W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Sep 25, 2023 – 02:40 AM EDT

PDB ID	:	5VPN
Title	:	E. coli Quinol fumarate reductase FrdA E245Q mutation
Authors	:	Starbird, C.A.; Maklashina, E.; Sharma, P.; Qualls-Histed, S.; Cecchini, G.; Iverson, T.M.
Deposited on	:	2017-05-05
Resolution	:	4.22 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

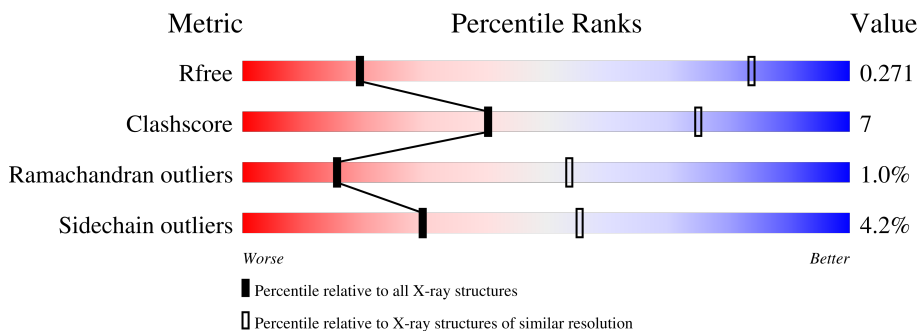|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 4.22 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	Percentile Ranks	Value
Rfree		0.271
Clashscore		7
Ramachandran outliers		1.0%
Sidechain outliers		4.2%

Worse   *Better*

▌ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	1008 (4.66-3.78)
Clashscore	141614	1047 (4.62-3.80)
Ramachandran outliers	138981	1003 (4.62-3.80)
Sidechain outliers	138945	1010 (4.66-3.78)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	585	83% 15% ••
1	E	585	82% 15% •
2	B	243	75% 23% •
2	F	243	77% 21% •
3	C	130	86% 12% •
3	G	130	77% 22% •
4	D	119	82% 16% ••

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Mol	Chain	Length	Quality of chain
4	H	119	82% 16% ·

2 Entry composition ⓘ

There are 8 unique types of molecules in this entry. The entry contains 16845 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 Fumarate reductase flavoprotein subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	577	Total 4448	C 2775	N 803	O 839	S 31	0	0	0
1	E	585	Total 4509	C 2813	N 815	O 850	S 31	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	245	GLN	GLU	engineered mutation	UNP P00363
E	245	GLN	GLU	engineered mutation	UNP P00363

- Molecule 2 is a protein called Succinate dehydrogenase iron-sulfur subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	243	Total 1888	C 1189	N 323	O 357	S 19	0	0	0
2	F	243	Total 1888	C 1189	N 323	O 357	S 19	0	0	0

- Molecule 3 is a protein called Fumarate reductase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	130	Total 1058	C 720	N 166	O 169	S 3	0	0	0
3	G	130	Total 1058	C 720	N 166	O 169	S 3	0	0	0

- Molecule 4 is a protein called Fumarate reductase subunit D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	119	Total 926	C 626	N 151	O 142	S 7	0	0	0

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WORLDWIDE
wwPDB
PROTEIN DATA BANK

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	H	119	926	626	151	142	7	0	0	0

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).
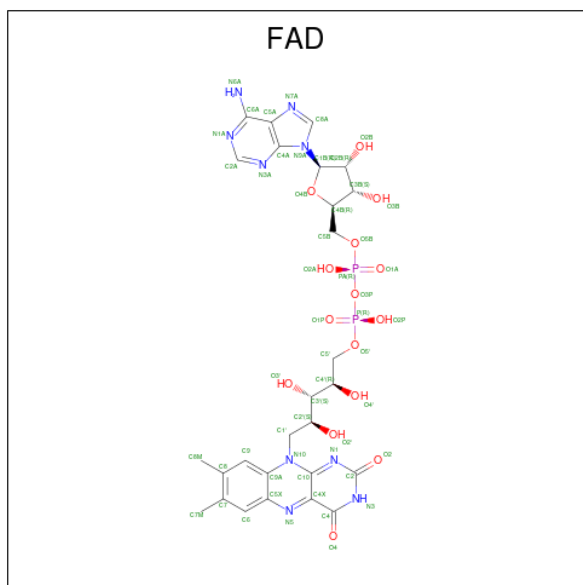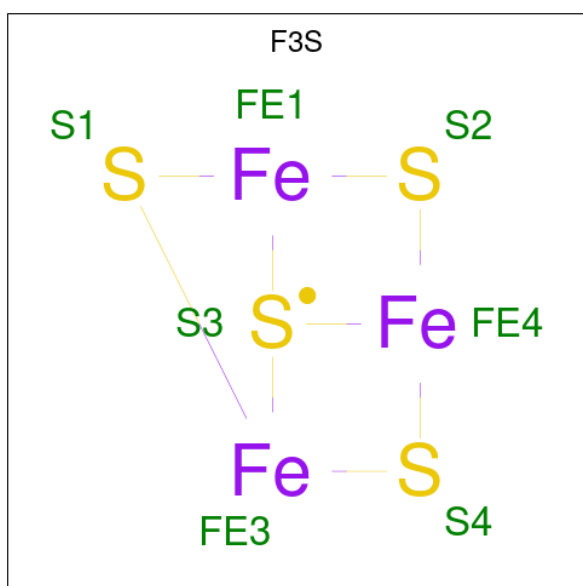

