



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:31 PM UTC

PDB ID : 8OG6 / pdb_00008og6
Title : Crystal structure of human DCAF1 WD40 repeats (Q1250L) in complex with compound 1
Authors : Schroeder, M.; Vulpetti, A.; Renatus, M.
Deposited on : 2023-03-19
Resolution : 2.25 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

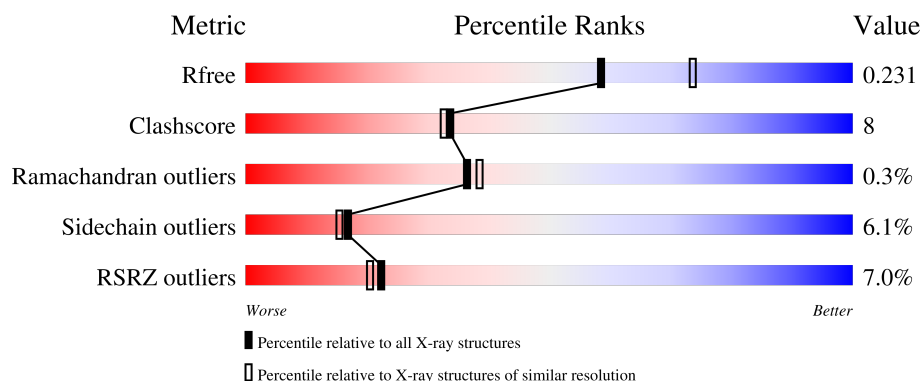
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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}	180053	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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 $\leq 5\%$. 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	367	6% 56% 22% • 18%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5007 atoms, of which 2350 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.

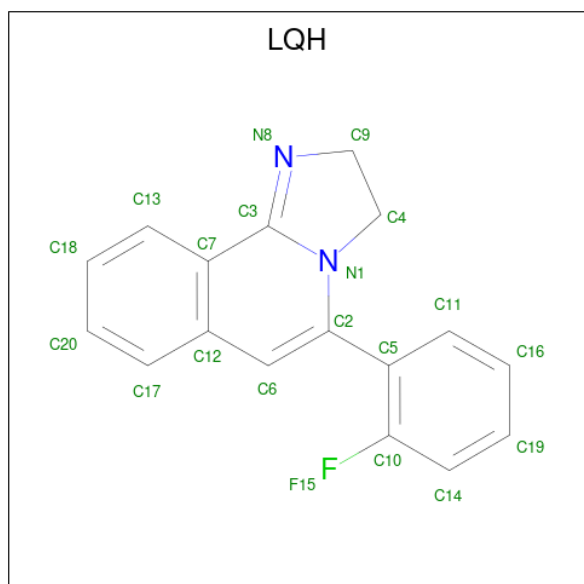
- Molecule 1 is a protein called DDB1- and CUL4-associated factor 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	301	4763	1531	2347	413	454	18	87	4	0

There are 5 discrepancies between the modelled and reference sequences:

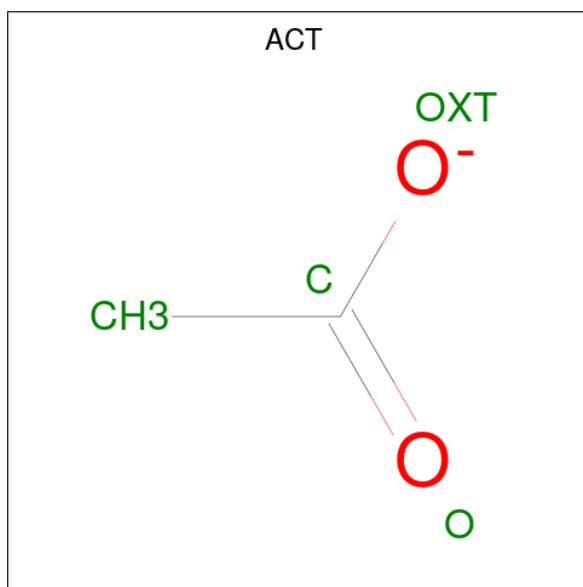
Chain	Residue	Modelled	Actual	Comment	Reference
A	1035	GLY	-	expression tag	UNP Q9Y4B6
A	1036	GLY	-	expression tag	UNP Q9Y4B6
A	1037	GLY	-	expression tag	UNP Q9Y4B6
A	1038	ARG	-	expression tag	UNP Q9Y4B6
A	1250	LEU	GLN	engineered mutation	UNP Q9Y4B6

- Molecule 2 is 5-(2-fluorophenyl)-2,3-dihydroimidazo[2,1-a]isoquinoline (CCD ID: LQH) (formula: C₁₇H₁₃FN₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	F	N	0	0
			20	17	1	2		
2	A	1	Total	C	F	N	0	0
			20	17	1	2		

- Molecule 3 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	197	Total	O	0	0
			197	197		

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.

