Full wwPDB X-ray Structure Validation Report (i)

Mar 5, 2026 – 04:40 PM UTC

PDB ID	:	6WLE / pdb_00006wle
Title	:	Crystal structure of the Zeitlupe light-state mimic G46A
Authors	:	Zoltowski, B.; Green, R.
Deposited on	:	2020-04-20
Resolution	:	3.00 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 (i) 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 (i)) were used in the production of this report:

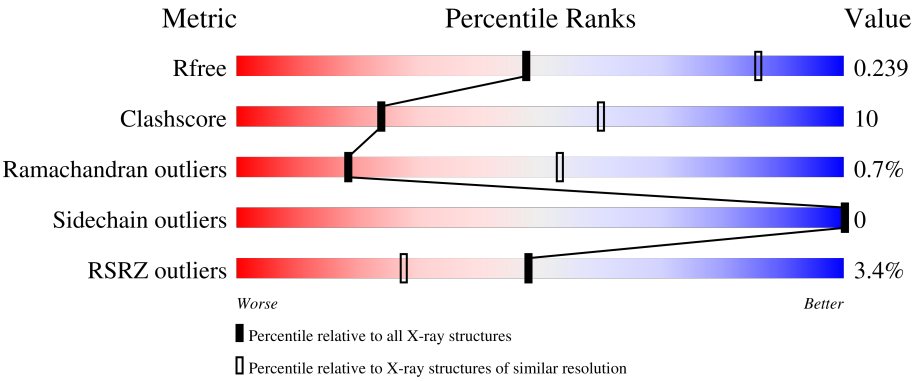
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



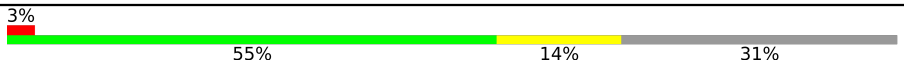
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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% 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	190	2% 56% 12% 32%
1	B	190	2% 58% 10% 32%
1	C	190	2% 55% 14% 31%
1	D	190	3% 52% 17% 32%
1	E	190	3% 56% 12% 32%

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Mol	Chain	Length	Quality of chain
1	F	190	
1	G	190	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 14875 atoms, of which 7301 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.

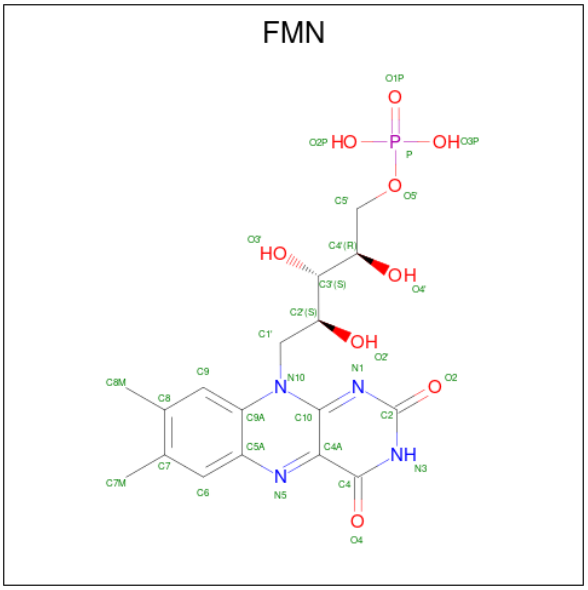
- Molecule 1 is a protein called Adagio protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	130	Total	C	H	N	O	S	0	0	0
			2054	656	1022	178	191	7			
1	A	130	Total	C	H	N	O	S	0	0	0
			2046	656	1014	178	191	7			
1	C	131	Total	C	H	N	O	S	0	0	0
			2060	661	1021	179	192	7			
1	D	130	Total	C	H	N	O	S	0	0	0
			2058	656	1026	178	191	7			
1	E	130	Total	C	H	N	O	S	0	0	0
			2054	656	1022	178	191	7			
1	F	131	Total	C	H	N	O	S	0	0	0
			2075	665	1031	179	193	7			
1	G	130	Total	C	H	N	O	S	0	0	0
			2046	656	1014	178	191	7			

There are 14 discrepancies between the modelled and reference sequences:

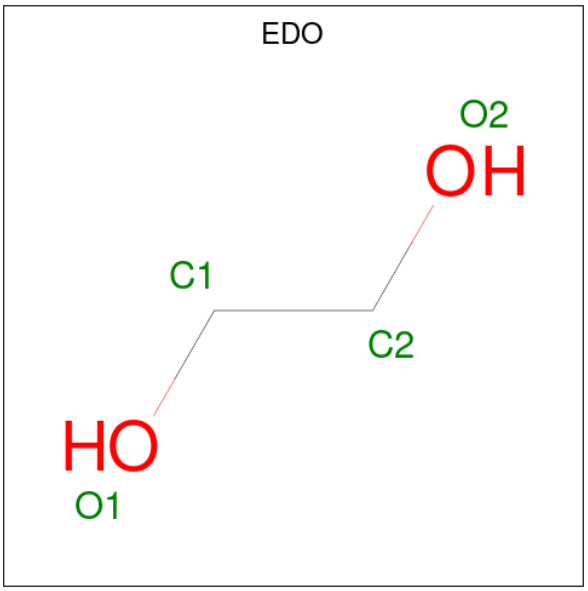
Chain	Residue	Modelled	Actual	Comment	Reference
B	18	ALA	GLY	engineered mutation	UNP Q94BT6
B	52	ARG	GLY	conflict	UNP Q94BT6
A	18	ALA	GLY	engineered mutation	UNP Q94BT6
A	52	ARG	GLY	conflict	UNP Q94BT6
C	18	ALA	GLY	engineered mutation	UNP Q94BT6
C	52	ARG	GLY	conflict	UNP Q94BT6
D	18	ALA	GLY	engineered mutation	UNP Q94BT6
D	52	ARG	GLY	conflict	UNP Q94BT6
E	18	ALA	GLY	engineered mutation	UNP Q94BT6
E	52	ARG	GLY	conflict	UNP Q94BT6
F	18	ALA	GLY	engineered mutation	UNP Q94BT6
F	52	ARG	GLY	conflict	UNP Q94BT6
G	18	ALA	GLY	engineered mutation	UNP Q94BT6
G	52	ARG	GLY	conflict	UNP Q94BT6

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		
2	A	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		
2	C	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		
2	D	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		
2	E	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		
2	F	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		
2	G	1	Total	C	H	N	O	P	0	0
			50	17	19	4	9	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C H O 10 2 6 2	0	0
3	D	1	Total C H O 10 2 6 2	0	0
3	E	1	Total C H O 10 2 6 2	0	0

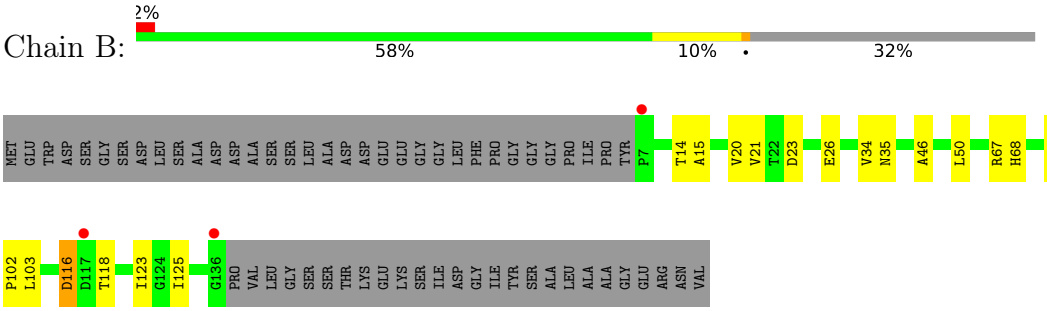
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	29	Total O 29 29	0	0
4	A	10	Total O 10 10	0	0
4	C	8	Total O 8 8	0	0
4	D	10	Total O 10 10	0	0
4	E	15	Total O 15 15	0	0
4	F	21	Total O 21 21	0	0
4	G	9	Total O 9 9	0	0

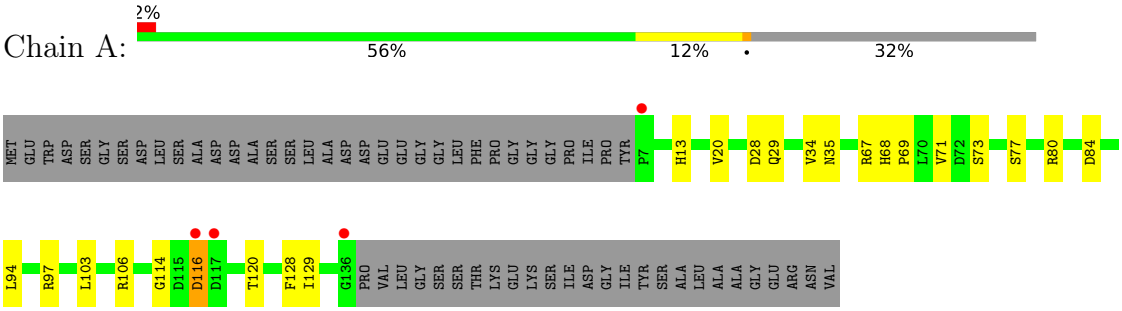
3 Residue-property plots (i)

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.

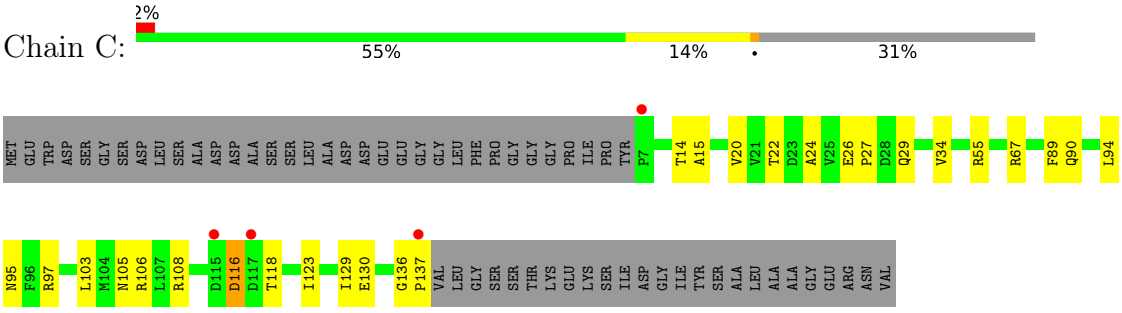
• Molecule 1: Adagio protein 1



• Molecule 1: Adagio protein 1

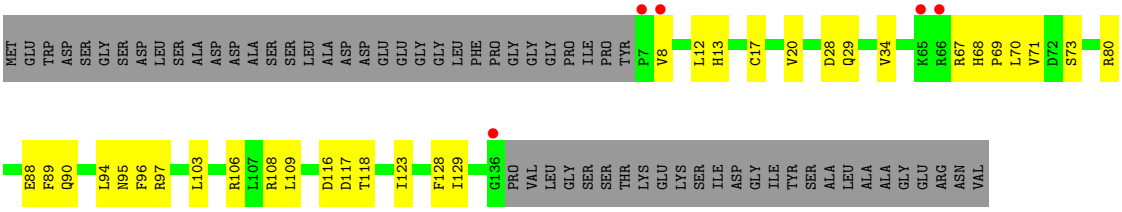


• Molecule 1: Adagio protein 1



• Molecule 1: Adagio protein 1

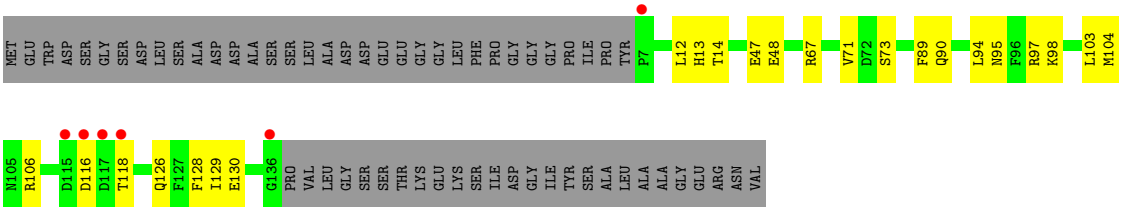




• Molecule 1: Adagio protein 1

Chain E:

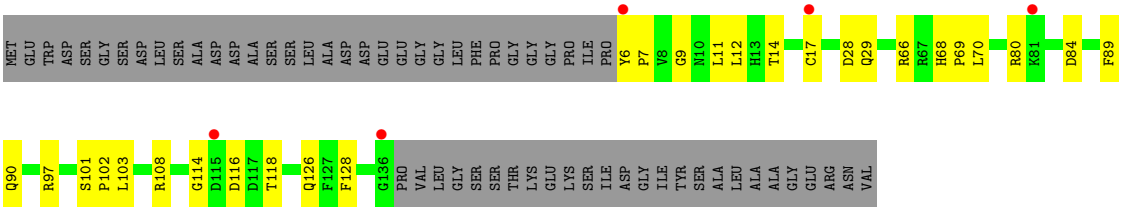




• Molecule 1: Adagio protein 1

Chain F:

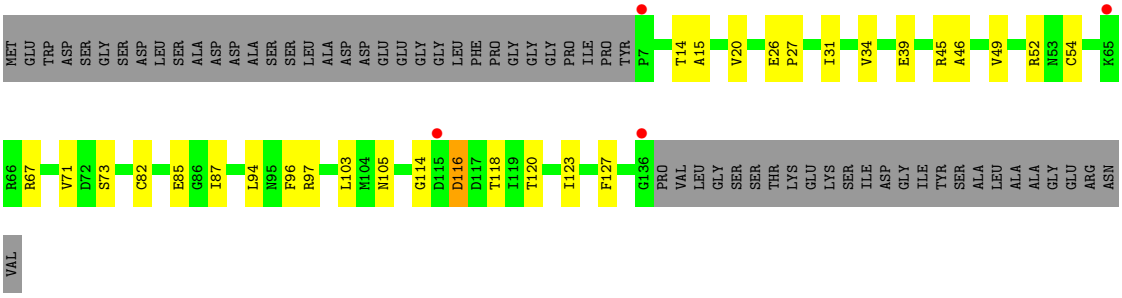




• Molecule 1: Adagio protein 1

Chain G:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, α, β, γ	265.82Å 265.82Å 265.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.59 – 3.00 45.59 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.59-3.00) 94.4 (45.59-3.00)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.65 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.203 , 0.242 0.204 , 0.239	Depositor DCC
R_{free} test set	1999 reflections (3.21%)	wwPDB-VP
Wilson B-factor (Å^2)	49.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 56.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -l,-k,-h	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	14875	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.75% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, FMN

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	0.65	0/1053	0.82	0/1427
1	B	0.77	0/1053	0.89	0/1427
1	C	0.73	0/1061	0.87	0/1439
1	D	0.69	1/1053 (0.1%)	0.84	1/1427 (0.1%)
1	E	0.79	0/1053	0.93	1/1427 (0.1%)
1	F	0.78	0/1066	0.85	0/1446
1	G	0.67	0/1053	0.77	0/1427
All	All	0.73	1/7392 (0.0%)	0.86	2/10020 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	17	CYS	CB-SG	-5.40	1.63	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	104	MET	CG-SD-CE	-6.10	87.48	100.90
1	D	17	CYS	CA-CB-SG	-5.59	101.54	114.40

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	1032	1014	1025	19	0
1	B	1032	1022	1025	18	0
1	C	1039	1021	1032	23	0
1	D	1032	1026	1025	26	0
1	E	1032	1022	1025	23	0
1	F	1044	1031	1034	23	3
1	G	1032	1014	1025	23	0
2	A	31	19	19	0	0
2	B	31	19	19	0	0
2	C	31	19	19	4	0
2	D	31	19	19	1	0
2	E	31	19	19	0	0
2	F	31	19	19	1	0
2	G	31	19	19	0	0
3	C	4	6	6	1	0
3	D	4	6	6	0	0
3	E	4	6	6	0	0
4	A	10	0	0	0	0
4	B	29	0	0	1	0
4	C	8	0	0	0	0
4	D	10	0	0	0	0
4	E	15	0	0	1	0
4	F	21	0	0	1	0
4	G	9	0	0	0	0
All	All	7574	7301	7342	149	3

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 10.

All (149) 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:F:116:ASP:HB2	1:F:118:THR:HG22	1.39	1.00
1:E:12:LEU:HD22	1:E:14:THR:O	1.75	0.86
1:D:103:LEU:HD23	1:D:128:PHE:HB3	1.59	0.84
1:B:116:ASP:HB2	1:B:118:THR:HG22	1.60	0.82
1:G:20:VAL:HG22	1:G:34:VAL:HG12	1.64	0.79
1:F:66:ARG:NH2	4:F:5301:HOH:O	2.18	0.76
1:F:102:PRO:O	1:F:103:LEU:HD12	1.84	0.76
1:G:116:ASP:HB3	1:G:118:THR:H	1.50	0.76
1:B:14:THR:HG22	1:B:15:ALA:H	1.51	0.73
1:E:12:LEU:HD23	1:E:14:THR:H	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:103:LEU:HG	1:E:128:PHE:HB3	1.70	0.72
1:G:116:ASP:HB2	1:G:118:THR:HG22	1.71	0.72
1:D:90:GLN:HG3	1:D:108:ARG:HD3	1.72	0.72
1:E:106:ARG:NH2	1:E:129:ILE:HD11	2.06	0.71
1:B:116:ASP:CB	1:B:118:THR:HG22	2.19	0.70
1:D:116:ASP:O	1:D:118:THR:N	2.25	0.69
1:F:6:TYR:HB2	1:F:7:PRO:CD	2.22	0.69
1:C:116:ASP:HB3	1:C:118:THR:H	1.56	0.69
1:F:80:ARG:NH1	2:F:5201:FMN:O3P	2.25	0.69
1:G:116:ASP:CB	1:G:118:THR:HG22	2.24	0.68
1:D:103:LEU:CD2	1:D:128:PHE:HB3	2.26	0.66
1:D:103:LEU:HD23	1:D:128:PHE:CB	2.26	0.66
1:D:103:LEU:HD23	1:D:128:PHE:CG	2.30	0.65
1:F:90:GLN:HG3	1:F:108:ARG:HD3	1.80	0.63
1:A:67:ARG:HD2	1:A:71:VAL:CG2	2.30	0.61
1:C:55:ARG:NE	2:C:5302:FMN:O2P	2.31	0.60
1:D:71:VAL:HG12	1:D:94:LEU:HB3	1.84	0.59
1:D:80:ARG:NH1	2:D:5302:FMN:O3P	2.36	0.59
1:E:106:ARG:CZ	1:E:129:ILE:HD11	2.33	0.59
1:D:103:LEU:HD23	1:D:128:PHE:CD1	2.37	0.59
1:B:20:VAL:HG22	1:B:34:VAL:HG12	1.86	0.58
1:A:13:HIS:CE1	1:E:106:ARG:HD2	2.38	0.58
1:E:12:LEU:CD2	1:E:14:THR:H	2.17	0.58
1:G:97:ARG:CZ	1:G:103:LEU:HD11	2.35	0.57
1:G:67:ARG:HD3	1:G:71:VAL:HG21	1.89	0.55
1:E:12:LEU:HD23	1:E:13:HIS:N	2.22	0.54
1:A:67:ARG:HD2	1:A:71:VAL:HG22	1.90	0.54
1:E:116:ASP:HB3	1:E:118:THR:HG22	1.89	0.54
1:D:97:ARG:CZ	1:D:103:LEU:HD11	2.37	0.53
1:F:12:LEU:HD23	1:F:14:THR:H	1.71	0.53
1:C:106:ARG:CZ	1:C:129:ILE:HD11	2.38	0.53
1:B:123:ILE:HD11	1:D:123:ILE:CD1	2.39	0.53
1:E:71:VAL:HG12	1:E:94:LEU:HB3	1.91	0.52
1:C:106:ARG:NH2	1:C:129:ILE:HD11	2.26	0.51
1:D:20:VAL:HG22	1:D:34:VAL:HG12	1.92	0.51
1:E:12:LEU:HD23	1:E:14:THR:N	2.25	0.51
1:A:20:VAL:HG22	1:A:34:VAL:HG12	1.91	0.51
1:G:71:VAL:HG12	1:G:94:LEU:HB3	1.92	0.50
1:G:114:GLY:HA3	1:G:120:THR:CG2	2.41	0.50
1:A:67:ARG:NH1	1:A:73:SER:HB3	2.26	0.50
1:G:114:GLY:HA3	1:G:120:THR:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:LEU:HD22	1:B:96:PHE:CZ	2.47	0.50
1:C:15:ALA:HB2	1:G:127:PHE:CE2	2.47	0.50
1:E:12:LEU:HD22	1:E:14:THR:C	2.36	0.50
1:C:55:ARG:NH2	2:C:5302:FMN:O2P	2.44	0.50
1:C:14:THR:HG22	1:C:15:ALA:H	1.77	0.49
1:G:14:THR:OG1	1:G:15:ALA:N	2.46	0.49
1:A:116:ASP:OD2	1:A:116:ASP:N	2.27	0.49
1:C:136:GLY:O	1:C:137:PRO:O	2.31	0.49
1:G:67:ARG:NH1	1:G:73:SER:HB3	2.28	0.48
1:A:71:VAL:HG12	1:A:94:LEU:HB3	1.95	0.48
1:A:106:ARG:NH2	1:A:129:ILE:CD1	2.76	0.48
1:G:82:CYS:HB3	1:G:87:ILE:HG13	1.95	0.48
1:F:6:TYR:HB2	1:F:7:PRO:HD3	1.92	0.48
1:F:68:HIS:CG	1:F:69:PRO:HD2	2.47	0.48
1:B:14:THR:HG22	1:B:15:ALA:N	2.25	0.48
1:D:106:ARG:CZ	1:D:129:ILE:HD11	2.44	0.48
1:G:39:GLU:OE2	1:G:46:ALA:HB2	2.14	0.48
1:B:123:ILE:HD11	1:D:123:ILE:HD13	1.96	0.48
1:D:94:LEU:HD22	1:D:96:PHE:CZ	2.48	0.48
1:F:68:HIS:ND1	1:F:70:LEU:HB2	2.28	0.48
1:D:67:ARG:NH1	1:D:73:SER:HB3	2.29	0.48
1:E:97:ARG:HG3	1:E:103:LEU:HD22	1.96	0.48
1:G:105:ASN:OD1	1:G:105:ASN:C	2.54	0.47
1:D:88:GLU:HG3	1:D:109:LEU:O	2.14	0.47
1:F:126:GLN:HB3	1:F:128:PHE:CE2	2.50	0.47
1:F:89:PHE:CG	1:F:90:GLN:N	2.82	0.47
1:F:114:GLY:C	1:F:116:ASP:H	2.22	0.47
1:C:22:THR:HG23	2:C:5302:FMN:C7M	2.44	0.47
1:E:129:ILE:HG22	1:E:130:GLU:O	2.15	0.47
1:C:67:ARG:HH22	3:C:5301:EDO:H21	1.81	0.46
1:G:67:ARG:HD3	1:G:71:VAL:CG2	2.46	0.46
1:C:123:ILE:HD11	1:G:123:ILE:HD11	1.98	0.46
1:E:12:LEU:CD2	1:E:14:THR:N	2.79	0.46
1:E:48:GLU:OE1	1:E:98:LYS:HE3	2.16	0.46
1:E:90:GLN:NE2	4:E:5401:HOH:O	2.38	0.46
1:E:126:GLN:HB3	1:E:128:PHE:CE2	2.51	0.46
1:C:94:LEU:HD23	1:C:95:ASN:N	2.31	0.46
1:D:68:HIS:HE1	1:D:70:LEU:HD12	1.81	0.46
1:B:14:THR:CG2	1:B:15:ALA:H	2.24	0.45
1:E:47:GLU:HG3	1:E:48:GLU:N	2.30	0.45
1:D:94:LEU:HD23	1:D:95:ASN:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:67:ARG:HD3	1:D:71:VAL:CG2	2.46	0.45
1:B:102:PRO:O	1:B:103:LEU:HD12	2.16	0.45
1:A:67:ARG:HH12	1:A:73:SER:HB3	1.81	0.45
1:A:80:ARG:O	1:A:84:ASP:HB2	2.16	0.45
1:C:14:THR:HG22	1:C:15:ALA:N	2.33	0.44
1:A:103:LEU:HD23	1:A:128:PHE:HB3	1.99	0.44
1:C:26:GLU:HB3	1:C:27:PRO:CD	2.47	0.44
1:B:20:VAL:HG12	1:B:21:VAL:N	2.32	0.44
1:A:114:GLY:HA3	1:A:120:THR:HG21	2.00	0.44
1:B:46:ALA:O	1:B:50:LEU:HG	2.17	0.44
1:C:97:ARG:CZ	1:C:103:LEU:HD11	2.48	0.44
1:D:68:HIS:CG	1:D:69:PRO:HD2	2.53	0.43
1:F:80:ARG:O	1:F:84:ASP:HB2	2.18	0.43
1:C:116:ASP:HB2	1:C:118:THR:HG22	2.00	0.43
1:C:90:GLN:HG3	1:C:108:ARG:HD3	2.00	0.43
1:D:28:ASP:O	1:D:29:GLN:C	2.62	0.43
1:F:11:LEU:HD12	1:F:11:LEU:H	1.82	0.43
1:E:67:ARG:NH1	1:E:73:SER:HB3	2.33	0.43
1:F:97:ARG:HD2	1:F:101:SER:OG	2.19	0.43
1:F:102:PRO:C	1:F:103:LEU:CD1	2.92	0.43
1:A:68:HIS:CG	1:A:69:PRO:HD2	2.53	0.42
1:F:102:PRO:C	1:F:103:LEU:HD12	2.44	0.42
1:G:45:ARG:HG3	1:G:45:ARG:NH1	2.35	0.42
1:F:28:ASP:O	1:F:29:GLN:C	2.62	0.42
1:G:31:ILE:HD11	1:G:54:CYS:SG	2.59	0.42
1:E:94:LEU:HD23	1:E:95:ASN:N	2.34	0.42
1:F:11:LEU:HD12	1:F:11:LEU:N	2.35	0.42
1:G:94:LEU:HD22	1:G:96:PHE:CZ	2.55	0.42
1:B:23:ASP:OD2	1:B:26:GLU:HG2	2.20	0.42
1:D:116:ASP:O	1:D:118:THR:HG22	2.20	0.42
1:F:9:GLY:HA2	1:F:11:LEU:HD11	2.00	0.42
1:B:123:ILE:CD1	1:D:123:ILE:HD13	2.49	0.42
1:A:35:ASN:OD1	1:A:35:ASN:C	2.62	0.42
1:C:20:VAL:HG22	1:C:34:VAL:HG12	2.02	0.41
1:F:12:LEU:CD2	1:F:14:THR:H	2.33	0.41
1:G:85:GLU:O	1:G:87:ILE:HG23	2.21	0.41
1:B:26:GLU:HB3	4:B:5305:HOH:O	2.21	0.41
1:B:35:ASN:OD1	1:B:35:ASN:C	2.61	0.41
1:B:123:ILE:HG22	1:B:125:ILE:CD1	2.50	0.41
1:C:22:THR:HG23	2:C:5302:FMN:HM73	2.02	0.41
1:D:89:PHE:CG	1:D:90:GLN:N	2.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:49:VAL:HA	1:G:52:ARG:HD3	2.02	0.41
1:A:67:ARG:CD	1:A:71:VAL:CG2	2.98	0.41
1:A:28:ASP:O	1:A:29:GLN:C	2.64	0.41
1:A:77:SER:OG	1:A:80:ARG:NH2	2.54	0.41
1:C:89:PHE:CG	1:C:90:GLN:N	2.89	0.41
1:C:105:ASN:OD1	1:C:105:ASN:C	2.63	0.41
1:E:89:PHE:CG	1:E:90:GLN:N	2.88	0.41
1:G:26:GLU:HB3	1:G:27:PRO:CD	2.51	0.41
1:B:67:ARG:HG3	1:B:68:HIS:N	2.36	0.40
1:E:97:ARG:O	1:E:98:LYS:C	2.64	0.40
1:C:24:ALA:HA	1:C:29:GLN:OE1	2.21	0.40
1:C:129:ILE:HG22	1:C:130:GLU:O	2.20	0.40
1:F:102:PRO:O	1:F:103:LEU:CD1	2.62	0.40
1:A:71:VAL:HG12	1:A:94:LEU:CB	2.52	0.40
1:A:97:ARG:CZ	1:A:103:LEU:HD11	2.52	0.40
1:D:12:LEU:HD23	1:D:13:HIS:H	1.87	0.40

