



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 05:54 am BST

PDB ID : 1GXF
Title : CRYSTAL STRUCTURE OF TRYPANOSOMA CRUZI TRYPANOTHIONE
REDUCTASE IN COMPLEX WITH THE INHIBITOR QUINACRINE MUS-
TARD
Authors : Bond, C.S.; Peterson, M.R.; Vickers, T.J.; Fairlamb, A.H.; Hunter, W.N.
Deposited on : 2002-04-04
Resolution : 2.70 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 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

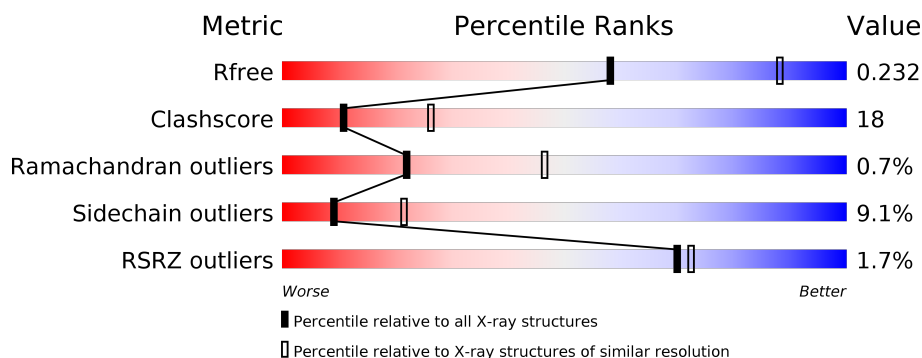
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	492	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> % 67% 27% • • </div> </div>
1	B	492	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red, orange, yellow, green);"></div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 3% 62% 31% 5% • </div> </div>

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
4	QUM	A	1501	-	-	X	X
4	QUM	A	1502	-	-	X	X
4	QUM	B	1501	-	-	X	X
4	QUM	B	1502	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7726 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 TRYPTOPHAN REDUCTASE (OXIDIZED FORM).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	485	Total	C	N	O	S	0	0	1
			3727	2370	635	701	21			
1	B	484	Total	C	N	O	S	0	0	1
			3718	2364	633	700	21			

There are 14 discrepancies between the modelled and reference sequences:

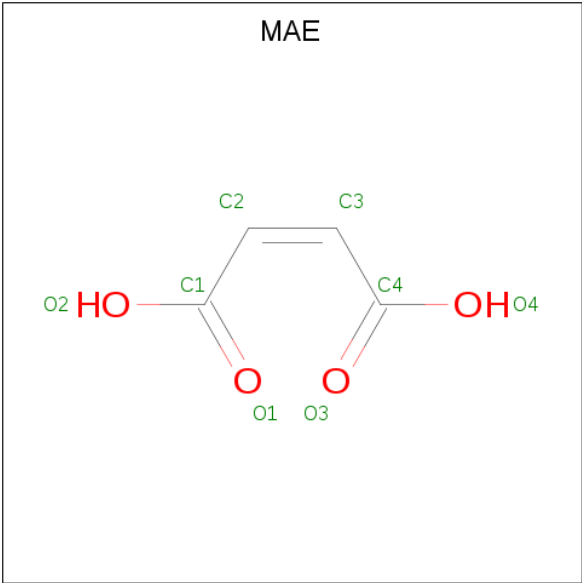
Chain	Residue	Modelled	Actual	Comment	Reference
A	95	ASN	LYS	variant	UNP P28593
A	112	ASP	GLU	variant	UNP P28593
A	156	HIS	ASN	variant	UNP P28593
A	353	THR	ASN	variant	UNP P28593
A	402	LYS	ASN	variant	UNP P28593
A	403	VAL	ILE	variant	UNP P28593
A	441	ILE	VAL	variant	UNP P28593
B	95	ASN	LYS	variant	UNP P28593
B	112	ASP	GLU	variant	UNP P28593
B	156	HIS	ASN	variant	UNP P28593
B	353	THR	ASN	variant	UNP P28593
B	402	LYS	ASN	variant	UNP P28593
B	403	VAL	ILE	variant	UNP P28593
B	441	ILE	VAL	variant	UNP P28593

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



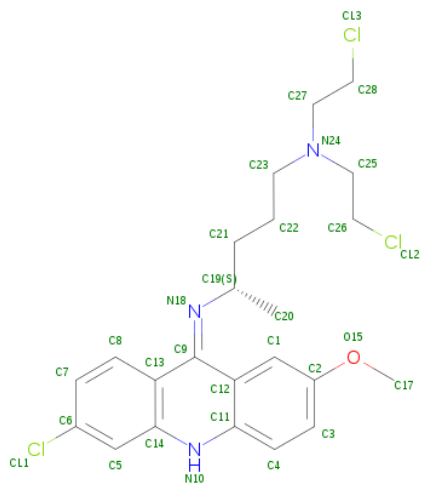
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 53	C 27	N 9	O 15	P 2	0	0
2	B	1	Total 53	C 27	N 9	O 15	P 2	0	0

- Molecule 3 is MALEIC ACID (three-letter code: MAE) (formula: C₄H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 4 is QUINACRINE MUSTARD (three-letter code: QUM) (formula: C₂₃H₂₈Cl₃N₃O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 28	C 23	Cl 1	N 3	O 1	0	0
4	A	1	Total 29	C 23	Cl 2	N 3	O 1	0	0
4	B	1	Total 28	C 23	Cl 1	N 3	O 1	0	0
4	B	1	Total 29	C 23	Cl 2	N 3	O 1	0	0

