



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 08:21 AM UTC

PDB ID : 6MYQ / pdb_00006myq
Title : Avian mitochondrial complex II with ferulenol bound
Authors : Berry, E.A.; Huang, L.-S.
Deposited on : 2018-11-02
Resolution : 1.97 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

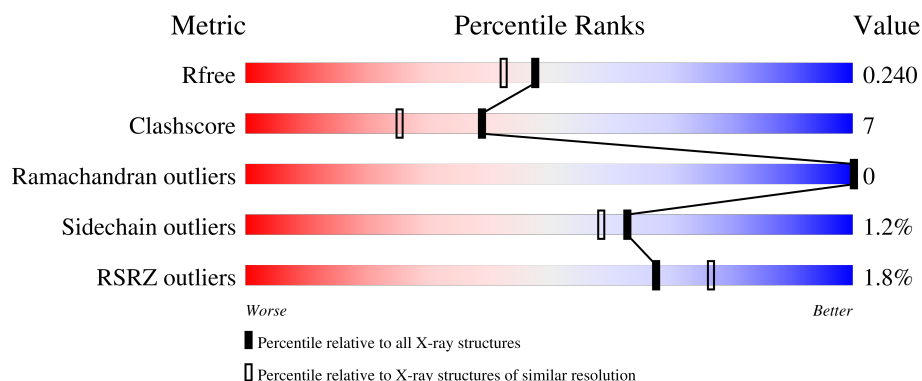
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	621	2% 83% 15% .
2	B	252	2% 82% 13% 5%
3	C	140	3% 86% 13% .
4	D	103	2% 83% 17% .

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
6	Y3P	A	1002	-	X	X	-
8	UNL	D	203	-	-	X	-

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 9426 atoms, of which 2 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 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	611	Total	C	N	O	S	0	1	0
			4723	2956	843	895	29			

- Molecule 2 is a protein called Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	239	Total	C	N	O	S	0	0	0
			1921	1215	325	359	22			

- Molecule 3 is a protein called Succinate dehydrogenase cytochrome b, large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	139	Total	C	N	O	S	0	0	0
			1076	707	178	186	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	139	ALA	SER	conflict	UNP D0VWW3
C	140	MET	GLU	conflict	UNP D0VWW3

- Molecule 4 is a protein called Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial.

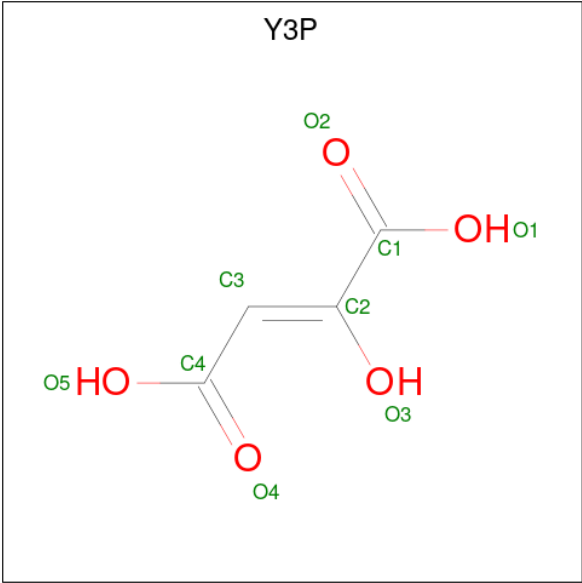
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	102	Total	C	N	O	S	0	0	0
			771	508	122	138	3			

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



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

- Molecule 6 is ({Z})-2-oxidanylbut-2-enedioic acid (CCD ID: Y3P) (formula: C₄H₄O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			11	4	2	5		

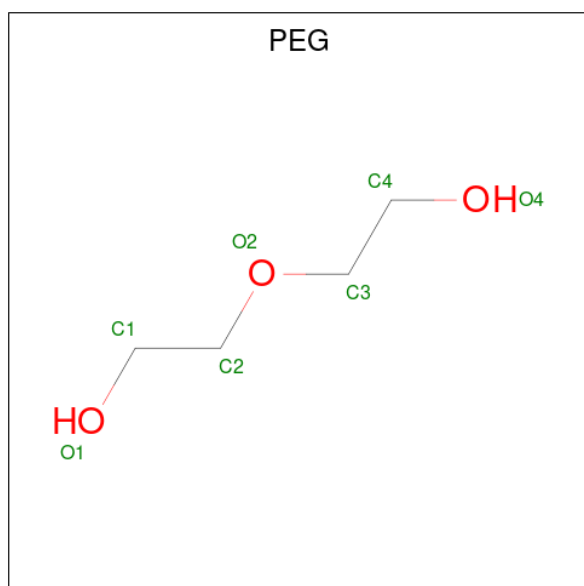
- Molecule 7 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total K 1 1	0	0
7	B	1	Total K 1 1	0	0

- Molecule 8 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

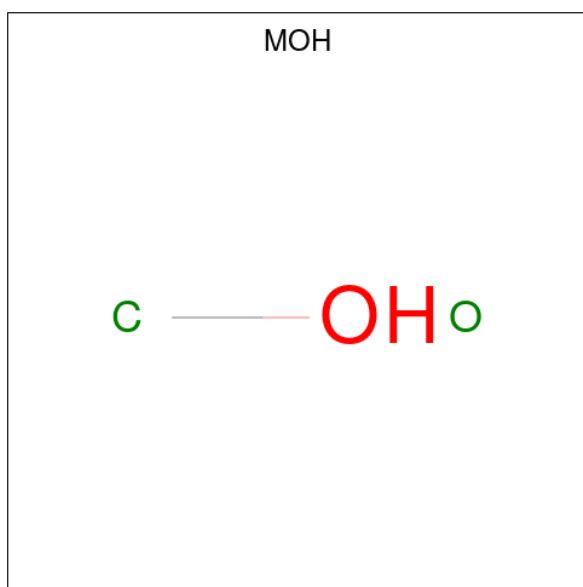
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	21	Total C Mn N O S 58 14 1 17 24 2	0	0
8	B	15	Total C N O S 42 9 12 20 1	0	1
8	C	19	Total C N O S 78 39 5 32 2	0	0
8	D	10	Total C O P 59 29 29 1	0	0

- Molecule 9 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



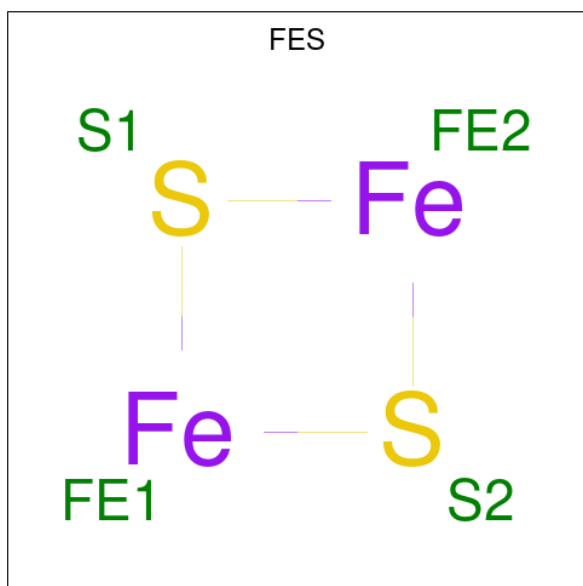
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C O 5 3 2	0	0

- Molecule 10 is METHANOL (CCD ID: MOH) (formula: CH₄O).



