



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:13 PM UTC

PDB ID : 4N7K / pdb_00004n7k
Title : Zinc Substituted Reaction Center of the Rhodobacter sphaeroides
Authors : Hardjasa, A.; Murphy, M.E.P.
Deposited on : 2013-10-15
Resolution : 2.85 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 : 9.0.010 (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

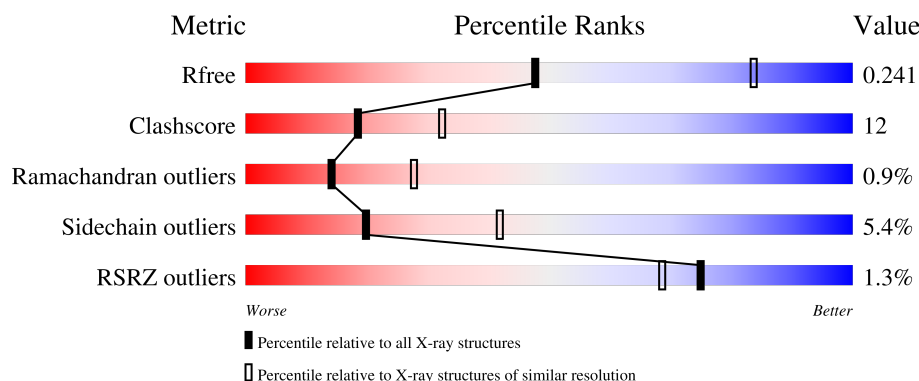
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	H	241	2% 81% 16% .
2	L	281	% 77% 21% .
3	M	303	2% 74% 25% .

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
7	LDA	L	303	-	-	-	X

2 Entry composition [i](#)

There are 15 unique types of molecules in this entry. The entry contains 7634 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 Reaction Center H Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	241	Total	C	N	O	S	0	5	1
			1849	1183	320	337	9			

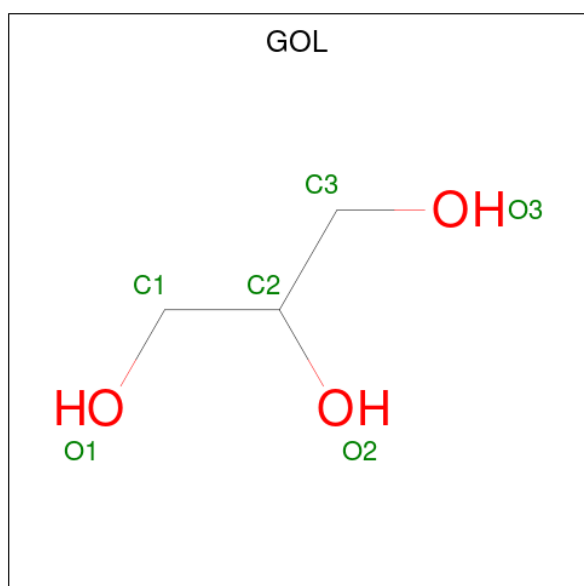
- Molecule 2 is a protein called Reaction center protein L chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	281	Total	C	N	O	S	0	2	0
			2239	1513	355	363	8			

- Molecule 3 is a protein called Reaction center protein M chain.

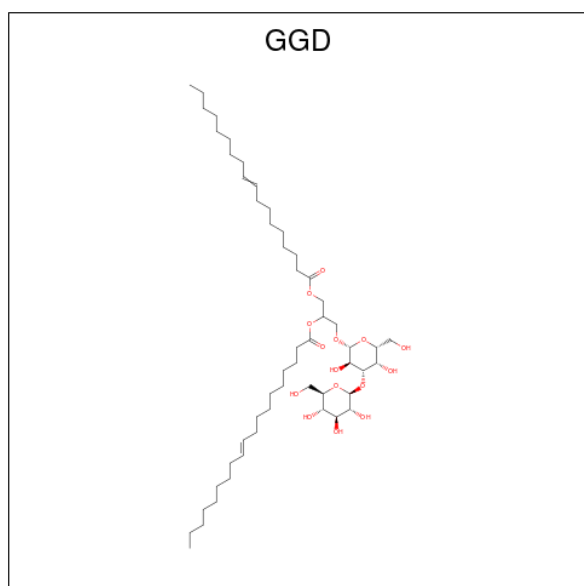
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	303	Total	C	N	O	S	0	1	1
			2411	1607	396	398	10			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



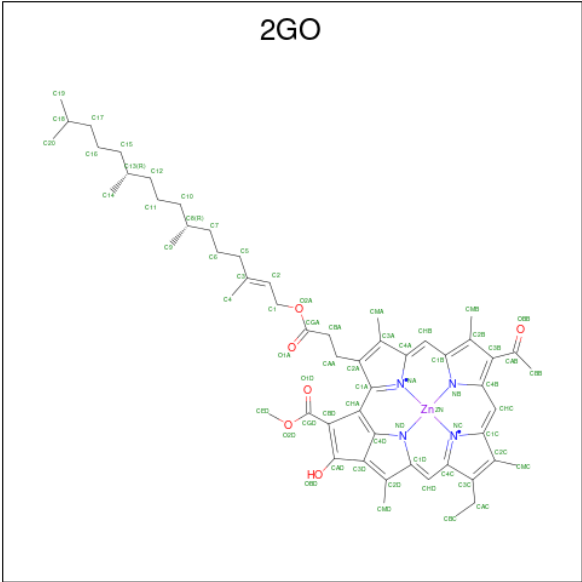
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is NONADEC-10-ENOIC ACID 2-[3,4-DIHYDROXY-6-HYDROXYMETHYL-5-(3,4,5-TRIHYDROXY-6-HYDROXYMETHYL-TETRAHYDRO-PYRAN-2-YLOXY)-TETRAHYDRO-PYRAN-2-YLOXY] -1-OCTADEC-9-ENOYLOXYMETHYL-ETHYL ESTER (CCD ID: GGD) (formula: C₅₂H₉₄O₁₅).



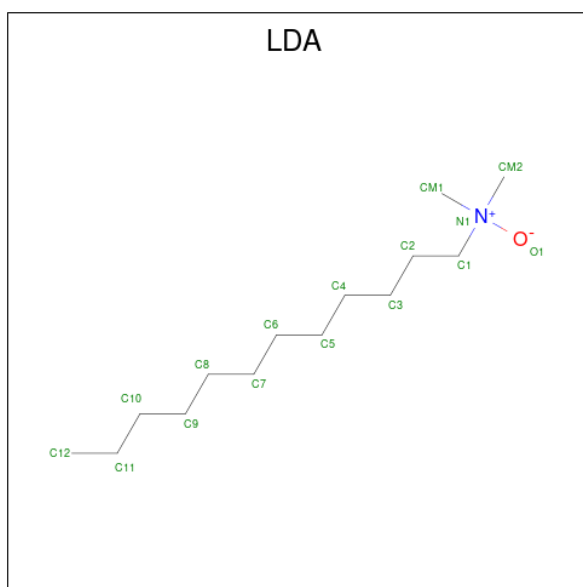
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	C	O	0	0
			57	42	15		

- Molecule 6 is [methyl 9-acetyl-14-ethyl-20-hydroxy-4,8,13,18-tetramethyl-3-{3-oxo-3-[(3,7,11,15-tetramethylhexadec-2-en-1-yl)oxy]propyl}-3,4,20,21-tetradecahydrophorbine-21-carboxylato(2-)-kappa 4 N 23 ,N 24 ,N 25 ,N 26]zinc (CCD ID: 2GO) (formula: C₅₅H₇₀N₄O₆Zn).



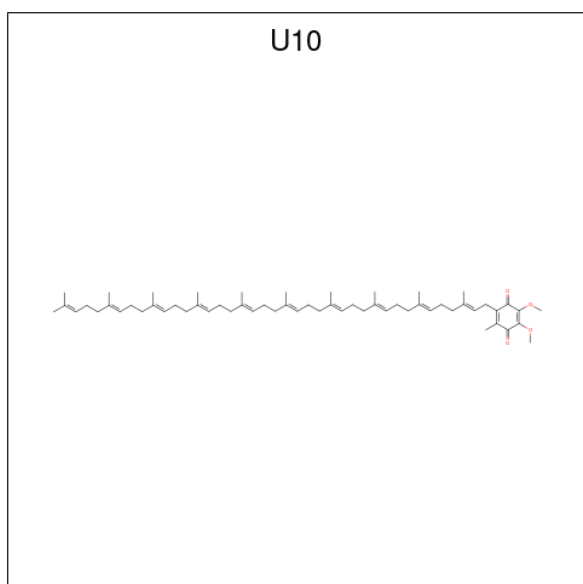
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	L	1	Total	C	N	O	Zn	0	0
			66	55	4	6	1		
6	L	1	Total	C	N	O	Zn	0	0
			66	55	4	6	1		
6	L	1	Total	C	N	O	Zn	0	0
			66	55	4	6	1		
6	M	1	Total	C	N	O	Zn	0	0
			66	55	4	6	1		
6	M	1	Total	C	N	O	Zn	0	0
			66	55	4	6	1		
6	M	1	Total	C	N	O	Zn	0	0
			66	55	4	6	1		

- Molecule 7 is LAURYL DIMETHYLAMINE-N-OXIDE (CCD ID: LDA) (formula: C₁₄H₃₁NO).



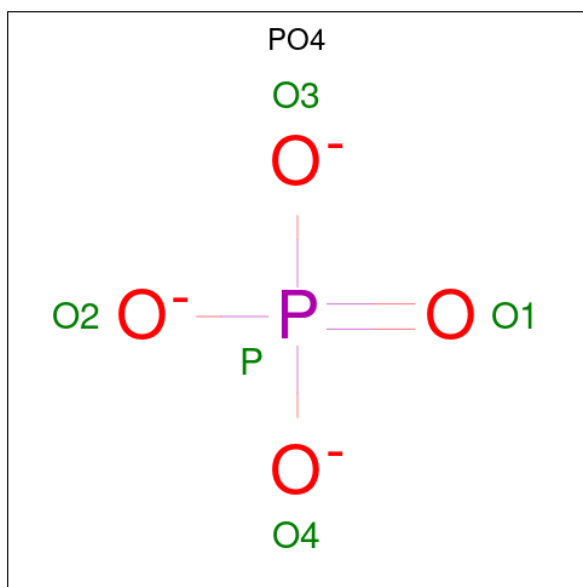
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	L	1	Total	C	N	O	0	0
			16	14	1	1		
7	L	1	Total	C	N	O	0	0
			16	14	1	1		
7	L	1	Total	C	N	O	0	0
			16	14	1	1		
7	M	1	Total	C	N	O	0	0
			16	14	1	1		
7	M	1	Total	C	N	O	0	0
			16	14	1	1		

- Molecule 8 is UBIQUINONE-10 (CCD ID: U10) (formula: $C_{59}H_{90}O_4$).