All (3) 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)
1:F:17:CYS:SG	1:F:17:CYS:HG[15_455]	1.19	0.41
1:F:17:CYS:CB	1:F:17:CYS:SG[15_455]	1.79	0.41
1:F:17:CYS:CB	1:F:17:CYS:HG[15_455]	1.25	0.35

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	128/190 (67%)	116 (91%)	11 (9%)	1 (1%)	16 50
1	B	128/190 (67%)	122 (95%)	5 (4%)	1 (1%)	16 50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	129/190 (68%)	120 (93%)	8 (6%)	1 (1%)	16 50
1	D	128/190 (67%)	120 (94%)	6 (5%)	2 (2%)	7 34
1	E	128/190 (67%)	122 (95%)	6 (5%)	0	100 100
1	F	129/190 (68%)	120 (93%)	9 (7%)	0	100 100
1	G	128/190 (67%)	117 (91%)	10 (8%)	1 (1%)	16 50
All	All	898/1330 (68%)	837 (93%)	55 (6%)	6 (1%)	18 53

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	116	ASP
1	C	116	ASP
1	D	117	ASP
1	G	116	ASP
1	A	116	ASP
1	D	8	VAL

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	115/160 (72%)	115 (100%)	0	100 100
1	B	115/160 (72%)	115 (100%)	0	100 100
1	C	116/160 (72%)	116 (100%)	0	100 100
1	D	115/160 (72%)	115 (100%)	0	100 100
1	E	115/160 (72%)	115 (100%)	0	100 100
1	F	116/160 (72%)	116 (100%)	0	100 100
1	G	115/160 (72%)	115 (100%)	0	100 100
All	All	807/1120 (72%)	807 (100%)	0	100 100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	29	GLN
1	E	13	HIS

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)

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	$\#\|Z\| > 2$
2	FMN	A	5201	-	33,33,33	1.19	3 (9%)	48,50,50	1.28	5 (10%)
2	FMN	G	5201	-	33,33,33	1.05	2 (6%)	48,50,50	1.52	11 (22%)
2	FMN	E	5302	-	33,33,33	1.17	3 (9%)	48,50,50	1.65	10 (20%)
2	FMN	C	5302	-	33,33,33	1.09	2 (6%)	48,50,50	1.32	7 (14%)
3	EDO	C	5301	-	3,3,3	0.51	0	2,2,2	0.56	0
3	EDO	D	5301	-	3,3,3	0.48	0	2,2,2	0.56	0
2	FMN	D	5302	-	33,33,33	1.19	2 (6%)	48,50,50	1.50	10 (20%)
2	FMN	F	5201	-	33,33,33	1.20	3 (9%)	48,50,50	1.32	7 (14%)
3	EDO	E	5301	-	3,3,3	0.64	0	2,2,2	0.61	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	FMN	B	5201	-	33,33,33	1.25	4 (12%)	48,50,50	1.54	9 (18%)

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	FMN	A	5201	-	-	1/18/18/18	0/3/3/3
2	FMN	G	5201	-	-	2/18/18/18	0/3/3/3
2	FMN	E	5302	-	-	3/18/18/18	0/3/3/3
2	FMN	C	5302	-	-	5/18/18/18	0/3/3/3
3	EDO	C	5301	-	-	1/1/1/1	-
3	EDO	D	5301	-	-	1/1/1/1	-
2	FMN	D	5302	-	-	1/18/18/18	0/3/3/3
2	FMN	F	5201	-	-	1/18/18/18	0/3/3/3
3	EDO	E	5301	-	-	1/1/1/1	-
2	FMN	B	5201	-	-	1/18/18/18	0/3/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5302	FMN	C4A-N5	3.59	1.38	1.30
2	C	5302	FMN	C4A-N5	3.53	1.38	1.30
2	F	5201	FMN	C4A-N5	3.11	1.37	1.30
2	F	5201	FMN	C5'-C4'	3.11	1.56	1.51
2	A	5201	FMN	C4A-N5	2.98	1.37	1.30
2	G	5201	FMN	C4A-N5	2.77	1.36	1.30
2	D	5302	FMN	C10-N1	2.72	1.38	1.33
2	B	5201	FMN	C4A-N5	2.71	1.36	1.30
2	C	5302	FMN	C10-N1	2.70	1.38	1.33
2	A	5201	FMN	C10-N1	2.66	1.38	1.33
2	E	5302	FMN	C10-N1	2.44	1.38	1.33
2	E	5302	FMN	C4A-N5	2.43	1.36	1.30
2	G	5201	FMN	C10-N1	2.41	1.38	1.33
2	F	5201	FMN	C10-N1	2.36	1.38	1.33
2	A	5201	FMN	C5'-C4'	2.35	1.55	1.51
2	B	5201	FMN	C10-N1	2.28	1.37	1.33
2	B	5201	FMN	C5'-C4'	2.20	1.54	1.51
2	B	5201	FMN	C9-C8	-2.04	1.36	1.39
2	E	5302	FMN	C4A-C4	-2.03	1.37	1.44

