



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 06:44 PM UTC

PDB ID : 5XTC / pdb_00005xtc
EMDB ID : EMD-6772
Title : Cryo-EM structure of human respiratory complex I transmembrane arm
Authors : Gu, J.; Wu, M.; Yang, M.
Deposited on : 2017-06-19
Resolution : 3.70 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:

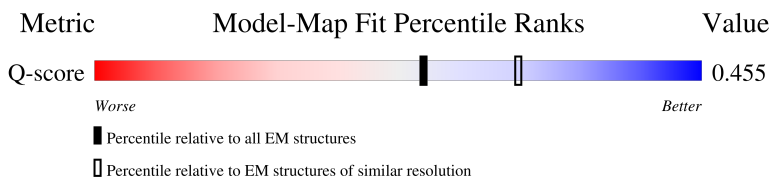
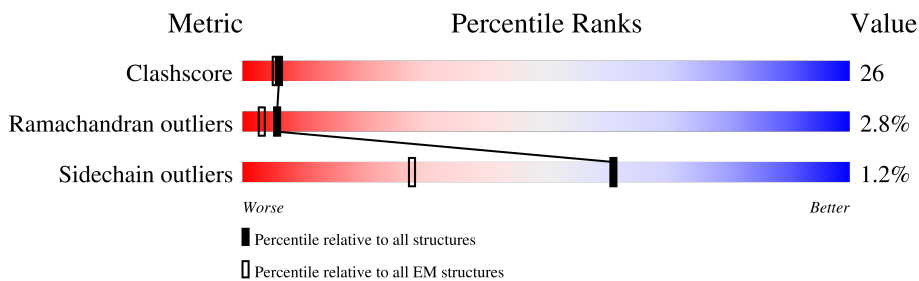
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.70 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	11569 (3.20 - 4.20)

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	Q	46	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>89%</p> <p>52%</p> </div> <div style="text-align: center;"> <p>43%</p> </div> </div>
2	S	70	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>13%</p> <p>66%</p> </div> <div style="text-align: center;"> <p>31%</p> </div> </div>
3	U	83	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>16%</p> <p>75%</p> </div> <div style="text-align: center;"> <p>25%</p> </div> </div>
4	V	140	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>31%</p> <p>64%</p> </div> <div style="text-align: center;"> <p>35%</p> </div> </div>

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Mol	Chain	Length	Quality of chain
5	W	116	8% 67% 31%
6	X	85	5% 53% 44%
7	Y	59	7% 31% 47% 19%
8	Z	80	15% 74% 26%
9	a	138	59% 36%
10	b	128	28% 42% 45% 9%
11	c	153	7% 50% 48%
12	d	171	6% 63% 33%
13	e	97	10% 71% 29%
14	f	47	30% 62% 34%
15	g	119	49% 49%
16	h	104	9% 48% 47% 5%
17	i	347	7% 51% 46%
18	j	115	50% 49% 48%
19	k	97	18% 47% 47%
20	l	603	9% 50% 44% 5%
21	m	174	26% 47% 49%
22	n	56	21% 59% 39%
23	o	128	5% 66% 33%
24	p	172	5% 58% 37% 5%
25	r	459	60% 39%
26	s	318	16% 49% 47%
27	u	169	62% 36%
28	v	122	18% 44% 44% 9%
29	w	320	57% 55% 42%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
30	PLX	b	201	-	-	X	-
32	PEE	V	202	-	-	X	-
32	PEE	l	701	-	-	X	-

2 Entry composition [i](#)

There are 33 unique types of molecules in this entry. The entry contains 38835 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] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Q	46	381	247	65	68	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	S	70	568	367	101	96	4	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	U	83	647	427	105	113	2	0	0

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	V	140	1038	668	178	187	5	0	0

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	W	116	956	614	167	170	5	0	0

- Molecule 6 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	X	85	686	442	101	138	5	0	0

- Molecule 7 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	Y	59	533	354	87	91	1	0	0

- Molecule 8 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	Z	80	648	426	110	110	2	0	0

- Molecule 9 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	a	138	1174	771	199	202	2	0	0

- Molecule 10 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	b	124	1059	697	181	176	5	0	0

- Molecule 11 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	c	153	1236	795	208	222	11	0	0

- Molecule 12 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	d	171	1418	885	262	259	12	0	0

- Molecule 13 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	e	97	810	522	132	152	4	0	0

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	f	47	405	269	69	67	0	0

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	g	119	1004	658	173	169	4	0	0

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	h	104	863	546	161	150	6	0	0

- Molecule 17 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	i	347	2735	1819	421	470	25	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	j	115	919	626	132	152	9	0	0

- Molecule 19 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	k	97	740	487	113	127	13	0	0

- Molecule 20 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	l	603	4717	3119	742	823	33	0	0

- Molecule 21 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	m	174	1313	879	194	229	11	0	0

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	n	56	473	305	85	80	3	0	0

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	o	128	1066	685	192	187	2	0	0

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	p	172	1495	961	265	261	8	0	0

- Molecule 25 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	r	459	3629	2411	569	619	30	0	0

- Molecule 26 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	s	318	2509	1678	380	435	16	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	u	169	1394	886	247	252	9	0	0

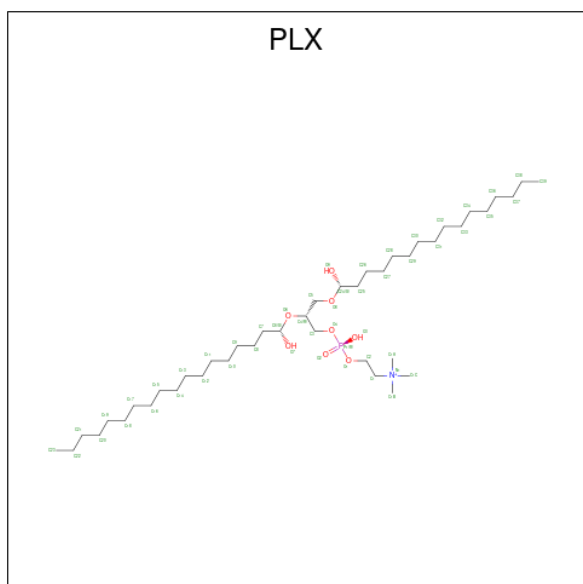
- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	v	111	921	569	187	156	9	0	0

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

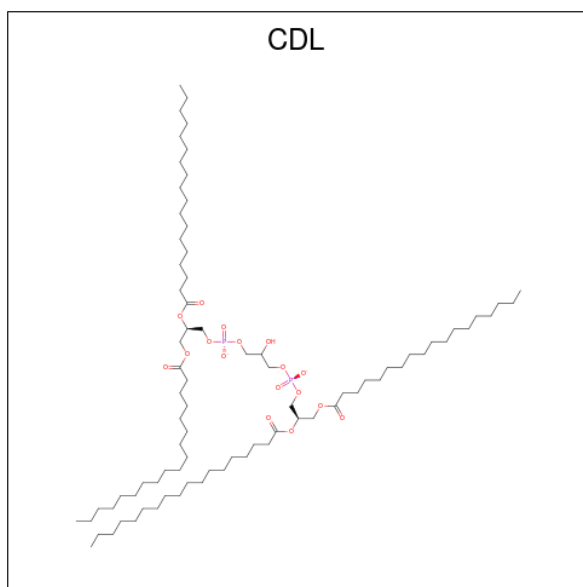
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	w	320	2474	1573	429	464	8	0	0

- Molecule 30 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).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
30	U	1	Total 52	C 42	N 1	O 8	P 1	0
30	V	1	Total 52	C 42	N 1	O 8	P 1	0
30	b	1	Total 52	C 42	N 1	O 8	P 1	0
30	g	1	Total 52	C 42	N 1	O 8	P 1	0
30	g	1	Total 52	C 42	N 1	O 8	P 1	0
30	g	1	Total 52	C 42	N 1	O 8	P 1	0
30	r	1	Total 52	C 42	N 1	O 8	P 1	0
30	r	1	Total 52	C 42	N 1	O 8	P 1	0
30	s	1	Total 52	C 42	N 1	O 8	P 1	0

- Molecule 31 is CARDIOLIPIN (CCD ID: CDL) (formula: $C_{81}H_{156}O_{17}P_2$).



