wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 10:19 AM EDT

PDB ID	:	2X6J
Title	:	THE CRYSTAL STRUCTURE OF THE DROSOPHILA CLASS III PI3-KINASE VPS34 IN COMPLEX WITH PIK-93
Authors	:	Miller, S.; Tavshanjian, B.; Oleksy, A.; Perisic, O.; Houseman, B.T.; Shokat, K.M.; Williams, R.L.
Deposited on	:	2010-02-17
Resolution	:	3.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

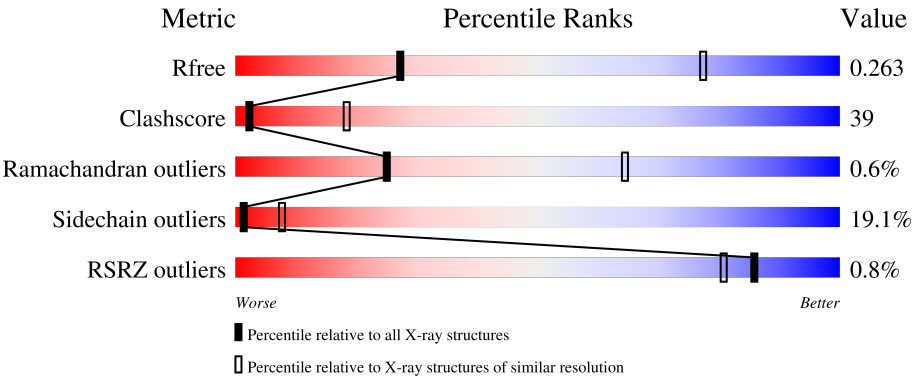
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	696	34% 34% 10% 22%
1	B	696	% 34% 34% 10% 22%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	093	B	1950	-	X	-	-

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8967 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.

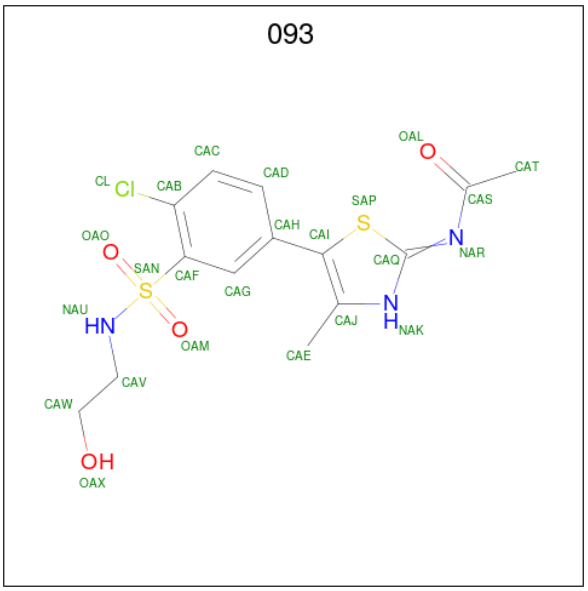
- Molecule 1 is a protein called PHOSPHOTIDYLINOSITOL 3 KINASE 59F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	0	0
			4457	2882	757	791	27			
1	B	546	Total	C	N	O	S	0	0	0
			4462	2886	759	790	27			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	254	GLY	-	expression tag	UNP Q9W1M7
A	255	SER	-	expression tag	UNP Q9W1M7
A	256	HIS	-	expression tag	UNP Q9W1M7
A	257	MET	-	expression tag	UNP Q9W1M7
A	455	ALA	GLY	engineered mutation	UNP Q9W1M7
B	254	GLY	-	expression tag	UNP Q9W1M7
B	255	SER	-	expression tag	UNP Q9W1M7
B	256	HIS	-	expression tag	UNP Q9W1M7
B	257	MET	-	expression tag	UNP Q9W1M7
B	455	ALA	GLY	engineered mutation	UNP Q9W1M7

- Molecule 2 is N-(5-(4-CHLORO-3-(2-HYDROXY-ETHYLSULFAMOYL)- PHENYLTHIAZOLE-2-YL)-ACETAMIDE (three-letter code: 093) (formula: $C_{14}H_{16}ClN_3O_4S_2$).



