Full wwPDB X-ray Structure Validation Report (i)

Sep 2, 2023 – 10:05 PM EDT

PDB ID	:	3QK0
Title	:	Crystal structure of PI3K-gamma in complex with benzothiazole 82
Authors	:	Whittington, D.A.; Tang, J.; Yakowec, P.
Deposited on	:	2011-01-31
Resolution	:	2.85 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:

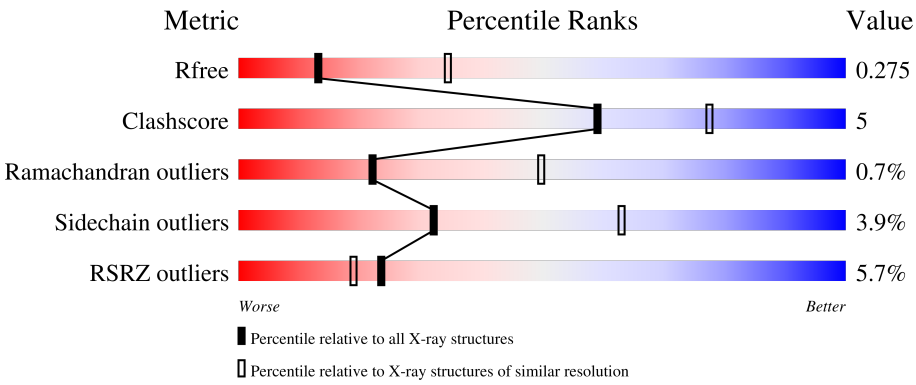
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	960	5% 73% 12% • 15%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6691 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.

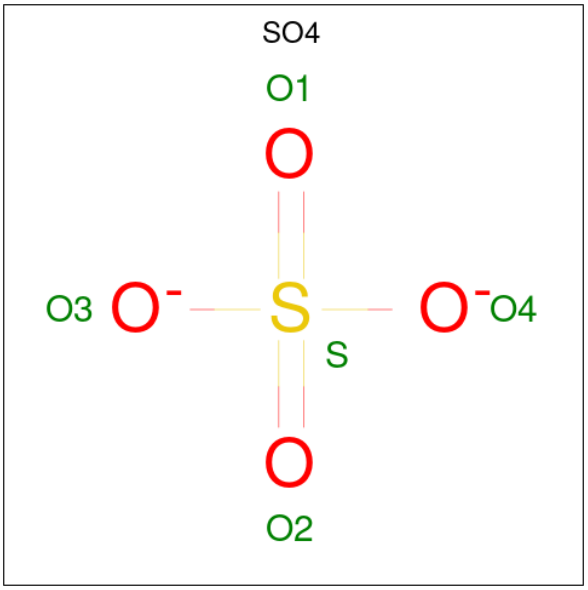
- Molecule 1 is a protein called Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	820	6638	4267	1132	1205	34	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	GLY	-	expression tag	UNP P48736

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



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

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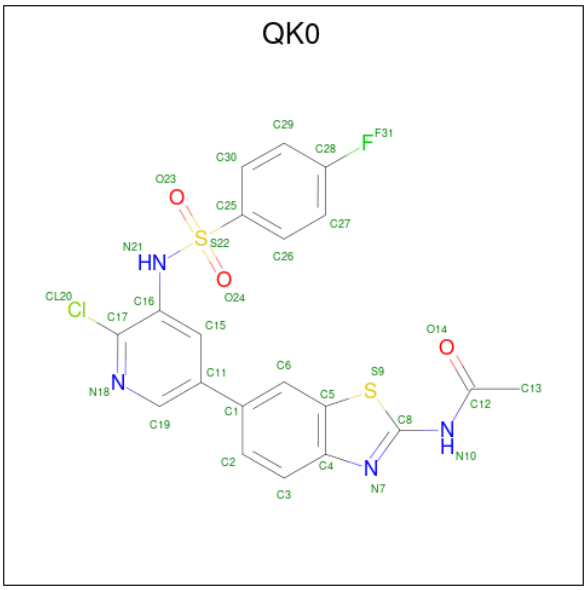
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is N-[6-(6-chloro-5-{[(4-fluorophenyl)sulfonyl]amino}pyridin-3-yl)-1,3-benzothiazol-2-yl]acetamide (three-letter code: QK0) (formula: $C_{20}H_{14}ClFN_4O_3S_2$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	Cl	F	N	O	S		
3	A	1	31	20	1	1	4	3	2	0	0

- Molecule 4 is water.