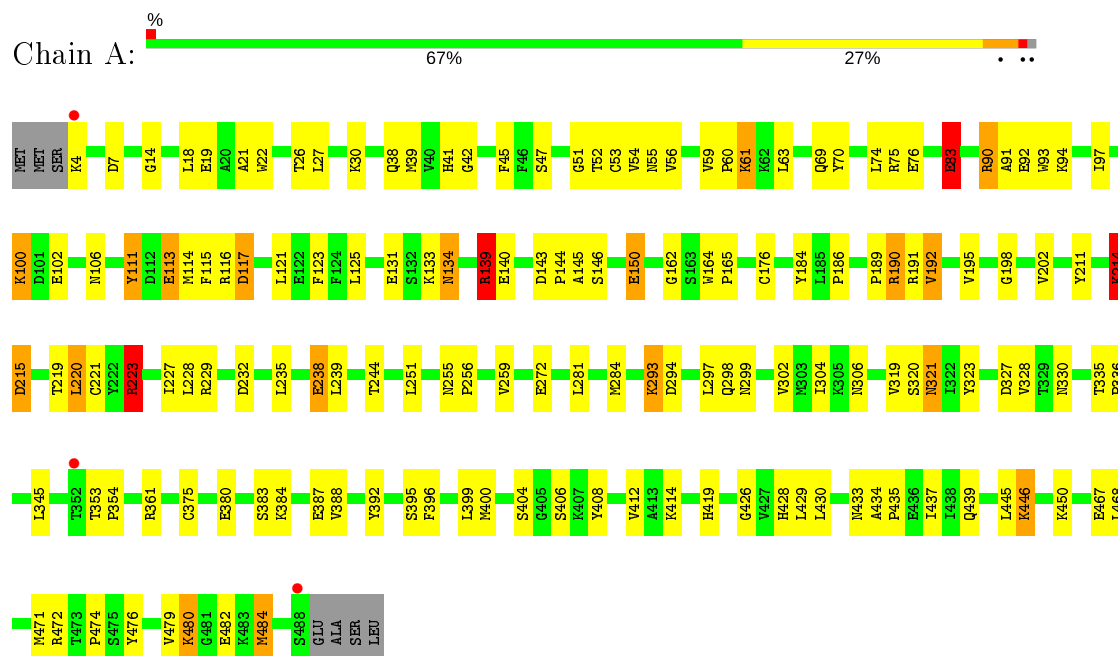
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	28	Total O 28 28	0	0
5	B	25	Total O 25 25	0	0

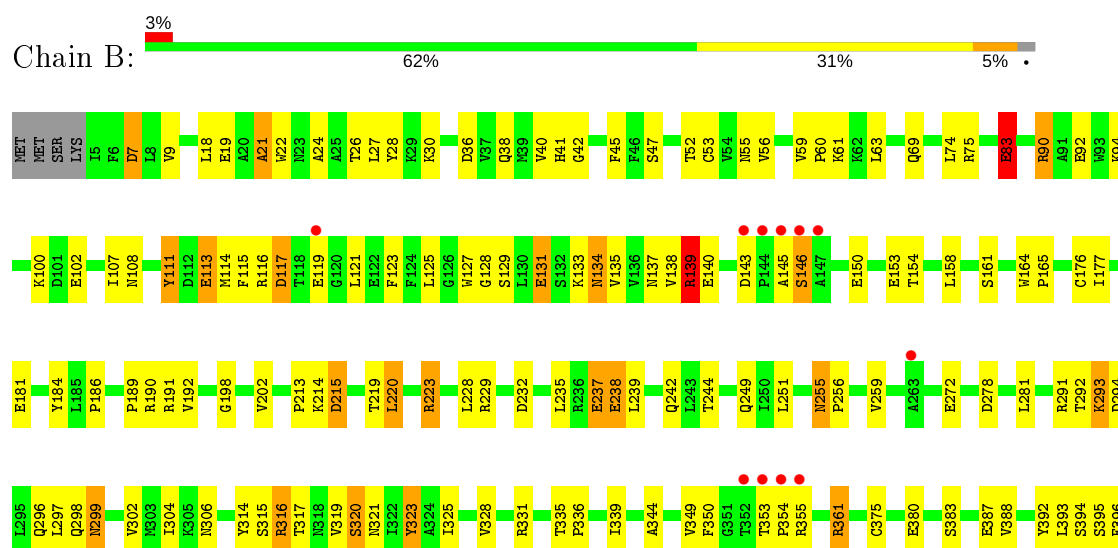
3 Residue-property plots [i](#)

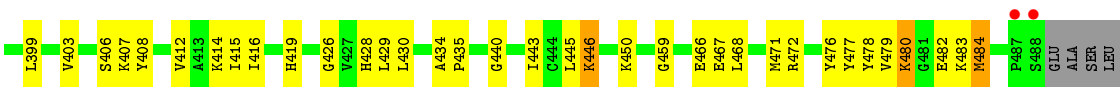
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: TRYPTANOTHIONE REDUCTASE (OXIDIZED FORM)



• Molecule 1: TRYPTANOTHIONE REDUCTASE (OXIDIZED FORM)





4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	93.10 Å 93.10 Å 156.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.00 – 2.70 29.96 – 2.70	Depositor EDS
% Data completeness (in resolution range)	79.0 (21.00-2.70) 79.5 (29.96-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.50 (at 2.68 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.190 , 0.250 0.188 , 0.232	Depositor DCC
R_{free} test set	1466 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.056 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7726	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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: QUM, MAE, 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	0.41	0/3804	1.15	23/5154 (0.4%)
1	B	0.41	0/3795	1.20	23/5143 (0.4%)
All	All	0.41	0/7599	1.18	46/10297 (0.4%)

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	472	ARG	CD-NE-CZ	26.14	160.19	123.60
1	A	472	ARG	CD-NE-CZ	23.57	156.60	123.60
1	B	361	ARG	NE-CZ-NH2	11.73	126.17	120.30
1	A	139	ARG	CD-NE-CZ	11.66	139.92	123.60
1	B	139	ARG	CD-NE-CZ	10.80	138.72	123.60

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	3727	0	3739	130	1
1	B	3718	0	3726	142	1
2	A	53	0	31	1	0
2	B	53	0	31	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	8	0	2	3	0
4	A	57	0	48	33	0
4	B	57	0	48	14	0
5	A	28	0	0	4	0
5	B	25	0	0	5	0
All	All	7726	0	7625	278	1

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.

