



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:52 pm BST

PDB ID : 6GVF
Title : Crystal structure of PI3K alpha in complex with 3-(2-Amino-benzooxazol-5-yl)-1-isopropyl-1H-pyrazolo[3,4-d]pyrimidin-4-ylamine
Authors : Ouvry, G.; Aurelly, M.; Bonnary, L.; Borde, E.; Bouix-Peter, C.; Chantalat, L.; Clary, L.; Defoin-Platel, C.; Deret, S.; Forissier, M.; Harris, C.S.; Isabet, T.; Lamy, L.; Luzy, A.P.; Pascau, J.; Soulet, C.; Taddei, A.; Taquet, N.; Tomas, L.; Thoreau, E.; Varvier, E.; Vial, E.; Hennequin, L.F.
Deposited on : 2018-06-21
Resolution : 2.50 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

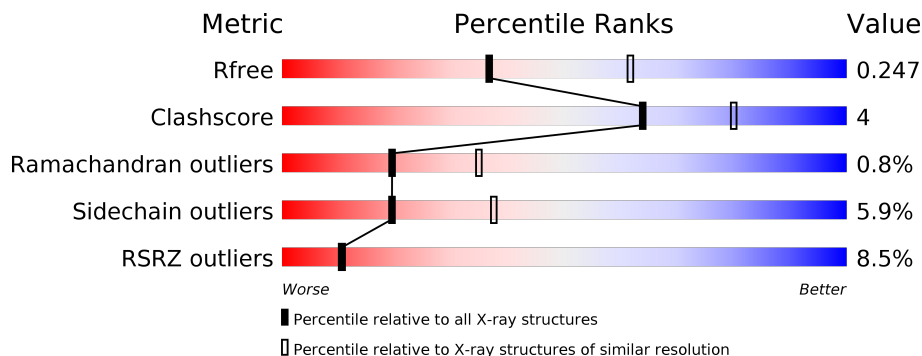
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 $\leq 5\%$. 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	945	

2 Entry composition i

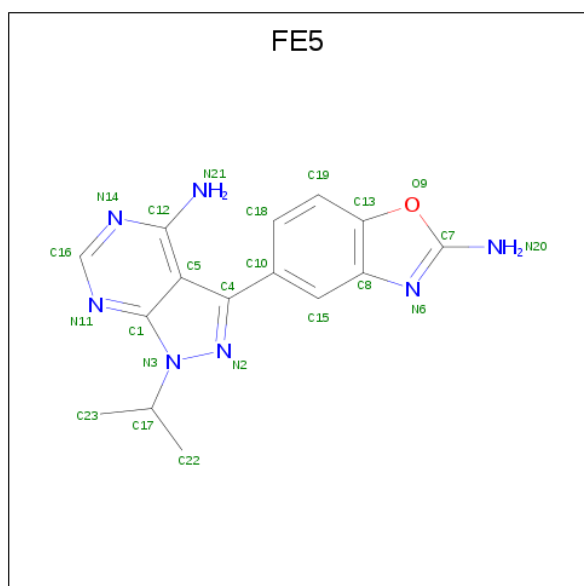
There are 3 unique types of molecules in this entry. The entry contains 7480 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 sub-unit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	910	7388	4710	1266	1350	62	25	1	0

- Molecule 2 is 5-(4-azanyl-1-propan-2-yl-pyrazolo[3,4-d]pyrimidin-3-yl)-1,3-benzoxazol-2-amine (three-letter code: FE5) (formula: C₁₅H₁₅N₇O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	23	15	7	1	0	0

