



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 03:23 PM UTC

PDB ID : 8D3K / pdb_00008d3k
Title : Crystal structure of human Apoptosis-Inducing Factor (AIF) complexed with 8-fluoro-2-methylquinolin-4-amine
Authors : Brosey, C.A.; Tainer, J.A.
Deposited on : 2022-06-01
Resolution : 2.30 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	:	4-5-2 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

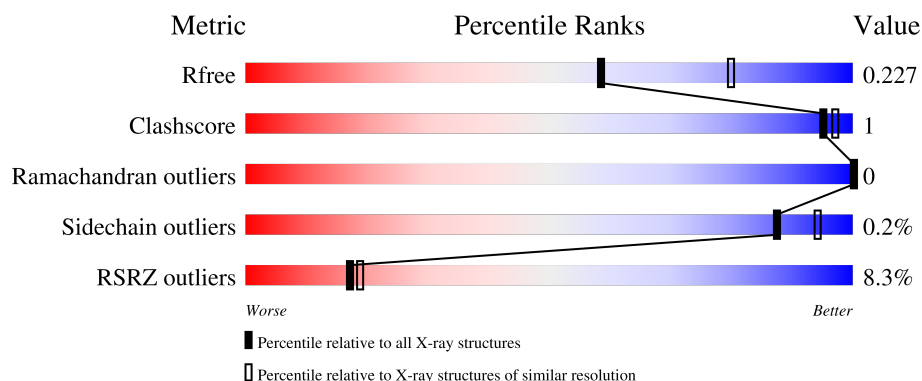
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

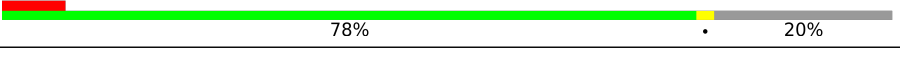
The reported resolution of this entry is 2.30 Å.

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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	
2	B	543	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 13489 atoms, of which 6529 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	437	6497	2093	3216	577	600	11	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	MET	-	initiating methionine	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

- Molecule 2 is a protein called Apoptosis-inducing factor 1, mitochondrial.

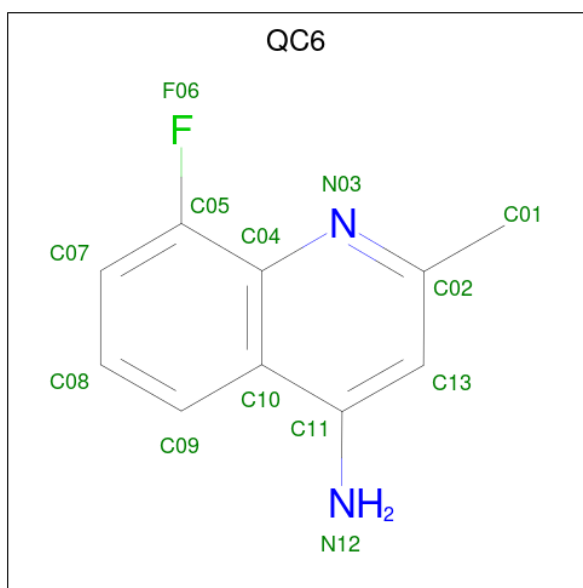
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	436	6501	2094	3228	569	599	11	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	77	MET	-	initiating methionine	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

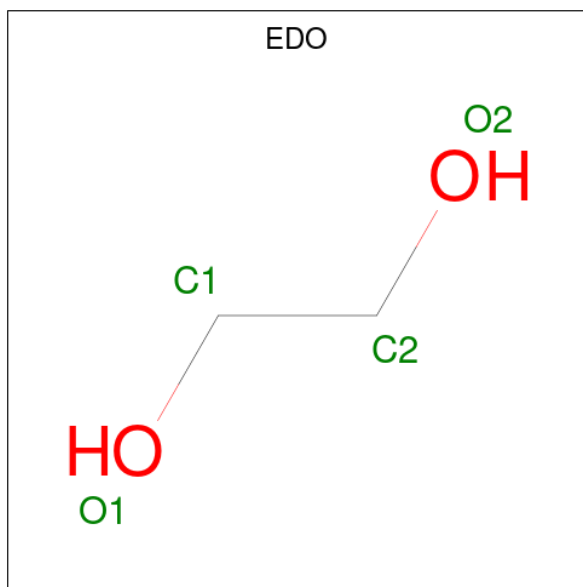
- Molecule 3 is 8-fluoro-2-methylquinolin-4-amine (CCD ID: QC6) (formula: C₁₀H₉FN₂)

(labeled as "Ligand of Interest" by depositor).



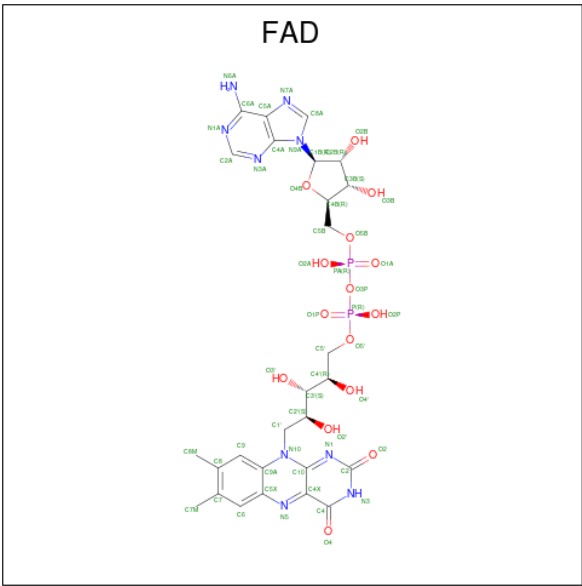
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	H	N	0	0
			22	10	1	9	2		
3	B	1	Total	C	F	H	N	0	0
			22	10	1	9	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



