



wwPDB EM Validation Summary Report ⓘ

Aug 6, 2026 – 09:42 AM JST

PDB ID : 7W4J / pdb_00007w4j
EMDB ID : EMD-32305
Title : Deactive state CI from Q1-NADH dataset, Subclass 1
Authors : Gu, J.; Yang, M.
Deposited on : 2021-11-28
Resolution : 3.20 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

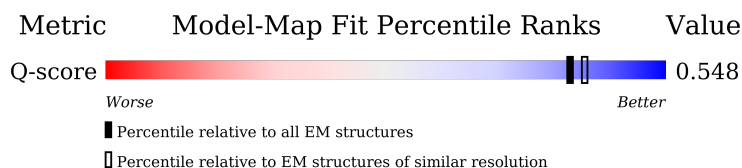
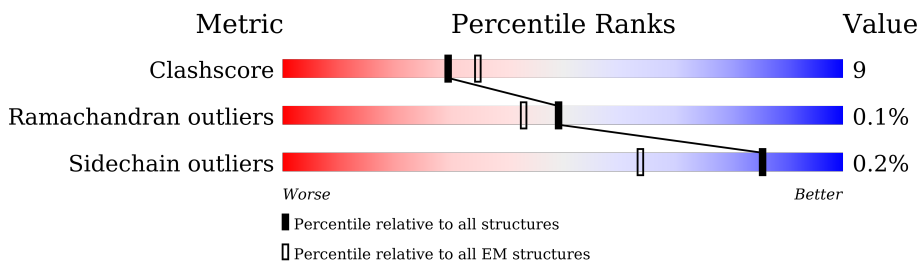
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	433	14% 78% 21%
2	B	176	80% 20%
3	C	156	72% 27%
4	E	115	12% 81% 19%

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Mol	Chain	Length	Quality of chain
5	F	86	
6	G	88	
6	X	88	
7	H	112	
8	I	112	
9	J	342	
10	K	43	
11	L	125	
12	M	690	
13	N	144	
14	O	217	
15	P	208	
16	Q	430	
17	S	70	
18	T	96	
19	U	83	
20	V	140	
21	W	142	
22	Y	70	
23	Z	84	
24	a	140	
25	b	126	
26	c	156	
27	d	175	
28	e	107	

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Mol	Chain	Length	Quality of chain
29	f	49	
30	g	122	
31	h	105	
32	i	347	
33	j	115	
34	k	98	
35	l	603	
36	m	175	
37	n	56	
38	o	128	
39	p	178	
40	r	459	
41	s	318	
42	u	171	
43	v	124	
44	w	320	

2 Entry composition [i](#)

There are 57 unique types of molecules in this entry. The entry contains 66607 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	431	Total	C	N	O	S	0	0
			3318	2095	591	612	20		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	176	Total	C	N	O	S	0	0
			1412	887	243	269	13		

- Molecule 3 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	156	Total	C	N	O	S	0	0
			1244	792	227	211	14		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	115	Total	C	N	O	S	0	0
			971	619	179	168	5		

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	86	Total	C	N	O	S	0	0
			691	434	129	126	2		

- Molecule 6 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	88	Total	C	N	O	S	0	0
			693	447	102	139	5		
6	X	88	Total	C	N	O	S	0	0
			696	449	103	139	5		

- Molecule 7 is a protein called Complex I subunit B13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	112	Total	C	N	O	S	0	0
			910	588	154	165	3		

- Molecule 8 is a protein called Complex I-B14.5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	97	Total	C	N	O	S	0	0
			780	491	147	139	3		

- Molecule 9 is a protein called NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	297	Total	C	N	O	S	0	0
			2359	1514	421	416	8		

- Molecule 10 is a protein called Complex I-9kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	42	Total	C	N	O	S	0	0
			355	219	67	68	1		

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	125	Total	C	N	O	S	0	0
			1016	642	181	190	3		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	690	Total	C	N	O	S	0	0
			5296	3320	923	1014	39		

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	144	Total	C	N	O	S	0	0
			1204	770	218	212	4		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	217	Total	C	N	O	S	0	0
			1671	1065	281	315	10		

- Molecule 15 is a protein called Complex I-30kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	208	Total	C	N	O	S	0	0
			1738	1124	298	314	2		

- Molecule 16 is a protein called Complex I-49kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	419	Total	C	N	O	S	0	0
			3377	2162	578	613	24		

- Molecule 17 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	S	70	Total	C	N	O	S	0	0
			567	364	104	94	5		

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	T	96	Total	C	N	O	S	0	0
			741	452	140	146	3		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	U	83	Total	C	N	O	S	0	0
			643	417	110	115	1		

- Molecule 20 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	140	Total	C	N	O	S	0	0
			1009	645	168	190	6		

- Molecule 21 is a protein called Complex I-B16.6.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	142	Total	C	N	O	S	0	0
			1173	755	203	206	9		

- Molecule 22 is a protein called Complex I-AGGG.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	70	Total	C	N	O	S	0	0
			597	392	98	106	1		

- Molecule 23 is a protein called Complex I-B12.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Z	84	Total	C	N	O	S	0	0
			671	436	116	118	1		

- Molecule 24 is a protein called Complex I-SGDH.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	a	140	Total	C	N	O	S	0	0
			1165	762	199	201	3		

- Molecule 25 is a protein called Complex I-B17.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	103	Total	C	N	O	S	0	0
			868	567	157	143	1		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	c	156	Total	C	N	O	S	0	0
			1315	853	213	241	8		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	d	175	Total	C	N	O	S	0	0
			1461	916	265	272	8		

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	e	107	Total	C	N	O	S	0	0
			890	568	145	173	4		

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	f	42	Total	C	N	O	0	0
			342	225	58	59		

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	g	121	Total	C	N	O	S	0	0
			1000	650	173	171	6		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	h	105	Total	C	N	O	S	0	0
			867	550	161	150	6		

- Molecule 32 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	i	347	Total	C	N	O	S	0	0
			2710	1782	420	462	46		

- Molecule 33 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	j	99	Total	C	N	O	S	0	0
			800	545	118	132	5		

- Molecule 34 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	k	98	Total	C	N	O	S	0	0
			748	493	113	128	14		

- Molecule 35 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	l	603	Total	C	N	O	S	0	0
			4780	3172	740	817	51		

- Molecule 36 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	129	Total	C	N	O	S	0	0
			948	636	138	166	8		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	n	56	Total	C	N	O	S	0	0
			479	311	88	79	1		

- Molecule 38 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	o	128	Total	C	N	O	S	0	0
			1058	689	182	187			

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	p	178	Total	C	N	O	S	0	0
			1534	982	279	265	8		

- Molecule 40 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	r	459	Total	C	N	O	S	0	0
			3631	2412	572	609	38		

- Molecule 41 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	s	303	Total	C	N	O	S	0	0
			2394	1607	369	397	21		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	u	171	Total	C	N	O	S	0	0
			1398	887	250	251	10		

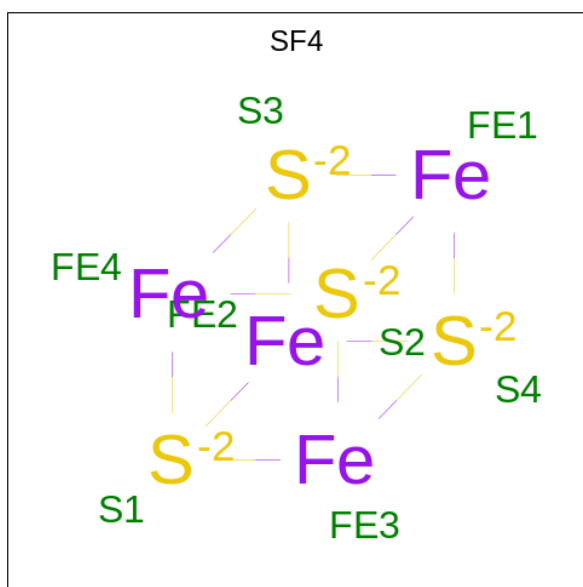
- Molecule 43 is a protein called Complex I-B18.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	v	124	Total	C	N	O	S	0	0
			1028	642	195	182	9		

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

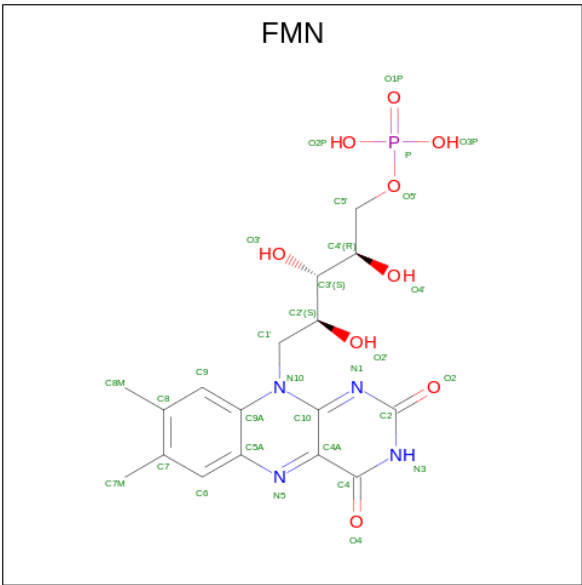
Mol	Chain	Residues	Atoms					AltConf	Trace
44	w	320	Total	C	N	O	S	0	0
			2582	1643	438	491	10		

- Molecule 45 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



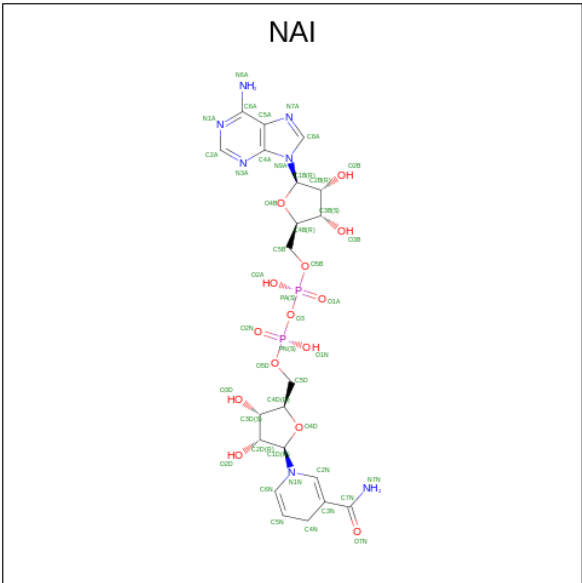
Mol	Chain	Residues	Atoms			AltConf
45	A	1	Total	Fe	S	0
			8	4	4	
45	B	1	Total	Fe	S	0
			8	4	4	
45	B	1	Total	Fe	S	0
			8	4	4	
45	C	1	Total	Fe	S	0
			8	4	4	
45	M	1	Total	Fe	S	0
			8	4	4	
45	M	1	Total	Fe	S	0
			8	4	4	

- Molecule 46 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
46	A	1	Total	C	N	O	P	0
			31	17	4	9	1	

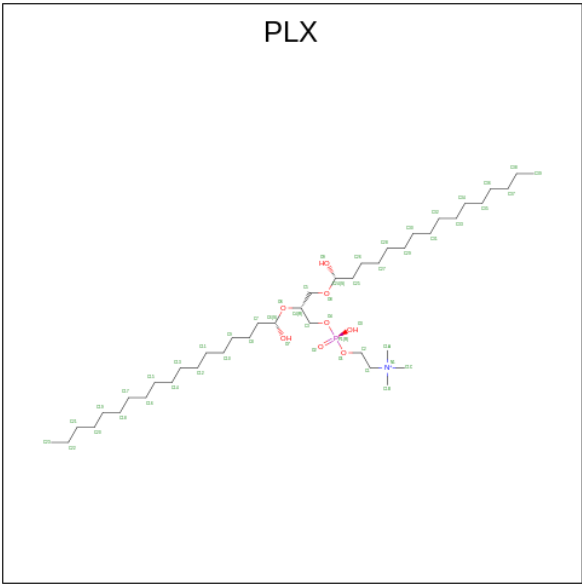
- Molecule 47 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
47	A	1	Total	C	N	O	P	0
			44	21	7	14	2	

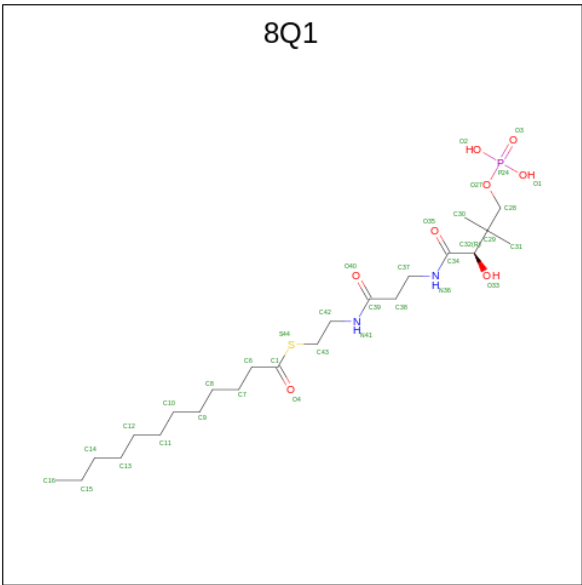
- Molecule 48 is (9R,11S)-9-([(1S)-1-HYDROXYHEXADECYL]OXY)METHYL)-2,2-DIMETHYL-5,7,10-TRIOXA-2LAMBDA 5 -AZA-6LAMBDA 5 -PHOSPHAOCTACOSANE-

6,6,11-TRIOL (CCD ID: PLX) (formula: C₄₂H₈₉NO₈P) (labeled as "Ligand of Interest" by depositor).



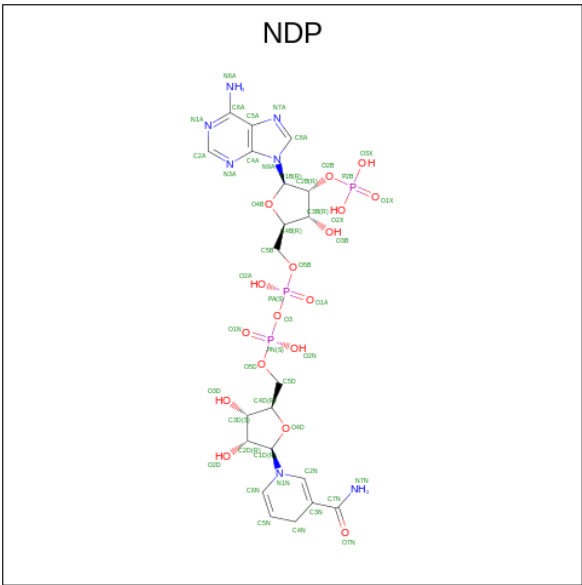
Mol	Chain	Residues	Atoms					AltConf
48	C	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	a	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	i	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	j	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	l	1	Total	C	N	O	P	0
			52	42	1	8	1	
48	r	1	Total	C	N	O	P	0
			52	42	1	8	1	

- Molecule 49 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonooxy)butanoyl]-beta-a
lanyl}amino)ethyl] dodecanethioate (CCD ID: 8Q1) (formula: C₂₃H₄₅N₂O₈PS) (labeled as
"Ligand of Interest" by depositor).



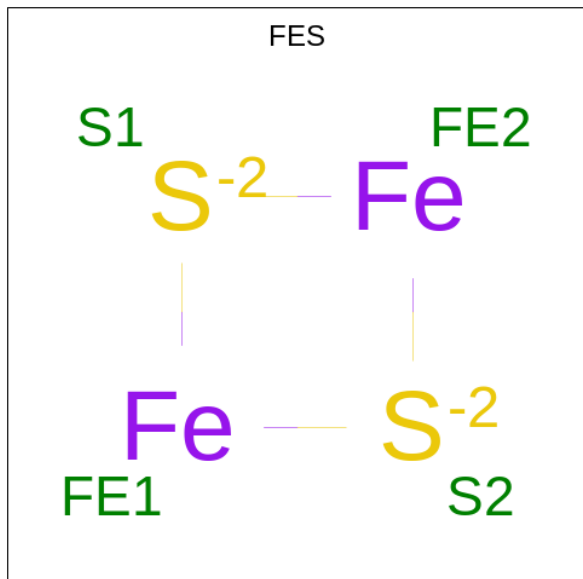
Mol	Chain	Residues	Atoms						AltConf
49	G	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	
49	X	1	Total	C	N	O	P	S	0
			35	23	2	8	1	1	

- Molecule 50 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
50	J	1	Total	C	N	O	P	0
			48	21	7	17	3	

- Molecule 51 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).

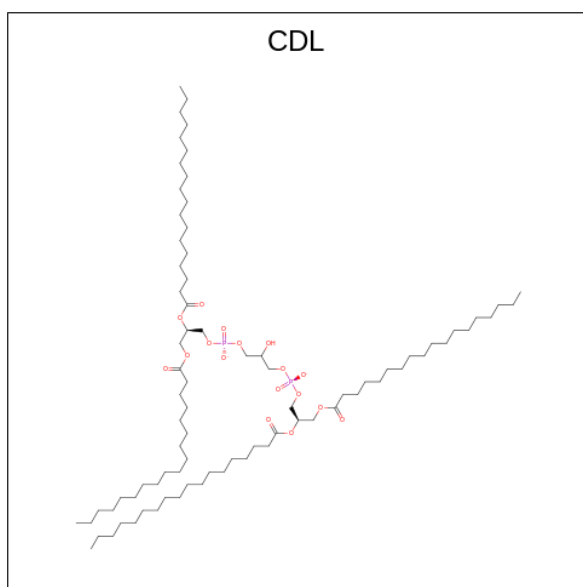


Mol	Chain	Residues	Atoms			AltConf
51	M	1	Total	Fe	S	0
			4	2	2	
51	O	1	Total	Fe	S	0
			4	2	2	

- Molecule 52 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
52	M	1	Total	Mg	0
			1	1	

- Molecule 53 is CARDIOLIPIN (CCD ID: CDL) (formula: $\text{C}_{81}\text{H}_{156}\text{O}_{17}\text{P}_2$) (labeled as "Ligand of Interest" by depositor).

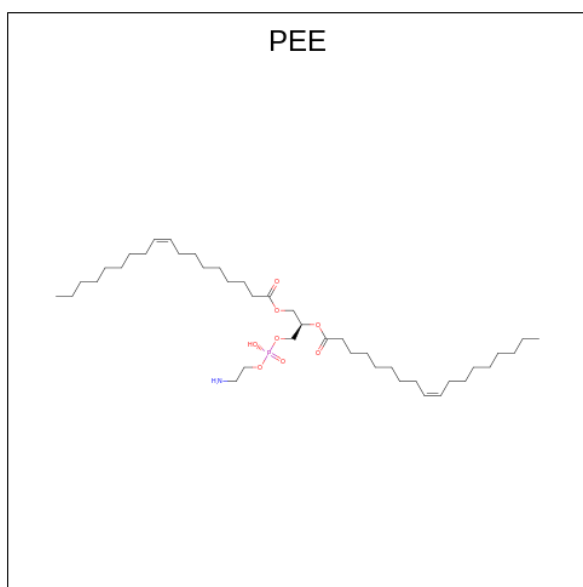


Mol	Chain	Residues	Atoms				AltConf
53	N	1	Total	C	O	P	0
			51	32	17	2	
53	V	1	Total	C	O	P	0
			71	52	17	2	
53	a	1	Total	C	O	P	0
			91	72	17	2	
53	i	1	Total	C	O	P	0
			66	47	17	2	
53	l	1	Total	C	O	P	0
			100	81	17	2	
53	r	1	Total	C	O	P	0
			100	81	17	2	

- Molecule 54 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

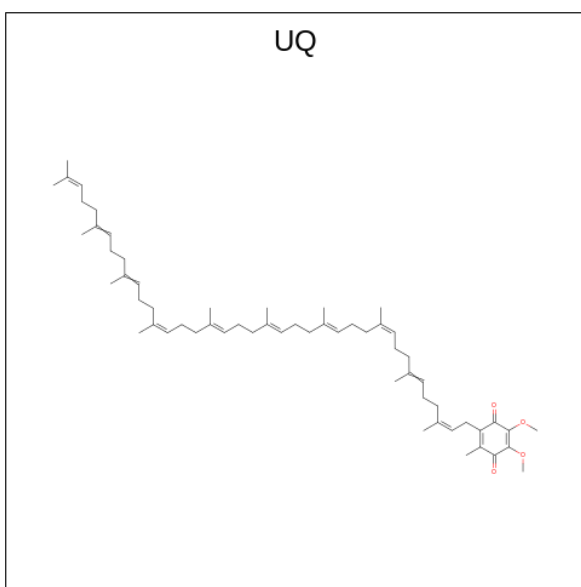
Mol	Chain	Residues	Atoms		AltConf
54	T	1	Total	Zn	0
			1	1	

- Molecule 55 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: C₄₁H₇₈NO₈P) (labeled as "Ligand of Interest" by depositor).



