



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:38 AM UTC

PDB ID : 7KKN / pdb_00007kkn
Title : Structure of the catalytic domain of tankyrase 1 in complex with talazoparib
Authors : Gajiwala, K.S.; Ryan, K.
Deposited on : 2020-10-27
Resolution : 1.48 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

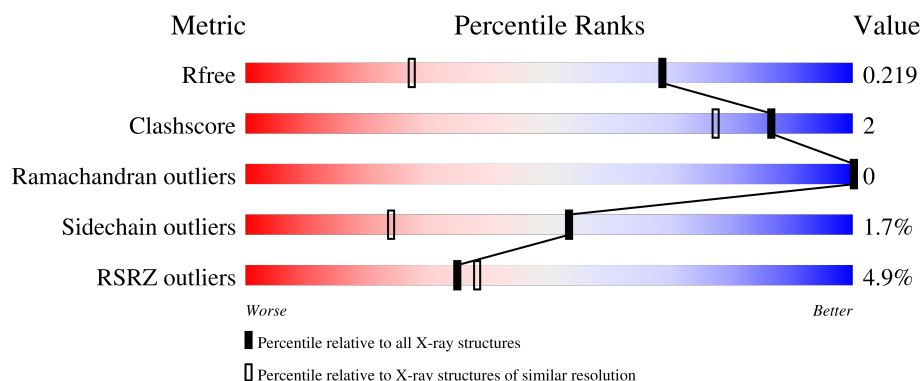
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.48 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	6779 (1.50-1.46)
Clashscore	190562	7025 (1.50-1.46)
Ramachandran outliers	187476	6917 (1.50-1.46)
Sidechain outliers	187428	6914 (1.50-1.46)
RSRZ outliers	180081	6781 (1.50-1.46)

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	213	2% 92% 6% .
1	B	213	2% 93% 5% .
1	C	213	12% 91% 6% .
1	D	213	3% 94% 5% .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7871 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 Poly [ADP-ribose] polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	3	0
			1686	1059	309	305	13			
1	B	210	Total	C	N	O	S	0	1	0
			1697	1067	310	307	13			
1	C	207	Total	C	N	O	S	0	1	0
			1682	1062	306	302	12			
1	D	210	Total	C	N	O	S	0	3	0
			1715	1079	313	310	13			

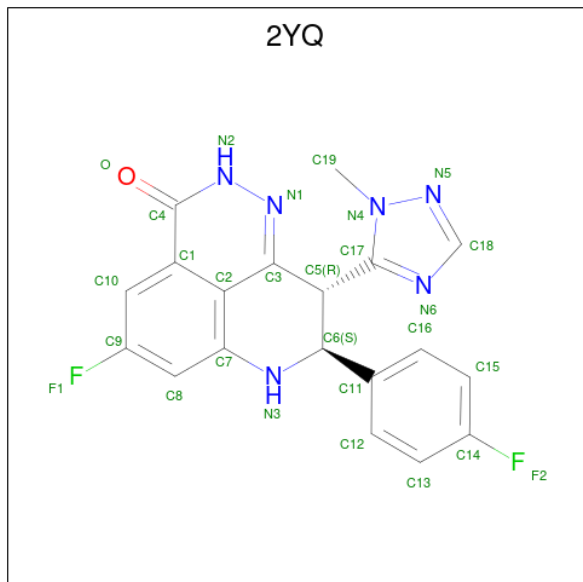
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1102	GLY	-	expression tag	UNP Q59FX0
A	1103	SER	-	expression tag	UNP Q59FX0
B	1102	GLY	-	expression tag	UNP Q59FX0
B	1103	SER	-	expression tag	UNP Q59FX0
C	1102	GLY	-	expression tag	UNP Q59FX0
C	1103	SER	-	expression tag	UNP Q59FX0
D	1102	GLY	-	expression tag	UNP Q59FX0
D	1103	SER	-	expression tag	UNP Q59FX0

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

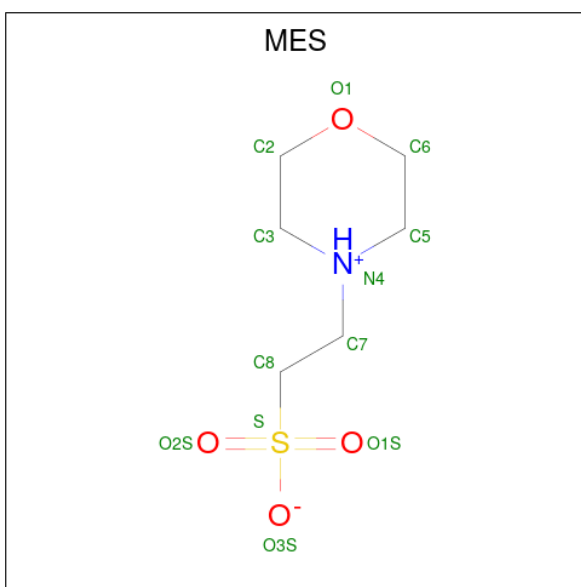
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is (8S,9R)-5-fluoro-8-(4-fluorophenyl)-9-(1-methyl-1H-1,2,4-triazol-5-yl)-2,7,8,9-tetrahydro-3H-pyrido[4,3,2-de]phthalazin-3-one (CCD ID: 2YQ) (formula: C₁₉H₁₄F₂N₆O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			28	19	2	6	1		
3	B	1	Total	C	F	N	O	0	0
			28	19	2	6	1		
3	C	1	Total	C	F	N	O	0	0
			28	19	2	6	1		
3	D	1	Total	C	F	N	O	0	0
			28	19	2	6	1		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

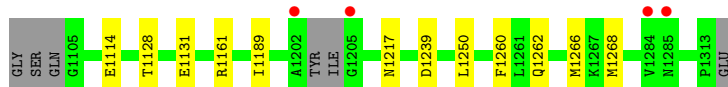
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	290	Total	O	0	0
			290	290		
5	B	288	Total	O	0	0
			288	288		
5	C	159	Total	O	0	0
			159	159		
5	D	214	Total	O	0	0
			214	214		

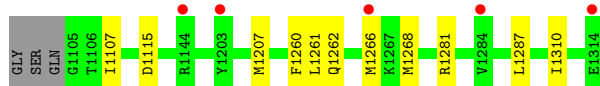
3 Residue-property plots [i](#)

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.