The worst 5 of 278 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)
4:A:1502:QUM:H1	4:A:1502:QUM:C20	1.28	1.61
4:A:1502:QUM:C1	4:A:1502:QUM:C20	2.22	1.18
1:B:232:ASP:HB3	1:B:235:LEU:HD12	1.21	1.12
1:A:232:ASP:HB3	1:A:235:LEU:HD12	1.26	1.10
4:A:1502:QUM:H1	4:A:1502:QUM:H203	1.15	1.08

All (1) 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)
1:A:299:ASN:ND2	1:B:407:LYS:NZ[3_554]	2.18	0.02

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	483/492 (98%)	450 (93%)	30 (6%)	3 (1%)	25	50
1	B	482/492 (98%)	442 (92%)	36 (8%)	4 (1%)	19	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	965/984 (98%)	892 (92%)	66 (7%)	7 (1%)	22	46

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	214	LYS
1	B	299	ASN
1	A	41	HIS
1	B	320	SER
1	B	21	ALA

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	405/412 (98%)	369 (91%)	36 (9%)	9	22
1	B	404/412 (98%)	366 (91%)	38 (9%)	8	20
All	All	809/824 (98%)	735 (91%)	74 (9%)	9	21

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	450	LYS
1	B	90	ARG
1	B	395	SER
1	A	480	LYS
1	B	47	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	69	GLN
1	B	106	ASN
1	B	255	ASN

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Mol	Chain	Res	Type
1	B	55	ASN
1	B	299	ASN

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 ⓘ

7 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
4	QUM	B	1501	1	26,30,32	0.89	1 (3%)	34,41,43	1.94	4 (11%)
4	QUM	A	1501	1	26,30,32	0.89	1 (3%)	34,41,43	1.83	5 (14%)
3	MAE	A	1500	-	1,7,7	0.51	0	2,8,8	1.41	0
4	QUM	A	1502	1	27,31,32	1.06	2 (7%)	34,42,43	2.35	6 (17%)
4	QUM	B	1502	1	27,31,32	1.08	2 (7%)	34,42,43	1.86	5 (14%)
2	FAD	A	1492	-	51,58,58	1.52	7 (13%)	60,89,89	1.85	7 (11%)
2	FAD	B	1492	-	51,58,58	1.52	8 (15%)	60,89,89	1.92	10 (16%)

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	QUM	B	1501	1	-	6/14/16/18	0/3/3/3
4	QUM	A	1501	1	-	6/14/16/18	0/3/3/3
3	MAE	A	1500	-	-	0/0/5/5	-
4	QUM	A	1502	1	-	12/15/17/18	0/3/3/3
4	QUM	B	1502	1	-	12/15/17/18	0/3/3/3
2	FAD	A	1492	-	-	4/30/50/50	0/6/6/6
2	FAD	B	1492	-	-	4/30/50/50	0/6/6/6

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1492	FAD	C4-C4X	5.50	1.50	1.41
2	A	1492	FAD	C4-C4X	5.44	1.50	1.41
2	B	1492	FAD	C1'-N10	4.28	1.52	1.48
2	A	1492	FAD	C1'-N10	3.91	1.52	1.48
2	A	1492	FAD	C2B-C1B	-3.91	1.47	1.53

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1502	QUM	C13-C14-N10	-9.20	118.61	123.60
2	A	1492	FAD	C4-N3-C2	8.58	122.39	115.14
2	B	1492	FAD	C4-N3-C2	8.55	122.36	115.14
4	B	1502	QUM	C13-C14-N10	-7.37	119.60	123.60
4	A	1502	QUM	C13-C9-C12	-6.92	116.83	120.16

There are no chirality outliers.

5 of 44 torsion outliers are listed below:

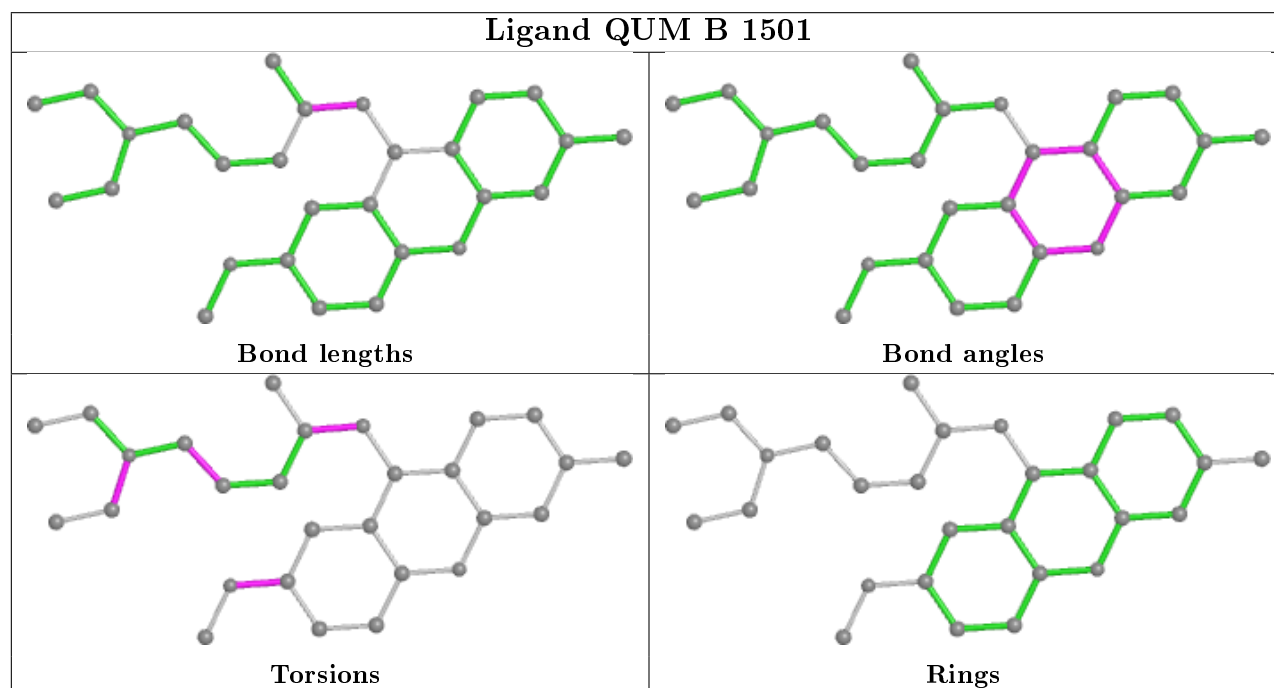
Mol	Chain	Res	Type	Atoms
4	B	1501	QUM	C20-C19-N18-C9
4	A	1501	QUM	C20-C19-N18-C9
4	A	1502	QUM	C20-C19-N18-C9
4	A	1502	QUM	N24-C27-C28-CL3
4	B	1502	QUM	C20-C19-N18-C9

There are no ring outliers.

