



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 10:27 PM UTC

PDB ID : 4YFF / pdb_00004yff
Title : TNNI3K complexed with inhibitor 2
Authors : Shewchuk, L.M.; Wang, L.; Lawhorn, B.G.
Deposited on : 2015-02-25
Resolution : 3.07 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

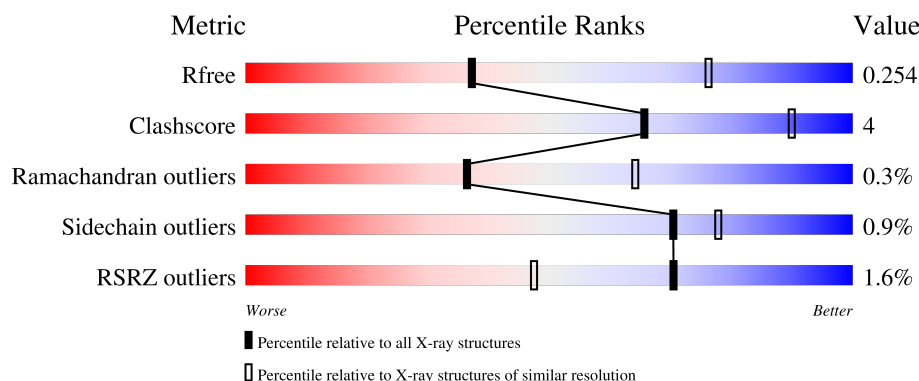
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.07 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	2010 (3.10-3.06)
Clashscore	190562	2102 (3.10-3.06)
Ramachandran outliers	187476	1982 (3.10-3.06)
Sidechain outliers	187428	1981 (3.10-3.06)
RSRZ outliers	180081	2010 (3.10-3.06)

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	311	2% 80% 15%
1	B	311	77% 8% 15%
1	C	311	2% 73% 9% 17%
1	D	311	2% 77% 5% 17%

2 Entry composition [i](#)

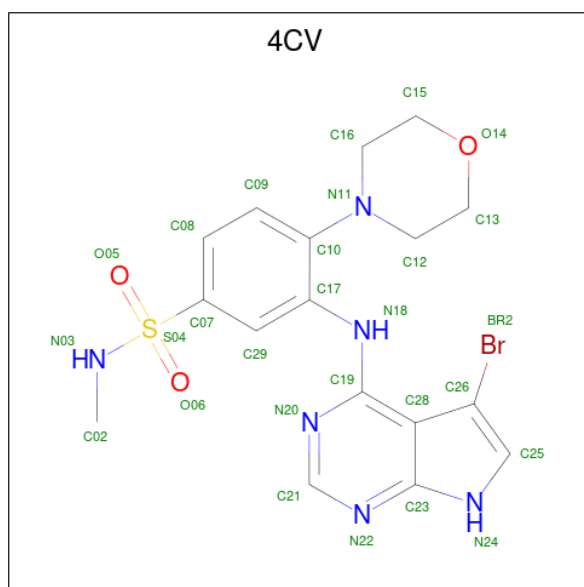
There are 3 unique types of molecules in this entry. The entry contains 8223 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Serine/threonine-protein kinase TNNI3K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	0	0
			2051	1322	350	364	15			
1	B	264	Total	C	N	O	S	0	0	0
			2043	1323	345	361	14			
1	C	258	Total	C	N	O	S	0	0	0
			2006	1289	346	356	15			
1	D	257	Total	C	N	O	S	0	1	0
			1992	1283	339	354	16			

- Molecule 2 is 3-[(5-bromo-7H-pyrrolo[2,3-d]pyrimidin-4-yl)amino]-N-methyl-4-(morpholin-4-yl)benzenesulfonamide (CCD ID: 4CV) (formula: C₁₇H₁₉BrN₆O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	Br	C	N	O	S	0
			28	1	17	6	3	1	
2	B	1	Total	Br	C	N	O	S	0
			28	1	17	6	3	1	

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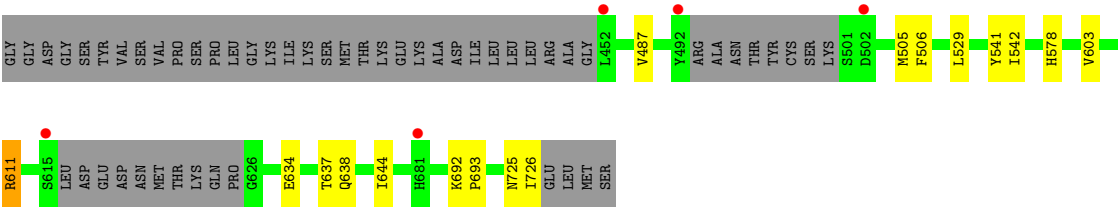
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	C	1	Total	Br	C	N	O	S	0	0
			28	1	17	6	3	1		
2	D	1	Total	Br	C	N	O	S	0	0
			28	1	17	6	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	5	Total	O	0	0
			5	5		
3	C	2	Total	O	0	0
			2	2		
3	D	7	Total	O	0	0
			7	7		

- Molecule 1: Serine/threonine-protein kinase TNNT3K





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.45Å 106.07Å 93.24Å 90.00° 93.78° 90.00°	Depositor
Resolution (Å)	20.00 – 3.07 20.00 – 3.07	Depositor EDS
% Data completeness (in resolution range)	95.8 (20.00-3.07) 95.9 (20.00-3.07)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.45 (at 3.06Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.209 , 0.251 0.213 , 0.254	Depositor DCC
R_{free} test set	1512 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	83.6	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 27.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8223	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.16 % 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 2.8528e-04. 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: 4CV

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	0.57	0/2100	0.87	3/2849 (0.1%)
1	B	0.56	0/2093	0.86	3/2841 (0.1%)
1	C	0.57	0/2054	0.84	0/2787
1	D	0.58	0/2043	0.84	0/2772
All	All	0.57	0/8290	0.85	6/11249 (0.1%)