- Chain A:
-
- 6% 56% 22% 18%
- GLY GLY GLY ARG GLU PRO LYS GLN ARG ARG GLN ALA PRO ILE ASN PHE THR SER ARG LEU ASN ARG ARG ALA SER PHE PRO LYS TVR GLY VAL ASP GLY CYS PHE ASP ARG HIS LEU TLE PHE SER ARG F1080 I1083 S1084 V1085 N1090 E1091 D1092 S1093 E1094 G1095 F1096 F1097
- R1106 M1109 T1112 G1115 Q1116 L1117 N1121 E1128 A1129 S1130 Y1131 N1132 C1133 T1138 T1139 L1140 L1141 S1144 R1145 T1152 W1156 P1159 A1162 G1165 S1168 M1172 K1173 H1174 S1175 F1176 T1177 F1184 S1185 R1186 H1187 D1190 R1191 T1199 A1200 H1201 L1202 Y1203 D1204 N1205 Q1206 G1208 N1209 K1210 L1211 T1233 D1234 D1235 N1239 W1244 D1245 V1246 R1247 S1248 A1249 L1250 A1251 I1252 N1259 G1264 H1267 P1268 R1269 G1270 V1273 D1281 H1286 S1288 H1289 R1298 V1299 V1300 H1303 T1306 Q1314 ASP T1315 ASP GLU ASP ASP LEU MET GLU

4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	82.23Å 82.23Å 237.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.68 – 2.25 45.68 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.68-2.25) 100.0 (45.68-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.203 , 0.231 0.203 , 0.231	Depositor DCC
R_{free} test set	1139 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	41.3	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5007	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.33% 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: ACT, LQH

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	1.74	53/2478 (2.1%)	1.56	24/3359 (0.7%)

The worst 5 of 53 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1247	ARG	C-O	11.16	1.38	1.24
1	A	1094	SER	C-O	10.83	1.36	1.23
1	A	1201	HIS	CD2-NE2	9.90	1.48	1.37
1	A	1289	HIS	C-O	9.46	1.35	1.23
1	A	1386	LEU	C-O	9.35	1.34	1.24

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1239	ASN	CA-CB-CG	-7.72	104.88	112.60
1	A	1281	ASP	CA-CB-CG	7.66	120.26	112.60
1	A	1247	ARG	CB-CA-C	-7.36	97.01	110.63
1	A	1306	THR	CA-CB-OG1	-7.31	98.64	109.60
1	A	1233	THR	CA-CB-OG1	-7.07	98.99	109.60

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	2416	2347	2331	36	0
2	A	40	0	0	3	0
3	A	4	3	3	0	0
4	A	197	0	0	2	2
All	All	2657	2350	2334	37	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 8.

The worst 5 of 37 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:1117[B]:LEU:HD12	1:A:1133:CYS:SG	2.12	0.89
1:A:1117[B]:LEU:HD11	1:A:1152:THR:HG21	1.57	0.85
1:A:1156:TRP:O	1:A:1156:TRP:CE3	2.34	0.81
1:A:1314:GLN:HE21	1:A:1314:GLN:HA	1.47	0.78
1:A:1117[B]:LEU:HD11	1:A:1152:THR:CG2	2.16	0.76

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)
4:A:1789:HOH:O	4:A:1789:HOH:O[7_555]	1.98	0.22
4:A:1792:HOH:O	4:A:1792:HOH:O[12_555]	2.15	0.05

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	301/367 (82%)	288 (96%)	12 (4%)	1 (0%)	36 38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1168	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	268/321 (84%)	252 (94%)	16 (6%)	17	16

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1374	SER
1	A	1359	THR
1	A	1299	VAL
1	A	1336	THR
1	A	1273	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1314	GLN
1	A	1353	ASN
1	A	1379	ASN
1	A	1132	ASN
1	A	1126	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	LQH	A	1501	-	23,23,23	1.86	5 (21%)	27,33,33	1.77	4 (14%)
3	ACT	A	1503	-	3,3,3	1.02	0	3,3,3	0.90	0
2	LQH	A	1502	-	23,23,23	1.97	5 (21%)	27,33,33	1.14	3 (11%)