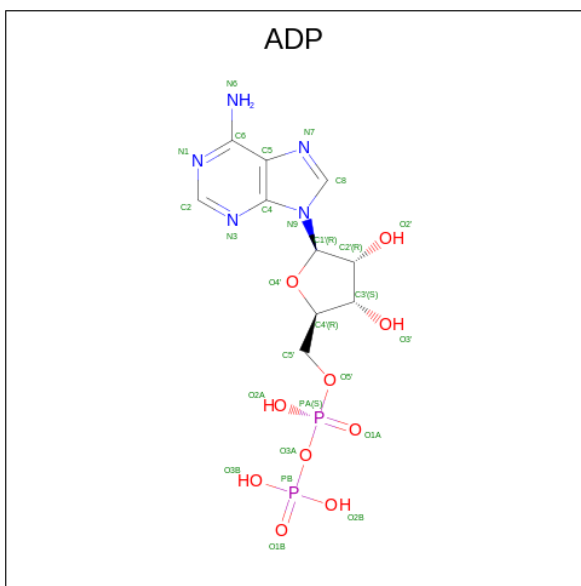
Mol	Chain	Residues	Atoms					AltConf
55	U	1	Total	C	N	O	P	0
			51	41	1	8	1	
55	i	1	Total	C	N	O	P	0
			47	37	1	8	1	
55	j	1	Total	C	N	O	P	0
			47	37	1	8	1	
55	l	1	Total	C	N	O	P	0
			46	36	1	8	1	
55	l	1	Total	C	N	O	P	0
			46	36	1	8	1	
55	m	1	Total	C	N	O	P	0
			41	31	1	8	1	
55	r	1	Total	C	N	O	P	0
			51	41	1	8	1	
55	s	1	Total	C	N	O	P	0
			51	41	1	8	1	

- Molecule 56 is Coenzyme Q10, (2Z,6E,10Z,14E,18E,22E,26Z)-isomer (CCD ID: UQ) (formula: C₅₉H₉₀O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
56	s	1	Total	C	O	0
			28	24	4	

- Molecule 57 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

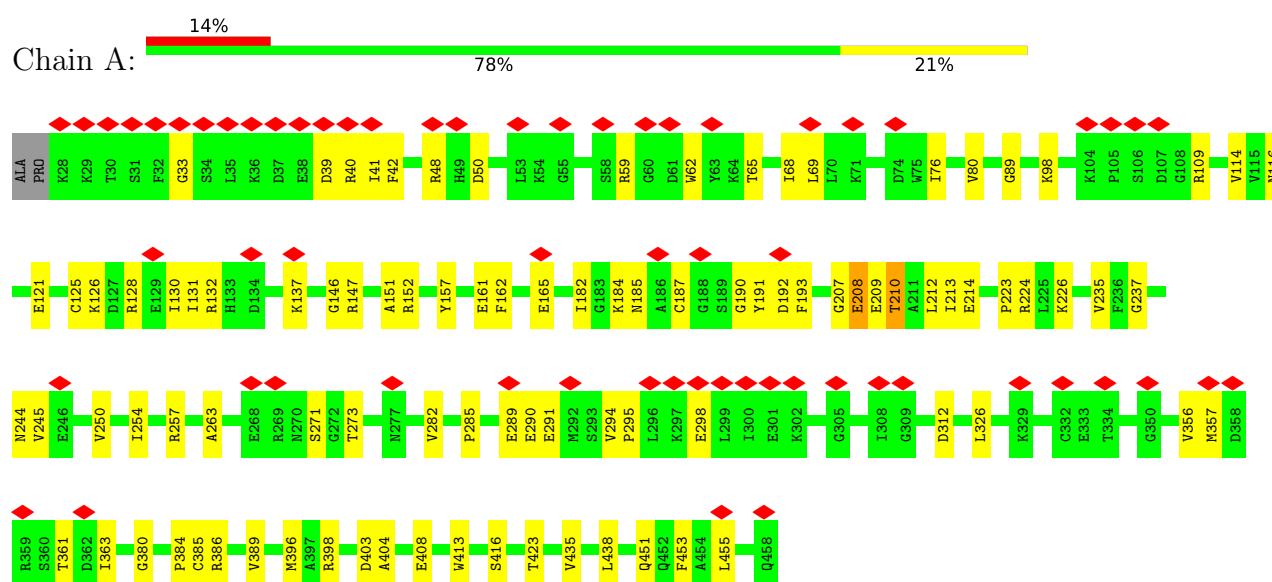


Mol	Chain	Residues	Atoms					AltConf
57	w	1	Total	C	N	O	P	0
			27	10	5	10	2	

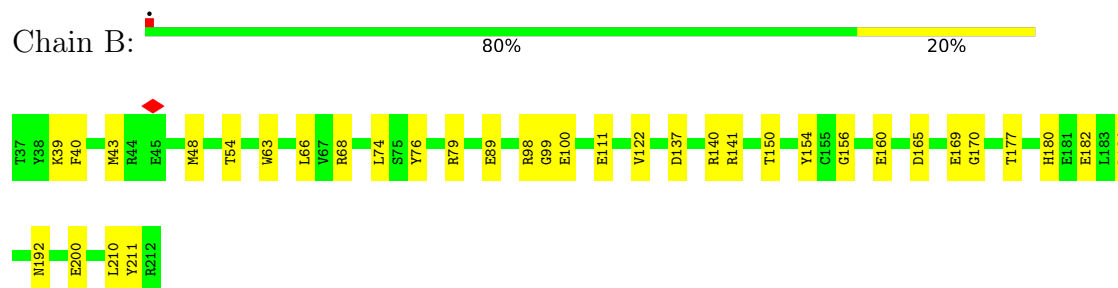
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

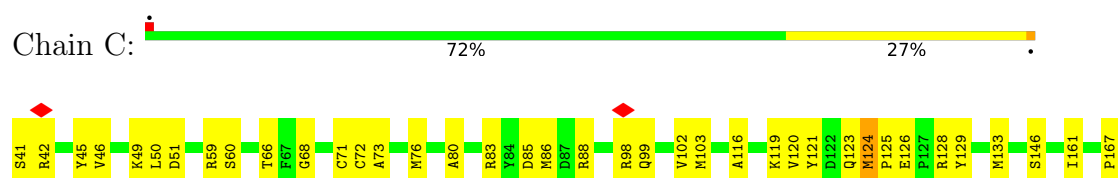
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial

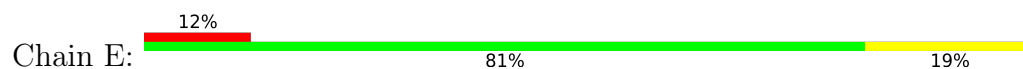


- Molecule 3: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial

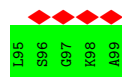
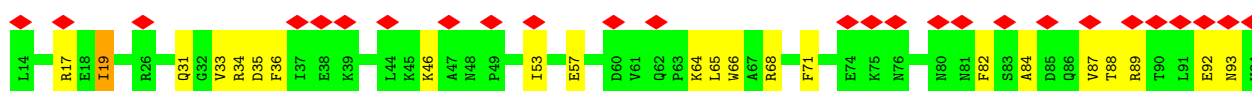
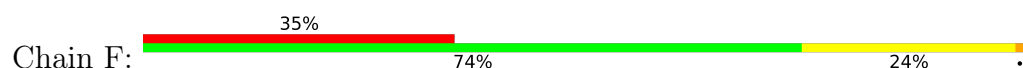




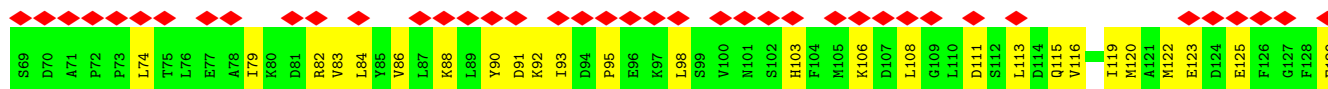
- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



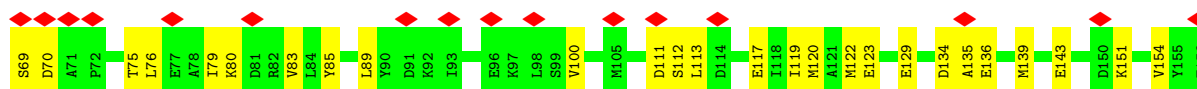
- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



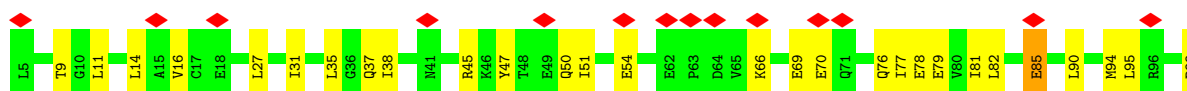
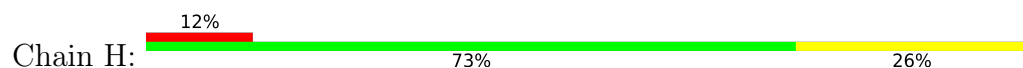
- Molecule 6: Acyl carrier protein



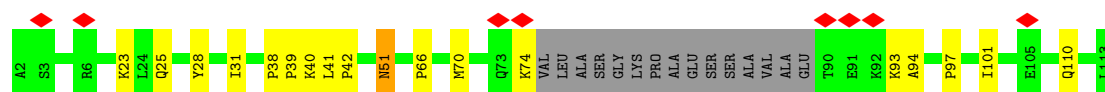
- Molecule 6: Acyl carrier protein



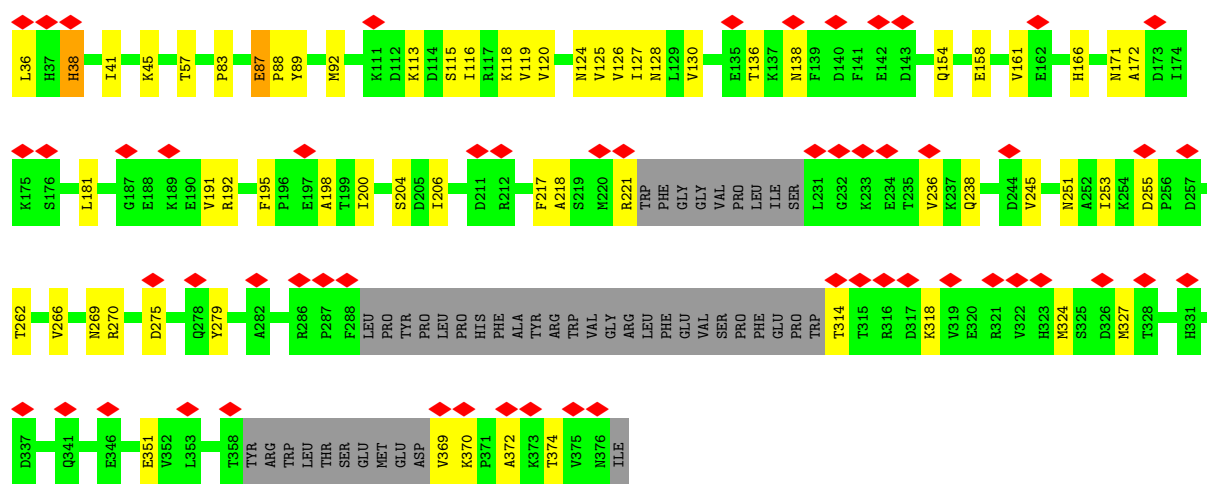
- Molecule 7: Complex I subunit B13



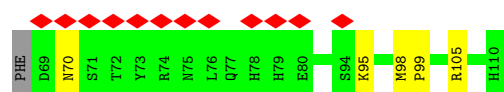
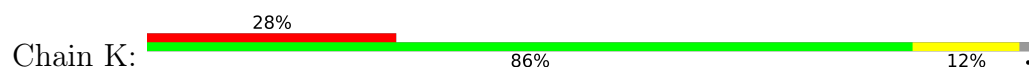
- Molecule 8: Complex I-B14.5a



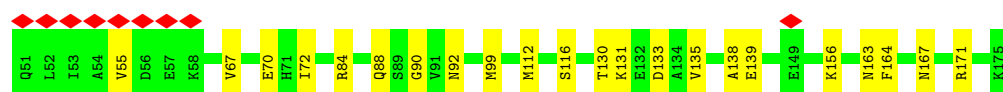
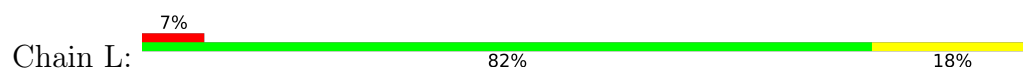
- Molecule 9: NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 9, mitochondrial



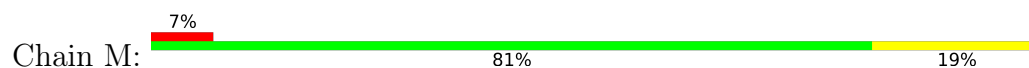
- Molecule 10: Complex I-9kD

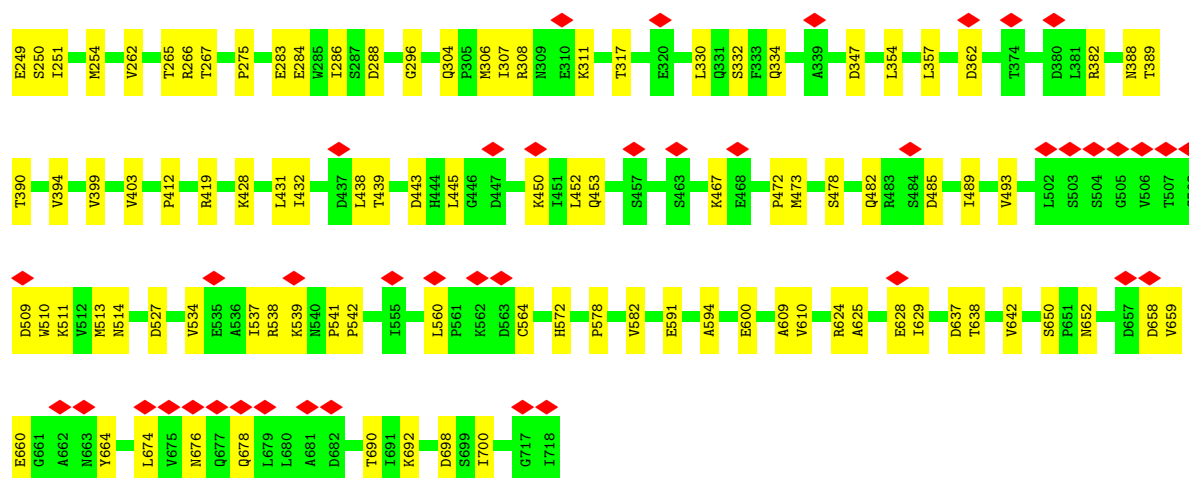


- Molecule 11: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

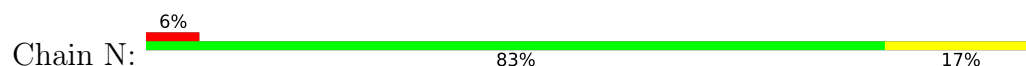


- Molecule 12: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

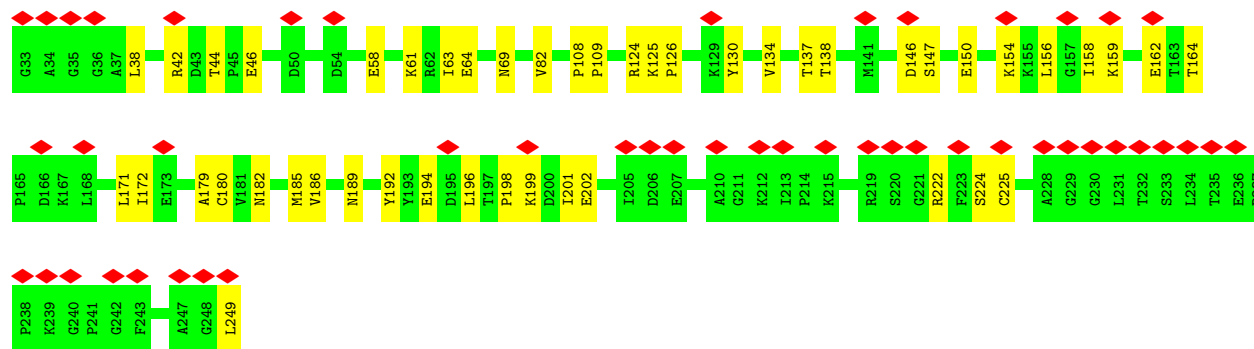
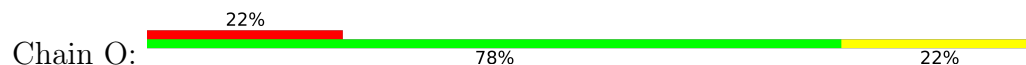




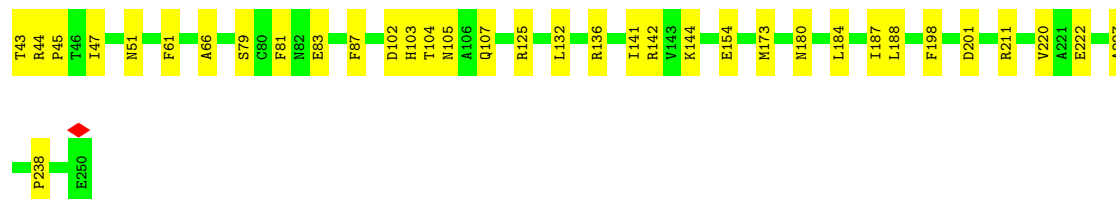
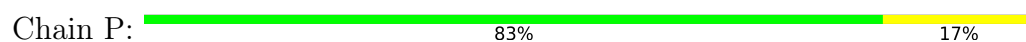
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



- Molecule 14: NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial

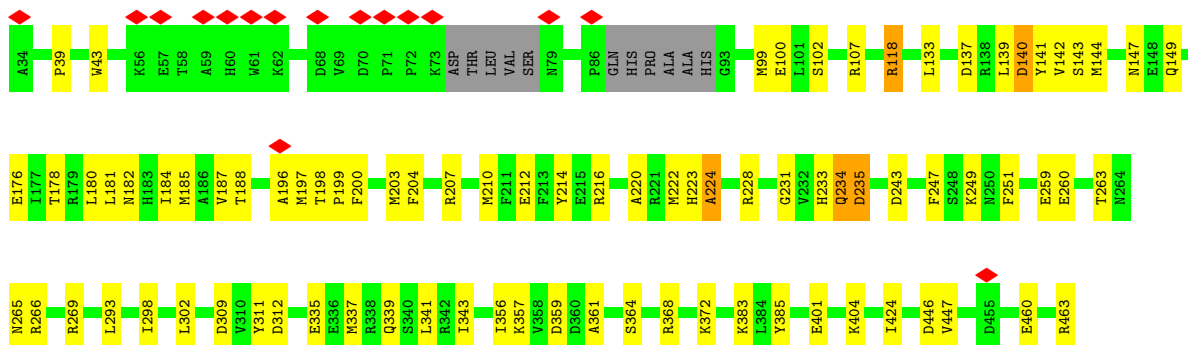


- Molecule 15: Complex I-30kD



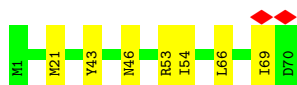
- Molecule 16: Complex I-49kD

Chain Q:  78% 18%

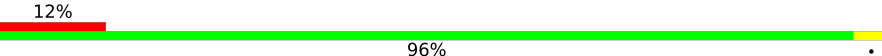


- Molecule 17: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

Chain S:  90% 10%



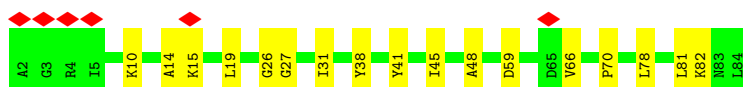
- Molecule 18: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial

Chain T:  12% 96%



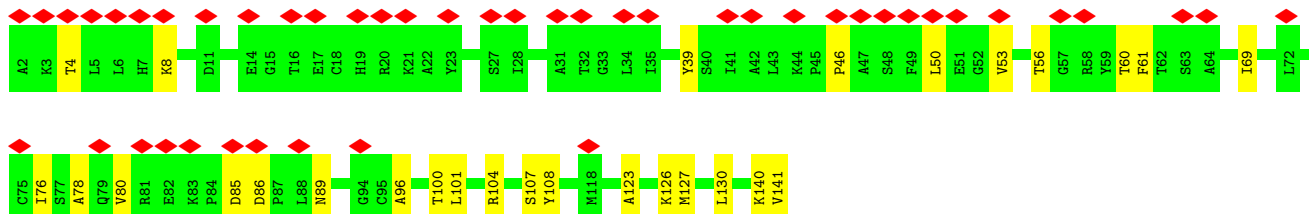
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

Chain U:  7% 80% 20%



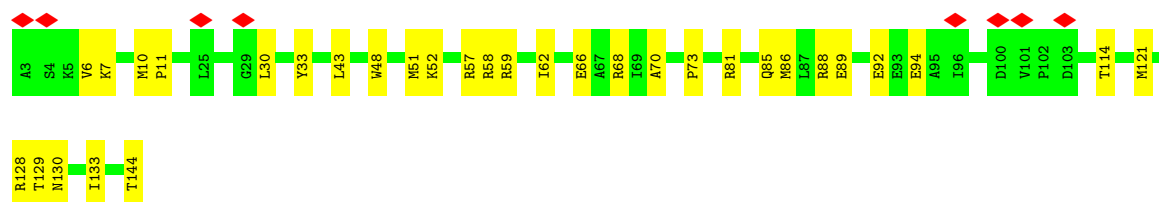
- Molecule 20: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

Chain V:  33% 80% 20%

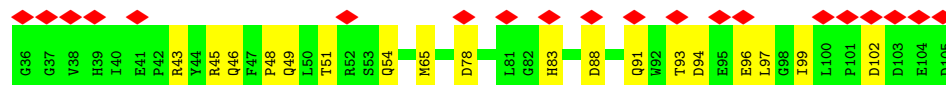
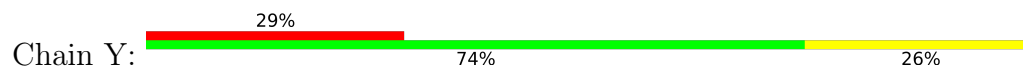


- Molecule 21: Complex I-B16.6

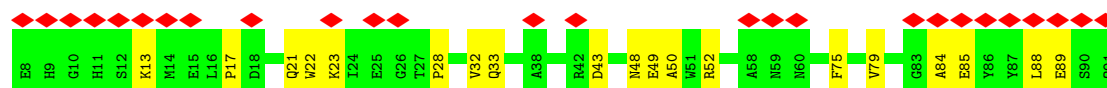
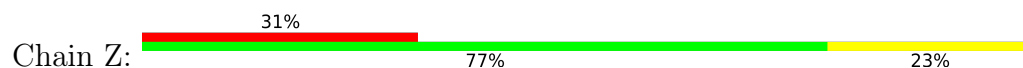
Chain W:  6% 77% 23%