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

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	491	ARG	NE-CZ-NH2	-11.95	108.45	119.20
1	B	491	ARG	NE-CZ-NH2	10.17	128.35	119.20
1	B	491	ARG	NE-CZ-NH1	-10.15	111.35	121.50
1	A	491	ARG	CD-NE-CZ	10.13	138.59	124.40
1	B	491	ARG	CD-NE-CZ	6.35	133.29	124.40
1	A	491	ARG	NE-CZ-NH1	6.17	127.67	121.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	491	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	2051	0	2006	10	0
1	B	2043	0	1997	27	0
1	C	2006	0	1969	31	0
1	D	1992	0	1946	12	0
2	A	28	0	19	1	0
2	B	28	0	19	2	0
2	C	28	0	19	3	0
2	D	28	0	19	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	2	0	0	0	0
3	D	7	0	0	0	0
All	All	8223	0	7994	61	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 4.

All (61) 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:629:ARG:NH2	1:C:664:PRO:O	2.12	0.80
1:B:629:ARG:NH1	1:C:668:LEU:O	2.23	0.70
1:A:637:THR:CG2	1:D:634:GLU:HA	2.25	0.65
1:A:640:THR:O	1:D:638:GLN:NE2	2.30	0.64
1:A:637:THR:HB	1:D:637:THR:HG21	1.78	0.64
1:B:674:ALA:HB1	1:C:636:PHE:CG	2.36	0.60
1:B:657:GLU:OE1	1:C:630:TRP:NE1	2.34	0.59
1:C:578:HIS:CE1	1:C:644:ILE:HB	2.39	0.57
2:B:801:4CV:N20	2:B:801:4CV:H19	2.20	0.57
1:A:637:THR:HG21	1:D:634:GLU:HA	1.87	0.57
2:A:801:4CV:N20	2:A:801:4CV:H19	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:578:HIS:CE1	1:D:644:ILE:HB	2.40	0.56
1:B:670:PRO:CG	1:C:626:GLY:HA2	2.36	0.56
1:A:550:LEU:C	1:A:550:LEU:HD23	2.32	0.55
1:C:452:LEU:HD22	1:C:510:VAL:HG11	1.88	0.55
1:A:638:GLN:HA	1:D:638:GLN:HG2	1.89	0.55
1:A:659:LEU:HD11	1:A:694:ILE:HG21	1.91	0.53
1:B:649:PHE:CD1	1:C:632:ALA:HA	2.44	0.53
2:D:801:4CV:N20	2:D:801:4CV:H19	2.23	0.53
1:B:629:ARG:HH22	1:C:665:PHE:C	2.16	0.52
2:C:801:4CV:N20	2:C:801:4CV:H19	2.24	0.52
1:B:550:LEU:C	1:B:550:LEU:HD23	2.35	0.51
2:B:801:4CV:H2	2:B:801:4CV:BR2	2.66	0.51
1:B:659:LEU:HD11	1:B:694:ILE:HG21	1.91	0.51
1:B:664:PRO:O	1:C:629:ARG:HD3	2.11	0.50
1:C:506:PHE:HE2	1:C:529:LEU:HD23	1.77	0.49
1:B:629:ARG:HD3	1:C:664:PRO:O	2.12	0.49
1:B:649:PHE:CD2	1:B:702:TRP:HA	2.48	0.49
1:B:632:ALA:HA	1:C:649:PHE:CD1	2.47	0.49
1:B:649:PHE:CE1	1:C:633:PRO:HD3	2.49	0.48
1:D:506:PHE:HE2	1:D:529:LEU:HD23	1.79	0.48
1:B:649:PHE:CZ	1:C:633:PRO:HD3	2.49	0.48
1:B:633:PRO:HD3	1:C:649:PHE:CZ	2.48	0.47
1:B:636:PHE:CD1	1:C:674:ALA:HB1	2.50	0.47
1:D:725:ASN:O	1:D:726:ILE:C	2.58	0.46
1:A:649:PHE:CD2	1:A:702:TRP:HA	2.50	0.46
1:B:679:TYR:HB3	1:C:705:CYS:HA	1.97	0.45
1:C:452:LEU:O	1:C:453:PRO:C	2.59	0.45
1:C:452:LEU:HD22	1:C:510:VAL:CG1	2.46	0.45
1:C:487:VAL:C	1:C:541:TYR:HB2	2.41	0.45
1:B:718:LYS:O	1:B:721:GLU:HB2	2.17	0.44
1:D:487:VAL:C	1:D:541:TYR:HB2	2.42	0.44
1:B:632:ALA:HB2	1:C:649:PHE:HB3	2.00	0.43
1:B:653:LEU:HD13	1:C:630:TRP:HA	1.99	0.43
1:B:674:ALA:HB1	1:C:636:PHE:CD2	2.53	0.43
1:B:649:PHE:HB3	1:C:632:ALA:HB2	1.99	0.43
1:B:629:ARG:NH2	1:C:665:PHE:C	2.76	0.43
1:B:674:ALA:HB1	1:C:636:PHE:CD1	2.54	0.43
1:C:542:ILE:CD1	1:C:603:VAL:HG21	2.50	0.42
1:D:505:MET:HE3	1:D:611:ARG:HH12	1.83	0.42
1:D:542:ILE:CD1	1:D:603:VAL:HG21	2.50	0.42
2:C:801:4CV:H14	2:C:801:4CV:H11	1.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:656:TRP:CE2	1:A:660:THR:HG21	2.56	0.41
1:B:656:TRP:CE2	1:B:660:THR:HG21	2.56	0.41
2:C:801:4CV:BR2	2:C:801:4CV:H2	2.75	0.41
1:B:659:LEU:CD1	1:B:694:ILE:HG21	2.51	0.40
1:C:505:MET:HE3	1:C:611:ARG:HH12	1.86	0.40
1:C:692:LYS:N	1:C:693:PRO:CD	2.84	0.40
1:C:482:CYS:O	1:C:483:ARG:C	2.64	0.40
1:D:692:LYS:N	1:D:693:PRO:CD	2.85	0.40
1:A:659:LEU:CD1	1:A:694:ILE:HG21	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	258/311 (83%)	249 (96%)	8 (3%)	1 (0%)	30	58
1	B	258/311 (83%)	252 (98%)	5 (2%)	1 (0%)	30	58
1	C	252/311 (81%)	240 (95%)	11 (4%)	1 (0%)	30	58
1	D	252/311 (81%)	242 (96%)	10 (4%)	0	100	100
All	All	1020/1244 (82%)	983 (96%)	34 (3%)	3 (0%)	36	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	606	ASP
1	B	606	ASP
1	C	453	PRO

