



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 02:04 pm BST

PDB ID : 3R7R
Title : Structure-based design of thienobenzoxepin inhibitors of PI3-Kinase
Authors : Murray, J.M.; Wiesmann, C.
Deposited on : 2011-03-22
Resolution : 2.90 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

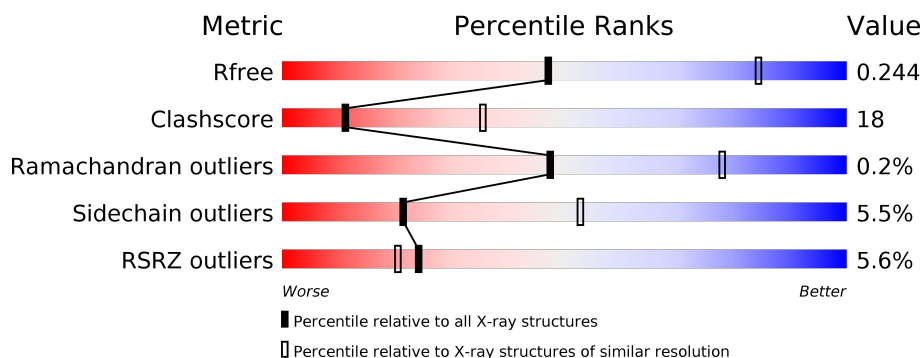
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	966	<div> <div>5%</div> <div>59%</div> <div>25%</div> <div>•</div> <div>13%</div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6804 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.

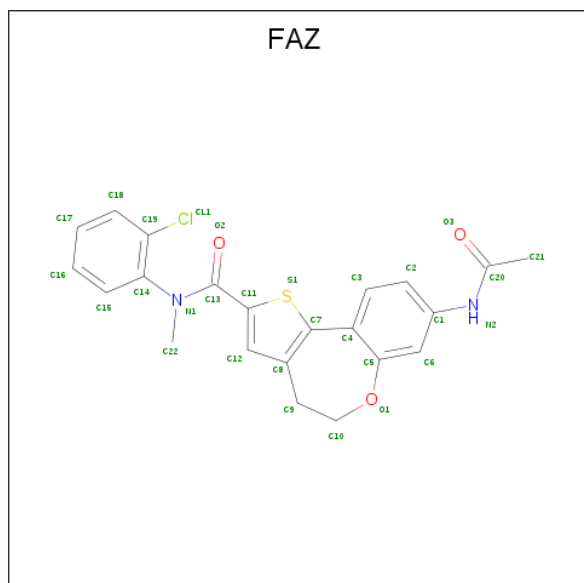
- Molecule 1 is a protein called Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	838	Total	C	N	O	S	0	0	0
			6775	4347	1155	1238	35			

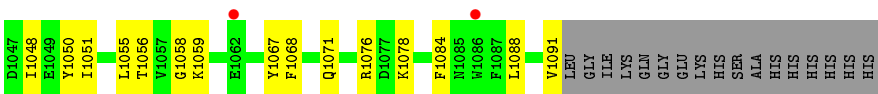
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	MET	-	INITIATING METHIONINE	UNP P48736
A	1103	HIS	-	EXPRESSION TAG	UNP P48736
A	1104	HIS	-	EXPRESSION TAG	UNP P48736
A	1105	HIS	-	EXPRESSION TAG	UNP P48736
A	1106	HIS	-	EXPRESSION TAG	UNP P48736
A	1107	HIS	-	EXPRESSION TAG	UNP P48736
A	1108	HIS	-	EXPRESSION TAG	UNP P48736

- Molecule 2 is 8-(acetylamino)-N-(2-chlorophenyl)-N-methyl-4,5-dihydrothieno[3,2-d][1]benzoxepine-2-carboxamide (three-letter code: FAZ) (formula: C₂₂H₁₉ClN₂O₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			29	22	1	2	3	1		



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	143.79 Å 67.87 Å 106.93 Å 90.00° 95.40° 90.00°	Depositor
Resolution (Å)	19.93 – 2.90 19.93 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (19.93-2.90) 99.7 (19.93-2.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.88 Å)	Xtriage
Refinement program	PHENIX dev_806, REFMAC	Depositor
R, R_{free}	0.207 , 0.253 0.201 , 0.244	Depositor DCC
R_{free} test set	1180 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	89.9	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 64.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6804	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.34% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FAZ

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	0.55	3/6920 (0.0%)	0.76	3/9362 (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	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	526	PRO	N-CD	-8.30	1.36	1.47
1	A	227	SER	CA-CB	6.01	1.61	1.52
1	A	526	PRO	N-CA	5.28	1.56	1.47

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	227	SER	CB-CA-C	-10.94	89.32	110.10
1	A	227	SER	N-CA-C	8.13	132.96	111.00
1	A	651	LEU	CA-CB-CG	7.16	131.76	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	167	ASN	Mainchain

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Mol	Chain	Res	Type	Group
1	A	278	ASP	Mainchain
1	A	373	LEU	Mainchain

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	A	6775	0	6793	239	0
2	A	29	0	19	7	0
All	All	6804	0	6812	243	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 18.

