Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:35 am BST

PDB ID	:	4WWN
Title	:	Crystal structure of human PI3K-gamma in complex with (S)-N-(1-(7-fluoro-2-(pyridin-2-yl)quinolin-3-yl)ethyl)-9H-purin-6-amine AMG319 inhibitor
Authors	:	Whittington, D.A.; Tang, J.; Yakowec, P.
Deposited on	:	2014-11-11
Resolution	:	2.70 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:

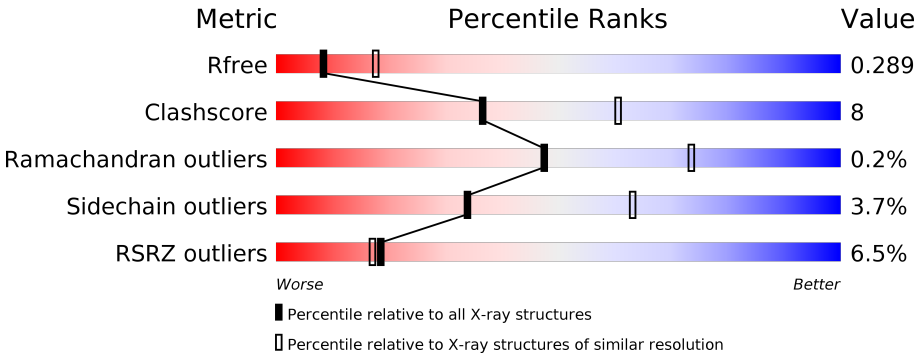
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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	959	6% 70% 15% • 13%

2 Entry composition

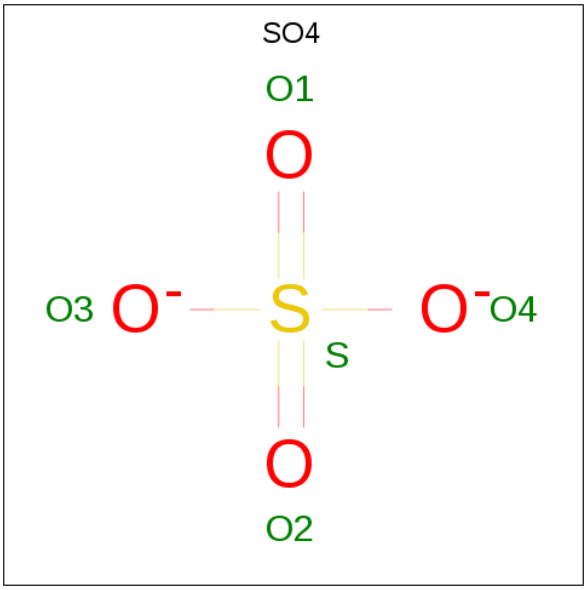
There are 4 unique types of molecules in this entry. The entry contains 6807 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

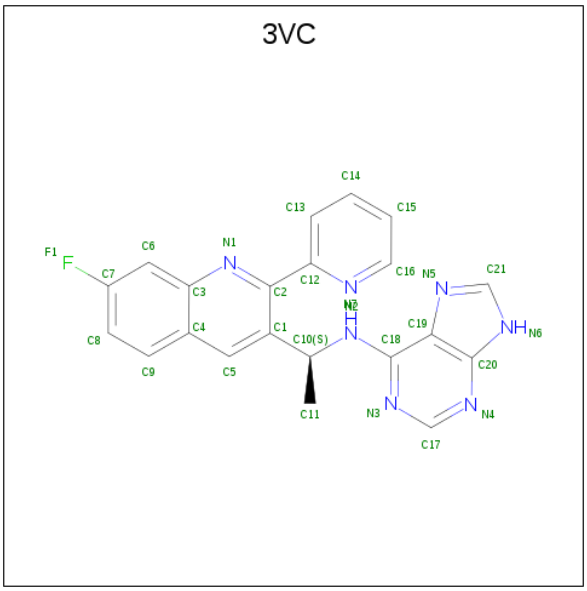
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	831	Total	C	N	O	S	0	0	0
			6729	4322	1148	1225	34			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	O	S		0	0
			5	4	1			
2	A	1	Total	O	S		0	0
			5	4	1			

- Molecule 3 is N-{(1S)-1-[7-fluoro-2-(pyridin-2-yl)quinolin-3-yl]ethyl}-9H-purin-6-amine (three-letter code: 3VC) (formula: $C_{21}H_{16}FN_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	N	0	0
			29	21	1	7		

- Molecule 4 is water.

