



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 28, 2020 – 02:54 PM EST

PDB ID : 7KK3
Title : Structure of the catalytic domain of PARP1 in complex with talazoparib
Authors : Gajiwala, K.S.; Ryan, K.
Deposited on : 2020-10-27
Resolution : 2.06 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.16
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.16

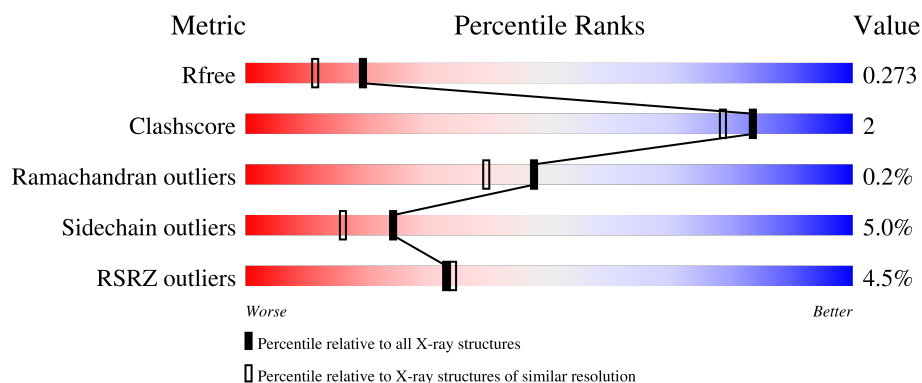
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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}	130704	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	352	 3% 86% 9% • 5%
1	B	352	 3% 85% 10% • •
1	C	352	 % 87% 9% • •
1	D	352	 10% 81% 12% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10984 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.

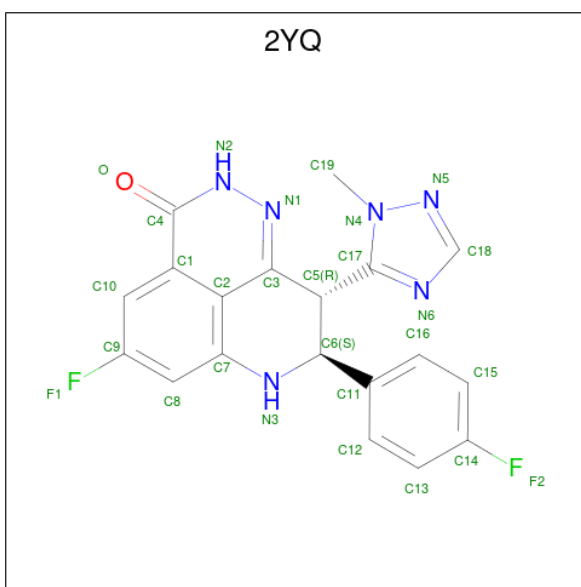
- Molecule 1 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2661	1699	450	502	10			
1	B	337	Total	C	N	O	S	0	0	0
			2661	1701	447	503	10			
1	C	340	Total	C	N	O	S	0	0	0
			2675	1701	451	513	10			
1	D	328	Total	C	N	O	S	0	0	0
			2594	1660	437	487	10			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	660	GLY	-	expression tag	UNP P09874
A	661	SER	-	expression tag	UNP P09874
B	660	GLY	-	expression tag	UNP P09874
B	661	SER	-	expression tag	UNP P09874
C	660	GLY	-	expression tag	UNP P09874
C	661	SER	-	expression tag	UNP P09874
D	660	GLY	-	expression tag	UNP P09874
D	661	SER	-	expression tag	UNP P09874

- Molecule 2 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 (three-letter code: 2YQ) (formula: C₁₉H₁₄F₂N₆O) (labeled as "Ligand of Interest" by depositor).



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

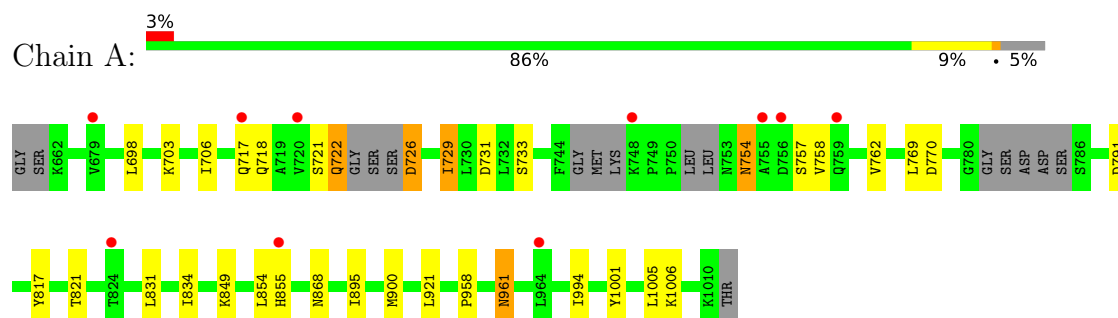
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	79	Total	O	0	0
			79	79		
3	B	56	Total	O	0	0
			56	56		
3	C	92	Total	O	0	0
			92	92		
3	D	54	Total	O	0	0
			54	54		

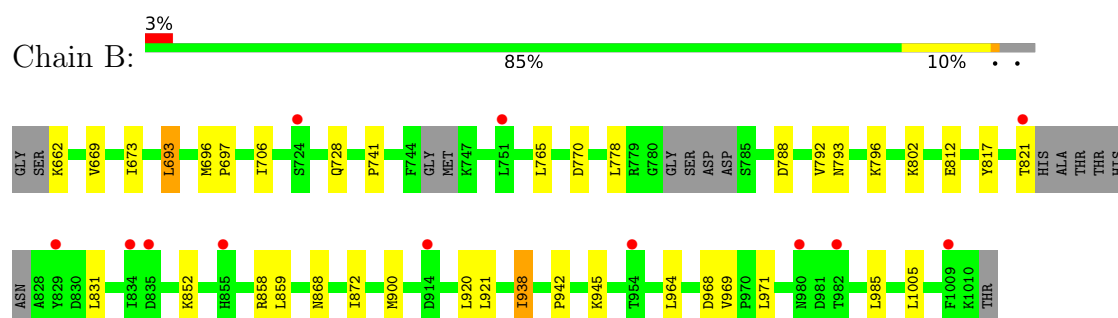
3 Residue-property plots [i](#)

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.

