wwPDB X-ray Structure Validation Summary Report (i)

Oct 5, 2023 – 03:58 AM EDT

PDB ID	:	6V6K
Title	:	EGFR(T790M/V948R) in complex with LN2057
Authors	:	Heppner, D.E.; Eck, M.J.
Deposited on	:	2019-12-05
Resolution	:	2.20 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	FAILED
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	FAILED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.20 Å.

There are no overall percentile quality scores available for this entry.

MolProbity and EDS failed to run properly - the sequence quality summary graphics cannot be shown.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	QQJ	F	1202	-	X	-	-
3	QQJ	H	1202	-	X	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 20750 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	D	314	Total	C	N	O	S	0	0	0
			2521	1614	427	461	19			
1	A	300	Total	C	N	O	S	0	1	0
			2420	1553	408	440	19			
1	B	301	Total	C	N	O	S	0	0	0
			2424	1554	411	440	19			
1	C	302	Total	C	N	O	S	0	1	0
			2440	1564	413	444	19			
1	E	303	Total	C	N	O	S	0	1	0
			2441	1565	413	444	19			
1	F	306	Total	C	N	O	S	0	0	0
			2453	1572	416	446	19			
1	G	314	Total	C	N	O	S	0	1	0
			2530	1619	428	464	19			
1	H	314	Total	C	N	O	S	0	1	0
			2530	1619	428	464	19			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	790	MET	THR	engineered mutation	UNP P00533
D	948	ARG	VAL	engineered mutation	UNP P00533
A	790	MET	THR	engineered mutation	UNP P00533
A	948	ARG	VAL	engineered mutation	UNP P00533
B	790	MET	THR	engineered mutation	UNP P00533
B	948	ARG	VAL	engineered mutation	UNP P00533
C	790	MET	THR	engineered mutation	UNP P00533
C	948	ARG	VAL	engineered mutation	UNP P00533
E	790	MET	THR	engineered mutation	UNP P00533
E	948	ARG	VAL	engineered mutation	UNP P00533
F	790	MET	THR	engineered mutation	UNP P00533
F	948	ARG	VAL	engineered mutation	UNP P00533
G	790	MET	THR	engineered mutation	UNP P00533

Continued on next page...

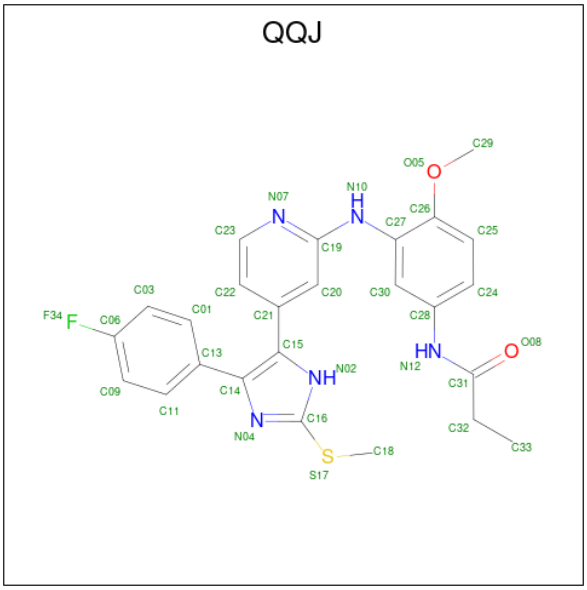
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	948	ARG	VAL	engineered mutation	UNP P00533
H	790	MET	THR	engineered mutation	UNP P00533
H	948	ARG	VAL	engineered mutation	UNP P00533

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Cl 1 1	0	0
2	A	1	Total Cl 1 1	0	0
2	B	1	Total Cl 1 1	0	0
2	C	1	Total Cl 1 1	0	0
2	E	1	Total Cl 1 1	0	0
2	F	1	Total Cl 1 1	0	0
2	G	1	Total Cl 1 1	0	0
2	H	1	Total Cl 1 1	0	0