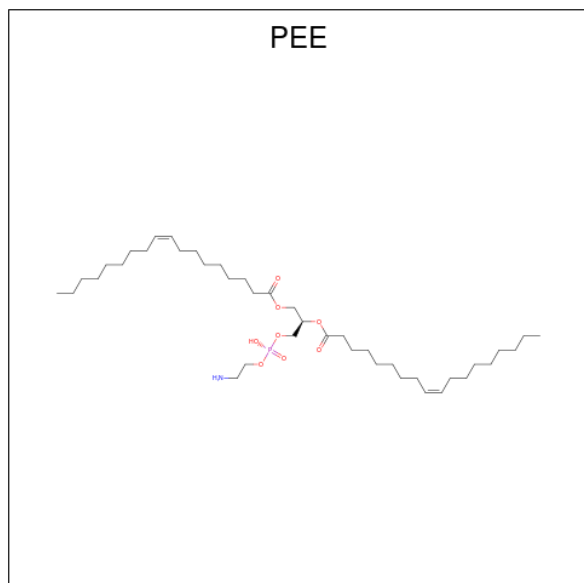
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
31	V	1	Total 63	C 44	O 17	P 2	0
31	i	1	Total 64	C 45	O 17	P 2	0
31	l	1	Total 64	C 45	O 17	P 2	0

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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
31	l	1	64	45	17	2	0
31	n	1	64	45	17	2	0

- Molecule 32 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



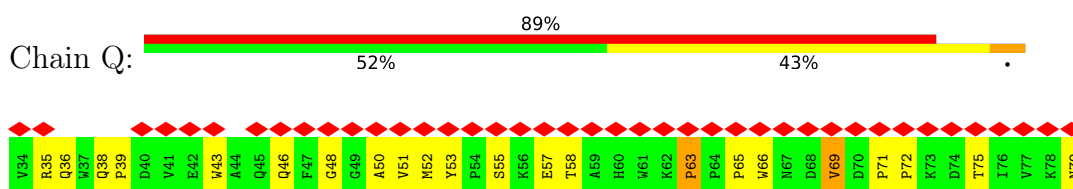
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
32	V	1	51	41	1	8	1	0
32	W	1	51	41	1	8	1	0
32	l	1	49	39	1	8	1	0
32	l	1	51	41	1	8	1	0

- Molecule 33 is S-[2-({N-[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]-beta-alanyl}amino)ethyl] dodecanethioate (CCD ID: 8Q1) (formula: $C_{23}H_{45}N_2O_8PS$).

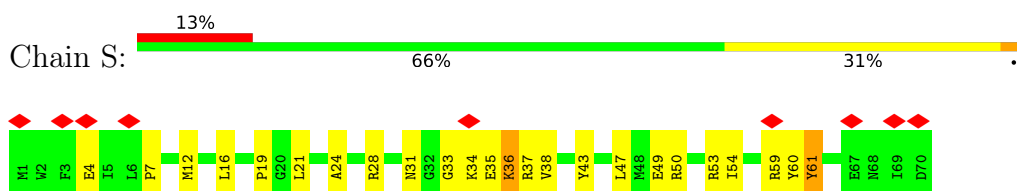
3 Residue-property plots [i](#)

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.

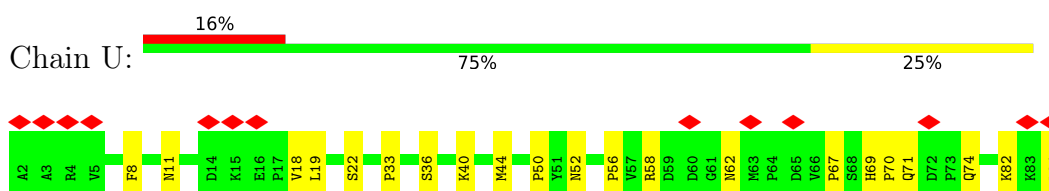
- Molecule 1: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



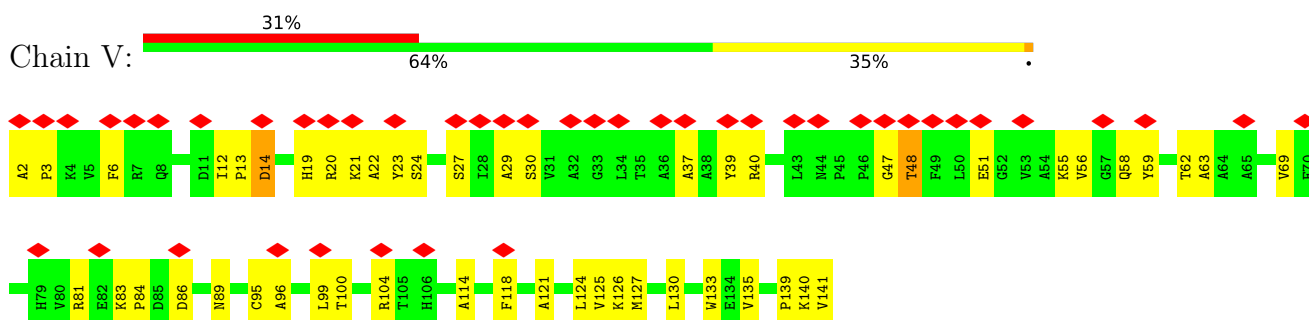
- Molecule 2: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1



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

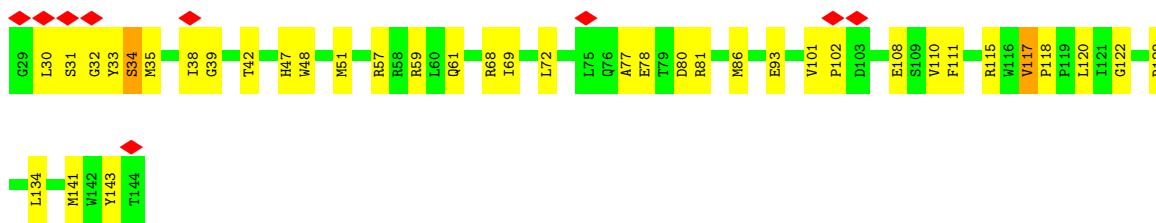


- Molecule 4: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11

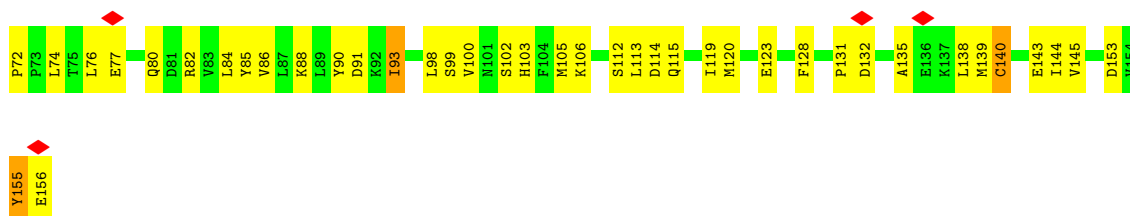


- Molecule 5: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

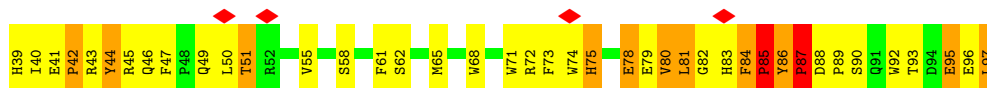




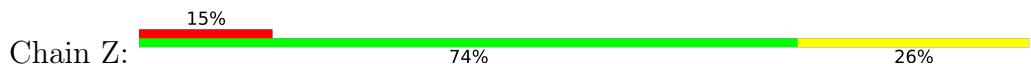
- Molecule 6: Acyl carrier protein, mitochondrial



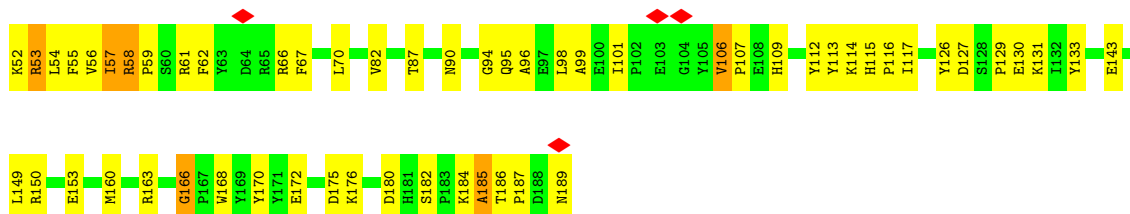
- Molecule 7: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial



- Molecule 8: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3

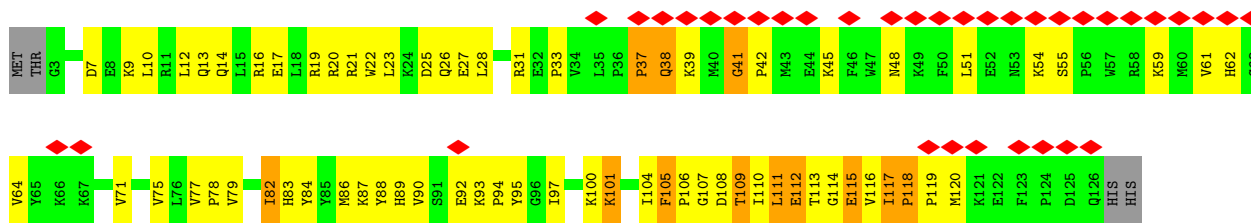


- Molecule 9: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial

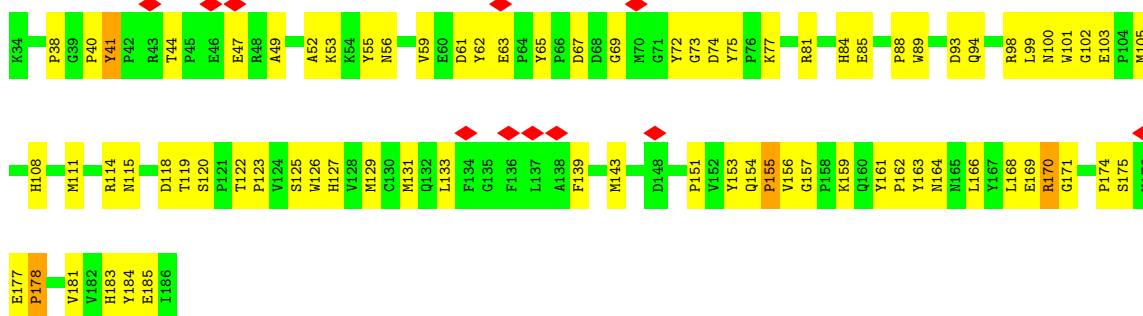


- Molecule 10: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6

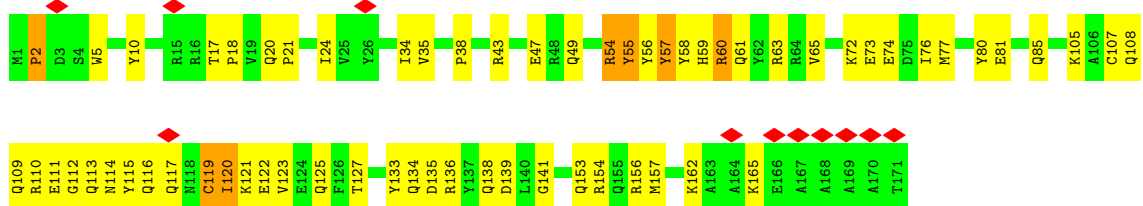




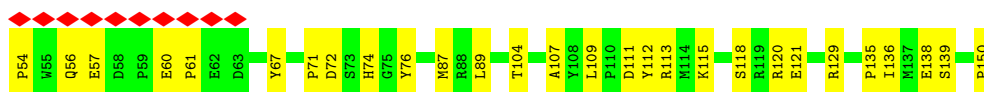
- Molecule 11: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial



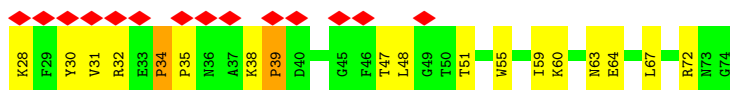
- Molecule 12: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10



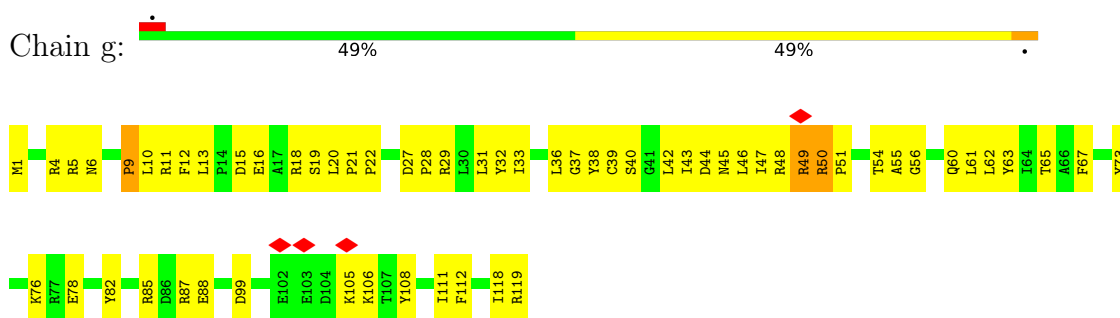
- Molecule 13: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



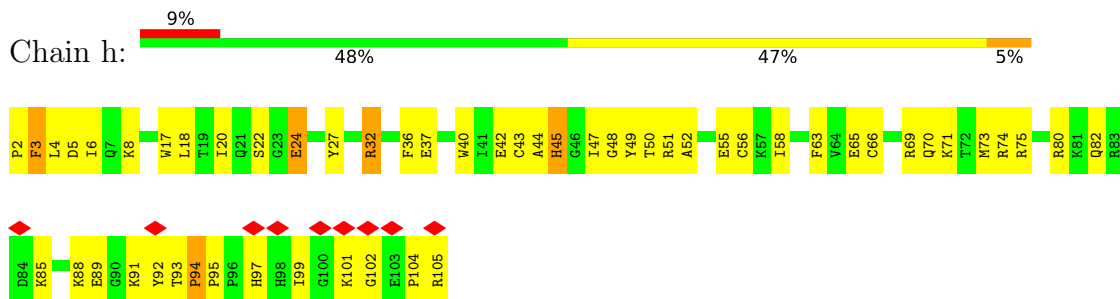
- Molecule 14: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial



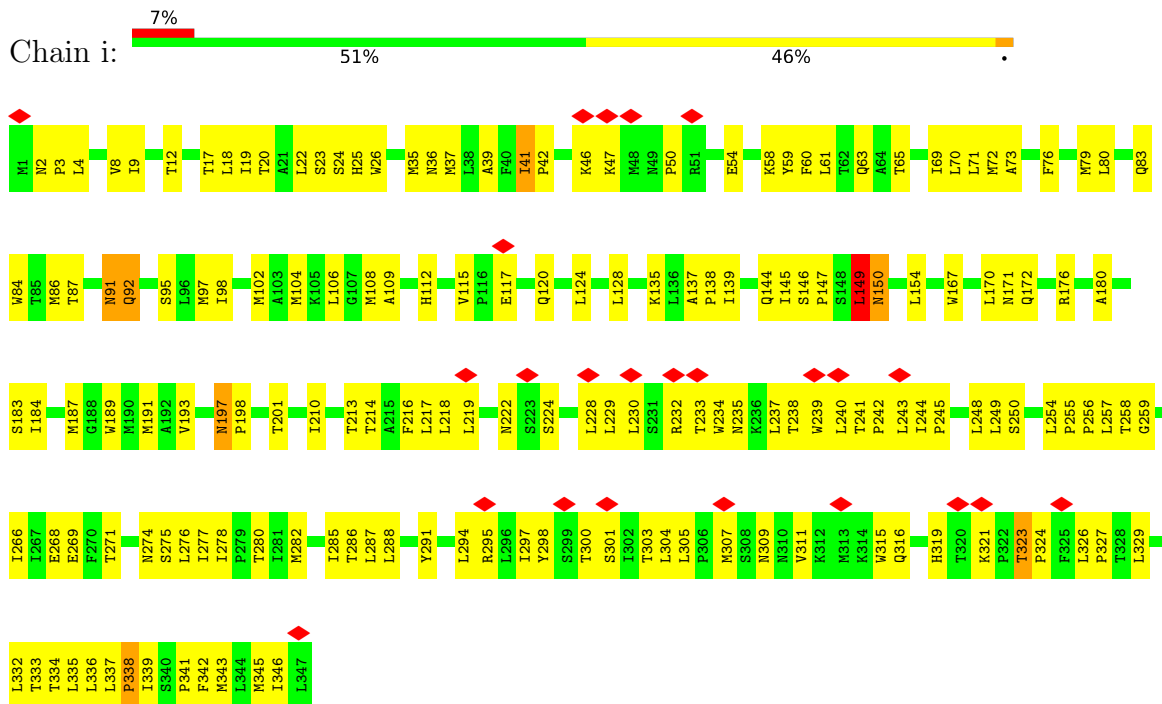
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 subunit C2



- Molecule 16: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5

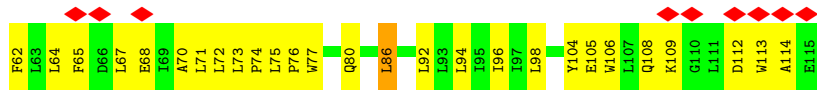
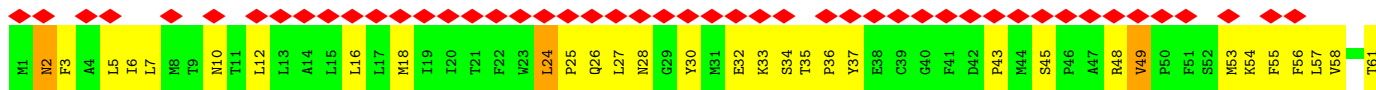


