Full wwPDB X-ray Structure Validation Report (i)

Aug 30, 2023 – 05:07 AM EDT

PDB ID	:	3MJW
Title	:	PI3 Kinase gamma with a benzofuranone inhibitor
Authors	:	Bard, J.; Svenson, K.
Deposited on	:	2010-04-13
Resolution	:	2.87 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 (i) 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 (i)) were used in the production of this report:

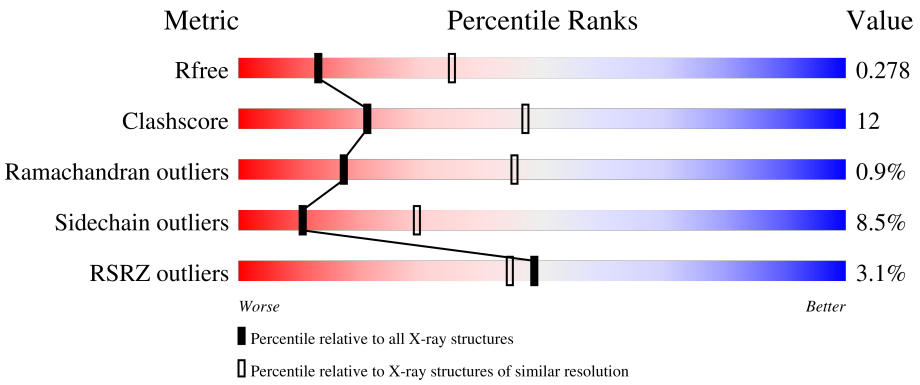
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.87 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	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

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 <=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	966	3% 59% 23% • 15%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6472 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.

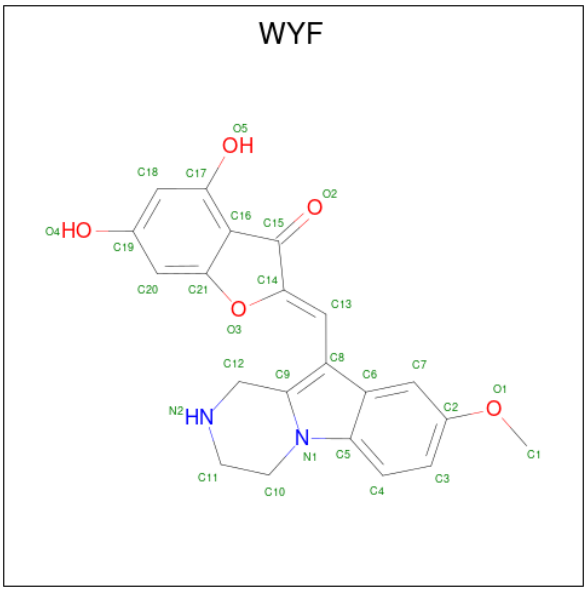
- Molecule 1 is a protein called Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	819	6444	4133	1102	1177	32	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	MET	-	expression tag	UNP P48736
A	459	ARG	GLN	conflict	UNP P48736
A	1103	HIS	-	expression tag	UNP P48736
A	1104	HIS	-	expression tag	UNP P48736
A	1105	HIS	-	expression tag	UNP P48736
A	1106	HIS	-	expression tag	UNP P48736
A	1107	HIS	-	expression tag	UNP P48736
A	1108	HIS	-	expression tag	UNP P48736

- Molecule 2 is (2Z)-4,6-dihydroxy-2-[(8-methoxy-1,2,3,4-tetrahydropyrazino[1,2-a]indol-10-yl)methylidene]-1-benzofuran-3(2H)-one (three-letter code: WYF) (formula: $C_{21}H_{18}N_2O_5$).