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	216/270 (80%)	214 (99%)	2 (1%)	70	78
1	B	214/270 (79%)	211 (99%)	3 (1%)	59	73
1	C	214/270 (79%)	212 (99%)	2 (1%)	70	78
1	D	212/270 (78%)	211 (100%)	1 (0%)	81	83
All	All	856/1080 (79%)	848 (99%)	8 (1%)	70	78

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	603	VAL
1	A	713	SER
1	B	445	ILE
1	B	603	VAL
1	B	713	SER
1	C	611	ARG
1	C	628	LEU
1	D	611	ARG

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

Mol	Chain	Res	Type
1	C	592	HIS
1	D	457	HIS
1	D	530	ASN
1	D	534	GLN
1	D	554	GLN
1	D	592	HIS

5.3.3 RNA

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](#)

4 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	4CV	C	801	-	30,31,31	1.85	4 (13%)	37,45,45	1.82	8 (21%)
2	4CV	A	801	-	30,31,31	1.68	4 (13%)	37,45,45	1.73	7 (18%)
2	4CV	B	801	-	30,31,31	1.64	3 (10%)	37,45,45	1.87	9 (24%)
2	4CV	D	801	-	30,31,31	1.75	3 (10%)	37,45,45	1.88	10 (27%)

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	4CV	C	801	-	-	7/17/25/25	0/4/4/4
2	4CV	A	801	-	-	7/17/25/25	0/4/4/4
2	4CV	B	801	-	-	7/17/25/25	0/4/4/4
2	4CV	D	801	-	-	7/17/25/25	0/4/4/4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	4CV	S04-N03	8.38	1.73	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	801	4CV	S04-N03	7.67	1.72	1.61
2	A	801	4CV	S04-N03	7.63	1.72	1.61
2	B	801	4CV	S04-N03	7.31	1.72	1.61
2	D	801	4CV	O05-S04	2.76	1.46	1.43
2	A	801	4CV	O06-S04	2.71	1.46	1.43
2	D	801	4CV	O06-S04	2.64	1.46	1.43
2	B	801	4CV	C19-N18	2.61	1.41	1.36
2	C	801	4CV	C19-N18	2.57	1.41	1.36
2	A	801	4CV	C19-N18	2.33	1.40	1.36
2	C	801	4CV	O06-S04	2.29	1.46	1.43
2	C	801	4CV	O05-S04	2.21	1.46	1.43
2	B	801	4CV	C28-C23	-2.06	1.38	1.41
2	A	801	4CV	O05-S04	2.05	1.45	1.43

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	4CV	C23-N24-C25	5.43	111.04	108.48
2	C	801	4CV	C07-S04-N03	-5.02	100.63	107.55
2	C	801	4CV	C23-N24-C25	4.79	110.74	108.48
2	B	801	4CV	C07-S04-N03	-4.62	101.19	107.55
2	D	801	4CV	O06-S04-O05	4.32	124.77	119.52
2	A	801	4CV	C23-N24-C25	4.21	110.47	108.48
2	D	801	4CV	O05-S04-C07	-3.88	103.08	107.98
2	D	801	4CV	C23-N24-C25	3.88	110.31	108.48
2	A	801	4CV	C07-S04-N03	-3.55	102.66	107.55
2	B	801	4CV	O05-S04-C07	-3.47	103.61	107.98
2	D	801	4CV	C07-S04-N03	-3.45	102.79	107.55
2	C	801	4CV	C12-N11-C10	-3.30	108.36	116.19
2	A	801	4CV	C02-N03-S04	-3.25	114.85	119.16
2	C	801	4CV	O05-S04-C07	-3.24	103.89	107.98
2	A	801	4CV	O06-S04-N03	3.18	112.92	107.06
2	D	801	4CV	C12-N11-C10	-3.14	108.73	116.19
2	A	801	4CV	C12-N11-C10	-3.03	108.99	116.19
2	A	801	4CV	O05-S04-C07	-3.01	104.19	107.98
2	A	801	4CV	N18-C19-N20	3.00	122.01	118.38
2	B	801	4CV	C26-C25-N24	-3.00	105.20	107.42
2	B	801	4CV	C12-N11-C10	-2.90	109.29	116.19
2	D	801	4CV	N18-C19-N20	2.84	121.82	118.38
2	B	801	4CV	O06-S04-N03	2.78	112.19	107.06
2	C	801	4CV	O06-S04-N03	2.76	112.15	107.06
2	D	801	4CV	C28-C19-N20	-2.56	116.50	120.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	801	4CV	O06-S04-O05	2.44	122.48	119.52
2	C	801	4CV	N18-C19-N20	2.43	121.32	118.38
2	D	801	4CV	C02-N03-S04	-2.39	115.99	119.16
2	D	801	4CV	C09-C08-C07	-2.21	117.30	119.44
2	B	801	4CV	C02-N03-S04	-2.18	116.27	119.16
2	B	801	4CV	C08-C07-S04	-2.17	117.37	119.76
2	C	801	4CV	C28-C19-N20	-2.10	117.29	120.91
2	D	801	4CV	O06-S04-N03	2.10	110.93	107.06
2	C	801	4CV	C16-N11-C10	-2.04	111.34	116.19

