



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 07:41 AM UTC

PDB ID : 7ZDM / pdb_00007zdm
EMDB ID : EMD-14658
Title : Complex I from *Ovis aries* at pH5.5, Closed state
Authors : Sazanov, L.; Petrova, O.
Deposited on : 2022-03-29
Resolution : 3.44 Å (reported)
Based on initial model : 6ZKC

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:

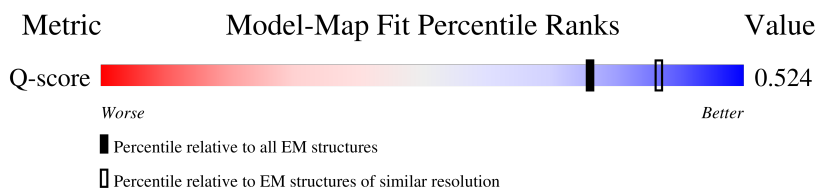
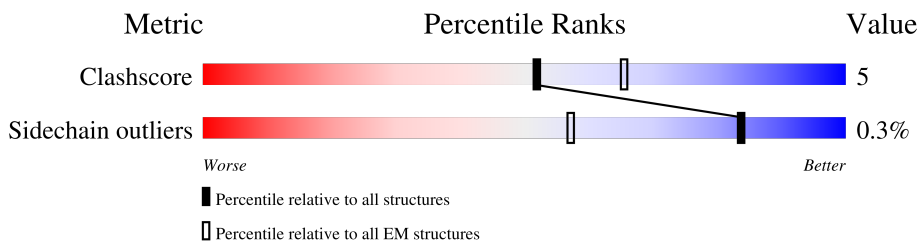
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.49

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 3.44 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13877 (2.94 - 3.94)

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	1	464	 78% 15% 7%
2	2	246	 75% 12% 13%
3	3	727	 82% 13% 5%
4	4	463	 5% 83% 10% 7%
5	5	266	 71% 7% 22%

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Mol	Chain	Length	Quality of chain
6	6	223	
7	9	217	
8	a	109	
9	b	124	
10	c	170	
11	d	380	
12	e	99	
13	f	116	
14	g	140	
15	h	114	
16	i	145	
17	X	157	
17	j	157	
18	A	115	
19	H	318	
20	J	175	
21	K	98	
22	L	606	
23	M	459	
24	N	347	
25	V	141	
26	W	189	
27	Y	171	
28	Z	175	
29	k	355	

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Mol	Chain	Length	Quality of chain
30	l	106	 77% 22%
31	m	84	 86% 10% 5%
32	n	98	 80% 19%
33	o	122	 87% 11%
34	p	130	 86% 12%
35	q	144	 83% 13%
36	r	128	 66% 11% 23% 5%
37	s	137	 73% 16% 11% 7%
38	t	179	 88% 11%
39	u	108	 49% 11% 40%
40	v	186	 74% 9% 17%
41	w	154	 53% 12% 34%
42	x	76	 62% 36% 5%
43	y	58	 78% 9% 14% 12%
44	z	70	 79% 21%

2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 67086 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
			Total	C	N	O	S		
1	1	430	3312	2086	593	613	20	0	0

- Molecule 2 is a protein called Mitochondrial complex I, 24 kDa subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	2	213	1655	1058	278	309	10	0	0

- Molecule 3 is a protein called NADH:ubiquinone oxidoreductase core subunit S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	688	5275	3301	922	1011	41	0	0

- Molecule 4 is a protein called Complex I-49kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	430	3457	2207	594	631	25	0	0

- Molecule 5 is a protein called NADH:ubiquinone oxidoreductase core subunit S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	208	1726	1112	296	315	3	0	0

- Molecule 6 is a protein called Complex I-20kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	6	156	1247	795	225	213	14	0	0

- Molecule 7 is a protein called Complex I-23kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	9	176	Total	C	N	O	S	0	0
			1414	889	243	270	12		

- Molecule 8 is a protein called Complex I-9kD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	a	44	Total	C	N	O	S	0	0
			371	233	66	71	1		

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	b	95	Total	C	N	O	S	0	0
			737	451	139	144	3		

- Molecule 10 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	c	126	Total	C	N	O	S	0	0
			1024	646	182	193	3		

- Molecule 11 is a protein called NADH:ubiquinone oxidoreductase subunit A9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	d	340	Total	C	N	O	S	0	0
			2748	1775	489	478	6		

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2.

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

- Molecule 13 is a protein called Mitochondrial complex I, B13 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	f	113	Total	C	N	O	S	0	0
			917	595	153	167	2		

- Molecule 14 is a protein called NADH:ubiquinone oxidoreductase subunit A6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	g	114	969	619	180	166	4	0	0

- Molecule 15 is a protein called Mitochondrial complex I, B14.5a subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	h	96	769	480	146	140	3	0	0

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	i	145	1209	778	216	210	5	0	0

- Molecule 17 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	j	82	660	425	98	132	5	0	0
17	X	87	701	451	103	142	5	0	0

- Molecule 18 is a protein called NADH-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	A	115	922	621	133	161	7	0	0

- Molecule 19 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	H	318	2528	1704	384	421	19	0	0

- Molecule 20 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	J	175	1344	904	192	235	13	0	0

- Molecule 21 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	K	98	749	490	112	132	15	0	0

- Molecule 22 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	L	606	4807	3188	746	829	44	0	0

- Molecule 23 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	M	459	3647	2429	571	607	40	0	0

- Molecule 24 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	N	347	2723	1808	416	459	40	0	0

- Molecule 25 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	V	140	1028	656	175	191	6	0	0

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	W	139	1155	761	194	198	2	0	0

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Y	171	1403	889	253	251	10	0	0

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	Z	171	1441	905	266	262	8	0	0

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	N	O	P	S		
29	k	320	2596	1659	432	494	1	10	0	0

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	l	105	874	551	164	153	6	0	0

- Molecule 31 is a protein called NADH:ubiquinone oxidoreductase subunit A3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	m	80	626	411	103	110	2	0	0

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	n	79	634	415	106	111	2	0	0

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
33	o	120	1004	652	175	172	5	0	0

- Molecule 34 is a protein called NADH:ubiquinone oxidoreductase subunit B4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	p	128	1059	675	189	194	1	0	0

- Molecule 35 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
35	q	139	1142	733	200	200	9	0	0

- Molecule 36 is a protein called Mitochondrial complex I, B17 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
36	r	99	846	554	149	142	1	0	0

- Molecule 37 is a protein called NADH:ubiquinone oxidoreductase subunit B7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
37	s	122	1047	653	199	186	9	0	0

- Molecule 38 is a protein called NADH:ubiquinone oxidoreductase subunit B9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	t	177	1520	973	279	262	6	0	0

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	u	65	563	372	93	97	1	0	0

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	v	155	1307	846	213	239	9	0	0

- Molecule 41 is a protein called Mitochondrial complex I, ESSS subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	w	101	846	542	140	160	4	0	0

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	x	49	412	271	70	71	0	0

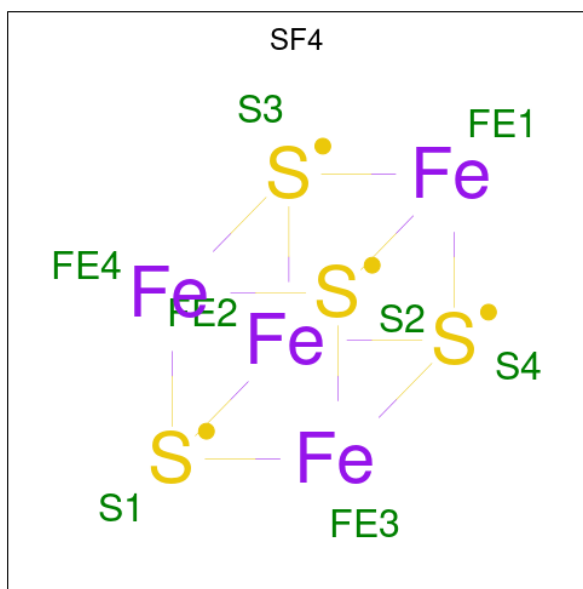
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
43	y	50	436	287	77	72	0	0

- Molecule 44 is a protein called Complex I-MWFE.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	z	70	576	369	106	96	5	0	0

- Molecule 45 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).



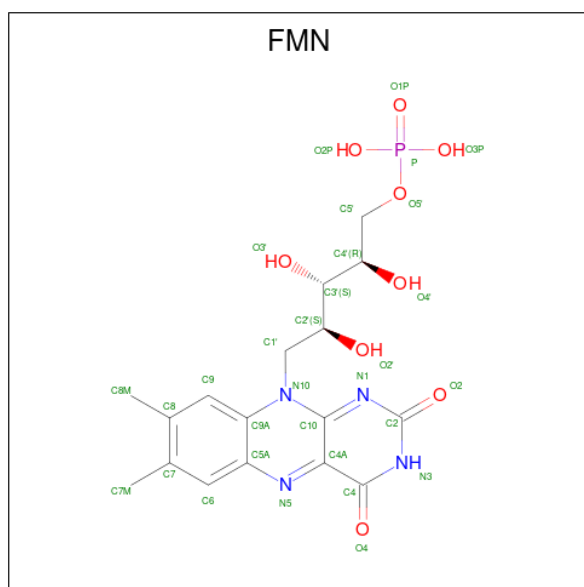
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
45	1	1	8	4	4	0
45	3	1	8	4	4	0
45	3	1	8	4	4	0

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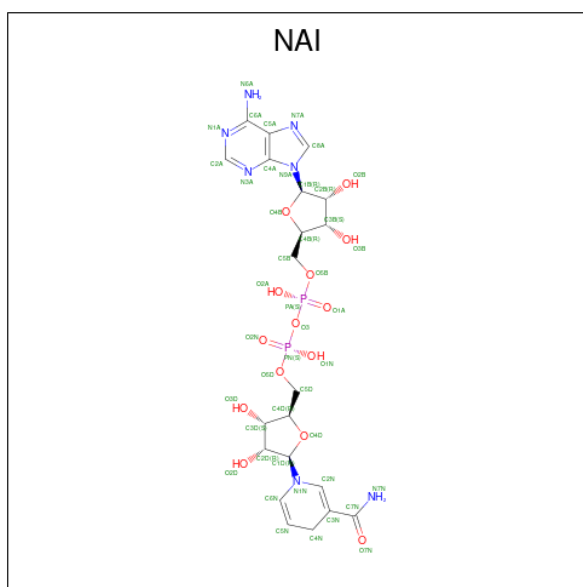
Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
45	6	1	8	4	4	0
45	9	1	8	4	4	0
45	9	1	8	4	4	0

- Molecule 46 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



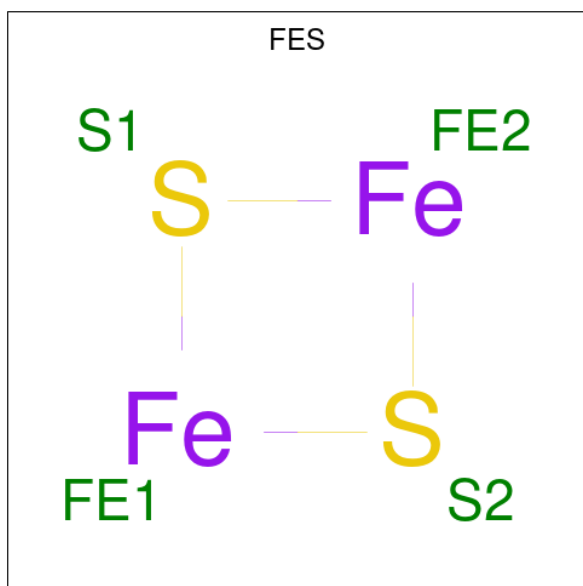
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
46	1	1	31	17	4	9	1	0

- Molecule 47 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



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

- Molecule 48 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).

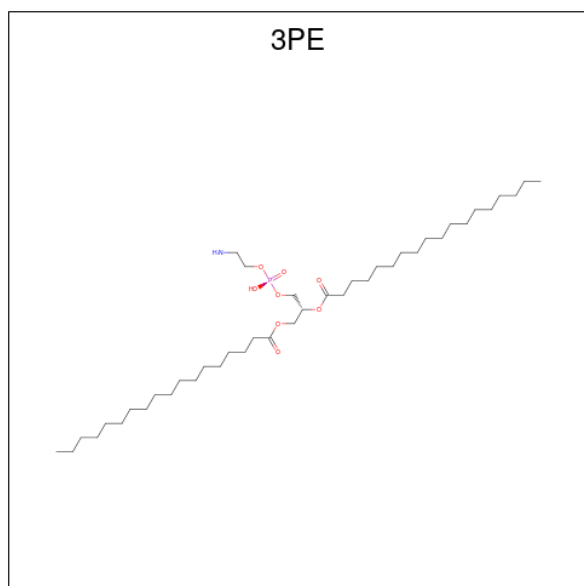


Mol	Chain	Residues	Atoms			AltConf
			Total	Fe	S	
48	2	1	4	2	2	0
48	3	1	4	2	2	0

- Molecule 49 is POTASSIUM ION (CCD ID: K) (formula: K).

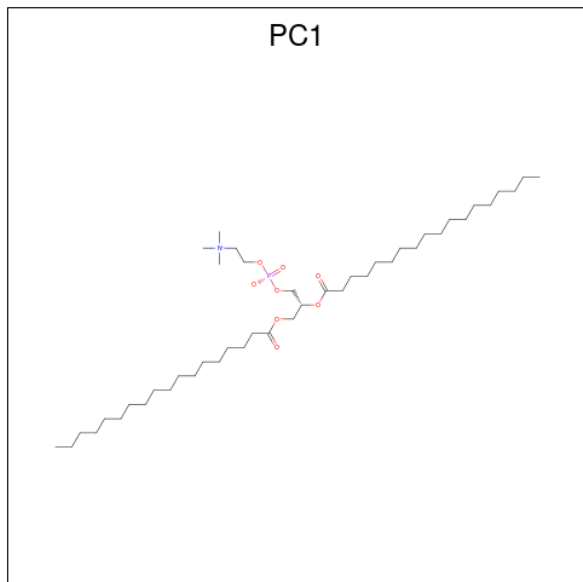
Mol	Chain	Residues	Atoms	AltConf
49	3	1	Total K 1 1	0

- Molecule 50 is 1,2-Distearoyl-sn-glycerophosphoethanolamine (CCD ID: 3PE) (formula: $C_{41}H_{82}NO_8P$).



Mol	Chain	Residues	Atoms	AltConf
50	4	1	Total C N O P 40 30 1 8 1	0
50	6	1	Total C N O P 51 41 1 8 1	0
50	A	1	Total C N O P 51 41 1 8 1	0
50	H	1	Total C N O P 51 41 1 8 1	0
50	J	1	Total C N O P 40 30 1 8 1	0
50	L	1	Total C N O P 51 41 1 8 1	0
50	M	1	Total C N O P 44 34 1 8 1	0
50	V	1	Total C O P 27 18 8 1	0
50	V	1	Total C N O P 37 27 1 8 1	0
50	o	1	Total C N O P 31 21 1 8 1	0

- Molecule 51 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: $C_{44}H_{88}NO_8P$).



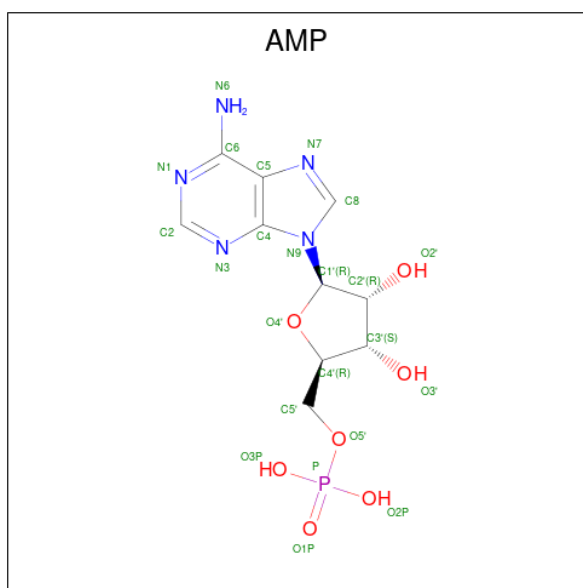
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
51	6	1	Total 46	C 36	N 1	O 8	P 1	0
51	9	1	Total 54	C 44	N 1	O 8	P 1	0
51	L	1	Total 54	C 44	N 1	O 8	P 1	0
51	L	1	Total 54	C 44	N 1	O 8	P 1	0
51	M	1	Total 54	C 44	N 1	O 8	P 1	0

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	b	1	Total 1	Zn 1	0

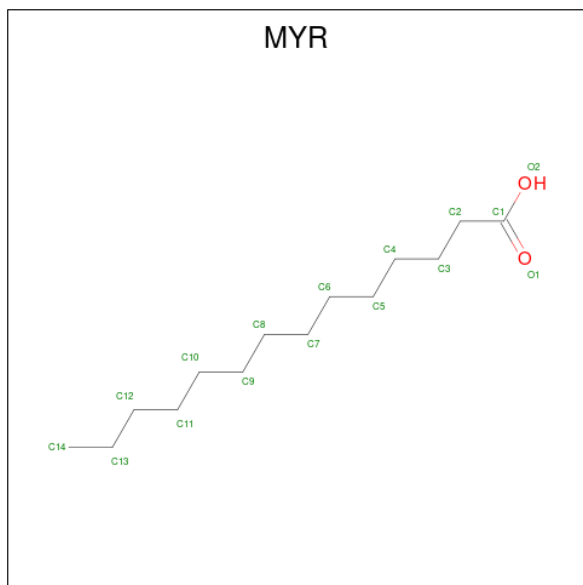
- Molecule 53 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).

