-tRNA ligase



• Molecule 1: Tryptophan-tRNA ligase



• Molecule 1: Tryptophan-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	184.95Å 66.75Å 100.17Å 90.00° 101.73° 90.00°	Depositor
Resolution (Å)	60.66 – 2.21 60.66 – 2.21	Depositor EDS
% Data completeness (in resolution range)	99.7 (60.66-2.21) 99.7 (60.66-2.21)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.212 , 0.220 0.211 , 0.218	Depositor DCC
R_{free} test set	2000 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.825	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7847	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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: A1EHN

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	0.40	0/2571	0.59	0/3466
1	B	0.42	0/2534	0.64	1/3420 (0.0%)
1	C	0.44	0/2539	0.67	1/3425 (0.0%)
All	All	0.42	0/7644	0.64	2/10311 (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	C	0	1
All	All	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	169	VAL	N-CA-C	-6.25	107.78	113.71
1	B	223	THR	CA-CB-OG1	-5.89	100.76	109.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	165	ARG	Sidechain
1	C	192	ARG	Sidechain

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	2527	0	2559	27	0
1	B	2491	0	2509	41	0
1	C	2496	0	2520	32	0
2	A	17	0	0	0	0
2	B	17	0	0	0	0
2	C	17	0	0	1	0
3	A	132	0	0	9	0
3	B	65	0	0	10	0
3	C	85	0	0	7	0
All	All	7847	0	7588	98	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 6.

