



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 10:57 PM EDT

PDB ID : 2FBW / pdb_00002fbw
Title : Avian respiratory complex II with carboxin bound
Authors : Huang, L.S.; Sun, G.; Cobessi, D.; Wang, A.C.; Shen, J.T.; Tung, E.Y.; Anderson, V.E.; Berry, E.A.
Deposited on : 2005-12-10
Resolution : 2.06 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) 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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

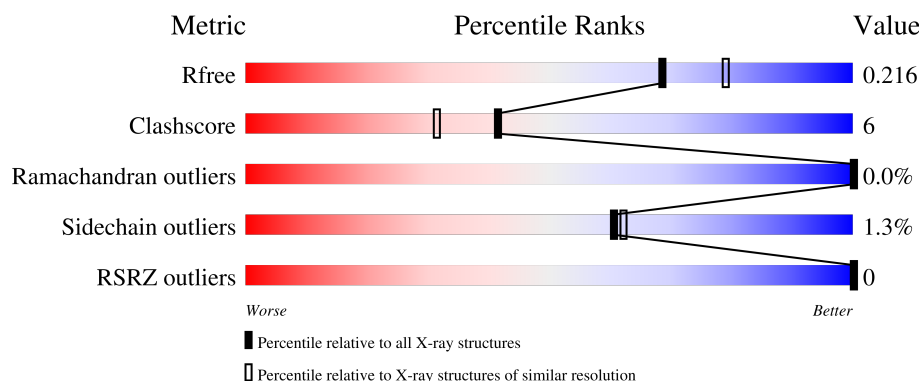
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	621	
1	N	621	
2	B	252	
2	O	252	
3	C	140	

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Mol	Chain	Length	Quality of chain
3	P	140	 81% 18% •
4	D	103	 83% 16% •
4	Q	103	 80% 18% •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	Y3P	A	1002	-	X	X	-
8	AZI	A	1004	-	X	-	-
8	AZI	B	1005	-	X	-	-
8	AZI	N	1004	-	X	-	-
9	UNL	A	1368	-	-	X	-

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 19296 atoms, of which 4 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 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	612	Total	C	N	O	S	1	4	0
			4737	2963	850	895	29			
1	N	612	Total	C	N	O	S	2	4	0
			4733	2962	847	895	29			

- Molecule 2 is a protein called Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	240	Total	C	N	O	S	1	2	0
			1944	1228	331	363	22			
2	O	241	Total	C	N	O	S	0	2	0
			1953	1234	333	364	22			

- Molecule 3 is a protein called Succinate dehydrogenase cytochrome b560 subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	139	Total	C	N	O	S	0	1	0
			1083	712	179	187	5			
3	P	139	Total	C	N	O	S	0	1	0
			1083	712	179	187	5			

- Molecule 4 is a protein called Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	101	Total	C	N	O	S	0	1	0
			767	505	122	137	3			
4	Q	101	Total	C	N	O	S	0	0	0
			766	505	121	137	3			

- # FAD

Y3P

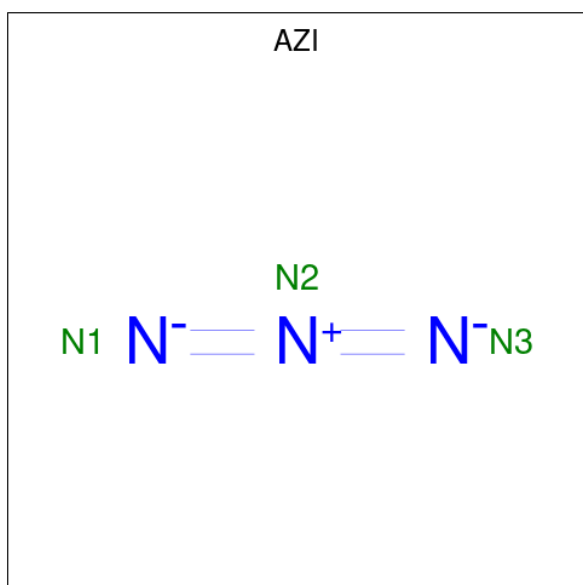
The chemical structure of Y3P is shown, featuring a central carbon-carbon double bond (C2=C3). C1 is a carboxylate group (COO-) attached to C2, with O1 as the hydroxyl oxygen and O2 as the carbonyl oxygen. C4 is a carboxylate group (COO-) attached to C3, with O4 as the carbonyl oxygen and O5 as the hydroxyl oxygen. The structure is labeled Y3P.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			11	4	2	5		
6	N	1	Total	C	H	O	0	0
			11	4	2	5		

- Molecule 7 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	K	0	0
			1	1		
7	N	1	Total	K	0	0
			1	1		

- Molecule 8 is AZIDE ION (CCD ID: AZI) (formula: N₃).

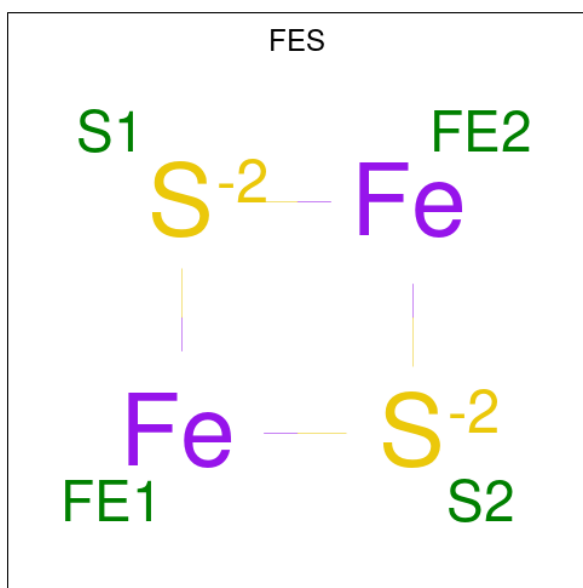


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	N	0	0
			3	3		
8	B	1	Total	N	0	0
			3	3		
8	N	1	Total	N	0	0
			3	3		

- Molecule 9 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

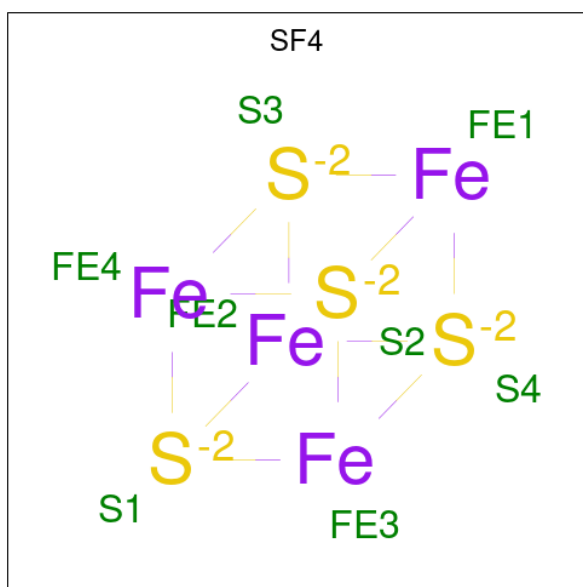
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	66	Total C N O S 129 30 15 83 1	0	8
9	B	43	Total C N O 77 11 15 51	0	5
9	C	19	Total C O 38 10 28	0	6
9	D	10	Total C O 52 29 23	0	1
9	N	64	Total C N O 142 31 21 90	0	11
9	O	36	Total C N O 84 20 12 52	0	9
9	P	9	Total C N O 43 26 3 14	0	0
9	Q	9	Total C O 74 45 29	0	1

- Molecule 10 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



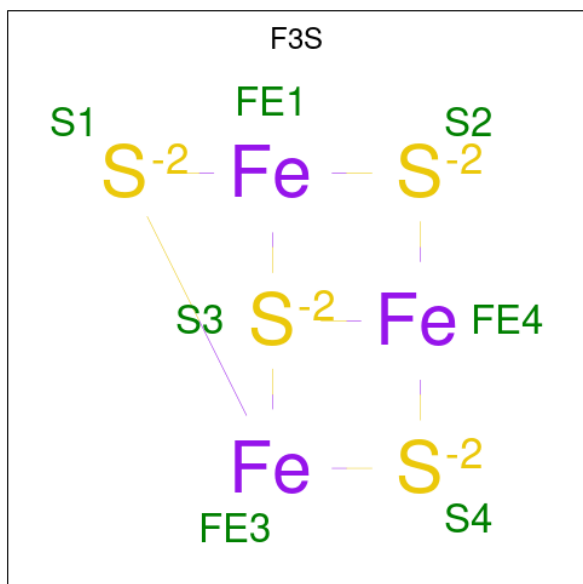
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	B	1	Total Fe S 4 2 2	0	0
10	O	1	Total Fe S 4 2 2	0	0

- Molecule 11 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
11	B	1	Total	Fe	S	0	0
			8	4	4		
11	O	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 12 is FE3-S4 CLUSTER (CCD ID: F3S) (formula: Fe_3S_4) (labeled as "Ligand of Interest" by depositor).



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

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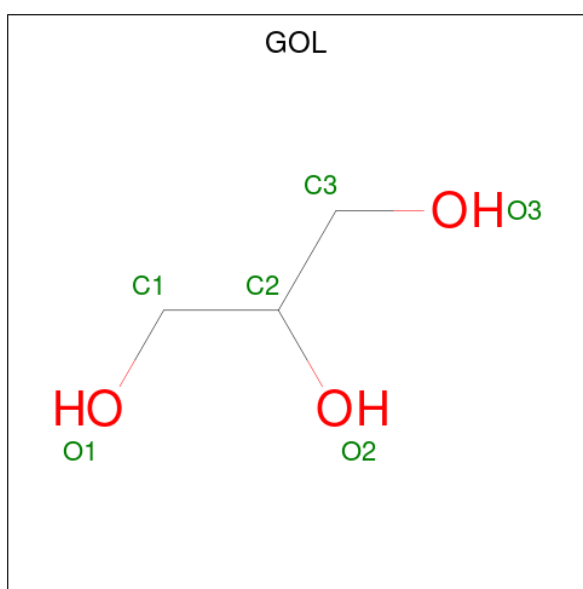
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	O	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 13 is SODIUM ION (CCD ID: NA) (formula: Na).

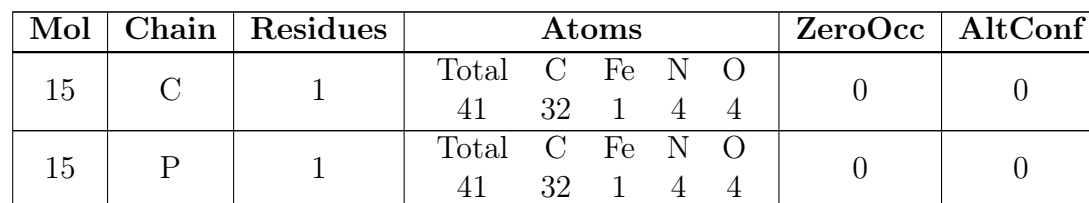
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	B	1	Total	Na	0	0
			1	1		

- Molecule 14 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	B	1	Total	C	O	0	0
			6	3	3		
14	N	1	Total	C	O	0	0
			6	3	3		

- Molecule 15 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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- Chemical structure of 2-(benzylthio)thiophene (CBE). The structure shows a thiophene ring (S4, C2-C6) connected at the 2-position to a methylene group (C8), which is further connected to a benzene ring (C11-C16). The nitrogen atom (N10) is part of the benzyl group. Atoms are color-coded: S4 is yellow, O7 and O9 are red, N10 is blue, and C1-C6 are green.

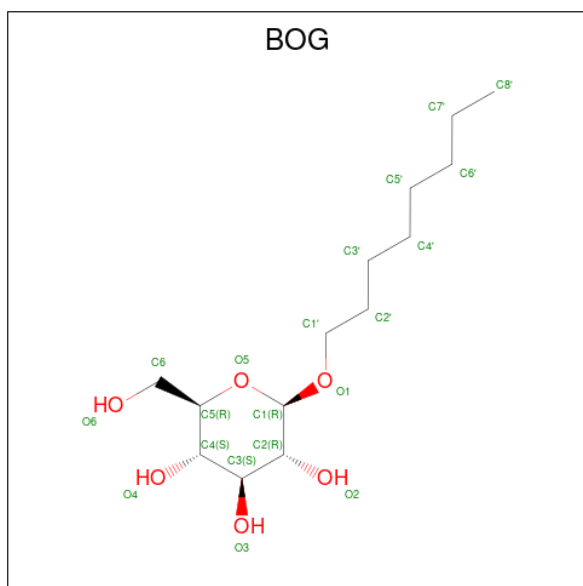
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
16	C	1	Total	C	N	O	S	0	0
			16	12	1	2	1		



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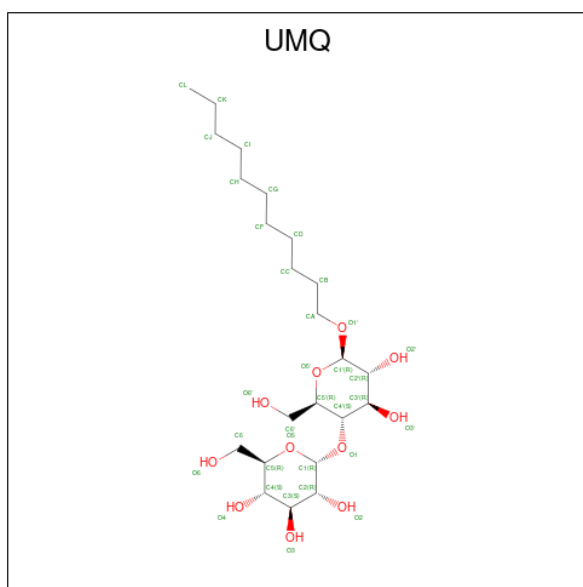
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
16	P	1	Total	C	N	O	S	0	0
			16	12	1	2	1		

- Molecule 17 is octyl beta-D-glucopyranoside (CCD ID: BOG) (formula: $C_{14}H_{28}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
17	C	1	Total	C	O	0	0
			18	12	6		
17	D	1	Total	C	O	0	0
			17	11	6		
17	P	1	Total	C	O	0	0
			20	14	6		

- Molecule 18 is UNDECYL-MALTOSIDE (CCD ID: UMQ) (formula: $C_{23}H_{44}O_{11}$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
18	P	1	Total	C	O	0	0
			26	16	10		

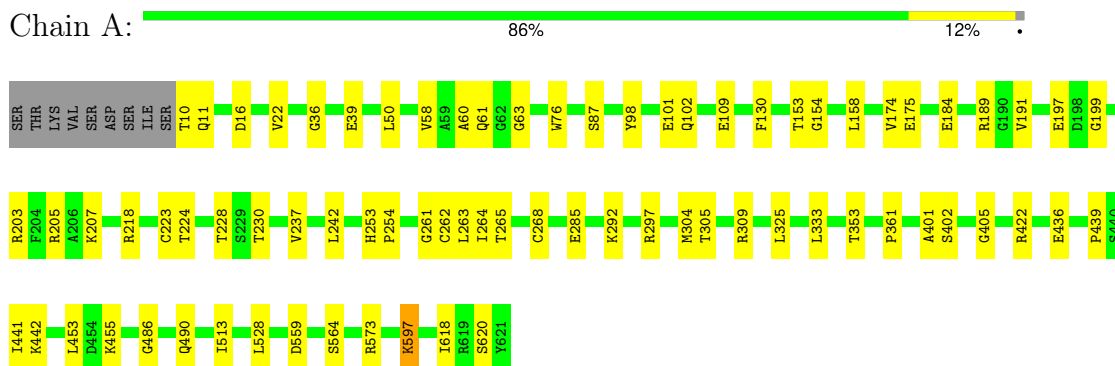
- Molecule 19 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
19	A	361	Total O 362 362	0	1
19	B	164	Total O 165 165	0	1
19	C	39	Total O 39 39	0	0
19	D	18	Total O 18 18	0	0
19	N	377	Total O 378 378	0	1
19	O	188	Total O 188 188	0	0
19	P	44	Total O 44 44	0	0
19	Q	12	Total O 12 12	0	0