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	5302	FMN	O3P-P-O5'	4.81	119.20	106.67
2	B	5201	FMN	C5A-C9A-N10	3.77	121.38	117.97
2	G	5201	FMN	C5'-C4'-C3'	3.72	119.23	112.22
2	E	5302	FMN	C5A-C9A-N10	3.56	121.19	117.97
2	E	5302	FMN	C4-N3-C2	-3.40	119.61	125.64
2	D	5302	FMN	C5'-C4'-C3'	3.39	118.62	112.22
2	F	5201	FMN	C4-N3-C2	-3.32	119.74	125.64
2	G	5201	FMN	C4-N3-C2	-3.27	119.84	125.64
2	D	5302	FMN	O3'-C3'-C4'	3.19	116.17	108.93
2	C	5302	FMN	C4A-C4-N3	3.11	121.16	113.25
2	A	5201	FMN	O2P-P-O5'	3.07	114.68	106.67
2	B	5201	FMN	C4A-C10-N10	3.00	120.78	116.48
2	C	5302	FMN	C4-N3-C2	-2.95	120.41	125.64
2	G	5201	FMN	C4A-C10-N10	2.90	120.63	116.48
2	D	5302	FMN	C5A-C9A-N10	2.89	120.58	117.97
2	B	5201	FMN	C4-N3-C2	-2.88	120.53	125.64
2	E	5302	FMN	O3'-C3'-C2'	2.87	115.44	108.93
2	E	5302	FMN	C4A-C4-N3	2.82	120.42	113.25
2	A	5201	FMN	C4-N3-C2	-2.80	120.67	125.64
2	E	5302	FMN	O4-C4-C4A	-2.73	119.31	126.53
2	A	5201	FMN	C4A-C4-N3	2.71	120.16	113.25
2	D	5302	FMN	O5'-P-O1P	-2.69	99.18	106.44
2	G	5201	FMN	O2P-P-O5'	2.66	113.61	106.67
2	D	5302	FMN	C4A-C4-N3	2.60	119.87	113.25
2	G	5201	FMN	O4-C4-C4A	-2.56	119.79	126.53
2	G	5201	FMN	O5'-P-O1P	-2.55	99.56	106.44
2	D	5302	FMN	C4-N3-C2	-2.51	121.19	125.64
2	E	5302	FMN	C4A-C10-N10	2.50	120.06	116.48
2	G	5201	FMN	C4A-C4-N3	2.49	119.60	113.25
2	D	5302	FMN	C9A-C5A-N5	-2.42	119.89	122.45
2	D	5302	FMN	O2P-P-O5'	2.39	112.90	106.67
2	G	5201	FMN	O3'-C3'-C4'	2.38	114.35	108.93
2	D	5302	FMN	C4A-C10-N10	2.36	119.86	116.48
2	F	5201	FMN	C4A-C10-N10	2.35	119.84	116.48
2	C	5302	FMN	O3'-C3'-C4'	-2.34	103.61	108.93
2	F	5201	FMN	C4A-C4-N3	2.34	119.21	113.25
2	B	5201	FMN	C5'-C4'-C3'	2.29	116.53	112.22
2	B	5201	FMN	C10-C4A-N5	-2.28	120.16	124.81
2	F	5201	FMN	C4-C4A-C10	2.26	120.81	116.93
2	E	5302	FMN	C4'-C3'-C2'	-2.26	109.81	113.57
2	G	5201	FMN	C4-C4A-C10	2.25	120.79	116.93
2	F	5201	FMN	O2P-P-O1P	2.25	119.60	110.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	5201	FMN	C1'-C2'-C3'	-2.23	103.60	109.66
2	C	5302	FMN	C4A-C10-N10	2.22	119.67	116.48
2	C	5302	FMN	C5A-C9A-N10	2.22	119.98	117.97
2	C	5302	FMN	O4-C4-C4A	-2.20	120.71	126.53
2	B	5201	FMN	C9-C9A-N10	-2.19	118.91	121.85
2	E	5302	FMN	C2'-C1'-N10	2.17	120.44	110.20
2	B	5201	FMN	C4A-C4-N3	2.15	118.73	113.25
2	A	5201	FMN	C9A-C5A-N5	-2.15	120.18	122.45
2	C	5302	FMN	O5'-C5'-C4'	-2.14	103.66	109.36
2	F	5201	FMN	O5'-C5'-C4'	2.13	115.05	109.36
2	G	5201	FMN	C10-C4A-N5	-2.12	120.48	124.81
2	F	5201	FMN	C10-C4A-N5	-2.10	120.51	124.81
2	G	5201	FMN	C4A-C10-N1	-2.10	119.43	124.59
2	E	5302	FMN	C9A-C5A-N5	-2.10	120.22	122.45
2	B	5201	FMN	O2P-P-O5'	2.07	112.08	106.67
2	B	5201	FMN	O3'-C3'-C2'	2.02	113.52	108.93
2	D	5302	FMN	C4A-C10-N1	-2.01	119.66	124.59

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	5302	FMN	C3'-C4'-C5'-O5'
2	C	5302	FMN	O4'-C4'-C5'-O5'
2	C	5302	FMN	C5'-O5'-P-O1P
2	C	5302	FMN	C5'-O5'-P-O2P
2	C	5302	FMN	C5'-O5'-P-O3P
2	G	5201	FMN	C4'-C5'-O5'-P
2	D	5302	FMN	C4'-C5'-O5'-P
2	F	5201	FMN	C4'-C5'-O5'-P
2	E	5302	FMN	N10-C1'-C2'-O2'
2	G	5201	FMN	N10-C1'-C2'-O2'
2	B	5201	FMN	C4'-C5'-O5'-P
2	A	5201	FMN	C4'-C5'-O5'-P
2	E	5302	FMN	C4'-C5'-O5'-P
3	C	5301	EDO	O1-C1-C2-O2
3	E	5301	EDO	O1-C1-C2-O2
2	E	5302	FMN	C5'-O5'-P-O3P
3	D	5301	EDO	O1-C1-C2-O2

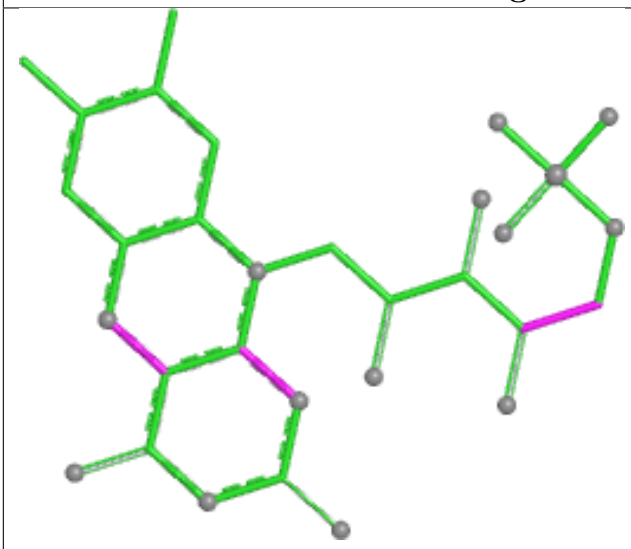
There are no ring outliers.

4 monomers are involved in 7 short contacts:

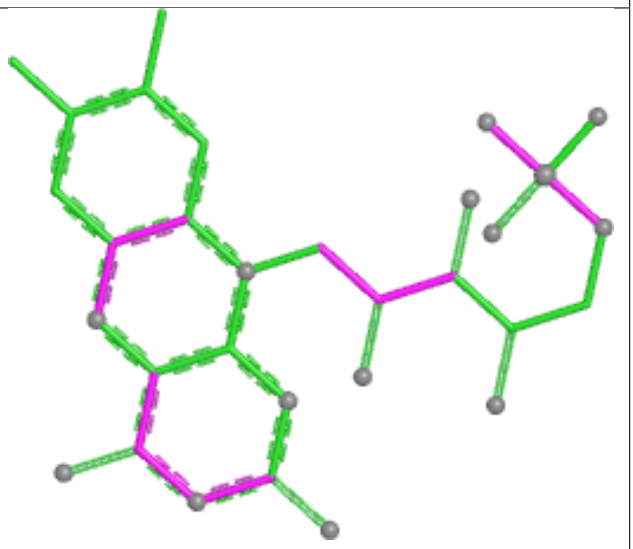
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	5302	FMN	4	0
3	C	5301	EDO	1	0
2	D	5302	FMN	1	0
2	F	5201	FMN	1	0

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 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.