All (98) 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:C:47:MET:HE3	1:C:123:LEU:HD11	1.55	0.87
1:A:183:ARG:HG2	3:A:513:HOH:O	1.80	0.80
1:A:252:MET:HG2	1:A:257:ILE:HG13	1.64	0.78
1:A:233:ARG:HG2	1:A:240:THR:HG21	1.65	0.78
1:B:47:MET:HG3	1:B:48:PRO:HD2	1.69	0.75
1:A:52:LEU:HD12	3:A:501:HOH:O	1.88	0.73
1:B:240:THR:HA	1:B:243:ILE:HD12	1.71	0.72
1:C:254:ILE:N	3:C:502:HOH:O	2.23	0.71
1:C:15:THR:HB	1:C:194:MET:HE2	1.74	0.70
1:B:224:ASP:N	3:B:503:HOH:O	2.25	0.68
1:C:19:TYR:HA	1:C:23:LEU:HB2	1.77	0.67
1:C:16:ILE:HG22	1:C:194:MET:HE1	1.76	0.67
1:B:202:LYS:HD3	3:B:530:HOH:O	1.97	0.65
1:C:144:VAL:HB	1:C:148:GLN:HG3	1.80	0.63
1:C:194:MET:HE3	1:C:205:ILE:H	1.63	0.63
1:A:294:SER:OG	1:A:296:LYS:HG2	2.00	0.61
1:C:148:GLN:HE22	2:C:401:A1EHN:C14	2.13	0.61
1:B:232:ASP:H	1:B:240:THR:CG2	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:ILE:HA	1:A:257:ILE:HD12	1.83	0.60
1:C:170:LEU:HA	3:C:504:HOH:O	2.01	0.60
1:C:56:LYS:HE2	1:C:60:GLN:NE2	2.16	0.60
1:C:171:VAL:N	3:C:504:HOH:O	2.27	0.59
1:C:287:LYS:NZ	3:C:505:HOH:O	2.35	0.59
1:B:188:GLN:HA	1:B:222:VAL:HG22	1.86	0.57
1:A:9:GLN:HE22	1:A:47:MET:HE1	1.70	0.57
1:B:19:TYR:HA	1:B:23:LEU:HB2	1.87	0.57
1:B:196:LYS:HB2	3:B:505:HOH:O	2.04	0.56
1:B:276:ILE:N	3:B:509:HOH:O	2.39	0.56
1:C:26:PHE:HA	1:C:29:VAL:HG22	1.87	0.56
1:B:56:LYS:HE3	1:B:60:GLN:HE21	1.70	0.56
1:B:236:LYS:O	1:B:240:THR:HG23	2.05	0.56
1:C:15:THR:CB	1:C:194:MET:HE2	2.36	0.55
1:A:190:PRO:HG3	3:A:516:HOH:O	2.07	0.55
1:B:232:ASP:H	1:B:240:THR:HG21	1.72	0.53
1:B:265:GLY:N	3:B:504:HOH:O	2.41	0.53
1:B:232:ASP:C	1:B:240:THR:HG21	2.33	0.53
1:C:253:PRO:O	1:C:257:ILE:HG13	2.08	0.52
1:C:253:PRO:HB3	3:C:502:HOH:O	2.09	0.52
1:C:42:GLN:HB2	1:C:80:GLN:NE2	2.24	0.52
1:A:246:TYR:HE1	1:A:252:MET:HE3	1.76	0.51
1:B:56:LYS:HE3	1:B:60:GLN:NE2	2.26	0.51
1:B:229:ILE:HD11	1:B:265:GLY:O	2.11	0.51
1:B:229:ILE:HG12	1:B:266:TYR:HE1	1.76	0.51
1:C:315:THR:HG22	1:C:319:MET:HE2	1.90	0.51
1:B:48:PRO:HA	3:B:537:HOH:O	2.10	0.51
1:B:229:ILE:HG12	1:B:266:TYR:CE1	2.46	0.51
1:B:262:GLU:CD	1:B:262:GLU:H	2.18	0.51
1:C:15:THR:HB	1:C:194:MET:CE	2.41	0.51
1:B:226:ASP:O	1:B:228:ILE:HG12	2.11	0.50
1:B:290:SER:O	1:B:294:SER:HB3	2.11	0.50
1:C:250:THR:C	1:C:252:MET:H	2.18	0.50
1:C:316:VAL:HA	1:C:319:MET:HE3	1.94	0.50
1:C:43:HIS:HE1	1:C:133:ASP:OD2	1.95	0.49
1:C:253:PRO:CA	3:C:502:HOH:O	2.61	0.49
1:A:19:TYR:HA	1:A:23:LEU:HB2	1.96	0.48
1:A:150:GLN:HE21	1:B:180:VAL:CG2	2.27	0.48
1:C:194:MET:CE	1:C:205:ILE:H	2.25	0.48
1:B:1:MET:HE3	1:B:34:ASP:HB2	1.96	0.47
1:A:260:LYS:NZ	3:A:509:HOH:O	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:PHE:HA	1:B:29:VAL:HG22	1.96	0.47
1:B:296:LYS:O	1:B:300:ILE:HG12	2.15	0.47
1:B:183:ARG:HG2	1:B:185:MET:CE	2.44	0.47
1:A:260:LYS:CE	3:A:509:HOH:O	2.62	0.47
1:B:243:ILE:HG23	1:B:257:ILE:HG21	1.97	0.46
1:B:232:ASP:H	1:B:240:THR:HG22	1.79	0.46
1:A:193:LYS:HB2	1:A:193:LYS:HE2	1.63	0.45
1:A:1:MET:HE2	1:A:32:ASP:C	2.42	0.45
1:A:14:PRO:HD2	1:A:64:ILE:HD13	1.99	0.45
1:C:163:ASN:OD1	1:C:168:ASP:HA	2.17	0.45
1:C:253:PRO:CB	3:C:502:HOH:O	2.64	0.44
1:B:183:ARG:HG2	1:B:185:MET:HE1	2.00	0.43
1:B:296:LYS:HB3	1:B:296:LYS:HE3	1.74	0.43
1:A:165:ARG:NH1	3:A:519:HOH:O	2.52	0.43
1:B:105:MET:HB2	3:B:516:HOH:O	2.18	0.43
1:A:252:MET:HB2	1:A:252:MET:HE2	1.73	0.43
1:A:295:ASP:OD1	1:A:295:ASP:N	2.51	0.43
1:B:273:LEU:C	3:B:509:HOH:O	2.61	0.43
1:B:125:THR:O	1:B:128:PRO:HD2	2.19	0.43
1:A:102:LEU:HD23	1:A:102:LEU:HA	1.79	0.43
1:A:53:LYS:NZ	3:A:518:HOH:O	2.51	0.42
1:A:255:LYS:HD3	3:A:532:HOH:O	2.19	0.42
1:B:260:LYS:HB3	1:B:260:LYS:HE3	1.58	0.42
1:B:276:ILE:HB	3:B:509:HOH:O	2.20	0.42
1:B:8:ILE:HG22	1:B:61:LEU:HD21	2.01	0.42
1:C:206:SER:O	1:C:209:ASP:HB2	2.20	0.42
1:C:186:SER:HB2	1:C:189:ASP:O	2.20	0.41
1:B:176:ARG:HD2	3:B:521:HOH:O	2.19	0.41
1:A:89:ALA:HA	1:A:92:MET:HE3	2.01	0.41
1:A:4:LEU:HD23	1:A:4:LEU:C	2.46	0.41
1:A:255:LYS:CD	3:A:532:HOH:O	2.68	0.41
1:C:252:MET:HG2	1:C:257:ILE:HG12	2.03	0.41
1:A:215:ALA:HB1	1:A:274:ALA:HB1	2.03	0.40
1:B:232:ASP:O	1:B:240:THR:HG21	2.21	0.40
1:C:50:ASP:CG	1:C:53:LYS:HD3	2.46	0.40
1:C:252:MET:HE2	1:C:252:MET:HB2	1.72	0.40
1:A:192:ARG:HG2	1:B:192:ARG:NH2	2.36	0.40
1:B:36:TYR:OH	1:B:311:VAL:HG21	2.22	0.40
1:C:228:ILE:HD13	1:C:228:ILE:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	317/335 (95%)	306 (96%)	11 (4%)	0	100	100
1	B	316/335 (94%)	297 (94%)	19 (6%)	0	100	100
1	C	315/335 (94%)	302 (96%)	13 (4%)	0	100	100
All	All	948/1005 (94%)	905 (96%)	43 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	276/289 (96%)	272 (99%)	4 (1%)	62	75
1	B	268/289 (93%)	263 (98%)	5 (2%)	52	65
1	C	272/289 (94%)	266 (98%)	6 (2%)	47	59
All	All	816/867 (94%)	801 (98%)	15 (2%)	54	67

