



Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 12:34 am BST

PDB ID : 6EFV
Title : The NADPH-dependent sulfite reductase flavoprotein adopts an extended conformation that is unique to this diflavin reductase
Authors : Tavorieri, A.M.; Askenasy, I.; Murray, D.T.; Pennington, J.M.; Stroupe, M.E.
Deposited on : 2018-08-17
Resolution : 2.34 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The 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

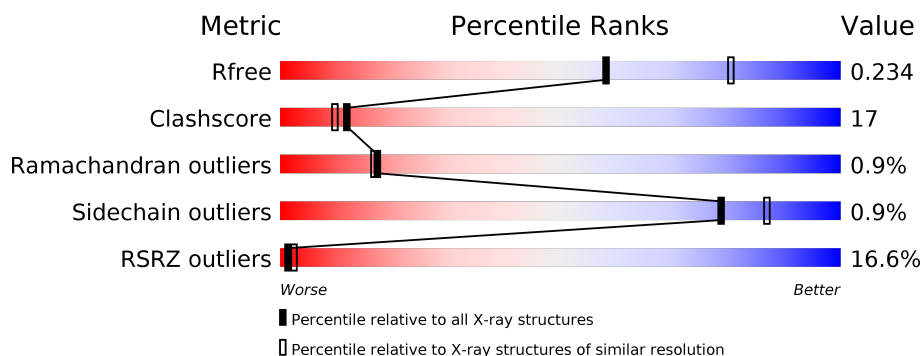
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	2096 (2.36-2.32)
Clashscore	141614	2193 (2.36-2.32)
Ramachandran outliers	138981	2159 (2.36-2.32)
Sidechain outliers	138945	2160 (2.36-2.32)
RSRZ outliers	127900	2067 (2.36-2.32)

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	569	<div> <div>15%</div> <div>69%</div> <div>23%</div> <div>7%</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	SO4	A	607	-	-	-	X
4	SO4	A	608	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	CXS	A	610	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4766 atoms, of which 36 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 Sulfite reductase [NADPH] flavoprotein alpha-component.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	530	Total	C	N	O	S	0	10	0
			4241	2684	735	815	7			

There are 45 discrepancies between the modelled and reference sequences:

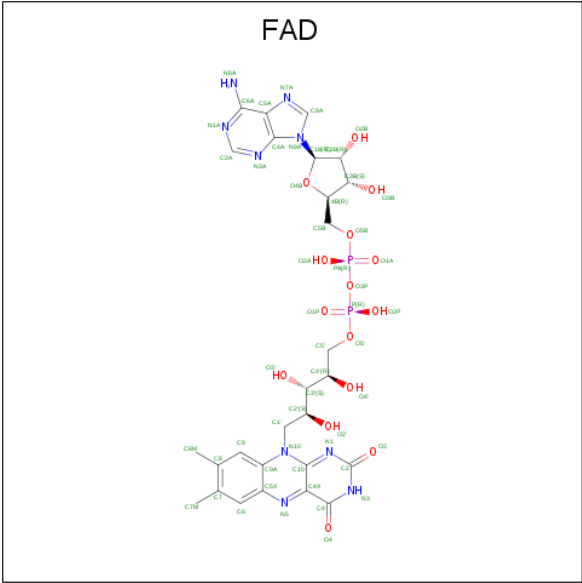
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	MET	-	expression tag	UNP W8SX42
A	26	GLY	-	expression tag	UNP W8SX42
A	27	GLY	-	expression tag	UNP W8SX42
A	28	SER	-	expression tag	UNP W8SX42
A	29	HIS	-	expression tag	UNP W8SX42
A	30	HIS	-	expression tag	UNP W8SX42
A	31	HIS	-	expression tag	UNP W8SX42
A	32	HIS	-	expression tag	UNP W8SX42
A	33	HIS	-	expression tag	UNP W8SX42
A	34	HIS	-	expression tag	UNP W8SX42
A	35	GLY	-	expression tag	UNP W8SX42
A	36	MET	-	expression tag	UNP W8SX42
A	37	ALA	-	expression tag	UNP W8SX42
A	38	SER	-	expression tag	UNP W8SX42
A	39	MET	-	expression tag	UNP W8SX42
A	40	THR	-	expression tag	UNP W8SX42
A	41	GLY	-	expression tag	UNP W8SX42
A	42	GLY	-	expression tag	UNP W8SX42
A	43	ASN	-	expression tag	UNP W8SX42
A	44	ASN	-	expression tag	UNP W8SX42
A	45	MET	-	expression tag	UNP W8SX42
A	46	GLY	-	expression tag	UNP W8SX42
A	47	ARG	-	expression tag	UNP W8SX42
A	48	ASP	-	expression tag	UNP W8SX42
A	49	LEU	-	expression tag	UNP W8SX42
A	50	TYR	-	expression tag	UNP W8SX42
A	51	ASP	-	expression tag	UNP W8SX42

