



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2023 – 12:18 PM EDT

PDB ID : 8D3E
Title : Crystal structure of human Apoptosis-Inducing Factor (AIF) W196A mutant complexed with 6-fluoroquinolin-4-amine
Authors : Brosey, C.A.; Tainer, J.A.
Deposited on : 2022-06-01
Resolution : 2.38 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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

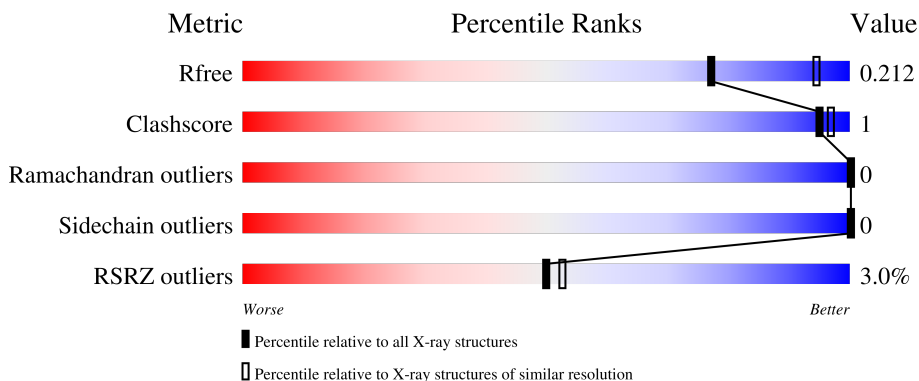
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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	543	 3% 77% 20%
1	B	543	 2% 78% 20%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13521 atoms, of which 6515 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 Apoptosis-inducing factor 1, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	433	6487	2078	3229	569	600	11	0	0	0
1	B	436	6472	2081	3207	575	598	11	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

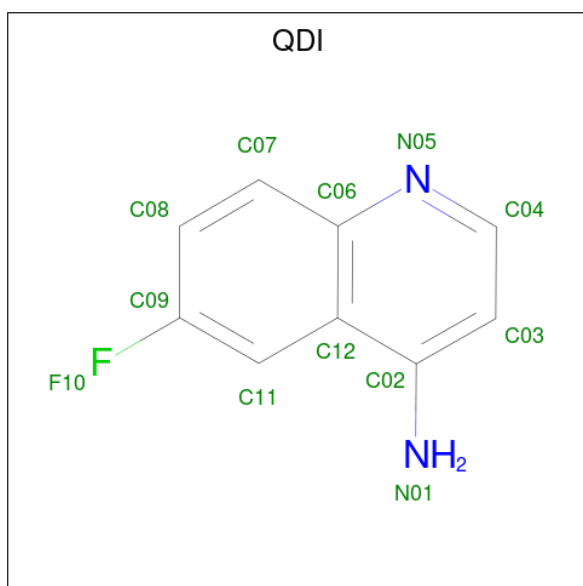
Chain	Residue	Modelled	Actual	Comment	Reference
A	77	MET	-	initiating methionine	UNP O95831
A	196	ALA	TRP	engineered mutation	UNP O95831
A	614	LEU	-	expression tag	UNP O95831
A	615	GLU	-	expression tag	UNP O95831
A	616	VAL	-	expression tag	UNP O95831
A	617	LEU	-	expression tag	UNP O95831
A	618	PHE	-	expression tag	UNP O95831
A	619	GLN	-	expression tag	UNP O95831
B	77	MET	-	initiating methionine	UNP O95831
B	196	ALA	TRP	engineered mutation	UNP O95831
B	614	LEU	-	expression tag	UNP O95831
B	615	GLU	-	expression tag	UNP O95831
B	616	VAL	-	expression tag	UNP O95831
B	617	LEU	-	expression tag	UNP O95831
B	618	PHE	-	expression tag	UNP O95831
B	619	GLN	-	expression tag	UNP O95831

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
2	A	1	83	27	30	9	15	2	0	0
2	B	1	83	27	30	9	15	2	0	0