- Molecule 3 is N-[3-({4-[4-(4-fluorophenyl)-2-(methylsulfanyl)-1H-imidazol-5-yl]pyridin-2-yl}amino)-4-methoxyphenyl]propanamide (three-letter code: QQJ) (formula: $C_{25}H_{24}FN_5O_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	D	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	A	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	B	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	C	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	E	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	F	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	G	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		
3	H	1	Total	C	F	N	O	S	0	0
			34	25	1	5	2	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	87	Total	O	0	0
			87	87		
4	A	81	Total	O	0	0
			81	81		
4	B	80	Total	O	0	0
			80	80		
4	C	103	Total	O	0	0
			103	103		
4	E	78	Total	O	0	0
			78	78		
4	F	85	Total	O	0	0
			85	85		
4	G	86	Total	O	0	0
			86	86		
4	H	111	Total	O	0	0
			111	111		

MolProbity and EDS failed to run properly - this section is therefore empty.

3 Data and refinement statistics (i)

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	71.60Å 102.45Å 174.04Å 90.00° 101.25° 90.00°	Depositor
Resolution (Å)	85.35 – 2.20	Depositor
% Data completeness (in resolution range)	93.7 (85.35-2.20)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.84 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.214 , 0.239	Depositor
Wilson B-factor (Å^2)	27.7	Xtriage
Anisotropy	0.717	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.005 for h,-k,-h-l	Xtriage
Total number of atoms	20750	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 66.40 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.0839e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

4 Model quality

4.1 Standard geometry

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles

4.3.1 Protein backbone

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains

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

4.5 Carbohydrates

There are no monosaccharides in this entry.

4.6 Ligand geometry

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
3	QQJ	G	1202	1	35,37,37	5.92	28 (80%)	42,51,51	1.62	9 (21%)
3	QQJ	D	1202	1	35,37,37	5.82	30 (85%)	42,51,51	1.61	10 (23%)
3	QQJ	E	1202	1	35,37,37	4.75	27 (77%)	42,51,51	2.65	12 (28%)
3	QQJ	F	1202	1	35,37,37	5.74	28 (80%)	42,51,51	1.71	12 (28%)
3	QQJ	C	1202	1	35,37,37	5.80	30 (85%)	42,51,51	1.60	11 (26%)
3	QQJ	B	1202	1	35,37,37	4.79	29 (82%)	42,51,51	2.00	9 (21%)
3	QQJ	H	1202	1	35,37,37	5.97	30 (85%)	42,51,51	2.07	10 (23%)
3	QQJ	A	1202	1	35,37,37	5.71	29 (82%)	42,51,51	1.73	8 (19%)

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
3	QQJ	G	1202	1	-	4/20/22/22	0/4/4/4
3	QQJ	D	1202	1	-	4/20/22/22	0/4/4/4
3	QQJ	E	1202	1	-	4/20/22/22	0/4/4/4
3	QQJ	F	1202	1	-	6/20/22/22	0/4/4/4
3	QQJ	C	1202	1	-	2/20/22/22	0/4/4/4
3	QQJ	B	1202	1	-	1/20/22/22	0/4/4/4
3	QQJ	H	1202	1	-	6/20/22/22	0/4/4/4
3	QQJ	A	1202	1	-	2/20/22/22	0/4/4/4

The worst 5 of 231 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1202	QQJ	C30-C28	9.96	1.55	1.39
3	C	1202	QQJ	C30-C28	9.91	1.55	1.39
3	A	1202	QQJ	C30-C28	9.61	1.55	1.39
3	G	1202	QQJ	C30-C28	9.54	1.55	1.39
3	C	1202	QQJ	C30-C27	9.51	1.54	1.39

The worst 5 of 81 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	1202	QQJ	C18-S17-C16	12.83	111.85	102.27
3	H	1202	QQJ	C18-S17-C16	8.17	108.36	102.27
3	B	1202	QQJ	C18-S17-C16	7.59	107.93	102.27
3	A	1202	QQJ	C18-S17-C16	6.16	106.86	102.27
3	H	1202	QQJ	C28-N12-C31	-5.11	118.56	127.50