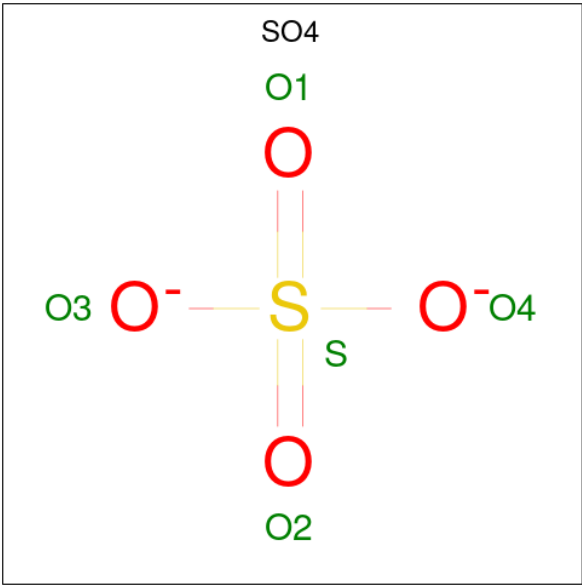
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	P	0	0
			83	27	30	9	15	2		
5	B	1	Total	C	H	N	O	P	0	0
			84	27	31	9	15	2		

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

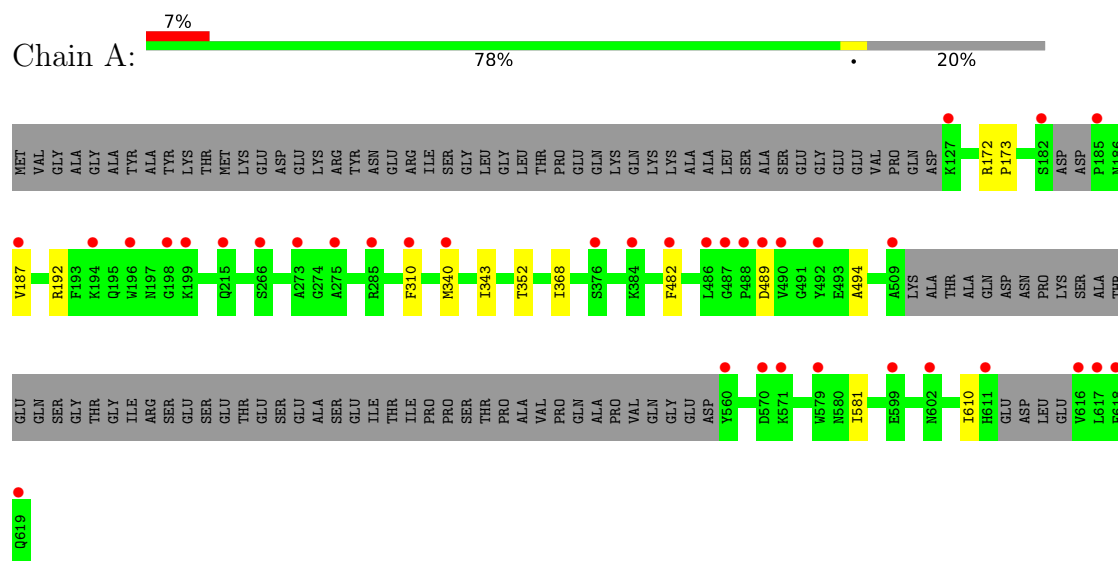
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	138	Total	O	0	0
			138	138		
7	B	107	Total	O	0	0
			107	107		

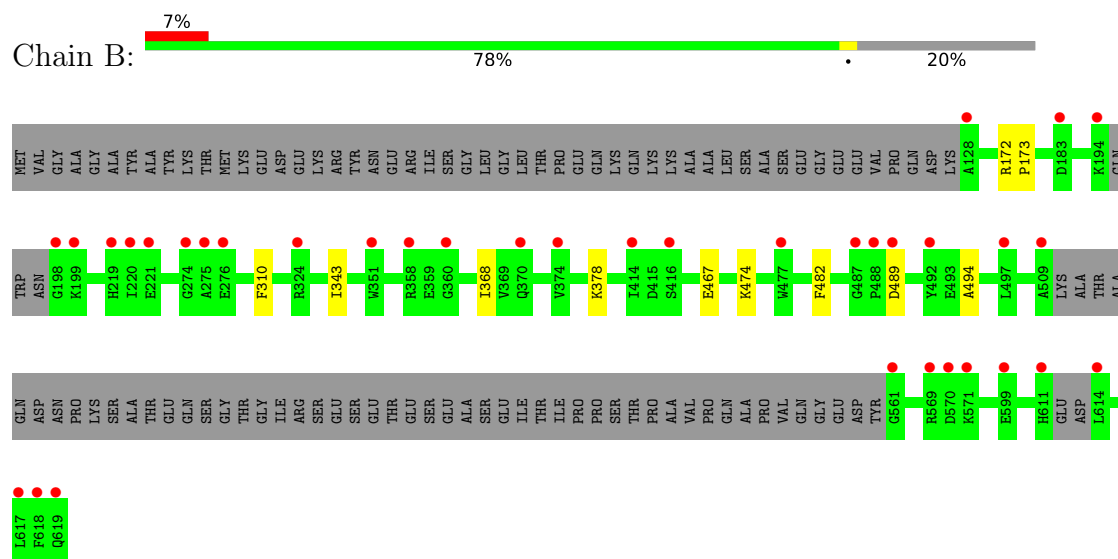
3 Residue-property plots [i](#)

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.