- Molecule 17: NADH-ubiquinone oxidoreductase chain 2

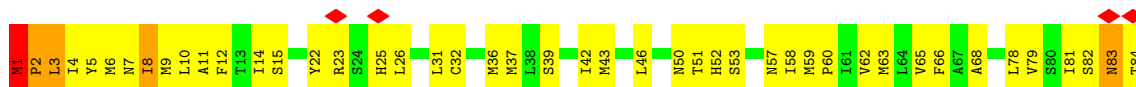


- Molecule 18: NADH-ubiquinone oxidoreductase chain 3

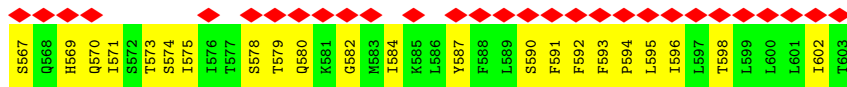
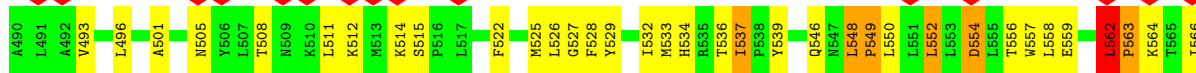
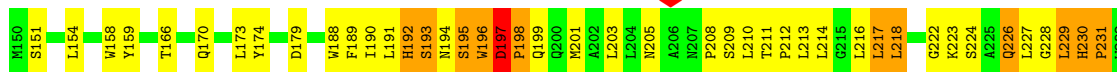
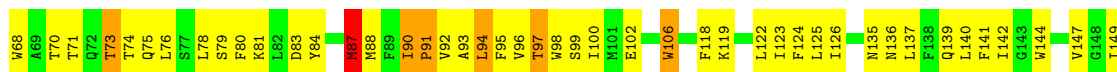




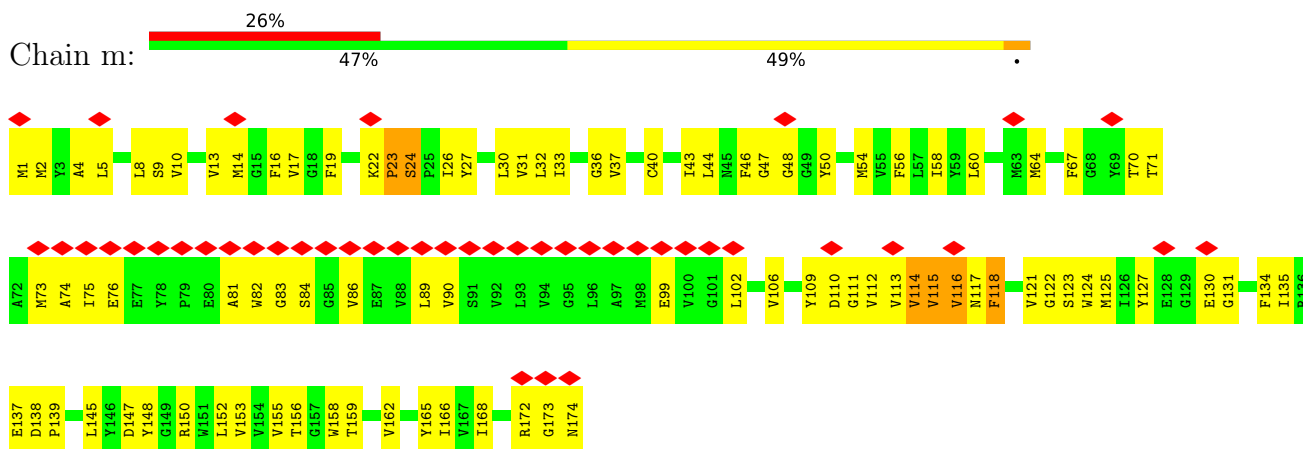
• Molecule 19: NADH-ubiquinone oxidoreductase chain 4L



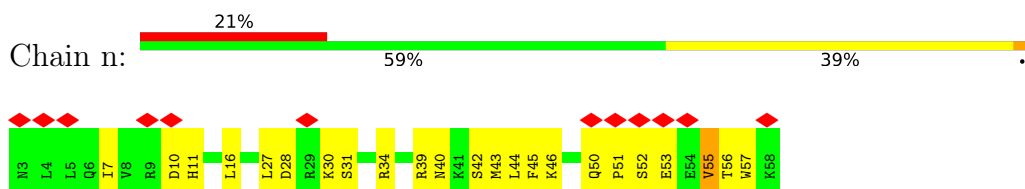
• Molecule 20: NADH-ubiquinone oxidoreductase chain 5



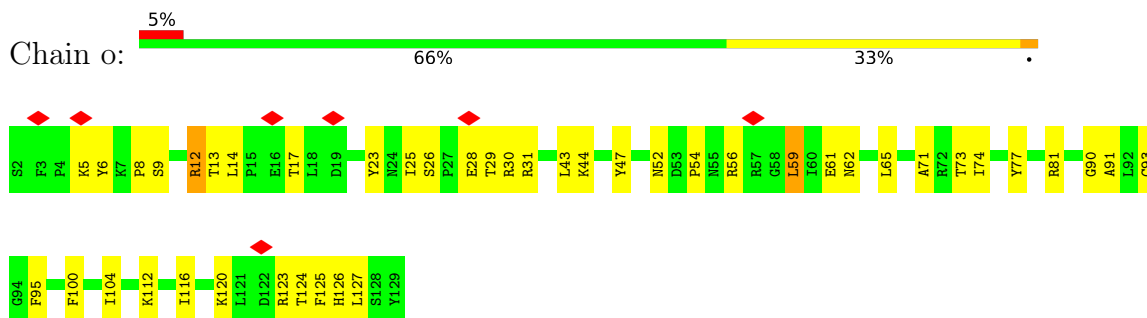
- Molecule 21: NADH-ubiquinone oxidoreductase chain 6



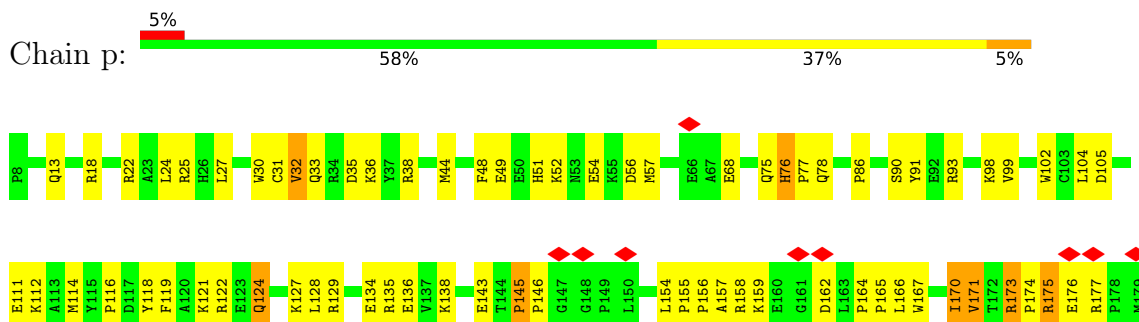
- Molecule 22: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1