All (243) 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:224:ILE:HD11	1:A:248:PHE:CE1	1.67	1.27
1:A:224:ILE:CD1	1:A:248:PHE:CE1	2.18	1.26
1:A:1000:LYS:HA	1:A:1076:ARG:NH2	1.55	1.21
1:A:1000:LYS:CA	1:A:1076:ARG:HH21	1.53	1.20
1:A:568:THR:HG22	1:A:571:ASP:CG	1.67	1.14
1:A:568:THR:HG22	1:A:571:ASP:OD2	1.49	1.10
1:A:525:HIS:HB3	1:A:526:PRO:HD3	1.26	1.08
1:A:525:HIS:HB3	1:A:526:PRO:CD	1.87	1.05
1:A:525:HIS:CB	1:A:526:PRO:HD3	1.89	1.03
1:A:224:ILE:HD11	1:A:248:PHE:HE1	0.99	0.99
1:A:373:LEU:O	1:A:373:LEU:HD12	1.65	0.96
1:A:888:ILE:HG22	1:A:949:ASN:OD1	1.67	0.94
1:A:233:ILE:HD11	1:A:248:PHE:HD1	1.34	0.92
1:A:1000:LYS:CA	1:A:1076:ARG:NH2	2.21	0.92
1:A:1000:LYS:HA	1:A:1076:ARG:HH21	0.76	0.90
1:A:1039:MET:HB3	1:A:1040:PRO:HD2	1.53	0.90
1:A:743:GLN:HG3	1:A:876:ILE:HD12	1.52	0.89
1:A:395:CYS:HG	1:A:417:SER:HG	1.17	0.88
1:A:568:THR:HG23	1:A:571:ASP:H	1.37	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:947:ARG:NH2	1:A:963:ILE:O	2.08	0.86
1:A:886:THR:CG2	1:A:890:LYS:HD3	2.07	0.85
1:A:888:ILE:CG2	1:A:949:ASN:OD1	2.24	0.84
1:A:564:LEU:CD1	1:A:1048:ILE:HG22	2.11	0.80
1:A:224:ILE:HD13	1:A:248:PHE:CE1	2.17	0.80
1:A:1002:THR:HG22	1:A:1003:SER:H	1.46	0.79
1:A:564:LEU:HD11	1:A:1048:ILE:CG2	2.13	0.78
1:A:889:ALA:HA	1:A:949:ASN:ND2	2.00	0.77
1:A:568:THR:CG2	1:A:571:ASP:CG	2.52	0.76
1:A:233:ILE:HD11	1:A:248:PHE:CD1	2.20	0.75
1:A:175:PHE:HA	1:A:178:ARG:NH1	2.03	0.74
1:A:217:ASN:HD22	1:A:219:CYS:HB2	1.53	0.74
1:A:525:HIS:CB	1:A:526:PRO:CD	2.58	0.73
1:A:223:VAL:HG22	1:A:232:THR:HG23	1.72	0.72
1:A:874:ASP:O	1:A:876:ILE:HG22	1.90	0.72
1:A:182:THR:HB	1:A:183:PRO:HD3	1.72	0.71
1:A:244:ILE:HD11	1:A:272:LEU:CD1	2.20	0.71
1:A:237:PRO:HA	1:A:287:ILE:HD11	1.71	0.71
1:A:373:LEU:HD12	1:A:373:LEU:C	2.10	0.71
1:A:886:THR:HG23	1:A:890:LYS:HD3	1.70	0.71
1:A:170:ASP:OD2	1:A:476:ARG:NH2	2.22	0.71
1:A:379:LEU:HD13	1:A:380:THR:H	1.55	0.70
1:A:174:GLU:OE2	1:A:177:ARG:NH1	2.23	0.70
1:A:1000:LYS:CB	1:A:1076:ARG:NH2	2.56	0.69
1:A:202:VAL:HG12	1:A:203:THR:N	2.08	0.69
1:A:819:ASP:OD1	1:A:821:THR:OG1	2.12	0.67
1:A:1067:TYR:O	1:A:1071:GLN:HG2	1.95	0.66
1:A:477:ARG:HA	1:A:520:LEU:HB3	1.77	0.66
1:A:1003:SER:O	1:A:1007:GLN:HG3	1.95	0.66