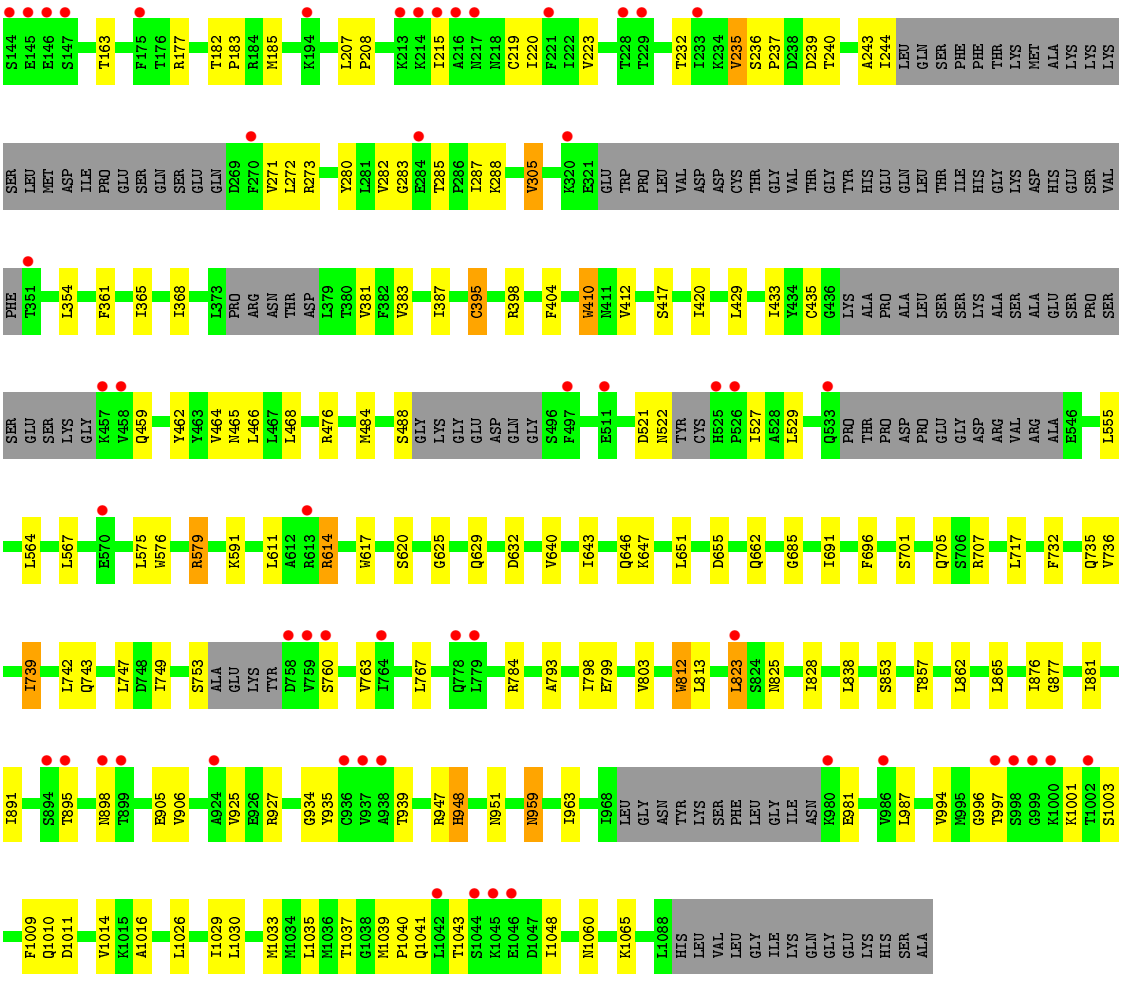
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	39	Total	O	0	0
			39	39		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	143.87Å 68.21Å 106.69Å 90.00° 94.81° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 28.71 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.2 (30.00-2.70) 95.3 (28.71-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 2.72Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.216 , 0.291 0.216 , 0.289	Depositor DCC
R_{free} test set	1951 reflections (7.16%)	wwPDB-VP
Wilson B-factor (Å^2)	71.7	Xtriage
Anisotropy	0.118	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 47.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6807	wwPDB-VP
Average B, all atoms (Å^2)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, 3VC

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	0.53	1/6872 (0.0%)	0.61	0/9296

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	812	TRP	CD2-CE2	5.36	1.47	1.41

There are no bond angle outliers.