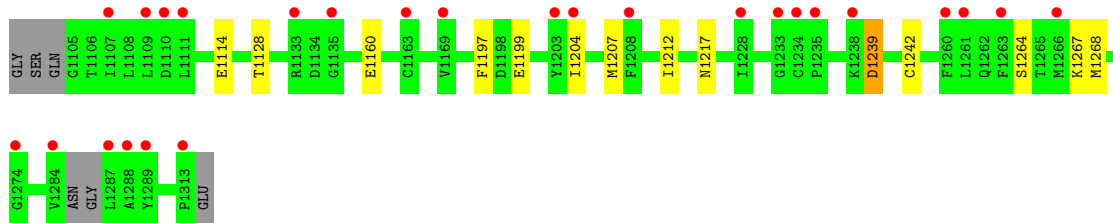
- Molecule 1: Poly [ADP-ribose] polymerase



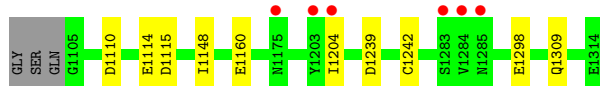
- Molecule 1: Poly [ADP-ribose] polymerase



- Molecule 1: Poly [ADP-ribose] polymerase



- Molecule 1: Poly [ADP-ribose] polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.66Å 113.86Å 83.35Å 90.00° 91.03° 90.00°	Depositor
Resolution (Å)	21.52 – 1.48 21.52 – 1.48	Depositor EDS
% Data completeness (in resolution range)	72.8 (21.52-1.48) 73.1 (21.52-1.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 1.48Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.184 , 0.215 0.187 , 0.219	Depositor DCC
R_{free} test set	5403 reflections (3.57%)	wwPDB-VP
Wilson B-factor (Å ²)	15.7	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.065 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7871	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% 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: ZN, 2YQ, MES

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	0.83	0/1727	1.06	1/2319 (0.0%)
1	B	0.85	0/1740	1.10	2/2339 (0.1%)
1	C	0.83	0/1725	1.12	2/2318 (0.1%)
1	D	0.82	0/1758	1.08	2/2363 (0.1%)
All	All	0.83	0/6950	1.09	7/9339 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	1115	ASP	CA-CB-CG	6.70	119.30	112.60
1	B	1115	ASP	CA-CB-CG	6.62	119.22	112.60
1	D	1160	GLU	CB-CG-CD	5.93	122.68	112.60
1	B	1310	ILE	N-CA-C	-5.74	103.79	110.05
1	A	1239	ASP	CA-CB-CG	5.49	118.09	112.60
1	C	1199	GLU	CB-CG-CD	5.40	121.77	112.60
1	C	1239	ASP	CA-CB-CG	5.33	117.93	112.60

There are no chirality outliers.

There are no planarity outliers.

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	1686	0	1620	12	0
1	B	1697	0	1630	10	0
1	C	1682	0	1618	4	0
1	D	1715	0	1649	2	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	28	0	14	0	0
3	B	28	0	14	0	0
3	C	28	0	14	0	0
3	D	28	0	14	0	0
4	A	12	0	13	0	0
4	B	12	0	13	0	0
5	A	290	0	0	0	0
5	B	288	0	0	0	0
5	C	159	0	0	0	0
5	D	214	0	0	0	0
All	All	7871	0	6599	28	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 2.

All (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1266[B]:MET:HE3	1:A:1268:MET:CE	2.05	0.86
1:B:1266:MET:HE3	1:B:1268:MET:HE1	1.68	0.75
1:B:1266:MET:HE3	1:B:1268:MET:CE	2.16	0.75
1:A:1266[B]:MET:HE3	1:A:1268:MET:HE3	1.72	0.69
1:B:1260:PHE:CD2	1:B:1266:MET:HE1	2.30	0.67
1:B:1262:GLN:HG3	1:B:1266:MET:HE2	1.77	0.67
1:A:1266[B]:MET:HE3	1:A:1268:MET:HE1	1.79	0.64
1:A:1262:GLN:HG3	1:A:1266[B]:MET:HE2	1.78	0.64
1:B:1266:MET:CE	1:B:1268:MET:HE1	2.31	0.59
1:B:1260:PHE:HD2	1:B:1266:MET:HE1	1.65	0.58
1:A:1260:PHE:CD2	1:A:1266[B]:MET:HE1	2.41	0.54
1:A:1262:GLN:HG3	1:A:1266[B]:MET:CE	2.38	0.53
1:C:1204:ILE:HG13	1:C:1267:LYS:HD3	1.91	0.53
1:C:1128:THR:HB	1:C:1217:ASN:HA	1.93	0.51
1:A:1266[B]:MET:CE	1:A:1268:MET:HE1	2.40	0.51
1:A:1189:ILE:HD13	1:A:1250:LEU:HG	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1128:THR:HB	1:A:1217:ASN:HA	1.94	0.50
1:C:1239:ASP:HB3	1:C:1242:CYS:HB2	1.94	0.49
1:A:1260:PHE:HD2	1:A:1266[B]:MET:HE1	1.77	0.48
1:D:1148[B]:ILE:HD11	1:D:1309:GLN:HG3	1.96	0.47
1:A:1131[A]:GLU:H	1:A:1131[A]:GLU:CD	2.23	0.46
1:B:1207:MET:SD	1:B:1287:LEU:HD21	2.55	0.46
1:C:1197:PHE:HB3	1:C:1212:ILE:HD13	1.98	0.46
1:B:1261:LEU:HD21	1:B:1281:ARG:HG3	1.97	0.46
1:D:1239:ASP:HB3	1:D:1242:CYS:HB2	1.99	0.45
1:B:1266:MET:HE3	1:B:1268:MET:HE3	1.99	0.43
1:A:1260:PHE:HE2	1:A:1266[B]:MET:SD	2.44	0.41
1:B:1260:PHE:CE2	1:B:1266:MET:HE1	2.55	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	206/213 (97%)	203 (98%)	3 (2%)	0	100	100
1	B	209/213 (98%)	205 (98%)	4 (2%)	0	100	100
1	C	204/213 (96%)	203 (100%)	1 (0%)	0	100	100
1	D	211/213 (99%)	210 (100%)	1 (0%)	0	100	100
All	All	830/852 (97%)	821 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	178/180 (99%)	176 (99%)	2 (1%)	65	40
1	B	179/180 (99%)	178 (99%)	1 (1%)	78	60
1	C	177/180 (98%)	172 (97%)	5 (3%)	38	10
1	D	181/180 (101%)	177 (98%)	4 (2%)	45	16
All	All	715/720 (99%)	703 (98%)	12 (2%)	53	24