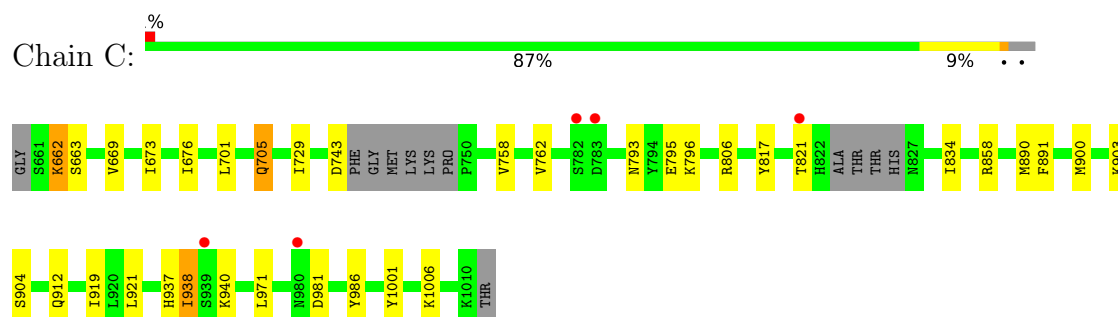
- Molecule 1: Poly [ADP-ribose] polymerase 1



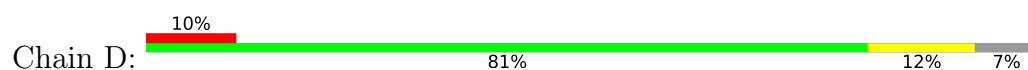
- Molecule 1: Poly [ADP-ribose] polymerase 1

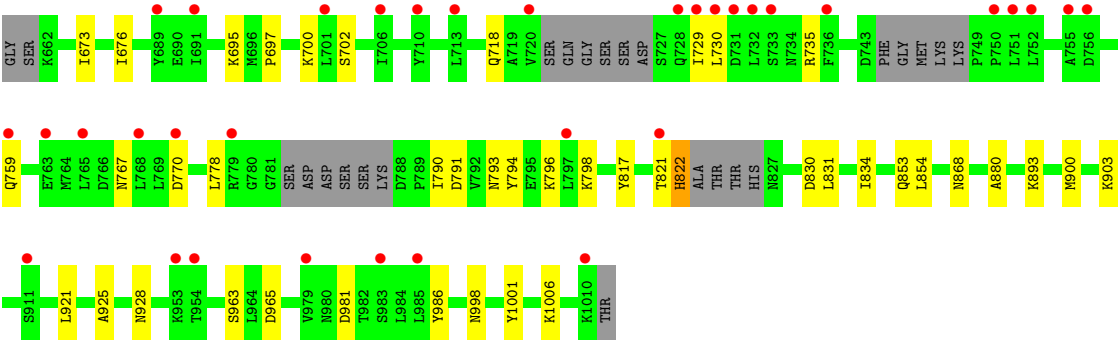


- Molecule 1: Poly [ADP-ribose] polymerase 1



- Molecule 1: Poly [ADP-ribose] polymerase 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.48Å 107.68Å 143.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	86.12 – 2.06 86.12 – 2.06	Depositor EDS
% Data completeness (in resolution range)	79.1 (86.12-2.06) 79.2 (86.12-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.07Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.213 , 0.259 0.218 , 0.273	Depositor DCC
R_{free} test set	4066 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.009 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10984	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 2YQ

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	0.51	0/2709	0.68	0/3652
1	B	0.50	0/2708	0.67	0/3649
1	C	0.52	0/2722	0.71	1/3670 (0.0%)
1	D	0.48	0/2640	0.68	0/3559
All	All	0.50	0/10779	0.68	1/14530 (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	C	937	HIS	C-N-CA	5.62	135.75	121.70