- Molecule 55 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	N	O		P
55	k	1	23	10	5	7	1	0

- Molecule 56 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).

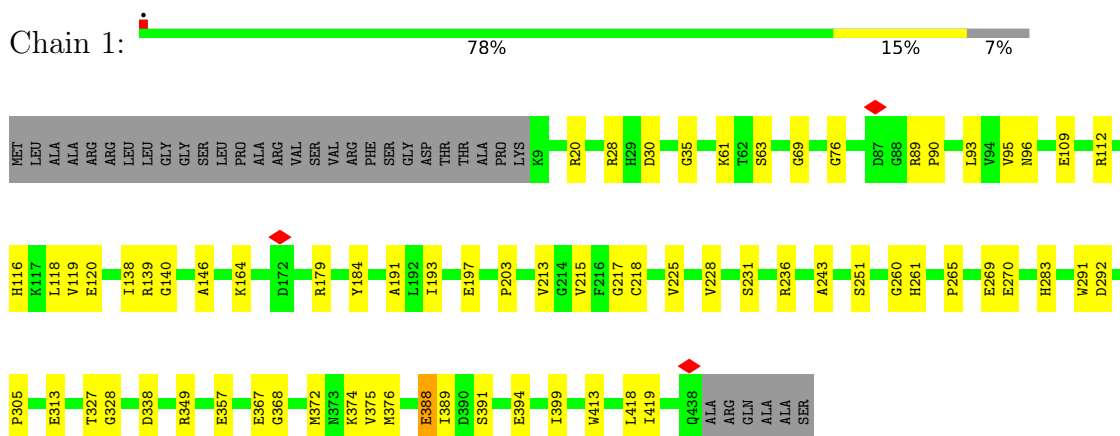


Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
56	s	1	15	14	1	0

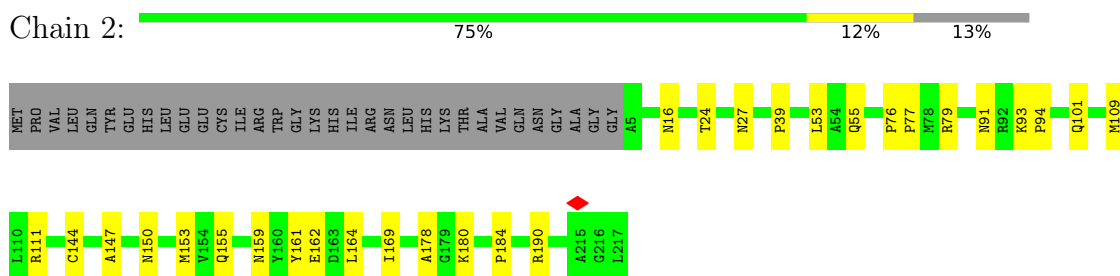
3 Residue-property plots [i](#)

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

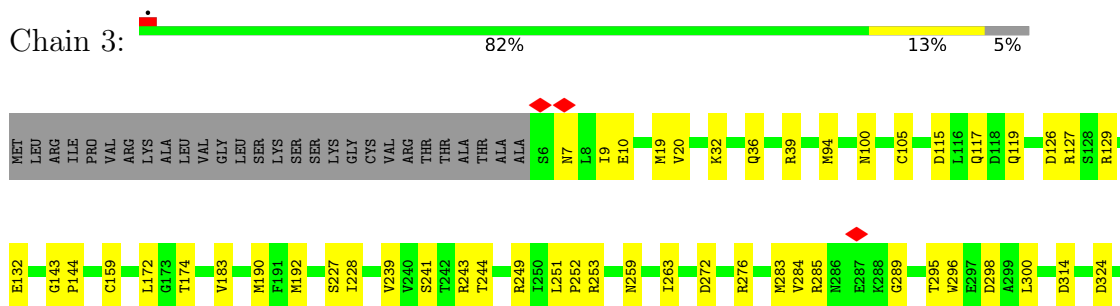
- Molecule 1: NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial



- Molecule 2: Mitochondrial complex I, 24 kDa subunit

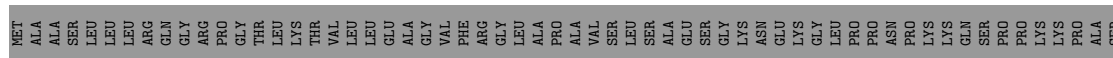
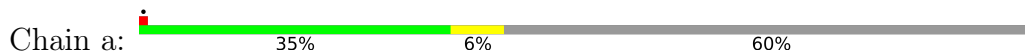


- Molecule 3: NADH:ubiquinone oxidoreductase core subunit S1

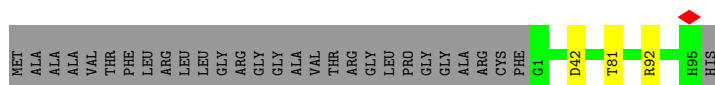
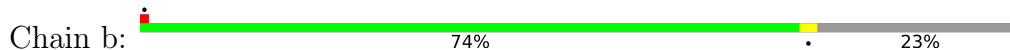




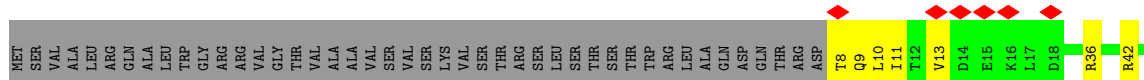
- Molecule 8: Complex I-9kD



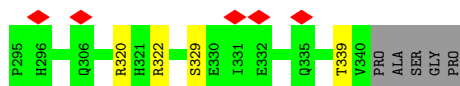
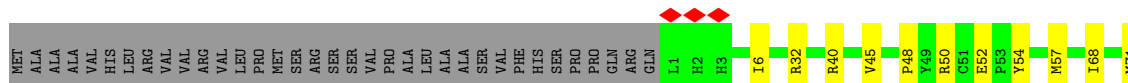
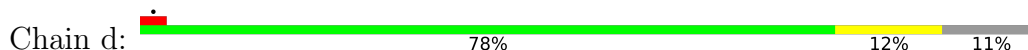
- Molecule 9: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



- Molecule 10: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial

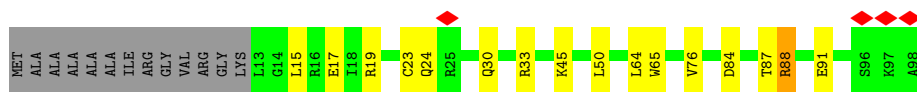


- Molecule 11: NADH:ubiquinone oxidoreductase subunit A9

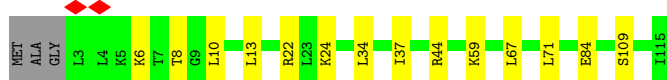
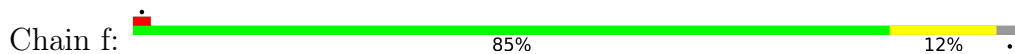


- Molecule 12: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2





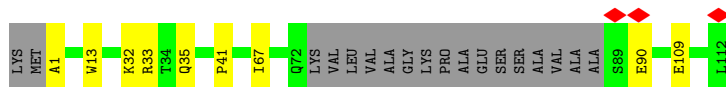
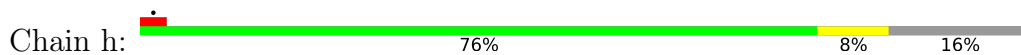
- Molecule 13: Mitochondrial complex I, B13 subunit



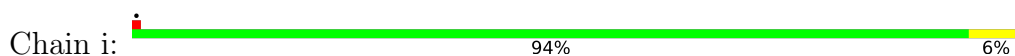
- Molecule 14: NADH:ubiquinone oxidoreductase subunit A6



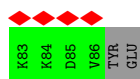
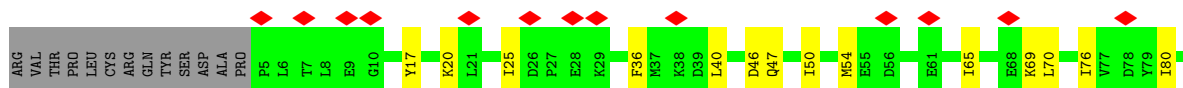
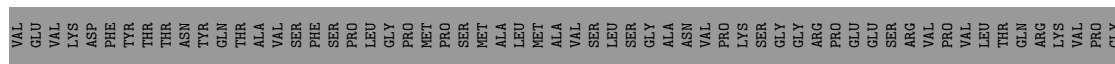
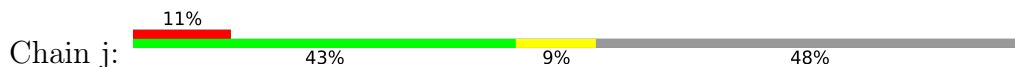
- Molecule 15: Mitochondrial complex I, B14.5a subunit



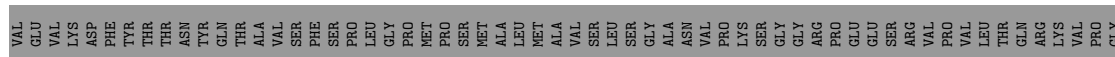
- Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12



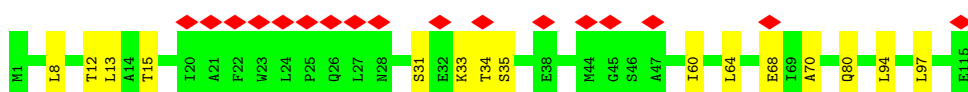
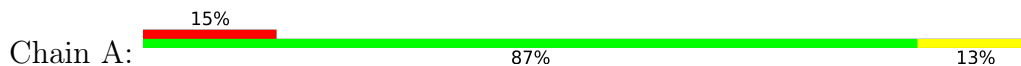
- Molecule 17: Acyl carrier protein



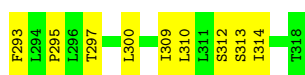
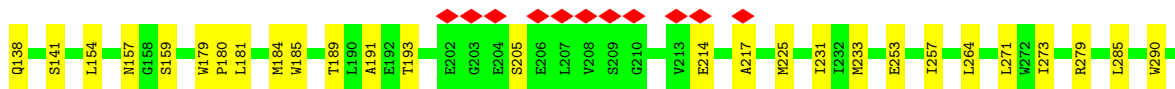
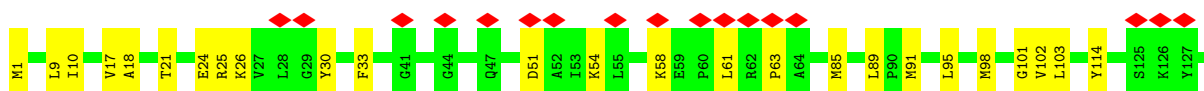
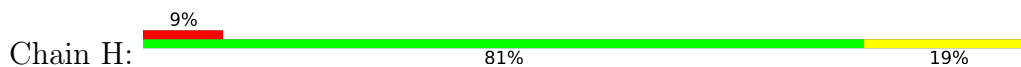
• Molecule 17: Acyl carrier protein



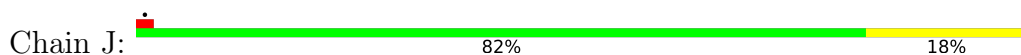
• Molecule 18: NADH-ubiquinone oxidoreductase chain 3



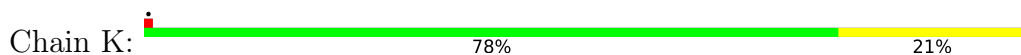
• Molecule 19: NADH-ubiquinone oxidoreductase chain 1



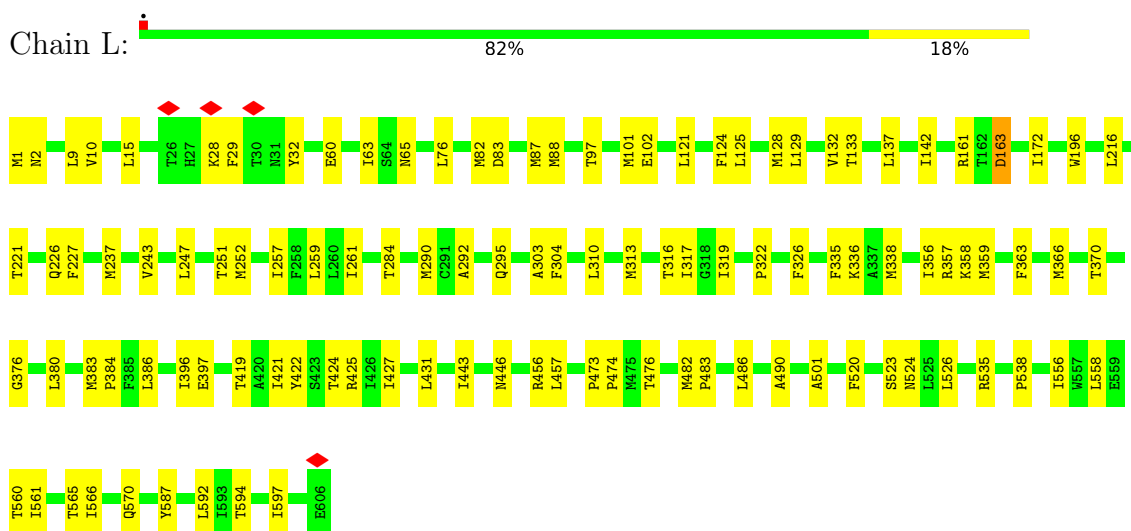
• Molecule 20: NADH-ubiquinone oxidoreductase chain 6



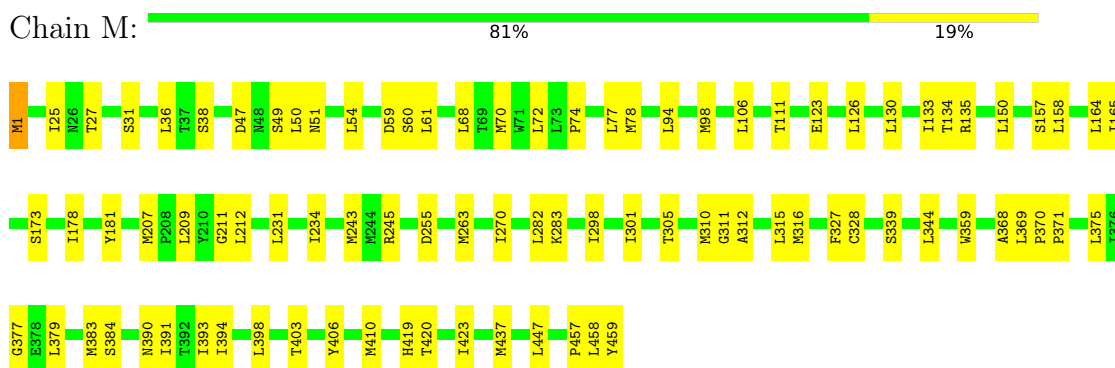
• Molecule 21: NADH-ubiquinone oxidoreductase chain 4L