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	6729	0	6768	107	0
2	A	10	0	0	0	0
3	A	29	0	16	0	0
4	A	39	0	0	0	0
All	All	6807	0	6784	107	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 8.

All (107) 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:767:LEU:HD22	1:A:803:VAL:HG23	1.37	1.06
1:A:235:VAL:HG11	1:A:244:ILE:HD13	1.52	0.91
1:A:767:LEU:HD22	1:A:803:VAL:CG2	2.10	0.81
1:A:767:LEU:CD2	1:A:803:VAL:HG23	2.14	0.78
1:A:925:VAL:HG13	1:A:994:VAL:HG12	1.65	0.77
1:A:272:LEU:HB3	1:A:305:VAL:HG21	1.66	0.76
1:A:273:ARG:O	1:A:305:VAL:HG23	1.86	0.75
1:A:215:ILE:HD12	1:A:220:ILE:HG22	1.68	0.73
1:A:743:GLN:HG3	1:A:876:ILE:HD13	1.71	0.72
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.71	0.70
1:A:240:THR:HG23	1:A:243:ALA:H	1.57	0.69
1:A:651:LEU:HD22	1:A:655:ASP:HB3	1.74	0.68
1:A:564:LEU:CD1	1:A:1048:ILE:HG22	2.23	0.68
1:A:576:TRP:CZ3	1:A:579:ARG:HD2	2.31	0.66
1:A:629:GLN:HG2	1:A:1029:ILE:HG13	1.76	0.66
1:A:235:VAL:HG12	1:A:239:ASP:OD2	1.95	0.65
1:A:466:LEU:HD11	1:A:476:ARG:HD3	1.79	0.64
1:A:996:GLY:O	1:A:1003:SER:OG	2.11	0.64
1:A:395:CYS:SG	1:A:417:SER:OG	2.56	0.64
1:A:735:GLN:O	1:A:739:ILE:HG23	1.99	0.61
1:A:838:LEU:HD12	1:A:877:GLY:HA3	1.82	0.61
1:A:611:LEU:O	1:A:614:ARG:CD	2.51	0.58
1:A:611:LEU:O	1:A:614:ARG:HD2	2.03	0.58
1:A:215:ILE:HD12	1:A:220:ILE:CG2	2.34	0.58
1:A:935:TYR:O	1:A:939:THR:HG23	2.04	0.58
1:A:891:ILE:HG22	1:A:906:VAL:HG12	1.87	0.57
1:A:271:VAL:CG2	1:A:282:VAL:HG22	2.36	0.56
1:A:812:TRP:CE2	1:A:881:ILE:HD13	2.41	0.56
1:A:925:VAL:HG13	1:A:994:VAL:CG1	2.35	0.56
1:A:280:TYR:HB3	1:A:282:VAL:HG23	1.89	0.55
1:A:685:GLY:HA2	1:A:691:ILE:HG22	1.89	0.55
1:A:521:ASP:OD1	1:A:522:ASN:N	2.39	0.55
1:A:1033:MET:O	1:A:1037:THR:HG23	2.07	0.55
1:A:749:ILE:CD1	1:A:767:LEU:HD13	2.38	0.54
1:A:368:ILE:HG21	1:A:433:ILE:HD11	1.90	0.54
1:A:207:LEU:HD12	1:A:208:PRO:HD2	1.90	0.54
1:A:625:GLY:O	1:A:629:GLN:HG3	2.08	0.53
1:A:743:GLN:CG	1:A:876:ILE:HD13	2.38	0.53
1:A:798:ILE:H	1:A:798:ILE:HD12	1.74	0.52
1:A:987:LEU:HD13	1:A:1009:PHE:CZ	2.44	0.52
1:A:223:VAL:HG22	1:A:232:THR:HG23	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1010:GLN:O	1:A:1014:VAL:HG23	2.11	0.51
1:A:361:PHE:HA	1:A:420:ILE:HD11	1.91	0.51
1:A:387:ILE:HD12	1:A:468:LEU:HD11	1.91	0.51
1:A:1035:LEU:HB3	1:A:1043:THR:HG21	1.91	0.51
1:A:235:VAL:HG12	1:A:239:ASP:CG	2.31	0.51
1:A:576:TRP:CH2	1:A:579:ARG:HD2	2.46	0.50
1:A:947:ARG:NH2	1:A:963:ILE:O	2.43	0.50
1:A:862:LEU:HD21	1:A:1016:ALA:HB2	1.94	0.50
1:A:555:LEU:HD11	1:A:575:LEU:HD23	1.92	0.50
1:A:354:LEU:HD12	1:A:527:ILE:HG22	1.93	0.50
1:A:853:SER:O	1:A:857:THR:HG23	2.12	0.50