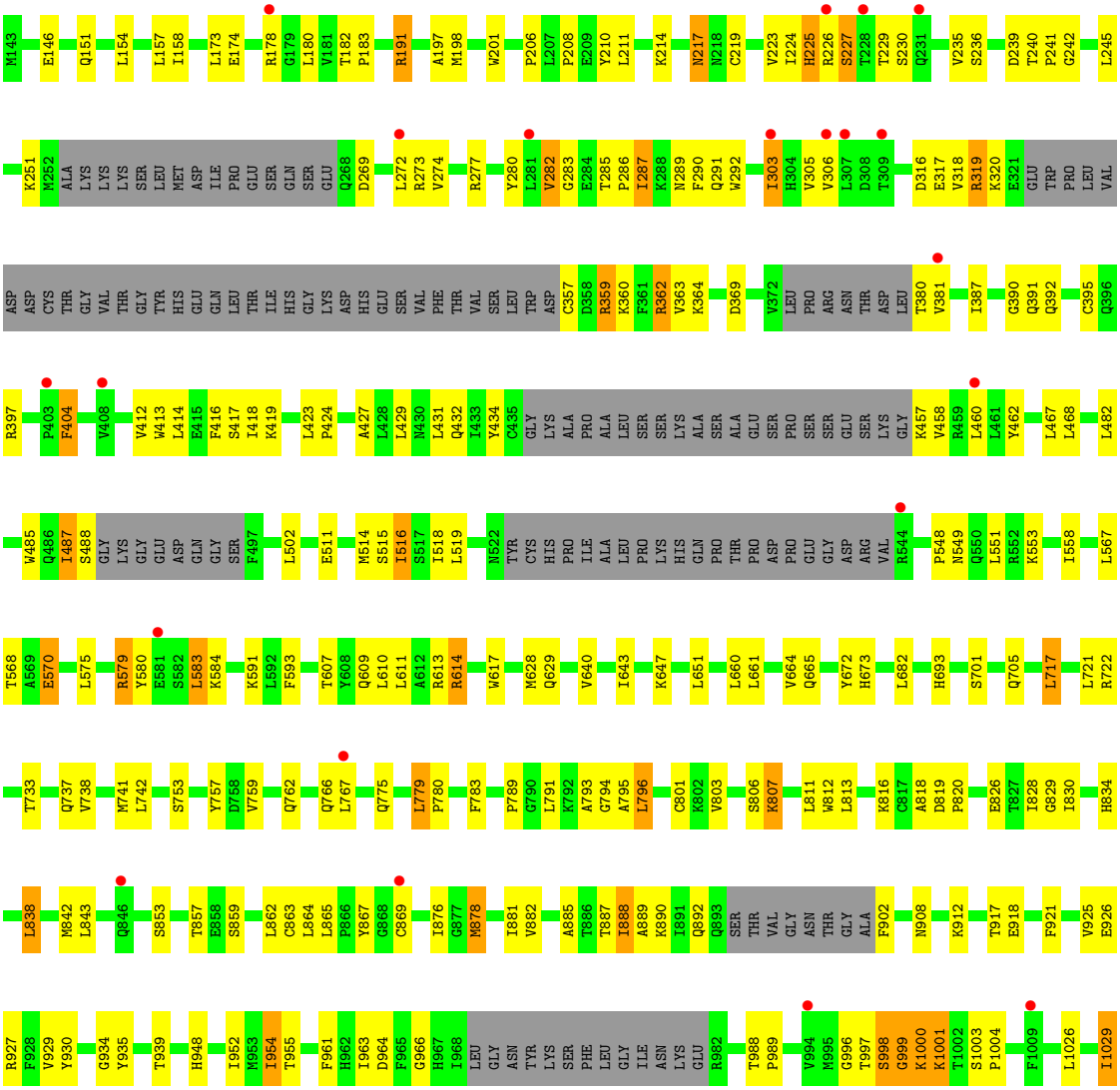
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	28	21	2	5	0	0

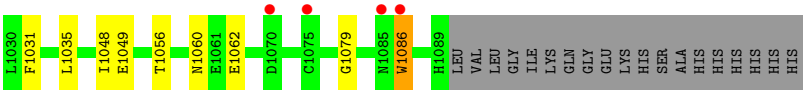
3 Residue-property plots (i)

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: Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform

