



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 7, 2020 – 04:56 am BST

PDB ID : 6J61
Title : Crystal Structure of Thymidylate Synthase, Thy1, from *Thermus thermophilus* having an Extra C Terminal Domain
Authors : Ogawa, A.; Sampei, G.; Kawai, G.
Deposited on : 2019-01-12
Resolution : 2.50 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

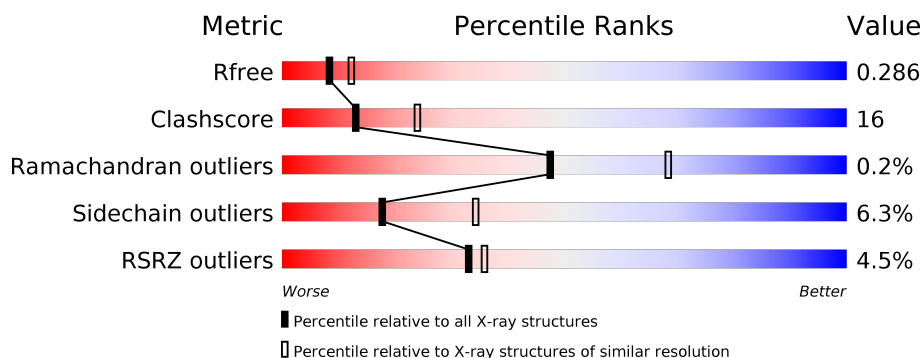
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	270	<div> <div>2%</div> <div> <div></div> <div>63%</div> <div>24%</div> <div>•</div> <div>10%</div> </div> </div>
1	B	270	<div> <div>5%</div> <div> <div></div> <div>58%</div> <div>27%</div> <div>•</div> <div>11%</div> </div> </div>
1	C	270	<div> <div>3%</div> <div> <div></div> <div>57%</div> <div>30%</div> <div>•</div> <div>11%</div> </div> </div>
1	D	270	<div> <div>5%</div> <div> <div></div> <div>57%</div> <div>29%</div> <div>•</div> <div>10%</div> </div> </div>

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 8244 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 Flavin-dependent thymidylate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	0	0	0
			1990	1287	355	343	5			
1	B	239	Total	C	N	O	S	0	0	0
			1968	1274	350	339	5			
1	C	240	Total	C	N	O	S	0	0	0
			1972	1276	351	340	5			
1	D	242	Total	C	N	O	S	0	0	0
			1990	1287	355	343	5			

- 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
			53	27	9	15	2	
2	B	1	Total	C	N	O	P	0
			53	27	9	15	2	

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

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).

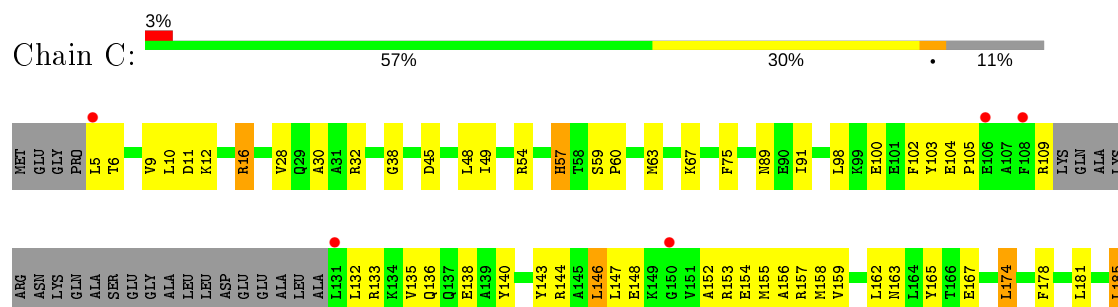
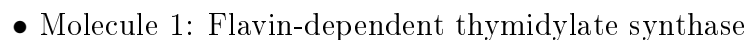


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 4 is water.

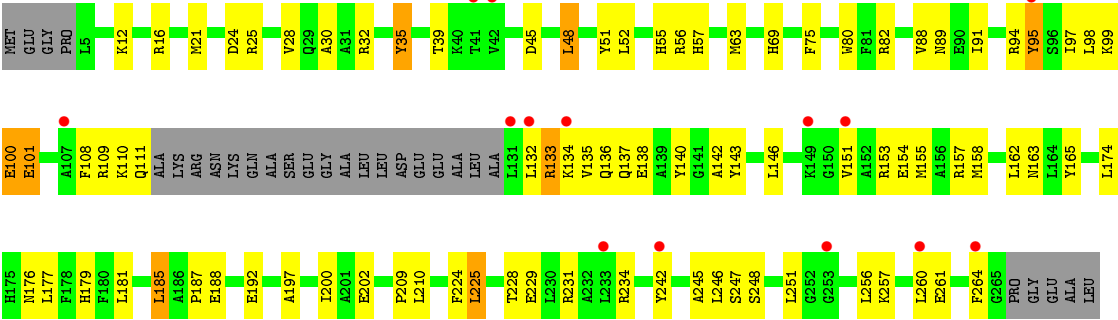
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	21	Total 21	O 21	0	0
4	B	12	Total 12	O 12	0	0
4	C	22	Total 22	O 22	0	0
4	D	17	Total 17	O 17	0	0

- Molecule 1: Flavin-dependent thymidylate synthase





● Molecule 1: Flavin-dependent thymidylate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.03Å 68.36Å 134.08Å 90.00° 115.12° 90.00°	Depositor
Resolution (Å)	49.37 – 2.50 49.37 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.3 (49.37-2.50) 97.1 (49.37-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.51Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.223 , 0.279 0.230 , 0.286	Depositor DCC
R_{free} test set	7335 reflections (9.18%)	wwPDB-VP
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.534	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 55.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8244	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% 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: PO4, 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	0/2035	0.62	0/2742
1	B	0.38	0/2013	0.61	0/2714
1	C	0.39	0/2017	0.62	0/2719
1	D	0.39	0/2035	0.62	0/2742
All	All	0.39	0/8100	0.62	0/10917

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	1990	0	2019	65	0
1	B	1968	0	1995	77	0
1	C	1972	0	1998	78	0
1	D	1990	0	2019	96	0
2	A	53	0	31	0	0
2	B	53	0	31	0	0
2	C	53	0	31	0	0
2	D	53	0	31	1	0
3	A	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	0	0
3	C	10	0	0	0	0
3	D	10	0	0	1	0
4	A	21	0	0	0	0
4	B	12	0	0	2	0
4	C	22	0	0	1	0
4	D	17	0	0	0	0
All	All	8244	0	8155	268	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 16.