- Molecule 23: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

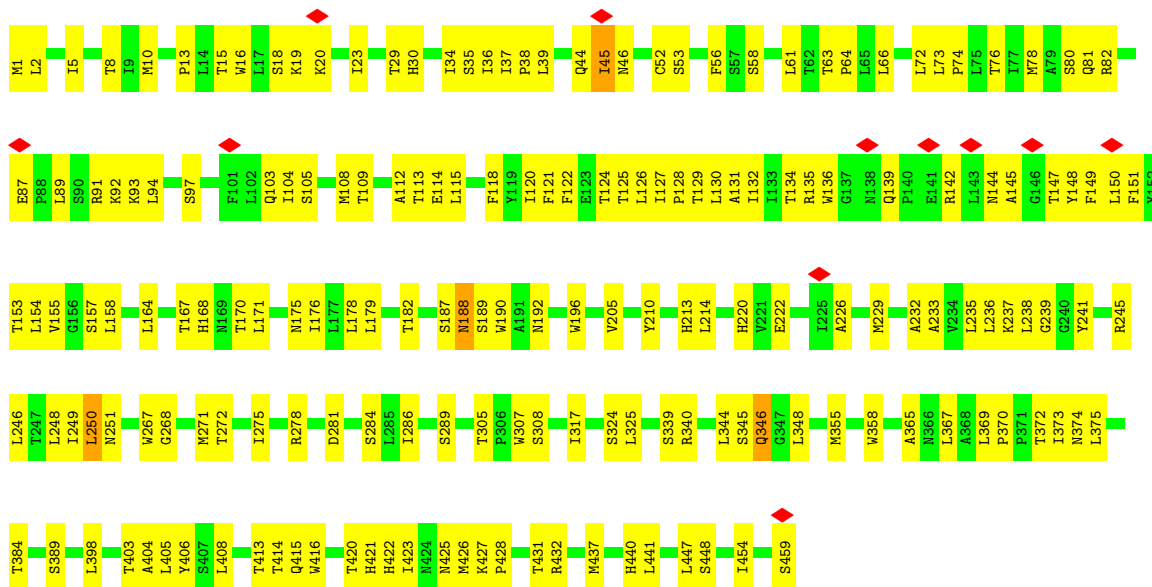


- Molecule 24: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

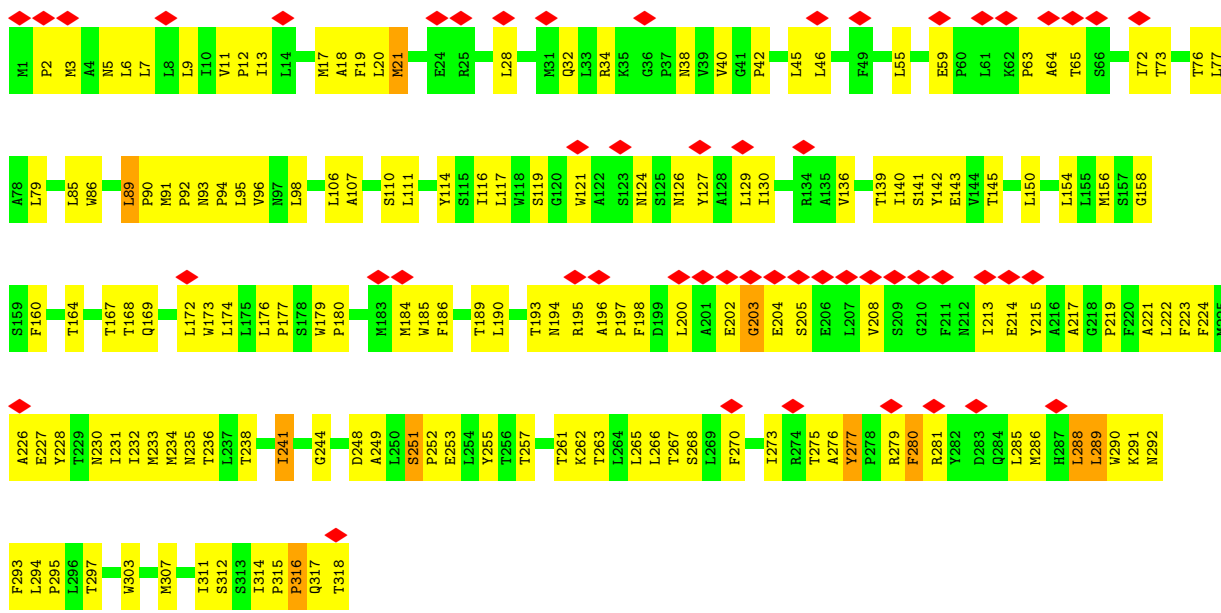


- Molecule 25: NADH-ubiquinone oxidoreductase chain 4

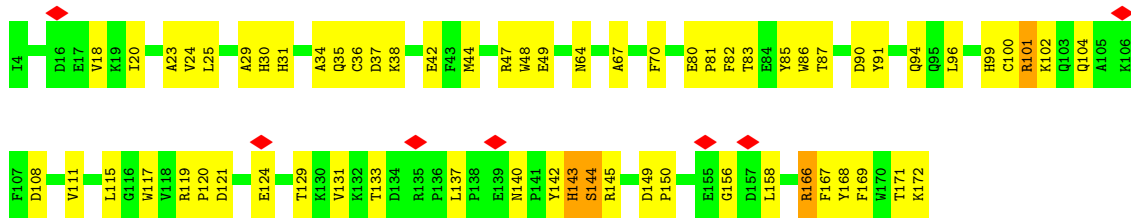




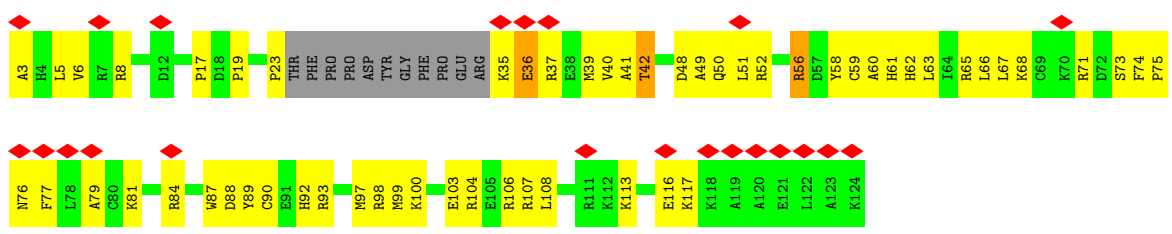
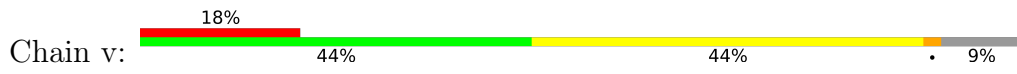
• Molecule 26: NADH-ubiquinone oxidoreductase chain 1



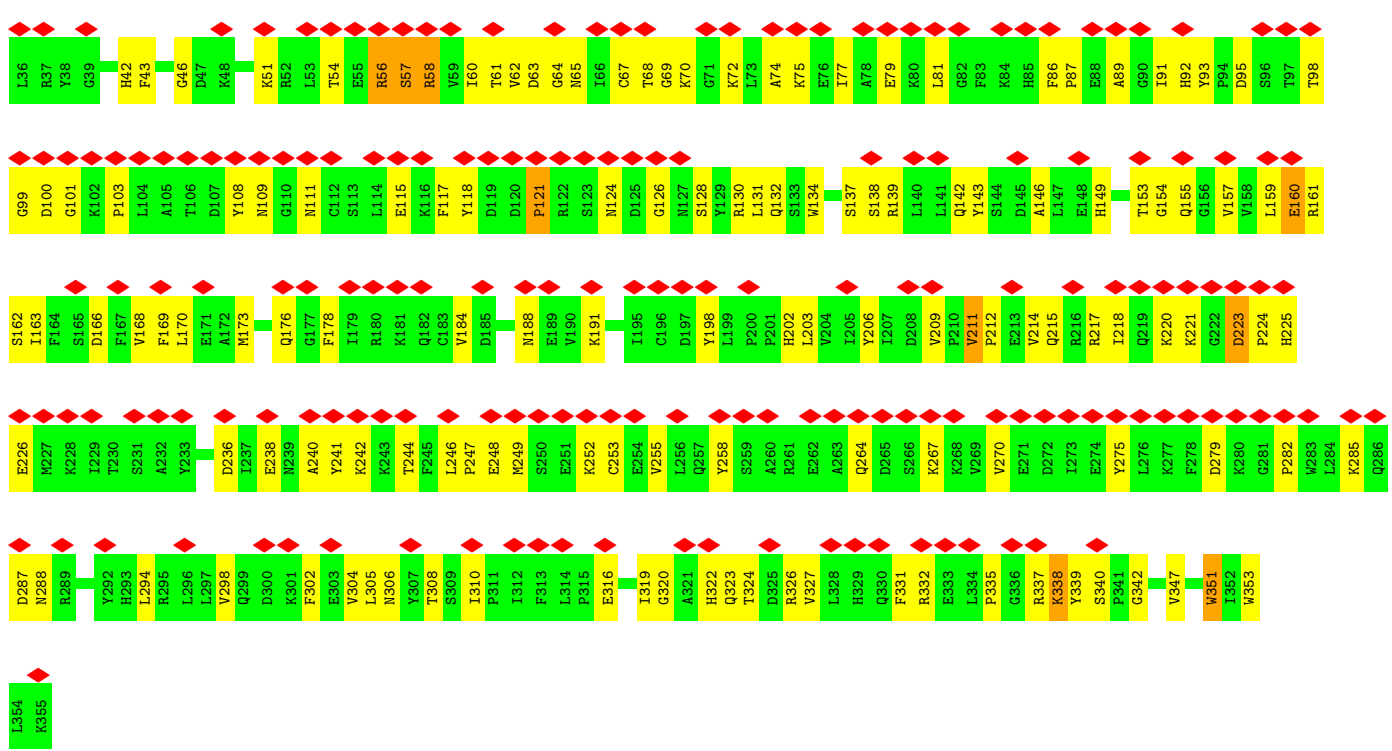
• Molecule 27: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8



• Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



• Molecule 29: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	167761	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.305	Depositor
Minimum map value	-0.154	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.0677	Depositor
Map size (\AA)	519.83997, 519.83997, 519.83997	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.083, 1.083, 1.083	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: CDL, 8Q1, PEE, PLX

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	Q	0.48	0/398	1.01	3/548 (0.5%)
2	S	0.81	0/583	0.94	1/785 (0.1%)
3	U	0.69	0/670	1.05	4/920 (0.4%)
4	V	0.64	0/1065	0.90	4/1450 (0.3%)
5	W	0.77	1/980 (0.1%)	0.95	3/1327 (0.2%)
6	X	0.71	0/698	0.89	0/942
7	Y	0.61	0/559	1.16	7/763 (0.9%)
8	Z	0.56	0/669	0.82	0/899
9	a	0.85	0/1209	0.99	6/1639 (0.4%)
10	b	0.71	3/1095 (0.3%)	1.08	6/1480 (0.4%)
11	c	0.69	0/1287	0.99	10/1761 (0.6%)
12	d	0.78	0/1445	0.98	3/1945 (0.2%)
13	e	0.76	0/835	0.95	0/1134
14	f	0.65	0/418	0.87	1/566 (0.2%)
15	g	0.78	0/1035	0.97	4/1398 (0.3%)
16	h	0.79	0/884	0.98	3/1182 (0.3%)
17	i	0.92	1/2808 (0.0%)	1.08	11/3843 (0.3%)
18	j	0.76	0/945	1.01	3/1292 (0.2%)
19	k	0.95	1/751 (0.1%)	1.04	3/1019 (0.3%)
20	l	0.84	6/4840 (0.1%)	1.03	29/6611 (0.4%)
21	m	0.82	0/1346	0.99	5/1832 (0.3%)
22	n	0.63	0/484	0.99	0/652
23	o	0.71	0/1093	0.89	0/1479
24	p	0.70	0/1549	1.00	11/2098 (0.5%)
25	r	0.96	1/3723 (0.0%)	1.02	2/5089 (0.0%)
26	s	0.83	0/2580	1.09	15/3539 (0.4%)
27	u	0.70	0/1433	0.96	2/1937 (0.1%)
28	v	0.63	0/934	1.00	4/1241 (0.3%)
29	w	0.53	1/2533 (0.0%)	0.91	7/3440 (0.2%)
All	All	0.78	14/38849 (0.0%)	1.00	147/52811 (0.3%)