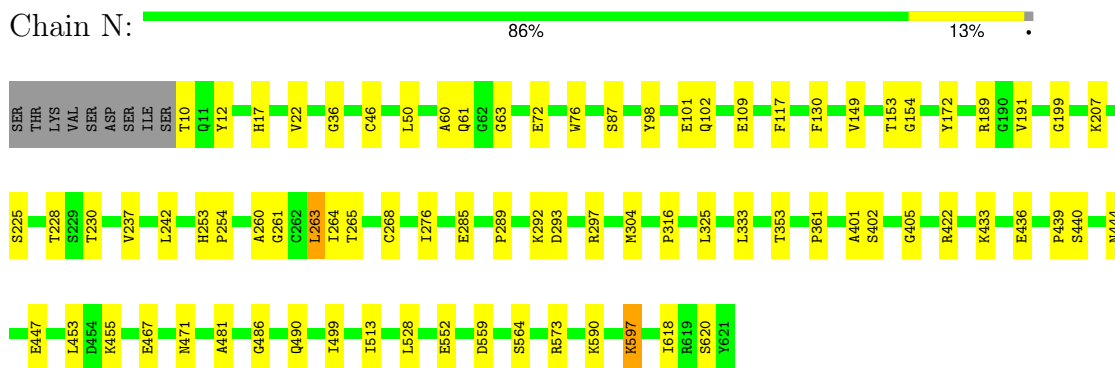
3 Residue-property plots

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

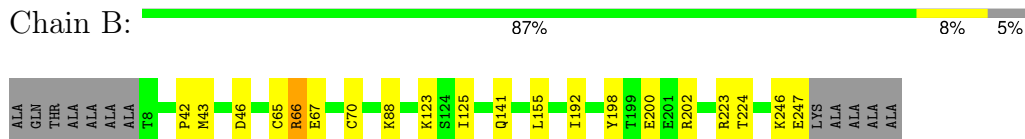
- Molecule 1: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial



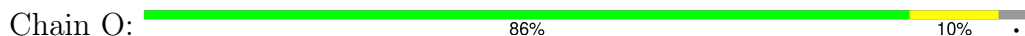
- Molecule 1: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial



- Molecule 2: Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial

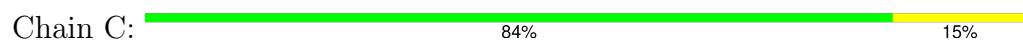


- Molecule 2: Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial

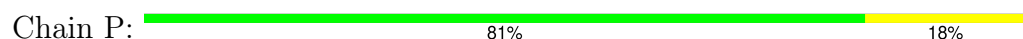




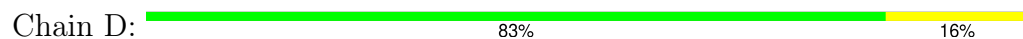
- Molecule 3: Succinate dehydrogenase cytochrome b560 subunit, mitochondrial



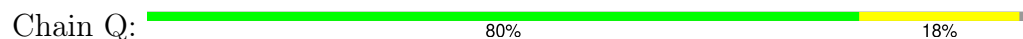
- Molecule 3: Succinate dehydrogenase cytochrome b560 subunit, mitochondrial



- Molecule 4: Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial



- Molecule 4: Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	118.70Å 200.75Å 67.63Å 90.00° 90.06° 90.00°	Depositor
Resolution (Å)	64.09 – 2.06 64.09 – 2.06	Depositor EDS
% Data completeness (in resolution range)	85.2 (64.09-2.06) 85.6 (64.09-2.06)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.62 (at 2.05Å)	Xtriage
Refinement program	PHENIX dev_3150	Depositor
R, R_{free}	0.171 , 0.215 0.171 , 0.216	Depositor DCC
R_{free} test set	8237 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.525	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.287 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	19296	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: NA, GOL, CBE, AZI, Y3P, FES, HEM, FAD, K, UMQ, SF4, UNL, F3S, BOG

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	0.34	0/4845	0.53	0/6559
1	N	0.34	0/4848	0.54	0/6564
2	B	0.34	0/1987	0.49	0/2678
2	O	0.32	0/1996	0.49	0/2689
3	C	0.21	0/1112	0.38	0/1511
3	P	0.21	0/1112	0.37	0/1511
4	D	0.18	0/798	0.29	0/1093
4	Q	0.17	0/789	0.28	0/1082
All	All	0.31	0/17487	0.49	0/23687

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	4737	0	4614	58	0
1	N	4733	0	4616	56	0
2	B	1944	0	1937	28	0
2	O	1953	0	1950	26	0
3	C	1083	0	1125	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	P	1083	0	1125	22	0
4	D	767	0	752	10	0
4	Q	766	0	761	15	0
5	A	53	0	29	3	0
5	N	53	0	29	4	0
6	A	9	2	0	4	0
6	N	9	2	0	2	0
7	A	1	0	0	0	0
7	N	1	0	0	0	0
8	A	3	0	0	0	0
8	B	3	0	0	0	0
8	N	3	0	0	0	0
9	A	129	0	0	9	0
9	B	77	0	0	4	0
9	C	38	0	0	3	0
9	D	52	0	0	1	0
9	N	142	0	0	7	0
9	O	84	0	0	3	0
9	P	43	0	0	0	0
9	Q	74	0	0	2	0
10	B	4	0	0	0	0
10	O	4	0	0	0	0
11	B	8	0	0	0	0
11	O	8	0	0	0	0
12	B	7	0	0	0	0
12	O	7	0	0	0	0
13	B	1	0	0	0	0
14	B	6	0	8	0	0
14	N	6	0	8	3	0
15	C	41	0	24	1	0
15	P	41	0	24	2	0
16	C	16	0	13	1	0
16	P	16	0	13	2	0
17	C	18	0	21	0	0
17	D	17	0	19	2	0
17	P	20	0	28	4	0
18	P	26	0	25	7	0
19	A	362	0	0	7	0
19	B	165	0	0	0	0
19	C	39	0	0	0	0
19	D	18	0	0	0	0
19	N	378	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	O	188	0	0	3	0
19	P	44	0	0	0	0
19	Q	12	0	0	0	0
All	All	19292	4	17121	226	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 6.

The worst 5 of 226 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:N:189:ARG:HD3	1:N:439:PRO:HB2	1.34	1.07
1:A:189:ARG:HD3	1:A:439:PRO:HB2	1.37	1.07
1:A:223:CYS:O	2:B:66[B]:ARG:NH2	2.02	0.93
1:A:218[A]:ARG:HH22	2:B:66[A]:ARG:HH21	1.19	0.90
1:A:297:ARG:HH22	6:A:1002:Y3P:C3	1.86	0.88

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	614/621 (99%)	594 (97%)	20 (3%)	0	100	100
1	N	614/621 (99%)	596 (97%)	18 (3%)	0	100	100
2	B	240/252 (95%)	234 (98%)	6 (2%)	0	100	100
2	O	241/252 (96%)	234 (97%)	6 (2%)	1 (0%)	30	23
3	C	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
3	P	138/140 (99%)	137 (99%)	1 (1%)	0	100	100
4	D	100/103 (97%)	99 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	Q	99/103 (96%)	97 (98%)	2 (2%)	0	100	100
All	All	2184/2232 (98%)	2128 (97%)	55 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	O	247	GLU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	496/506 (98%)	491 (99%)	5 (1%)	68	71
1	N	497/506 (98%)	488 (98%)	9 (2%)	51	51
2	B	218/219 (100%)	213 (98%)	5 (2%)	44	41
2	O	219/219 (100%)	216 (99%)	3 (1%)	59	60
3	C	118/118 (100%)	118 (100%)	0	100	100
3	P	118/118 (100%)	118 (100%)	0	100	100
4	D	79/79 (100%)	78 (99%)	1 (1%)	61	62
4	Q	78/79 (99%)	77 (99%)	1 (1%)	61	62
All	All	1823/1844 (99%)	1799 (99%)	24 (1%)	61	62

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	191	VAL
1	N	293	ASP
1	N	263	LEU
1	N	597	LYS
2	B	66[B]	ARG

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

Mol	Chain	Res	Type
4	D	69	ASN
1	N	324	GLN
4	Q	69	ASN
4	Q	60	HIS
1	A	324	GLN

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](#)

Of 323 ligands modelled in this entry, 3 are monoatomic and 297 are unknown - leaving 23 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	$\# Z > 2$
8	AZI	B	1005	-	2,2,2	3.20	2 (100%)	0,1,1	-	-
14	GOL	N	1005	-	5,5,5	0.06	0	5,5,5	0.27	0
16	CBE	P	202	-	16,17,17	1.48	2 (12%)	17,22,22	2.02	3 (17%)
11	SF4	O	1002	2	0,12,12	-	-	-	-	-
17	BOG	D	201	-	17,17,20	0.69	1 (5%)	22,22,25	0.73	1 (4%)
5	FAD	A	1001	-	58,58,58	0.88	2 (3%)	85,89,89	0.93	2 (2%)
14	GOL	B	1006	-	5,5,5	0.08	0	5,5,5	0.32	0
5	FAD	N	1001	1	58,58,58	0.95	3 (5%)	85,89,89	1.01	5 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	FES	B	1001	2	0,4,4	-	-	-		
17	BOG	C	203	-	18,18,20	0.55	0	23,23,25	0.66	0
8	AZI	N	1004	-	2,2,2	3.18	2 (100%)	0,1,1	-	-
6	Y3P	A	1002	-	8,8,8	2.62	5 (62%)	9,10,10	1.53	3 (33%)
17	BOG	P	204	-	20,20,20	0.50	0	25,25,25	0.69	1 (4%)
8	AZI	A	1004	-	2,2,2	3.19	2 (100%)	0,1,1	-	-
15	HEM	C	201	4,3	48,48,50	1.36	7 (14%)	66,80,82	1.14	5 (7%)
6	Y3P	N	1002	-	8,8,8	2.68	6 (75%)	9,10,10	1.08	0
15	HEM	P	201	4,3	48,48,50	1.36	7 (14%)	66,80,82	1.11	5 (7%)
16	CBE	C	202	-	16,17,17	1.52	3 (18%)	17,22,22	2.02	4 (23%)
18	UMQ	P	203	-	27,27,35	0.24	0	37,37,46	0.45	0
10	FES	O	1001	2	0,4,4	-	-	-		
12	F3S	B	1003	2	0,9,9	-	-	-		
11	SF4	B	1002	2	0,12,12	-	-	-		
12	F3S	O	1003	2	0,9,9	-	-	-		

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
14	GOL	N	1005	-	-	0/4/4/4	-
16	CBE	P	202	-	-	2/6/19/19	0/2/2/2
11	SF4	O	1002	2	-	-	0/6/5/5
17	BOG	D	201	-	-	1/8/28/31	0/1/1/1
5	FAD	A	1001	-	-	6/34/50/50	0/6/6/6
14	GOL	B	1006	-	-	0/4/4/4	-
5	FAD	N	1001	1	-	5/34/50/50	0/6/6/6
10	FES	B	1001	2	-	-	0/1/1/1
17	BOG	C	203	-	-	4/9/29/31	0/1/1/1
6	Y3P	A	1002	-	-	4/8/8/8	-
17	BOG	P	204	-	-	1/11/31/31	0/1/1/1
15	HEM	C	201	4,3	-	1/10/50/54	-
6	Y3P	N	1002	-	-	4/8/8/8	-
15	HEM	P	201	4,3	-	1/10/50/54	-
16	CBE	C	202	-	-	2/6/19/19	0/2/2/2
18	UMQ	P	203	-	-	3/12/49/60	0/2/2/2
10	FES	O	1001	2	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	F3S	B	1003	2	-	-	0/3/3/3
11	SF4	B	1002	2	-	-	0/6/5/5
12	F3S	O	1003	2	-	-	0/3/3/3

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	N	1002	Y3P	C2-C1	4.78	1.55	1.48
6	A	1002	Y3P	C2-C1	4.72	1.55	1.48
16	P	202	CBE	C3-S4	-3.80	1.67	1.74
6	A	1002	Y3P	O2-C1	3.68	1.31	1.22
16	C	202	CBE	C11-N10	-3.62	1.34	1.41

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	P	202	CBE	O7-C2-C1	6.92	117.48	109.30
16	C	202	CBE	O7-C2-C1	6.80	117.34	109.30
5	N	1001	FAD	O3P-PA-O1A	-2.87	102.06	110.70
16	C	202	CBE	C6-O7-C2	2.78	123.39	115.85
5	N	1001	FAD	O2A-PA-O3P	2.61	114.32	107.27

There are no chirality outliers.

5 of 34 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1001	FAD	N10-C1'-C2'-O2'
5	A	1001	FAD	N10-C1'-C2'-C3'
5	N	1001	FAD	N10-C1'-C2'-O2'
5	N	1001	FAD	N10-C1'-C2'-C3'
6	A	1002	Y3P	O1-C1-C2-O3

There are no ring outliers.