1:A:701:SER:O	1:A:705:GLN:HG2	2.11	0.50
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.94	0.49
1:A:272:LEU:CB	1:A:305:VAL:HG21	2.39	0.48
1:A:163:THR:HG22	1:A:177:ARG:NH1	2.28	0.48
1:A:696:PHE:CD1	1:A:717:LEU:HD11	2.49	0.48
1:A:747:LEU:HD21	1:A:876:ILE:HD12	1.95	0.48
1:A:220:ILE:HG12	1:A:287:ILE:HD13	1.96	0.47
1:A:823:LEU:H	1:A:823:LEU:HD22	1.80	0.47
1:A:1026:LEU:O	1:A:1030:LEU:HG	2.14	0.47
1:A:742:LEU:HD22	1:A:813:LEU:CD1	2.46	0.46
1:A:862:LEU:HD23	1:A:934:GLY:N	2.30	0.46
1:A:219:CYS:HA	1:A:235:VAL:O	2.16	0.46
1:A:237:PRO:HA	1:A:287:ILE:HD12	1.98	0.46
1:A:361:PHE:HA	1:A:420:ILE:CD1	2.46	0.46
1:A:611:LEU:O	1:A:614:ARG:HD3	2.15	0.46
1:A:895:THR:HB	1:A:906:VAL:HG13	1.99	0.45
1:A:237:PRO:HA	1:A:287:ILE:CD1	2.47	0.45
1:A:567:LEU:HD21	1:A:591:LYS:HG2	2.00	0.44
1:A:564:LEU:HD13	1:A:1048:ILE:HG22	2.00	0.44
1:A:948:HIS:ND1	1:A:951:ASN:ND2	2.53	0.44
1:A:235:VAL:CG1	1:A:239:ASP:OD2	2.65	0.44
1:A:365:ILE:HD12	1:A:383:VAL:HG11	1.99	0.44
1:A:564:LEU:HD11	1:A:1048:ILE:CG2	2.44	0.44
1:A:614:ARG:HG2	1:A:614:ARG:O	2.17	0.44
1:A:280:TYR:HB3	1:A:282:VAL:CG2	2.48	0.44
1:A:732:PHE:O	1:A:736:VAL:HG23	2.18	0.43
1:A:640:VAL:O	1:A:643:ILE:HG12	2.17	0.43
1:A:760:SER:HB2	1:A:763:VAL:HB	1.99	0.43
1:A:1014:VAL:HG11	1:A:1065:LYS:HG3	1.99	0.43
1:A:381:VAL:HG23	1:A:404:PHE:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:SER:O	1:A:647:LYS:NZ	2.51	0.43
1:A:617:TRP:CE2	1:A:643:ILE:HD12	2.53	0.43
1:A:793:ALA:HA	1:A:828:ILE:HD12	1.98	0.43
1:A:1041:GLN:HG2	1:A:1043:THR:HG23	2.00	0.43
1:A:433:ILE:HD12	1:A:484:MET:HE1	2.00	0.43
1:A:282:VAL:HG12	1:A:283:GLY:N	2.34	0.42
1:A:632:ASP:C	1:A:632:ASP:OD1	2.57	0.42
1:A:927:ARG:NH2	1:A:959:ASN:OD1	2.51	0.42
1:A:354:LEU:HD22	1:A:529:LEU:HD13	2.00	0.42
1:A:466:LEU:HD11	1:A:476:ARG:CD	2.48	0.42
1:A:464:VAL:HG22	1:A:465:ASN:N	2.35	0.42
1:A:862:LEU:CD2	1:A:934:GLY:HA2	2.50	0.42
1:A:799:GLU:CD	1:A:799:GLU:H	2.23	0.42
1:A:215:ILE:CD1	1:A:220:ILE:CG2	2.98	0.41
1:A:235:VAL:HG13	1:A:244:ILE:HG21	2.02	0.41
1:A:235:VAL:CG1	1:A:244:ILE:HD13	2.38	0.41
1:A:462:TYR:HB2	1:A:484:MET:HE1	2.02	0.41
1:A:237:PRO:HB3	1:A:288:LYS:HB3	2.02	0.41
1:A:381:VAL:HG22	1:A:435:CYS:HB3	2.02	0.41
1:A:997:THR:HG23	1:A:1001:LYS:HB2	2.02	0.40
1:A:354:LEU:HD12	1:A:527:ILE:CG2	2.51	0.40
1:A:1029:ILE:HG23	1:A:1029:ILE:HD12	1.85	0.40
1:A:361:PHE:HB2	1:A:420:ILE:HD12	2.04	0.40
1:A:410:TRP:HB3	1:A:412:VAL:HG22	2.03	0.40
1:A:182:THR:HB	1:A:183:PRO:HD3	2.04	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	811/959 (85%)	769 (95%)	40 (5%)	2 (0%)	47 73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	579	ARG
1	A	1040	PRO

