



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 17, 2021 – 08:39 AM EDT

PDB ID : 1ICP
Title : CRYSTAL STRUCTURE OF 12-OXOPHYTODIENOATE REDUCTASE 1 FROM TOMATO COMPLEXED WITH PEG400
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Deposited on : 2001-04-02
Resolution : 1.90 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 : 2.23.2
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) : 2.23.2

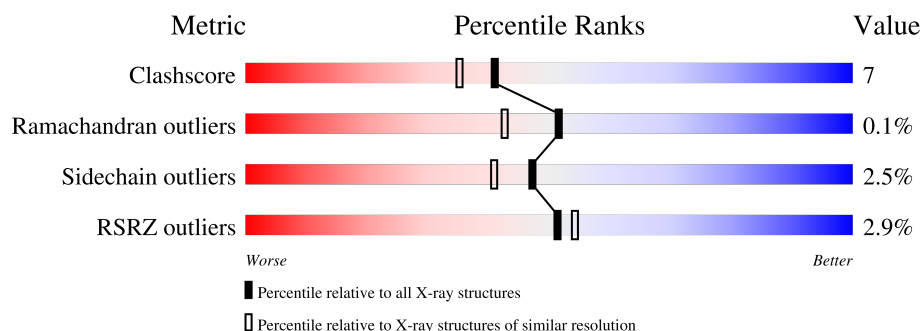
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	376	
1	B	376	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6250 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 12-OXOPHYTODIENOATE REDUCTASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	0	0
			2819	1785	495	526	13			
1	B	358	Total	C	N	O	S	0	0	0
			2819	1785	496	525	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	142	MET	ARG	engineered mutation	UNP Q9XG54
B	142	MET	ARG	engineered mutation	UNP Q9XG54

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

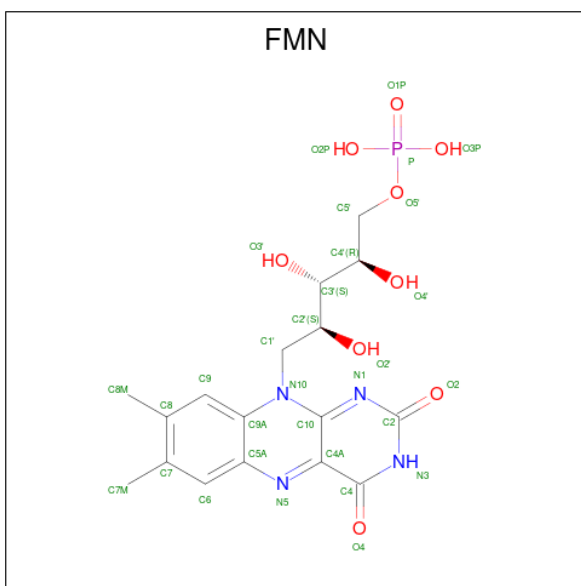
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

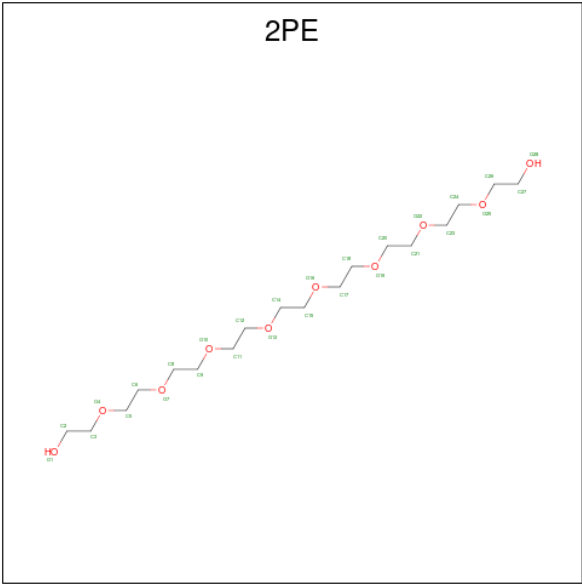


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



- Molecule 5 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: C₁₈H₃₈O₁₀).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			28	18	10		
5	B	1	Total	C	O	0	0
			28	18	10		

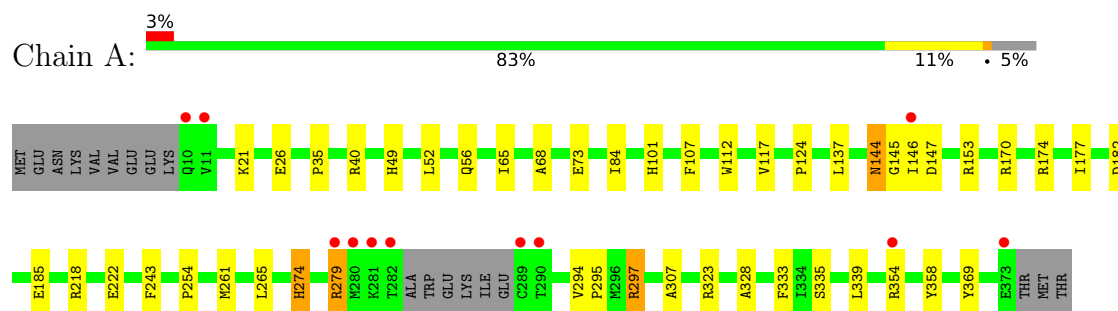
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	248	Total	O	0	0
			248	248		
6	B	235	Total	O	0	0
			235	235		