12 monomers are involved in 31 short contacts:

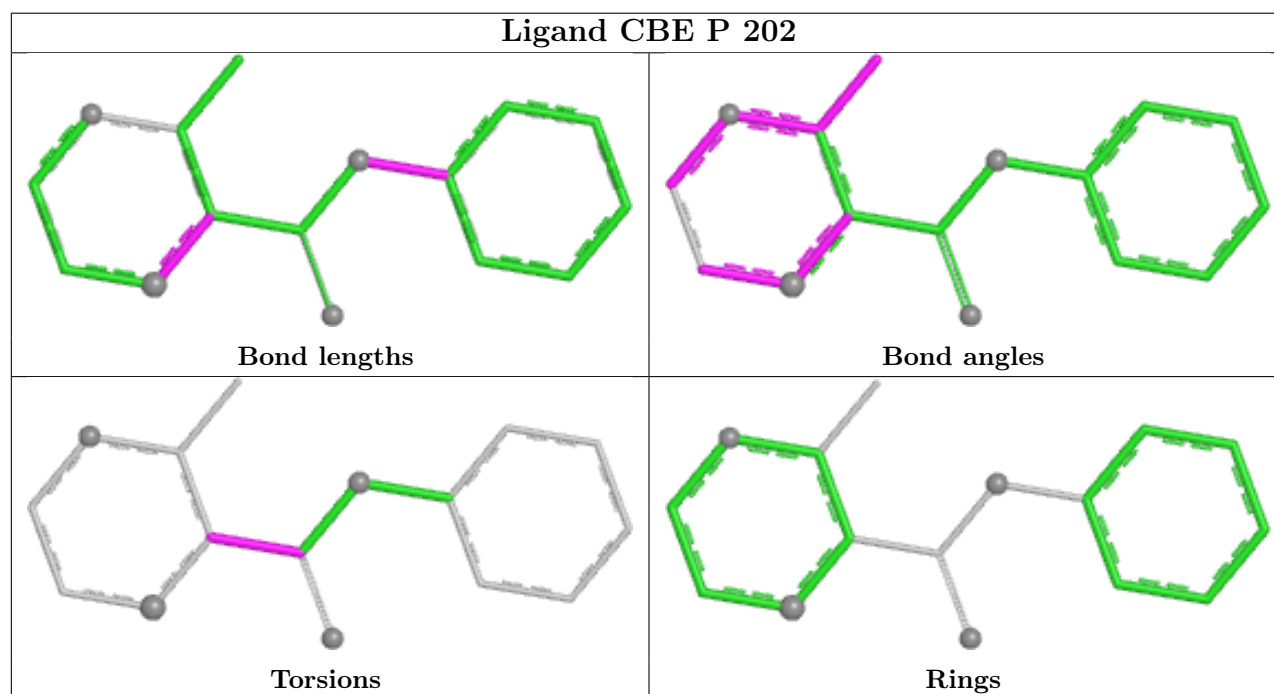
Mol	Chain	Res	Type	Clashes	Symm-Clashes
14	N	1005	GOL	3	0
16	P	202	CBE	2	0
17	D	201	BOG	2	0
5	A	1001	FAD	3	0
5	N	1001	FAD	4	0

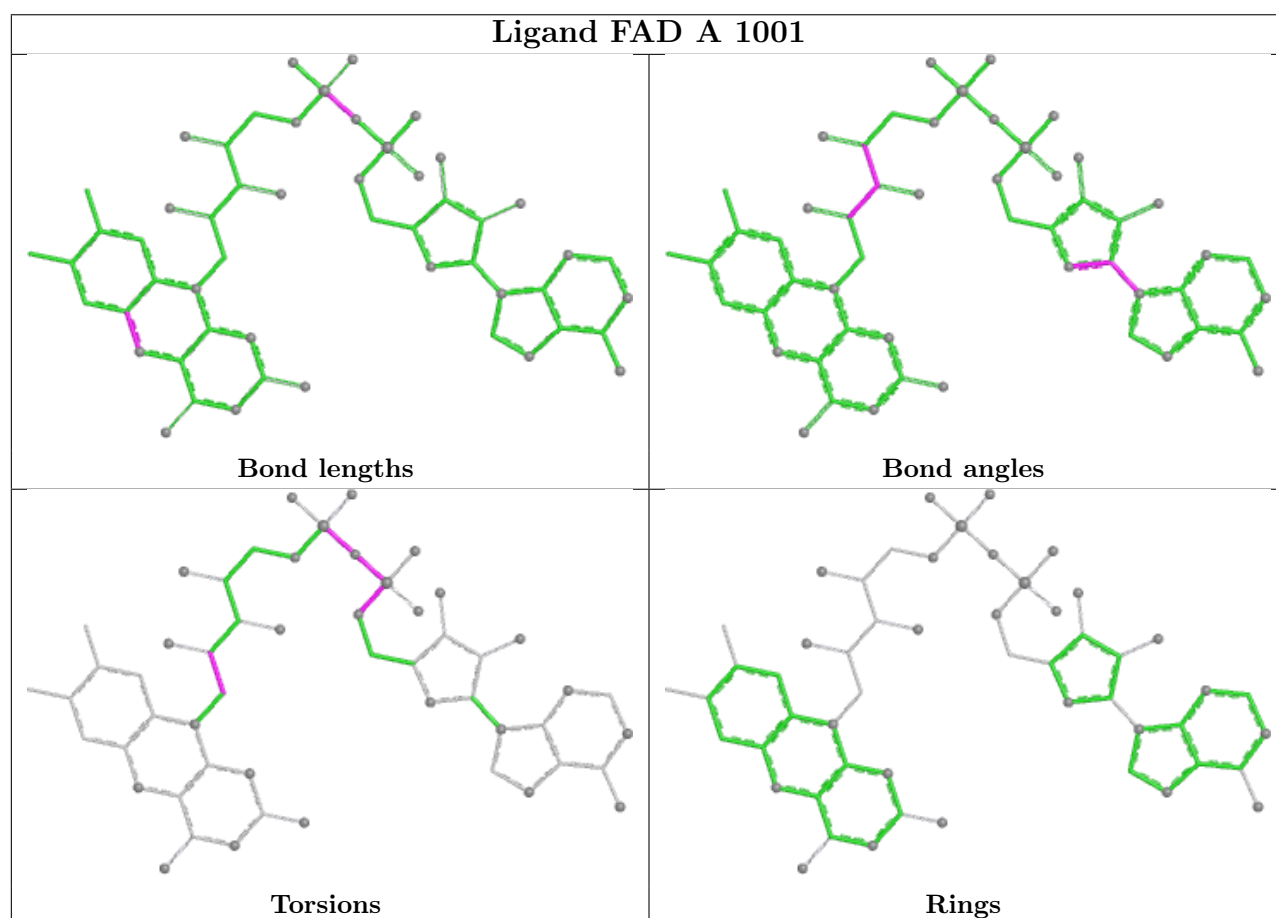
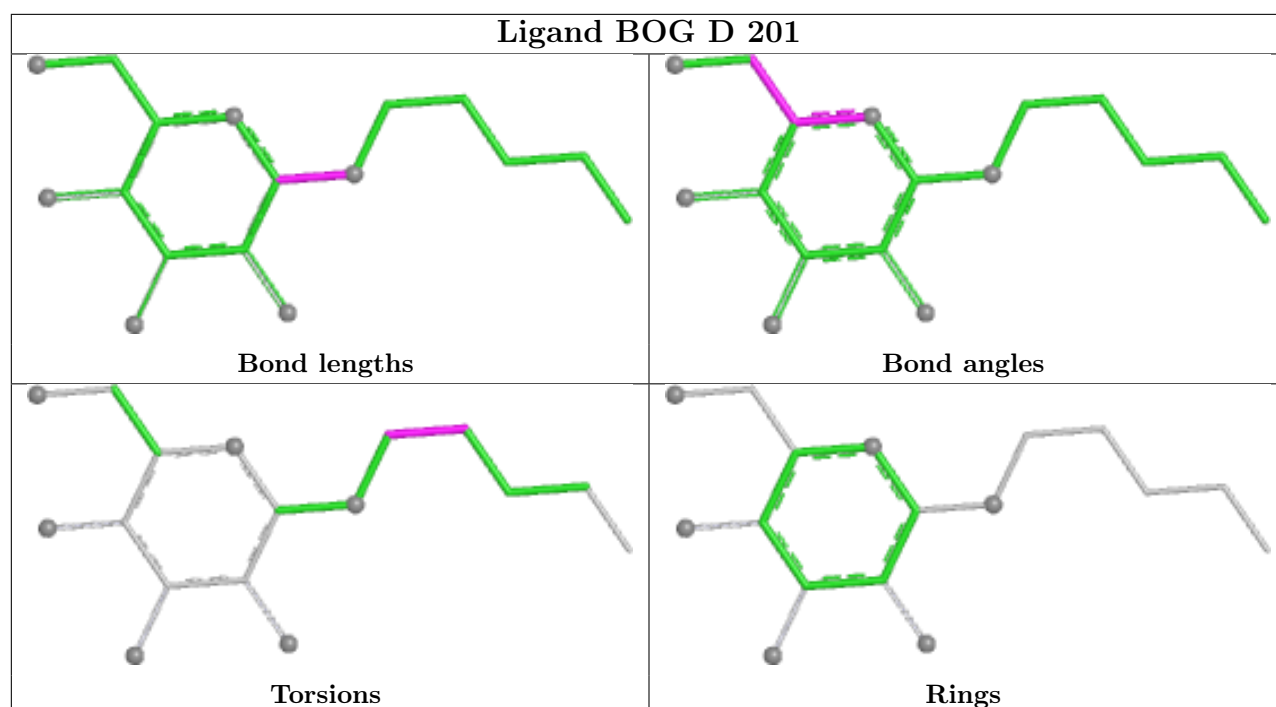
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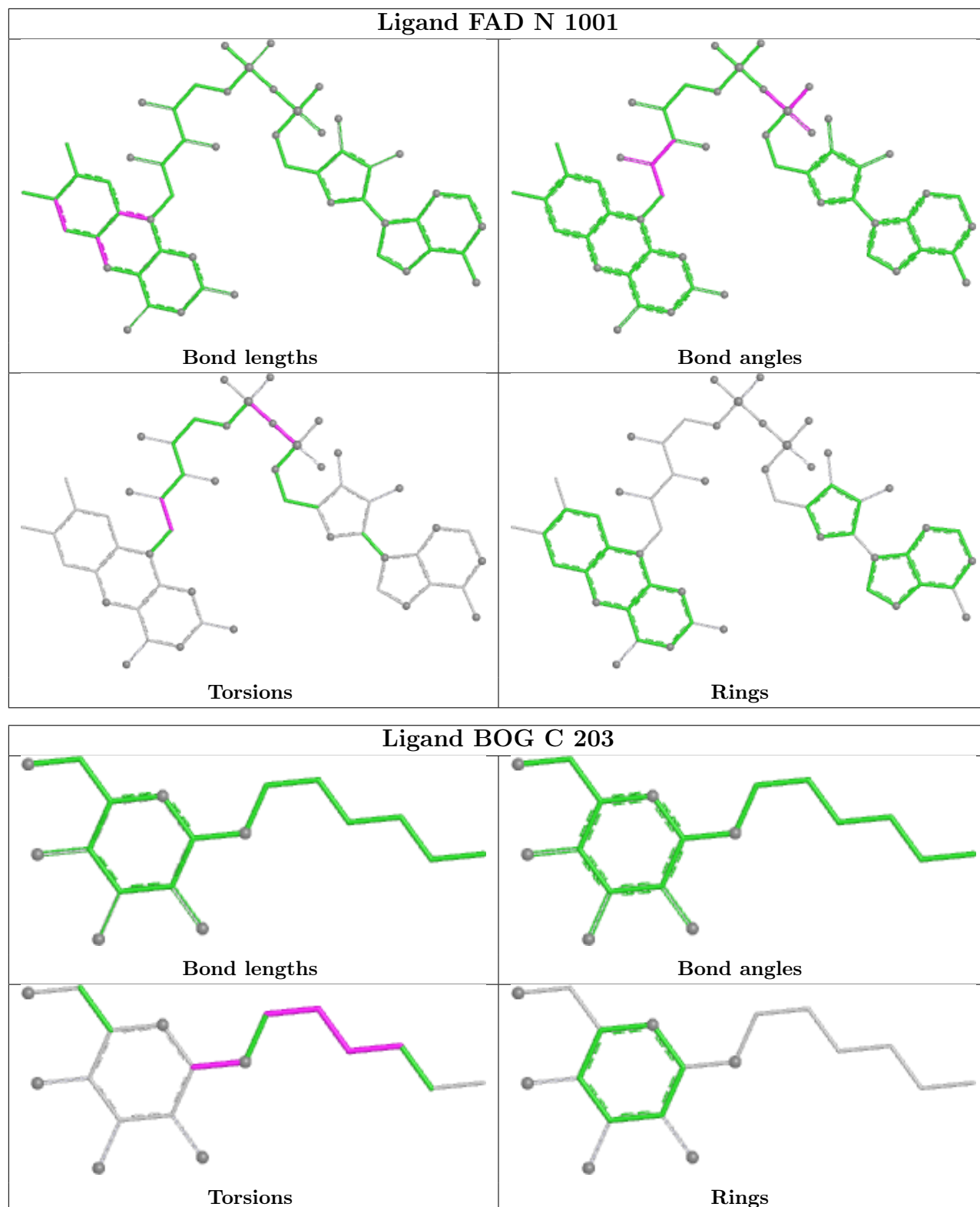
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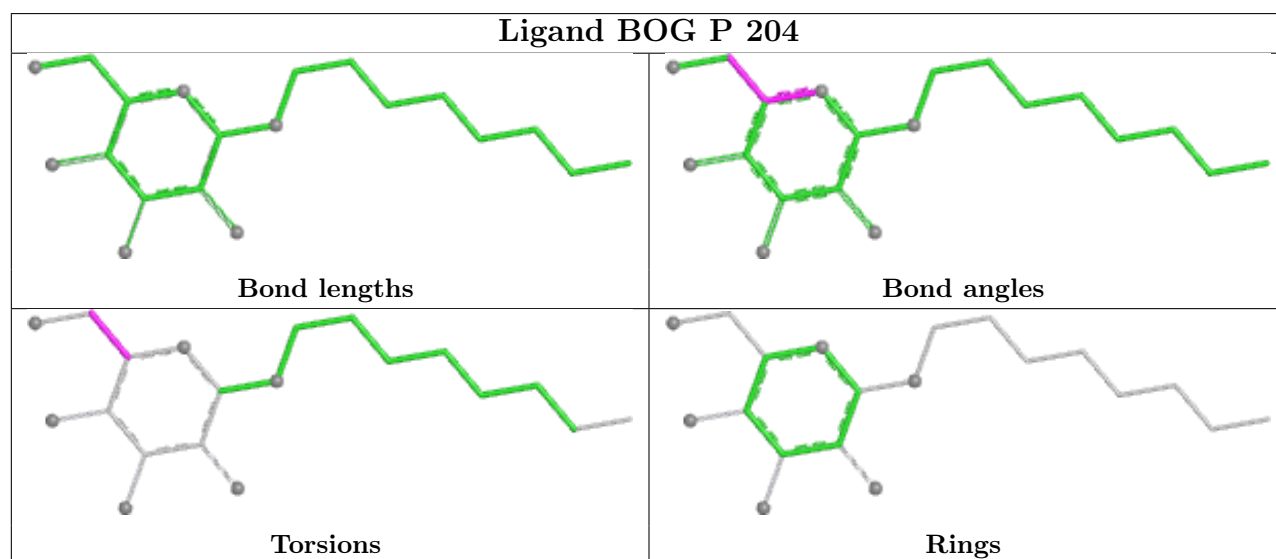
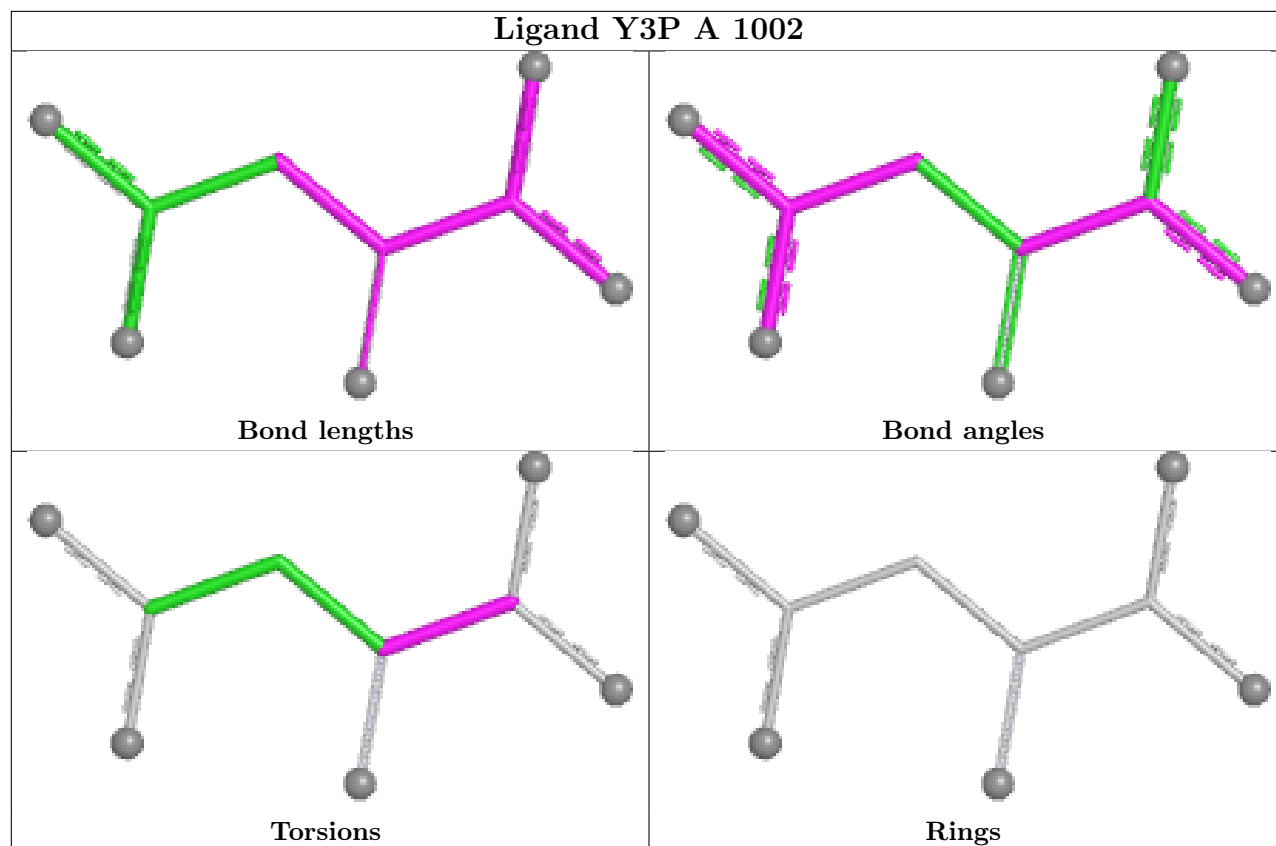
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1002	Y3P	4	0
17	P	204	BOG	4	0
15	C	201	HEM	1	0
6	N	1002	Y3P	2	0
15	P	201	HEM	2	0
16	C	202	CBE	1	0
18	P	203	UMQ	7	0