- Molecule 1: Apoptosis-inducing factor 1, mitochondrial



- Molecule 2: Apoptosis-inducing factor 1, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.39Å 115.02Å 124.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.55 – 2.30 71.55 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (71.55-2.30) 99.9 (71.55-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.41 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.189 , 0.220 0.197 , 0.227	Depositor DCC
R_{free} test set	2958 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.822	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13489	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.82% 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, QC6, CSX, SO4, 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	0.14	0/3331	0.32	0/4517
2	B	0.13	0/3334	0.31	0/4519
All	All	0.13	0/6665	0.32	0/9036

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	3281	3216	3214	10	0
2	B	3273	3228	3223	6	0
3	A	13	9	0	0	0
3	B	13	9	0	0	0
4	A	4	6	6	0	0
5	A	53	30	31	0	0
5	B	53	31	31	0	0
6	A	15	0	0	0	0
6	B	10	0	0	0	0
7	A	138	0	0	0	0
7	B	107	0	0	1	0
All	All	6960	6529	6505	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:310:PHE:CZ	1:A:343:ILE:HD13	2.24	0.72
1:A:340:MET:CE	1:A:352:THR:HG21	2.30	0.62
1:A:340:MET:HE1	1:A:352:THR:HG21	1.84	0.58
2:B:172:ARG:N	2:B:173:PRO:CD	2.75	0.50
1:A:187:VAL:HG23	1:A:192:ARG:O	2.12	0.50
1:A:581:ILE:HD11	1:A:610:ILE:HD11	1.93	0.49
1:A:172:ARG:N	1:A:173:PRO:CD	2.76	0.49
1:A:482:PHE:CE2	1:A:494:ALA:HB3	2.49	0.47
2:B:310:PHE:CZ	2:B:343:ILE:HD13	2.50	0.47
1:A:368:ILE:N	1:A:368:ILE:HD12	2.32	0.44
1:A:489:ASP:OD1	1:A:489:ASP:N	2.50	0.43
2:B:467:GLU:OE1	2:B:474:LYS:NZ	2.47	0.43
1:A:482:PHE:CZ	1:A:494:ALA:HB3	2.54	0.42
2:B:482:PHE:CZ	2:B:494:ALA:HB3	2.54	0.42
2:B:368:ILE:N	2:B:368:ILE:HD12	2.35	0.42
2:B:378:LYS:NZ	7:B:811:HOH:O	2.55	0.40

There are no symmetry-related clashes.

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	428/543 (79%)	413 (96%)	15 (4%)	0	100	100
2	B	428/543 (79%)	414 (97%)	14 (3%)	0	100	100
All	All	856/1086 (79%)	827 (97%)	29 (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	328/443 (74%)	328 (100%)	0	100	100
2	B	330/444 (74%)	329 (100%)	1 (0%)	86	93
All	All	658/887 (74%)	657 (100%)	1 (0%)	87	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	489	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	235	GLN
1	A	366	ASN
1	A	432	ASN
1	A	598	HIS
1	A	602	ASN
2	B	350	ASN
2	B	366	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSX	A	256	1	3,6,7	1.05	0	1,6,8	0.51	0
1	CSX	A	441	1	3,6,7	1.01	0	1,6,8	0.13	0
2	CSX	B	441	2	3,6,7	1.00	0	1,6,8	0.46	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
1	CSX	A	256	1	-	0/2/5/7	-
1	CSX	A	441	1	-	0/2/5/7	-
2	CSX	B	441	2	-	0/2/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

10 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
6	SO4	B	703	-	4,4,4	0.26	0	6,6,6	0.11	0
5	FAD	B	702	-	58,58,58	1.43	4 (6%)	85,89,89	0.89	3 (3%)
6	SO4	A	706	-	4,4,4	0.23	0	6,6,6	0.10	0
5	FAD	A	703	-	58,58,58	1.44	4 (6%)	85,89,89	0.89	2 (2%)
4	EDO	A	702	-	3,3,3	0.41	0	2,2,2	0.52	0
6	SO4	A	704	-	4,4,4	0.24	0	6,6,6	0.08	0
6	SO4	A	705	-	4,4,4	0.23	0	6,6,6	0.09	0
3	QC6	A	701	-	14,14,14	2.58	8 (57%)	18,20,20	2.01	3 (16%)
6	SO4	B	704	-	4,4,4	0.24	0	6,6,6	0.06	0
3	QC6	B	701	-	14,14,14	2.69	9 (64%)	18,20,20	1.69	4 (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
5	FAD	B	702	-	-	3/34/50/50	0/6/6/6
5	FAD	A	703	-	-	3/34/50/50	0/6/6/6
4	EDO	A	702	-	-	0/1/1/1	-
3	QC6	A	701	-	-	-	0/2/2/2
3	QC6	B	701	-	-	-	0/2/2/2

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	702	FAD	C9-C9A	6.19	1.49	1.39
5	A	703	FAD	C9-C9A	6.15	1.49	1.39
5	A	703	FAD	C6-C5X	6.06	1.49	1.40
3	A	701	QC6	C05-C04	6.02	1.47	1.41
5	B	702	FAD	C6-C5X	5.89	1.48	1.40
3	B	701	QC6	C05-C04	5.82	1.47	1.41
3	B	701	QC6	C13-C02	3.40	1.45	1.38
3	B	701	QC6	C08-C07	3.34	1.44	1.38
5	B	702	FAD	O5'-C5'	3.26	1.57	1.44
5	A	703	FAD	O5'-C5'	3.26	1.56	1.44
3	A	701	QC6	C13-C02	3.20	1.44	1.38
3	A	701	QC6	C08-C07	2.98	1.44	1.38
3	B	701	QC6	C04-N03	2.79	1.42	1.37
3	B	701	QC6	C01-C02	2.72	1.56	1.50
3	A	701	QC6	F06-C05	2.56	1.40	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	701	QC6	F06-C05	2.54	1.40	1.36
3	A	701	QC6	C04-N03	2.44	1.42	1.37
3	A	701	QC6	C01-C02	2.42	1.55	1.50
3	B	701	QC6	C07-C05	2.31	1.39	1.36
5	A	703	FAD	C1'-C2'	2.20	1.55	1.52
3	A	701	QC6	C02-N03	2.19	1.37	1.33
5	B	702	FAD	C1'-C2'	2.18	1.55	1.52
3	A	701	QC6	C07-C05	2.07	1.38	1.36
3	B	701	QC6	C02-N03	2.07	1.37	1.33
3	B	701	QC6	C09-C10	2.04	1.46	1.42