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	LQH	A	1501	-	-	0/4/10/10	0/4/4/4
2	LQH	A	1502	-	-	2/4/10/10	0/4/4/4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1502	LQH	C3-N1	-4.43	1.31	1.38
2	A	1502	LQH	C12-C6	4.34	1.52	1.43
2	A	1501	LQH	C3-N1	-4.33	1.31	1.38
2	A	1501	LQH	C12-C6	4.28	1.52	1.43
2	A	1502	LQH	C7-C3	3.85	1.53	1.45

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1501	LQH	C9-C4-N1	-5.26	97.50	101.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1501	LQH	C14-C10-C5	-4.13	118.62	123.07
2	A	1501	LQH	C11-C5-C10	3.33	120.40	116.70
2	A	1501	LQH	C12-C6-C2	-3.21	118.56	122.19
2	A	1502	LQH	C9-C4-N1	-2.76	99.30	101.30

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1502	LQH	N1-C2-C5-C11
2	A	1502	LQH	N1-C2-C5-C10

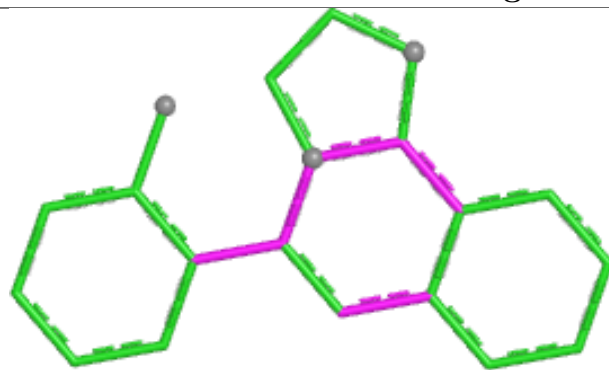
There are no ring outliers.

1 monomer is involved in 3 short contacts:

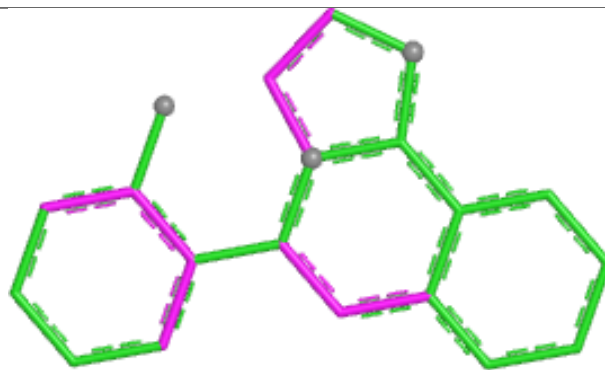
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1501	LQH	3	0

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.

