



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 02:04 am BST

PDB ID : 6N7Z
Title : Crystal structure of human FPPS in complex with an allosteric inhibitor YF-02037
Authors : Park, J.; Berghuis, A.M.
Deposited on : 2018-11-28
Resolution : 2.55 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

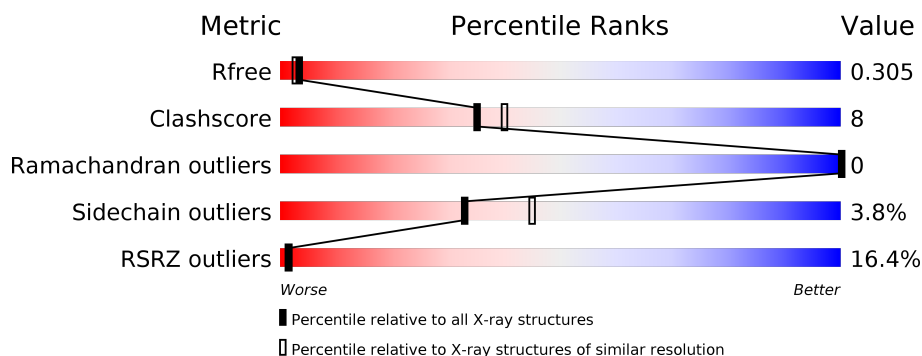
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	F	375	<div> <div>15%</div> <div>71%</div> <div>17%</div> <div>• 10%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2751 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 Farnesyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	336	Total	C	N	O	S	0	2	0
			2641	1712	431	487	11			

There are 22 discrepancies between the modelled and reference sequences:

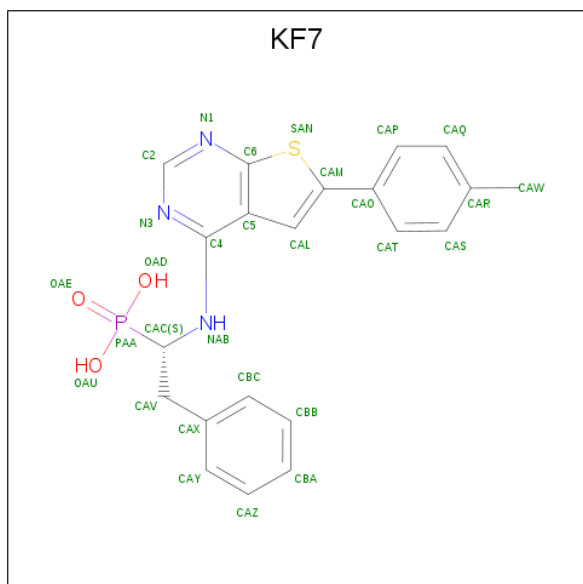
Chain	Residue	Modelled	Actual	Comment	Reference
F	-21	MET	-	initiating methionine	UNP P14324
F	-20	GLY	-	expression tag	UNP P14324
F	-19	SER	-	expression tag	UNP P14324
F	-18	SER	-	expression tag	UNP P14324
F	-17	HIS	-	expression tag	UNP P14324
F	-16	HIS	-	expression tag	UNP P14324
F	-15	HIS	-	expression tag	UNP P14324
F	-14	HIS	-	expression tag	UNP P14324
F	-13	HIS	-	expression tag	UNP P14324
F	-12	HIS	-	expression tag	UNP P14324
F	-11	SER	-	expression tag	UNP P14324
F	-10	SER	-	expression tag	UNP P14324
F	-9	GLY	-	expression tag	UNP P14324
F	-8	ARG	-	expression tag	UNP P14324
F	-7	GLU	-	expression tag	UNP P14324
F	-6	ASN	-	expression tag	UNP P14324
F	-5	LEU	-	expression tag	UNP P14324
F	-4	TYR	-	expression tag	UNP P14324
F	-3	PHE	-	expression tag	UNP P14324
F	-2	GLN	-	expression tag	UNP P14324
F	-1	GLY	-	expression tag	UNP P14324
F	0	HIS	-	expression tag	UNP P14324

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is [(1S)-1-{[6-(4-methylphenyl)thieno[2,3-d]pyrimidin-4-yl]amino}-2-phenylethyl] phosphonic acid (three-letter code: KF7) (formula: C₂₁H₂₀N₃O₃PS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	F	1	Total	C	N	O	P	S	0	0
			29	21	3	3	1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	F	1	Total	Cl	0	0
			1	1		