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	VAL
1	A	53	LYS
1	A	212	ASN
1	A	295	ASP
1	B	223	THR

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Mol	Chain	Res	Type
1	B	226	ASP
1	B	260	LYS
1	B	262	GLU
1	B	316	VAL
1	C	2	GLU
1	C	29	VAL
1	C	168	ASP
1	C	169	VAL
1	C	252	MET
1	C	255	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	107	GLN
1	A	150	GLN
1	A	235	ASN
1	B	43	HIS
1	B	303	GLN
1	C	43	HIS
1	C	80	GLN
1	C	148	GLN
1	C	235	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 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	A1EHN	C	401	-	17,19,19	1.13	1 (5%)	16,30,30	1.16	2 (12%)
2	A1EHN	B	401	-	17,19,19	1.23	1 (5%)	16,30,30	1.19	3 (18%)
2	A1EHN	A	401	-	17,19,19	1.30	1 (5%)	16,30,30	1.27	2 (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
2	A1EHN	C	401	-	-	0/3/20/20	0/2/3/3
2	A1EHN	B	401	-	-	0/3/20/20	0/2/3/3
2	A1EHN	A	401	-	-	0/3/20/20	0/2/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	A1EHN	C4-C17	3.47	1.44	1.40
2	B	401	A1EHN	C4-C17	3.15	1.44	1.40
2	C	401	A1EHN	C4-C17	2.78	1.43	1.40

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	A1EHN	O16-C14-C13	-2.42	117.48	122.44
2	C	401	A1EHN	O16-C14-C13	-2.31	117.71	122.44
2	B	401	A1EHN	O16-C14-C13	-2.29	117.74	122.44
2	B	401	A1EHN	C10-C11-C17	-2.26	117.75	120.50
2	A	401	A1EHN	C10-C11-S12	2.24	123.06	117.95
2	C	401	A1EHN	C10-C11-S12	2.14	122.83	117.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	A1EHN	C10-C11-S12	2.00	122.52	117.95

There are no chirality outliers.