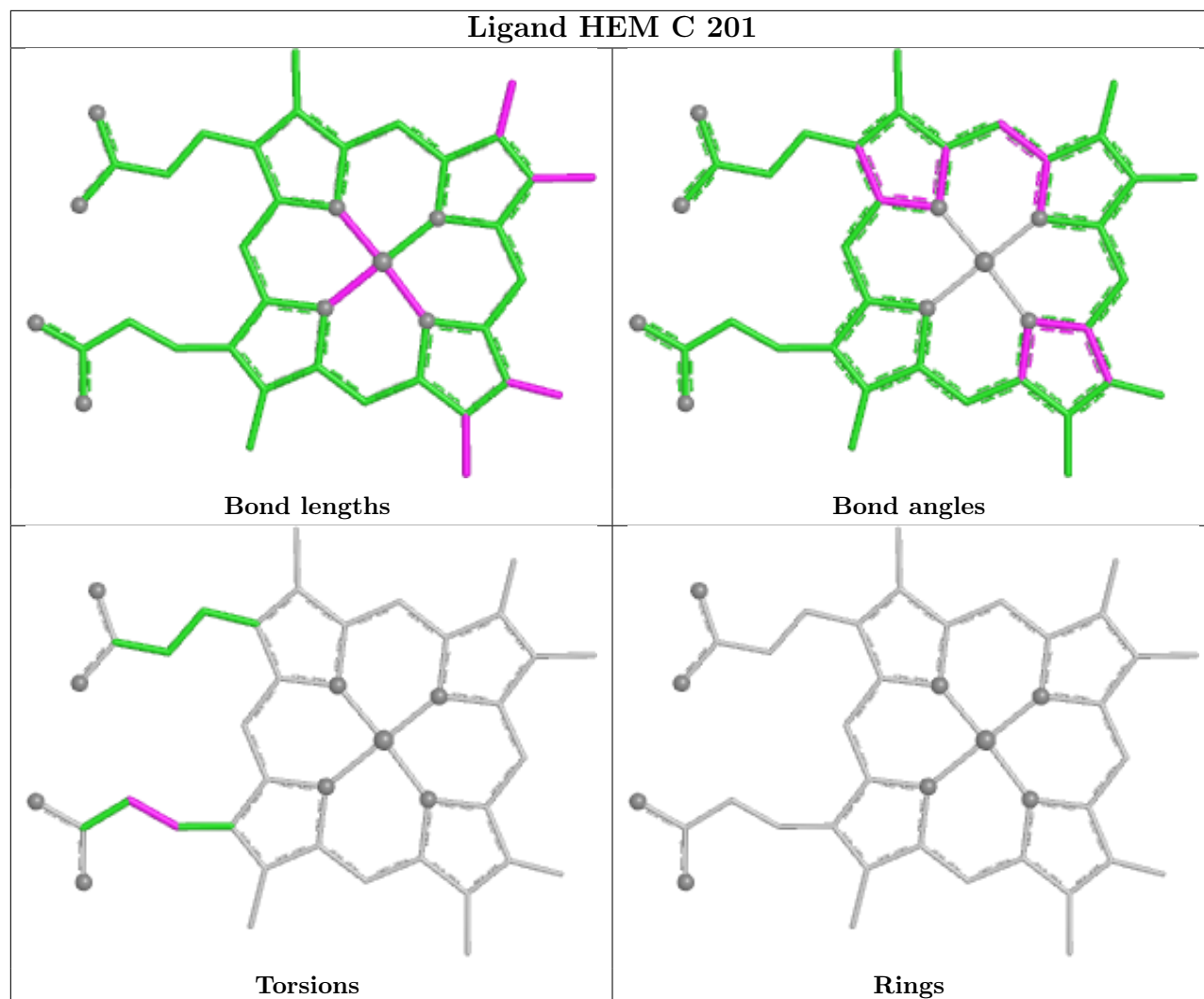
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