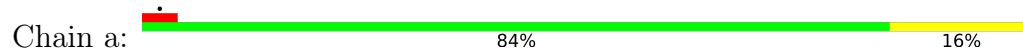
• Molecule 22: Complex I-AGGG



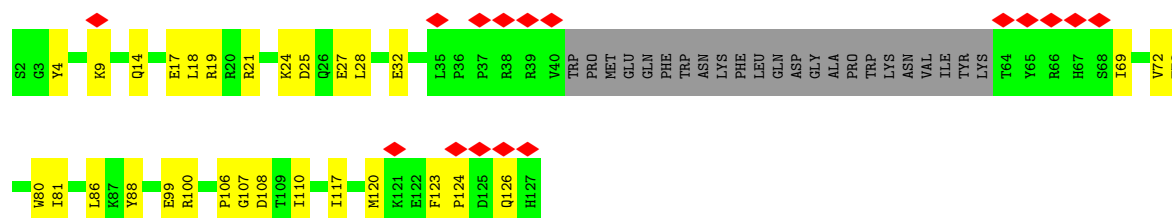
• Molecule 23: Complex I-B12



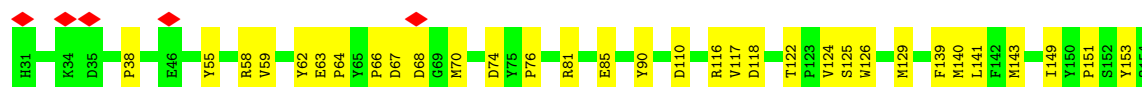
• Molecule 24: Complex I-SGDH



• Molecule 25: Complex I-B17

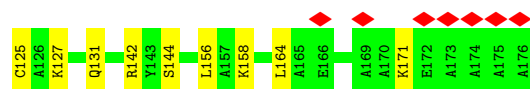
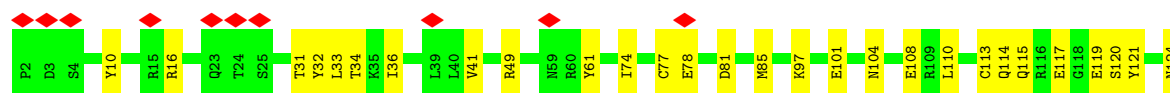
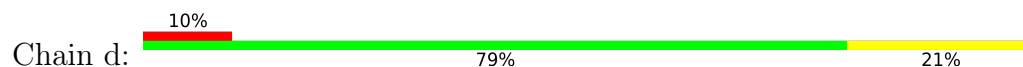


• Molecule 26: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial





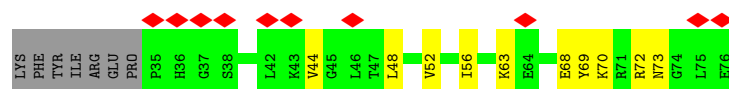
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



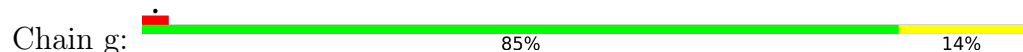
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



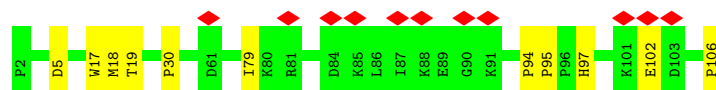
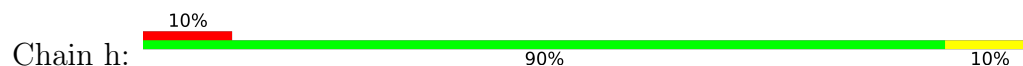
- Molecule 29: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



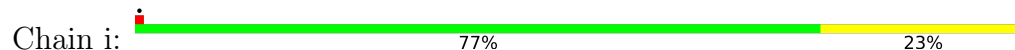
- Molecule 30: NADH dehydrogenase [ubiquinone] 1 subunit C2

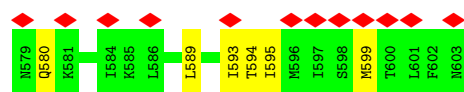


- Molecule 31: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

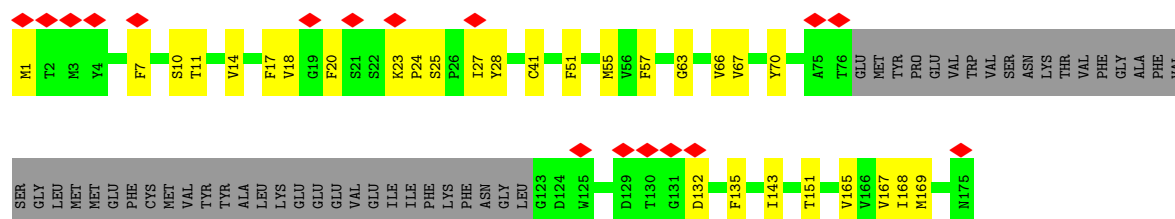


- Molecule 32: NADH-ubiquinone oxidoreductase chain 2

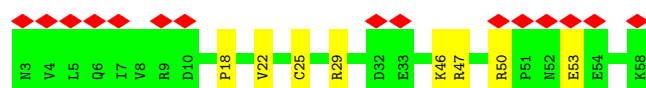
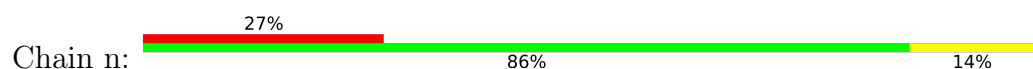




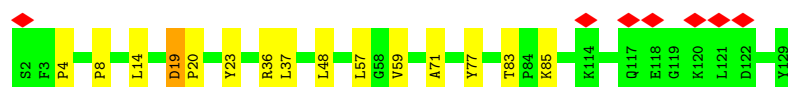
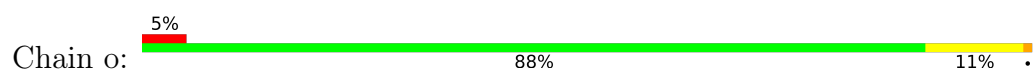
- Molecule 36: NADH-ubiquinone oxidoreductase chain 6



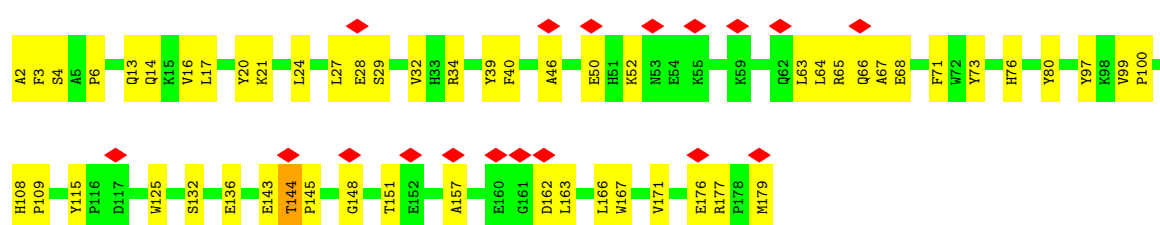
- Molecule 37: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



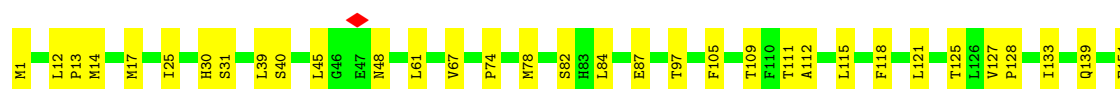
- Molecule 38: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

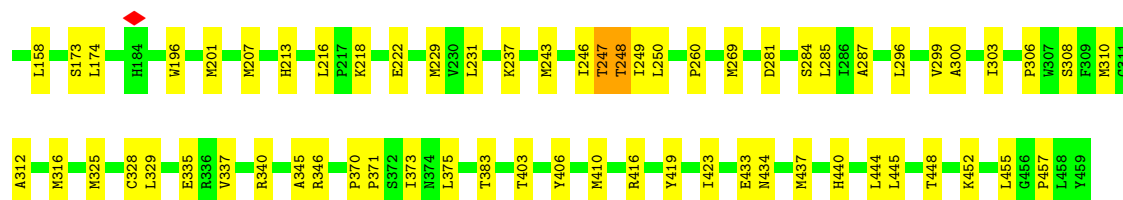


- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

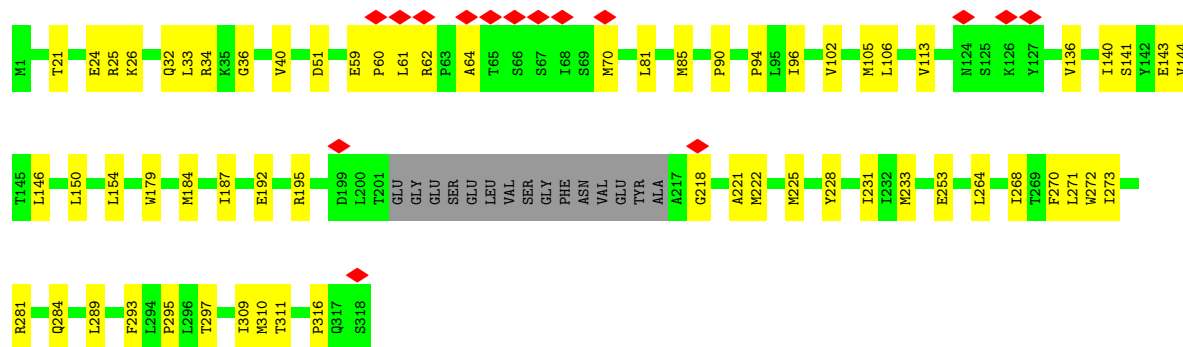
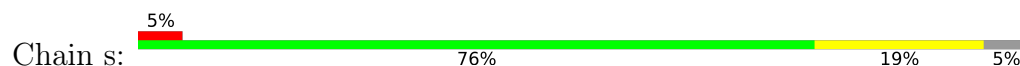


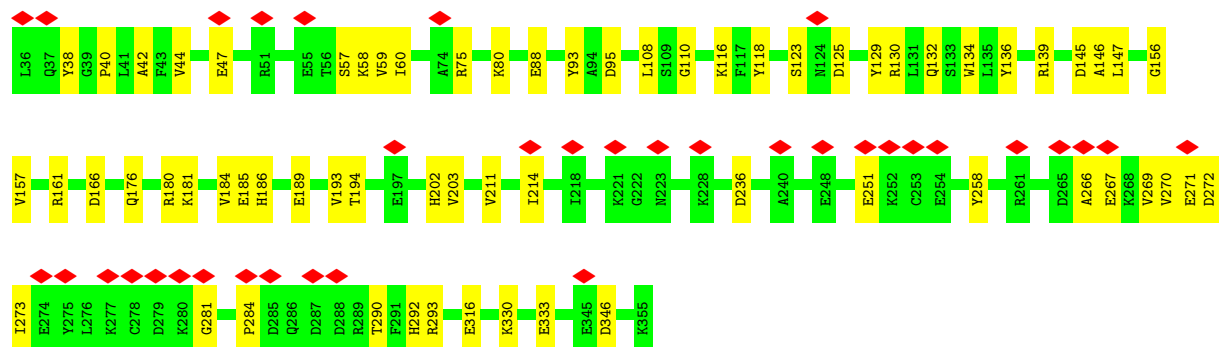
- Molecule 40: NADH-ubiquinone oxidoreductase chain 4





• Molecule 41: NADH-ubiquinone oxidoreductase chain 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32329	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.228	Depositor
Minimum map value	-0.105	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0298	Depositor
Map size ($\text{\AA}$)	333.7616, 333.7616, 333.7616	wwPDB
Map dimensions	304, 304, 304	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0979, 1.0979, 1.0979	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PLX, UQ, ADP, ZN, FES, 2MR, FMN, 8Q1, CDL, NDP, SF4, PEE, NAI

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	0.13	0/3393	0.35	0/4584
2	B	0.11	0/1443	0.28	0/1952
3	C	0.14	0/1275	0.41	2/1725 (0.1%)
4	E	0.11	0/995	0.28	0/1340
5	F	0.12	0/702	0.33	0/945
6	G	0.18	0/705	0.44	0/956
6	X	0.11	0/708	0.31	0/959
7	H	0.12	0/929	0.35	0/1258
8	I	0.14	0/798	0.37	0/1079
9	J	0.13	0/2411	0.34	2/3254 (0.1%)
10	K	0.09	0/365	0.27	0/493
11	L	0.10	0/1039	0.28	0/1403
12	M	0.11	0/5384	0.31	0/7295
13	N	0.10	0/1245	0.29	0/1694
14	O	0.12	0/1711	0.36	0/2328
15	P	0.12	0/1789	0.33	0/2436
16	Q	0.19	0/3451	0.49	6/4672 (0.1%)
17	S	0.15	0/582	0.37	0/783
18	T	0.08	0/755	0.25	0/1018
19	U	0.11	0/664	0.34	0/912
20	V	0.21	0/1030	0.49	2/1397 (0.1%)
21	W	0.13	0/1204	0.28	0/1624
22	Y	0.13	0/623	0.32	0/853
23	Z	0.10	0/692	0.33	0/935
24	a	0.12	0/1199	0.34	0/1623
25	b	0.14	0/895	0.45	0/1219
26	c	0.15	0/1371	0.35	0/1875
27	d	0.19	0/1494	0.44	2/2015 (0.1%)
28	e	0.16	0/916	0.46	0/1246
29	f	0.14	0/350	0.34	0/473
30	g	0.11	0/1031	0.26	0/1394
31	h	0.12	0/889	0.30	0/1190

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	i	0.14	0/2773	0.33	0/3768
33	j	0.17	0/819	0.42	0/1117
34	k	0.16	0/759	0.36	0/1029
35	l	0.15	0/4909	0.39	2/6677 (0.0%)
36	m	0.15	0/970	0.40	0/1316
37	n	0.18	0/491	0.39	0/663
38	o	0.15	0/1088	0.45	2/1476 (0.1%)
39	p	0.15	0/1590	0.49	7/2155 (0.3%)
40	r	0.15	0/3723	0.36	2/5078 (0.0%)
41	s	0.15	0/2464	0.36	0/3369
42	u	0.12	0/1436	0.34	0/1938
43	v	0.14	0/1052	0.38	0/1411
44	w	0.12	0/2642	0.32	0/3580
All	All	0.14	0/66754	0.37	27/90507 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	1

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	233	HIS	N-CA-C	10.10	122.29	111.28
16	Q	140	ASP	N-CA-C	-7.71	95.70	108.34
35	l	429	PHE	N-CA-C	6.75	118.72	111.36
16	Q	224	ALA	N-CA-C	6.61	118.56	111.36
35	l	432	LEU	N-CA-C	6.51	118.38	111.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	126	GLU	Peptide

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	3318	0	3280	73	0
2	B	1412	0	1363	30	0
3	C	1244	0	1250	31	0
4	E	971	0	975	16	0
5	F	691	0	704	16	0
6	G	693	0	671	44	0
6	X	696	0	680	19	0
7	H	910	0	950	19	0
8	I	780	0	808	17	0
9	J	2359	0	2402	41	0
10	K	355	0	329	5	0
11	L	1016	0	1016	18	0
12	M	5296	0	5326	85	0
13	N	1204	0	1162	18	0
14	O	1671	0	1673	31	0
15	P	1738	0	1693	26	0
16	Q	3377	0	3319	62	0
17	S	567	0	565	7	0
18	T	741	0	702	3	0
19	U	643	0	642	16	0
20	V	1009	0	1005	20	0
21	W	1173	0	1166	29	0
22	Y	597	0	537	12	0
23	Z	671	0	641	12	0
24	a	1165	0	1174	20	0
25	b	868	0	882	35	0
26	c	1315	0	1208	31	0
27	d	1461	0	1431	38	0
28	e	890	0	837	19	0
29	f	342	0	341	8	0
30	g	1000	0	994	13	0
31	h	867	0	871	12	0
32	i	2710	0	2874	60	0
33	j	800	0	855	23	0
34	k	748	0	799	19	0
35	l	4780	0	4923	147	0
36	m	948	0	960	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	n	479	0	486	6	0
38	o	1058	0	1068	12	0
39	p	1534	0	1470	46	0
40	r	3631	0	3839	69	0
41	s	2394	0	2508	55	0
42	u	1398	0	1378	31	0
43	v	1028	0	980	41	0
44	w	2582	0	2531	40	0
45	A	8	0	0	1	0
45	B	16	0	0	0	0
45	C	8	0	0	1	0
45	M	16	0	0	0	0
46	A	31	0	19	7	0
47	A	44	0	27	6	0
48	C	52	0	88	5	0
48	a	52	0	88	2	0
48	i	52	0	88	5	0
48	j	52	0	88	3	0
48	l	52	0	88	5	0
48	r	52	0	88	3	0
49	G	35	0	0	0	0
49	X	35	0	0	8	0
50	J	48	0	24	1	0
51	M	4	0	0	0	0
51	O	4	0	0	0	0
52	M	1	0	0	0	0
53	N	51	0	46	0	0
53	V	71	0	92	7	0
53	a	91	0	132	4	0
53	i	66	0	76	2	0
53	l	100	0	156	6	0
53	r	100	0	156	10	0
54	T	1	0	0	0	0
55	U	51	0	82	5	0
55	i	47	0	71	5	0
55	j	47	0	71	3	0
55	l	92	0	138	4	0
55	m	41	0	59	0	0
55	r	51	0	82	2	0
55	s	51	0	82	10	0
56	s	28	0	31	4	0
57	w	27	0	11	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	66607	0	67151	1226	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 9.

The worst 5 of 1226 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)
6:X:112:SER:CB	49:X:201:8Q1:O1	1.66	1.42
50:J:401:NDP:O4D	50:J:401:NDP:C4D	1.69	1.12
47:A:503:NAI:C1B	47:A:503:NAI:O4B	1.63	1.07
39:p:64:LEU:O	39:p:68:GLU:HG2	1.55	1.05
16:Q:235:ASP:HB2	16:Q:356:ILE:HD13	1.40	1.01

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 PDB entries followed by that with respect to all EM entries.

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	429/433 (99%)	415 (97%)	14 (3%)	0	100	100
2	B	174/176 (99%)	172 (99%)	2 (1%)	0	100	100
3	C	154/156 (99%)	148 (96%)	6 (4%)	0	100	100
4	E	113/115 (98%)	110 (97%)	3 (3%)	0	100	100
5	F	84/86 (98%)	80 (95%)	4 (5%)	0	100	100
6	G	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
6	X	86/88 (98%)	83 (96%)	3 (4%)	0	100	100
7	H	110/112 (98%)	101 (92%)	9 (8%)	0	100	100
8	I	93/112 (83%)	83 (89%)	10 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	J	289/342 (84%)	277 (96%)	11 (4%)	1 (0%)	36	68
10	K	40/43 (93%)	40 (100%)	0	0	100	100
11	L	123/125 (98%)	119 (97%)	4 (3%)	0	100	100
12	M	688/690 (100%)	665 (97%)	22 (3%)	1 (0%)	48	79
13	N	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
14	O	215/217 (99%)	208 (97%)	7 (3%)	0	100	100
15	P	206/208 (99%)	195 (95%)	11 (5%)	0	100	100
16	Q	412/430 (96%)	399 (97%)	12 (3%)	1 (0%)	43	73
17	S	68/70 (97%)	65 (96%)	3 (4%)	0	100	100
18	T	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
19	U	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
20	V	138/140 (99%)	131 (95%)	6 (4%)	1 (1%)	18	52
21	W	140/142 (99%)	136 (97%)	4 (3%)	0	100	100
22	Y	68/70 (97%)	64 (94%)	4 (6%)	0	100	100
23	Z	82/84 (98%)	79 (96%)	3 (4%)	0	100	100
24	a	138/140 (99%)	135 (98%)	3 (2%)	0	100	100
25	b	99/126 (79%)	94 (95%)	4 (4%)	1 (1%)	12	45
26	c	154/156 (99%)	144 (94%)	8 (5%)	2 (1%)	9	40
27	d	173/175 (99%)	172 (99%)	1 (1%)	0	100	100
28	e	105/107 (98%)	101 (96%)	4 (4%)	0	100	100
29	f	40/49 (82%)	39 (98%)	1 (2%)	0	100	100
30	g	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
31	h	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
32	i	345/347 (99%)	331 (96%)	14 (4%)	0	100	100
33	j	95/115 (83%)	89 (94%)	6 (6%)	0	100	100
34	k	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
35	l	601/603 (100%)	573 (95%)	28 (5%)	0	100	100
36	m	125/175 (71%)	111 (89%)	14 (11%)	0	100	100
37	n	54/56 (96%)	54 (100%)	0	0	100	100
38	o	126/128 (98%)	121 (96%)	5 (4%)	0	100	100
39	p	176/178 (99%)	168 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	r	457/459 (100%)	440 (96%)	16 (4%)	1 (0%)	43	73
41	s	299/318 (94%)	291 (97%)	8 (3%)	0	100	100
42	u	169/171 (99%)	165 (98%)	4 (2%)	0	100	100
43	v	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
44	w	318/320 (99%)	304 (96%)	14 (4%)	0	100	100
All	All	8029/8322 (96%)	7715 (96%)	306 (4%)	8 (0%)	49	79

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	Q	235	ASP
40	r	248	THR
12	M	283	GLU
26	c	64	PRO
25	b	126	GLN

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 PDB entries followed by that with respect to all EM entries.