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	2661	0	2703	12	0
1	B	2661	0	2718	15	0
1	C	2675	0	2712	12	0
1	D	2594	0	2646	12	0
2	A	28	0	14	0	0
2	B	28	0	14	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	28	0	14	0	0
2	D	28	0	14	0	0
3	A	79	0	0	0	0
3	B	56	0	0	0	0
3	C	92	0	0	0	0
3	D	54	0	0	0	0
All	All	10984	0	10835	50	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 (50) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:821:THR:HB	1:C:900:MET:HA	1.63	0.78
1:B:821:THR:HB	1:B:900:MET:HA	1.72	0.72
1:B:942:PRO:HG2	1:B:945:LYS:HG3	1.75	0.68
1:C:903:LYS:HD2	1:C:986:TYR:HB2	1.75	0.68
1:D:697:PRO:HD2	1:D:700:LYS:HB2	1.77	0.66
1:C:834:ILE:HD11	1:C:1006:LYS:HB2	1.81	0.61
1:A:821:THR:HB	1:A:900:MET:HA	1.83	0.60
1:C:669:VAL:O	1:C:673:ILE:HG12	2.01	0.60
1:A:758:VAL:O	1:A:762:VAL:HG23	2.02	0.59
1:D:821:THR:HB	1:D:900:MET:HA	1.85	0.59
1:D:903:LYS:HD2	1:D:986:TYR:HB2	1.83	0.58
1:C:890:MET:HG2	1:C:891:PHE:CE2	2.39	0.58
1:D:921:LEU:HB2	1:D:1001:TYR:HB2	1.86	0.57
1:B:858:ARG:HG2	1:B:968:ASP:HB2	1.86	0.56
1:A:921:LEU:HB2	1:A:1001:TYR:HB2	1.88	0.55
1:C:758:VAL:O	1:C:762:VAL:HG23	2.07	0.54
1:C:921:LEU:HB2	1:C:1001:TYR:HB2	1.92	0.51
1:B:831:LEU:HD22	1:B:1005:LEU:HD13	1.92	0.51
1:C:662:LYS:HE2	1:C:663:SER:H	1.76	0.50
1:B:693:LEU:HD23	1:B:697:PRO:HA	1.93	0.50
1:A:726:ASP:HA	1:A:729:ILE:HG23	1.94	0.49
1:A:754:ASN:HD22	1:A:757:SER:HB3	1.78	0.49
1:C:904:SER:HB3	1:C:919:ILE:HD11	1.95	0.49
1:D:822:HIS:HE1	1:D:831:LEU:H	1.60	0.48
1:B:669:VAL:O	1:B:673:ILE:HG12	2.13	0.47
1:B:696:MET:HB2	1:B:741:PRO:HD2	1.96	0.47
1:A:834:ILE:HD11	1:A:1006:LYS:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:958:PRO:O	1:A:961:ASN:HB2	2.15	0.46
1:A:770:ASP:HB3	1:A:868:ASN:HA	1.98	0.46
1:D:673:ILE:HD11	1:D:794:TYR:HD1	1.80	0.46
1:D:834:ILE:HD11	1:D:1006:LYS:HB2	1.98	0.45
1:A:706:ILE:HG21	1:A:769:LEU:HG	1.99	0.45
1:B:793:ASN:HA	1:B:796:LYS:HD2	1.99	0.45
1:B:706:ILE:HG23	1:B:765:LEU:HD22	1.99	0.45
1:D:880:ALA:HB3	1:D:893:LYS:HG2	1.99	0.45
1:B:964:LEU:HD12	1:B:969:VAL:HG21	1.99	0.44
1:A:718:GLN:O	1:A:722:GLN:HB2	2.18	0.44
1:A:895:ILE:HD11	1:A:994:ILE:HG22	2.00	0.44
1:D:793:ASN:HA	1:D:796:LYS:HD2	2.00	0.43
1:B:770:ASP:HB2	1:B:868:ASN:HD22	1.82	0.43
1:C:793:ASN:HA	1:C:796:LYS:HD2	2.01	0.43
1:B:872:ILE:HG21	1:B:920:LEU:HD11	1.99	0.43
1:B:938:ILE:HD12	1:D:965:ASP:HA	2.01	0.43
1:C:701:LEU:HA	1:C:705:GLN:HE22	1.83	0.42
1:D:854:LEU:HD23	1:D:925:ALA:HB1	2.01	0.42
1:B:788:ASP:O	1:B:792:VAL:HG23	2.19	0.42
1:D:770:ASP:HB3	1:D:868:ASN:HA	2.01	0.42
1:A:831:LEU:HD22	1:A:1005:LEU:HD13	2.01	0.41
1:B:859:LEU:HG	1:B:921:LEU:HD22	2.02	0.41
1:C:938:ILE:HB	1:C:940:LYS:H	1.85	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	326/352 (93%)	317 (97%)	8 (2%)	1 (0%)	41	32
1	B	329/352 (94%)	317 (96%)	12 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	334/352 (95%)	327 (98%)	6 (2%)	1 (0%)	41	32
1	D	318/352 (90%)	311 (98%)	7 (2%)	0	100	100
All	All	1307/1408 (93%)	1272 (97%)	33 (2%)	2 (0%)	47	39

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	754	ASN
1	C	938	ILE

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	297/309 (96%)	282 (95%)	15 (5%)	24	15
1	B	298/309 (96%)	287 (96%)	11 (4%)	34	27
1	C	300/309 (97%)	288 (96%)	12 (4%)	31	24
1	D	289/309 (94%)	268 (93%)	21 (7%)	14	6
All	All	1184/1236 (96%)	1125 (95%)	59 (5%)	24	16

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	698	LEU
1	A	703	LYS
1	A	717	GLN
1	A	721	SER
1	A	722	GLN
1	A	726	ASP
1	A	729	ILE
1	A	731	ASP
1	A	733	SER
1	A	791	ASP

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Mol	Chain	Res	Type
1	A	817	TYR
1	A	849	LYS
1	A	854	LEU
1	A	855	HIS
1	A	961	ASN
1	B	662	LYS
1	B	693	LEU
1	B	728	GLN
1	B	778	LEU
1	B	802	LYS
1	B	812	GLU
1	B	817	TYR
1	B	852	LYS
1	B	938	ILE
1	B	971	LEU
1	B	985	LEU
1	C	662	LYS
1	C	676	ILE
1	C	705	GLN
1	C	729	ILE
1	C	743	ASP
1	C	795	GLU
1	C	806	ARG
1	C	817	TYR
1	C	858	ARG
1	C	912	GLN
1	C	971	LEU
1	C	981	ASP
1	D	676	ILE
1	D	695	LYS
1	D	702	SER
1	D	718	GLN
1	D	729	ILE
1	D	730	LEU
1	D	735	ARG
1	D	759	GLN
1	D	767	ASN
1	D	778	LEU
1	D	790	ILE
1	D	791	ASP
1	D	798	LYS
1	D	817	TYR