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	53	27	9	15	2	0	0
5	E	1	53	27	9	15	2	0	0

- Molecule 6 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).

FES

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

• Molecule 7 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe_3S_4).

F3S

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

- Molecule 8 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).
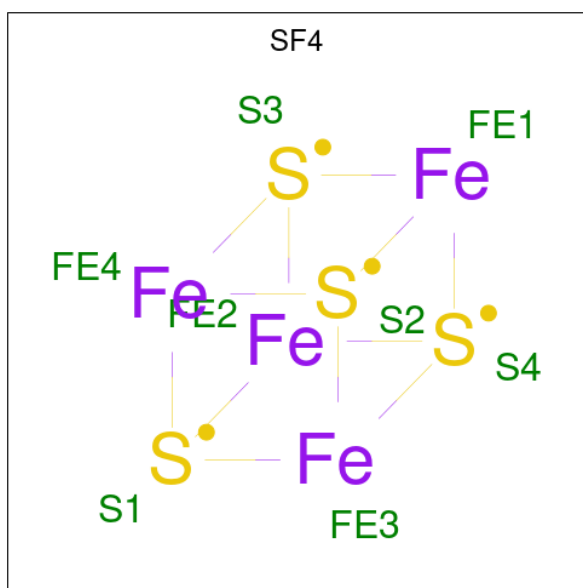
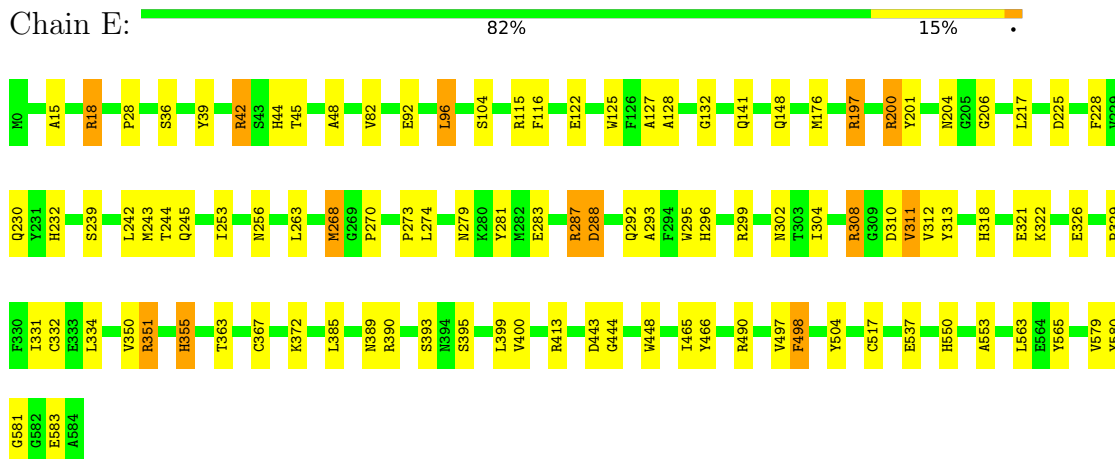| Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total 8	Fe 4	S 4	0	0
8	F	1	Total 8	Fe 4	S 4	0	0