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	345/346 (100%)	343 (99%)	2 (1%)	78	84
2	B	151/151 (100%)	151 (100%)	0	100	100
3	C	131/132 (99%)	131 (100%)	0	100	100
4	E	107/107 (100%)	107 (100%)	0	100	100
5	F	76/76 (100%)	75 (99%)	1 (1%)	61	78
6	G	76/81 (94%)	76 (100%)	0	100	100
6	X	77/81 (95%)	77 (100%)	0	100	100
7	H	99/99 (100%)	98 (99%)	1 (1%)	68	80
8	I	87/97 (90%)	85 (98%)	2 (2%)	44	70
9	J	255/296 (86%)	255 (100%)	0	100	100
10	K	41/42 (98%)	40 (98%)	1 (2%)	43	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	L	113/113 (100%)	113 (100%)	0	100	100
12	M	580/580 (100%)	580 (100%)	0	100	100
13	N	130/130 (100%)	130 (100%)	0	100	100
14	O	183/183 (100%)	183 (100%)	0	100	100
15	P	190/190 (100%)	190 (100%)	0	100	100
16	Q	361/370 (98%)	361 (100%)	0	100	100
17	S	58/58 (100%)	58 (100%)	0	100	100
18	T	79/79 (100%)	79 (100%)	0	100	100
19	U	69/69 (100%)	69 (100%)	0	100	100
20	V	99/101 (98%)	98 (99%)	1 (1%)	68	80
21	W	123/123 (100%)	123 (100%)	0	100	100
22	Y	62/63 (98%)	62 (100%)	0	100	100
23	Z	64/65 (98%)	64 (100%)	0	100	100
24	a	122/122 (100%)	122 (100%)	0	100	100
25	b	95/119 (80%)	95 (100%)	0	100	100
26	c	141/141 (100%)	139 (99%)	2 (1%)	59	77
27	d	155/155 (100%)	155 (100%)	0	100	100
28	e	99/99 (100%)	99 (100%)	0	100	100
29	f	35/45 (78%)	35 (100%)	0	100	100
30	g	108/109 (99%)	108 (100%)	0	100	100
31	h	93/93 (100%)	93 (100%)	0	100	100
32	i	311/311 (100%)	310 (100%)	1 (0%)	86	88
33	j	88/100 (88%)	88 (100%)	0	100	100
34	k	85/85 (100%)	85 (100%)	0	100	100
35	l	534/537 (99%)	530 (99%)	4 (1%)	76	83
36	m	98/141 (70%)	98 (100%)	0	100	100
37	n	53/53 (100%)	53 (100%)	0	100	100
38	o	112/113 (99%)	112 (100%)	0	100	100
39	p	159/159 (100%)	159 (100%)	0	100	100
40	r	410/410 (100%)	410 (100%)	0	100	100
41	s	263/275 (96%)	263 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	u	153/153 (100%)	153 (100%)	0	100	100
43	v	104/111 (94%)	104 (100%)	0	100	100
44	w	281/283 (99%)	281 (100%)	0	100	100
All	All	7055/7246 (97%)	7040 (100%)	15 (0%)	85	89

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	V	107	SER
35	l	488	MET
26	c	59	VAL
35	l	575	ILE
35	l	177	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
35	l	400	ASN
41	s	47	GLN
35	l	471	ASN
39	p	13	GLN
14	O	41	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
16	2MR	Q	118	16	10,12,13	1.98	1 (10%)	5,13,15	6.06	3 (60%)

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
16	2MR	Q	118	16	-	2/10/13/15	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	Q	118	2MR	CZ-NE	5.69	1.46	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	Q	118	2MR	NE-CZ-NH2	12.38	130.82	119.48
16	Q	118	2MR	CD-NE-CZ	4.49	131.82	123.41
16	Q	118	2MR	CQ2-NH2-CZ	3.06	130.62	123.86

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
16	Q	118	2MR	NE-CD-CG-CB
16	Q	118	2MR	CA-CB-CG-CD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
16	Q	118	2MR	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 37 ligands modelled in this entry, 2 are monoatomic - leaving 35 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
53	CDL	r	503	-	99,99,99	1.09	8 (8%)	105,111,111	0.85	4 (3%)
48	PLX	j	202	-	51,51,51	1.15	4 (7%)	55,59,59	0.60	1 (1%)
48	PLX	a	202	-	51,51,51	1.15	4 (7%)	55,59,59	0.60	1 (1%)
55	PEE	l	703	-	45,45,50	1.23	6 (13%)	48,50,55	0.98	2 (4%)
48	PLX	C	302	-	51,51,51	1.15	4 (7%)	55,59,59	0.61	1 (1%)
55	PEE	r	501	-	50,50,50	1.16	6 (12%)	53,55,55	0.95	2 (3%)
45	SF4	M	802	12	0,12,12	-	-	-	-	-
49	8Q1	G	201	6	31,34,34	1.72	6 (19%)	40,43,43	1.56	6 (15%)
53	CDL	N	201	-	50,50,99	1.41	8 (16%)	56,62,111	1.12	4 (7%)
57	ADP	w	401	-	27,29,29	2.96	8 (29%)	42,45,45	2.01	10 (23%)
48	PLX	r	502	-	51,51,51	1.14	4 (7%)	55,59,59	0.61	1 (1%)
50	NDP	J	401	-	49,52,52	4.40	23 (46%)	66,80,80	2.18	14 (21%)
45	SF4	A	501	1	0,12,12	-	-	-	-	-
51	FES	M	803	12	0,4,4	-	-	-	-	-
47	NAI	A	503	-	45,48,48	3.91	20 (44%)	60,73,73	1.77	12 (20%)
53	CDL	V	201	-	70,70,99	1.22	8 (11%)	76,82,111	0.96	4 (5%)
55	PEE	s	401	-	50,50,50	1.15	6 (12%)	53,55,55	1.01	2 (3%)
46	FMN	A	502	-	33,33,33	1.08	2 (6%)	48,50,50	1.21	8 (16%)
55	PEE	i	403	-	46,46,50	1.21	6 (13%)	49,51,55	1.00	2 (4%)
53	CDL	l	702	-	99,99,99	1.09	9 (9%)	105,111,111	0.84	4 (3%)
49	8Q1	X	201	-	31,34,34	1.70	6 (19%)	40,43,43	1.53	6 (15%)
45	SF4	C	301	3,16	0,12,12	-	-	-	-	-
53	CDL	i	401	-	65,65,99	1.28	9 (13%)	71,77,111	1.01	4 (5%)
45	SF4	M	801	12	0,12,12	-	-	-	-	-
45	SF4	B	301	2	0,12,12	-	-	-	-	-
53	CDL	a	201	-	90,90,99	1.13	8 (8%)	96,102,111	0.92	4 (4%)
55	PEE	l	704	-	45,45,50	1.22	6 (13%)	48,50,55	0.97	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	UQ	s	402	-	28,28,63	3.28	7 (25%)	34,37,79	2.73	10 (29%)
48	PLX	i	402	-	51,51,51	1.14	3 (5%)	55,59,59	0.60	1 (1%)
55	PEE	m	201	-	40,40,50	1.15	5 (12%)	43,45,55	0.98	2 (4%)
55	PEE	U	101	-	50,50,50	1.16	6 (12%)	53,55,55	0.95	2 (3%)
51	FES	O	301	14	0,4,4	-	-	-	-	-
48	PLX	l	701	-	51,51,51	1.15	4 (7%)	55,59,59	0.58	1 (1%)
45	SF4	B	302	2	0,12,12	-	-	-	-	-
55	PEE	j	201	-	46,46,50	1.21	6 (13%)	49,51,55	0.96	2 (4%)

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
53	CDL	r	503	-	-	64/110/110/110	-
48	PLX	j	202	-	-	27/55/55/55	-
48	PLX	a	202	-	-	23/55/55/55	-
55	PEE	l	703	-	-	23/49/49/54	-
48	PLX	C	302	-	-	26/55/55/55	-
55	PEE	r	501	-	-	29/54/54/54	-
45	SF4	M	802	12	-	-	0/6/5/5
49	8Q1	G	201	6	-	19/41/41/41	-
53	CDL	N	201	-	-	35/61/61/110	-
57	ADP	w	401	-	-	4/16/32/32	0/3/3/3
48	PLX	r	502	-	-	27/55/55/55	-
50	NDP	J	401	-	-	14/34/77/77	0/4/5/5
45	SF4	A	501	1	-	-	0/6/5/5
53	CDL	V	201	-	-	51/81/81/110	-
47	NAI	A	503	-	-	10/29/72/72	0/5/5/5
51	FES	M	803	12	-	-	0/1/1/1
55	PEE	s	401	-	-	26/54/54/54	-
46	FMN	A	502	-	-	2/18/18/18	0/3/3/3
55	PEE	i	403	-	-	24/50/50/54	-
53	CDL	l	702	-	-	60/110/110/110	-
49	8Q1	X	201	-	-	19/41/41/41	-
45	SF4	C	301	3,16	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
53	CDL	i	401	-	-	43/76/76/110	-
53	CDL	a	201	-	-	45/101/101/110	-
55	PEE	l	704	-	-	21/49/49/54	-
56	UQ	s	402	-	-	7/21/45/87	0/1/1/1
45	SF4	B	301	2	-	-	0/6/5/5
45	SF4	M	801	12	-	-	0/6/5/5
48	PLX	i	402	-	-	25/55/55/55	-
55	PEE	m	201	-	-	24/44/44/54	-
55	PEE	U	101	-	-	23/54/54/54	-
51	FES	O	301	14	-	-	0/1/1/1
48	PLX	l	701	-	-	38/55/55/55	-
45	SF4	B	302	2	-	-	0/6/5/5
55	PEE	j	201	-	-	25/50/50/54	-

The worst 5 of 192 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	J	401	NDP	C3B-C2B	-12.79	1.24	1.52
50	J	401	NDP	C6N-C5N	12.41	1.55	1.33
50	J	401	NDP	O4D-C4D	10.75	1.69	1.45
47	A	503	NAI	C3D-C4D	-10.20	1.26	1.53
50	J	401	NDP	C3D-C4D	-9.86	1.27	1.53

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	s	402	UQ	C7-C8-C9	-9.37	111.19	126.79
50	J	401	NDP	C3N-C2N-N1N	-7.49	112.41	123.10
50	J	401	NDP	C1D-N1N-C2N	-7.30	108.96	121.11
49	G	201	8Q1	C6-C1-S44	5.96	120.39	113.46
56	s	402	UQ	C12-C13-C14	-5.92	113.39	127.66

There are no chirality outliers.

5 of 734 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
46	A	502	FMN	N10-C1'-C2'-O2'
46	A	502	FMN	N10-C1'-C2'-C3'
47	A	503	NAI	C5B-O5B-PA-O3

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Mol	Chain	Res	Type	Atoms
48	C	302	PLX	O7-C6-C7-C8
48	C	302	PLX	C3-O4-P1-O1

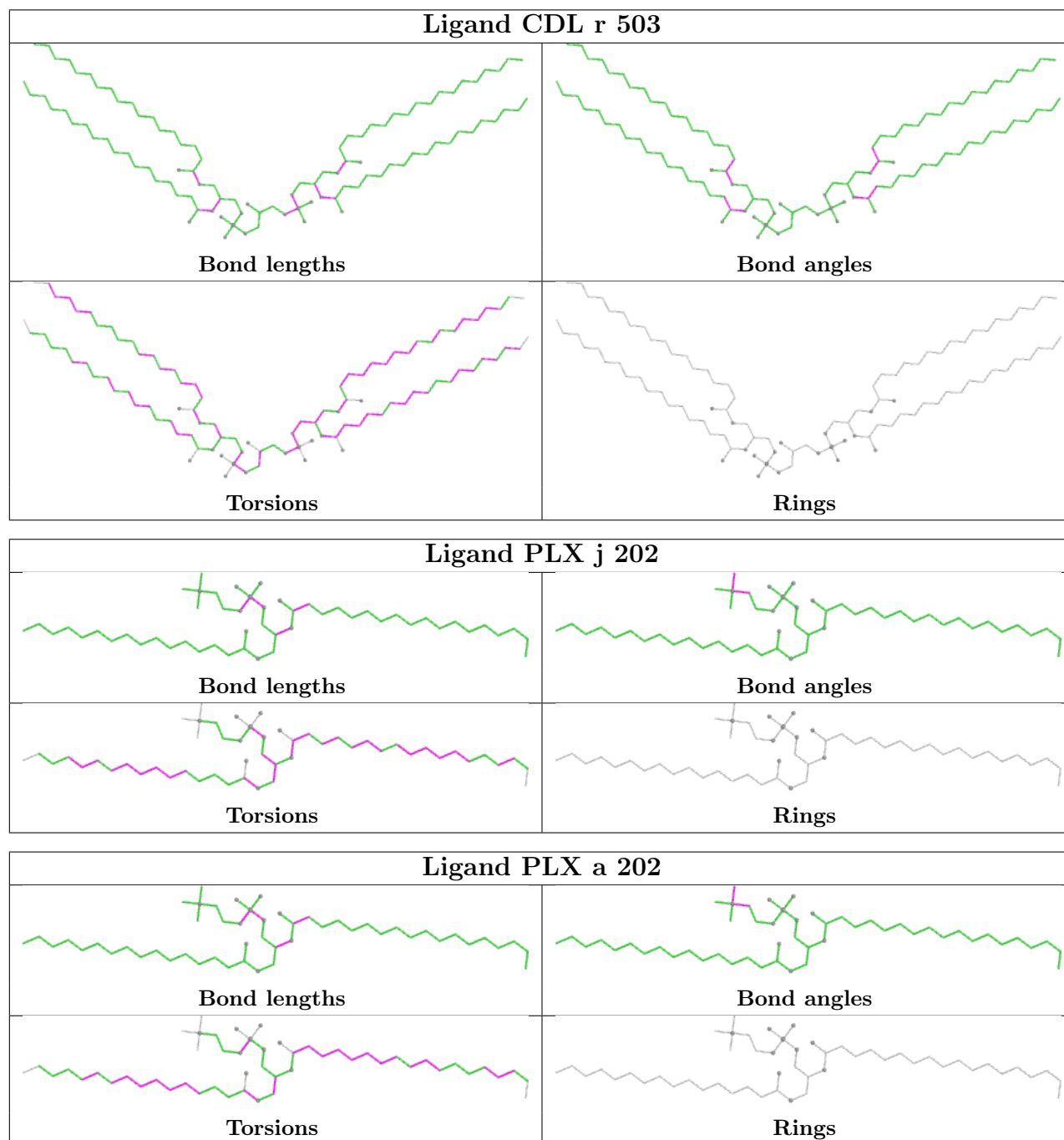
There are no ring outliers.

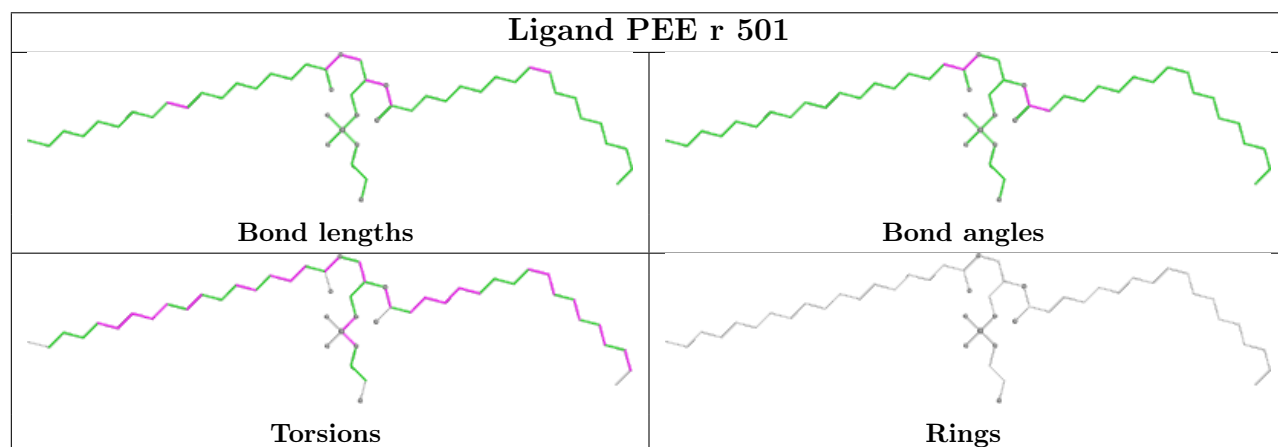
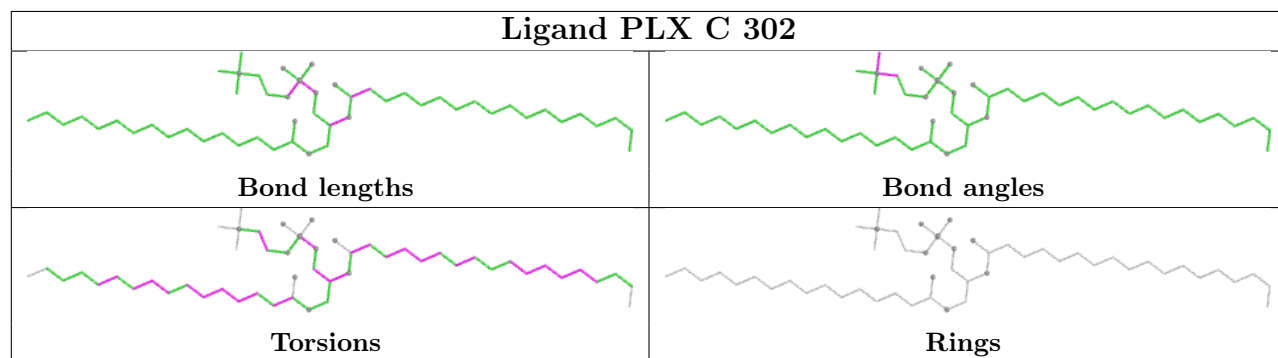
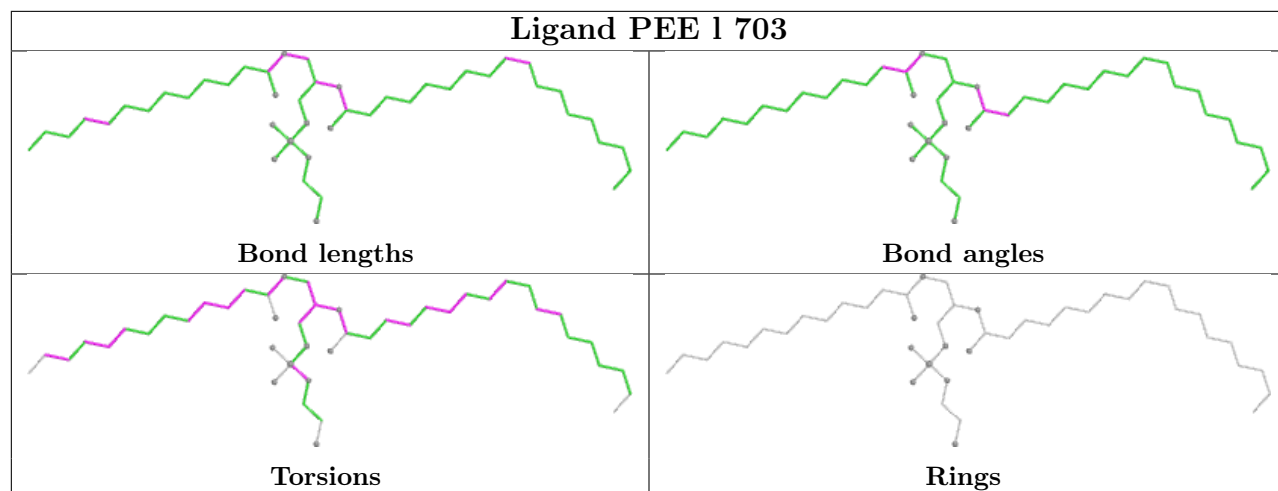
26 monomers are involved in 106 short contacts:

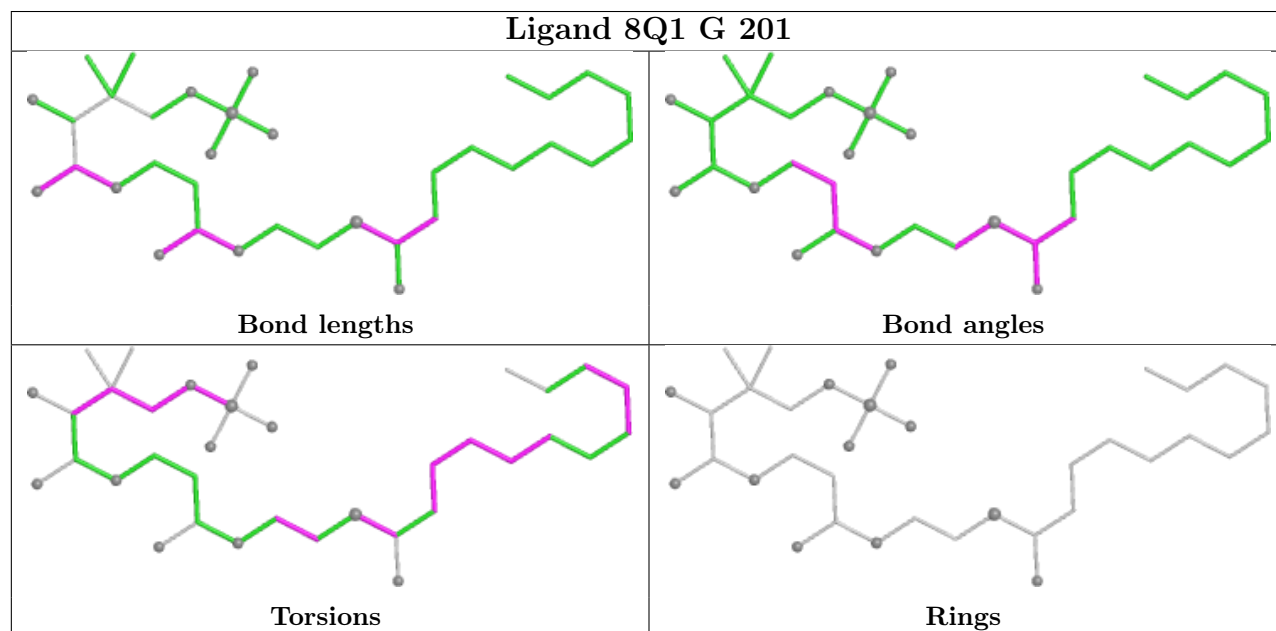
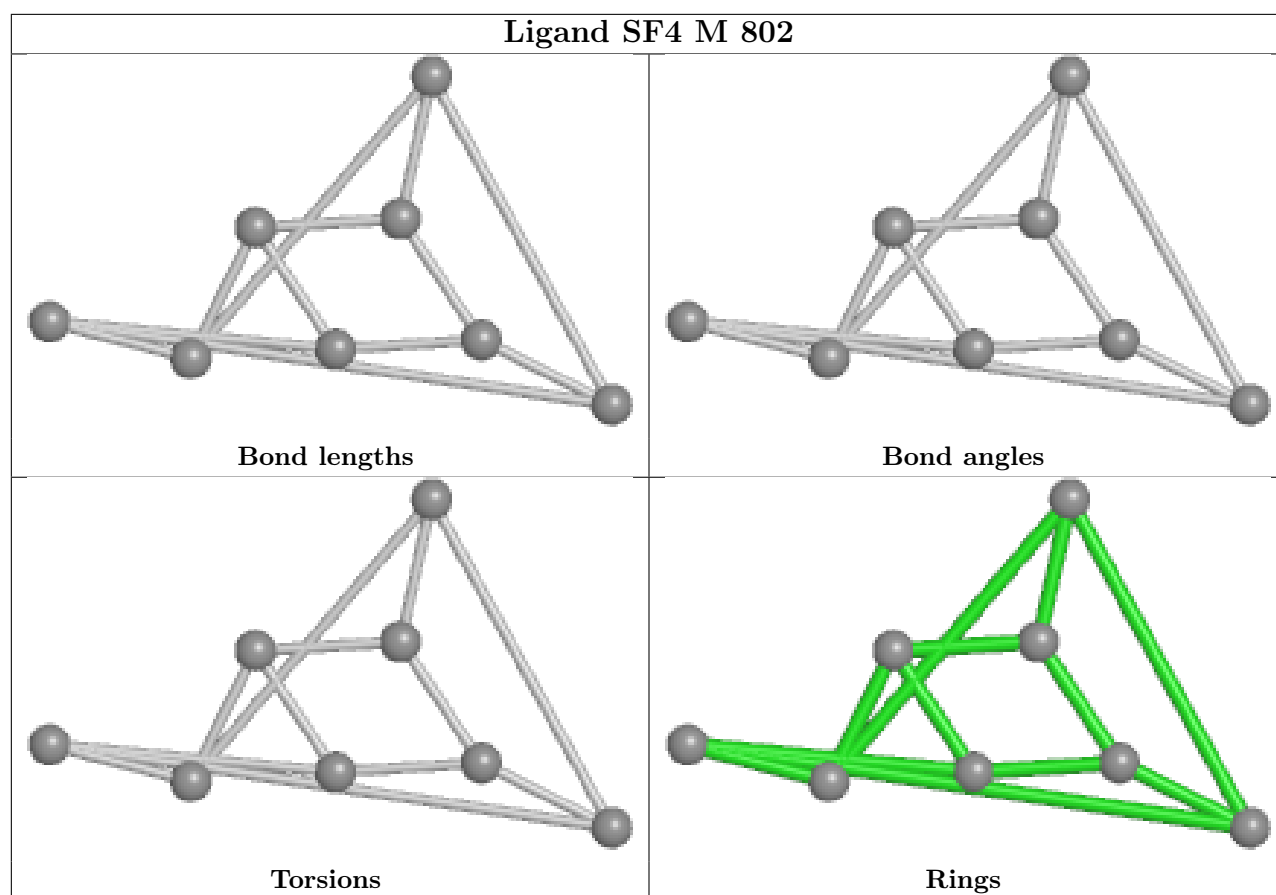
Mol	Chain	Res	Type	Clashes	Symm-Clashes
53	r	503	CDL	10	0
48	j	202	PLX	3	0
48	a	202	PLX	2	0
55	l	703	PEE	2	0
48	C	302	PLX	5	0
55	r	501	PEE	2	0
57	w	401	ADP	2	0
48	r	502	PLX	3	0
50	J	401	NDP	1	0
45	A	501	SF4	1	0
47	A	503	NAI	6	0
53	V	201	CDL	7	0
55	s	401	PEE	10	0
46	A	502	FMN	7	0
55	i	403	PEE	5	0
53	l	702	CDL	6	0
49	X	201	8Q1	8	0
45	C	301	SF4	1	0
53	i	401	CDL	2	0
53	a	201	CDL	4	0
55	l	704	PEE	2	0
56	s	402	UQ	4	0
48	i	402	PLX	5	0
55	U	101	PEE	5	0
48	l	701	PLX	5	0
55	j	201	PEE	3	0