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	QC6	F06-C05-C04	5.83	119.79	117.37
3	B	701	QC6	F06-C05-C04	3.99	119.02	117.37
3	A	701	QC6	C05-C04-N03	3.71	122.78	119.42
3	B	701	QC6	C07-C05-C04	3.67	125.28	123.17
3	A	701	QC6	C07-C05-C04	3.15	124.98	123.17
3	B	701	QC6	C05-C04-N03	3.04	122.17	119.42
5	A	703	FAD	C4-N3-C2	-2.54	121.13	125.64
5	B	702	FAD	C4-N3-C2	-2.47	121.25	125.64
5	B	702	FAD	C5'-C4'-C3'	-2.10	108.26	112.22
5	B	702	FAD	O3B-C3B-C4B	-2.05	105.19	111.08
3	B	701	QC6	C13-C02-N03	-2.02	120.30	122.60
5	A	703	FAD	C5'-C4'-C3'	-2.00	108.44	112.22

There are no chirality outliers.

All (6) torsion outliers are listed below:

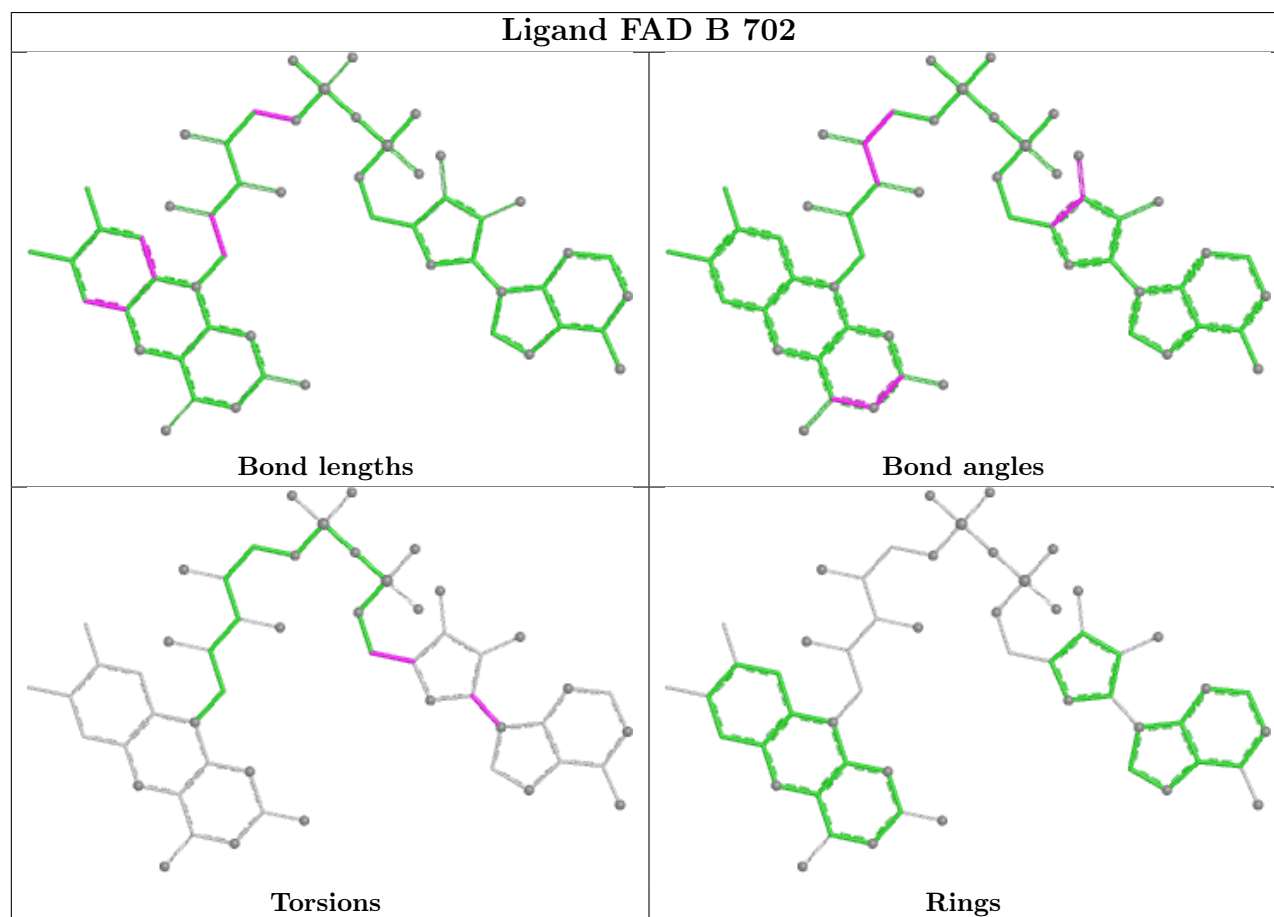
Mol	Chain	Res	Type	Atoms
5	A	703	FAD	C3B-C4B-C5B-O5B
5	A	703	FAD	O4B-C4B-C5B-O5B
5	B	702	FAD	C3B-C4B-C5B-O5B
5	B	702	FAD	O4B-C4B-C5B-O5B
5	B	702	FAD	C2B-C1B-N9A-C8A
5	A	703	FAD	C2B-C1B-N9A-C8A