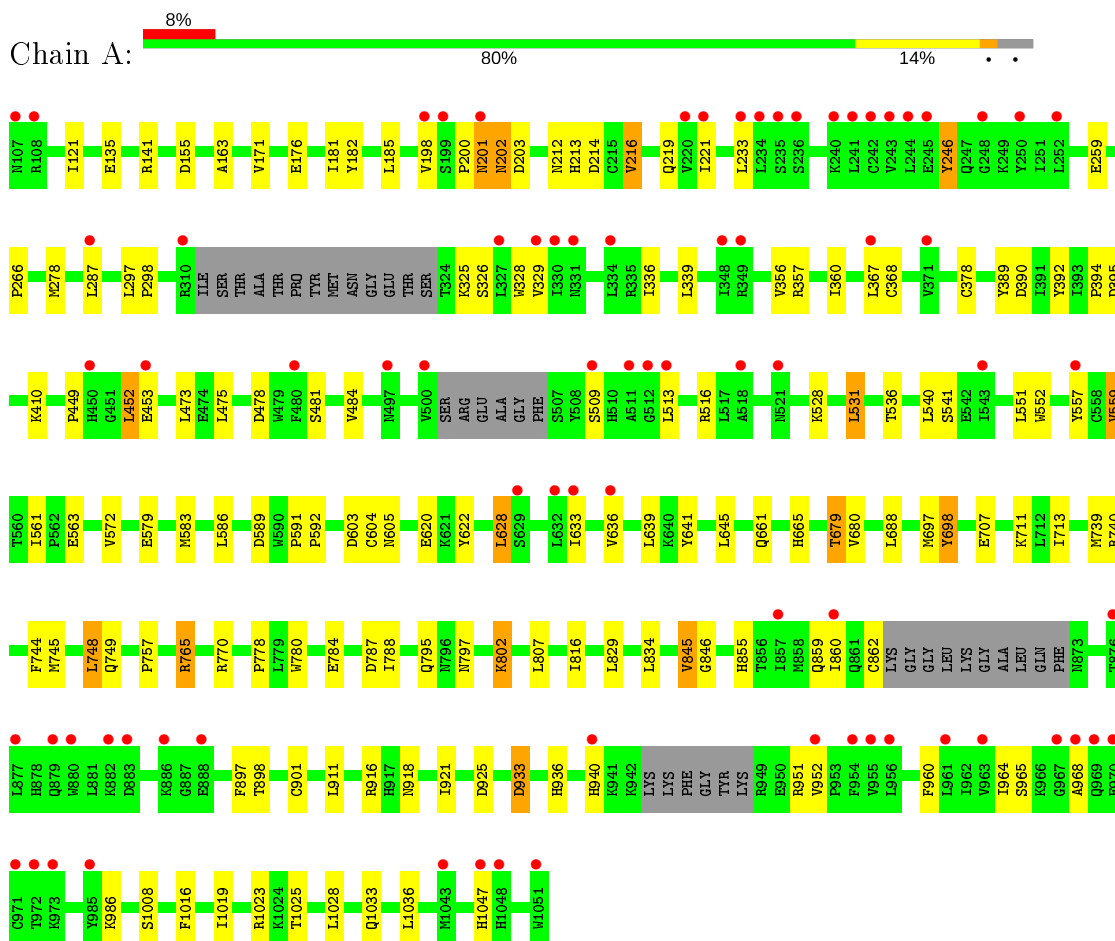
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	69	Total	O	0	0
			69	69		

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	59.42Å 136.00Å 143.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.72 – 2.50 45.71 – 2.50	Depositor EDS
% Data completeness (in resolution range)	68.0 (45.72-2.50) 68.0 (45.71-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.193 , 0.244 0.203 , 0.247	Depositor DCC
R_{free} test set	1337 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	84.6	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 71.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.004 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7480	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: FE5

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	0.51	0/7552	0.70	0/10219

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	7388	0	7298	62	0
2	A	23	0	0	0	0
3	A	69	0	0	1	0
All	All	7480	0	7298	62	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 4.