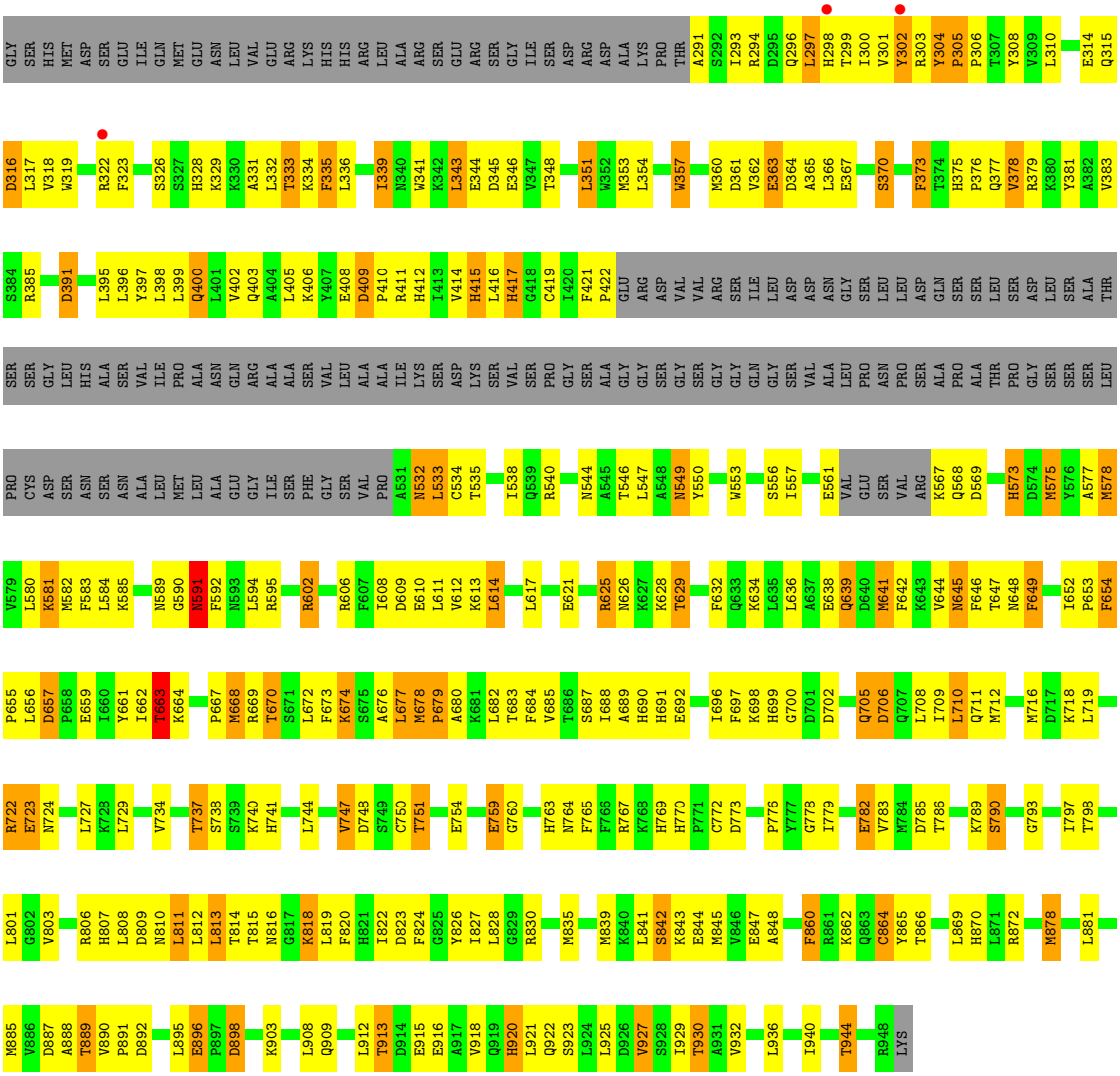
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			24	14	1	3	4	2		
2	B	1	Total	C	Cl	N	O	S	0	0
			24	14	1	3	4	2		

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.