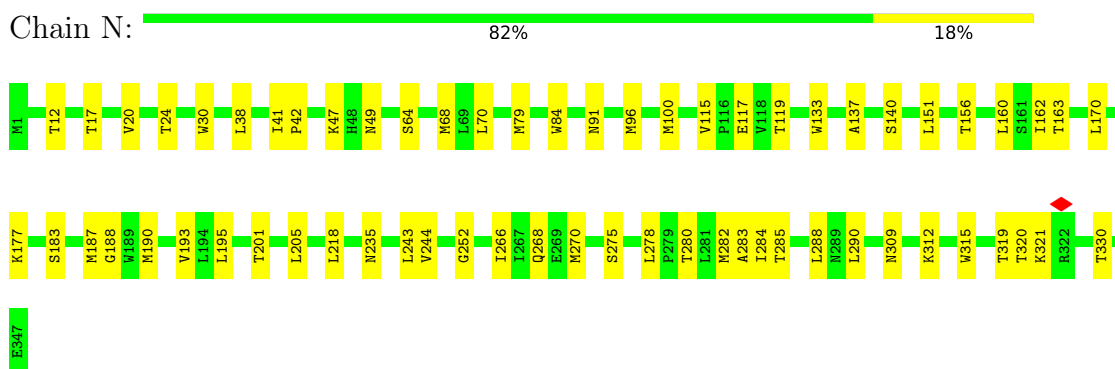
- Molecule 22: NADH-ubiquinone oxidoreductase chain 5



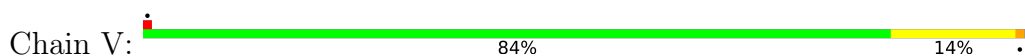
- Molecule 23: NADH-ubiquinone oxidoreductase chain 4



- Molecule 24: NADH-ubiquinone oxidoreductase chain 2

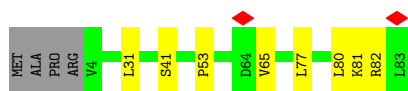
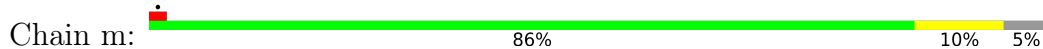


- Molecule 25: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

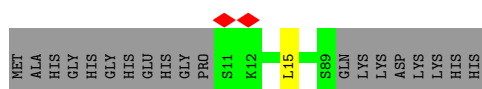
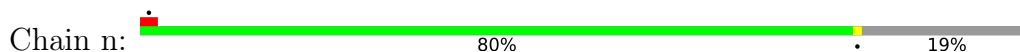




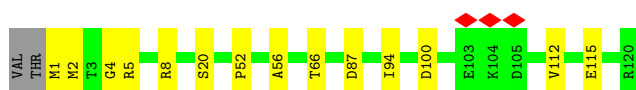
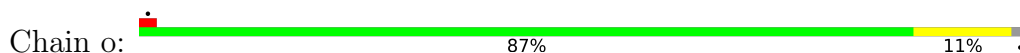
- Molecule 31: NADH:ubiquinone oxidoreductase subunit A3



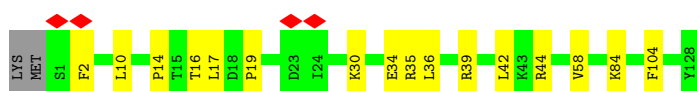
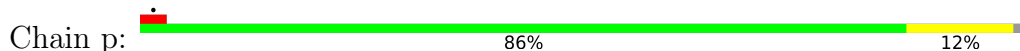
- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



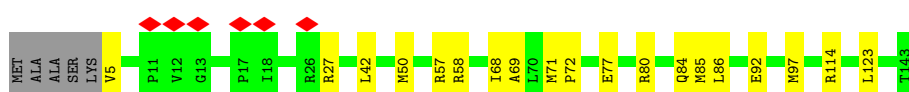
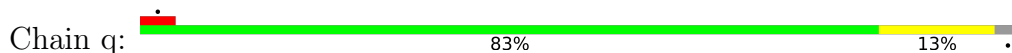
- Molecule 33: NADH dehydrogenase [ubiquinone] 1 subunit C2



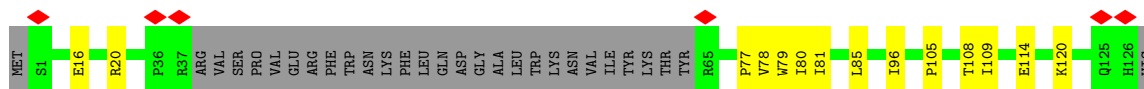
- Molecule 34: NADH:ubiquinone oxidoreductase subunit B4



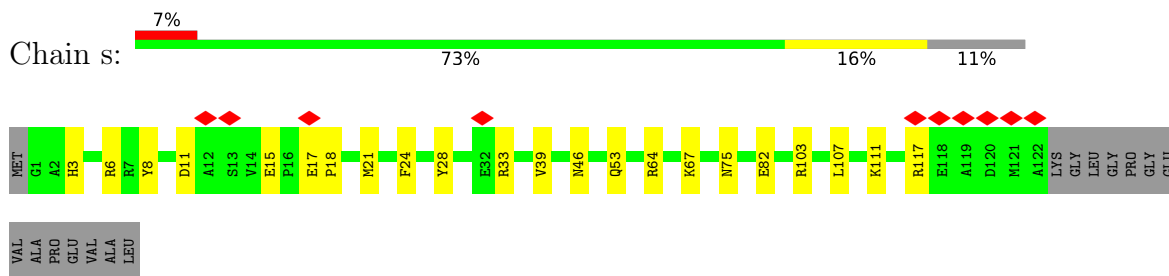
- Molecule 35: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13



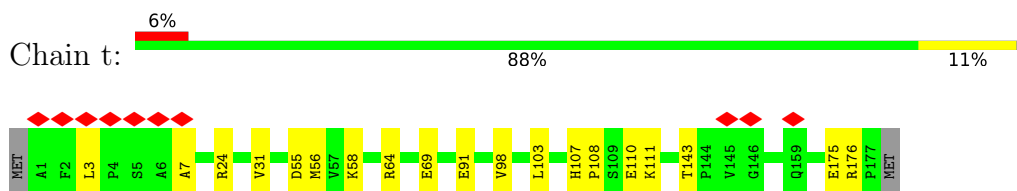
- Molecule 36: Mitochondrial complex I, B17 subunit



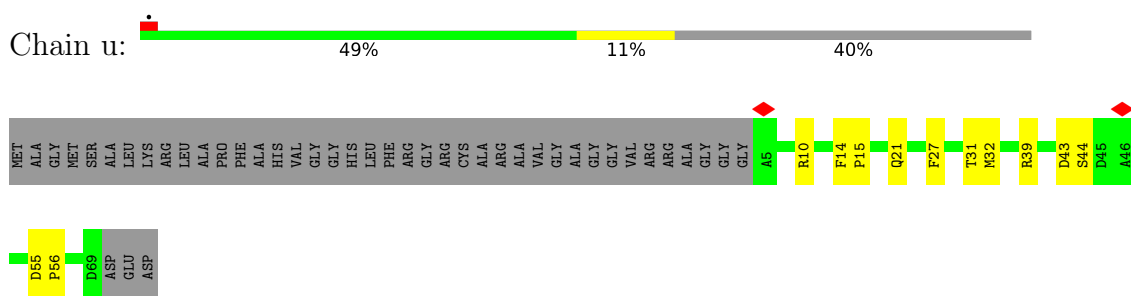
- Molecule 37: NADH:ubiquinone oxidoreductase subunit B7



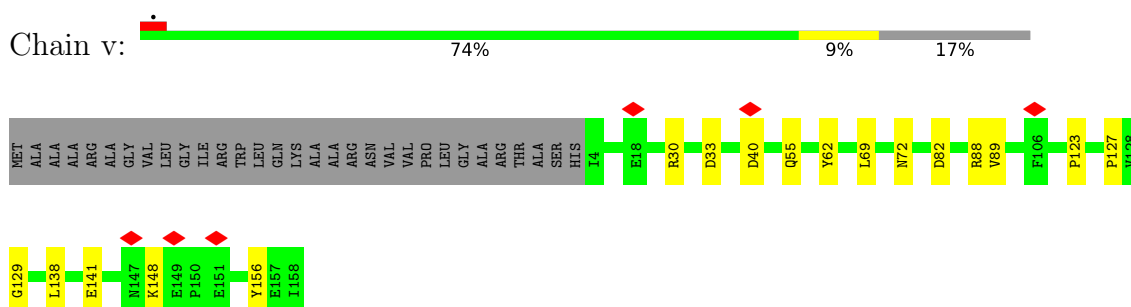
• Molecule 38: NADH:ubiquinone oxidoreductase subunit B9



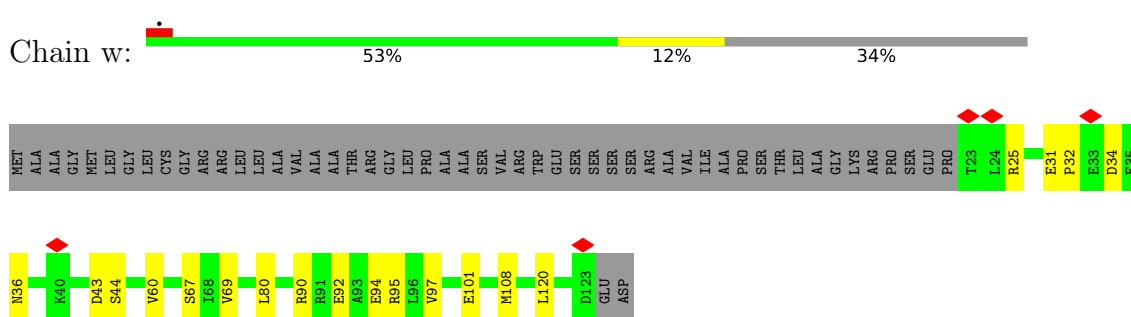
• Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



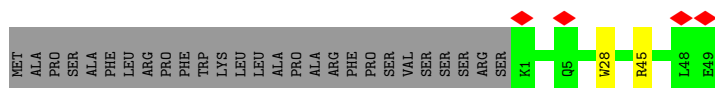
• Molecule 40: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



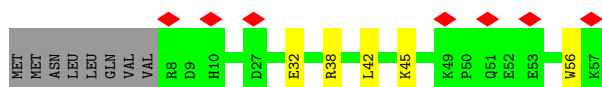
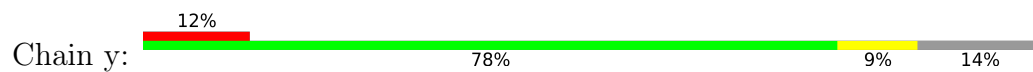
• Molecule 41: Mitochondrial complex I, ESSS subunit



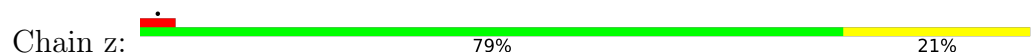
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



- Molecule 43: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



- Molecule 44: Complex I-MWFE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	32982	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	90	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.561	Depositor
Minimum map value	-0.069	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	173.24, 197.64, 285.48	wwPDB
Map dimensions	162, 142, 234	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.22, 1.22, 1.22	Depositor

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: SEP, FES, MYR, PC1, ZMP, SF4, K, FME, AMP, NDP, ZN, FMN, AYA, 3PE, 2MR, 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	1	0.21	0/3386	0.40	0/4575
2	2	0.19	0/1695	0.42	0/2306
3	3	0.19	0/5362	0.37	0/7266
4	4	0.22	0/3535	0.39	0/4791
5	5	0.21	0/1776	0.40	0/2417
6	6	0.22	0/1278	0.38	0/1728
7	9	0.22	0/1445	0.39	0/1956
8	a	0.17	0/383	0.34	0/518
9	b	0.17	0/749	0.29	0/1009
10	c	0.21	0/1047	0.42	0/1415
11	d	0.18	0/2824	0.37	0/3830
12	e	0.24	0/702	0.52	1/945 (0.1%)
13	f	0.21	0/937	0.36	0/1271
14	g	0.22	0/993	0.40	0/1336
15	h	0.18	0/779	0.38	0/1053
16	i	0.20	0/1250	0.38	0/1698
17	X	0.23	0/713	0.45	0/963
17	j	0.24	0/670	0.52	0/902
18	A	0.23	0/947	0.46	0/1296
19	H	0.25	0/2603	0.49	0/3561
20	J	0.27	0/1378	0.56	0/1868
21	K	0.29	0/749	0.52	0/1014
22	L	0.26	0/4925	0.49	0/6700
23	M	0.28	0/3731	0.49	0/5085
24	N	0.28	0/2787	0.49	0/3795
25	V	0.20	0/1041	0.38	0/1412
26	W	0.22	0/1188	0.37	0/1607
27	Y	0.20	0/1440	0.38	0/1942
28	Z	0.22	0/1475	0.37	0/1989
29	k	0.20	0/2646	0.33	0/3579
30	l	0.22	0/896	0.46	0/1200
31	m	0.20	0/647	0.47	0/890

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	n	0.18	0/653	0.34	0/882
33	o	0.22	0/1035	0.33	0/1398
34	p	0.21	0/1085	0.36	0/1467
35	q	0.21	0/1171	0.35	0/1579
36	r	0.22	0/874	0.40	0/1188
37	s	0.22	0/1072	0.50	1/1436 (0.1%)
38	t	0.21	0/1573	0.37	0/2130
39	u	0.20	0/590	0.43	0/810
40	v	0.21	0/1361	0.42	0/1861
41	w	0.23	0/872	0.48	0/1185
42	x	0.18	0/425	0.34	0/576
43	y	0.18	0/449	0.33	0/605
44	z	0.24	0/591	0.51	0/795
All	All	0.22	0/67728	0.42	2/91829 (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	3	0	1
4	4	0	1
20	J	0	1
All	All	0	3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	s	117	ARG	CB-CG-CD	5.55	124.07	111.30
12	e	88	ARG	CA-CB-CG	5.03	124.16	114.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	3	259	ASN	Peptide
4	4	275	TYR	Peptide
20	J	115	ILE	Peptide

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	1	3312	0	3266	42	0
2	2	1655	0	1668	20	0
3	3	5275	0	5300	61	0
4	4	3457	0	3398	33	0
5	5	1726	0	1676	14	0
6	6	1247	0	1256	22	0
7	9	1414	0	1371	25	0
8	a	371	0	344	5	0
9	b	737	0	710	1	0
10	c	1024	0	1023	19	0
11	d	2748	0	2763	28	0
12	e	691	0	706	11	0
13	f	917	0	958	9	0
14	g	969	0	980	15	0
15	h	769	0	780	7	0
16	i	1209	0	1182	5	0
17	X	701	0	692	10	0
17	j	660	0	662	10	0
18	A	922	0	953	16	0
19	H	2528	0	2641	46	0
20	J	1344	0	1364	25	0
21	K	749	0	793	22	0
22	L	4807	0	4949	79	0
23	M	3647	0	3849	65	0
24	N	2723	0	2930	44	0
25	V	1028	0	1036	13	0
26	W	1155	0	1177	23	0
27	Y	1403	0	1392	25	0
28	Z	1441	0	1419	21	0
29	k	2596	0	2559	21	0
30	l	874	0	869	22	0
31	m	626	0	635	8	0
32	n	634	0	616	0	0
33	o	1004	0	995	11	0
34	p	1059	0	1062	14	0
35	q	1142	0	1137	17	0
36	r	846	0	864	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
37	s	1047	0	1013	16	0
38	t	1520	0	1477	16	0
39	u	563	0	509	8	0
40	v	1307	0	1207	15	0
41	w	846	0	792	16	0
42	x	412	0	411	2	0
43	y	436	0	437	3	0
44	z	576	0	570	13	0
45	1	8	0	0	0	0
45	3	16	0	0	0	0
45	6	8	0	0	0	0
45	9	16	0	0	0	0
46	1	31	0	19	0	0
47	1	44	0	27	3	0
48	2	4	0	0	0	0
48	3	4	0	0	0	0
49	3	1	0	0	0	0
50	4	40	0	54	0	0
50	6	51	0	82	1	0
50	A	51	0	82	1	0
50	H	51	0	82	1	0
50	J	40	0	54	2	0
50	L	51	0	82	1	0
50	M	44	0	65	0	0
50	V	64	0	75	2	0
50	o	31	0	36	0	0
51	6	46	0	69	0	0
51	9	54	0	88	0	0
51	L	108	0	176	3	0
51	M	54	0	88	4	0
52	b	1	0	0	0	0
53	d	48	0	26	3	0
54	X	31	0	34	0	0
54	j	34	0	40	1	0
55	k	23	0	12	3	0
56	s	15	0	26	0	0
All	All	67086	0	67608	730	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 5.