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

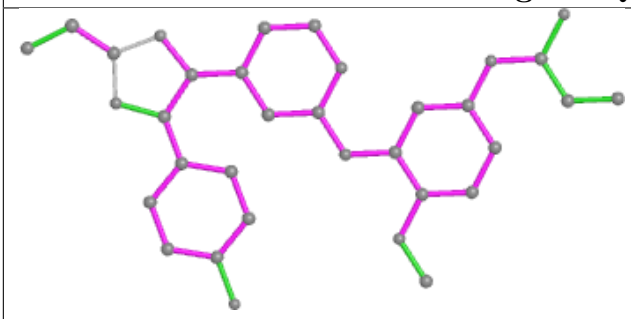
Mol	Chain	Res	Type	Atoms
3	A	1202	QQJ	C01-C13-C14-N04
3	H	1202	QQJ	C27-C26-O05-C29
3	F	1202	QQJ	C27-C26-O05-C29
3	H	1202	QQJ	C25-C26-O05-C29
3	D	1202	QQJ	C25-C26-O05-C29

There are no ring outliers.

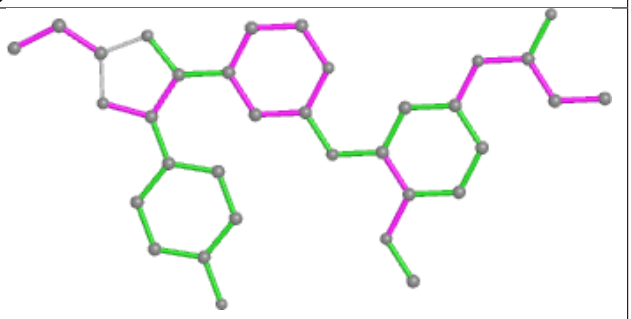
No monomer is involved in short contacts.

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 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.