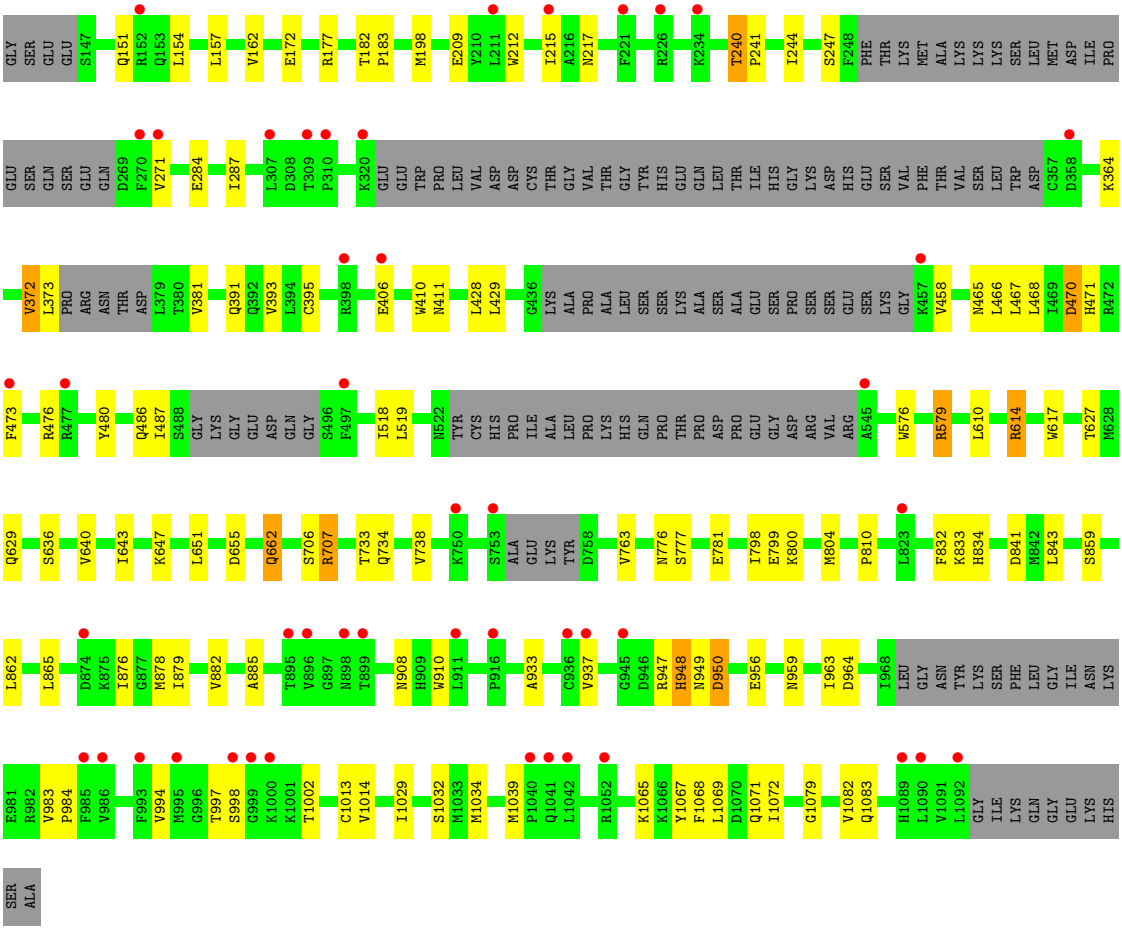
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	7	7	7	0	0

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:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	144.53Å 67.83Å 107.10Å 90.00° 95.34° 90.00°	Depositor
Resolution (Å)	30.00 – 2.85 29.18 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.4 (30.00-2.85) 99.4 (29.18-2.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.23 (at 2.85Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.226 , 0.277 0.223 , 0.275	Depositor DCC
R_{free} test set	1432 reflections (5.92%)	wwPDB-VP
Wilson B-factor (Å^2)	80.8	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 49.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6691	wwPDB-VP
Average B, all atoms (Å^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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: QK0, SO4

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	0.40	0/6778	0.53	0/9169

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	6638	0	6692	63	0
2	A	15	0	0	0	0
3	A	31	0	14	3	0
4	A	7	0	0	0	0
All	All	6691	0	6706	63	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 5.