All (62) 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:200:PRO:HA	1:A:202:ASN:N	1.98	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:PRO:HA	1:A:202:ASN:H	1.51	0.76
1:A:592:PRO:HB2	1:A:622:TYR:HE2	1.54	0.72
1:A:572:VAL:HG21	1:A:583:MET:HG2	1.74	0.68
1:A:745:MET:O	1:A:749:GLN:HG2	1.94	0.68
1:A:936:HIS:HB2	1:A:940:HIS:HB3	1.82	0.62
1:A:807:LEU:HD12	1:A:846:GLY:HA3	1.81	0.60
1:A:135:GLU:HG2	1:A:645:LEU:HD12	1.84	0.59
1:A:368:CYS:HB2	1:A:390:ASP:HB3	1.84	0.58
1:A:965:SER:HB3	1:A:968:ALA:HB3	1.86	0.58
1:A:163:ALA:HA	1:A:297:LEU:HD21	1.86	0.57
1:A:898:THR:HG22	1:A:964:ILE:HG12	1.85	0.57
1:A:392:TYR:HB3	1:A:395:ASP:HB2	1.87	0.56
1:A:449:PRO:HD2	1:A:452:LEU:HD13	1.87	0.56
1:A:1023:ARG:HG3	1:A:1028:LEU:HD12	1.90	0.54
1:A:1016:PHE:HA	1:A:1019:ILE:HD12	1.90	0.53
1:A:182:TYR:HA	1:A:185:LEU:HD12	1.90	0.53
1:A:216:VAL:HB	1:A:219:GLN:HE21	1.74	0.53
1:A:531:LEU:HD23	1:A:551:LEU:HD23	1.92	0.52
1:A:897:PHE:O	1:A:901:CYS:HB2	2.11	0.51
1:A:829:LEU:HD11	1:A:986:LYS:HB3	1.93	0.51
1:A:221:ILE:HG23	1:A:287:LEU:HD11	1.93	0.51
1:A:713:ILE:HG12	1:A:845:VAL:HG11	1.94	0.50
1:A:744:PHE:CZ	1:A:748:LEU:HD13	2.47	0.50
1:A:328:TRP:HA	1:A:394:PRO:HB3	1.94	0.50
1:A:298:PRO:HG2	1:A:697:MET:HG2	1.93	0.49
1:A:765:ARG:HD3	1:A:784:GLU:HG3	1.95	0.48
1:A:661:GLN:OE1	1:A:698:TYR:HB2	2.14	0.47
1:A:326:SER:O	1:A:329:VAL:HG22	2.14	0.47
1:A:739:MET:HA	1:A:744:PHE:CD1	2.50	0.47
1:A:360:ILE:HG22	1:A:367:LEU:HD12	1.96	0.47
1:A:636:VAL:O	1:A:639:LEU:HB2	2.14	0.47
1:A:855:HIS:HB3	1:A:859:GLN:HG3	1.96	0.46
1:A:816:ILE:HG21	1:A:911:LEU:HD21	1.97	0.46
1:A:198:VAL:HG12	1:A:203:ASP:HB2	1.97	0.46
1:A:711:LYS:HB2	1:A:748:LEU:HD11	1.97	0.45
1:A:778:PRO:HB3	1:A:802:LYS:HG3	1.98	0.45
1:A:325:LYS:O	1:A:484:VAL:HA	2.16	0.45
1:A:665:HIS:CG	1:A:757:PRO:HG3	2.52	0.45
1:A:897:PHE:HZ	1:A:960:PHE:HD1	1.63	0.44
1:A:181:ILE:HG12	1:A:278:MET:HG2	1.99	0.44
1:A:559:VAL:HG22	1:A:591:PRO:HD3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ILE:HG22	1:A:688:LEU:HB3	2.00	0.44
1:A:940:HIS:NE2	1:A:951:ARG:HD2	2.33	0.44
1:A:516:ARG:HB3	1:A:552:TRP:HD1	1.82	0.44
1:A:679:THR:HG22	1:A:680:VAL:HG13	1.98	0.44
1:A:185:LEU:HD21	1:A:213:HIS:HB3	1.99	0.43
1:A:552:TRP:HZ3	1:A:583:MET:HE2	1.82	0.43
1:A:707:GLU:HB3	3:A:1214:HOH:O	2.18	0.43
1:A:356:VAL:HG21	1:A:473:LEU:HD11	2.00	0.43
1:A:336:ILE:HD12	1:A:389:TYR:CE2	2.54	0.43
1:A:214:ASP:HA	1:A:266:PRO:HB3	2.00	0.42
1:A:604:CYS:HB3	1:A:641:TYR:CZ	2.54	0.42
1:A:770:ARG:HG3	1:A:780:TRP:HB3	2.00	0.42
1:A:528:LYS:HG2	1:A:557:TYR:CZ	2.55	0.42
1:A:1033:GLN:HE22	1:A:1036:LEU:HD22	1.84	0.42
1:A:855:HIS:HB2	1:A:860:ILE:HD11	2.02	0.41
1:A:916:ARG:HB3	1:A:921:ILE:HD11	2.03	0.41
1:A:540:LEU:HD21	1:A:1016:PHE:HD1	1.86	0.41
1:A:952:VAL:HG11	1:A:1047:HIS:HE1	1.85	0.41
1:A:603:ASP:OD1	1:A:605:ASN:HB2	2.21	0.40
1:A:628:LEU:O	1:A:628:LEU:HD12	2.22	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	901/945 (95%)	845 (94%)	49 (5%)	7 (1%)	19 35