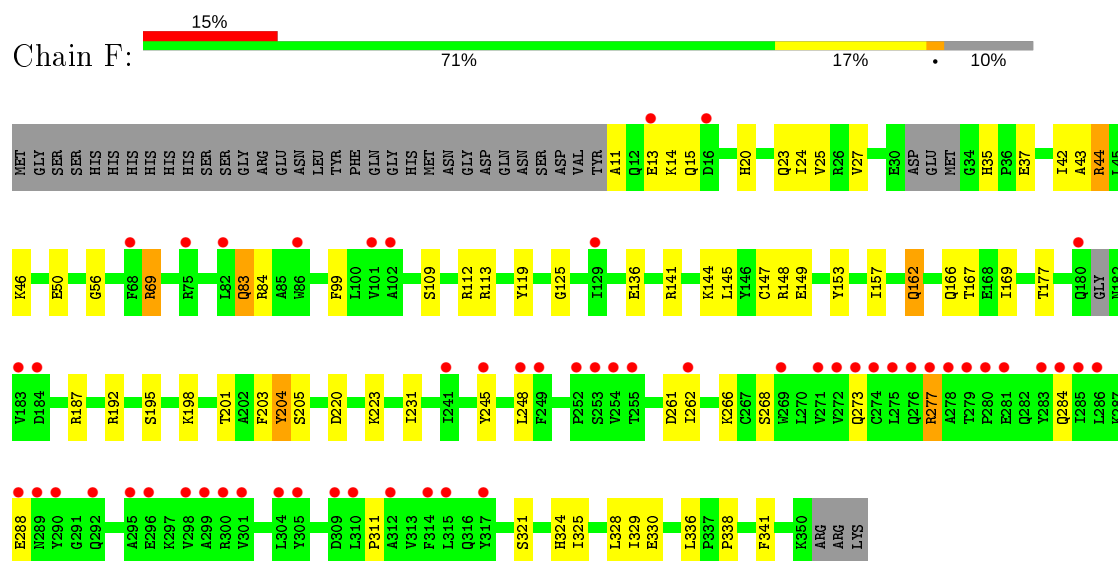
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	74	Total	O	0	2
			74	74		

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: Farnesyl pyrophosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	110.86 Å 110.86 Å 75.04 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.63 – 2.55 44.59 – 2.55	Depositor EDS
% Data completeness (in resolution range)	98.0 (44.63-2.55) 98.0 (44.59-2.55)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.54 Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.232 , 0.281 0.244 , 0.305	Depositor DCC
R_{free} test set	726 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.634	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.38$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2751	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: KF7, GOL, CL

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	F	0.67	2/2698 (0.1%)	0.77	0/3666

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	F	0	6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	136	GLU	CD-OE1	10.75	1.37	1.25
1	F	37	GLU	CD-OE2	5.99	1.32	1.25

There are no bond angle outliers.

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	112	ARG	Sidechain
1	F	141[A]	ARG	Sidechain
1	F	277	ARG	Sidechain
1	F	44	ARG	Sidechain
1	F	69	ARG	Sidechain
1	F	84	ARG	Sidechain