The worst 5 of 730 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)
29:k:94:TYR:HH	29:k:151:HIS:HD1	1.31	0.77
2:2:79:ARG:HE	10:c:131:SER:HB3	1.58	0.68
22:L:356:ILE:HA	22:L:359:MET:HE2	1.75	0.68
3:3:36:GLN:HE22	10:c:49:VAL:H	1.39	0.67
3:3:126:ASP:HB2	4:4:328:ALA:HB3	1.77	0.67

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	1	344/368 (94%)	341 (99%)	3 (1%)	70	76
2	2	183/210 (87%)	183 (100%)	0	100	100
3	3	578/608 (95%)	578 (100%)	0	100	100
4	4	370/391 (95%)	370 (100%)	0	100	100
5	5	189/230 (82%)	189 (100%)	0	100	100
6	6	132/181 (73%)	132 (100%)	0	100	100
7	9	151/179 (84%)	150 (99%)	1 (1%)	76	78
8	a	43/93 (46%)	43 (100%)	0	100	100
9	b	79/97 (81%)	78 (99%)	1 (1%)	61	72
10	c	113/150 (75%)	113 (100%)	0	100	100
11	d	294/326 (90%)	293 (100%)	1 (0%)	86	84
12	e	76/82 (93%)	76 (100%)	0	100	100
13	f	101/102 (99%)	101 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	g	107/124 (86%)	107 (100%)	0	100	100
15	h	84/96 (88%)	83 (99%)	1 (1%)	63	73
16	i	131/131 (100%)	130 (99%)	1 (1%)	73	77
17	X	80/141 (57%)	80 (100%)	0	100	100
17	j	76/141 (54%)	76 (100%)	0	100	100
18	A	103/103 (100%)	103 (100%)	0	100	100
19	H	278/278 (100%)	276 (99%)	2 (1%)	76	78
20	J	144/144 (100%)	142 (99%)	2 (1%)	59	71
21	K	86/86 (100%)	86 (100%)	0	100	100
22	L	538/538 (100%)	537 (100%)	1 (0%)	87	85
23	M	411/411 (100%)	411 (100%)	0	100	100
24	N	315/315 (100%)	314 (100%)	1 (0%)	86	84
25	V	101/102 (99%)	100 (99%)	1 (1%)	68	75
26	W	122/160 (76%)	122 (100%)	0	100	100
27	Y	154/154 (100%)	153 (99%)	1 (1%)	78	80
28	Z	155/157 (99%)	155 (100%)	0	100	100
29	k	283/309 (92%)	281 (99%)	2 (1%)	76	78
30	l	94/95 (99%)	93 (99%)	1 (1%)	65	74
31	m	69/72 (96%)	69 (100%)	0	100	100
32	n	61/76 (80%)	60 (98%)	1 (2%)	55	70
33	o	107/109 (98%)	105 (98%)	2 (2%)	50	67
34	p	114/116 (98%)	114 (100%)	0	100	100
35	q	119/122 (98%)	118 (99%)	1 (1%)	73	77
36	r	95/122 (78%)	94 (99%)	1 (1%)	65	74
37	s	110/120 (92%)	110 (100%)	0	100	100
38	t	159/161 (99%)	159 (100%)	0	100	100
39	u	59/84 (70%)	59 (100%)	0	100	100
40	v	140/160 (88%)	140 (100%)	0	100	100
41	w	92/130 (71%)	91 (99%)	1 (1%)	65	74
42	x	44/67 (66%)	44 (100%)	0	100	100
43	y	46/54 (85%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	z	59/59 (100%)	59 (100%)	0	100	100
All	All	7189/7954 (90%)	7164 (100%)	25 (0%)	84	84

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
25	V	84	ASP
29	k	262	LEU
41	w	36	ASN
29	k	44	GLU
30	l	76	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
22	L	175	ASN
38	t	13	GLN
23	M	338	HIS
38	t	12	GLN
44	z	44	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

7 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
29	SEP	k	36	29	8,9,10	1.56	1 (12%)	7,12,14	1.33	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	FME	M	1	23	8,9,10	1.08	1 (12%)	8,9,11	1.14	1 (12%)
4	2MR	4	85	4	10,12,13	2.45	2 (20%)	5,13,15	0.99	0
25	AYA	V	1	25	6,7,8	1.27	1 (16%)	6,8,10	1.83	2 (33%)
22	FME	L	1	22	8,9,10	0.99	0	8,9,11	0.96	1 (12%)
15	AYA	h	1	15	6,7,8	1.31	1 (16%)	6,8,10	1.24	1 (16%)
21	FME	K	1	21	8,9,10	0.99	0	8,9,11	1.04	1 (12%)

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
29	SEP	k	36	29	-	3/6/8/10	-
23	FME	M	1	23	-	4/7/9/11	-
4	2MR	4	85	4	-	3/10/13/15	-
25	AYA	V	1	25	-	3/5/6/8	-
22	FME	L	1	22	-	2/7/9/11	-
15	AYA	h	1	15	-	0/5/6/8	-
21	FME	K	1	21	-	3/7/9/11	-

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	4	85	2MR	CZ-NH2	5.15	1.44	1.33
4	4	85	2MR	CZ-NE	5.08	1.45	1.34
29	k	36	SEP	P-O1P	3.42	1.61	1.50
15	h	1	AYA	CA-N	-2.56	1.43	1.46
25	V	1	AYA	CA-N	-2.52	1.43	1.46

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	V	1	AYA	CB-CA-N	3.46	113.59	109.68
29	k	36	SEP	OG-CB-CA	2.86	110.93	108.14
15	h	1	AYA	CB-CA-N	2.80	112.84	109.68
25	V	1	AYA	CA-N-CT	2.46	124.68	121.50
21	K	1	FME	C-CA-N	2.10	113.56	109.50

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	4	85	2MR	C-CA-CB-CG
23	M	1	FME	C-CA-CB-CG
25	V	1	AYA	O-C-CA-CB
23	M	1	FME	CA-CB-CG-SD
25	V	1	AYA	OT-CT-N-CA

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	M	1	FME	2	0
21	K	1	FME	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 32 ligands modelled in this entry, 2 are monoatomic - leaving 30 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	$\# Z > 2$
50	3PE	V	201	-	26,26,50	0.48	0	29,31,55	0.50	1 (3%)
50	3PE	A	201	-	50,50,50	0.30	0	53,55,55	0.33	0
54	ZMP	X	101	17	25,30,36	0.79	1 (4%)	29,37,45	1.02	2 (6%)
50	3PE	H	401	-	50,50,50	0.31	0	53,55,55	0.34	0
45	SF4	6	201	6	0,12,12	-	-	-	-	-
50	3PE	o	501	-	30,30,50	0.38	0	33,35,55	0.37	0
45	SF4	1	501	1	0,12,12	-	-	-	-	-
50	3PE	6	203	-	50,50,50	0.30	0	53,55,55	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	3PE	L	1001	-	50,50,50	0.30	0	53,55,55	0.32	0
55	AMP	k	501	-	25,25,25	1.41	4 (16%)	37,38,38	1.93	9 (24%)
45	SF4	9	403	7	0,12,12	-	-	-	-	-
45	SF4	9	402	7	0,12,12	-	-	-	-	-
50	3PE	M	501	-	43,43,50	0.32	0	46,48,55	0.33	0
51	PC1	9	401	-	53,53,53	0.30	0	59,61,61	0.46	0
51	PC1	L	1002	-	53,53,53	0.30	0	59,61,61	0.53	1 (1%)
53	NDP	d	401	-	51,52,52	0.34	0	71,80,80	0.37	0
50	3PE	J	201	-	39,39,50	0.35	0	42,44,55	0.32	0
56	MYR	s	201	37	13,14,15	0.15	0	12,13,15	0.15	0
48	FES	3	803	3	0,4,4	-	-	-	-	-
51	PC1	6	202	-	45,45,53	0.31	0	51,53,61	0.32	0
51	PC1	L	1003	-	53,53,53	0.29	0	59,61,61	0.33	0
45	SF4	3	801	3	0,12,12	-	-	-	-	-
48	FES	2	300	2	0,4,4	-	-	-	-	-
50	3PE	V	202	-	36,36,50	0.35	0	39,41,55	0.30	0
45	SF4	3	802	3	0,12,12	-	-	-	-	-
51	PC1	M	502	-	53,53,53	0.30	0	59,61,61	0.35	0
50	3PE	4	501	-	39,39,50	0.33	0	42,44,55	0.35	0
46	FMN	1	502	-	33,33,33	1.06	2 (6%)	48,50,50	1.27	7 (14%)
54	ZMP	j	101	17	28,33,36	0.66	1 (3%)	32,40,45	1.10	3 (9%)
47	NAI	1	503	-	47,48,48	0.40	1 (2%)	64,73,73	1.79	4 (6%)

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
50	3PE	V	201	-	-	2/27/27/54	-
50	3PE	A	201	-	-	13/54/54/54	-
54	ZMP	X	101	17	-	15/35/37/43	-
50	3PE	H	401	-	-	7/54/54/54	-
50	3PE	o	501	-	-	5/34/34/54	-
45	SF4	6	201	6	-	-	0/6/5/5
45	SF4	1	501	1	-	-	0/6/5/5
50	3PE	6	203	-	-	11/54/54/54	-
50	3PE	L	1001	-	-	12/54/54/54	-
55	AMP	k	501	-	-	0/10/26/26	0/3/3/3
45	SF4	9	403	7	-	-	0/6/5/5

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	SF4	9	402	7	-	-	0/6/5/5
50	3PE	M	501	-	-	8/47/47/54	-
51	PC1	9	401	-	-	8/57/57/57	-
51	PC1	L	1002	-	-	14/57/57/57	-
53	NDP	d	401	-	-	10/34/77/77	0/5/5/5
50	3PE	J	201	-	-	9/43/43/54	-
56	MYR	s	201	37	-	0/12/12/13	-
48	FES	3	803	3	-	-	0/1/1/1
51	PC1	6	202	-	-	9/49/49/57	-
51	PC1	L	1003	-	-	8/57/57/57	-
45	SF4	3	801	3	-	-	0/6/5/5
48	FES	2	300	2	-	-	0/1/1/1
50	3PE	V	202	-	-	12/40/40/54	-
45	SF4	3	802	3	-	-	0/6/5/5
51	PC1	M	502	-	-	13/57/57/57	-
50	3PE	4	501	-	-	5/43/43/54	-
46	FMN	1	502	-	-	7/18/18/18	0/3/3/3
54	ZMP	j	101	17	-	10/38/40/43	-
47	NAI	1	503	-	-	8/29/72/72	0/5/5/5

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	k	501	AMP	C5-C4	4.66	1.47	1.39
46	1	502	FMN	C4A-N5	3.19	1.37	1.30
55	k	501	AMP	C5-C6	2.77	1.48	1.41
54	j	101	ZMP	C9-C10	2.42	1.53	1.50
54	X	101	ZMP	C9-C10	2.32	1.53	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	1	503	NAI	O5B-PA-O1A	-9.60	70.88	108.94
47	1	503	NAI	O2A-PA-O1A	-8.25	74.05	112.44
55	k	501	AMP	C5-C4-N3	-6.05	118.39	126.72
47	1	503	NAI	O3-PA-O1A	-5.83	93.18	110.70
55	k	501	AMP	N3-C4-N9	4.70	135.16	127.17

There are no chirality outliers.

5 of 186 torsion outliers are listed below:

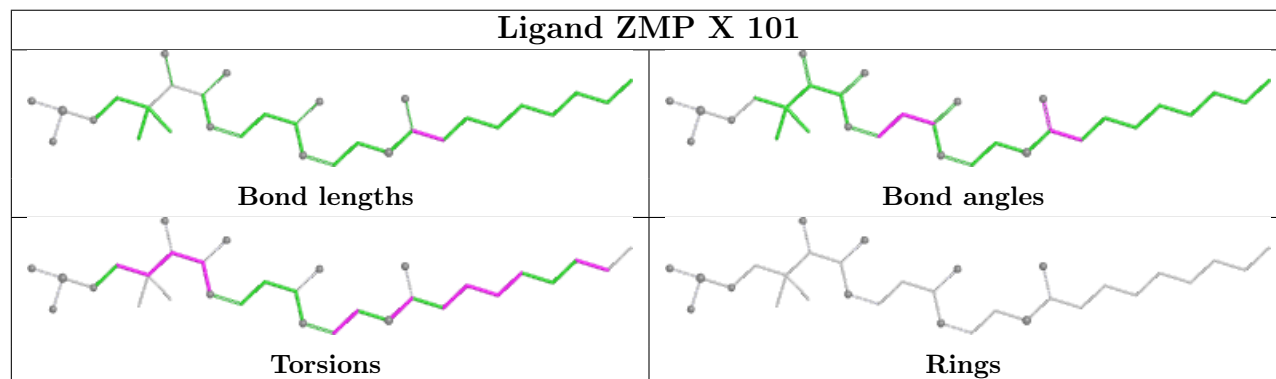
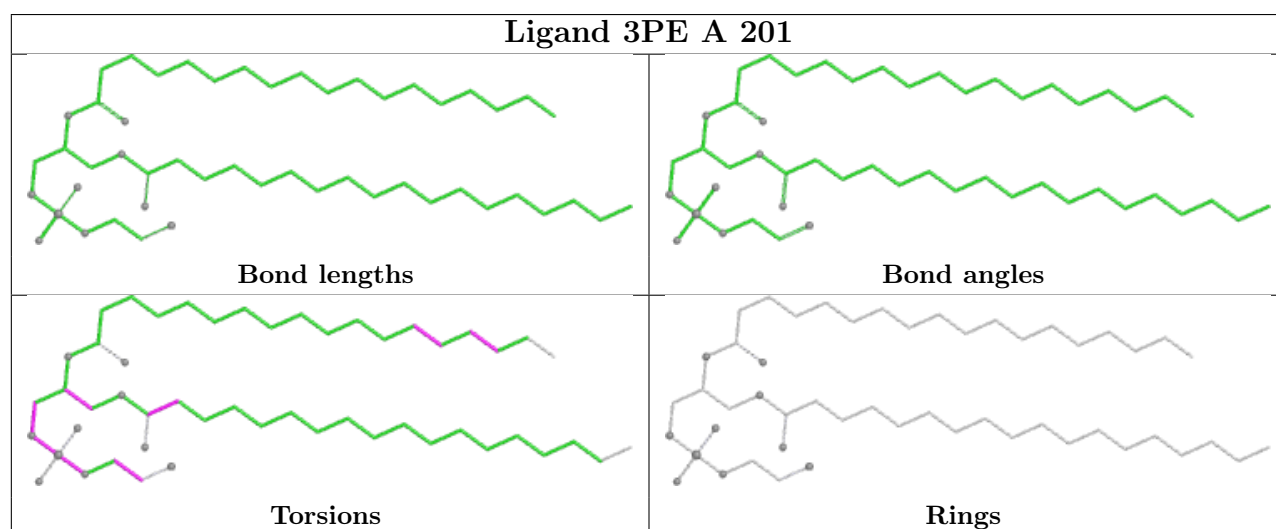
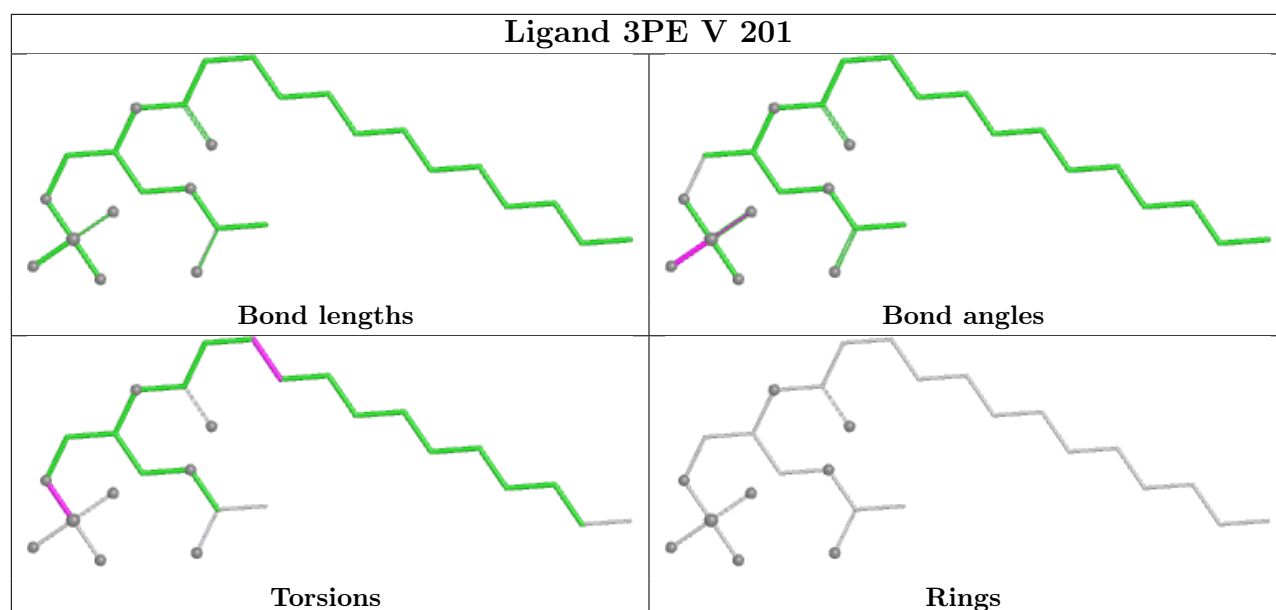
Mol	Chain	Res	Type	Atoms
46	1	502	FMN	N10-C1'-C2'-O2'
46	1	502	FMN	N10-C1'-C2'-C3'
46	1	502	FMN	C5'-O5'-P-O2P
46	1	502	FMN	C5'-O5'-P-O3P
50	4	501	3PE	C11-O13-P-O12