All (268) 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:D:146:LEU:HD12	1:D:151:VAL:HG21	1.38	1.05
1:A:54:ARG:HD3	1:A:255:ARG:HD3	1.48	0.94
1:A:203:ILE:O	1:A:207:ARG:HG2	1.70	0.92
1:C:28:VAL:HG22	1:C:48:LEU:HD12	1.52	0.92
1:D:231:ARG:HA	1:D:234:ARG:HH12	1.32	0.91
1:C:155:MET:O	1:C:158:MET:HG2	1.74	0.88
1:B:158:MET:HG2	1:D:163:ASN:HB3	1.57	0.87
1:A:181:LEU:O	1:A:185:LEU:HB2	1.76	0.86
1:B:231:ARG:HA	1:B:234:ARG:NH1	1.93	0.83
1:D:231:ARG:HA	1:D:234:ARG:NH1	1.96	0.81
1:A:5:LEU:HD23	1:A:6:THR:H	1.46	0.80
1:C:89:ASN:HD21	1:D:57:HIS:HE1	1.30	0.79
1:B:56:ARG:NH1	1:B:56:ARG:HA	1.99	0.78
1:C:181:LEU:O	1:C:185:LEU:HB2	1.85	0.76
1:C:57:HIS:HE1	1:D:89:ASN:HD21	1.33	0.76
1:C:54:ARG:HD2	1:C:258:GLU:OE1	1.85	0.76
1:B:246:LEU:HG	1:B:251:LEU:HD12	1.65	0.76
1:A:187:PRO:HG2	1:A:188:GLU:OE1	1.90	0.71
1:B:158:MET:CG	1:D:163:ASN:HB3	2.21	0.71
1:C:57:HIS:CE1	1:D:89:ASN:HD21	2.10	0.69
1:C:188:GLU:H	1:C:188:GLU:CD	1.96	0.69
1:D:98:LEU:H	1:D:98:LEU:HD22	1.57	0.69
1:D:110:LYS:O	1:D:111:GLN:HG3	1.93	0.68
1:B:100:GLU:HB2	1:B:140:TYR:CZ	2.29	0.68
1:B:231:ARG:HA	1:B:234:ARG:HH12	1.58	0.68
1:C:12:LYS:HB2	1:C:165:TYR:CE2	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:TRP:HD1	1:B:194:ARG:HH21	1.42	0.66
1:C:242:TYR:O	1:C:246:LEU:HD13	1.95	0.66
1:D:181:LEU:O	1:D:185:LEU:HB2	1.95	0.66
1:C:91:ILE:HD13	1:C:167:GLU:HB2	1.77	0.66
1:C:28:VAL:CG1	1:C:32:ARG:NH1	2.59	0.66
1:C:89:ASN:HD21	1:D:57:HIS:CE1	2.14	0.66
1:C:143:TYR:O	1:C:147:LEU:HD13	1.96	0.65
1:A:56:ARG:HA	1:A:56:ARG:HE	1.60	0.65
1:A:131:LEU:O	1:A:135:VAL:HG13	1.96	0.65
1:C:98:LEU:HD22	1:C:98:LEU:N	2.12	0.65
1:B:155:MET:HG3	1:D:109:ARG:HH12	1.63	0.64
1:A:89:ASN:HD21	1:B:57:HIS:CE1	2.16	0.64
1:C:98:LEU:HD22	1:C:98:LEU:H	1.62	0.64
1:D:16:ARG:NH1	1:D:69:HIS:ND1	2.46	0.64
1:A:56:ARG:NE	1:A:56:ARG:HA	2.13	0.63
1:D:132:LEU:O	1:D:135:VAL:HG12	1.99	0.62
1:B:181:LEU:O	1:B:185:LEU:HB2	1.99	0.62
1:A:132:LEU:O	1:A:136:GLN:HG3	1.99	0.62
1:A:111:GLN:C	1:C:152:ALA:HA	2.19	0.62
1:A:89:ASN:HD21	1:B:57:HIS:HE1	1.48	0.61
1:B:190:GLN:OE1	1:D:154:GLU:HB2	1.99	0.61
1:C:57:HIS:HE1	1:D:89:ASN:ND2	1.99	0.61
1:A:217:GLU:OE2	1:D:228:THR:HG23	2.00	0.61
1:D:97:ILE:HG12	1:D:153:ARG:NH1	2.16	0.61
1:B:56:ARG:HA	1:B:56:ARG:HH11	1.66	0.61
1:D:242:TYR:HD2	1:D:260:LEU:HD23	1.66	0.60
1:D:133:ARG:O	1:D:137:GLN:HG3	2.01	0.60
1:B:12:LYS:HB2	1:B:165:TYR:CE2	2.37	0.60
1:B:41:THR:OG1	1:B:44:GLU:HG3	2.02	0.59
1:C:256:LEU:O	1:C:256:LEU:HD12	2.02	0.59
1:D:100:GLU:HB2	1:D:140:TYR:CE2	2.36	0.59
1:D:35:TYR:CD1	1:D:35:TYR:N	2.70	0.59
1:A:100:GLU:HB2	1:A:140:TYR:CZ	2.37	0.58
1:C:144:ARG:O	1:C:148:GLU:HG3	2.02	0.58
1:A:109:ARG:NH2	1:A:191:TRP:HB3	2.19	0.58
1:D:99:LYS:O	1:D:101:GLU:N	2.36	0.58
1:D:16:ARG:HG2	1:D:69:HIS:HB3	1.85	0.58
1:A:131:LEU:HD23	1:C:146:LEU:HD13	1.85	0.58
1:D:97:ILE:HG12	1:D:153:ARG:HH12	1.68	0.58
1:B:9:VAL:HG12	1:B:10:LEU:HG	1.85	0.57
1:A:57:HIS:CE1	1:B:89:ASN:HD21	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:153:ARG:HG2	1:D:153:ARG:HH11	1.69	0.57
1:A:25:ARG:O	1:A:28:VAL:HG12	2.05	0.57
1:B:41:THR:HG23	1:B:44:GLU:OE2	2.04	0.57
1:C:238:THR:OG1	1:C:241:VAL:HG23	2.05	0.57
1:B:109:ARG:HB2	1:B:109:ARG:CZ	2.35	0.57
1:D:100:GLU:HB2	1:D:140:TYR:CZ	2.40	0.57
1:D:155:MET:O	1:D:158:MET:HG2	2.05	0.57
1:D:257:LYS:HE3	1:D:261:GLU:OE2	2.05	0.57
1:B:228:THR:HG23	1:C:217:GLU:OE2	2.05	0.56
1:D:185:LEU:HD13	1:D:197:ALA:HB1	1.88	0.56
1:C:59:SER:HB2	1:D:89:ASN:HD22	1.71	0.56
1:B:82:ARG:HD2	4:C:418:HOH:O	2.05	0.56
1:C:89:ASN:ND2	1:D:57:HIS:HE1	2.02	0.55
1:B:217:GLU:OE2	1:C:228:THR:HG23	2.06	0.55
1:A:134:LYS:HE3	1:A:138:GLU:OE1	2.06	0.55
1:B:54:ARG:NH1	1:B:258:GLU:OE1	2.39	0.55
1:C:59:SER:HB2	1:C:60:PRO:HD3	1.88	0.54
1:A:5:LEU:CD2	1:A:6:THR:H	2.19	0.54
1:B:188:GLU:CD	1:B:188:GLU:H	2.11	0.54
1:D:187:PRO:HG2	1:D:188:GLU:OE1	2.06	0.54
1:C:132:LEU:O	1:C:136:GLN:HG3	2.07	0.54
1:C:91:ILE:CD1	1:C:167:GLU:HB2	2.38	0.54
1:C:258:GLU:O	1:C:262:LYS:HG3	2.06	0.54
1:C:256:LEU:O	1:C:260:LEU:HG	2.08	0.54
1:D:142:ALA:O	1:D:146:LEU:HD23	2.08	0.53
1:D:146:LEU:CD1	1:D:151:VAL:HG21	2.24	0.53
1:A:109:ARG:NH2	1:A:192:GLU:OE2	2.41	0.53
1:A:240:GLU:OE1	1:A:244:LYS:HE3	2.09	0.53
1:B:69:HIS:HE2	1:B:167:GLU:HG2	1.74	0.53
1:A:188:GLU:N	1:A:188:GLU:OE1	2.42	0.53
1:A:82:ARG:HH11	1:A:82:ARG:HG3	1.73	0.53
1:D:56:ARG:NE	1:D:56:ARG:HA	2.25	0.52
1:D:28:VAL:CG1	1:D:32:ARG:NH1	2.72	0.52
1:A:224:PHE:HD2	1:D:224:PHE:CD2	2.28	0.52
1:C:257:LYS:O	1:C:261:GLU:HG3	2.10	0.52
1:D:132:LEU:HG	1:D:136:GLN:NE2	2.24	0.52
1:D:257:LYS:O	1:D:261:GLU:HG3	2.09	0.52
1:C:188:GLU:OE2	1:C:188:GLU:N	2.43	0.52
1:C:30:ALA:CB	1:C:63:MET:HG3	2.40	0.52
1:D:247:SER:HA	1:D:251:LEU:O	2.09	0.52
1:A:257:LYS:O	1:A:261:GLU:HG3	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:186:ALA:HB1	1:B:188:GLU:OE1	2.11	0.51
1:C:231:ARG:HA	1:C:234:ARG:HH12	1.74	0.51
1:D:242:TYR:CE1	1:D:246:LEU:HD11	2.46	0.51
1:B:187:PRO:HG2	1:B:188:GLU:OE2	2.11	0.51
1:A:238:THR:OG1	1:A:241:VAL:HG23	2.11	0.51
1:C:16:ARG:NH2	1:D:35:TYR:HA	2.26	0.51
1:A:54:ARG:HD3	1:A:255:ARG:CD	2.33	0.50
1:C:45:ASP:O	1:C:49:ILE:HG13	2.11	0.50
1:D:225:LEU:HD12	1:D:229:GLU:HB3	1.93	0.50
1:B:30:ALA:CB	1:B:63:MET:HG3	2.41	0.50
1:B:238:THR:OG1	1:B:241:VAL:HG23	2.11	0.50
1:B:157:ARG:HD2	1:B:158:MET:N	2.27	0.50
1:D:109:ARG:HH11	1:D:109:ARG:HB2	1.77	0.50
1:B:100:GLU:HG3	1:B:102:PHE:HE1	1.76	0.50
1:C:100:GLU:HB2	1:C:140:TYR:CZ	2.47	0.50
1:A:153:ARG:HH11	1:A:153:ARG:HG2	1.77	0.49
1:C:231:ARG:HA	1:C:234:ARG:NH1	2.27	0.49
1:D:135:VAL:HG13	1:D:136:GLN:N	2.27	0.49
1:C:234:ARG:HB3	1:C:234:ARG:HH11	1.77	0.49
1:A:224:PHE:HD2	1:D:224:PHE:HD2	1.61	0.49
1:C:135:VAL:HG13	1:C:136:GLN:N	2.27	0.49
1:D:176:ASN:O	1:D:179:HIS:HB3	2.13	0.49
1:B:78:ARG:HD3	4:B:404:HOH:O	2.12	0.49
1:A:30:ALA:CB	1:A:63:MET:HG3	2.43	0.49
1:D:153:ARG:HG2	1:D:153:ARG:NH1	2.28	0.49