- Molecule 3 is 6-fluoroquinolin-4-amine (three-letter code: QDI) (formula: $C_9H_7FN_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	F	H			N
3	A	1	19	9	1	7	2	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		
4	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	186	Total	O	0	0
			186	186		
6	B	170	Total	O	0	0
			170	170		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.79Å 114.33Å 120.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.34 – 2.38 29.34 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.3 (29.34-2.38) 99.4 (29.34-2.38)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.180 , 0.212 0.180 , 0.212	Depositor DCC
R_{free} test set	2437 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtrriage
Anisotropy	0.234	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.003 for -h,l,k	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13521	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: EDO, CL, QDI, FAD

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	0.24	0/3324	0.43	0/4507
1	B	0.24	0/3331	0.43	0/4520
All	All	0.24	0/6655	0.43	0/9027

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

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	3258	3229	3229	10	0
1	B	3265	3207	3206	6	0
2	A	53	30	31	0	0
2	B	53	30	31	0	0
3	A	12	7	0	0	0
4	A	4	6	6	0	0
4	B	4	6	6	0	0
5	A	1	0	0	0	0
6	A	186	0	0	0	0
6	B	170	0	0	0	0
All	All	7006	6515	6509	16	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 1.

All (16) 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:581:ILE:HD11	1:A:610:ILE:HD11	1.79	0.63
1:B:267:LEU:HD11	1:B:306:ILE:HG21	1.84	0.58
1:A:482:PHE:CZ	1:A:494:ALA:HB3	2.40	0.55
1:A:267:LEU:HD11	1:A:306:ILE:HG21	1.89	0.54
1:B:191:LEU:HD13	1:B:203:ILE:HD11	1.93	0.51
1:B:172:ARG:N	1:B:173:PRO:CD	2.74	0.50
1:B:158:ARG:NH1	1:B:217:LEU:O	2.43	0.50
1:A:172:ARG:N	1:A:173:PRO:CD	2.75	0.50
1:A:191:LEU:HD13	1:A:203:ILE:HD11	1.97	0.47
1:A:158:ARG:NH1	1:A:217:LEU:O	2.50	0.43
1:B:270:ILE:HD13	1:B:281:THR:HG21	2.02	0.42
1:A:340:MET:CE	1:A:352:THR:HG21	2.48	0.42
1:A:482:PHE:CE1	1:A:494:ALA:HB3	2.55	0.42
1:A:452:VAL:HG13	1:A:454:HIS:CE1	2.55	0.41
1:B:402:PRO:HG3	1:B:451:ARG:CZ	2.50	0.41
1:A:454:HIS:CE1	1:A:482:PHE:CD2	3.09	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	429/543 (79%)	418 (97%)	11 (3%)	0	100	100
1	B	432/543 (80%)	420 (97%)	12 (3%)	0	100	100
All	All	861/1086 (79%)	838 (97%)	23 (3%)	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	A	334/444 (75%)	334 (100%)	0	100	100
1	B	328/444 (74%)	328 (100%)	0	100	100
All	All	662/888 (74%)	662 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	A	454	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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$
4	EDO	A	703	-	3,3,3	0.45	0	2,2,2	0.40	0
2	FAD	A	701	-	53,58,58	1.53	4 (7%)	68,89,89	1.04	3 (4%)
3	QDI	A	702	-	13,13,13	1.49	3 (23%)	18,18,18	1.34	2 (11%)
2	FAD	B	701	-	53,58,58	1.53	4 (7%)	68,89,89	1.05	4 (5%)
4	EDO	B	702	-	3,3,3	0.46	0	2,2,2	0.23	0