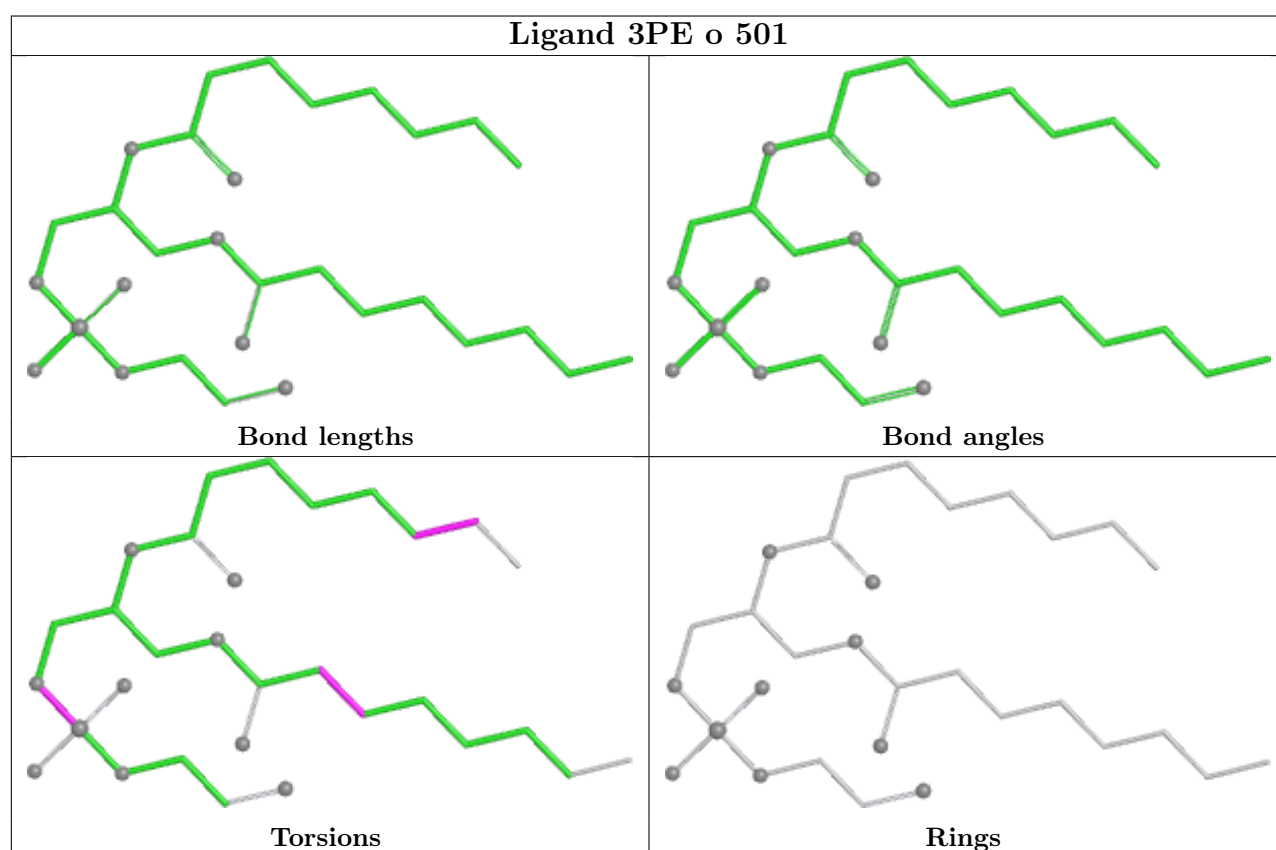
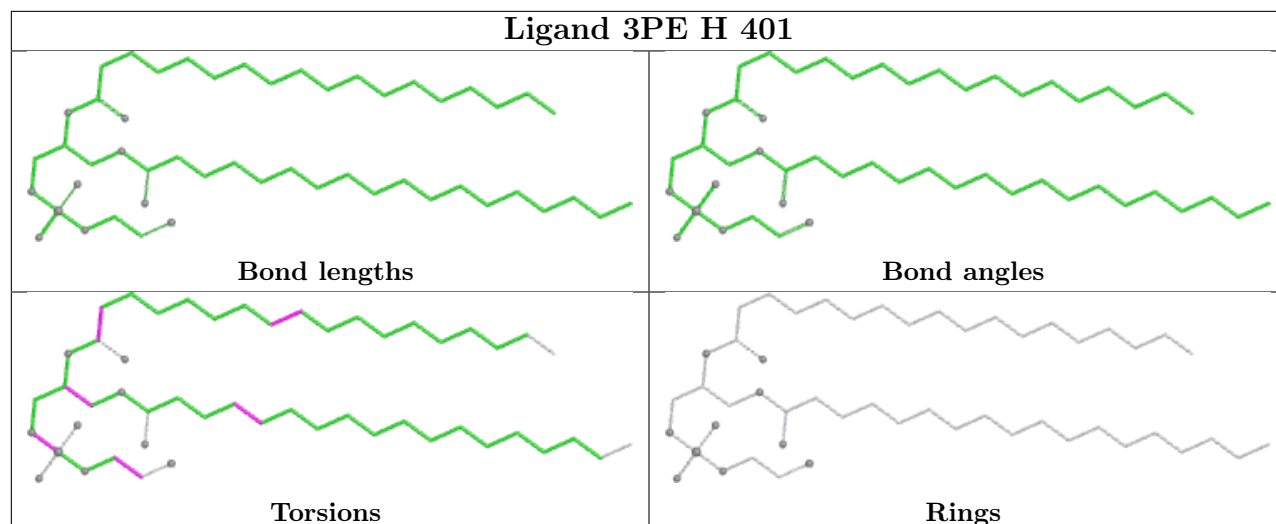
There are no ring outliers.

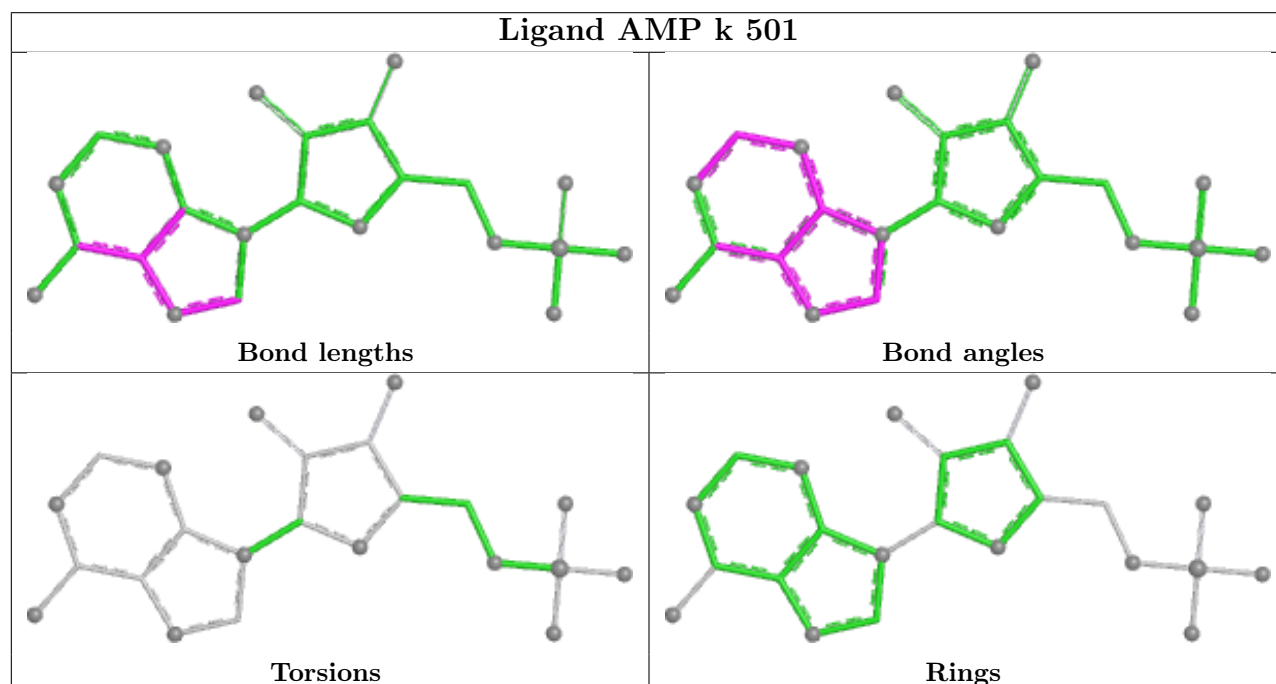
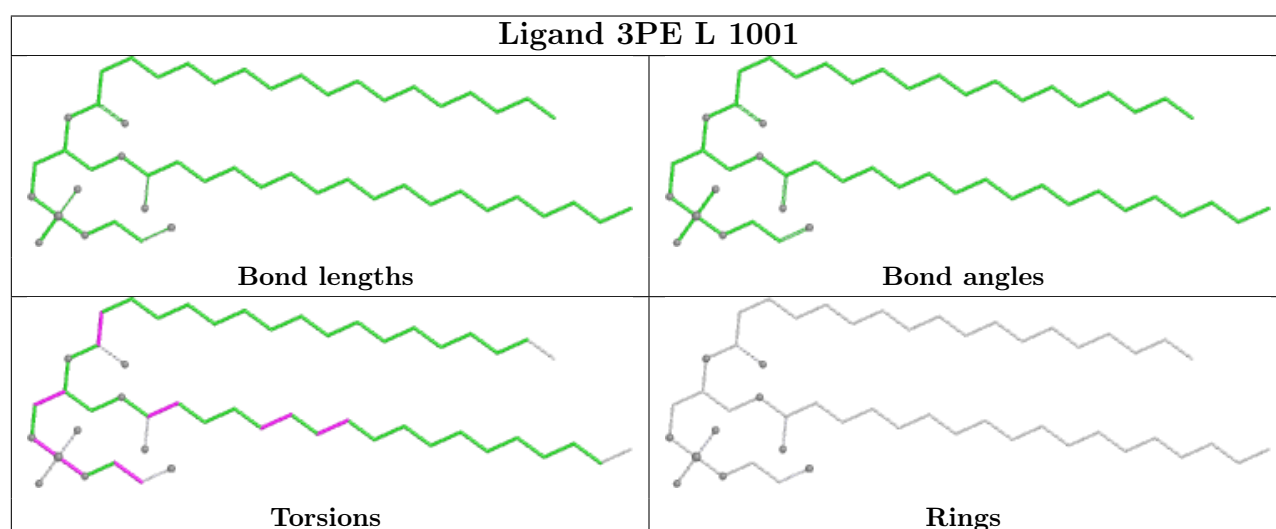
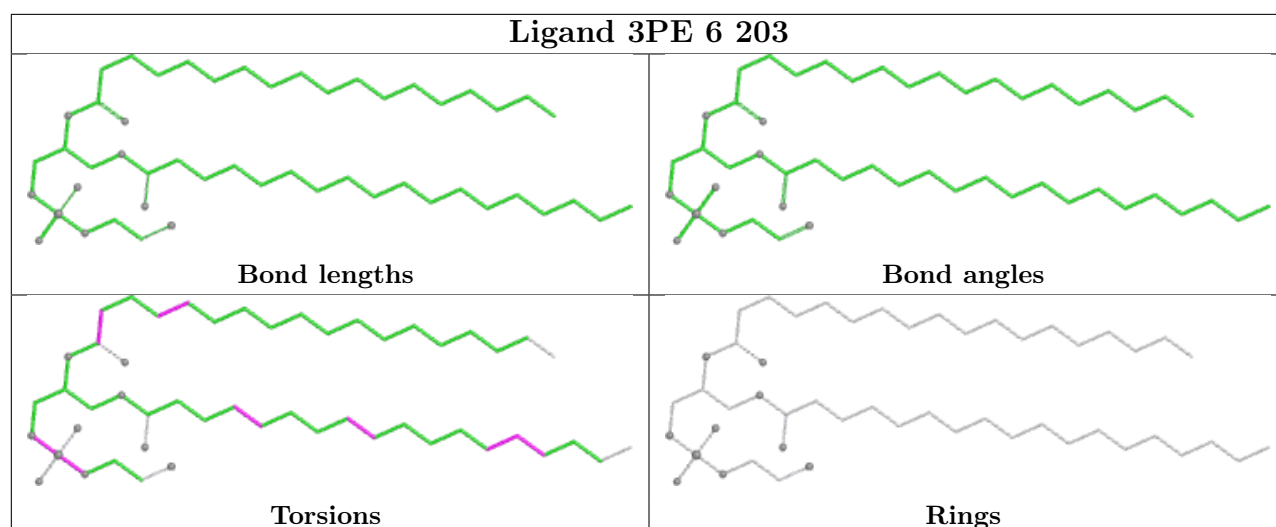
13 monomers are involved in 24 short contacts:

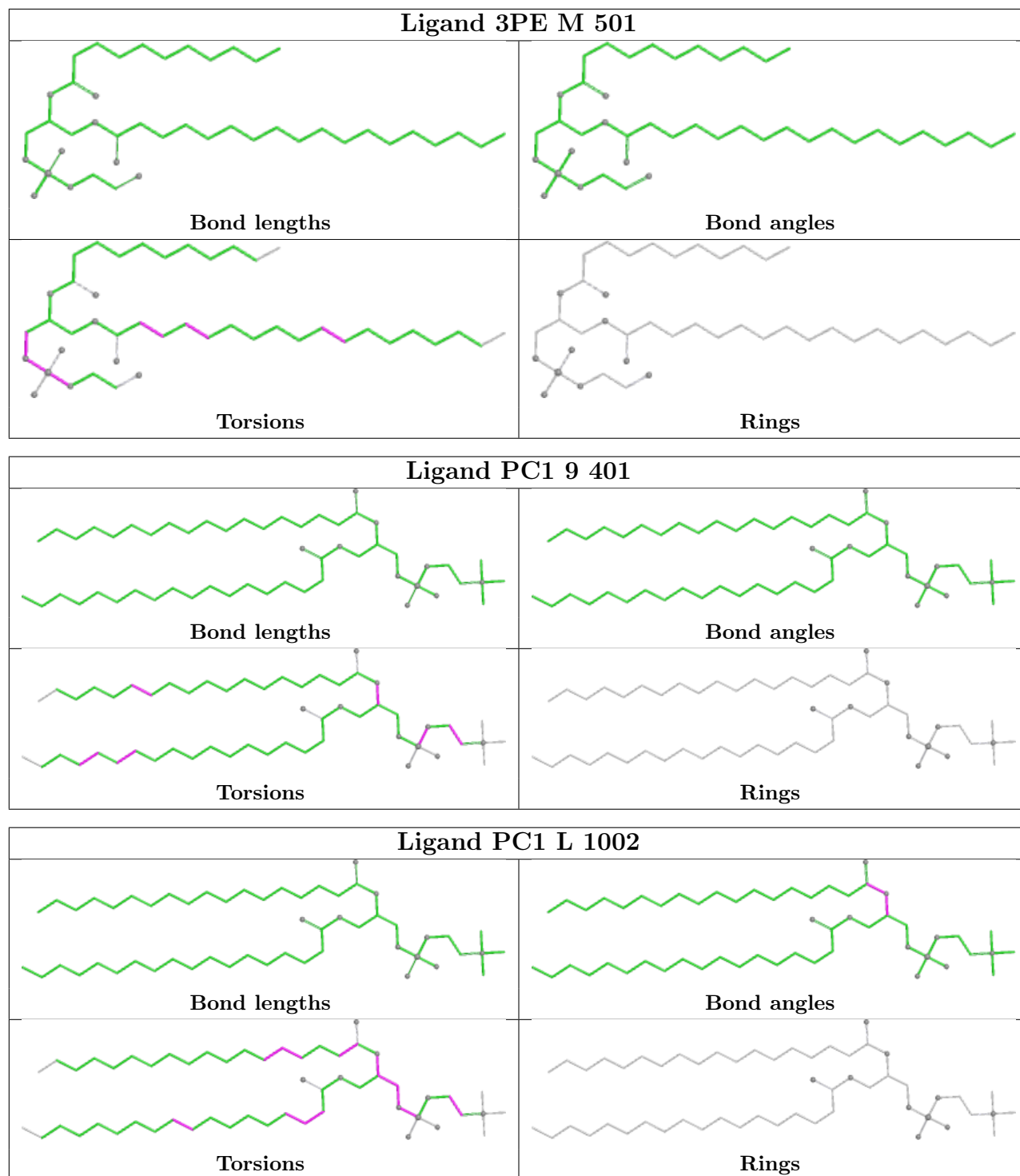
Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	A	201	3PE	1	0
50	H	401	3PE	1	0
50	6	203	3PE	1	0
50	L	1001	3PE	1	0
55	k	501	AMP	3	0
51	L	1002	PC1	2	0
53	d	401	NDP	3	0
50	J	201	3PE	2	0
51	L	1003	PC1	2	0
50	V	202	3PE	2	0
51	M	502	PC1	4	0
54	j	101	ZMP	1	0
47	1	503	NAI	3	0