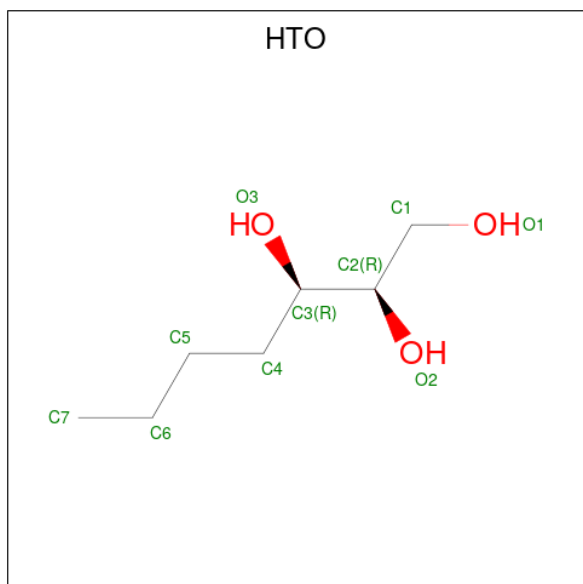
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	L	1	Total	C	O	0	1
			46	38	8		
8	M	1	Total	C	O	0	0
			48	44	4		

- Molecule 9 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	L	1	Total	O	P	0	0
			5	4	1		

- Molecule 10 is HEPTANE-1,2,3-TRIOL (CCD ID: HTO) (formula: $C_7H_{16}O_3$).

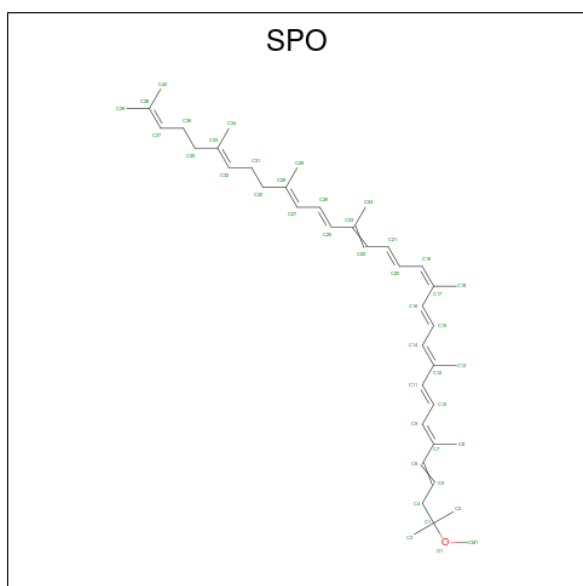


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	L	1	Total	C	O	0	0
			10	7	3		
10	L	1	Total	C	O	0	0
			10	7	3		

- Molecule 11 is FE (III) ION (CCD ID: FE) (formula: Fe).

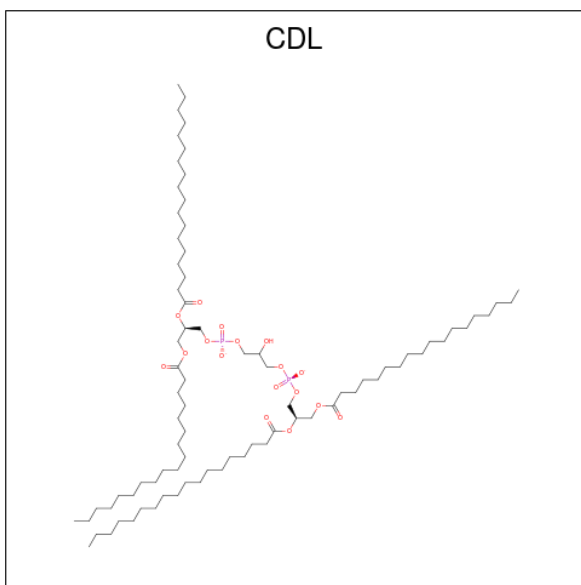
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	M	1	Total	Fe	0	0
			1	1		

- Molecule 12 is SPHEROIDENE (CCD ID: SPO) (formula: C₄₁H₆₀O).



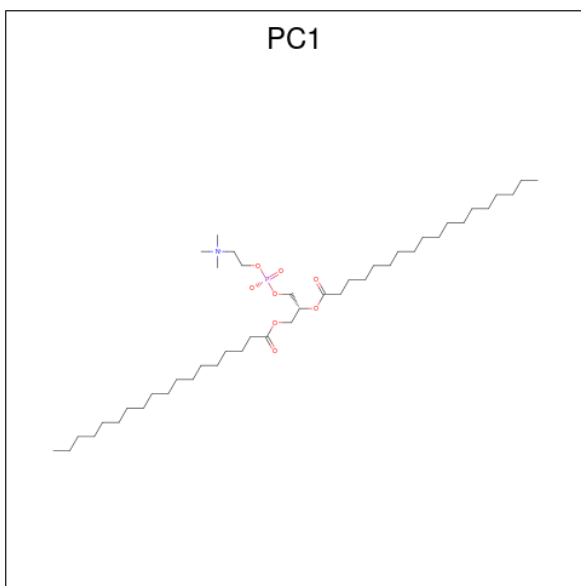
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	1	Total	C	O	0	0
			42	41	1		

- Molecule 13 is CARDIOLIPIN (CCD ID: CDL) (formula: C₈₁H₁₅₆O₁₇P₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	M	1	Total	C	O	P	0	0
			81	62	17	2		

- Molecule 14 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
14	M	1	Total	C	N	O	P	0	0
			43	33	1	8	1		

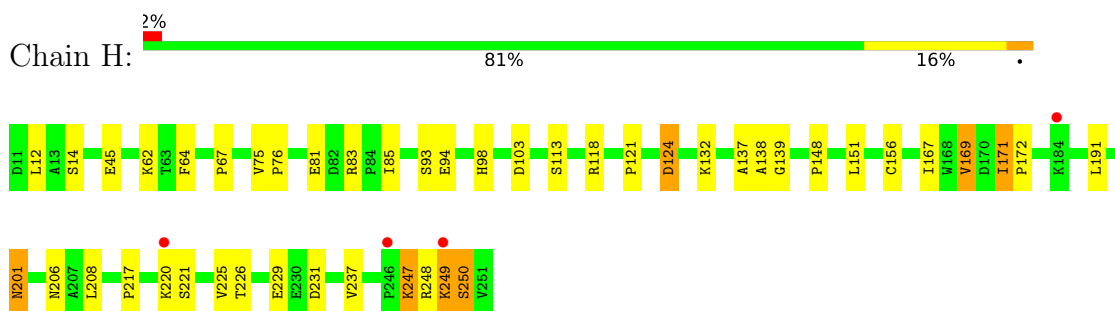
- Molecule 15 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	H	109	Total 109	O 109	0	0
15	L	81	Total 81	O 81	0	0
15	M	84	Total 84	O 84	0	0

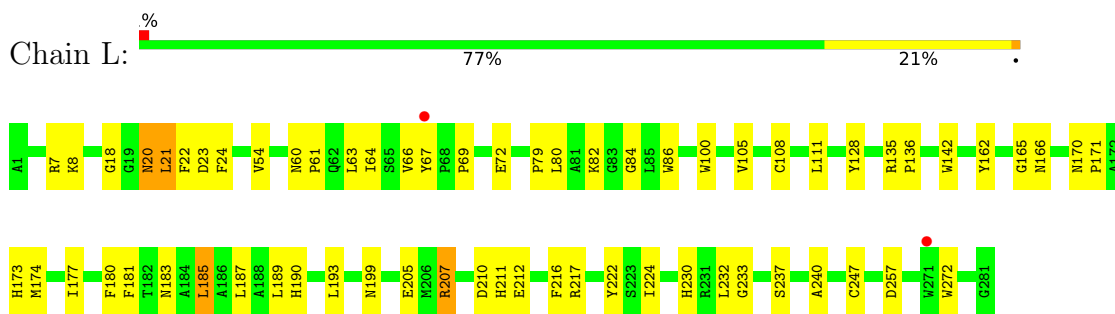
3 Residue-property plots

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.

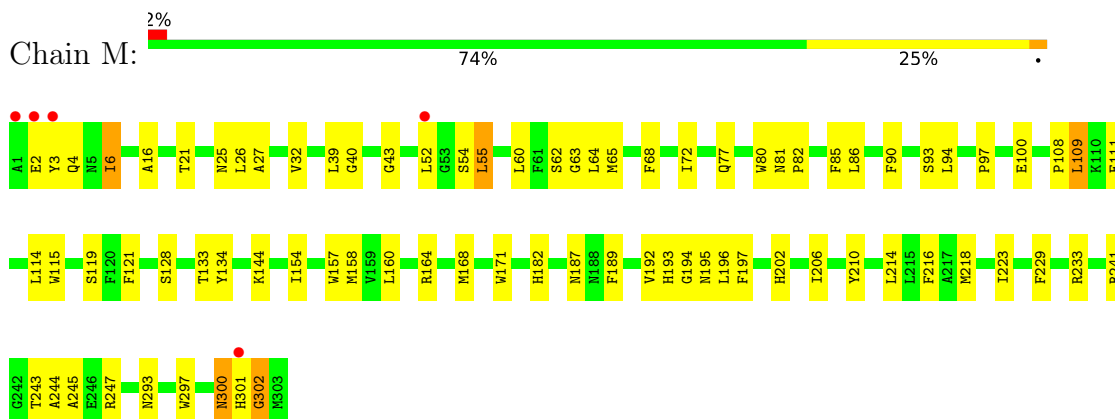
- Molecule 1: Reaction Center H Chain



- Molecule 2: Reaction center protein L chain



- Molecule 3: Reaction center protein M chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	139.45Å 139.45Å 184.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.91 – 2.85 36.91 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.0 (36.91-2.85) 96.0 (36.91-2.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 2.85Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.182 , 0.243 0.182 , 0.241	Depositor DCC
R_{free} test set	2368 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	61.9	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 53.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.012 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7634	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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: CDL, PC1, LDA, GOL, GGD, HTO, SPO, U10, PO4, FE, 2GO

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	H	0.76	0/1929	1.04	0/2619
2	L	0.69	0/2339	0.96	1/3203 (0.0%)
3	M	0.72	0/2508	1.02	3/3424 (0.1%)
All	All	0.72	0/6776	1.01	4/9246 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	81	ASN	CA-C-N	9.68	129.31	119.24
3	M	81	ASN	C-N-CA	9.68	129.31	119.24
3	M	160	LEU	N-CA-C	5.95	117.44	111.07
2	L	210	ASP	N-CA-C	-5.71	105.14	111.36

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	H	1849	0	1872	35	0
2	L	2239	0	2185	63	0
3	M	2411	0	2319	63	0
4	H	24	0	32	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	18	0	24	3	0
5	H	57	0	68	2	0
6	L	198	0	207	15	0
6	M	198	0	207	27	0
7	L	48	0	93	0	0
7	M	32	0	62	1	0
8	L	46	0	46	13	0
8	M	48	0	63	3	0
9	L	5	0	0	1	0
10	L	20	0	32	0	0
11	M	1	0	0	0	0
12	M	42	0	60	5	0
13	M	81	0	106	2	0
14	M	43	0	60	0	0
15	H	109	0	0	6	0
15	L	81	0	0	3	0
15	M	84	0	0	5	0
All	All	7634	0	7436	178	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 12.