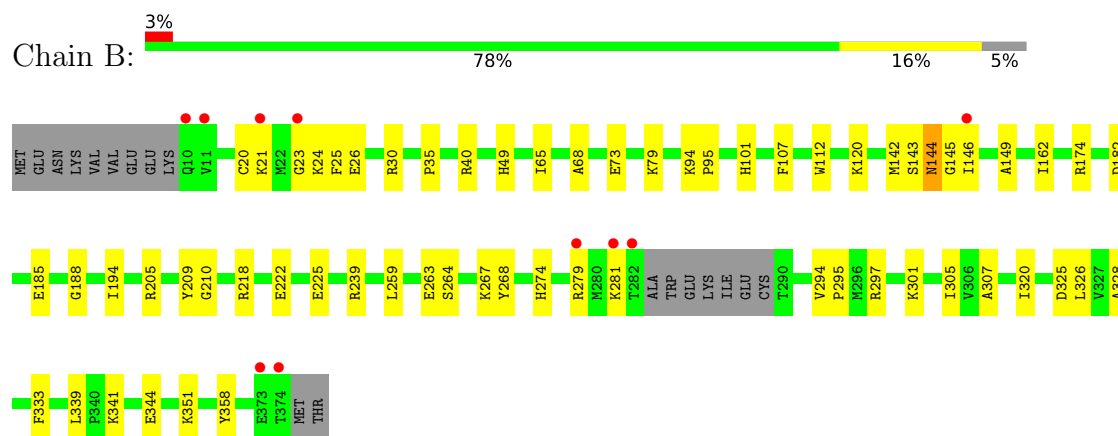
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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: 12-OXOPHYTODIENOATE REDUCTASE 1



• Molecule 1: 12-OXOPHYTODIENOATE REDUCTASE 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.39Å 71.32Å 71.53Å 63.71° 83.85° 77.36°	Depositor
Resolution (Å)	22.90 – 1.90 22.85 – 1.90	Depositor EDS
% Data completeness (in resolution range)	91.8 (22.90-1.90) 91.5 (22.85-1.90)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 1.89Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.182 , 0.222 0.176 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	22.3	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 49.9	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	0.96	EDS
Total number of atoms	6250	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.92% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, SO4, 2PE, 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	0.37	0/2886	0.63	0/3915
1	B	0.37	0/2886	0.63	0/3913
All	All	0.37	0/5772	0.63	0/7828