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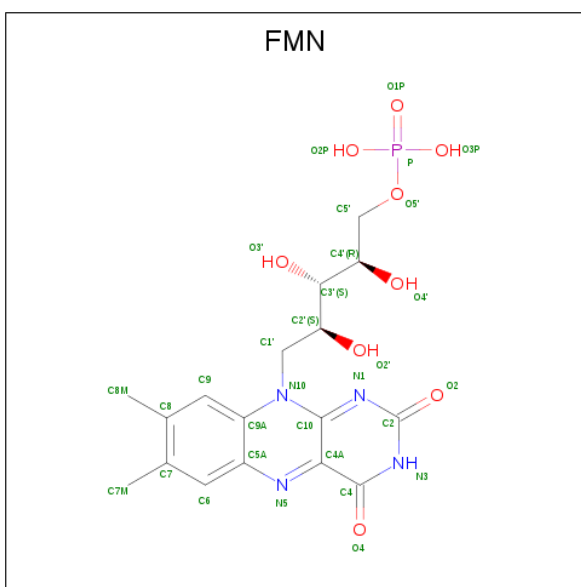
Chain	Residue	Modelled	Actual	Comment	Reference
A	52	ASP	-	expression tag	UNP W8SX42
A	53	ASP	-	expression tag	UNP W8SX42
A	54	ASP	-	expression tag	UNP W8SX42
A	55	LYS	-	expression tag	UNP W8SX42
A	56	ASP	-	expression tag	UNP W8SX42
A	57	ARG	-	expression tag	UNP W8SX42
A	58	TRP	-	expression tag	UNP W8SX42
A	59	GLY	-	expression tag	UNP W8SX42
A	60	SER	-	expression tag	UNP W8SX42
A	61	GLU	-	expression tag	UNP W8SX42
A	62	LEU	-	expression tag	UNP W8SX42
A	63	GLU	-	expression tag	UNP W8SX42
A	?	-	ALA	deletion	UNP W8SX42
A	?	-	ALA	deletion	UNP W8SX42
A	?	-	PRO	deletion	UNP W8SX42
A	?	-	SER	deletion	UNP W8SX42
A	?	-	GLN	deletion	UNP W8SX42
A	?	-	SER	deletion	UNP W8SX42

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



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

- Molecule 3 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 4 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



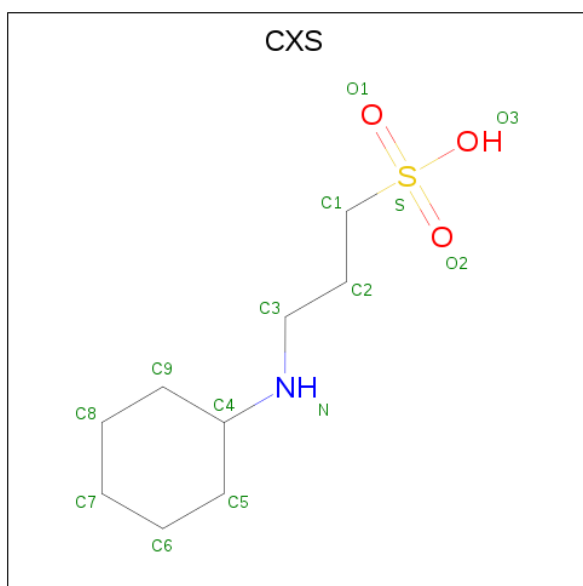
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 5 is 3-CYCLOHEXYL-1-PROPYLSULFONIC ACID (three-letter code: CXS) (formula: $C_9H_{19}NO_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	S	0	0
			32	9	18	1	3	1		
5	A	1	Total	C	H	N	O	S	0	0
			32	9	18	1	3	1		

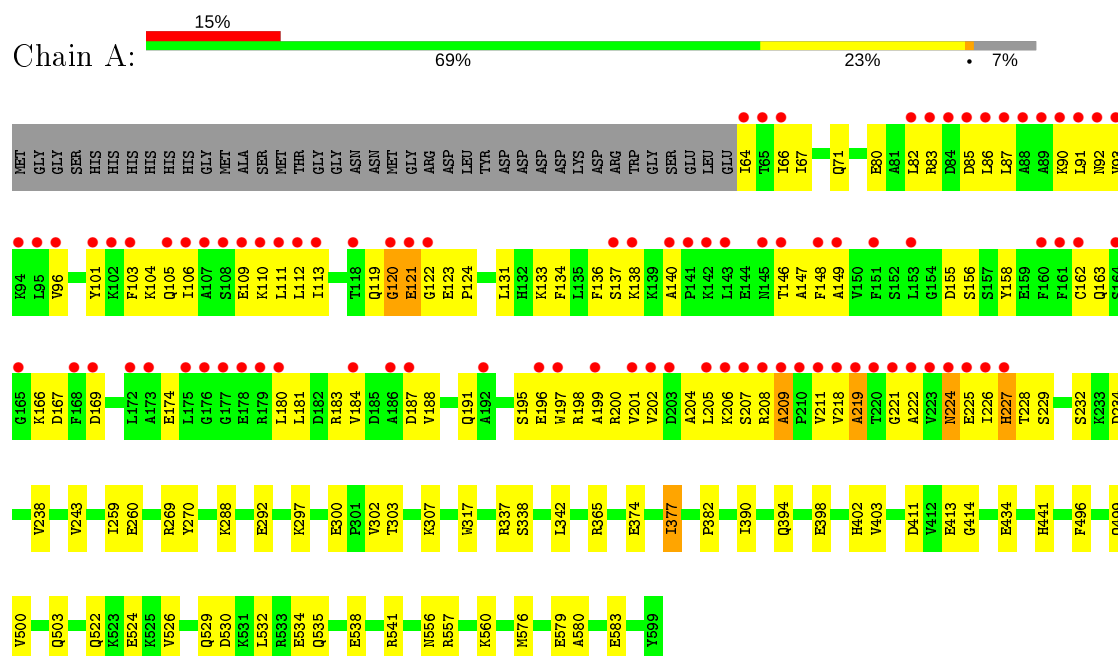
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	347	Total	O	0	0
			347	347		

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: Sulfite reductase [NADPH] flavoprotein alpha-component



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.48Å 99.74Å 103.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.95 – 2.34 45.95 – 2.34	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.95-2.34) 99.6 (45.95-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.85 (at 2.34Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.167 , 0.234 0.167 , 0.234	Depositor DCC
R_{free} test set	1992 reflections (7.38%)	wwPDB-VP
Wilson B-factor (Å ²)	24.5	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4766	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.83% 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: FMN, CXS, SO4, FAD

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.39	0/4350	0.55	0/5902

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	4241	0	4191	147	1
2	A	53	0	31	0	0
3	A	31	0	19	1	0
4	A	30	0	0	1	0
5	A	28	36	38	1	0
6	A	347	0	0	15	1
All	All	4730	36	4279	150	2

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 17.