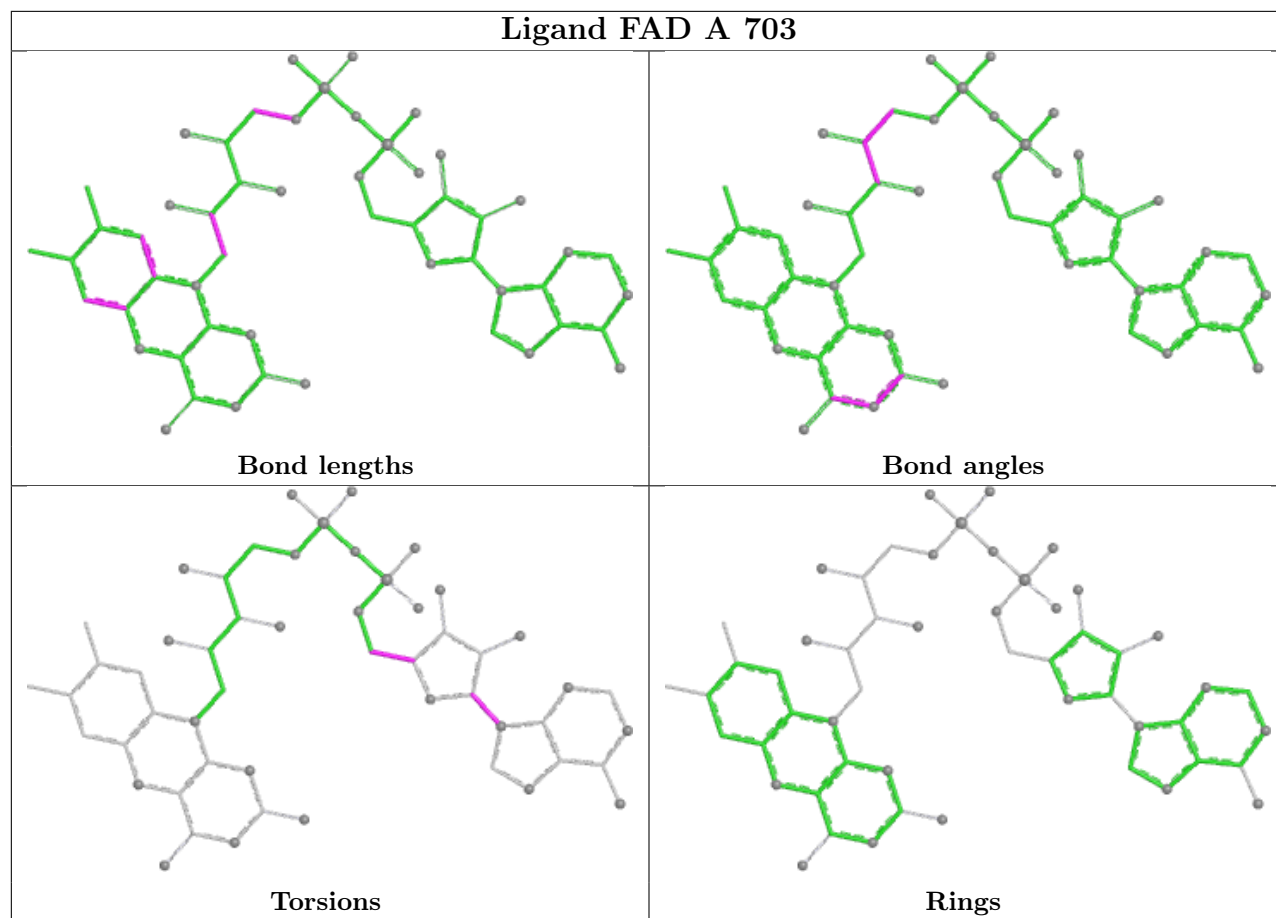
There are no ring outliers.

No monomer is involved in short contacts.

