

Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 – 06:24 am BST

PDB ID : 6GVH

Title: Crystal structure of PI3K alpha in complex with 3-(2-Amino-benzooxazol-5-y

1)-4-chloro-1-isopropyl-1H-pyrazolo[3,4-d]pyrimidin-6-ylamine

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Deposited on : 2018-06-21

Resolution : 2.74 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 following versions of software and data (see references (1)) 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)

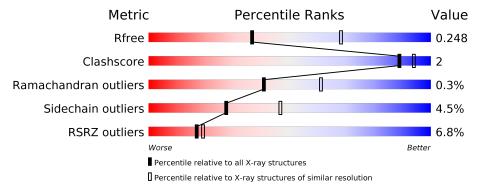
Validation Pipeline (wwPDB-VP) : 2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.74 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$egin{aligned} ext{Similar resolution} \ (\# ext{Entries}, ext{resolution range}(ext{Å})) \end{aligned}$
R_{free}	130704	$1271 \ (2.76 - 2.72)$
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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		
			6%		
1	A	962	86%	8%	5%



2 Entry composition (i)

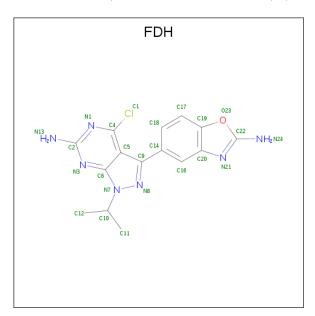
There are 3 unique types of molecules in this entry. The entry contains 7577 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 alpha isoform.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	913	Total 7426	C 4733	N 1271	O 1360	S 62	3	2	0

• Molecule 2 is 5-(6-azanyl-4-chloranyl-1-propan-2-yl-pyrazolo[3,4-d]pyrimidin-3-yl)-1,3-benzo xazol-2-amine (three-letter code: FDH) (formula: $C_{15}H_{14}ClN_7O$).



Mol	Chain	Residues	${f Atoms}$			ZeroOcc	AltConf		
2	A	1	Total 24	C 15	Cl 1	N 7	O 1	0	0

• Molecule 3 is water.

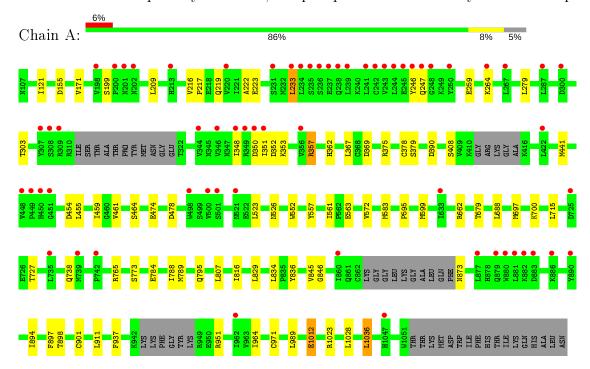
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
3	A	127	Total O 127 127	0	0



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 alpha isoform





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	58.11Å 133.60Å 141.16Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.50 - 2.74	Depositor
Resolution (A)	44.86 - 2.74	EDS
% Data completeness	90.2 (32.50-2.74)	Depositor
(in resolution range)	90.1 (44.86-2.74)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.12 (at 2.73Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
D D.	0.190 , 0.246	Depositor
R, R_{free}	0.200 , 0.248	DCC
R_{free} test set	1292 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	74.5	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.32,60.4	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	7577	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.84% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: FDH

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).

Mal	Chain	Bond	lengths	Bond angles		
Mol Chain	RMSZ	# Z >5	RMSZ	# Z > 5		
1	A	0.51	0/7591	0.66	0/10272	

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	7426	0	7330	28	0
2	A	24	0	0	1	0
3	A	127	0	0	1	0
All	All	7577	0	7330	28	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 (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:662:ARG:HD3	3:A:1238:HOH:O	2.05	0.56