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Mol	Chain	Res	Type
1	D	822	HIS
1	D	830	ASP
1	D	853	GLN
1	D	928	ASN
1	D	963	SER
1	D	981	ASP
1	D	998	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	754	ASN
1	A	767	ASN
1	A	868	ASN
1	A	934	HIS
1	B	868	ASN
1	C	670	GLN
1	C	705	GLN
1	C	718	GLN
1	C	722	GLN
1	C	767	ASN
1	C	868	ASN
1	D	767	ASN
1	D	822	HIS
1	D	934	HIS
1	D	998	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry

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	2YQ	A	9001	-	27,32,32	1.55	3 (11%)	30,48,48	2.11	5 (16%)
2	2YQ	C	9001	-	27,32,32	1.89	2 (7%)	30,48,48	2.03	6 (20%)
2	2YQ	B	9001	-	27,32,32	1.09	2 (7%)	30,48,48	2.08	7 (23%)
2	2YQ	D	9001	-	27,32,32	1.18	1 (3%)	30,48,48	2.12	6 (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
2	2YQ	A	9001	-	-	0/4/20/20	0/4/5/5
2	2YQ	C	9001	-	-	0/4/20/20	0/4/5/5
2	2YQ	B	9001	-	-	0/4/20/20	0/4/5/5
2	2YQ	D	9001	-	-	0/4/20/20	0/4/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	9001	2YQ	C3-C5	-8.51	1.48	1.51
2	A	9001	2YQ	C3-C5	-5.90	1.49	1.51
2	D	9001	2YQ	C3-C2	3.87	1.48	1.43
2	B	9001	2YQ	C3-C2	3.47	1.47	1.43
2	A	9001	2YQ	C3-C2	3.39	1.47	1.43
2	C	9001	2YQ	C3-C2	2.77	1.46	1.43
2	B	9001	2YQ	N2-N1	2.33	1.40	1.34
2	A	9001	2YQ	N2-N1	2.19	1.39	1.34

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	9001	2YQ	C4-N2-N1	8.34	126.98	119.32
2	C	9001	2YQ	C4-N2-N1	7.99	126.66	119.32
2	B	9001	2YQ	C4-N2-N1	7.97	126.64	119.32
2	A	9001	2YQ	C4-N2-N1	7.74	126.43	119.32
2	D	9001	2YQ	C2-C7-N3	5.02	120.74	117.45
2	A	9001	2YQ	C2-C7-N3	5.02	120.73	117.45
2	B	9001	2YQ	C2-C7-N3	4.91	120.66	117.45
2	C	9001	2YQ	C2-C7-N3	4.77	120.57	117.45
2	A	9001	2YQ	C5-C3-N1	4.11	122.52	118.18
2	A	9001	2YQ	C3-C5-C6	3.91	116.73	109.81
2	B	9001	2YQ	C5-C3-N1	3.50	121.88	118.18
2	D	9001	2YQ	C5-C3-N1	3.44	121.81	118.18
2	D	9001	2YQ	C19-N4-C17	2.66	132.00	128.84
2	C	9001	2YQ	C3-C5-C6	2.65	114.51	109.81
2	D	9001	2YQ	C3-C5-C6	2.64	114.49	109.81
2	C	9001	2YQ	C19-N4-C17	2.62	131.95	128.84
2	B	9001	2YQ	C9-C10-C1	-2.60	117.58	119.43
2	B	9001	2YQ	C3-C5-C6	2.53	114.29	109.81
2	C	9001	2YQ	C5-C3-N1	2.37	120.68	118.18
2	A	9001	2YQ	C19-N4-C17	2.36	131.64	128.84
2	C	9001	2YQ	C9-C10-C1	-2.18	117.88	119.43
2	B	9001	2YQ	C19-N4-C17	2.12	131.36	128.84
2	B	9001	2YQ	C10-C1-C2	2.03	120.81	118.94
2	D	9001	2YQ	C9-C10-C1	-2.02	117.99	119.43