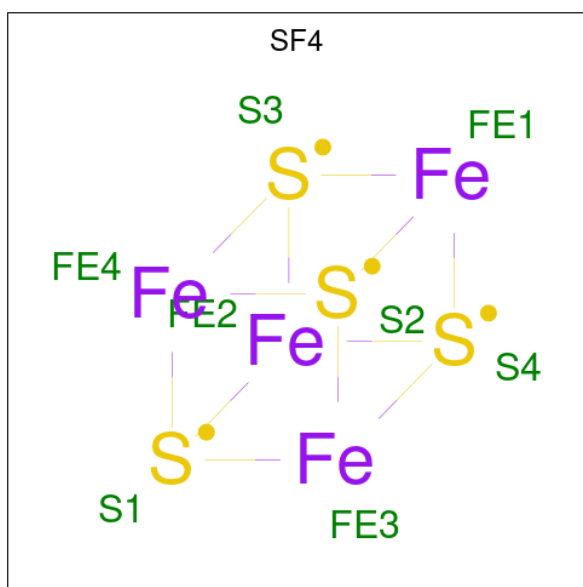
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			2	1	1		

- Molecule 11 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



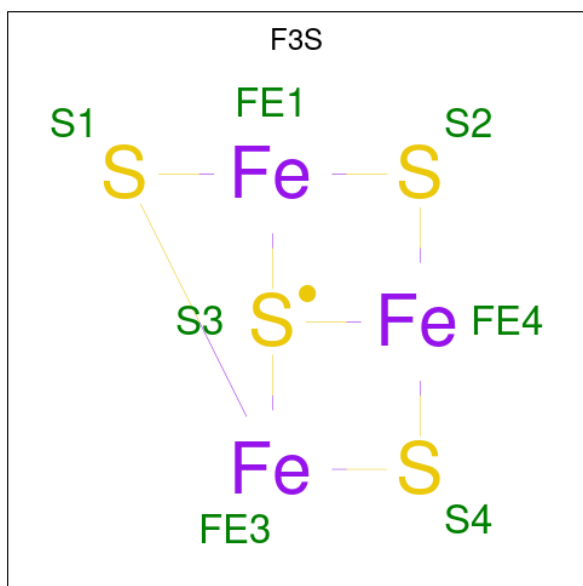
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 12 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



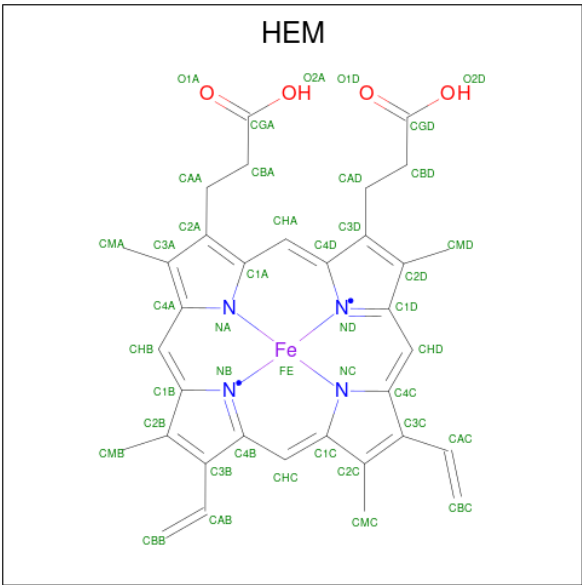
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	B	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 13 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe_3S_4).



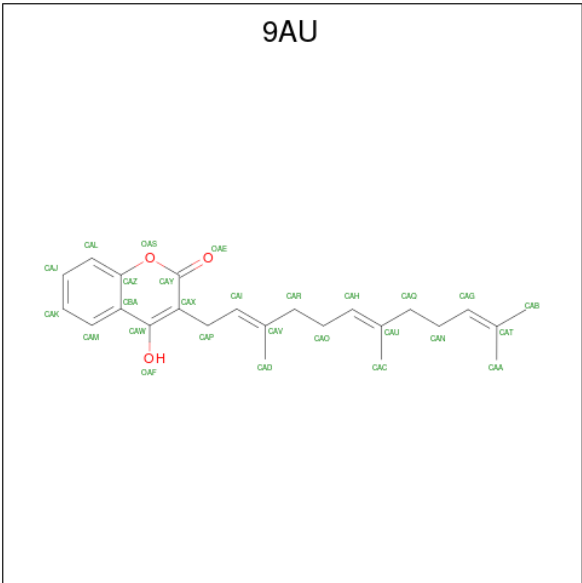
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 14 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $\text{C}_{34}\text{H}_{32}\text{FeN}_4\text{O}_4$).



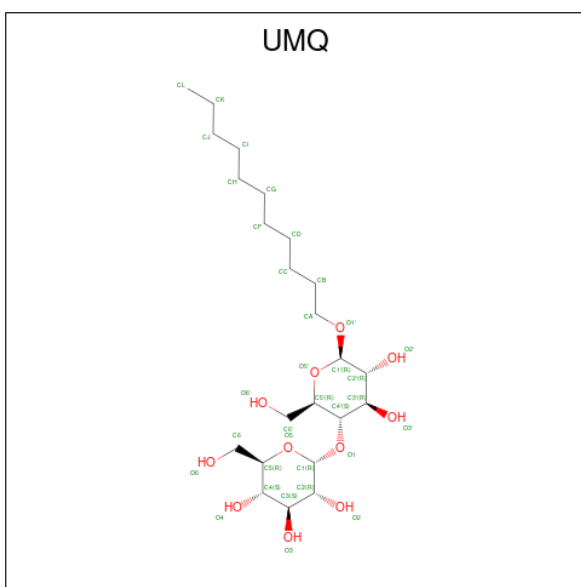
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	C	1	Total	C	Fe	N	O	0	0
			41	32	1	4	4		

- Molecule 15 is 4-oxidanyl-3-[(2 {E},6 {E})-3,7,11-trimethyldodeca-2,6,10-trienyl]chromen-2-one (CCD ID: 9AU) (formula: C₂₄H₃₀O₃) (labeled as "Ligand of Interest" by depositor).



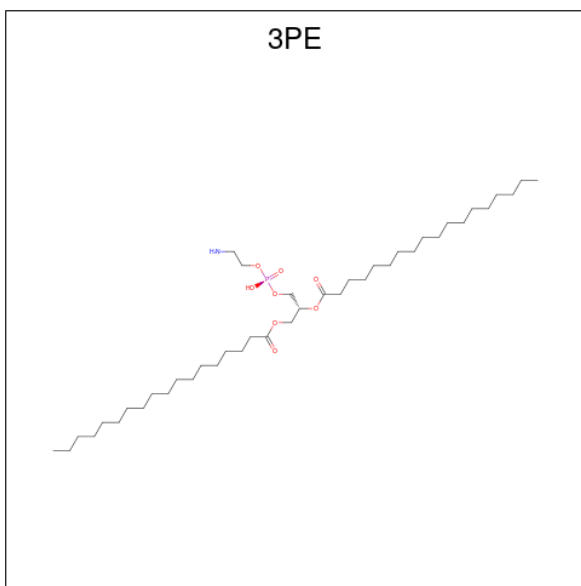
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
15	C	1	Total	C	O	0	0
			19	16	3		

- Molecule 16 is UNDECYL-MALTOSIDE (CCD ID: UMQ) (formula: C₂₃H₄₄O₁₁).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
16	C	1	Total	C	O	0	0
			34	23	11		

- Molecule 17 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
17	D	1	Total	C	N	O	P	0	0
			42	32	1	8	1		