The worst 5 of 178 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)
3:M:197:PHE:HZ	6:M:402:2GO:H21	1.33	0.93
1:H:118[B]:ARG:HD2	15:M:566:HOH:O	1.72	0.89
3:M:197:PHE:CZ	6:M:402:2GO:H21	2.08	0.88
2:L:69:PRO:HG2	2:L:142:TRP:HB2	1.58	0.86
6:M:402:2GO:CBB	6:M:402:2GO:H19	2.05	0.86

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	H	245/241 (102%)	230 (94%)	11 (4%)	4 (2%)	7	17
2	L	281/281 (100%)	262 (93%)	17 (6%)	2 (1%)	18	35
3	M	302/303 (100%)	277 (92%)	23 (8%)	2 (1%)	18	35
All	All	828/825 (100%)	769 (93%)	51 (6%)	8 (1%)	14	25

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	250	SER
3	M	301	HIS
1	H	249[A]	LYS
1	H	249[B]	LYS
3	M	302	GLY

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	H	199/196 (102%)	184 (92%)	15 (8%)	12	26
2	L	221/220 (100%)	214 (97%)	7 (3%)	34	59
3	M	237/237 (100%)	222 (94%)	15 (6%)	16	34
All	All	657/653 (101%)	620 (94%)	37 (6%)	20	40

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	M	72	ILE
3	M	214	LEU
3	M	94	LEU
3	M	133	THR
1	H	221	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	4	GLN
3	M	77	GLN
3	M	300	ASN
3	M	187	ASN
2	L	20	ASN

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 29 ligands modelled in this entry, 1 is monoatomic - leaving 28 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	$\# Z > 2$
6	2GO	M	401	3	73,74,74	2.25	23 (31%)	91,115,115	3.43	34 (37%)
4	GOL	H	303	-	5,5,5	0.53	0	5,5,5	0.45	0
8	U10	M	407	-	48,48,63	1.51	4 (8%)	60,61,79	1.52	12 (20%)
7	LDA	L	302	-	13,15,15	2.00	1 (7%)	14,17,17	0.61	0
14	PC1	M	410	-	42,42,53	1.17	2 (4%)	48,50,61	2.48	11 (22%)
4	GOL	H	301	-	5,5,5	0.43	0	5,5,5	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	U10	L	306[A]	-	23,23,63	2.12	2 (8%)	30,31,79	1.41	5 (16%)
7	LDA	L	303	-	13,15,15	1.95	1 (7%)	14,17,17	0.45	0
10	HTO	L	309	-	9,9,9	0.79	0	10,10,10	0.82	0
13	CDL	M	409	-	80,80,99	3.97	5 (6%)	86,92,111	1.27	8 (9%)
6	2GO	M	406	-	73,74,74	2.24	24 (32%)	91,115,115	3.49	39 (42%)
7	LDA	M	404	-	13,15,15	2.07	2 (15%)	14,17,17	0.60	0
5	GGD	H	305	-	58,58,68	1.04	3 (5%)	72,72,82	1.53	12 (16%)
9	PO4	L	308	-	4,4,4	1.03	0	6,6,6	0.40	0
6	2GO	L	307	2	73,74,74	2.22	23 (31%)	91,115,115	3.53	38 (41%)
4	GOL	H	304	-	5,5,5	0.45	0	5,5,5	0.60	0
7	LDA	M	403	-	13,15,15	2.04	1 (7%)	14,17,17	0.71	0
4	GOL	H	302	-	5,5,5	0.80	0	5,5,5	1.11	0
6	2GO	L	305	-	73,74,74	2.34	24 (32%)	91,115,115	3.40	43 (47%)
10	HTO	L	310	-	9,9,9	0.74	0	10,10,10	0.60	0
4	GOL	L	312	-	5,5,5	0.34	0	5,5,5	0.45	0
6	2GO	L	301	2	73,74,74	2.28	23 (31%)	91,115,115	3.47	46 (50%)
8	U10	L	306[B]	-	23,23,63	1.99	2 (8%)	30,31,79	1.36	5 (16%)
12	SPO	M	408	-	41,41,41	0.79	0	47,50,50	1.55	12 (25%)
6	2GO	M	402	3	73,74,74	2.18	25 (34%)	91,115,115	3.70	39 (42%)
7	LDA	L	304	-	13,15,15	2.00	1 (7%)	14,17,17	0.63	0
4	GOL	L	311	-	5,5,5	0.44	0	5,5,5	0.42	0
4	GOL	L	313	-	5,5,5	0.36	0	5,5,5	0.58	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
6	2GO	M	401	3	-	14/41/97/97	-
4	GOL	H	303	-	-	3/4/4/4	-
8	U10	M	407	-	-	9/45/69/87	0/1/1/1
7	LDA	L	302	-	-	6/13/13/13	-
14	PC1	M	410	-	-	23/46/46/57	-
4	GOL	H	301	-	-	3/4/4/4	-
8	U10	L	306[A]	-	-	3/15/39/87	0/1/1/1
7	LDA	L	303	-	-	5/13/13/13	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	HTO	L	309	-	-	6/10/10/10	-
13	CDL	M	409	-	-	50/91/91/110	-
6	2GO	M	406	-	-	20/41/97/97	-
7	LDA	M	404	-	-	6/13/13/13	-
5	GGD	H	305	-	-	12/47/87/97	0/2/2/2
6	2GO	L	307	2	-	7/41/97/97	-
4	GOL	H	304	-	-	2/4/4/4	-
7	LDA	M	403	-	-	4/13/13/13	-
4	GOL	H	302	-	-	2/4/4/4	-
6	2GO	L	305	-	-	18/41/97/97	-
10	HTO	L	310	-	-	3/10/10/10	-
4	GOL	L	312	-	-	4/4/4/4	-
6	2GO	L	301	2	-	13/41/97/97	-
8	U10	L	306[B]	-	-	5/15/39/87	0/1/1/1
12	SPO	M	408	-	-	10/47/47/47	-
6	2GO	M	402	3	-	12/41/97/97	-
7	LDA	L	304	-	-	7/13/13/13	-
4	GOL	L	311	-	-	2/4/4/4	-
4	GOL	L	313	-	-	2/4/4/4	-

The worst 5 of 166 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	M	409	CDL	C35-C34	33.75	3.19	1.51
8	L	306[A]	U10	C6-C1	8.69	1.50	1.35
8	L	306[B]	U10	C6-C1	8.29	1.50	1.35
8	M	407	U10	C6-C1	7.28	1.48	1.35
7	M	403	LDA	O1-N1	-6.98	1.25	1.42

The worst 5 of 304 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	307	2GO	CAC-C3C-C4C	-12.38	108.68	124.79
6	M	402	2GO	CAA-C2A-C3A	-11.98	105.43	127.87
6	M	402	2GO	CAC-C3C-C4C	-11.71	109.56	124.79
6	M	406	2GO	CAC-C3C-C2C	-11.07	107.22	127.56
6	M	406	2GO	CAC-C3C-C4C	-10.33	111.35	124.79

There are no chirality outliers.

5 of 251 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	H	301	GOL	O1-C1-C2-O2
4	H	301	GOL	O1-C1-C2-C3
4	H	302	GOL	C1-C2-C3-O3
4	H	303	GOL	C1-C2-C3-O3
4	H	304	GOL	O1-C1-C2-C3

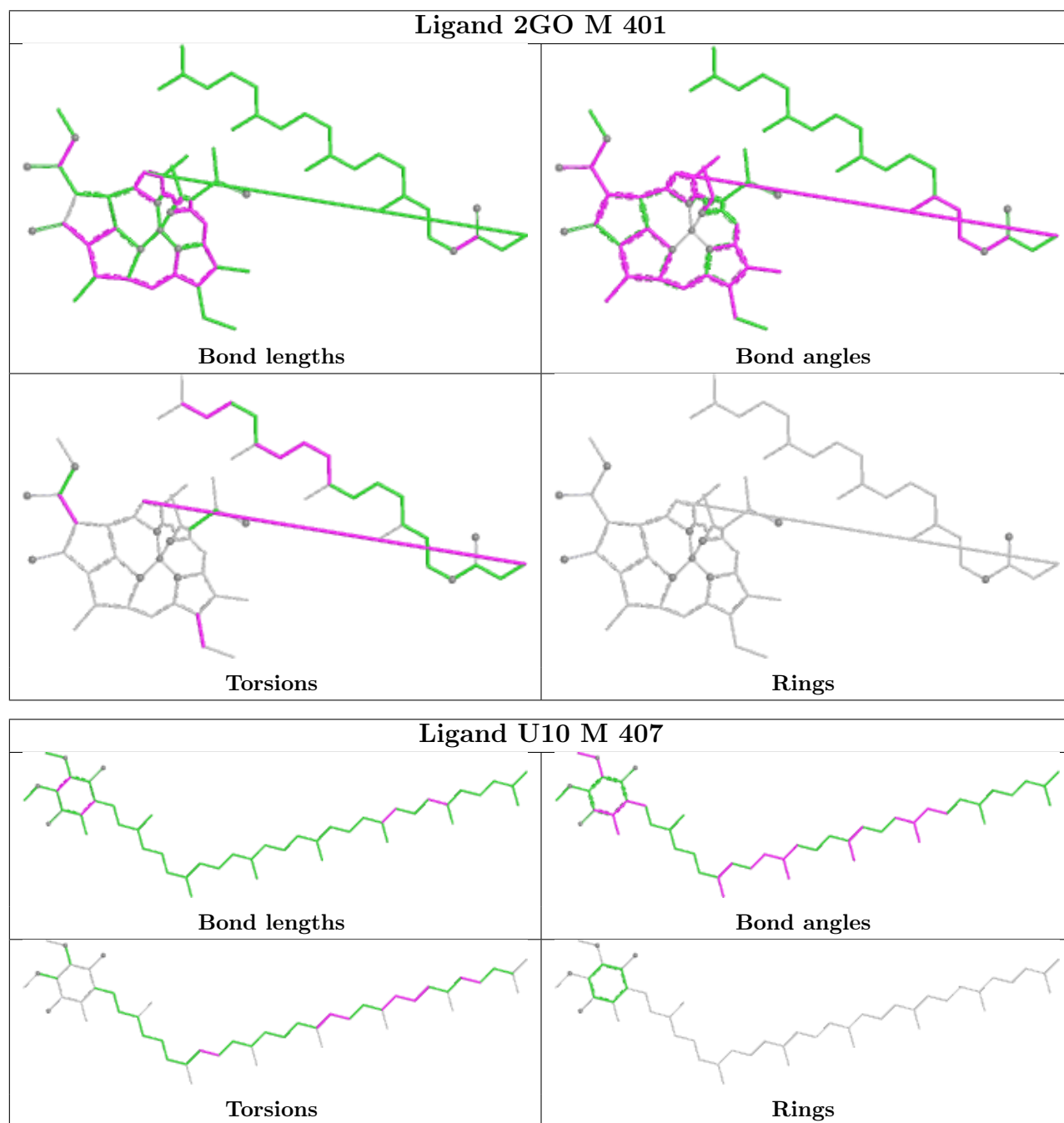
There are no ring outliers.