3 Residue-property plots ⓘ

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. 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. 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.
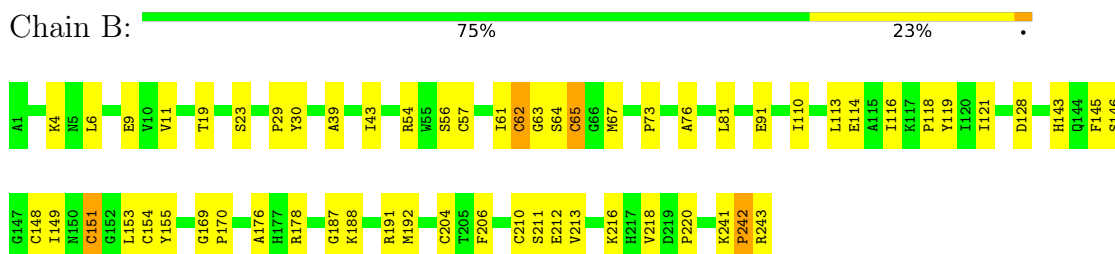
• Molecule 1: Fumarate reductase flavoprotein subunit
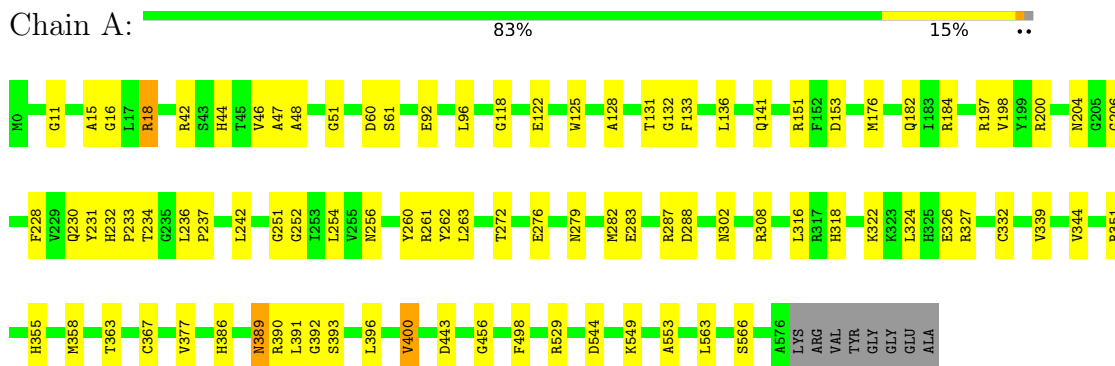
Chain A:

• Molecule 1: Fumarate reductase flavoprotein subunit
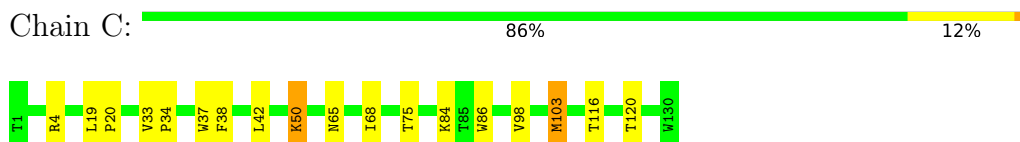
Chain E:

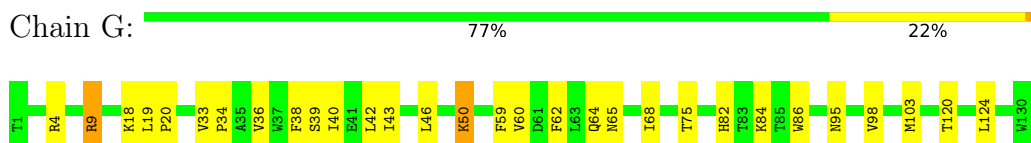• Molecule 2: Succinate dehydrogenase iron-sulfur subunit

Chain B:

• Molecule 2: Succinate dehydrogenase iron-sulfur subunit
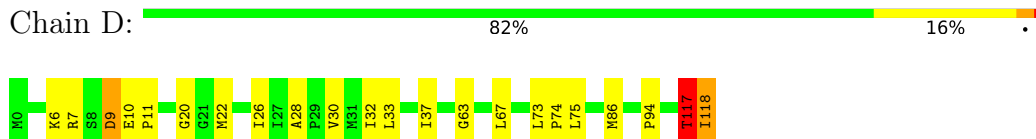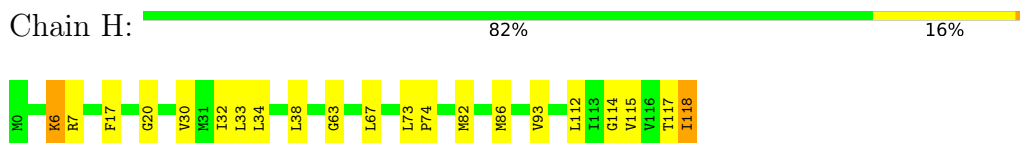
Chain F:
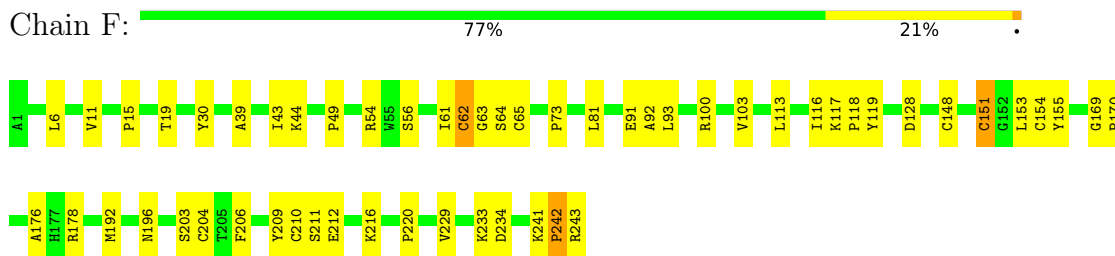
• Molecule 3: Fumarate reductase subunit C

Chain C:

• Molecule 3: Fumarate reductase subunit C

Chain G:

• Molecule 4: Fumarate reductase subunit D

Chain D:

• Molecule 4: Fumarate reductase subunit D

Chain H:

4　Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	133.56Å　138.13Å　220.08Å 90.00°　　90.00°　　90.00°	Depositor
Resolution (Å)	22.96　–　4.22 50.29　–　4.21	Depositor EDS
% Data completeness (in resolution range)	95.9 (22.96-4.22) 80.5 (50.29-4.21)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.24 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.215　,　0.270 0.215　,　0.271	Depositor DCC
R_{free} test set	1437 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	135.1	Xtriage
Anisotropy	0.680	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 144.0	EDS
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.017 for k,h,-l	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	16845	wwPDB-VP
Average B, all atoms (Å^2)	214.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.37% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: F3S, SF4, FES, 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	0.26	0/4540	0.45	0/6139
1	E	0.27	0/4602	0.46	0/6221
2	B	0.27	0/1931	0.44	0/2617
2	F	0.27	0/1931	0.45	0/2617
3	C	0.28	0/1094	0.43	0/1496
3	G	0.28	0/1094	0.47	0/1496
4	D	0.27	0/956	0.41	0/1303
4	H	0.30	0/956	0.42	0/1303
All	All	0.27	0/17104	0.45	0/23192

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	4448	0	4337	57	0
1	E	4509	0	4398	75	0
2	B	1888	0	1848	37	0
2	F	1888	0	1847	34	0
3	C	1058	0	1108	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1058	0	1108	24	0
4	D	926	0	971	17	0
4	H	926	0	971	15	0
5	A	53	0	31	5	0
5	E	53	0	31	11	0
6	B	4	0	0	0	0
6	F	4	0	0	0	0
7	B	7	0	0	0	0
7	F	7	0	0	0	0
8	B	8	0	0	0	0
8	F	8	0	0	0	0
All	All	16845	0	16650	240	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 240 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:96:LEU:HD11	1:E:400:VAL:HG11	1.54	0.87
3:G:65:ASN:HB3	3:G:68:ILE:H	1.50	0.76
2:B:62:CYS:SG	2:B:63:GLY:N	2.60	0.74
1:E:28:PRO:HA	1:E:148:GLN:HE21	1.52	0.74
1:E:176:MET:HB3	3:G:4:ARG:HD3	1.69	0.74

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	575/585 (98%)	540 (94%)	31 (5%)	4 (1%)	22	62

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	583/585 (100%)	538 (92%)	37 (6%)	8 (1%)	11	47
2	B	241/243 (99%)	225 (93%)	13 (5%)	3 (1%)	13	50
2	F	241/243 (99%)	230 (95%)	8 (3%)	3 (1%)	13	50
3	C	128/130 (98%)	122 (95%)	6 (5%)	0	100	100
3	G	128/130 (98%)	121 (94%)	6 (5%)	1 (1%)	19	60
4	D	117/119 (98%)	110 (94%)	6 (5%)	1 (1%)	17	56
4	H	117/119 (98%)	111 (95%)	5 (4%)	1 (1%)	17	56
All	All	2130/2154 (99%)	1997 (94%)	112 (5%)	21 (1%)	15	54