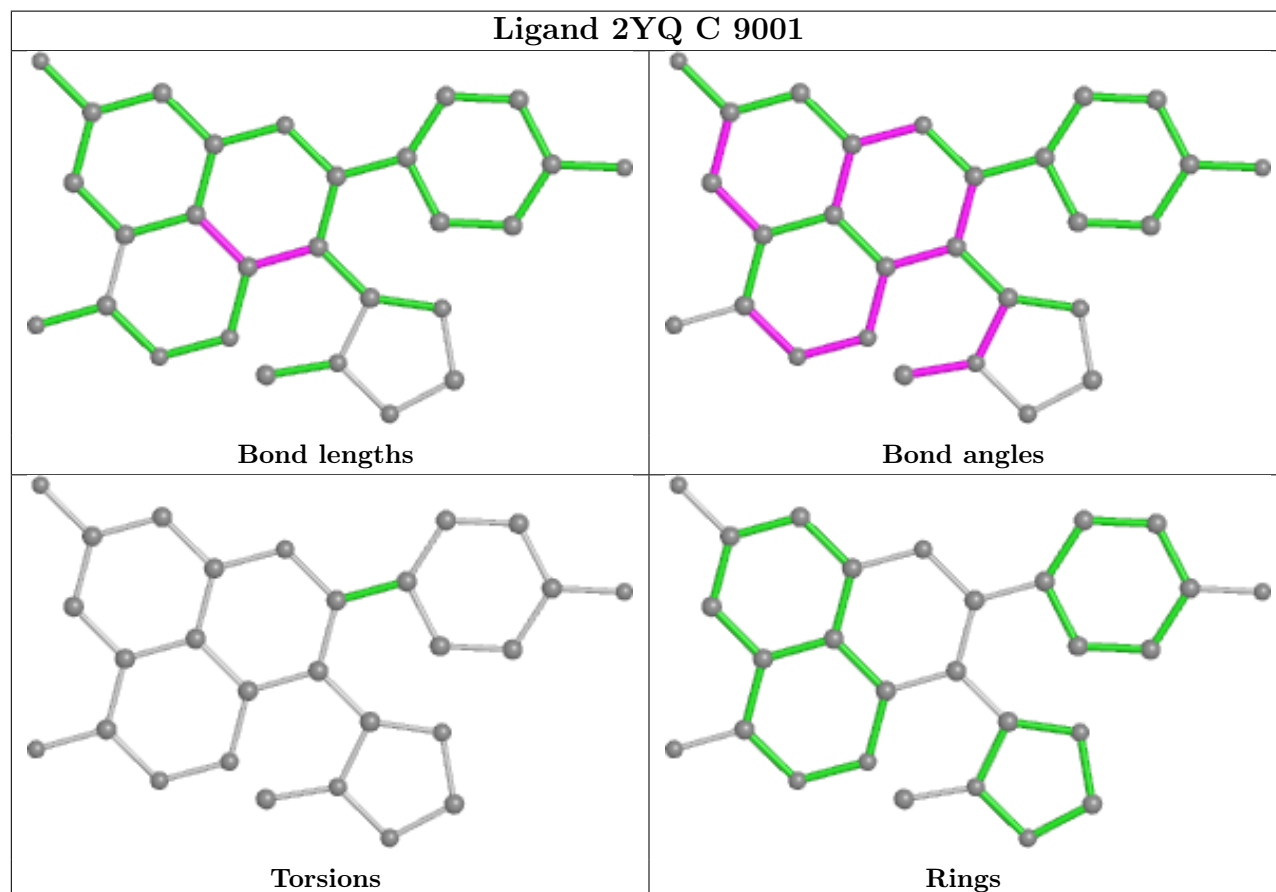
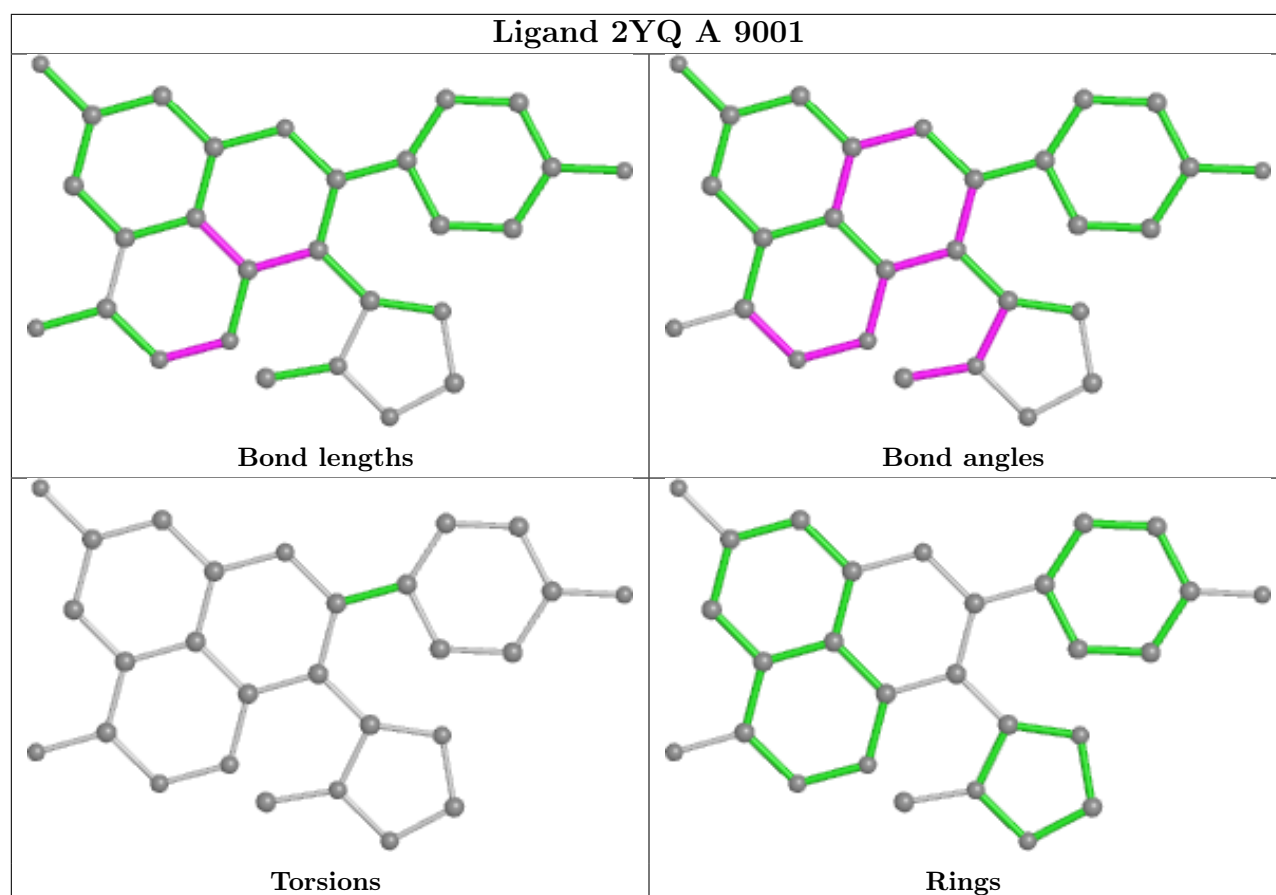
There are no chirality outliers.