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
4	EDO	A	703	-	-	0/1/1/1	-
2	FAD	A	701	-	-	3/30/50/50	0/6/6/6
3	QDI	A	702	-	-	-	0/2/2/2
2	FAD	B	701	-	-	3/30/50/50	0/6/6/6
4	EDO	B	702	-	-	0/1/1/1	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	FAD	C9-C9A	6.20	1.49	1.39
2	A	701	FAD	C9-C9A	6.16	1.49	1.39
2	B	701	FAD	C6-C5X	5.89	1.49	1.40
2	A	701	FAD	C6-C5X	5.88	1.49	1.40
2	B	701	FAD	O5'-C5'	3.17	1.57	1.44
2	A	701	FAD	O5'-C5'	3.16	1.56	1.44
3	A	702	QDI	C08-C09	3.01	1.43	1.37
3	A	702	QDI	C03-C04	2.47	1.43	1.38
3	A	702	QDI	F10-C09	-2.27	1.30	1.36
2	B	701	FAD	C1'-C2'	2.15	1.55	1.52
2	A	701	FAD	C1'-C2'	2.11	1.55	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	QDI	C09-C11-C12	3.66	121.66	118.80
3	A	702	QDI	C08-C09-C11	-3.46	119.41	123.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	FAD	C4-N3-C2	-2.61	120.82	125.64
2	A	701	FAD	O4B-C1B-C2B	-2.61	103.11	106.93
2	B	701	FAD	O4B-C1B-C2B	-2.54	103.22	106.93
2	B	701	FAD	C4-N3-C2	-2.50	121.03	125.64
2	A	701	FAD	C5A-C6A-N6A	2.29	123.83	120.35
2	B	701	FAD	C5A-C6A-N6A	2.28	123.82	120.35
2	B	701	FAD	C5'-C4'-C3'	-2.14	108.07	112.20

There are no chirality outliers.

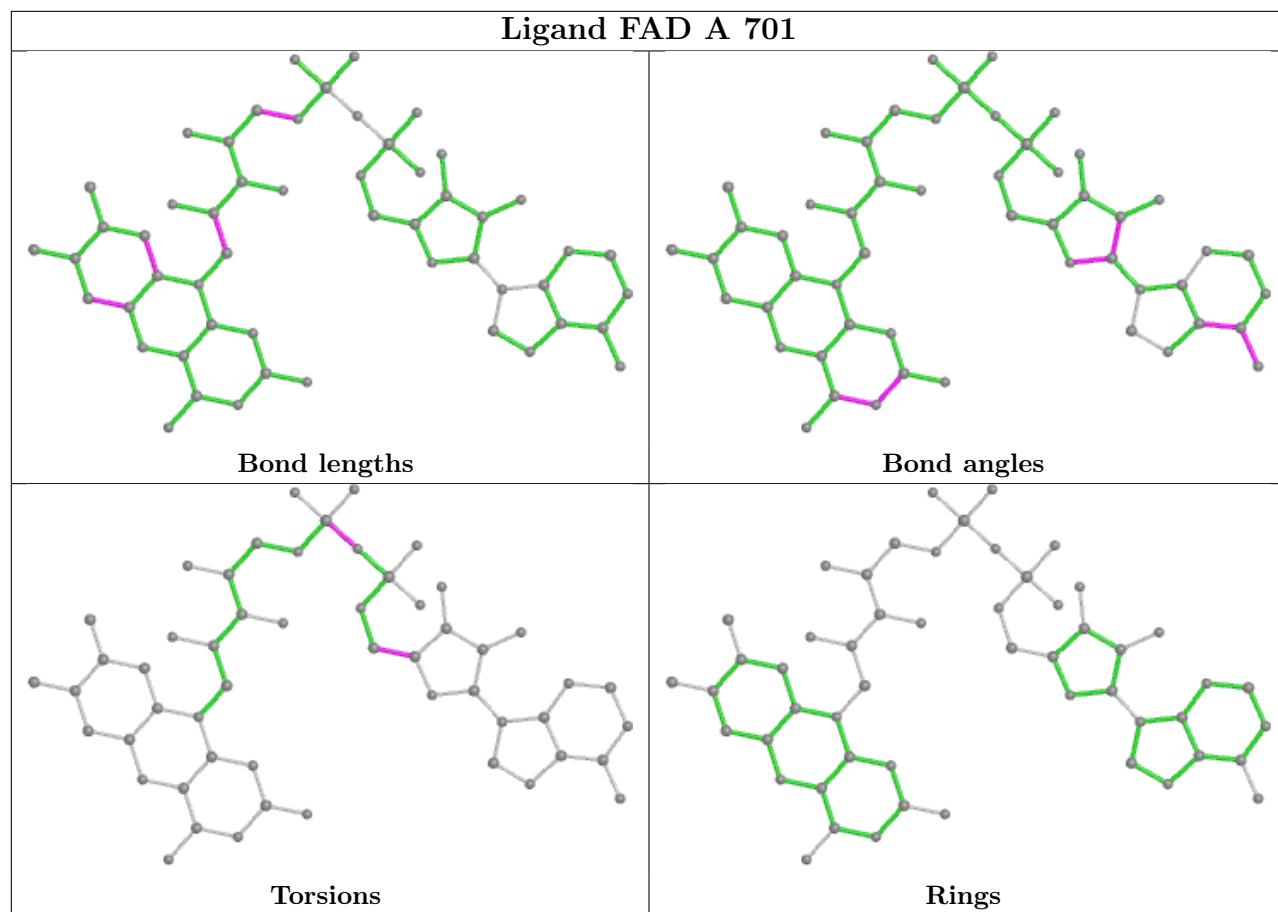
All (6) torsion outliers are listed below:

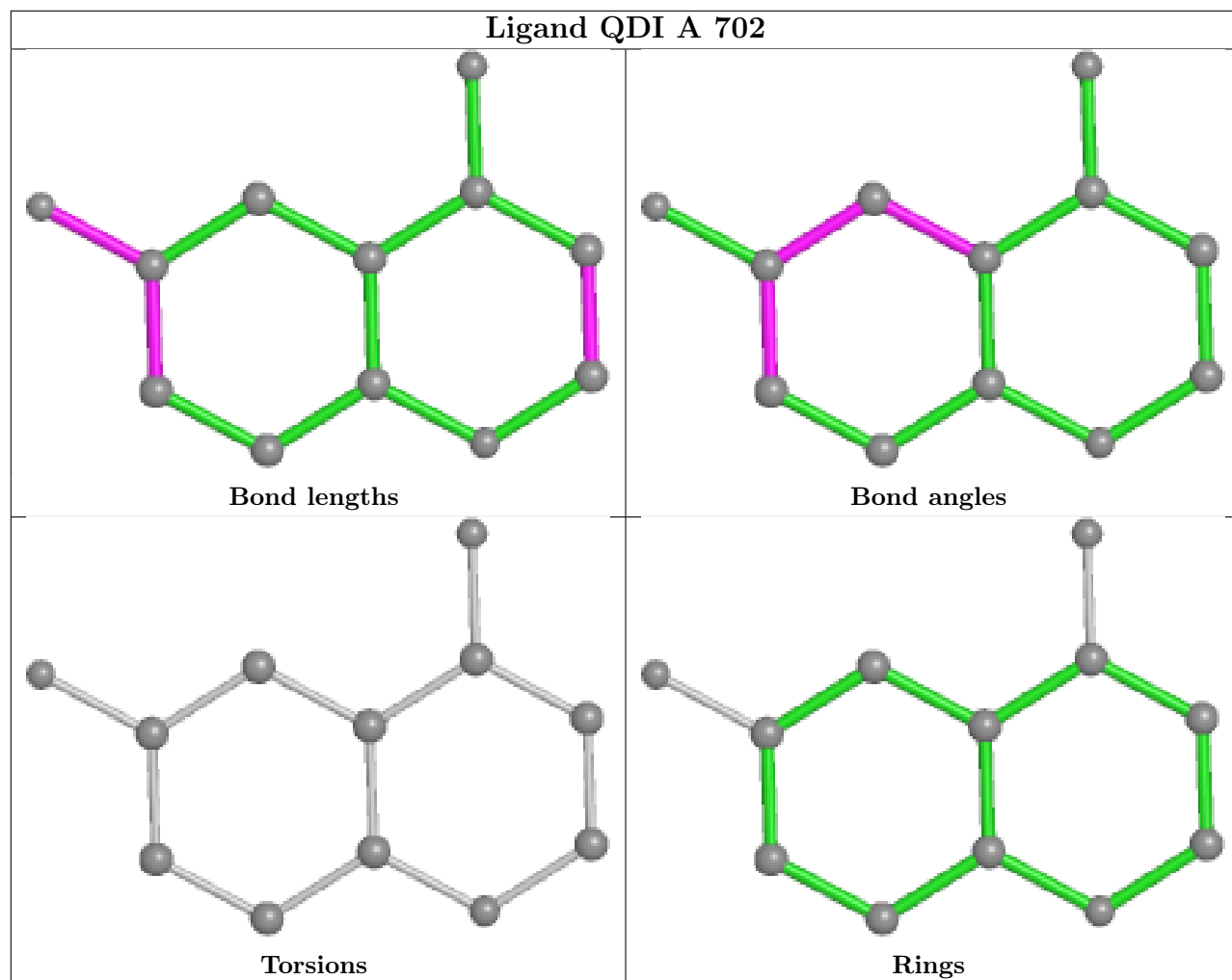
Mol	Chain	Res	Type	Atoms
2	A	701	FAD	PA-O3P-P-O5'
2	B	701	FAD	PA-O3P-P-O5'
2	B	701	FAD	O4B-C4B-C5B-O5B
2	A	701	FAD	O4B-C4B-C5B-O5B
2	A	701	FAD	C3B-C4B-C5B-O5B
2	B	701	FAD	C3B-C4B-C5B-O5B