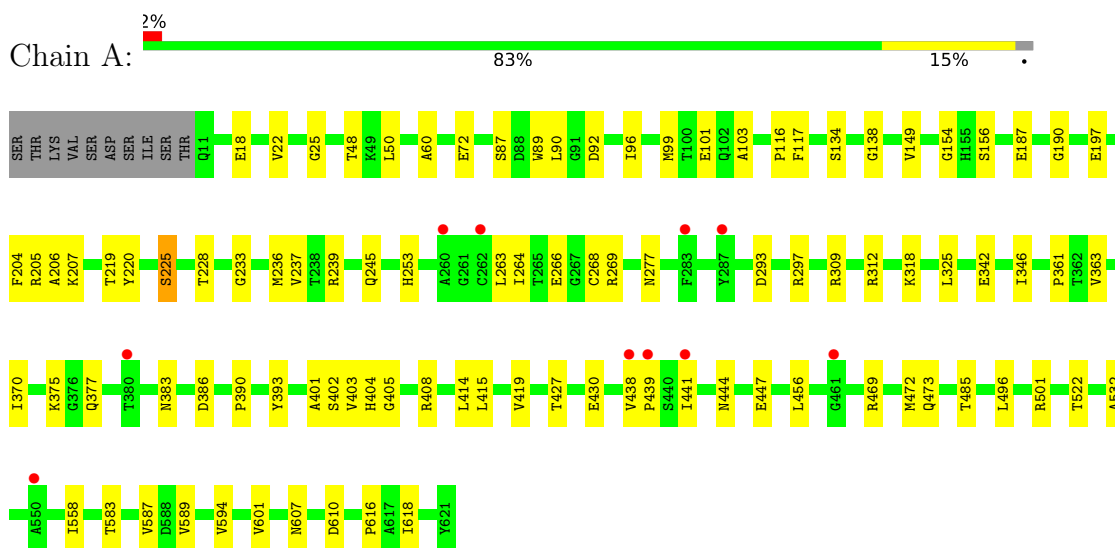
- Molecule 18 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
18	A	1	Total O 2 2	0	1
18	A	234	Total O 237 237	0	3
18	B	145	Total O 146 146	0	1
18	C	1	Total O 2 2	0	1
18	C	1	Total O 1 1	0	0
18	C	51	Total O 51 51	0	0
18	D	31	Total O 31 31	0	0

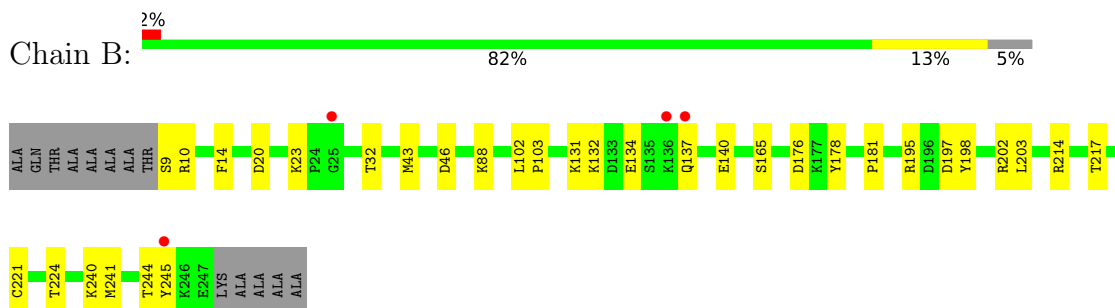
3 Residue-property plots [i](#)

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.

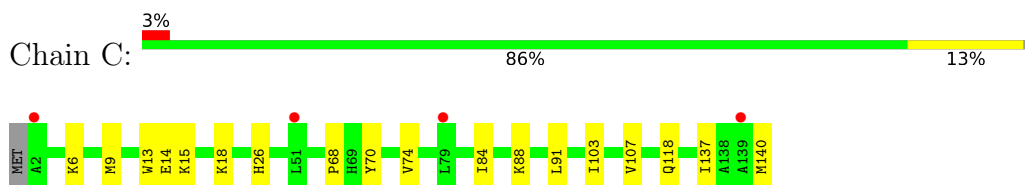
- Molecule 1: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial



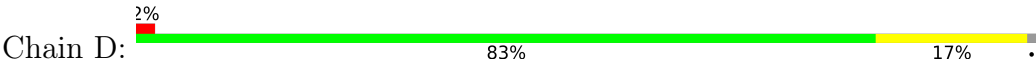
- Molecule 2: Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial



- Molecule 3: Succinate dehydrogenase cytochrome b, large subunit



- Molecule 4: Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	69.91Å 84.55Å 290.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.62 – 1.97 29.62 – 1.97	Depositor EDS
% Data completeness (in resolution range)	93.7 (29.62-1.97) 82.9 (29.62-1.97)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.48 (at 1.96Å)	Xtriage
Refinement program	PHENIX dev_3150	Depositor
R, R_{free}	0.208 , 0.239 0.208 , 0.240	Depositor DCC
R_{free} test set	2334 reflections (1.90%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.326	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9426	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.97% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, FAD, K, FES, 3PE, UNL, F3S, MLZ, MOH, 9AU, HEM, UMQ, Y3P, PEG

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	0.35	0/4824	0.55	0/6531
2	B	0.38	0/1963	0.54	0/2646
3	C	0.32	0/1094	0.53	0/1486
4	D	0.32	0/794	0.45	0/1089
All	All	0.35	0/8675	0.54	0/11752

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 [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	4723	0	4608	69	0
2	B	1921	0	1913	22	0
3	C	1076	0	1116	15	0
4	D	771	0	763	16	0
5	A	53	0	29	5	0
6	A	9	2	0	6	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	58	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	42	0	0	3	0
8	C	78	0	0	1	0
8	D	59	0	0	3	0
9	A	5	0	5	3	0
10	A	2	0	0	1	0
11	B	4	0	0	0	0
12	B	8	0	0	0	0
13	B	7	0	0	0	0
14	C	41	0	24	0	0
15	C	19	0	0	0	0
16	C	34	0	44	0	0
17	D	42	0	61	2	0
18	A	239	0	0	9	0
18	B	146	0	0	3	0
18	C	54	0	0	0	0
18	D	31	0	0	2	0
All	All	9424	2	8563	119	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 7.

The worst 5 of 119 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:297:ARG:HH22	6:A:1002:Y3P:C3	1.67	1.07
1:A:187:GLU:HG2	1:A:390:PRO:HB2	1.65	0.77
3:C:68:PRO:HA	4:D:99:MET:HE1	1.74	0.69
3:C:118:GLN:OE1	8:C:1019:UNL:O	2.11	0.68
1:A:219:THR:HA	1:A:472:MET:HE3	1.76	0.67

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	610/621 (98%)	590 (97%)	20 (3%)	0	100	100
2	B	237/252 (94%)	232 (98%)	5 (2%)	0	100	100
3	C	136/140 (97%)	135 (99%)	1 (1%)	0	100	100
4	D	100/103 (97%)	98 (98%)	2 (2%)	0	100	100
All	All	1083/1116 (97%)	1055 (97%)	28 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	496/506 (98%)	488 (98%)	8 (2%)	55	50
2	B	215/219 (98%)	214 (100%)	1 (0%)	81	79
3	C	116/117 (99%)	116 (100%)	0	100	100
4	D	78/79 (99%)	76 (97%)	2 (3%)	40	32
All	All	905/921 (98%)	894 (99%)	11 (1%)	63	58

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	618	ILE
2	B	217	THR
4	D	19	LEU
4	D	14	ARG
1	A	441	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	150	GLN
3	C	69	HIS
4	D	69	ASN
3	C	118	GLN
1	A	607	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
3	MLZ	C	15	3	8,9,10	0.62	0	4,9,11	1.80	1 (25%)

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	MLZ	C	15	3	-	2/7/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	15	MLZ	CM-NZ-CE	3.39	121.45	112.01

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	15	MLZ	CG-CD-CE-NZ
3	C	15	MLZ	CE-CD-CG-CB

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](#)

Of 79 ligands modelled in this entry, 2 are monoatomic and 66 are unknown - leaving 11 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	$\# Z > 2$
13	F3S	B	1003	2	0,9,9	-	-	-		
11	FES	B	1001	2	0,4,4	-	-	-		
17	3PE	D	201	-	41,41,50	1.09	2 (4%)	44,46,55	1.11	4 (9%)
6	Y3P	A	1002	-	8,8,8	2.47	4 (50%)	9,10,10	2.23	3 (33%)
9	PEG	A	1005	-	4,4,6	0.60	0	3,3,5	0.11	0
14	HEM	C	201	4,3	48,48,50	1.61	7 (14%)	66,80,82	1.34	8 (12%)
5	FAD	A	1001	1	58,58,58	1.12	6 (10%)	85,89,89	1.56	16 (18%)
10	MOH	A	1011	-	1,1,1	0.08	0	-		
15	9AU	C	202	-	20,20,28	3.01	8 (40%)	25,27,37	2.12	10 (40%)
16	UMQ	C	1002	-	35,35,35	0.55	0	46,46,46	0.92	2 (4%)
12	SF4	B	1002	2	0,12,12	-	-	-		