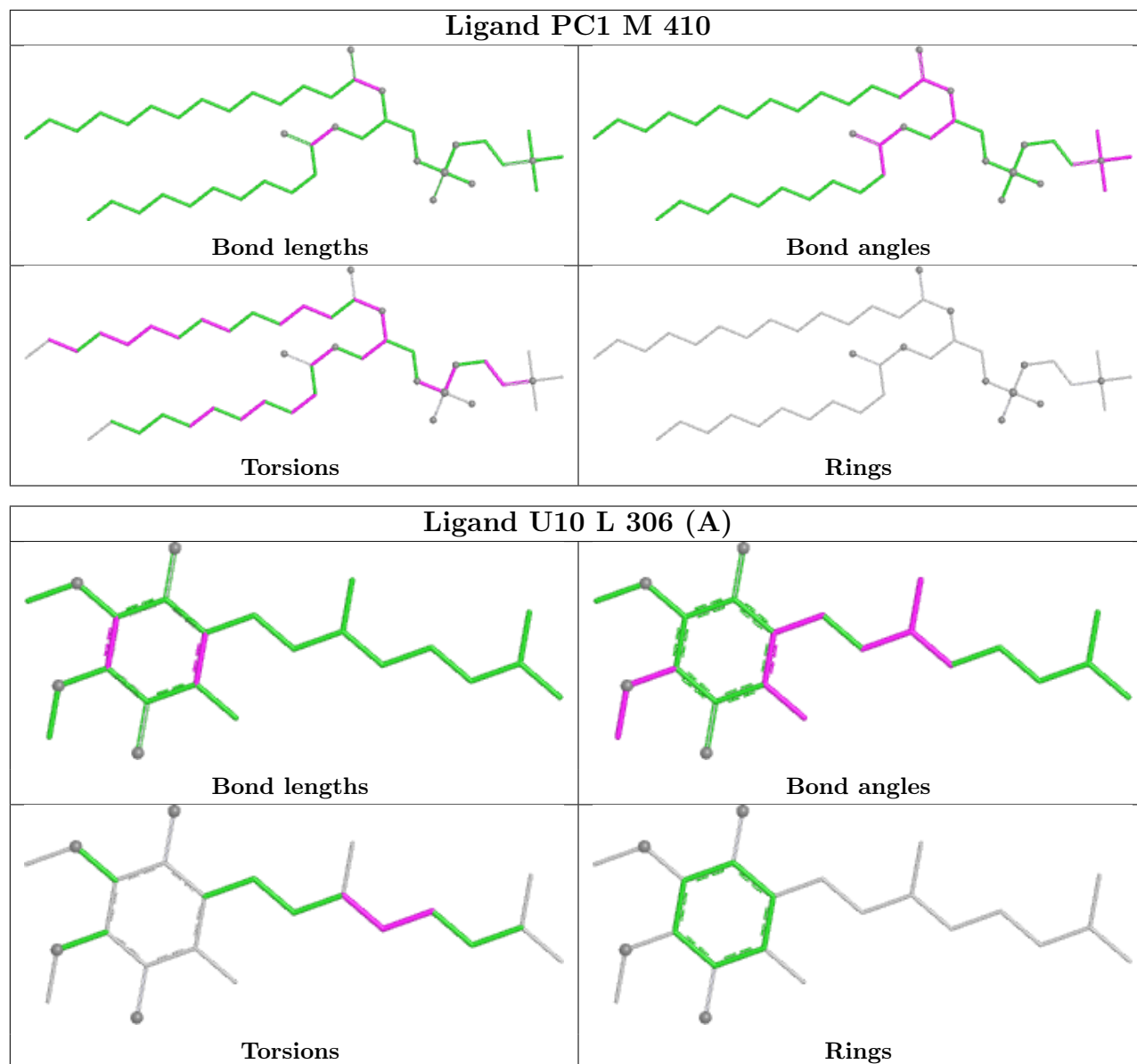
19 monomers are involved in 67 short contacts:

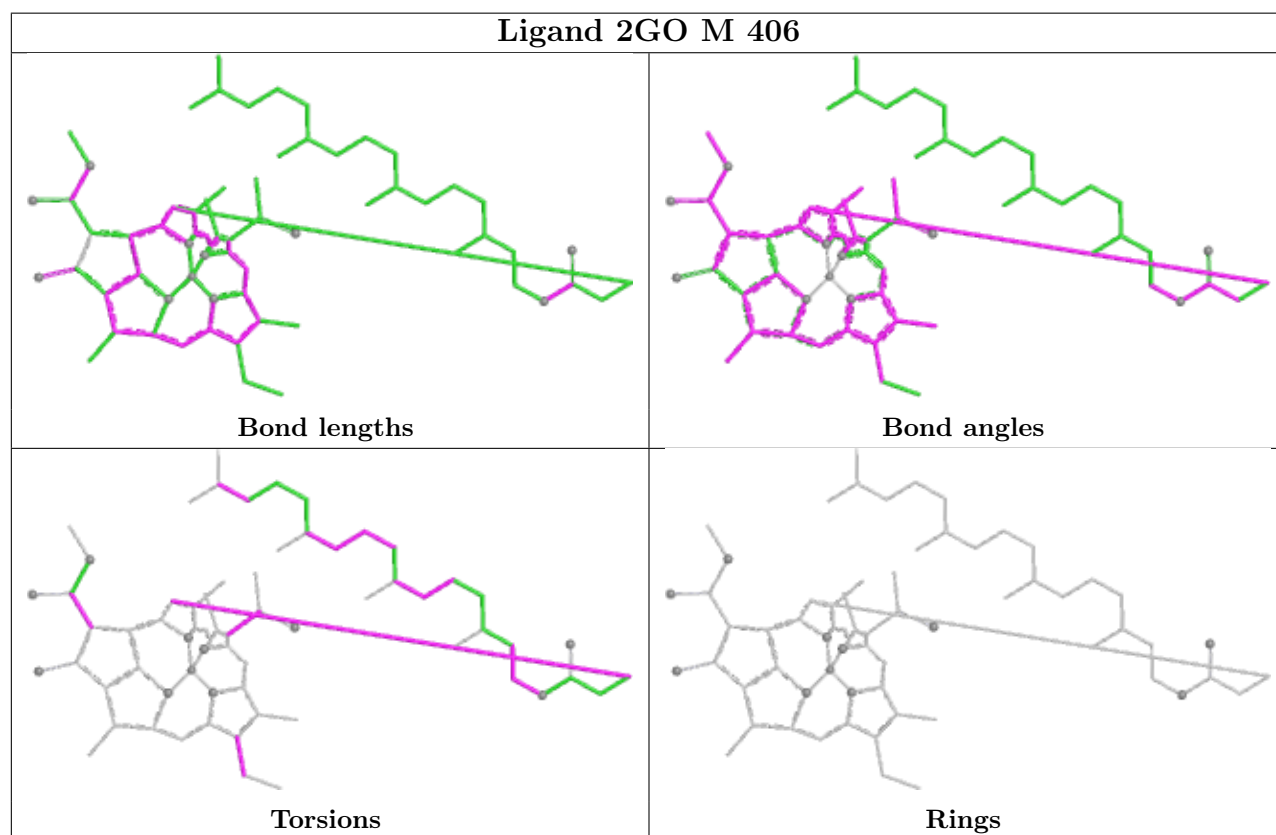
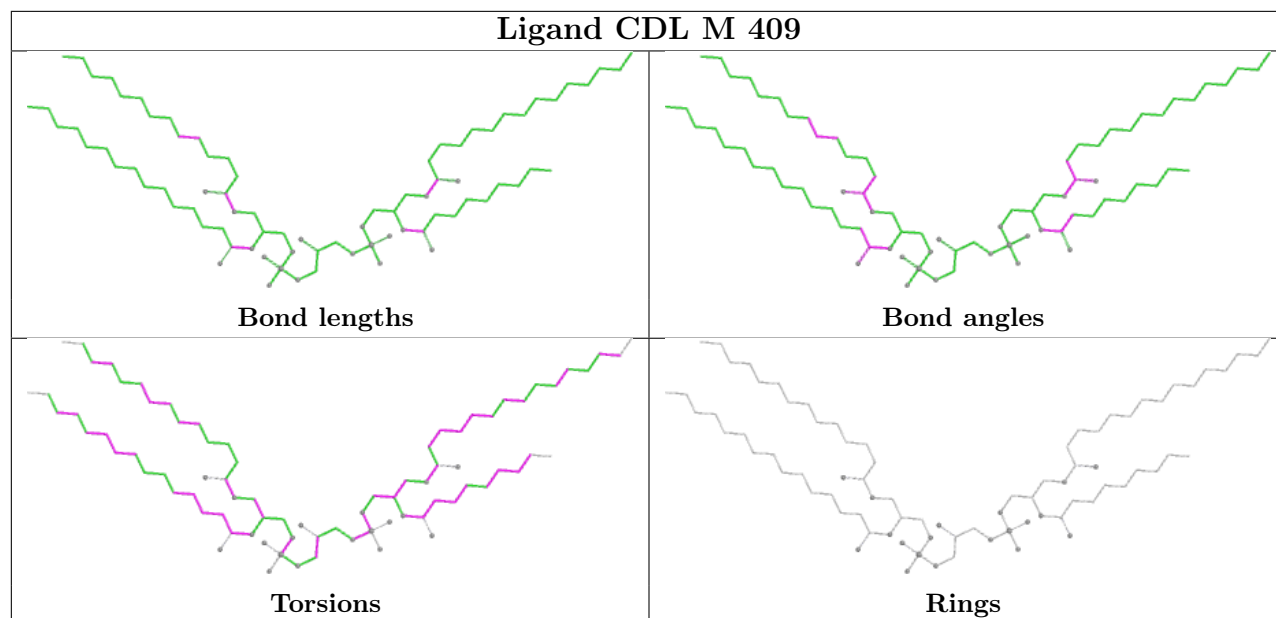
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	M	401	2GO	10	0
4	H	303	GOL	1	0
8	M	407	U10	3	0
4	H	301	GOL	1	0
8	L	306[A]	U10	7	0
13	M	409	CDL	2	0
6	M	406	2GO	8	0
5	H	305	GGD	2	0
9	L	308	PO4	1	0
6	L	307	2GO	2	0
7	M	403	LDA	1	0
6	L	305	2GO	8	0
4	L	312	GOL	1	0
6	L	301	2GO	6	0
8	L	306[B]	U10	6	0
12	M	408	SPO	5	0
6	M	402	2GO	10	0
4	L	311	GOL	1	0
4	L	313	GOL	1	0