There are no torsion outliers.

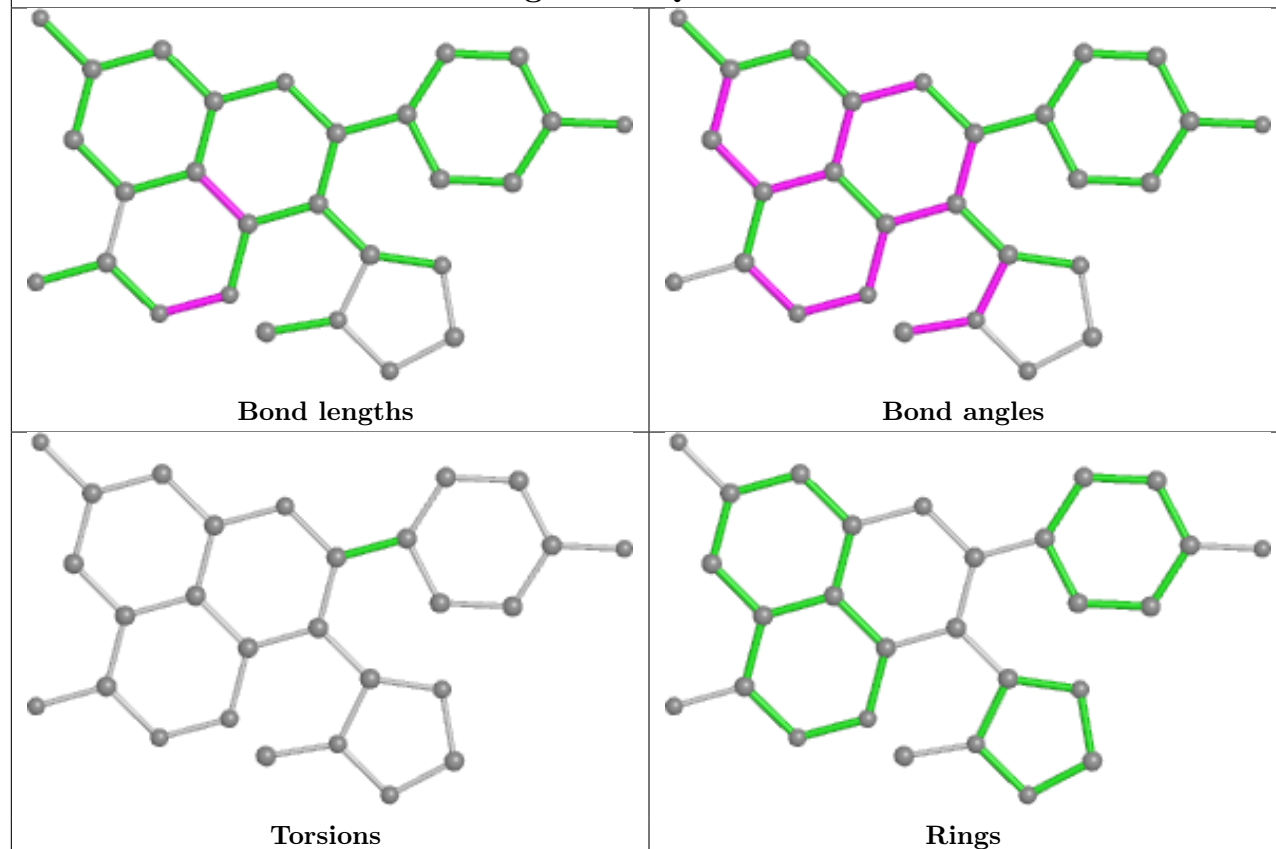
There are no ring outliers.

No monomer is involved in short contacts.

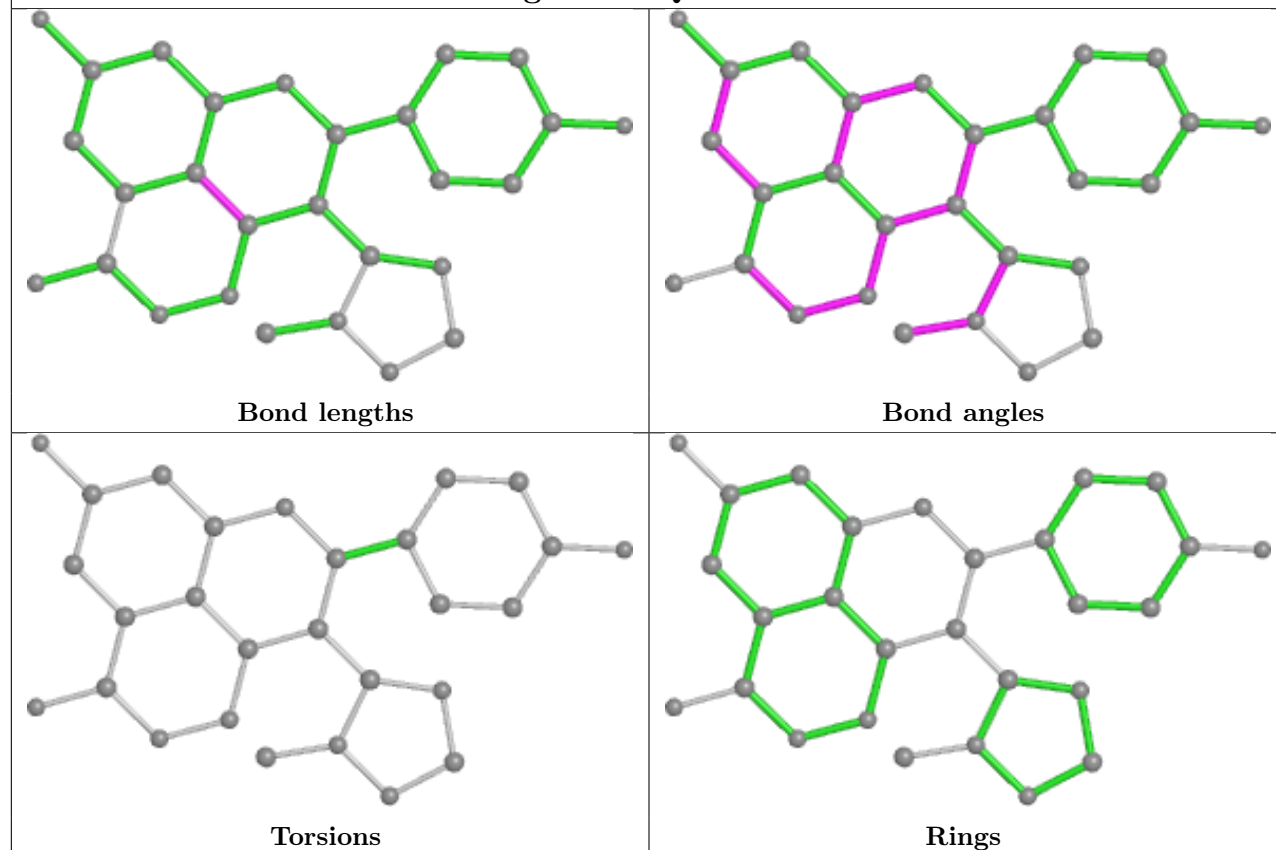
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 B 9001