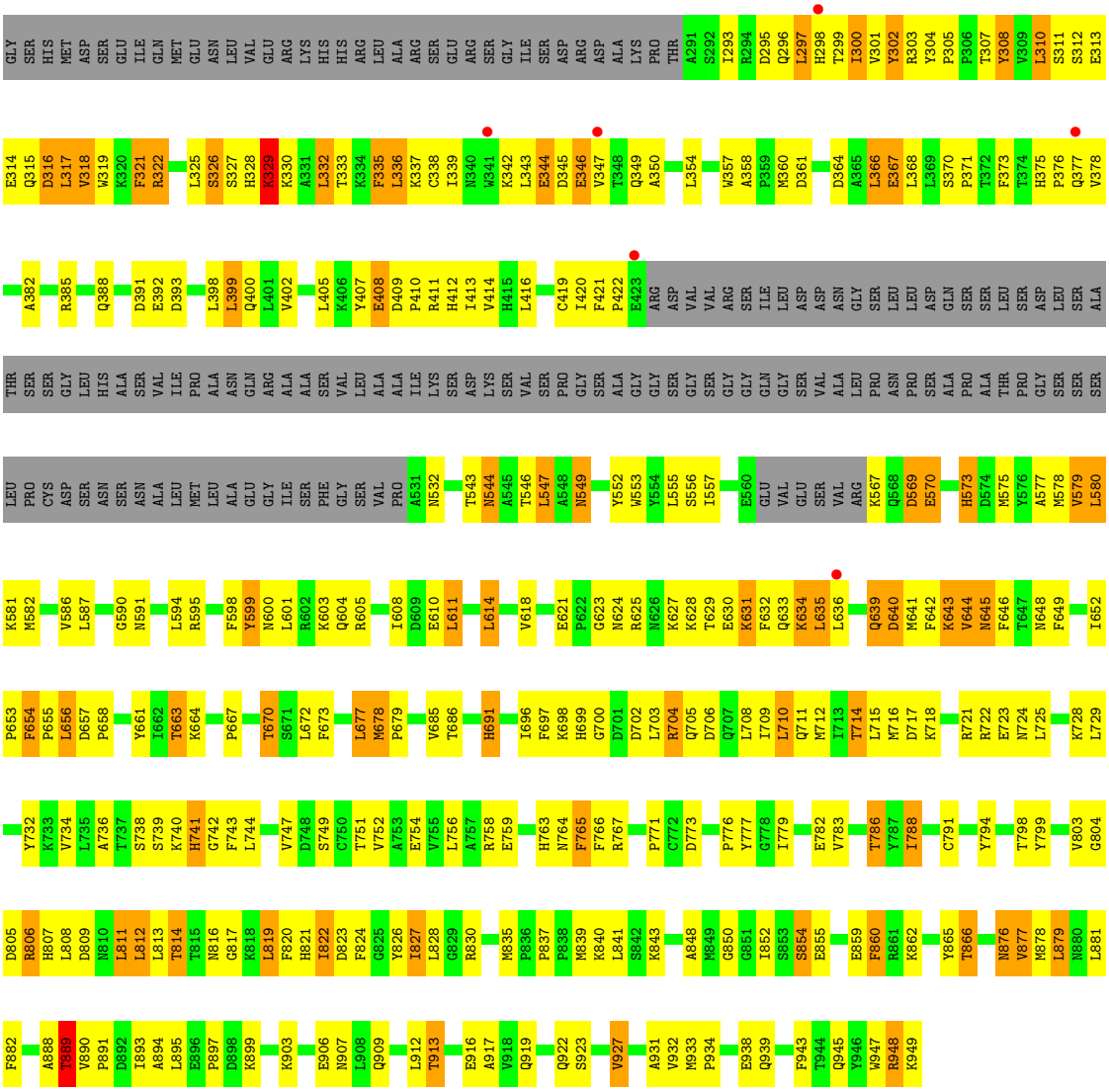
• Molecule 1: PHOSPHOTIDYLINOSITOL 3 KINASE 59F

Chain A:



• Molecule 1: PHOSPHOTIDYLINOSITOL 3 KINASE 59F

Chain B:


GLY SER HIS MET ASP SER GLU ILE GLN MET GLU ASN LEU VAL GLU ARG LYS HIS HIS ARG LEU ALA ARG SER GLU ARG SER GLY ILE SER ASP ARG ASP ALA LYS PRO THR A291 S292 I293 R294 D295 Q296 L297 H298 T299 I300 V301 Y302 R303 Y304 P305 P306 T307 Y308 V309 L310 S311 S312 E313
E314 Q315 D316 L317 V318 W319 K320 F321 R322 L325 S326 S327 H328 K329 K330 A331 L332 T333 K334 F335 L336 K337 C338 I339 N340 W341 K342 L343 E344 D345 E346 V347 T348 Q349 A350 L354 W357 A358 P359 M360 D361 D364 A365 L366 E367 L368 L369 S370 P371 T372 F373 T374 H375 P376 Q377 V378
A382 R385 Q388 D391 E392 D393 L398 L399 Q400 L401 V402 L405 K406 Y407 E408 D409 P410 R411 H412 I413 V414 H415 L416 C419 I420 F421 P422 E423 ARG ASP VAL VAL ARG SER ILE LEU ASP ASP ASN GLY SER LEU LEU ASP GLN SER SER LEU SER ASP LEU SER ALA
THR SER SER GLY LEU HIS ALA SER VAL ILE PRO ALA ASN GLN ARG ALA ALA SER VAL LEU ALA ALA ILE LYS SER ASP LYS SER VAL SER PRO GLY SER ALA GLY GLY SER GLY SER GLY GLY GLN GLY SER VAL ALA LEU PRO ASN PRO SER ALA PRO ALA THR PRO GLY SER SER SER
LEU PRO CYS ASP SER ASN SER ASN ALA LEU MET LEU ALA GLU GLY ILE SER PHE GLY SER VAL PRO A531 N532 T543 N544 A545 T546 L547 A548 N549 Y552 W553 Y554 L555 S556 I557 E560 GLU VAL GLU SER VAL ARG K567 Q568 D569 E570 H573 D574 M575 Y576 A577 M578 V579 L580
K581 M582 V586 L587 G590 N591 L594 R595 F598 Y599 N600 L601 R602 K603 Q604 R605 I608 D609 E610 L611 L614 V618 E621 P622 G623 N624 R625 N626 K627 K628 T629 E630 K631 F632 Q633 K634 L635 L636 Q639 D640 M641 F642 K643 V644 N645 F646 T647 N648 F649 I652
P653 F654 P655 L656 D657 P658 Y661 I662 T663 K664 P667 T670 S671 L672 F673 L677 M678 P679 V685 T686 H691 I696 F697 K698 H699 G700 D701 D702 L703 R704 Q705 D706 Q707 L708 I709 L710 Q711 M712 I713 T714 L715 M716 D717 K718 R721 R722 E723 N724 L725 K728 L729
Y732 K733 V734 L735 A736 T737 S738 S739 K740 H741 G742 F743 L744 V747 D748 S749 C750 T751 V752 A753 E754 V755 L756 A757 R758 E759 H763 N764 F765 F766 R767 P771 C772 D773 P776 Y777 G778 I779 E782 V783 T786 Y787 I788 C791 Y794 T798 Y799 V803 G804
D805 R806 H807 L808 D809 N810 L811 L812 L813 T814 T815 N816 G817 K818 L819 P820 H821 I822 D823 F824 G825 Y826 I827 L828 G829 R830 M835 P836 P837 P838 M839 K840 L841 S842 K843 A848 M849 G850 G851 I852 S853 S854 E855 E859 F860 R861 K862 Y865 T866 N876 V877 M878 L879 N880 L881
F882 A888 T889 V890 P891 D892 I893 A894 L895 E896 P897 D898 K899 K903 E906 N907 L908 Q909 L912 T913 E916 A917 V918 Q919 Q922 S923 V927 A931 V932 M933 P934 E938 Q939 F943 T944 Q945 Y946 W947 R948 K949

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	109.95Å 156.33Å 242.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	61.62 – 3.50 61.62 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (61.62-3.50) 99.5 (61.62-3.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.04 (at 3.49Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.230 , 0.272 0.225 , 0.263	Depositor DCC
R_{free} test set	1313 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	93.2	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 58.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	8967	wwPDB-VP
Average B, all atoms (Å^2)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: 093

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	0.61	1/4566 (0.0%)	0.84	1/6183 (0.0%)
1	B	0.48	0/4571	0.69	2/6189 (0.0%)
All	All	0.55	1/9137 (0.0%)	0.77	3/12372 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	864	CYS	CB-SG	-6.21	1.71	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	329	LYS	CD-CE-NZ	-5.49	99.07	111.70
1	A	818	LYS	N-CA-C	-5.24	96.86	111.00
1	B	710	LEU	CA-CB-CG	-5.02	103.75	115.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	589	ASN	Peptide

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Mol	Chain	Res	Type	Group
1	A	591	ASN	Mainchain
1	A	663	THR	Mainchain
1	A	680	ALA	Peptide
1	A	737	THR	Mainchain

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	4457	0	4490	348	1
1	B	4462	0	4499	348	1
2	A	24	0	16	8	0
2	B	24	0	16	6	0
All	All	8967	0	9021	697	2

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 39.

