



wwPDB X-ray Structure Validation Summary Report

Mar 9, 2026 – 07:08 AM UTC

PDB ID : 2WS3 / pdb_00002ws3
Title : Crystal structure of the E. coli succinate:quinone oxidoreductase (SQR) SdhD Tyr83Phe mutant
Authors : Ruprecht, J.; Yankovskaya, V.; Maklashina, E.; Iwata, S.; Cecchini, G.
Deposited on : 2009-09-03
Resolution : 3.20 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the  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)
Xtrriage (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

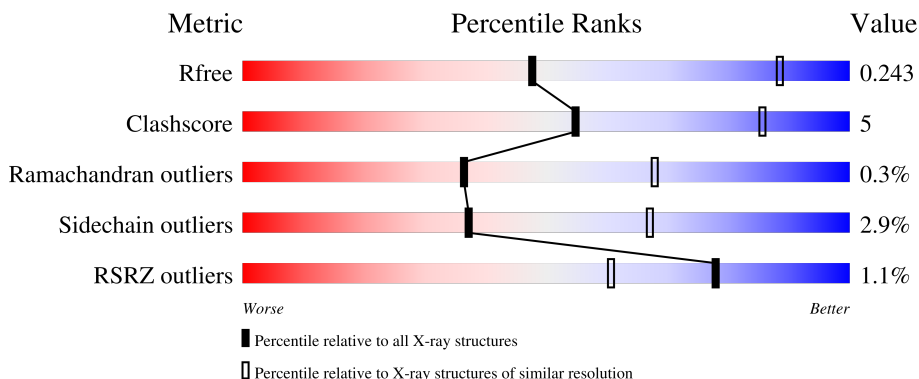
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	588	
1	E	588	
1	I	588	
2	B	238	
2	F	238	

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Mol	Chain	Length	Quality of chain
2	J	238	
3	C	129	
3	G	129	
3	K	129	
4	D	115	
4	H	115	
4	L	115	

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
10	F3S	F	304	-	-	X	-
7	TEO	E	1590	-	-	X	-
7	TEO	I	1590	-	-	X	-
9	SF4	J	303	-	-	X	-

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 24900 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 SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	588	Total 4522	C 2812	N 821	O 861	S 28	0	0	0
1	E	588	Total 4522	C 2812	N 821	O 861	S 28	0	0	0
1	I	588	Total 4522	C 2812	N 821	O 861	S 28	0	0	0

- Molecule 2 is a protein called SUCCINATE DEHYDROGENASE IRON-SULFUR SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	238	Total 1869	C 1172	N 329	O 348	S 20	0	0	0
2	F	238	Total 1869	C 1172	N 329	O 348	S 20	0	0	0
2	J	238	Total 1869	C 1172	N 329	O 348	S 20	0	0	0

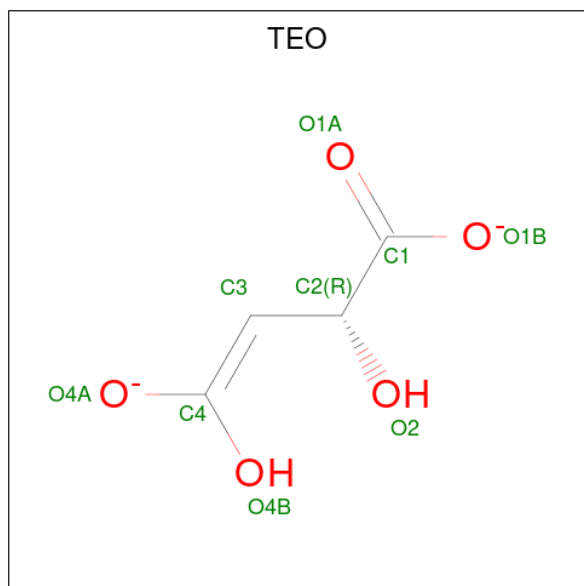
- Molecule 3 is a protein called SUCCINATE DEHYDROGENASE CYTOCHROME B-556 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	121	Total 933	C 619	N 151	O 158	S 5	0	0	0
3	G	121	Total 933	C 619	N 151	O 158	S 5	0	0	0
3	K	121	Total 933	C 619	N 151	O 158	S 5	0	0	0

- Molecule 4 is a protein called SUCCINATE DEHYDROGENASE HYDROPHOBIC MEMBRANE ANCHOR SUBUNIT.

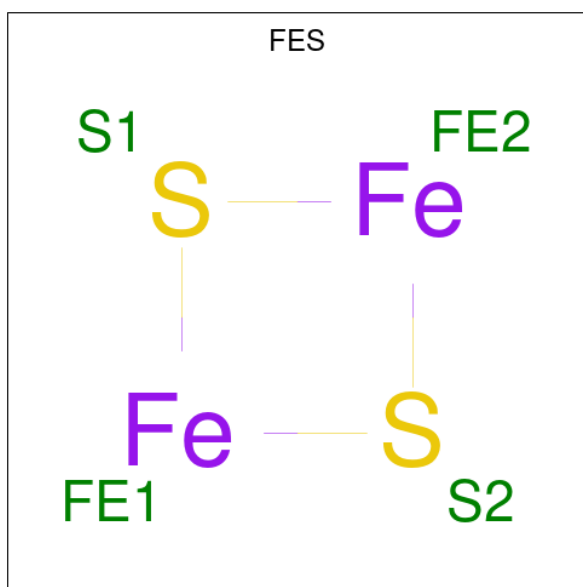
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Na 1 1	0	0
6	E	1	Total Na 1 1	0	0
6	I	1	Total Na 1 1	0	0

- Molecule 7 is MALATE LIKE INTERMEDIATE (CCD ID: TEO) (formula: $C_4H_4O_5$).



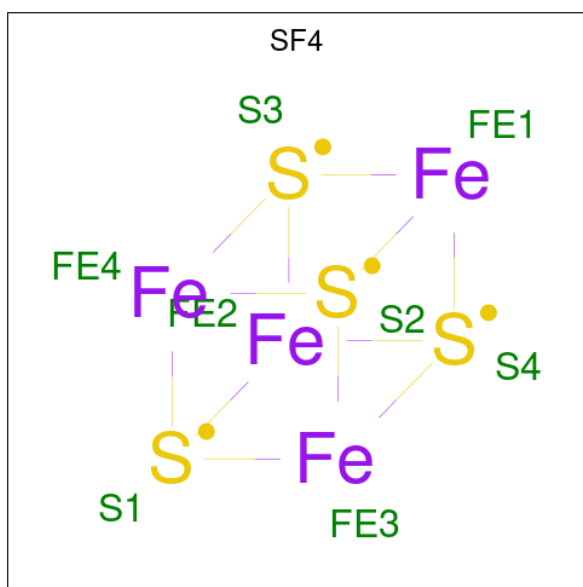
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 9 4 5	0	0
7	E	1	Total C O 9 4 5	0	0
7	I	1	Total C O 9 4 5	0	0

- Molecule 8 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			4	2	2		
8	F	1	Total	Fe	S	0	0
			4	2	2		
8	J	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 9 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



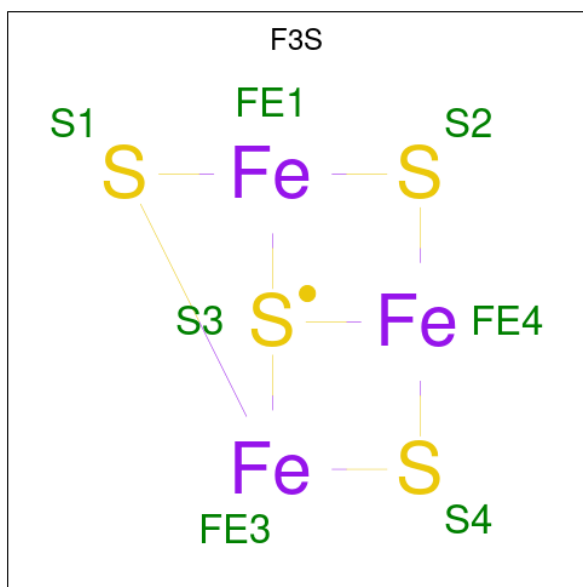
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Fe	S	0	0
			8	4	4		

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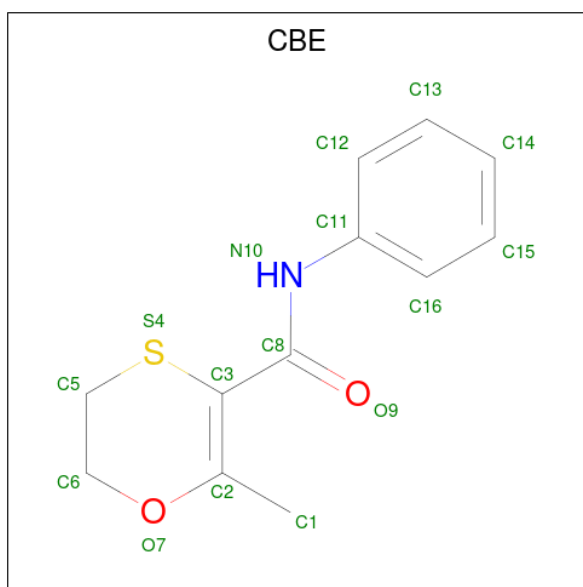
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	F	1	Total	Fe	S	0	0
			8	4	4		
9	J	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 10 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe₃S₄).