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	202	ASN

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Mol	Chain	Res	Type
1	A	246	TYR
1	A	925	ASP
1	A	933	ASP
1	A	339	LEU
1	A	201	ASN
1	A	481	SER

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	820/859 (96%)	771 (94%)	49 (6%)	19 37

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	ARG
1	A	155	ASP
1	A	171	VAL
1	A	176	GLU
1	A	201	ASN
1	A	212	ASN
1	A	216	VAL
1	A	233	LEU
1	A	246	TYR
1	A	259[A]	GLU
1	A	259[B]	GLU
1	A	357	ARG
1	A	378	CYS
1	A	410	LYS
1	A	452	LEU
1	A	453	GLU
1	A	475	LEU
1	A	478	ASP
1	A	509	SER
1	A	513	LEU

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Mol	Chain	Res	Type
1	A	531	LEU
1	A	536	THR
1	A	541	SER
1	A	559	VAL
1	A	561	ILE
1	A	563	GLU
1	A	579	GLU
1	A	586	LEU
1	A	589	ASP
1	A	620	GLU
1	A	628	LEU
1	A	633	ILE
1	A	679	THR
1	A	698	TYR
1	A	740	ARG
1	A	748	LEU
1	A	765	ARG
1	A	787	ASP
1	A	788	ILE
1	A	795	GLN
1	A	797	ASN
1	A	802	LYS
1	A	834	LEU
1	A	845	VAL
1	A	862	CYS
1	A	918	ASN
1	A	933	ASP
1	A	1008	SER
1	A	1025	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	189	GLN
1	A	212	ASN
1	A	219	GLN
1	A	374	GLN
1	A	643	GLN
1	A	721	GLN
1	A	1033	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 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	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FE5	A	1101	-	21,26,26	1.08	2 (9%)	20,39,39	1.55	3 (15%)

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	FE5	A	1101	-	-	2/8/8/8	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	FE5	C4-N2	-2.96	1.32	1.35
2	A	1101	FE5	C7-N6	-2.41	1.31	1.35

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	FE5	N20-C7-N6	3.75	128.04	123.19
2	A	1101	FE5	C10-C15-C8	-3.51	118.37	121.44
2	A	1101	FE5	C4-N2-N3	2.22	106.95	105.17

There are no chirality outliers.