The worst 5 of 697 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:375:HIS:CD2	1:A:377:GLN:H	1.54	1.24
1:B:311:SER:HB3	1:B:314:GLU:CB	1.76	1.15
1:B:299:THR:HB	1:B:303:ARG:HH11	1.10	1.14
1:A:705:GLN:HG2	1:A:890:VAL:HG13	1.22	1.13
1:A:629:THR:HB	1:A:672:LEU:HD12	1.18	1.10

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:TYR:OH	1:A:782:GLU:OE1[6_555]	2.07	0.13
1:B:391:ASP:OD2	1:B:724:ASN:ND2[8_565]	2.18	0.02

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	539/696 (77%)	505 (94%)	30 (6%)	4 (1%)	22	61
1	B	540/696 (78%)	517 (96%)	20 (4%)	3 (1%)	25	64
All	All	1079/1392 (78%)	1022 (95%)	50 (5%)	7 (1%)	25	64

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	326	SER
1	A	305	PRO
1	B	408	GLU
1	A	304	TYR
1	A	591	ASN

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	490/612 (80%)	398 (81%)	92 (19%)	1	8
1	B	490/612 (80%)	395 (81%)	95 (19%)	1	7
All	All	980/1224 (80%)	793 (81%)	187 (19%)	1	8

5 of 187 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	398	LEU

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Mol	Chain	Res	Type
1	B	654	PHE
1	B	544	ASN
1	B	599	TYR
1	B	704	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	810	ASN
1	B	907	ASN
1	B	403	GLN
1	B	807	HIS
1	A	922	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)

2 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	093	B	1950	-	19,25,25	4.25	14 (73%)	23,36,36	3.12	11 (47%)
2	093	A	1949	-	19,25,25	4.02	12 (63%)	23,36,36	2.89	11 (47%)

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	093	B	1950	-	-	9/13/19/19	0/2/2/2
2	093	A	1949	-	-	2/13/19/19	0/2/2/2

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1950	093	CAG-CAF	11.88	1.49	1.37
2	A	1949	093	CAG-CAF	10.80	1.48	1.37
2	A	1949	093	SAN-NAU	7.86	1.73	1.61
2	B	1950	093	SAN-NAU	7.48	1.72	1.61
2	B	1950	093	CAD-CAC	5.17	1.47	1.36

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1949	093	OAO-SAN-OAM	-8.88	108.74	119.52
2	B	1950	093	OAO-SAN-OAM	-7.10	110.90	119.52
2	B	1950	093	CAT-CAS-NAR	6.79	124.91	114.84
2	B	1950	093	CAB-CAF-SAN	-5.44	119.44	123.19
2	B	1950	093	CAF-CAB-CL	-5.27	117.70	121.52

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1950	093	OAL-CAS-NAR-CAQ
2	B	1950	093	CAT-CAS-NAR-CAQ
2	B	1950	093	NAU-CAV-CAW-OAX
2	B	1950	093	CAV-NAU-SAN-OAM
2	B	1950	093	CAV-NAU-SAN-OAO

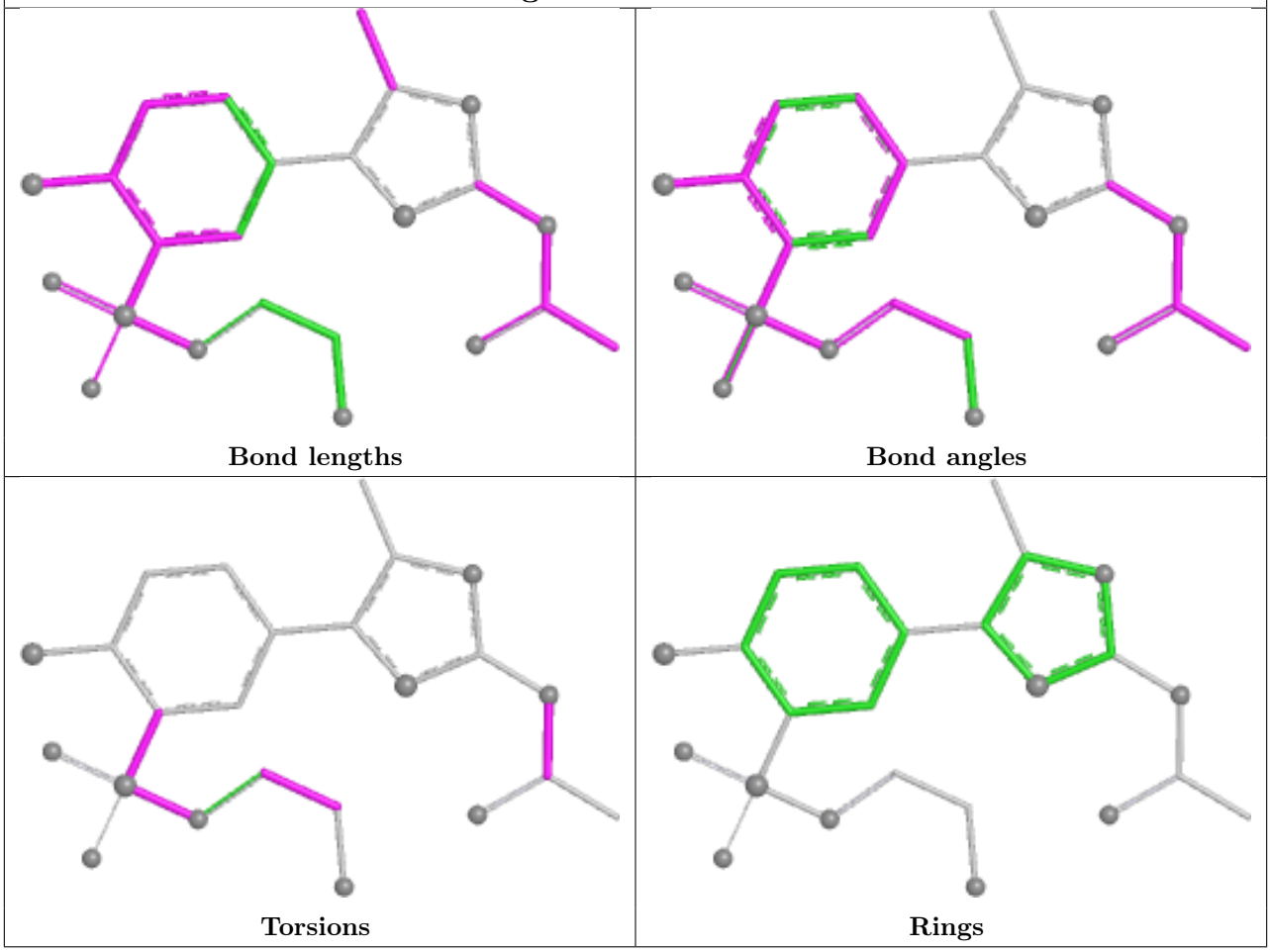
There are no ring outliers.