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	F	2641	0	2539	43	0
2	F	6	0	8	0	0
3	F	29	0	0	0	0
4	F	1	0	0	0	0
5	F	74	0	0	7	0
All	All	2751	0	2547	43	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 (43) 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:F:177:THR:O	1:F:187:ARG:HD3	1.82	0.79
1:F:13:GLU:CB	1:F:69:ARG:HH22	1.97	0.78
1:F:220:ASP:OD1	1:F:220:ASP:N	2.25	0.67
1:F:261:ASP:HA	1:F:266:LYS:HG3	1.80	0.62
1:F:15:GLN:CB	5:F:518:HOH:O	2.47	0.61
1:F:20:HIS:CE1	1:F:83:GLN:OE1	2.53	0.61
1:F:113:ARG:NH2	5:F:502:HOH:O	2.34	0.60
1:F:231:ILE:HG21	1:F:341:PHE:CD1	2.40	0.57
1:F:144:LYS:NZ	5:F:501:HOH:O	2.40	0.55
1:F:83:GLN:OE1	1:F:83:GLN:HA	2.07	0.54
1:F:321:SER:O	1:F:325:ILE:HG12	2.08	0.53
1:F:273:GLN:OE1	1:F:277:ARG:NH1	2.40	0.53
1:F:177:THR:OG1	1:F:192:ARG:NH1	2.42	0.52
1:F:248:LEU:HD22	1:F:262:ILE:HD11	1.89	0.52
1:F:166:GLN:NE2	1:F:203[A]:PHE:CD1	2.73	0.52
1:F:99:PHE:CE2	1:F:167:THR:HG21	2.47	0.50
1:F:324:HIS:CE1	1:F:328:LEU:HD11	2.47	0.49
1:F:42:ILE:O	1:F:43:ALA:C	2.52	0.47
1:F:11:ALA:HA	1:F:14:LYS:HB3	1.97	0.47
1:F:119:TYR:O	1:F:125:GLY:HA2	2.15	0.47
1:F:27:VAL:CG1	1:F:145:LEU:HD13	2.45	0.47
1:F:35:HIS:ND1	5:F:503:HOH:O	2.36	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:20:HIS:HB2	5:F:510:HOH:O	2.15	0.46
1:F:204:TYR:C	1:F:204:TYR:CD2	2.90	0.45
1:F:284:GLN:O	1:F:288:GLU:N	2.50	0.45
1:F:248:LEU:CD2	1:F:262:ILE:HD11	2.48	0.44
1:F:166:GLN:NE2	1:F:203[B]:PHE:CZ	2.87	0.43
1:F:245:TYR:HE1	1:F:311:PRO:HA	1.82	0.43
1:F:162:GLN:O	1:F:166:GLN:HG2	2.19	0.43
1:F:46:LYS:O	1:F:50:GLU:HG2	2.20	0.42
1:F:153:TYR:CZ	1:F:157:ILE:HD11	2.54	0.42
1:F:25:VAL:CG1	1:F:46:LYS:HG3	2.50	0.41
1:F:329:ILE:HD11	1:F:341:PHE:HB3	2.01	0.41
1:F:162:GLN:NE2	5:F:504:HOH:O	2.42	0.41
1:F:338:PRO:O	1:F:341:PHE:N	2.52	0.41
1:F:23:GLN:O	1:F:24:ILE:C	2.58	0.41
1:F:169:ILE:HA	1:F:169:ILE:HD13	1.80	0.41
1:F:201:THR:O	1:F:205:SER:HB2	2.21	0.41
1:F:147:CYS:O	1:F:148:ARG:C	2.59	0.41
1:F:198:LYS:HE2	1:F:203[B]:PHE:CZ	2.55	0.41
1:F:248:LEU:HD13	1:F:262:ILE:HD12	2.02	0.40
1:F:149:GLU:HA	1:F:149:GLU:OE2	2.21	0.40
1:F:56:GLY:HA2	5:F:512:HOH:O	2.21	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	F	332/375 (88%)	308 (93%)	24 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	F	263 / 322 (82%)	253 (96%)	10 (4%)	33	45

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	44	ARG
1	F	83	GLN
1	F	109	SER
1	F	162	GLN
1	F	195	SER
1	F	204	TYR
1	F	223	LYS
1	F	268	SER
1	F	330	GLU
1	F	336	LEU

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

Mol	Chain	Res	Type
1	F	20	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

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	GOL	F	401	-	5,5,5	0.49	0	5,5,5	0.33	0
3	KF7	F	402	-	27,32,32	3.09	12 (44%)	34,46,46	2.15	9 (26%)

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	GOL	F	401	-	-	4/4/4/4	-
3	KF7	F	402	-	-	2/18/18/18	0/4/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	402	KF7	PAA-OAE	7.30	1.61	1.49
3	F	402	KF7	C4-C5	-6.94	1.36	1.44
3	F	402	KF7	C2-N1	4.82	1.39	1.32
3	F	402	KF7	CAV-CAX	-4.58	1.40	1.51
3	F	402	KF7	PAA-OAU	4.14	1.61	1.54
3	F	402	KF7	PAA-OAD	-3.85	1.48	1.54
3	F	402	KF7	PAA-CAC	3.81	1.88	1.84
3	F	402	KF7	C5-C6	-3.78	1.36	1.42
3	F	402	KF7	CAM-SAN	-3.65	1.67	1.72
3	F	402	KF7	CAC-NAB	3.43	1.48	1.45
3	F	402	KF7	C2-N3	3.12	1.39	1.33
3	F	402	KF7	CAW-CAR	-3.11	1.40	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	402	KF7	N1-C2-N3	-7.10	117.58	128.68
3	F	402	KF7	C5-C6-SAN	-4.41	107.70	112.24
3	F	402	KF7	C5-C4-NAB	-3.74	117.10	120.63
3	F	402	KF7	OAE-PAA-CAC	-3.72	106.43	113.80
3	F	402	KF7	C2-N3-C4	3.67	119.73	116.59
3	F	402	KF7	OAU-PAA-OAE	-2.99	105.94	113.45
3	F	402	KF7	C2-N1-C6	2.85	120.12	113.45
3	F	402	KF7	CAT-CAO-CAM	2.40	124.15	120.21
3	F	402	KF7	OAU-PAA-OAD	2.24	113.67	107.64

There are no chirality outliers.