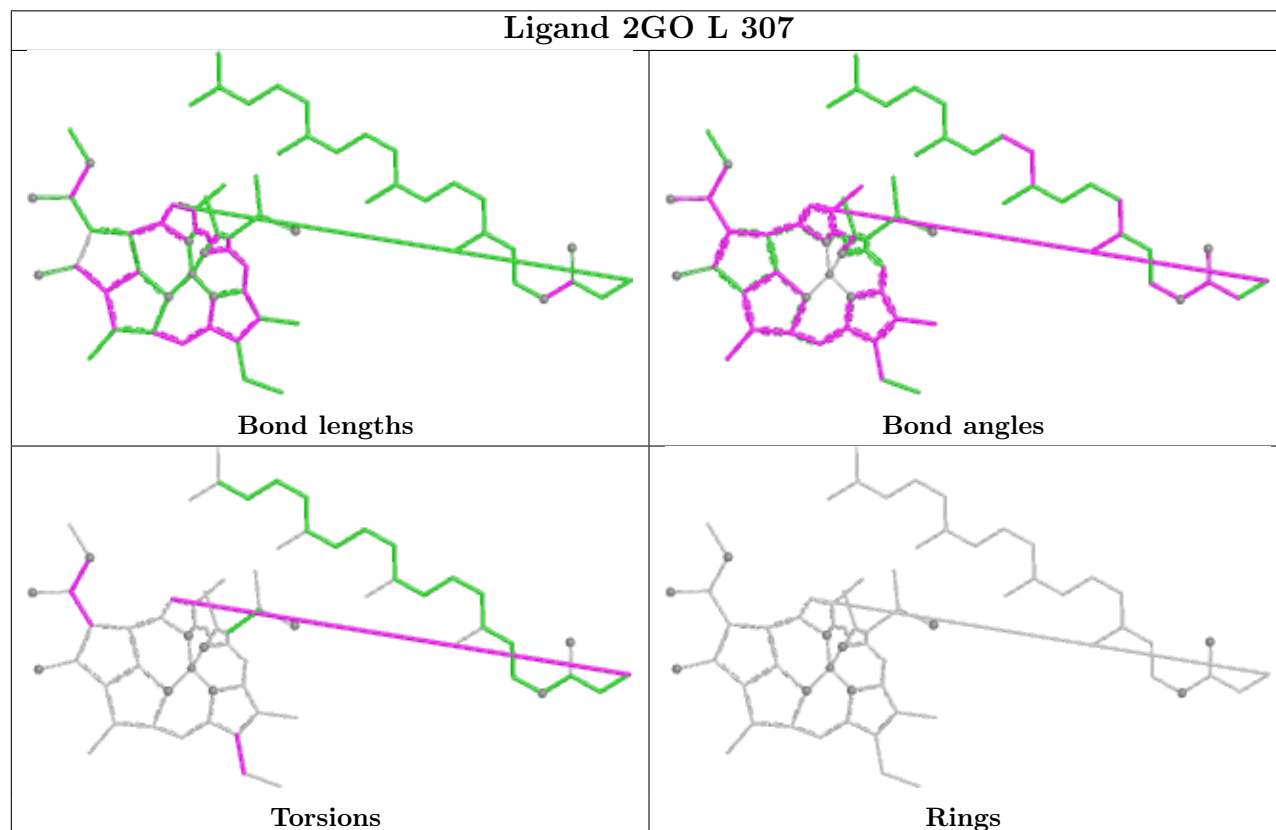
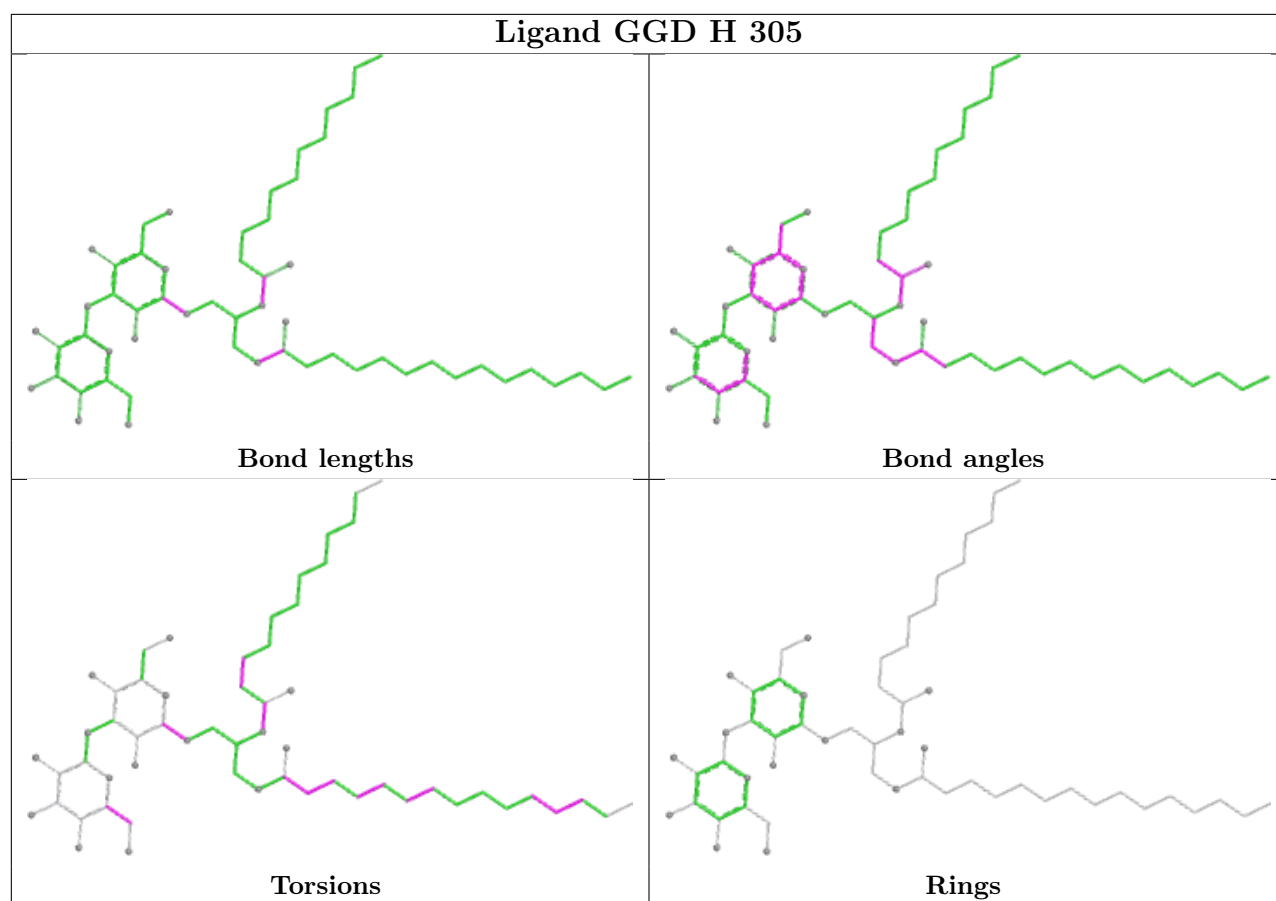
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