Ligand 2YQ D 9001



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	336/352 (95%)	0.42	10 (2%) 50 53	31, 54, 92, 115	0
1	B	337/352 (95%)	0.38	12 (3%) 42 45	36, 58, 90, 117	0
1	C	340/352 (96%)	0.29	5 (1%) 73 75	31, 50, 83, 118	0
1	D	328/352 (93%)	0.71	34 (10%) 6 6	38, 67, 121, 149	0
All	All	1341/1408 (95%)	0.45	61 (4%) 33 34	31, 56, 102, 149	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	752	LEU	6.6
1	D	706	ILE	6.6
1	D	730	LEU	5.6
1	D	755	ALA	5.1
1	D	751	LEU	4.9
1	D	779	ARG	4.9
1	D	763	GLU	4.7
1	A	755	ALA	4.3
1	B	821	THR	3.7
1	A	824	THR	3.5
1	A	720	VAL	3.5
1	B	855	HIS	3.4
1	D	701	LEU	3.4
1	A	717	GLN	3.3
1	D	759	GLN	3.3
1	D	985	LEU	3.3
1	D	732	LEU	3.3
1	D	954	THR	3.1
1	D	983	SER	3.1
1	B	724	SER	3.0
1	D	756	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	821	THR	3.0
1	C	783	ASP	2.9
1	B	980	ASN	2.9
1	B	1009	PHE	2.8
1	D	691	ILE	2.8
1	A	748	LYS	2.8
1	C	939	SER	2.8
1	D	731	ASP	2.7
1	B	829	TYR	2.7
1	D	733	SER	2.7
1	A	964	LEU	2.7
1	D	729	ILE	2.7
1	D	1010	LYS	2.7
1	D	770	ASP	2.6
1	D	750	PRO	2.6
1	A	756	ASP	2.6
1	D	710	TYR	2.6
1	B	914	ASP	2.5
1	C	821	THR	2.5
1	C	980	ASN	2.5
1	D	736	PHE	2.5
1	D	689	TYR	2.5
1	B	835	ASP	2.4
1	B	751	LEU	2.4
1	D	765	LEU	2.4
1	D	720	VAL	2.4
1	D	797	LEU	2.3
1	D	713	LEU	2.3
1	D	728	GLN	2.2
1	B	982	THR	2.2
1	C	782	SER	2.1
1	B	834	ILE	2.1
1	D	768	LEU	2.1
1	D	911	SER	2.1
1	A	679	VAL	2.1
1	B	954	THR	2.1
1	A	759	GLN	2.1
1	D	979	VAL	2.1
1	A	855	HIS	2.0
1	D	953	LYS	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 monosaccharides in this entry.

6.4 Ligands [i](#)

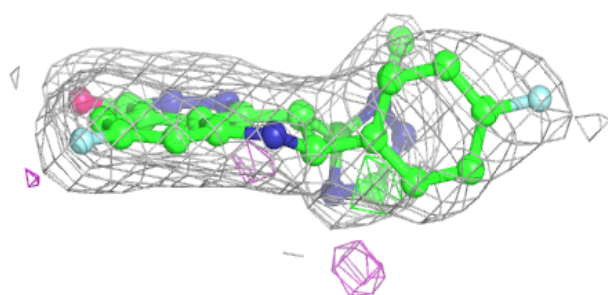
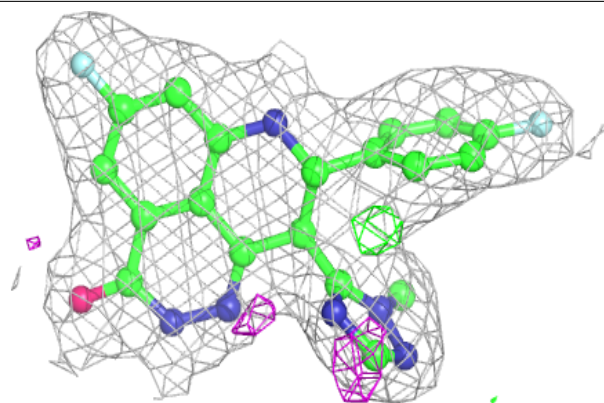
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	2YQ	C	9001	28/28	0.96	0.13	31,41,54,57	0
2	2YQ	B	9001	28/28	0.96	0.14	35,44,64,68	0
2	2YQ	D	9001	28/28	0.96	0.15	43,45,54,61	0
2	2YQ	A	9001	28/28	0.98	0.13	28,35,42,45	0