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	PRO
1	E	579	VAL
1	A	261	ARG
2	B	242	PRO
1	E	329	PRO

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	460/465 (99%)	450 (98%)	10 (2%)	52	70
1	E	465/465 (100%)	442 (95%)	23 (5%)	25	52
2	B	205/205 (100%)	194 (95%)	11 (5%)	22	50
2	F	205/205 (100%)	192 (94%)	13 (6%)	18	45
3	C	111/111 (100%)	108 (97%)	3 (3%)	44	66
3	G	111/111 (100%)	107 (96%)	4 (4%)	35	60
4	D	97/97 (100%)	92 (95%)	5 (5%)	23	50
4	H	97/97 (100%)	93 (96%)	4 (4%)	30	56
All	All	1751/1756 (100%)	1678 (96%)	73 (4%)	30	55

5 of 73 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	151	CYS
4	H	86	MET
2	F	203	SER
3	G	9	ARG
4	D	7	ARG

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

Mol	Chain	Res	Type
1	E	230	GLN
1	E	232	HIS
3	G	95	ASN
1	E	389	ASN
1	E	204	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

8 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	$\#\lvert Z\rvert > 2$	Counts	RMSZ	$\#\lvert Z\rvert > 2$
5	FAD	A	601	-	53,58,58	0.46	0	68,89,89	0.54	2 (2%)
6	FES	B	301	-	0,4,4	-	-	-		
8	SF4	F	303	2	0,12,12	-	-	-		
8	SF4	B	303	-	0,12,12	-	-	-		
6	FES	F	301	-	0,4,4	-	-	-		
7	F3S	B	302	-	0,9,9	-	-	-		
7	F3S	F	302	-	0,9,9	-	-	-		
5	FAD	E	601	-	53,58,58	0.47	0	68,89,89	0.56	2 (2%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	FAD	A	601	-	-	14/30/50/50	0/6/6/6
6	FES	B	301	-	-	-	0/1/1/1
8	SF4	F	303	2	-	-	0/6/5/5
8	SF4	B	303	-	-	-	0/6/5/5
6	FES	F	301	-	-	-	0/1/1/1
7	F3S	B	302	-	-	-	0/3/3/3
7	F3S	F	302	-	-	-	0/3/3/3
5	FAD	E	601	-	-	15/30/50/50	0/6/6/6

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	601	FAD	P-O3P-PA	-2.58	123.97	132.83
5	E	601	FAD	P-O3P-PA	-2.49	124.29	132.83
5	E	601	FAD	C5A-C6A-N6A	2.25	123.77	120.35
5	A	601	FAD	C5A-C6A-N6A	2.24	123.76	120.35

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	601	FAD	N10-C1'-C2'-O2'
5	A	601	FAD	N10-C1'-C2'-C3'
5	A	601	FAD	C2'-C3'-C4'-O4'