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	747/857 (87%)	719 (96%)	28 (4%)	34 63

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	185	MET
1	A	235	VAL
1	A	236	SER
1	A	285	THR
1	A	305	VAL
1	A	395	CYS
1	A	398	ARG
1	A	410	TRP
1	A	459	GLN
1	A	488	SER
1	A	614	ARG
1	A	646	GLN
1	A	662	GLN
1	A	707	ARG
1	A	739	ILE
1	A	753	SER
1	A	784	ARG
1	A	823	LEU
1	A	825	ASN
1	A	865	LEU
1	A	898	ASN
1	A	905	GLU
1	A	948	HIS

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Mol	Chain	Res	Type
1	A	959	ASN
1	A	981	GLU
1	A	1011	ASP
1	A	1039	MET
1	A	1060	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	898	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 carbohydrates in this entry.

5.6 Ligand geometry

3 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	SO4	A	1202	-	4,4,4	0.40	0	6,6,6	0.38	0
2	SO4	A	1201	-	4,4,4	0.34	0	6,6,6	0.11	0
3	3VC	A	1203	-	29,33,33	1.92	4 (13%)	33,47,47	1.95	8 (24%)

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	3VC	A	1203	-	-	4/12/12/12	0/5/5/5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1203	3VC	C2-C12	-7.87	1.38	1.49
3	A	1203	3VC	C3-N1	-2.40	1.33	1.37
3	A	1203	3VC	C6-C7	2.23	1.39	1.36
3	A	1203	3VC	C20-N4	-2.22	1.34	1.37

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1203	3VC	C17-N3-C18	5.47	121.28	116.59
3	A	1203	3VC	C11-C10-C1	-3.62	106.39	111.60
3	A	1203	3VC	N4-C17-N3	-3.50	123.21	128.68
3	A	1203	3VC	N7-C18-N3	2.98	122.59	118.06
3	A	1203	3VC	C8-C7-C6	-2.79	120.15	123.23
3	A	1203	3VC	C16-N2-C12	2.67	120.97	117.23
3	A	1203	3VC	C20-C19-N5	-2.44	106.86	109.40
3	A	1203	3VC	C17-N4-C20	2.09	118.35	113.45

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1203	3VC	N2-C12-C2-C1
3	A	1203	3VC	C13-C12-C2-C1
3	A	1203	3VC	N2-C12-C2-N1
3	A	1203	3VC	C13-C12-C2-N1

