



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:17 PM UTC

PDB ID : 9V84 / pdb_00009v84
Title : Crystal structure of complex Hit-1 with YTHDC1
Authors : Zhang, H.; Yang, S.Y.
Deposited on : 2025-05-29
Resolution : 2.40 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

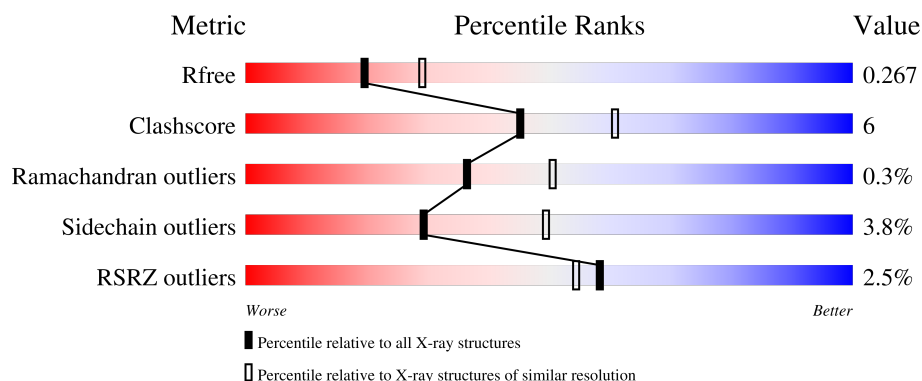
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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.



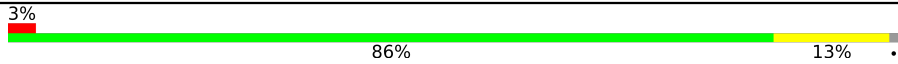
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	163	% 83% 15% ..
1	B	163	3% 88% 9% ..
1	C	163	% 88% 11% ..
1	D	163	2% 83% 15% ..
1	E	163	3% 88% 12% .

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Mol	Chain	Length	Quality of chain
1	F	163	
1	G	163	
1	H	163	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	605	-	-	X	-

2 Entry composition

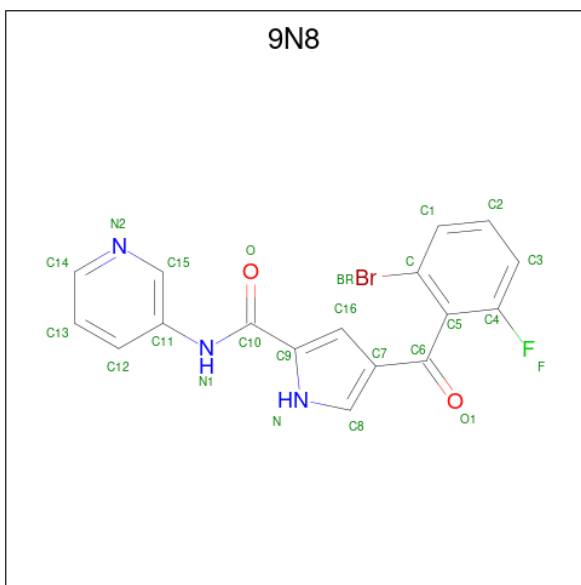
There are 4 unique types of molecules in this entry. The entry contains 10507 atoms, of which 88 are hydrogens and 0 are deuteriums.

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 YTH domain-containing protein 1.

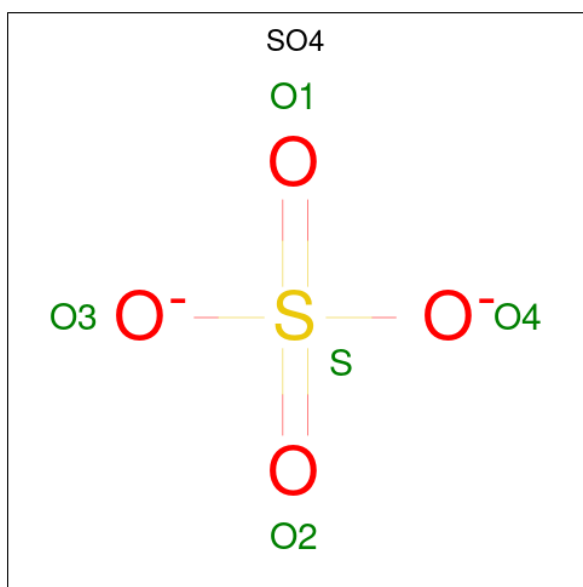
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	160	Total	C	N	O	S	0	0	0
			1240	800	219	215	6			
1	A	162	Total	C	N	O	S	0	0	0
			1236	797	214	219	6			
1	C	162	Total	C	N	O	S	0	0	0
			1249	809	217	217	6			
1	D	161	Total	C	N	O	S	0	0	0
			1228	794	211	217	6			
1	E	162	Total	C	N	O	S	0	0	0
			1219	789	208	216	6			
1	F	162	Total	C	N	O	S	0	0	0
			1240	802	216	216	6			
1	G	162	Total	C	N	O	S	0	0	0
			1215	788	204	217	6			
1	H	163	Total	C	N	O	S	0	0	0
			1260	814	216	224	6			

- Molecule 2 is 4-(2-bromanyl-6-fluoranyl-phenyl)carbonyl- {N}-pyridin-3-yl-1 {H}-pyrrole-2-carboxamide (CCD ID: 9N8) (formula: C₁₇H₁₁BrFN₃O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	B	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	A	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	C	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	D	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	E	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	F	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	G	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		
2	H	1	Total	Br	C	F	H	N	O	0	0
			35	1	17	1	11	3	2		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

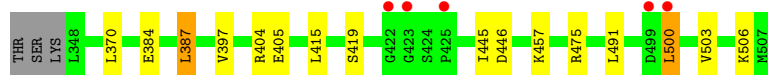
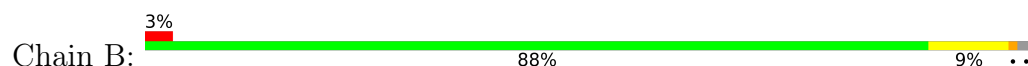
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	22	Total	O	0	0
			22	22		
4	A	27	Total	O	0	0
			27	27		
4	C	28	Total	O	0	0
			28	28		
4	D	37	Total	O	0	0
			37	37		
4	E	18	Total	O	0	0
			18	18		
4	F	28	Total	O	0	0
			28	28		
4	G	21	Total	O	0	0
			21	21		
4	H	39	Total	O	0	0
			39	39		

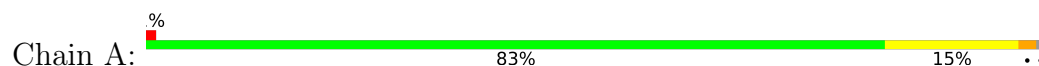
3 Residue-property plots [i](#)

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.

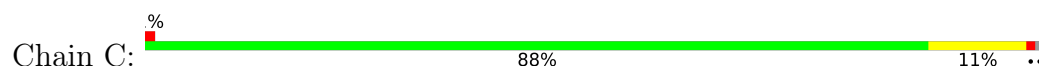
- Molecule 1: YTH domain-containing protein 1



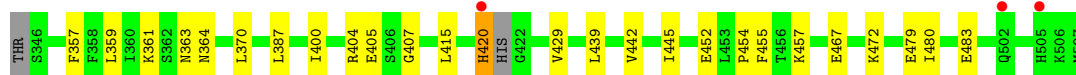
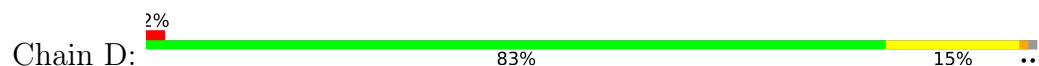
- Molecule 1: YTH domain-containing protein 1



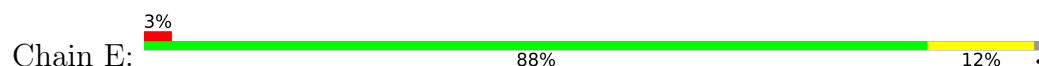
- Molecule 1: YTH domain-containing protein 1



- Molecule 1: YTH domain-containing protein 1



- Molecule 1: YTH domain-containing protein 1



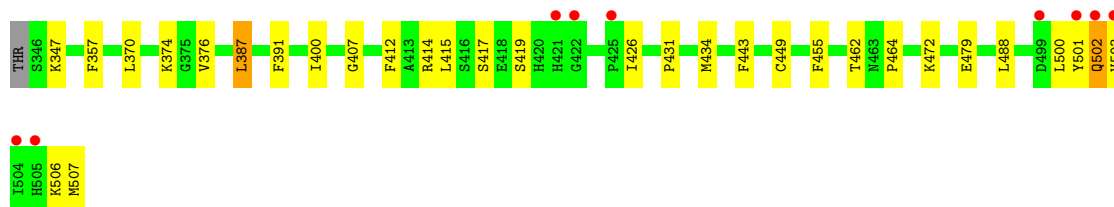
- Molecule 1: YTH domain-containing protein 1

Chain F:  3% 86% 13%



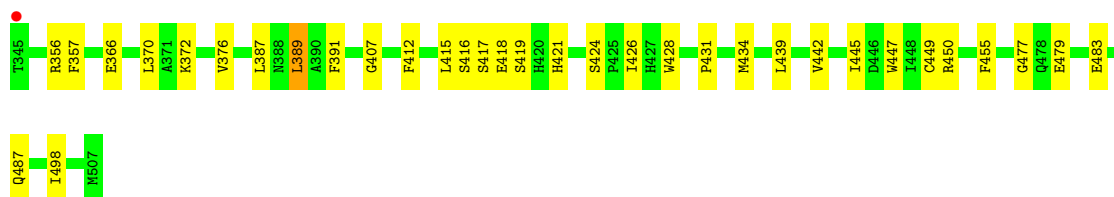
• Molecule 1: YTH domain-containing protein 1

Chain G:  6% 80% 18%



• Molecule 1: YTH domain-containing protein 1

Chain H:  0% 79% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.16Å 77.38Å 105.24Å 112.72° 93.18° 104.43°	Depositor
Resolution (Å)	29.47 – 2.40 29.47 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.7 (29.47-2.40) 97.6 (29.47-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.82 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.228 , 0.267 0.229 , 0.267	Depositor DCC
R_{free} test set	3436 reflections (4.71%)	wwPDB-VP
Wilson B-factor (Å ²)	29.9	Xtrriage
Anisotropy	0.084	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 24.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10507	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 73.96 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6698e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4, 9N8