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
13	F3S	B	1003	2	-	-	0/3/3/3
17	3PE	D	201	-	-	15/45/45/54	-
11	FES	B	1001	2	-	-	0/1/1/1
6	Y3P	A	1002	-	-	4/8/8/8	-
9	PEG	A	1005	-	-	1/2/2/4	-
14	HEM	C	201	4,3	-	3/10/50/54	-
5	FAD	A	1001	1	-	4/34/50/50	0/6/6/6
15	9AU	C	202	-	-	3/8/8/17	0/2/2/2
16	UMQ	C	1002	-	-	8/20/60/60	0/2/2/2
12	SF4	B	1002	2	-	-	0/6/5/5

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	C	202	9AU	OAS-CAZ	8.01	1.50	1.38
15	C	202	9AU	CAW-CAX	5.90	1.48	1.36
14	C	201	HEM	FE-ND	5.82	2.12	1.94
15	C	202	9AU	OAS-CAY	5.20	1.45	1.38
6	A	1002	Y3P	C2-C1	4.72	1.55	1.48

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	C	202	9AU	CAZ-OAS-CAY	-4.86	117.62	122.26
5	A	1001	FAD	C5A-C4A-N3A	-4.40	120.66	126.72
6	A	1002	Y3P	O2-C1-C2	-4.37	115.11	120.12
5	A	1001	FAD	C4-N3-C2	-3.93	118.66	125.64
15	C	202	9AU	CBA-CAW-CAX	-3.81	118.70	120.99

There are no chirality outliers.

5 of 38 torsion outliers are listed below:

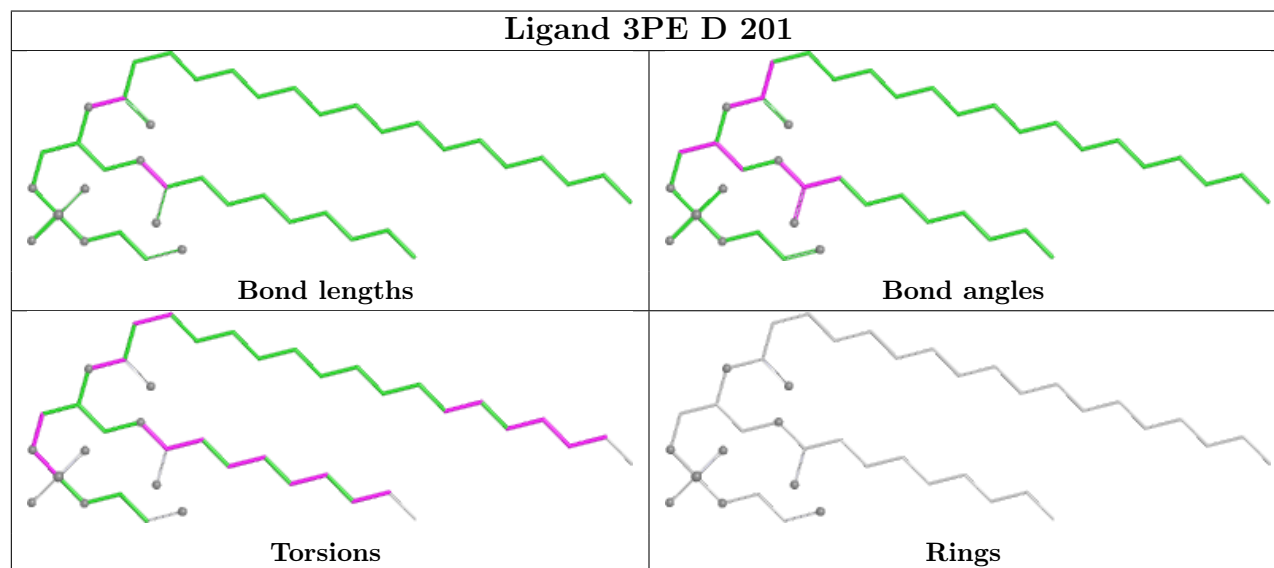
Mol	Chain	Res	Type	Atoms
5	A	1001	FAD	N10-C1'-C2'-O2'
5	A	1001	FAD	N10-C1'-C2'-C3'
6	A	1002	Y3P	O1-C1-C2-O3
6	A	1002	Y3P	O2-C1-C2-O3
17	D	201	3PE	C1-O11-P-O14

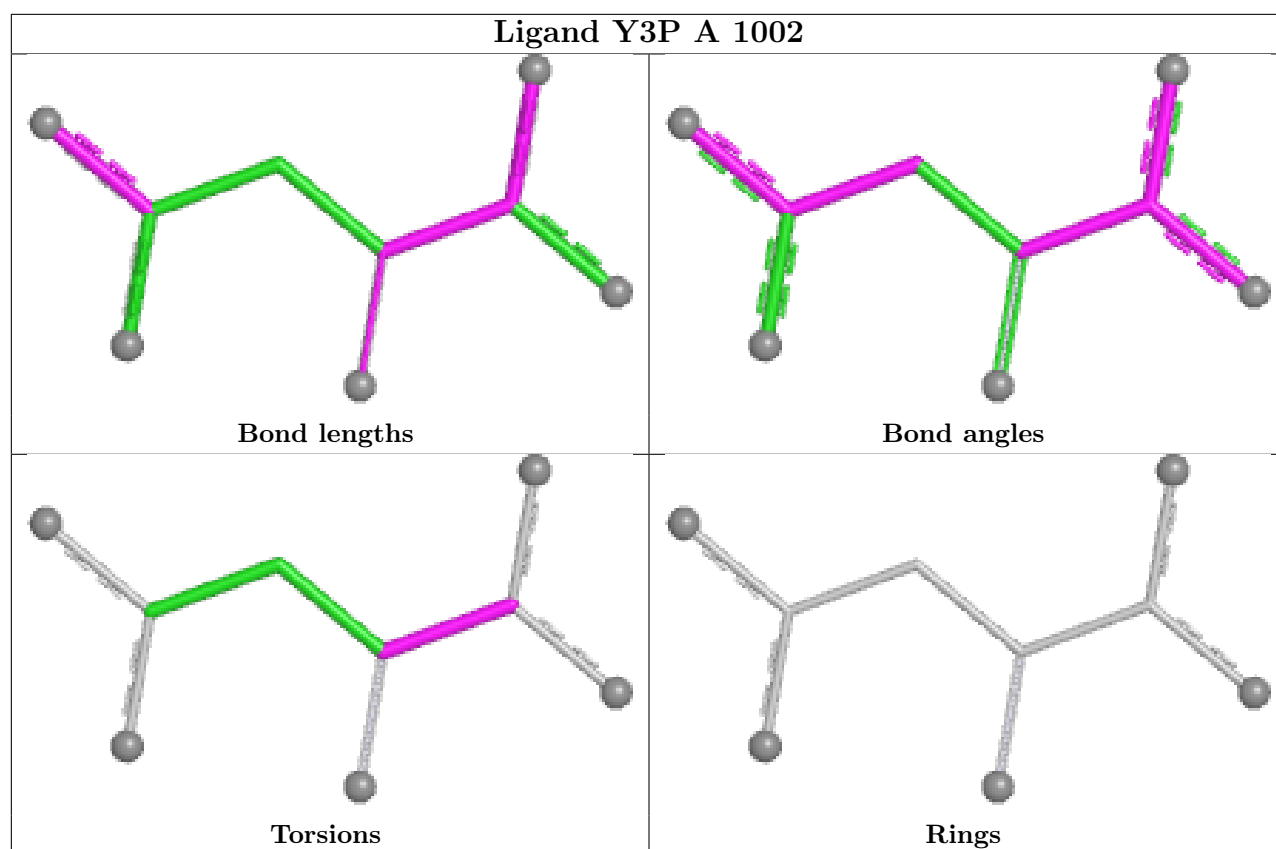
There are no ring outliers.