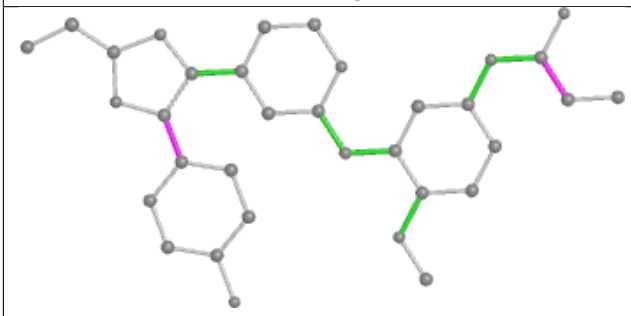
Ligand QQJ G 1202



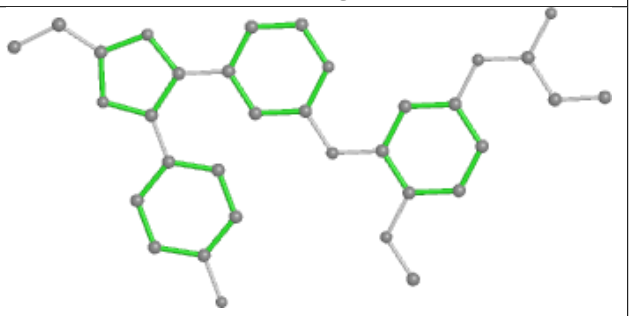
Bond lengths



Bond angles

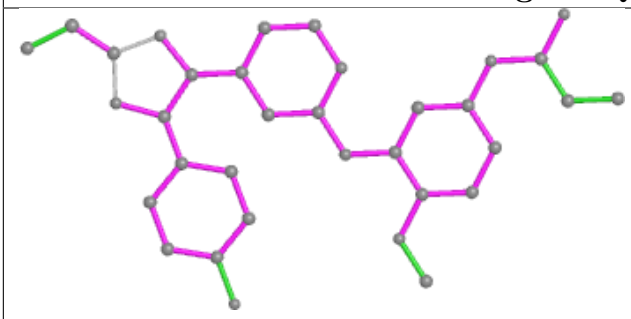


Torsions

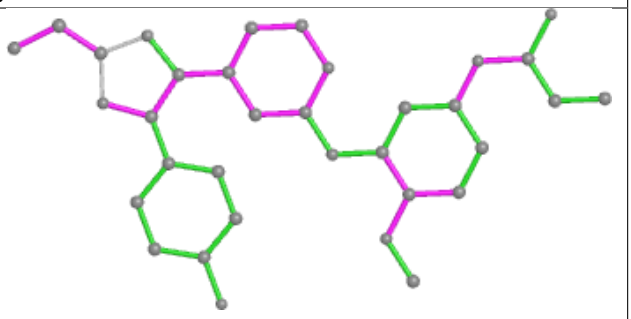


Rings

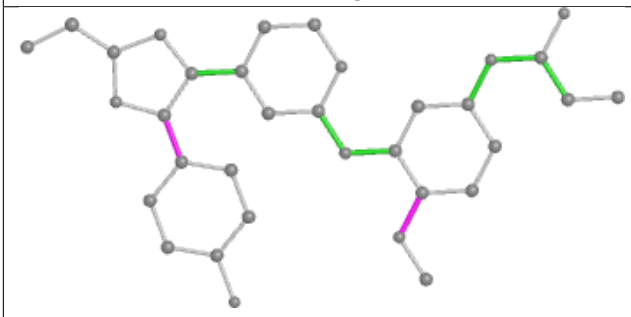
Ligand QQJ D 1202



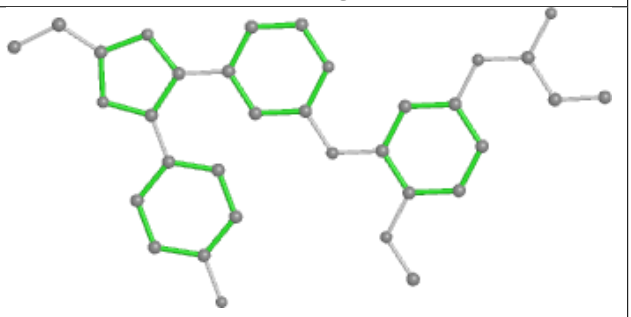
Bond lengths