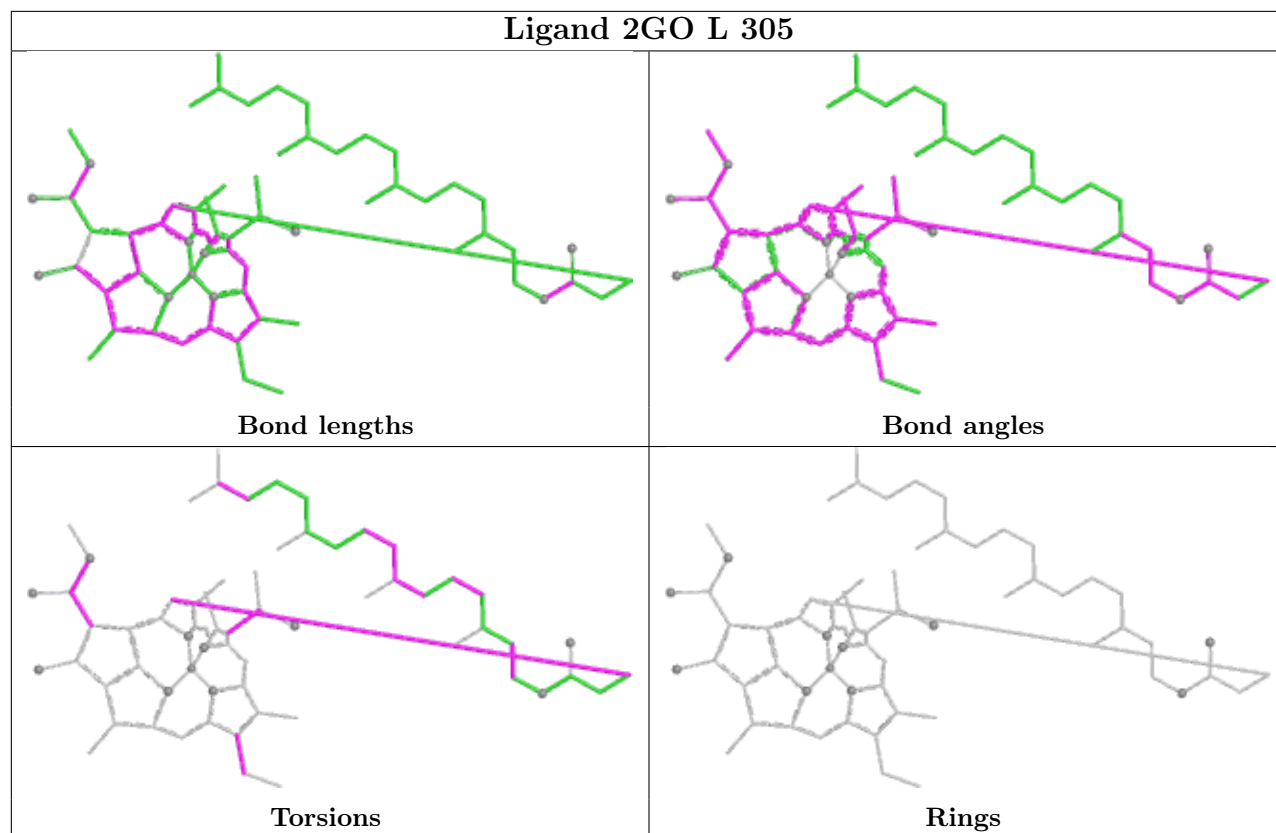




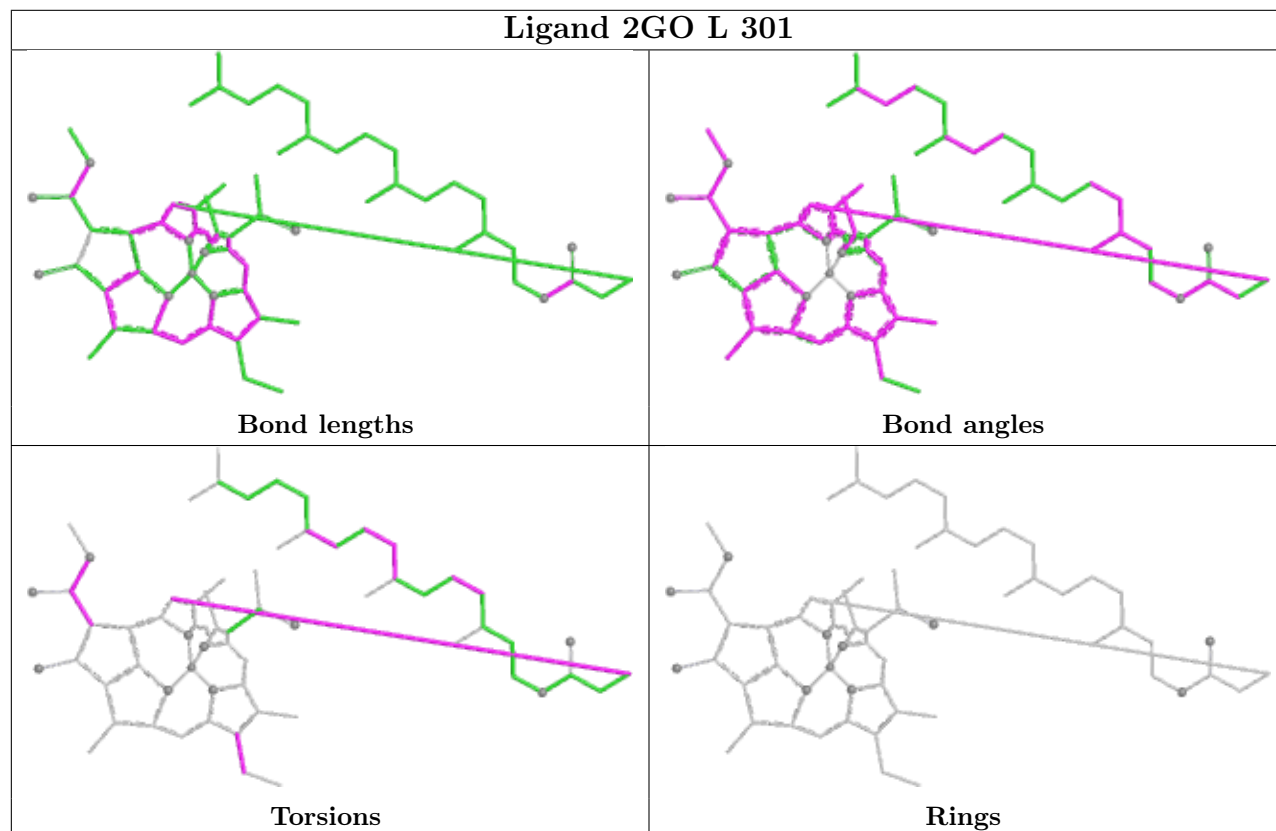


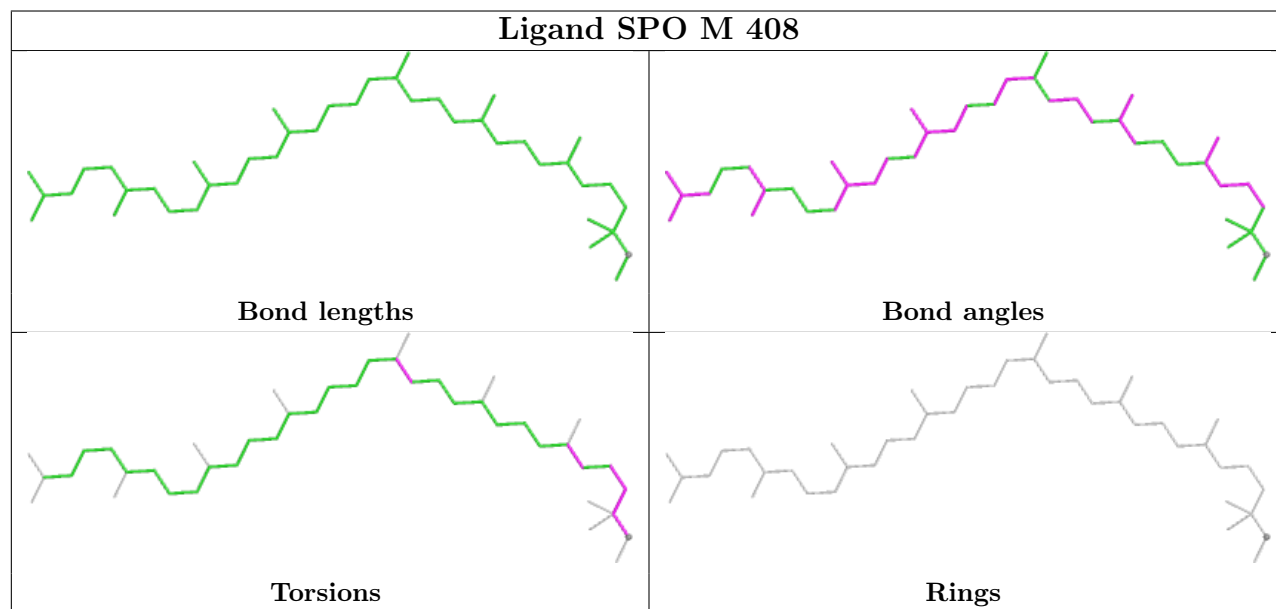
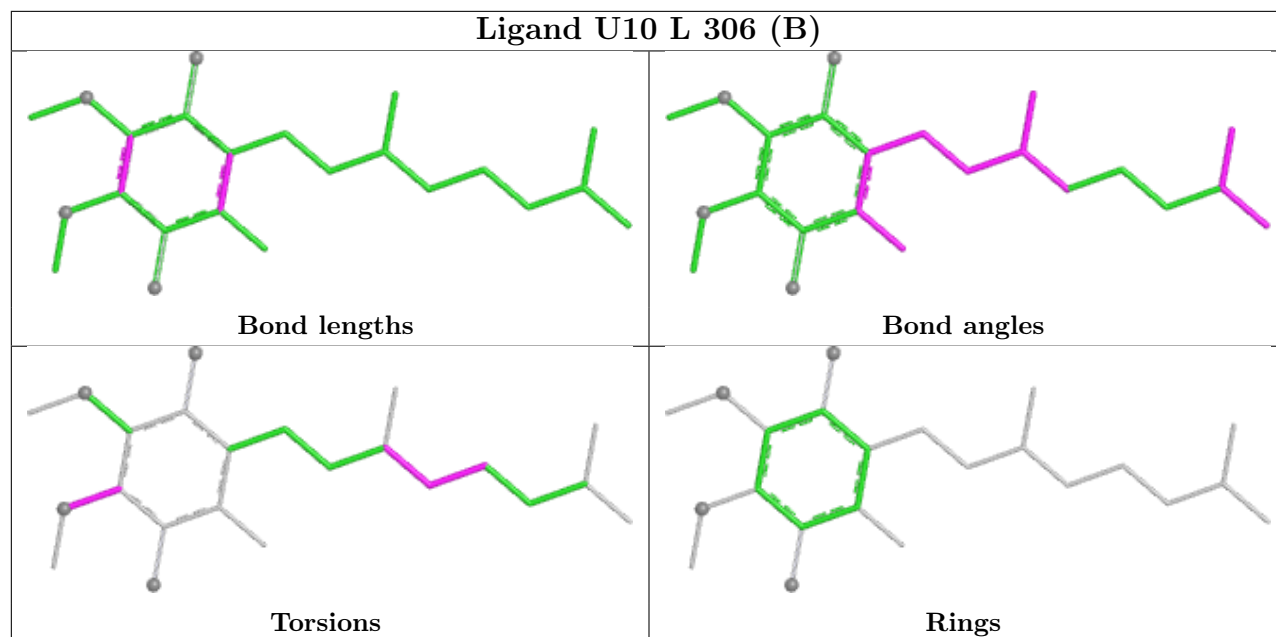


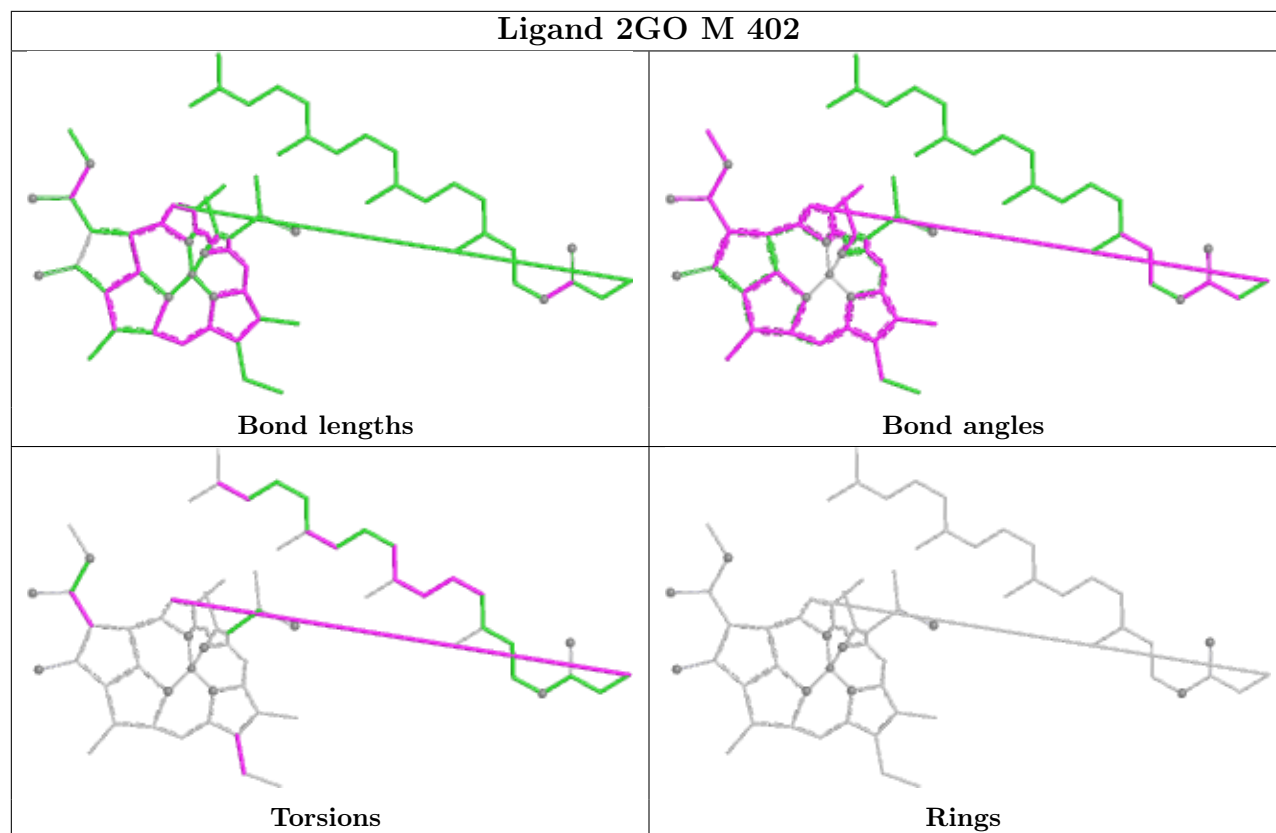
Ligand 2GO L 305



Ligand 2GO L 301







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	H	241/241 (100%)	-0.40	4 (1%) 69 63	32, 53, 76, 161	8 (3%)
2	L	281/281 (100%)	-0.40	2 (0%) 84 80	37, 52, 79, 101	2 (0%)
3	M	303/303 (100%)	-0.30	5 (1%) 69 63	37, 55, 80, 123	7 (2%)
All	All	825/825 (100%)	-0.36	11 (1%) 75 68	32, 54, 80, 161	17 (2%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	M	1	ALA	12.8
3	M	2	GLU	7.2
1	H	249[A]	LYS	5.5
1	H	246	PRO	3.5
3	M	301	HIS	3.3

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](#)