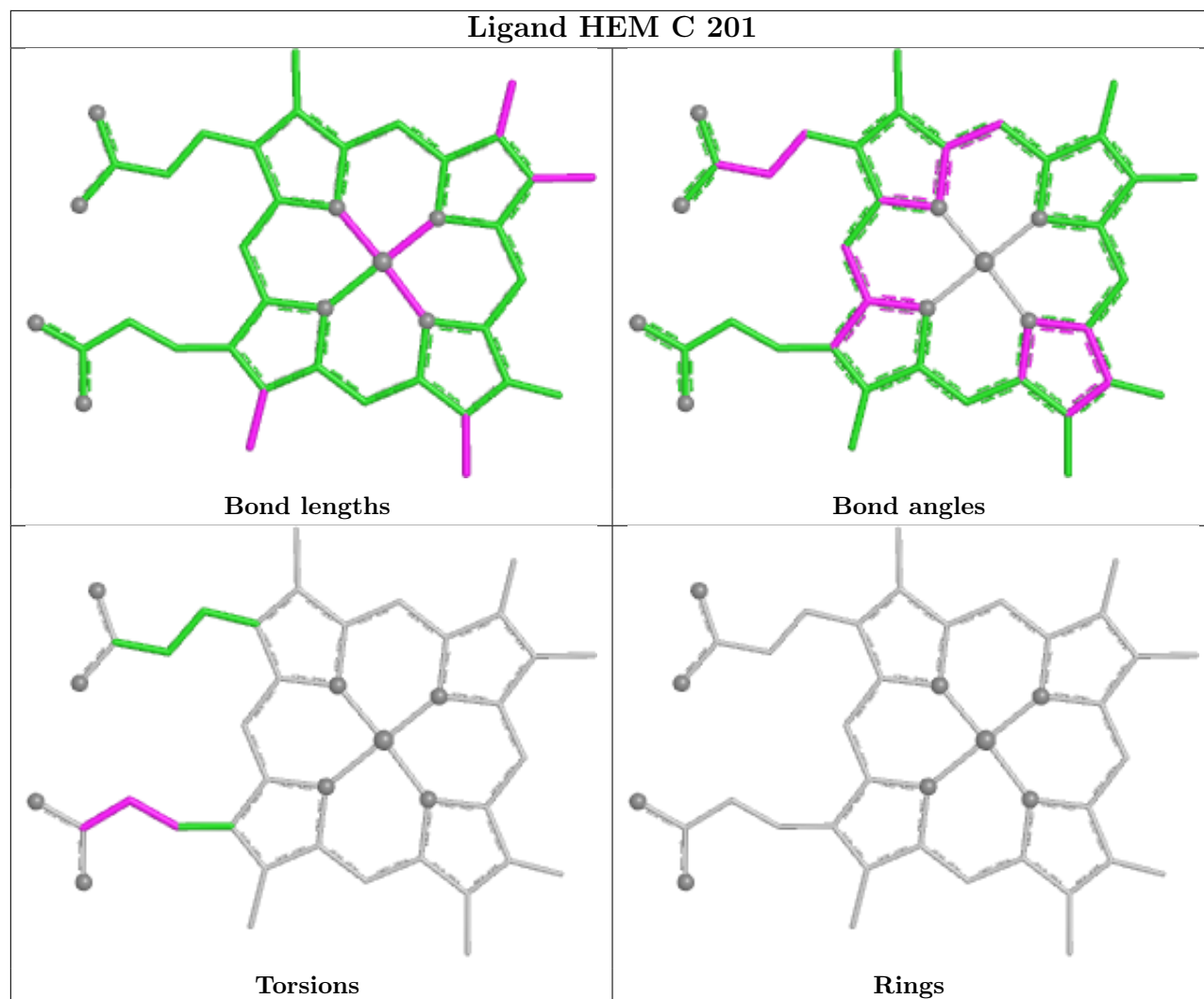
5 monomers are involved in 17 short contacts:

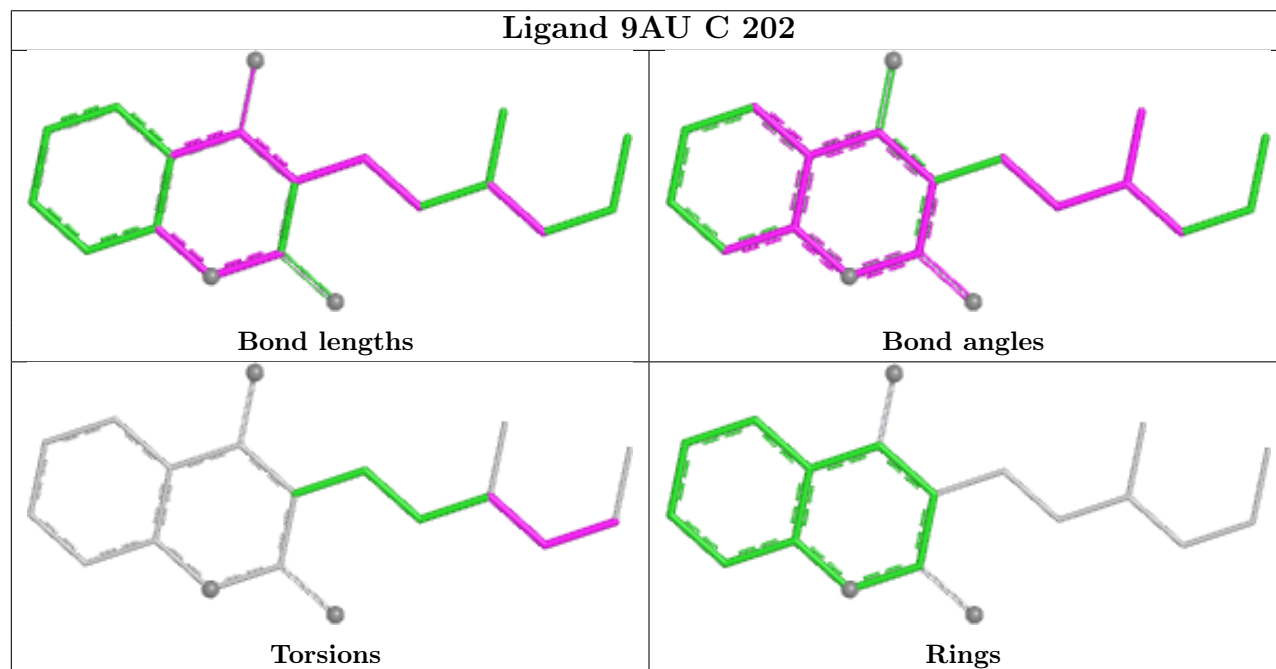
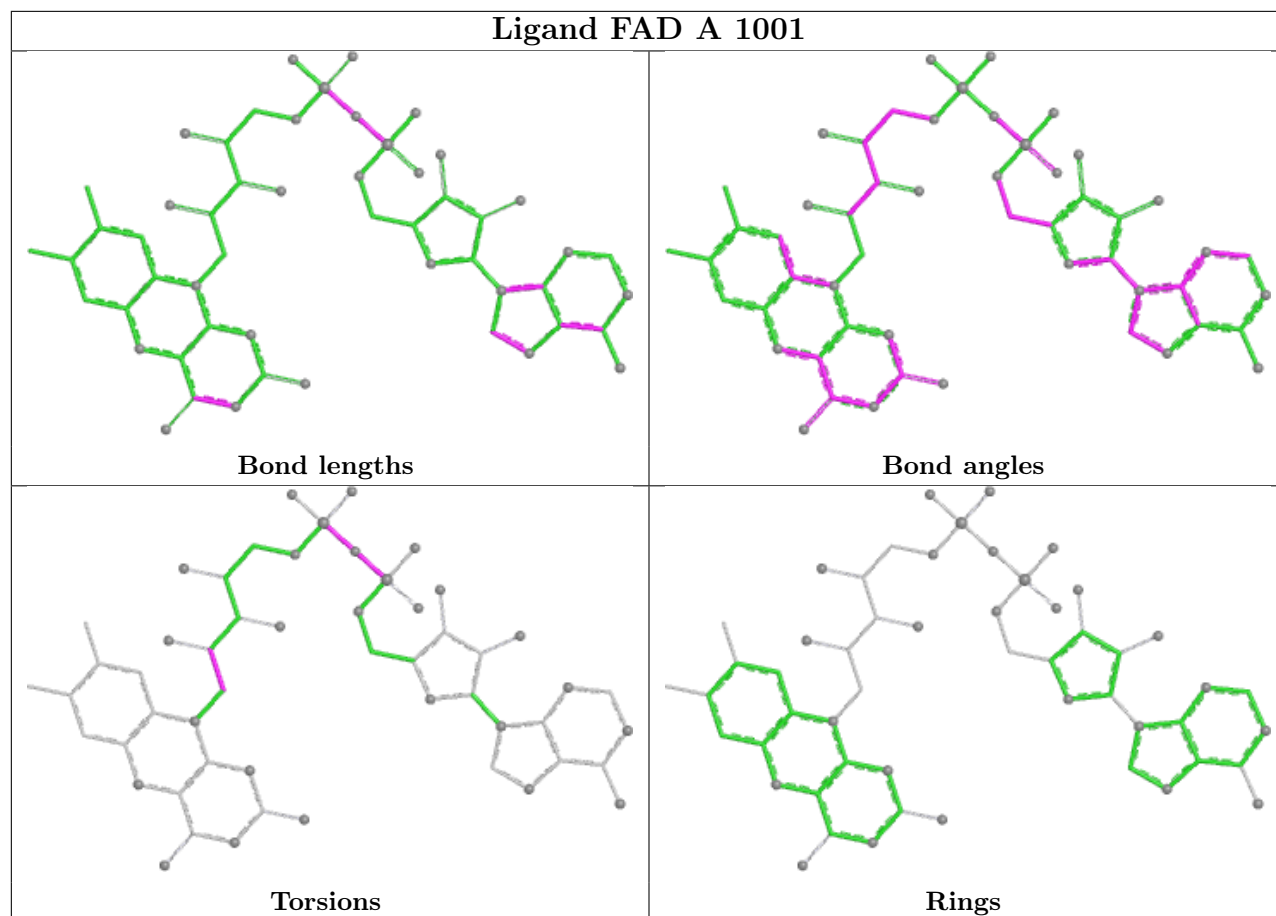
Mol	Chain	Res	Type	Clashes	Symm-Clashes
17	D	201	3PE	2	0
6	A	1002	Y3P	6	0
9	A	1005	PEG	3	0
5	A	1001	FAD	5	0
10	A	1011	MOH	1	0