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	0.13	0/1269	0.34	0/1725
1	B	0.12	0/1273	0.30	0/1725
1	C	0.12	0/1282	0.32	0/1736
1	D	0.12	0/1258	0.32	0/1706
1	E	0.12	0/1249	0.31	0/1698
1	F	0.12	0/1272	0.33	1/1727 (0.1%)
1	G	0.11	0/1247	0.29	0/1697
1	H	0.13	0/1293	0.31	0/1753
All	All	0.12	0/10143	0.31	1/13767 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	448	ILE	N-CA-C	-5.20	107.76	112.96

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	1236	0	1179	20	0
1	B	1240	0	1205	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1249	0	1234	13	0
1	D	1228	0	1191	20	0
1	E	1219	0	1172	9	0
1	F	1240	0	1200	15	0
1	G	1215	0	1160	19	0
1	H	1260	0	1233	18	0
2	A	24	11	0	1	0
2	B	24	11	0	0	0
2	C	24	11	0	0	0
2	D	24	11	0	0	0
2	E	24	11	0	1	0
2	F	24	11	0	0	0
2	G	24	11	0	0	0
2	H	24	11	0	1	0
3	A	25	0	0	2	0
3	B	15	0	0	0	0
3	C	15	0	0	1	0
3	D	15	0	0	1	0
3	E	20	0	0	0	0
3	F	15	0	0	0	0
3	G	10	0	0	0	0
3	H	5	0	0	0	0
4	A	27	0	0	1	0
4	B	22	0	0	0	0
4	C	28	0	0	0	0
4	D	37	0	0	1	0
4	E	18	0	0	0	0
4	F	28	0	0	1	0
4	G	21	0	0	1	0
4	H	39	0	0	1	0
All	All	10419	88	9574	116	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 (116) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:404:ARG:HD2	1:D:404:ARG:HD3	1.63	0.80
1:F:359:LEU:HD21	1:F:361:LYS:HE2	1.68	0.75
1:C:415:LEU:HD23	1:C:445:ILE:HG22	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:420:HIS:HB3	1:D:442:VAL:H	1.52	0.73
1:G:347:LYS:HB2	1:G:500:LEU:HD13	1.73	0.71
1:E:376:VAL:HG21	1:E:426:ILE:HD13	1.73	0.69
1:D:364:ASN:HD21	1:D:429:VAL:HG23	1.60	0.67
1:A:421:HIS:ND1	3:A:605:SO4:O2	2.29	0.64
1:H:356:ARG:NE	1:H:479:GLU:OE2	2.21	0.64
1:C:364:ASN:HD21	1:C:429:VAL:HG23	1.63	0.63
1:A:430:LEU:HB3	1:A:434:MET:HE2	1.82	0.62
1:H:407:GLY:HA2	1:H:455:PHE:CE2	2.35	0.62
1:A:404:ARG:HD2	1:C:404:ARG:HD3	1.81	0.61
1:C:429:VAL:HG23	1:C:429:VAL:O	2.00	0.61
1:G:347:LYS:HB2	1:G:500:LEU:CD1	2.30	0.61
1:G:414:ARG:HD3	1:G:503:VAL:CG1	2.32	0.60
1:D:364:ASN:ND2	1:D:429:VAL:HG23	2.16	0.59
1:G:407:GLY:HA2	1:G:455:PHE:CD2	2.36	0.59
1:A:364:ASN:ND2	1:A:429:VAL:HG22	2.19	0.57
1:F:429:VAL:HG23	1:F:429:VAL:O	2.05	0.57
1:A:434:MET:HE1	2:A:601:9N8:BR	2.60	0.57
1:D:420:HIS:N	1:D:442:VAL:O	2.35	0.57
1:G:414:ARG:HD3	1:G:503:VAL:HG11	1.87	0.56
1:G:419:SER:HB3	1:G:443:PHE:CZ	2.40	0.56
1:F:359:LEU:CD2	1:F:361:LYS:HE2	2.35	0.56
1:D:452:GLU:HG3	3:D:603:SO4:O4	2.06	0.56
1:C:364:ASN:ND2	1:C:429:VAL:HG23	2.21	0.55
1:F:364:ASN:HD21	1:F:429:VAL:HG23	1.72	0.55
1:E:376:VAL:HG21	1:E:426:ILE:CD1	2.36	0.55
1:E:503:VAL:O	1:E:507:MET:HG3	2.07	0.55
1:D:359:LEU:HD21	1:D:361:LYS:HE3	1.88	0.54
1:A:347:LYS:O	1:A:351:VAL:HG23	2.09	0.53
1:G:472:LYS:HB3	4:G:712:HOH:O	2.07	0.52
1:D:467:GLU:HG2	1:F:465:TRP:CD1	2.45	0.52
1:G:391:PHE:CZ	1:G:417:SER:HA	2.44	0.51
1:A:405:GLU:OE1	1:C:405:GLU:N	2.38	0.51
1:D:429:VAL:HG23	1:D:429:VAL:O	2.10	0.51
1:G:407:GLY:HA2	1:G:455:PHE:CE2	2.46	0.51
1:H:426:ILE:HG21	1:H:428:TRP:CZ2	2.46	0.51
1:H:421:HIS:HA	4:H:723:HOH:O	2.10	0.51
1:A:429:VAL:HG22	1:A:429:VAL:O	2.11	0.50
1:E:434:MET:HE1	2:E:601:9N8:BR	2.67	0.50
1:E:487:GLN:HG3	1:H:389:LEU:HD11	1.92	0.50
1:D:363:ASN:OD1	1:D:404:ARG:HD2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:391:PHE:CZ	1:H:417:SER:HA	2.47	0.50
1:B:446:ASP:CB	1:B:503:VAL:HG22	2.41	0.50
1:A:357:PHE:HB2	1:A:480:ILE:HB	1.95	0.49
1:G:412:PHE:CE1	1:G:449:CYS:HB3	2.47	0.49
1:A:346:SER:O	1:A:347:LYS:CB	2.60	0.49
1:G:387:LEU:HG	1:G:415:LEU:HD11	1.95	0.49
1:H:407:GLY:HA2	1:H:455:PHE:CD2	2.47	0.48
1:H:431:PRO:HB2	1:H:434:MET:HE3	1.95	0.48
1:B:387:LEU:HG	1:B:415:LEU:HD11	1.96	0.48
1:F:451:ARG:NH1	1:F:494:PRO:O	2.46	0.47
1:B:397:VAL:HG11	1:B:415:LEU:HD12	1.96	0.47
1:A:457:LYS:HE3	4:A:709:HOH:O	2.14	0.47
1:B:384:GLU:OE2	1:B:419:SER:OG	2.20	0.47
1:H:415:LEU:HD23	1:H:445:ILE:HG22	1.96	0.47
1:C:431:PRO:HG2	1:C:434:MET:HE1	1.96	0.47
1:B:415:LEU:HD23	1:B:445:ILE:HG22	1.96	0.47
1:H:412:PHE:CE1	1:H:449:CYS:HB3	2.50	0.46
1:A:505:HIS:O	1:A:505:HIS:ND1	2.43	0.46
1:C:372:LYS:HA	1:C:447:TRP:NE1	2.31	0.46
1:C:467:GLU:HA	1:E:465:TRP:CZ2	2.50	0.46
1:B:446:ASP:CG	1:B:506:LYS:HZ2	2.24	0.45
1:A:353:GLN:HB3	1:A:395:ARG:NH1	2.32	0.45
1:C:451:ARG:HB3	3:C:603:SO4:O4	2.17	0.45
1:F:481:GLU:CD	1:F:483:GLU:H	2.24	0.45
1:F:389:LEU:HD23	1:F:392:ARG:NH2	2.32	0.45
1:B:446:ASP:HB3	1:B:503:VAL:HG22	1.99	0.45
1:H:426:ILE:HG21	1:H:428:TRP:CE2	2.52	0.44
1:A:387:LEU:HG	1:A:415:LEU:HD11	2.00	0.44
1:G:501:TYR:O	1:G:502:GLN:CB	2.64	0.44
1:H:357:PHE:O	1:H:479:GLU:HG3	2.17	0.44
1:B:500:LEU:HD12	1:B:500:LEU:HA	1.79	0.44
1:F:391:PHE:CZ	1:F:417:SER:HA	2.52	0.44
1:H:477:GLY:HA3	2:H:601:9N8:C13	2.48	0.44
1:A:472:LYS:HG2	1:A:473:ILE:HG12	1.99	0.43
1:B:457:LYS:O	1:B:491:LEU:HD13	2.17	0.43
1:C:429:VAL:O	1:C:429:VAL:CG2	2.66	0.43
1:D:415:LEU:HD23	1:D:445:ILE:HG22	1.99	0.43
1:E:471:VAL:HG21	1:E:488:LEU:HD22	2.00	0.43
1:F:364:ASN:ND2	1:F:429:VAL:HG23	2.34	0.43
1:F:419:SER:HB3	1:F:443:PHE:CZ	2.54	0.43
1:D:357:PHE:O	1:D:479:GLU:HG3	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:407:GLY:HA2	1:D:455:PHE:CD2	2.54	0.42
1:D:407:GLY:HA2	1:D:455:PHE:CE2	2.54	0.42
1:A:421:HIS:HB3	3:A:605:SO4:O2	2.20	0.42
1:D:472:LYS:HB3	4:D:706:HOH:O	2.18	0.42
1:H:419:SER:HA	1:H:442:VAL:O	2.19	0.42
1:G:400:ILE:HD13	1:G:488:LEU:HD23	2.01	0.42
1:G:357:PHE:O	1:G:479:GLU:HG3	2.20	0.42
1:G:431:PRO:HB2	1:G:434:MET:HE3	2.02	0.42
1:G:503:VAL:O	1:G:507:MET:HG3	2.19	0.42
1:H:483:GLU:OE2	1:H:487:GLN:NE2	2.49	0.42
1:A:376:VAL:HG21	1:A:426:ILE:CD1	2.50	0.42
1:G:387:LEU:HD12	1:G:387:LEU:HA	1.85	0.42
1:D:400:ILE:HD12	1:D:480:ILE:HD12	2.02	0.41
1:F:475:ARG:HA	4:F:703:HOH:O	2.19	0.41
1:G:374:LYS:O	1:G:376:VAL:HG13	2.20	0.41
1:H:372:LYS:HA	1:H:447:TRP:NE1	2.35	0.41
1:A:359:LEU:HD21	1:A:361:LYS:NZ	2.35	0.41
1:F:376:VAL:HA	1:F:443:PHE:O	2.20	0.41
1:G:462:THR:O	1:G:464:PRO:HD3	2.20	0.41
1:A:376:VAL:HG21	1:A:426:ILE:HD13	2.02	0.41
1:E:359:LEU:HD21	1:E:361:LYS:HE2	2.01	0.41
1:D:467:GLU:HA	1:F:465:TRP:CZ2	2.56	0.41
1:H:376:VAL:HG21	1:H:426:ILE:HD13	2.02	0.41
1:H:450:ARG:CZ	1:H:498:ILE:HD11	2.50	0.41
1:B:405:GLU:OE1	1:D:405:GLU:N	2.49	0.41
1:D:467:GLU:HG2	1:F:465:TRP:CG	2.56	0.41
1:C:423:GLY:O	1:C:424:SER:O	2.39	0.40
1:D:454:PRO:HG2	1:D:457:LYS:HG2	2.02	0.40
1:E:391:PHE:CZ	1:E:417:SER:HA	2.56	0.40
1:C:464:PRO:HD2	1:C:481:GLU:HB3	2.03	0.40
1:A:359:LEU:HD21	1:A:361:LYS:HZ2	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	160/163 (98%)	155 (97%)	4 (2%)	1 (1%)	21	32
1	B	158/163 (97%)	156 (99%)	2 (1%)	0	100	100
1	C	160/163 (98%)	157 (98%)	2 (1%)	1 (1%)	21	32
1	D	157/163 (96%)	156 (99%)	1 (1%)	0	100	100
1	E	160/163 (98%)	158 (99%)	1 (1%)	1 (1%)	21	32
1	F	160/163 (98%)	159 (99%)	1 (1%)	0	100	100
1	G	160/163 (98%)	154 (96%)	5 (3%)	1 (1%)	21	32
1	H	161/163 (99%)	157 (98%)	4 (2%)	0	100	100
All	All	1276/1304 (98%)	1252 (98%)	20 (2%)	4 (0%)	36	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	347	LYS
1	C	424	SER
1	G	502	GLN
1	E	423	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	126/143 (88%)	121 (96%)	5 (4%)	28	47
1	B	127/143 (89%)	123 (97%)	4 (3%)	35	57
1	C	131/143 (92%)	127 (97%)	4 (3%)	35	57
1	D	126/143 (88%)	121 (96%)	5 (4%)	28	47
1	E	123/143 (86%)	118 (96%)	5 (4%)	27	46
1	F	126/143 (88%)	122 (97%)	4 (3%)	34	56
1	G	123/143 (86%)	119 (97%)	4 (3%)	33	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	133/143 (93%)	125 (94%)	8 (6%)	17	31
All	All	1015/1144 (89%)	976 (96%)	39 (4%)	29	49