All (63) 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:834:HIS:HB2	1:A:876:ILE:HD12	1.46	0.93
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.58	0.85
1:A:947:ARG:NH2	1:A:963:ILE:O	2.24	0.70
1:A:162:VAL:HG12	1:A:177:ARG:HD2	1.74	0.69
1:A:244:ILE:HA	1:A:247:SER:HB2	1.73	0.68
1:A:372:VAL:HG12	1:A:373:LEU:H	1.56	0.68
1:A:629:GLN:HG2	1:A:1029:ILE:HG13	1.74	0.68
1:A:486:GLN:HG2	1:A:487:ILE:H	1.59	0.68
1:A:908:ASN:HD22	1:A:994:VAL:HA	1.62	0.64
1:A:162:VAL:CG1	1:A:177:ARG:HD2	2.29	0.63
1:A:576:TRP:O	1:A:579:ARG:HD3	1.98	0.62
1:A:182:THR:HB	1:A:183:PRO:HD3	1.80	0.62
1:A:428:LEU:HD22	1:A:465:ASN:HB3	1.81	0.61
1:A:798:ILE:HD12	1:A:798:ILE:H	1.66	0.59
1:A:364:LYS:HE2	1:A:411:ASN:OD1	2.05	0.56
1:A:209:GLU:HB2	1:A:859:SER:HB3	1.88	0.56
1:A:640:VAL:O	1:A:643:ILE:HG12	2.06	0.56
1:A:429:LEU:CB	1:A:468:LEU:HD21	2.35	0.54
1:A:1014:VAL:HG11	1:A:1065:LYS:HG3	1.90	0.53
1:A:1013:CYS:HB3	1:A:1068:PHE:HE2	1.74	0.52
1:A:707:ARG:H	1:A:707:ARG:HH11	1.56	0.52
1:A:614:ARG:HG2	1:A:614:ARG:O	2.11	0.51
1:A:466:LEU:HD11	1:A:476:ARG:HD3	1.94	0.50
1:A:364:LYS:HB3	1:A:519:LEU:HB3	1.94	0.50
1:A:950:ASP:OD1	1:A:950:ASP:N	2.40	0.49
1:A:947:ARG:HH11	1:A:948:HIS:CE1	2.30	0.48
1:A:372:VAL:HG12	1:A:373:LEU:N	2.27	0.48
1:A:1013:CYS:HB3	1:A:1068:PHE:CE2	2.49	0.48
1:A:964:ASP:HA	3:A:1103:QK0:CL20	2.51	0.47
1:A:151:GLN:HA	1:A:154:LEU:HD12	1.97	0.47
1:A:617:TRP:O	1:A:647:LYS:NZ	2.47	0.47
1:A:240:THR:HG22	1:A:241:PRO:HD2	1.97	0.46
1:A:651:LEU:HD22	1:A:655:ASP:HB3	1.97	0.46
1:A:172:GLU:HG3	1:A:471:HIS:ND1	2.30	0.46
1:A:198:MET:SD	1:A:271:VAL:HG11	2.55	0.46
1:A:910:TRP:CH2	1:A:956:GLU:HA	2.51	0.45
1:A:212:TRP:HA	1:A:215:ILE:HD12	1.97	0.44
1:A:833:LYS:O	1:A:876:ILE:HG13	2.17	0.44
1:A:579:ARG:HG2	1:A:610:LEU:HD22	2.00	0.44
1:A:983:VAL:HB	1:A:1082:VAL:HG21	1.98	0.44
1:A:882:VAL:O	3:A:1103:QK0:H13	2.18	0.43
1:A:949:ASN:HB2	1:A:1083:GLN:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:ASP:HB2	1:A:476:ARG:NH2	2.34	0.43
1:A:480:TYR:HB2	1:A:518:ILE:HG13	2.01	0.43
1:A:734:GLN:O	1:A:738:VAL:HG23	2.19	0.43
1:A:983:VAL:HA	1:A:984:PRO:HD2	1.83	0.43
1:A:862:LEU:N	1:A:862:LEU:HD12	2.34	0.43
1:A:997:THR:HG22	1:A:998:SER:N	2.33	0.43
1:A:1067:TYR:O	1:A:1071:GLN:HG2	2.19	0.42
1:A:1069:LEU:HD23	1:A:1072:ILE:HD12	2.01	0.42
1:A:614:ARG:NH2	1:A:643:ILE:HG22	2.34	0.42
1:A:576:TRP:CD2	1:A:579:ARG:HD2	2.55	0.42
1:A:157:LEU:HD21	1:A:733:THR:HA	2.02	0.42
1:A:467:LEU:O	1:A:476:ARG:HD2	2.20	0.42
1:A:804:MET:HB2	1:A:810:PRO:HD2	2.01	0.42
1:A:885:ALA:O	3:A:1103:QK0:H13B	2.20	0.41
1:A:878:MET:C	1:A:879:ILE:HG13	2.41	0.41
1:A:662:GLN:HE21	1:A:662:GLN:HB3	1.72	0.41
1:A:933:ALA:O	1:A:937:VAL:HG23	2.20	0.41
1:A:287:ILE:H	1:A:287:ILE:HG13	1.70	0.40
1:A:865:LEU:HD23	1:A:865:LEU:HA	1.96	0.40
1:A:372:VAL:CG1	1:A:373:LEU:H	2.28	0.40
1:A:843:LEU:HD13	1:A:1034:MET:HG3	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	802/960 (84%)	745 (93%)	51 (6%)	6 (1%)	22 50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	777	SER
1	A	1079	GLY
1	A	217	ASN
1	A	406	GLU
1	A	579	ARG
1	A	372	VAL