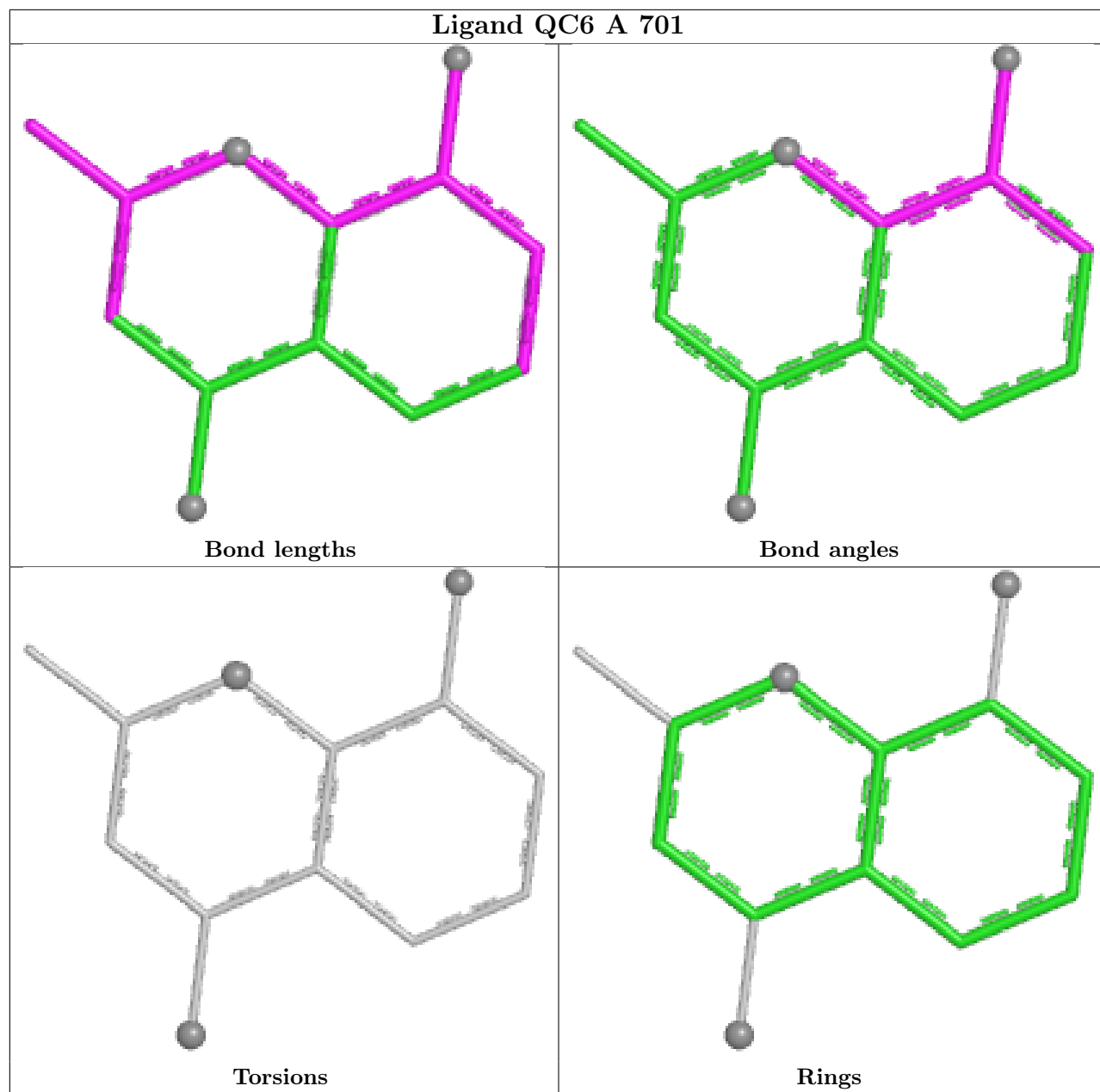
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

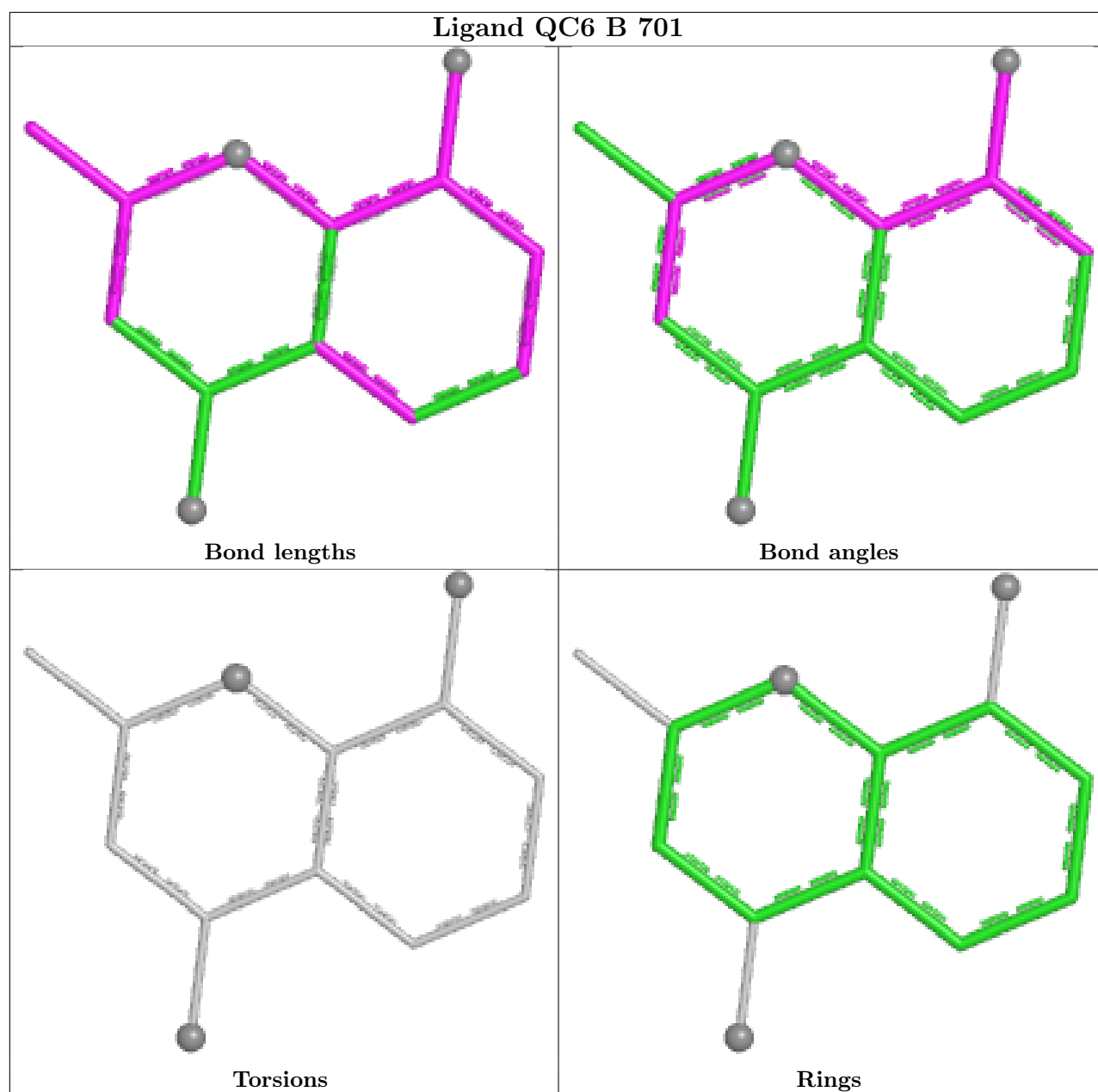
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.