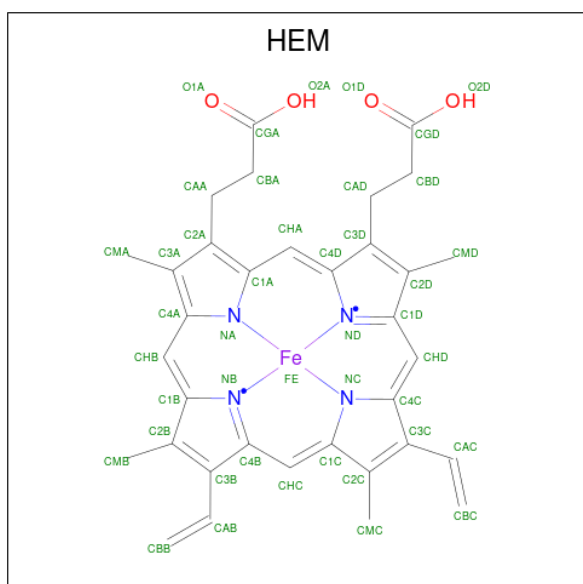
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	Fe	S	0	0
			7	3	4		
10	F	1	Total	Fe	S	0	0
			7	3	4		
10	J	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 11 is 2-METHYL-N-PHENYL-5,6-DIHYDRO-1,4-OXATHIINE-3-CARBOXAMIDE (CCD ID: CBE) (formula: C₁₂H₁₃NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	C	1	Total	C	N	O	S	0	0
			16	12	1	2	1		
11	G	1	Total	C	N	O	S	0	0
			16	12	1	2	1		
11	K	1	Total	C	N	O	S	0	0
			16	12	1	2	1		

- Molecule 12 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

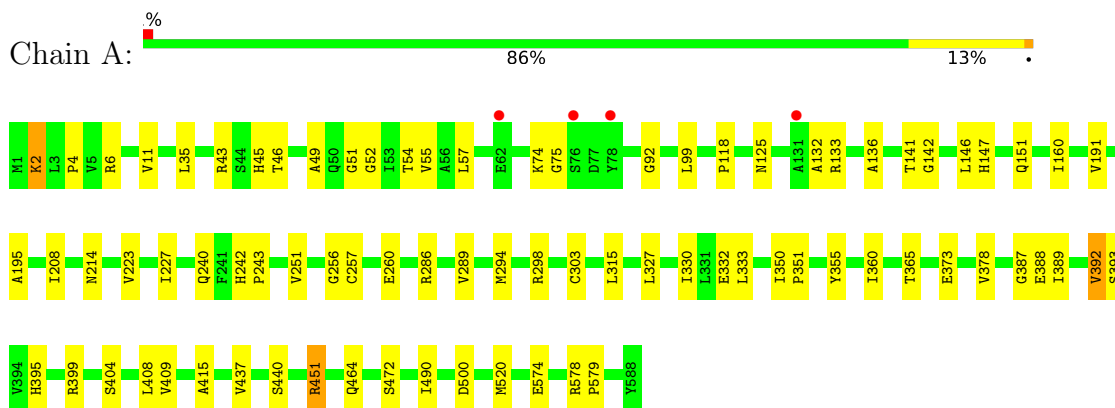


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
12	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
12	G	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
12	K	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

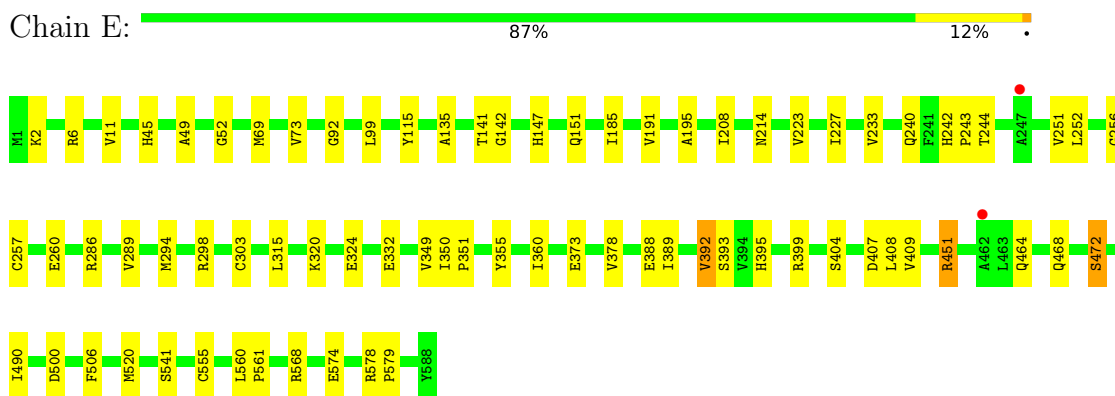
3 Residue-property plots [i](#)

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.

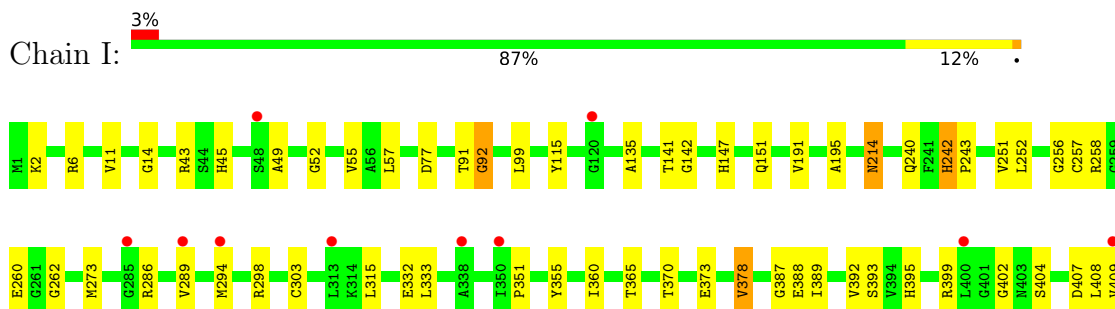
- Molecule 1: SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT

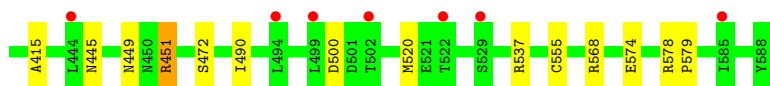


- Molecule 1: SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT

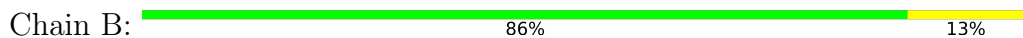


- Molecule 1: SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT

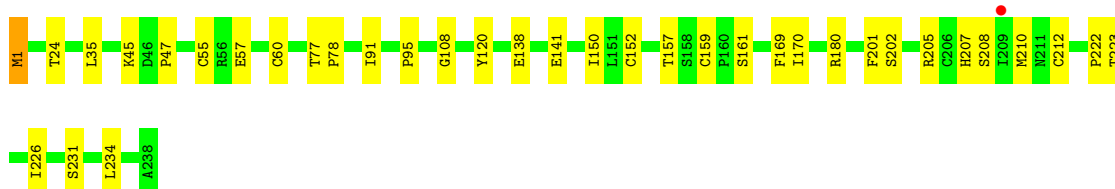
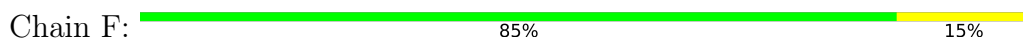