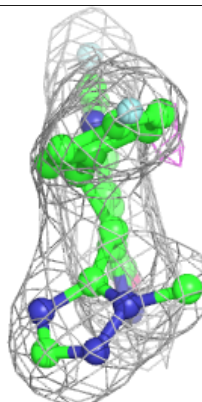
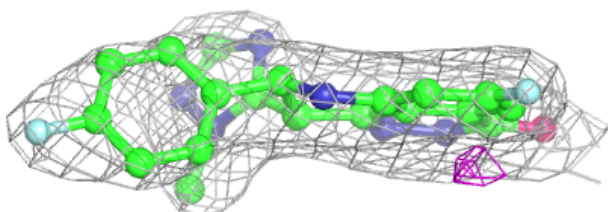
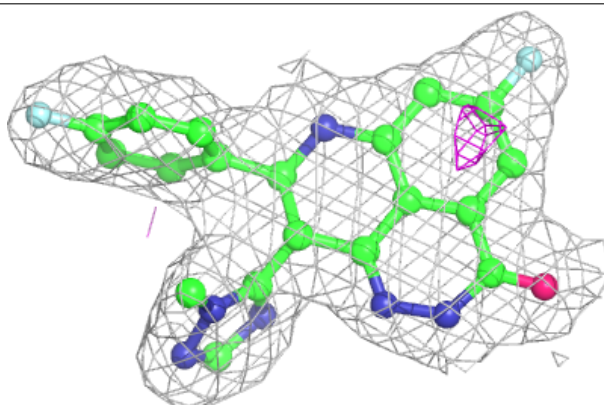
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 2YQ C 9001:

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

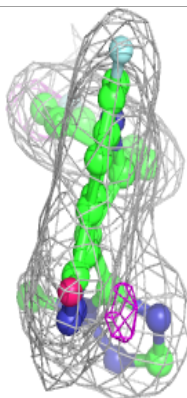
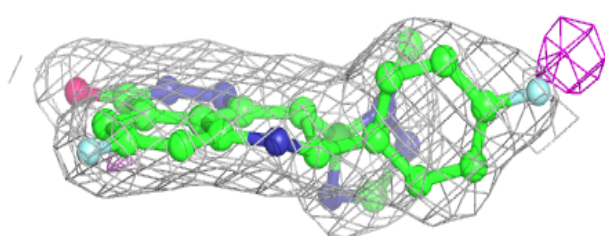
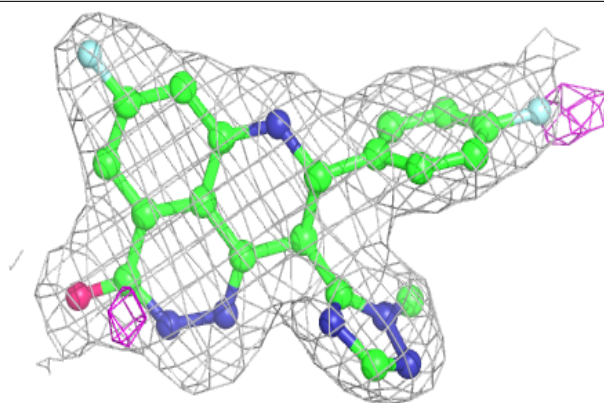
**Electron density around 2YQ B 9001:**

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

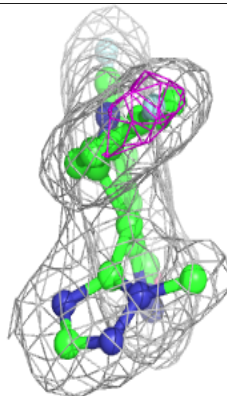
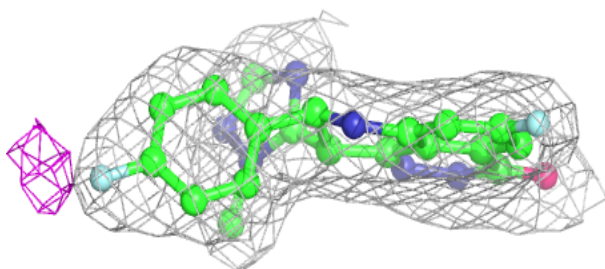
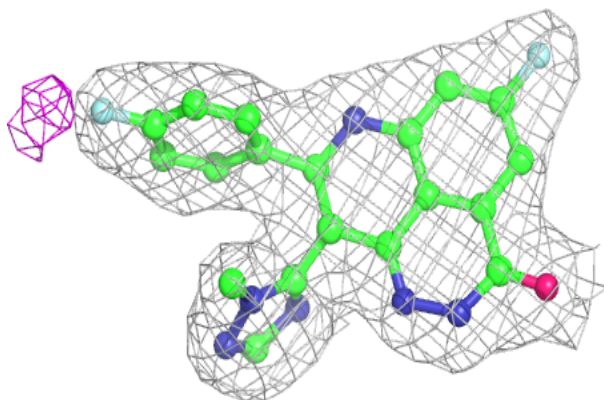


Electron density around 2YQ D 9001:

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

**Electron density around 2YQ A 9001:**

$2mF_o-DF_c$ (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.