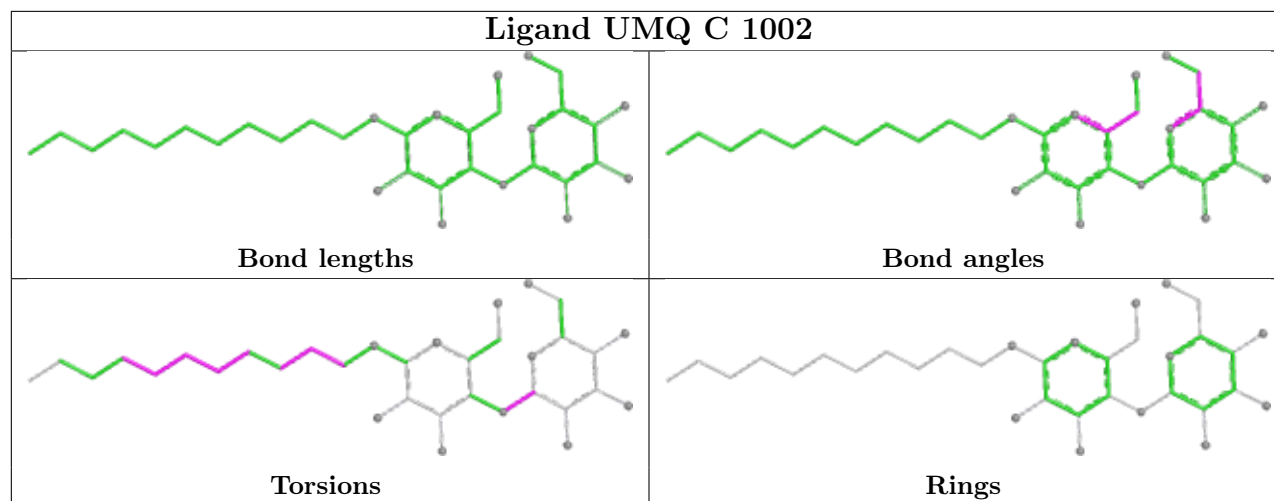
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











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	611/621 (98%)	0.41	10 (1%) 70 79	22, 51, 75, 101	1 (0%)
2	B	239/252 (94%)	0.22	4 (1%) 69 78	31, 42, 71, 89	0
3	C	138/140 (98%)	0.45	4 (2%) 53 63	35, 48, 74, 81	0
4	D	102/103 (99%)	0.42	2 (1%) 65 74	36, 48, 66, 86	0
All	All	1090/1116 (97%)	0.38	20 (1%) 67 76	22, 49, 73, 101	1 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	441	ILE	4.2
3	C	2	ALA	4.1
1	A	439	PRO	4.0
4	D	73	TYR	3.8
2	B	25	GLY	3.3

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
3	MLZ	C	15	10/11	0.91	0.12	50,59,65,65	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

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
8	UNL	C	1010	15/-	0.61	0.23	74,76,93,94	15
8	UNL	A	1025	1/-	0.63	0.19	73,73,73,73	0
8	UNL	A	1022	1/-	0.66	0.12	76,76,76,76	0
8	UNL	B	1012	2/-	0.68	0.26	85,85,85,86	0
8	UNL	D	208	12/-	0.71	0.21	72,76,79,80	0
8	UNL	D	207	12/-	0.72	0.20	75,81,89,90	0
10	MOH	A	1011	2/2	0.72	0.31	79,79,79,81	0
8	UNL	C	1008	3/-	0.73	0.15	51,51,59,60	0
8	UNL	D	206	5/-	0.74	0.20	74,74,79,79	0
8	UNL	C	1003	3/-	0.74	0.28	47,47,52,56	0
8	UNL	B	1014	4/-	0.75	0.08	89,91,91,92	0
8	UNL	B	1007	3/-	0.76	0.19	58,58,65,65	0
8	UNL	C	1007	5/-	0.76	0.21	54,55,60,62	0
8	UNL	A	1012	2/-	0.77	0.23	70,70,70,71	0
8	UNL	B	1017	1/-	0.78	0.18	47,47,47,47	0
9	PEG	A	1005	5/7	0.79	0.19	67,67,72,74	0
8	UNL	C	1022	1/-	0.79	0.12	66,66,66,66	0
15	9AU	C	202	19/27	0.79	0.14	38,57,67,69	0
8	UNL	A	1019	3/-	0.80	0.32	64,64,66,66	0
8	UNL	B	1009	3/-	0.81	0.13	42,42,43,46	3
8	UNL	A	1010	4/-	0.81	0.18	68,68,72,80	0
8	UNL	D	212	1/-	0.81	0.29	63,63,63,63	0
8	UNL	C	1012	3/-	0.81	0.17	73,73,74,76	0
8	UNL	C	1005	15/-	0.81	0.18	52,72,78,78	15
8	UNL	A	1018	2/-	0.81	0.29	53,53,53,60	0
17	3PE	D	201	42/51	0.81	0.16	66,82,115,119	0
8	UNL	A	1027	1/-	0.82	0.16	49,49,49,49	1
8	UNL	A	1023	1/-	0.83	0.13	72,72,72,72	0
8	UNL	A	1024	1/-	0.83	0.10	48,48,48,48	0
8	UNL	A	1021	3/-	0.84	0.22	44,44,60,64	0
8	UNL	A	1017	2/-	0.84	0.20	80,80,80,82	0
8	UNL	C	1016	1/-	0.84	0.12	55,55,55,55	0
8	UNL	A	1020	3/-	0.84	0.24	39,39,46,53	0
8	UNL	B	1015	1/-	0.85	0.24	64,64,64,64	0
8	UNL	D	203	11/-	0.85	0.10	56,74,78,79	0
8	UNL	B	1008	3/-	0.85	0.18	40,40,50,53	0
8	UNL	B	1006	3/-	0.85	0.17	64,64,66,67	0