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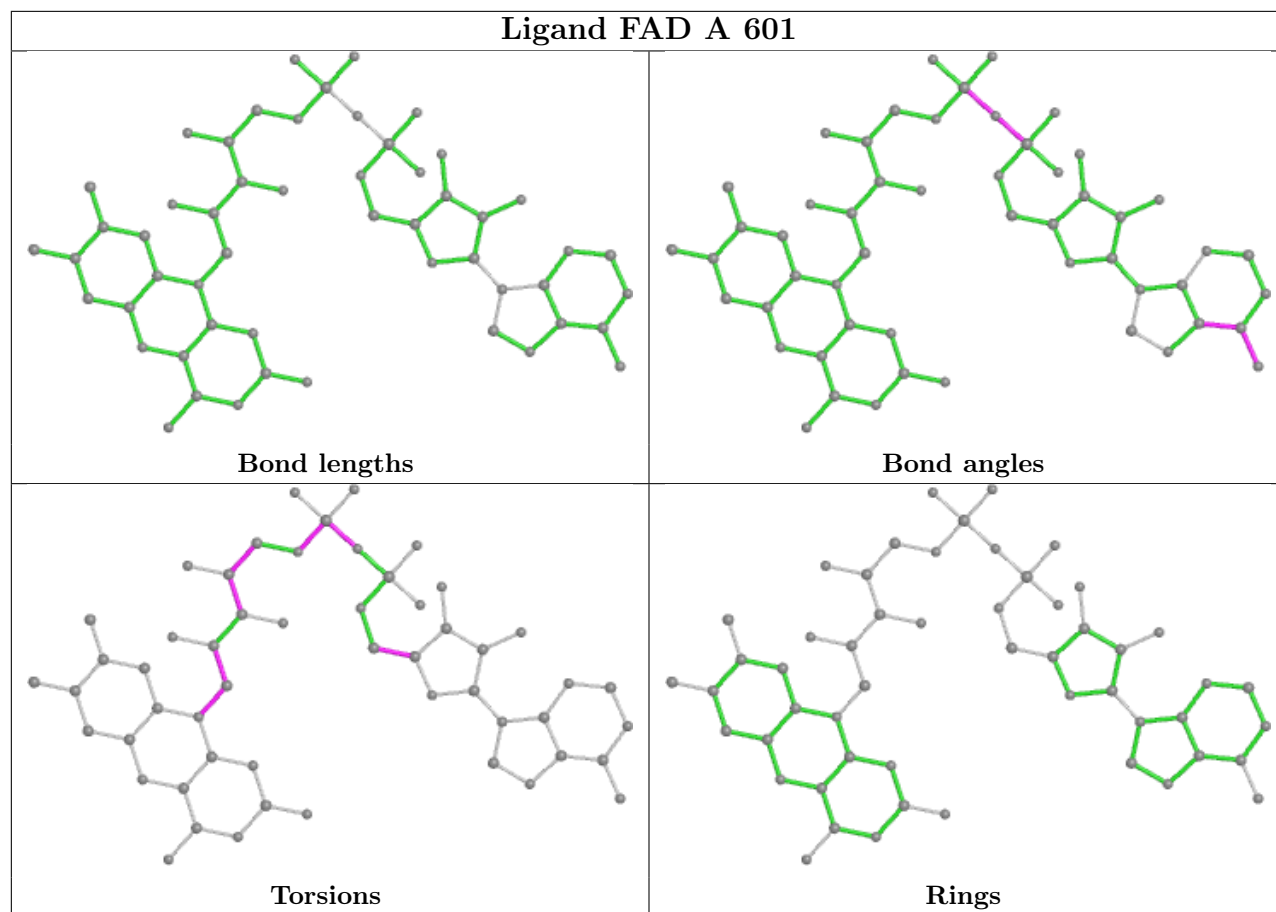| Mol	Chain	Res	Type	Atoms
5	A	601	FAD	C2'-C3'-C4'-C5'
5	A	601	FAD	O3'-C3'-C4'-O4'

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	601	FAD	5	0
5	E	601	FAD	11	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 then 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 FAD A 601