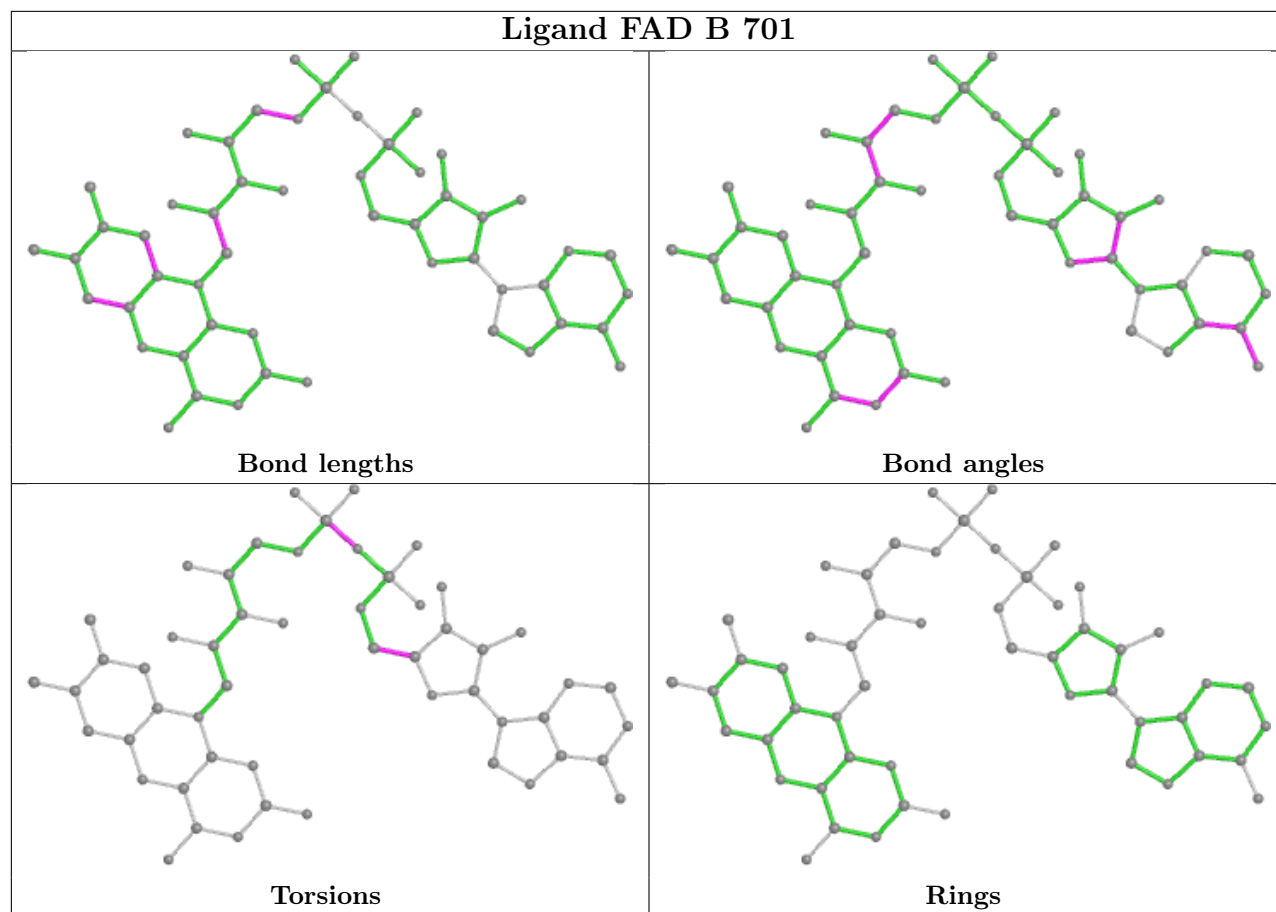
There are no ring outliers.