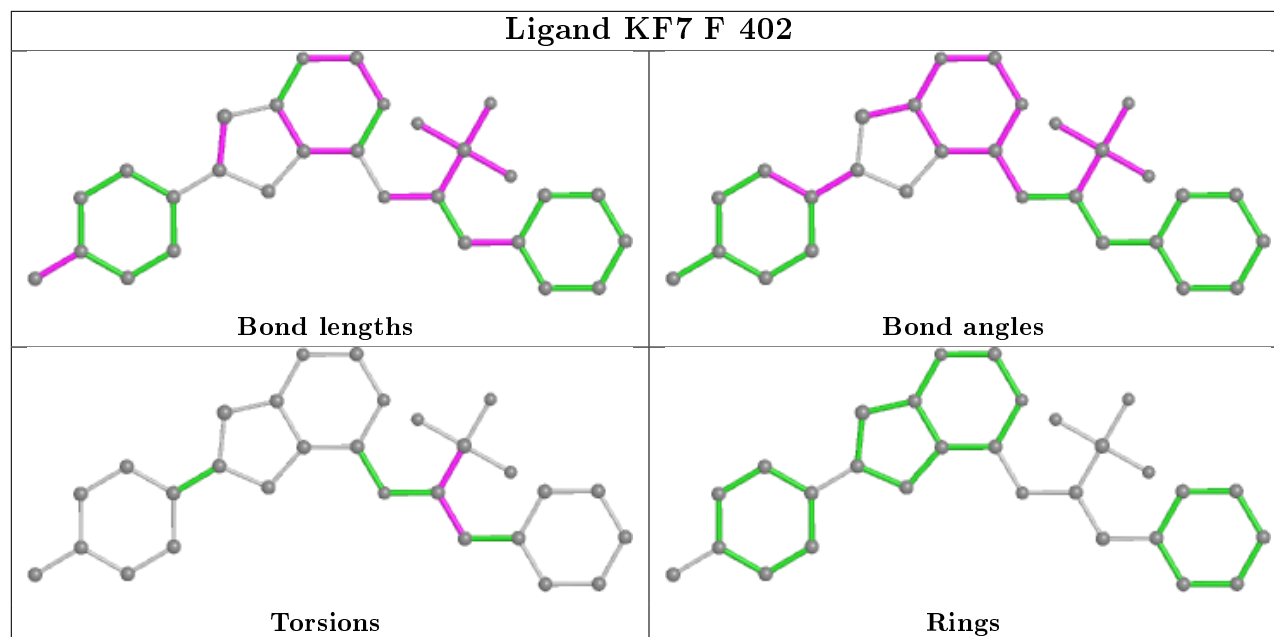
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	401	GOL	O1-C1-C2-C3
2	F	401	GOL	C1-C2-C3-O3
2	F	401	GOL	O2-C2-C3-O3
2	F	401	GOL	O1-C1-C2-O2
3	F	402	KF7	CAV-CAC-PAA-OAE
3	F	402	KF7	NAB-CAC-CAV-CAX

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	F	336/375 (89%)	0.96	55 (16%) 1 1	40, 70, 130, 148	0

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	254	VAL	8.5
1	F	290	TYR	6.5
1	F	255	THR	5.8
1	F	286	LEU	5.0
1	F	278	ALA	4.9
1	F	277	ARG	4.9
1	F	275	LEU	4.9
1	F	305	TYR	4.9
1	F	248	LEU	4.7
1	F	310	LEU	4.7
1	F	249	PHE	4.5
1	F	262	ILE	4.1
1	F	283	TYR	3.9
1	F	252	PRO	3.9
1	F	288	GLU	3.8
1	F	281	GLU	3.8
1	F	245	TYR	3.7
1	F	289	ASN	3.7
1	F	298	VAL	3.4
1	F	86	TRP	3.4
1	F	285	ILE	3.3
1	F	315	LEU	3.2
1	F	300	ARG	3.0
1	F	301	VAL	2.9
1	F	184	ASP	2.9
1	F	279	THR	2.9
1	F	273	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	309	ASP	2.8
1	F	13	GLU	2.7
1	F	253	SER	2.7
1	F	180	GLN	2.6
1	F	102	ALA	2.6
1	F	272	VAL	2.6
1	F	304	LEU	2.5
1	F	183	VAL	2.5
1	F	16	ASP	2.5
1	F	314	PHE	2.5
1	F	296	GLU	2.5
1	F	276	GLN	2.5
1	F	68	PHE	2.4
1	F	129	ILE	2.4
1	F	274	CYS	2.4
1	F	284	GLN	2.4
1	F	312	ALA	2.4
1	F	82	LEU	2.3
1	F	280	PRO	2.3
1	F	292	GLN	2.3
1	F	317	TYR	2.3
1	F	299	ALA	2.2
1	F	75	ARG	2.2
1	F	101	VAL	2.2
1	F	269	TRP	2.1
1	F	241	ILE	2.1
1	F	271	VAL	2.0
1	F	295	ALA	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.