Bond lengths

Bond angles

Torsions

Rings

Ligand FAD E 601

Bond lengths

Bond angles

Torsions

Rings
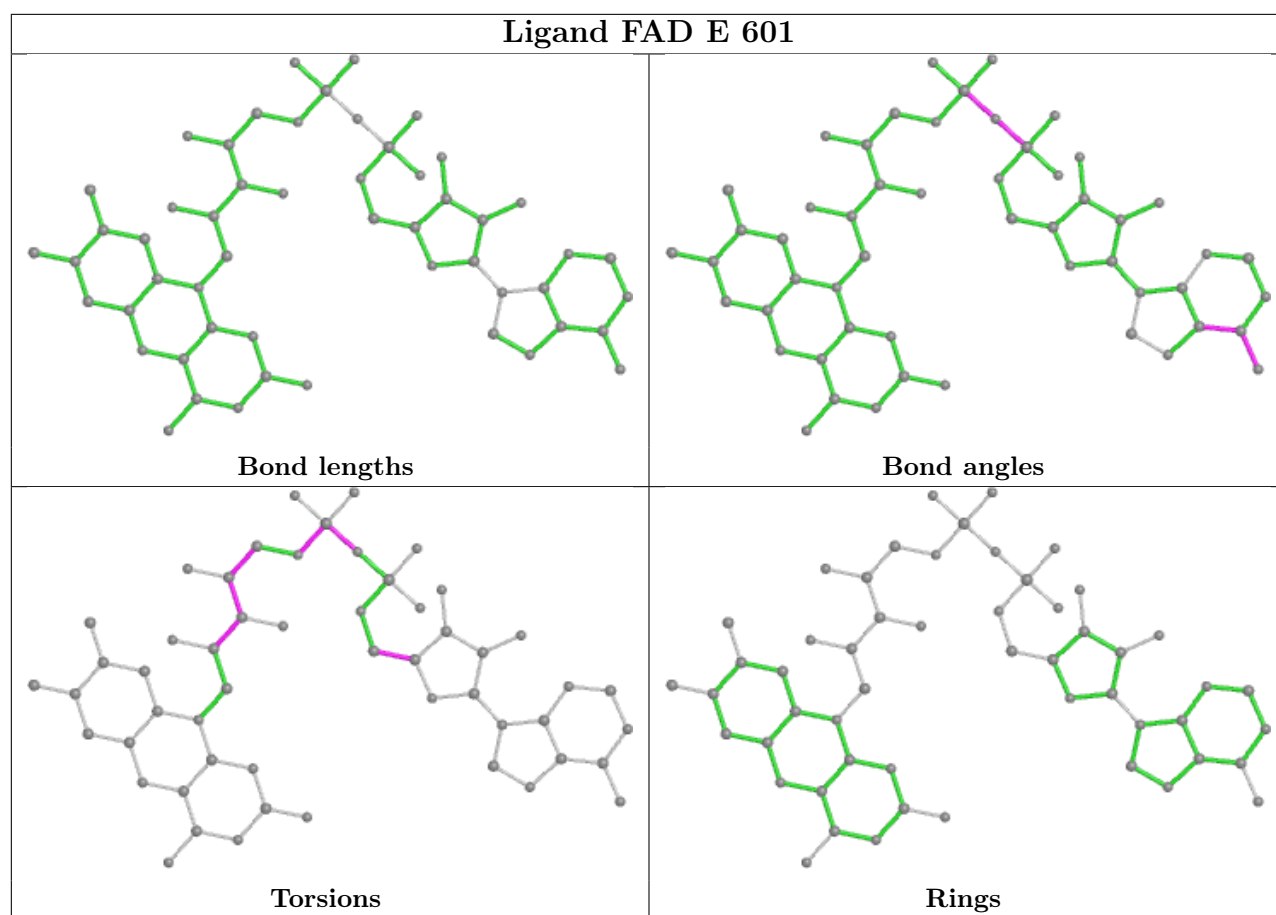
5.7 Other polymers (i)