Chain A: 3% 59% 23% • 15%




L1030
F1031
L1035
I1048
E1049
T1056
N1060
E1061
E1062
D1070
G1075
G1079
N1085
W1086
H1089
LEU
VAL
LEU
GLY
ILE
LYS
GLN
GLY
GLU
LYS
HIS
SER
ALA
HIS
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	145.60Å 68.57Å 107.25Å 90.00° 95.02° 90.00°	Depositor
Resolution (Å)	36.23 – 2.87 41.24 – 2.86	Depositor EDS
% Data completeness (in resolution range)	86.3 (36.23-2.87) 86.3 (41.24-2.86)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.48 (at 2.86Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.225 , 0.281 0.231 , 0.278	Depositor DCC
R_{free} test set	2000 reflections (9.00%)	wwPDB-VP
Wilson B-factor (Å^2)	70.4	Xtriage
Anisotropy	0.374	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 46.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	6472	wwPDB-VP
Average B, all atoms (Å^2)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: WYF

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	0.22	0/6579	0.40	0/8926

There are no bond length outliers.

There are no bond angle outliers.

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	6444	0	6306	153	0
2	A	28	0	17	3	0
All	All	6472	0	6323	155	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 12.

All (155) 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:217:ASN:HD22	1:A:219:CYS:HB3	1.52	0.75
1:A:404:PHE:CD1	1:A:404:PHE:N	2.55	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:887:THR:HG22	1:A:889:ALA:H	1.54	0.72
1:A:487:ILE:HG22	1:A:488:SER:H	1.59	0.67
1:A:613:ARG:HA	1:A:614:ARG:CB	2.26	0.65
1:A:240:THR:HG23	1:A:241:PRO:HD2	1.80	0.64
1:A:793:ALA:HB2	1:A:828:ILE:HD12	1.80	0.63
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.82	0.62
1:A:219:CYS:HA	1:A:235:VAL:O	2.00	0.62
1:A:272:LEU:HB3	1:A:305:VAL:HG11	1.82	0.61
1:A:285:THR:HG22	1:A:289:ASN:HB2	1.82	0.61
1:A:404:PHE:N	1:A:404:PHE:HD1	1.97	0.61
1:A:303:ILE:HD12	1:A:303:ILE:H	1.66	0.60
1:A:174:GLU:O	1:A:178:ARG:HD2	2.01	0.60
1:A:613:ARG:HA	1:A:614:ARG:HB3	1.83	0.60
1:A:182:THR:HB	1:A:183:PRO:HD3	1.84	0.60
1:A:998:SER:H	1:A:1001:LYS:HG3	1.66	0.59
1:A:240:THR:HG22	1:A:242:GLY:H	1.68	0.58
1:A:239:ASP:O	1:A:286:PRO:HA	2.04	0.57
1:A:380:THR:HA	1:A:404:PHE:CD1	2.39	0.57
1:A:482:LEU:HB2	1:A:516:ILE:HG22	1.87	0.56
1:A:568:THR:HG22	1:A:570:GLU:H	1.69	0.56
1:A:629:GLN:HG2	1:A:1029:ILE:HG13	1.88	0.56
1:A:693:HIS:CD2	1:A:789:PRO:HG3	2.41	0.56
1:A:640:VAL:O	1:A:643:ILE:HG12	2.07	0.55
1:A:432:GLN:HB3	1:A:460:LEU:HD11	1.87	0.55
1:A:998:SER:H	1:A:1001:LYS:CG	2.19	0.55
1:A:660:LEU:O	1:A:664:VAL:HG23	2.06	0.55
1:A:273:ARG:HG2	1:A:274:VAL:N	2.22	0.54
1:A:834:HIS:HB2	1:A:876:ILE:HD12	1.89	0.54
1:A:1003:SER:HB2	1:A:1004:PRO:HD2	1.88	0.54
1:A:225:HIS:ND1	1:A:225:HIS:N	2.55	0.54