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

Mol	Chain	Res	Type
1	A	1114	GLU
1	A	1161	ARG
1	B	1107	ILE
1	C	1114	GLU
1	C	1160	GLU
1	C	1207	MET
1	C	1264	SER
1	C	1268	MET
1	D	1110	ASP
1	D	1114	GLU
1	D	1204	ILE
1	D	1298	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1248	GLN
1	A	1285	ASN
1	B	1174	HIS
1	B	1177	HIS
1	B	1248	GLN
1	C	1151	GLN
1	C	1166	GLN
1	C	1190	ASN
1	C	1248	GLN
1	C	1262	GLN
1	D	1151	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	1248	GLN
1	D	1262	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	2YQ	A	9002	-	31,32,32	1.22	3 (9%)	34,48,48	1.67	6 (17%)
3	2YQ	B	9002	-	31,32,32	1.09	1 (3%)	34,48,48	1.52	6 (17%)
3	2YQ	C	9002	-	31,32,32	1.23	1 (3%)	34,48,48	1.52	4 (11%)
4	MES	B	9003	-	12,12,12	0.78	0	15,16,16	0.37	0
4	MES	A	9003	-	12,12,12	0.76	0	15,16,16	0.41	0
3	2YQ	D	9002	-	31,32,32	1.14	2 (6%)	34,48,48	1.47	7 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	2YQ	A	9002	-	-	0/6/20/20	0/5/5/5
3	2YQ	B	9002	-	-	0/6/20/20	0/5/5/5
3	2YQ	C	9002	-	-	0/6/20/20	0/5/5/5
4	MES	B	9003	-	-	1/6/14/14	0/1/1/1
4	MES	A	9003	-	-	0/6/14/14	0/1/1/1
3	2YQ	D	9002	-	-	0/6/20/20	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	9002	2YQ	C17-N4	3.41	1.37	1.34
3	B	9002	2YQ	C17-N4	3.06	1.36	1.34
3	D	9002	2YQ	C17-N4	2.89	1.36	1.34
3	C	9002	2YQ	C17-N4	2.51	1.36	1.34
3	A	9002	2YQ	C4-N2	2.35	1.39	1.35
3	A	9002	2YQ	C5-C17	2.23	1.52	1.50
3	D	9002	2YQ	C4-N2	2.10	1.38	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	9002	2YQ	C16-C11-C12	4.54	123.94	118.30
3	C	9002	2YQ	C11-C6-N3	4.41	119.76	111.04
3	C	9002	2YQ	C1-C2-C7	4.33	122.96	118.86
3	B	9002	2YQ	C16-C11-C12	4.06	123.33	118.30
3	A	9002	2YQ	C1-C2-C7	3.79	122.44	118.86
3	A	9002	2YQ	C15-C16-C11	-3.56	117.63	121.18
3	D	9002	2YQ	C16-C11-C12	3.43	122.55	118.30
3	B	9002	2YQ	C1-C2-C7	3.33	122.01	118.86
3	D	9002	2YQ	O-C4-N2	3.27	125.07	120.88
3	B	9002	2YQ	C15-C16-C11	-3.05	118.13	121.18
3	A	9002	2YQ	C13-C12-C11	-3.02	118.16	121.18
3	B	9002	2YQ	C13-C12-C11	-2.84	118.35	121.18
3	D	9002	2YQ	C13-C12-C11	-2.76	118.43	121.18
3	A	9002	2YQ	O-C4-N2	2.72	124.35	120.88
3	C	9002	2YQ	O-C4-N2	2.53	124.12	120.88
3	B	9002	2YQ	O-C4-N2	2.50	124.07	120.88
3	D	9002	2YQ	C1-C2-C7	2.39	121.12	118.86
3	D	9002	2YQ	C12-C11-C6	-2.36	117.03	120.78
3	D	9002	2YQ	C15-C16-C11	-2.24	118.95	121.18
3	A	9002	2YQ	C11-C6-N3	2.10	115.19	111.04
3	C	9002	2YQ	C16-C11-C12	2.09	120.89	118.30
3	B	9002	2YQ	C12-C11-C6	-2.04	117.53	120.78

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	9002	2YQ	O-C4-C1	-2.00	119.70	123.27

There are no chirality outliers.