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	370	LEU
1	B	387	LEU
1	B	475	ARG
1	B	500	LEU
1	A	370	LEU
1	A	387	LEU
1	A	429	VAL
1	A	439	LEU
1	A	496	GLU
1	C	370	LEU
1	C	387	LEU
1	C	424	SER
1	C	439	LEU
1	D	370	LEU
1	D	387	LEU
1	D	420	HIS
1	D	439	LEU
1	D	483	GLU
1	E	370	LEU
1	E	387	LEU
1	E	395	ARG
1	E	405	GLU
1	E	439	LEU
1	F	370	LEU
1	F	387	LEU
1	F	424	SER
1	F	503	VAL
1	G	370	LEU
1	G	387	LEU
1	G	426	ILE
1	G	506	LYS
1	H	366	GLU
1	H	370	LEU
1	H	387	LEU
1	H	389	LEU
1	H	416	SER

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Mol	Chain	Res	Type
1	H	418	GLU
1	H	424	SER
1	H	439	LEU

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

Mol	Chain	Res	Type
1	B	420	HIS
1	A	383	ASN
1	C	364	ASN
1	E	478	GLN
1	F	365	HIS
1	G	365	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 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
3	SO4	A	602	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	B	602	-	4,4,4	0.25	0	6,6,6	0.07	0
3	SO4	F	603	-	4,4,4	0.25	0	6,6,6	0.13	0
3	SO4	A	604	-	4,4,4	0.24	0	6,6,6	0.11	0
3	SO4	E	603	-	4,4,4	0.22	0	6,6,6	0.10	0
3	SO4	H	602	-	4,4,4	0.26	0	6,6,6	0.07	0
2	9N8	E	601	-	26,26,26	1.69	5 (19%)	32,36,36	1.32	3 (9%)
3	SO4	G	602	-	4,4,4	0.22	0	6,6,6	0.08	0
3	SO4	E	604	-	4,4,4	0.24	0	6,6,6	0.12	0
2	9N8	A	601	-	26,26,26	1.69	5 (19%)	32,36,36	1.28	3 (9%)
3	SO4	C	604	-	4,4,4	0.27	0	6,6,6	0.07	0
3	SO4	B	603	-	4,4,4	0.27	0	6,6,6	0.11	0
2	9N8	C	601	-	26,26,26	1.80	7 (26%)	32,36,36	1.23	2 (6%)
2	9N8	F	601	-	26,26,26	1.72	6 (23%)	32,36,36	1.20	2 (6%)
3	SO4	F	602	-	4,4,4	0.21	0	6,6,6	0.10	0
3	SO4	D	604	-	4,4,4	0.27	0	6,6,6	0.10	0
3	SO4	D	603	-	4,4,4	0.25	0	6,6,6	0.09	0
2	9N8	H	601	-	26,26,26	1.74	6 (23%)	32,36,36	1.35	4 (12%)
3	SO4	E	602	-	4,4,4	0.24	0	6,6,6	0.06	0
2	9N8	B	601	-	26,26,26	1.71	6 (23%)	32,36,36	1.29	4 (12%)
3	SO4	E	605	-	4,4,4	0.26	0	6,6,6	0.08	0
3	SO4	C	602	-	4,4,4	0.23	0	6,6,6	0.12	0
3	SO4	A	603	-	4,4,4	0.26	0	6,6,6	0.09	0
3	SO4	B	604	-	4,4,4	0.26	0	6,6,6	0.05	0
3	SO4	A	606	-	4,4,4	0.27	0	6,6,6	0.06	0
2	9N8	G	601	-	26,26,26	1.69	5 (19%)	32,36,36	1.35	4 (12%)
2	9N8	D	601	-	26,26,26	1.73	6 (23%)	32,36,36	1.23	3 (9%)
3	SO4	A	605	-	4,4,4	0.24	0	6,6,6	0.10	0
3	SO4	D	602	-	4,4,4	0.21	0	6,6,6	0.11	0
3	SO4	G	603	-	4,4,4	0.25	0	6,6,6	0.10	0
3	SO4	C	603	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	F	604	-	4,4,4	0.27	0	6,6,6	0.08	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
2	9N8	E	601	-	-	6/16/16/16	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	9N8	A	601	-	-	6/16/16/16	0/3/3/3
2	9N8	B	601	-	-	6/16/16/16	0/3/3/3
2	9N8	G	601	-	-	6/16/16/16	0/3/3/3
2	9N8	H	601	-	-	6/16/16/16	0/3/3/3
2	9N8	D	601	-	-	5/16/16/16	0/3/3/3
2	9N8	C	601	-	-	6/16/16/16	0/3/3/3
2	9N8	F	601	-	-	6/16/16/16	0/3/3/3

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	9N8	C10-N1	4.88	1.45	1.35
2	H	601	9N8	C10-N1	4.73	1.45	1.35
2	G	601	9N8	C10-N1	4.72	1.45	1.35
2	B	601	9N8	C10-N1	4.69	1.45	1.35
2	F	601	9N8	C10-N1	4.68	1.45	1.35
2	A	601	9N8	C10-N1	4.64	1.45	1.35
2	E	601	9N8	C10-N1	4.60	1.45	1.35
2	D	601	9N8	C10-N1	4.58	1.45	1.35
2	C	601	9N8	C9-N	-4.10	1.32	1.37
2	E	601	9N8	C9-N	-4.02	1.32	1.37
2	D	601	9N8	C9-N	-3.97	1.32	1.37
2	F	601	9N8	C9-N	-3.96	1.32	1.37
2	H	601	9N8	C9-N	-3.79	1.32	1.37
2	G	601	9N8	C9-N	-3.76	1.32	1.37
2	B	601	9N8	C9-N	-3.74	1.32	1.37
2	A	601	9N8	C9-N	-3.71	1.32	1.37
2	C	601	9N8	C7-C6	3.62	1.53	1.47
2	H	601	9N8	C7-C6	3.43	1.53	1.47
2	D	601	9N8	C7-C6	3.21	1.52	1.47
2	F	601	9N8	C7-C6	3.13	1.52	1.47
2	B	601	9N8	C7-C6	3.03	1.52	1.47
2	G	601	9N8	C7-C6	3.01	1.52	1.47
2	A	601	9N8	C7-C6	2.99	1.52	1.47
2	E	601	9N8	C7-C6	2.97	1.52	1.47
2	D	601	9N8	O-C10	-2.55	1.18	1.23
2	A	601	9N8	O-C10	-2.49	1.18	1.23
2	B	601	9N8	O-C10	-2.47	1.18	1.23
2	E	601	9N8	O-C10	-2.42	1.19	1.23
2	F	601	9N8	O-C10	-2.41	1.19	1.23
2	H	601	9N8	O-C10	-2.35	1.19	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	601	9N8	O1-C6	-2.30	1.18	1.23
2	C	601	9N8	O-C10	-2.30	1.19	1.23
2	B	601	9N8	O1-C6	-2.26	1.18	1.23
2	G	601	9N8	O-C10	-2.25	1.19	1.23
2	F	601	9N8	O1-C6	-2.24	1.18	1.23
2	A	601	9N8	O1-C6	-2.24	1.18	1.23
2	H	601	9N8	O1-C6	-2.20	1.18	1.23
2	C	601	9N8	O1-C6	-2.17	1.18	1.23
2	D	601	9N8	O1-C6	-2.17	1.18	1.23
2	C	601	9N8	C9-C10	2.14	1.53	1.48
2	G	601	9N8	O1-C6	-2.14	1.18	1.23
2	H	601	9N8	C9-C10	2.10	1.53	1.48
2	C	601	9N8	C11-N1	2.09	1.45	1.41
2	D	601	9N8	BR-C	2.04	1.94	1.89
2	F	601	9N8	C8-N	-2.02	1.32	1.36
2	B	601	9N8	C8-N	-2.01	1.32	1.36