Bond angles

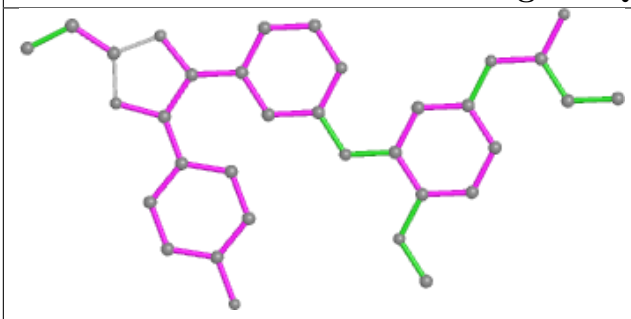


Torsions

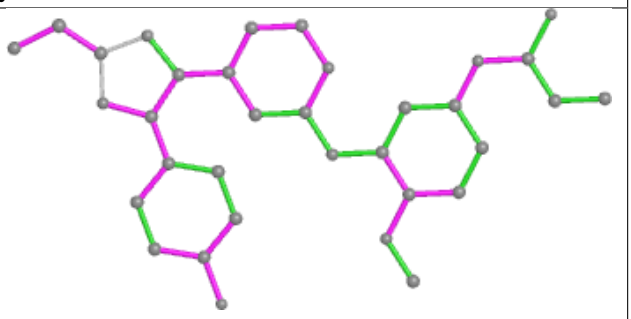


Rings

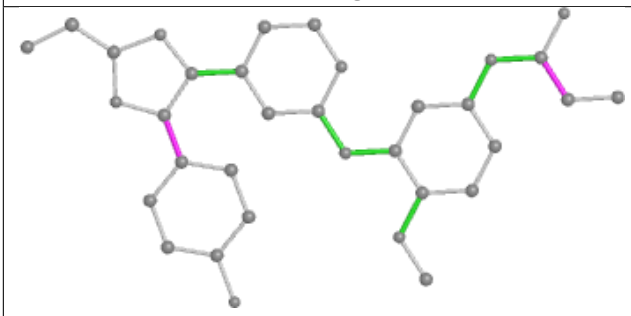
Ligand QQJ E 1202



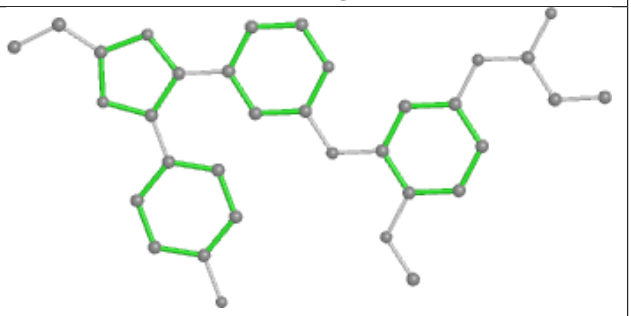
Bond lengths



Bond angles

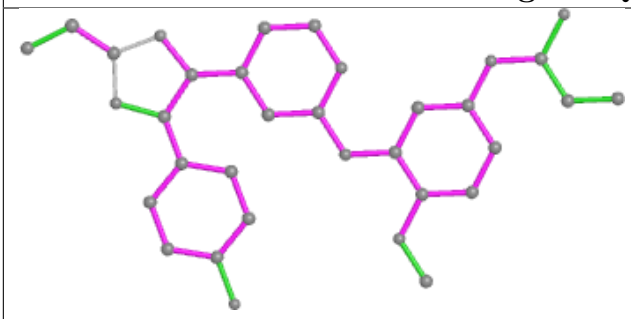


Torsions

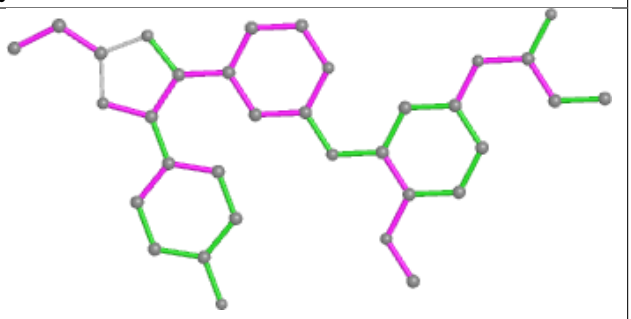


Rings