All (1) torsion outliers are listed below:

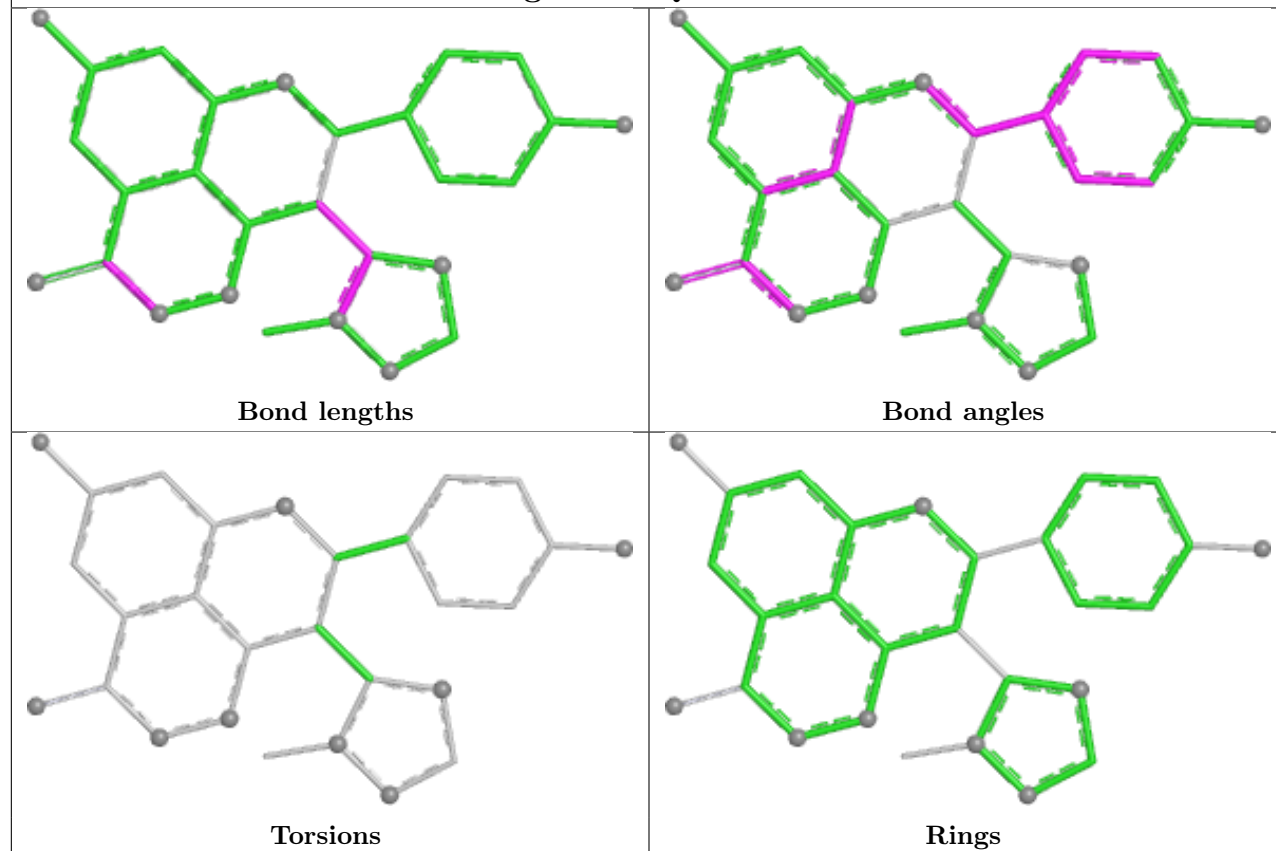
Mol	Chain	Res	Type	Atoms
4	B	9003	MES	C8-C7-N4-C3

There are no ring outliers.