1:A:467:LEU:HD13	1:A:672:TYR:CE2	2.43	0.54
1:A:737:GLN:O	1:A:741:MET:HG3	2.08	0.53
1:A:434:TYR:CZ	1:A:460:LEU:HD13	2.44	0.53
1:A:1035:LEU:HD12	1:A:1048:ILE:HG12	1.89	0.53
1:A:173:LEU:HD23	1:A:673:HIS:CD2	2.44	0.52
1:A:362:ARG:HG3	1:A:413:TRP:CE3	2.45	0.52
1:A:811:LEU:HB3	1:A:813:LEU:CD1	2.40	0.52
1:A:779:LEU:HD12	1:A:796:LEU:HD12	1.92	0.52
1:A:948:HIS:HB2	1:A:1086:TRP:HD1	1.75	0.52
1:A:794:GLY:HA3	1:A:818:ALA:HB2	1.92	0.51
1:A:224:ILE:HD12	1:A:224:ILE:N	2.25	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:842:MET:HG2	1:A:869:CYS:O	2.11	0.51
1:A:229:THR:HG22	1:A:230:SER:N	2.26	0.51
1:A:395:CYS:SG	1:A:417:SER:HB2	2.50	0.51
1:A:583:LEU:HD21	1:A:614:ARG:H	1.75	0.51
1:A:753:SER:HB2	1:A:757:TYR:CB	2.40	0.51
1:A:701:SER:O	1:A:705:GLN:HG2	2.11	0.50
1:A:424:PRO:HD2	1:A:427:ALA:HB2	1.94	0.50
1:A:303:ILE:HD12	1:A:303:ILE:N	2.26	0.50
1:A:287:ILE:HA	1:A:290:PHE:CD1	2.47	0.50
1:A:549:ASN:O	1:A:553:LYS:HG2	2.12	0.50
1:A:795:ALA:HB3	1:A:816:LYS:HE3	1.95	0.49
1:A:210:TYR:HE2	1:A:859:SER:C	2.16	0.49
1:A:395:CYS:SG	1:A:418:ILE:HG13	2.53	0.49
1:A:567:LEU:HD21	1:A:591:LYS:HD2	1.95	0.49
1:A:807:LYS:CD	1:A:807:LYS:H	2.25	0.49
1:A:174:GLU:HB3	1:A:178:ARG:NH1	2.28	0.49
1:A:882:VAL:HG12	1:A:885:ALA:HB2	1.95	0.49
1:A:359:ARG:HG3	1:A:360:LYS:N	2.28	0.49
1:A:277:ARG:NH1	1:A:791:LEU:HG	2.28	0.48
1:A:198:MET:HE2	1:A:282:VAL:HG21	1.94	0.48
1:A:829:GLY:HA3	1:A:881:ILE:HD12	1.96	0.48
1:A:558:ILE:HG21	1:A:575:LEU:HD21	1.96	0.48
1:A:779:LEU:HD22	1:A:780:PRO:O	2.14	0.48
1:A:853:SER:O	1:A:857:THR:HG23	2.13	0.48
2:A:1:WYF:O3	2:A:1:WYF:H7	2.14	0.47
1:A:282:VAL:HG23	1:A:283:GLY:N	2.28	0.47
1:A:180:LEU:C	1:A:183:PRO:HD2	2.35	0.47
1:A:548:PRO:HG2	1:A:551:LEU:HD12	1.97	0.47
1:A:210:TYR:CD1	1:A:211:LEU:HG	2.50	0.47
1:A:1060:ASN:C	1:A:1062:GLU:H	2.18	0.47
1:A:997:THR:HA	1:A:1001:LYS:HD2	1.96	0.47
1:A:807:LYS:HD2	1:A:807:LYS:N	2.30	0.46
1:A:390:GLY:O	1:A:391:GLN:HB2	2.13	0.46
1:A:912:LYS:HE2	1:A:918:GLU:OE2	2.15	0.46
1:A:280:TYR:HB3	1:A:282:VAL:HG13	1.97	0.46
1:A:151:GLN:OE1	1:A:722:ARG:NH2	2.48	0.46
1:A:274:VAL:HG21	1:A:292:TRP:CD1	2.50	0.46
1:A:457:LYS:HA	1:A:458:VAL:HA	1.79	0.46
1:A:273:ARG:O	1:A:305:VAL:HG13	2.16	0.46
1:A:387:ILE:HD12	1:A:418:ILE:HD12	1.97	0.46
1:A:888:ILE:HD11	1:A:952:ILE:CG2	2.46	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:948:HIS:HB2	1:A:1086:TRP:CD1	2.50	0.46
1:A:948:HIS:CB	1:A:1086:TRP:HD1	2.28	0.46
1:A:580:TYR:O	1:A:584:LYS:HD3	2.16	0.46
1:A:593:PHE:CE2	1:A:611:LEU:HD21	2.51	0.46
1:A:964:ASP:HA	2:A:1:WYF:C18	2.46	0.46
1:A:287:ILE:N	1:A:287:ILE:HD13	2.30	0.46
1:A:413:TRP:CH2	1:A:519:LEU:HD23	2.51	0.45
1:A:762:GLN:O	1:A:766:GLN:HG2	2.17	0.45
1:A:364:LYS:HA	1:A:412:VAL:O	2.16	0.45
1:A:418:ILE:HG22	1:A:419:LYS:O	2.17	0.45