1:A:614:ARG:HG2	1:A:617:TRP:HB3	1.78	0.65
1:A:564:LEU:HD13	1:A:1048:ILE:HG22	1.77	0.65
1:A:251:LYS:HD3	1:A:251:LYS:O	1.97	0.64
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.77	0.64
1:A:525:HIS:CG	1:A:526:PRO:HD3	2.32	0.64
1:A:1084:PHE:CE2	1:A:1088:LEU:HD11	2.34	0.63
1:A:217:ASN:ND2	1:A:219:CYS:HB2	2.14	0.63
2:A:1:FAZ:S1	2:A:1:FAZ:C14	2.87	0.63
1:A:1002:THR:HG22	1:A:1003:SER:N	2.13	0.62
1:A:244:ILE:HD11	1:A:272:LEU:HD11	1.81	0.62
1:A:564:LEU:CD1	1:A:1048:ILE:CG2	2.72	0.62
1:A:660:LEU:O	1:A:664:VAL:HG23	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:ILE:CD1	1:A:248:PHE:CZ	2.80	0.61
1:A:916:PRO:HD2	1:A:920:LYS:HD3	1.82	0.61
1:A:202:VAL:CG1	1:A:203:THR:N	2.63	0.60
1:A:804:MET:HE3	1:A:810:PRO:HG2	1.84	0.60
1:A:775:GLN:HE22	1:A:796:LEU:N	1.99	0.60
1:A:240:THR:HG23	1:A:241:PRO:HD2	1.83	0.60
1:A:1000:LYS:CB	1:A:1076:ARG:HH21	2.12	0.59
1:A:997:THR:HG22	1:A:998:SER:N	2.18	0.59
1:A:175:PHE:HA	1:A:178:ARG:HH12	1.68	0.59
1:A:207:LEU:HD23	1:A:212:TRP:CE2	2.38	0.58
1:A:311:PRO:O	1:A:313:PRO:HD3	2.02	0.58
1:A:303:ILE:HD12	1:A:303:ILE:N	2.19	0.58
1:A:997:THR:HG23	1:A:1001:LYS:HB3	1.85	0.57
1:A:180:LEU:C	1:A:183:PRO:HD2	2.24	0.57
1:A:229:THR:HG22	1:A:230:SER:N	2.18	0.57
1:A:272:LEU:HB3	1:A:305:VAL:HG11	1.86	0.57
1:A:625:GLY:O	1:A:629:GLN:HG3	2.04	0.57
1:A:151:GLN:OE1	1:A:722:ARG:NH2	2.37	0.57
1:A:373:LEU:O	1:A:373:LEU:CD1	2.45	0.57
1:A:287:ILE:HD12	1:A:288:LYS:N	2.20	0.57
1:A:184:ARG:NH2	1:A:321:GLU:OE1	2.30	0.57
1:A:1068:PHE:O	1:A:1071:GLN:HB2	2.04	0.56
1:A:565:ASN:OD1	1:A:566:PRO:HD2	2.06	0.56
1:A:1056:THR:HG23	1:A:1056:THR:O	2.07	0.55
1:A:274:VAL:HG11	1:A:292:TRP:CE2	2.42	0.55
1:A:1000:LYS:HB3	1:A:1076:ARG:NH2	2.21	0.55
1:A:775:GLN:HE22	1:A:796:LEU:H	1.54	0.55
1:A:739:ILE:HD13	1:A:872:THR:HB	1.88	0.55
1:A:657:LEU:HD11	1:A:690:ARG:HD3	1.88	0.55
1:A:249:PHE:O	1:A:253:ALA:N	2.40	0.54
1:A:371:PRO:HG2	1:A:511:GLU:O	2.07	0.54
1:A:379:LEU:HD13	1:A:380:THR:HG22	1.89	0.54
1:A:525:HIS:HB3	1:A:526:PRO:HD2	1.82	0.54
1:A:248:PHE:HD2	1:A:249:PHE:HD1	1.55	0.54
1:A:720:TYR:OH	1:A:728:MET:HE2	2.08	0.54
1:A:379:LEU:CD1	1:A:380:THR:H	2.19	0.54
1:A:720:TYR:OH	1:A:728:MET:CE	2.56	0.54