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

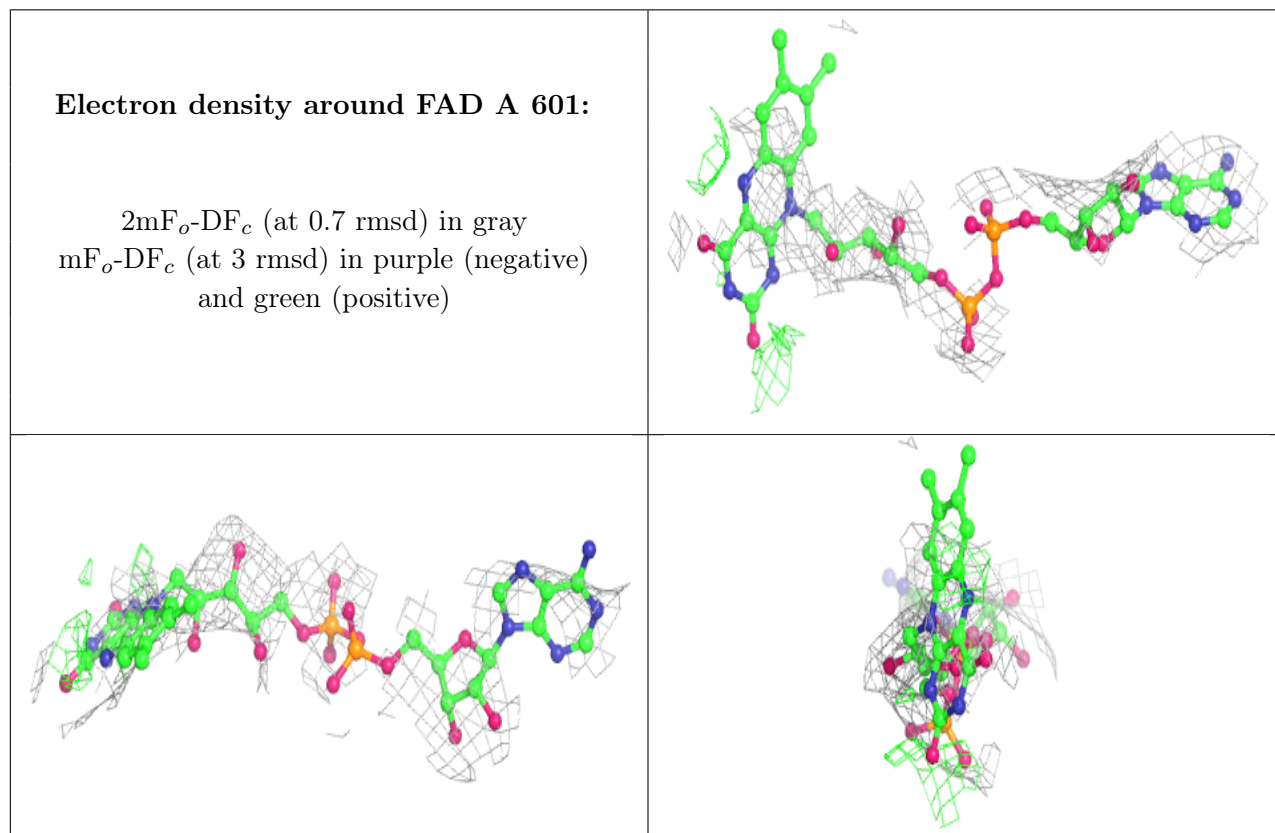Unable to reproduce the depositors R factor - this section is therefore empty.
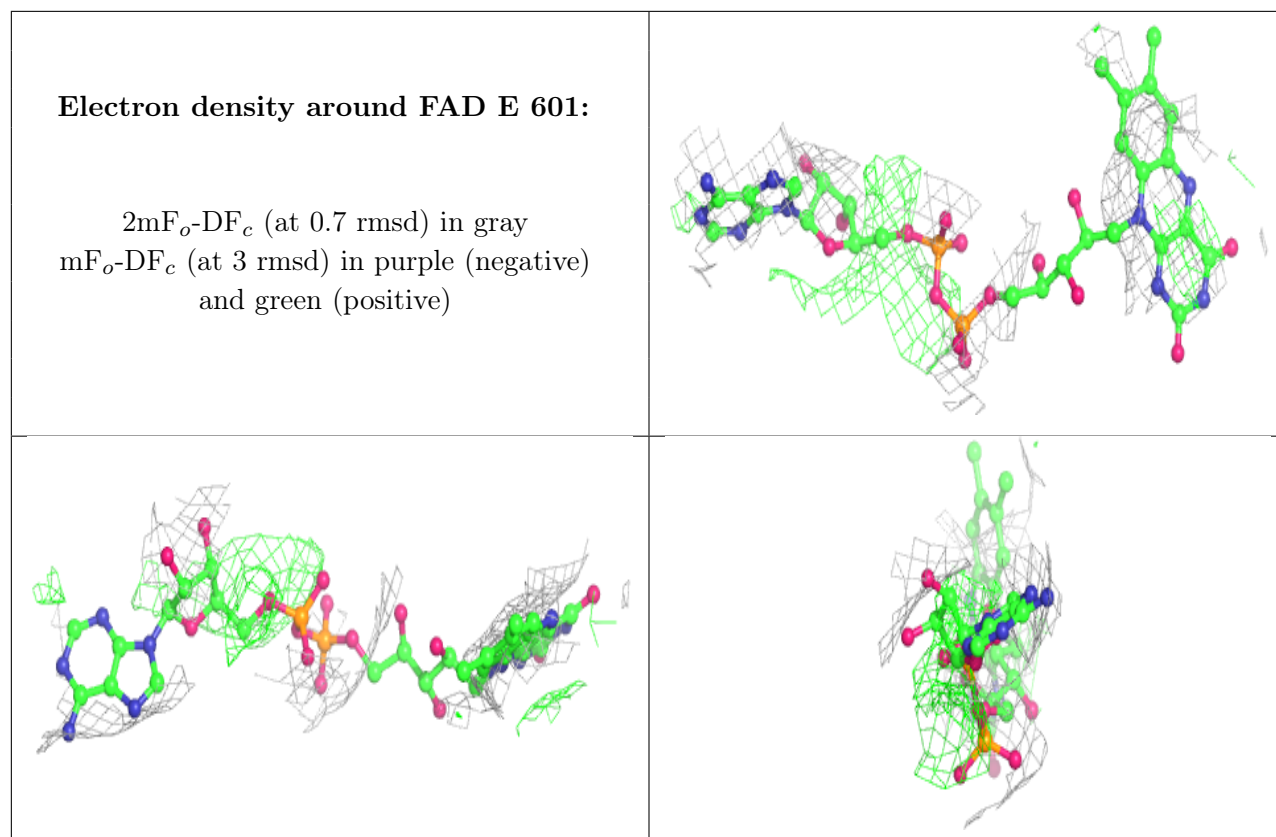
6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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 A 601:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (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)

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.