All (150) 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:110:LYS:HB3	1:A:211:VAL:CG1	1.45	1.43
1:A:110:LYS:CB	1:A:211:VAL:HG11	1.54	1.38
1:A:111:LEU:HD13	1:A:205:LEU:HD11	1.55	0.88
1:A:110:LYS:CB	1:A:211:VAL:CG1	2.31	0.83
1:A:66:ILE:HD13	1:A:113:ILE:HB	1.60	0.82
1:A:111:LEU:HG	1:A:211:VAL:HG21	1.60	0.82
1:A:66:ILE:CD1	1:A:113:ILE:HB	2.12	0.79
1:A:413:GLU:OE2	6:A:701:HOH:O	2.02	0.77
1:A:181:LEU:HD11	1:A:204:ALA:HB3	1.67	0.76
1:A:224:ASN:HB3	1:A:232:SER:HB2	1.69	0.74
1:A:113:ILE:HD12	1:A:149:ALA:HB3	1.69	0.74
1:A:302:VAL:HG21	1:A:377:ILE:CD1	2.18	0.73
1:A:90:LYS:HE2	1:A:206:LYS:HG3	1.70	0.73
1:A:206:LYS:HG2	1:A:207:SER:H	1.54	0.72
1:A:500:VAL:HG12	6:A:925:HOH:O	1.88	0.72
1:A:225:GLU:O	1:A:226:ILE:HG13	1.90	0.71
1:A:111:LEU:HD21	1:A:211:VAL:HG23	1.74	0.70
1:A:83:ARG:O	1:A:87:LEU:HB2	1.92	0.70
1:A:522:GLN:NE2	1:A:524:GLU:O	2.25	0.69
4:A:604:SO4:O4	6:A:702:HOH:O	2.11	0.69
1:A:110:LYS:HD2	1:A:211:VAL:HG12	1.73	0.69
1:A:198:ARG:O	1:A:202:VAL:HG23	1.94	0.68
1:A:64:ILE:HG21	1:A:86:LEU:HD13	1.75	0.68
1:A:181:LEU:HD11	1:A:204:ALA:CB	2.24	0.68
1:A:90:LYS:HE3	1:A:206:LYS:HA	1.78	0.66
1:A:111:LEU:CG	1:A:211:VAL:HG21	2.27	0.65
1:A:302:VAL:HG21	1:A:377:ILE:HD13	1.79	0.65
1:A:398[A]:GLU:OE1	6:A:704:HOH:O	2.15	0.64
1:A:226:ILE:HD13	6:A:876:HOH:O	1.97	0.63
1:A:111:LEU:HG	1:A:211:VAL:CG2	2.28	0.63
1:A:530:ASP:O	1:A:534:GLU:HG3	1.99	0.62
1:A:204:ALA:O	1:A:209:ALA:HB3	1.99	0.61
1:A:181:LEU:HD22	1:A:201:VAL:HG22	1.80	0.61
1:A:111:LEU:HD23	1:A:147:ALA:HB3	1.82	0.61
1:A:64:ILE:HD12	1:A:92:ASN:HB2	1.83	0.60
1:A:158:TYR:OH	6:A:703:HOH:O	2.13	0.60
1:A:111:LEU:HD21	1:A:211:VAL:CG2	2.31	0.60
1:A:224:ASN:O	1:A:225:GLU:HG3	2.02	0.59
1:A:64:ILE:N	1:A:92:ASN:HB3	2.18	0.59
1:A:71:GLN:HG3	1:A:119:GLN:NE2	2.19	0.58
1:A:91:LEU:O	1:A:91:LEU:HD23	2.03	0.57
1:A:64:ILE:HD13	1:A:205:LEU:HD21	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:ASN:ND2	1:A:218:VAL:HB	2.19	0.57
1:A:111:LEU:CD2	1:A:211:VAL:HG21	2.35	0.57
1:A:224:ASN:HB3	1:A:232:SER:CB	2.34	0.57
1:A:411:ASP:HB2	6:A:829:HOH:O	2.05	0.56
1:A:556:ASN:O	1:A:560:LYS:HE3	2.05	0.56
1:A:579:GLU:O	1:A:583:GLU:HG3	2.06	0.55
1:A:101:TYR:CE2	1:A:103:PHE:HA	2.41	0.55
1:A:110:LYS:HB3	1:A:211:VAL:HG11	0.62	0.54
1:A:71:GLN:HG3	1:A:119:GLN:CG	2.37	0.54
5:A:610:CXS:H71	6:A:953:HOH:O	2.07	0.54
1:A:64:ILE:CD1	1:A:92:ASN:HB2	2.36	0.54
1:A:288:LYS:O	1:A:292:GLU:HG3	2.07	0.54
1:A:224:ASN:CB	1:A:232:SER:HB2	2.37	0.53
1:A:226:ILE:HD12	1:A:232:SER:HA	1.91	0.53
1:A:524:GLU:OE1	1:A:524:GLU:N	2.33	0.53
1:A:85:ASP:OD2	1:A:198:ARG:HG2	2.08	0.53
1:A:133:LYS:O	1:A:137:SER:HB2	2.09	0.53
1:A:111:LEU:CD2	1:A:211:VAL:CG2	2.86	0.53
1:A:110:LYS:CG	1:A:211:VAL:CG1	2.86	0.53
1:A:110:LYS:HD2	1:A:211:VAL:CG1	2.39	0.52
1:A:181:LEU:HD22	1:A:201:VAL:CG2	2.40	0.52
1:A:208:ARG:O	1:A:209:ALA:HB2	2.10	0.52
1:A:120[B]:GLY:O	1:A:123:GLU:HB2	2.10	0.52
1:A:111:LEU:CG	1:A:211:VAL:CG2	2.87	0.52
1:A:90:LYS:CE	1:A:206:LYS:HA	2.39	0.52
1:A:64:ILE:HG21	1:A:205:LEU:HD21	1.91	0.52
3:A:602:FMN:H9	3:A:602:FMN:H2'	1.91	0.51
1:A:64:ILE:HA	1:A:111:LEU:HB2	1.92	0.51
1:A:191:GLN:O	1:A:195:SER:HB2	2.11	0.51
1:A:112:LEU:O	1:A:148:PHE:HA	2.10	0.50
1:A:66:ILE:HD12	1:A:82:LEU:HD23	1.93	0.50
1:A:86:LEU:HD12	1:A:93:VAL:HG23	1.93	0.50
1:A:136:PHE:CZ	1:A:167:ASP:HB3	2.46	0.50