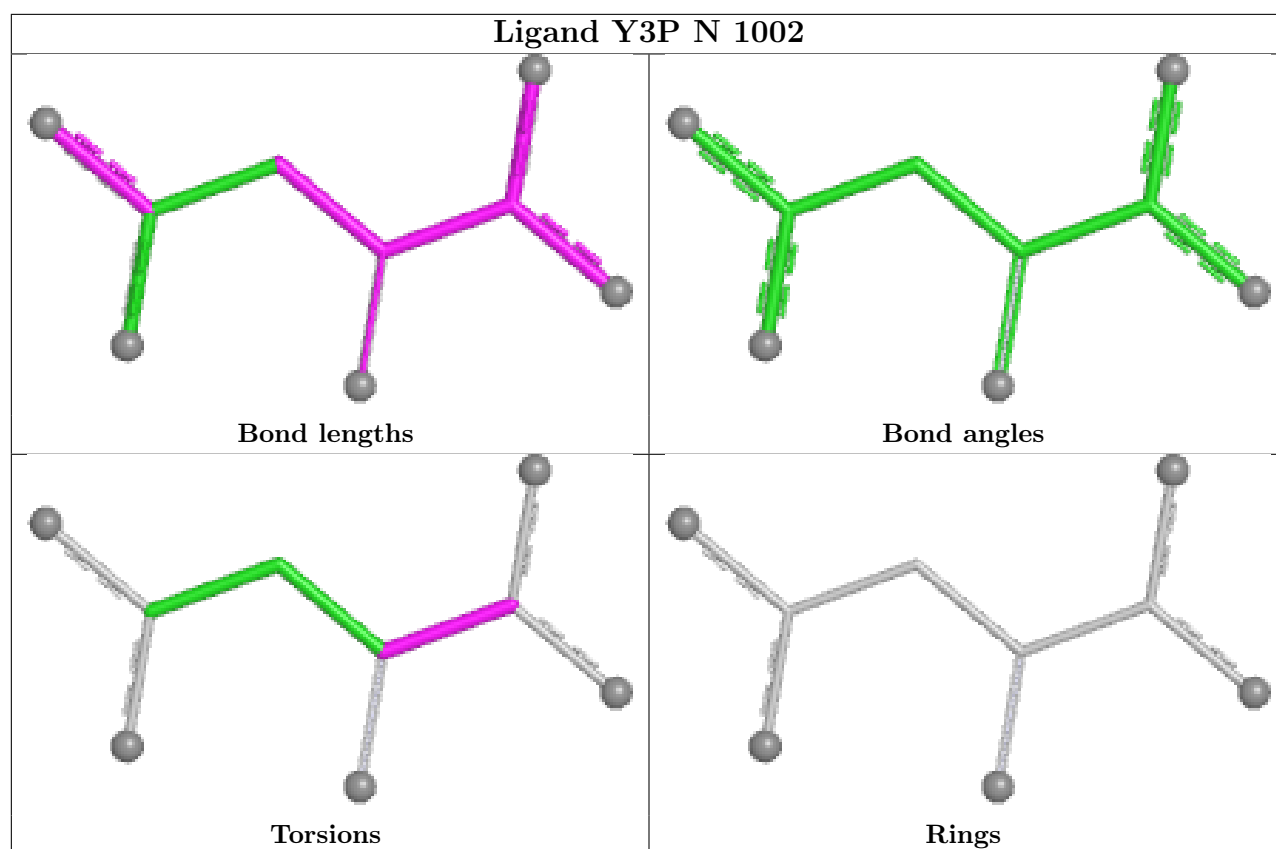


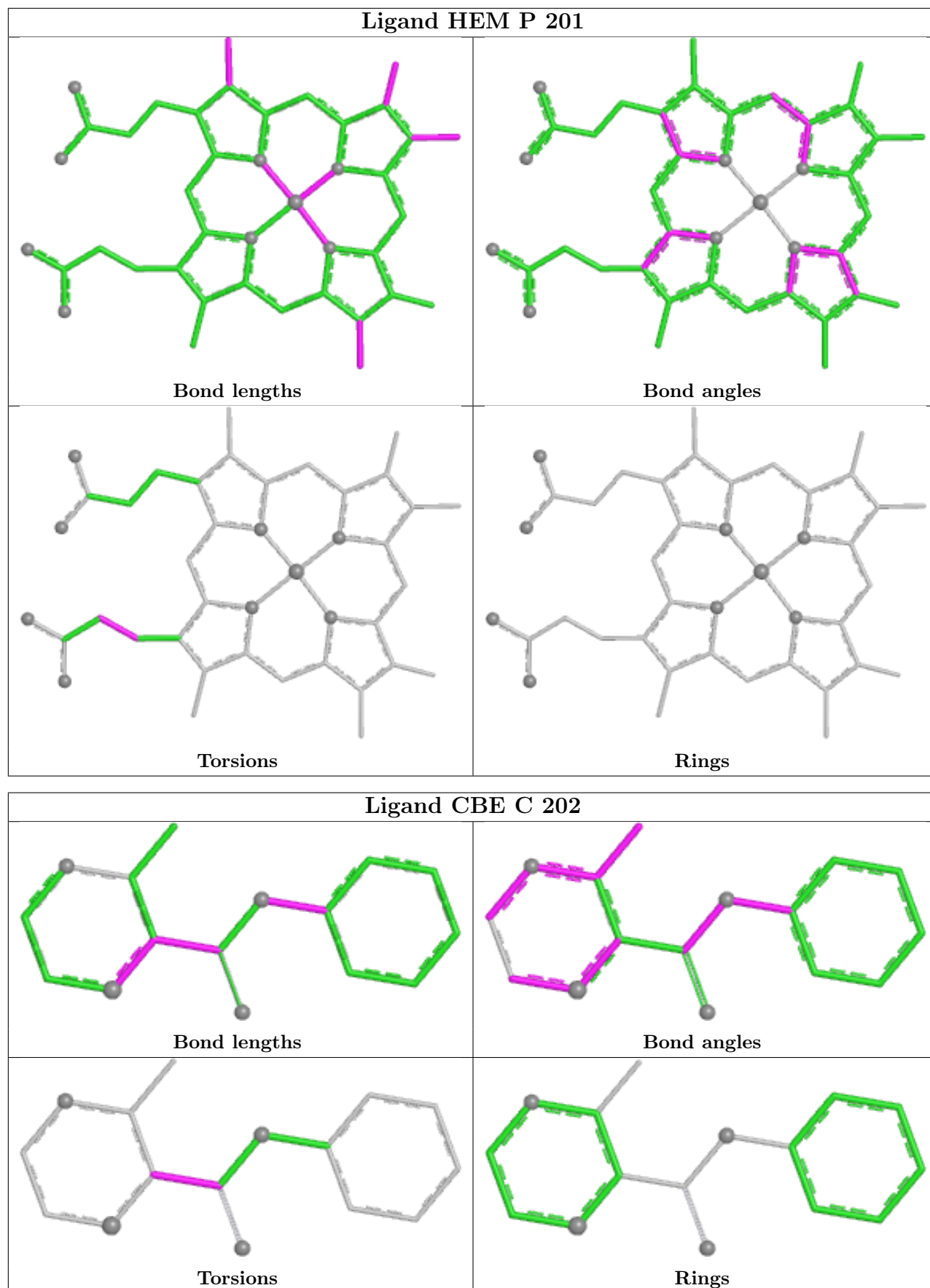


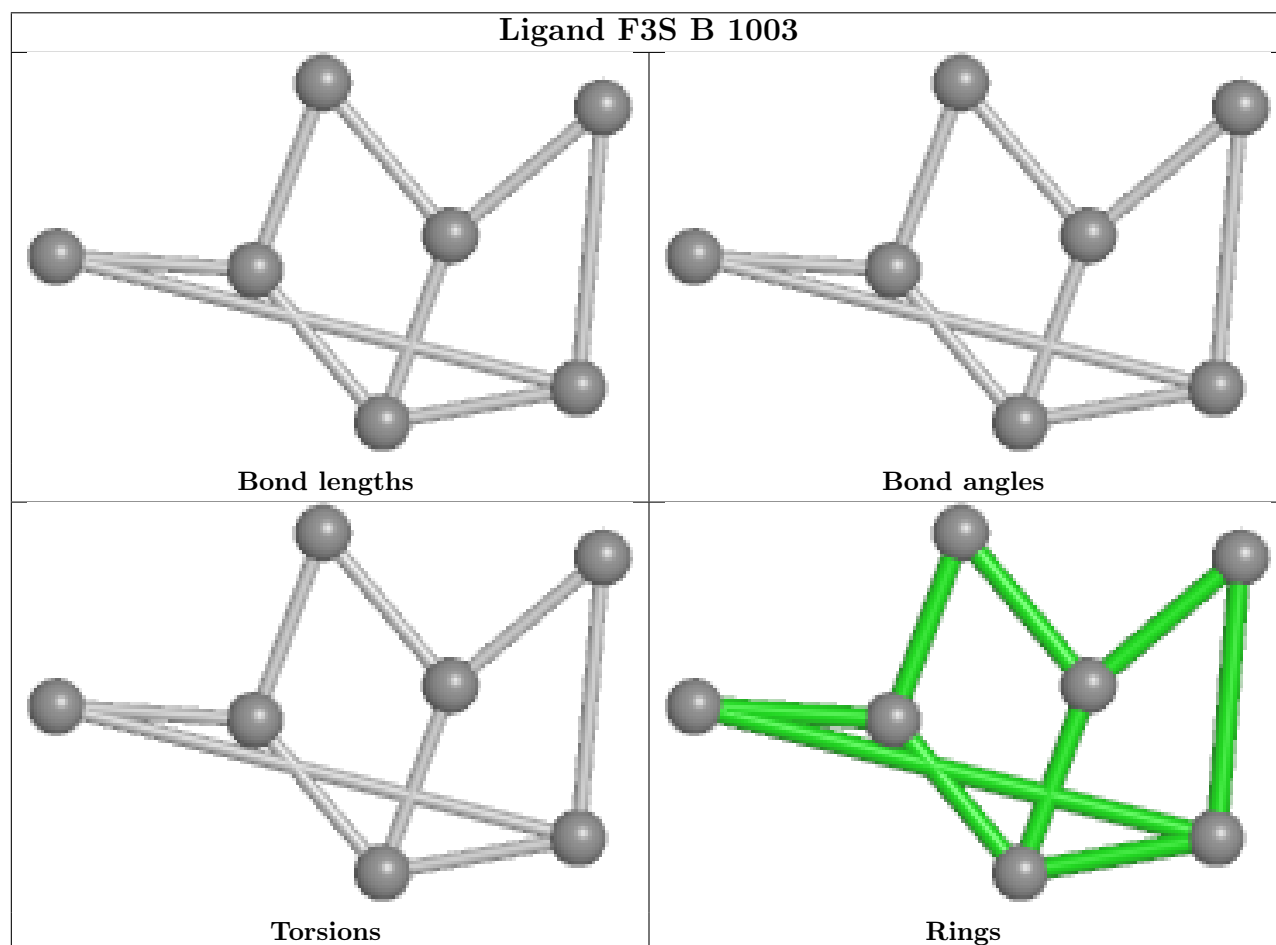
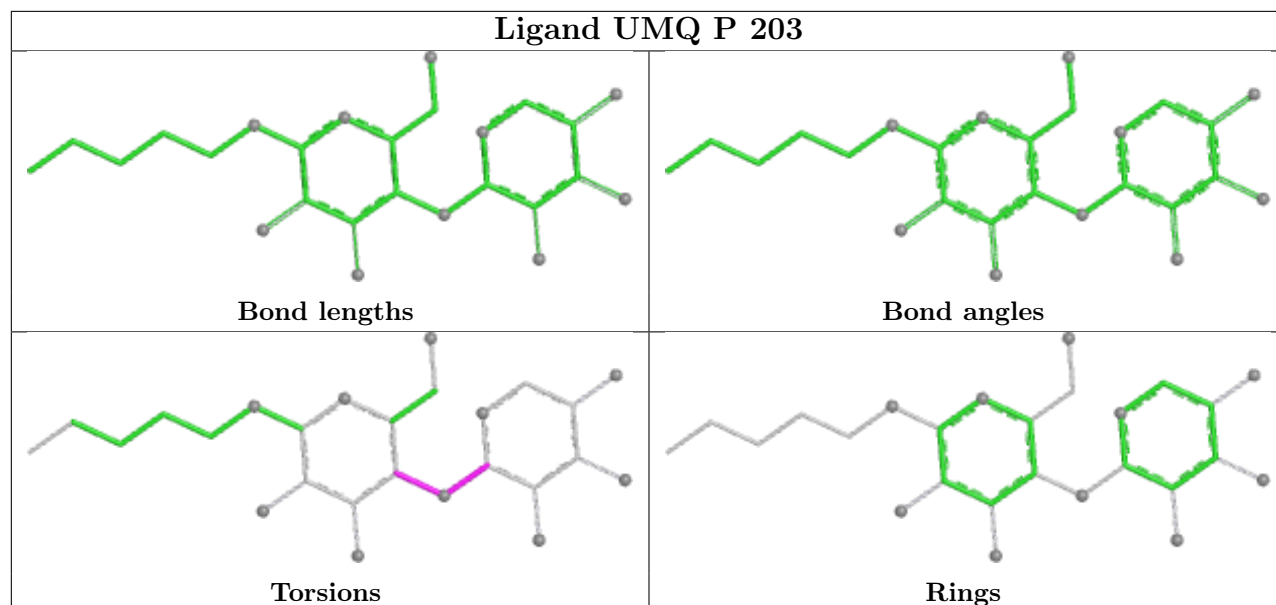


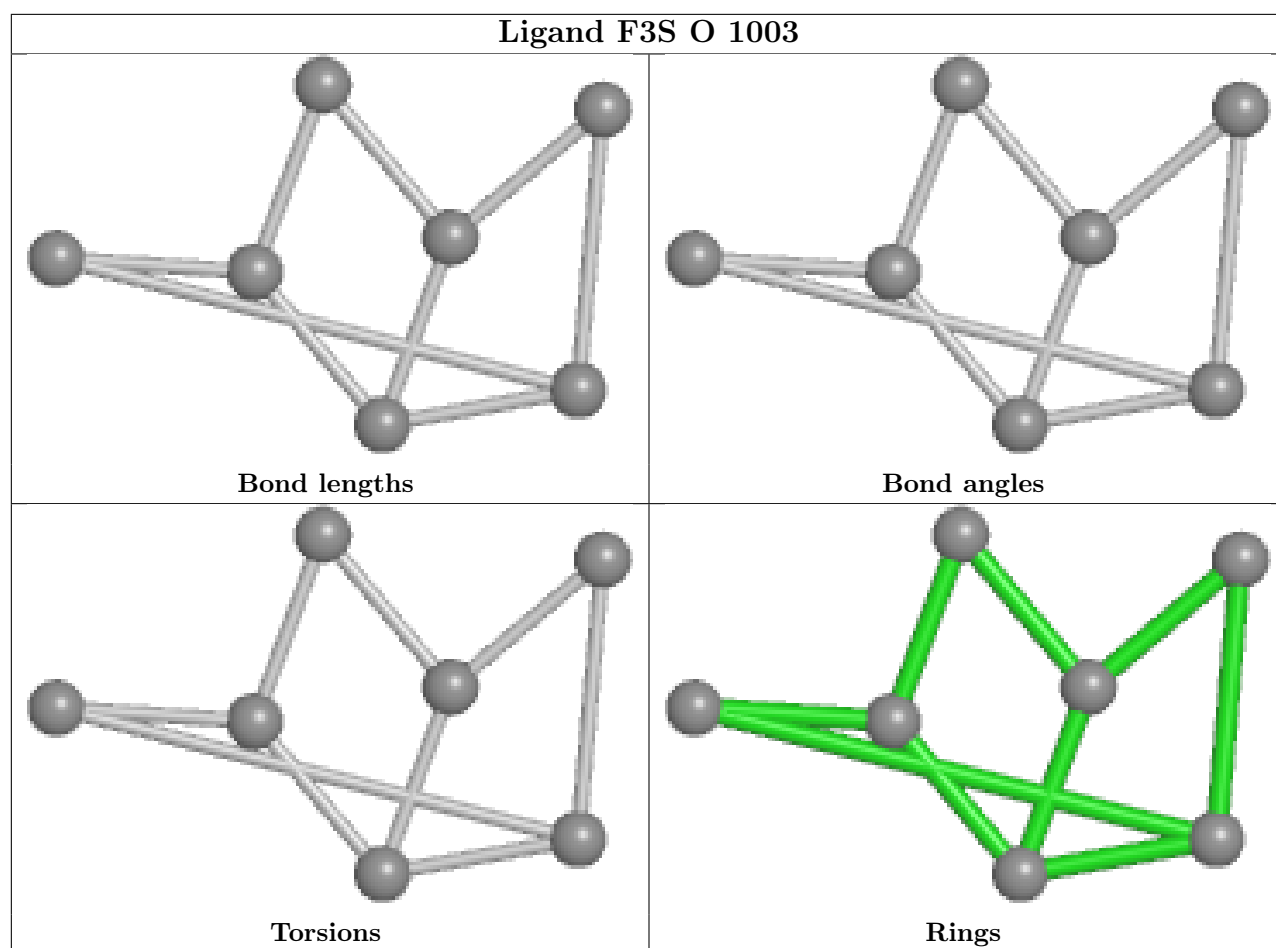












5.7 Other polymers [i](#)

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	612/621 (98%)	-1.41	0 100 100	16, 31, 54, 93	8 (1%)
1	N	612/621 (98%)	-1.44	0 100 100	18, 30, 54, 96	10 (1%)
2	B	240/252 (95%)	-1.41	0 100 100	11, 32, 50, 112	3 (1%)
2	O	241/252 (95%)	-1.45	0 100 100	10, 31, 51, 109	2 (0%)
3	C	139/140 (99%)	-1.03	0 100 100	27, 45, 80, 88	2 (1%)
3	P	139/140 (99%)	-0.93	0 100 100	27, 45, 87, 102	1 (0%)
4	D	101/103 (98%)	-0.93	0 100 100	34, 53, 78, 86	1 (0%)
4	Q	101/103 (98%)	-0.83	0 100 100	36, 55, 78, 93	0
All	All	2185/2232 (97%)	-1.32	0 100 100	10, 33, 66, 112	27 (1%)

There are no RSRZ outliers to report.