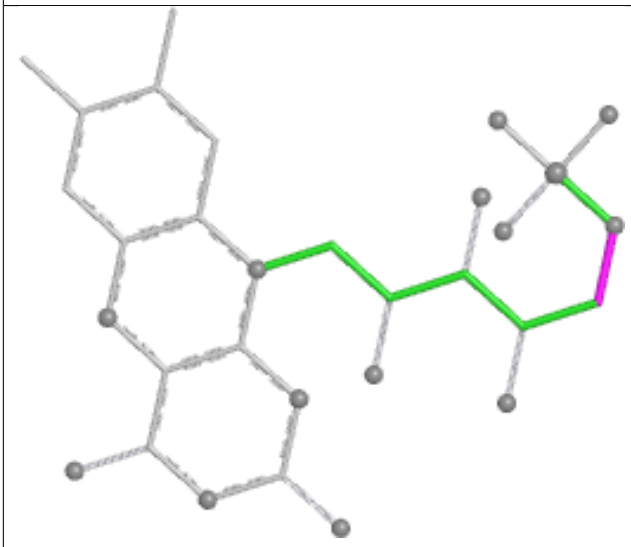
Ligand FMN A 5201



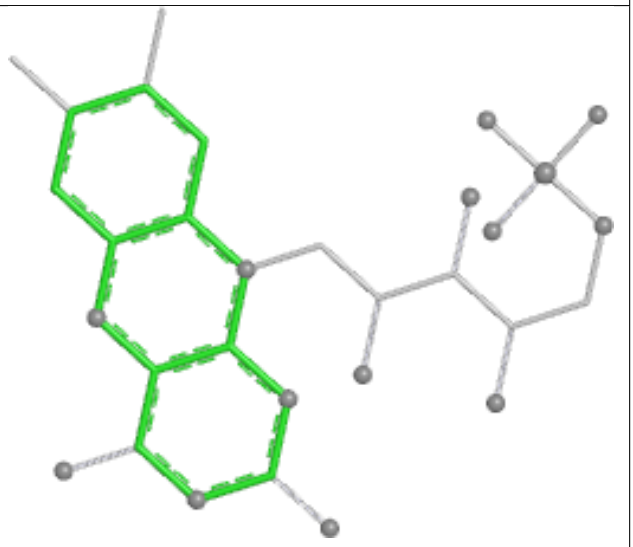
Bond lengths



Bond angles

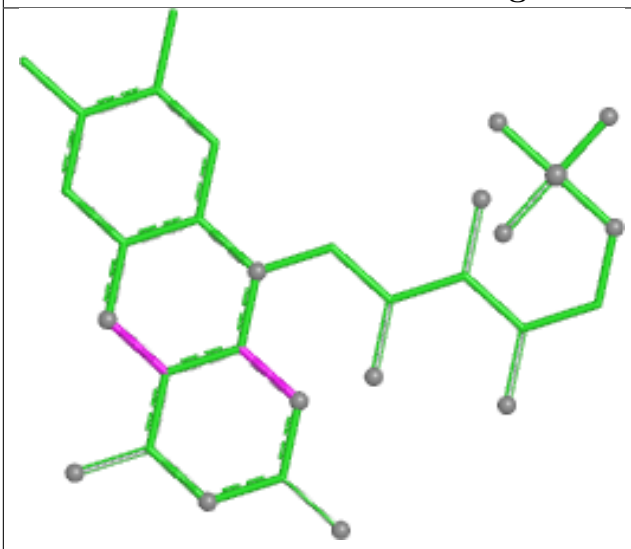


Torsions

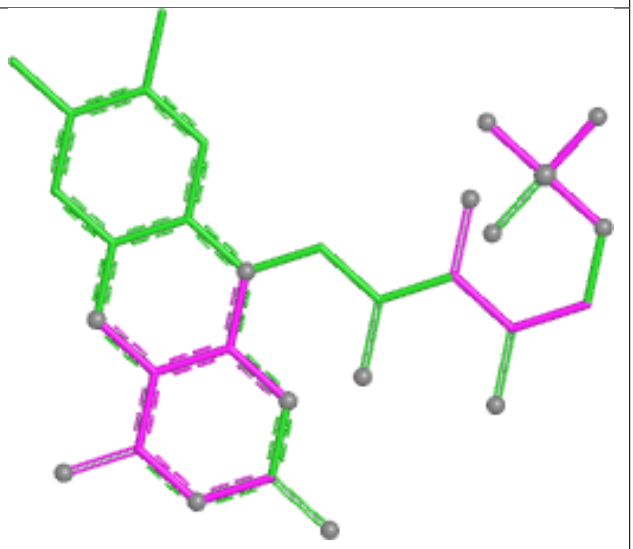


Rings

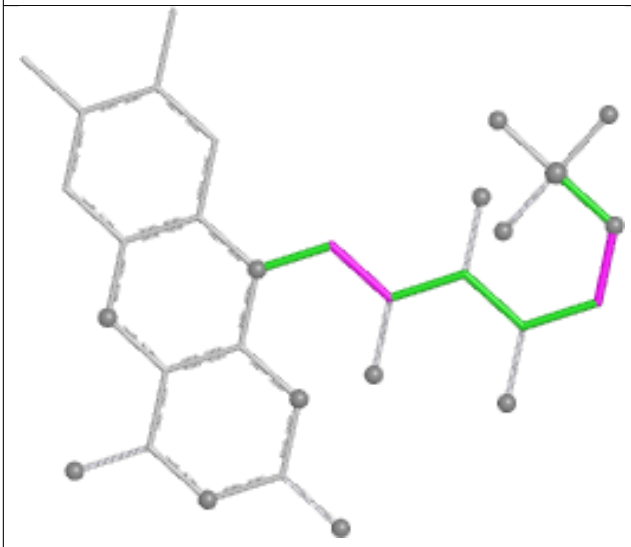
Ligand FMN G 5201



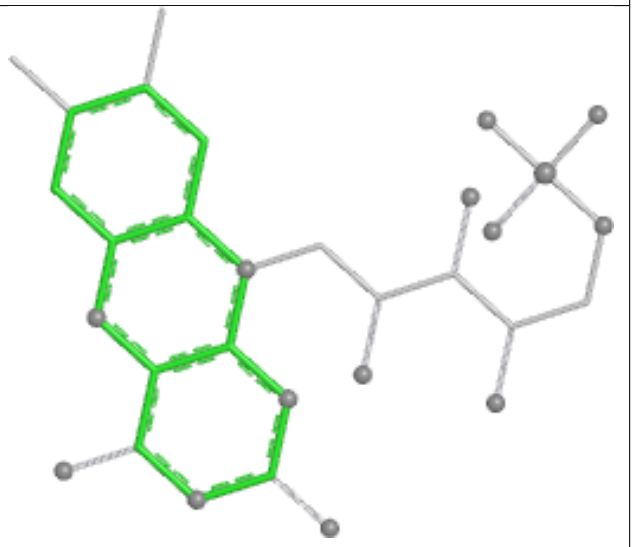
Bond lengths



Bond angles

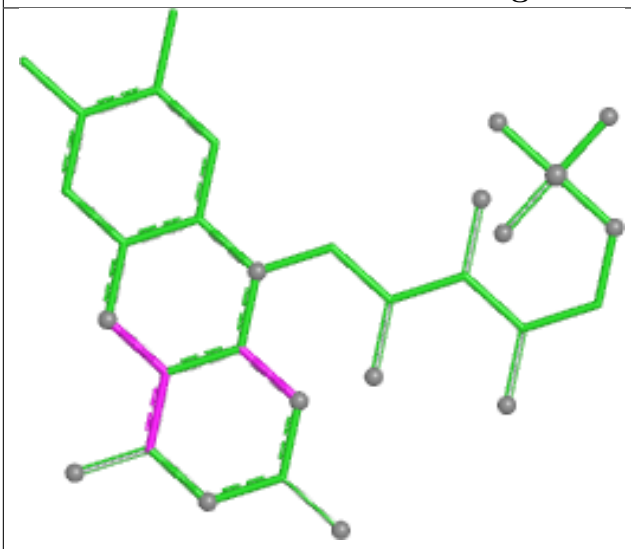


Torsions

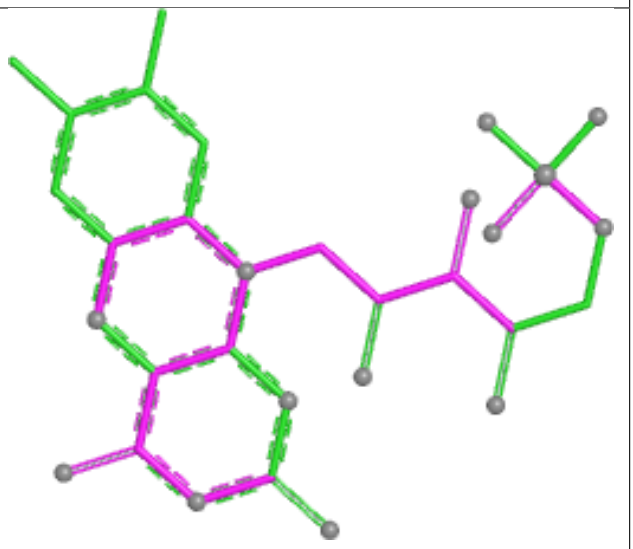


Rings

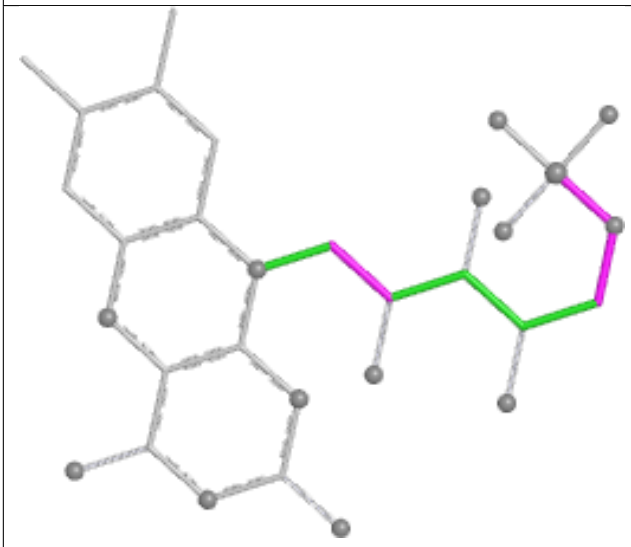
Ligand FMN E 5302



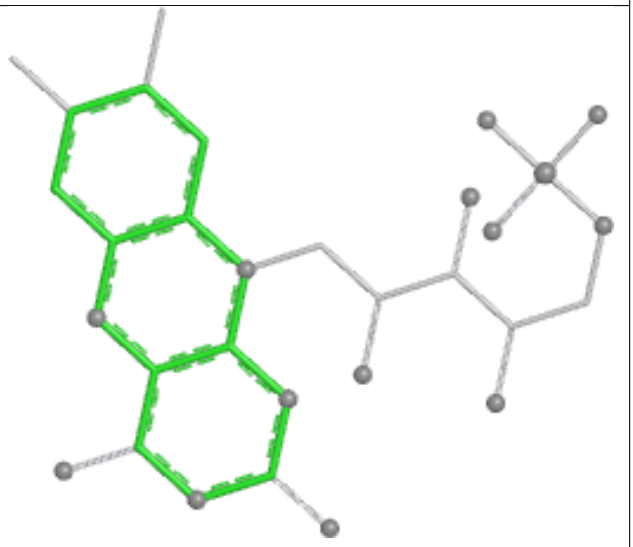
Bond lengths



Bond angles

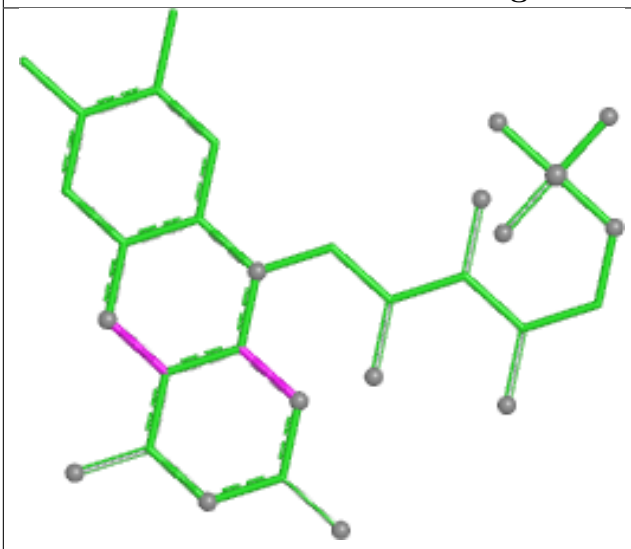


Torsions

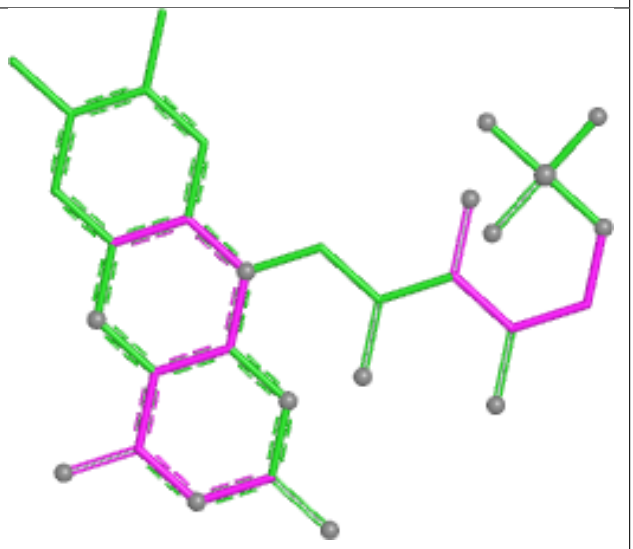


Rings

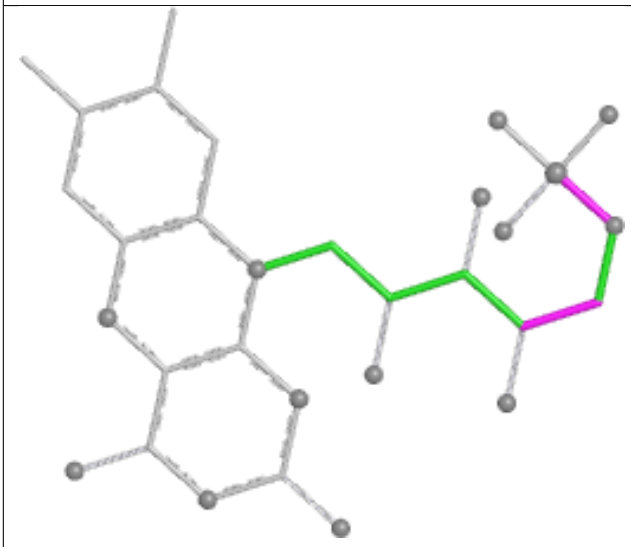
Ligand FMN C 5302



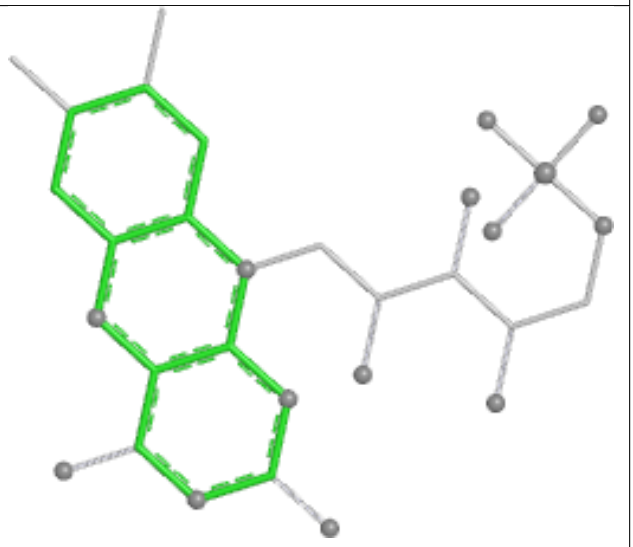
Bond lengths



Bond angles

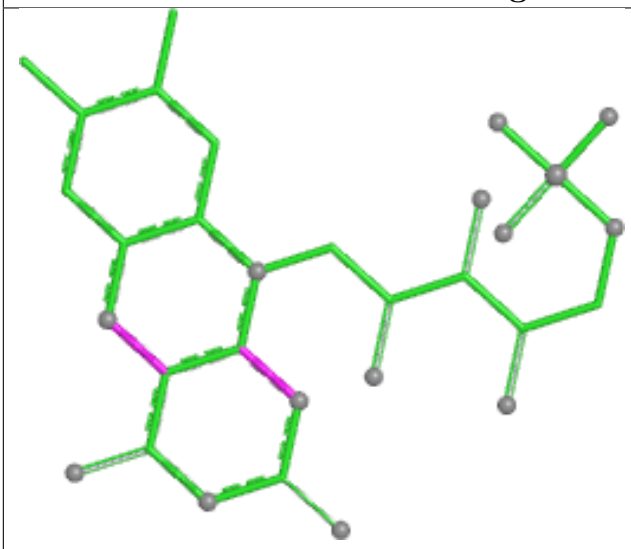


Torsions

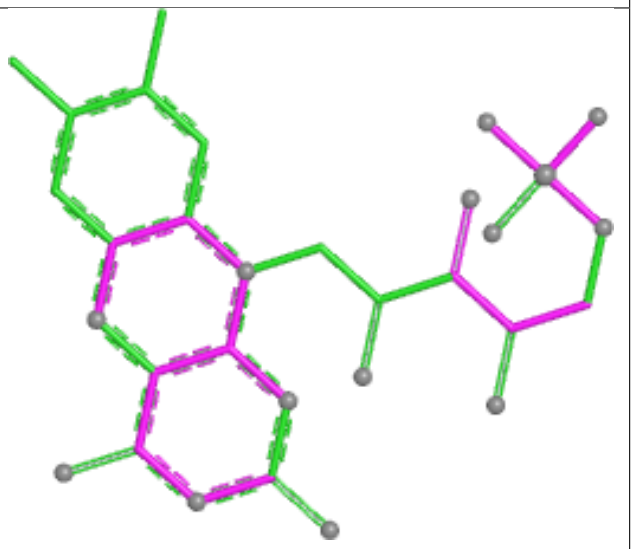


Rings

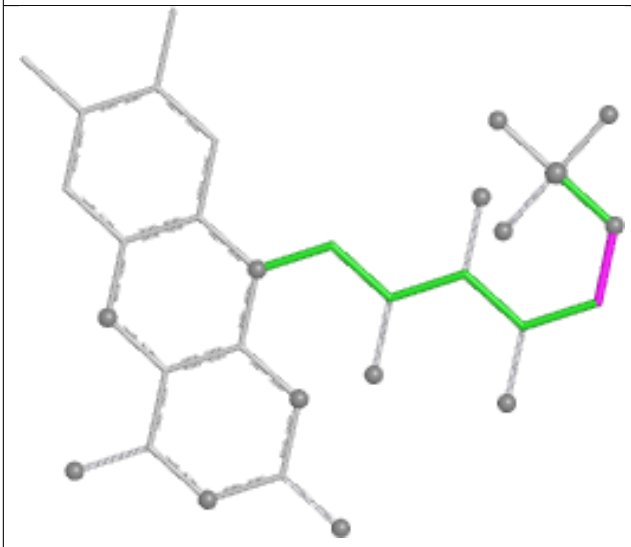
Ligand FMN D 5302



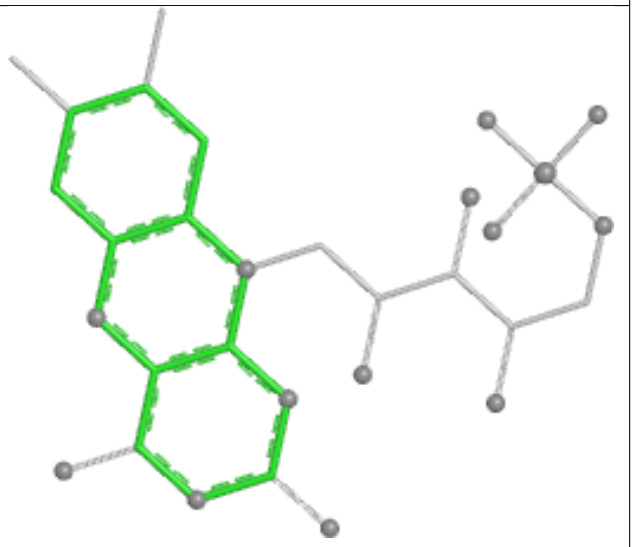
Bond lengths



Bond angles

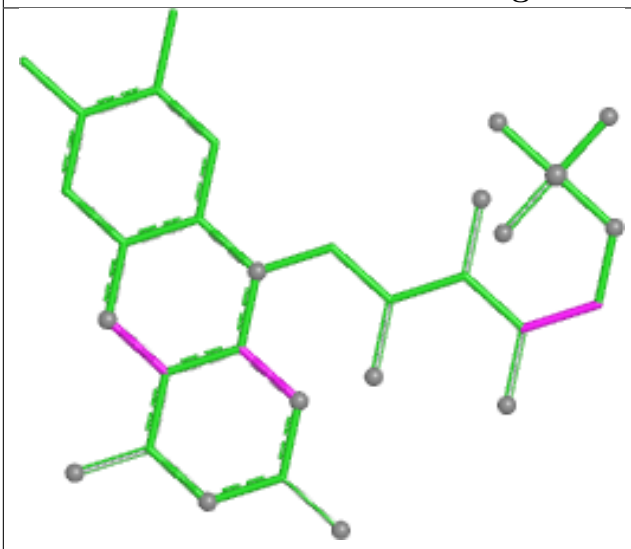


Torsions

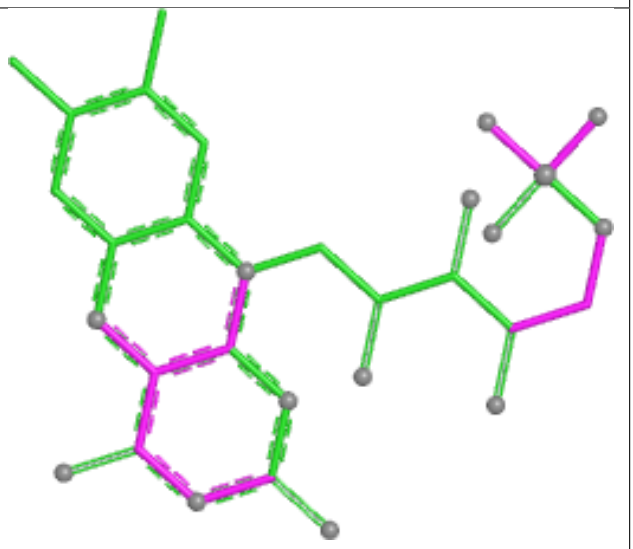