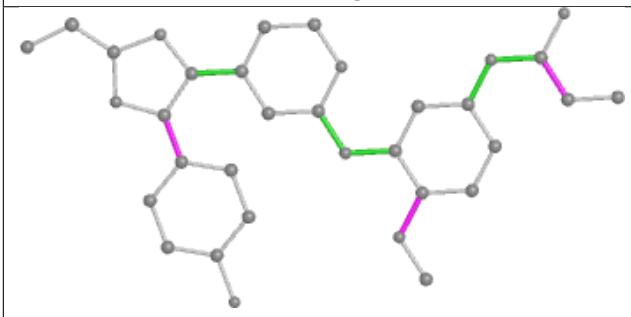
Ligand QQJ F 1202



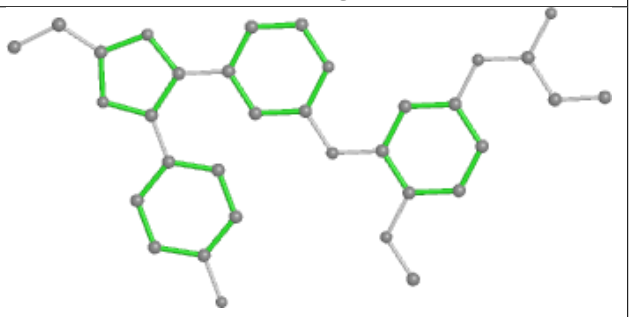
Bond lengths



Bond angles

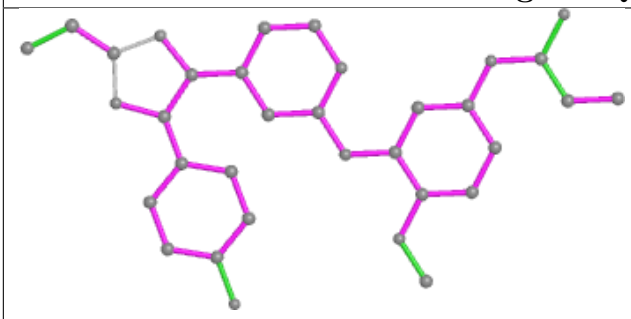


Torsions

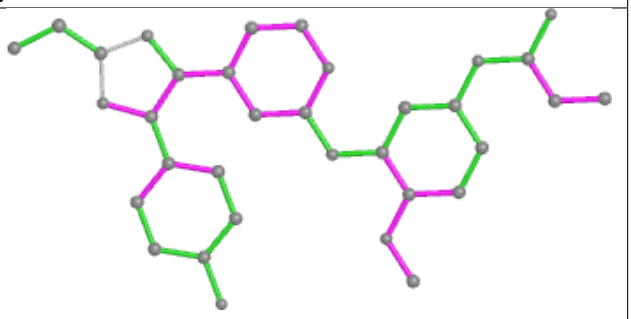


Rings

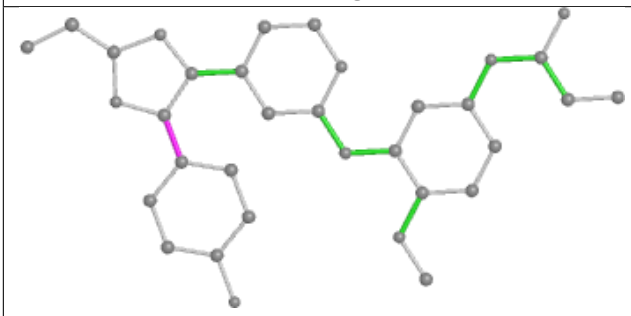
Ligand QQJ C 1202



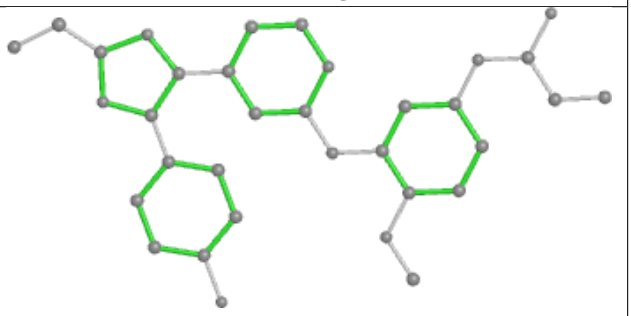
Bond lengths



Bond angles