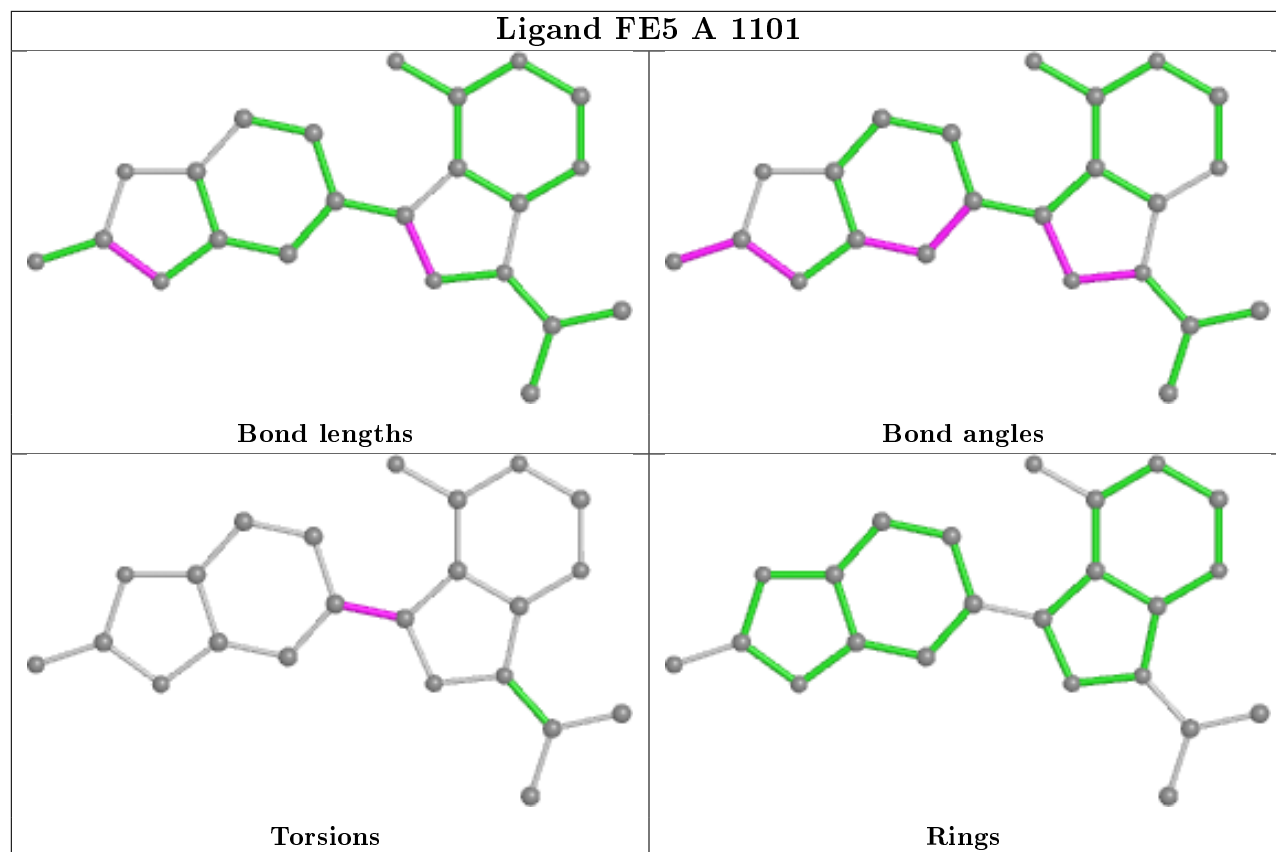
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	FE5	C15-C10-C4-N2
2	A	1101	FE5	C18-C10-C4-N2

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 than 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

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, 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	910/945 (96%)	0.51	77 (8%) 10 10	49, 97, 173, 214	9 (0%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	244	LEU	7.6
1	A	513	LEU	7.6
1	A	500	VAL	6.6
1	A	511	ALA	6.0
1	A	450	HIS	6.0
1	A	236	SER	5.9
1	A	969	GLN	5.8
1	A	235	SER	5.7
1	A	348	ILE	5.6
1	A	331	ASN	5.3
1	A	1051	TRP	5.2
1	A	512	GLY	5.0
1	A	1047	HIS	4.9
1	A	971	CYS	4.6
1	A	233	LEU	4.6
1	A	242	CYS	4.3
1	A	250	TYR	4.2
1	A	241	LEU	4.1
1	A	970	GLU	4.1
1	A	956	LEU	3.9
1	A	252	LEU	3.9
1	A	234	LEU	3.8
1	A	972	THR	3.8
1	A	857	ILE	3.7
1	A	518	ALA	3.6
1	A	961	LEU	3.5
1	A	955	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	940	HIS	3.5
1	A	330	ILE	3.4
1	A	557	TYR	3.3
1	A	973	LYS	3.3
1	A	334	LEU	3.3
1	A	880	TRP	3.3
1	A	879	GLN	3.1
1	A	633	ILE	3.0
1	A	968	ALA	3.0
1	A	220	VAL	2.9
1	A	199	SER	2.9
1	A	367	LEU	2.9
1	A	240	LYS	2.9
1	A	243	VAL	2.8
1	A	480	PHE	2.8
1	A	198	VAL	2.8
1	A	245	GLU	2.8
1	A	287	LEU	2.8
1	A	883	ASP	2.8
1	A	632	LEU	2.7
1	A	886	LYS	2.7
1	A	543	ILE	2.7
1	A	888	GLU	2.6
1	A	349	ARG	2.5
1	A	497	ASN	2.5
1	A	107	ASN	2.5
1	A	329	VAL	2.5
1	A	221	ILE	2.4
1	A	629	SER	2.4
1	A	1048	HIS	2.4
1	A	876	THR	2.4
1	A	453	GLU	2.4
1	A	954	PHE	2.4
1	A	201	ASN	2.3
1	A	967	GLY	2.3
1	A	108	ARG	2.3
1	A	963	VAL	2.2
1	A	882	LYS	2.2
1	A	985	TYR	2.2
1	A	509	SER	2.2
1	A	636	VAL	2.2
1	A	327	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	310	ARG	2.2
1	A	248	GLY	2.2
1	A	860	ILE	2.1
1	A	371	VAL	2.1
1	A	521	ASN	2.1
1	A	1043	MET	2.0
1	A	952	VAL	2.0
1	A	877	LEU	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](#)