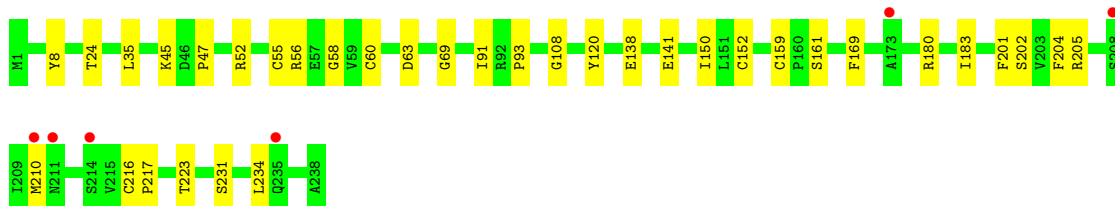
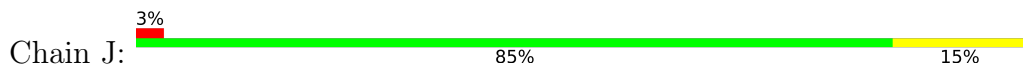
● Molecule 2: SUCCINATE DEHYDROGENASE IRON-SULFUR SUBUNIT



● Molecule 2: SUCCINATE DEHYDROGENASE IRON-SULFUR SUBUNIT



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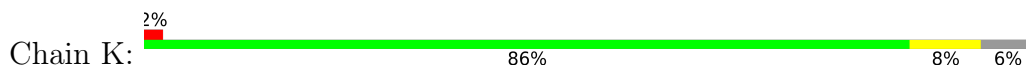
● Molecule 3: SUCCINATE DEHYDROGENASE CYTOCHROME B-556 SUBUNIT



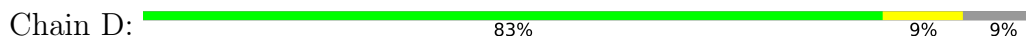
● Molecule 3: SUCCINATE DEHYDROGENASE CYTOCHROME B-556 SUBUNIT



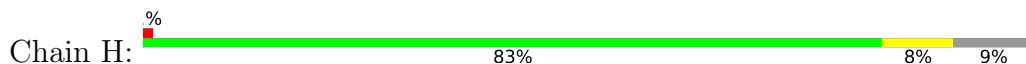
● Molecule 3: SUCCINATE DEHYDROGENASE CYTOCHROME B-556 SUBUNIT



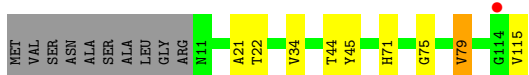
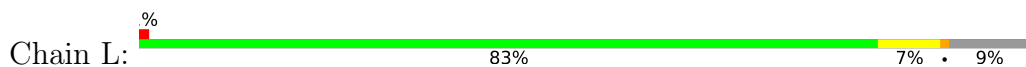
- Molecule 4: SUCCINATE DEHYDROGENASE HYDROPHOBIC MEMBRANE ANCHOR SUBUNIT



- Molecule 4: SUCCINATE DEHYDROGENASE HYDROPHOBIC MEMBRANE ANCHOR SUBUNIT



- Molecule 4: SUCCINATE DEHYDROGENASE HYDROPHOBIC MEMBRANE ANCHOR SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	119.85Å 184.71Å 203.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.03 – 3.20 49.03 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.03-3.20) 99.7 (49.03-3.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.19Å)	Xtrriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.219 , 0.253 0.210 , 0.243	Depositor DCC
R_{free} test set	3797 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	84.8	Xtrriage
Anisotropy	0.360	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	24900	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.11% 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: FAD, HEM, FES, SF4, CBE, NA, F3S, TEO

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	0.81	0/4611	0.96	3/6237 (0.0%)
1	E	0.72	0/4611	0.93	1/6237 (0.0%)
1	I	0.59	0/4611	0.89	2/6237 (0.0%)
2	B	0.90	0/1908	0.94	2/2578 (0.1%)
2	F	0.78	0/1908	0.95	0/2578
2	J	0.65	0/1908	0.86	1/2578 (0.0%)
3	C	0.76	0/953	0.92	0/1293
3	G	0.71	0/953	0.92	0/1293
3	K	0.68	1/953 (0.1%)	0.92	0/1293
4	D	0.73	0/858	0.94	0/1173
4	H	0.70	0/858	0.94	0/1173
4	L	0.67	0/858	0.97	0/1173
All	All	0.73	1/24990 (0.0%)	0.93	9/33843 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	25	ILE	CA-CB	5.05	1.60	1.54

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	392	VAL	N-CA-C	6.55	116.69	110.53
1	I	242	HIS	CA-C-N	5.84	125.31	119.24
1	I	242	HIS	C-N-CA	5.84	125.31	119.24
1	E	392	VAL	N-CA-C	5.63	115.82	110.53
1	A	125	ASN	N-CA-C	5.34	118.76	111.39

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	4522	0	4426	54	0
1	E	4522	0	4426	44	0
1	I	4522	0	4426	46	0
2	B	1869	0	1850	14	0
2	F	1869	0	1850	17	0
2	J	1869	0	1850	17	0
3	C	933	0	979	5	0
3	G	933	0	979	5	0
3	K	933	0	979	6	0
4	D	835	0	875	7	0
4	H	835	0	875	5	0
4	L	835	0	875	6	0
5	A	53	0	31	10	0
5	E	53	0	31	10	0
5	I	53	0	31	16	0
6	A	1	0	0	0	0
6	E	1	0	0	0	0
6	I	1	0	0	0	0
7	A	9	0	3	3	0
7	E	9	0	3	5	0
7	I	9	0	3	6	0
8	B	4	0	0	0	0
8	F	4	0	0	0	0
8	J	4	0	0	1	0
9	B	8	0	0	0	0
9	F	8	0	0	0	0
9	J	8	0	0	3	0
10	B	7	0	0	1	0
10	F	7	0	0	2	0
10	J	7	0	0	1	0
11	C	16	0	13	2	0
11	G	16	0	13	0	0
11	K	16	0	13	2	0
12	C	43	0	30	7	0
12	G	43	0	30	6	0
12	K	43	0	30	12	0
All	All	24900	0	24621	239	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 5.

The worst 5 of 239 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:E:45:HIS:NE2	5:E:601:FAD:HM82	1.13	1.41
1:A:45:HIS:NE2	5:A:601:FAD:HM82	1.07	1.36
1:A:45:HIS:NE2	5:A:601:FAD:C8M	1.94	1.30
1:E:45:HIS:NE2	5:E:601:FAD:C8M	2.08	1.15
1:A:45:HIS:CE1	5:A:601:FAD:HM82	1.86	1.09

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	586/588 (100%)	560 (96%)	24 (4%)	2 (0%)	36	68
1	E	586/588 (100%)	558 (95%)	26 (4%)	2 (0%)	36	68
1	I	586/588 (100%)	561 (96%)	23 (4%)	2 (0%)	36	68
2	B	236/238 (99%)	223 (94%)	12 (5%)	1 (0%)	30	62
2	F	236/238 (99%)	220 (93%)	15 (6%)	1 (0%)	30	62
2	J	236/238 (99%)	223 (94%)	12 (5%)	1 (0%)	30	62
3	C	119/129 (92%)	114 (96%)	5 (4%)	0	100	100
3	G	119/129 (92%)	115 (97%)	4 (3%)	0	100	100
3	K	119/129 (92%)	116 (98%)	3 (2%)	0	100	100
4	D	103/115 (90%)	98 (95%)	5 (5%)	0	100	100
4	H	103/115 (90%)	98 (95%)	5 (5%)	0	100	100
4	L	103/115 (90%)	98 (95%)	5 (5%)	0	100	100
All	All	3132/3210 (98%)	2984 (95%)	139 (4%)	9 (0%)	36	68

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	92	GLY
1	E	92	GLY
1	I	92	GLY
1	A	472	SER
1	E	472	SER