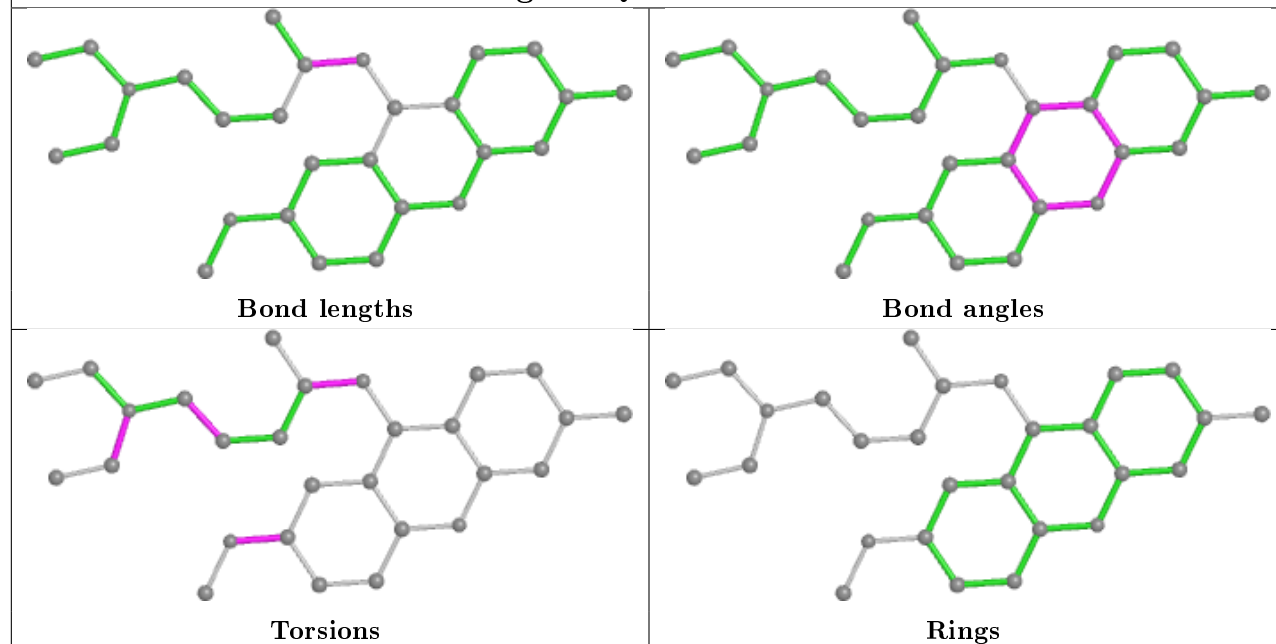
7 monomers are involved in 54 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1501	QUM	12	0
4	A	1501	QUM	18	0
3	A	1500	MAE	3	0
4	A	1502	QUM	18	0
4	B	1502	QUM	5	0
2	A	1492	FAD	1	0
2	B	1492	FAD	3	0

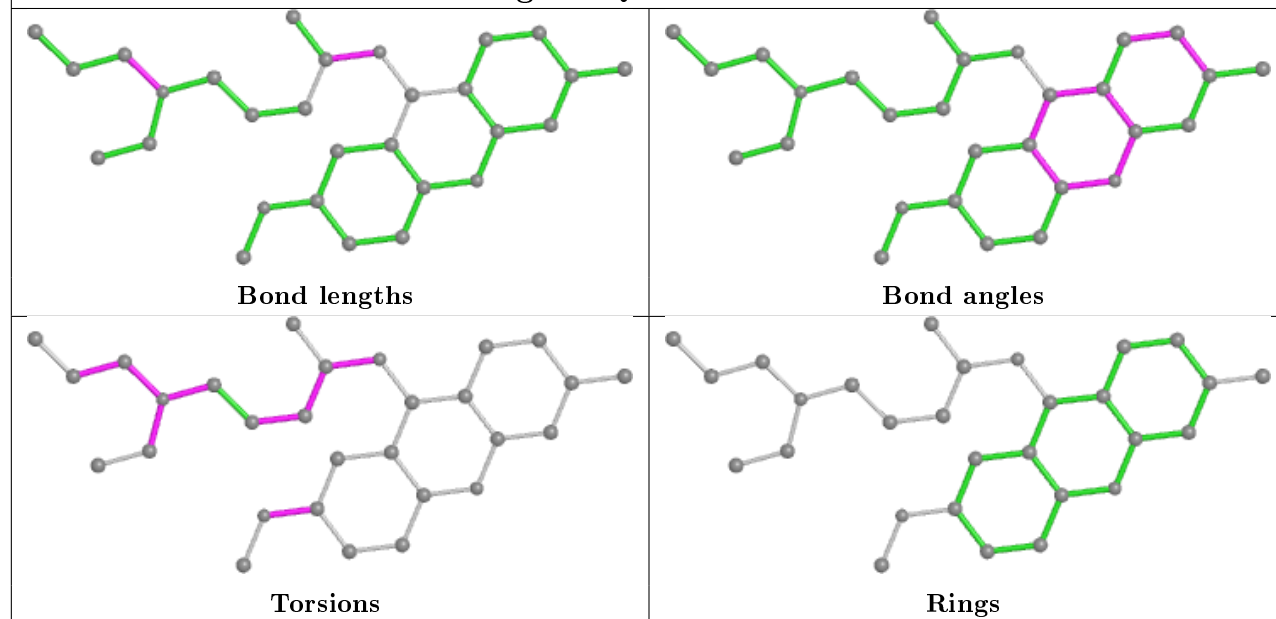
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.