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	601	9N8	C4-C5-C	3.92	120.33	115.27
2	G	601	9N8	C4-C5-C	3.88	120.27	115.27
2	E	601	9N8	C4-C5-C	3.75	120.10	115.27
2	C	601	9N8	C4-C5-C	3.57	119.88	115.27
2	F	601	9N8	C4-C5-C	3.56	119.86	115.27
2	A	601	9N8	C4-C5-C	3.44	119.71	115.27
2	B	601	9N8	C4-C5-C	3.36	119.60	115.27
2	D	601	9N8	C4-C5-C	3.33	119.56	115.27
2	E	601	9N8	C14-N2-C15	2.95	122.02	116.85
2	B	601	9N8	C14-N2-C15	2.92	121.97	116.85
2	F	601	9N8	C14-N2-C15	2.85	121.84	116.85
2	H	601	9N8	C14-N2-C15	2.82	121.79	116.85
2	D	601	9N8	C14-N2-C15	2.74	121.65	116.85
2	C	601	9N8	C14-N2-C15	2.72	121.61	116.85
2	G	601	9N8	C14-N2-C15	2.71	121.60	116.85
2	A	601	9N8	C14-N2-C15	2.66	121.50	116.85
2	A	601	9N8	C10-C9-N	2.46	125.69	120.11
2	H	601	9N8	C-C5-C6	-2.36	119.11	123.87
2	B	601	9N8	C10-C9-N	2.32	125.36	120.11
2	G	601	9N8	C-C5-C6	-2.14	119.55	123.87
2	D	601	9N8	C10-C9-N	2.11	124.90	120.11
2	H	601	9N8	C3-C4-C5	-2.09	119.65	123.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	601	9N8	C3-C4-C5	-2.08	119.67	123.48
2	B	601	9N8	C11-N1-C10	-2.06	123.80	127.45
2	E	601	9N8	C12-C11-C15	2.02	119.75	117.78

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	9N8	O1-C6-C7-C16
2	C	601	9N8	N1-C10-C9-N
2	D	601	9N8	O1-C6-C7-C16
2	H	601	9N8	O-C10-C9-N
2	H	601	9N8	N1-C10-C9-N
2	C	601	9N8	O-C10-C9-C16
2	E	601	9N8	O-C10-C9-C16
2	F	601	9N8	O-C10-C9-C16
2	G	601	9N8	O-C10-C9-C16
2	H	601	9N8	O-C10-C9-C16
2	A	601	9N8	O-C10-C9-N
2	C	601	9N8	O-C10-C9-N
2	E	601	9N8	O-C10-C9-N
2	F	601	9N8	O-C10-C9-N
2	G	601	9N8	O-C10-C9-N
2	C	601	9N8	N1-C10-C9-C16
2	E	601	9N8	N1-C10-C9-C16
2	F	601	9N8	N1-C10-C9-C16
2	G	601	9N8	N1-C10-C9-C16
2	H	601	9N8	N1-C10-C9-C16
2	A	601	9N8	N1-C10-C9-N
2	E	601	9N8	N1-C10-C9-N
2	F	601	9N8	N1-C10-C9-N
2	G	601	9N8	N1-C10-C9-N
2	A	601	9N8	O-C10-C9-C16
2	A	601	9N8	N1-C10-C9-C16
2	B	601	9N8	O-C10-C9-C16
2	B	601	9N8	N1-C10-C9-C16
2	B	601	9N8	O1-C6-C7-C8
2	C	601	9N8	O1-C6-C7-C8
2	E	601	9N8	O1-C6-C7-C8
2	G	601	9N8	O1-C6-C7-C8
2	H	601	9N8	O1-C6-C7-C8
2	B	601	9N8	N1-C10-C9-N

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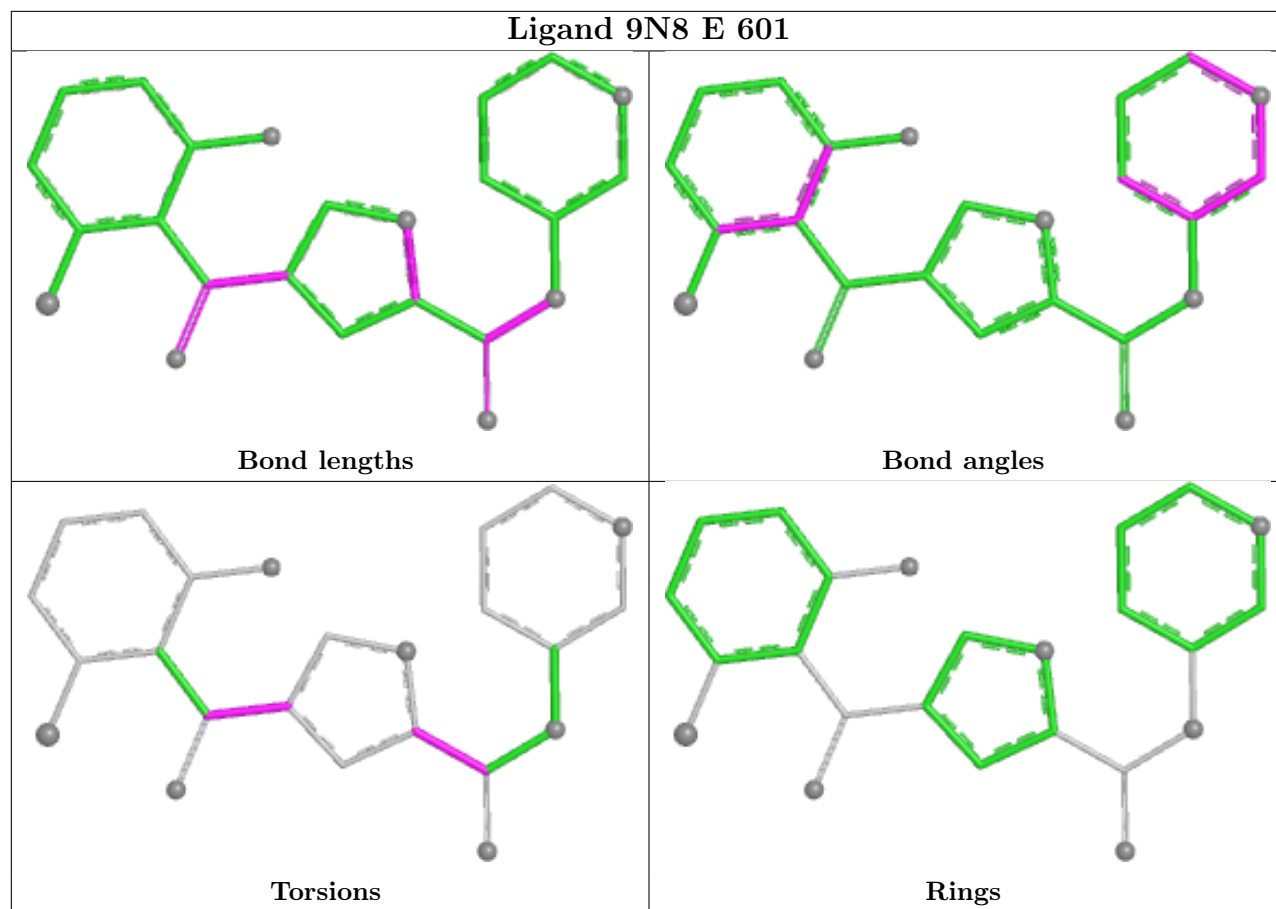
Mol	Chain	Res	Type	Atoms
2	B	601	9N8	O1-C6-C7-C16
2	C	601	9N8	O1-C6-C7-C16
2	E	601	9N8	O1-C6-C7-C16
2	F	601	9N8	O1-C6-C7-C16
2	G	601	9N8	O1-C6-C7-C16
2	H	601	9N8	O1-C6-C7-C16
2	B	601	9N8	O-C10-C9-N
2	D	601	9N8	O-C10-C9-C16
2	D	601	9N8	N1-C10-C9-C16
2	D	601	9N8	N1-C10-C9-N
2	D	601	9N8	O-C10-C9-N
2	A	601	9N8	O1-C6-C7-C8
2	F	601	9N8	O1-C6-C7-C8

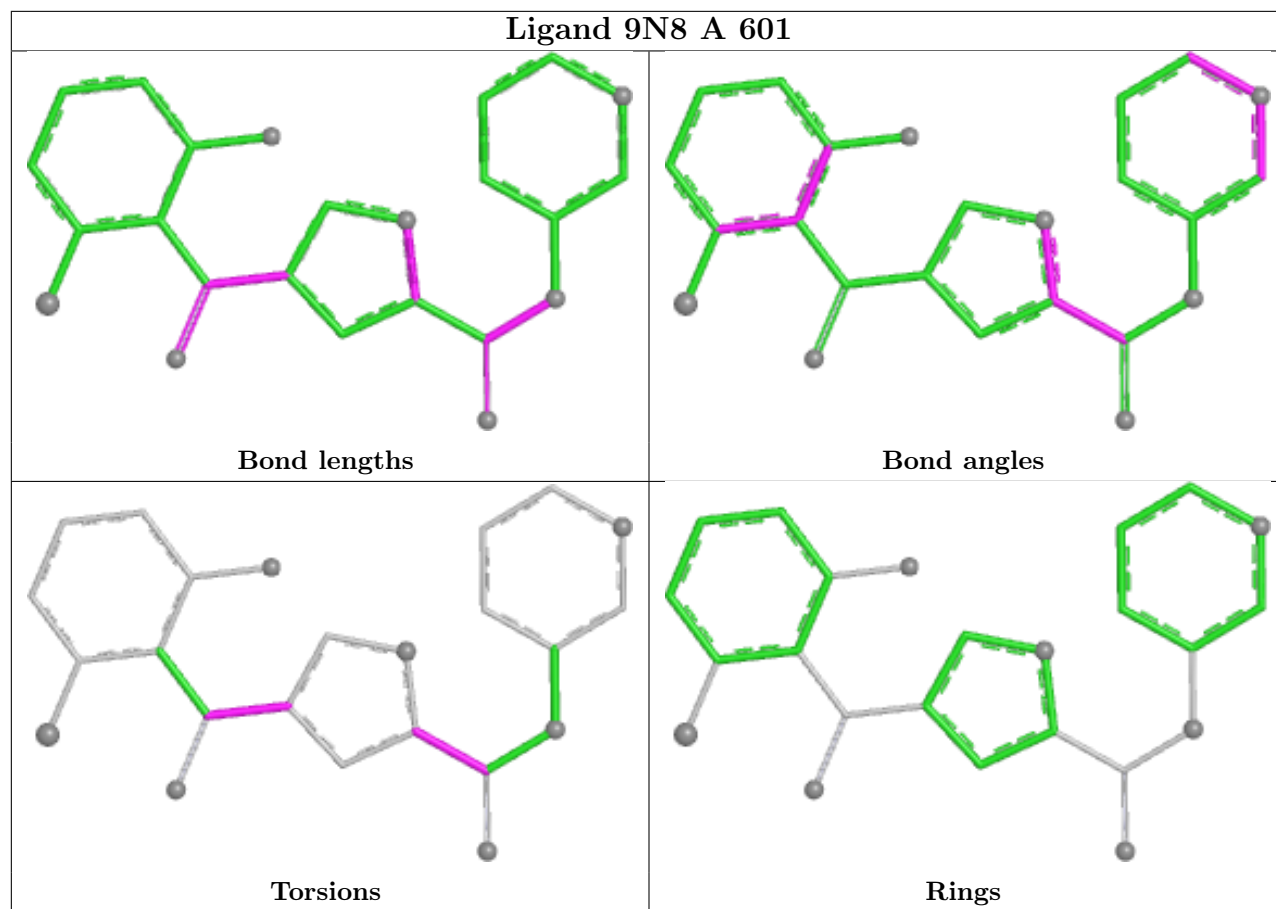
There are no ring outliers.