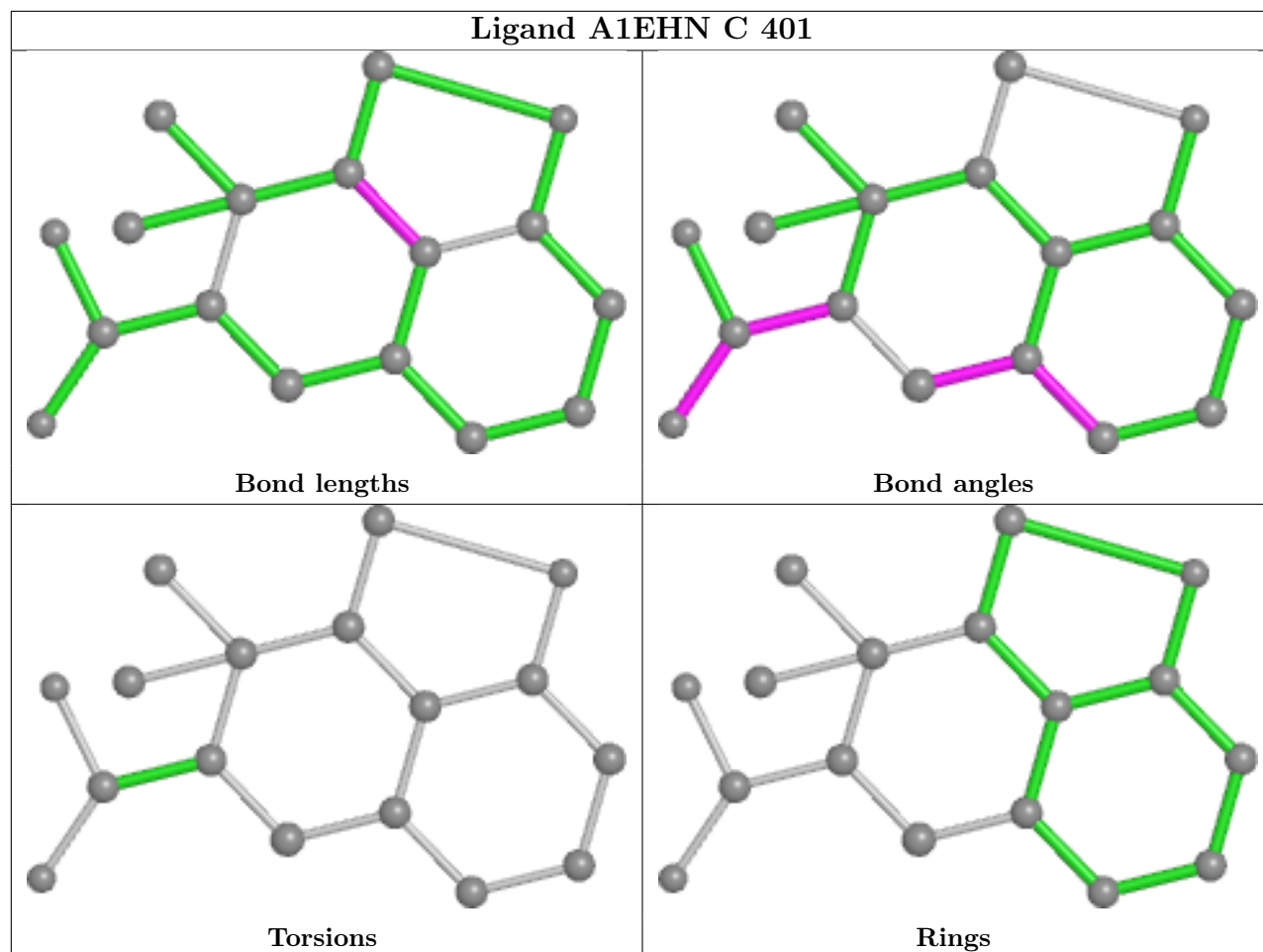
There are no torsion outliers.

There are no ring outliers.