1:A:227:SER:O	1:A:228:THR:CG2	2.56	0.54
1:A:889:ALA:CA	1:A:949:ASN:ND2	2.69	0.53
1:A:825:ASN:N	1:A:825:ASN:OD1	2.42	0.53
1:A:214:LYS:NZ	1:A:300:GLY:HA2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1058:GLY:C	1:A:1059:LYS:HD3	2.30	0.52
1:A:373:LEU:N	1:A:374:PRO:CD	2.71	0.52
1:A:391:GLN:HG3	1:A:502:LEU:HD21	1.91	0.52
1:A:874:ASP:O	1:A:876:ILE:CG2	2.56	0.52
1:A:888:ILE:HG22	1:A:949:ASN:CG	2.28	0.52
1:A:181:VAL:HG12	1:A:185:MET:CE	2.40	0.52
1:A:223:VAL:HG12	1:A:225:HIS:NE2	2.25	0.52
1:A:240:THR:HG22	1:A:242:GLY:H	1.75	0.52
1:A:798:ILE:HD12	1:A:798:ILE:H	1.75	0.51
1:A:145:GLU:HA	1:A:148:GLN:OE1	2.11	0.51
1:A:624:VAL:O	1:A:628:MET:HG2	2.10	0.51
1:A:887:THR:HG22	1:A:889:ALA:H	1.74	0.51
1:A:916:PRO:HD2	1:A:920:LYS:CD	2.40	0.51
1:A:180:LEU:O	1:A:183:PRO:HD2	2.11	0.51
1:A:568:THR:CG2	1:A:571:ASP:H	2.16	0.51
1:A:202:VAL:CG1	1:A:285:THR:HG21	2.40	0.51
1:A:583:LEU:O	1:A:583:LEU:HD23	2.11	0.51
1:A:804:MET:CE	1:A:831:ILE:HG12	2.41	0.51
1:A:988:THR:HB	1:A:989:PRO:HD2	1.93	0.50
1:A:983:VAL:HG22	1:A:984:PRO:HD2	1.93	0.50
1:A:552:ARG:HH21	1:A:581:GLU:CD	2.13	0.50
1:A:225:HIS:ND1	1:A:230:SER:HB3	2.27	0.50
1:A:705:GLN:HG3	1:A:839:ARG:CZ	2.41	0.50
1:A:225:HIS:CE1	1:A:230:SER:CB	2.95	0.50
1:A:228:THR:OG1	1:A:229:THR:N	2.44	0.50
1:A:207:LEU:HD11	1:A:211:LEU:HB3	1.94	0.50
1:A:886:THR:HG22	1:A:887:THR:N	2.27	0.49
1:A:1042:LEU:CD1	1:A:1042:LEU:H	2.25	0.49
1:A:308:ASP:N	1:A:308:ASP:OD1	2.44	0.49
1:A:1008:LYS:O	1:A:1012:ILE:HG13	2.12	0.49
1:A:886:THR:HG22	1:A:887:THR:H	1.78	0.49
1:A:839:ARG:HA	1:A:842:MET:HE2	1.95	0.49
1:A:1001:LYS:NZ	1:A:1001:LYS:HB3	2.27	0.49
1:A:389:HIS:O	1:A:392:GLN:HB3	2.13	0.49
1:A:149:ALA:O	1:A:152:ARG:HB3	2.13	0.48
2:A:1:FAZ:C19	2:A:1:FAZ:S1	3.02	0.48
1:A:964:ASP:CB	2:A:1:FAZ:H19	2.44	0.48
1:A:226:ARG:O	1:A:227:SER:HB2	2.14	0.48
1:A:733:THR:O	1:A:737:GLN:HG3	2.14	0.48
1:A:880:GLU:O	2:A:1:FAZ:H8	2.14	0.47
1:A:467:LEU:O	1:A:476:ARG:HD2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:VAL:CG1	1:A:225:HIS:NE2	2.77	0.47
1:A:381:VAL:HG21	1:A:404:PHE:CG	2.50	0.47
1:A:583:LEU:HG	1:A:589:TYR:OH	2.15	0.47
1:A:610:LEU:HD23	1:A:610:LEU:HA	1.68	0.47
1:A:905:GLU:HG3	1:A:993:PHE:CE2	2.49	0.47