1:D:24:ASP:OD1	1:D:210:LEU:HB2	2.12	0.49
1:A:89:ASN:HD22	1:B:59:SER:HB2	1.78	0.48
1:C:247:SER:C	1:C:249:LEU:H	2.16	0.48
1:B:192:GLU:N	1:B:192:GLU:OE1	2.42	0.48
1:B:80:TRP:CZ2	1:B:200:ILE:HD11	2.47	0.48
1:B:59:SER:HB2	1:B:60:PRO:HD3	1.96	0.48
1:B:132:LEU:HD22	1:B:136:GLN:OE1	2.12	0.48
1:D:30:ALA:CB	1:D:63:MET:HG3	2.44	0.48
1:B:14:PHE:C	1:B:14:PHE:CD1	2.87	0.48
1:C:242:TYR:CE1	1:C:246:LEU:HD11	2.48	0.48
1:D:28:VAL:HG21	1:D:45:ASP:HB3	1.96	0.48
1:A:109:ARG:HH22	1:A:192:GLU:CD	2.16	0.48
1:D:242:TYR:CD2	1:D:260:LEU:HD23	2.46	0.48
1:D:91:ILE:O	1:D:91:ILE:HG13	2.13	0.48
1:B:28:VAL:HG21	1:B:45:ASP:HB3	1.96	0.47
1:B:155:MET:SD	1:D:109:ARG:NH1	2.87	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:231:ARG:O	1:D:234:ARG:O	2.32	0.47
1:A:190:GLN:HG3	1:C:154:GLU:CD	2.34	0.47
1:C:174:LEU:HD22	1:C:178:PHE:CE2	2.48	0.47
1:D:12:LYS:HB2	1:D:165:TYR:CE2	2.49	0.47
1:A:190:GLN:OE1	1:C:154:GLU:HB2	2.14	0.47
1:B:69:HIS:HE2	1:B:167:GLU:CG	2.28	0.47
1:D:95:TYR:CD1	1:D:95:TYR:N	2.82	0.47
1:D:98:LEU:N	1:D:98:LEU:HD22	2.28	0.47
1:D:245:ALA:O	1:D:248:SER:HB3	2.14	0.47
1:D:109:ARG:NH1	1:D:109:ARG:HB2	2.30	0.47
1:A:110:LYS:O	1:A:111:GLN:CB	2.62	0.46
1:B:159:VAL:HG12	1:D:132:LEU:CD1	2.46	0.46
1:B:159:VAL:HG12	1:D:132:LEU:HD12	1.96	0.46
1:A:219:LEU:HD22	1:A:219:LEU:N	2.30	0.46
1:A:110:LYS:O	1:A:111:GLN:HB2	2.15	0.46
1:B:133:ARG:HH11	1:B:133:ARG:HG3	1.81	0.46
1:A:21:MET:HB2	1:B:21:MET:HB2	1.96	0.46
1:C:9:VAL:HG12	1:C:10:LEU:HG	1.97	0.46
1:B:160:LEU:HD13	1:B:164:LEU:HD22	1.97	0.46
1:C:257:LYS:HD3	1:C:257:LYS:HA	1.82	0.46
1:B:131:LEU:HD23	1:B:131:LEU:C	2.37	0.46
1:A:87:SER:HB2	1:A:171:LYS:HB3	1.98	0.46
1:D:134:LYS:NZ	1:D:138:GLU:HG3	2.32	0.45
1:A:83:HIS:HA	2:D:301:FAD:O1A	2.15	0.45
1:C:205:LYS:HG3	1:C:212:TRP:CD1	2.51	0.45
1:B:131:LEU:HD23	1:B:131:LEU:O	2.15	0.45
1:C:187:PRO:HD2	1:C:188:GLU:OE2	2.16	0.45
1:D:242:TYR:O	1:D:246:LEU:HD13	2.16	0.45
1:C:194:ARG:HG3	1:C:194:ARG:HH11	1.82	0.45
1:D:51:TYR:CE1	1:D:55:HIS:CD2	3.05	0.44
1:A:65:VAL:HG11	1:A:171:LYS:HD3	1.99	0.44
1:A:218:HIS:C	1:A:219:LEU:HD22	2.37	0.44
1:A:57:HIS:HE1	1:B:89:ASN:ND2	2.15	0.44
1:B:54:ARG:NH1	1:B:258:GLU:CD	2.71	0.44
1:B:12:LYS:HZ2	1:B:102:PHE:H	1.66	0.44
1:C:67:LYS:HE2	1:D:21:MET:CE	2.47	0.44
1:B:135:VAL:HG13	1:B:136:GLN:N	2.32	0.44
1:B:155:MET:CG	1:D:109:ARG:HH12	2.28	0.44
1:D:134:LYS:HZ3	1:D:138:GLU:HG3	1.82	0.44
1:B:30:ALA:HB1	1:B:63:MET:HG3	2.00	0.44
1:C:12:LYS:HB2	1:C:165:TYR:CZ	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:LEU:HD21	1:D:142:ALA:HB1	1.99	0.44
1:B:72:ALA:HA	1:B:196:TYR:OH	2.17	0.43
1:C:187:PRO:HB2	1:C:188:GLU:OE2	2.18	0.43
1:C:28:VAL:HG12	1:C:38:GLY:O	2.18	0.43
1:D:185:LEU:HD13	1:D:197:ALA:CB	2.48	0.43
1:D:35:TYR:HD1	1:D:35:TYR:N	2.14	0.43
1:A:28:VAL:HG22	1:A:32:ARG:NH1	2.33	0.43
1:B:185:LEU:HD13	1:B:197:ALA:HB1	1.99	0.43
1:C:98:LEU:H	1:C:98:LEU:CD2	2.27	0.43
1:A:28:VAL:HG23	1:A:48:LEU:CD1	2.48	0.43
1:C:28:VAL:HG11	1:C:32:ARG:NH1	2.33	0.43
1:B:138:GLU:HG3	1:D:138:GLU:OE1	2.18	0.43
1:A:89:ASN:ND2	1:B:57:HIS:HE1	2.13	0.43
1:B:109:ARG:HH12	1:D:155:MET:CG	2.32	0.43
1:D:234:ARG:HB3	1:D:234:ARG:NH1	2.34	0.43
1:D:82:ARG:NH1	3:D:302:PO4:O2	2.52	0.43
1:D:98:LEU:H	1:D:98:LEU:CD2	2.29	0.43
1:A:154:GLU:OE2	1:C:109:ARG:NH2	2.41	0.43
1:A:180:PHE:CE1	1:A:184:ARG:HG3	2.54	0.43
1:A:9:VAL:HG12	1:A:10:LEU:HG	2.01	0.43
1:B:19:ASP:OD1	1:B:20:GLN:N	2.50	0.42
1:C:156:ALA:O	1:C:159:VAL:HG22	2.19	0.42
1:A:138:GLU:HG3	1:C:138:GLU:OE1	2.18	0.42
1:A:72:ALA:O	1:A:166:THR:HG22	2.19	0.42
1:B:185:LEU:HD13	1:B:197:ALA:CB	2.49	0.42
1:C:98:LEU:CD2	1:C:98:LEU:N	2.81	0.42
1:D:24:ASP:OD2	1:D:209:PRO:HD2	2.20	0.42
1:D:94:ARG:HB2	1:D:95:TYR:CD1	2.54	0.42
1:C:102:PHE:HB3	1:C:163:ASN:ND2	2.34	0.42
1:C:11:ASP:OD2	1:C:12:LYS:HG3	2.19	0.42
1:C:5:LEU:HD22	1:C:6:THR:OG1	2.19	0.42
1:A:35:TYR:HA	1:B:16:ARG:NH1	2.35	0.42
1:C:251:LEU:HD21	1:C:255:ARG:CZ	2.50	0.42
1:C:75:PHE:HB3	1:C:162:LEU:HB3	2.02	0.42
1:A:68:PHE:O	1:A:169:TYR:HA	2.20	0.42
1:B:192:GLU:HB2	4:B:401:HOH:O	2.18	0.42
1:D:24:ASP:CG	1:D:210:LEU:HB2	2.40	0.42
1:B:33:VAL:O	1:B:33:VAL:HG12	2.20	0.42
1:A:57:HIS:HE1	1:B:89:ASN:HD21	1.65	0.42
1:C:240:GLU:O	1:C:244:LYS:HG3	2.20	0.42
1:C:231:ARG:HG3	1:C:234:ARG:HH12	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:188:GLU:N	1:C:188:GLU:CD	2.68	0.41
1:A:190:GLN:CD	1:C:154:GLU:HB2	2.41	0.41
1:A:75:PHE:CZ	1:C:158:MET:HE2	2.55	0.41
1:B:223:ALA:HB3	1:C:230:LEU:HD11	2.03	0.41
1:B:48:LEU:HD22	1:B:52:LEU:HG	2.02	0.41
1:A:110:LYS:O	1:A:111:GLN:HG3	2.20	0.41
1:A:157:ARG:C	1:A:157:ARG:HD2	2.40	0.41
1:C:103:TYR:O	1:C:105:PRO:HD3	2.21	0.41
1:D:142:ALA:O	1:D:146:LEU:CD2	2.69	0.41
1:B:100:GLU:HB2	1:B:140:TYR:CE2	2.55	0.41
1:B:219:LEU:O	1:B:220:LEU:C	2.58	0.41
1:D:242:TYR:CZ	1:D:246:LEU:HD11	2.55	0.41
1:D:82:ARG:HH11	1:D:82:ARG:HG3	1.85	0.41
1:A:30:ALA:HB2	1:A:63:MET:HG3	2.03	0.41
1:C:67:LYS:HE2	1:D:21:MET:HE1	2.02	0.41
1:C:186:ALA:HB1	1:C:188:GLU:OE1	2.21	0.41
1:D:25:ARG:HG2	1:D:39:THR:HG21	2.02	0.41
1:A:258:GLU:O	1:A:262:LYS:HG3	2.20	0.41
1:B:162:LEU:HD12	1:D:162:LEU:HD23	2.02	0.41
1:D:48:LEU:O	1:D:52:LEU:HG	2.21	0.41
1:A:100:GLU:HG2	1:A:100:GLU:O	2.21	0.40
1:B:151:VAL:HG11	1:D:108:PHE:CD1	2.55	0.40
1:B:257:LYS:HA	1:B:257:LYS:HD3	1.88	0.40
1:C:234:ARG:C	1:C:236:LEU:H	2.22	0.40
1:D:80:TRP:CZ2	1:D:200:ILE:HD11	2.56	0.40
1:A:174:LEU:HD11	1:A:178:PHE:CZ	2.56	0.40
1:C:185:LEU:HD13	1:C:197:ALA:HB1	2.02	0.40
1:D:140:TYR:O	1:D:143:TYR:HB3	2.21	0.40
1:D:234:ARG:HG3	1:D:264:PHE:CD1	2.56	0.40
1:D:75:PHE:HZ	1:D:192:GLU:HG2	1.87	0.40
1:A:233:LEU:HD23	1:A:233:LEU:HA	1.87	0.40
1:D:246:LEU:HB3	1:D:256:LEU:HD12	2.02	0.40
1:A:159:VAL:HG12	1:C:132:LEU:HD12	2.03	0.40
1:B:102:PHE:N	1:B:102:PHE:CD1	2.90	0.40
1:B:109:ARG:NH1	1:D:155:MET:SD	2.95	0.40
1:D:202:GLU:OE2	1:D:202:GLU:HA	2.21	0.40
1:B:188:GLU:N	1:B:188:GLU:CD	2.72	0.40