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	4CV	C02-N03-S04-O05
2	A	801	4CV	C02-N03-S04-O06
2	A	801	4CV	C02-N03-S04-C07
2	B	801	4CV	C02-N03-S04-O06
2	B	801	4CV	C02-N03-S04-C07
2	C	801	4CV	C02-N03-S04-O05
2	C	801	4CV	C02-N03-S04-O06
2	C	801	4CV	C02-N03-S04-C07
2	D	801	4CV	C02-N03-S04-O06
2	D	801	4CV	C02-N03-S04-C07
2	C	801	4CV	C29-C07-S04-O05
2	A	801	4CV	C29-C07-S04-O05
2	C	801	4CV	C08-C07-S04-O05
2	D	801	4CV	C29-C07-S04-O05
2	A	801	4CV	C08-C07-S04-O05
2	B	801	4CV	C29-C07-S04-O05
2	D	801	4CV	C08-C07-S04-O05
2	B	801	4CV	C08-C07-S04-O05
2	C	801	4CV	C29-C07-S04-N03
2	B	801	4CV	C02-N03-S04-O05
2	D	801	4CV	C02-N03-S04-O05
2	A	801	4CV	C29-C07-S04-N03
2	C	801	4CV	C08-C07-S04-N03
2	D	801	4CV	C29-C07-S04-N03
2	A	801	4CV	C08-C07-S04-N03
2	B	801	4CV	C29-C07-S04-N03
2	D	801	4CV	C08-C07-S04-N03
2	B	801	4CV	C08-C07-S04-N03

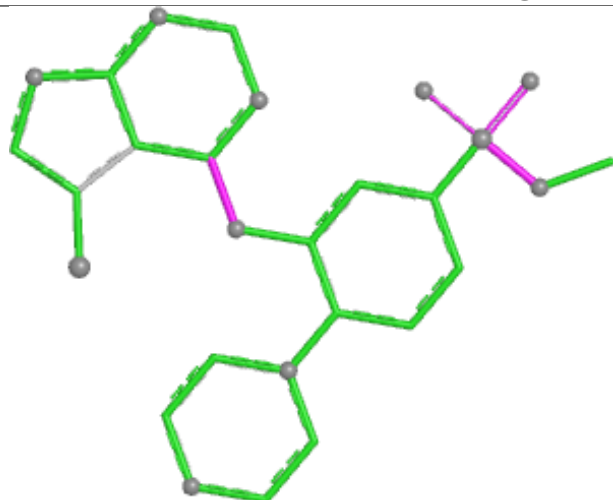
There are no ring outliers.

4 monomers are involved in 7 short contacts:

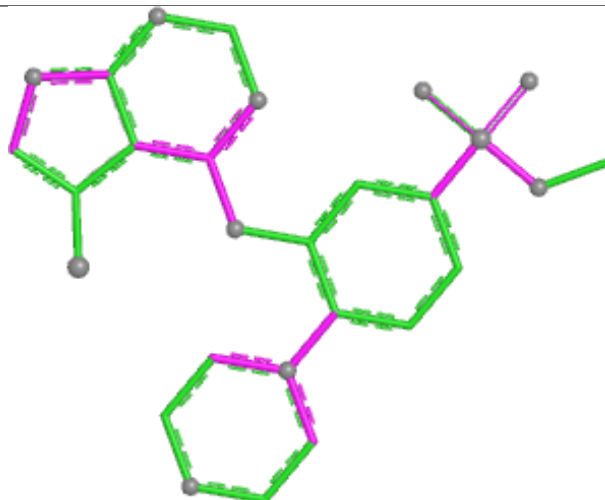
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	801	4CV	3	0
2	A	801	4CV	1	0
2	B	801	4CV	2	0
2	D	801	4CV	1	0

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.