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	433/543 (79%)	0.16	15 (3%) 44 47	30, 46, 73, 138	0
1	B	436/543 (80%)	0.07	11 (2%) 57 59	27, 44, 77, 95	0
All	All	869/1086 (80%)	0.11	26 (2%) 50 53	27, 45, 75, 138	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	196	ALA	4.1
1	B	488	PRO	3.9
1	A	196	ALA	3.5
1	A	128	ALA	3.4
1	A	488	PRO	3.3
1	A	275	ALA	3.1
1	B	386	GLY	3.0
1	A	351	TRP	2.9
1	B	379	LEU	2.7
1	A	195	GLN	2.7
1	B	198	GLY	2.5
1	A	579	TRP	2.5
1	A	600	ASP	2.5
1	A	153	ARG	2.4
1	B	272	ARG	2.3
1	B	579	TRP	2.3
1	A	597	GLN	2.3
1	B	434	TRP	2.2
1	A	197	ASN	2.2
1	A	274	GLY	2.2
1	A	187	VAL	2.2
1	B	197	ASN	2.1
1	A	184	ASP	2.1
1	A	489	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	510	LYS	2.0
1	B	509	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 monosaccharides in this entry.

6.4 Ligands [i](#)

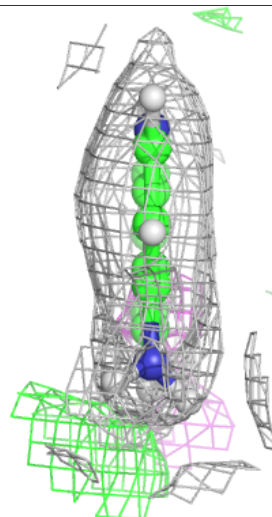
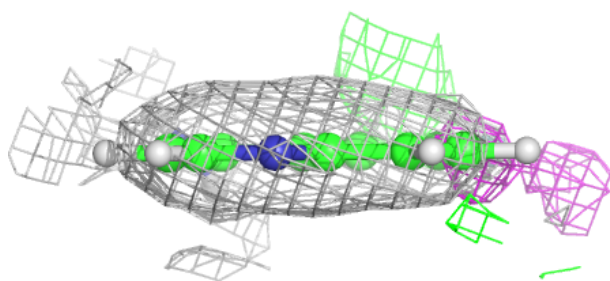
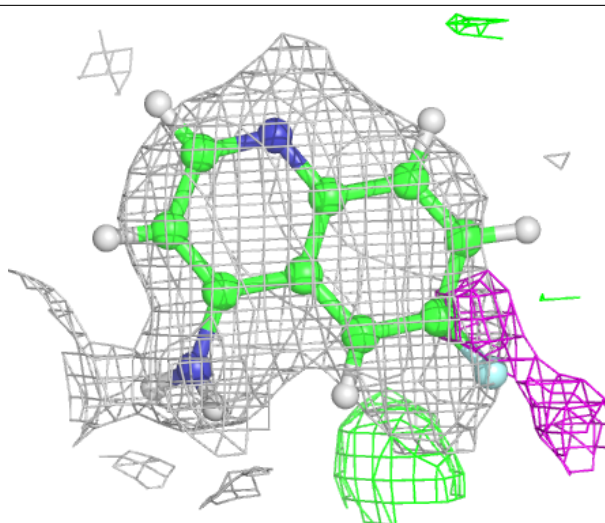
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	QDI	A	702	12/12	0.89	0.24	42,50,67,70	0
4	EDO	A	703	4/4	0.91	0.28	42,50,54,64	0
4	EDO	B	702	4/4	0.91	0.20	36,43,51,51	0
5	CL	A	704	1/1	0.92	0.07	69,69,69,69	0
2	FAD	A	701	53/53	0.97	0.18	30,37,45,54	0
2	FAD	B	701	53/53	0.98	0.12	26,34,44,56	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.