There are no symmetry-related clashes.

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	238/270 (88%)	230 (97%)	8 (3%)	0	100	100
1	B	235/270 (87%)	219 (93%)	15 (6%)	1 (0%)	34	54
1	C	236/270 (87%)	223 (94%)	13 (6%)	0	100	100
1	D	238/270 (88%)	215 (90%)	22 (9%)	1 (0%)	34	54
All	All	947/1080 (88%)	887 (94%)	58 (6%)	2 (0%)	47	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	100	GLU
1	B	220	LEU

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	203/222 (91%)	191 (94%)	12 (6%)	19	37
1	B	201/222 (90%)	185 (92%)	16 (8%)	12	23
1	C	201/222 (90%)	189 (94%)	12 (6%)	19	37
1	D	203/222 (91%)	192 (95%)	11 (5%)	22	42
All	All	808/888 (91%)	757 (94%)	51 (6%)	18	34

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	39	THR
1	A	41	THR
1	A	48	LEU
1	A	57	HIS
1	A	88	VAL
1	A	106	GLU
1	A	135	VAL
1	A	157	ARG
1	A	185	LEU
1	A	255	ARG
1	A	256	LEU
1	B	48	LEU
1	B	57	HIS
1	B	88	VAL
1	B	104	GLU
1	B	106	GLU
1	B	132	LEU
1	B	133	ARG
1	B	148	GLU
1	B	157	ARG
1	B	174	LEU
1	B	177	LEU
1	B	185	LEU
1	B	193	ILE
1	B	208	VAL
1	B	221	GLU
1	B	246	LEU
1	C	16	ARG
1	C	57	HIS
1	C	104	GLU
1	C	133	ARG
1	C	146	LEU
1	C	153	ARG
1	C	157	ARG
1	C	174	LEU
1	C	185	LEU
1	C	188	GLU
1	C	254	SER
1	C	256	LEU
1	D	35	TYR
1	D	48	LEU
1	D	88	VAL

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Mol	Chain	Res	Type
1	D	95	TYR
1	D	101	GLU
1	D	133	ARG
1	D	157	ARG
1	D	174	LEU
1	D	177	LEU
1	D	185	LEU
1	D	225	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	HIS
1	A	89	ASN
1	B	57	HIS
1	B	89	ASN
1	B	195	GLN
1	C	57	HIS
1	C	79	GLN
1	C	89	ASN
1	D	55	HIS
1	D	57	HIS
1	D	89	ASN
1	D	136	GLN
1	D	195	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

12 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
3	PO4	A	302	-	4,4,4	1.70	0	6,6,6	0.42	0
3	PO4	B	303	-	4,4,4	1.56	0	6,6,6	0.42	0
3	PO4	D	303	-	4,4,4	1.71	0	6,6,6	0.43	0
3	PO4	D	302	-	4,4,4	1.62	0	6,6,6	0.42	0
3	PO4	B	302	-	4,4,4	1.58	0	6,6,6	0.44	0
3	PO4	A	303	-	4,4,4	1.66	0	6,6,6	0.41	0
2	FAD	D	301	-	51,58,58	2.30	7 (13%)	60,89,89	2.15	12 (20%)
2	FAD	A	301	-	51,58,58	2.20	6 (11%)	60,89,89	2.19	11 (18%)
2	FAD	C	301	-	51,58,58	2.36	7 (13%)	60,89,89	2.16	13 (21%)
3	PO4	C	303	-	4,4,4	1.68	0	6,6,6	0.44	0
2	FAD	B	301	-	51,58,58	2.23	7 (13%)	60,89,89	2.19	11 (18%)
3	PO4	C	302	-	4,4,4	1.65	0	6,6,6	0.43	0

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
2	FAD	A	301	-	-	5/30/50/50	0/6/6/6
2	FAD	C	301	-	-	3/30/50/50	0/6/6/6
2	FAD	B	301	-	-	1/30/50/50	0/6/6/6
2	FAD	D	301	-	-	0/30/50/50	0/6/6/6