1:A:235:VAL:HG12	1:A:236:SER:N	2.30	0.47
1:A:224:ILE:HD13	1:A:248:PHE:CD1	2.49	0.47
1:A:888:ILE:HD13	1:A:952:ILE:HG22	1.95	0.47
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.97	0.47
1:A:888:ILE:CD1	1:A:952:ILE:HG22	2.45	0.47
2:A:1:FAZ:O3	2:A:1:FAZ:H1	2.14	0.47
1:A:739:ILE:HG13	1:A:740:GLU:N	2.30	0.47
1:A:947:ARG:NH2	1:A:964:ASP:O	2.46	0.47
1:A:214:LYS:HZ1	1:A:300:GLY:HA2	1.80	0.46
1:A:910:TRP:CH2	1:A:956:GLU:HG2	2.50	0.46
1:A:737:GLN:O	1:A:741:MET:HG3	2.15	0.46
1:A:1039:MET:HB3	1:A:1040:PRO:CD	2.34	0.46
1:A:497:PHE:CD1	1:A:497:PHE:N	2.83	0.46
1:A:170:ASP:OD1	1:A:170:ASP:C	2.54	0.46
1:A:379:LEU:HB3	1:A:435:CYS:SG	2.55	0.46
2:A:1:FAZ:O3	2:A:1:FAZ:C2	2.63	0.46
1:A:373:LEU:N	1:A:374:PRO:HD2	2.31	0.46
1:A:224:ILE:HD12	1:A:248:PHE:CZ	2.50	0.46
1:A:905:GLU:O	1:A:905:GLU:HG2	2.16	0.46
1:A:248:PHE:HD2	1:A:249:PHE:CD1	2.34	0.45
1:A:229:THR:CG2	1:A:230:SER:N	2.79	0.45
1:A:293:VAL:O	1:A:297:LEU:HG	2.15	0.45
1:A:207:LEU:HD12	1:A:208:PRO:HD2	1.99	0.45
1:A:361:PHE:HA	1:A:420:ILE:HD11	1.97	0.45
1:A:361:PHE:HB2	1:A:420:ILE:HD13	1.99	0.45
1:A:273:ARG:NH2	1:A:821:THR:OG1	2.50	0.45
1:A:274:VAL:HG21	1:A:292:TRP:CD1	2.52	0.44
1:A:614:ARG:HD2	1:A:618:ASP:OD1	2.17	0.44
1:A:895:THR:O	1:A:896:VAL:C	2.54	0.44
1:A:1035:LEU:HA	1:A:1039:MET:HG2	2.00	0.44
1:A:202:VAL:CG1	1:A:203:THR:H	2.30	0.44
1:A:434:TYR:CE1	1:A:460:LEU:HB2	2.53	0.44
1:A:498:ASN:OD1	1:A:498:ASN:C	2.55	0.44
1:A:270:PHE:HB3	1:A:307:LEU:HD11	2.00	0.44
1:A:593:PHE:CZ	1:A:611:LEU:HD21	2.51	0.44
1:A:220:ILE:N	1:A:235:VAL:O	2.41	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:583:LEU:C	1:A:583:LEU:HD23	2.38	0.44
1:A:227:SER:O	1:A:228:THR:HG23	2.18	0.44
1:A:569:ALA:O	1:A:573:GLU:HG3	2.18	0.43
1:A:202:VAL:HG11	1:A:285:THR:HG21	1.99	0.43
1:A:1043:THR:HG22	1:A:1045:LYS:H	1.83	0.43
1:A:507:ASN:HA	1:A:508:PRO:HD3	1.86	0.43
1:A:997:THR:CG2	1:A:998:SER:N	2.81	0.43
1:A:651:LEU:HD22	1:A:655:ASP:HB3	2.01	0.43
1:A:485:TRP:CH2	1:A:508:PRO:HD3	2.53	0.43
1:A:568:THR:HG23	1:A:571:ASP:N	2.18	0.43
1:A:1059:LYS:N	1:A:1059:LYS:HD3	2.33	0.43
1:A:367:GLY:HA3	1:A:409:LEU:HD23	2.00	0.43
1:A:373:LEU:C	1:A:373:LEU:CD1	2.84	0.43
1:A:424:PRO:HG2	1:A:427:ALA:HB2	1.99	0.43