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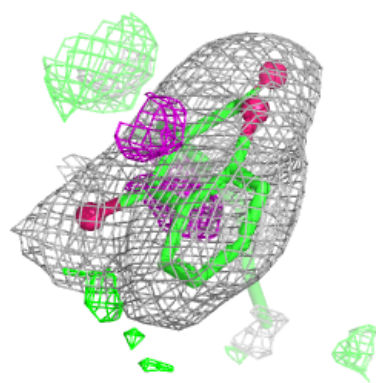
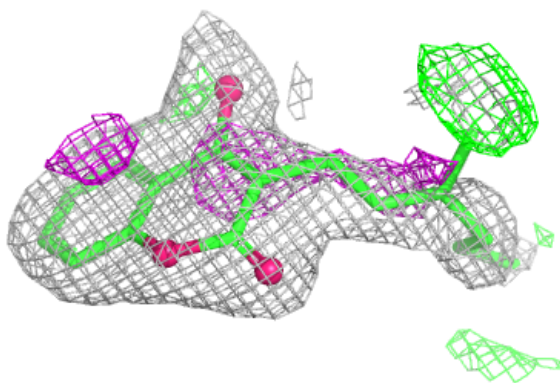
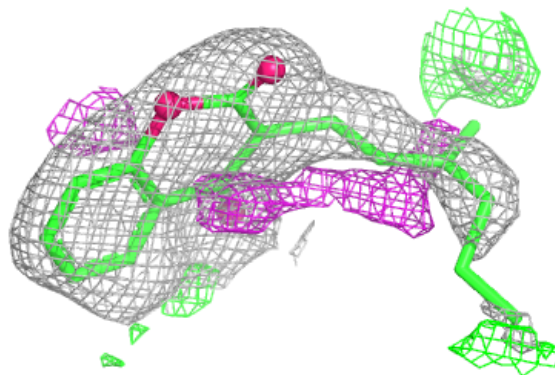
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	UNL	C	1017	1/-	0.85	0.16	54,54,54,54	0
8	UNL	C	1006	12/-	0.86	0.14	63,73,75,75	0
8	UNL	A	1009	4/-	0.86	0.14	65,65,66,73	0
8	UNL	A	1013	3/-	0.86	0.22	37,37,37,49	3
8	UNL	D	205	1/-	0.86	0.13	65,65,65,65	0
8	UNL	A	1008	4/-	0.87	0.11	63,66,67,69	0
8	UNL	B	1019	1/-	0.87	0.24	56,56,56,56	0
8	UNL	C	1009	4/-	0.88	0.10	75,75,76,76	0
8	UNL	A	1015	3/-	0.88	0.16	65,65,68,69	0
8	UNL	B	1011	4/-	0.89	0.09	69,73,74,78	0
7	K	B	1004	1/1	0.89	0.19	84,84,84,84	0
8	UNL	D	204	5/-	0.89	0.16	45,48,49,51	5
8	UNL	B	1016	1/-	0.90	0.11	59,59,59,59	0
8	UNL	D	211	1/-	0.90	0.08	61,61,61,61	0
8	UNL	A	1006	7/-	0.90	0.15	68,70,71,72	0
8	UNL	B	1018[A]	1/-	0.90	0.07	29,29,29,29	1
8	UNL	B	1018[B]	1/-	0.90	0.07	28,28,28,28	1
8	UNL	B	1013	4/-	0.90	0.11	45,46,47,50	4
8	UNL	C	1019	1/-	0.90	0.07	53,53,53,53	0
8	UNL	B	1005	4/-	0.91	0.14	51,54,57,63	0
8	UNL	B	1010	6/-	0.91	0.15	61,64,65,67	6
8	UNL	C	1018	1/-	0.91	0.14	57,57,57,57	0
8	UNL	D	209	10/-	0.91	0.11	60,70,71,73	0
16	UMQ	C	1002	34/34	0.91	0.11	40,61,78,83	0
8	UNL	C	1015	1/-	0.91	0.08	44,44,44,44	0
8	UNL	C	1021	1/-	0.92	0.12	60,60,60,60	0
8	UNL	A	1026	1/-	0.92	0.11	56,56,56,56	0
8	UNL	C	1004	3/-	0.92	0.17	50,50,52,54	0
8	UNL	C	1011	4/-	0.92	0.13	67,67,71,80	0
8	UNL	D	210	1/-	0.93	0.09	45,45,45,45	0
8	UNL	A	1016	2/-	0.94	0.12	64,64,64,64	0
8	UNL	A	1004	6/-	0.94	0.11	66,67,69,77	4
6	Y3P	A	1002	9/9	0.94	0.07	41,53,64,66	0
8	UNL	A	1007	4/-	0.94	0.09	69,71,73,76	0
8	UNL	C	1013	3/-	0.95	0.14	68,68,68,68	0
8	UNL	C	1014	1/-	0.95	0.11	49,49,49,49	0
14	HEM	C	201	41/43	0.97	0.08	34,42,51,53	0
5	FAD	A	1001	53/53	0.97	0.06	32,39,46,49	0
7	K	A	1003	1/1	0.98	0.05	53,53,53,53	0
12	SF4	B	1002	8/8	0.98	0.04	30,36,41,41	0
11	FES	B	1001	4/4	0.99	0.03	36,38,38,39	0
13	F3S	B	1003	7/7	0.99	0.04	31,35,36,36	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.

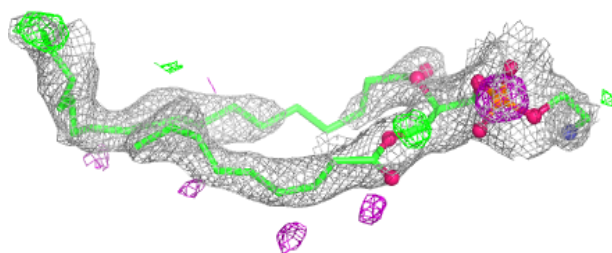
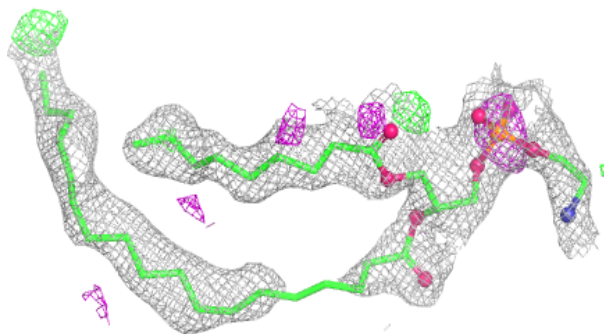
Electron density around 9AU C 202:

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

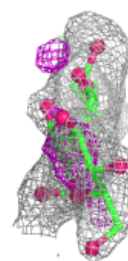
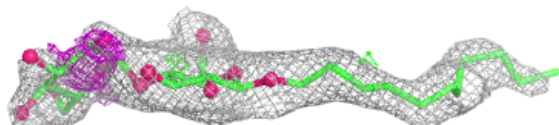
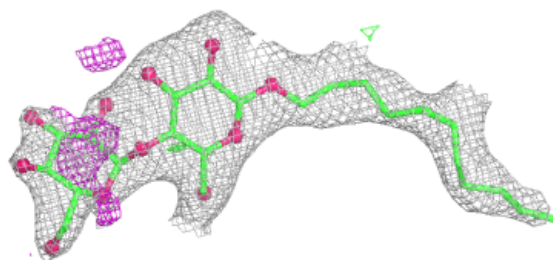


Electron density around 3PE D 201:

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and green (positive)