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
29	w	0	1

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	i	278	ILE	CA-CB	-7.69	1.50	1.54
10	b	117	ILE	C-N	6.55	1.41	1.33
5	W	117	VAL	CA-CB	-6.13	1.49	1.54
25	r	37	ILE	CA-CB	-5.94	1.51	1.54
10	b	105	PHE	C-N	5.77	1.41	1.33

The worst 5 of 147 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	s	314	ILE	CA-C-N	9.73	126.77	119.66
26	s	314	ILE	C-N-CA	9.73	126.77	119.66
17	i	323	THR	CA-C-N	8.50	147.40	127.00
17	i	323	THR	C-N-CA	8.50	147.40	127.00
7	Y	86	TYR	C-N-CD	8.43	139.15	120.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
29	w	338	LYS	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	Q	381	0	355	29	0
2	S	568	0	567	37	0
3	U	647	0	653	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	V	1038	0	1027	36	0
5	W	956	0	949	41	0
6	X	686	0	676	33	0
7	Y	533	0	475	97	0
8	Z	648	0	627	18	0
9	a	1174	0	1177	104	0
10	b	1059	0	1079	125	0
11	c	1236	0	1092	81	0
12	d	1418	0	1375	121	0
13	e	810	0	772	32	0
14	f	405	0	407	19	0
15	g	1004	0	1008	63	0
16	h	863	0	861	66	0
17	i	2735	0	2893	185	0
18	j	919	0	968	58	0
19	k	740	0	792	90	0
20	l	4717	0	4893	399	0
21	m	1313	0	1330	121	0
22	n	473	0	480	30	0
23	o	1066	0	1086	51	0
24	p	1495	0	1440	93	0
25	r	3629	0	3825	164	0
26	s	2509	0	2617	134	0
27	u	1394	0	1367	59	0
28	v	921	0	892	90	0
29	w	2474	0	2304	117	0
30	U	52	0	88	3	0
30	V	52	0	88	5	0
30	b	52	0	88	38	0
30	g	156	0	264	13	0
30	r	104	0	176	22	0
30	s	52	0	88	2	0
31	V	63	0	68	8	0
31	i	64	0	72	3	0
31	l	128	0	144	5	0
31	n	64	0	72	10	0
32	V	51	0	82	21	0
32	W	51	0	82	18	0
32	l	100	0	157	68	0
33	p	35	0	0	12	0
All	All	38835	0	39456	2064	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 26.

The worst 5 of 2064 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)
9:a:55:PHE:CE2	24:p:118:TYR:CE2	1.82	1.65
20:l:533:MET:CE	32:l:702:PEE:H36	1.25	1.58
20:l:37:LYS:HE2	20:l:98:TRP:CD1	1.40	1.57
9:a:55:PHE:HE2	24:p:118:TYR:CE2	1.17	1.56
9:a:55:PHE:CE2	24:p:118:TYR:CD2	1.91	1.55

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	Q	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	18
2	S	68/70 (97%)	61 (90%)	5 (7%)	2 (3%)	3	26
3	U	81/83 (98%)	76 (94%)	4 (5%)	1 (1%)	10	40
4	V	138/140 (99%)	129 (94%)	6 (4%)	3 (2%)	5	31
5	W	114/116 (98%)	109 (96%)	4 (4%)	1 (1%)	14	45
6	X	83/85 (98%)	73 (88%)	6 (7%)	4 (5%)	2	17
7	Y	57/59 (97%)	50 (88%)	1 (2%)	6 (10%)	0	5
8	Z	78/80 (98%)	73 (94%)	5 (6%)	0	100	100
9	a	136/138 (99%)	121 (89%)	12 (9%)	3 (2%)	5	31
10	b	122/128 (95%)	107 (88%)	10 (8%)	5 (4%)	2	20
11	c	151/153 (99%)	129 (85%)	15 (10%)	7 (5%)	2	18
12	d	169/171 (99%)	165 (98%)	3 (2%)	1 (1%)	21	52
13	e	95/97 (98%)	84 (88%)	8 (8%)	3 (3%)	3	25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	f	45/47 (96%)	43 (96%)	1 (2%)	1 (2%)	5	31
15	g	117/119 (98%)	105 (90%)	6 (5%)	6 (5%)	1	17
16	h	102/104 (98%)	87 (85%)	9 (9%)	6 (6%)	1	15
17	i	345/347 (99%)	324 (94%)	15 (4%)	6 (2%)	7	34
18	j	113/115 (98%)	103 (91%)	7 (6%)	3 (3%)	4	27
19	k	95/97 (98%)	88 (93%)	4 (4%)	3 (3%)	3	25
20	l	601/603 (100%)	551 (92%)	38 (6%)	12 (2%)	6	32
21	m	172/174 (99%)	150 (87%)	12 (7%)	10 (6%)	1	15
22	n	54/56 (96%)	50 (93%)	2 (4%)	2 (4%)	2	22
23	o	126/128 (98%)	113 (90%)	9 (7%)	4 (3%)	3	25
24	p	170/172 (99%)	157 (92%)	10 (6%)	3 (2%)	6	34
25	r	457/459 (100%)	420 (92%)	28 (6%)	9 (2%)	6	32
26	s	316/318 (99%)	286 (90%)	21 (7%)	9 (3%)	4	27
27	u	167/169 (99%)	152 (91%)	10 (6%)	5 (3%)	3	26
28	v	107/122 (88%)	90 (84%)	14 (13%)	3 (3%)	4	27
29	w	318/320 (99%)	281 (88%)	28 (9%)	9 (3%)	4	27
All	All	4641/4716 (98%)	4217 (91%)	295 (6%)	129 (3%)	6	27

5 of 129 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	S	60	TYR
3	U	71	GLN
5	W	34	SER
6	X	155	TYR
7	Y	84	PHE

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	Q	41/41 (100%)	41 (100%)	0	100	100
2	S	59/59 (100%)	59 (100%)	0	100	100
3	U	72/72 (100%)	72 (100%)	0	100	100
4	V	102/102 (100%)	102 (100%)	0	100	100
5	W	100/100 (100%)	100 (100%)	0	100	100
6	X	78/79 (99%)	77 (99%)	1 (1%)	61	71
7	Y	57/57 (100%)	50 (88%)	7 (12%)	4	22
8	Z	62/63 (98%)	62 (100%)	0	100	100
9	a	124/124 (100%)	123 (99%)	1 (1%)	73	76
10	b	118/122 (97%)	113 (96%)	5 (4%)	26	51
11	c	124/137 (90%)	124 (100%)	0	100	100
12	d	145/154 (94%)	137 (94%)	8 (6%)	19	46
13	e	90/90 (100%)	90 (100%)	0	100	100
14	f	43/43 (100%)	43 (100%)	0	100	100
15	g	105/105 (100%)	105 (100%)	0	100	100
16	h	90/90 (100%)	90 (100%)	0	100	100
17	i	314/314 (100%)	313 (100%)	1 (0%)	86	83
18	j	102/103 (99%)	101 (99%)	1 (1%)	68	74
19	k	85/85 (100%)	81 (95%)	4 (5%)	23	48
20	l	531/532 (100%)	512 (96%)	19 (4%)	31	54
21	m	137/137 (100%)	137 (100%)	0	100	100
22	n	53/53 (100%)	53 (100%)	0	100	100
23	o	114/114 (100%)	114 (100%)	0	100	100
24	p	157/157 (100%)	155 (99%)	2 (1%)	61	71
25	r	416/416 (100%)	416 (100%)	0	100	100
26	s	278/278 (100%)	278 (100%)	0	100	100
27	u	153/153 (100%)	153 (100%)	0	100	100
28	v	89/111 (80%)	89 (100%)	0	100	100
29	w	249/288 (86%)	249 (100%)	0	100	100
All	All	4088/4179 (98%)	4039 (99%)	49 (1%)	61	72

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	l	25	ASN
20	l	193	SER
20	l	59	GLN
20	l	97	THR
20	l	196	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 96 such sidechains are listed below:

Mol	Chain	Res	Type
20	l	446	ASN
25	r	390	ASN
20	l	569	HIS
23	o	126	HIS
26	s	97	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