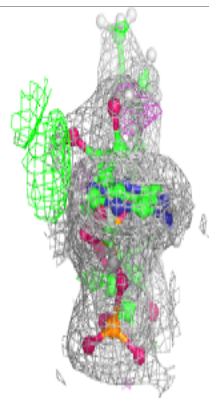
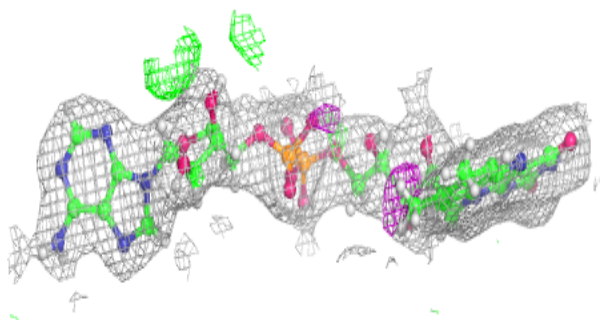
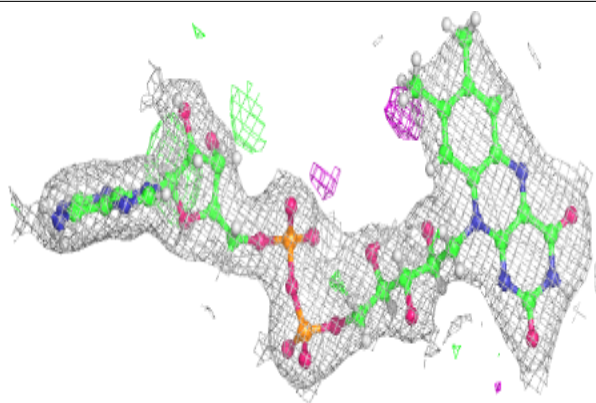
Electron density around QDI A 702:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

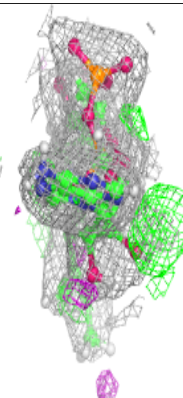
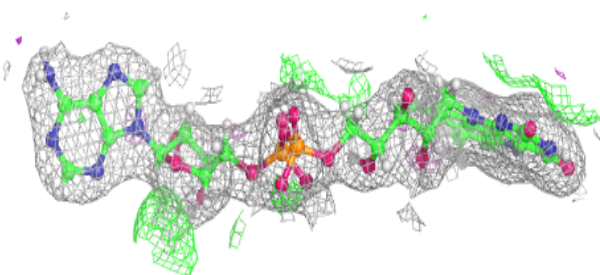
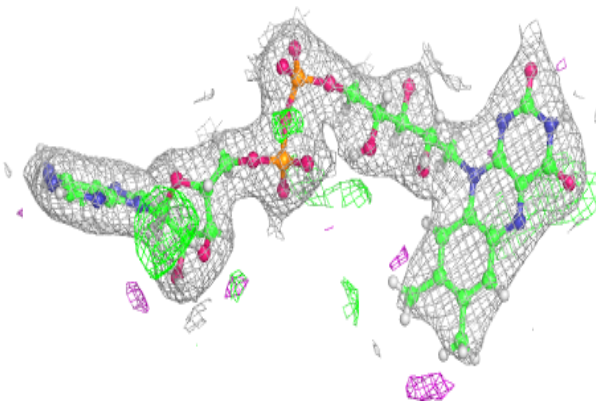


Electron density around FAD A 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around FAD B 701:**

$2mF_o-DF_c$ (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.