2 monomers are involved in 14 short contacts:

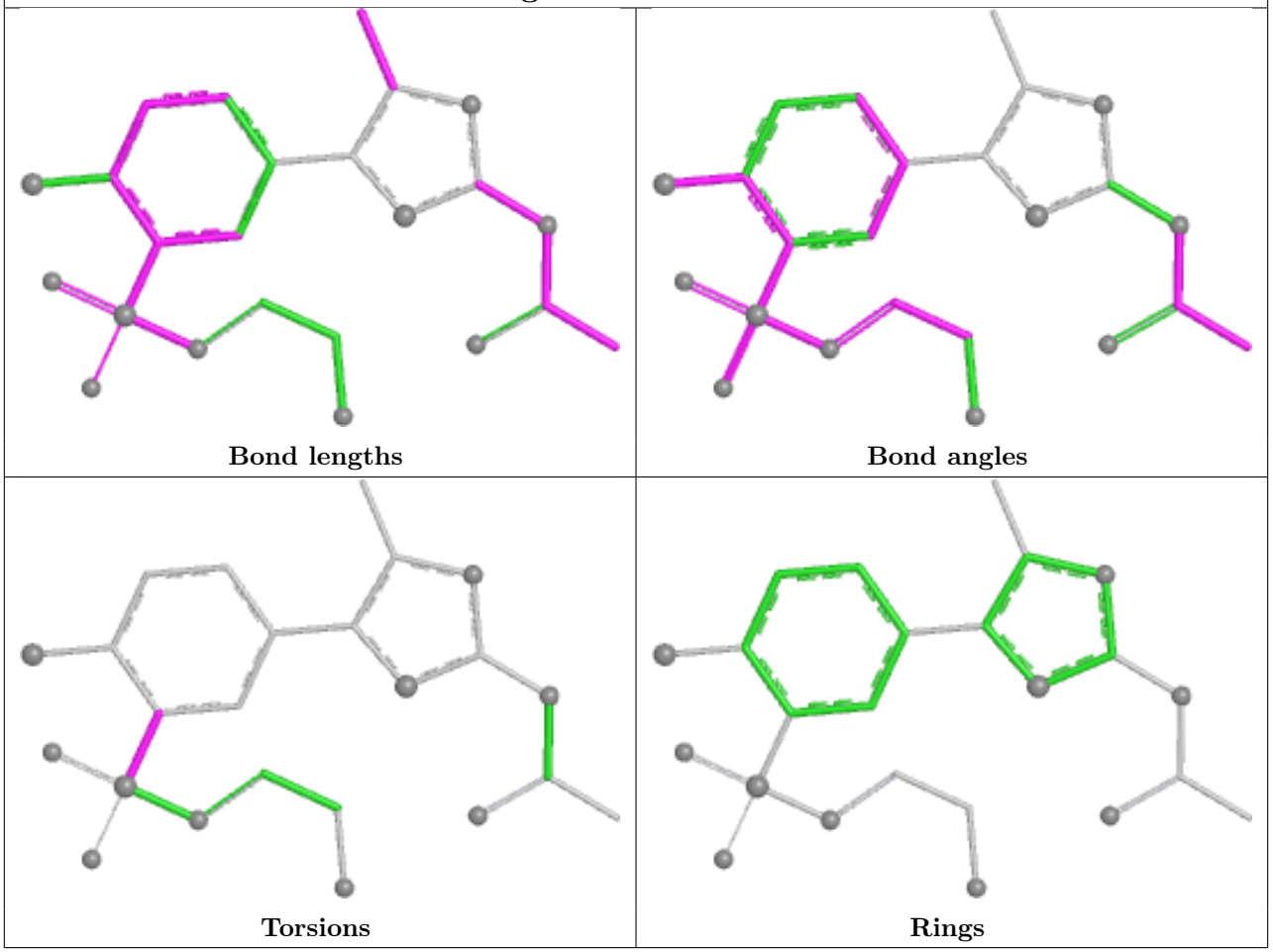
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1950	093	6	0
2	A	1949	093	8	0