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, 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($\text{\AA}^2$)	Q<0.9
9	UNL	D	227	1/-	0.92	0.07	75,75,75,75	0
9	UNL	A	1428	1/-	0.93	0.06	69,69,69,69	0
9	UNL	P	257	1/-	0.93	0.04	66,66,66,66	0
9	UNL	C	251[A]	1/-	0.95	0.08	11,11,11,11	1
9	UNL	C	251[B]	1/-	0.95	0.08	37,37,37,37	1
9	UNL	D	220	13/-	0.95	0.14	50,72,97,97	0
9	UNL	D	224	6/-	0.95	0.07	81,86,87,92	0
9	UNL	D	226[A]	1/-	0.95	0.09	47,47,47,47	1
9	UNL	D	226[B]	1/-	0.95	0.09	15,15,15,15	1
9	UNL	A	1416	1/-	0.95	0.05	66,66,66,66	0
9	UNL	A	1368	4/-	0.95	0.10	33,37,38,40	4
9	UNL	A	1418	1/-	0.96	0.05	65,65,65,65	0
9	UNL	A	1429	1/-	0.96	0.08	66,66,66,66	0
9	UNL	B	1181	3/-	0.96	0.16	54,54,59,61	0
9	UNL	B	1185	1/-	0.96	0.08	59,59,59,59	0
9	UNL	B	1193	1/-	0.96	0.07	53,53,53,53	0
9	UNL	B	1209	1/-	0.96	0.06	52,52,52,52	0
9	UNL	B	1211	1/-	0.96	0.10	61,61,61,61	0
9	UNL	N	1392	2/-	0.96	0.15	55,55,55,61	0
9	UNL	O	1195	3/-	0.96	0.12	48,48,63,78	0
9	UNL	C	244	3/-	0.96	0.12	45,45,59,60	0
9	UNL	C	255[B]	1/-	0.97	0.04	29,29,29,29	1
9	UNL	C	261	1/-	0.97	0.07	55,55,55,55	0
9	UNL	B	1180	3/-	0.97	0.06	57,57,66,79	0
9	UNL	D	221	14/-	0.97	0.10	62,91,106,111	0
9	UNL	A	1367	15/-	0.97	0.08	40,59,71,77	15
9	UNL	B	1213	1/-	0.97	0.06	42,42,42,42	0
9	UNL	A	1431	1/-	0.97	0.05	47,47,47,47	0
9	UNL	C	245	2/-	0.97	0.08	68,68,68,82	0
9	UNL	N	1383	2/-	0.97	0.15	56,56,56,58	0
9	UNL	B	1178	3/-	0.97	0.12	54,54,55,59	0
9	UNL	N	1406	2/-	0.97	0.05	28,28,28,31	2
9	UNL	N	1408	4/-	0.97	0.11	57,59,60,67	0
9	UNL	N	1422[A]	1/-	0.97	0.08	25,25,25,25	1
9	UNL	N	1422[B]	1/-	0.97	0.08	28,28,28,28	1
9	UNL	N	1439	1/-	0.97	0.04	17,17,17,17	1
9	UNL	N	1444	1/-	0.97	0.06	59,59,59,59	0
9	UNL	B	1202	1/-	0.97	0.05	50,50,50,50	0
9	UNL	O	1196	3/-	0.97	0.06	63,63,73,83	0
9	UNL	O	1197	3/-	0.97	0.05	71,71,76,79	0
9	UNL	O	1200	3/-	0.97	0.05	81,81,90,92	0
9	UNL	O	1209[A]	1/-	0.97	0.14	45,45,45,45	1
9	UNL	O	1209[B]	1/-	0.97	0.14	24,24,24,24	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	UNL	O	1226	1/-	0.97	0.04	55,55,55,55	0
9	UNL	P	253	3/-	0.97	0.08	83,83,85,91	0
9	UNL	C	255[A]	1/-	0.97	0.04	28,28,28,28	1
9	UNL	Q	213	7/-	0.97	0.08	71,81,89,93	7
9	UNL	Q	215	3/-	0.97	0.10	38,38,61,64	0
9	UNL	Q	216	9/-	0.97	0.09	59,64,75,76	0
9	UNL	Q	218	12/-	0.97	0.10	58,80,96,103	0
17	BOG	P	204	20/20	0.97	0.09	64,83,102,104	0
9	UNL	C	246	3/-	0.98	0.08	52,52,58,66	0
9	UNL	A	1410	1/-	0.98	0.06	57,57,57,57	0
9	UNL	A	1415	1/-	0.98	0.05	60,60,60,60	0
9	UNL	A	1366	3/-	0.98	0.11	47,47,64,65	0
9	UNL	A	1370	4/-	0.98	0.07	40,45,55,91	0
9	UNL	C	257	1/-	0.98	0.03	58,58,58,58	0
9	UNL	C	258	1/-	0.98	0.03	49,49,49,49	0
9	UNL	C	259	1/-	0.98	0.14	60,60,60,60	0
9	UNL	C	260	1/-	0.98	0.10	55,55,55,55	0
9	UNL	A	1424	1/-	0.98	0.05	58,58,58,58	0
9	UNL	A	1426	1/-	0.98	0.10	55,55,55,55	0
9	UNL	A	1371	2/-	0.98	0.09	35,35,35,43	0
9	UNL	A	1376	3/-	0.98	0.04	61,61,66,73	0
9	UNL	A	1377	4/-	0.98	0.06	75,76,79,81	0
9	UNL	B	1174	3/-	0.98	0.10	62,62,63,74	0
9	UNL	A	1390	1/-	0.98	0.21	37,37,37,37	0
9	UNL	D	228	1/-	0.98	0.05	59,59,59,59	0
9	UNL	A	1397[A]	1/-	0.98	0.07	25,25,25,25	1
9	UNL	N	1387	3/-	0.98	0.10	47,47,56,59	0
9	UNL	N	1388	14/-	0.98	0.07	36,54,70,72	14
9	UNL	N	1390	2/-	0.98	0.05	51,51,51,63	0
9	UNL	N	1391	3/-	0.98	0.04	46,46,59,59	0
9	UNL	A	1397[B]	1/-	0.98	0.07	18,18,18,18	1
9	UNL	N	1398	2/-	0.98	0.15	53,53,53,57	0
9	UNL	N	1405	3/-	0.98	0.11	42,42,57,59	0
9	UNL	A	1398[A]	1/-	0.98	0.07	31,31,31,31	1
9	UNL	B	1188	1/-	0.98	0.04	48,48,48,48	0
9	UNL	N	1412[A]	1/-	0.98	0.07	21,21,21,21	1
9	UNL	N	1412[B]	1/-	0.98	0.07	35,35,35,35	1
9	UNL	N	1414[A]	1/-	0.98	0.05	14,14,14,14	1
9	UNL	N	1414[B]	1/-	0.98	0.05	0,0,0,0	1
9	UNL	N	1415[A]	1/-	0.98	0.03	16,16,16,16	1
9	UNL	N	1415[B]	1/-	0.98	0.03	22,22,22,22	1
9	UNL	N	1417[A]	1/-	0.98	0.08	22,22,22,22	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	UNL	N	1417[B]	1/-	0.98	0.08	21,21,21,21	1
9	UNL	N	1419[A]	1/-	0.98	0.07	0,0,0,0	1
9	UNL	N	1419[B]	1/-	0.98	0.07	41,41,41,41	1
9	UNL	N	1421[A]	1/-	0.98	0.10	33,33,33,33	1
9	UNL	N	1421[B]	1/-	0.98	0.10	24,24,24,24	1
9	UNL	B	1190	1/-	0.98	0.04	53,53,53,53	0
9	UNL	B	1191	1/-	0.98	0.08	51,51,51,51	0
9	UNL	N	1427	1/-	0.98	0.12	45,45,45,45	0
9	UNL	N	1433	1/-	0.98	0.04	60,60,60,60	0
9	UNL	A	1398[B]	1/-	0.98	0.07	21,21,21,21	1
9	UNL	N	1443	1/-	0.98	0.06	51,51,51,51	0
9	UNL	B	1200	1/-	0.98	0.03	56,56,56,56	0
9	UNL	N	1446	1/-	0.98	0.09	59,59,59,59	0
9	UNL	O	1192	3/-	0.98	0.07	36,36,49,59	0
9	UNL	B	1201[A]	1/-	0.98	0.10	17,17,17,17	1
9	UNL	B	1201[B]	1/-	0.98	0.10	42,42,42,42	1
9	UNL	A	1401[A]	1/-	0.98	0.08	29,29,29,29	1
9	UNL	O	1199	5/-	0.98	0.09	37,46,55,64	0
9	UNL	B	1204	1/-	0.98	0.05	20,20,20,20	1
9	UNL	O	1202	5/-	0.98	0.08	53,65,68,69	0
9	UNL	B	1205	1/-	0.98	0.07	44,44,44,44	0
9	UNL	B	1206	1/-	0.98	0.06	63,63,63,63	0
9	UNL	O	1212[A]	1/-	0.98	0.06	41,41,41,41	1
9	UNL	O	1212[B]	1/-	0.98	0.06	33,33,33,33	1
9	UNL	O	1216[A]	1/-	0.98	0.08	44,44,44,44	1
9	UNL	O	1216[B]	1/-	0.98	0.08	35,35,35,35	1
9	UNL	O	1218	1/-	0.98	0.08	56,56,56,56	0
9	UNL	O	1220	1/-	0.98	0.06	56,56,56,56	0
9	UNL	O	1222	1/-	0.98	0.06	73,73,73,73	0
9	UNL	O	1223	1/-	0.98	0.14	54,54,54,54	0
9	UNL	O	1224	1/-	0.98	0.06	60,60,60,60	0
9	UNL	B	1208	1/-	0.98	0.06	51,51,51,51	0
9	UNL	O	1227	1/-	0.98	0.04	67,67,67,67	0
9	UNL	A	1401[B]	1/-	0.98	0.08	4,4,4,4	1
9	UNL	P	254	1/-	0.98	0.05	56,56,56,56	0
9	UNL	B	1210	1/-	0.98	0.16	48,48,48,48	0
9	UNL	A	1402[A]	1/-	0.98	0.04	14,14,14,14	1
9	UNL	Q	214[A]	17/-	0.98	0.07	20,42,49,49	17
9	UNL	Q	214[B]	16/-	0.98	0.07	37,46,55,58	16
9	UNL	A	1402[B]	1/-	0.98	0.04	12,12,12,12	1
9	UNL	C	243	9/-	0.98	0.09	54,66,84,84	0
9	UNL	A	1408	1/-	0.98	0.06	58,58,58,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	UNL	Q	221	1/-	0.98	0.03	51,51,51,51	0
17	BOG	C	203	18/20	0.98	0.06	56,77,95,104	0
9	UNL	A	1409	1/-	0.98	0.10	44,44,44,44	0
18	UMQ	P	203	26/34	0.98	0.07	42,58,107,113	0
9	UNL	C	250[B]	1/-	0.99	0.03	24,24,24,24	1
9	UNL	A	1378	2/-	0.99	0.07	64,64,64,67	0
9	UNL	A	1379	3/-	0.99	0.06	21,21,42,58	3
9	UNL	C	252[A]	1/-	0.99	0.08	32,32,32,32	1
9	UNL	C	252[B]	1/-	0.99	0.08	34,34,34,34	1
9	UNL	C	253	1/-	0.99	0.03	28,28,28,28	1
9	UNL	C	254	1/-	0.99	0.04	33,33,33,33	0
9	UNL	A	1380	7/-	0.99	0.07	20,52,57,66	7
9	UNL	A	1411	1/-	0.99	0.04	52,52,52,52	0
9	UNL	C	256	1/-	0.99	0.07	47,47,47,47	0
9	UNL	A	1413	1/-	0.99	0.03	49,49,49,49	0
9	UNL	A	1414	1/-	0.99	0.04	47,47,47,47	0
9	UNL	A	1381	3/-	0.99	0.07	31,31,55,67	0
9	UNL	A	1382	3/-	0.99	0.05	26,26,31,50	3
9	UNL	A	1417	1/-	0.99	0.05	60,60,60,60	0
9	UNL	A	1383	5/-	0.99	0.05	65,66,72,73	0
9	UNL	A	1419	1/-	0.99	0.04	60,60,60,60	0
9	UNL	D	222	9/-	0.99	0.04	52,61,65,66	0
9	UNL	D	223	4/-	0.99	0.06	60,60,67,74	0
9	UNL	A	1420	1/-	0.99	0.05	50,50,50,50	0
9	UNL	D	225	1/-	0.99	0.14	48,48,48,48	0
9	UNL	A	1421	1/-	0.99	0.05	49,49,49,49	0
9	UNL	A	1422	1/-	0.99	0.05	54,54,54,54	0
9	UNL	A	1423	1/-	0.99	0.07	64,64,64,64	0
9	UNL	A	1384	2/-	0.99	0.04	55,55,55,63	0
9	UNL	D	229	1/-	0.99	0.02	55,55,55,55	0
9	UNL	A	1425	1/-	0.99	0.03	53,53,53,53	0
9	UNL	N	1384	2/-	0.99	0.06	67,67,67,71	0
9	UNL	N	1385	4/-	0.99	0.04	72,75,76,82	0
9	UNL	N	1386	2/-	0.99	0.05	23,23,23,43	2
9	UNL	A	1385[A]	1/-	0.99	0.09	45,45,45,45	1
9	UNL	A	1427	1/-	0.99	0.09	59,59,59,59	0
9	UNL	N	1389	2/-	0.99	0.05	63,63,63,73	0
9	UNL	A	1385[B]	1/-	0.99	0.09	21,21,21,21	1
9	UNL	A	1387	1/-	0.99	0.06	47,47,47,47	0
9	UNL	A	1430	1/-	0.99	0.04	51,51,51,51	0
9	UNL	N	1393	3/-	0.99	0.04	64,64,69,73	0
9	UNL	N	1394	2/-	0.99	0.07	58,58,58,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	UNL	N	1395	6/-	0.99	0.04	51,57,61,70	6
9	UNL	N	1396	3/-	0.99	0.07	27,27,41,50	0
9	UNL	N	1397	3/-	0.99	0.03	50,50,56,74	0
9	UNL	A	1388	1/-	0.99	0.04	35,35,35,35	0
9	UNL	N	1400	2/-	0.99	0.04	66,66,66,75	0
9	UNL	N	1401	3/-	0.99	0.06	49,49,57,73	0
9	UNL	N	1402	3/-	0.99	0.03	24,24,31,41	3
9	UNL	N	1403	3/-	0.99	0.04	15,15,21,33	3
9	UNL	N	1404	7/-	0.99	0.05	37,62,71,71	0
9	UNL	B	1171	7/-	0.99	0.06	54,72,78,79	0
9	UNL	B	1172	4/-	0.99	0.04	68,71,74,77	0
9	UNL	N	1407	3/-	0.99	0.06	38,38,45,53	3
9	UNL	B	1173	3/-	0.99	0.03	42,42,47,64	0
9	UNL	N	1409	4/-	0.99	0.05	70,70,73,77	0
9	UNL	N	1410	4/-	0.99	0.04	17,25,27,37	4
9	UNL	N	1411	2/-	0.99	0.08	55,55,55,57	0
9	UNL	A	1389	1/-	0.99	0.24	45,45,45,45	0
9	UNL	B	1175	3/-	0.99	0.06	53,53,65,66	0
9	UNL	N	1413[A]	1/-	0.99	0.03	16,16,16,16	1
9	UNL	N	1413[B]	1/-	0.99	0.03	23,23,23,23	1
9	UNL	B	1176	4/-	0.99	0.04	68,70,76,76	4
9	UNL	B	1177	3/-	0.99	0.06	55,55,64,65	0
9	UNL	A	1369	4/-	0.99	0.05	41,45,46,53	0
9	UNL	B	1179	4/-	0.99	0.06	63,70,73,73	0
9	UNL	A	1391	1/-	0.99	0.03	60,60,60,60	0
9	UNL	A	1392	1/-	0.99	0.04	62,62,62,62	0
9	UNL	N	1418[A]	1/-	0.99	0.03	28,28,28,28	1
9	UNL	N	1418[B]	1/-	0.99	0.03	33,33,33,33	1
9	UNL	B	1182[A]	1/-	0.99	0.03	21,21,21,21	1
9	UNL	B	1182[B]	1/-	0.99	0.03	4,4,4,4	1
9	UNL	N	1420[A]	1/-	0.99	0.07	26,26,26,26	1
9	UNL	N	1420[B]	1/-	0.99	0.07	8,8,8,8	1
9	UNL	B	1183[A]	1/-	0.99	0.04	24,24,24,24	1
9	UNL	B	1183[B]	1/-	0.99	0.04	6,6,6,6	1
9	UNL	B	1184[A]	1/-	0.99	0.08	22,22,22,22	1
9	UNL	B	1184[B]	1/-	0.99	0.08	36,36,36,36	1
9	UNL	N	1423	1/-	0.99	0.08	42,42,42,42	0
9	UNL	N	1424	1/-	0.99	0.07	47,47,47,47	0
9	UNL	N	1426	1/-	0.99	0.03	55,55,55,55	0
9	UNL	A	1394	1/-	0.99	0.05	62,62,62,62	0
9	UNL	N	1428	1/-	0.99	0.11	47,47,47,47	0
9	UNL	N	1429	1/-	0.99	0.04	54,54,54,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	UNL	N	1430	1/-	0.99	0.04	41,41,41,41	0
9	UNL	N	1431	1/-	0.99	0.04	45,45,45,45	0
9	UNL	N	1432	1/-	0.99	0.10	51,51,51,51	0
9	UNL	B	1186[A]	1/-	0.99	0.06	12,12,12,12	1
9	UNL	N	1434	1/-	0.99	0.13	58,58,58,58	0
9	UNL	N	1435	1/-	0.99	0.10	56,56,56,56	0
9	UNL	N	1437	1/-	0.99	0.05	52,52,52,52	0
9	UNL	N	1438	1/-	0.99	0.05	58,58,58,58	0
9	UNL	B	1186[B]	1/-	0.99	0.06	4,4,4,4	1
9	UNL	N	1440	1/-	0.99	0.06	57,57,57,57	0
9	UNL	N	1441	1/-	0.99	0.05	52,52,52,52	0
9	UNL	N	1442	1/-	0.99	0.03	51,51,51,51	0
9	UNL	B	1187	1/-	0.99	0.04	49,49,49,49	0
9	UNL	A	1395	1/-	0.99	0.04	44,44,44,44	0
9	UNL	N	1445	1/-	0.99	0.05	50,50,50,50	0
9	UNL	B	1189	1/-	0.99	0.05	47,47,47,47	0
9	UNL	A	1396[A]	1/-	0.99	0.08	20,20,20,20	1
9	UNL	O	1193	7/-	0.99	0.07	57,62,66,72	7
9	UNL	O	1194	6/-	0.99	0.04	35,43,53,56	0
9	UNL	A	1396[B]	1/-	0.99	0.08	36,36,36,36	1
9	UNL	B	1192	1/-	0.99	0.05	53,53,53,53	0
8	AZI	N	1004	3/3	0.99	0.07	40,40,48,59	0
9	UNL	O	1198	4/-	0.99	0.03	52,60,61,70	0
9	UNL	B	1194	1/-	0.99	0.06	52,52,52,52	0
9	UNL	B	1195	1/-	0.99	0.02	45,45,45,45	0
9	UNL	O	1201	3/-	0.99	0.04	54,54,67,71	0
9	UNL	B	1196	1/-	0.99	0.08	46,46,46,46	0
9	UNL	O	1203	4/-	0.99	0.04	46,47,49,53	4
9	UNL	O	1204	3/-	0.99	0.06	54,54,55,66	0
9	UNL	O	1205	1/-	0.99	0.06	49,49,49,49	0
9	UNL	O	1206[A]	1/-	0.99	0.11	33,33,33,33	1
9	UNL	O	1206[B]	1/-	0.99	0.11	17,17,17,17	1
9	UNL	O	1208[A]	1/-	0.99	0.03	19,19,19,19	1
9	UNL	O	1208[B]	1/-	0.99	0.03	20,20,20,20	1
9	UNL	B	1198	1/-	0.99	0.07	50,50,50,50	0
9	UNL	B	1199	1/-	0.99	0.06	45,45,45,45	0
9	UNL	O	1210	1/-	0.99	0.10	50,50,50,50	0
9	UNL	O	1211[A]	1/-	0.99	0.05	33,33,33,33	1
9	UNL	O	1211[B]	1/-	0.99	0.05	8,8,8,8	1
6	Y3P	A	1002	9/9	0.99	0.03	22,31,41,50	0
9	UNL	A	1372	2/-	0.99	0.05	34,34,34,53	0
9	UNL	O	1213[A]	1/-	0.99	0.04	22,22,22,22	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
9	UNL	O	1213[B]	1/-	0.99	0.04	21,21,21,21	1
9	UNL	O	1214[A]	1/-	0.99	0.06	27,27,27,27	1
9	UNL	O	1214[B]	1/-	0.99	0.06	29,29,29,29	1
9	UNL	O	1215	1/-	0.99	0.04	47,47,47,47	0
9	UNL	A	1373	3/-	0.99	0.06	39,39,57,70	0
9	UNL	A	1399[A]	1/-	0.99	0.08	24,24,24,24	1
9	UNL	O	1217	1/-	0.99	0.15	42,42,42,42	0
9	UNL	B	1203	1/-	0.99	0.07	44,44,44,44	0
9	UNL	A	1399[B]	1/-	0.99	0.08	29,29,29,29	1
9	UNL	O	1221	1/-	0.99	0.08	36,36,36,36	0
9	UNL	A	1400[A]	1/-	0.99	0.03	26,26,26,26	1
9	UNL	A	1400[B]	1/-	0.99	0.03	24,24,24,24	1
9	UNL	A	1374	2/-	0.99	0.04	54,54,54,63	2
9	UNL	O	1225	1/-	0.99	0.08	42,42,42,42	0
9	UNL	A	1375	3/-	0.99	0.05	74,74,76,85	0
8	AZI	A	1004	3/3	0.99	0.03	41,41,47,59	0
9	UNL	P	249	9/-	0.99	0.07	58,72,86,93	0
9	UNL	P	250	6/-	0.99	0.04	69,74,80,82	0
9	UNL	P	251	2/-	0.99	0.13	59,59,59,70	0
9	UNL	P	252	19/-	0.99	0.07	42,61,85,88	19
8	AZI	B	1005	3/3	0.99	0.08	54,54,65,71	0
9	UNL	B	1212	1/-	0.99	0.05	51,51,51,51	0
9	UNL	P	255	1/-	0.99	0.07	54,54,54,54	0
9	UNL	P	256	1/-	0.99	0.11	57,57,57,57	0
9	UNL	A	1403	1/-	0.99	0.05	50,50,50,50	0
9	UNL	A	1404	1/-	0.99	0.03	57,57,57,57	0
9	UNL	A	1405	1/-	0.99	0.05	44,44,44,44	0
9	UNL	A	1406	1/-	0.99	0.05	47,47,47,47	0
9	UNL	A	1407	1/-	0.99	0.04	35,35,35,35	0
9	UNL	C	247	1/-	0.99	0.04	48,48,48,48	0
9	UNL	Q	217	3/-	0.99	0.05	52,52,64,64	0
9	UNL	C	248[A]	1/-	0.99	0.04	28,28,28,28	1
9	UNL	Q	219	5/-	0.99	0.05	47,50,74,79	0
9	UNL	Q	220	1/-	0.99	0.10	60,60,60,60	0
9	UNL	C	248[B]	1/-	0.99	0.04	31,31,31,31	1
14	GOL	N	1005	6/6	0.99	0.05	35,36,38,49	6
9	UNL	C	249[A]	1/-	0.99	0.05	27,27,27,27	1
17	BOG	D	201	17/20	0.99	0.05	61,67,79,82	0
9	UNL	C	249[B]	1/-	0.99	0.05	19,19,19,19	1
9	UNL	C	250[A]	1/-	0.99	0.03	23,23,23,23	1
9	UNL	O	1207[A]	1/-	1.00	0.03	13,13,13,13	1
9	UNL	O	1207[B]	1/-	1.00	0.03	30,30,30,30	1