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

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	2819	0	2743	37	0
1	B	2819	0	2742	43	0
2	A	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	31	0	19	2	0
4	B	31	0	19	1	0
5	A	28	0	38	1	0
5	B	28	0	38	3	0
6	A	248	0	0	4	0
6	B	235	0	0	5	0
All	All	6250	0	5599	81	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (81) 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:B:23:GLY:HA3	6:B:670:HOH:O	1.85	0.75
1:A:279:ARG:HG2	1:A:279:ARG:HH11	1.54	0.73
1:B:225:GLU:HG2	1:B:268:TYR:CE2	2.26	0.71
1:A:101:HIS:HD2	6:A:738:HOH:O	1.76	0.69
1:A:21:LYS:HD2	1:A:26:GLU:OE1	1.95	0.66
1:B:101:HIS:HE1	1:B:182:ASP:OD2	1.80	0.65
1:A:73:GLU:HB3	1:A:124:PRO:HG3	1.79	0.65
1:A:101:HIS:HE1	1:A:182:ASP:OD2	1.81	0.64
1:A:153:ARG:HB2	1:A:153:ARG:NH1	2.13	0.64
1:B:21:LYS:HD3	1:B:26:GLU:OE2	1.99	0.63
1:B:301:LYS:HA	1:B:301:LYS:HE2	1.83	0.61
1:A:354:ARG:HG2	1:A:354:ARG:HH11	1.65	0.60
1:B:149:ALA:HB2	5:B:504:2PE:H262	1.84	0.59
4:A:501:FMN:H1'2	5:A:503:2PE:H82	1.83	0.59
1:B:101:HIS:HD2	6:B:603:HOH:O	1.84	0.59
1:A:144:ASN:HD21	1:A:147:ASP:H	1.49	0.58
1:B:40:ARG:O	1:B:49:HIS:HE1	1.88	0.57
1:A:144:ASN:HD22	1:A:145:GLY:N	2.03	0.56
1:A:279:ARG:HG2	1:A:279:ARG:NH1	2.18	0.56
1:B:35:PRO:HG3	1:B:65:ILE:HG21	1.88	0.56
1:A:294:VAL:HB	1:A:295:PRO:HD3	1.87	0.56
1:B:144:ASN:HD22	1:B:145:GLY:N	2.05	0.55
1:B:142:MET:HA	5:B:504:2PE:H241	1.88	0.55
1:B:264:SER:O	1:B:267:LYS:HG2	2.08	0.54
1:A:218:ARG:O	1:A:222:GLU:HG3	2.06	0.54
1:A:35:PRO:HG3	1:A:65:ILE:HG21	1.89	0.54
1:B:358:TYR:CZ	4:B:502:FMN:HM72	2.43	0.54
1:B:144:ASN:HD22	1:B:144:ASN:C	2.11	0.53
1:A:144:ASN:ND2	1:A:146:ILE:H	2.06	0.53
1:A:358:TYR:CZ	4:A:501:FMN:HM72	2.44	0.53
1:B:20:CYS:HB2	1:B:30:ARG:NE	2.24	0.51
1:B:68:ALA:HB1	1:B:112:TRP:CE3	2.44	0.51
1:A:68:ALA:HB1	1:A:112:TRP:CD2	2.45	0.51
1:A:254:PRO:HD2	6:A:542:HOH:O	2.11	0.51
1:A:297:ARG:HG3	1:A:323:ARG:O	2.11	0.51
1:B:21:LYS:HE3	1:B:23:GLY:O	2.11	0.51
1:A:49:HIS:HD2	6:A:592:HOH:O	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:LYS:HD2	1:A:26:GLU:CD	2.32	0.50
1:A:35:PRO:HG3	1:A:65:ILE:CG2	2.42	0.49
1:B:49:HIS:HD2	6:B:527:HOH:O	1.95	0.49
1:B:279:ARG:O	1:B:281:LYS:HD2	2.13	0.48
1:A:117:VAL:HG22	1:A:137:LEU:HD11	1.96	0.48
1:B:68:ALA:HB1	1:B:112:TRP:CD2	2.49	0.47
1:A:40:ARG:O	1:A:49:HIS:HE1	1.98	0.47
1:A:243:PHE:CE2	1:A:254:PRO:HB2	2.49	0.47
1:A:68:ALA:HB1	1:A:112:TRP:CE3	2.50	0.47
1:B:94:LYS:HB2	1:B:95:PRO:HD3	1.97	0.47
1:A:170:ARG:HD2	6:A:613:HOH:O	2.15	0.46
1:A:261:MET:O	1:A:265:LEU:HG	2.16	0.46
1:B:142:MET:HG2	5:B:504:2PE:H262	1.97	0.46
1:B:259:LEU:O	1:B:263:GLU:HG3	2.16	0.45
1:B:144:ASN:ND2	1:B:146:ILE:H	2.14	0.45
1:B:174:ARG:HD3	1:B:174:ARG:O	2.16	0.45
1:B:281:LYS:HD2	1:B:281:LYS:N	2.33	0.44
1:B:73:GLU:HG3	6:B:533:HOH:O	2.18	0.44
1:B:205:ARG:HB2	1:B:210:GLY:HA3	2.00	0.43
1:B:24:LYS:HD2	1:B:25:PHE:CZ	2.53	0.43
1:A:144:ASN:HD22	1:A:144:ASN:C	2.19	0.43
1:B:162:ILE:HD12	1:B:209:TYR:CD2	2.53	0.43
1:B:120:LYS:NZ	6:B:582:HOH:O	2.44	0.43
1:B:218:ARG:O	1:B:222:GLU:HG3	2.19	0.43
1:A:335:SER:HA	1:A:369:TYR:CG	2.54	0.43
1:A:185:GLU:OE2	1:A:274:HIS:HD2	2.02	0.43
1:A:307:ALA:HB2	1:A:328:ALA:HB3	2.01	0.42
1:B:30:ARG:HD2	1:B:325:ASP:O	2.19	0.42
1:B:188:GLY:HA2	1:B:194:ILE:HB	2.02	0.42
1:A:153:ARG:HB2	1:A:153:ARG:HH11	1.85	0.42
1:B:239:ARG:HA	1:B:274:HIS:O	2.19	0.42
1:B:185:GLU:OE2	1:B:274:HIS:HD2	2.03	0.42
1:A:52:LEU:O	1:A:56:GLN:HG3	2.20	0.42
1:B:341:LYS:HD2	1:B:344:GLU:OE1	2.20	0.42
1:A:354:ARG:HH11	1:A:354:ARG:CG	2.33	0.41
1:B:144:ASN:HD22	1:B:146:ILE:H	1.68	0.41
1:B:307:ALA:HB2	1:B:328:ALA:HB3	2.03	0.41
1:B:305:ILE:HG12	1:B:326:LEU:HB2	2.03	0.41
1:A:21:LYS:HD2	1:A:26:GLU:OE2	2.20	0.41
1:A:174:ARG:NH2	1:A:177:ILE:HG21	2.36	0.41
1:B:294:VAL:HB	1:B:295:PRO:HD3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:351:LYS:HA	1:B:351:LYS:HE2	2.02	0.40
1:A:354:ARG:HG2	1:A:354:ARG:NH1	2.36	0.40
1:B:35:PRO:HG3	1:B:65:ILE:CG2	2.50	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	354/376 (94%)	345 (98%)	8 (2%)	1 (0%)	41	31
1	B	354/376 (94%)	343 (97%)	11 (3%)	0	100	100
All	All	708/752 (94%)	688 (97%)	19 (3%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	ILE