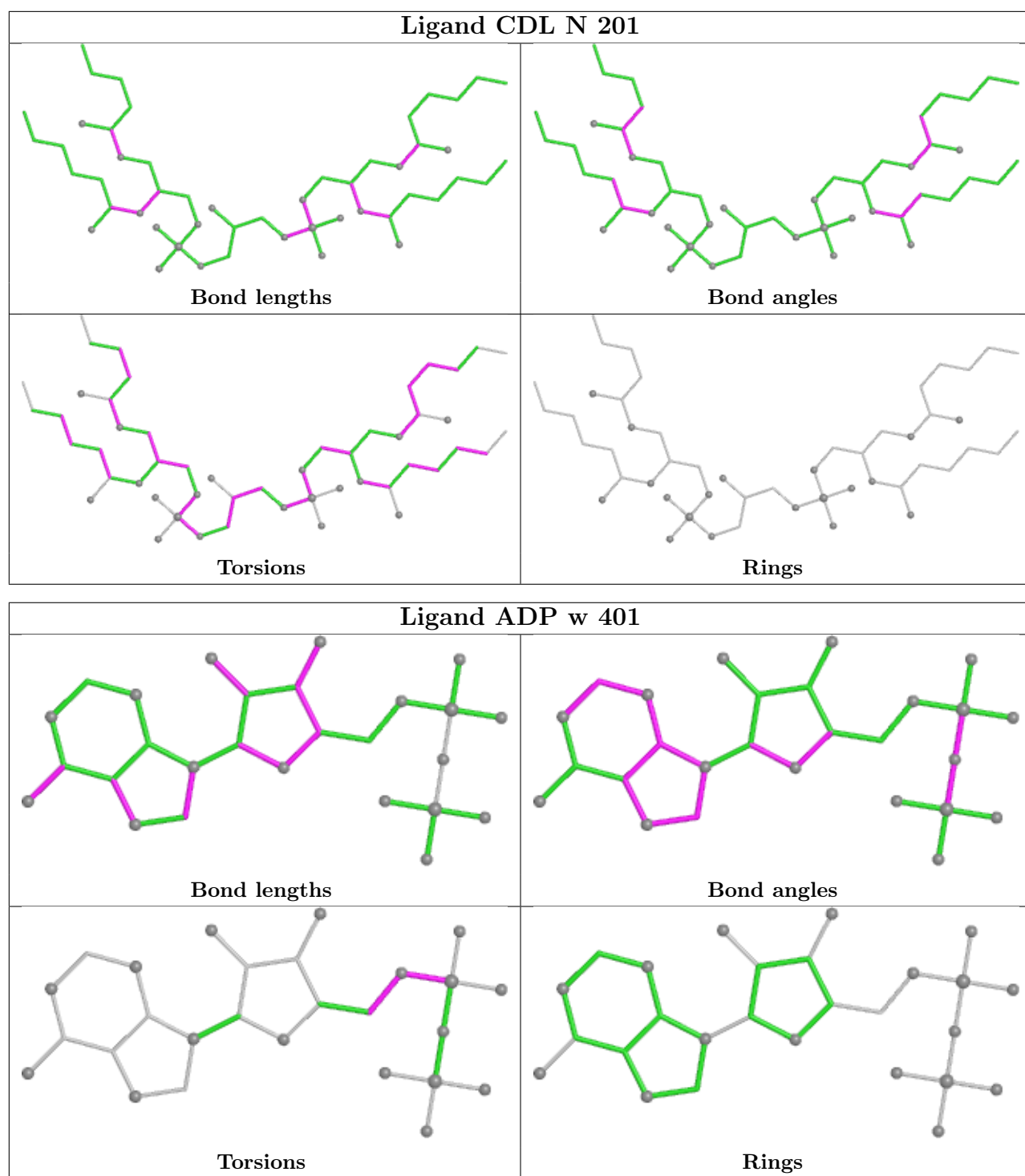
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

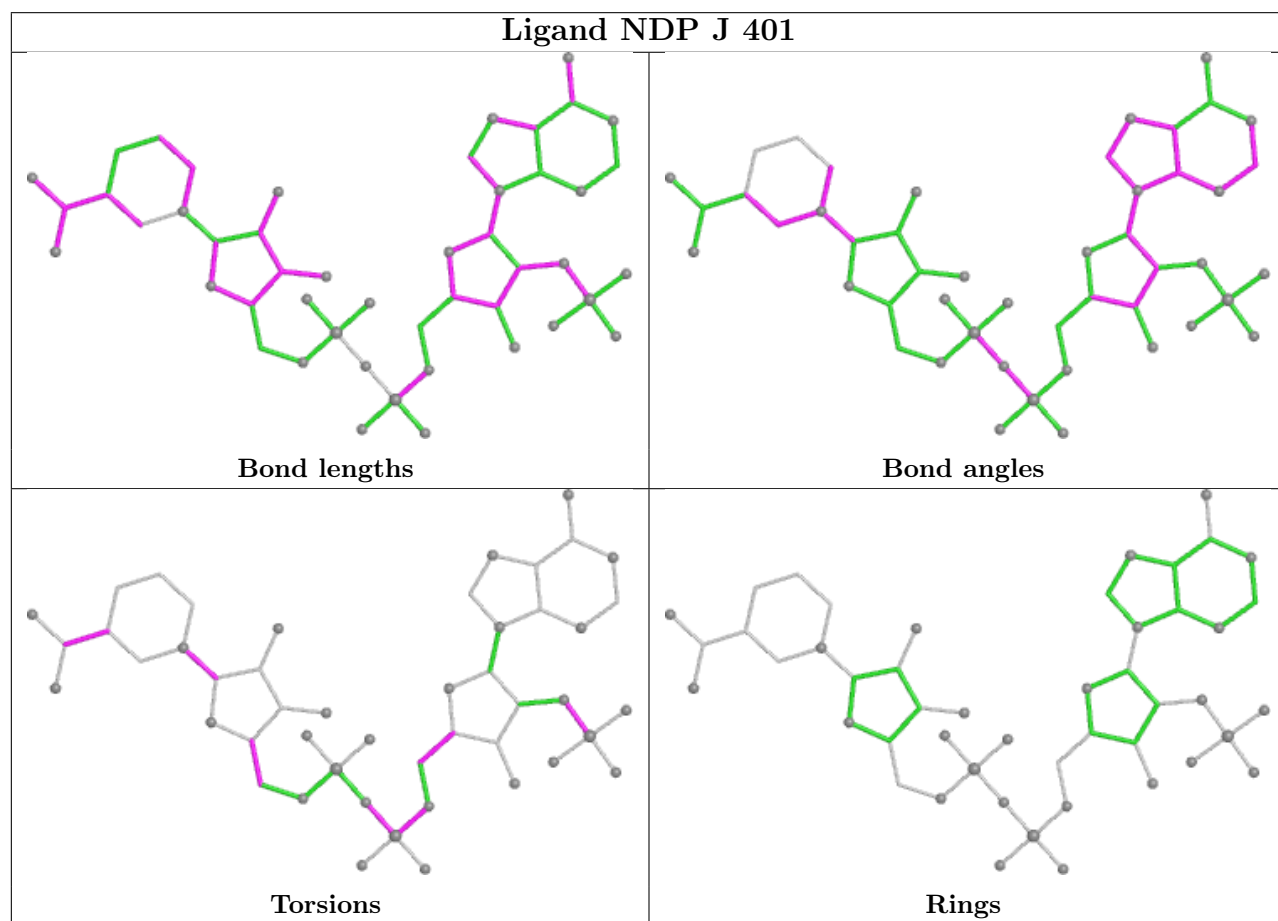
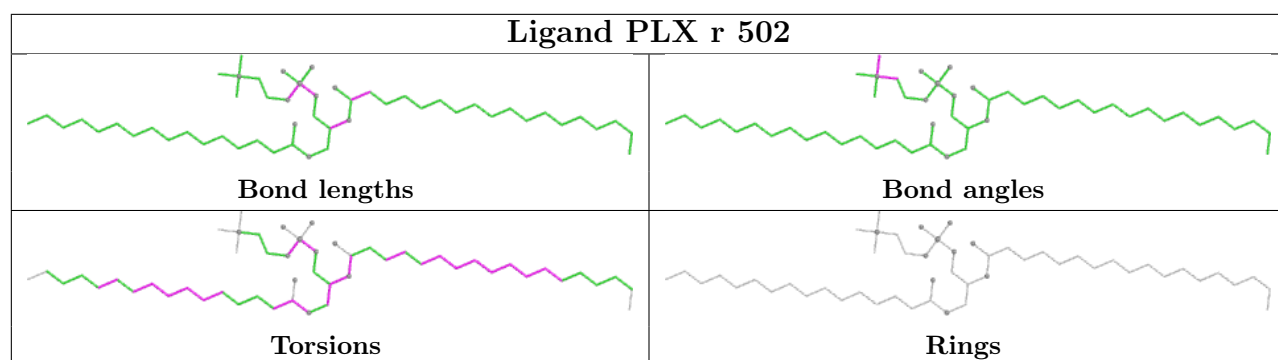
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

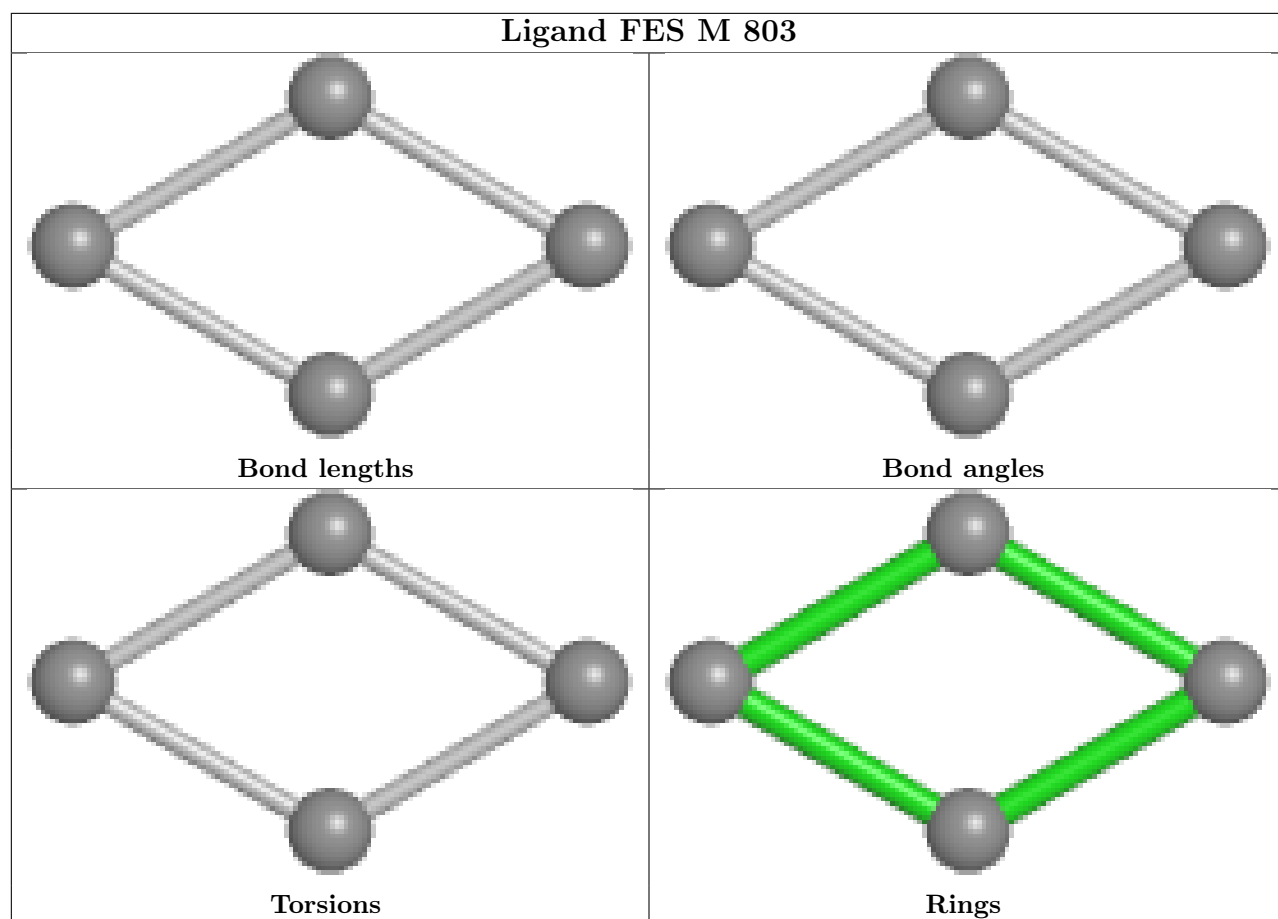
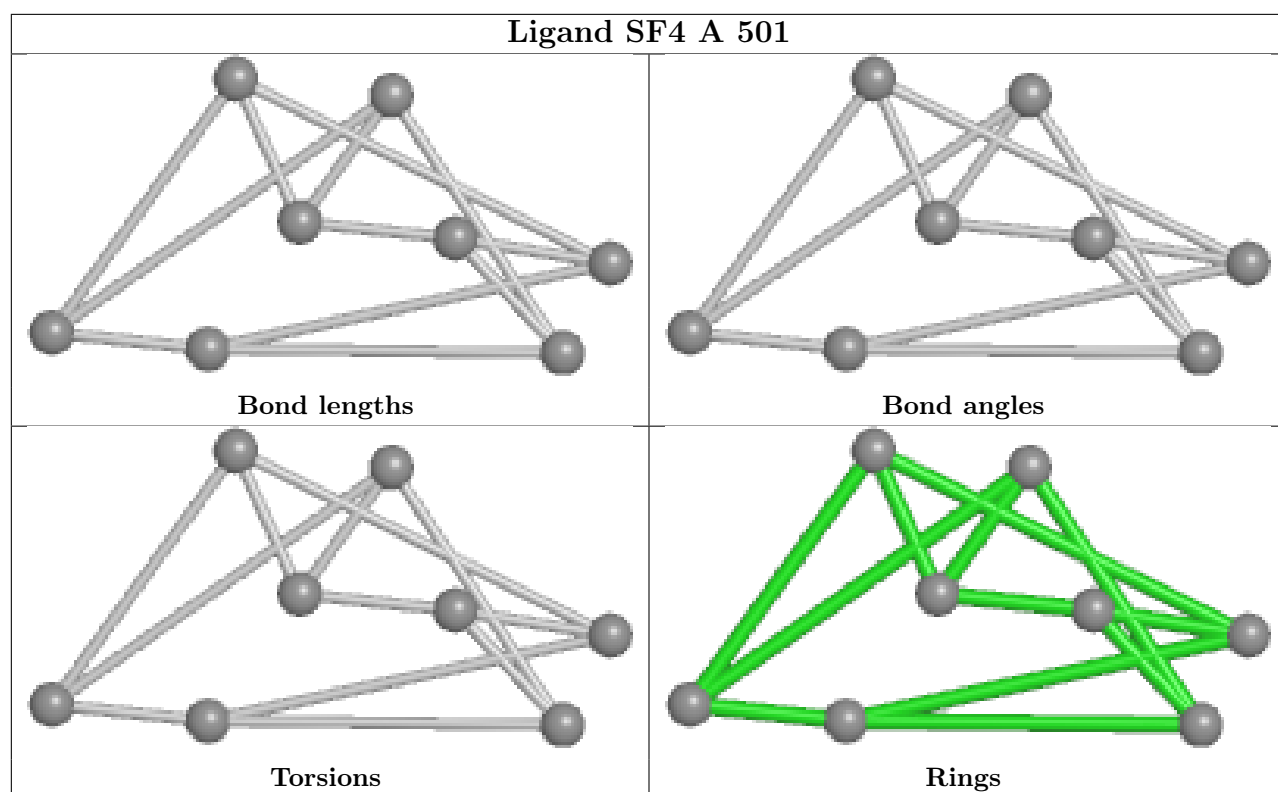