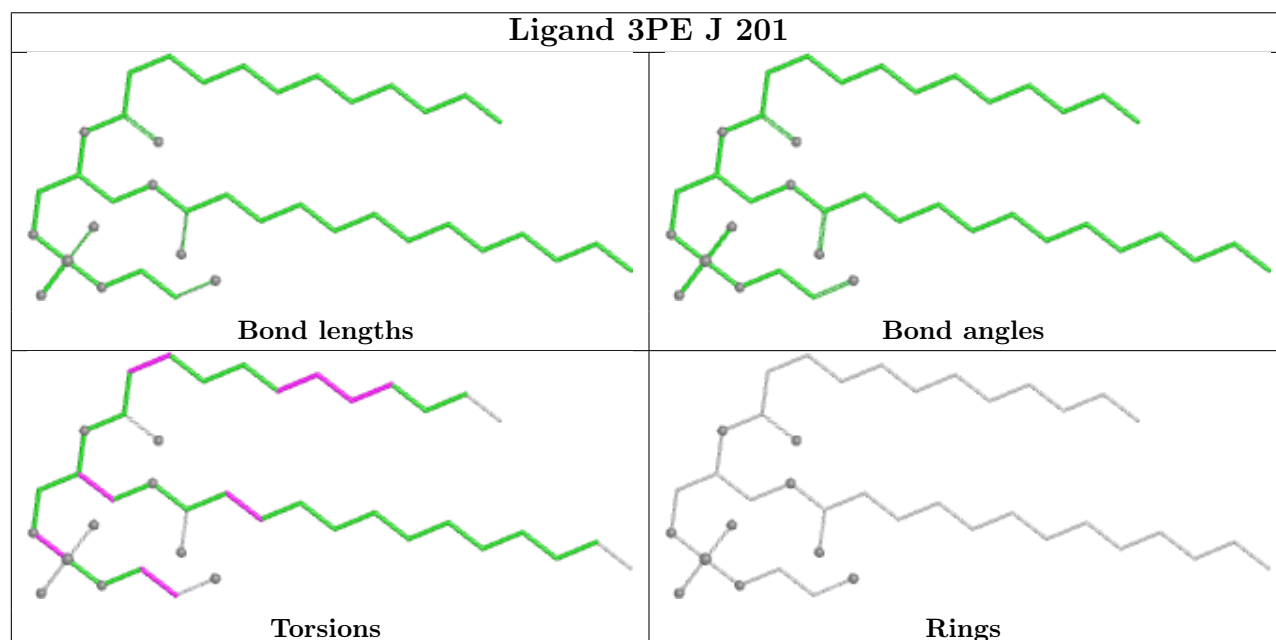
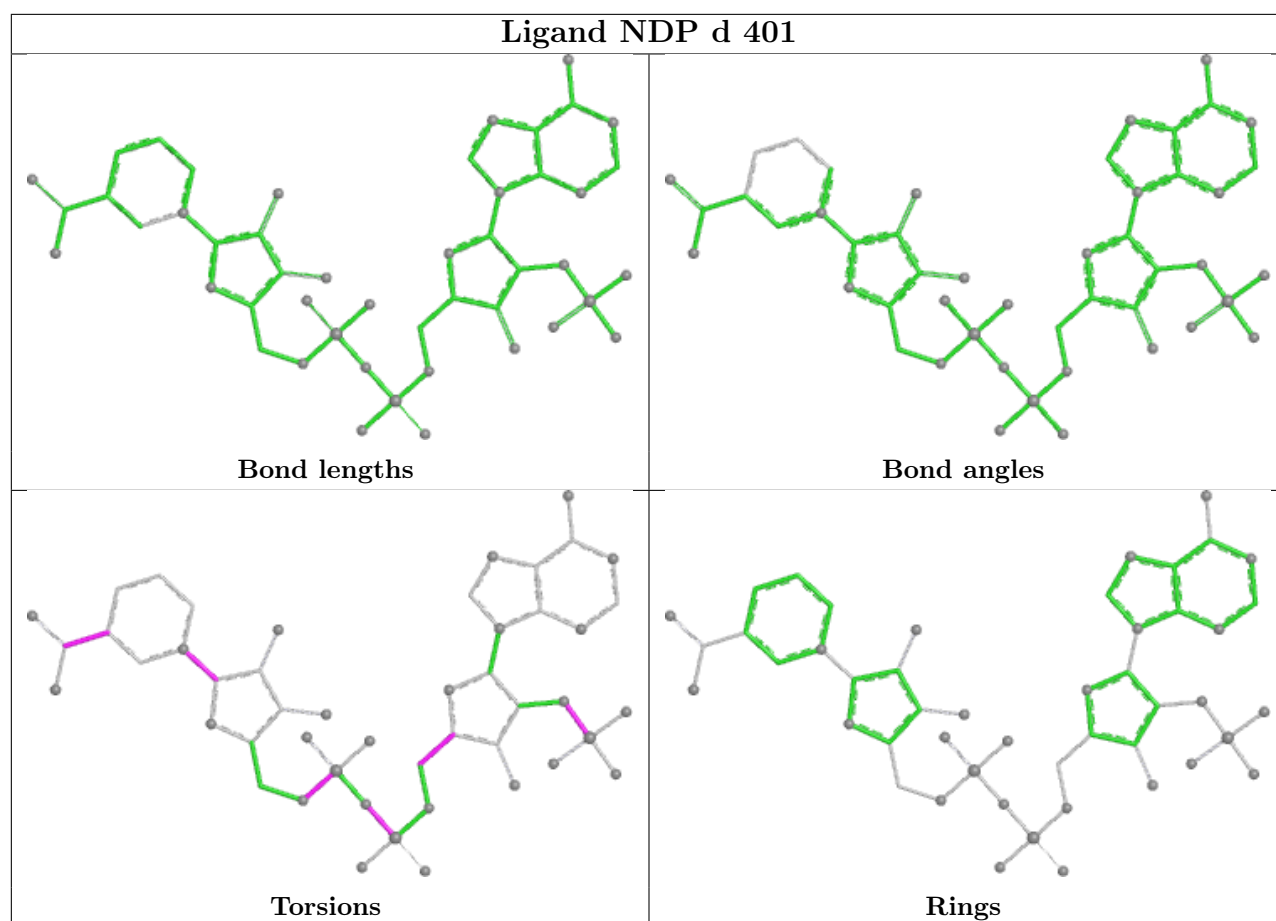
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