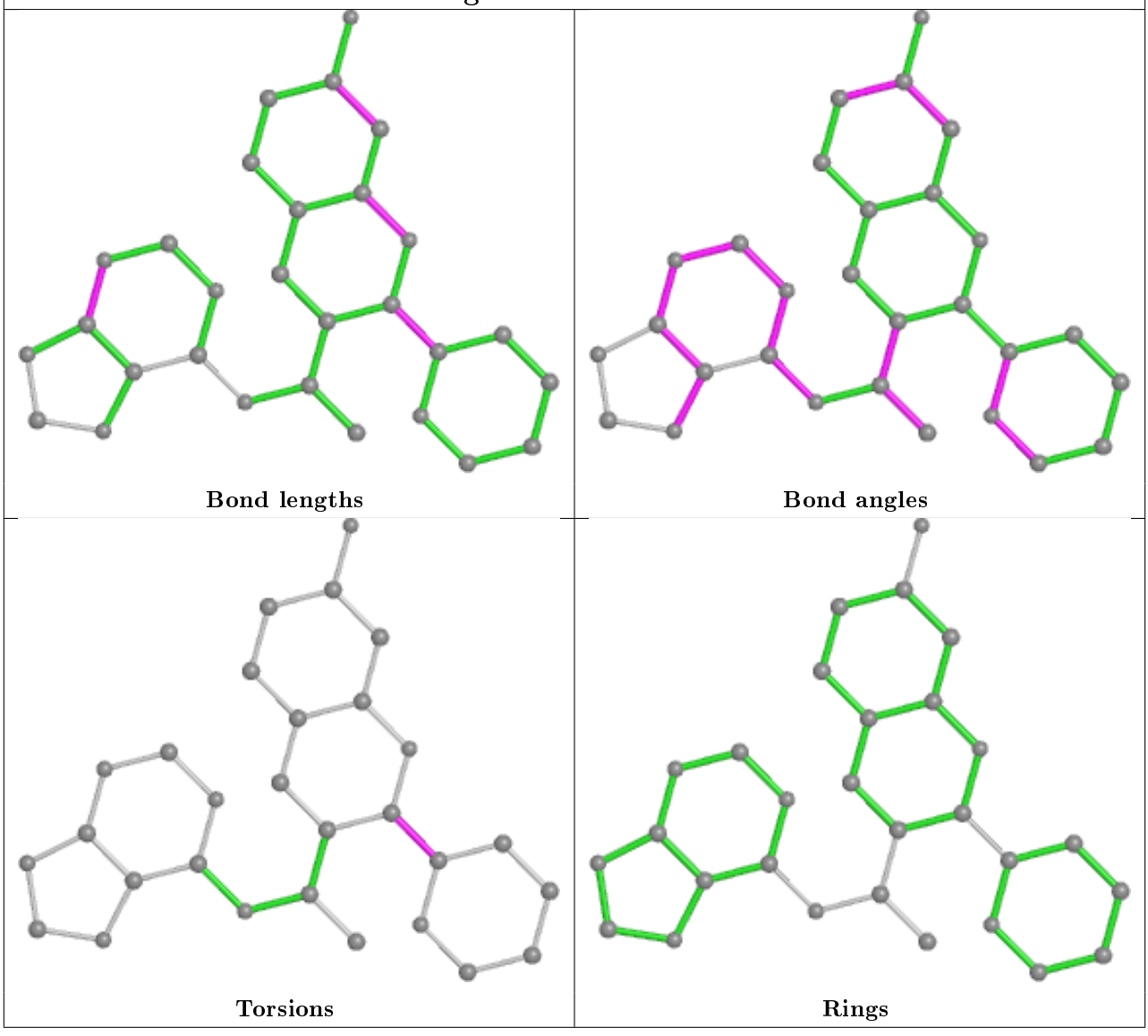
There are no ring outliers.