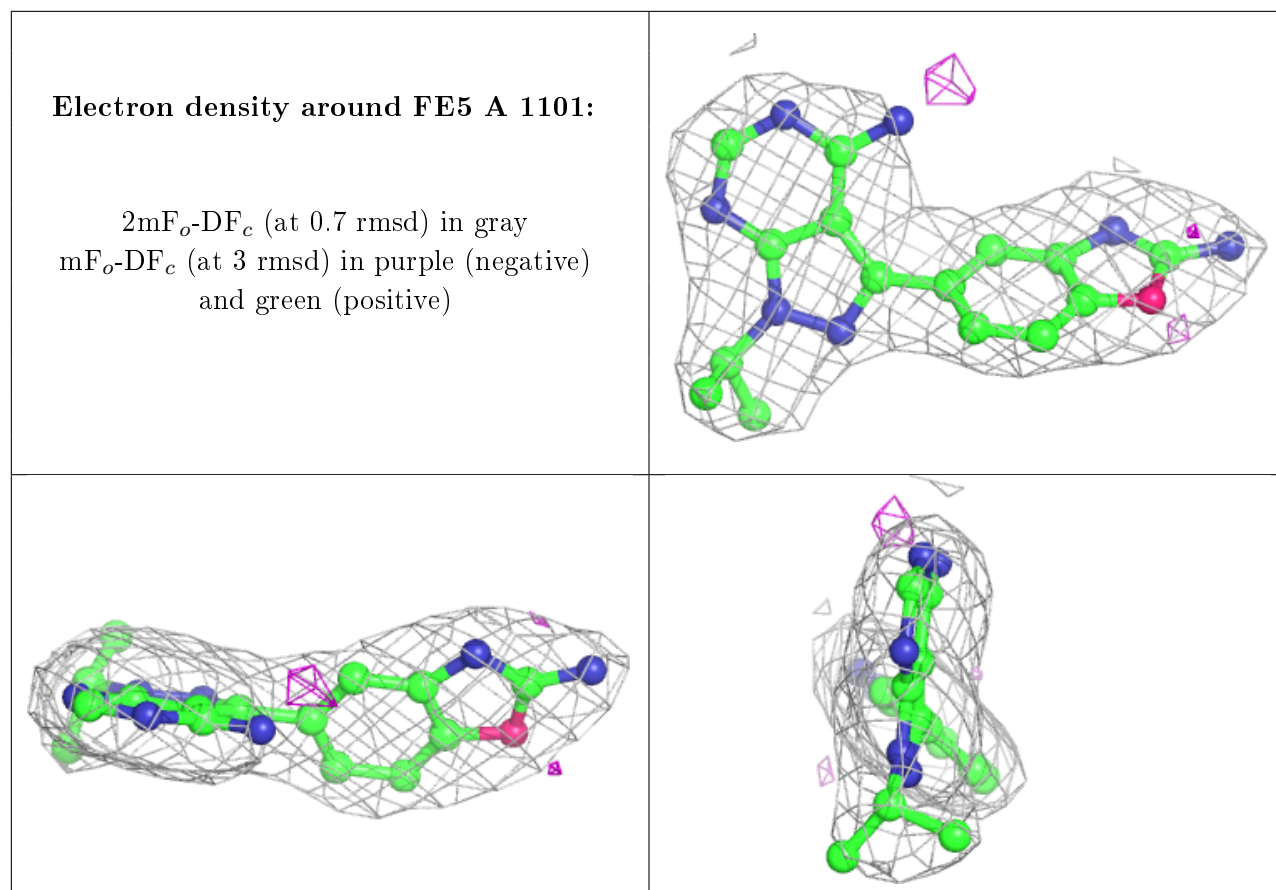
There are no carbohydrates in this entry.

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, 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	FE5	A	1101	23/23	0.98	0.16	50,69,80,80	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 ⓘ

There are no such residues in this entry.