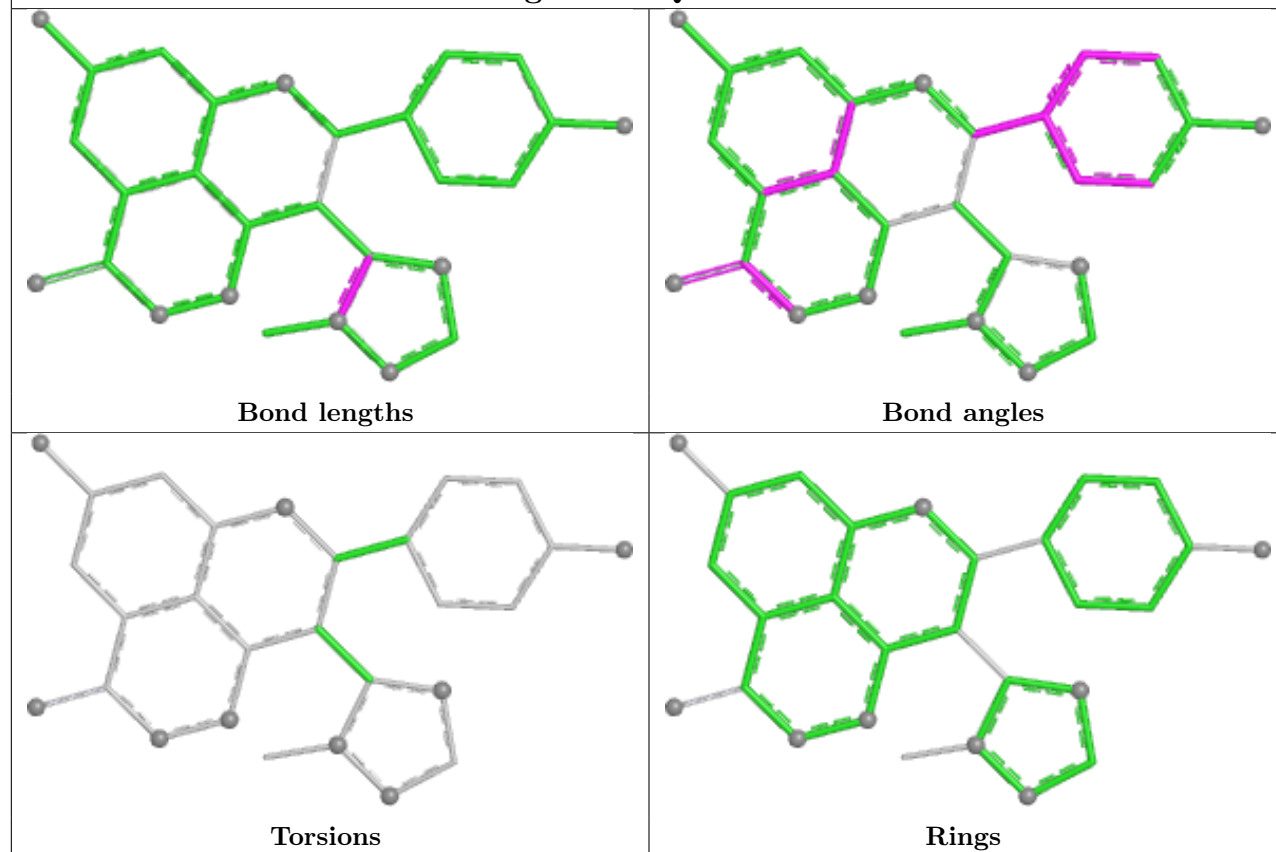
No monomer is involved in short contacts.