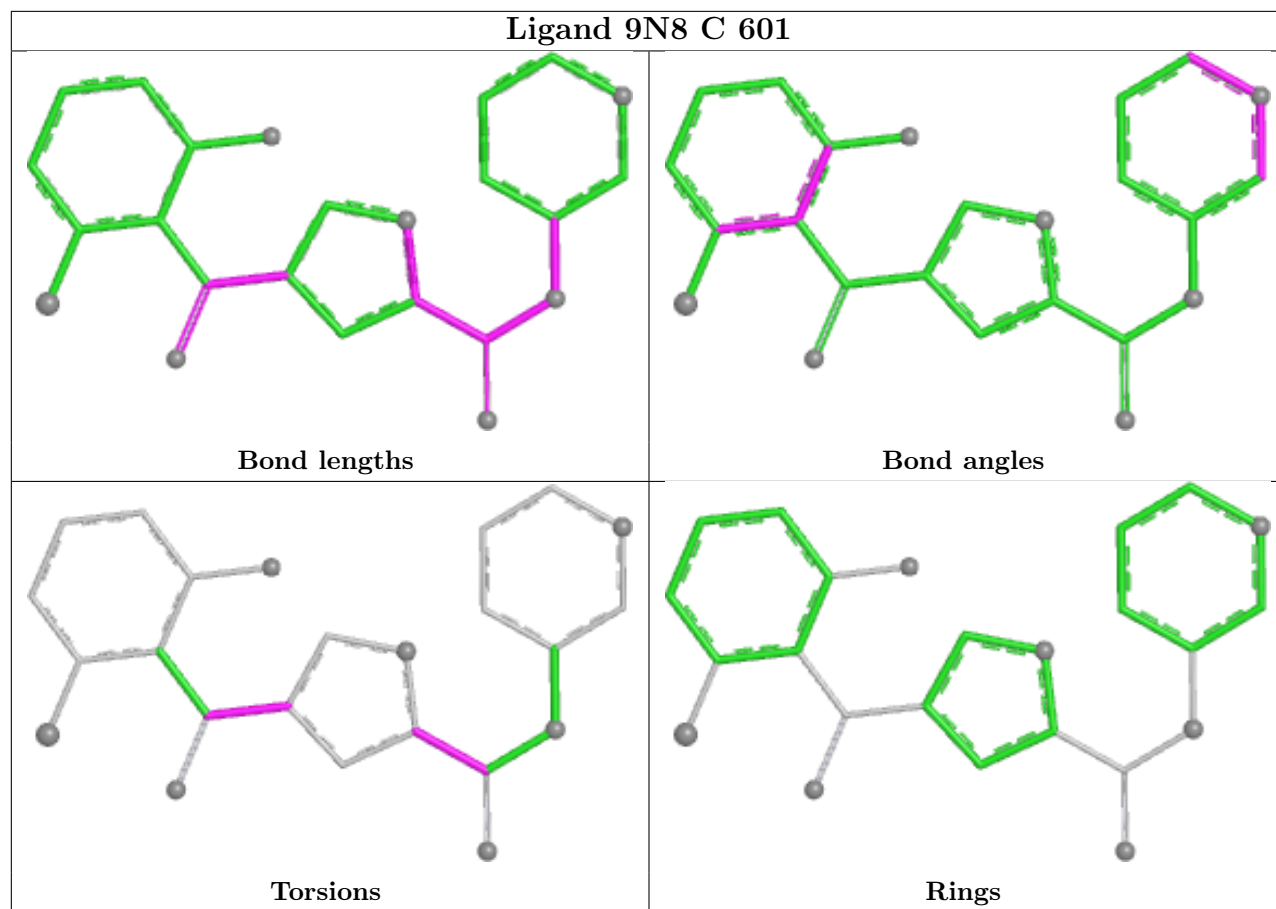
6 monomers are involved in 7 short contacts:

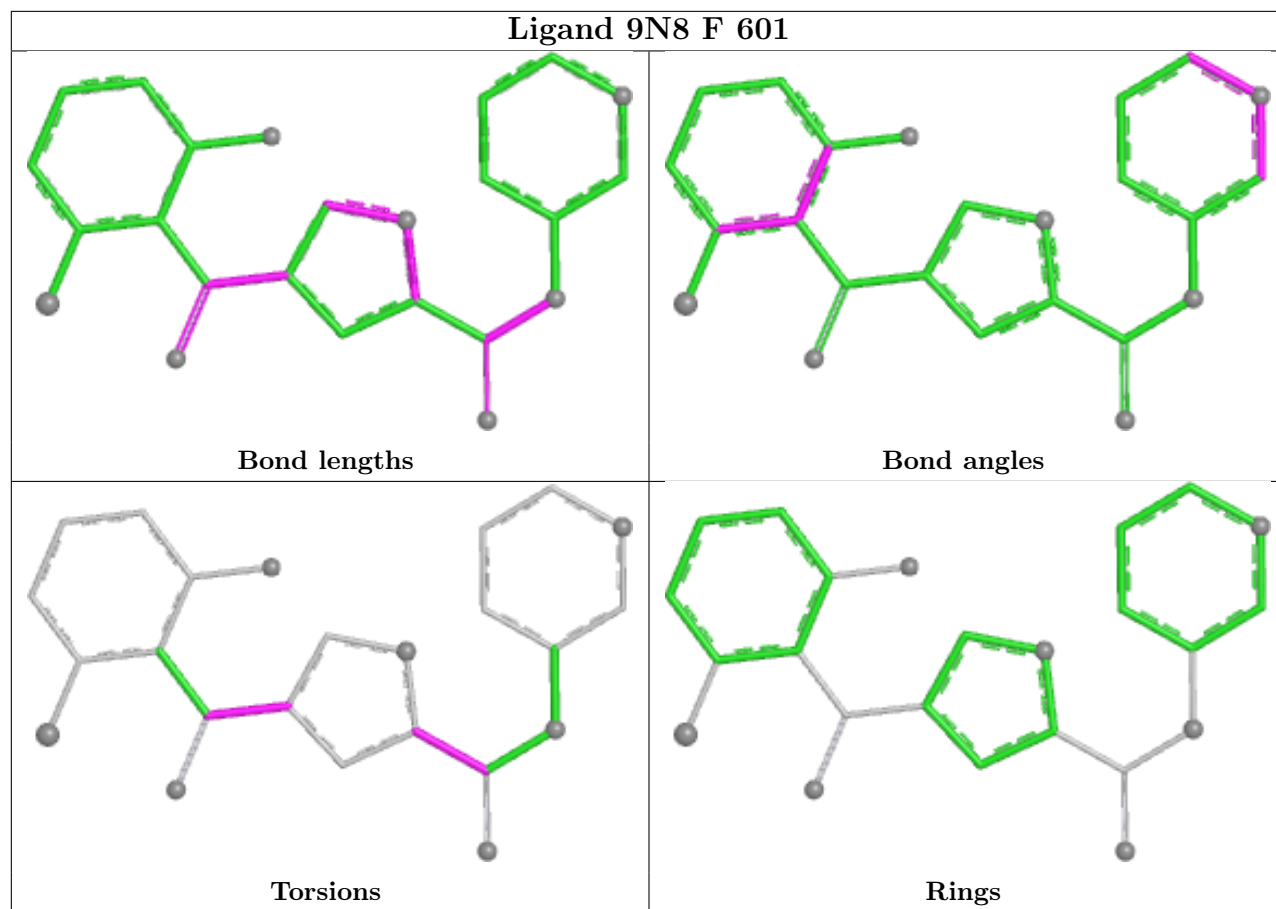
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	601	9N8	1	0
2	A	601	9N8	1	0
3	D	603	SO4	1	0
2	H	601	9N8	1	0
3	A	605	SO4	2	0
3	C	603	SO4	1	0