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	299/320 (93%)	292 (98%)	7 (2%)	50	45
1	B	298/320 (93%)	290 (97%)	8 (3%)	44	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	597/640 (93%)	582 (98%)	15 (2%)	47 41

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	107	PHE
1	A	144	ASN
1	A	274	HIS
1	A	279	ARG
1	A	297	ARG
1	A	333	PHE
1	A	339	LEU
1	B	79	LYS
1	B	107	PHE
1	B	143	SER
1	B	144	ASN
1	B	297	ARG
1	B	320	ILE
1	B	333	PHE
1	B	339	LEU

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

Mol	Chain	Res	Type
1	A	47	GLN
1	A	49	HIS
1	A	101	HIS
1	A	144	ASN
1	A	167	ASN
1	A	274	HIS
1	B	39	GLN
1	B	47	GLN
1	B	49	HIS
1	B	101	HIS
1	B	144	ASN
1	B	150	HIS
1	B	274	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	FMN	A	501	-	31,33,33	2.45	8 (25%)	40,50,50	2.93	11 (27%)
5	2PE	B	504	-	27,27,27	0.68	0	26,26,26	0.50	0
3	SO4	B	506	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	A	507	-	4,4,4	0.25	0	6,6,6	0.11	0
4	FMN	B	502	-	31,33,33	2.36	7 (22%)	40,50,50	2.76	12 (30%)
5	2PE	A	503	-	27,27,27	0.64	0	26,26,26	0.54	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
4	FMN	B	502	-	-	4/18/18/18	0/3/3/3
4	FMN	A	501	-	-	6/18/18/18	0/3/3/3
5	2PE	B	504	-	-	14/25/25/25	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	2PE	A	503	-	-	13/25/25/25	-

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	FMN	C4A-C10	10.37	1.49	1.38
4	B	502	FMN	C4A-C10	9.69	1.48	1.38
4	B	502	FMN	C9A-N10	3.94	1.43	1.38
4	A	501	FMN	C9A-N10	3.68	1.43	1.38
4	A	501	FMN	C6-C5A	3.30	1.47	1.41
4	B	502	FMN	C4-C4A	3.20	1.46	1.41
4	A	501	FMN	C4-N3	3.03	1.38	1.33
4	B	502	FMN	C6-C5A	3.02	1.46	1.41
4	A	501	FMN	C8-C7	3.02	1.48	1.40
4	A	501	FMN	C2-N3	2.85	1.43	1.38
4	A	501	FMN	C4-C4A	2.84	1.46	1.41
4	B	502	FMN	C2-N3	2.83	1.43	1.38
4	B	502	FMN	C8-C7	2.70	1.47	1.40
4	B	502	FMN	C4-N3	2.67	1.37	1.33
4	A	501	FMN	C5A-N5	2.45	1.39	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	502	FMN	C4-N3-C2	11.95	125.23	115.14
4	A	501	FMN	C4-N3-C2	11.77	125.08	115.14
4	A	501	FMN	P-O5'-C5'	7.92	140.11	118.30
4	B	502	FMN	C4-C4A-C10	-5.36	116.40	119.95
4	A	501	FMN	C4-C4A-C10	-5.35	116.41	119.95
4	A	501	FMN	C4A-C4-N3	-5.25	116.25	123.43
4	B	502	FMN	C4A-C4-N3	-5.15	116.39	123.43
4	B	502	FMN	C4A-C10-N10	-3.79	116.40	120.30
4	B	502	FMN	C1'-C2'-C3'	3.39	119.27	109.79
4	A	501	FMN	C4A-C10-N10	-3.37	116.84	120.30
4	B	502	FMN	C5A-C9A-N10	-3.19	115.40	117.72
4	A	501	FMN	C5A-C9A-N10	-3.17	115.42	117.72
4	B	502	FMN	O2'-C2'-C3'	-2.75	102.40	109.10
4	B	502	FMN	C4A-N5-C5A	2.69	119.46	116.77
4	B	502	FMN	P-O5'-C5'	2.68	125.68	118.30
4	A	501	FMN	C1'-C2'-C3'	2.67	117.26	109.79
4	B	502	FMN	C5'-C4'-C3'	-2.29	107.79	112.20
4	B	502	FMN	C6-C5A-C9A	-2.17	116.20	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	FMN	C6-C5A-C9A	-2.16	116.22	119.05
4	B	502	FMN	C4-C4A-N5	2.14	121.05	118.60
4	A	501	FMN	C4A-N5-C5A	2.12	118.89	116.77
4	A	501	FMN	C4-C4A-N5	2.07	120.96	118.60
4	A	501	FMN	C1'-N10-C9A	2.07	119.92	118.29