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	737/857 (86%)	708 (96%)	29 (4%)	32 63

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	240	THR
1	A	284	GLU
1	A	381	VAL
1	A	391	GLN
1	A	393	VAL
1	A	395	CYS
1	A	410	TRP
1	A	458	VAL
1	A	470	ASP
1	A	473	PHE
1	A	614	ARG
1	A	627	THR
1	A	636	SER
1	A	662	GLN
1	A	706	SER
1	A	707	ARG
1	A	763	VAL
1	A	776	ASN
1	A	781	GLU
1	A	799	GLU
1	A	800	LYS

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Mol	Chain	Res	Type
1	A	832	PHE
1	A	841	ASP
1	A	948	HIS
1	A	950	ASP
1	A	959	ASN
1	A	1002	THR
1	A	1032	SER
1	A	1039	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	391	GLN
1	A	459	GLN
1	A	554	GLN
1	A	662	GLN
1	A	711	GLN
1	A	743	GLN
1	A	846	GLN
1	A	908	ASN
1	A	949	ASN
1	A	951	ASN
1	A	1007	GLN
1	A	1010	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)

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	$\#\|Z\| > 2$
3	QK0	A	1103	-	30,34,34	2.10	4 (13%)	35,50,50	2.30	9 (25%)
2	SO4	A	2	-	4,4,4	0.15	0	6,6,6	0.10	0
2	SO4	A	1	-	4,4,4	0.13	0	6,6,6	0.13	0
2	SO4	A	3	-	4,4,4	0.16	0	6,6,6	0.13	0

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	QK0	A	1103	-	-	2/13/19/19	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1103	QK0	O23-S22	6.48	1.50	1.43
3	A	1103	QK0	O24-S22	6.15	1.50	1.43
3	A	1103	QK0	C16-N21	-4.73	1.34	1.42
3	A	1103	QK0	C17-N18	2.03	1.35	1.32