1:A:184:VAL:CG2	1:A:200:ARG:HH22	2.24	0.50
1:A:300:GLU:N	1:A:300:GLU:OE1	2.32	0.50
1:A:227:HIS:CG	1:A:228:THR:H	2.30	0.50
1:A:90:LYS:CE	1:A:206:LYS:HG3	2.38	0.50
1:A:92:ASN:HD21	1:A:219:ALA:H	1.60	0.49
1:A:238:VAL:HG13	1:A:434:GLU:HG3	1.94	0.49
1:A:260:GLU:HG2	1:A:402:HIS:CD2	2.46	0.49
1:A:259:ILE:HB	1:A:403:VAL:HG23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:ILE:CG2	1:A:205:LEU:HD21	2.42	0.49
1:A:535:GLN:HA	1:A:535:GLN:OE1	2.13	0.49
1:A:80:GLU:HG2	1:A:83:ARG:NH2	2.28	0.49
1:A:109:GLU:O	1:A:146:THR:HG23	2.14	0.48
1:A:226:ILE:CD1	1:A:232:SER:HA	2.43	0.48
1:A:119:GLN:HG3	6:A:939:HOH:O	2.13	0.47
1:A:112:LEU:O	1:A:148:PHE:HB2	2.14	0.47
1:A:365:ARG:HD3	6:A:747:HOH:O	2.13	0.47
1:A:538:GLU:OE1	1:A:541:ARG:NH1	2.47	0.47
1:A:101:TYR:OH	1:A:106:ILE:HG13	2.14	0.47
1:A:187:ASP:CG	1:A:188:VAL:H	2.19	0.46
1:A:156:SER:N	1:A:187:ASP:OD1	2.44	0.46
1:A:87:LEU:HD13	1:A:93:VAL:CG1	2.45	0.46
1:A:207:SER:HB2	1:A:221:GLY:O	2.16	0.46
1:A:113:ILE:CD1	1:A:149:ALA:HB3	2.43	0.46
1:A:224:ASN:OD1	1:A:234:ASP:N	2.37	0.46
1:A:64:ILE:HD13	1:A:205:LEU:CD2	2.46	0.46
1:A:92:ASN:HD21	1:A:219:ALA:N	2.14	0.46
1:A:541:ARG:HD2	6:A:707:HOH:O	2.17	0.45
1:A:104[C]:LYS:HG3	1:A:105:GLN:OE1	2.16	0.45
1:A:303:THR:HA	1:A:307:LYS:O	2.16	0.45
1:A:270:TYR:CZ	1:A:394:GLN:HG3	2.52	0.45
1:A:155:ASP:HB3	1:A:158:TYR:HD2	1.82	0.45
1:A:64:ILE:HG13	1:A:92:ASN:CB	2.47	0.45
1:A:64:ILE:N	1:A:92:ASN:O	2.50	0.45
1:A:288:LYS:HE2	1:A:292:GLU:OE2	2.17	0.45
1:A:196:GLU:O	1:A:199:ALA:HB3	2.17	0.44
1:A:227:HIS:HD2	6:A:955:HOH:O	2.01	0.44
1:A:83:ARG:HA	1:A:93:VAL:HG21	1.99	0.44
1:A:243:VAL:HB	1:A:260:GLU:HB2	2.00	0.44
1:A:184:VAL:HG21	1:A:200:ARG:NH2	2.33	0.44
1:A:123:GLU:HG3	1:A:124:PRO:HD2	1.99	0.44
1:A:110:LYS:HE3	6:A:997:HOH:O	2.17	0.44
1:A:180:LEU:C	1:A:181:LEU:HD12	2.38	0.43
1:A:522:GLN:NE2	1:A:526:VAL:HG23	2.33	0.43
1:A:499:GLN:O	1:A:503:GLN:HG3	2.17	0.43
1:A:224:ASN:CB	1:A:232:SER:CB	2.96	0.43
1:A:64:ILE:HG21	1:A:86:LEU:CD1	2.46	0.43
1:A:211:VAL:HG12	1:A:218:VAL:HG23	2.01	0.43
1:A:174:GLU:O	1:A:174:GLU:HG2	2.18	0.43
1:A:226:ILE:HG22	1:A:229:SER:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:ASP:CB	1:A:183:ARG:HD3	2.49	0.43
1:A:302:VAL:HA	1:A:374[B]:GLU:OE2	2.19	0.43
1:A:576:MET:HB2	1:A:580:ALA:HB3	2.01	0.43
1:A:122:GLY:CA	1:A:163:GLN:HB3	2.48	0.42
1:A:557:ARG:HA	1:A:557:ARG:HD2	1.88	0.42
1:A:122:GLY:HA2	1:A:163:GLN:HB3	2.02	0.42
1:A:270:TYR:CE1	1:A:390:ILE:HG21	2.55	0.42
1:A:162:CYS:O	1:A:166:LYS:HG3	2.20	0.42
1:A:337[A]:ARG:NE	6:A:705:HOH:O	2.24	0.42
1:A:382:PRO:HD2	6:A:968:HOH:O	2.20	0.41
1:A:103:PHE:HB3	1:A:131:LEU:HD13	2.02	0.41
1:A:138:LYS:O	1:A:138:LYS:HG2	2.19	0.41
1:A:224:ASN:C	1:A:225:GLU:HG3	2.39	0.41
1:A:64:ILE:CD1	1:A:205:LEU:HD21	2.51	0.41
1:A:269:ARG:HA	1:A:394:GLN:OE1	2.21	0.41
1:A:134:PHE:O	1:A:140:ALA:HB2	2.21	0.41
1:A:67:ILE:CD1	1:A:112:LEU:HD11	2.50	0.41
1:A:297:LYS:HG2	1:A:300:GLU:OE2	2.20	0.41
1:A:92:ASN:ND2	1:A:219:ALA:H	2.19	0.41
1:A:184:VAL:HG21	1:A:197:TRP:HD1	1.85	0.41
1:A:411:ASP:OD1	1:A:414:GLY:CA	2.69	0.41
1:A:221:GLY:O	1:A:222:ALA:HB3	2.21	0.40
1:A:226:ILE:HG23	1:A:441:HIS:NE2	2.36	0.40
1:A:338:SER:O	1:A:342:LEU:HG	2.22	0.40
1:A:529:GLN:HA	1:A:532:LEU:HD12	2.02	0.40
1:A:96:VAL:HG21	1:A:101:TYR:HD1	1.85	0.40