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A 4 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}({\rm \AA})$	$overlap (\AA)$
1:A:557:TYR:HE1	1:A:561:ILE:HD11	1.74	0.53
1:A:209:LEU:HD13	1:A:223:GLU:HB3	1.90	0.52
1:A:989:LEU:HD11	1:A:1036:LEU:HD12	1.94	0.50
1:A:461:VAL:HB	1:A:679:THR:HG23	1.95	0.47
1:A:216:VAL:HB	1:A:219:GLN:HE21	1.80	0.46
1:A:572:VAL:HG21	1:A:583:MET:HG2	1.96	0.46
1:A:898:THR:HG22	1:A:964:ILE:HG12	1.98	0.46
1:A:362:HIS:HB2	1:A:367:LEU:HD11	1.99	0.45
1:A:1023:ARG:HG2	1:A:1028:LEU:HD12	1.99	0.44
1:A:353:LYS:HD3	1:A:375:ARG:HB3	1.98	0.44
1:A:894:ILE:O	1:A:898:THR:HG23	2.19	0.43
1:A:697:MET:SD	1:A:700:LYS:HD2	2.59	0.42
1:A:552:TRP:HZ3	1:A:583:MET:HE2	1.84	0.42
1:A:816:ILE:HG21	1:A:911:LEU:HD21	2.02	0.42
1:A:715:LEU:HD21	1:A:738:GLN:HG2	2.01	0.42
1:A:595:PRO:O	1:A:599:MET:HG3	2.20	0.42
1:A:765:ARG:HD3	1:A:784:GLU:HG3	2.01	0.42
1:A:897:PHE:O	1:A:901:CYS:HB2	2.19	0.42
1:A:357:ARG:HD3	1:A:455:LEU:HB2	2.02	0.42
1:A:216:VAL:HG13	1:A:217:PRO:HD2	2.02	0.41
1:A:523:LEU:HD21	1:A:557:TYR:CD2	2.56	0.41
1:A:1012:GLU:H	1:A:1012:GLU:HG2	1.67	0.41
1:A:121:ILE:HG22	1:A:688:LEU:HB3	2.02	0.41
1:A:836:TYR:OH	2:A:1101:FDH:N21	2.54	0.41
1:A:351:ILE:HG23	1:A:408:SER:HB2	2.02	0.41
1:A:807:LEU:HD12	1:A:846:GLY:HA3	2.02	0.41
1:A:222:ALA:HB2	1:A:247:GLN:HG2	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	905/962 (94%)	866 (96%)	36 (4%)	3 (0%)	41 61

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	246	TYR
1	A	233	LEU
1	A	264	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	Analysed Rotameric Out		Percentiles
1	A	826/875 (94%)	788 (95%)	38 (5%)	27 46

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	155	ASP
1	A	171	VAL
1	A	199	SER
1	A	233	LEU
1	A	259[A]	GLU
1	A	259[B]	GLU
1	A	279	LEU
1	A	303	THR
1	A	348	ILE
1	A	350	ASP
1	A	352	ASP
1	A	357	ARG
1	A	369	ASP
1	A	378	CYS
1	A	379	SER
1	A	390	ASP
1	A	441	MET
1	A	454	ASP



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Mol	Chain	Res	Type
1	A	459	ILE
1	A	464	SER
1	A	474	GLU
1	A	478	ASP
1	A	526	ASN
1	A	563	GLU
1	A	727	THR
1	A	773	SER
1	A	788	ILE
1	A	789	MET
1	A	795	GLN
1	A	829	LEU
1	A	834	LEU
1	A	845	VAL
1	A	873	ASN
1	A	937	PHE
1	A	951	ARG
1	A	971	CYS
1	A	1012	GLU
1	A	1036	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	183	ASN
1	A	219	GLN
1	A	362	HIS
1	A	370	ASN
1	A	372	ASN
1	A	797	ASN
1	A	825	GLN
1	A	940	HIS
1	A	981	GLN
1	A	994	HIS

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 carbohydrates 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		Chain Res L		Bond lengths		Bond angles			
	MIOI	туре	Chain	res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
Ī	2	FDH	A	1101	-	21,27,27	1.04	2 (9%)	21,41,41	1.45	3 (14%)

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	FDH	A	1101	-	=	3/8/8/8	0/4/4/4

All (2) bond length outliers are listed below:

ľ	Mol	Chain	${f Res}$	Type	Atoms	\mathbf{Z}	${f Observed(\AA)}$	$\operatorname{Ideal}(ext{\AA})$
	2	A	1101	FDH	C22-N21	-2.60	1.31	1.35
	2	A	1101	FDH	C9-N8	-2.57	1.33	1.35

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
2	A	1101	FDH	N24-C22-N21	3.80	128.11	123.19
2	A	1101	FDH	C14-C16-C20	-3.42	118.44	121.44



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Mol	Chain	Res	Type	${f Atoms}$	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	A	1101	FDH	C9-N8-N7	2.08	106.83	105.17

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	FDH	C11-C10-N7-C6
2	A	1101	FDH	C16-C14-C9-N8
2	A	1101	FDH	C18-C14-C9-N8