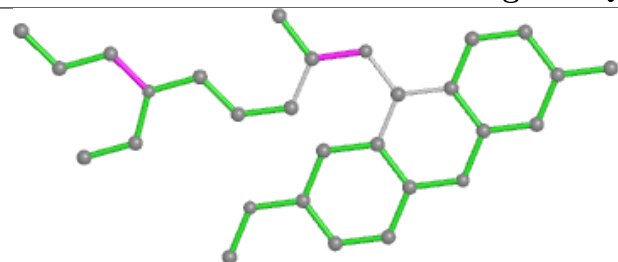
Ligand QUM A 1501



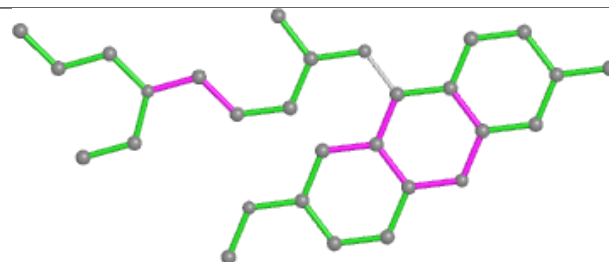
Ligand QUM A 1502



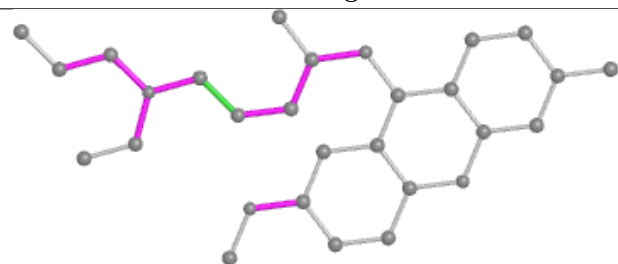
Ligand QUM B 1502



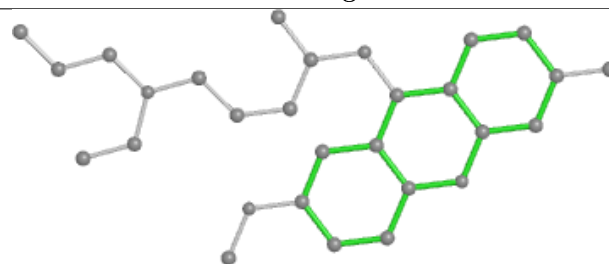
Bond lengths



Bond angles

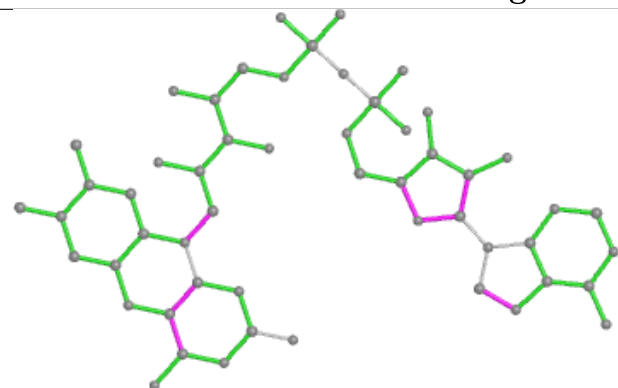


Torsions

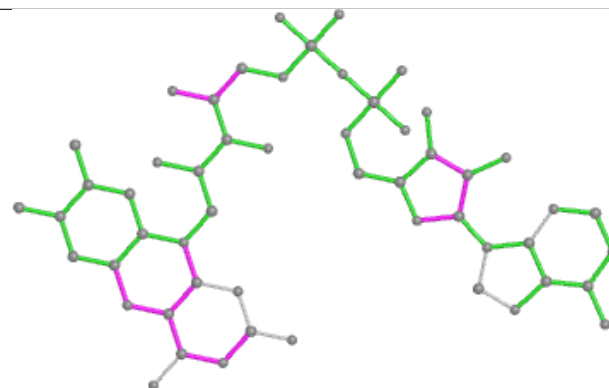


Rings

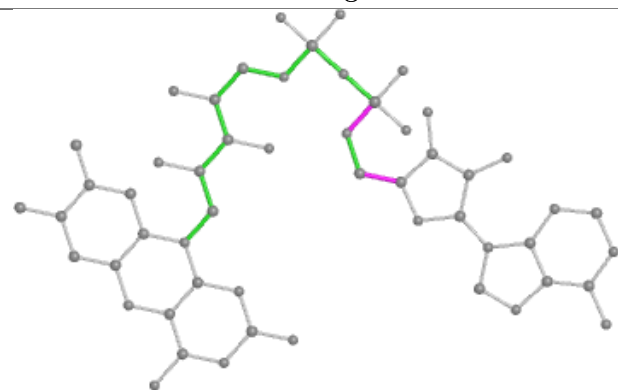
Ligand FAD A 1492



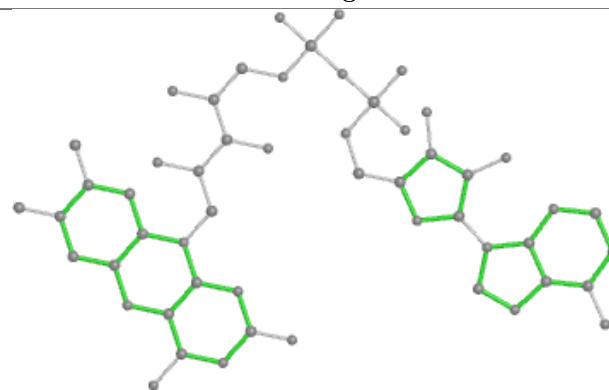
Bond lengths



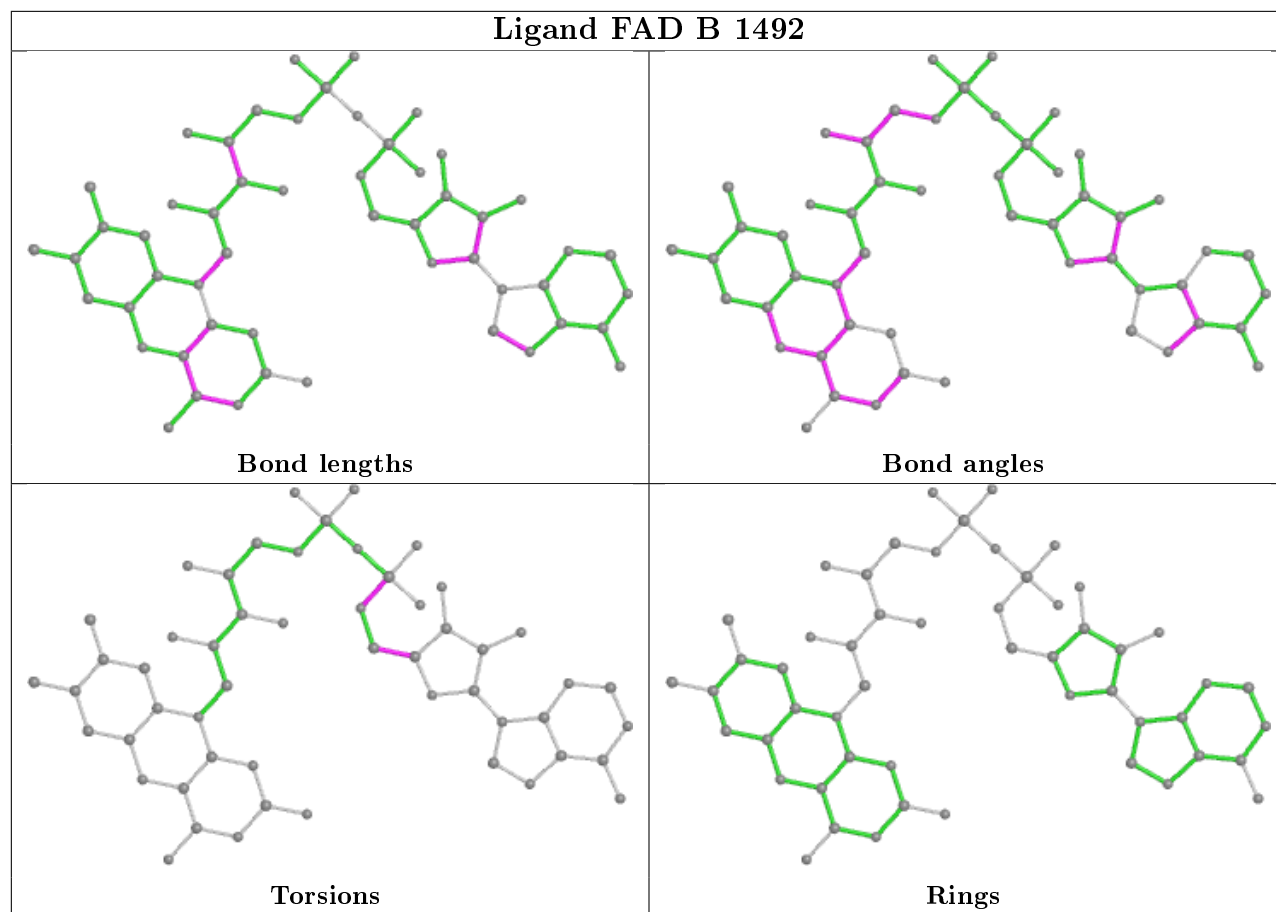
Bond angles