All (2) 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)
6:A:818:HOH:O	6:A:926:HOH:O[4_444]	1.85	0.35
1:A:121:GLU:OE2	1:A:560:LYS:NZ[4_444]	1.94	0.26

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	538/569 (95%)	505 (94%)	27 (5%)	6 (1%)	14 13

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	120[A]	GLY
1	A	120[B]	GLY
1	A	209	ALA
1	A	219	ALA
1	A	227	HIS
1	A	121	GLU

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	449/471 (95%)	445 (99%)	4 (1%)	78 87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	224	ASN
1	A	317	TRP
1	A	377	ILE
1	A	496	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	GLN

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 ⓘ

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	605	-	4,4,4	0.13	0	6,6,6	0.07	0
2	FAD	A	601	-	51,58,58	1.31	6 (11%)	60,89,89	2.28	7 (11%)
5	CXS	A	609	-	14,14,14	1.34	3 (21%)	18,18,18	2.25	5 (27%)
4	SO4	A	607	-	4,4,4	0.21	0	6,6,6	0.09	0
4	SO4	A	608	-	4,4,4	0.17	0	6,6,6	0.10	0
3	FMN	A	602	-	31,33,33	1.49	4 (12%)	40,50,50	1.57	6 (15%)
4	SO4	A	603	-	4,4,4	0.18	0	6,6,6	0.13	0
4	SO4	A	604	-	4,4,4	0.17	0	6,6,6	0.18	0
4	SO4	A	606	-	4,4,4	0.14	0	6,6,6	0.06	0
5	CXS	A	610	-	14,14,14	1.46	3 (21%)	18,18,18	1.91	6 (33%)

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	FMN	A	602	-	-	9/18/18/18	0/3/3/3
2	FAD	A	601	-	-	1/30/50/50	0/6/6/6
5	CXS	A	610	-	-	2/8/16/16	0/1/1/1
5	CXS	A	609	-	-	2/8/16/16	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	FAD	C4X-C10	5.81	1.44	1.38
3	A	602	FMN	C10-N1	4.40	1.38	1.33
3	A	602	FMN	C4A-N5	3.96	1.39	1.33
5	A	610	CXS	C1-S	3.37	1.82	1.77
2	A	601	FAD	C4-N3	3.36	1.38	1.33
3	A	602	FMN	C4-N3	3.28	1.38	1.33
5	A	609	CXS	O1-S	2.88	1.53	1.45
5	A	610	CXS	O1-S	2.71	1.53	1.45
3	A	602	FMN	C1'-N10	2.70	1.51	1.48
2	A	601	FAD	C4X-N5	-2.67	1.29	1.33
5	A	609	CXS	C1-S	2.55	1.81	1.77
5	A	610	CXS	O2-S	2.54	1.52	1.45
2	A	601	FAD	C5X-N5	2.42	1.39	1.35
5	A	609	CXS	O2-S	2.28	1.51	1.45
2	A	601	FAD	C4-C4X	2.26	1.45	1.41
2	A	601	FAD	C9A-N10	2.19	1.41	1.38

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	FAD	C4-N3-C2	12.82	125.96	115.14
2	A	601	FAD	C4X-C4-N3	-7.09	113.73	123.43
3	A	602	FMN	C4-N3-C2	6.06	120.26	115.14
5	A	609	CXS	O2-S-C1	5.23	113.22	106.92
2	A	601	FAD	C10-C4X-N5	4.80	124.58	121.26
5	A	609	CXS	C2-C1-S	-4.52	106.32	113.25
5	A	610	CXS	O3-S-O2	-4.30	100.78	111.27
5	A	609	CXS	O3-S-O2	-3.98	101.55	111.27
2	A	601	FAD	C4-C4X-C10	-3.75	117.47	119.95
5	A	610	CXS	O2-S-C1	3.54	111.18	106.92
3	A	602	FMN	C4A-N5-C5A	3.53	120.30	116.77
2	A	601	FAD	C1'-N10-C9A	3.34	120.92	118.29
2	A	601	FAD	C4X-C10-N10	-3.24	116.98	120.30
5	A	609	CXS	O1-S-C1	3.22	110.79	106.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	FMN	C5A-C9A-N10	3.20	120.04	117.72
3	A	602	FMN	C1'-N10-C9A	3.17	120.79	118.29
5	A	610	CXS	O3-S-C1	2.98	110.58	105.77
5	A	610	CXS	C3-N-C4	-2.74	108.76	114.14
5	A	610	CXS	O1-S-C1	2.60	110.04	106.92
5	A	609	CXS	C6-C5-C4	2.53	115.88	111.11
5	A	610	CXS	C2-C1-S	-2.53	109.38	113.25
3	A	602	FMN	C4A-C4-N3	-2.42	120.12	123.43
2	A	601	FAD	C5A-C6A-N6A	2.35	123.92	120.35
3	A	602	FMN	C10-C4A-N5	-2.02	119.86	121.26