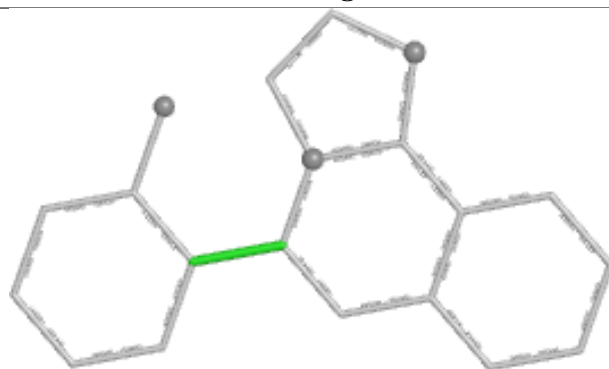
Ligand LQH A 1501



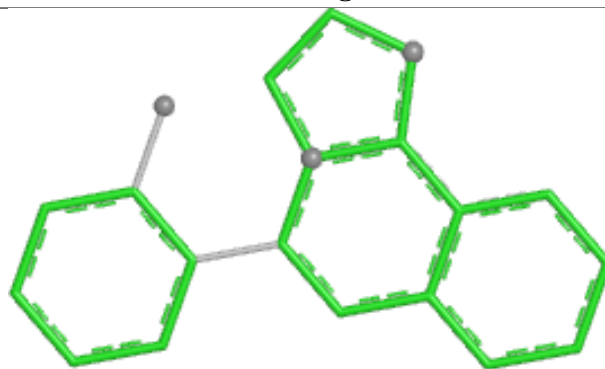
Bond lengths



Bond angles

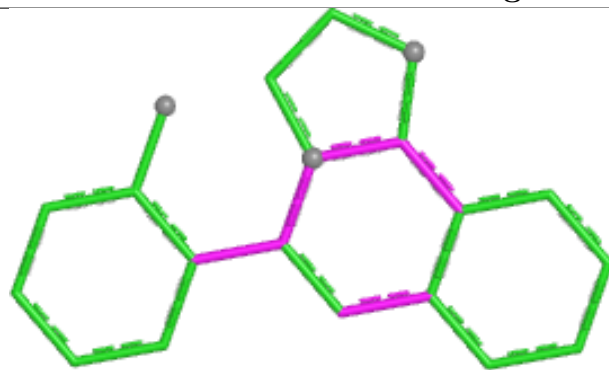


Torsions

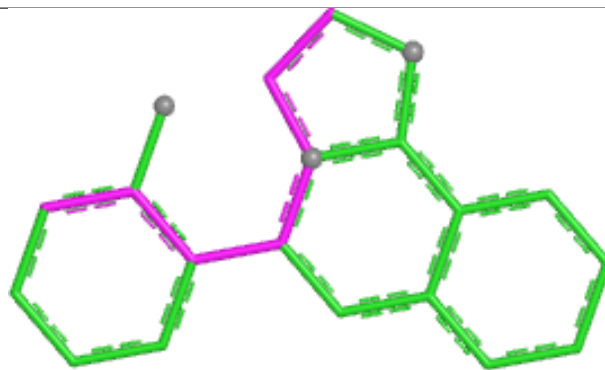


Rings

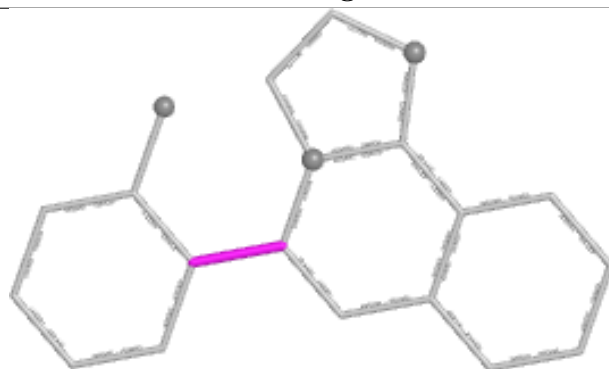
Ligand LQH A 1502



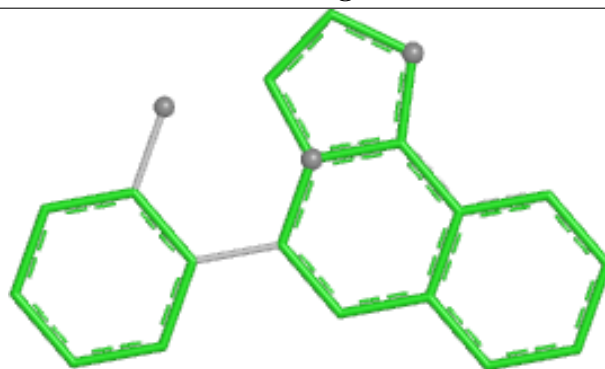
Bond lengths



Bond angles



Torsions



Rings

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, 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	301/367 (82%)	0.45	21 (6%) 22 20	16, 47, 81, 108	4 (1%)

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1390	GLY	6.6
1	A	1315	ALA	5.1
1	A	1303[A]	HIS	4.1
1	A	1375	MET	4.0
1	A	1247	ARG	3.8

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

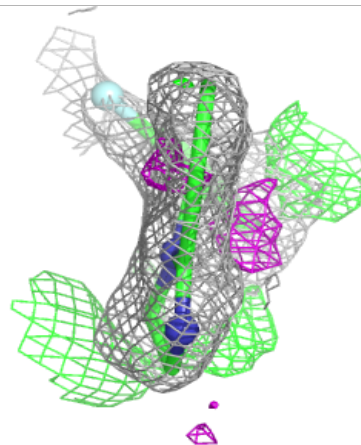
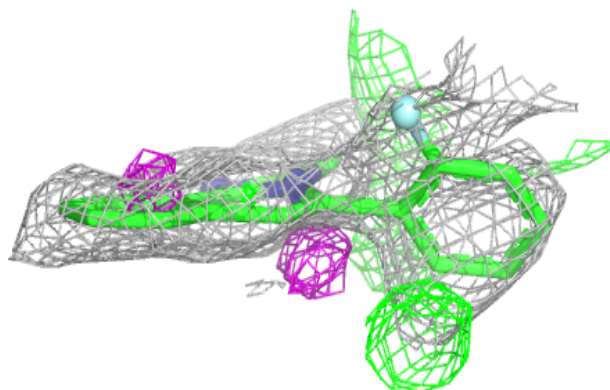
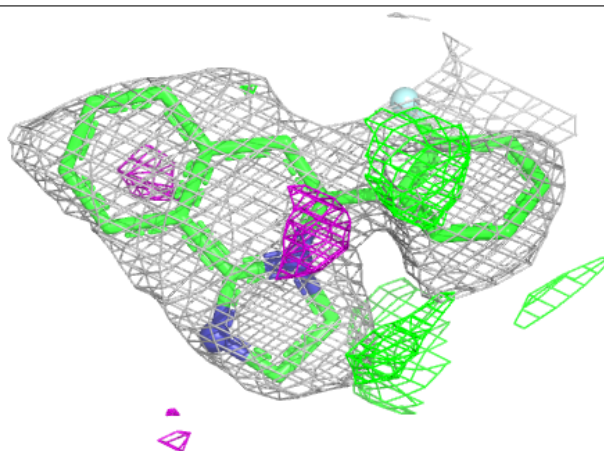
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