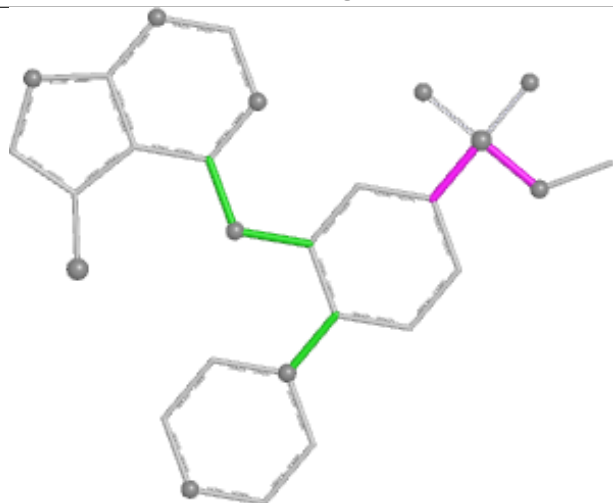
Ligand 4CV C 801



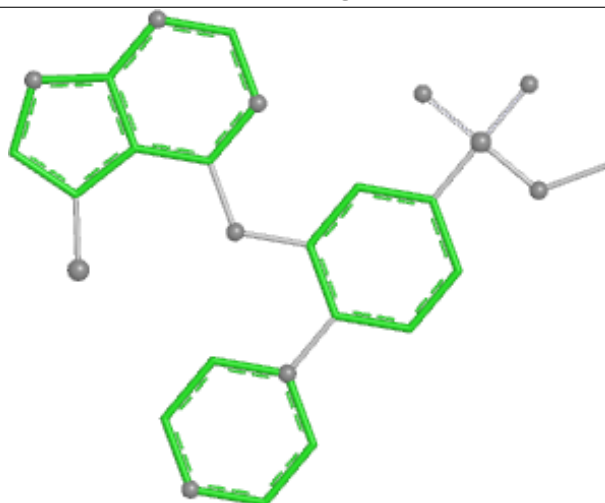
Bond lengths



Bond angles

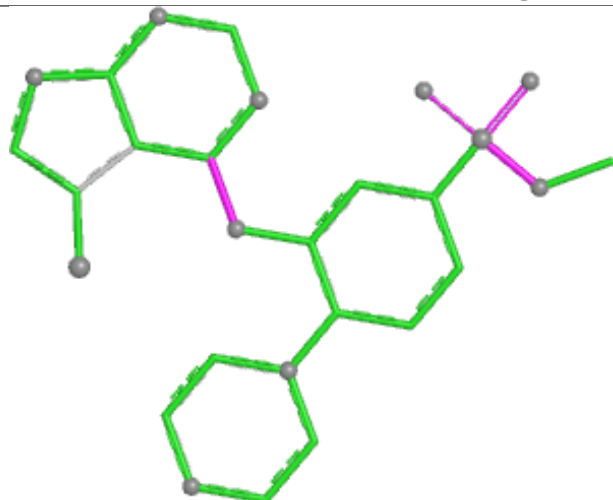


Torsions

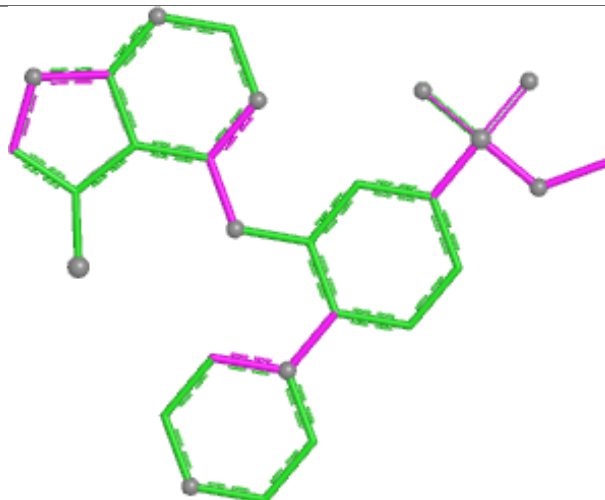


Rings

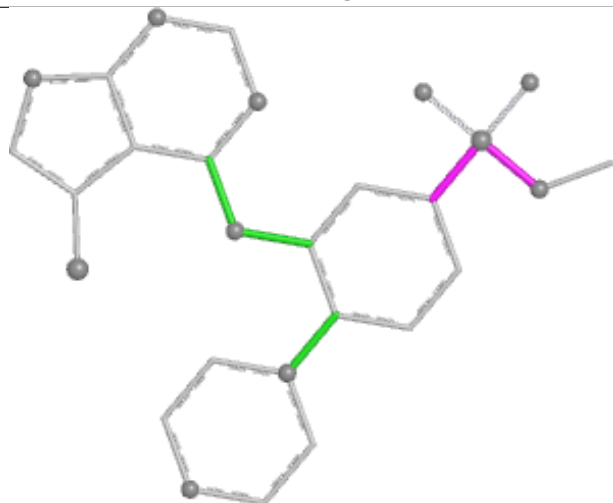
Ligand 4CV A 801



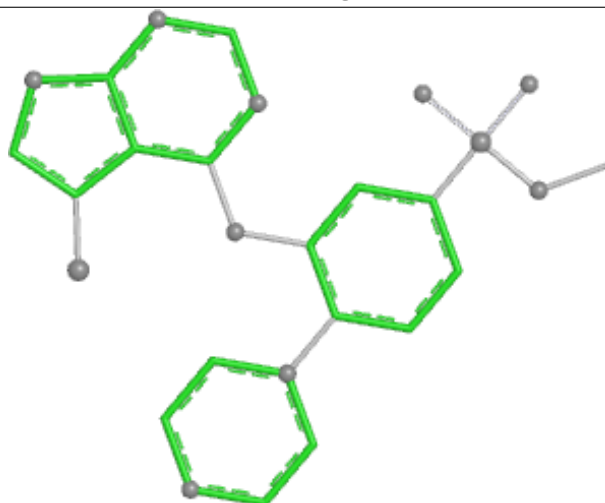
Bond lengths



Bond angles

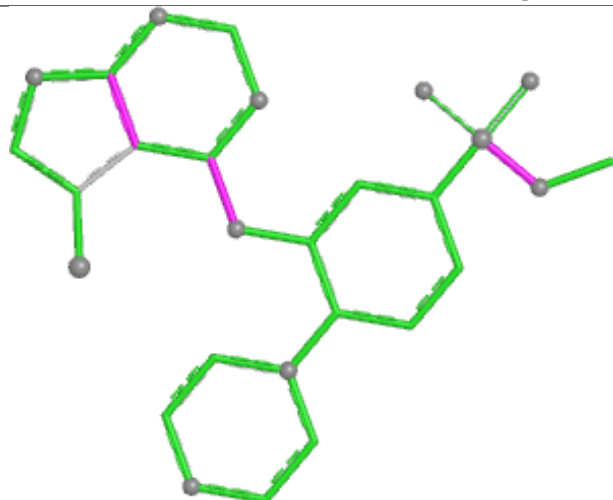


Torsions

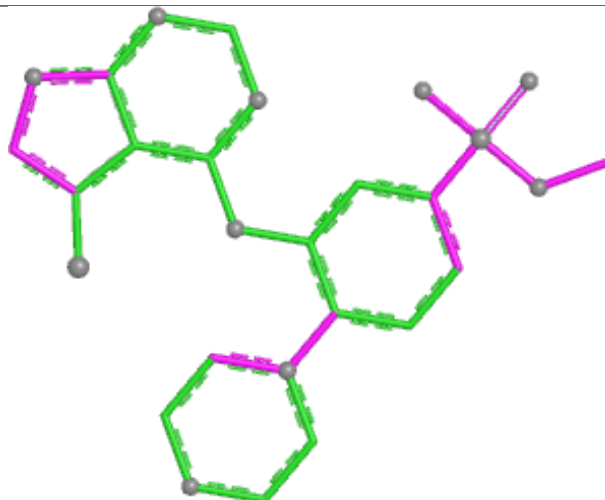


Rings

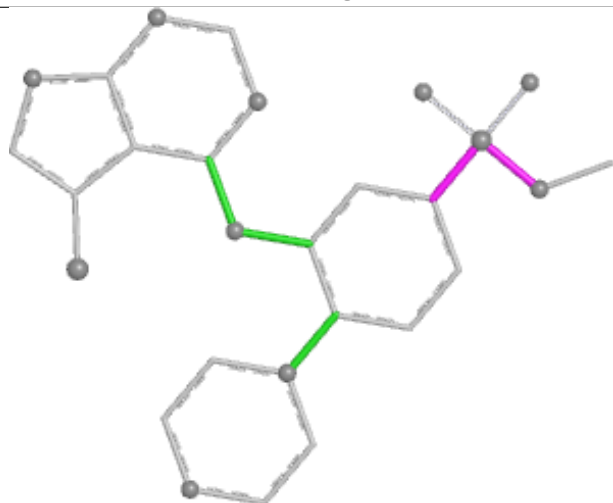
Ligand 4CV B 801



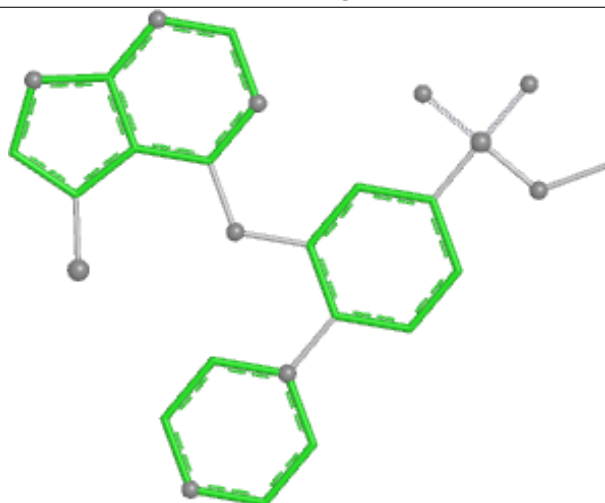
Bond lengths



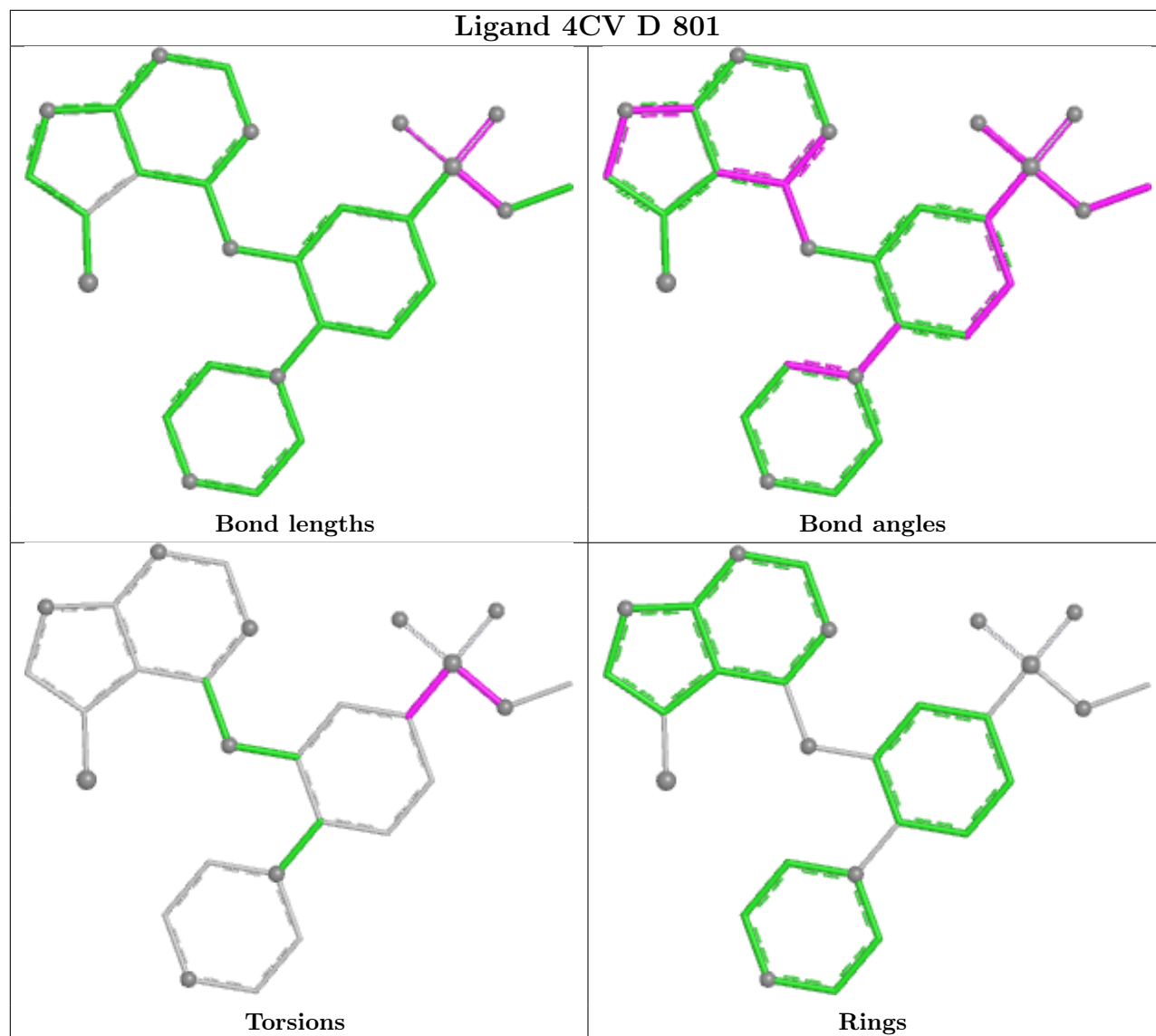
Bond angles



Torsions



Rings