1:A:208:PRO:HB3	1:A:210:TYR:CZ	2.51	0.45
1:A:613:ARG:CA	1:A:614:ARG:CB	2.94	0.45
1:A:287:ILE:HD13	1:A:287:ILE:H	1.82	0.44
1:A:397:ARG:HB3	1:A:414:LEU:HD22	1.99	0.44
1:A:191:ARG:O	1:A:191:ARG:HG3	2.18	0.44
1:A:198:MET:CE	1:A:282:VAL:HG21	2.47	0.44
1:A:223:VAL:HG12	1:A:225:HIS:CE1	2.53	0.44
1:A:989:PRO:HD3	1:A:1079:GLY:HA2	1.98	0.44
1:A:1003:SER:CB	1:A:1004:PRO:HD2	2.46	0.44
1:A:423:LEU:HA	1:A:424:PRO:HD3	1.81	0.44
1:A:317:GLU:HG2	1:A:318:VAL:N	2.33	0.44
1:A:629:GLN:CG	1:A:1029:ILE:HG13	2.47	0.44
1:A:462:TYR:HA	1:A:485:TRP:O	2.18	0.44
1:A:935:TYR:CE1	1:A:961:PHE:HA	2.52	0.44
1:A:157:LEU:HD21	1:A:733:THR:HA	2.00	0.44
1:A:1031:PHE:O	1:A:1035:LEU:HG	2.18	0.44
1:A:226:ARG:O	1:A:227:SER:HB2	2.18	0.43
1:A:661:LEU:O	1:A:665:GLN:HG2	2.19	0.43
1:A:742:LEU:HD22	1:A:813:LEU:HD21	2.01	0.43
1:A:954:ILE:HG13	1:A:955:THR:O	2.19	0.43
2:A:1:WYF:H7	2:A:1:WYF:H1B	1.78	0.43
1:A:363:VAL:HG12	1:A:416:PHE:HE1	1.84	0.43
1:A:838:LEU:O	1:A:842:MET:HG3	2.19	0.43
1:A:717:LEU:HD22	1:A:721:LEU:HG	2.01	0.42
1:A:579:ARG:H	1:A:579:ARG:HG3	1.55	0.42
1:A:867:TYR:OH	1:A:963:ILE:HA	2.20	0.42
1:A:926:GLU:O	1:A:929:VAL:HG22	2.20	0.42
1:A:794:GLY:CA	1:A:818:ALA:HB2	2.48	0.42
1:A:197:ALA:HB2	1:A:316:ASP:OD2	2.19	0.42
1:A:395:CYS:HB3	1:A:416:PHE:HD2	1.85	0.42
1:A:434:TYR:HB3	1:A:458:VAL:CG2	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ILE:HA	1:A:290:PHE:HD1	1.83	0.42
1:A:431:LEU:HD13	1:A:516:ILE:HD12	2.01	0.42
1:A:779:LEU:HD23	1:A:780:PRO:HD2	2.01	0.42
1:A:801:CYS:HA	1:A:812:TRP:O	2.20	0.42
1:A:201:TRP:CE2	1:A:291:GLN:HG3	2.55	0.41
1:A:738:VAL:HG21	1:A:783:PHE:CG	2.55	0.41
1:A:360:LYS:HB3	1:A:416:PHE:O	2.19	0.41
1:A:514:MET:HG3	1:A:515:SER:N	2.34	0.41
1:A:767:LEU:HG	1:A:803:VAL:CG2	2.51	0.41
1:A:607:THR:O	1:A:610:LEU:HB2	2.19	0.41
1:A:593:PHE:CZ	1:A:611:LEU:HD21	2.56	0.41
1:A:628:MET:HB2	1:A:1029:ILE:HG21	2.02	0.41
1:A:236:SER:HB3	1:A:239:ASP:OD1	2.21	0.41
1:A:583:LEU:HD12	1:A:610:LEU:HD22	2.03	0.41
1:A:999:GLY:O	1:A:1000:LYS:CB	2.68	0.41
1:A:862:LEU:HB3	1:A:934:GLY:HA3	2.03	0.41
1:A:996:GLY:O	1:A:1003:SER:HB3	2.21	0.41
1:A:954:ILE:HG13	1:A:955:THR:N	2.33	0.41
1:A:830:ILE:CG2	1:A:878:MET:HB2	2.50	0.40
1:A:921:PHE:O	1:A:925:VAL:HG23	2.19	0.40
1:A:935:TYR:O	1:A:939:THR:HG23	2.21	0.40
1:A:364:LYS:O	1:A:518:ILE:HA	2.21	0.40
1:A:863:CYS:SG	1:A:930:TYR:HB3	2.61	0.40
1:A:154:LEU:O	1:A:158:ILE:HG13	2.20	0.40
1:A:319:ARG:HG3	1:A:320:LYS:N	2.36	0.40
1:A:390:GLY:C	1:A:392:GLN:H	2.25	0.40
1:A:614:ARG:HG2	1:A:617:TRP:HB3	2.03	0.40
1:A:819:ASP:HA	1:A:820:PRO:HD3	1.86	0.40
1:A:998:SER:O	1:A:999:GLY:C	2.60	0.40
1:A:807:LYS:CD	1:A:807:LYS:N	2.84	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	801/966 (83%)	720 (90%)	74 (9%)	7 (1%)	17 45