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	FAD	C4X-C10	12.52	1.51	1.38
2	D	301	FAD	C4X-C10	11.92	1.50	1.38
2	A	301	FAD	C4X-C10	11.68	1.50	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	FAD	C4X-C10	11.34	1.50	1.38
2	D	301	FAD	C4-C4X	5.29	1.50	1.41
2	C	301	FAD	C4-C4X	5.20	1.50	1.41
2	B	301	FAD	C4-C4X	5.19	1.50	1.41
2	A	301	FAD	C4-C4X	4.94	1.49	1.41
2	D	301	FAD	O4B-C1B	4.83	1.47	1.41
2	C	301	FAD	O4B-C1B	4.76	1.47	1.41
2	B	301	FAD	O4B-C1B	4.68	1.47	1.41
2	C	301	FAD	C9A-N10	4.23	1.44	1.38
2	B	301	FAD	C9A-N10	4.14	1.44	1.38
2	D	301	FAD	C9A-N10	4.07	1.44	1.38
2	A	301	FAD	O4B-C1B	3.98	1.46	1.41
2	A	301	FAD	C9A-N10	3.86	1.43	1.38
2	B	301	FAD	C4-N3	3.40	1.39	1.33
2	C	301	FAD	C4-N3	3.23	1.38	1.33
2	D	301	FAD	C4-N3	3.21	1.38	1.33
2	A	301	FAD	C4-N3	3.07	1.38	1.33
2	A	301	FAD	C8A-N7A	-2.52	1.30	1.34
2	B	301	FAD	C8A-N7A	-2.20	1.30	1.34
2	C	301	FAD	C9A-C5X	2.17	1.46	1.42
2	C	301	FAD	C8A-N7A	-2.14	1.30	1.34
2	D	301	FAD	C8A-N7A	-2.10	1.31	1.34
2	D	301	FAD	C10-N1	2.09	1.36	1.33
2	B	301	FAD	C6-C5X	2.02	1.45	1.41

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	FAD	C4-N3-C2	8.24	122.09	115.14
2	C	301	FAD	C4-N3-C2	8.12	122.00	115.14
2	D	301	FAD	C4-N3-C2	8.10	121.98	115.14
2	B	301	FAD	C4-N3-C2	7.76	121.69	115.14
2	B	301	FAD	C1'-N10-C9A	6.10	123.10	118.29
2	A	301	FAD	P-O3P-PA	-5.61	113.58	132.83
2	B	301	FAD	P-O3P-PA	-5.52	113.87	132.83
2	C	301	FAD	C1'-N10-C9A	5.49	122.61	118.29
2	B	301	FAD	C4X-N5-C5X	5.47	122.23	116.77
2	C	301	FAD	P-O3P-PA	-5.45	114.14	132.83
2	D	301	FAD	P-O3P-PA	-5.43	114.19	132.83
2	A	301	FAD	C4-C4X-C10	-5.35	116.41	119.95
2	D	301	FAD	C4-C4X-C10	-5.31	116.44	119.95
2	D	301	FAD	C4X-N5-C5X	5.30	122.07	116.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	FAD	C4X-N5-C5X	5.29	122.05	116.77
2	A	301	FAD	C1'-N10-C9A	5.25	122.42	118.29
2	B	301	FAD	C4-C4X-C10	-5.21	116.50	119.95
2	D	301	FAD	C1'-N10-C9A	5.19	122.38	118.29
2	C	301	FAD	C4X-N5-C5X	5.19	121.95	116.77
2	C	301	FAD	C4-C4X-C10	-4.99	116.65	119.95
2	A	301	FAD	N3A-C2A-N1A	-4.72	121.30	128.68
2	B	301	FAD	N3A-C2A-N1A	-4.63	121.44	128.68
2	C	301	FAD	N3A-C2A-N1A	-4.59	121.51	128.68
2	A	301	FAD	C4X-C4-N3	-4.45	117.34	123.43
2	D	301	FAD	N3A-C2A-N1A	-4.45	121.72	128.68
2	C	301	FAD	C4X-C4-N3	-4.45	117.34	123.43
2	D	301	FAD	C4X-C4-N3	-4.35	117.48	123.43
2	B	301	FAD	C4X-C4-N3	-4.35	117.49	123.43
2	B	301	FAD	C4-C4X-N5	4.07	123.25	118.60
2	A	301	FAD	C4-C4X-N5	4.04	123.22	118.60
2	D	301	FAD	C4-C4X-N5	3.95	123.12	118.60
2	C	301	FAD	C4-C4X-N5	3.73	122.87	118.60
2	C	301	FAD	C9A-N10-C10	-2.63	118.47	121.91
2	D	301	FAD	C9A-N10-C10	-2.37	118.80	121.91
2	B	301	FAD	P-O5'-C5'	-2.29	108.28	121.68
2	A	301	FAD	C9A-N10-C10	-2.22	119.01	121.91
2	A	301	FAD	P-O5'-C5'	-2.17	108.95	121.68
2	C	301	FAD	C5X-C9A-N10	2.17	119.29	117.72
2	A	301	FAD	PA-O5B-C5B	-2.15	109.07	121.68
2	C	301	FAD	C4A-C5A-N7A	-2.15	107.16	109.40
2	C	301	FAD	P-O5'-C5'	-2.14	109.15	121.68
2	B	301	FAD	C9A-N10-C10	-2.13	119.11	121.91
2	D	301	FAD	P-O5'-C5'	-2.08	109.46	121.68
2	B	301	FAD	PA-O5B-C5B	-2.06	109.57	121.68
2	D	301	FAD	PA-O5B-C5B	-2.04	109.69	121.68
2	D	301	FAD	C5X-C9A-N10	2.03	119.18	117.72
2	C	301	FAD	PA-O5B-C5B	-2.01	109.89	121.68

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	FAD	P-O3P-PA-O5B
2	C	301	FAD	O4'-C4'-C5'-O5'
2	A	301	FAD	P-O3P-PA-O5B
2	C	301	FAD	P-O3P-PA-O5B

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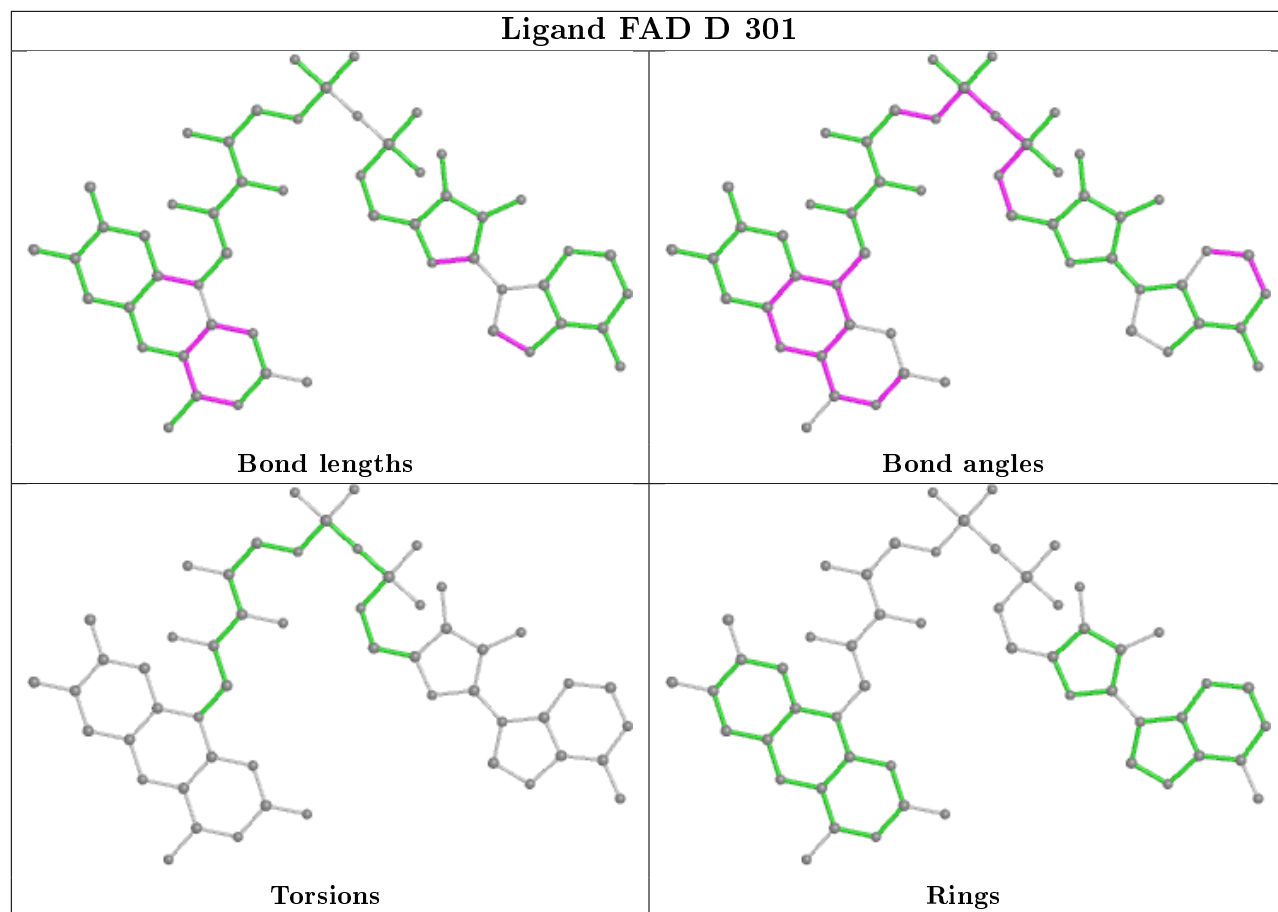
Mol	Chain	Res	Type	Atoms
2	C	301	FAD	C3'-C4'-C5'-O5'
2	A	301	FAD	C2'-C3'-C4'-O4'
2	A	301	FAD	O4'-C4'-C5'-O5'
2	A	301	FAD	C2'-C3'-C4'-C5'
2	A	301	FAD	O3'-C3'-C4'-C5'