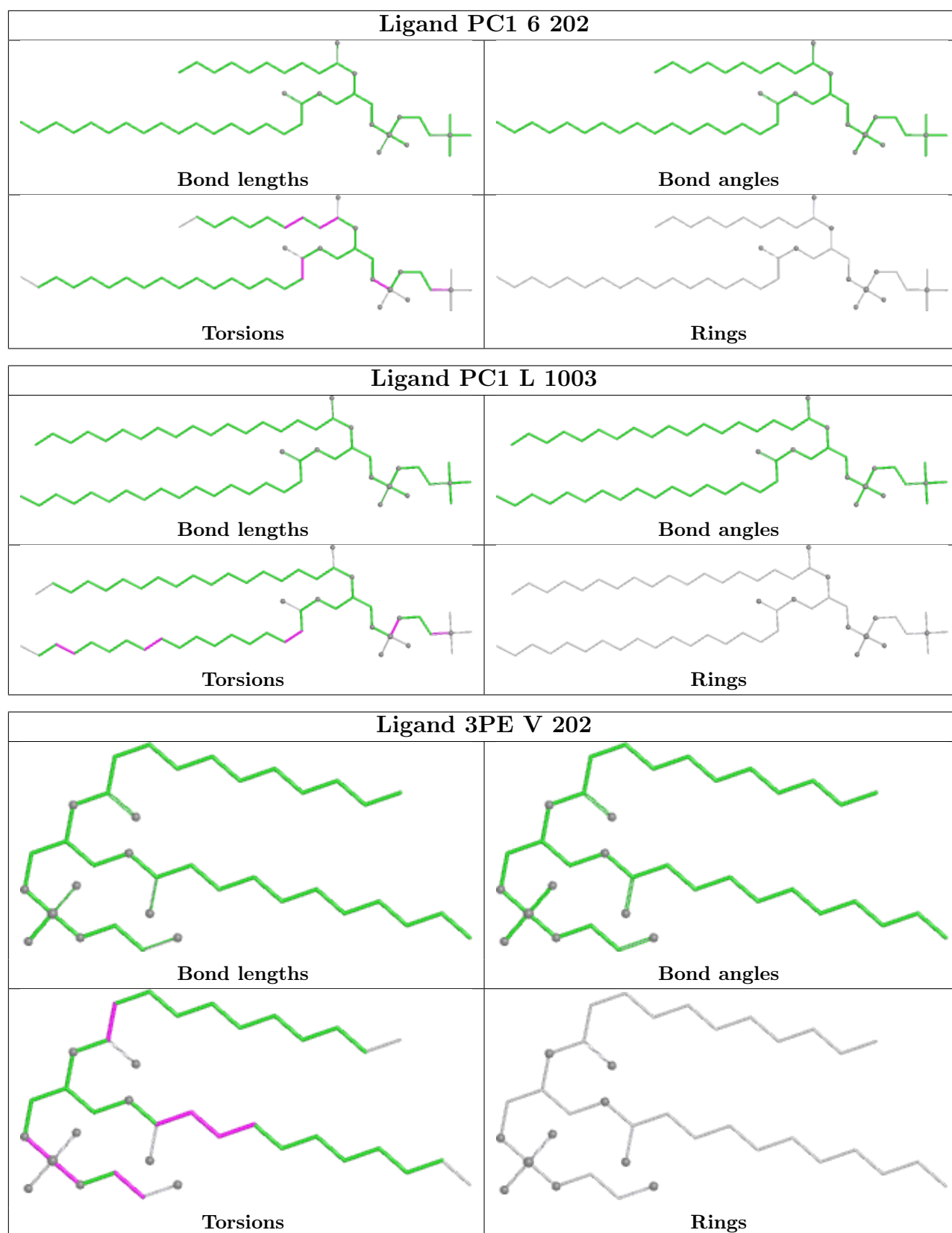


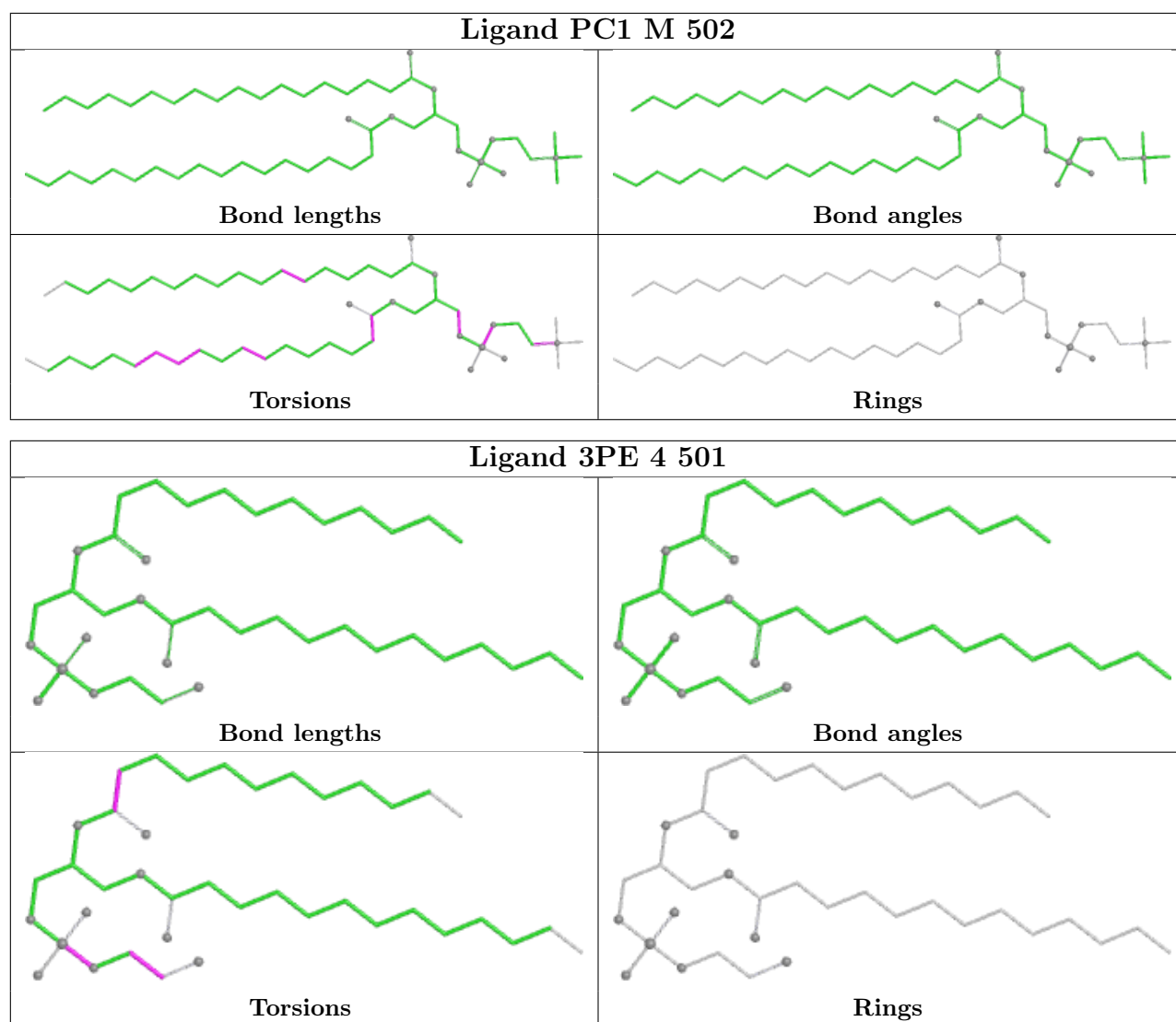


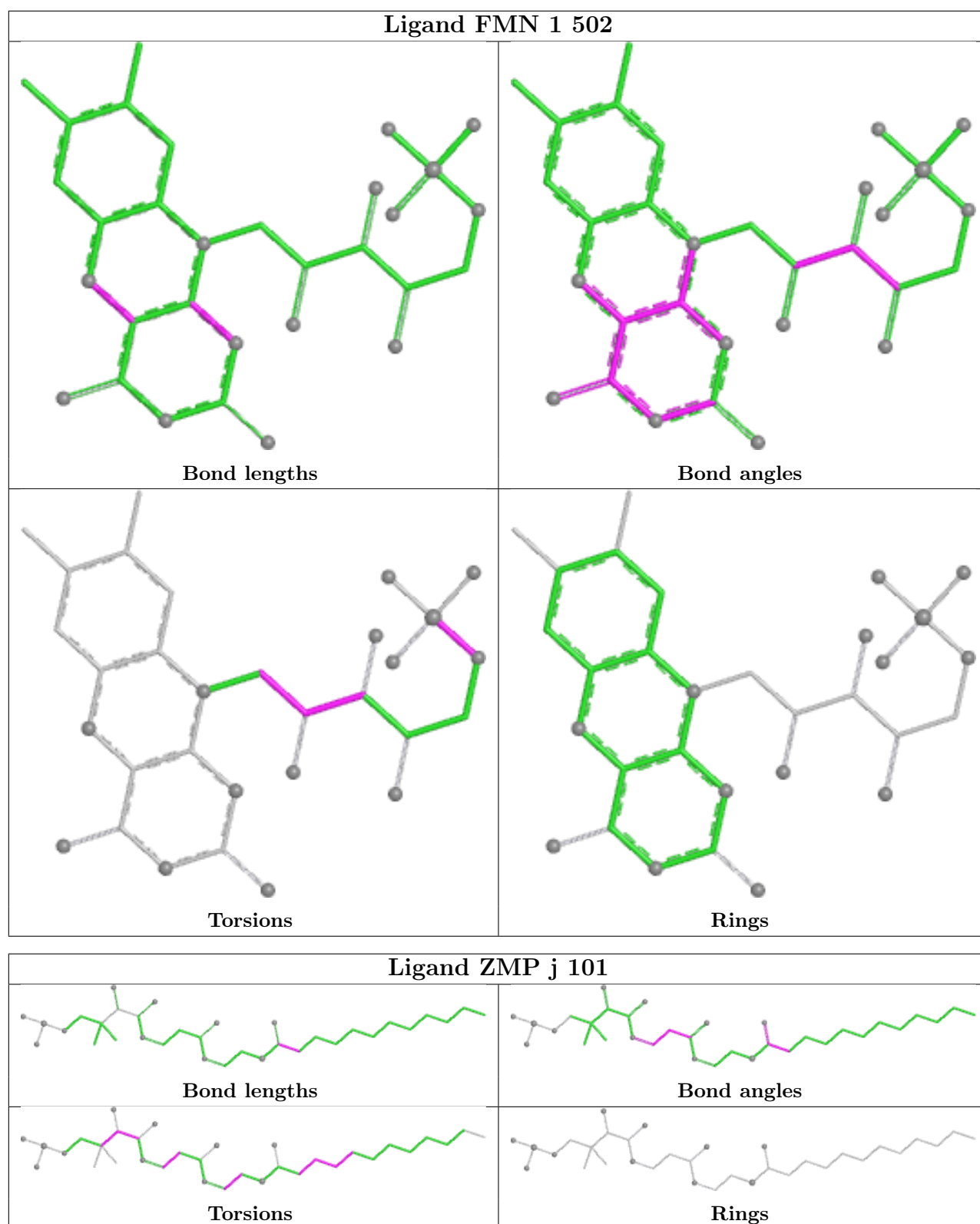


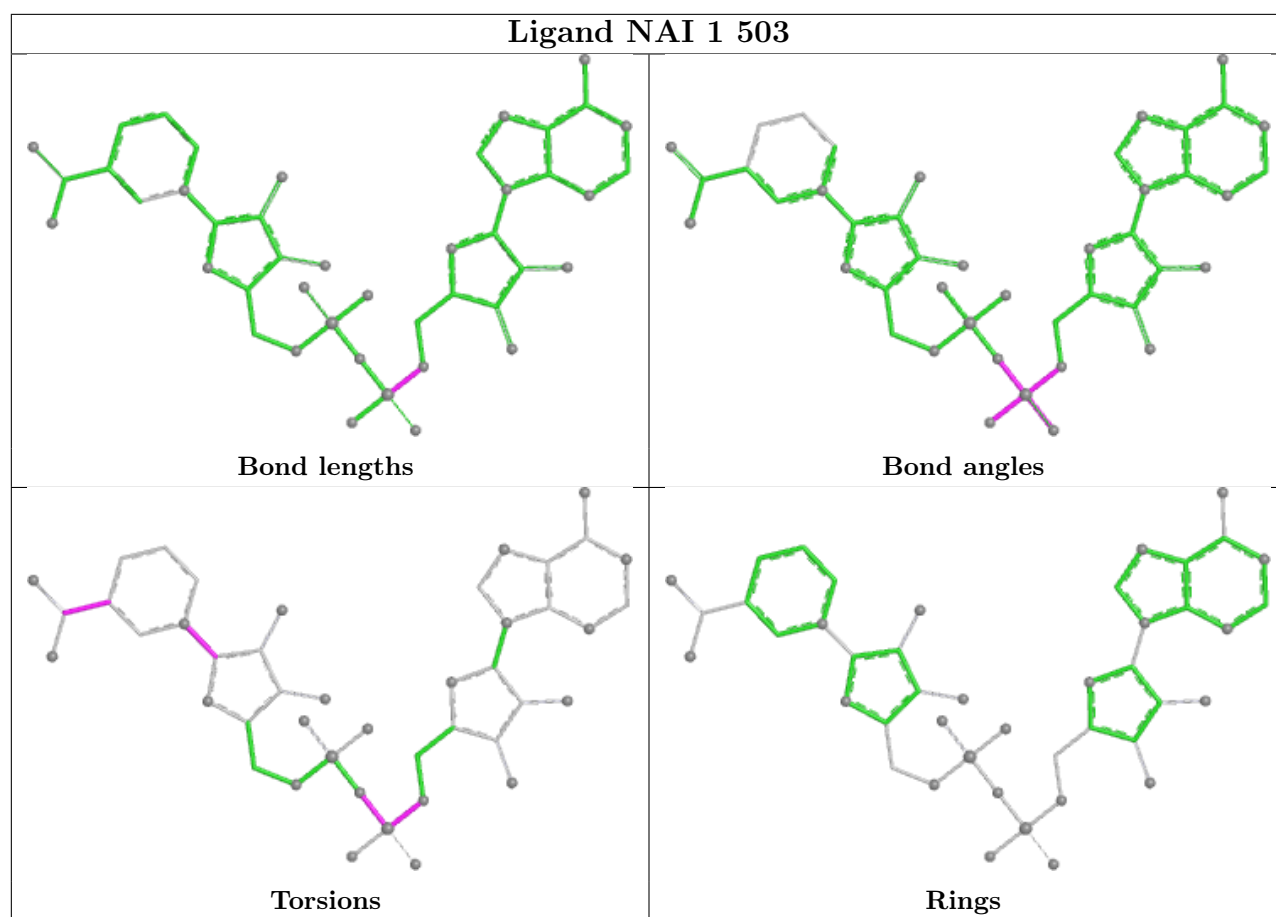












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

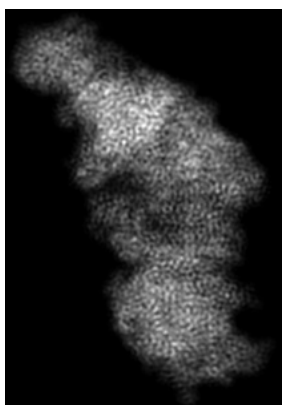
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14658. These allow visual inspection of the internal detail of the map and identification of artifacts.

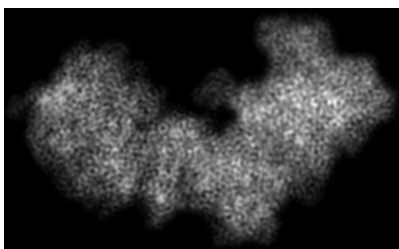
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

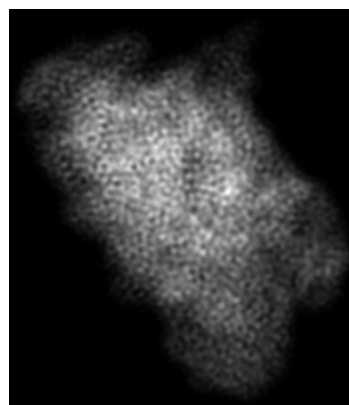
6.1.1 Primary map



X



Y



Z

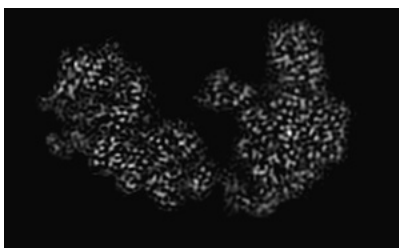
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 71



Y Index: 81



Z Index: 117

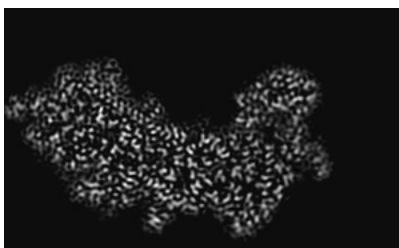
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

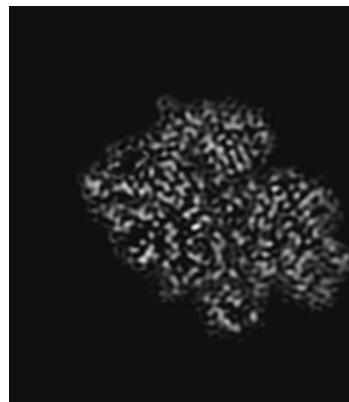
6.3.1 Primary map



X Index: 89



Y Index: 106

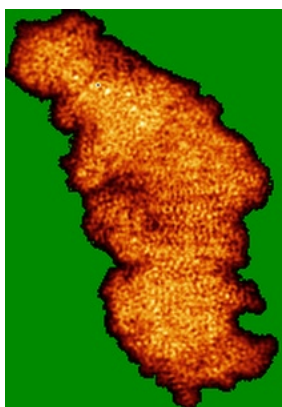


Z Index: 172

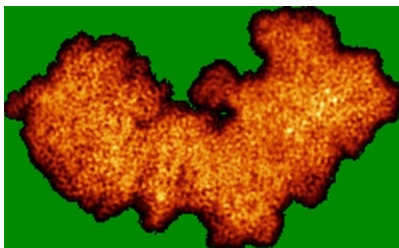
The images above show the largest variance slices of the map in three orthogonal directions.

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

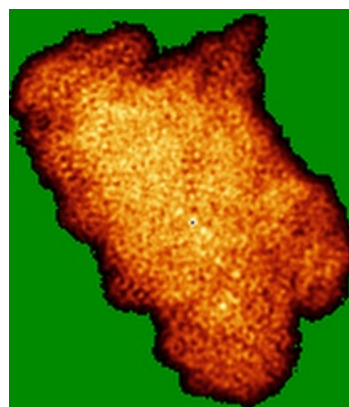
6.4.1 Primary map



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 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

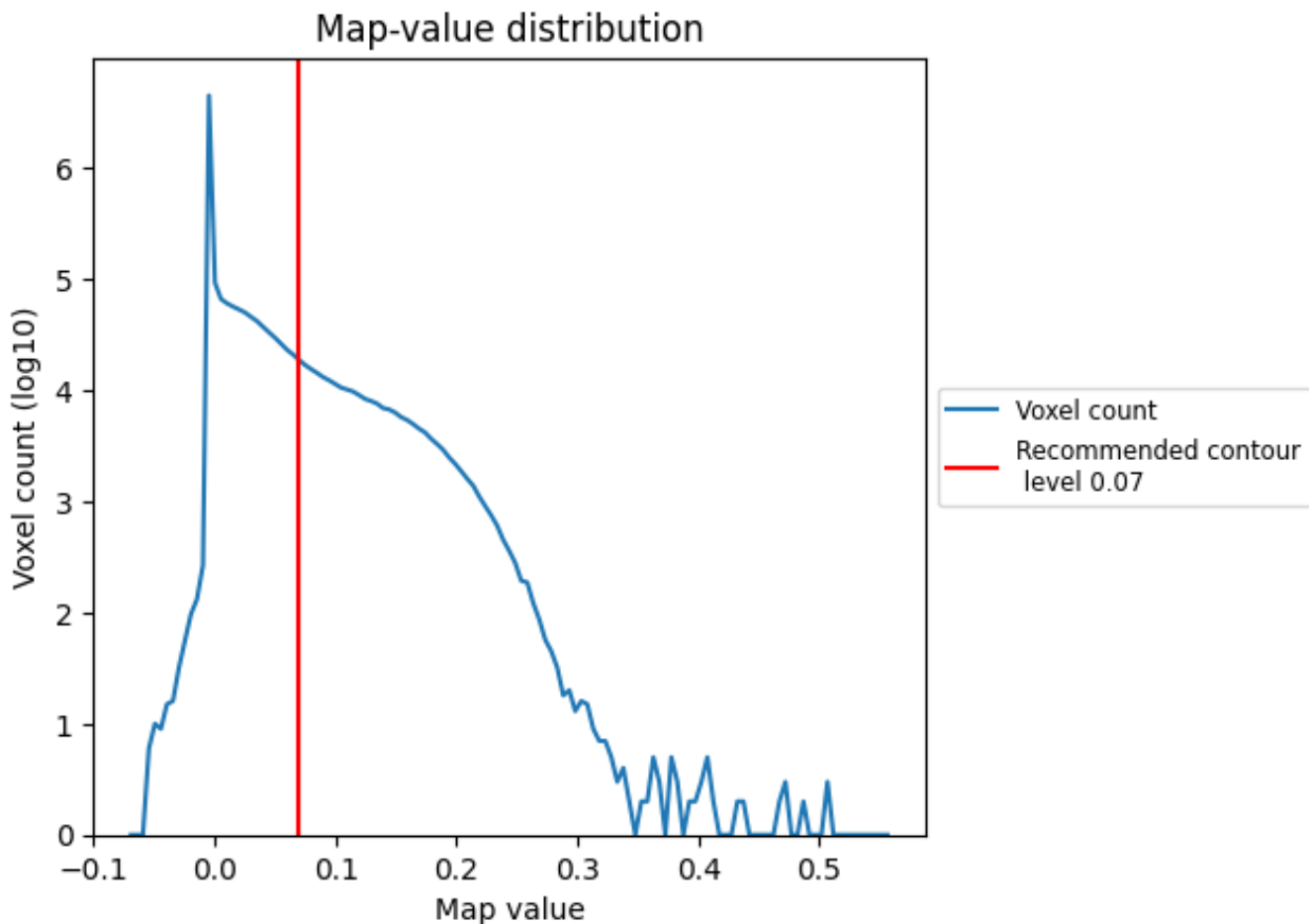
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

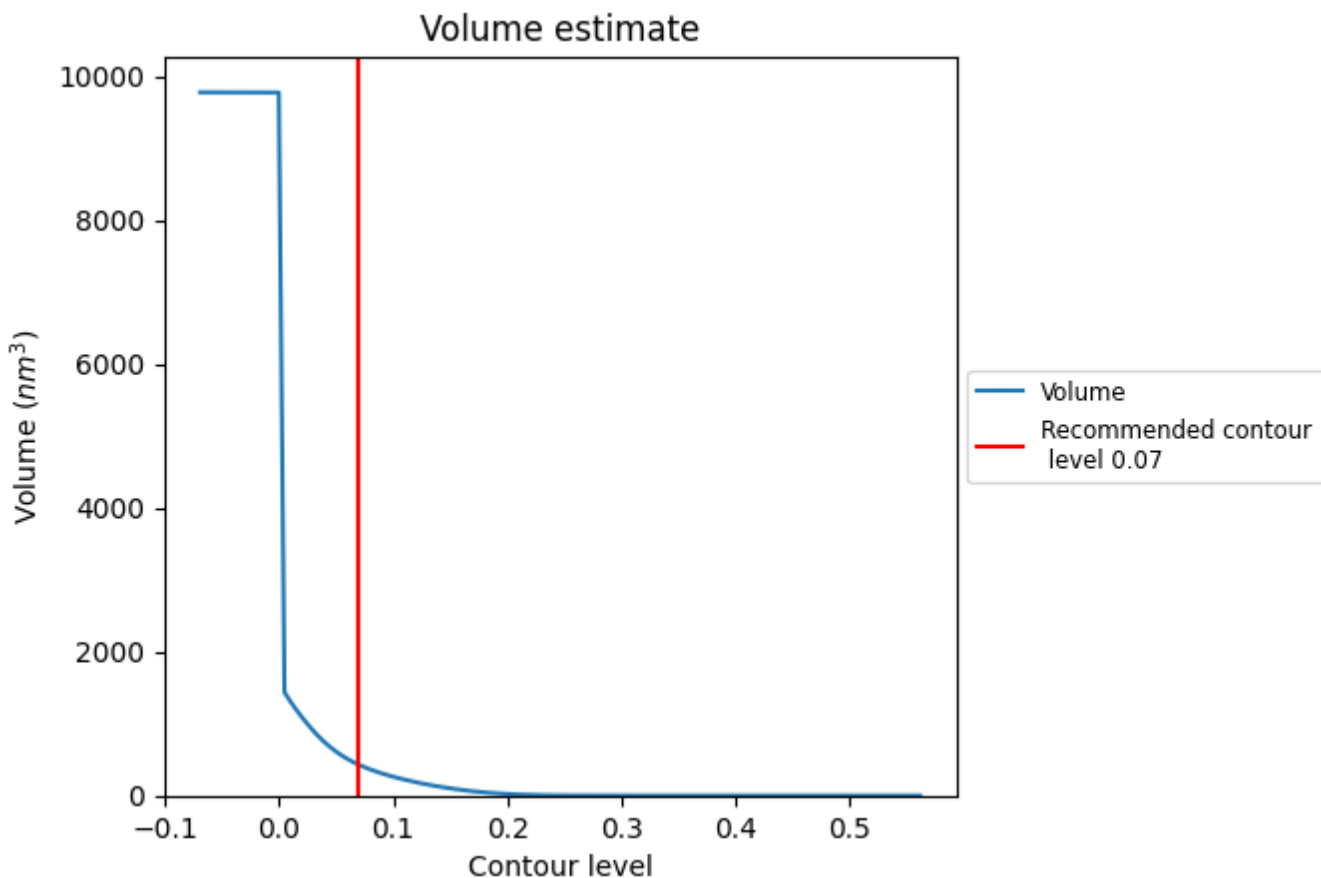
This section contains the results of statistical analysis of the map.