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

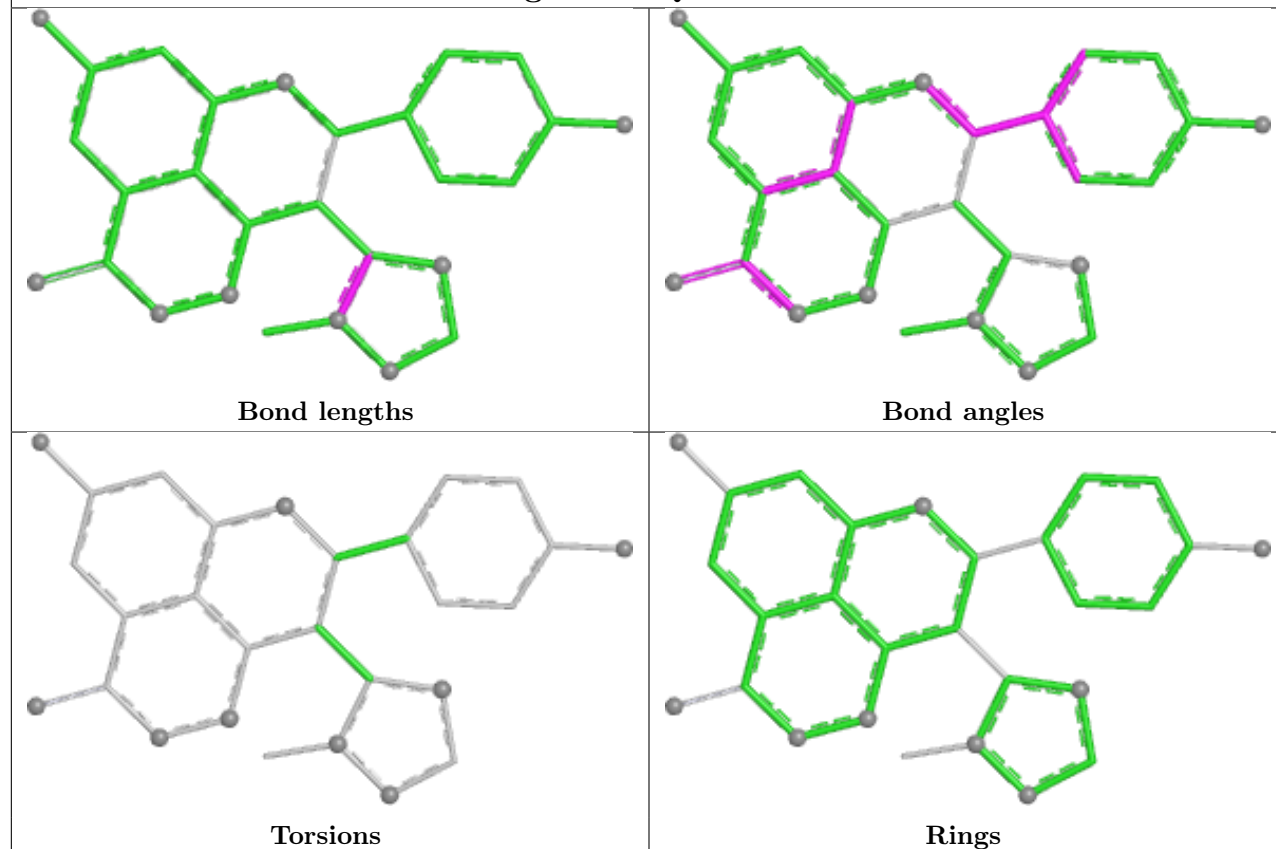
Ligand 2YQ A 9002



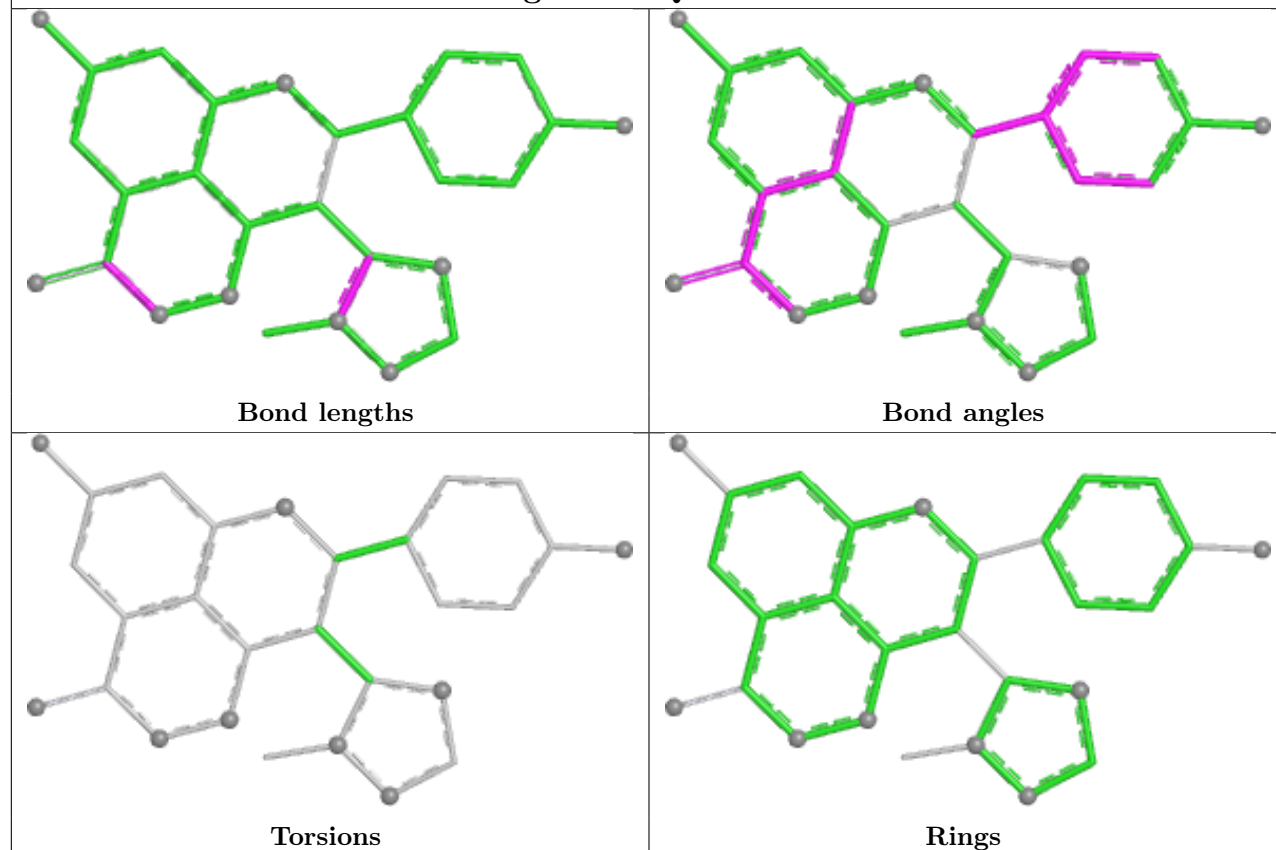
Ligand 2YQ B 9002



Ligand 2YQ C 9002



Ligand 2YQ D 9002



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	207/213 (97%)	-0.24	4 (1%)	66	70	6, 15, 31, 47	3 (1%)
1	B	210/213 (98%)	-0.16	5 (2%)	59	63	8, 15, 38, 57	1 (0%)
1	C	207/213 (97%)	1.02	26 (12%)	8	8	12, 26, 43, 63	1 (0%)
1	D	210/213 (98%)	0.14	6 (2%)	53	58	9, 19, 40, 52	3 (1%)
All	All	834/852 (97%)	0.19	41 (4%)	35	38	6, 19, 40, 63	8 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1284	VAL	5.7
1	B	1284	VAL	5.1
1	D	1284	VAL	4.7
1	B	1203	TYR	4.7
1	C	1228	ILE	3.9
1	D	1204	ILE	3.9
1	C	1203[A]	TYR	3.8
1	C	1169	VAL	3.5
1	C	1288	ALA	3.4
1	D	1203	TYR	3.3
1	C	1261	LEU	3.1
1	A	1284	VAL	3.1
1	C	1109	LEU	3.0
1	C	1204	ILE	2.9
1	C	1234	CYS	2.9
1	D	1285	ASN	2.8
1	B	1314	GLU	2.7
1	C	1135	GLY	2.7
1	C	1163	CYS	2.7
1	D	1283	SER	2.6
1	C	1263	PHE	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	1289	TYR	2.5
1	C	1111	LEU	2.5
1	C	1313	PRO	2.4
1	C	1266	MET	2.4
1	A	1285	ASN	2.4
1	C	1107	ILE	2.3
1	A	1205	GLY	2.3
1	A	1202	ALA	2.3
1	C	1235	PRO	2.3
1	C	1110	ASP	2.3
1	C	1233	GLY	2.2
1	B	1266	MET	2.2
1	C	1260	PHE	2.2
1	C	1133	ARG	2.1
1	C	1287	LEU	2.1
1	C	1238	LYS	2.1
1	C	1274	GLY	2.1
1	C	1208	PHE	2.0
1	D	1175	ASN	2.0
1	B	1144	ARG	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.