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	473/473 (100%)	465 (98%)	8 (2%)	53 75
1	E	473/473 (100%)	463 (98%)	10 (2%)	47 71
1	I	473/473 (100%)	463 (98%)	10 (2%)	47 71
2	B	208/208 (100%)	196 (94%)	12 (6%)	18 51
2	F	208/208 (100%)	198 (95%)	10 (5%)	23 56
2	J	208/208 (100%)	199 (96%)	9 (4%)	26 59
3	C	101/109 (93%)	98 (97%)	3 (3%)	36 66
3	G	101/109 (93%)	100 (99%)	1 (1%)	68 80
3	K	101/109 (93%)	99 (98%)	2 (2%)	48 72
4	D	88/96 (92%)	85 (97%)	3 (3%)	32 64
4	H	88/96 (92%)	84 (96%)	4 (4%)	24 58
4	L	88/96 (92%)	84 (96%)	4 (4%)	24 58
All	All	2610/2658 (98%)	2534 (97%)	76 (3%)	37 67

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	373	GLU
3	K	22	ILE
1	I	451	ARG
2	J	141	GLU

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Mol	Chain	Res	Type
4	L	115	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	135	GLN
4	H	14	HIS
2	J	211	ASN
3	G	91	HIS
1	I	25	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 3 are monoatomic - leaving 21 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
10	F3S	J	304	2	0,9,9	-	-	-		
7	TEO	A	1590	-	5,8,8	1.84	1 (20%)	4,10,10	2.71	3 (75%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	FAD	E	601	-	58,58,58	1.28	6 (10%)	85,89,89	1.84	22 (25%)
8	FES	F	302	2	0,4,4	-	-	-	-	-
12	HEM	C	1130	3,4	50,50,50	1.76	10 (20%)	67,82,82	1.47	15 (22%)
10	F3S	F	304	2	0,9,9	-	-	-	-	-
12	HEM	K	1130	3,4	50,50,50	2.25	12 (24%)	67,82,82	1.60	13 (19%)
7	TEO	I	1590	-	5,8,8	1.29	0	4,10,10	2.12	1 (25%)
8	FES	J	302	2	0,4,4	-	-	-	-	-
9	SF4	F	303	2	0,12,12	-	-	-	-	-
8	FES	B	302	2	0,4,4	-	-	-	-	-
11	CBE	K	1129	-	16,17,17	1.75	3 (18%)	17,22,22	2.24	3 (17%)
11	CBE	G	1129	-	16,17,17	1.47	2 (12%)	17,22,22	2.55	3 (17%)
11	CBE	C	1129	-	16,17,17	1.53	2 (12%)	17,22,22	2.69	3 (17%)
9	SF4	B	303	2	0,12,12	-	-	-	-	-
5	FAD	A	601	-	58,58,58	1.26	8 (13%)	85,89,89	1.66	17 (20%)
12	HEM	G	1130	3,4	50,50,50	1.97	10 (20%)	67,82,82	1.32	7 (10%)
9	SF4	J	303	2	0,12,12	-	-	-	-	-
7	TEO	E	1590	-	5,8,8	1.42	0	4,10,10	1.69	1 (25%)
5	FAD	I	601	-	58,58,58	1.38	8 (13%)	85,89,89	1.68	17 (20%)
10	F3S	B	304	2	0,9,9	-	-	-	-	-

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
10	F3S	J	304	2	-	-	0/3/3/3
7	TEO	A	1590	-	-	3/6/8/8	-
5	FAD	E	601	-	-	4/34/50/50	0/6/6/6
8	FES	F	302	2	-	-	0/1/1/1
12	HEM	C	1130	3,4	-	0/14/54/54	-
10	F3S	F	304	2	-	-	0/3/3/3
12	HEM	K	1130	3,4	-	8/14/54/54	-
7	TEO	I	1590	-	-	5/6/8/8	-
8	FES	J	302	2	-	-	0/1/1/1
9	SF4	F	303	2	-	-	0/6/5/5
8	FES	B	302	2	-	-	0/1/1/1
11	CBE	K	1129	-	-	3/6/19/19	0/2/2/2
11	CBE	G	1129	-	-	1/6/19/19	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	CBE	C	1129	-	-	1/6/19/19	0/2/2/2
9	SF4	B	303	2	-	-	0/6/5/5
5	FAD	A	601	-	-	1/34/50/50	0/6/6/6
12	HEM	G	1130	3,4	-	5/14/54/54	-
9	SF4	J	303	2	-	-	0/6/5/5
7	TEO	E	1590	-	-	2/6/8/8	-
5	FAD	I	601	-	-	17/34/50/50	0/6/6/6
10	F3S	B	304	2	-	-	0/3/3/3

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	G	1130	HEM	C3D-C2D	8.41	1.54	1.36
12	K	1130	HEM	C3D-C2D	8.08	1.54	1.36
12	K	1130	HEM	FE-NB	7.65	2.18	1.94
12	C	1130	HEM	C3D-C2D	7.25	1.52	1.36
5	I	601	FAD	P-O3P	4.86	1.64	1.59

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	G	1129	CBE	O7-C2-C1	8.92	119.83	109.30
11	C	1129	CBE	O7-C2-C1	8.87	119.78	109.30
11	K	1129	CBE	O7-C2-C1	8.17	118.95	109.30
5	A	601	FAD	N3A-C2A-N1A	-6.20	119.20	128.58
5	I	601	FAD	N3A-C2A-N1A	-5.84	119.75	128.58

There are no chirality outliers.

5 of 50 torsion outliers are listed below:

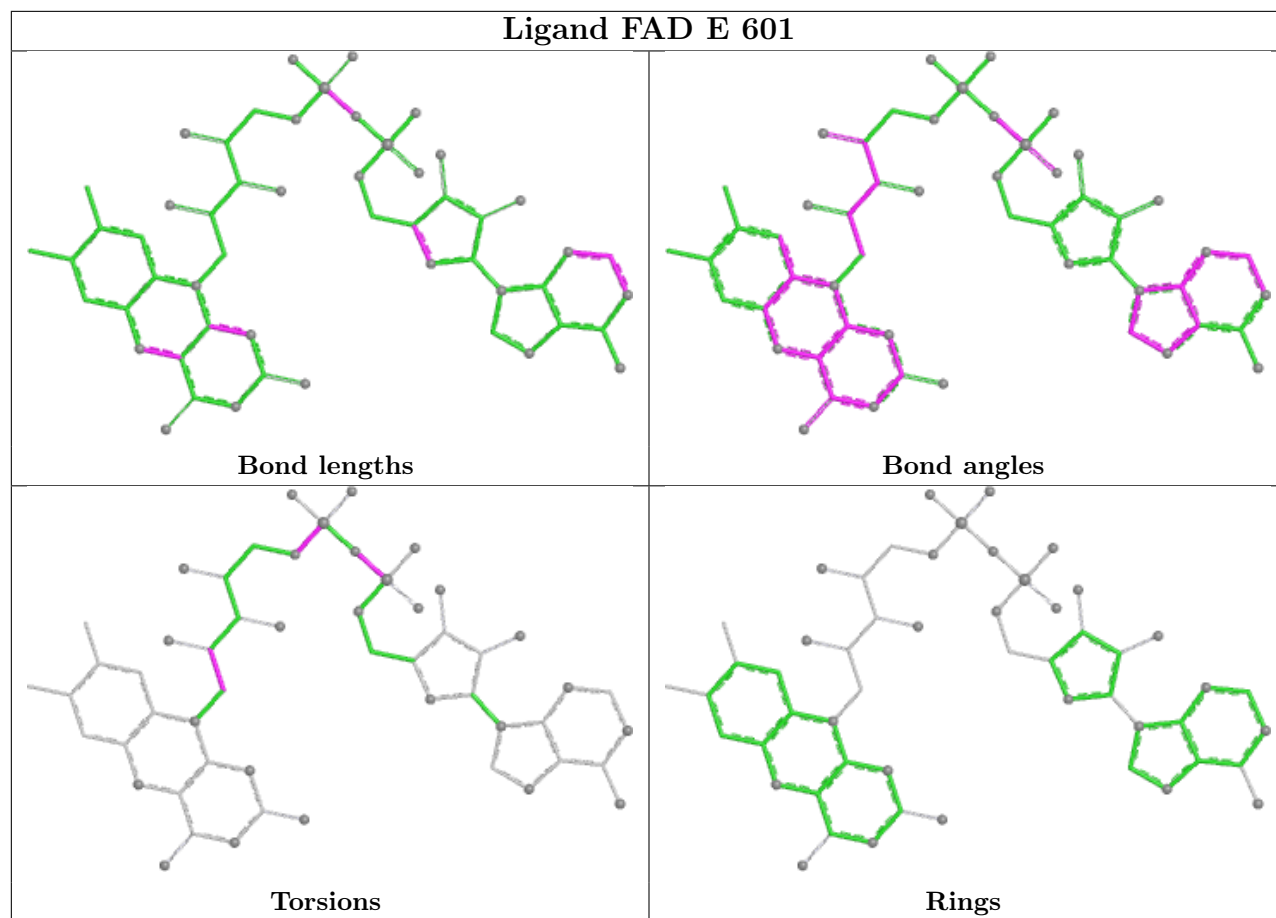
Mol	Chain	Res	Type	Atoms
5	E	601	FAD	C5'-O5'-P-O3P
5	I	601	FAD	N10-C1'-C2'-O2'
5	I	601	FAD	N10-C1'-C2'-C3'
5	I	601	FAD	C1'-C2'-C3'-O3'
5	I	601	FAD	C1'-C2'-C3'-C4'