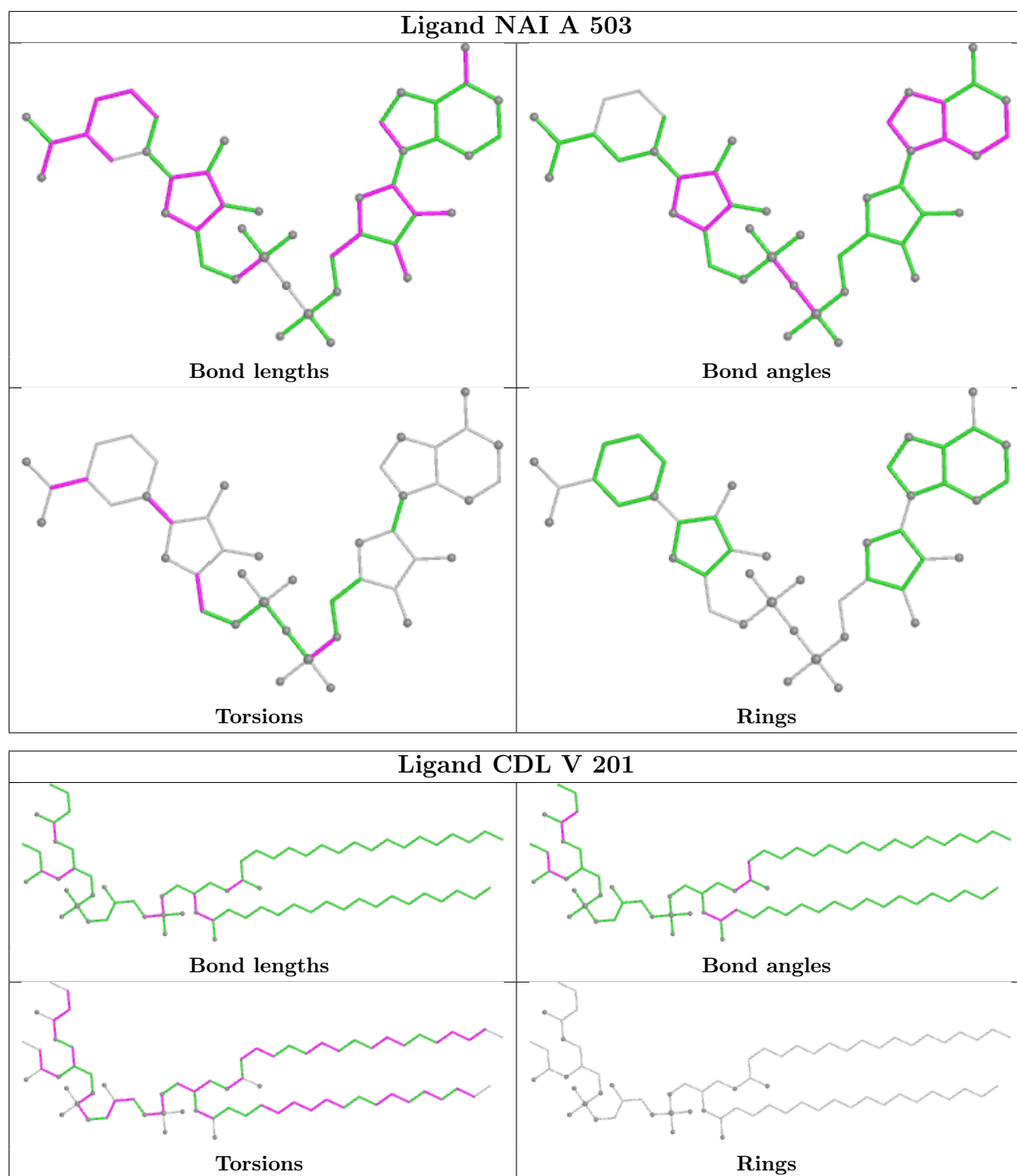


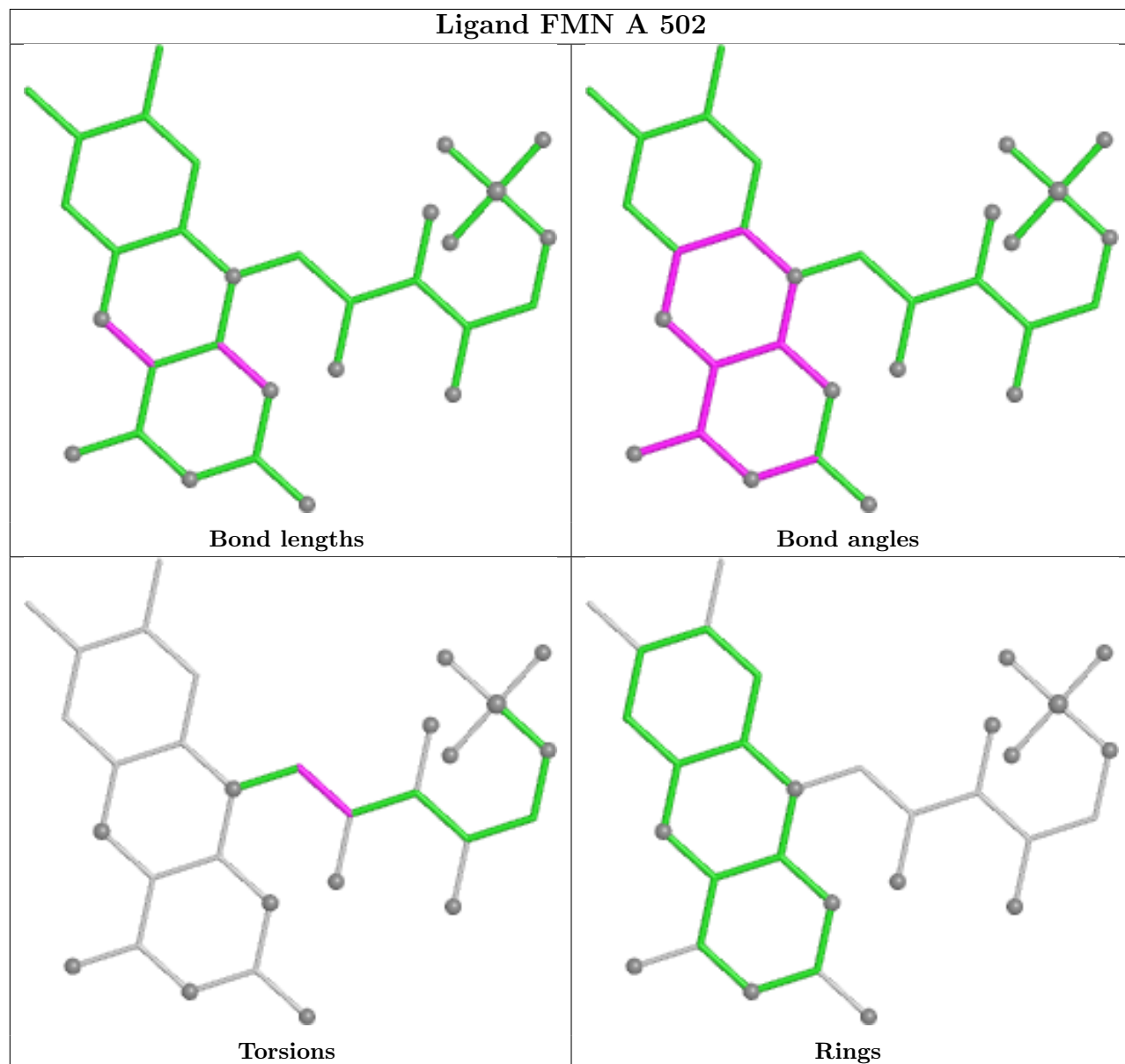
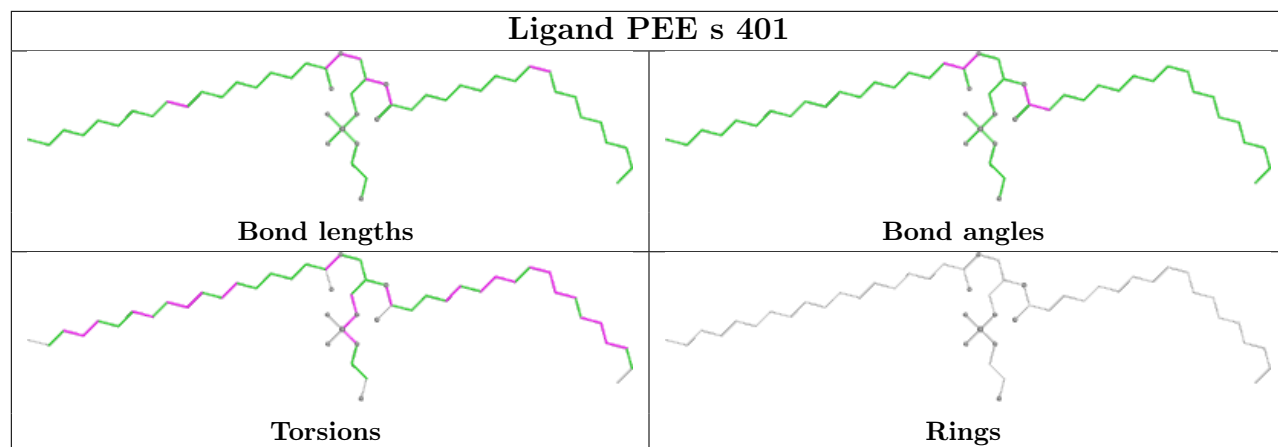


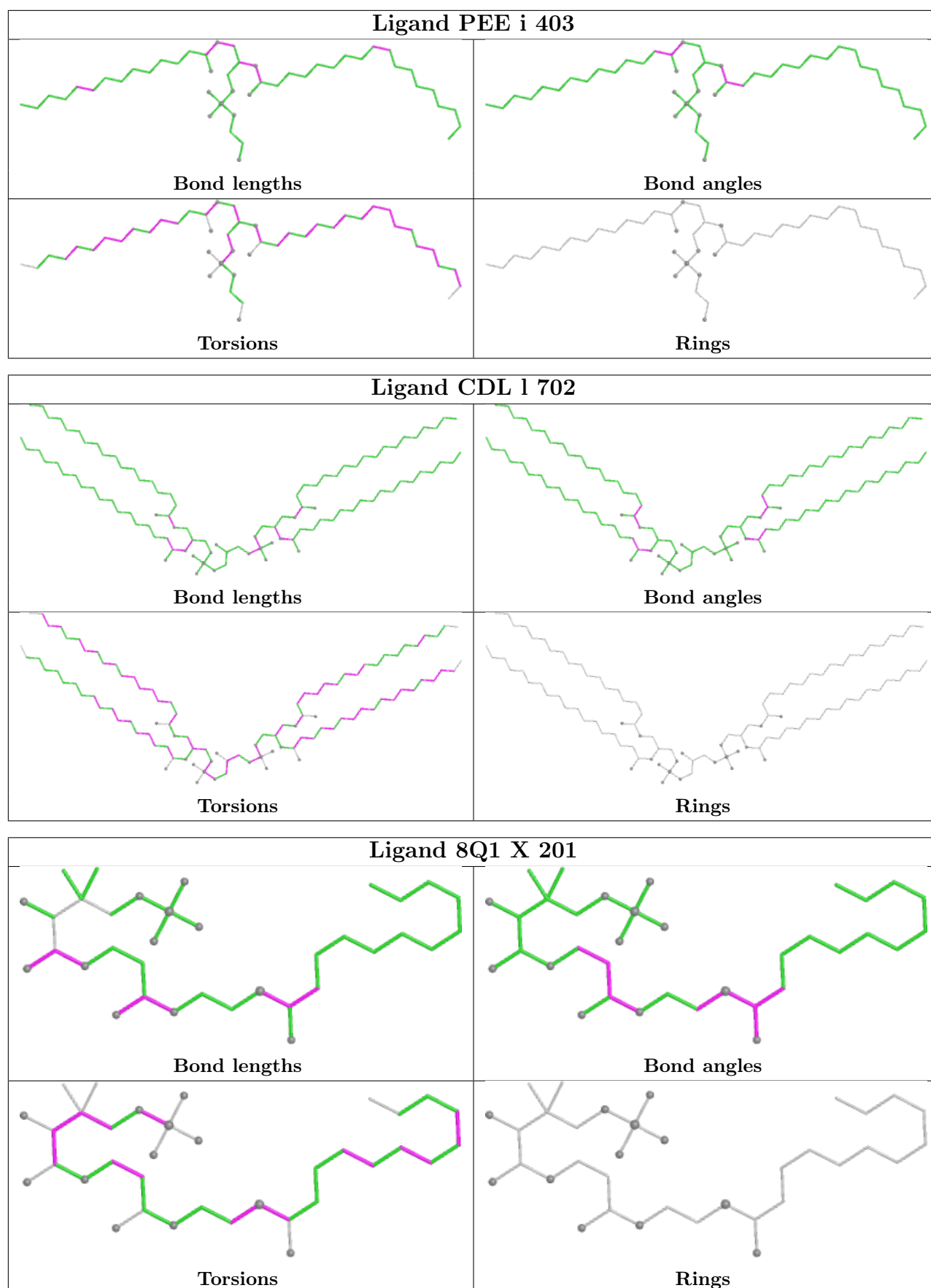


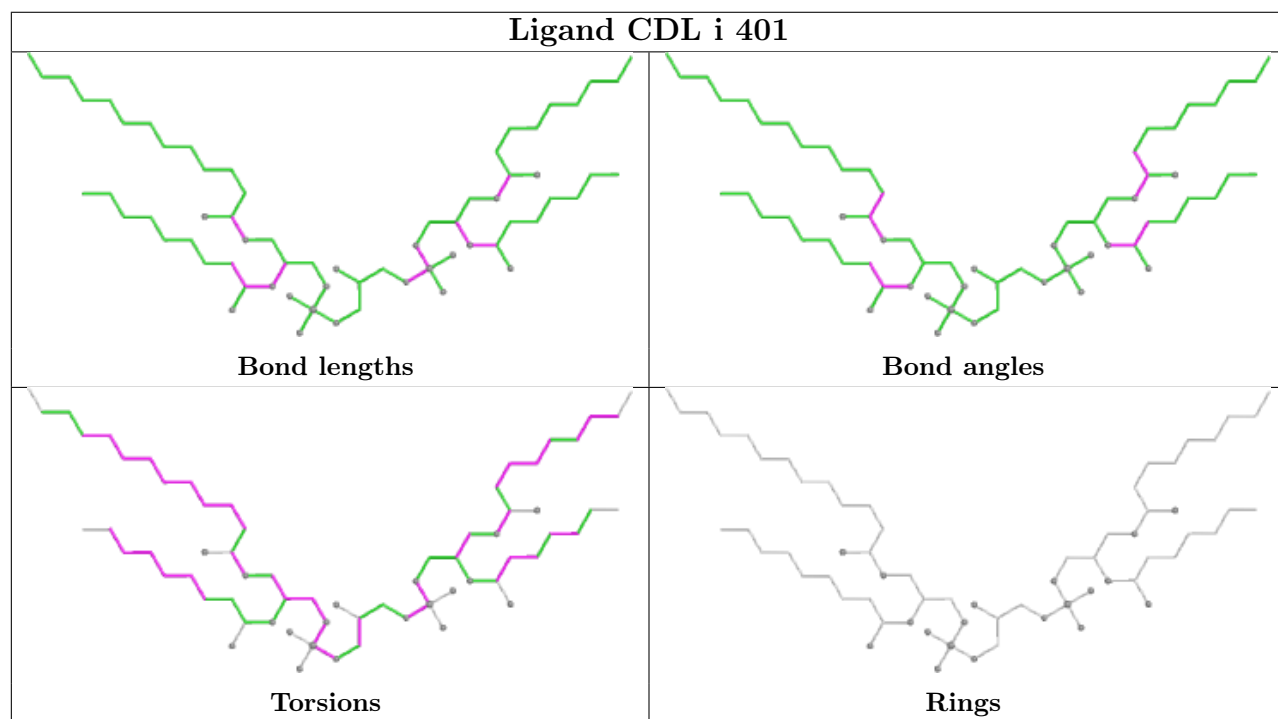
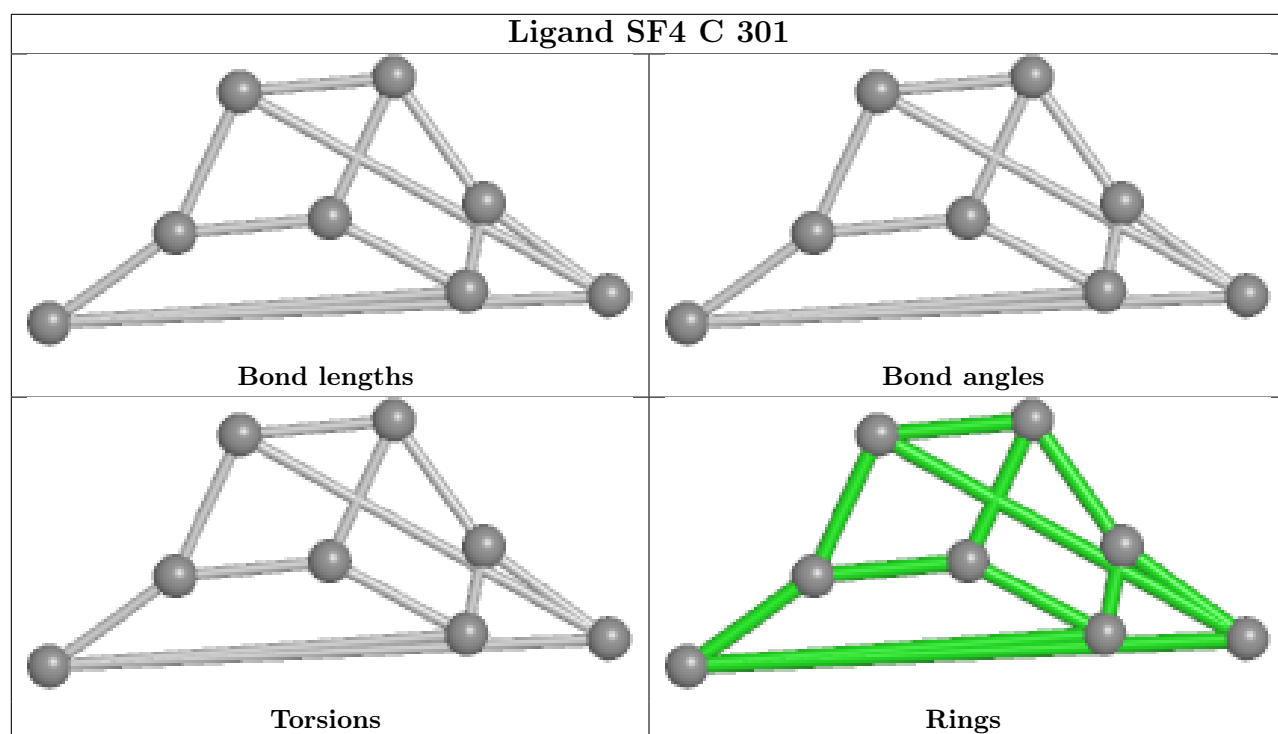


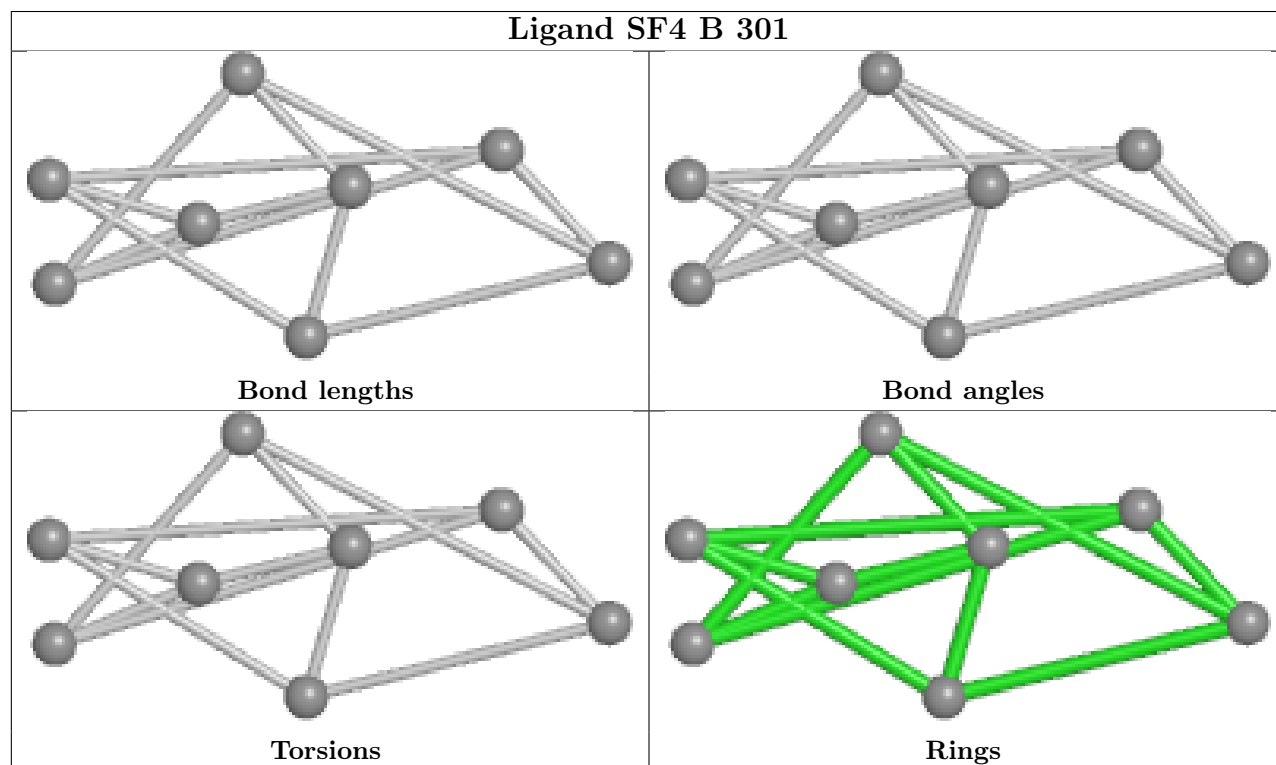
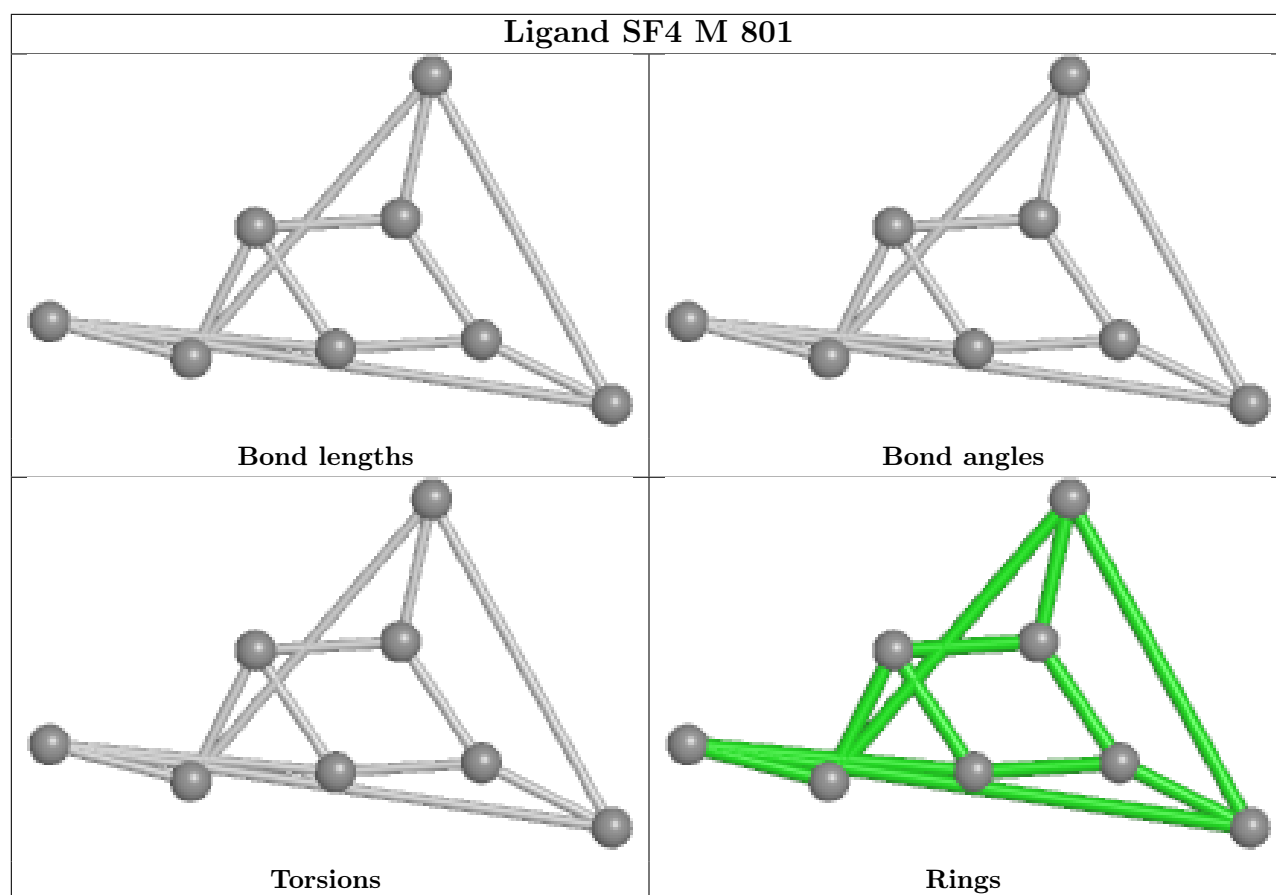