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	966	GLY
1	A	999	GLY
1	A	206	PRO
1	A	269	ASP
1	A	303	ILE
1	A	227	SER
1	A	1000	LYS

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	685/864 (79%)	627 (92%)	58 (8%)	10 29

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	GLU
1	A	191	ARG
1	A	214	LYS
1	A	217	ASN
1	A	225	HIS
1	A	245	LEU
1	A	251	LYS
1	A	282	VAL
1	A	287	ILE
1	A	306	VAL
1	A	319	ARG
1	A	357	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	359	ARG
1	A	362	ARG
1	A	369	ASP
1	A	381	VAL
1	A	404	PHE
1	A	487	ILE
1	A	502	LEU
1	A	511	GLU
1	A	516	ILE
1	A	570	GLU
1	A	579	ARG
1	A	583	LEU
1	A	609	GLN
1	A	614	ARG
1	A	647	LYS
1	A	651	LEU
1	A	682	LEU
1	A	717	LEU
1	A	759	VAL
1	A	775	GLN
1	A	779	LEU
1	A	796	LEU
1	A	806	SER
1	A	807	LYS
1	A	826	GLU
1	A	838	LEU
1	A	843	LEU
1	A	864	LEU
1	A	865	LEU
1	A	878	MET
1	A	888	ILE
1	A	890	LYS
1	A	892	GLN
1	A	902	PHE
1	A	908	ASN
1	A	917	THR
1	A	927	ARG
1	A	954	ILE
1	A	988	THR
1	A	998	SER
1	A	1001	LYS
1	A	1026	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1029	ILE
1	A	1049	GLU
1	A	1056	THR
1	A	1086	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	217	ASN
1	A	600	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	WYF	A	1	-	28,32,32	1.36	4 (14%)	35,48,48	1.74	9 (25%)

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	WYF	A	1	-	-	2/4/25/25	0/4/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	WYF	C12-N2	3.96	1.51	1.46
2	A	1	WYF	C10-N1	-2.54	1.46	1.49
2	A	1	WYF	C7-C2	2.42	1.41	1.37
2	A	1	WYF	C8-C13	-2.26	1.43	1.47