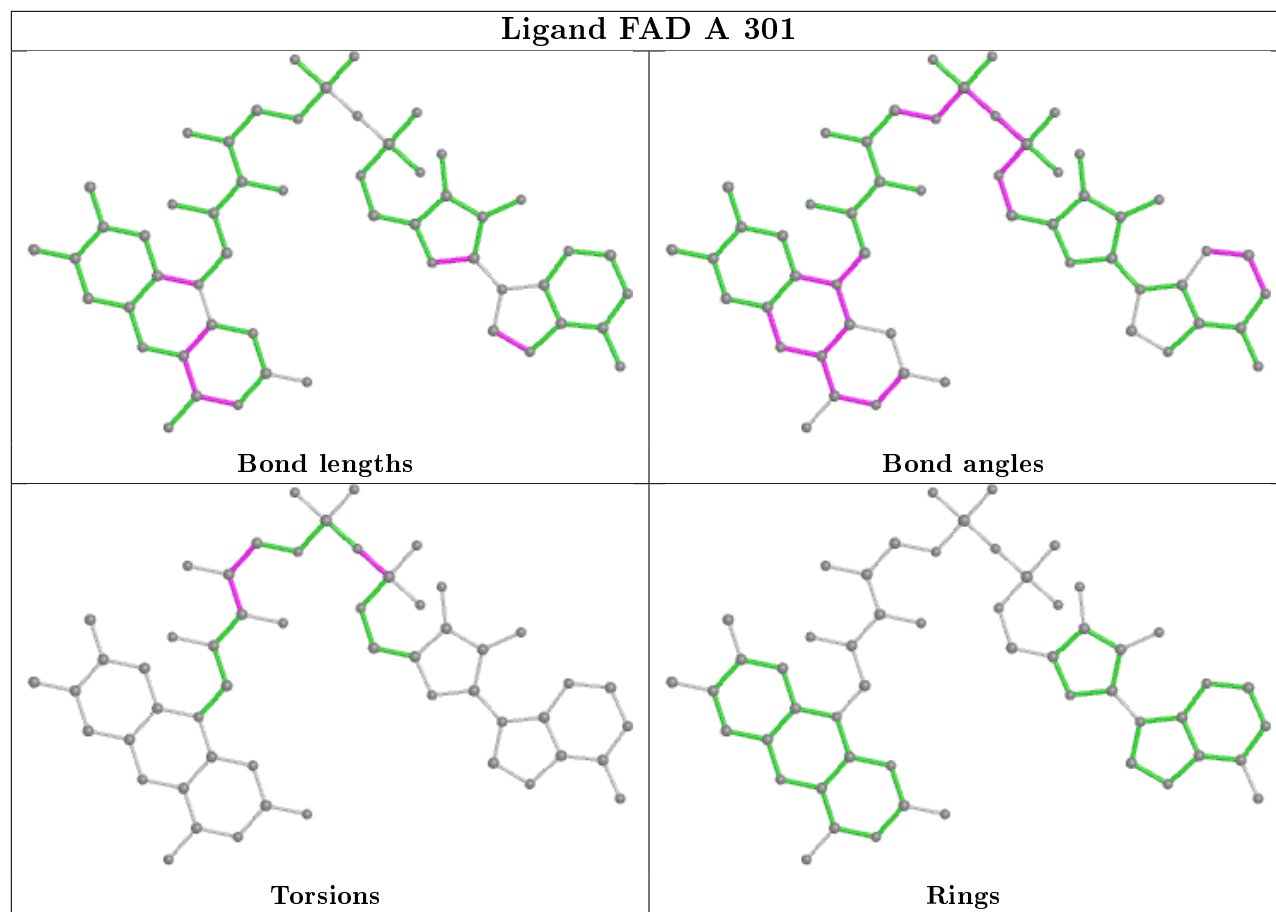
There are no ring outliers.

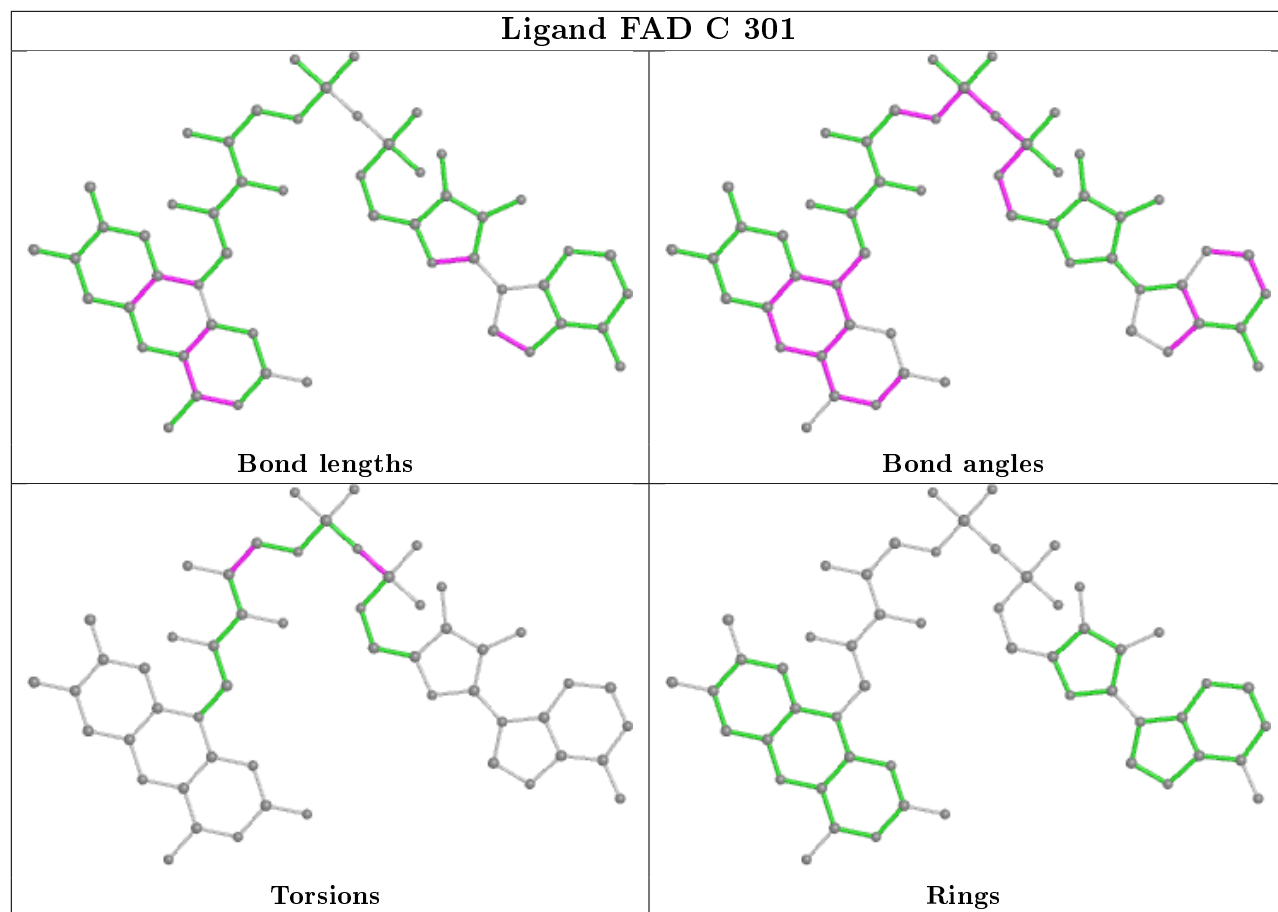
2 monomers are involved in 2 short contacts:

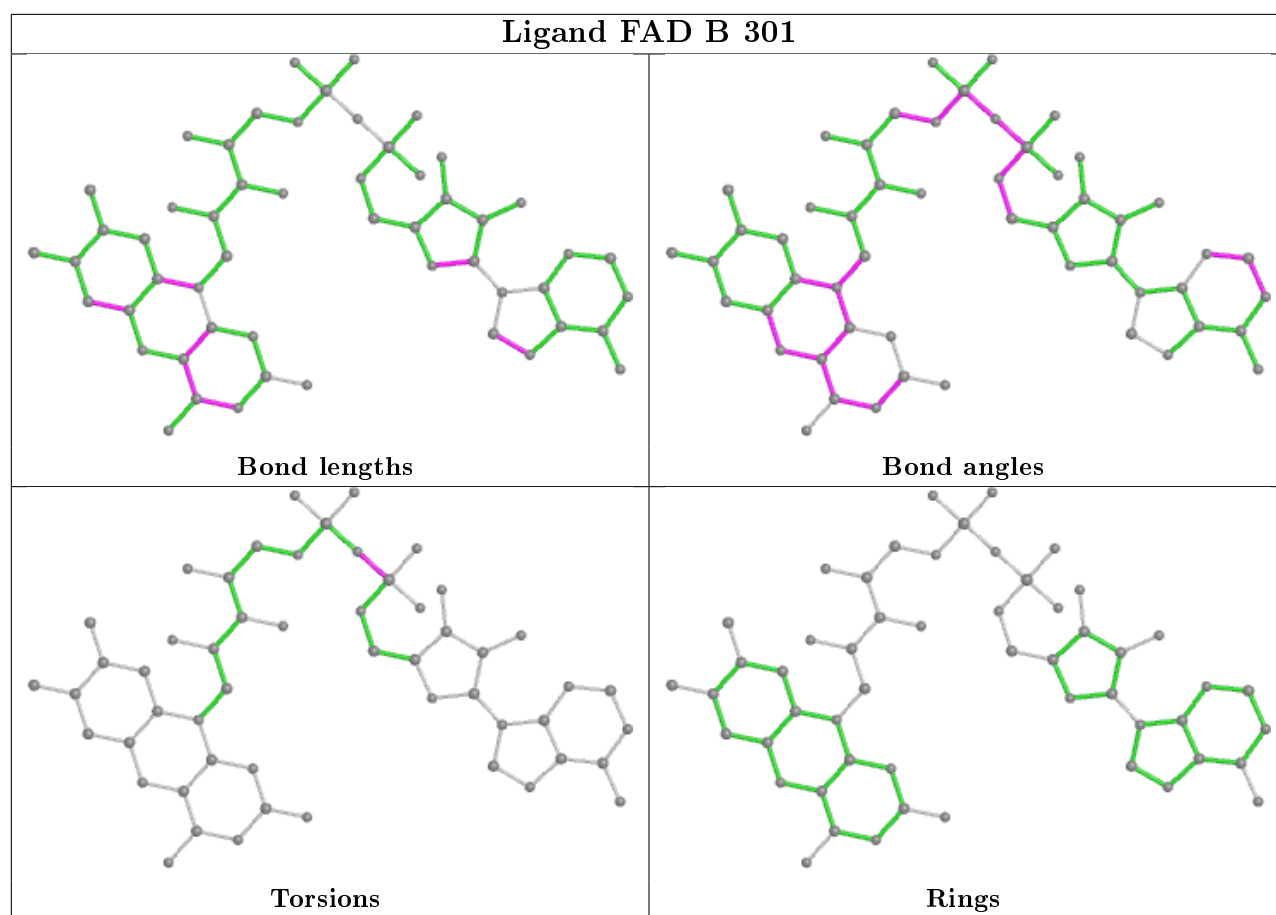
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	302	PO4	1	0
2	D	301	FAD	1	0

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	242/270 (89%)	0.04	6 (2%) 57 61	26, 44, 66, 84	0
1	B	239/270 (88%)	0.40	14 (5%) 22 23	33, 52, 75, 80	0
1	C	240/270 (88%)	0.21	9 (3%) 40 43	27, 44, 68, 84	0
1	D	242/270 (89%)	0.34	14 (5%) 23 24	24, 47, 73, 79	0
All	All	963/1080 (89%)	0.25	43 (4%) 33 36	24, 47, 71, 84	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	108	PHE	4.7
1	C	240	GLU	4.2
1	D	107	ALA	4.0
1	D	151	VAL	4.0
1	C	241	VAL	3.8
1	B	132	LEU	3.8
1	D	131	LEU	3.7
1	B	131	LEU	3.7
1	B	95	TYR	3.6
1	D	149	LYS	3.6
1	B	159	VAL	3.6
1	A	42	VAL	3.5
1	A	97	ILE	3.4
1	A	95	TYR	3.3
1	C	242	TYR	3.3
1	B	135	VAL	3.3
1	C	108	PHE	3.2
1	D	233	LEU	3.1
1	D	95	TYR	3.0
1	D	132	LEU	2.9
1	B	138	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	100	GLU	2.8
1	D	41	THR	2.8
1	C	5	LEU	2.8
1	B	134	LYS	2.7
1	D	242	TYR	2.6
1	C	150	GLY	2.6
1	A	244	LYS	2.6
1	D	260	LEU	2.5
1	C	244	LYS	2.4
1	D	134	LYS	2.4
1	B	146	LEU	2.3
1	B	102	PHE	2.3
1	B	105	PRO	2.2
1	D	42	VAL	2.2
1	B	30	ALA	2.1
1	D	264	PHE	2.1
1	A	5	LEU	2.1
1	C	131	LEU	2.1
1	D	253	GLY	2.1
1	B	100	GLU	2.0
1	B	148	GLU	2.0
1	C	106	GLU	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(Å ²)	Q<0.9
2	FAD	D	301	53/53	0.85	0.22	61,74,93,93	0

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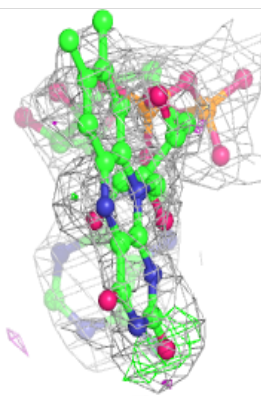
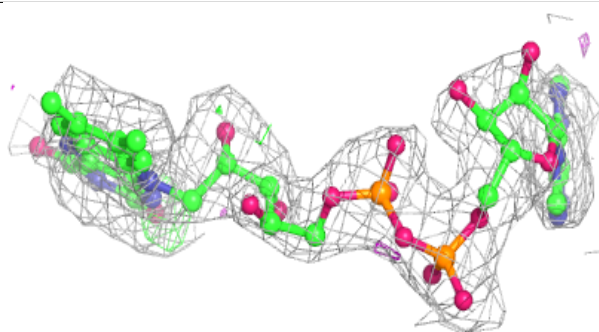
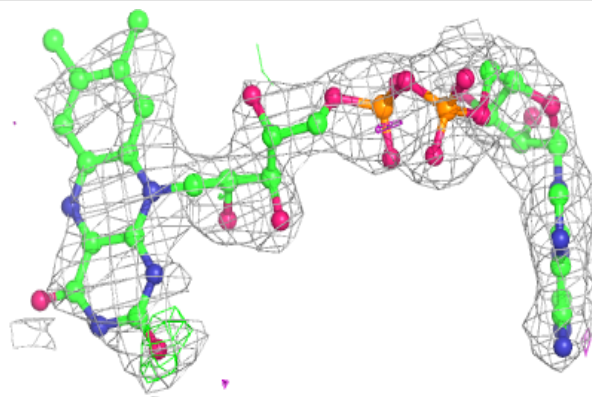
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PO4	C	302	5/5	0.86	0.19	92,93,93,93	0
2	FAD	B	301	53/53	0.88	0.21	56,61,66,67	0
2	FAD	C	301	53/53	0.90	0.24	59,65,72,74	0
2	FAD	A	301	53/53	0.91	0.20	55,64,74,75	0
3	PO4	A	303	5/5	0.92	0.16	98,98,98,98	0
3	PO4	D	302	5/5	0.93	0.17	77,77,78,78	0
3	PO4	B	302	5/5	0.93	0.24	82,83,84,85	0
3	PO4	A	302	5/5	0.94	0.18	73,74,74,75	0
3	PO4	D	303	5/5	0.95	0.16	69,69,70,71	0
3	PO4	B	303	5/5	0.97	0.11	62,64,66,66	0
3	PO4	C	303	5/5	0.97	0.13	52,52,53,54	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.