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	485/492 (98%)	-0.39	3 (0%) 89 91	19, 42, 73, 90	0
1	B	484/492 (98%)	-0.40	13 (2%) 54 55	19, 42, 73, 90	0
All	All	969/984 (98%)	-0.40	16 (1%) 70 72	19, 42, 73, 90	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	353	THR	4.0
1	B	263	ALA	3.7
1	B	354	PRO	3.3
1	B	488	SER	3.1
1	B	352	THR	3.1

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](#)

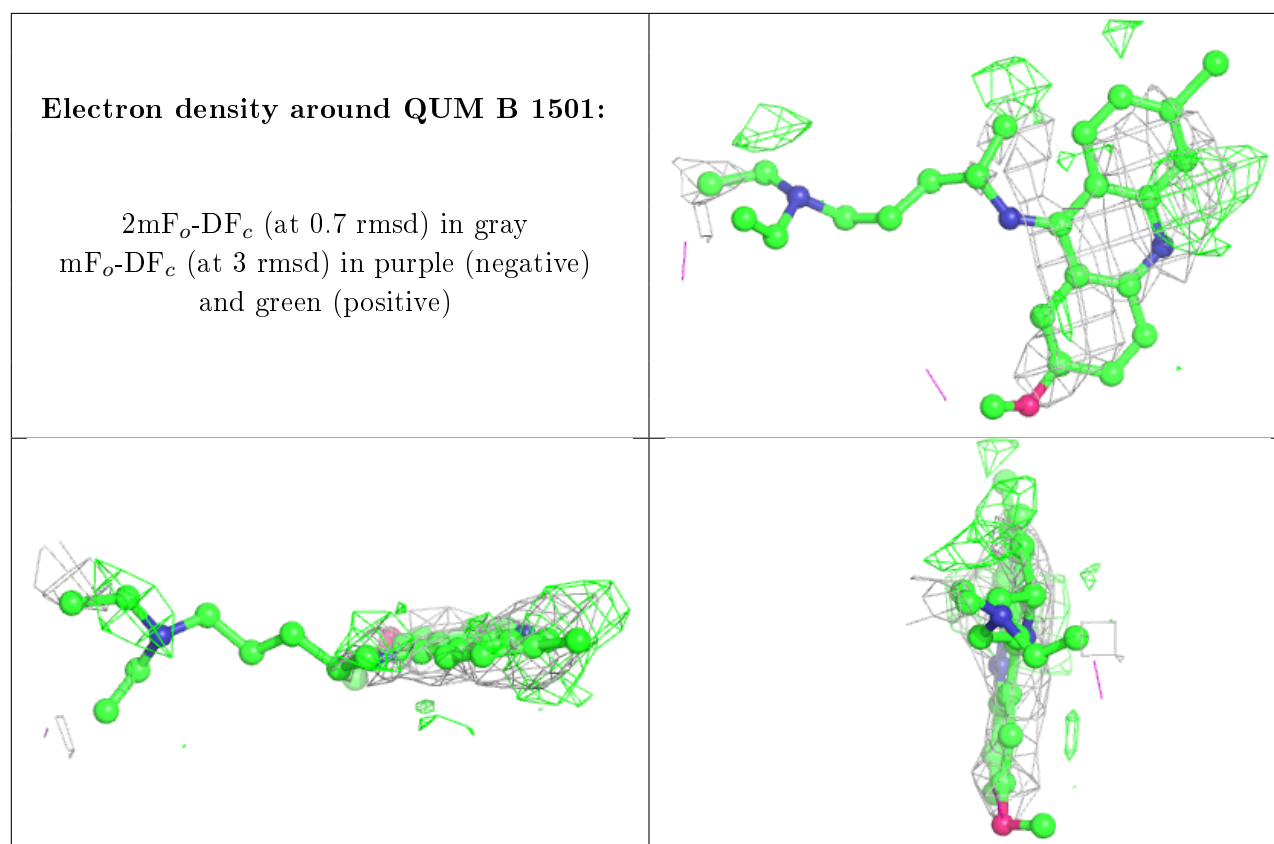
There are no carbohydrates in this entry.

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.