Ligand QC6 A 701





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	435/543 (80%)	0.47	36 (8%)	17 19	26, 54, 90, 115	1 (0%)
2	B	435/543 (80%)	0.55	36 (8%)	17 19	35, 60, 90, 114	0
All	All	870/1086 (80%)	0.51	72 (8%)	17 19	26, 57, 90, 115	1 (0%)

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	560	TYR	7.9
1	A	185	PRO	6.1
1	A	619	GLN	6.0
2	B	198	GLY	5.8
1	A	182	SER	5.1
2	B	128	ALA	5.0
1	A	127	LYS	4.8
2	B	194	LYS	4.8
2	B	599	GLU	4.7
1	A	489	ASP	4.7
1	A	616	VAL	4.7
1	A	196	TRP	4.5
2	B	614	LEU	4.1
2	B	570	ASP	4.1
1	A	617	LEU	4.0
2	B	509	ALA	3.8
1	A	492	TYR	3.7
2	B	488	PRO	3.6
2	B	276	GLU	3.6
2	B	358	ARG	3.5
2	B	561	GLY	3.5
1	A	618	PHE	3.4
2	B	477	TRP	3.4
1	A	310	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	489	ASP	3.4
2	B	324	ARG	3.3
2	B	221	GLU	3.3
1	A	487	GLY	3.2
2	B	569	ARG	3.2
2	B	618	PHE	3.2
1	A	482	PHE	3.1
2	B	492	TYR	3.0
1	A	488	PRO	3.0
2	B	617	LEU	2.9
1	A	215	GLN	2.9
1	A	198	GLY	2.9
2	B	619	GLN	2.9
1	A	199	LYS	2.8
1	A	490	VAL	2.8
1	A	273	ALA	2.7
1	A	570	ASP	2.7
2	B	611	HIS	2.6
2	B	199	LYS	2.6
1	A	599	GLU	2.6
1	A	509	ALA	2.6
1	A	187	VAL	2.6
1	A	194	LYS	2.6
1	A	275	ALA	2.5
1	A	486	LEU	2.5
2	B	220	ILE	2.4
2	B	351	TRP	2.4
2	B	183	ASP	2.4
1	A	571	LYS	2.4
1	A	266	SER	2.3
1	A	384	LYS	2.3
1	A	579	TRP	2.3
1	A	340	MET	2.3
2	B	370	GLN	2.3
2	B	374	VAL	2.3
2	B	416	SER	2.3
2	B	275	ALA	2.2
1	A	611	HIS	2.2
2	B	497	LEU	2.2
2	B	571	LYS	2.2
2	B	360	GLY	2.2
1	A	376	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	602	ASN	2.1
2	B	487	GLY	2.1
2	B	414	ILE	2.1
2	B	274	GLY	2.1
2	B	219	HIS	2.0
1	A	285	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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	CSX	B	441	7/8	0.91	0.15	30,36,43,59	0
1	CSX	A	256	7/8	0.95	0.10	31,39,47,48	0
1	CSX	A	441	7/8	0.97	0.10	32,35,42,60	0

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
6	SO4	A	704	5/5	0.71	0.12	87,96,103,103	0
6	SO4	B	704	5/5	0.82	0.10	91,96,100,105	0
6	SO4	A	706	5/5	0.85	0.12	69,73,91,97	0
3	QC6	A	701	13/13	0.89	0.16	40,46,63,63	22
6	SO4	A	705	5/5	0.89	0.15	51,59,71,123	0
6	SO4	B	703	5/5	0.93	0.14	49,56,66,70	0
4	EDO	A	702	4/4	0.95	0.12	37,44,52,60	0
3	QC6	B	701	13/13	0.95	0.09	41,47,58,58	0
5	FAD	B	702	53/53	0.97	0.07	32,42,52,62	0

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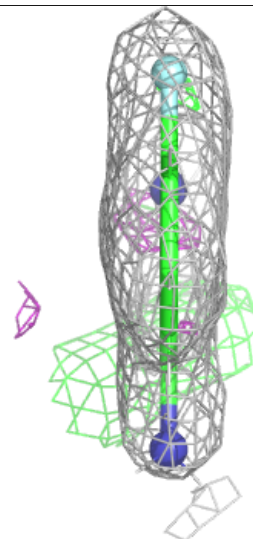
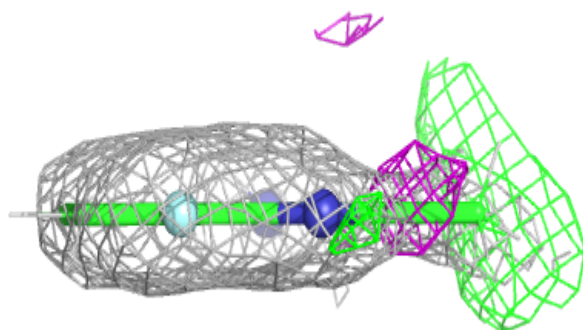
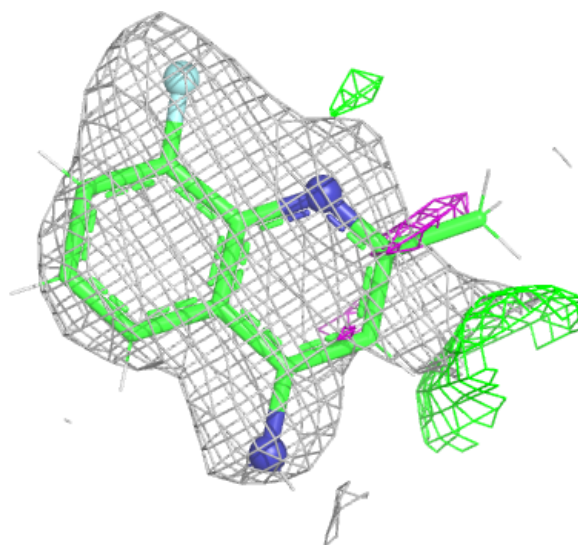
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	FAD	A	703	53/53	0.97	0.07	31,40,51,63	0