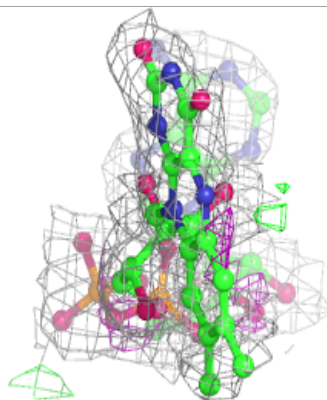
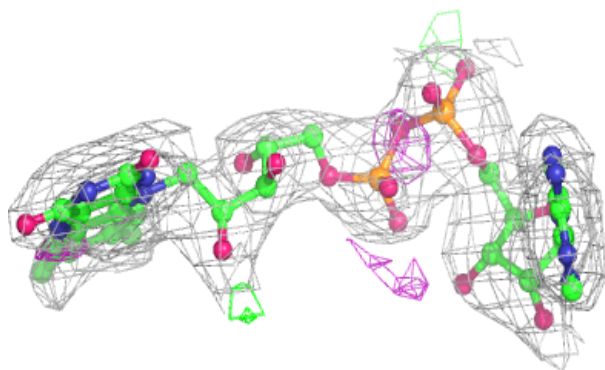
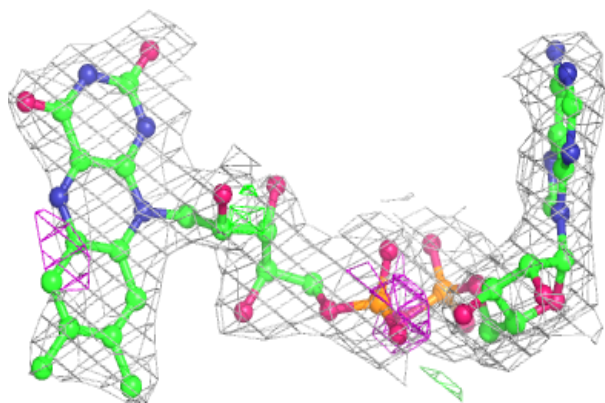
Electron density around FAD D 301:

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

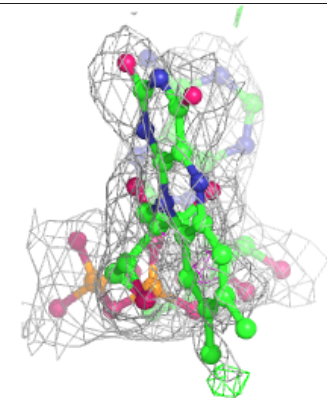
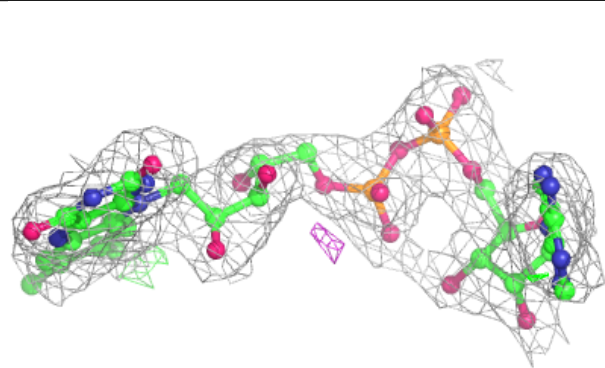
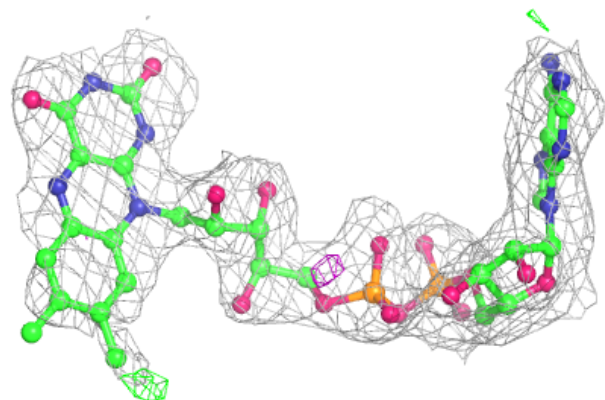


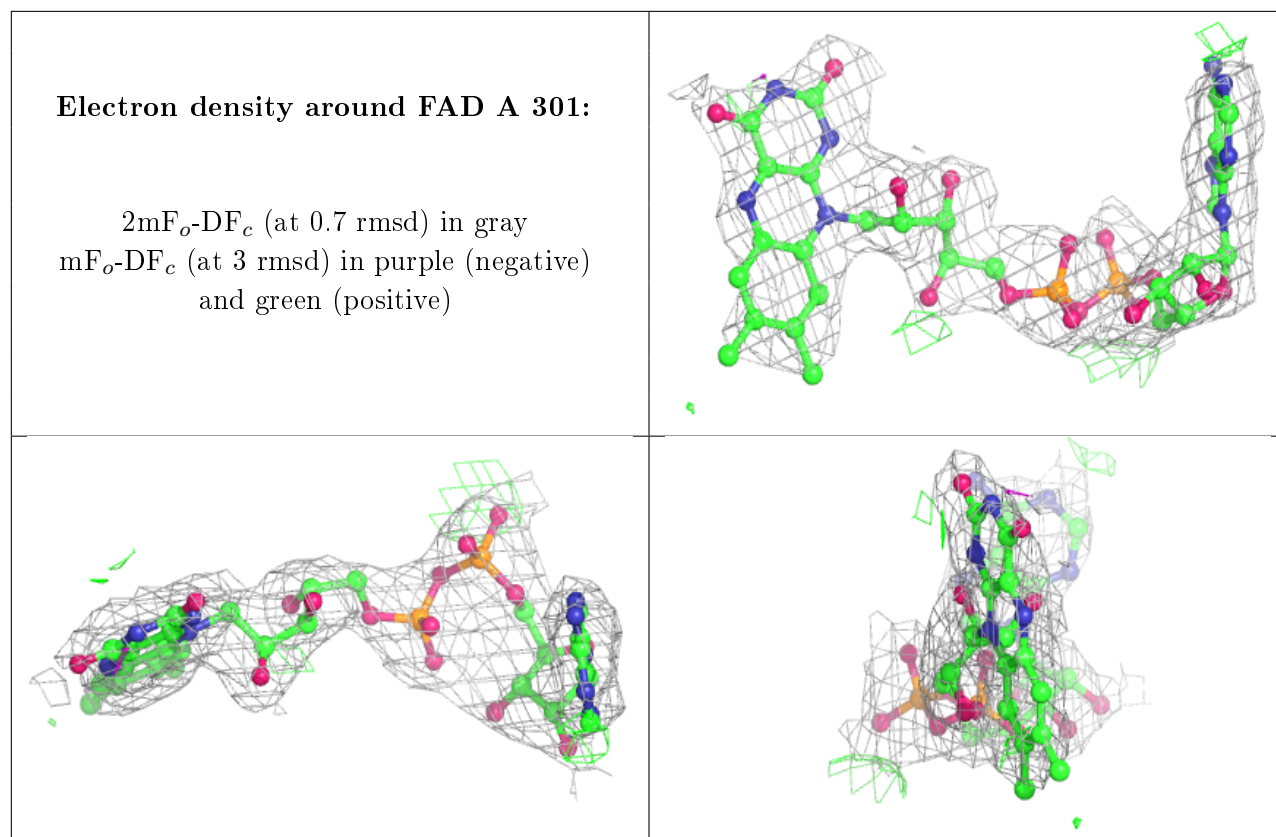
Electron density around FAD B 301:

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

**Electron density around FAD C 301:**

$2mF_o - DF_c$ (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.