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1103	QK0	O24-S22-O23	-7.96	109.77	119.55
3	A	1103	QK0	C19-N18-C17	6.41	121.91	117.47
3	A	1103	QK0	C4-C5-S9	-4.17	106.32	111.85
3	A	1103	QK0	C6-C5-S9	3.53	132.15	125.10
3	A	1103	QK0	C5-C4-N7	2.70	114.32	108.04
3	A	1103	QK0	C16-C17-CL20	2.25	120.57	118.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	1103	QK0	C15-C16-C17	2.10	118.31	116.06
3	A	1103	QK0	O14-C12-N10	2.09	125.79	123.04
3	A	1103	QK0	CL20-C17-N18	2.02	119.09	115.99

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1103	QK0	C26-C25-S22-O24
3	A	1103	QK0	C30-C25-S22-O24

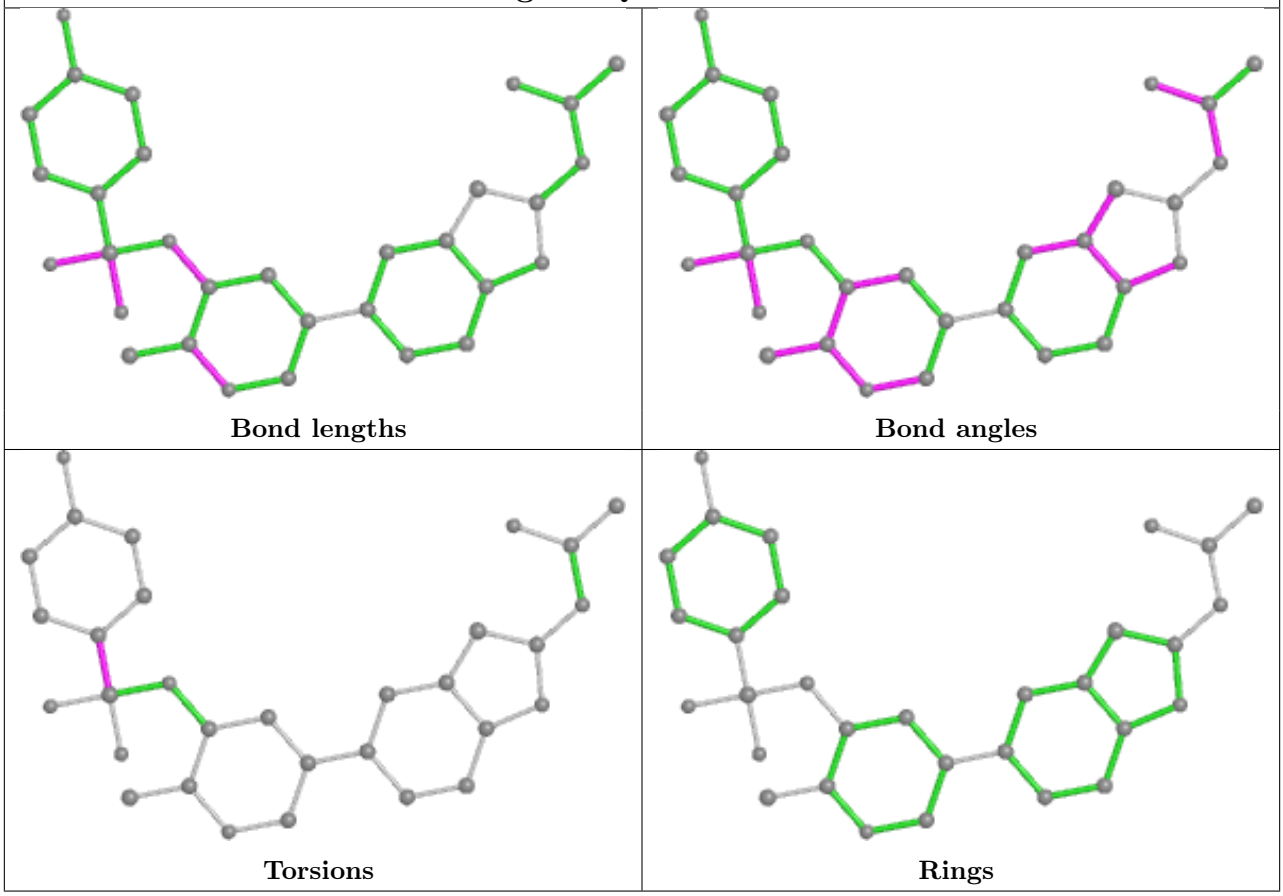
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1103	QK0	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 QK0 A 1103