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	264/311 (84%)	-0.18	5 (1%) 66 44	54, 79, 121, 173	0
1	B	264/311 (84%)	-0.29	0 100 100	55, 78, 125, 178	0
1	C	258/311 (82%)	-0.22	7 (2%) 56 33	64, 88, 126, 162	0
1	D	257/311 (82%)	-0.29	5 (1%) 66 44	57, 80, 120, 142	1 (0%)
All	All	1043/1244 (83%)	-0.24	17 (1%) 70 47	54, 80, 125, 178	1 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	626	GLY	4.0
1	D	492	TYR	3.7
1	A	445	ILE	3.6
1	D	615	SER	3.4
1	A	628	LEU	3.4
1	D	681	HIS	3.2
1	C	501	SER	3.1
1	D	452	LEU	3.1
1	C	502	ASP	3.0
1	C	615	SER	2.8
1	A	726	ILE	2.8
1	C	681	HIS	2.8
1	C	492	TYR	2.5
1	C	625	PRO	2.3
1	A	501	SER	2.1
1	D	502	ASP	2.1
1	A	474	PHE	2.1

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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

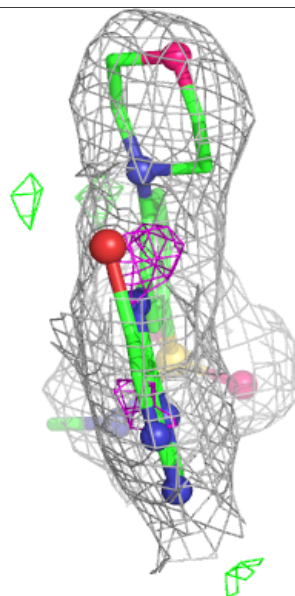
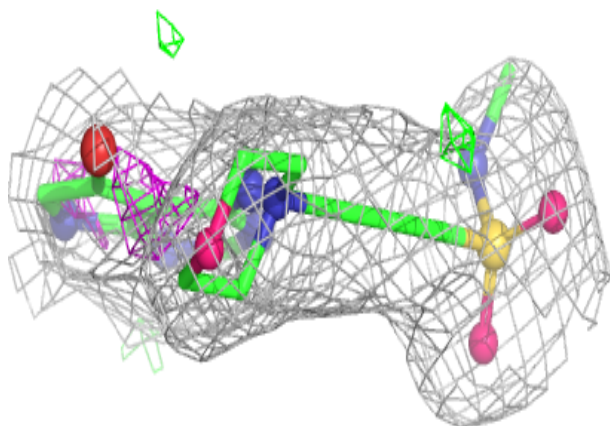
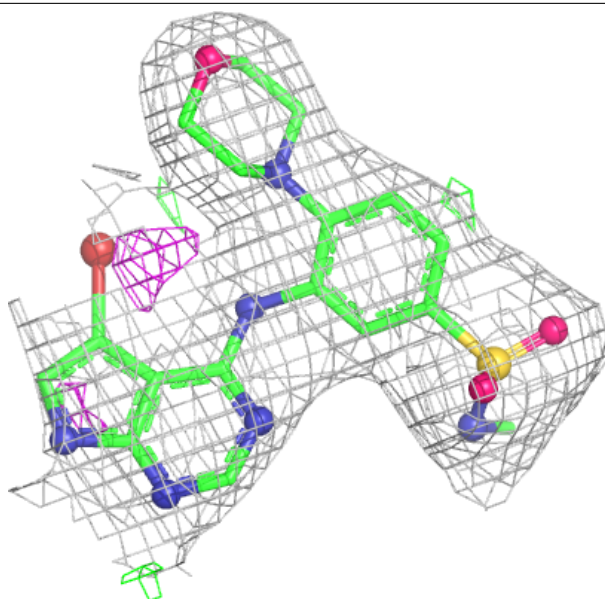
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	4CV	D	801	28/28	0.95	0.08	52,62,84,97	0
2	4CV	C	801	28/28	0.96	0.08	61,77,95,116	0
2	4CV	B	801	28/28	0.96	0.07	55,65,77,106	0
2	4CV	A	801	28/28	0.98	0.06	52,61,69,93	0

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

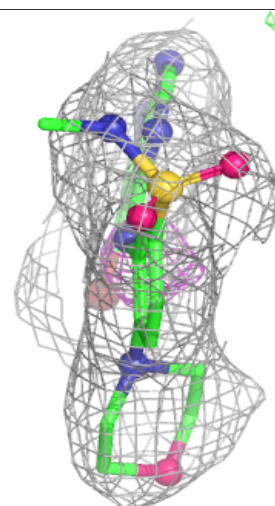
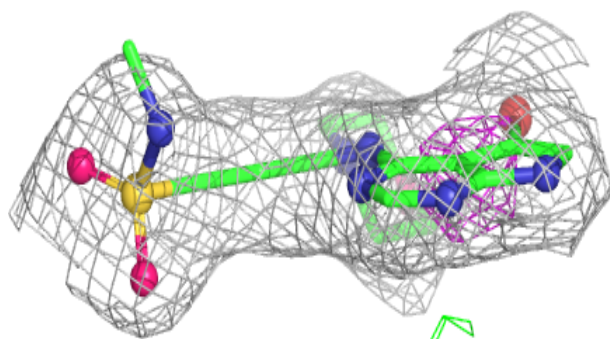
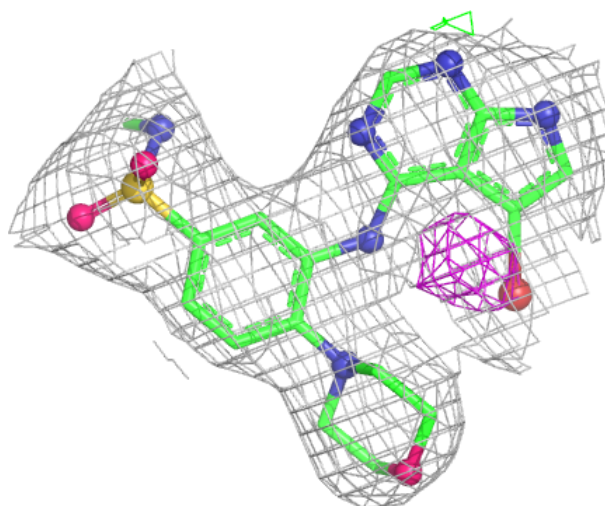
Electron density around 4CV D 801:

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



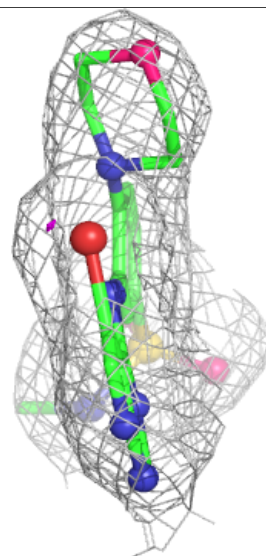
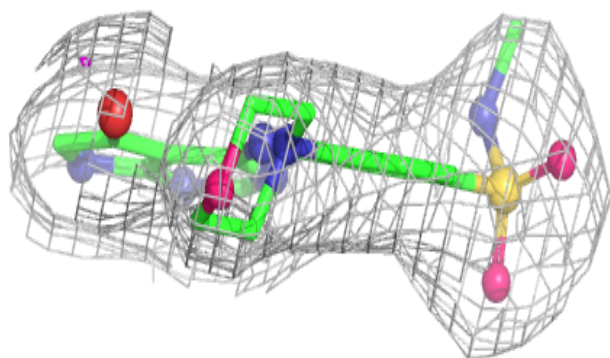
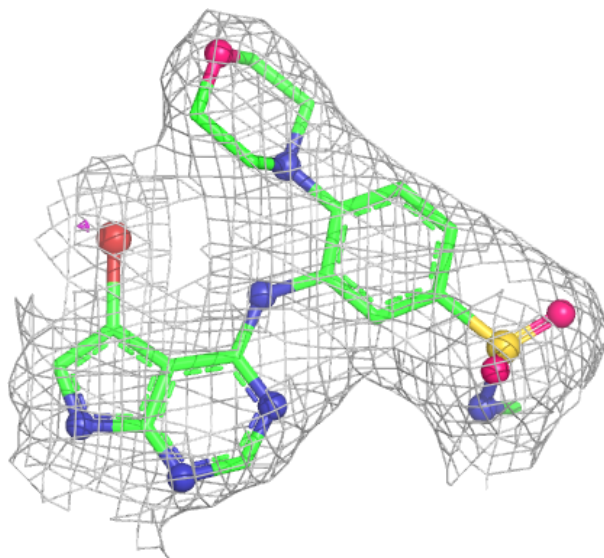
Electron density around 4CV C 801:

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



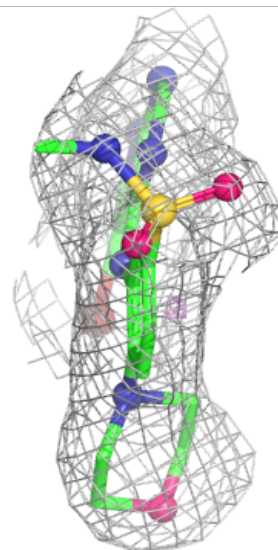
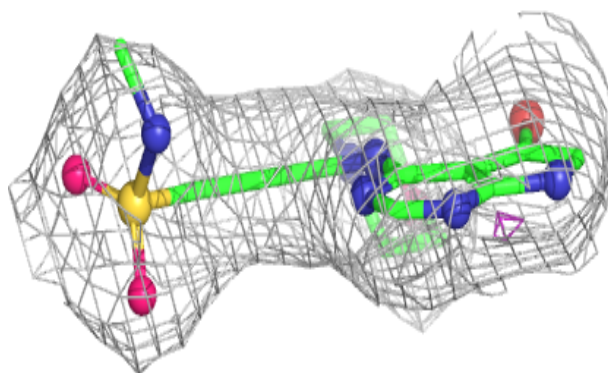
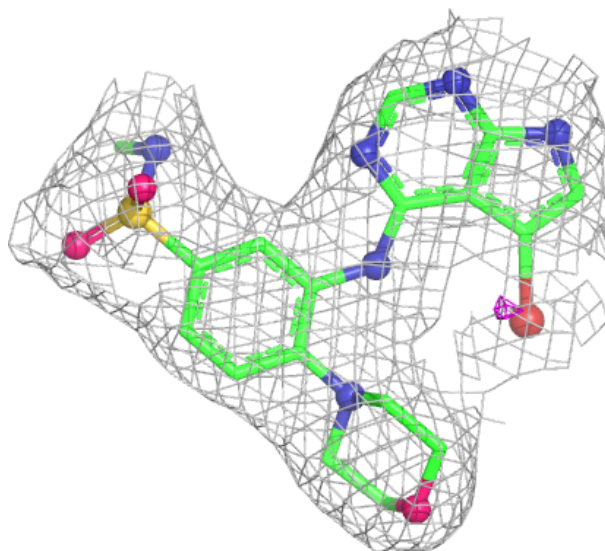
Electron density around 4CV B 801:

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



Electron density around 4CV A 801:

$2mF_o-DF_c$ (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.