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	FMN	C2'-C1'-N10-C10
3	A	602	FMN	C1'-C2'-C3'-O3'
3	A	602	FMN	C1'-C2'-C3'-C4'
3	A	602	FMN	C5'-O5'-P-O1P
3	A	602	FMN	C5'-O5'-P-O2P
3	A	602	FMN	C5'-O5'-P-O3P
3	A	602	FMN	O2'-C2'-C3'-C4'
5	A	609	CXS	C5-C4-N-C3
5	A	610	CXS	C5-C4-N-C3
3	A	602	FMN	O2'-C2'-C3'-O3'
5	A	609	CXS	C9-C4-N-C3
5	A	610	CXS	C9-C4-N-C3
2	A	601	FAD	O4B-C4B-C5B-O5B
3	A	602	FMN	O4'-C4'-C5'-O5'

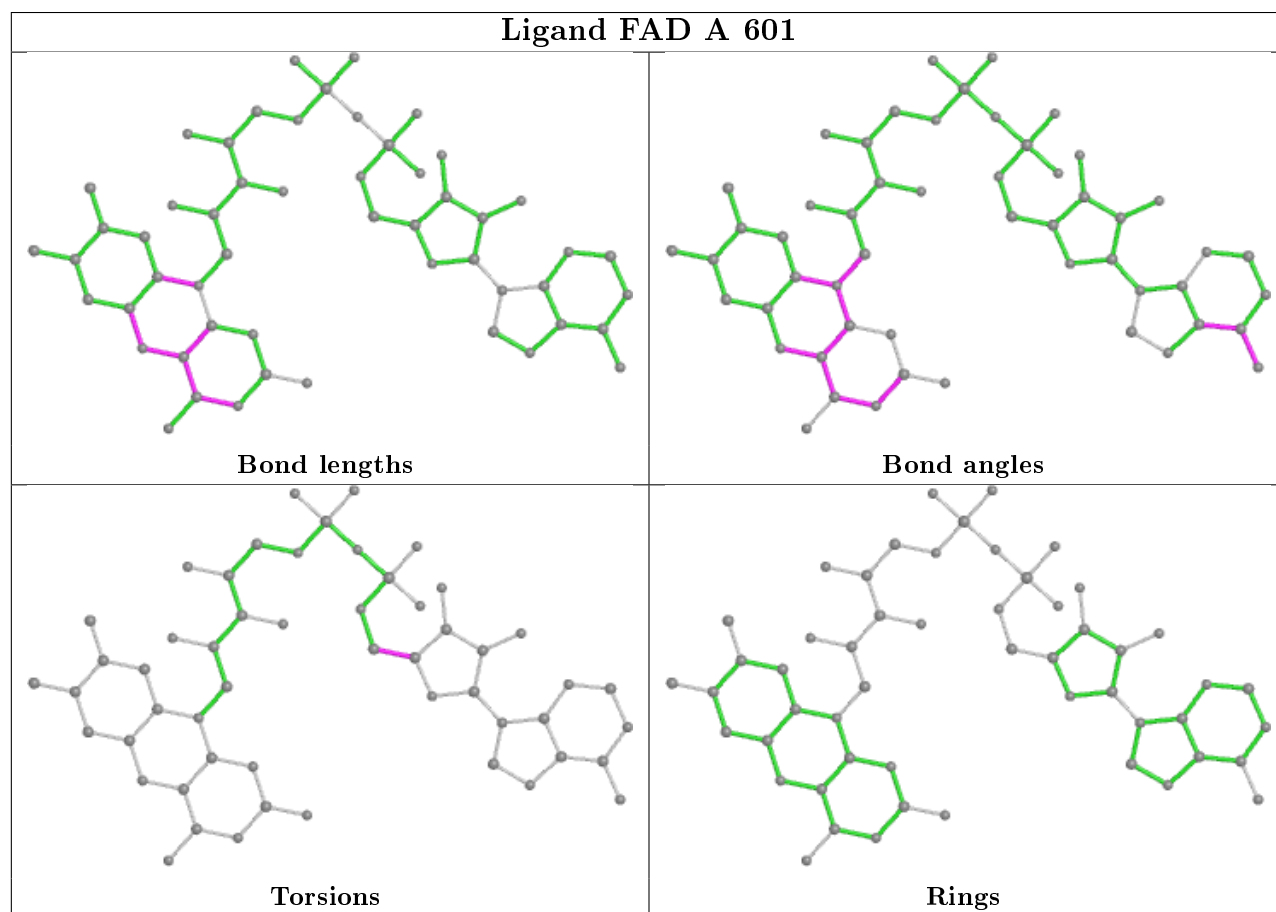
There are no ring outliers.