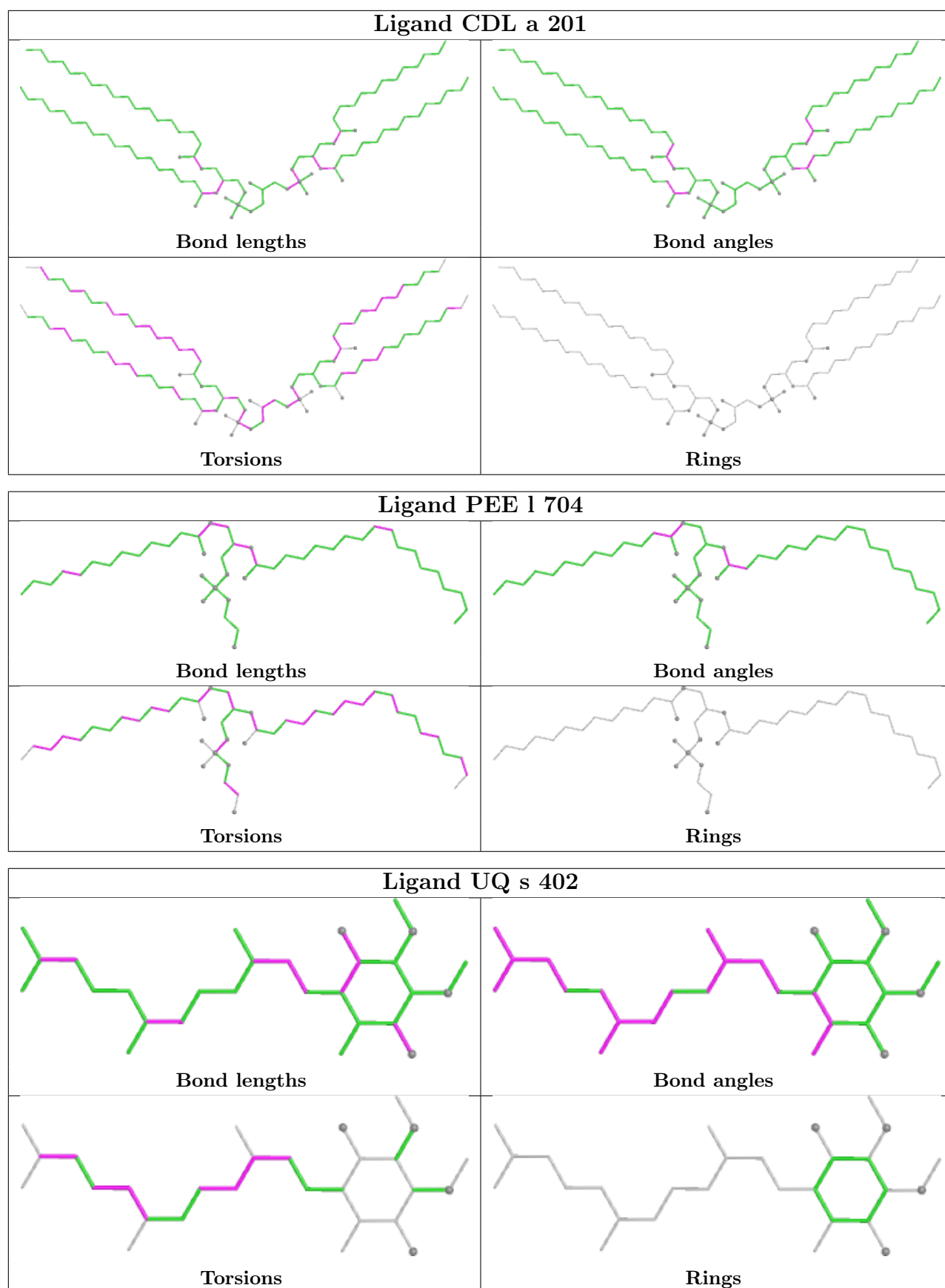


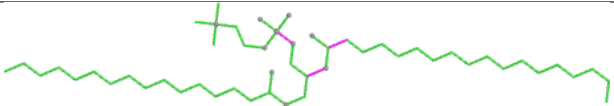
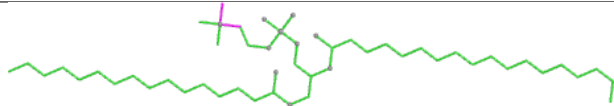
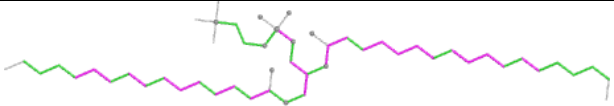
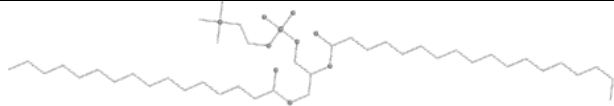


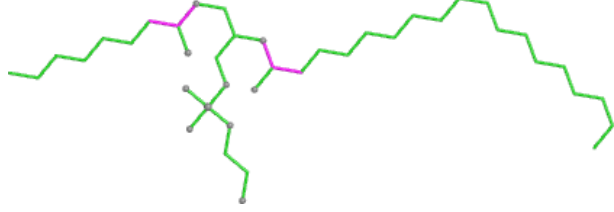
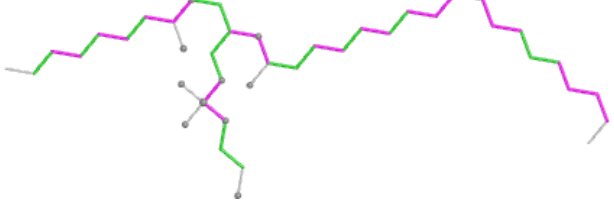
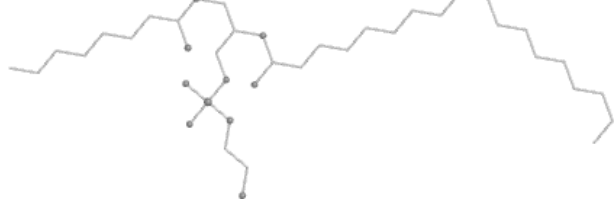


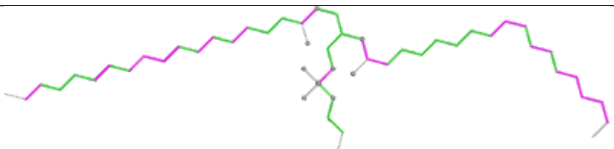
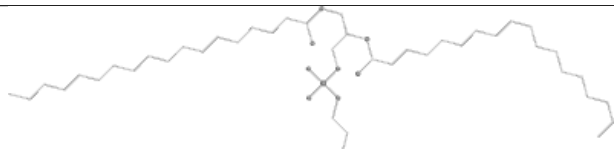


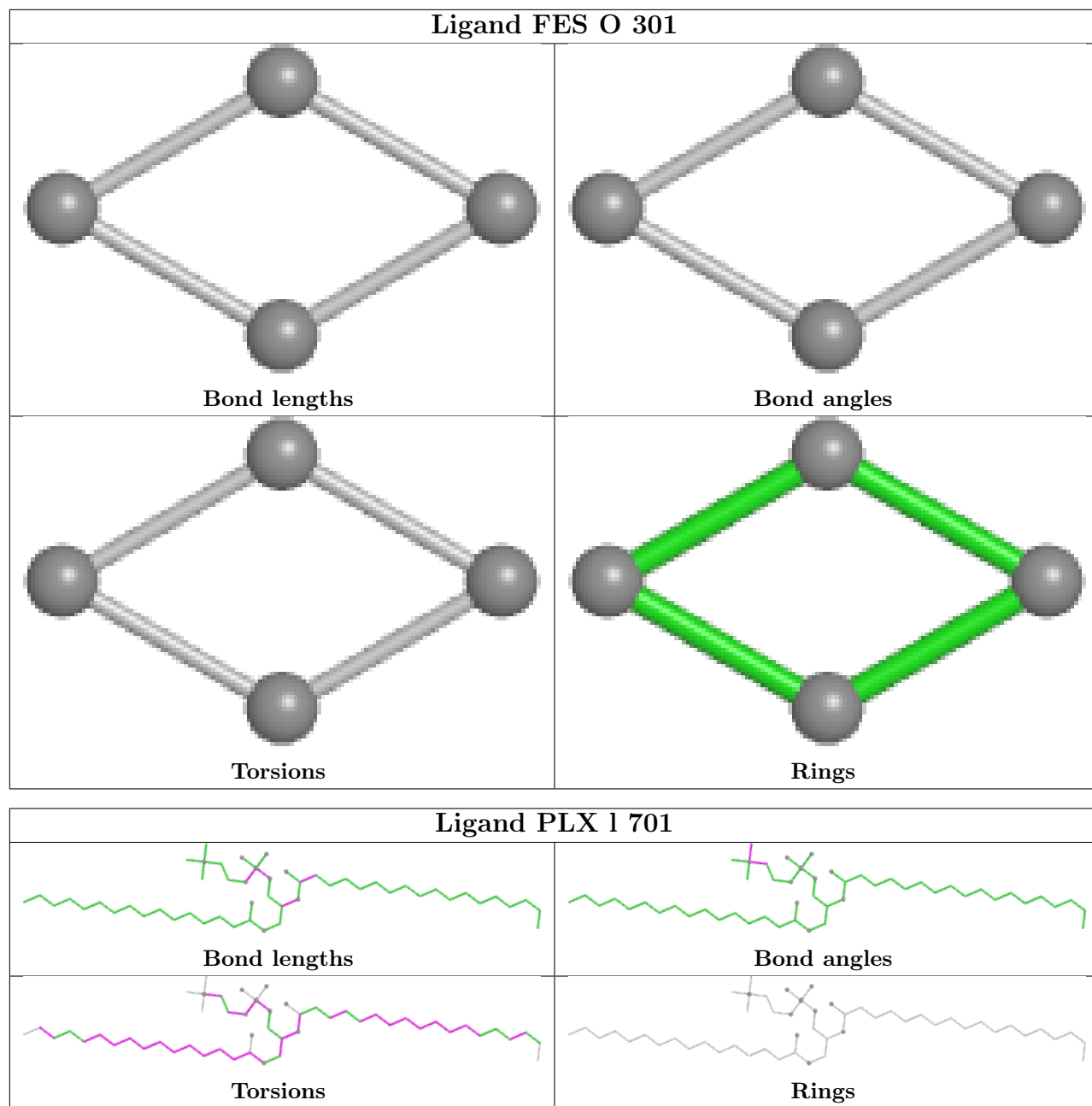


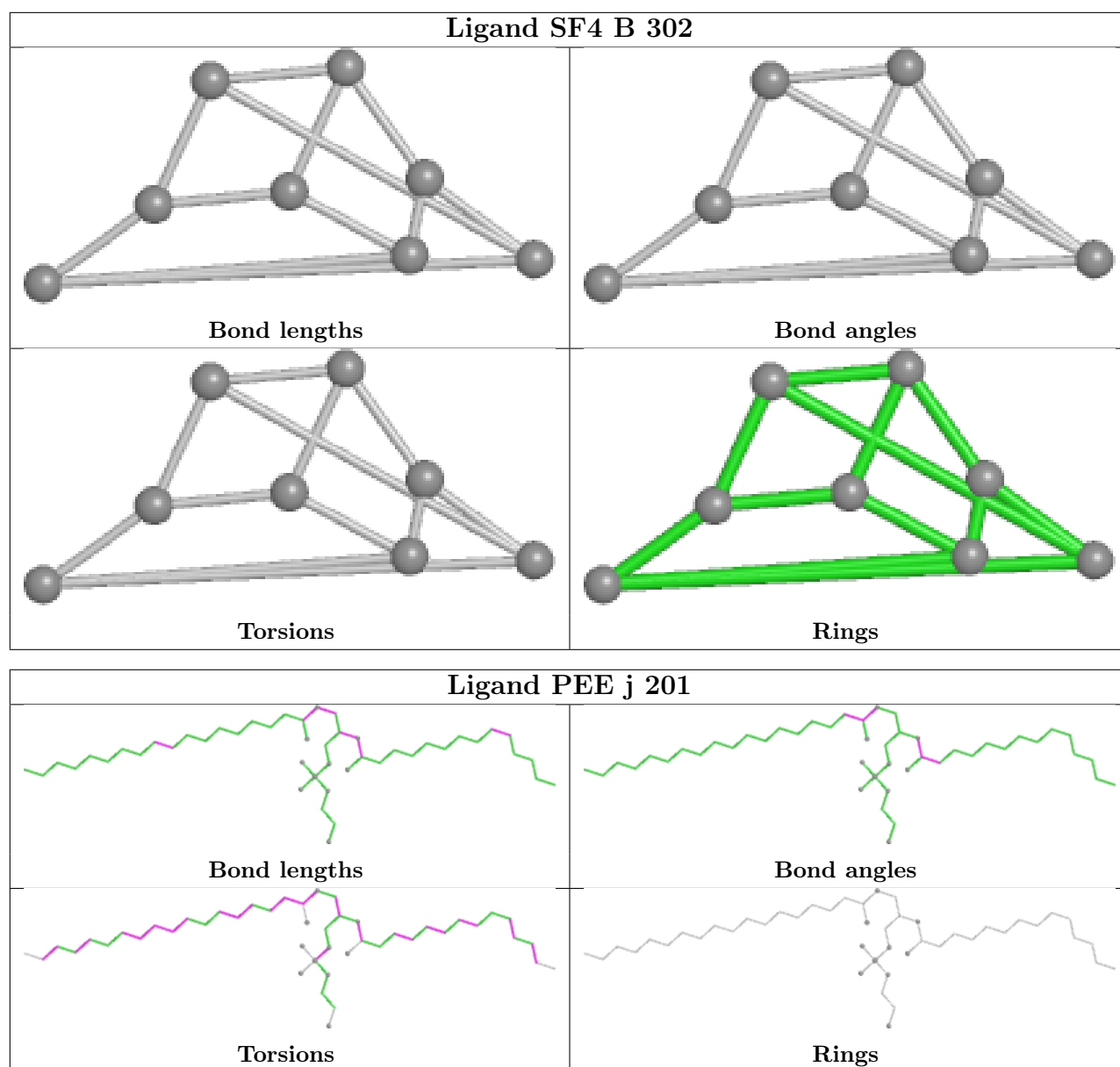


Ligand PLX i 402	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PEE m 201	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PEE U 101	
	
Bond lengths	Bond angles
	
Torsions	Rings





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.

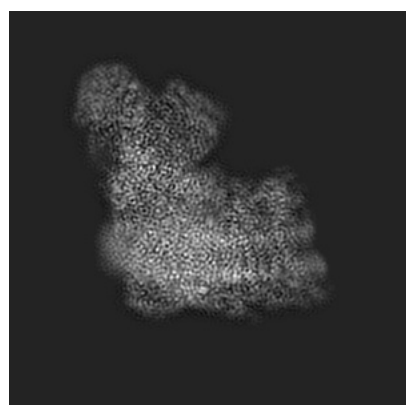
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32305. These allow visual inspection of the internal detail of the map and identification of artifacts.

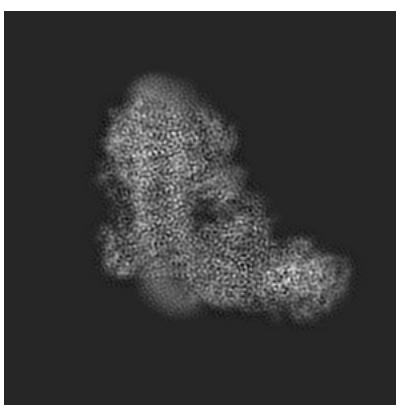
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

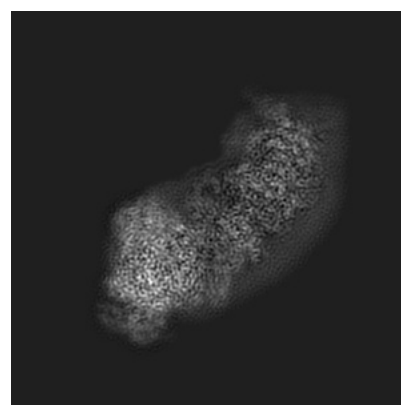
6.1.1 Primary map



X



Y

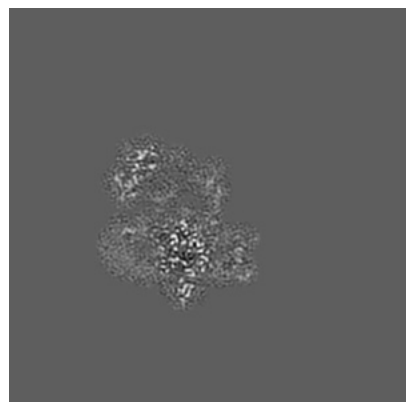


Z

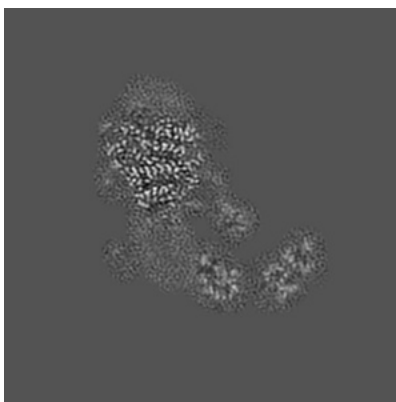
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

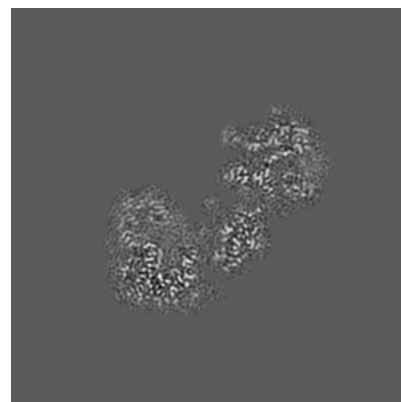
6.2.1 Primary map



X Index: 152



Y Index: 152

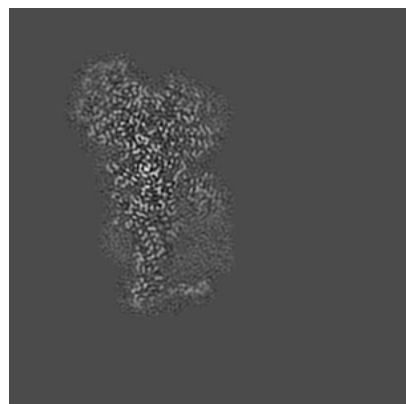


Z Index: 152

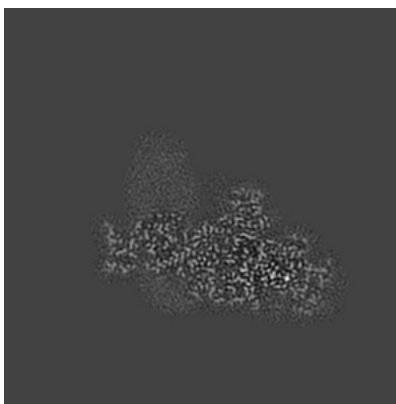
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

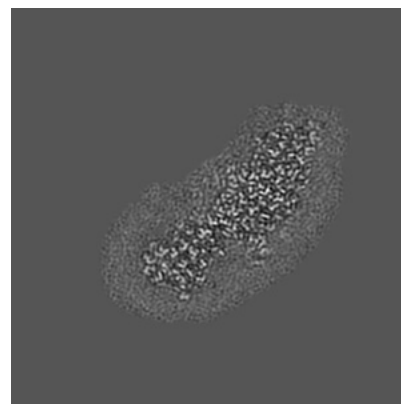
6.3.1 Primary map



X Index: 105



Y Index: 99

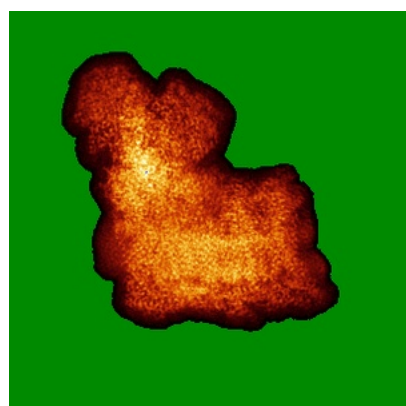


Z Index: 127

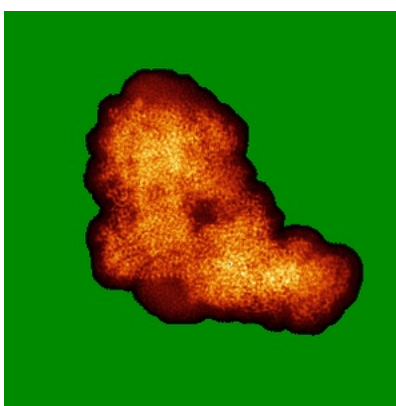
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

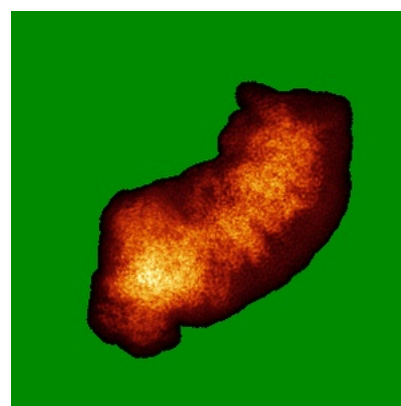
6.4.1 Primary map



X



Y

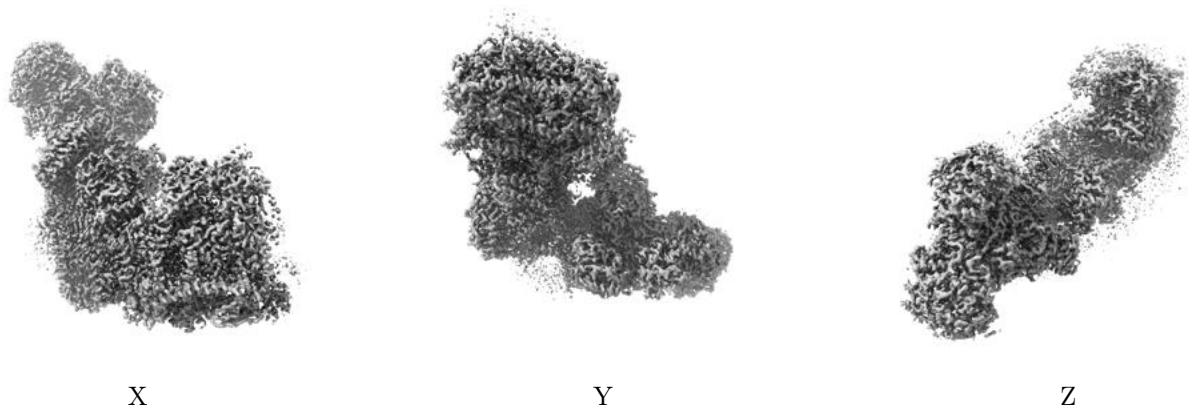


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0298. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