19 ligands 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
30	PLX	r	501	-	51,51,51	0.77	1 (1%)	53,59,59	0.67	1 (1%)
31	CDL	V	201	-	61,61,99	1.23	5 (8%)	64,71,111	0.95	3 (4%)
30	PLX	g	202	-	51,51,51	0.77	1 (1%)	53,59,59	0.62	1 (1%)
30	PLX	g	203	-	51,51,51	0.81	1 (1%)	53,59,59	0.59	1 (1%)
30	PLX	b	201	-	51,51,51	0.55	0	53,59,59	0.64	0
30	PLX	r	502	-	51,51,51	0.62	0	53,59,59	0.66	1 (1%)
30	PLX	U	101	-	51,51,51	0.76	1 (1%)	53,59,59	0.71	2 (3%)
31	CDL	n	101	-	63,63,99	1.25	5 (7%)	69,75,111	1.08	4 (5%)
33	8Q1	p	201	-	32,34,34	1.59	5 (15%)	39,43,43	1.59	6 (15%)
32	PEE	l	701	-	48,48,50	1.36	4 (8%)	51,53,55	0.98	2 (3%)
32	PEE	W	201	-	50,50,50	1.16	6 (12%)	53,55,55	0.99	2 (3%)
31	CDL	l	704	-	63,63,99	1.27	5 (7%)	69,75,111	1.02	4 (5%)
31	CDL	l	703	-	63,63,99	1.23	5 (7%)	69,75,111	1.08	4 (5%)
30	PLX	V	203	-	51,51,51	0.80	1 (1%)	53,59,59	0.60	1 (1%)
30	PLX	s	401	-	51,51,51	0.79	1 (1%)	53,59,59	0.69	1 (1%)
32	PEE	l	702	-	50,50,50	1.19	6 (12%)	53,55,55	1.00	2 (3%)
31	CDL	i	401	-	63,63,99	1.23	5 (7%)	69,75,111	1.06	5 (7%)
30	PLX	g	201	-	51,51,51	0.85	1 (1%)	53,59,59	0.70	1 (1%)
32	PEE	V	202	-	50,50,50	1.18	6 (12%)	53,55,55	0.92	2 (3%)

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
30	PLX	r	501	-	-	27/55/55/55	-
31	CDL	V	201	-	-	40/69/69/110	-
30	PLX	g	202	-	-	26/55/55/55	-
30	PLX	g	203	-	-	22/55/55/55	-
30	PLX	b	201	-	-	26/55/55/55	-
30	PLX	r	502	-	-	36/55/55/55	-
30	PLX	U	101	-	-	22/55/55/55	-
31	CDL	n	101	-	-	32/74/74/110	-
33	8Q1	p	201	-	-	20/41/41/41	-
32	PEE	l	701	-	-	31/52/52/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	PEE	W	201	-	-	29/54/54/54	-
31	CDL	l	704	-	-	42/74/74/110	-
31	CDL	l	703	-	-	36/74/74/110	-
30	PLX	V	203	-	-	26/55/55/55	-
30	PLX	s	401	-	-	22/55/55/55	-
32	PEE	l	702	-	-	27/54/54/54	-
31	CDL	i	401	-	-	39/74/74/110	-
30	PLX	g	201	-	-	24/55/55/55	-
32	PEE	V	202	-	-	26/54/54/54	-

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	p	201	8Q1	C39-N41	5.06	1.45	1.33
33	p	201	8Q1	C34-N36	4.93	1.45	1.33
31	l	704	CDL	OB8-CB7	4.36	1.46	1.33
31	n	101	CDL	OA6-CA5	4.30	1.46	1.34
31	l	703	CDL	OA6-CA5	4.29	1.46	1.34

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	p	201	8Q1	C6-C1-S44	5.93	120.47	113.40
32	l	702	PEE	O2-C10-C11	4.38	120.96	111.48
31	l	703	CDL	OA6-CA5-C11	4.17	120.51	111.48
31	i	401	CDL	OA6-CA5-C11	4.13	120.42	111.48
31	l	704	CDL	OA6-CA5-C11	4.11	120.36	111.48

There are no chirality outliers.

5 of 553 torsion outliers are listed below:

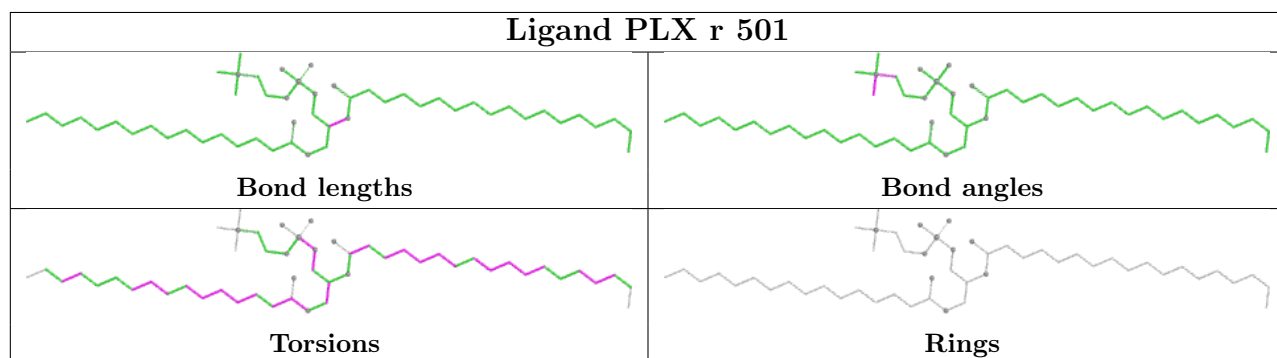
Mol	Chain	Res	Type	Atoms
30	U	101	PLX	O7-C6-C7-C8
30	U	101	PLX	O7-C6-O6-C4
30	U	101	PLX	C3-O4-P1-O1
30	U	101	PLX	C3-O4-P1-O2
30	U	101	PLX	N1-C1-C2-O1

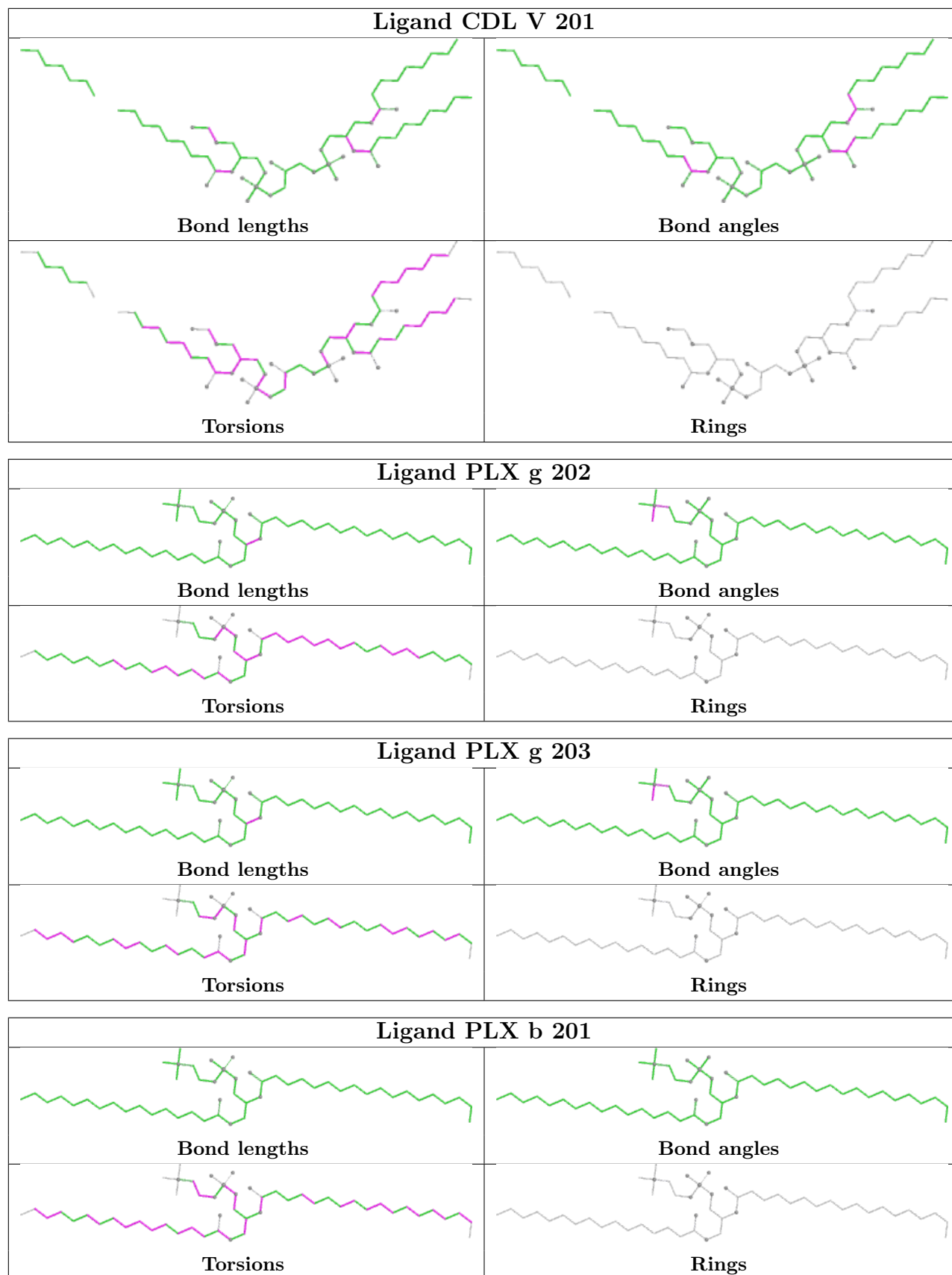
There are no ring outliers.