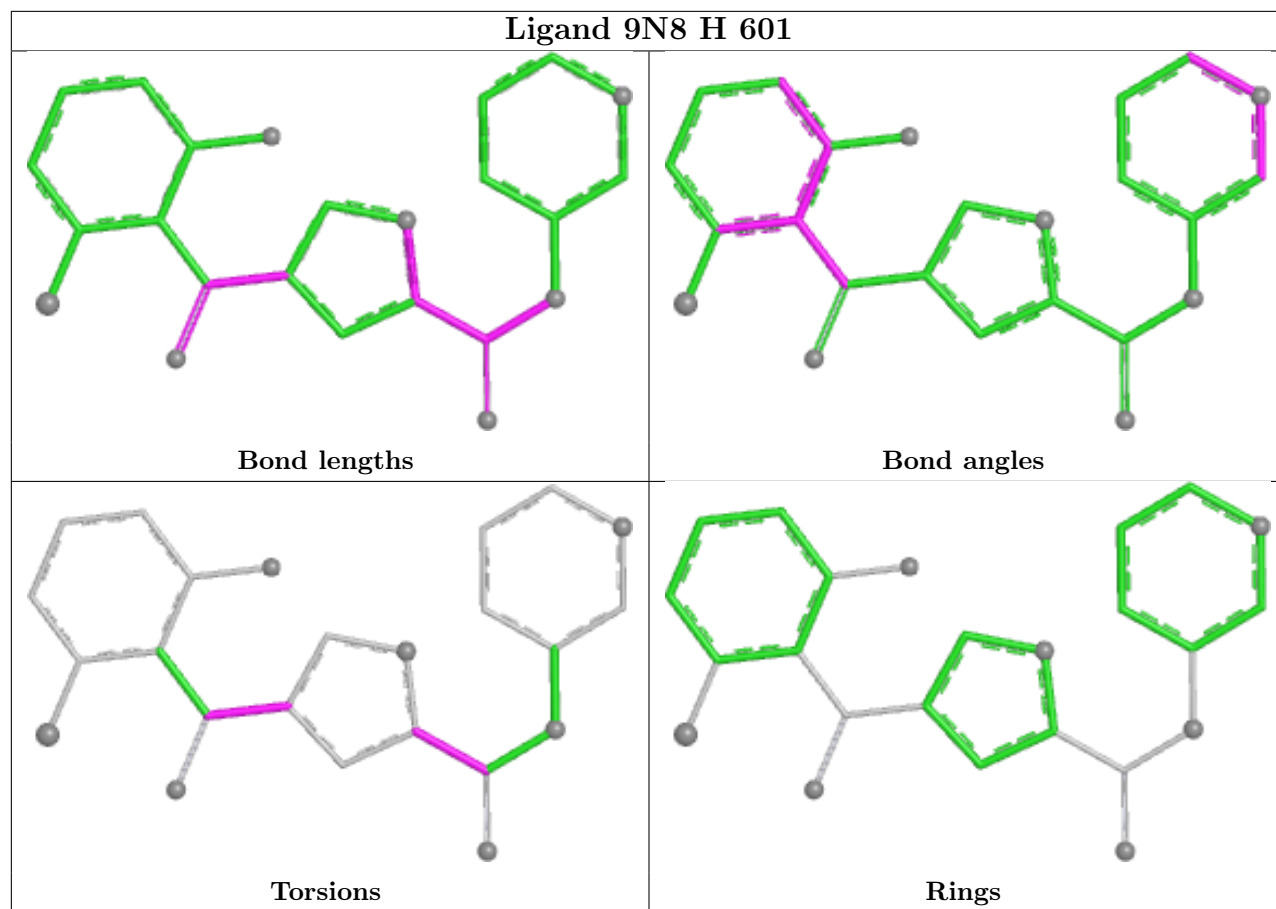
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