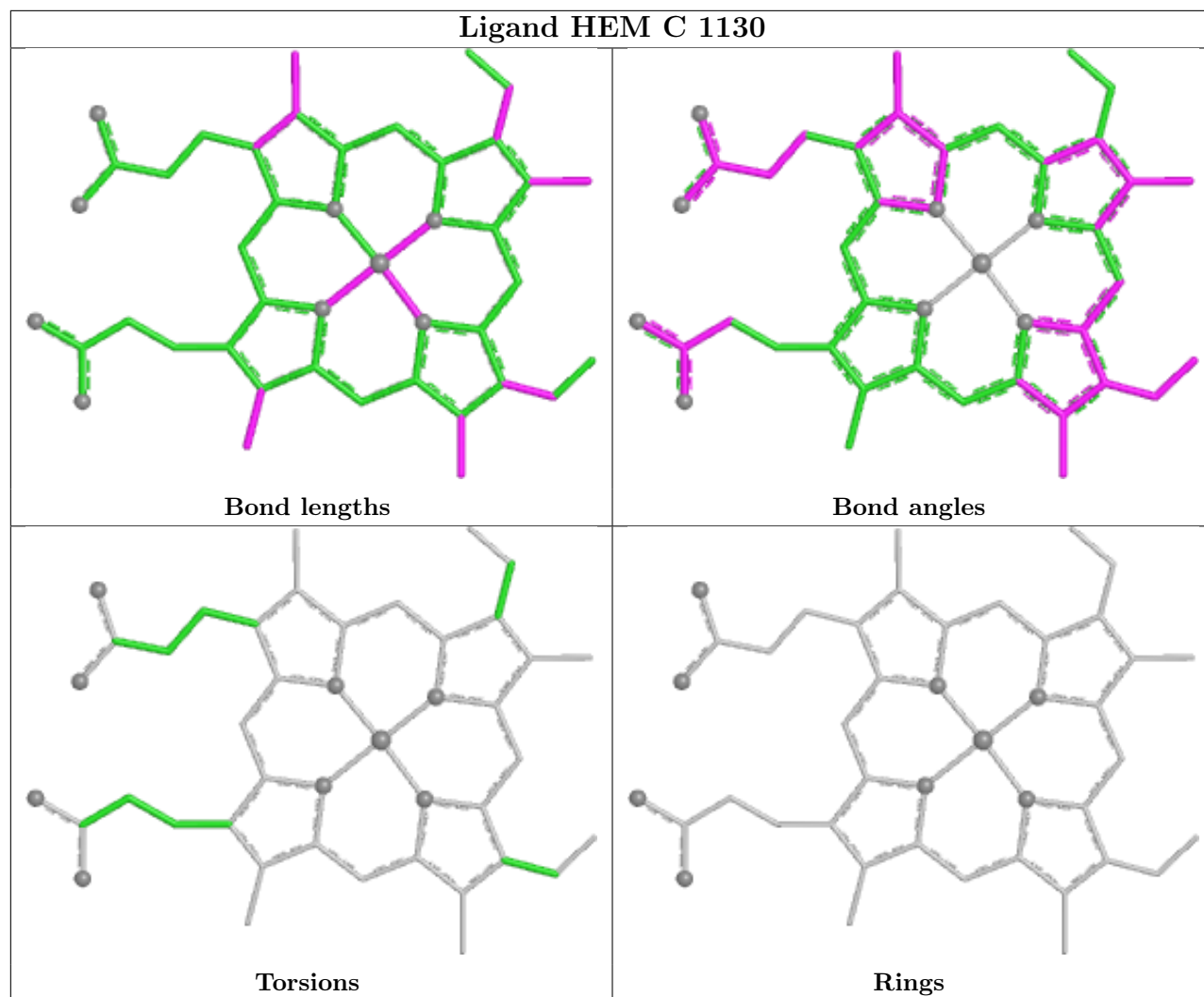
There are no ring outliers.

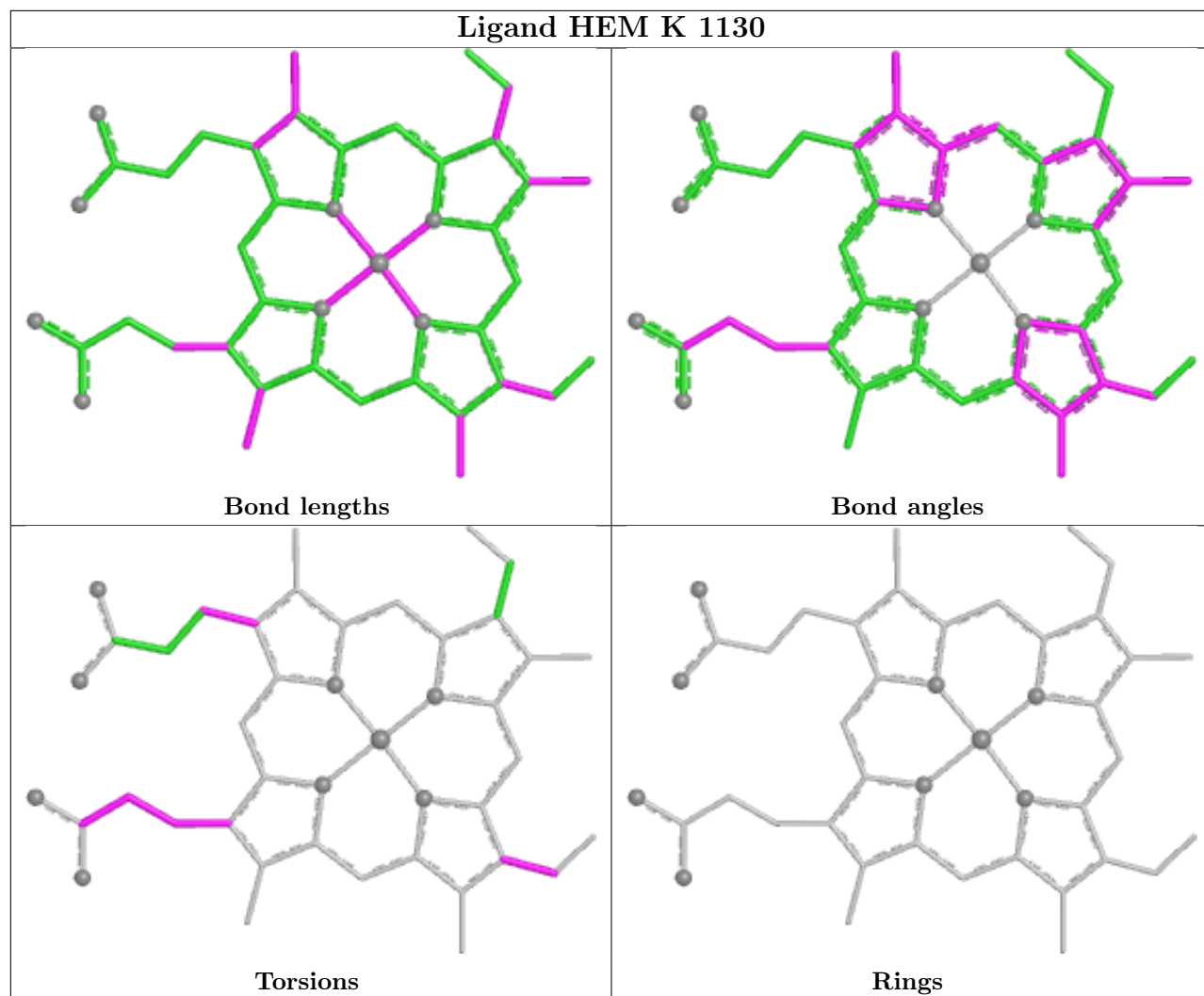
16 monomers are involved in 81 short contacts:

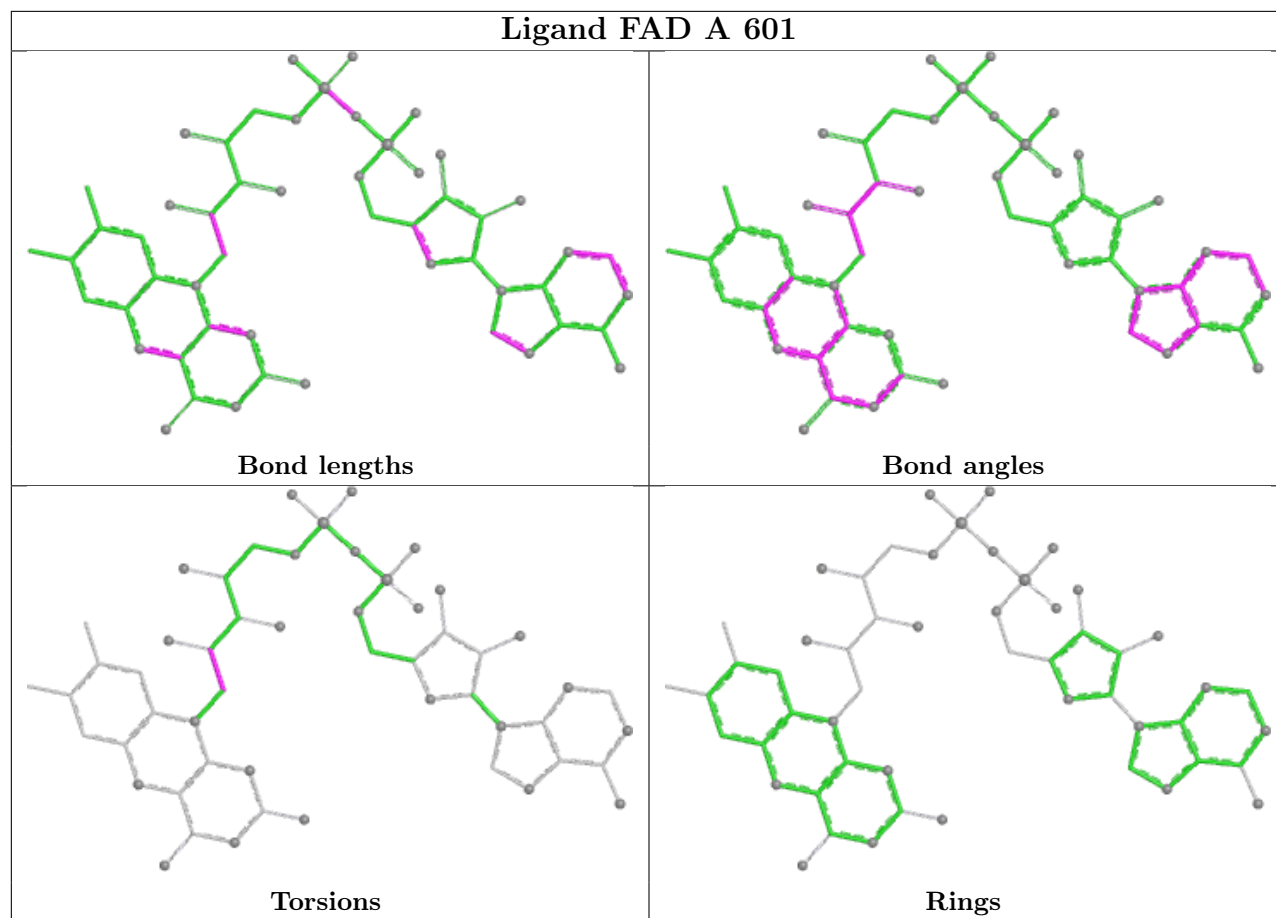
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	J	304	F3S	1	0
7	A	1590	TEO	3	0
5	E	601	FAD	10	0
12	C	1130	HEM	7	0
10	F	304	F3S	2	0
12	K	1130	HEM	12	0
7	I	1590	TEO	6	0
8	J	302	FES	1	0
11	K	1129	CBE	2	0
11	C	1129	CBE	2	0
5	A	601	FAD	10	0
12	G	1130	HEM	6	0
9	J	303	SF4	3	0
7	E	1590	TEO	5	0
5	I	601	FAD	16	0
10	B	304	F3S	1	0

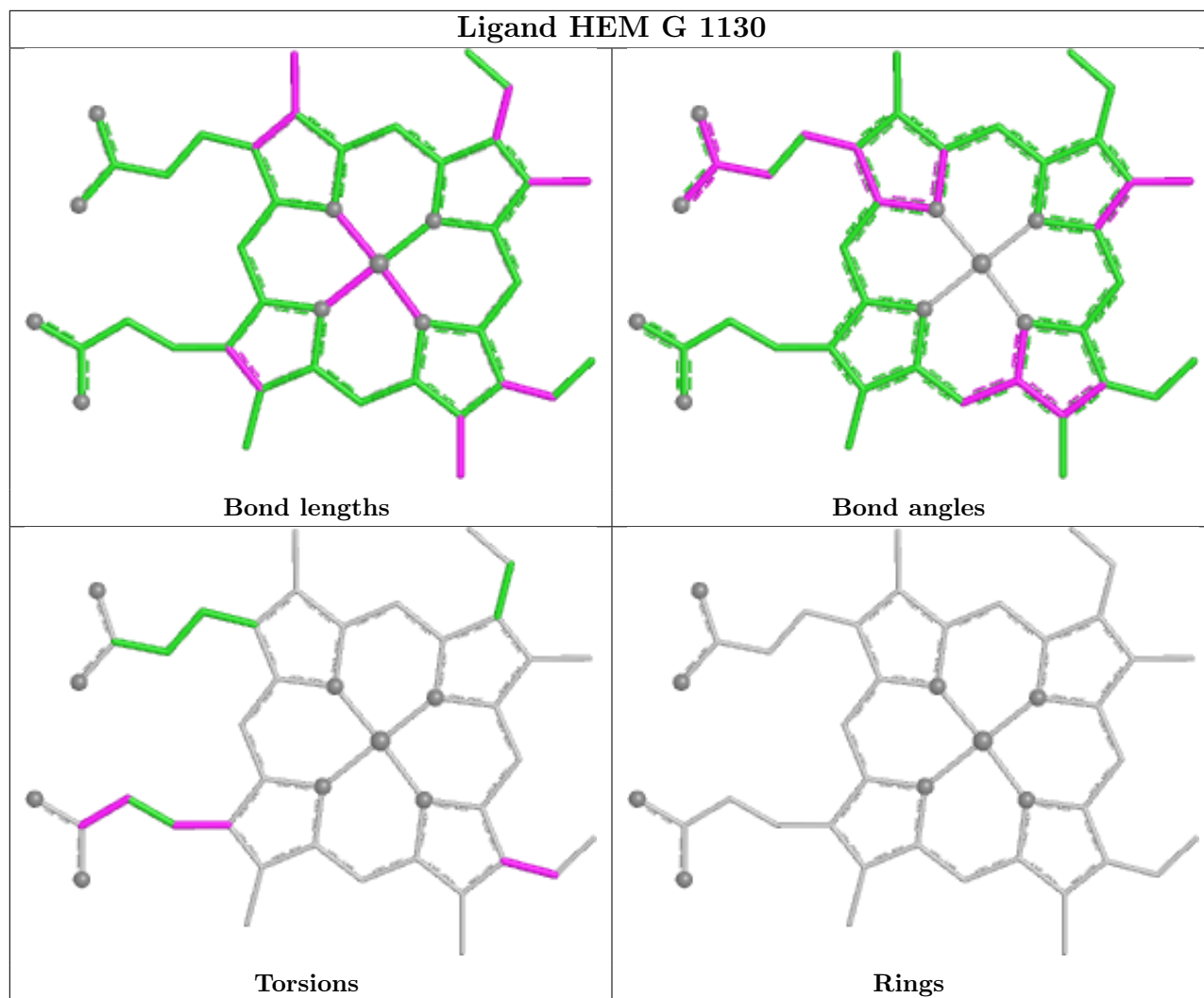
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