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	FMN	C3'-C4'-C5'-O5'
4	A	501	FMN	O4'-C4'-C5'-O5'
4	A	501	FMN	C4'-C5'-O5'-P
4	A	501	FMN	C5'-O5'-P-O1P
4	A	501	FMN	C5'-O5'-P-O3P
5	A	503	2PE	O7-C8-C9-O10
5	A	503	2PE	O19-C20-C21-O22
5	B	504	2PE	O4-C5-C6-O7
5	B	504	2PE	O22-C23-C24-O25
5	A	503	2PE	O22-C23-C24-O25
5	B	504	2PE	O19-C20-C21-O22
5	A	503	2PE	O4-C5-C6-O7
5	B	504	2PE	O7-C8-C9-O10
5	A	503	2PE	O10-C11-C12-O13
5	B	504	2PE	O13-C14-C15-O16
5	B	504	2PE	O1-C2-C3-O4
5	B	504	2PE	O10-C11-C12-O13
5	B	504	2PE	O16-C17-C18-O19
5	A	503	2PE	O13-C14-C15-O16
4	B	502	FMN	C4'-C5'-O5'-P
5	A	503	2PE	C20-C21-O22-C23
5	A	503	2PE	C15-C14-O13-C12
5	B	504	2PE	C20-C21-O22-C23
5	A	503	2PE	C23-C24-O25-C26
5	B	504	2PE	C6-C5-O4-C3
5	A	503	2PE	C5-C6-O7-C8
5	B	504	2PE	O25-C26-C27-O28
4	B	502	FMN	C5'-O5'-P-O1P
5	A	503	2PE	O1-C2-C3-O4
5	B	504	2PE	C15-C14-O13-C12
5	B	504	2PE	C17-C18-O19-C20
5	A	503	2PE	C12-C11-O10-C9

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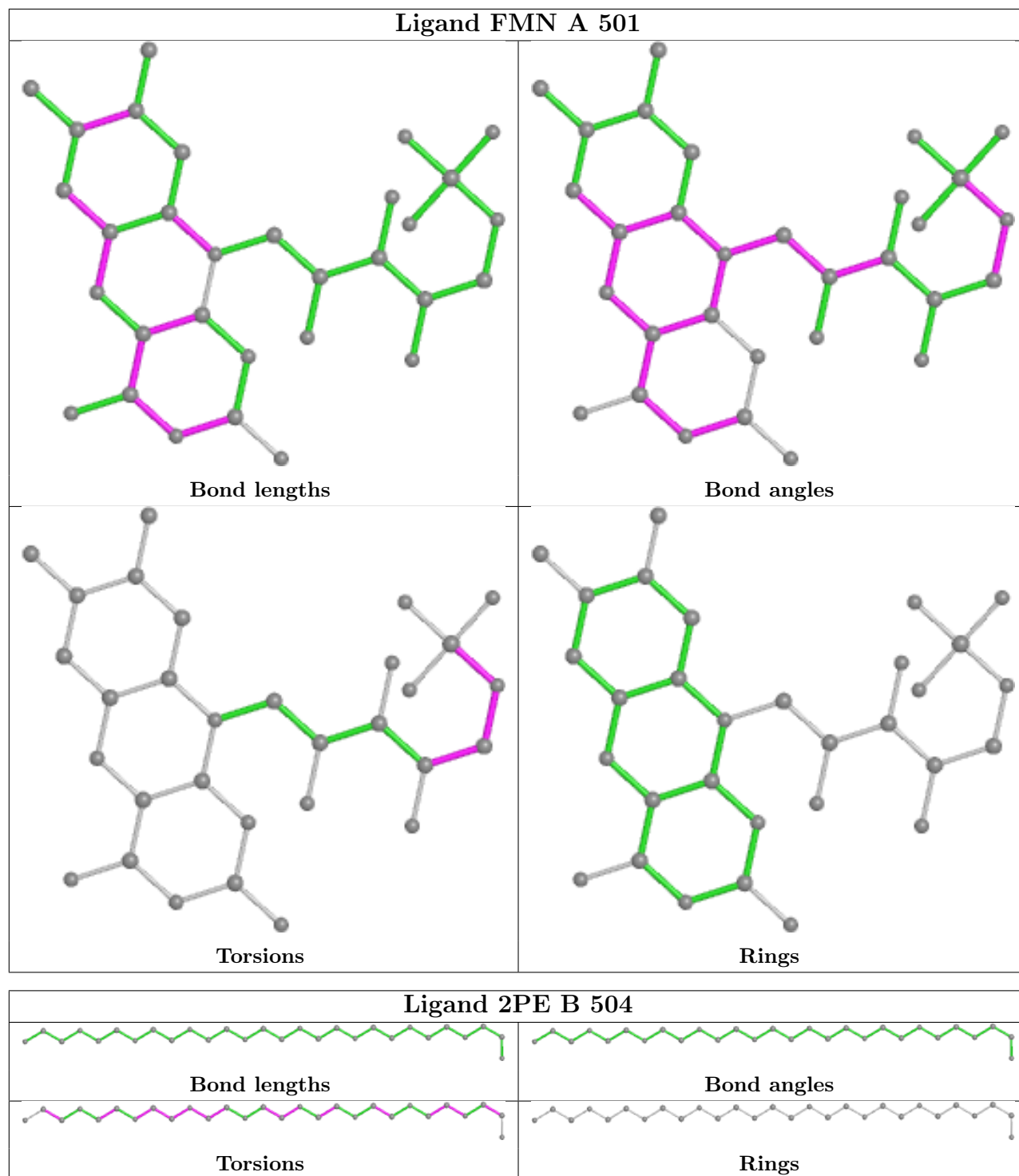
Mol	Chain	Res	Type	Atoms
4	A	501	FMN	C5'-O5'-P-O2P
4	B	502	FMN	O2'-C2'-C3'-C4'
4	B	502	FMN	O2'-C2'-C3'-O3'
5	A	503	2PE	C6-C5-O4-C3
5	B	504	2PE	C21-C20-O19-C18