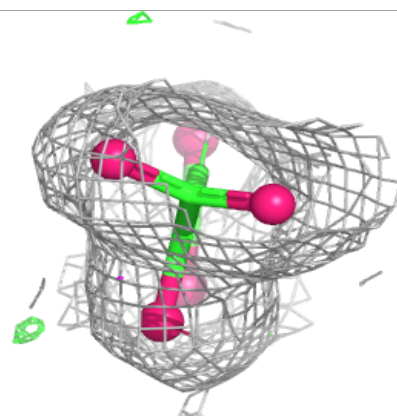
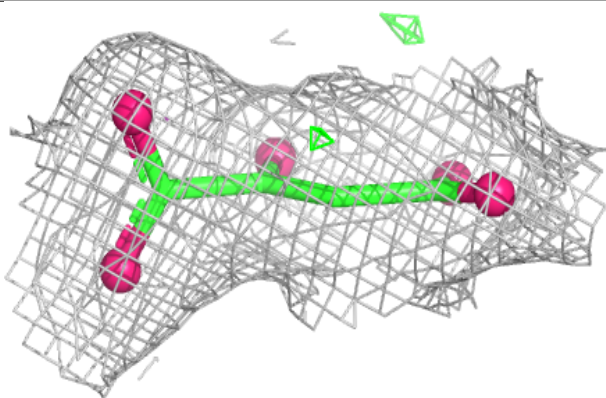
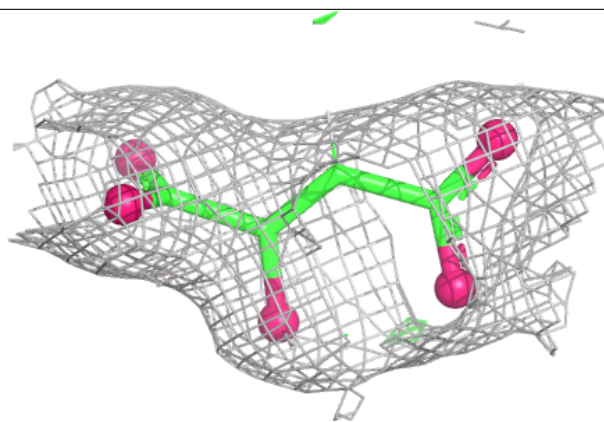
**Electron density around UMQ C 1002:**

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

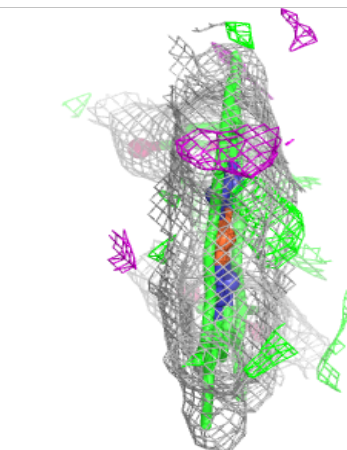
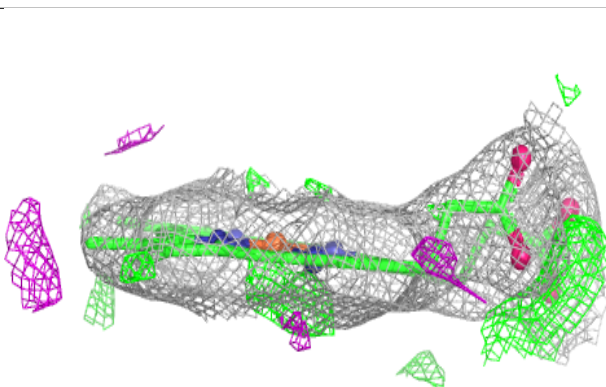
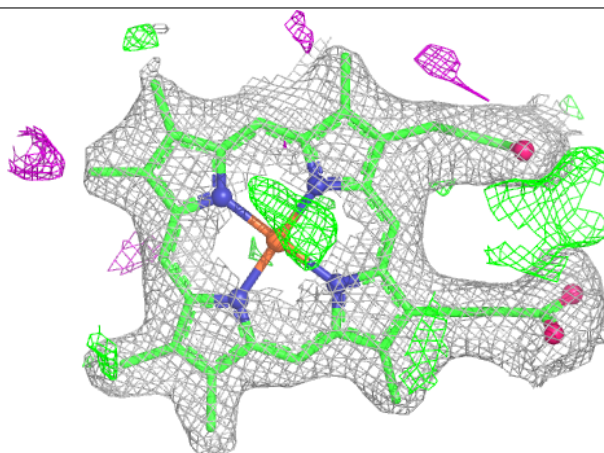


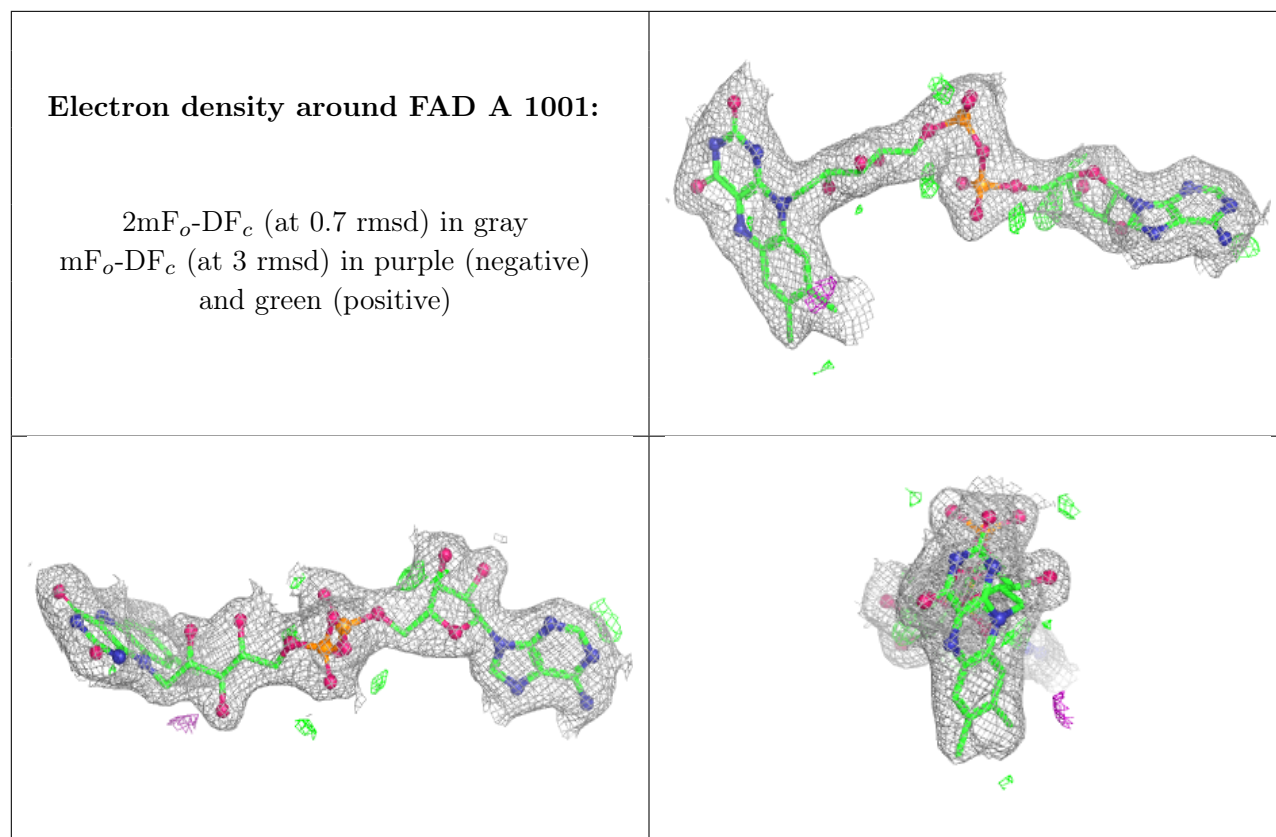
Electron density around Y3P A 1002:

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

**Electron density around HEM C 201:**

$2mF_o-DF_c$ (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.