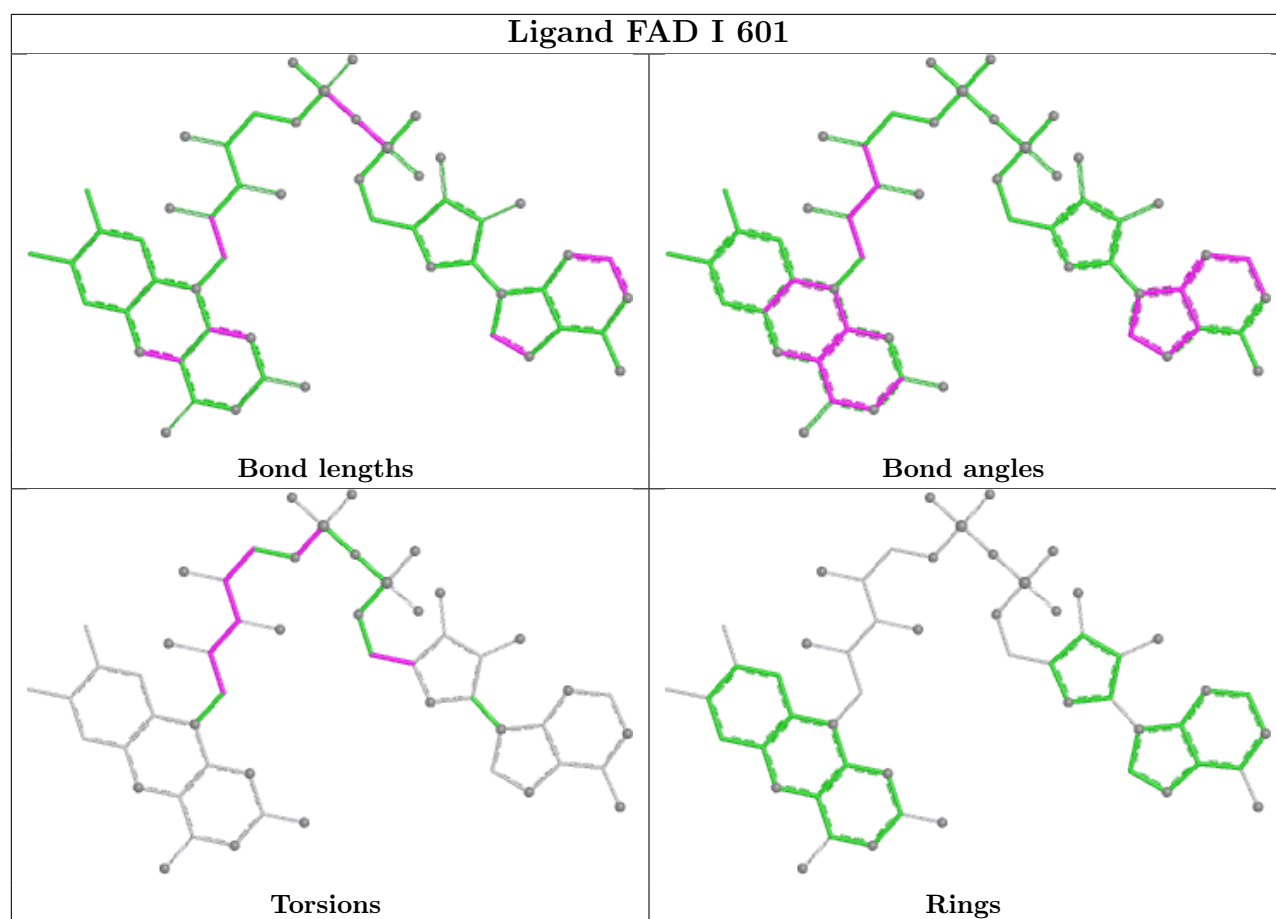












5.7 Other polymers [i](#)

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	588/588 (100%)	-0.47	4 (0%) 84 69	45, 63, 84, 97	0
1	E	588/588 (100%)	-0.40	2 (0%) 90 81	53, 72, 95, 112	0
1	I	588/588 (100%)	0.32	17 (2%) 53 35	91, 124, 168, 190	0
2	B	238/238 (100%)	-0.46	0 100 100	45, 61, 88, 107	0
2	F	238/238 (100%)	-0.29	1 (0%) 88 79	54, 72, 104, 123	0
2	J	238/238 (100%)	0.07	6 (2%) 58 39	75, 96, 164, 189	0
3	C	121/129 (93%)	-0.12	0 100 100	62, 76, 107, 120	0
3	G	121/129 (93%)	-0.02	0 100 100	71, 94, 119, 126	0
3	K	121/129 (93%)	0.14	2 (1%) 69 49	93, 118, 135, 144	0
4	D	105/115 (91%)	-0.18	0 100 100	55, 75, 109, 124	0
4	H	105/115 (91%)	-0.27	1 (0%) 79 63	63, 79, 137, 155	0
4	L	105/115 (91%)	-0.20	1 (0%) 79 63	73, 90, 142, 165	0
All	All	3156/3210 (98%)	-0.18	34 (1%) 78 61	45, 80, 147, 190	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	208	SER	3.6
1	A	62	GLU	3.1
2	J	210	MET	2.8
1	I	522	THR	2.8
1	I	585	ILE	2.7

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

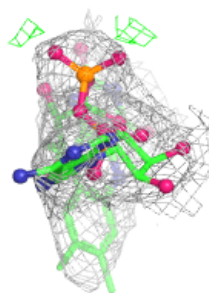
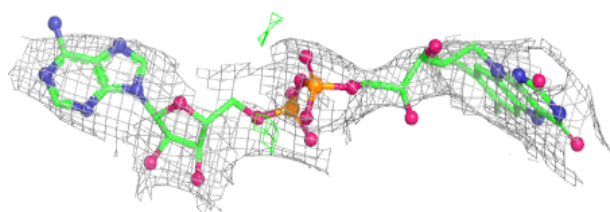
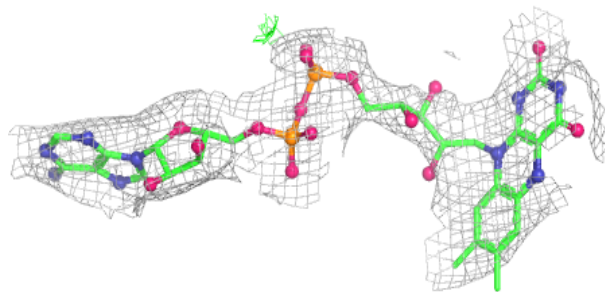
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	TEO	I	1590	9/9	0.78	0.08	109,112,114,114	0
11	CBE	K	1129	16/16	0.92	0.13	85,91,97,97	0
5	FAD	I	601	53/53	0.93	0.10	106,112,121,125	0
8	FES	J	302	4/4	0.94	0.07	108,110,116,117	0
6	NA	I	1589	1/1	0.94	0.04	53,53,53,53	0
11	CBE	G	1129	16/16	0.95	0.09	56,60,62,62	0
7	TEO	E	1590	9/9	0.95	0.07	50,52,53,55	0
7	TEO	A	1590	9/9	0.96	0.05	50,52,53,53	0
11	CBE	C	1129	16/16	0.96	0.07	53,55,56,56	0
12	HEM	K	1130	43/43	0.96	0.09	50,54,72,82	0
5	FAD	E	601	53/53	0.97	0.07	46,61,71,73	0
6	NA	A	1589	1/1	0.97	0.05	27,27,27,27	0
6	NA	E	1589	1/1	0.97	0.05	45,45,45,45	0
5	FAD	A	601	53/53	0.98	0.06	38,42,53,54	0
12	HEM	C	1130	43/43	0.98	0.07	40,48,62,67	0
12	HEM	G	1130	43/43	0.98	0.07	55,61,71,75	0
10	F3S	J	304	7/7	0.98	0.06	88,90,92,93	0
10	F3S	F	304	7/7	0.99	0.05	64,69,72,75	0
9	SF4	J	303	8/8	0.99	0.04	83,87,90,91	0
8	FES	F	302	4/4	1.00	0.03	54,55,56,58	0
10	F3S	B	304	7/7	1.00	0.03	49,54,58,59	0
8	FES	B	302	4/4	1.00	0.03	38,41,43,44	0
9	SF4	B	303	8/8	1.00	0.04	38,40,40,41	0
9	SF4	F	303	8/8	1.00	0.03	55,58,59,59	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.