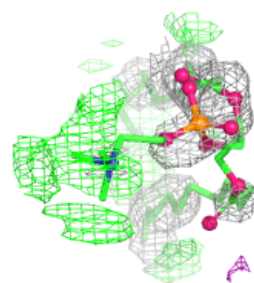
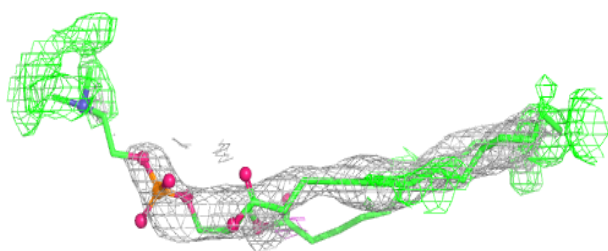
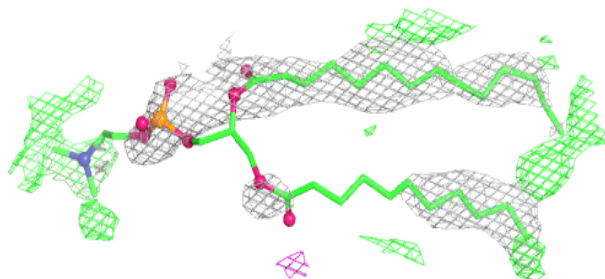
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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
14	PC1	M	410	43/54	0.74	0.35	78,117,175,190	0
7	LDA	L	303	16/16	0.75	0.43	76,95,143,148	0
7	LDA	L	304	16/16	0.83	0.25	68,96,124,125	0
10	HTO	L	309	10/10	0.85	0.30	88,103,117,127	0
10	HTO	L	310	10/10	0.85	0.28	86,114,140,156	0
4	GOL	H	301	6/6	0.85	0.17	94,109,111,112	0
13	CDL	M	409	81/100	0.86	0.23	70,101,156,164	0
5	GGD	H	305	57/67	0.86	0.22	49,107,216,221	0
7	LDA	L	302	16/16	0.87	0.23	42,105,140,143	0
7	LDA	M	404	16/16	0.88	0.18	67,87,102,106	0
4	GOL	L	311	6/6	0.90	0.16	60,73,85,104	0
8	U10	L	306[A]	23/63	0.91	0.23	50,71,86,91	23
8	U10	L	306[B]	23/63	0.91	0.23	43,68,73,75	23
4	GOL	H	304	6/6	0.91	0.12	74,85,89,94	0
4	GOL	H	303	6/6	0.92	0.14	73,85,90,96	0
4	GOL	H	302	6/6	0.92	0.14	56,65,69,81	0
8	U10	M	407	48/63	0.93	0.15	43,54,99,111	0
12	SPO	M	408	42/42	0.94	0.16	46,64,98,112	0
6	2GO	M	406	66/66	0.94	0.15	60,76,135,142	0
4	GOL	L	313	6/6	0.94	0.10	84,89,93,93	0
9	PO4	L	308	5/5	0.95	0.07	97,97,98,98	0
4	GOL	L	312	6/6	0.95	0.11	87,88,92,95	0
7	LDA	M	403	16/16	0.95	0.13	42,60,67,68	0
6	2GO	L	305	66/66	0.97	0.09	31,47,56,58	0
6	2GO	M	402	66/66	0.98	0.08	39,50,75,86	0
6	2GO	L	301	66/66	0.98	0.08	29,39,59,68	0
6	2GO	L	307	66/66	0.98	0.09	35,48,59,63	0
6	2GO	M	401	66/66	0.98	0.10	35,47,88,92	0
11	FE	M	405	1/1	1.00	0.01	46,46,46,46	0

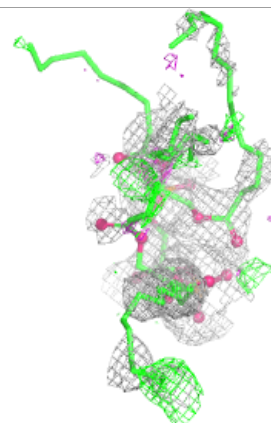
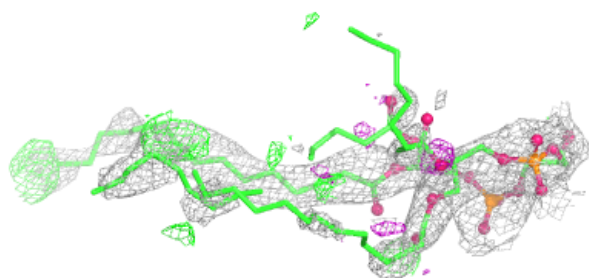
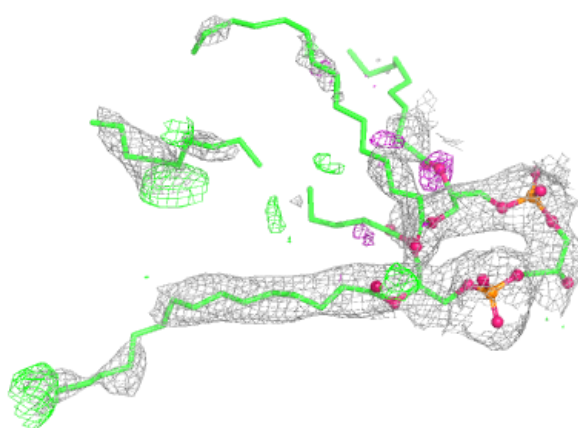
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PC1 M 410:

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

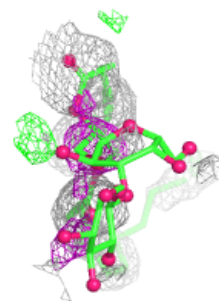
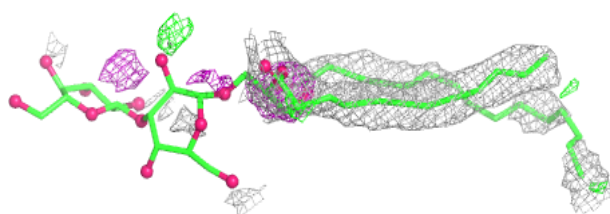
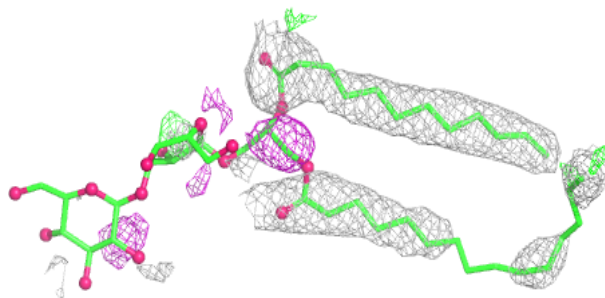
**Electron density around CDL M 409:**

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

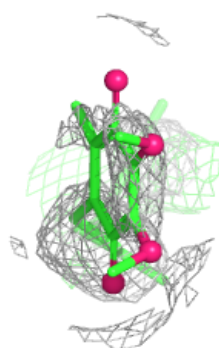
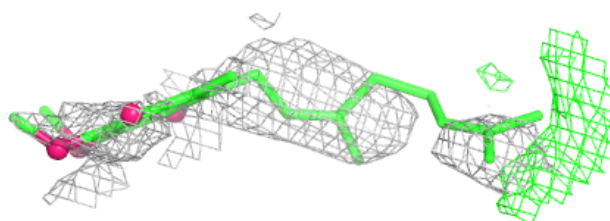
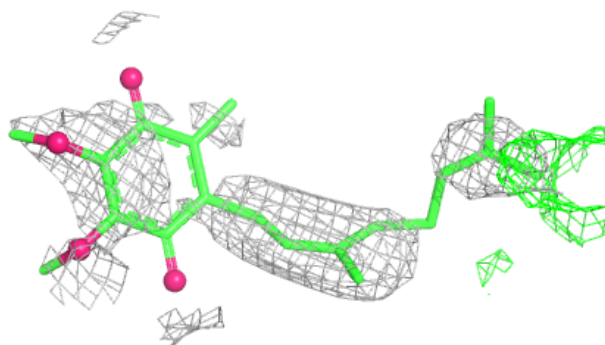


Electron density around GGD H 305:

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

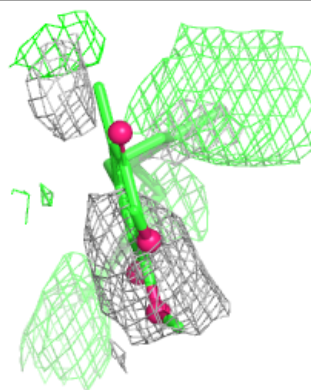
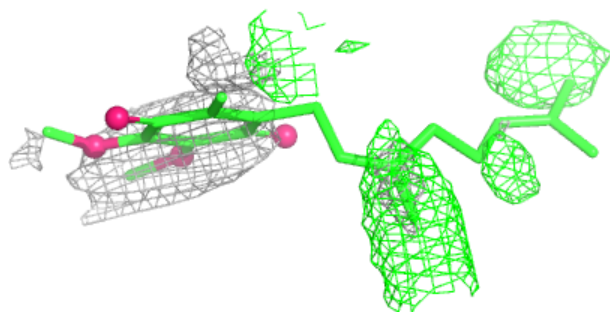
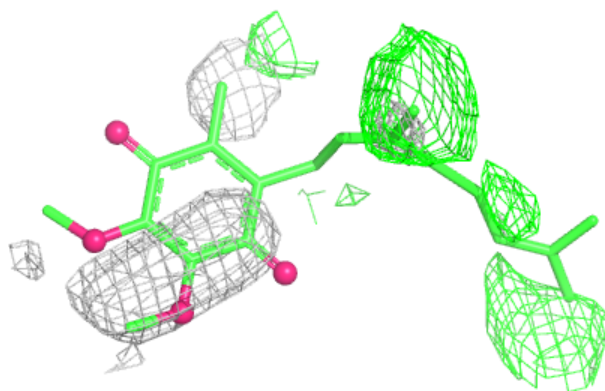
**Electron density around U10 L 306 (A):**

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

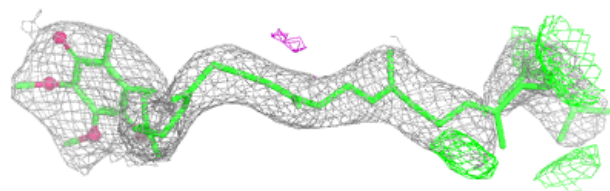
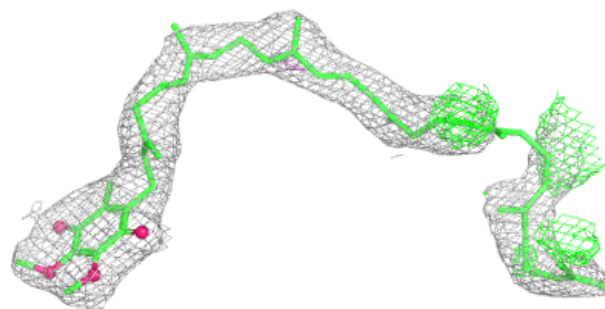


Electron density around U10 L 306 (B):