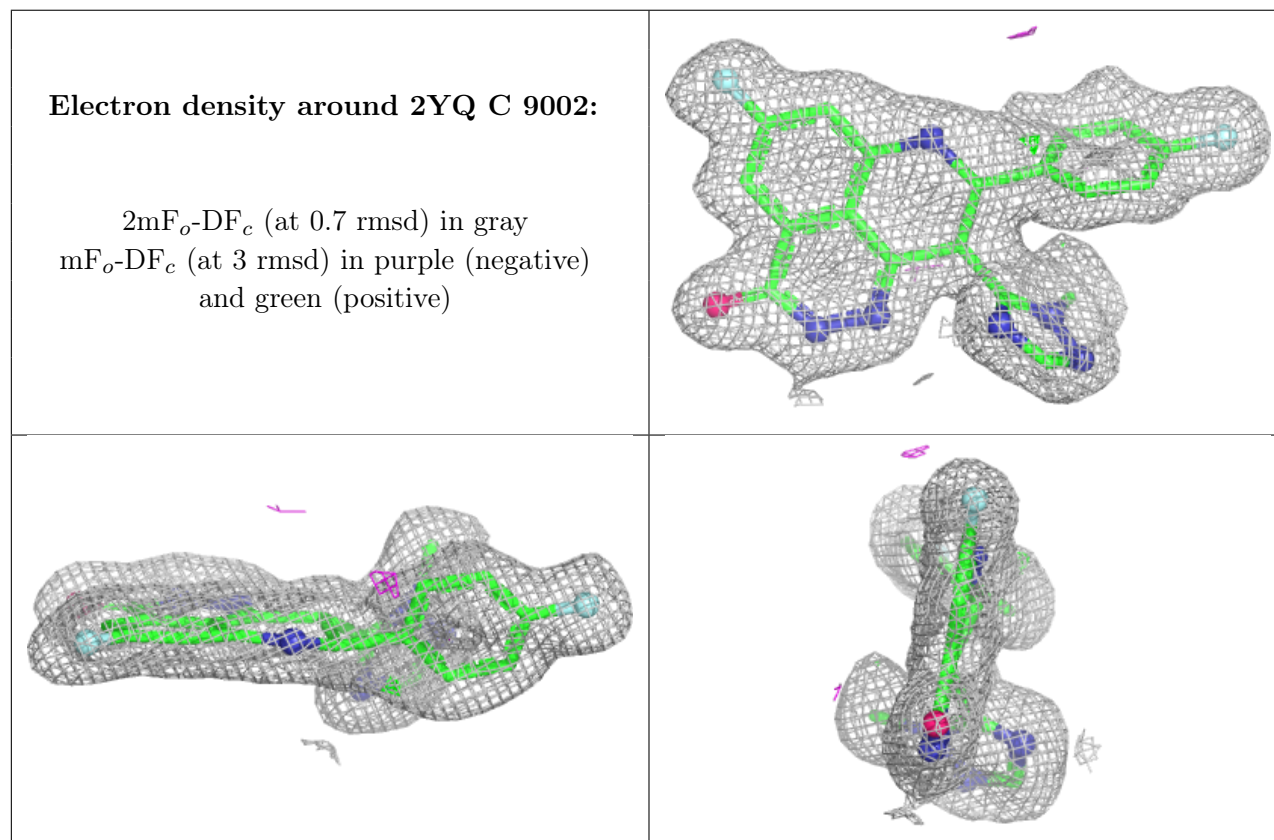
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MES	A	9003	12/12	0.93	0.12	22,32,40,41	0
4	MES	B	9003	12/12	0.93	0.13	22,29,44,44	0
3	2YQ	C	9002	28/28	0.94	0.08	11,19,30,32	0

Continued on next page...

Continued from previous page...

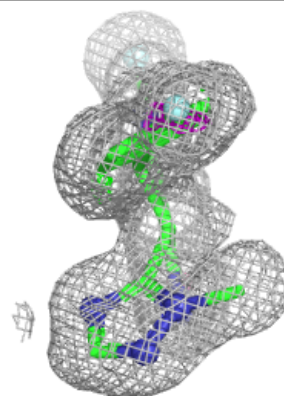
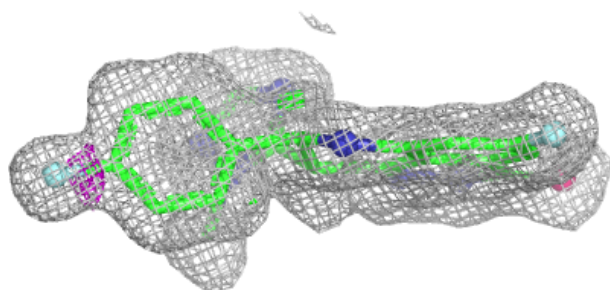
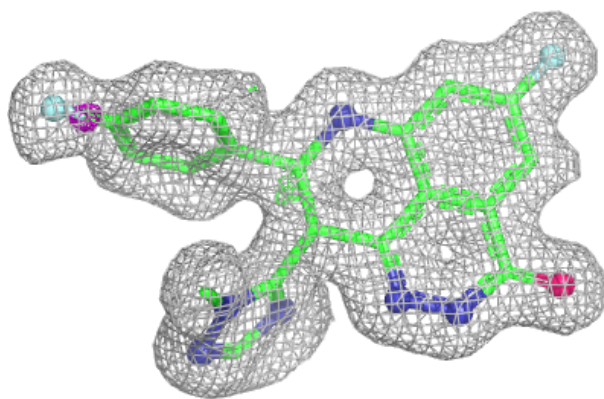
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	C	9001	1/1	0.95	0.06	28,28,28,28	0
3	2YQ	A	9002	28/28	0.96	0.05	7,12,16,26	0
3	2YQ	D	9002	28/28	0.96	0.06	9,15,21,28	0
3	2YQ	B	9002	28/28	0.98	0.04	7,11,18,25	0
2	ZN	B	9001	1/1	0.99	0.04	13,13,13,13	0
2	ZN	A	9001	1/1	0.99	0.03	15,15,15,15	0
2	ZN	D	9001	1/1	0.99	0.03	17,17,17,17	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.