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 427 nm³; this corresponds to an approximate mass of 385 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.

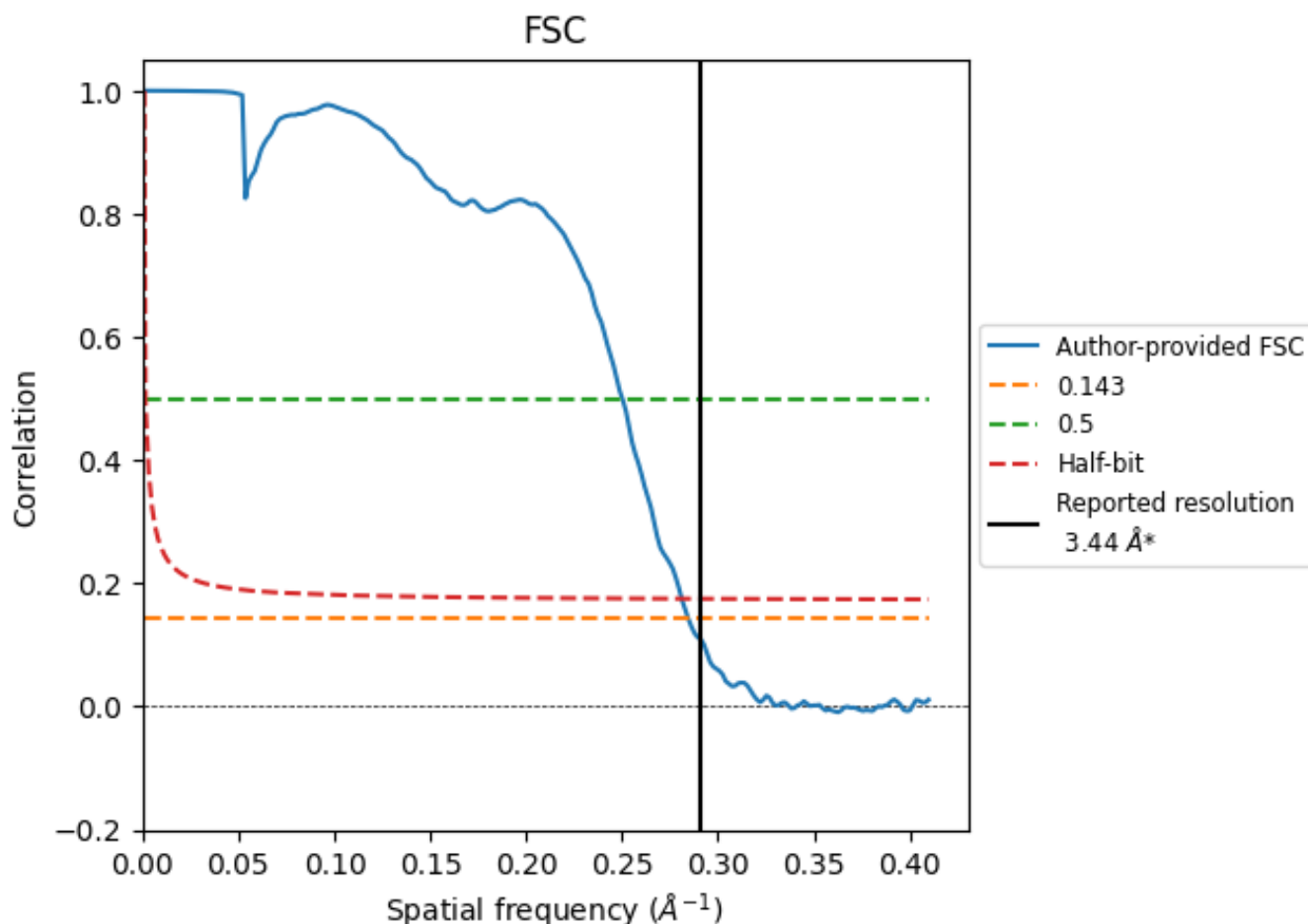
7.3 Rotationally averaged power spectrum [i](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.291 Å⁻¹

8.2 Resolution estimates [i](#)

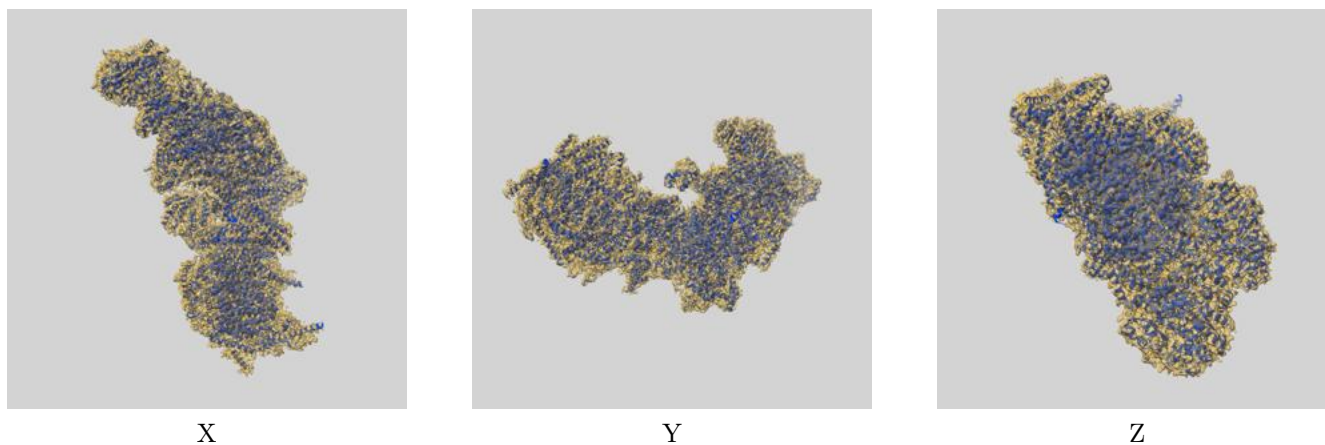
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.44	-	-
Author-provided FSC curve	3.51	4.00	3.56
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

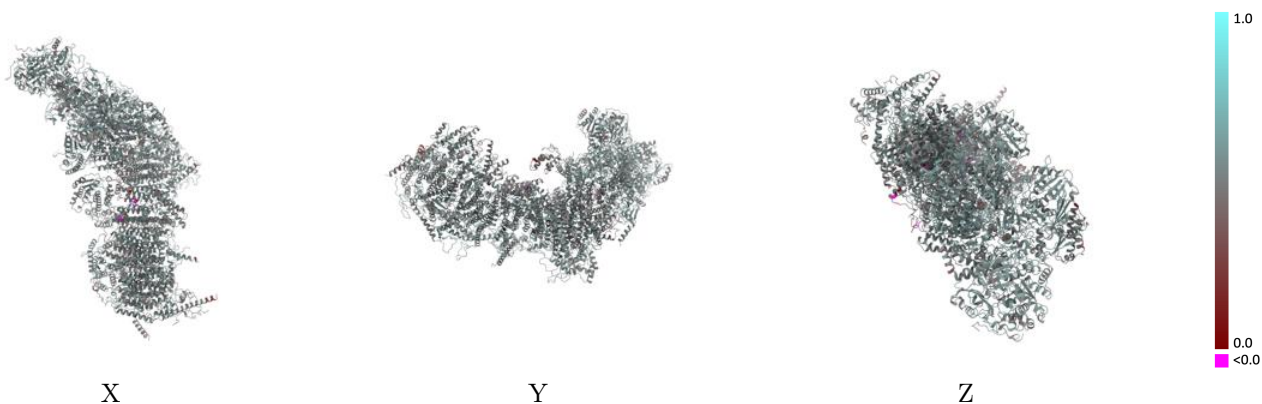
This section contains information regarding the fit between EMDB map EMD-14658 and PDB model 7ZDM. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



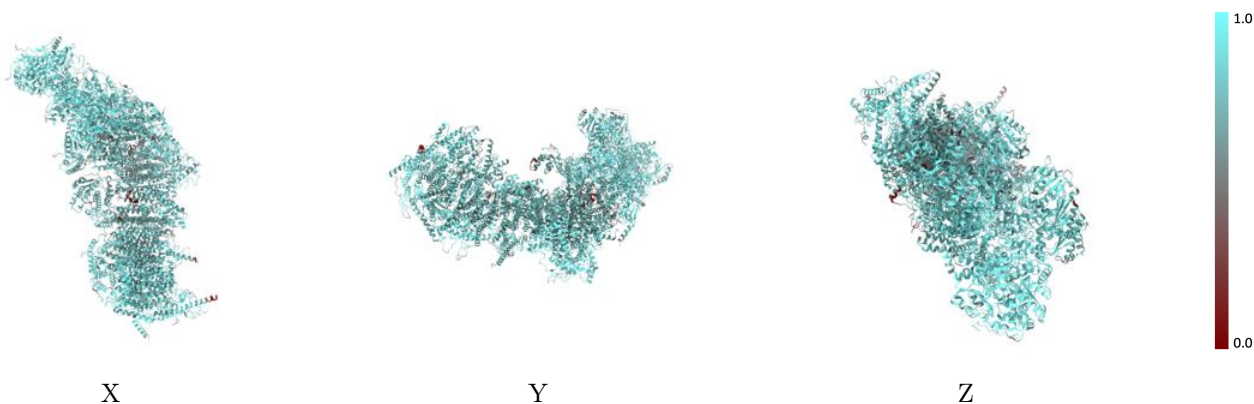
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



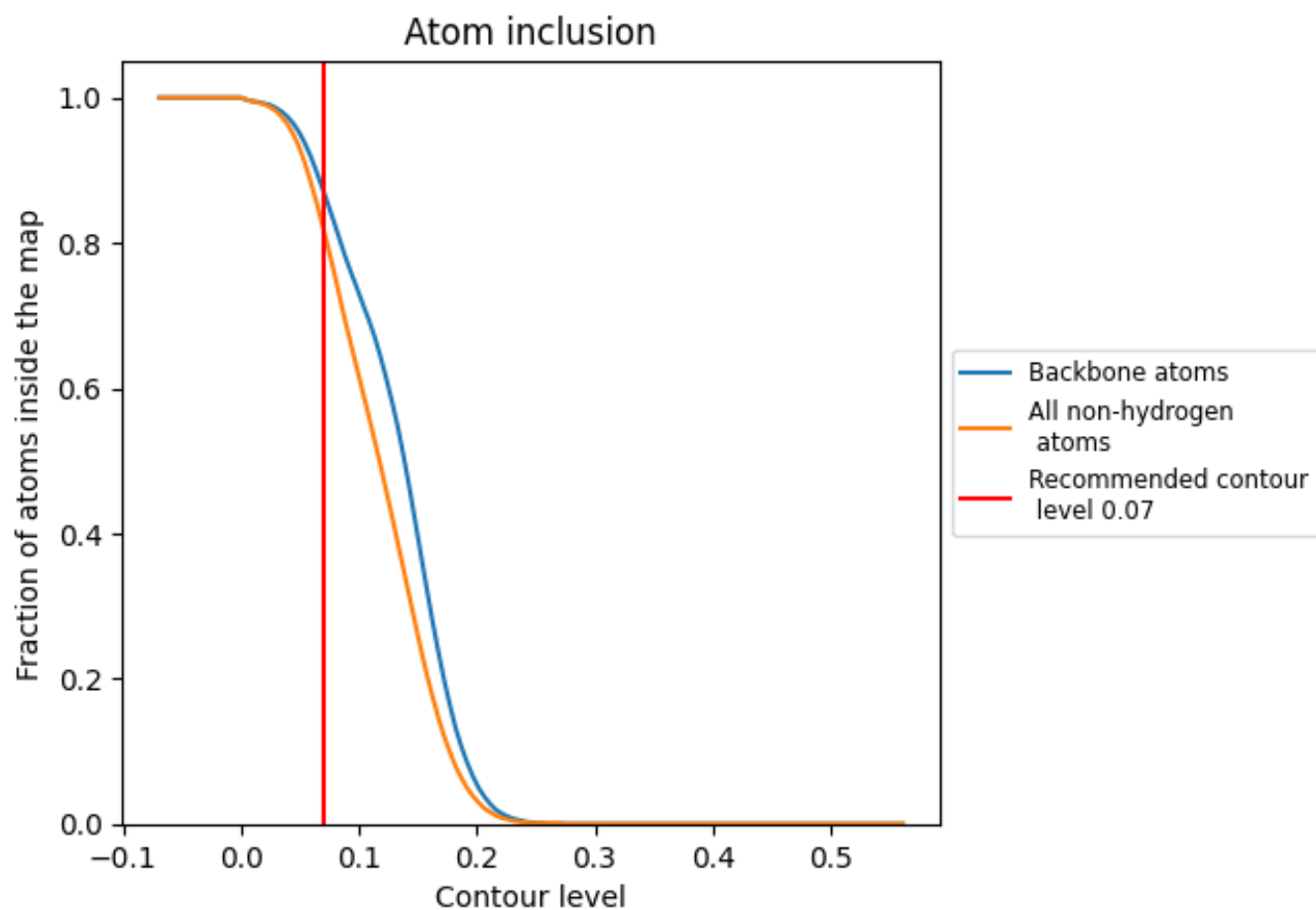
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 82% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.5240
1	 0.8900	 0.5310
2	 0.8620	 0.5300
3	 0.8460	 0.5330
4	 0.7970	 0.5180
5	 0.8610	 0.5550
6	 0.8400	 0.5440
9	 0.8320	 0.5280
A	 0.6360	 0.4750
H	 0.7410	 0.5040
J	 0.7750	 0.5110
K	 0.8060	 0.5270
L	 0.8200	 0.5220
M	 0.8440	 0.5460
N	 0.8450	 0.5390
V	 0.7690	 0.5060
W	 0.8670	 0.5430
X	 0.8280	 0.5100
Y	 0.8390	 0.5260
Z	 0.8250	 0.5240
a	 0.8400	 0.5190
b	 0.8190	 0.5480
c	 0.8040	 0.5410
d	 0.8250	 0.5320
e	 0.8230	 0.5090
f	 0.7960	 0.5220
g	 0.7890	 0.5290
h	 0.8180	 0.5260
i	 0.8430	 0.5450
j	 0.6360	 0.4420
k	 0.7960	 0.5200
l	 0.8170	 0.5200
m	 0.7900	 0.5100
n	 0.8090	 0.5030
o	 0.8330	 0.5330



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Chain	Atom inclusion	Q-score
p	 0.7910	 0.5190
q	 0.8210	 0.5130
r	 0.7970	 0.5170
s	 0.7990	 0.4910
t	 0.8240	 0.5170
u	 0.8430	 0.5040
v	 0.8180	 0.5240
w	 0.8030	 0.5250
x	 0.7590	 0.5110
y	 0.7230	 0.4980
z	 0.8160	 0.5020