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 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 3VC A 1203



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	831/959 (86%)	0.17	54 (6%)	18	17	46, 80, 132, 159	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	999	GLY	6.7
1	A	997	THR	6.4
1	A	998	SER	5.5
1	A	1044	SER	5.1
1	A	533	GLN	5.0
1	A	525	HIS	4.9
1	A	457	LYS	4.7
1	A	1000	LYS	4.7
1	A	228	THR	4.1
1	A	145	GLU	4.0
1	A	895	THR	3.9
1	A	147	SER	3.7
1	A	980	LYS	3.6
1	A	613	ARG	3.5
1	A	351	THR	3.5
1	A	778	GLN	3.5
1	A	320	LYS	3.4
1	A	146	GLU	3.4
1	A	758	ASP	3.4
1	A	1042	LEU	3.4
1	A	759	VAL	3.3
1	A	526	PRO	3.3
1	A	936	CYS	3.2
1	A	823	LEU	3.1
1	A	779	LEU	3.1
1	A	194	LYS	3.0
1	A	284	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	270	PHE	3.0
1	A	144	SER	2.9
1	A	221	PHE	2.9
1	A	764	ILE	2.9
1	A	497	PHE	2.9
1	A	899	THR	2.8
1	A	217	ASN	2.7
1	A	214	LYS	2.7
1	A	216	ALA	2.6
1	A	937	VAL	2.5
1	A	894	SER	2.5
1	A	175	PHE	2.5
1	A	213	LYS	2.4
1	A	511	GLU	2.4
1	A	1045	LYS	2.4
1	A	229	THR	2.3
1	A	938	ALA	2.2
1	A	570	GLU	2.2
1	A	215	ILE	2.2
1	A	760	SER	2.1
1	A	898	ASN	2.1
1	A	1046	GLU	2.1
1	A	233	ILE	2.1
1	A	458	VAL	2.1
1	A	986	VAL	2.1
1	A	924	ALA	2.1
1	A	1002	THR	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 carbohydrates 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,

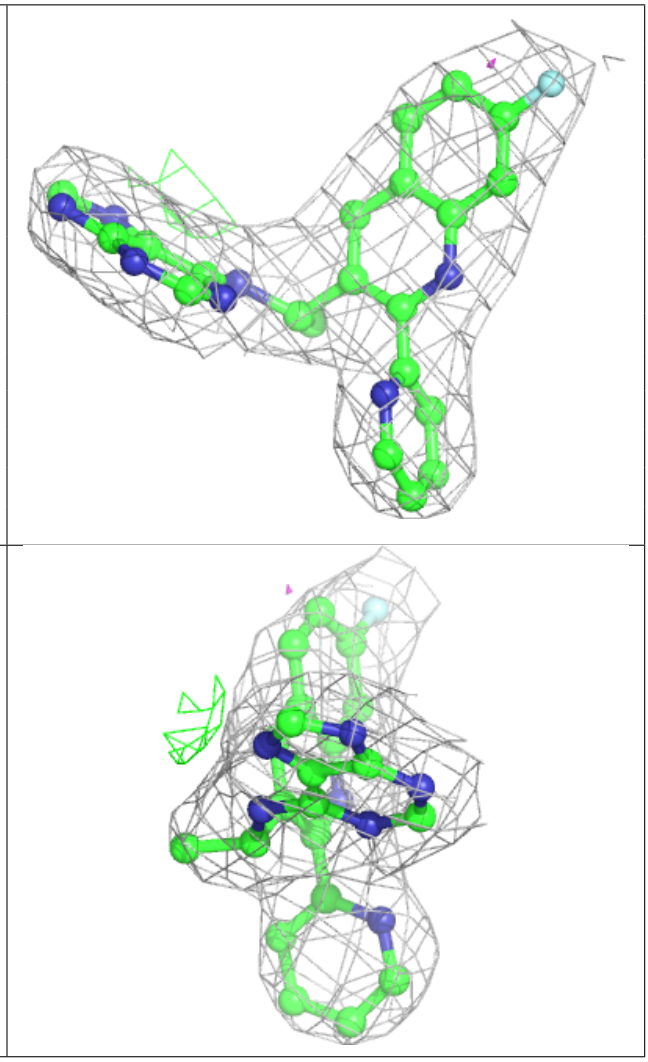
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	A	1202	5/5	0.96	0.11	64,65,79,81	0
3	3VC	A	1203	29/29	0.96	0.12	54,65,74,74	0
2	SO4	A	1201	5/5	0.97	0.11	84,91,96,105	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 3VC A 1203:

$2mF_o$-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

There are no such residues in this entry.