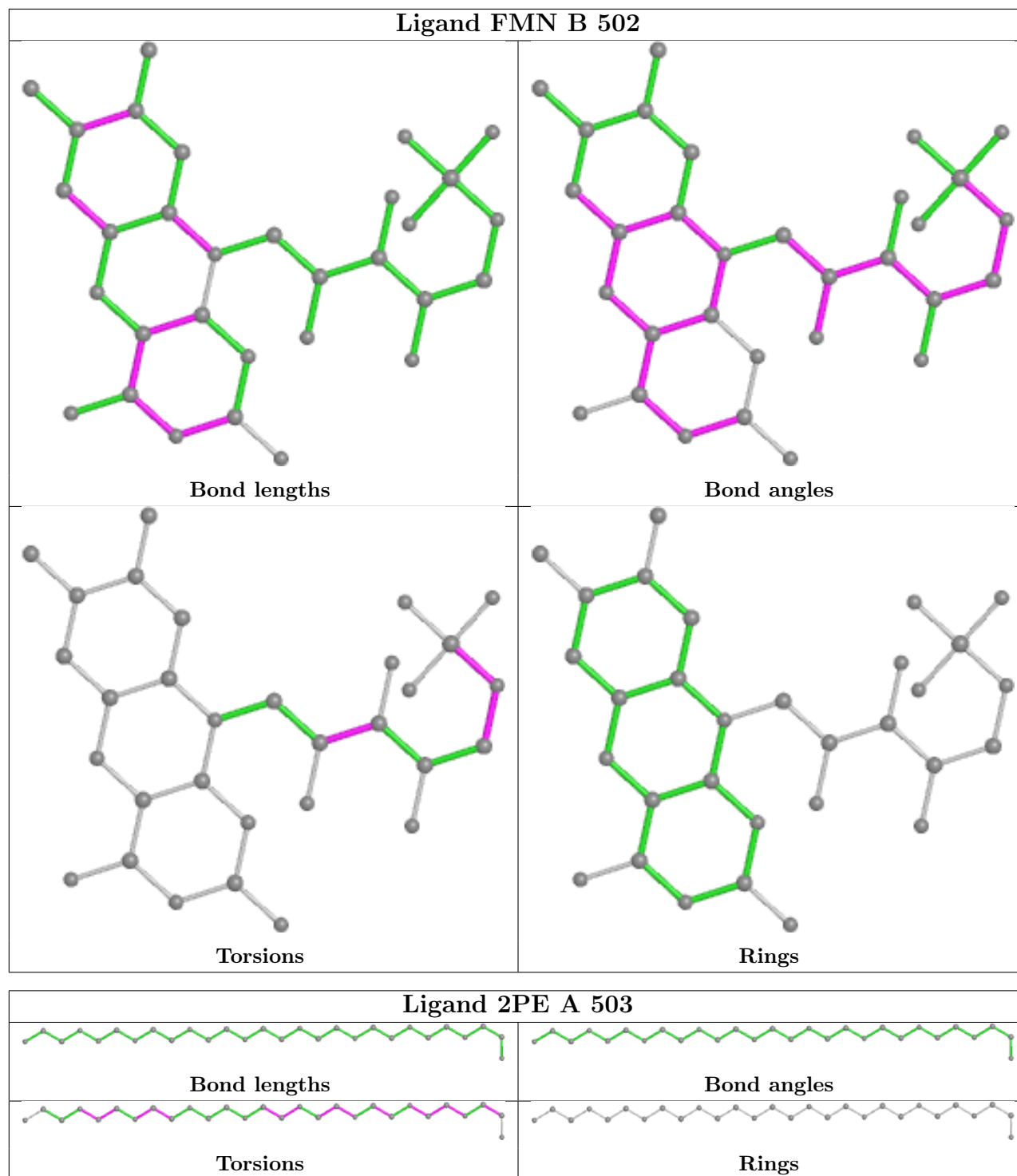
There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	FMN	2	0
5	B	504	2PE	3	0
4	B	502	FMN	1	0
5	A	503	2PE	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 ⓘ