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 093 B 1950



Ligand 093 A 1949



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, 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	545/696 (78%)	-0.29	3 (0%)	89	86	32, 55, 105, 116	0
1	B	546/696 (78%)	-0.18	6 (1%)	80	75	43, 65, 116, 123	0
All	All	1091/1392 (78%)	-0.23	9 (0%)	86	81	32, 61, 107, 123	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	341	TRP	3.1
1	A	302	TYR	2.7
1	B	636	LEU	2.5
1	A	322	ARG	2.2
1	A	298	HIS	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

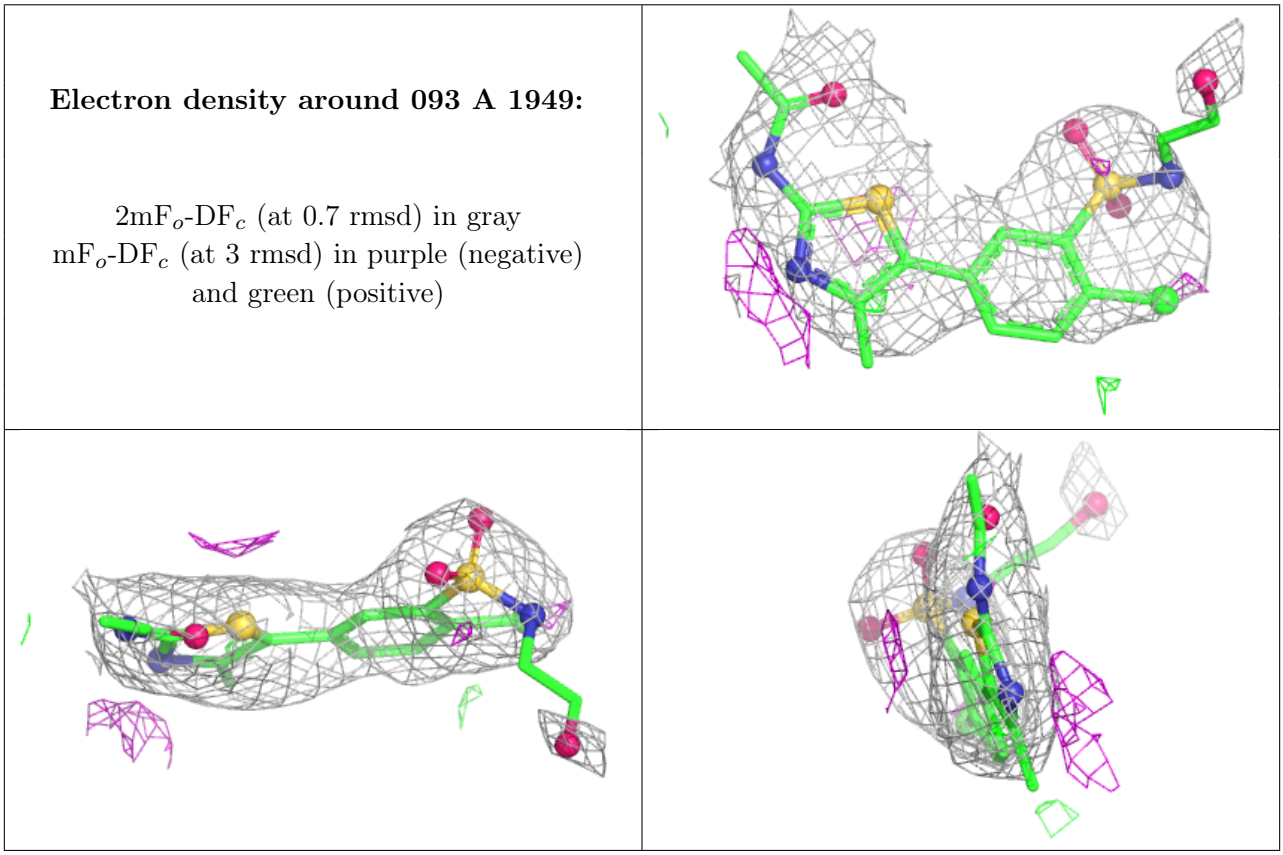
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	093	A	1949	24/24	0.89	0.31	87,97,104,107	0
2	093	B	1950	24/24	0.91	0.35	101,108,117,119	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.