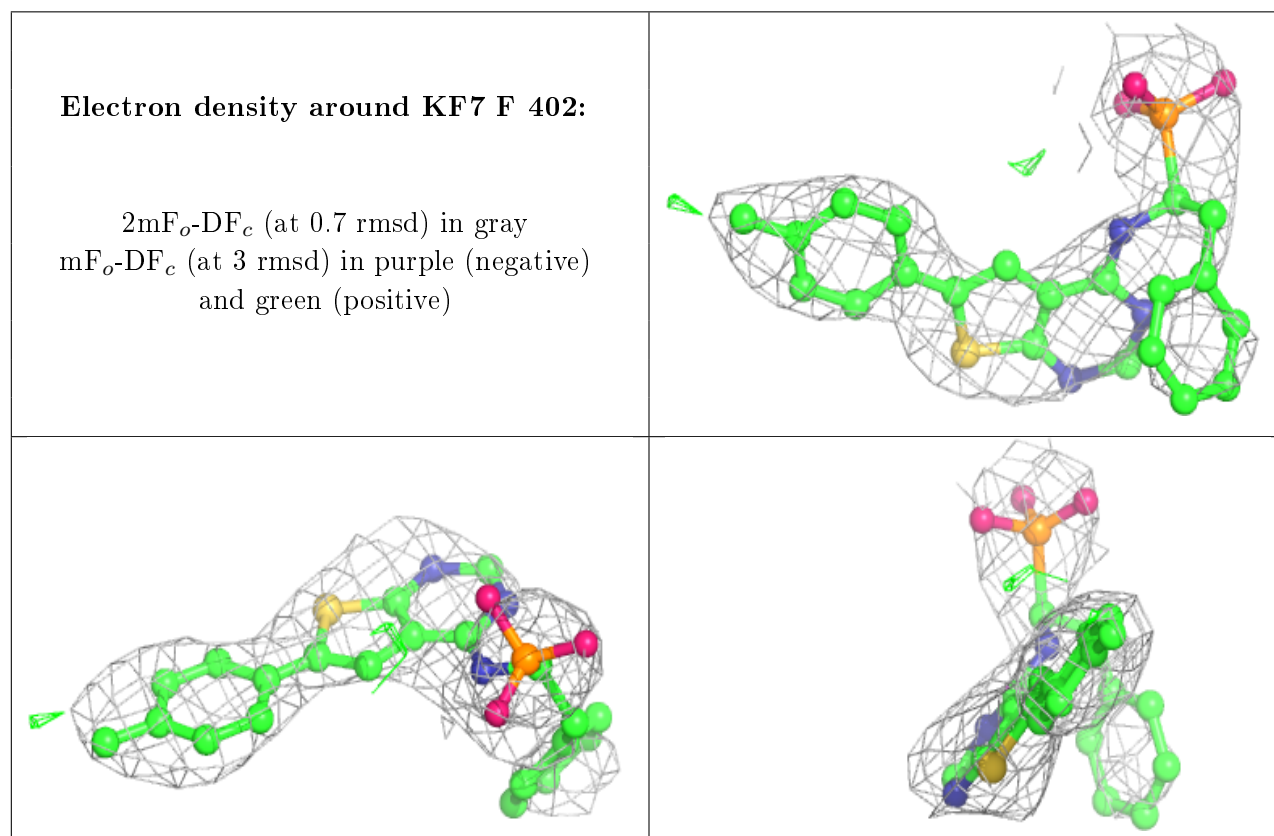
6.4 Ligands [i](#)

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
4	CL	F	403	1/1	0.70	0.28	92,92,92,92	0
3	KF7	F	402	29/29	0.86	0.30	64,114,129,136	0
2	GOL	F	401	6/6	0.94	0.26	71,76,79,83	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.