Rings

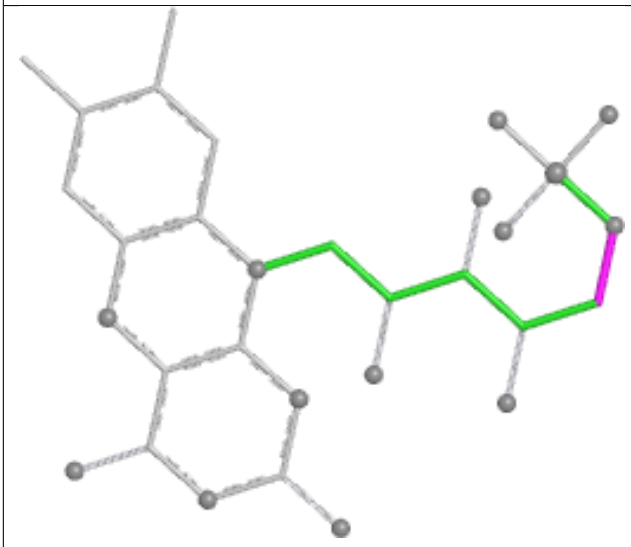
Ligand FMN F 5201



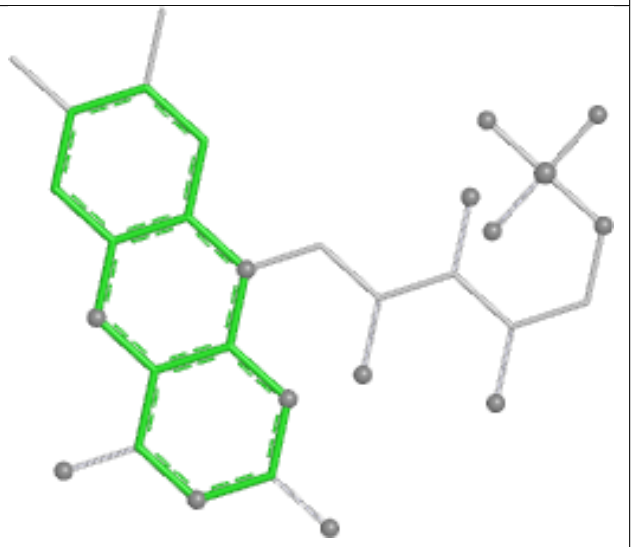
Bond lengths



Bond angles

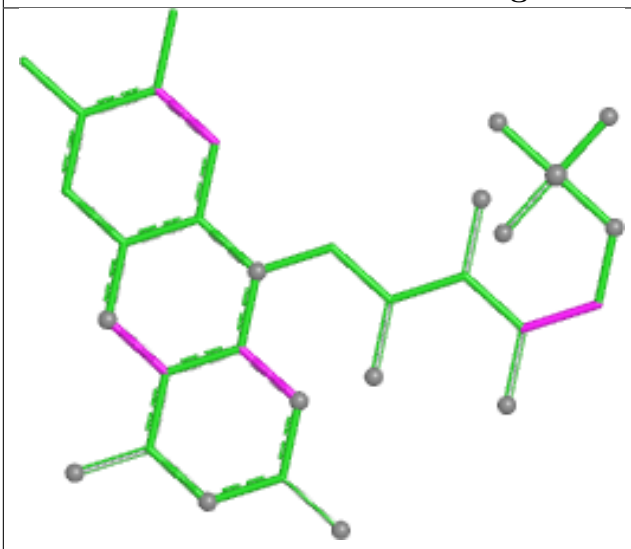


Torsions

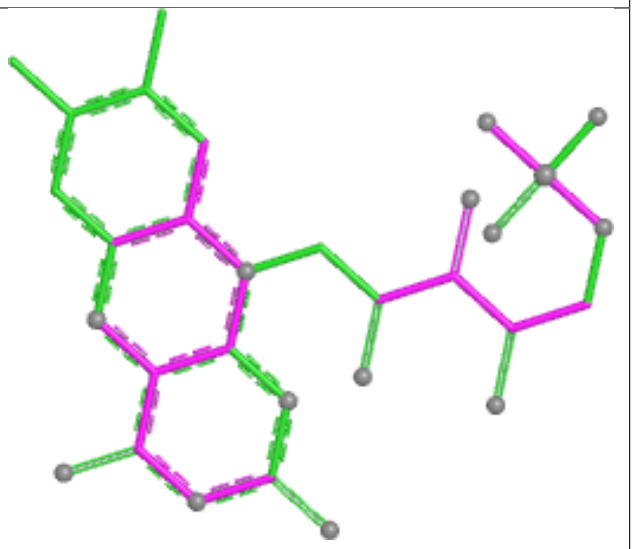


Rings

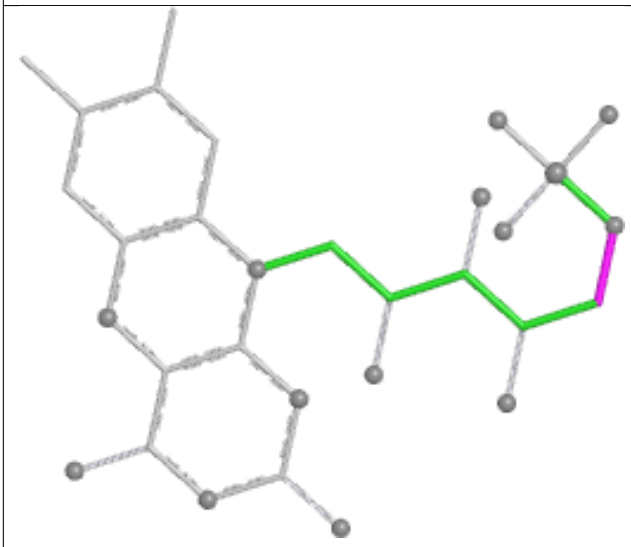
Ligand FMN B 5201



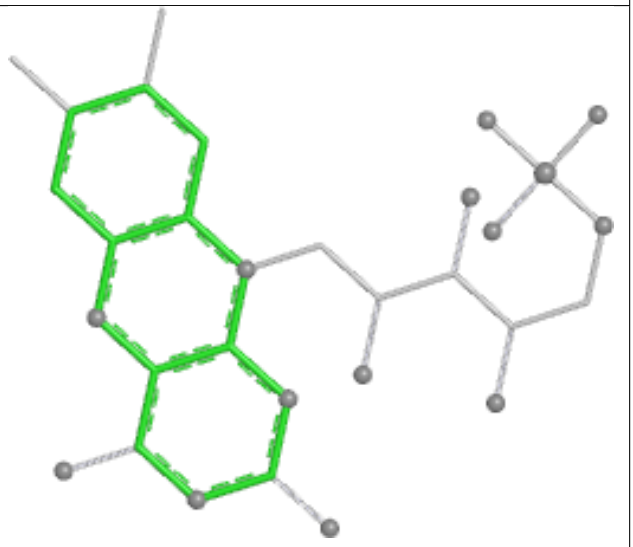
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	130/190 (68%)	-0.18	4 (3%)	51	30	39, 54, 85, 96	0
1	B	130/190 (68%)	-0.44	3 (2%)	61	38	33, 41, 73, 92	0
1	C	131/190 (68%)	-0.30	4 (3%)	51	30	35, 53, 80, 94	0
1	D	130/190 (68%)	-0.21	5 (3%)	44	24	37, 53, 80, 102	0
1	E	130/190 (68%)	-0.31	6 (4%)	37	20	33, 44, 74, 103	0
1	F	131/190 (68%)	-0.28	5 (3%)	44	24	34, 45, 80, 103	0
1	G	130/190 (68%)	-0.04	4 (3%)	51	30	39, 60, 92, 106	0
All	All	912/1330 (68%)	-0.25	31 (3%)	48	27	33, 50, 83, 106	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	136	GLY	7.9
1	F	136	GLY	6.3
1	D	136	GLY	6.1
1	B	136	GLY	5.8
1	F	6	TYR	5.1
1	E	136	GLY	4.7
1	C	117	ASP	4.1
1	G	7	PRO	4.1
1	G	136	GLY	4.0
1	G	115	ASP	3.9
1	E	7	PRO	3.9
1	E	117	ASP	3.9
1	D	7	PRO	3.9
1	C	137	PRO	3.8
1	E	116	ASP	3.3
1	B	7	PRO	3.3
1	E	115	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	116	ASP	3.0