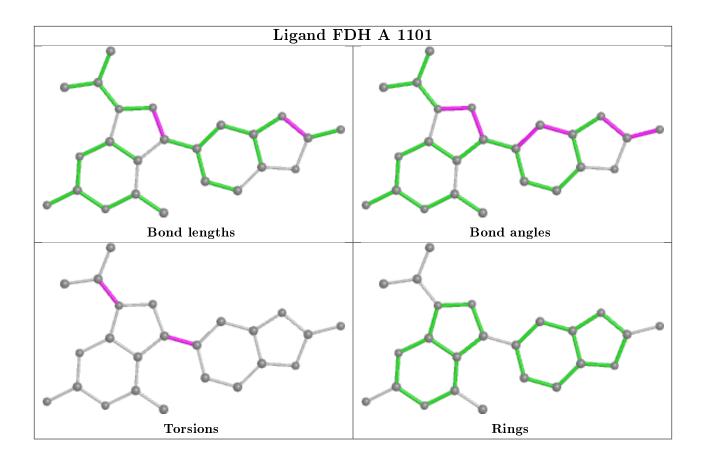
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	FDH	1	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.





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, 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(\AA^2)$	Q < 0.9
1	A	913/962 (94%)	0.43	62 (6%) 17 19	42, 81, 132, 206	1 (0%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	521	ASN	6.8	
1	A	235	SER	6.5	
1	A	244	LEU	6.2	
1	A	234	LEU	5.8	
1	A	243	VAL	5.5	
1	A	231	SER	5.0	
1	A	237	GLU	4.9	
1	A	346	VAL	4.6	
1	A	247	GLN	4.4	
1	A	349	ARG	4.4	
1	A	245	GLU	4.3	
1	A	886	LYS	4.2	
1	A	242	CYS	4.0	
1	A	725	ASP	3.9	
1	A	202	ASN	3.6	
1	A	233	LEU	3.5	
1	A	220	VAL	3.5	
1	A	239	LEU	3.4	
1	A	860	ILE	3.4	
1	A	250	TYR	3.4	
1	A	879	GLN	3.2	
1	A	348	ILE	3.2	
1	A	883	ASP	3.2	
1	A	236	SER	3.2	
1	A	500	VAL	3.2	
1	A	309	ARG	3.1	
1	A	198	VAL	3.1	



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Mol	Chain	Res	Type	RSRZ	
1	A	350	ASP	3.1	
1	A	450	HIS	3.1	
1	A	742	PRO	3.1	
1	A	241	LEU	3.0	
1	A	308	SER	3.0	
1	A	422	LEU	3.0	
1	A	877	LEU	3.0	
1	A	246	TYR	2.9	
1	A	287	LEU	2.9	
1	A	882	LYS	2.9	
1	A	213	HIS	2.7	
1	A	300	ASP	2.6	
1	A	449	PRO	2.6	
1	A	739	MET	2.6	
1	A	238	GLN	2.5	
1	A	881	LEU	2.5	
1	A	735	LEU	2.5	
1	A	448	VAL	2.5	
1	A	307	TYR	2.4	
1	A	880	TRP	2.4	
1	A	248	GLY	2.3	
1	A	351	ILE	2.3	
1	A	890	TYR	2.3	
1	A	201	ASN	2.3	
1	A	451	GLY	2.2	
1	A	200	PRO	2.2	
1	A	344	VAL	2.2	
1	A	633	ILE	2.1	
1	A	962	ILE	2.1	
1	A	498	TRP	2.1	
1	A	267	LEU	2.1	
1	A	356	VAL	2.1	
1	A	1047	HIS	2.1	
1	A	501	SER	2.1	
1	A	264	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)

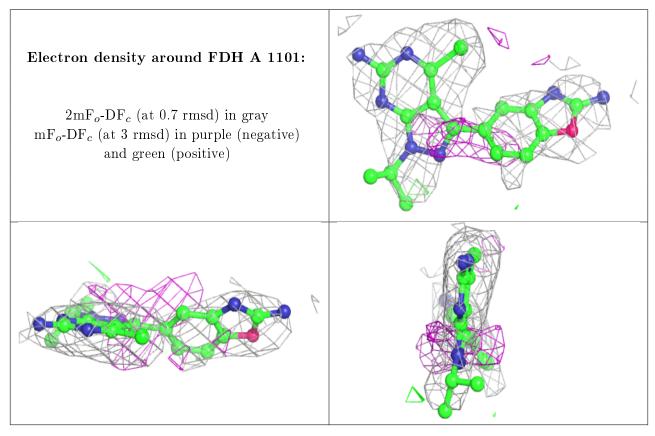
There are no carbohydrates in this entry.

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	${f B\text{-factors}}({f \AA}^2)$	Q<0.9
2	FDH	A	1101	24/24	0.86	0.31	82,95,101,103	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.



6.5 Other polymers (i)

There are no such residues in this entry.