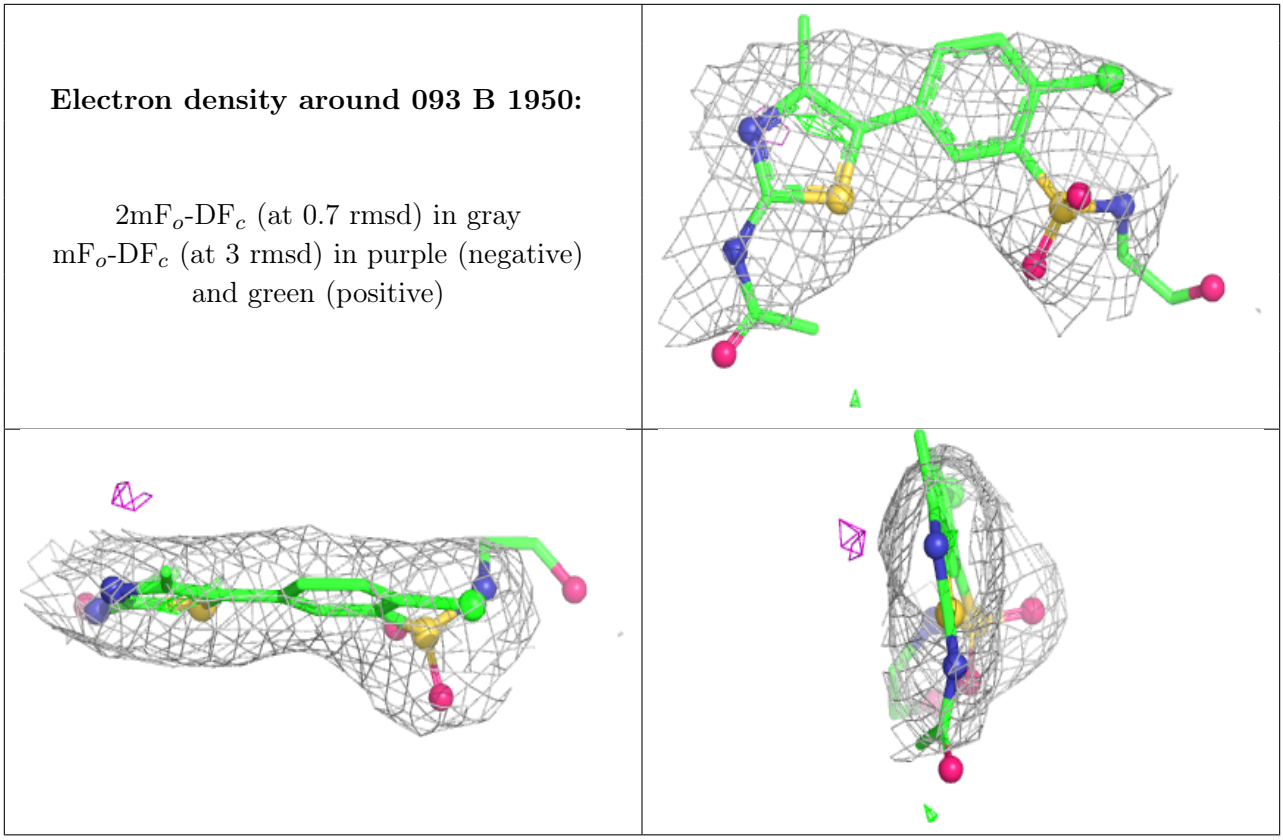
Electron density around 093 A 1949:

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



Electron density around 093 B 1950:

$2mF_o$-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.