1:A:1000:LYS:C	1:A:1076:ARG:NH2	2.70	0.43
1:A:250:THR:C	1:A:252:MET:H	2.22	0.43
1:A:466:LEU:HD11	1:A:476:ARG:HD3	2.00	0.43
1:A:173:LEU:O	1:A:177:ARG:HG3	2.18	0.43
1:A:181:VAL:HG12	1:A:185:MET:HE2	2.00	0.43
1:A:1029:ILE:HA	1:A:1029:ILE:HD12	1.80	0.43
1:A:214:LYS:HG2	1:A:214:LYS:O	2.19	0.42
1:A:551:LEU:HA	1:A:551:LEU:HD23	1.77	0.42
1:A:592:LEU:O	1:A:595:SER:HB2	2.20	0.42
1:A:853:SER:O	1:A:857:THR:HG23	2.19	0.42
1:A:692:GLY:HA3	1:A:720:TYR:OH	2.20	0.42
1:A:226:ARG:O	1:A:227:SER:CB	2.67	0.42
1:A:271:VAL:CG1	1:A:310:PRO:HG3	2.50	0.42
1:A:778:GLN:N	1:A:778:GLN:OE1	2.49	0.42
1:A:1055:LEU:O	1:A:1056:THR:HG22	2.20	0.42
1:A:274:VAL:HG11	1:A:292:TRP:CZ2	2.55	0.42
1:A:579:ARG:HG2	1:A:610:LEU:HD11	2.02	0.42
1:A:561:THR:OG1	1:A:591:LYS:HE2	2.20	0.42
1:A:845:LEU:HD13	1:A:965:PHE:CE1	2.55	0.42
1:A:1042:LEU:O	1:A:1042:LEU:HD13	2.19	0.42
1:A:964:ASP:HA	2:A:1:FAZ:H19	2.02	0.42
1:A:767:LEU:HD22	1:A:771:LEU:HG	2.02	0.42
1:A:1048:ILE:O	1:A:1051:ILE:HG22	2.20	0.41
1:A:1027:LEU:HA	1:A:1027:LEU:HD23	1.85	0.41
1:A:219:CYS:HA	1:A:235:VAL:O	2.20	0.41
1:A:872:THR:OG1	1:A:877:GLY:HA2	2.20	0.41
1:A:579:ARG:HD3	1:A:579:ARG:HH11	1.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1050:TYR:C	1:A:1050:TYR:CD2	2.93	0.41
1:A:245:LEU:HD23	1:A:245:LEU:HA	1.86	0.41
1:A:250:THR:C	1:A:252:MET:N	2.74	0.41
1:A:267:GLU:N	1:A:269:ASP:OD1	2.53	0.41
1:A:661:LEU:O	1:A:665:GLN:HG2	2.21	0.41
1:A:207:LEU:HD23	1:A:212:TRP:CD2	2.55	0.41
1:A:682:LEU:HD23	1:A:682:LEU:HA	1.85	0.41
1:A:386:ASN:OD1	1:A:396:GLN:HG3	2.20	0.41
1:A:848:LEU:HA	1:A:848:LEU:HD12	1.89	0.41
1:A:717:LEU:HA	1:A:717:LEU:HD23	1.83	0.41
1:A:983:VAL:CG2	1:A:984:PRO:HD2	2.51	0.40
1:A:990:ASP:OD1	1:A:990:ASP:N	2.53	0.40
1:A:476:ARG:HB3	1:A:520:LEU:HD23	2.03	0.40
1:A:568:THR:CG2	1:A:571:ASP:OD2	2.42	0.40
1:A:597:LYS:HB2	1:A:603:ILE:HD13	2.02	0.40
1:A:804:MET:HE3	1:A:810:PRO:CG	2.51	0.40
1:A:935:TYR:CE1	1:A:961:PHE:HA	2.56	0.40
1:A:381:VAL:HG21	1:A:404:PHE:CD2	2.56	0.40
1:A:910:TRP:CZ3	1:A:956:GLU:HA	2.56	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	822/966 (85%)	782 (95%)	38 (5%)	2 (0%)	47 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	896	VAL
1	A	758	ASP