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1	WYF	C13-C14-C15	-5.05	121.92	126.24
2	A	1	WYF	O3-C14-C13	3.54	127.61	124.43
2	A	1	WYF	O1-C2-C7	-3.50	114.89	124.43
2	A	1	WYF	C20-C21-C16	-2.72	121.65	124.81
2	A	1	WYF	O3-C21-C16	2.67	113.18	110.60
2	A	1	WYF	C18-C17-C16	-2.37	118.18	120.93
2	A	1	WYF	O2-C15-C14	2.36	128.34	126.16
2	A	1	WYF	C9-N1-C5	2.22	111.04	106.63
2	A	1	WYF	C11-C10-N1	2.12	113.40	109.07

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	WYF	C7-C2-O1-C1
2	A	1	WYF	C3-C2-O1-C1

There are no ring outliers.

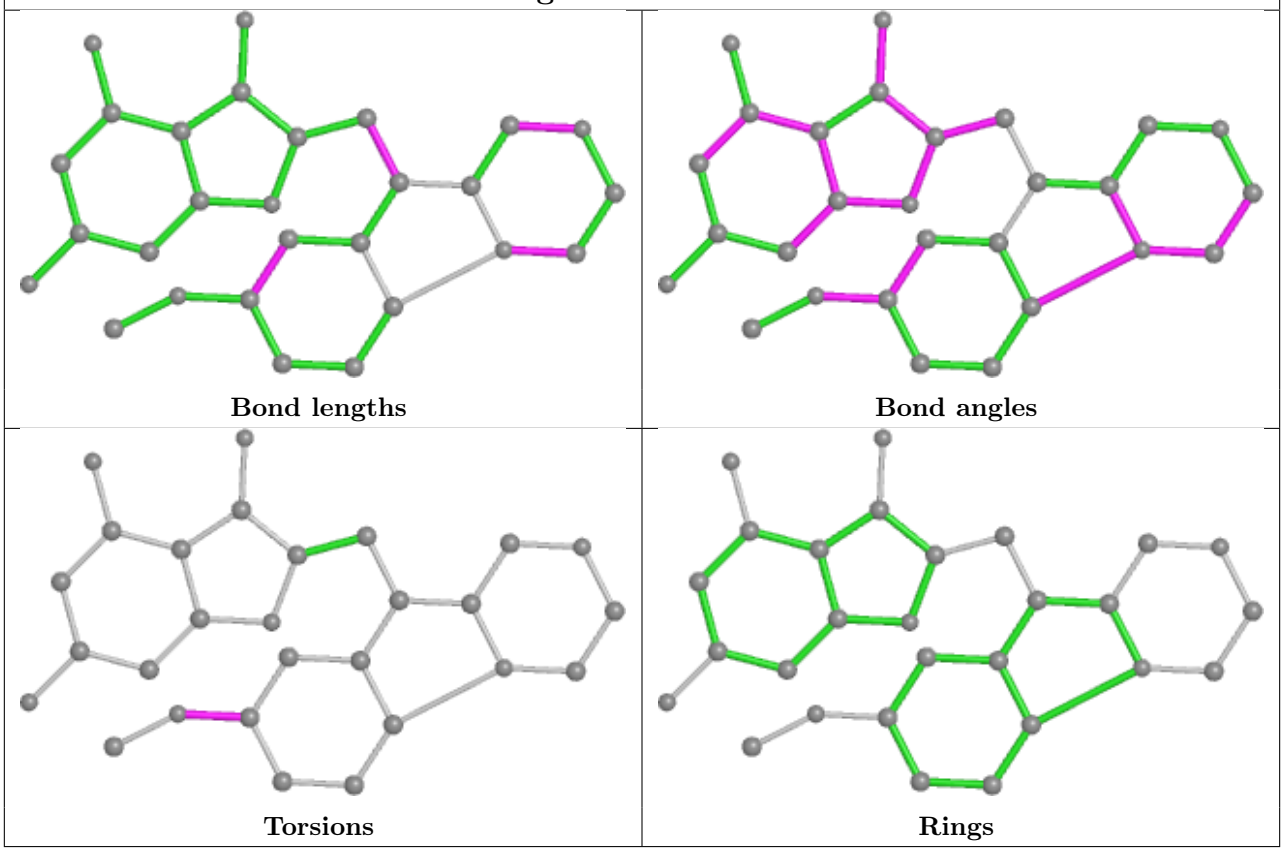
1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	WYF	3	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 then 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 WYF A 1