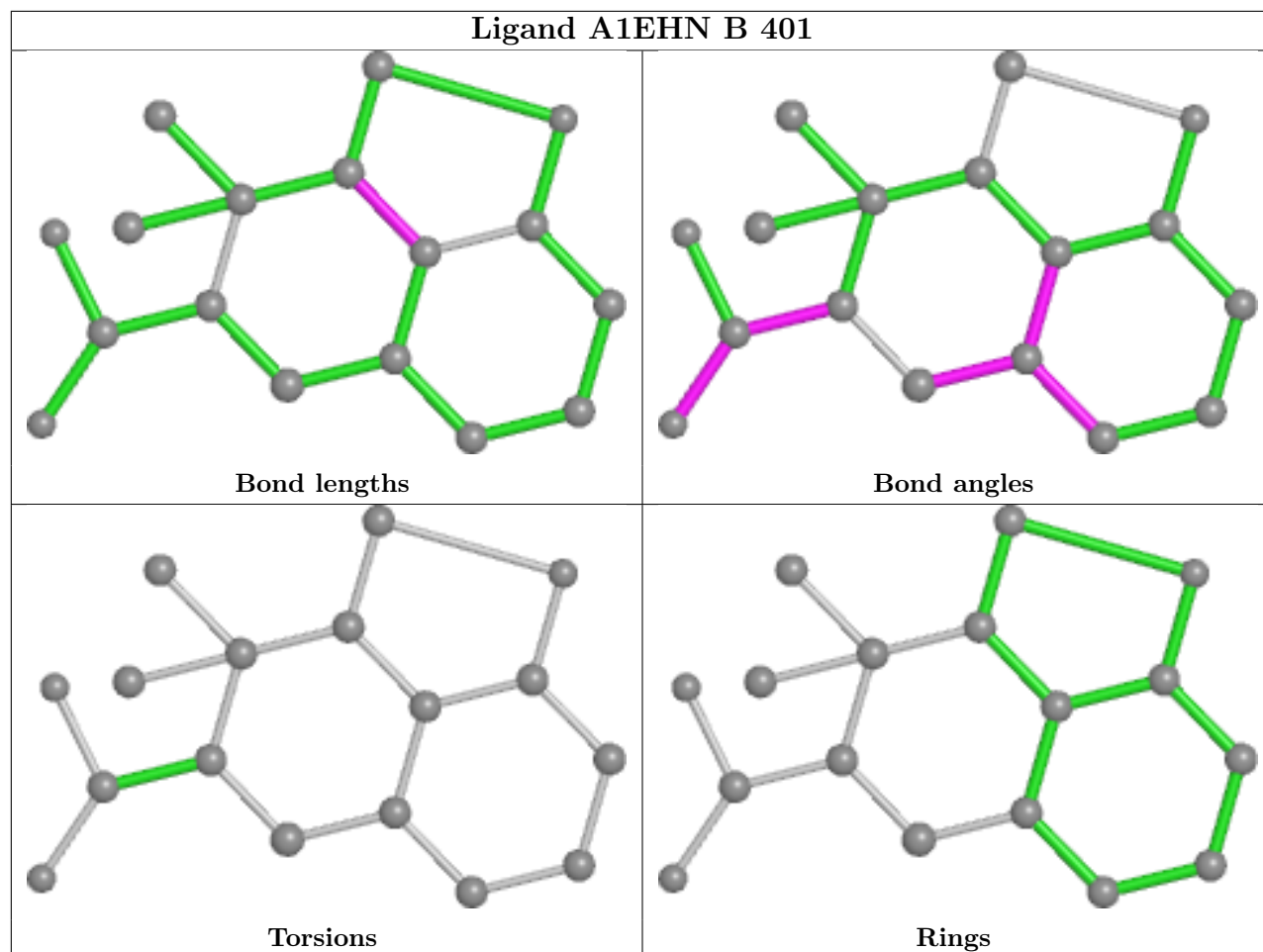
1 monomer is involved in 1 short contact:

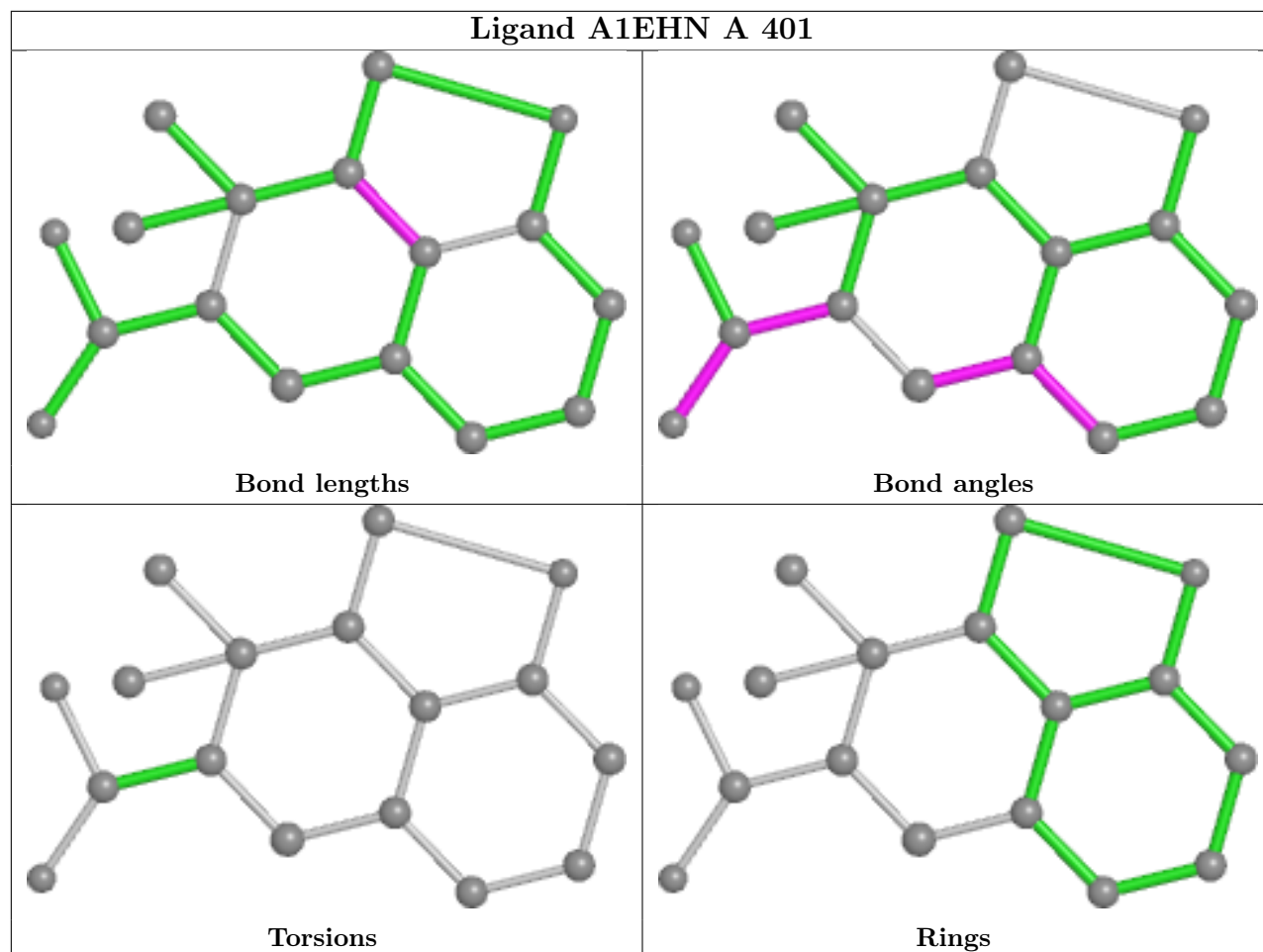
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	A1EHN	1	0

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.