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.

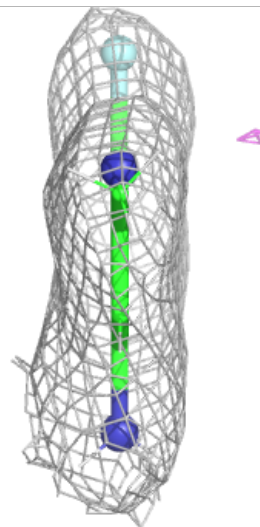
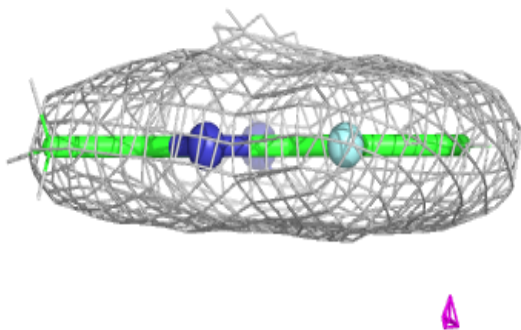
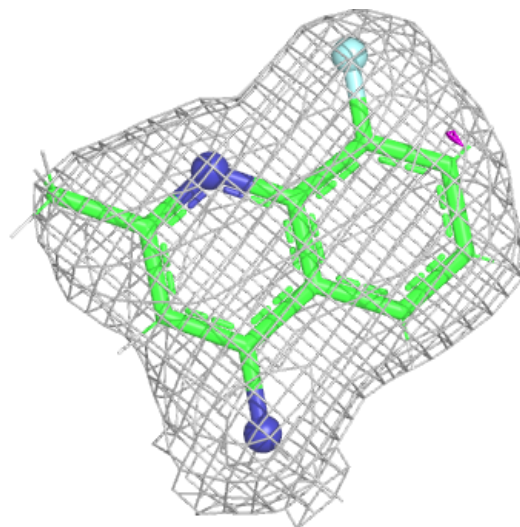
Electron density around QC6 A 701:

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



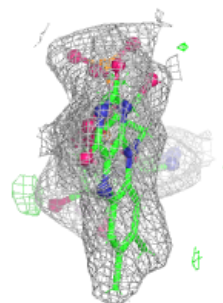
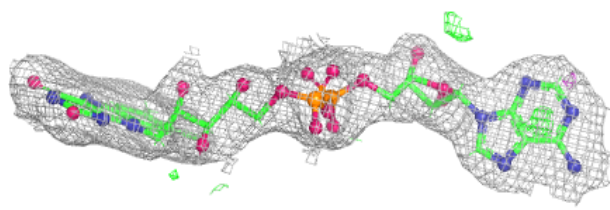
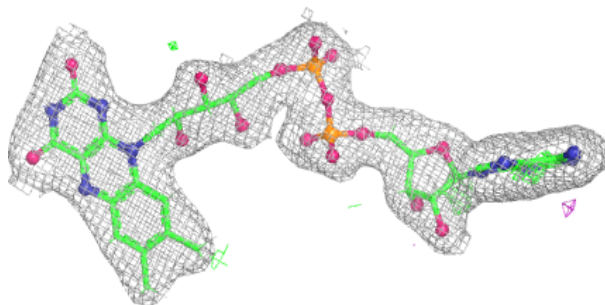
Electron density around QC6 B 701:

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

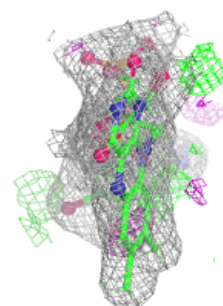
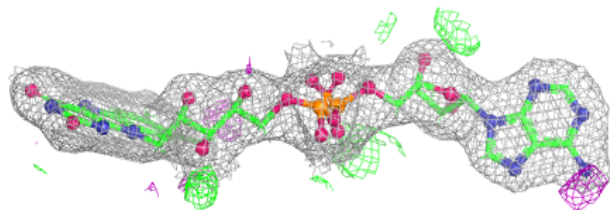
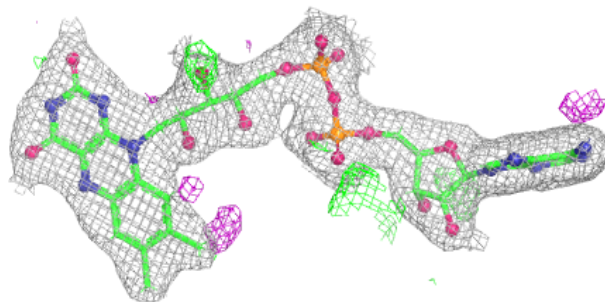


Electron density around FAD B 702:

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

**Electron density around FAD A 703:**

$2mF_o-DF_c$ (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.