1	G	65	LYS	2.8
1	C	115	ASP	2.7
1	E	118	THR	2.6
1	F	81	LYS	2.6
1	F	115	ASP	2.4
1	A	7	PRO	2.4
1	F	17	CYS	2.4
1	A	117	ASP	2.3
1	C	7	PRO	2.2
1	D	8	VAL	2.1
1	D	65	LYS	2.1
1	B	117	ASP	2.0
1	D	66	ARG	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 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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	EDO	D	5301	4/4	0.72	0.35	54,78,94,94	0
3	EDO	E	5301	4/4	0.72	0.28	55,67,92,92	0
3	EDO	C	5301	4/4	0.93	0.18	34,61,73,74	0
2	FMN	G	5201	31/31	0.97	0.08	39,57,71,76	0
2	FMN	D	5302	31/31	0.97	0.08	32,49,61,64	0
2	FMN	F	5201	31/31	0.98	0.06	30,39,50,55	0
2	FMN	A	5201	31/31	0.98	0.06	31,49,59,66	0
2	FMN	C	5302	31/31	0.98	0.07	34,49,59,62	0
2	FMN	B	5201	31/31	0.98	0.07	30,39,54,58	0

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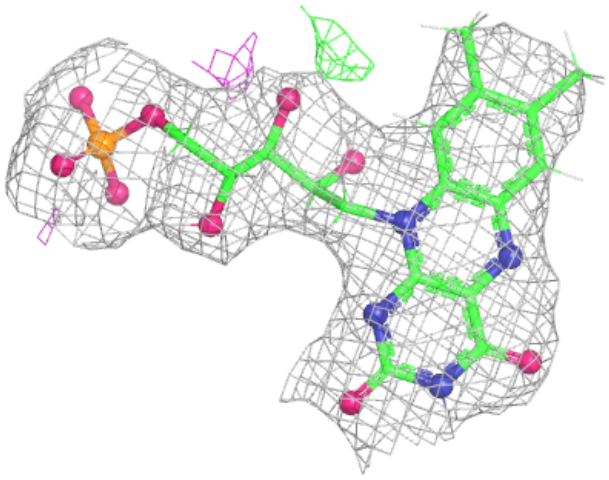
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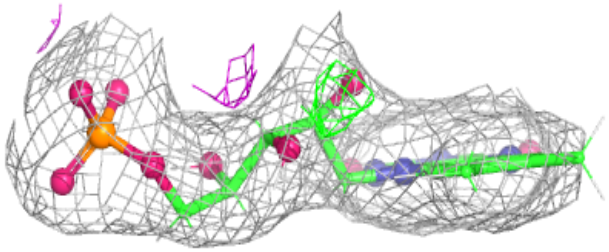
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	FMN	E	5302	31/31	0.98	0.06	30,39,50,51	0

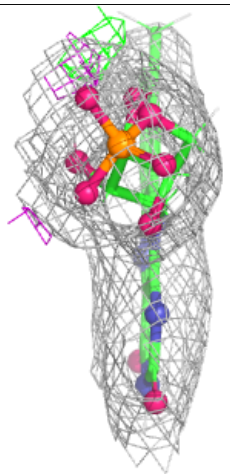
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around FMN G 5201:

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

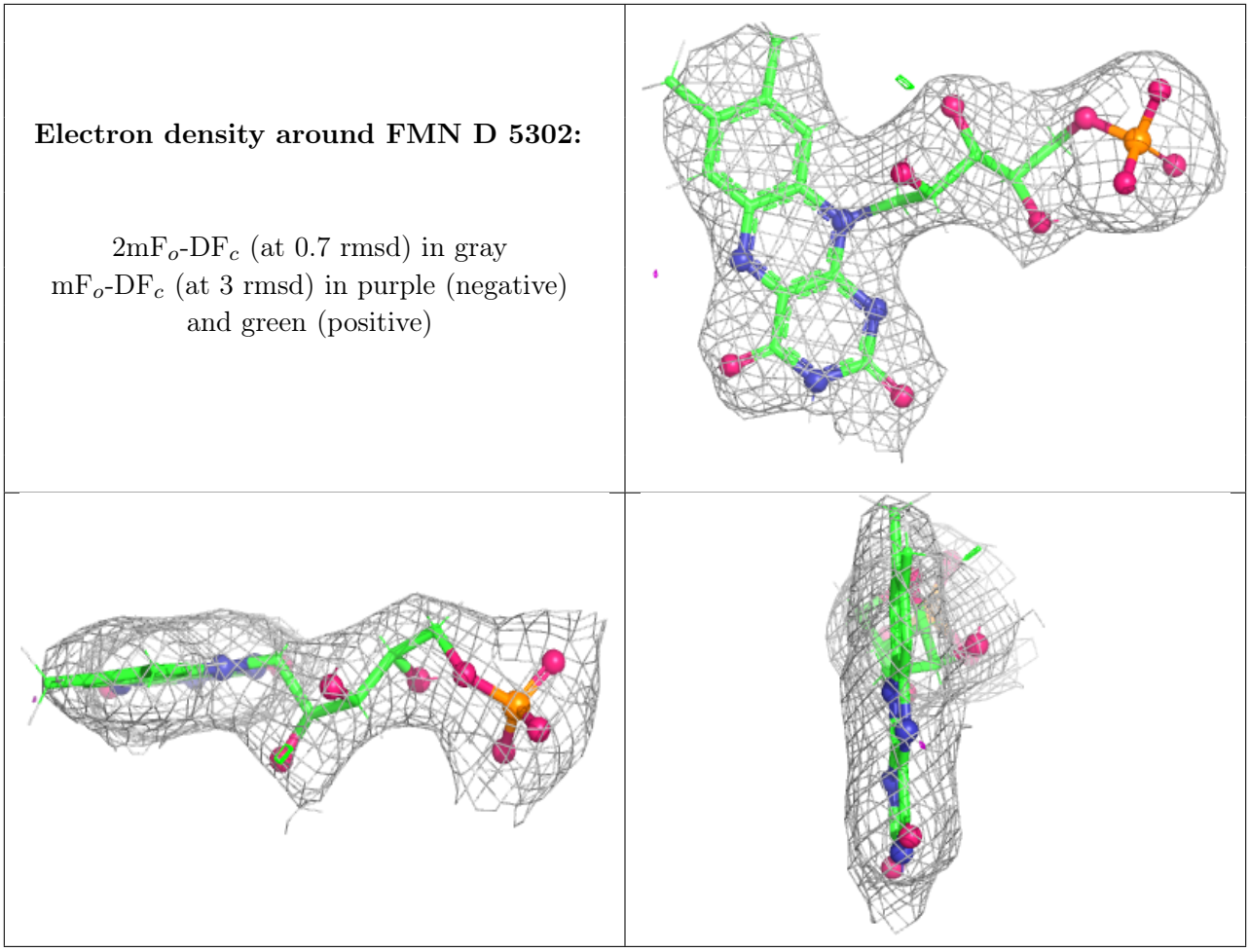






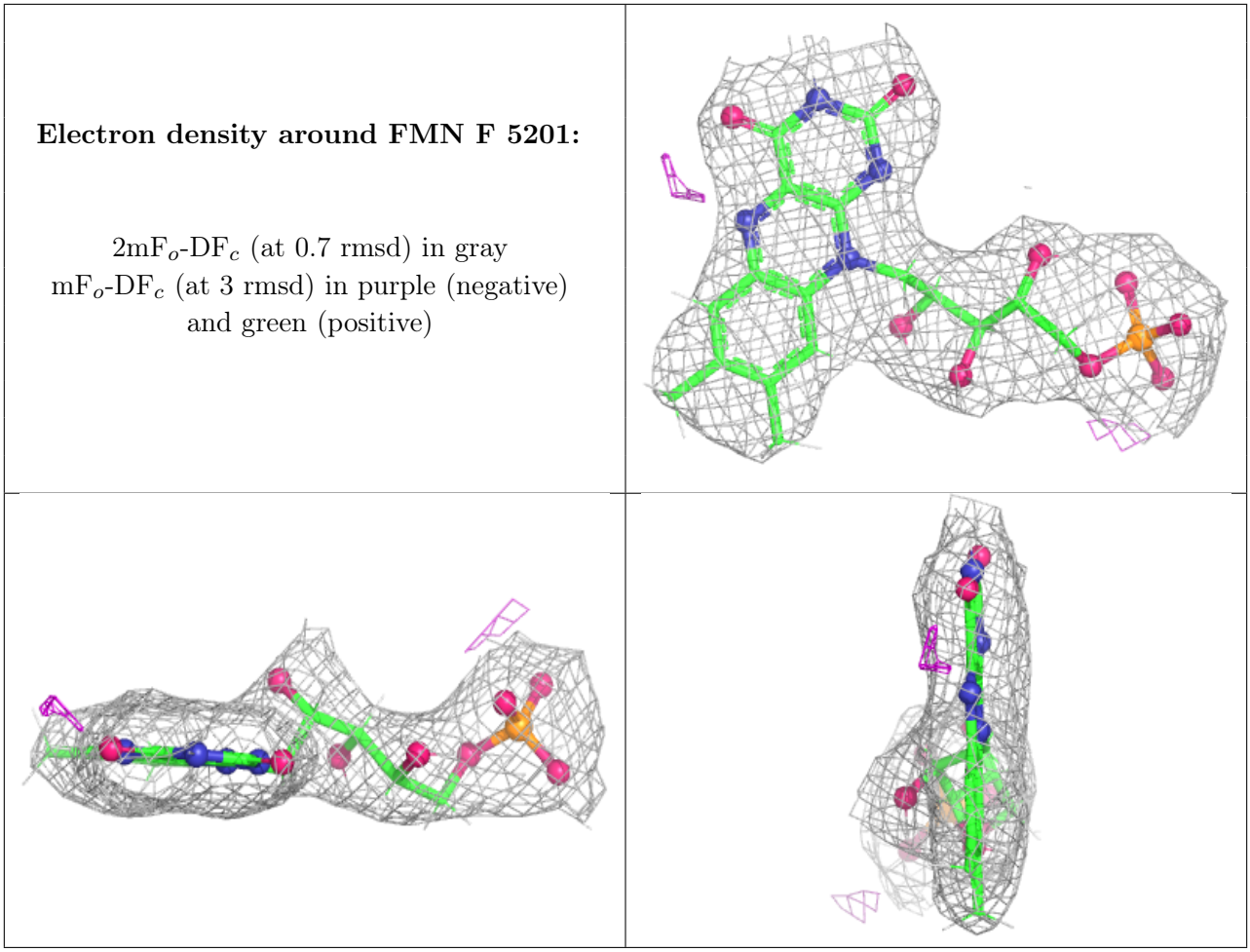
Electron density around FMN D 5302:

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



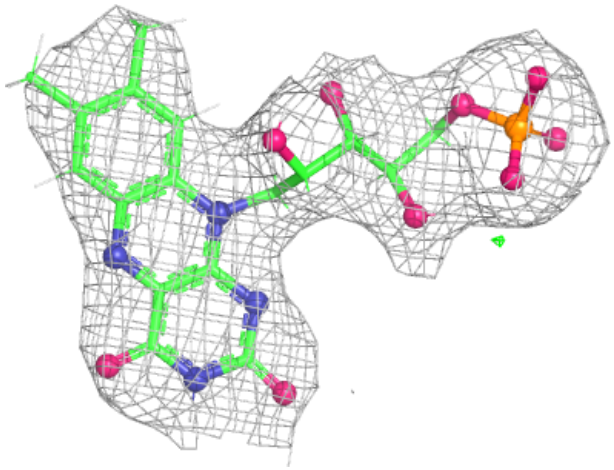
Electron density around FMN F 5201:

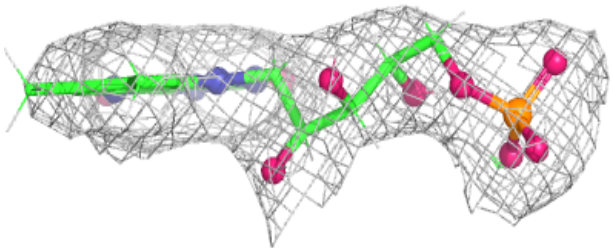
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

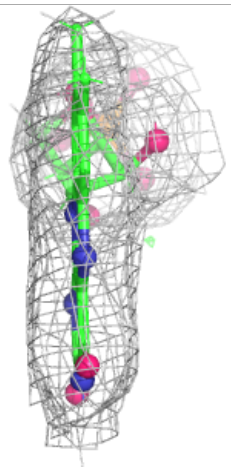


Electron density around FMN A 5201:

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

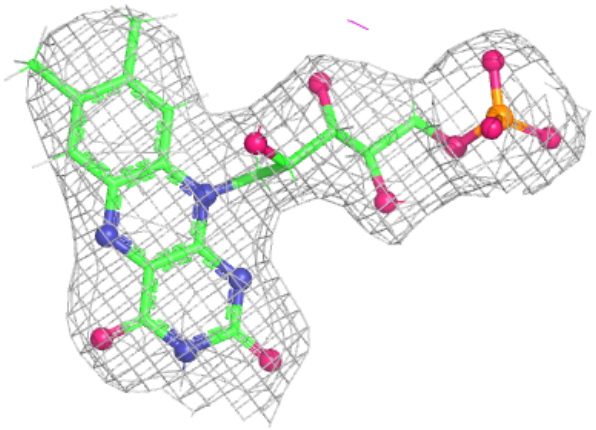


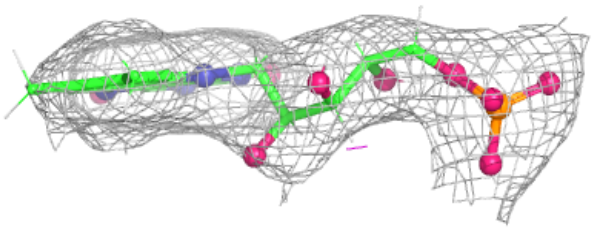


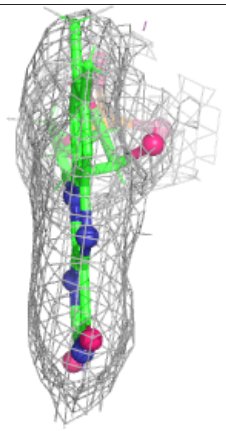


Electron density around FMN C 5302:

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

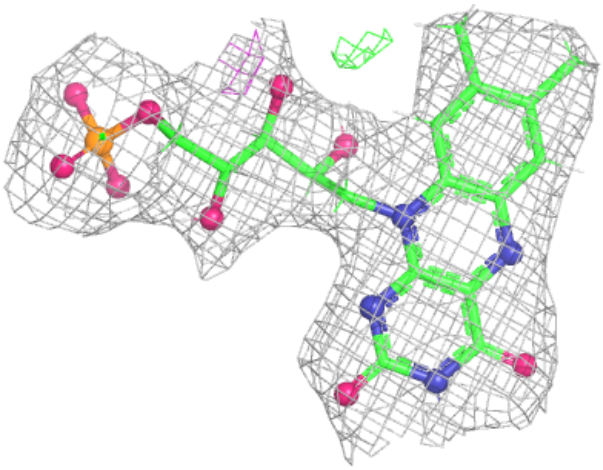


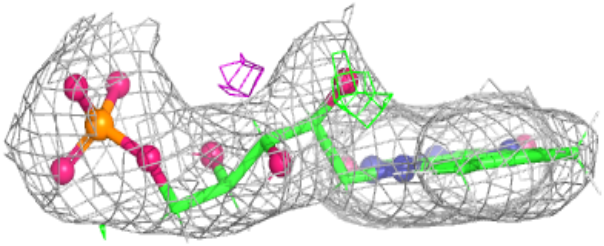


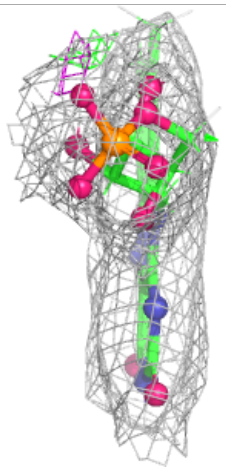


Electron density around FMN B 5201:

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

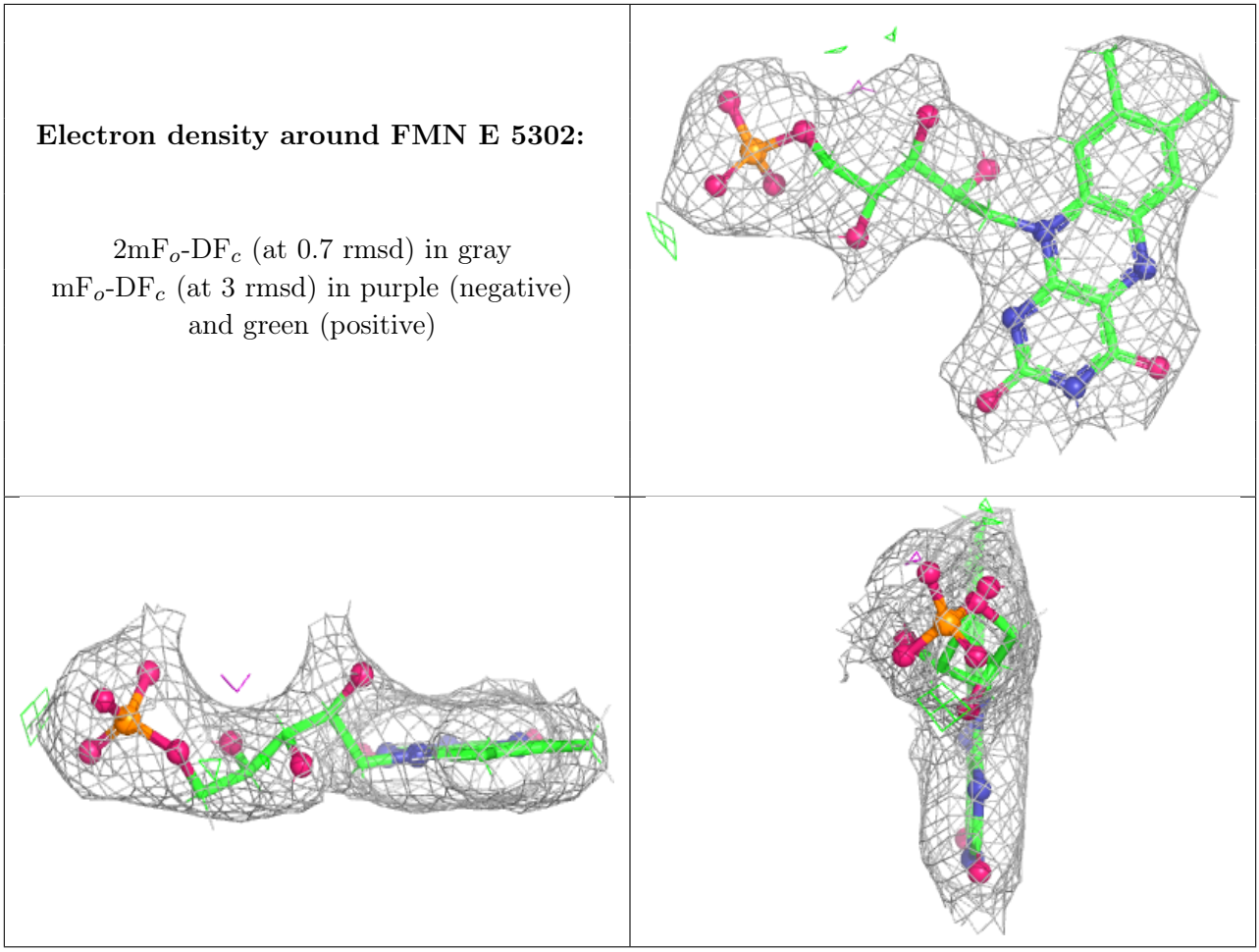






Electron density around FMN E 5302:

$2mF_o$-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

There are no such residues in this entry.