Ligand A1EHN B 401





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	321/335 (95%)	0.12	7 (2%) 62 59	25, 41, 58, 74	0
1	B	320/335 (95%)	0.72	40 (12%) 9 8	29, 52, 84, 94	0
1	C	319/335 (95%)	0.53	9 (2%) 55 52	34, 48, 67, 80	0
All	All	960/1005 (95%)	0.46	56 (5%) 30 27	25, 47, 73, 94	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	265	GLY	5.2
1	B	223	THR	5.0
1	B	266	TYR	5.0
1	B	224	ASP	4.9
1	B	108	TYR	4.7
1	B	229	ILE	4.2
1	B	227	GLY	3.9
1	B	261	TYR	3.8
1	C	168	ASP	3.8
1	C	167	ASN	3.6
1	B	191	THR	3.5
1	B	254	ILE	3.4
1	B	269	PHE	3.4
1	C	106	THR	3.3
1	A	48	PRO	3.3
1	B	267	GLY	3.3
1	B	234	ASP	3.3
1	B	231	PHE	3.2
1	B	228	ILE	3.2
1	C	180	VAL	3.1
1	A	108	TYR	3.1
1	B	180	VAL	3.1
1	B	329	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	253	PRO	3.0
1	B	47	MET	2.9
1	B	119	ILE	2.9
1	A	295	ASP	2.8
1	B	257	ILE	2.7
1	B	225	SER	2.6
1	B	256	ASP	2.6
1	B	222	VAL	2.5
1	B	48	PRO	2.5
1	C	329	ARG	2.5
1	B	255	LYS	2.4
1	C	169	VAL	2.4
1	B	239	ILE	2.4
1	B	262	GLU	2.4
1	B	236	LYS	2.4
1	B	253	PRO	2.3
1	C	117	GLU	2.3
1	B	263	GLY	2.3
1	B	271	GLY	2.2
1	B	52	LEU	2.2
1	B	212	ASN	2.2
1	A	107	GLN	2.2
1	B	268	LYS	2.2
1	A	329	ARG	2.2
1	B	244	SER	2.1
1	B	190	PRO	2.1
1	B	235	ASN	2.1
1	B	273	LEU	2.1
1	A	73	ASP	2.1
1	A	53	LYS	2.1
1	B	16	ILE	2.0
1	C	178	PRO	2.0
1	B	295	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

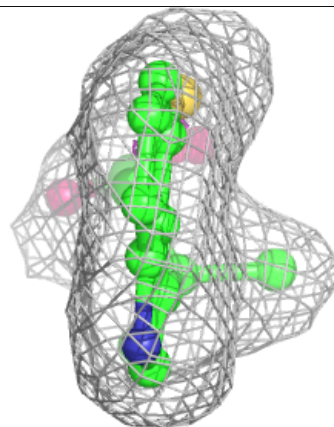
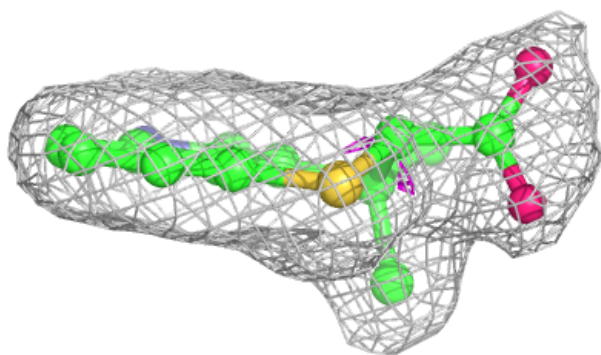
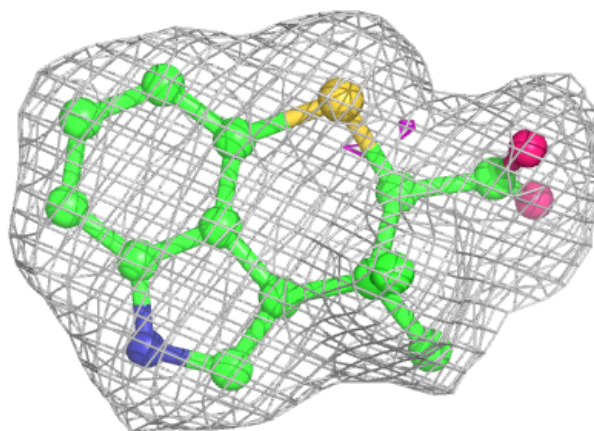
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	A1EHN	B	401	17/17	0.92	0.09	36,38,53,56	0
2	A1EHN	C	401	17/17	0.92	0.09	48,49,61,62	0
2	A1EHN	A	401	17/17	0.96	0.08	31,35,47,52	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.