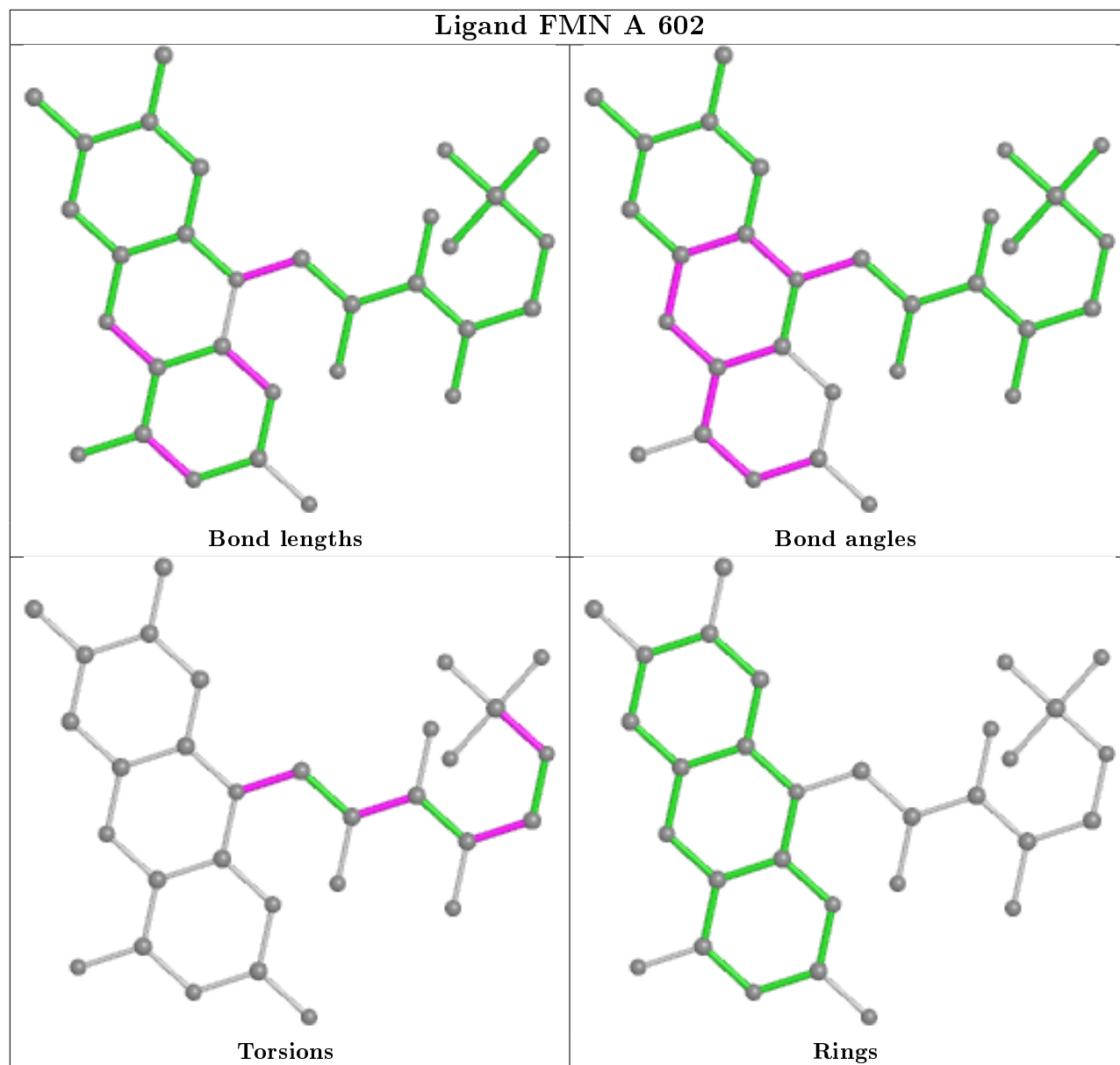
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	FMN	1	0
4	A	604	SO4	1	0
5	A	610	CXS	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	530/569 (93%)	0.67	88 (16%) ⓘ ⓘ	10, 27, 89, 143	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	210	PRO	13.0
1	A	211	VAL	12.5
1	A	209	ALA	11.0
1	A	221	GLY	10.7
1	A	91	LEU	10.3
1	A	226	ILE	10.2
1	A	225	GLU	8.8
1	A	220	THR	8.3
1	A	222	ALA	8.2
1	A	219	ALA	7.9
1	A	89	ALA	7.8
1	A	224	ASN	7.4
1	A	93	VAL	6.8
1	A	223	VAL	6.2
1	A	207	SER	6.2
1	A	106	ILE	6.0
1	A	90	LYS	5.8
1	A	122	GLY	5.5
1	A	92	ASN	5.4
1	A	141	PRO	5.1
1	A	88	ALA	5.0
1	A	172	LEU	4.9
1	A	202	VAL	4.9
1	A	218	VAL	4.8
1	A	140	ALA	4.8
1	A	227	HIS	4.7
1	A	107	ALA	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	143	LEU	4.4
1	A	64	ILE	4.3
1	A	84	ASP	4.3
1	A	206	LYS	4.3
1	A	108	SER	4.2
1	A	120[A]	GLY	4.2
1	A	87	LEU	4.2
1	A	205	LEU	4.0
1	A	113	ILE	4.0
1	A	165	GLY	4.0
1	A	186	ALA	4.0
1	A	160	PHE	3.8
1	A	142	LYS	3.8
1	A	199	ALA	3.8
1	A	176	GLY	3.8
1	A	94	LYS	3.8
1	A	162	CYS	3.8
1	A	95	LEU	3.7
1	A	138	LYS	3.7
1	A	149	ALA	3.6
1	A	197	TRP	3.5
1	A	203	ASP	3.5
1	A	201	VAL	3.3
1	A	103	PHE	3.3
1	A	65	THR	3.3
1	A	173	ALA	3.2
1	A	208	ARG	3.1
1	A	168	PHE	3.1
1	A	82	LEU	3.1
1	A	111	LEU	3.1
1	A	180	LEU	3.0
1	A	161	PHE	3.0
1	A	105	GLN	3.0
1	A	112	LEU	2.9
1	A	175	LEU	2.9
1	A	137	SER	2.9
1	A	83	ARG	2.8
1	A	96	VAL	2.7
1	A	148	PHE	2.7
1	A	187	ASP	2.6
1	A	86	LEU	2.6
1	A	151	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	192	ALA	2.6
1	A	85	ASP	2.5
1	A	164	SER	2.5
1	A	184	VAL	2.4
1	A	146	THR	2.4
1	A	177	GLY	2.3
1	A	110	LYS	2.3
1	A	179	ARG	2.3
1	A	66	ILE	2.3
1	A	101	TYR	2.2
1	A	121	GLU	2.2
1	A	118	THR	2.2
1	A	109	GLU	2.2
1	A	145	ASN	2.1
1	A	196	GLU	2.1
1	A	102	LYS	2.1
1	A	153	LEU	2.0
1	A	178	GLU	2.0
1	A	169	ASP	2.0

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	SO4	A	607	5/5	0.57	0.46	66,68,88,112	0
5	CXS	A	610	14/14	0.63	0.42	43,74,89,120	0
4	SO4	A	606	5/5	0.65	0.37	110,110,127,132	0
4	SO4	A	608	5/5	0.70	0.52	58,61,105,119	0