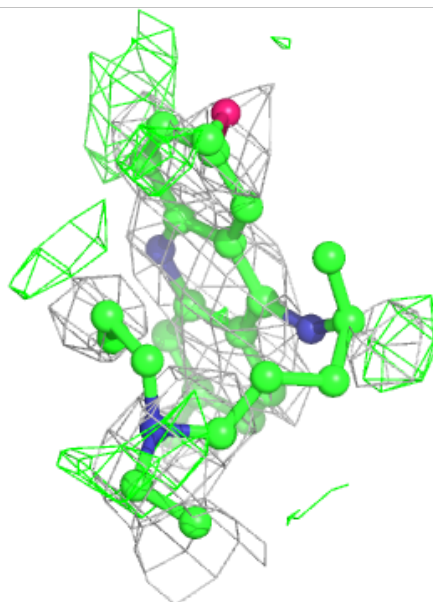
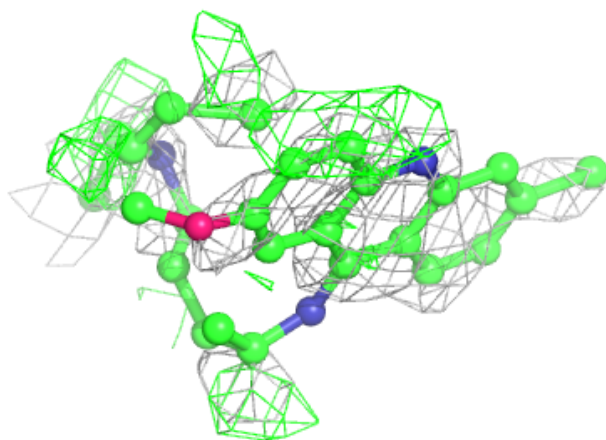
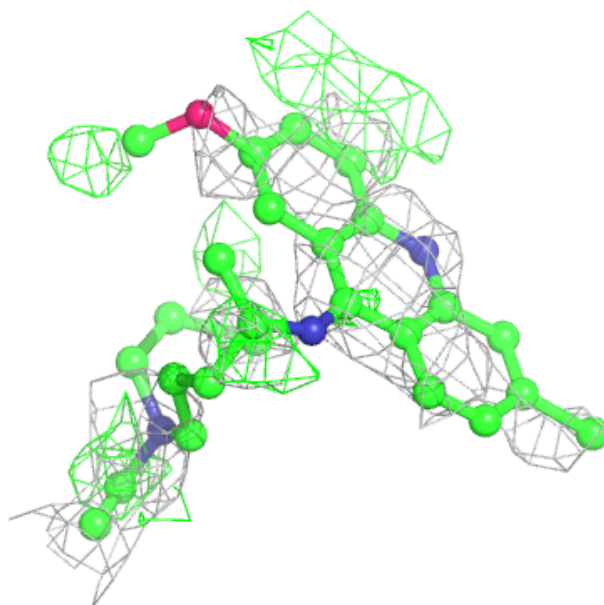
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	QUM	B	1501	28/30	0.58	0.53	53,55,68,71	28
4	QUM	A	1502	29/30	0.72	0.41	47,55,57,58	29
4	QUM	B	1502	29/30	0.74	0.40	47,55,57,58	29
4	QUM	A	1501	28/30	0.75	0.41	53,56,68,71	28
3	MAE	A	1500	8/8	0.94	0.20	29,31,33,35	0
2	FAD	A	1492	53/53	0.97	0.14	16,33,49,50	0
2	FAD	B	1492	53/53	0.97	0.12	17,33,49,50	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.



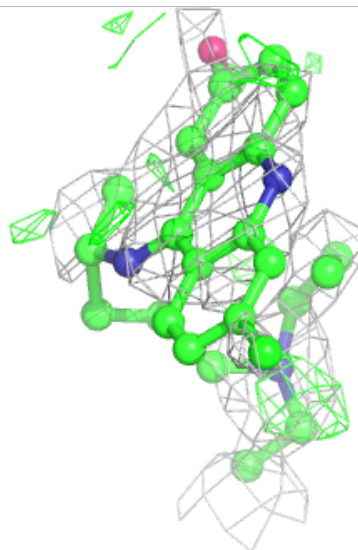
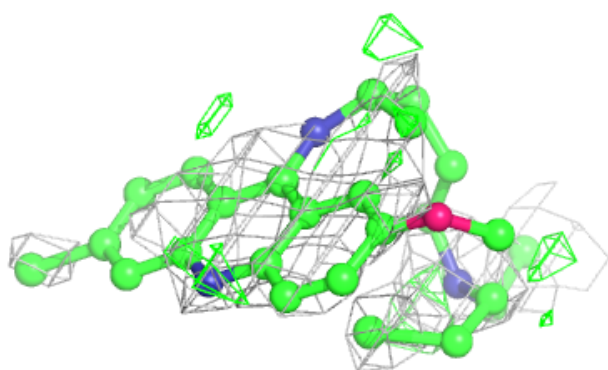
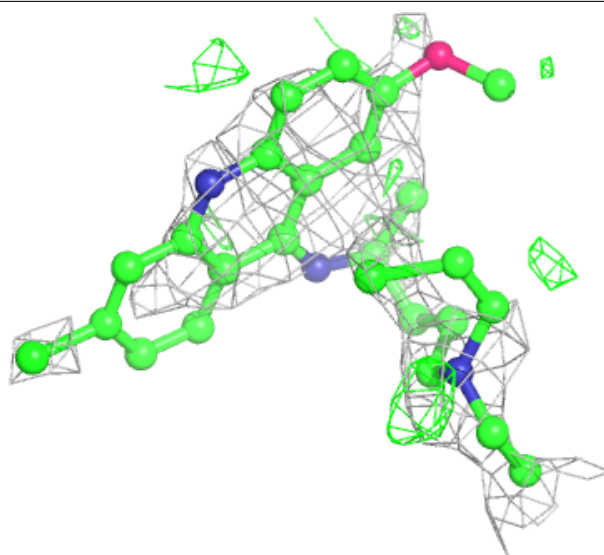
Electron density around QUM A 1502:

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



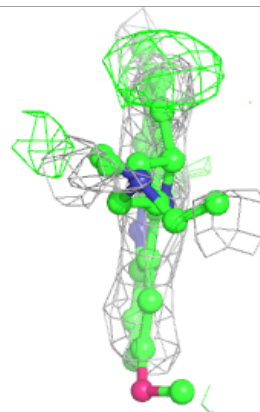
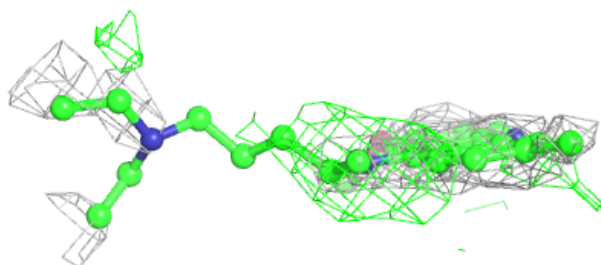
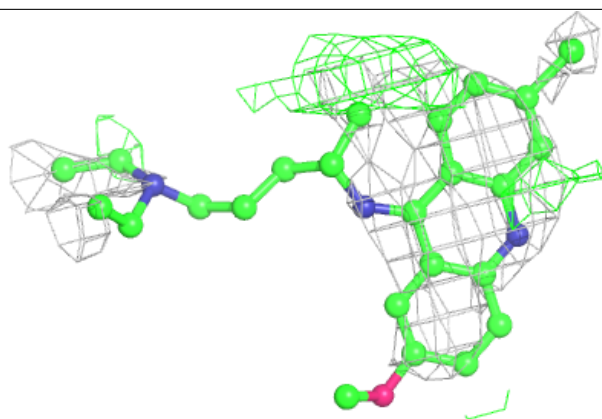
Electron density around QUM B 1502:

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

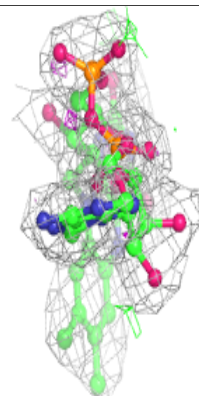
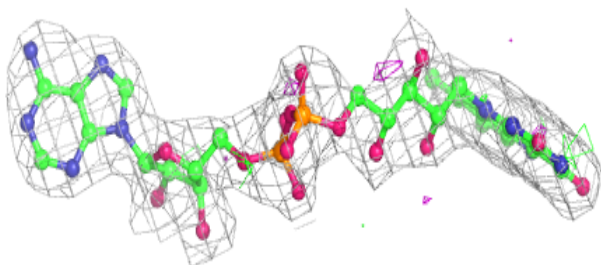
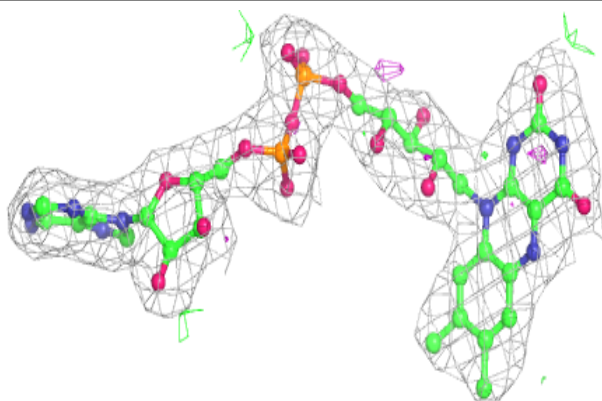


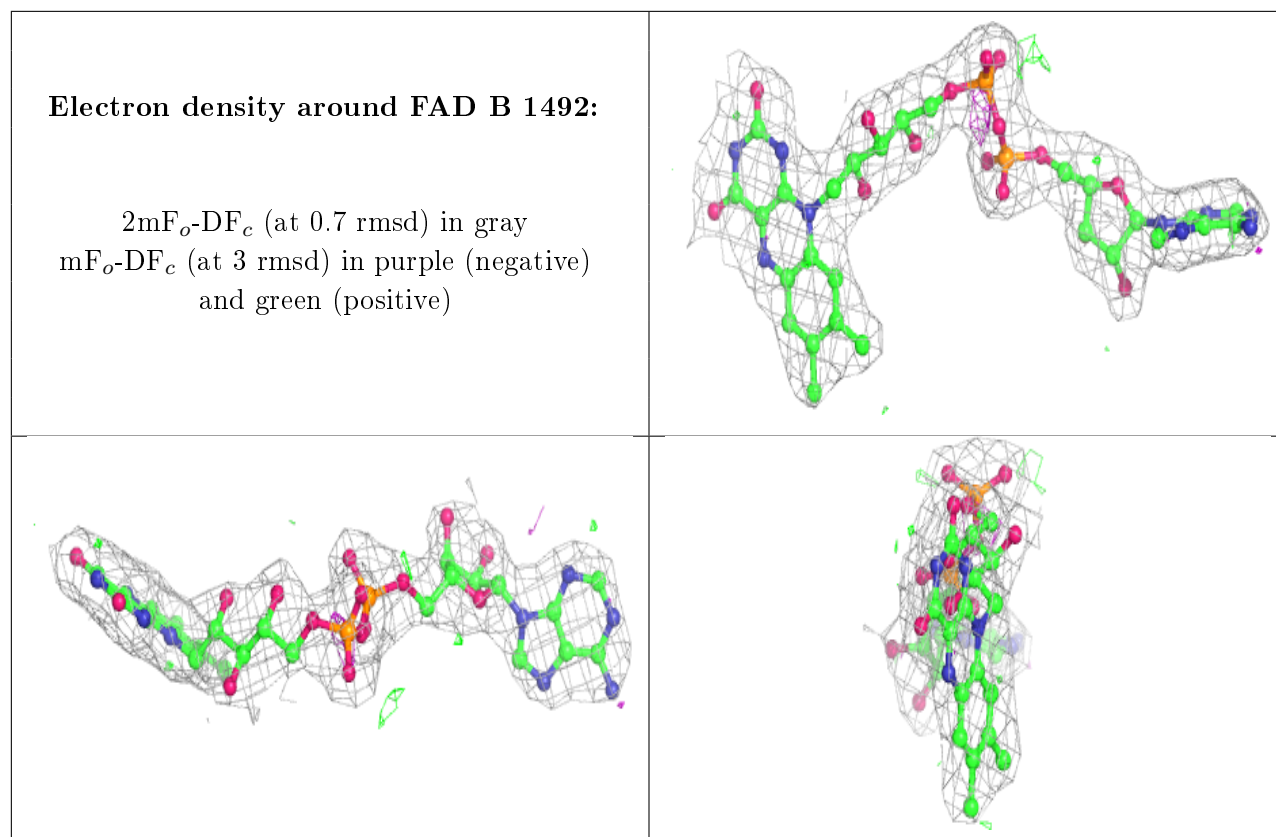
Electron density around QUM A 1501:

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

**Electron density around FAD A 1492:**

$2mF_o-DF_c$ (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.