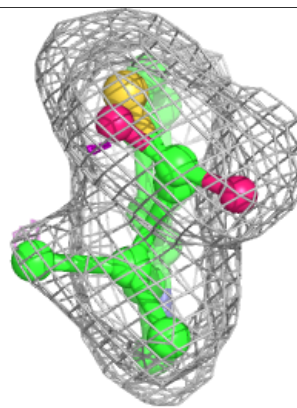
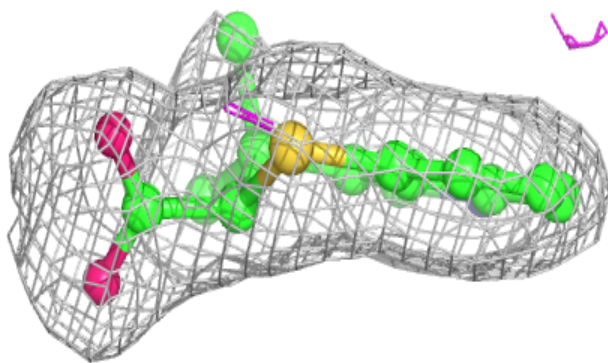
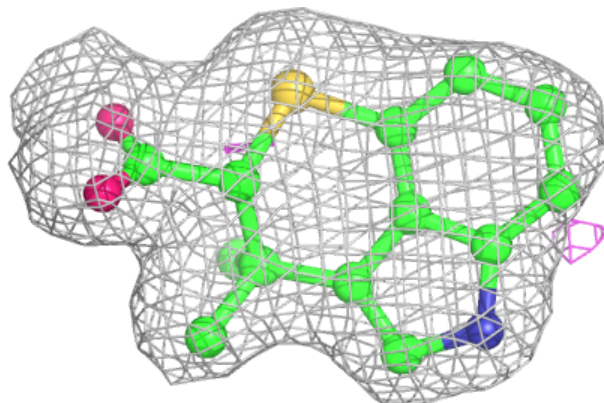
Electron density around A1EHN B 401:

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



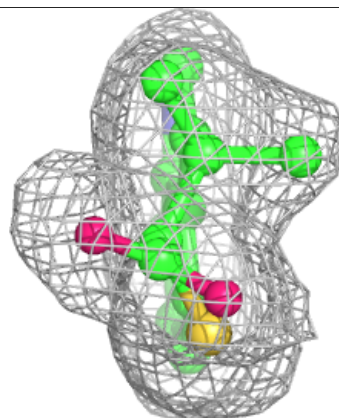
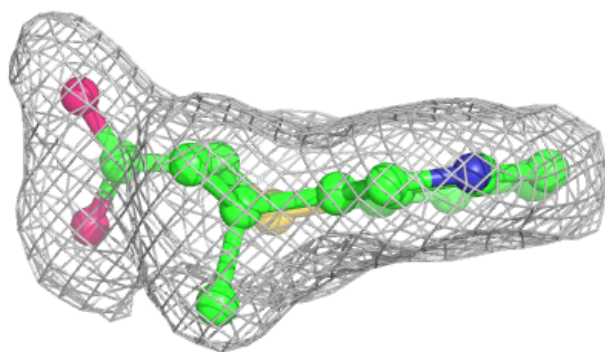
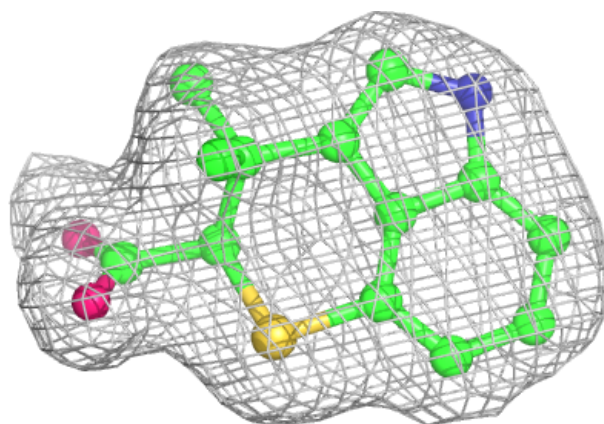
Electron density around A1EHN C 401:

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



Electron density around A1EHN A 401:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.