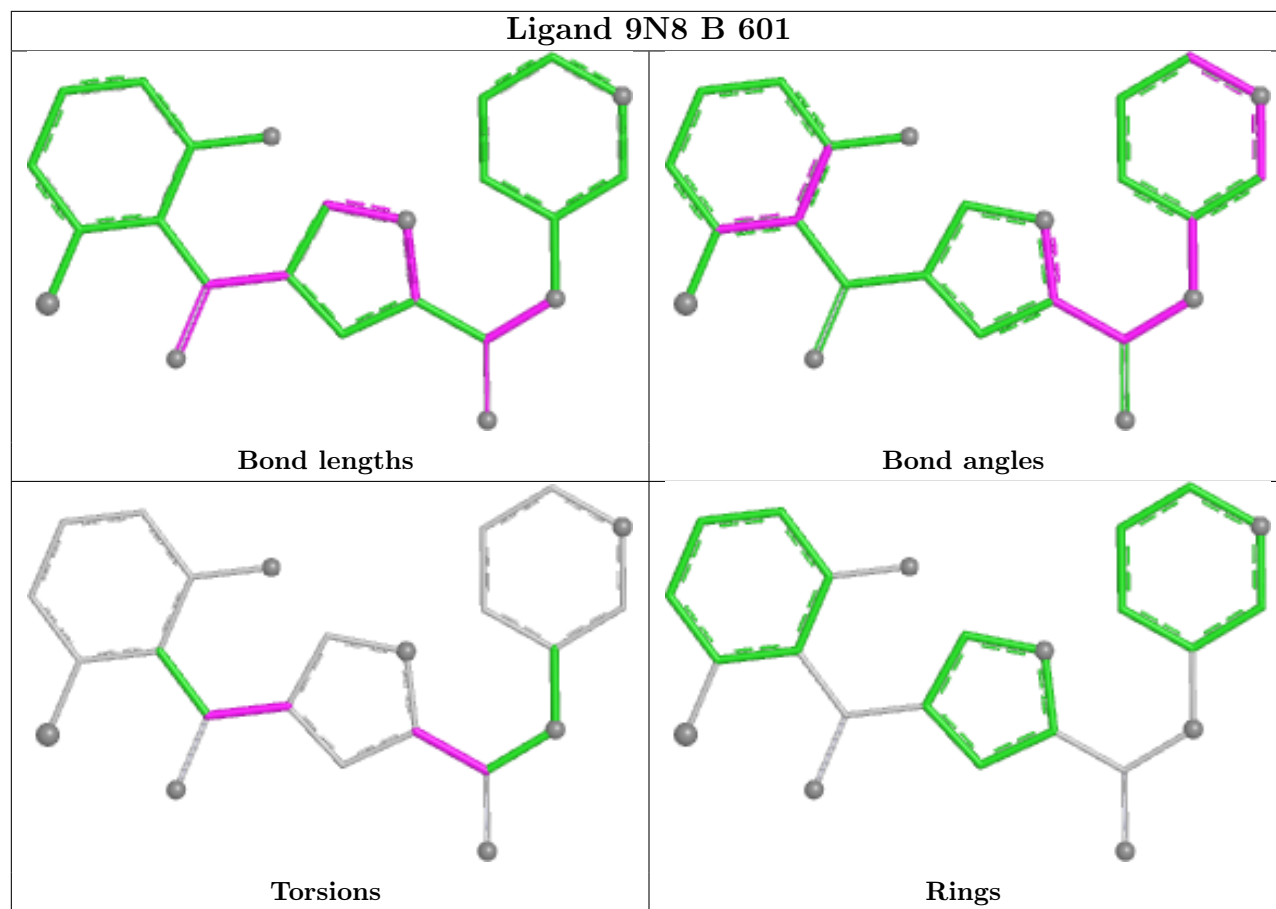


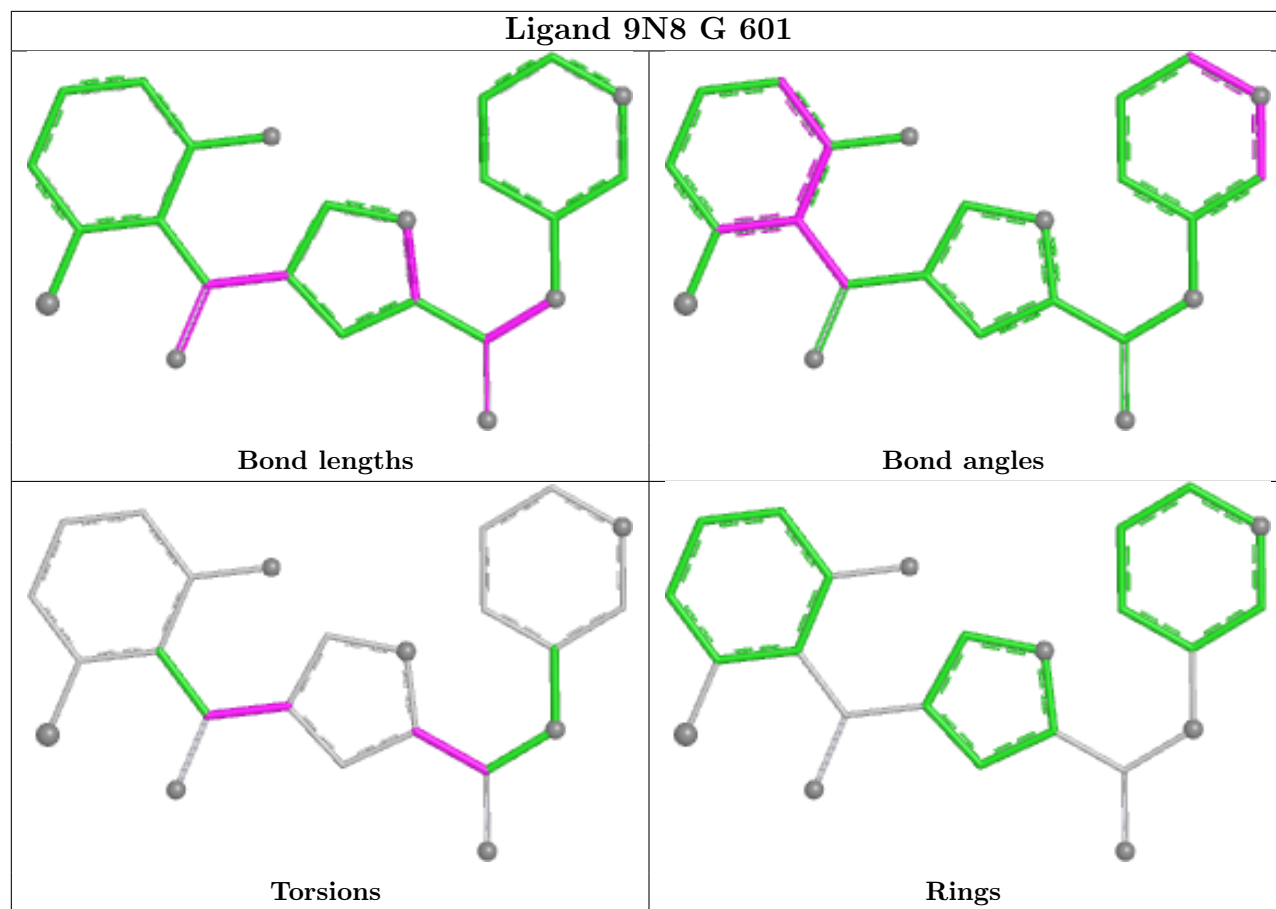


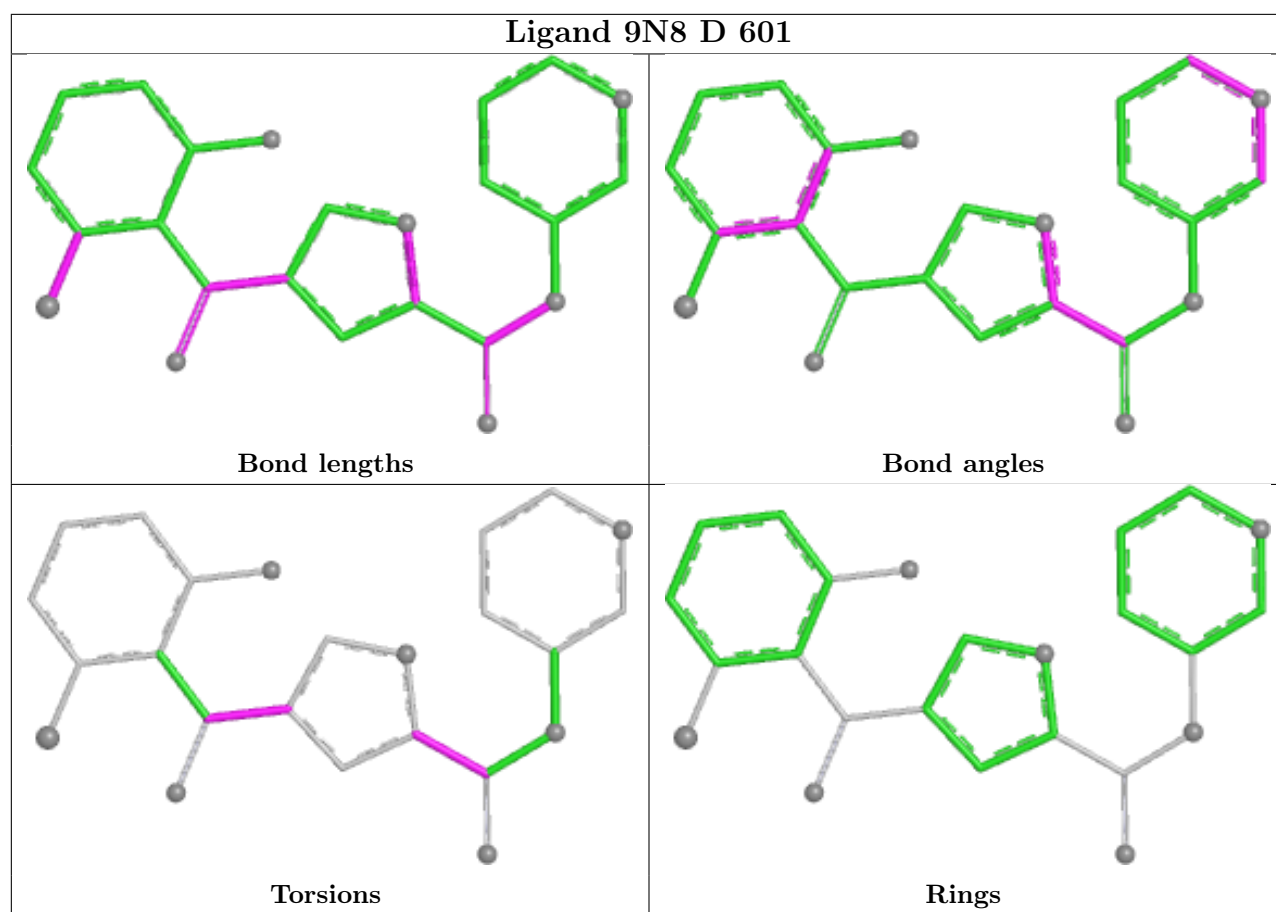












5.7 Other polymers [i](#)

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	162/163 (99%)	0.09	2 (1%) 76 73	19, 26, 38, 48	0
1	B	160/163 (98%)	0.32	5 (3%) 51 47	21, 31, 42, 53	0
1	C	162/163 (99%)	0.00	2 (1%) 76 73	19, 26, 37, 41	0
1	D	161/163 (98%)	0.13	3 (1%) 66 62	21, 30, 43, 49	0
1	E	162/163 (99%)	0.15	5 (3%) 51 47	20, 28, 47, 52	0
1	F	162/163 (99%)	0.34	5 (3%) 51 47	22, 32, 42, 65	0
1	G	162/163 (99%)	0.35	9 (5%) 30 26	24, 32, 48, 57	0
1	H	163/163 (100%)	0.03	1 (0%) 85 83	23, 27, 38, 41	0
All	All	1294/1304 (99%)	0.18	32 (2%) 58 54	19, 29, 42, 65	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	505	HIS	3.7
1	G	504	ILE	3.7
1	B	423	GLY	3.6
1	D	420	HIS	3.6
1	E	501	TYR	3.3
1	G	425	PRO	3.0
1	E	422	GLY	3.0
1	G	501	TYR	3.0
1	F	420	HIS	2.8
1	F	363	ASN	2.8
1	B	422	GLY	2.7
1	G	503	VAL	2.7
1	G	499	ASP	2.7
1	G	502	GLN	2.6
1	G	505	HIS	2.6
1	F	425	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	423	GLY	2.5
1	C	503	VAL	2.5
1	D	502	GLN	2.5
1	E	424	SER	2.4
1	B	499	ASP	2.4
1	E	505	HIS	2.4
1	A	501	TYR	2.4
1	E	502	GLN	2.4
1	F	429	VAL	2.3
1	C	423	GLY	2.2
1	B	500	LEU	2.2
1	B	425	PRO	2.2
1	G	421	HIS	2.1
1	H	345	THR	2.1
1	G	422	GLY	2.0
1	A	420	HIS	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 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
3	SO4	A	606	5/5	0.78	0.23	50,51,51,52	0
3	SO4	C	604	5/5	0.81	0.25	44,44,45,46	0
3	SO4	F	604	5/5	0.81	0.14	52,52,53,53	0
3	SO4	G	603	5/5	0.81	0.14	59,61,61,62	0
3	SO4	C	603	5/5	0.87	0.14	46,47,48,49	0
3	SO4	D	604	5/5	0.88	0.17	41,43,44,45	0
3	SO4	H	602	5/5	0.88	0.16	49,50,51,52	0

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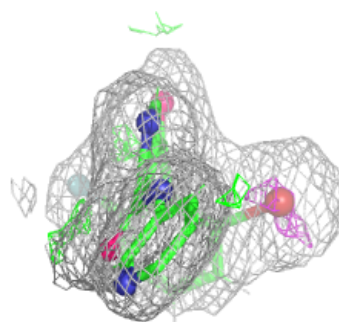
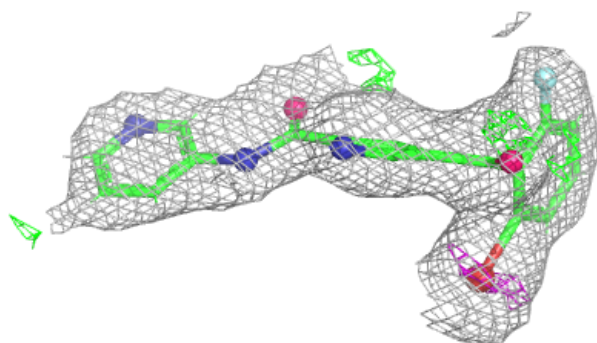
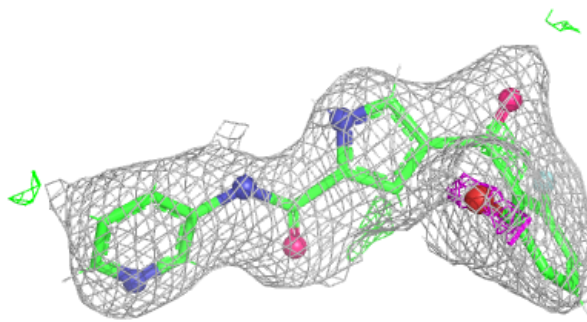
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	604	5/5	0.89	0.12	44,46,47,47	0
3	SO4	A	605	5/5	0.91	0.21	44,45,45,45	0
3	SO4	B	604	5/5	0.91	0.13	37,38,39,40	0
2	9N8	F	601	24/24	0.92	0.11	23,34,45,51	0
3	SO4	A	603	5/5	0.92	0.13	35,35,36,36	0
3	SO4	E	605	5/5	0.92	0.11	43,43,43,44	0
3	SO4	D	603	5/5	0.93	0.12	40,41,42,42	0
2	9N8	B	601	24/24	0.93	0.10	21,28,39,46	0
2	9N8	C	601	24/24	0.94	0.09	19,24,38,46	0
2	9N8	D	601	24/24	0.94	0.10	21,29,40,48	0
3	SO4	F	603	5/5	0.95	0.10	41,42,42,43	0
2	9N8	A	601	24/24	0.95	0.09	19,28,36,43	0
3	SO4	B	603	5/5	0.95	0.09	39,40,40,41	0
2	9N8	E	601	24/24	0.95	0.09	20,27,40,44	0
2	9N8	H	601	24/24	0.96	0.09	22,28,35,42	0
3	SO4	D	602	5/5	0.96	0.07	30,30,32,32	0
3	SO4	C	602	5/5	0.96	0.09	28,31,31,33	0
2	9N8	G	601	24/24	0.96	0.09	24,32,43,45	0
3	SO4	E	604	5/5	0.96	0.07	31,34,35,37	0
3	SO4	B	602	5/5	0.97	0.07	26,26,27,28	0
3	SO4	E	603	5/5	0.97	0.08	29,30,30,33	0
3	SO4	A	602	5/5	0.98	0.05	24,24,26,28	0
3	SO4	G	602	5/5	0.98	0.07	30,31,31,33	0
3	SO4	F	602	5/5	0.98	0.07	28,29,30,31	0
3	SO4	E	602	5/5	0.98	0.06	26,26,27,27	0

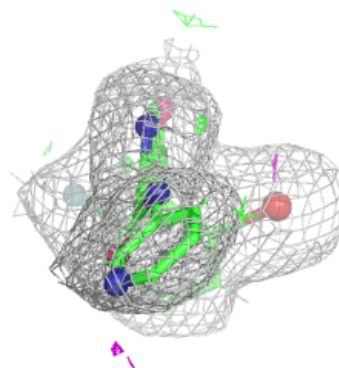
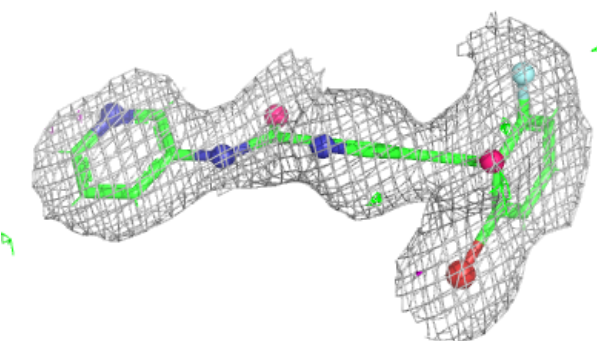
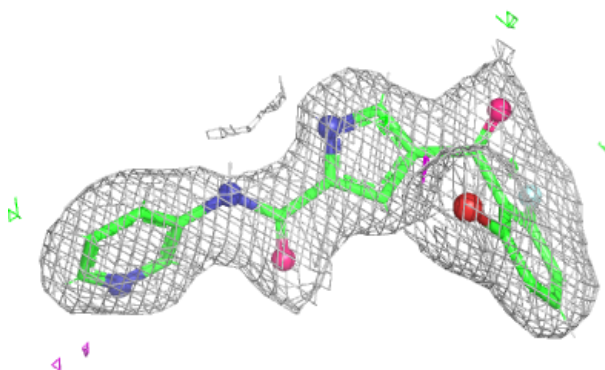
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 9N8 F 601:

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

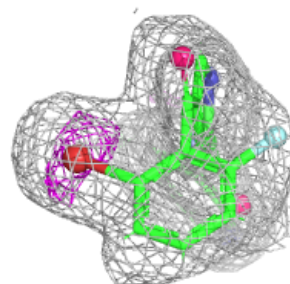
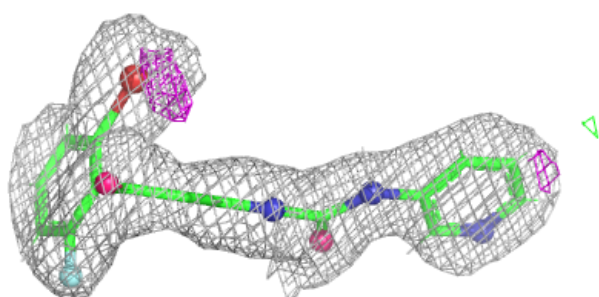
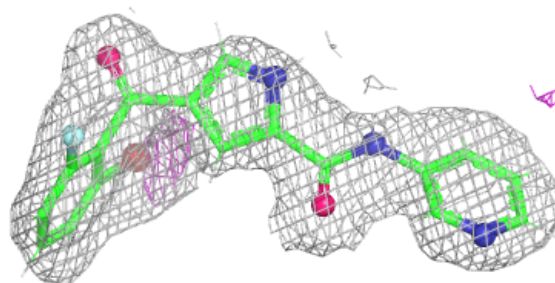
**Electron density around 9N8 B 601:**

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

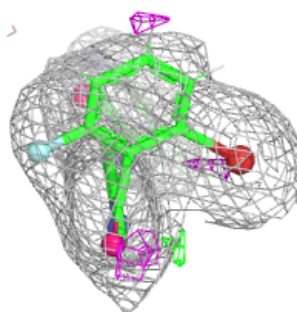
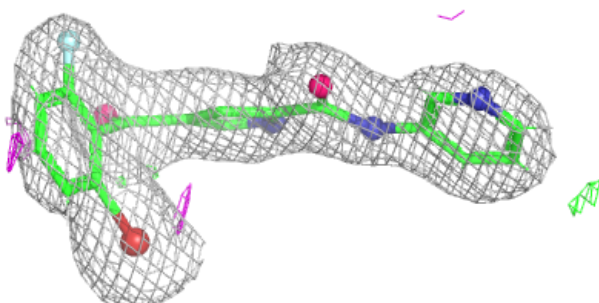
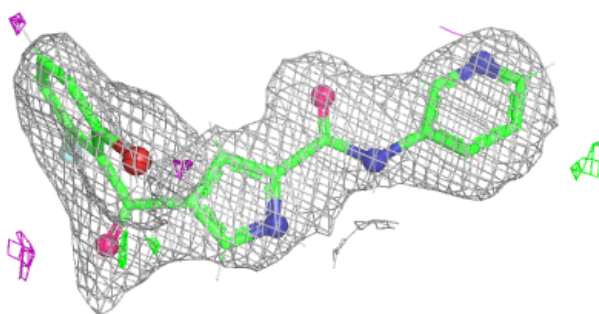


Electron density around 9N8 C 601:

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

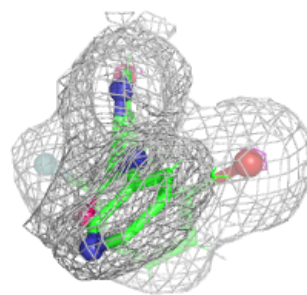
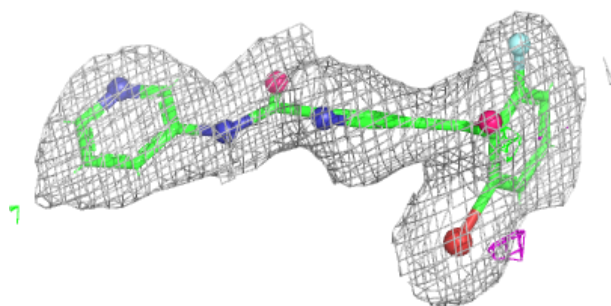
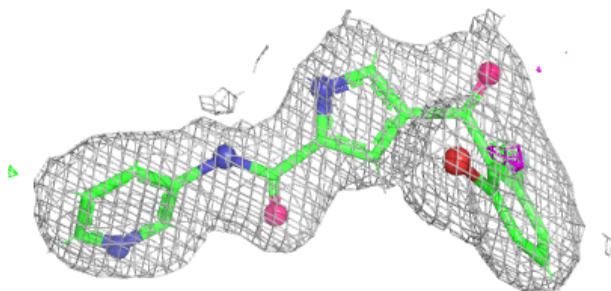
**Electron density around 9N8 D 601:**

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

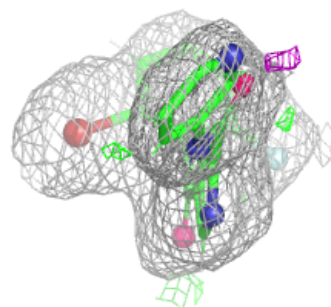
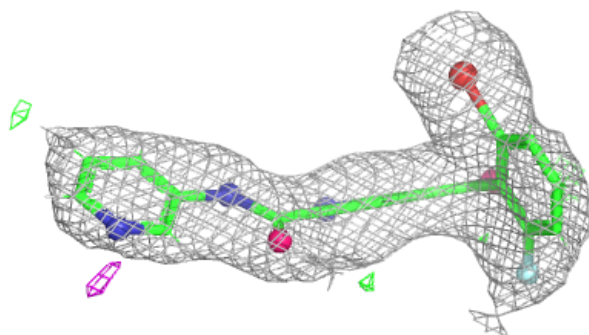
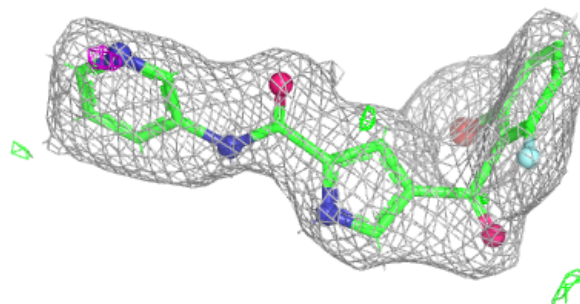


Electron density around 9N8 A 601:

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

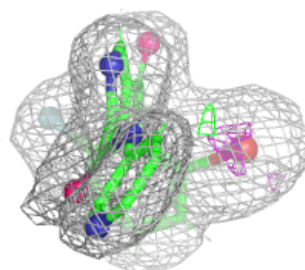
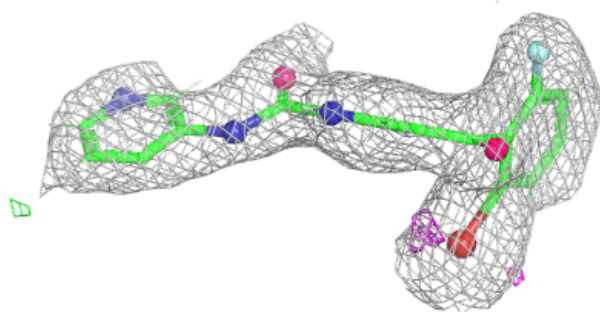
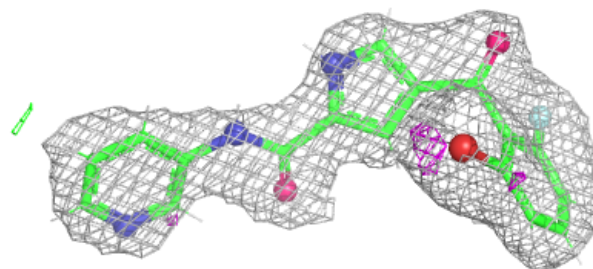
**Electron density around 9N8 E 601:**

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

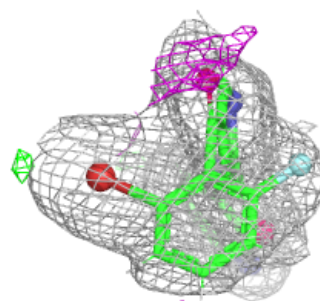
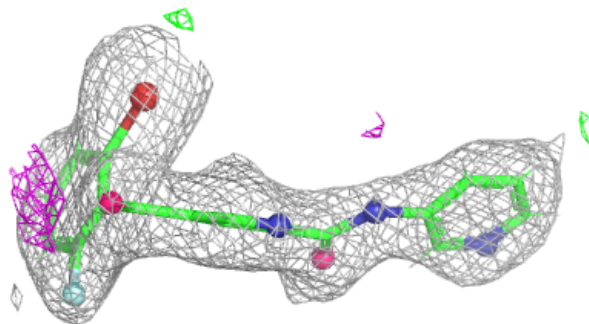
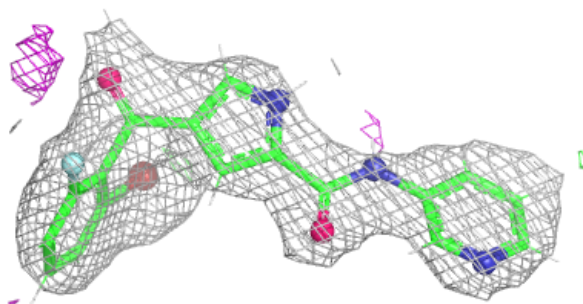


Electron density around 9N8 H 601:

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

**Electron density around 9N8 G 601:**

$2mF_o-DF_c$ (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.