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	358/376 (95%)	-0.23	11 (3%) 49 51	15, 23, 37, 56	0
1	B	358/376 (95%)	-0.20	10 (2%) 53 56	16, 23, 39, 60	0
All	All	716/752 (95%)	-0.22	21 (2%) 51 54	15, 23, 38, 60	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	10	GLN	6.4
1	B	374	THR	6.0
1	A	289	CYS	5.2
1	B	282	THR	4.5
1	A	280	MET	4.3
1	A	10	GLN	4.2
1	A	281	LYS	3.2
1	B	23	GLY	3.1
1	A	282	THR	3.0
1	A	11	VAL	2.9
1	B	146	ILE	2.8
1	B	11	VAL	2.8
1	A	146	ILE	2.6
1	B	279	ARG	2.6
1	A	279	ARG	2.5
1	A	290	THR	2.4
1	B	373	GLU	2.4
1	A	373	GLU	2.4
1	B	281	LYS	2.3
1	A	354	ARG	2.1
1	B	21	LYS	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 monosaccharides in this entry.

6.4 Ligands [i](#)

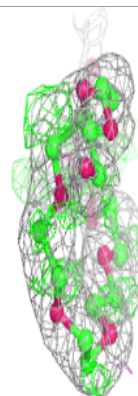
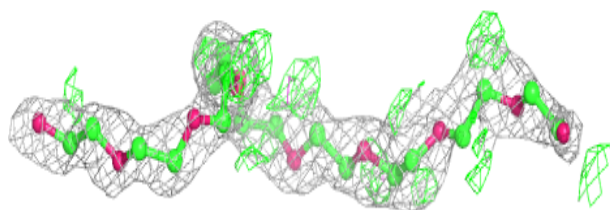
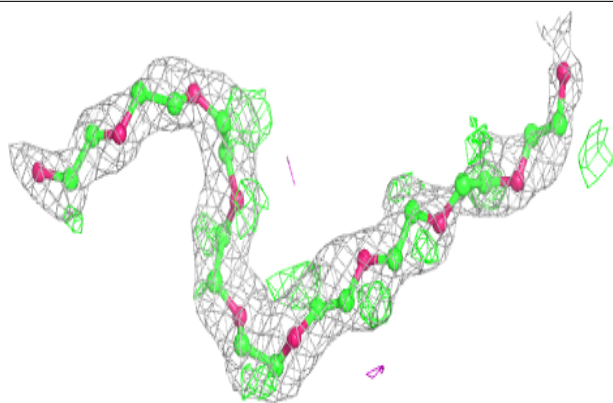
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	2PE	B	504	28/28	0.81	0.20	31,46,69,70	0
5	2PE	A	503	28/28	0.87	0.17	29,43,67,70	0
3	SO4	B	506	5/5	0.95	0.20	61,64,66,66	0
4	FMN	A	501	31/31	0.97	0.08	15,19,23,24	0
3	SO4	A	507	5/5	0.98	0.17	47,47,50,50	0
4	FMN	B	502	31/31	0.98	0.07	13,19,21,22	0
2	CL	A	505	1/1	0.99	0.09	27,27,27,27	0

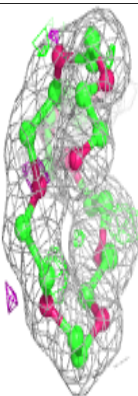
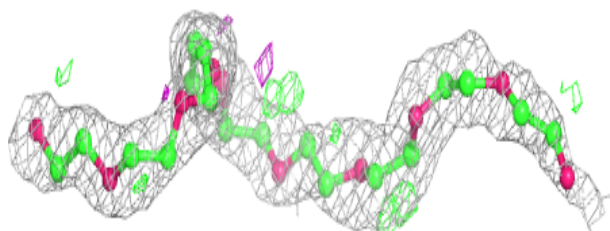
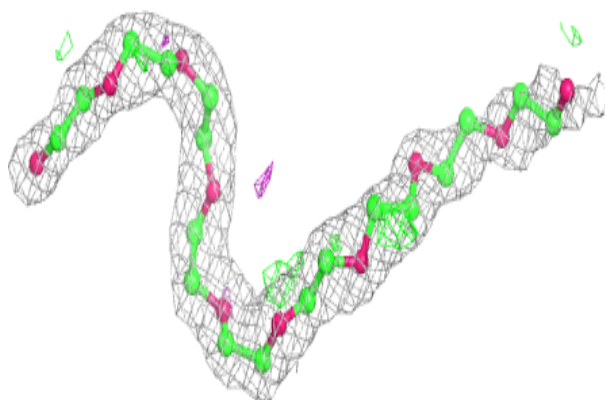
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 2PE B 504:

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

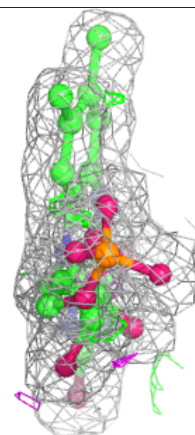
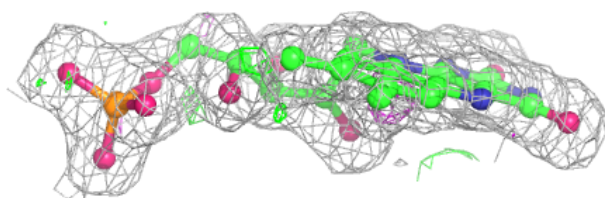
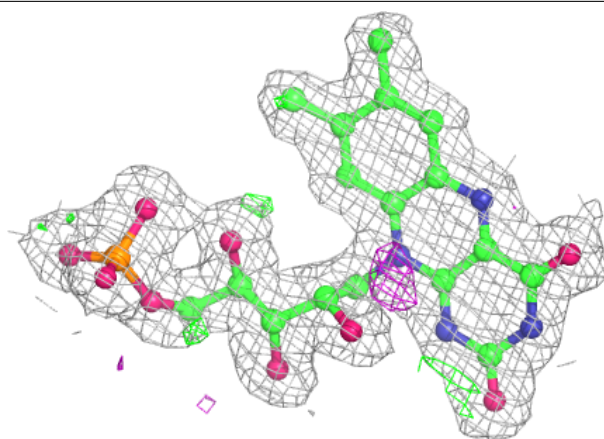
**Electron density around 2PE A 503:**

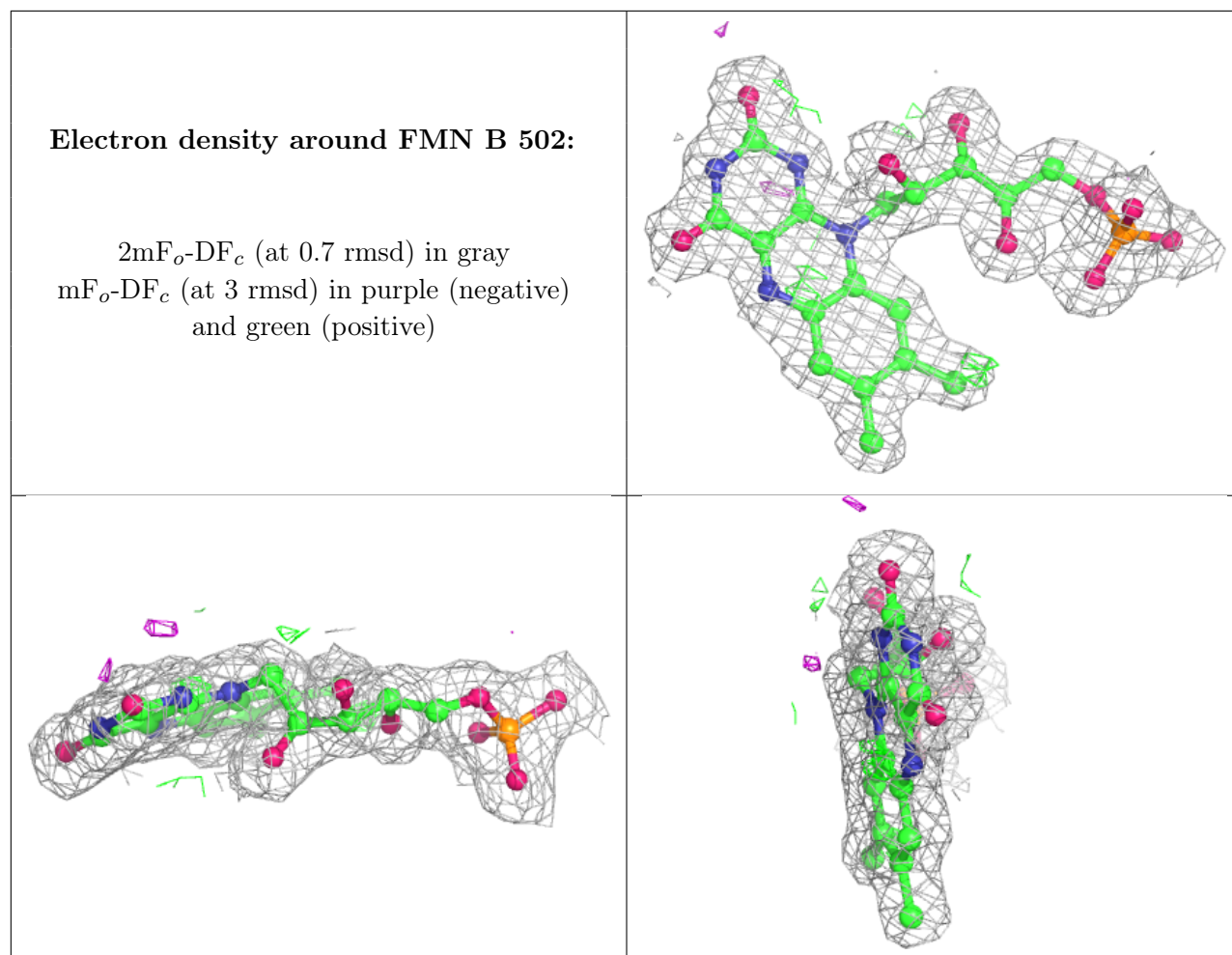
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FMN A 501:

$2mF_o-DF_c$ (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.