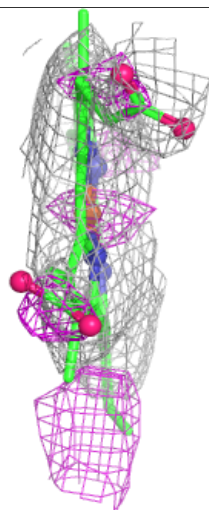
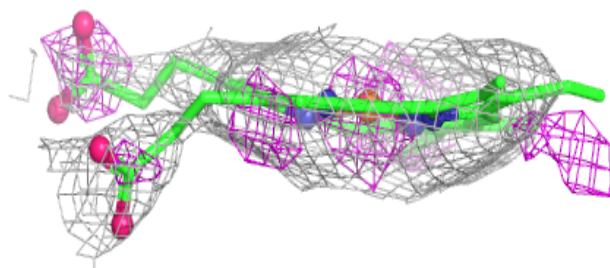
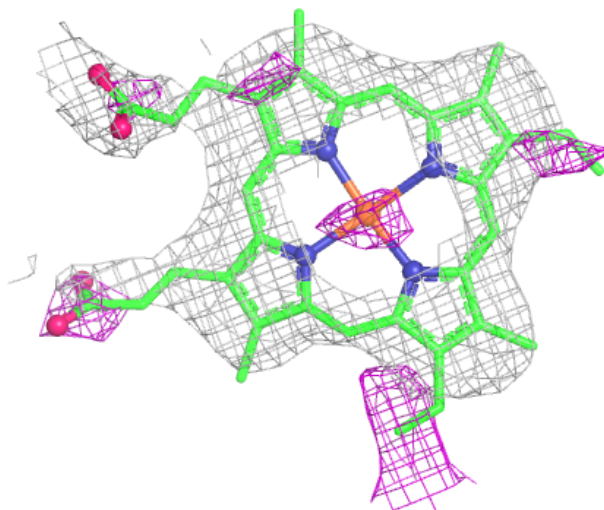
Electron density around FAD I 601:

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



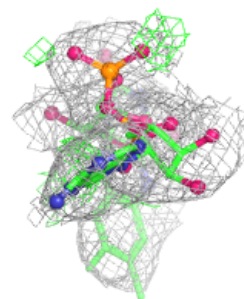
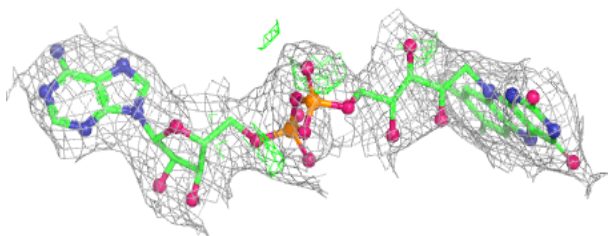
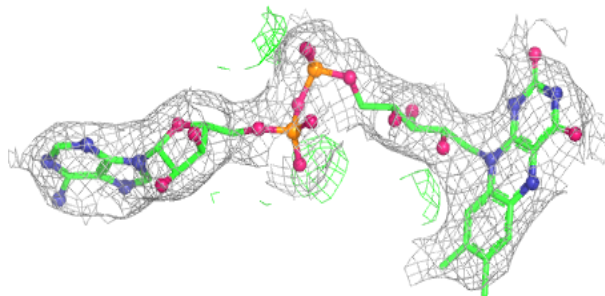
Electron density around HEM K 1130:

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

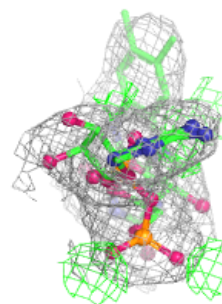
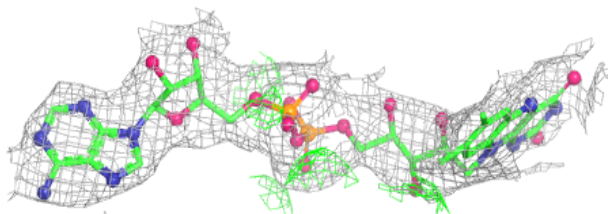
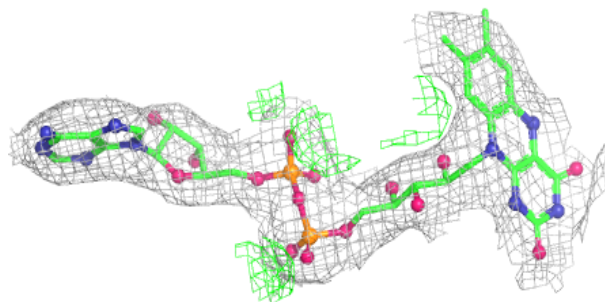


Electron density around FAD E 601:

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

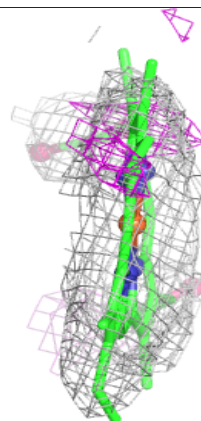
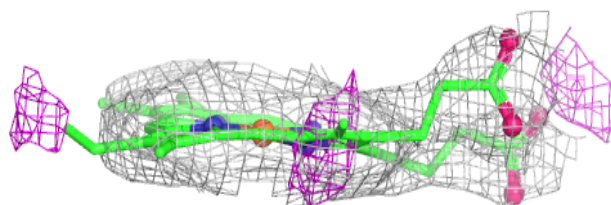
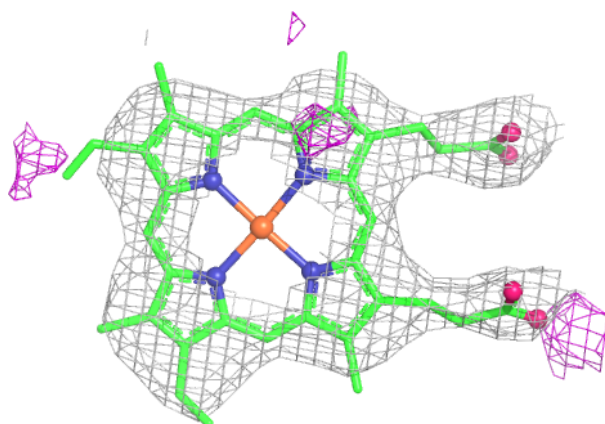
**Electron density around FAD A 601:**

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

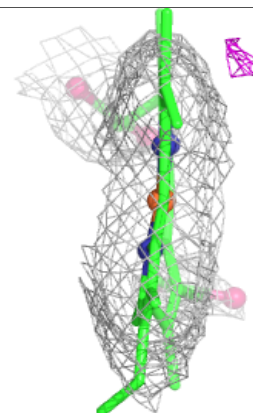
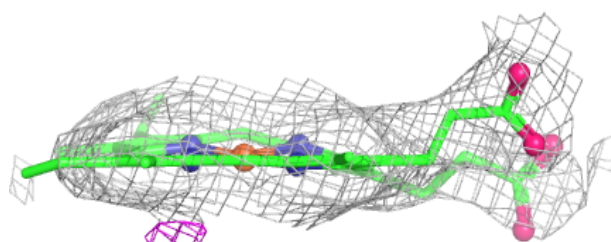
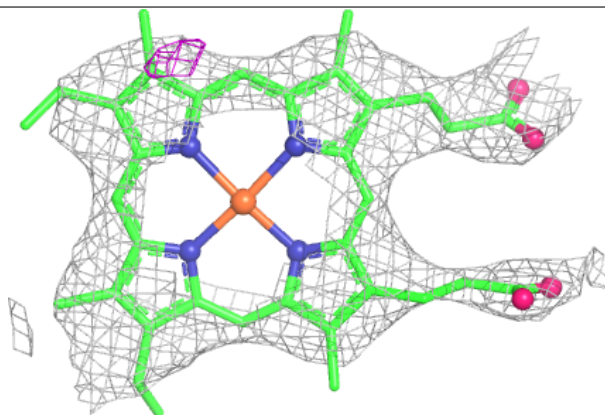


Electron density around HEM C 1130:

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

**Electron density around HEM G 1130:**

$2mF_o-DF_c$ (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.