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	820/960 (85%)	0.18	47 (5%) 23 19	49, 86, 135, 160	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	916	PRO	5.4
1	A	1090	LEU	4.3
1	A	320	LYS	4.2
1	A	998	SER	4.0
1	A	307	LEU	4.0
1	A	1042	LEU	3.9
1	A	1089	HIS	3.8
1	A	477	ARG	3.8
1	A	1000	LYS	3.7
1	A	895	THR	3.7
1	A	823	LEU	3.7
1	A	270	PHE	3.7
1	A	753	SER	3.5
1	A	545	ALA	3.4
1	A	999	GLY	3.4
1	A	1041	GLN	3.4
1	A	211	LEU	3.2
1	A	896	VAL	3.2
1	A	358	ASP	3.2
1	A	936	CYS	3.1
1	A	1092	LEU	3.1
1	A	406	GLU	3.0
1	A	234	LYS	3.0
1	A	310	PRO	2.9
1	A	226	ARG	2.8
1	A	457	LYS	2.7
1	A	899	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	985	PHE	2.7
1	A	986	VAL	2.7
1	A	497	PHE	2.7
1	A	152	ARG	2.6
1	A	271	VAL	2.6
1	A	993	PHE	2.5
1	A	398	ARG	2.5
1	A	995	MET	2.4
1	A	911	LEU	2.4
1	A	309	THR	2.4
1	A	937	VAL	2.3
1	A	898	ASN	2.2
1	A	1040	PRO	2.2
1	A	874	ASP	2.2
1	A	215	ILE	2.2
1	A	473	PHE	2.2
1	A	750	LYS	2.2
1	A	221	PHE	2.1
1	A	1052	ARG	2.0
1	A	945	GLY	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	SO4	A	3	5/5	0.78	0.23	144,144,144,144	0
3	QK0	A	1103	31/31	0.93	0.18	92,93,93,94	0
2	SO4	A	2	5/5	0.94	0.18	113,113,113,113	0

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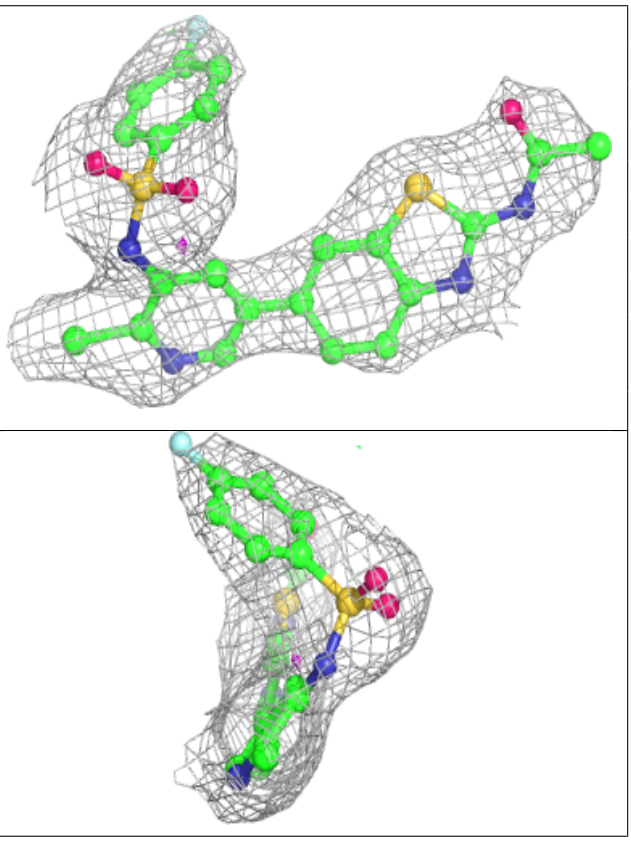
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	SO4	A	1	5/5	0.96	0.18	95,95,96,96	0

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 QK0 A 1103:

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.