5.3.2 Protein sidechains ⓘ

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	750/864 (87%)	709 (94%)	41 (6%)	21 53

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	MET
1	A	269	ASP
1	A	298	LYS
1	A	370	ILE
1	A	373	LEU
1	A	374	PRO
1	A	379	LEU
1	A	393	VAL
1	A	476	ARG
1	A	477	ARG
1	A	520	LEU
1	A	521	ASP
1	A	550	GLN
1	A	570	GLU
1	A	575	LEU
1	A	601	GLN
1	A	610	LEU
1	A	626	LEU
1	A	647	LYS
1	A	682	LEU
1	A	707	ARG
1	A	717	LEU
1	A	739	ILE
1	A	767	LEU
1	A	825	ASN
1	A	832	PHE
1	A	838	LEU
1	A	843	LEU
1	A	845	LEU
1	A	848	LEU

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Mol	Chain	Res	Type
1	A	865	LEU
1	A	876	ILE
1	A	907	LEU
1	A	926	GLU
1	A	959	ASN
1	A	967	HIS
1	A	989	PRO
1	A	1026	LEU
1	A	1042	LEU
1	A	1078	LYS
1	A	1091	VAL

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

Mol	Chain	Res	Type
1	A	775	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	FAZ	A	1	-	26,32,32	1.29	3 (11%)	35,46,46	1.66	8 (22%)

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	FAZ	A	1	-	-	0/12/26/26	0/3/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	FAZ	C14-N1	-4.44	1.38	1.44
2	A	1	FAZ	O1-C5	-2.24	1.34	1.38
2	A	1	FAZ	O1-C10	-2.12	1.41	1.44

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	FAZ	C5-C4-C7	3.97	125.45	119.69
2	A	1	FAZ	C10-O1-C5	3.67	121.13	116.03
2	A	1	FAZ	C1-N2-C20	-3.65	121.36	127.99
2	A	1	FAZ	C10-C9-C8	-3.04	106.48	114.47
2	A	1	FAZ	O2-C13-N1	-2.68	117.39	121.47
2	A	1	FAZ	C22-N1-C14	2.44	120.13	116.72
2	A	1	FAZ	C21-C20-N2	2.27	118.31	114.98
2	A	1	FAZ	C11-C13-N1	2.16	123.64	118.50

There are no chirality outliers.

There are no torsion outliers.

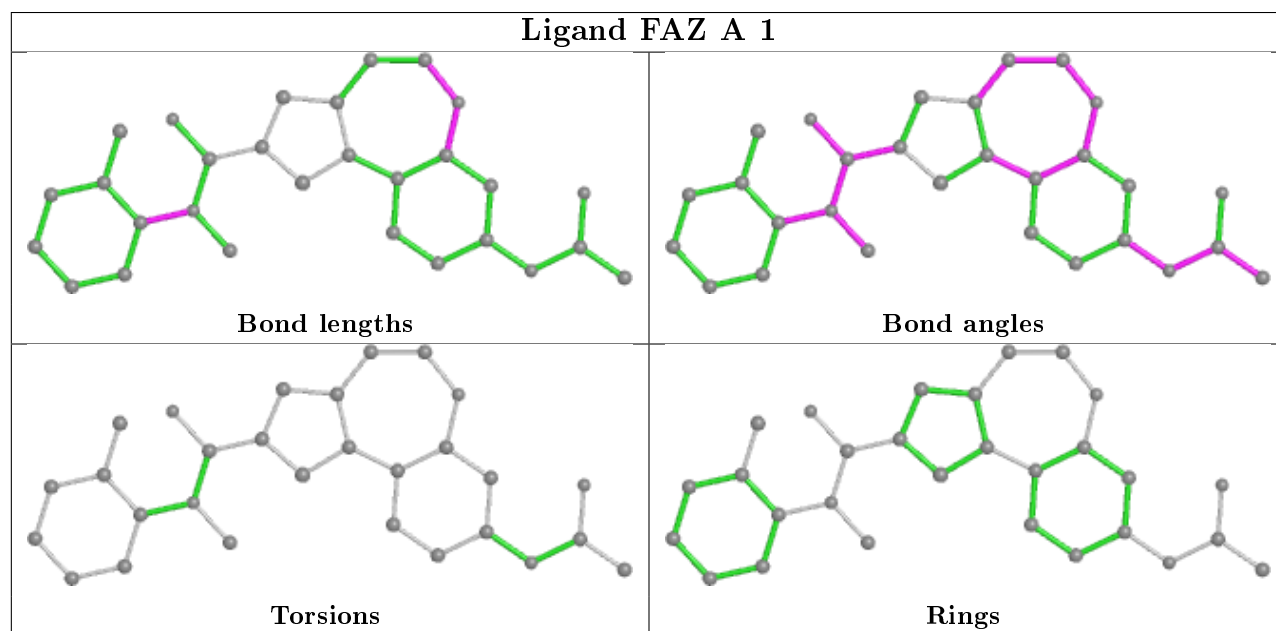
There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	FAZ	7	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 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	838/966 (86%)	0.05	47 (5%) 24 20	56, 114, 198, 279	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1044	SER	12.8
1	A	376	ASN	8.9
1	A	377	THR	7.7
1	A	755	GLU	6.7
1	A	375	ARG	6.0
1	A	378	ASP	4.5
1	A	823	LEU	4.3
1	A	747	LEU	4.3
1	A	825	ASN	4.0
1	A	250	THR	3.9
1	A	374	PRO	3.7
1	A	756	LYS	3.7
1	A	1086	TRP	3.7
1	A	322	GLU	3.6
1	A	253	ALA	3.2
1	A	489	GLY	3.1
1	A	143	MET	3.1
1	A	216	ALA	3.1
1	A	1062	GLU	2.8
1	A	981	GLU	2.8
1	A	896	VAL	2.8
1	A	998	SER	2.7
1	A	837	ASP	2.6
1	A	488	SER	2.6
1	A	996	GLY	2.6
1	A	999	GLY	2.6
1	A	147	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1043	THR	2.5
1	A	778	GLN	2.5
1	A	268	GLN	2.4
1	A	229	THR	2.4
1	A	1046	GLU	2.3
1	A	252	MET	2.3
1	A	832	PHE	2.3
1	A	987	LEU	2.3
1	A	320	LYS	2.2
1	A	824	SER	2.2
1	A	148	GLN	2.2
1	A	916	PRO	2.2
1	A	997	THR	2.2
1	A	1000	LYS	2.1
1	A	267	GLU	2.1
1	A	152	ARG	2.1
1	A	246	GLN	2.1
1	A	1041	GLN	2.1
1	A	895	THR	2.1
1	A	429	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.