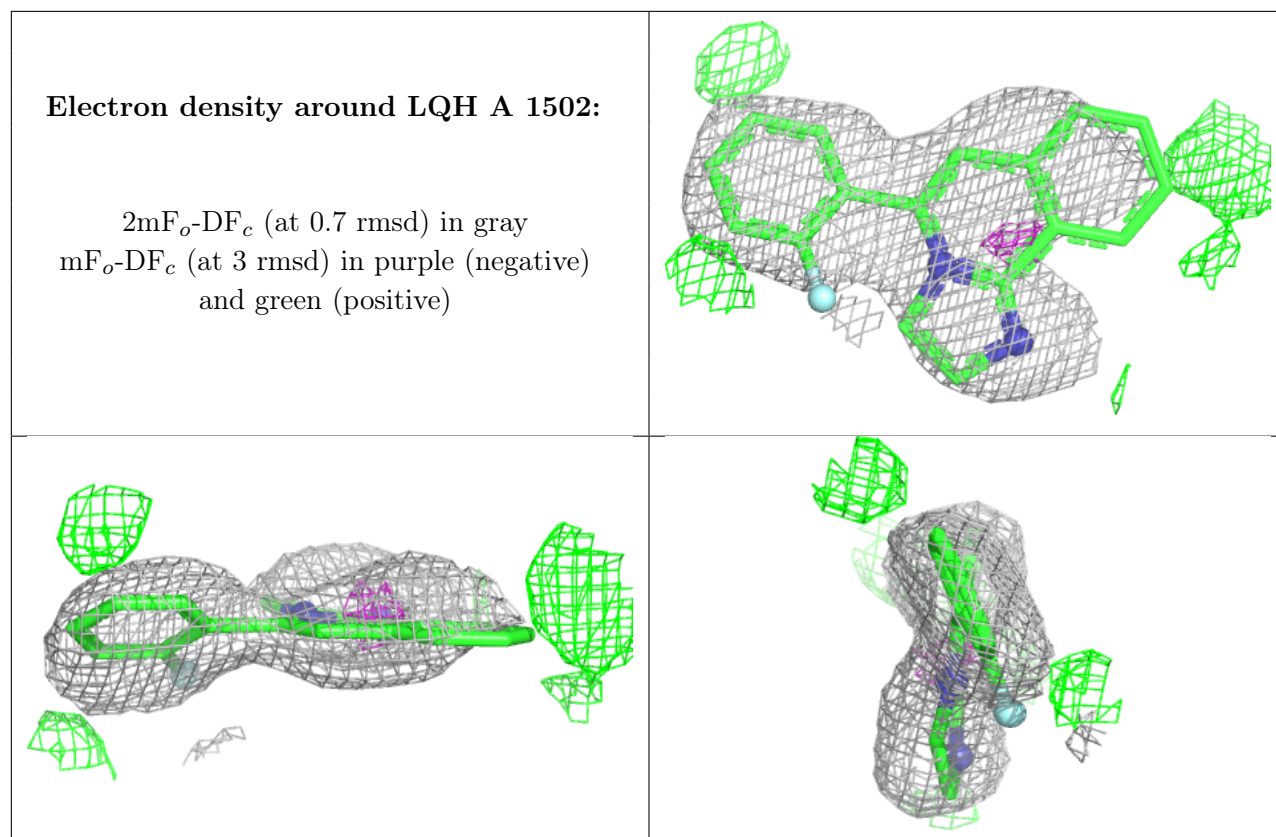
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	LQH	A	1501	20/20	0.76	0.23	61,77,93,95	0
2	LQH	A	1502	20/20	0.82	0.23	66,71,78,78	20
3	ACT	A	1503	4/4	0.98	0.05	27,28,29,29	7

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 LQH A 1501:

$2mF_o-DF_c$ (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.