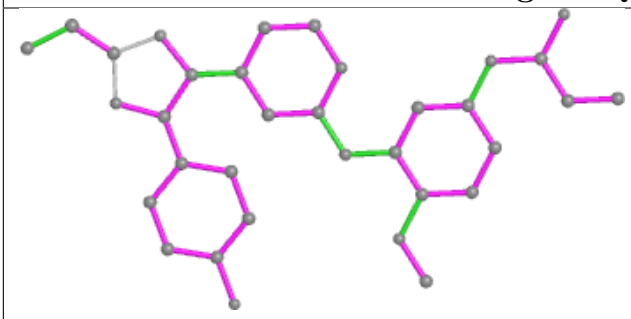


Torsions

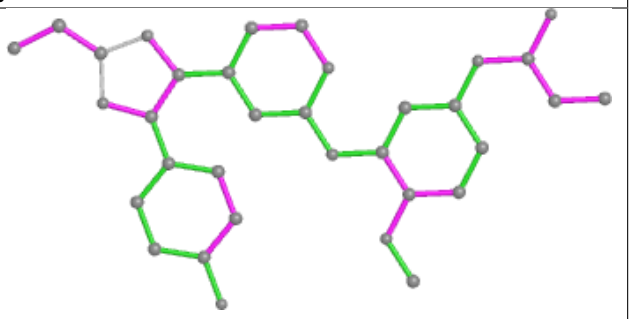


Rings

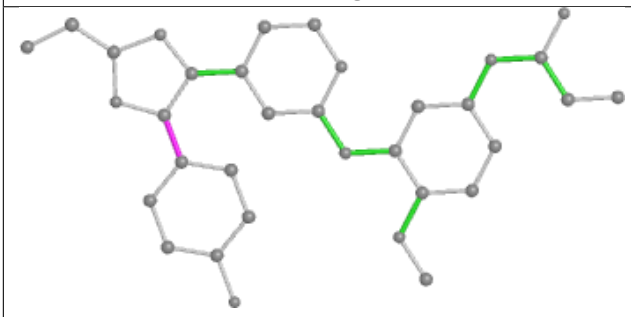
Ligand QQJ B 1202



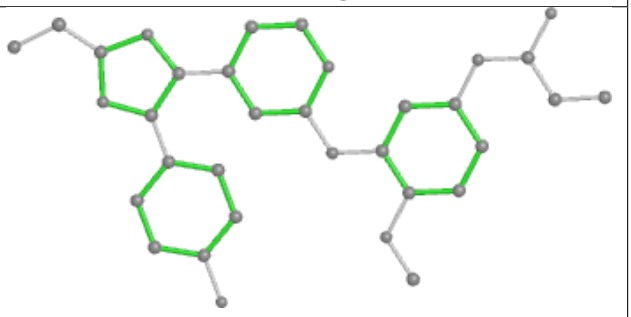
Bond lengths



Bond angles

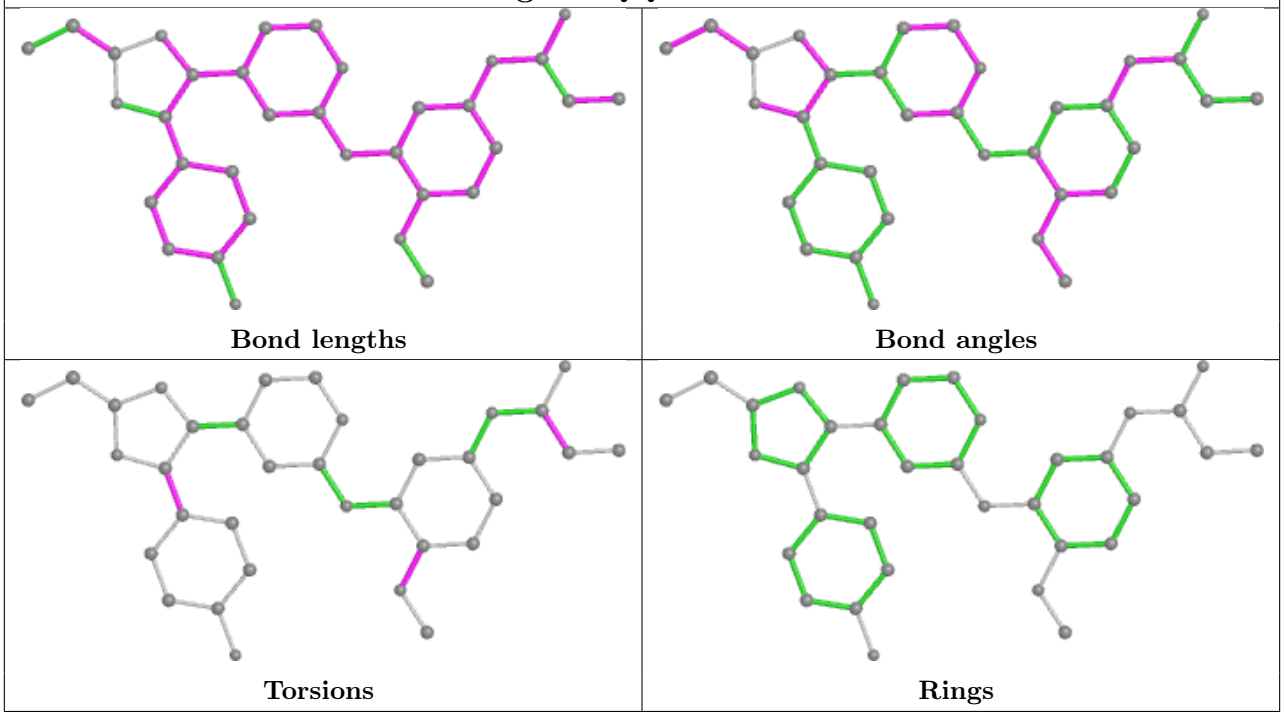


Torsions

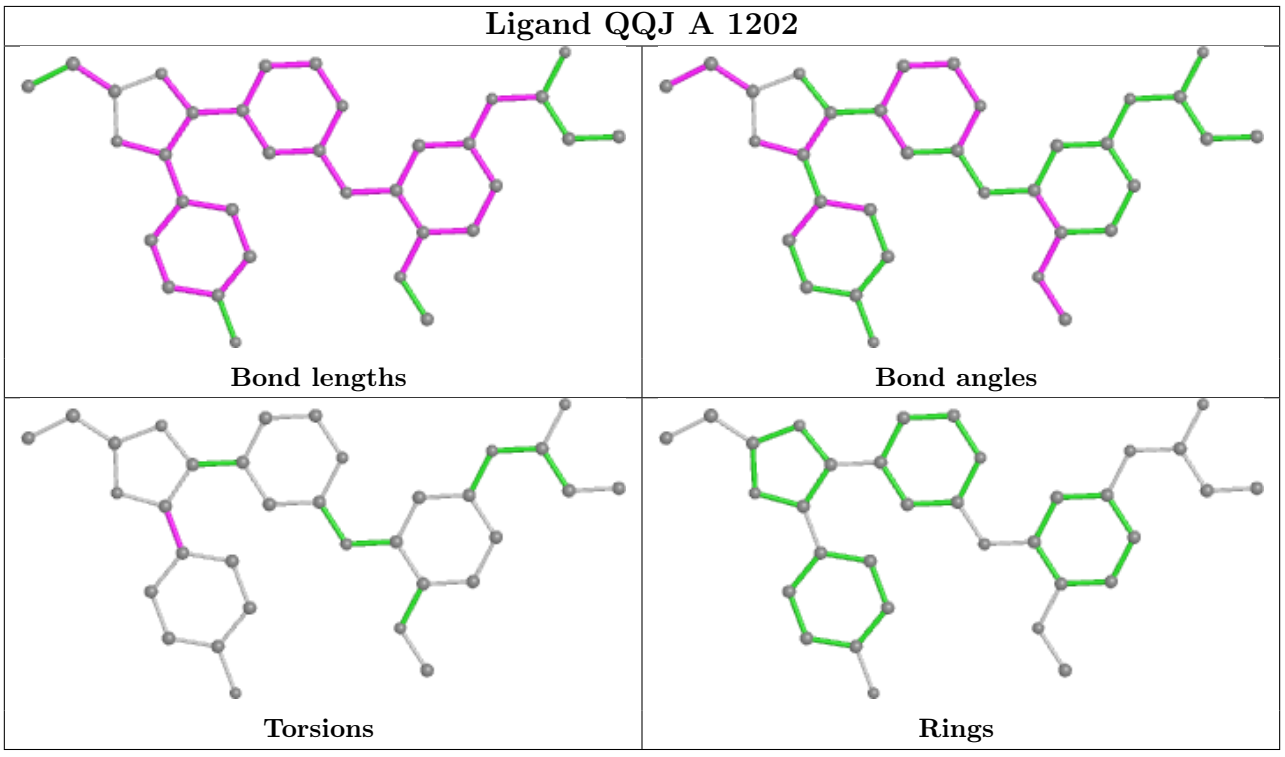


Rings

Ligand QQJ H 1202



Ligand QQJ A 1202



4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

5.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

5.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

5.4 Ligands

EDS failed to run properly - this section is therefore empty.

5.5 Other polymers

EDS failed to run properly - this section is therefore empty.