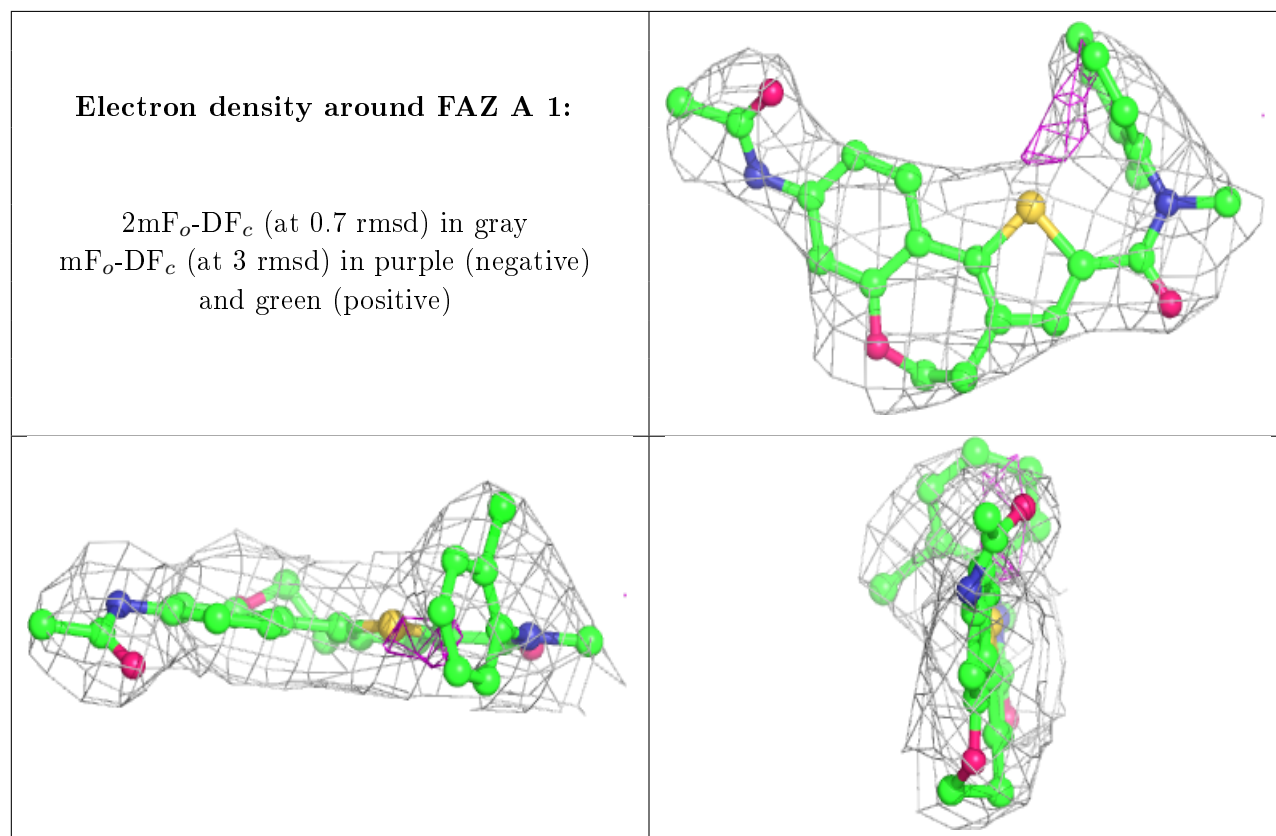
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
2	FAZ	A	1	29/29	0.94	0.16	81,101,116,138	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.