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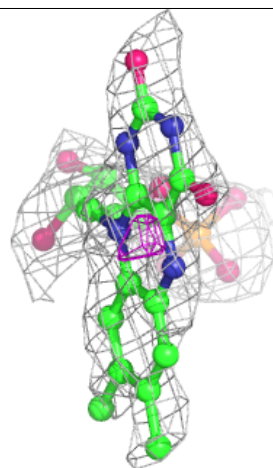
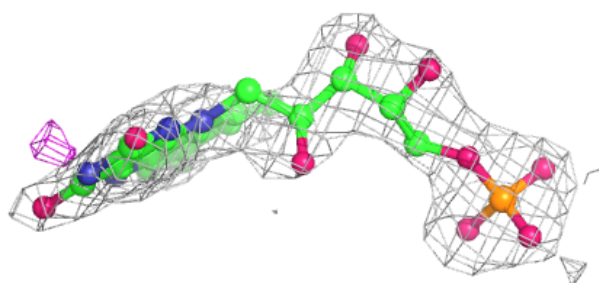
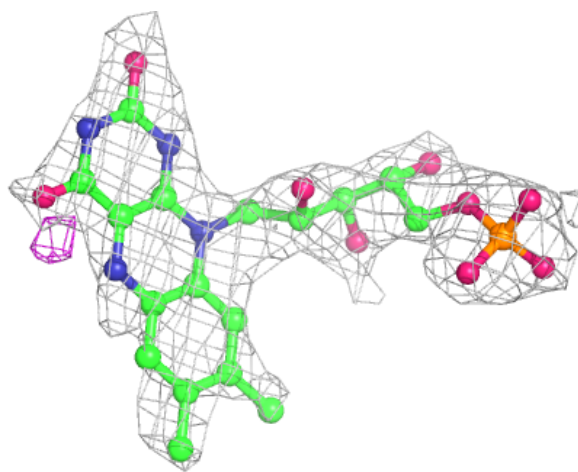
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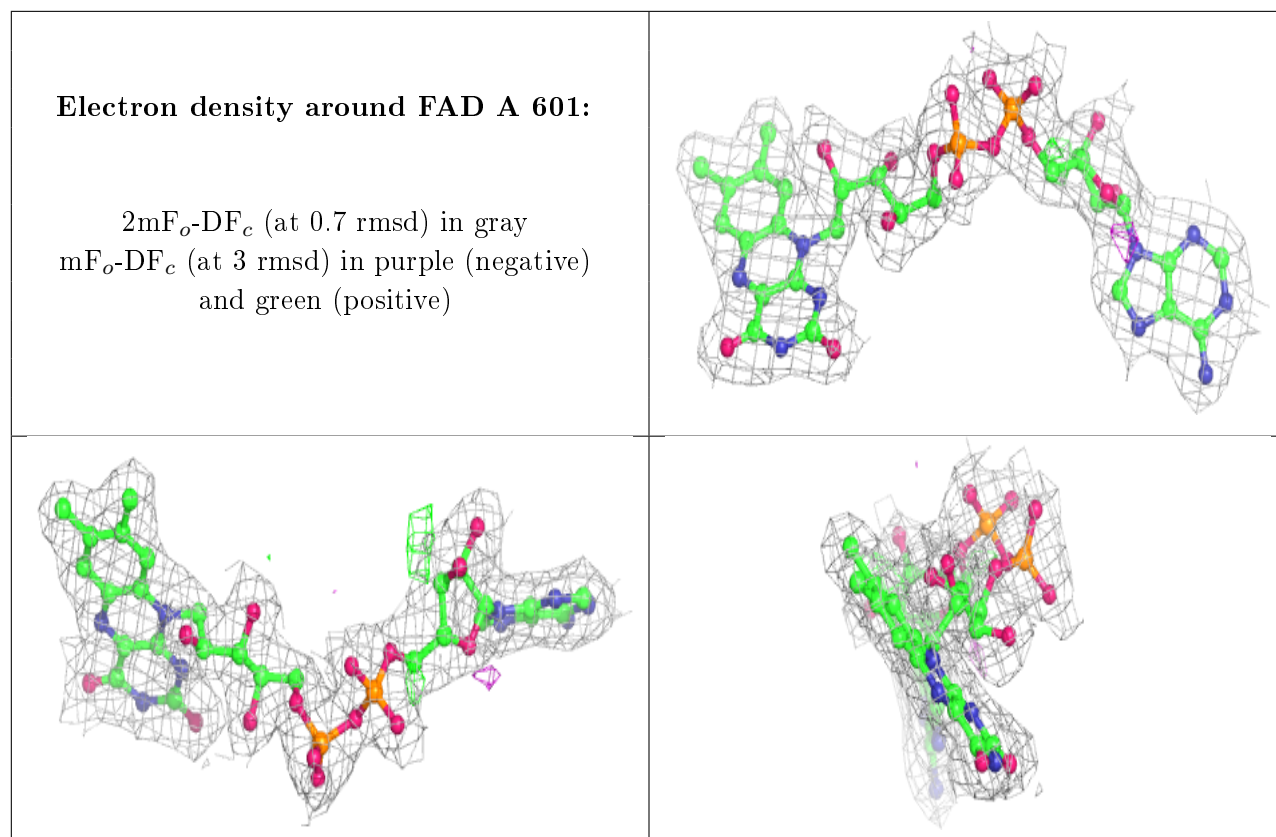
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	CXS	A	609	14/14	0.83	0.26	21,38,82,82	0
4	SO4	A	604	5/5	0.83	0.37	48,65,78,86	0
3	FMN	A	602	31/31	0.92	0.19	36,58,63,64	0
4	SO4	A	605	5/5	0.96	0.19	55,70,77,81	0
4	SO4	A	603	5/5	0.98	0.12	41,43,49,50	0
2	FAD	A	601	53/53	0.98	0.12	7,17,27,42	0

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 FMN A 602:

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.