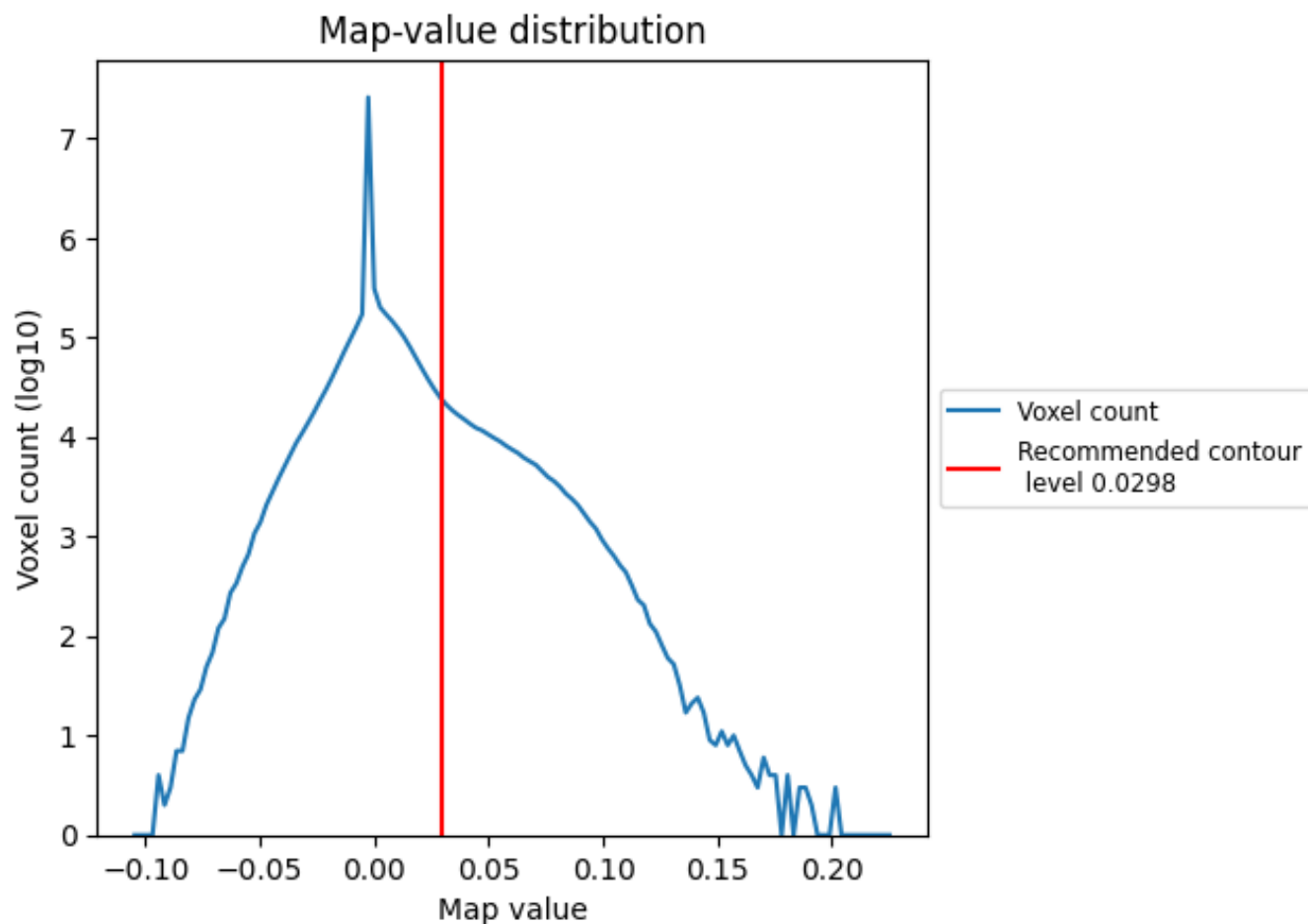
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

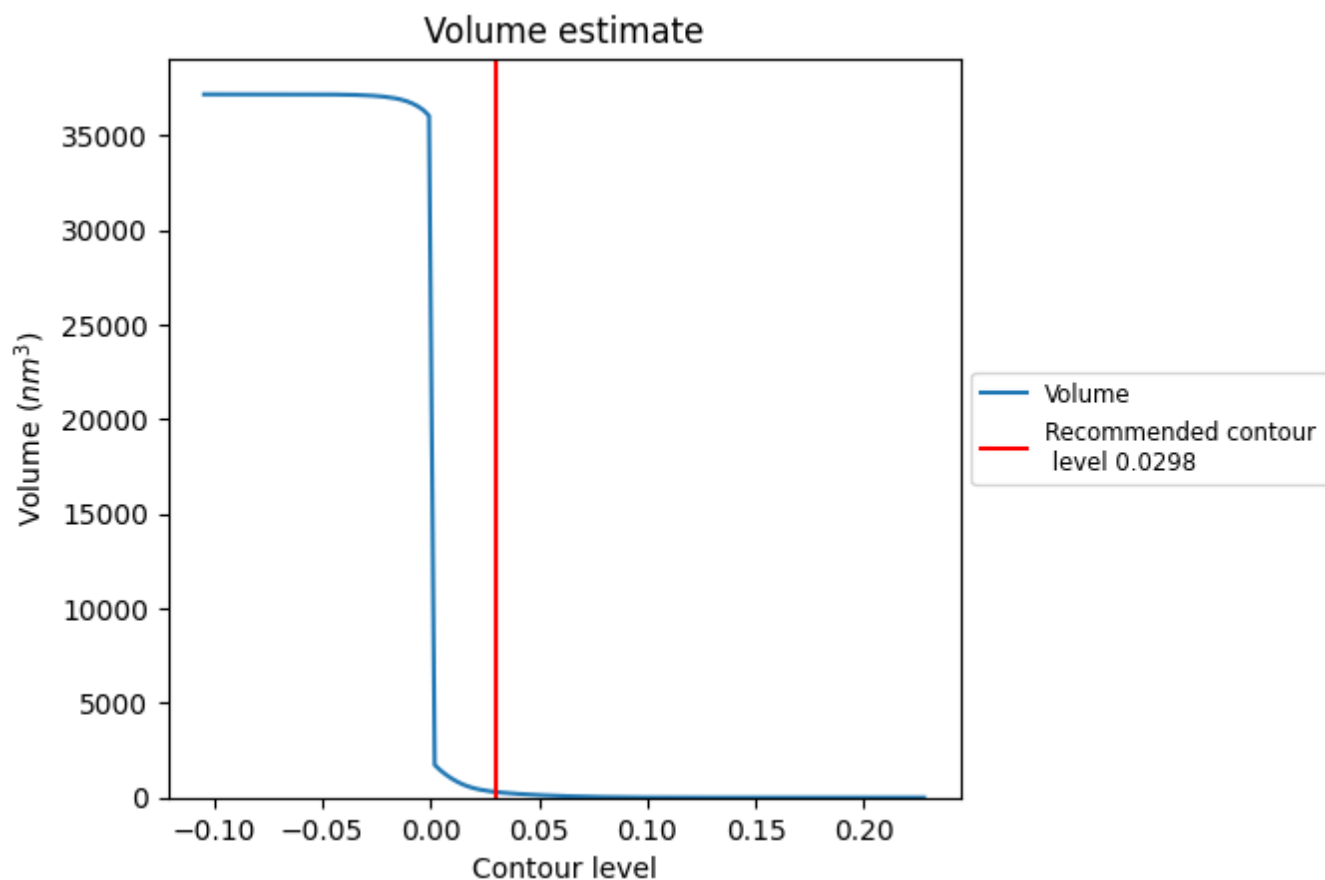
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

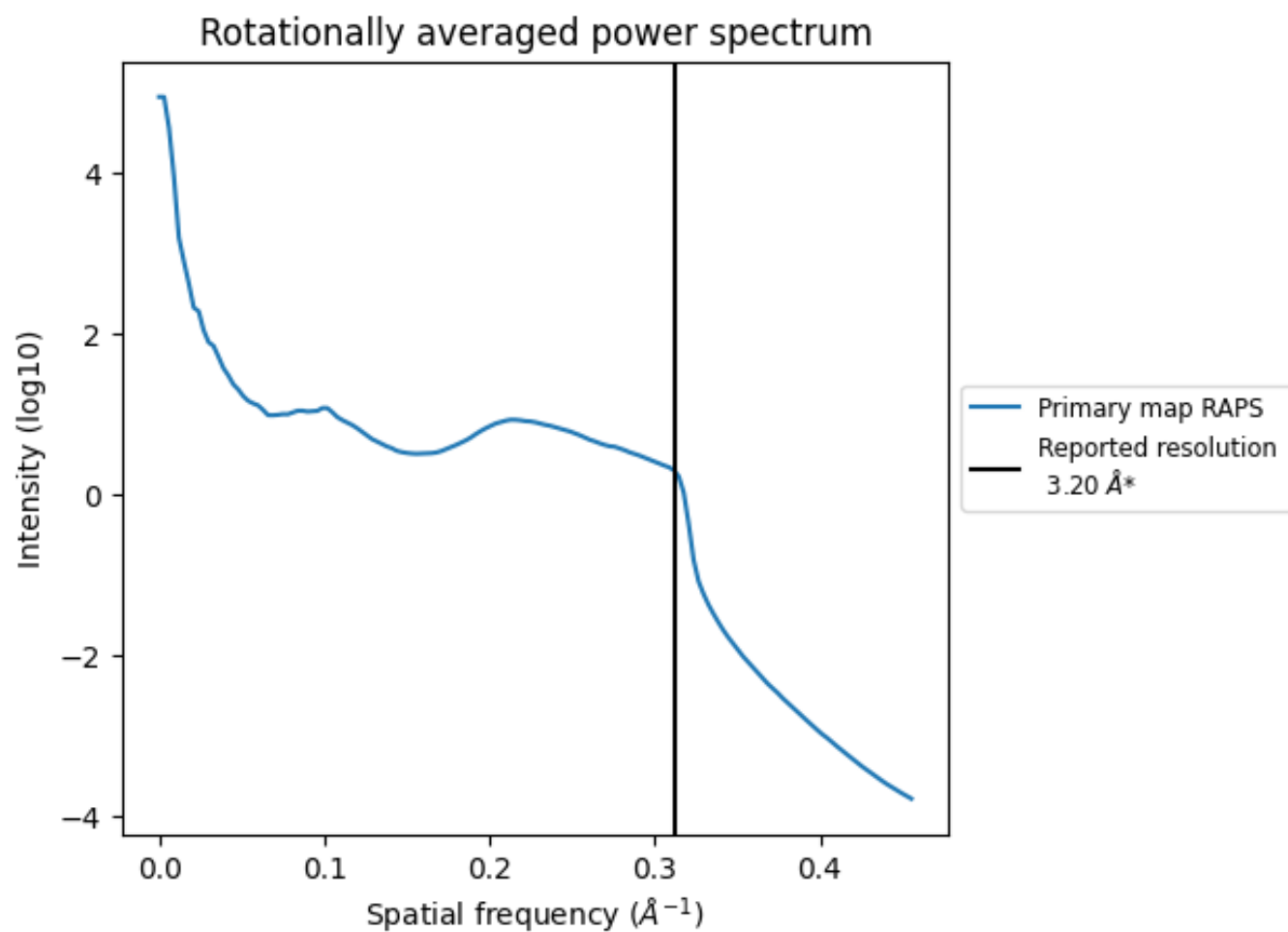
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 297 nm^3 ; this corresponds to an approximate mass of 269 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

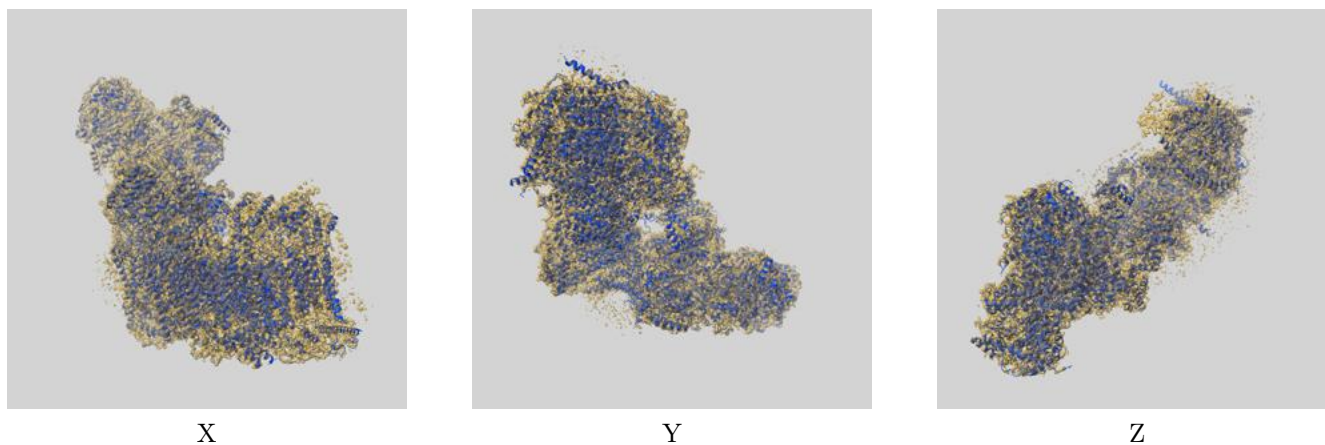
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

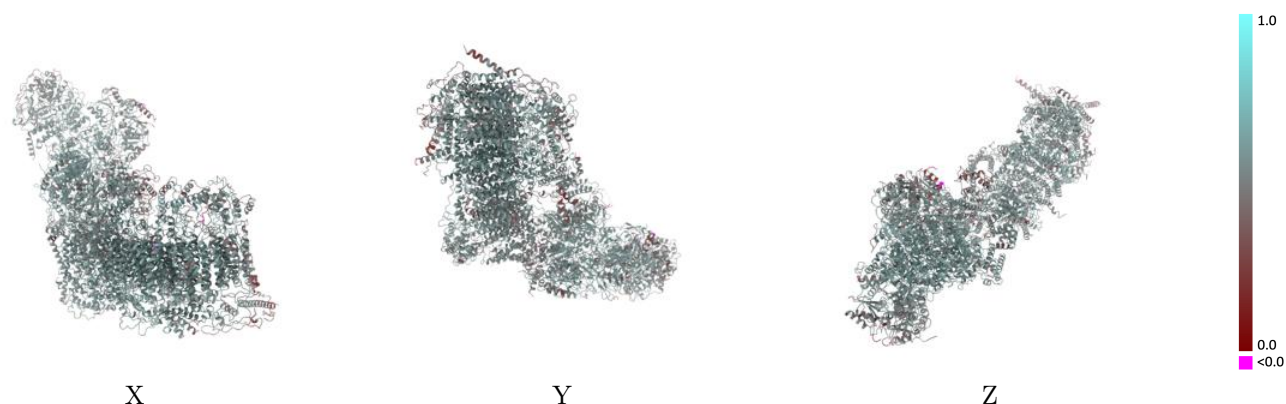
This section contains information regarding the fit between EMDB map EMD-32305 and PDB model 7W4J. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



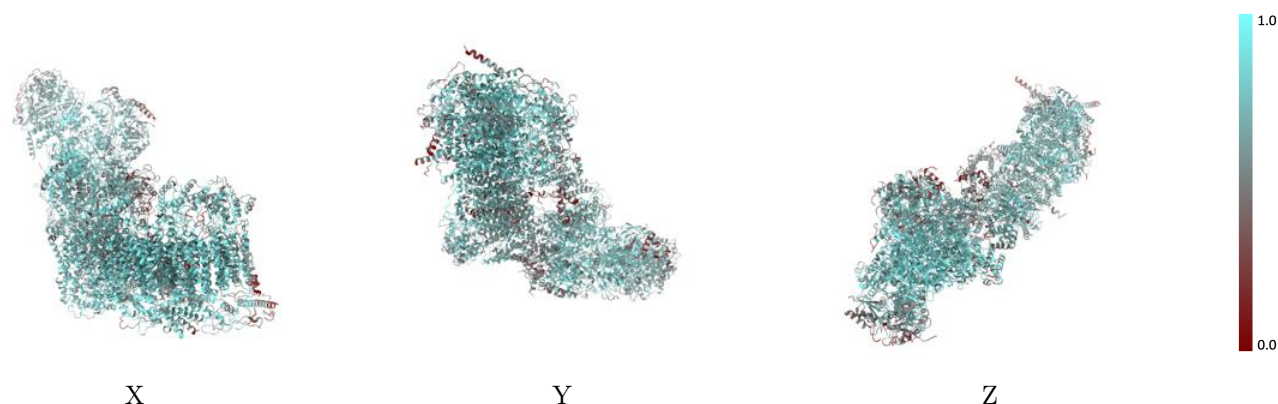
The images above show the 3D surface view of the map at the recommended contour level 0.0298 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



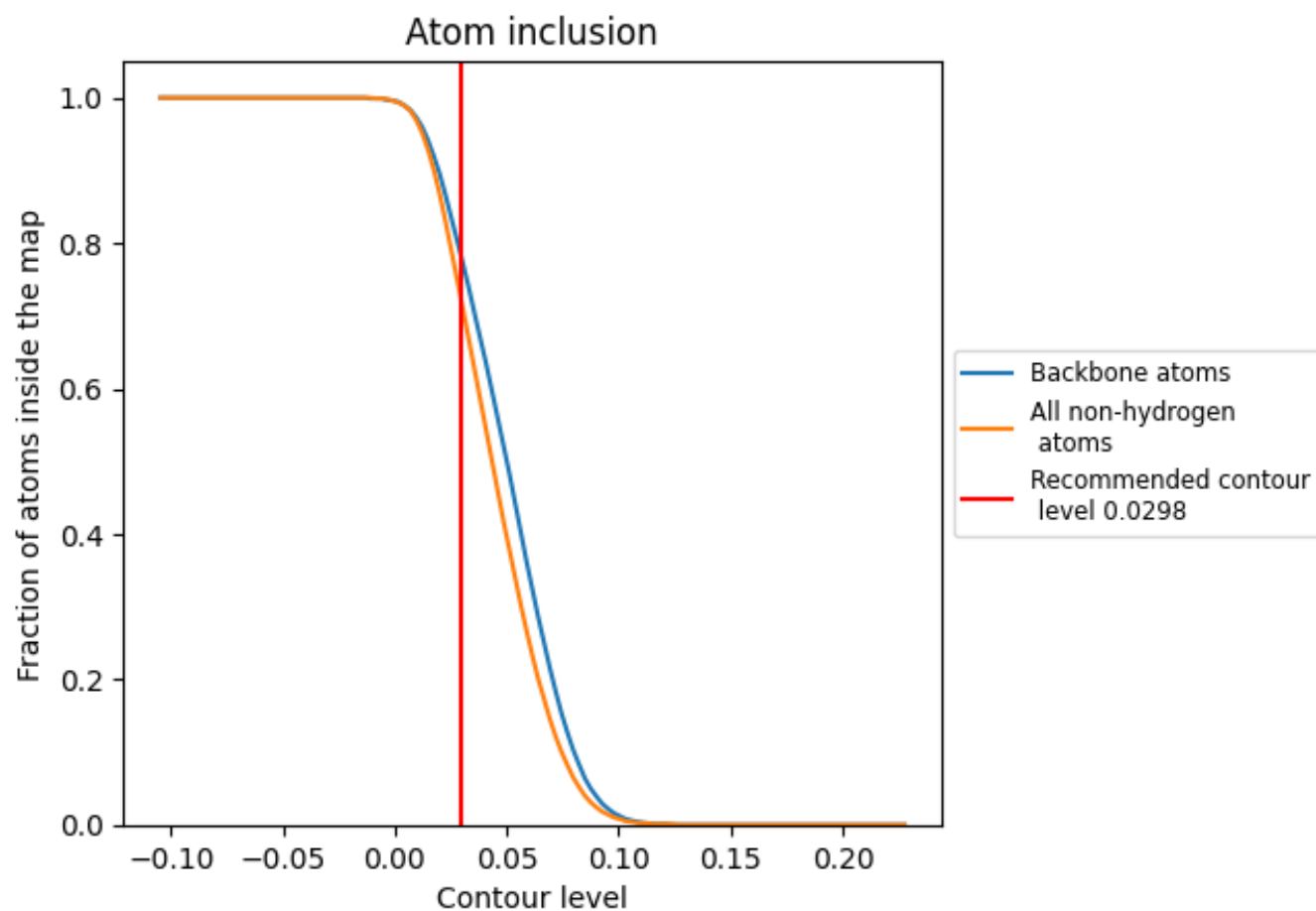
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0298).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0298) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7190	 0.5480
A	 0.6350	 0.5250
B	 0.8670	 0.5980
C	 0.8340	 0.5910
E	 0.6780	 0.5380
F	 0.5270	 0.4500
G	 0.3770	 0.3990
H	 0.6770	 0.5350
I	 0.7350	 0.5610
J	 0.6240	 0.5190
K	 0.5440	 0.4960
L	 0.7720	 0.5750
M	 0.7420	 0.5570
N	 0.7430	 0.5720
O	 0.5930	 0.5050
P	 0.8450	 0.5980
Q	 0.8270	 0.5910
S	 0.7900	 0.5640
T	 0.7230	 0.5590
U	 0.7150	 0.5310
V	 0.4780	 0.4920
W	 0.7610	 0.5580
X	 0.6450	 0.5100
Y	 0.5910	 0.4690
Z	 0.5270	 0.4350
a	 0.7440	 0.5700
b	 0.6430	 0.4970
c	 0.7370	 0.5540
d	 0.7140	 0.5400
e	 0.6690	 0.5320
f	 0.6410	 0.5130
g	 0.8000	 0.5760
h	 0.7280	 0.5560
i	 0.8060	 0.5820
j	 0.6030	 0.5210



Continued on next page...

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Chain	Atom inclusion	Q-score
k	 0.6940	 0.5560
l	 0.7560	 0.5620
m	 0.6580	 0.5320
n	 0.6100	 0.5260
o	 0.7250	 0.5580
p	 0.7290	 0.5370
r	 0.8130	 0.5820
s	 0.7710	 0.5590
u	 0.7460	 0.5510
v	 0.5940	 0.4880
w	 0.6840	 0.5340