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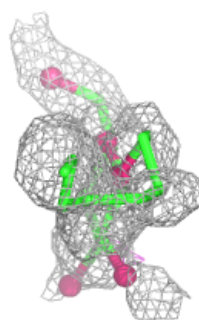
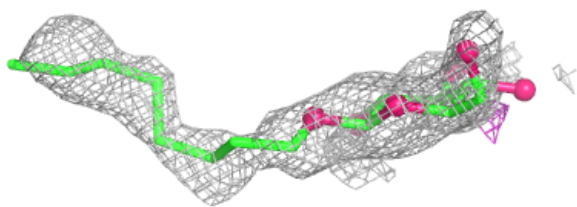
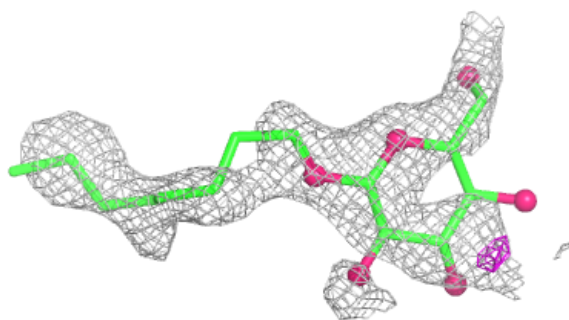
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	Y3P	N	1002	9/9	1.00	0.02	24,29,41,41	0
9	UNL	O	1219	1/-	1.00	0.02	26,26,26,26	1
9	UNL	A	1412	1/-	1.00	0.03	39,39,39,39	0
7	K	A	1003	1/1	1.00	0.01	33,33,33,33	0
9	UNL	N	1436	1/-	1.00	0.02	24,24,24,24	0
9	UNL	N	1416[A]	1/-	1.00	0.05	24,24,24,24	1
9	UNL	N	1416[B]	1/-	1.00	0.05	34,34,34,34	1
9	UNL	B	1197	1/-	1.00	0.02	46,46,46,46	0
9	UNL	N	1425	1/-	1.00	0.05	30,30,30,30	0
9	UNL	N	1399	1/-	1.00	0.02	40,40,40,40	0
9	UNL	A	1386	1/-	1.00	0.02	42,42,42,42	0
10	FES	B	1001	4/4	1.00	0.02	24,24,24,27	0
10	FES	O	1001	4/4	1.00	0.01	23,25,26,28	0
11	SF4	B	1002	8/8	1.00	0.01	24,26,28,30	0
11	SF4	O	1002	8/8	1.00	0.01	22,27,31,31	0
12	F3S	B	1003	7/7	1.00	0.02	27,28,30,34	0
12	F3S	O	1003	7/7	1.00	0.02	25,28,32,32	0
13	NA	B	1004	1/1	1.00	0.02	25,25,25,25	0
14	GOL	B	1006	6/6	1.00	0.03	32,40,43,45	0
9	UNL	B	1207	1/-	1.00	0.06	41,41,41,41	0
15	HEM	C	201	41/43	1.00	0.03	20,40,55,69	0
15	HEM	P	201	41/43	1.00	0.04	28,41,57,63	0
16	CBE	C	202	16/16	1.00	0.02	29,36,43,47	0
16	CBE	P	202	16/16	1.00	0.02	27,35,47,48	0
9	UNL	A	1393	1/-	1.00	0.06	55,55,55,55	0
7	K	N	1003	1/1	1.00	0.01	28,28,28,28	0
5	FAD	N	1001	53/53	1.00	0.02	10,21,29,34	0
5	FAD	A	1001	53/53	1.00	0.02	9,22,32,37	0

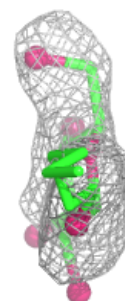
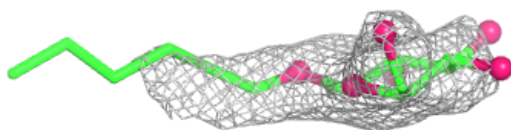
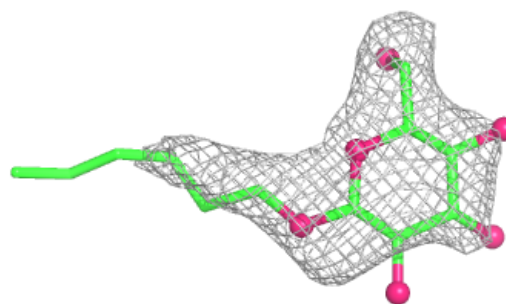
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around BOG P 204:

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

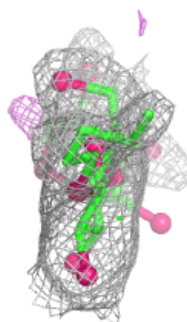
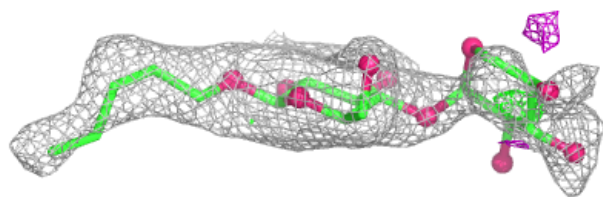
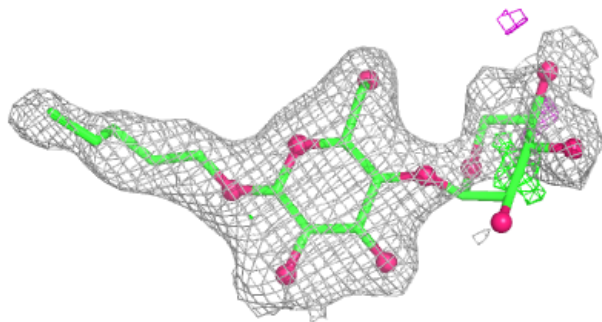
**Electron density around BOG C 203:**

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

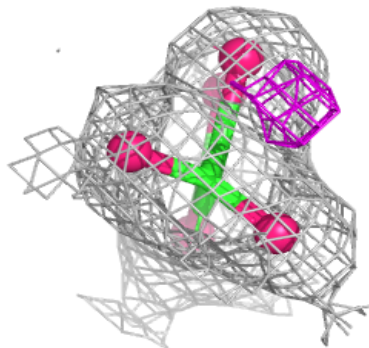
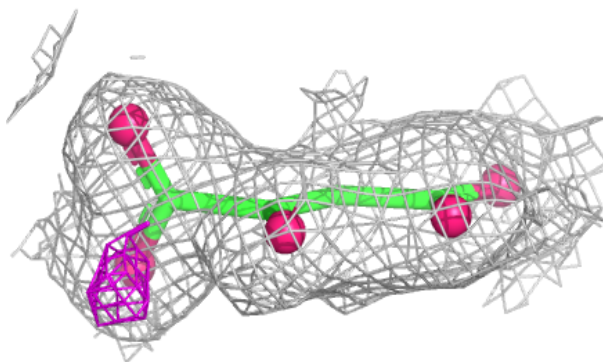
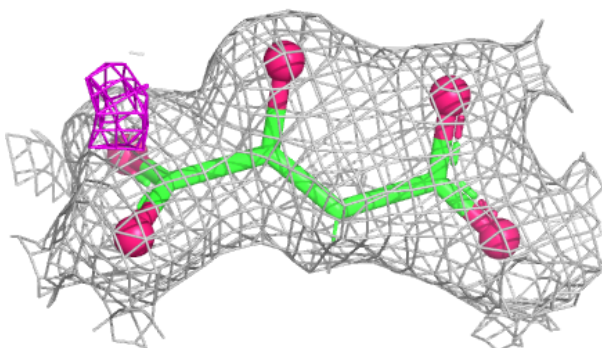


Electron density around UMQ P 203:

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

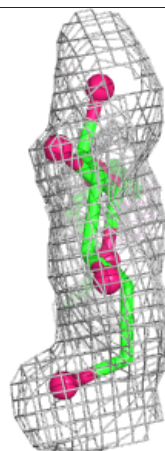
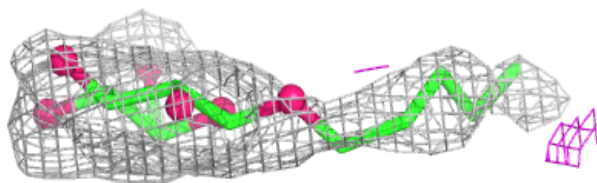
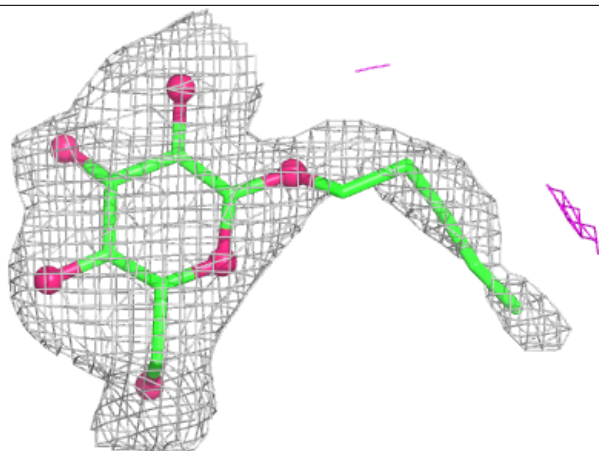
**Electron density around Y3P A 1002:**

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

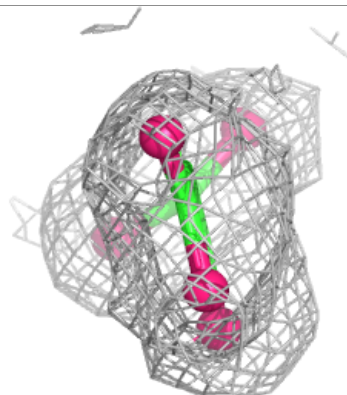
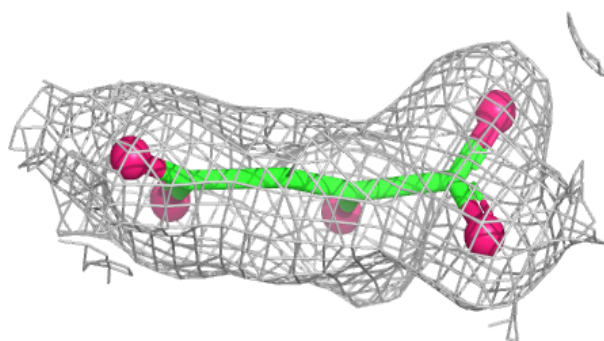
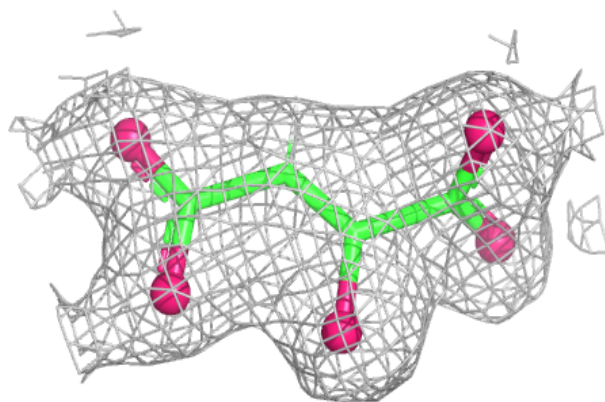


Electron density around BOG D 201:

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

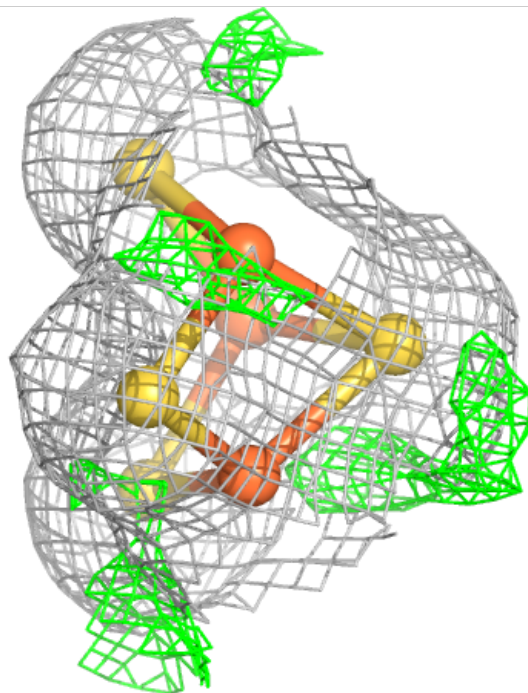
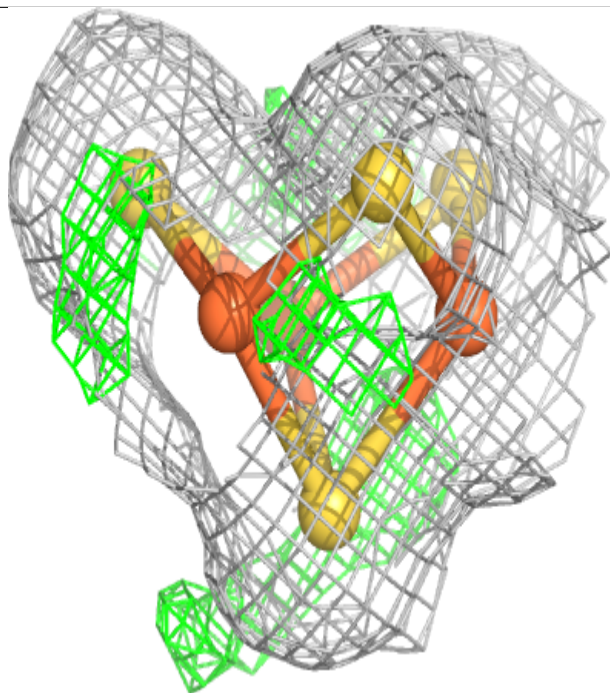
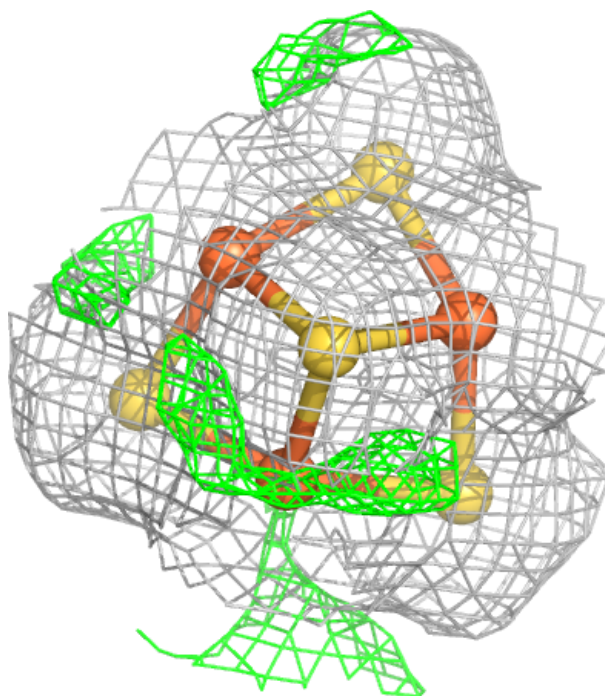
**Electron density around Y3P N 1002:**

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



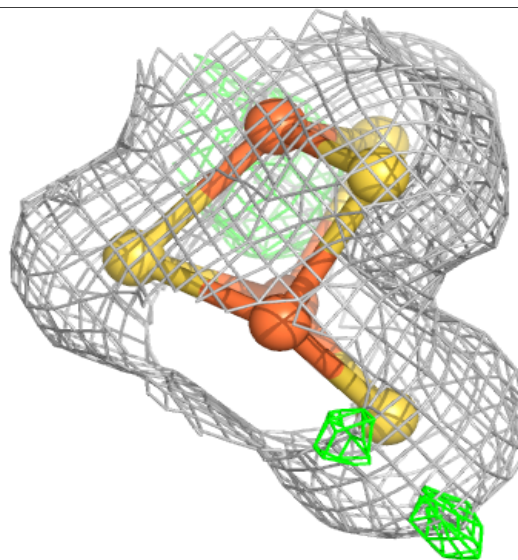
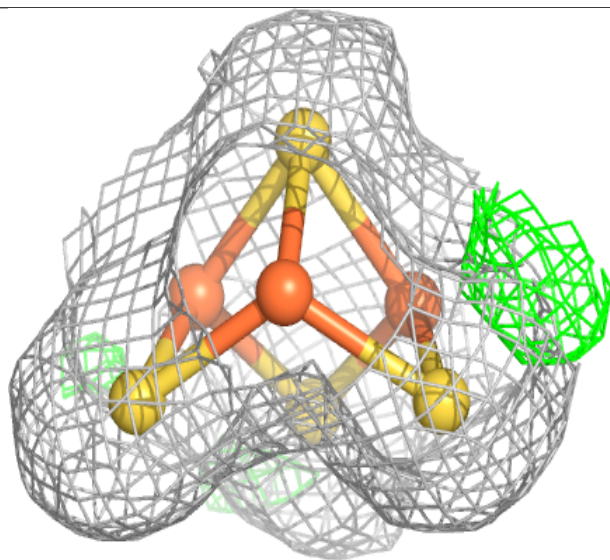
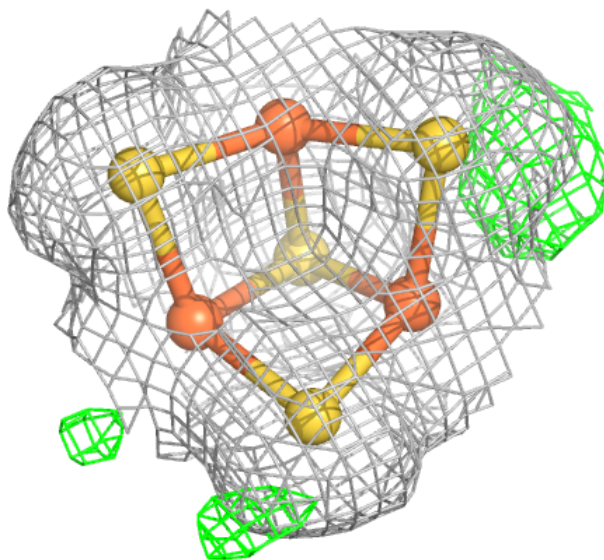
Electron density around F3S B 1003:

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



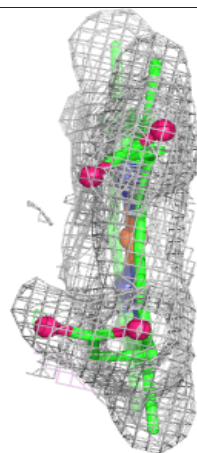
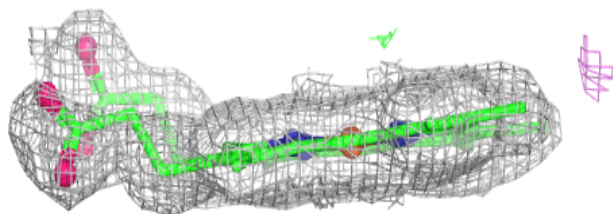
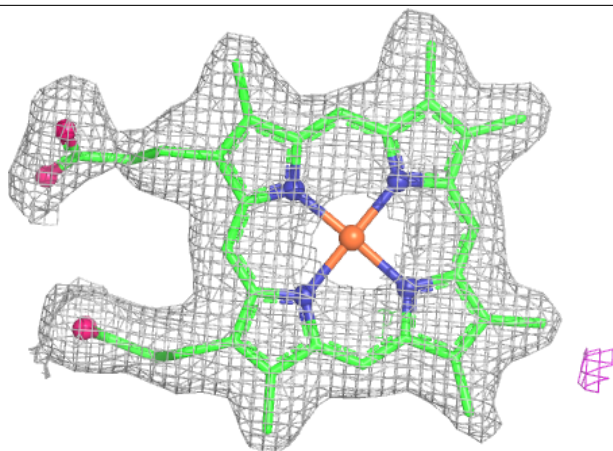
Electron density around F3S O 1003:

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



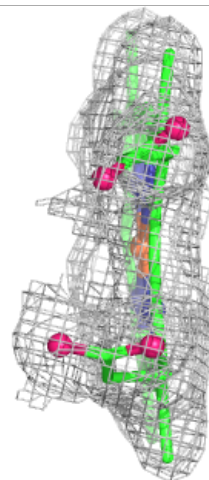
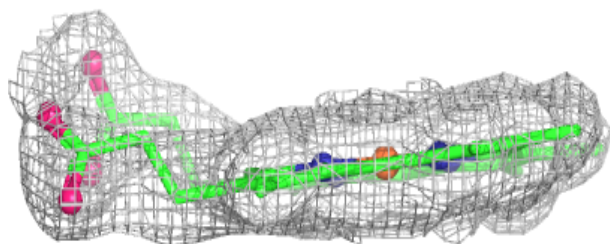
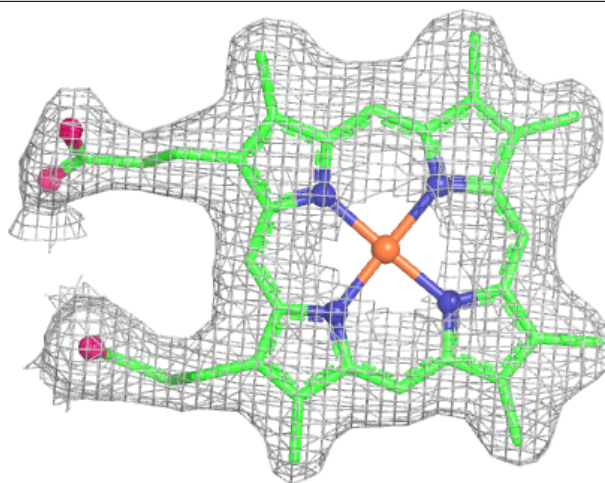
Electron density around HEM C 201:

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



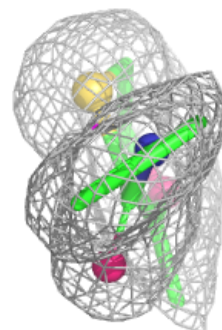
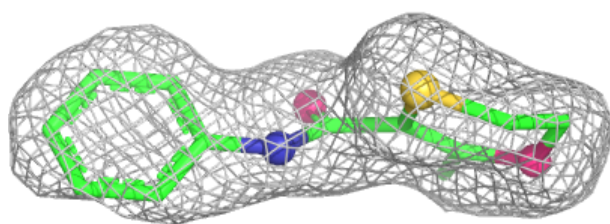
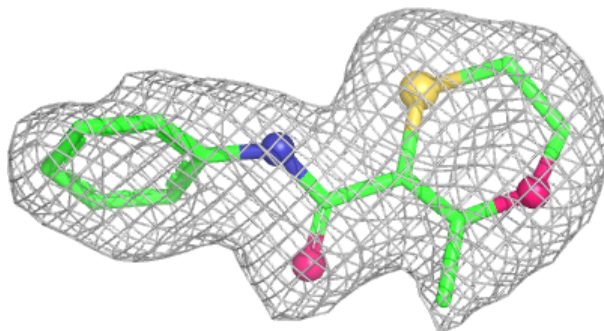
Electron density around HEM P 201:

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

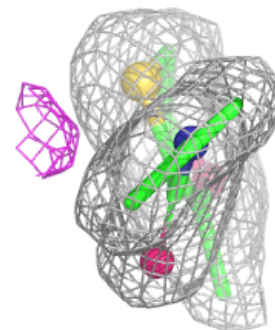
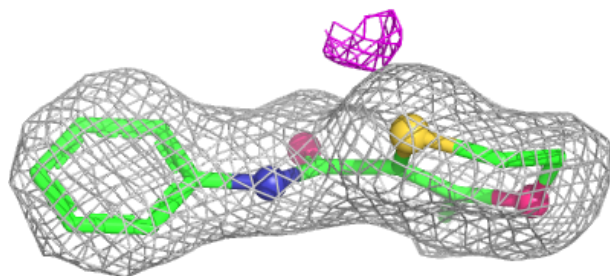
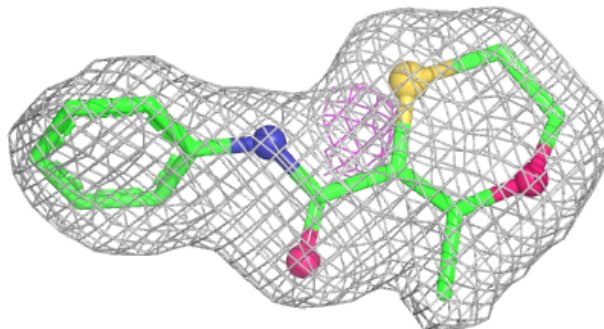


Electron density around CBE C 202:

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

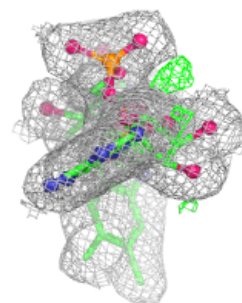
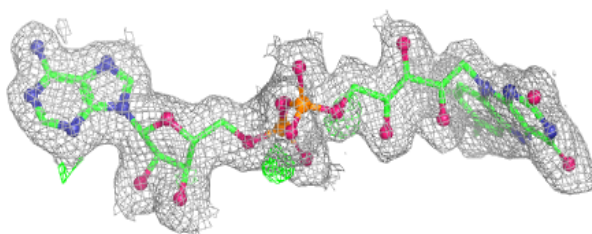
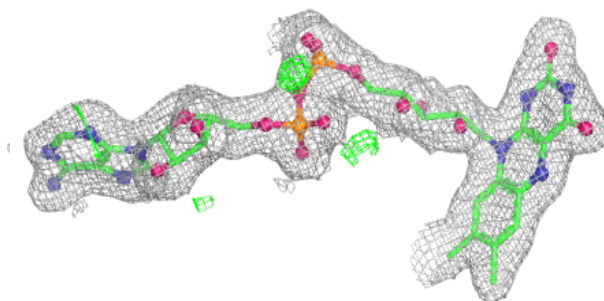
**Electron density around CBE P 202:**

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

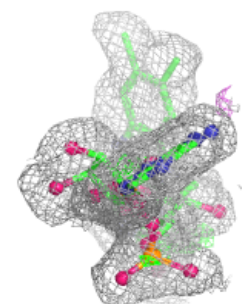
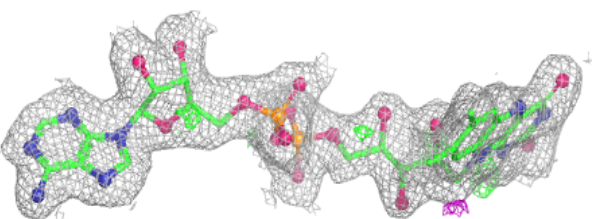
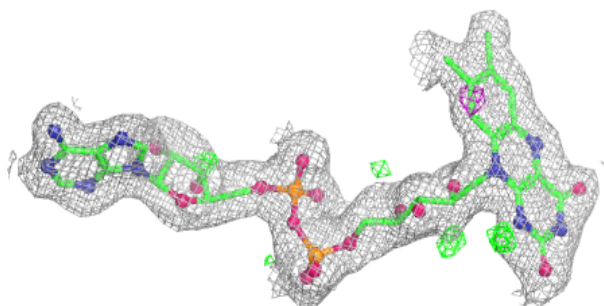


Electron density around FAD N 1001:

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

**Electron density around FAD A 1001:**

$2mF_o-DF_c$ (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.