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

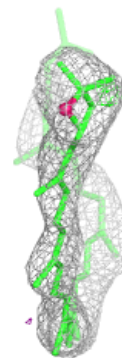
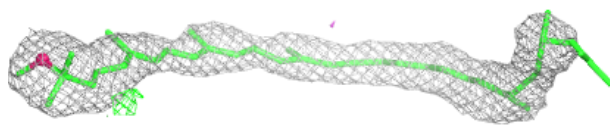
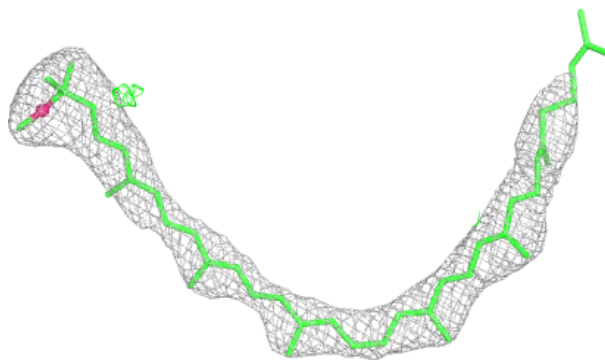
**Electron density around U10 M 407:**

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

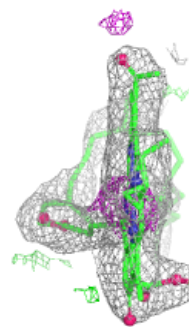
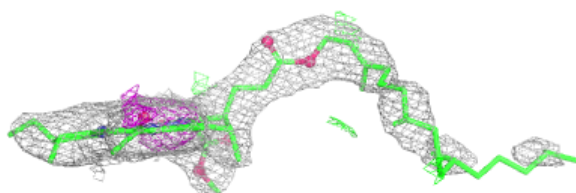
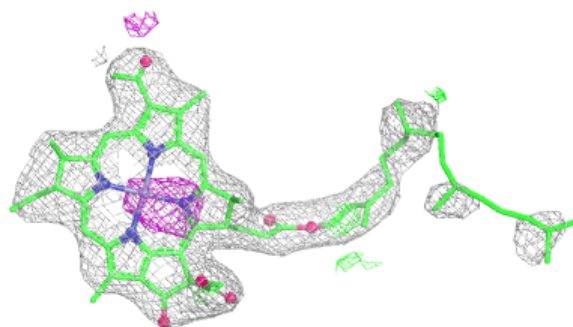


Electron density around SPO M 408:

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

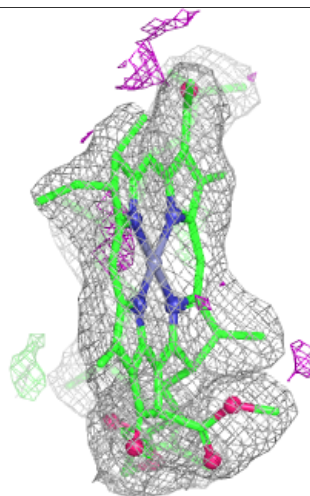
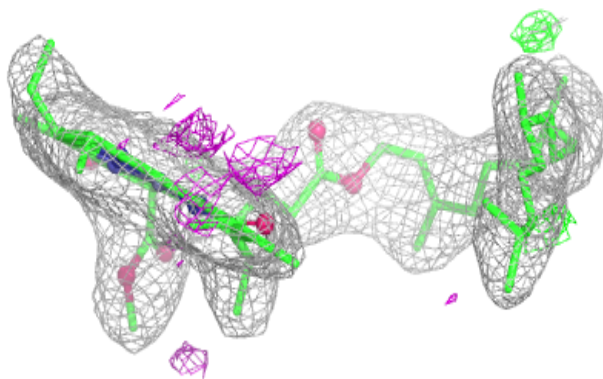
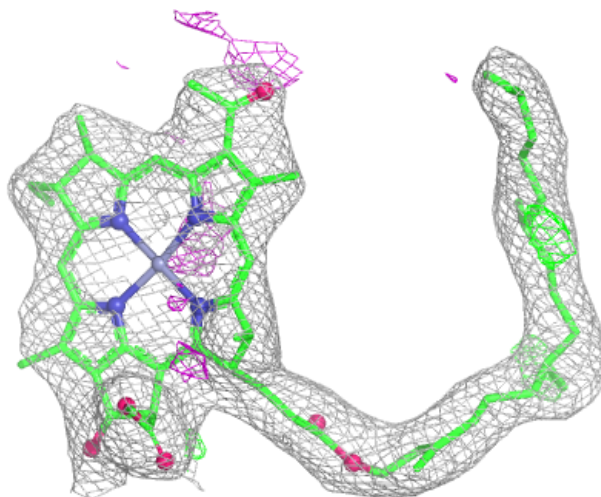
**Electron density around 2GO M 406:**

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



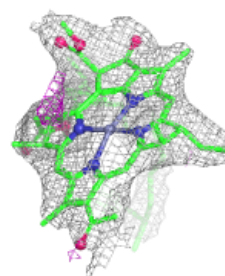
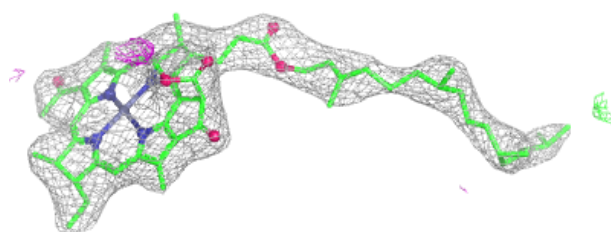
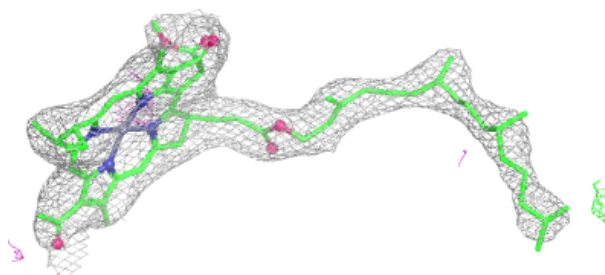
Electron density around 2GO L 305:

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

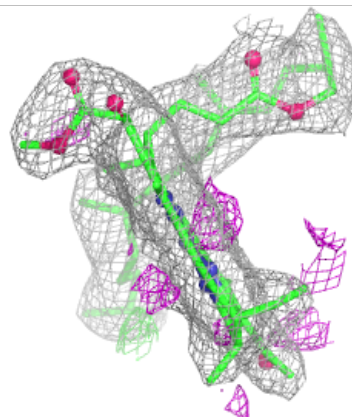
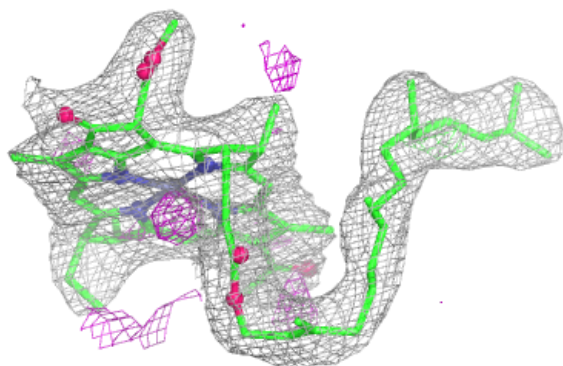
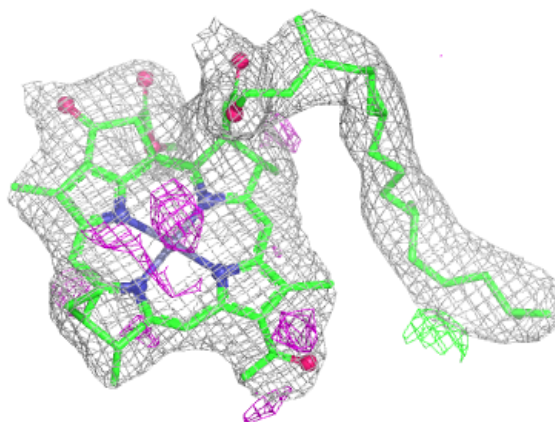


Electron density around 2GO M 402:

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

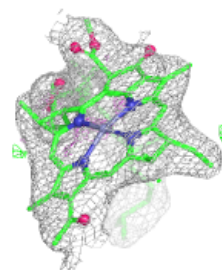
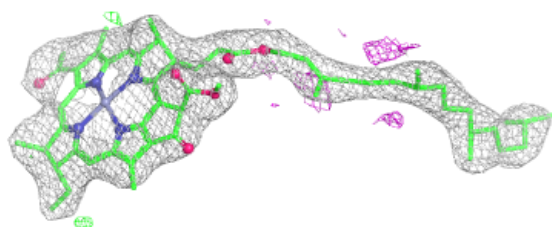
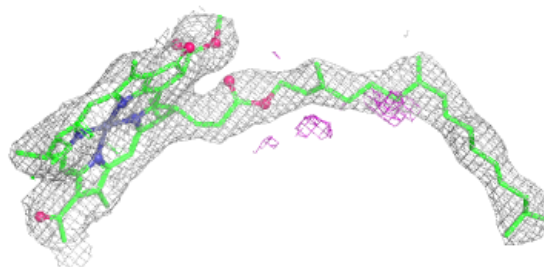
**Electron density around 2GO L 301:**

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

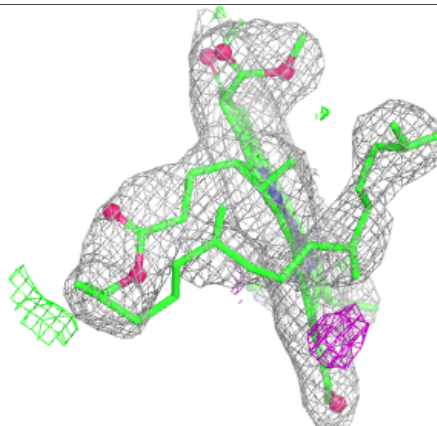
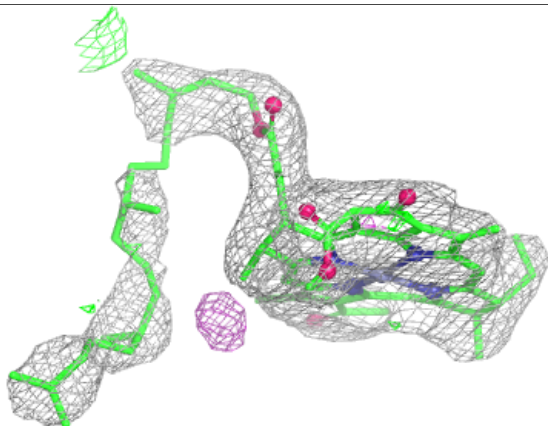
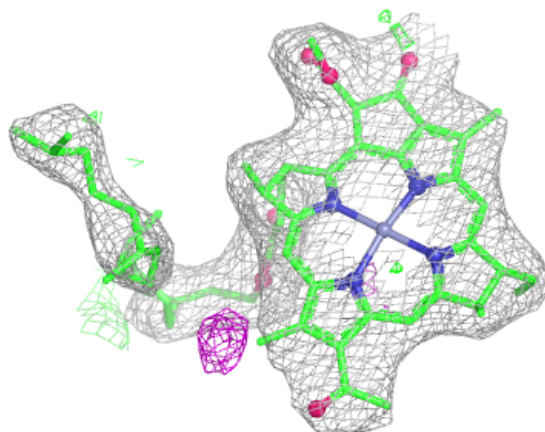


Electron density around 2GO L 307:

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

**Electron density around 2GO M 401:**

$2mF_o-DF_c$ (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.