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	819/966 (84%)	0.15	25 (3%) 49 45	41, 77, 115, 138	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	307	LEU	4.9
1	A	1075	CYS	4.6
1	A	272	LEU	3.9
1	A	403	PRO	3.2
1	A	1086	TRP	3.2
1	A	767	LEU	3.1
1	A	226	ARG	3.0
1	A	381	VAL	2.9
1	A	306	VAL	2.7
1	A	303	ILE	2.7
1	A	460	LEU	2.6
1	A	544	ARG	2.6
1	A	869	CYS	2.6
1	A	309	THR	2.6
1	A	1070	ASP	2.5
1	A	846	GLN	2.4
1	A	1085	ASN	2.4
1	A	281	LEU	2.3
1	A	408	VAL	2.3
1	A	231	GLN	2.2
1	A	228	THR	2.1
1	A	1009	PHE	2.1
1	A	581	GLU	2.0
1	A	178	ARG	2.0
1	A	994	VAL	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)

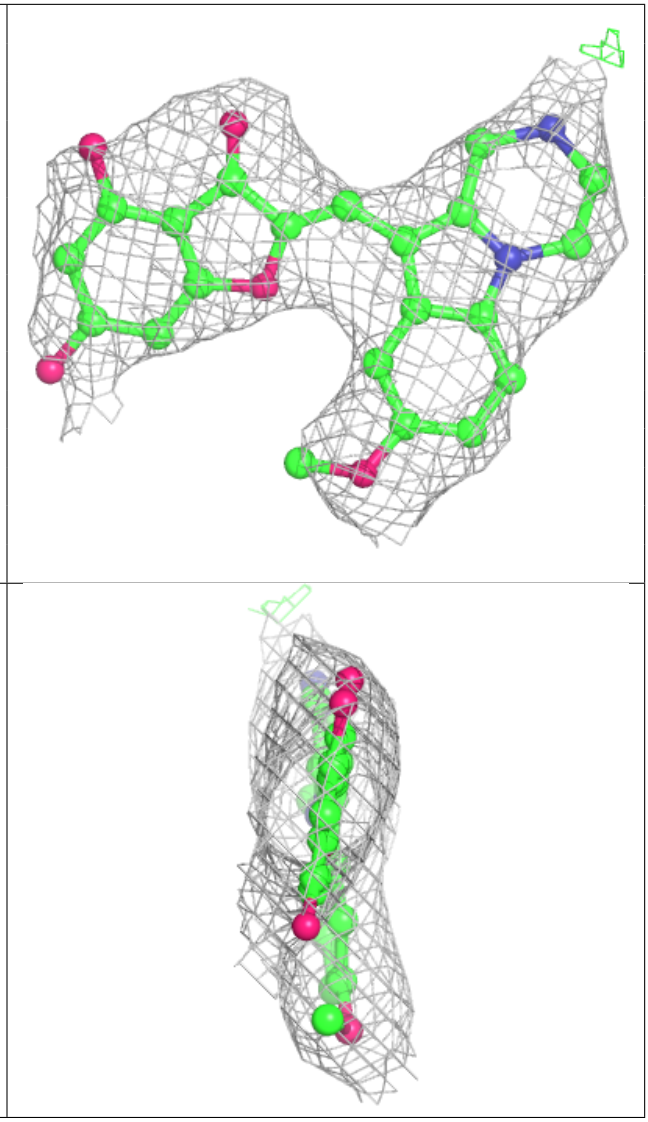
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	WYF	A	1	28/28	0.93	0.18	69,85,92,96	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 WYF A 1:

$2mF_o$-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.