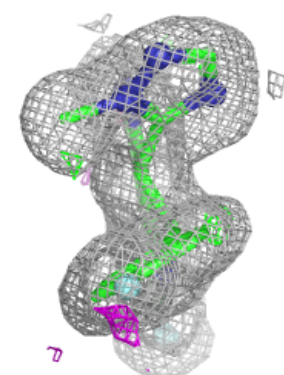
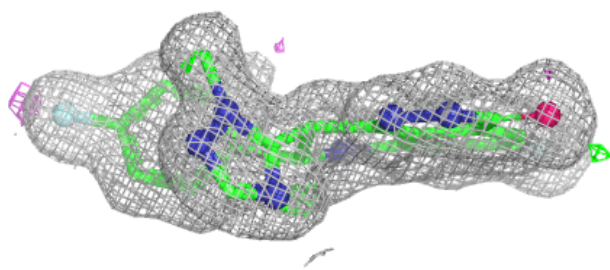
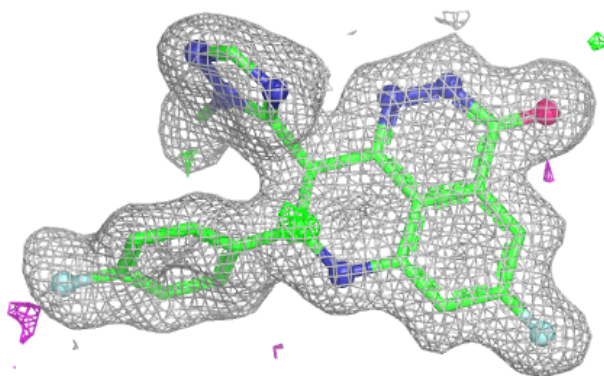


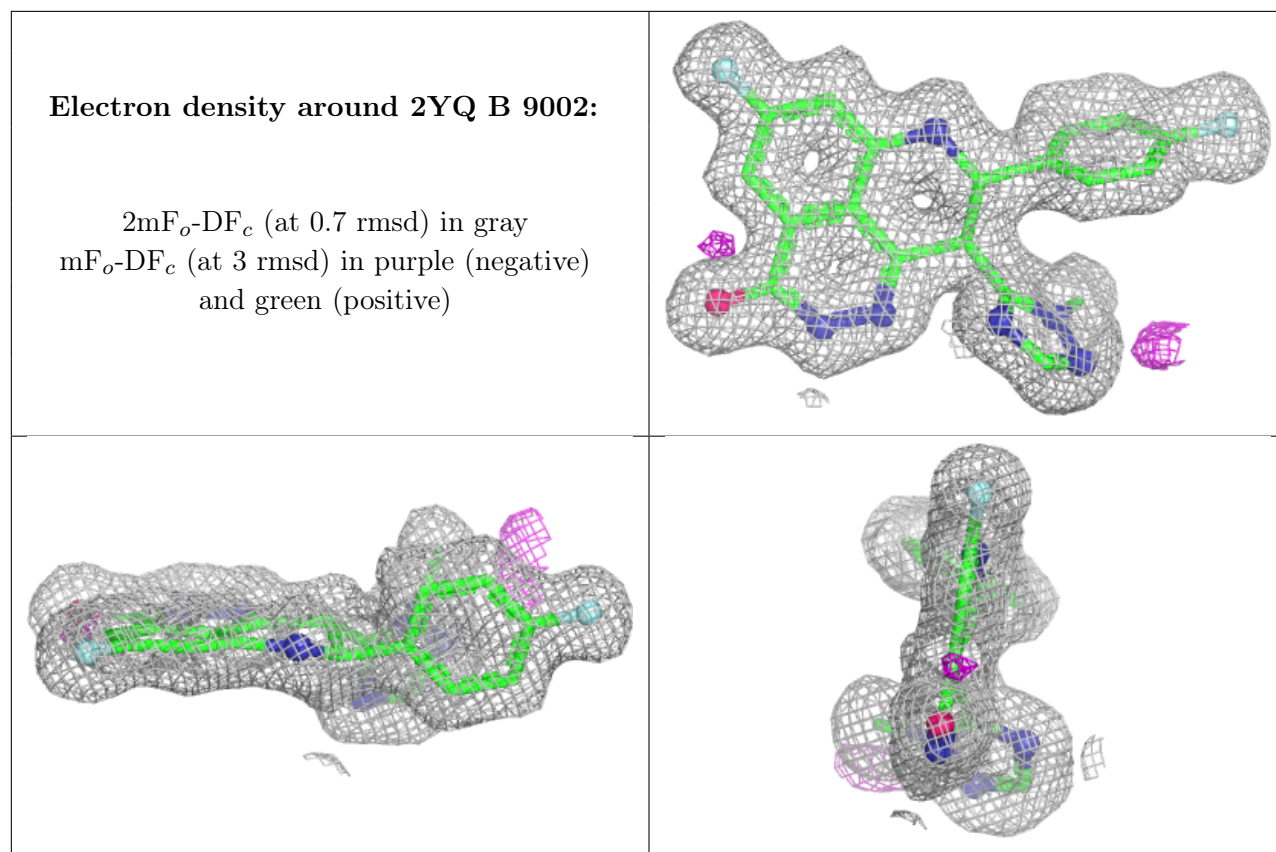
Electron density around 2YQ A 9002:

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

**Electron density around 2YQ D 9002:**

$2mF_o-DF_c$ (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.