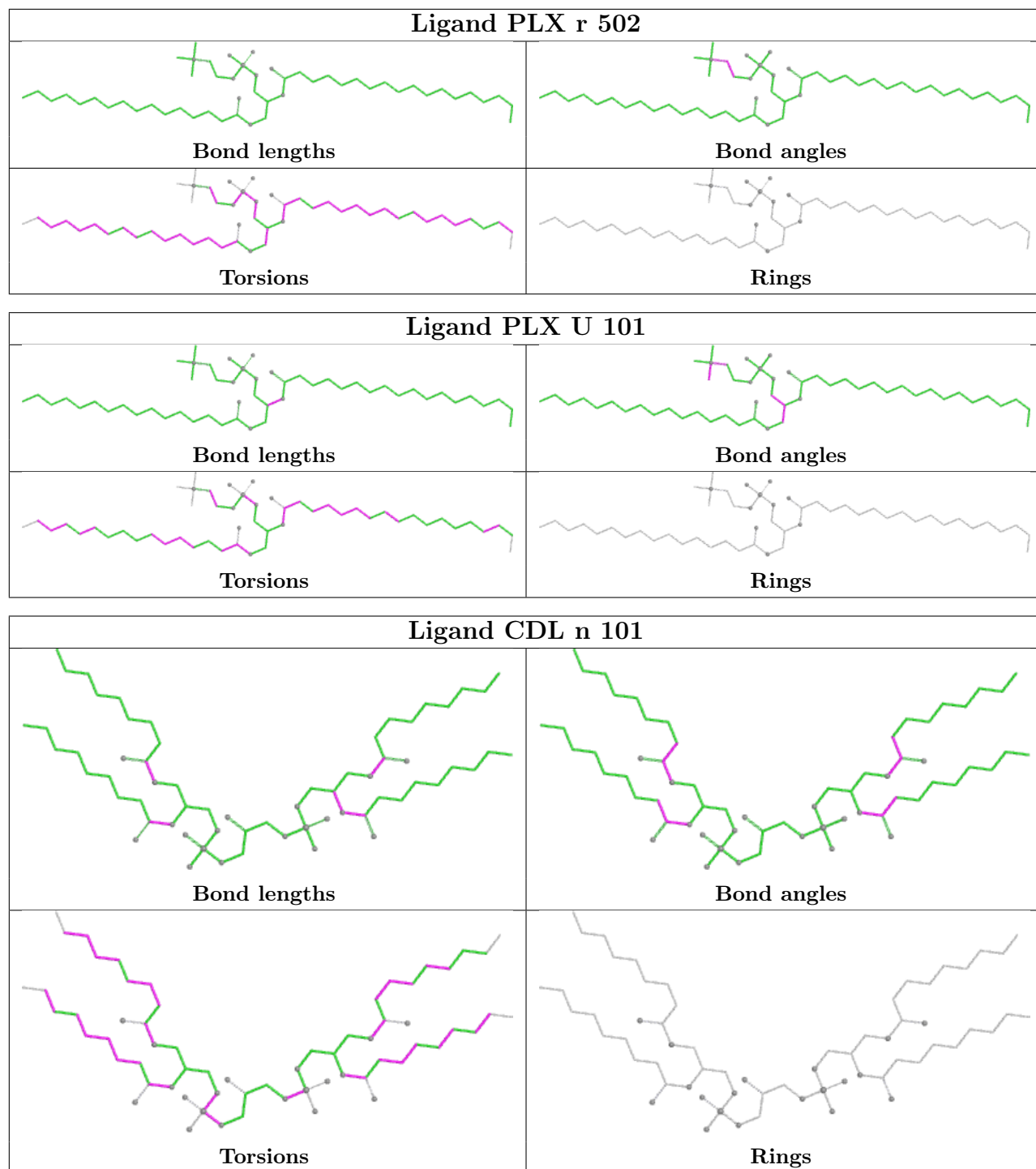
19 monomers are involved in 221 short contacts:

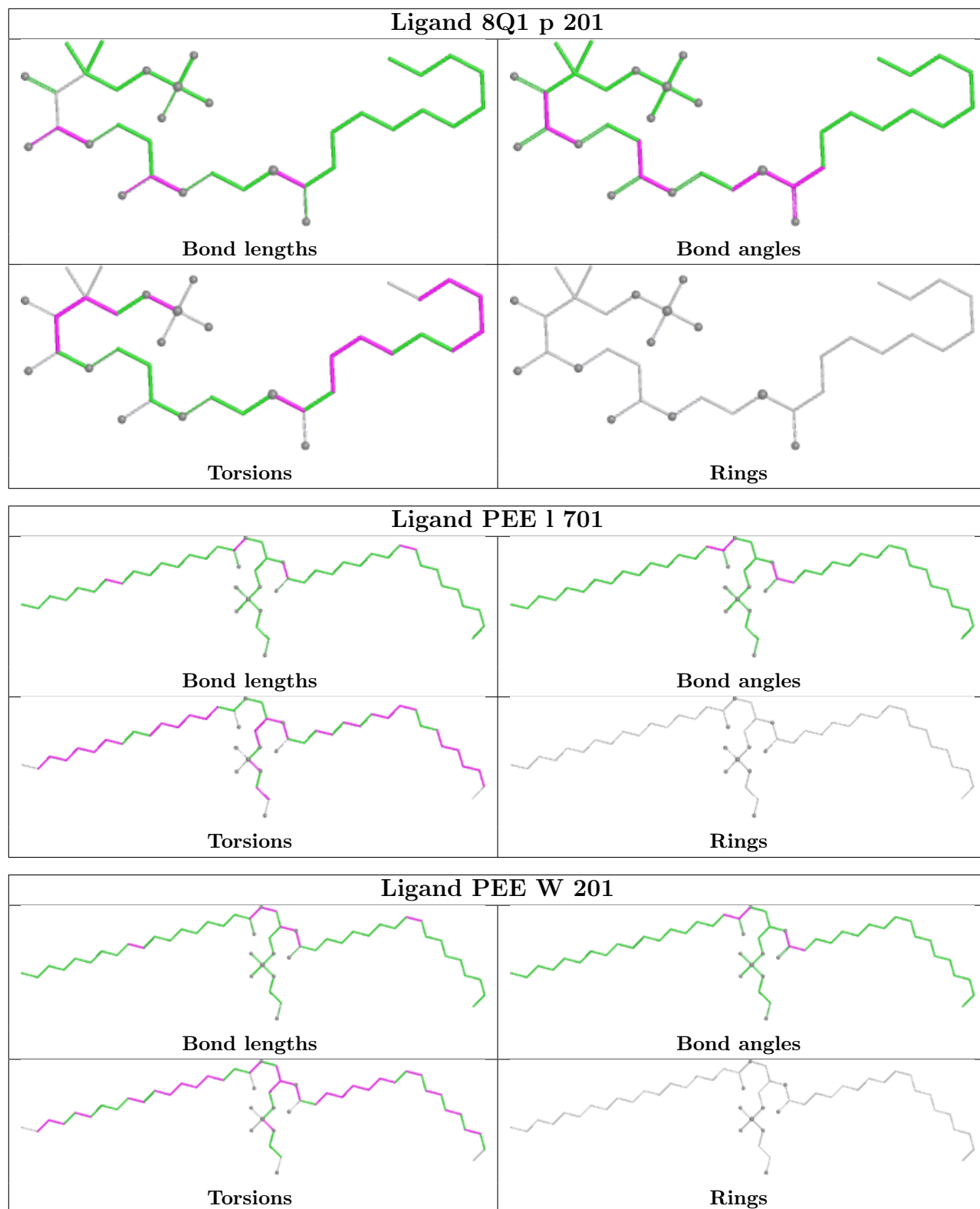
Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	r	501	PLX	6	0
31	V	201	CDL	8	0
30	g	202	PLX	3	0
30	g	203	PLX	8	0
30	b	201	PLX	38	0
30	r	502	PLX	16	0
30	U	101	PLX	3	0
31	n	101	CDL	10	0
33	p	201	8Q1	12	0
32	l	701	PEE	50	0
32	W	201	PEE	18	0
31	l	704	CDL	3	0
31	l	703	CDL	2	0
30	V	203	PLX	5	0
30	s	401	PLX	2	0
32	l	702	PEE	18	0
31	i	401	CDL	3	0
30	g	201	PLX	2	0
32	V	202	PEE	21	0

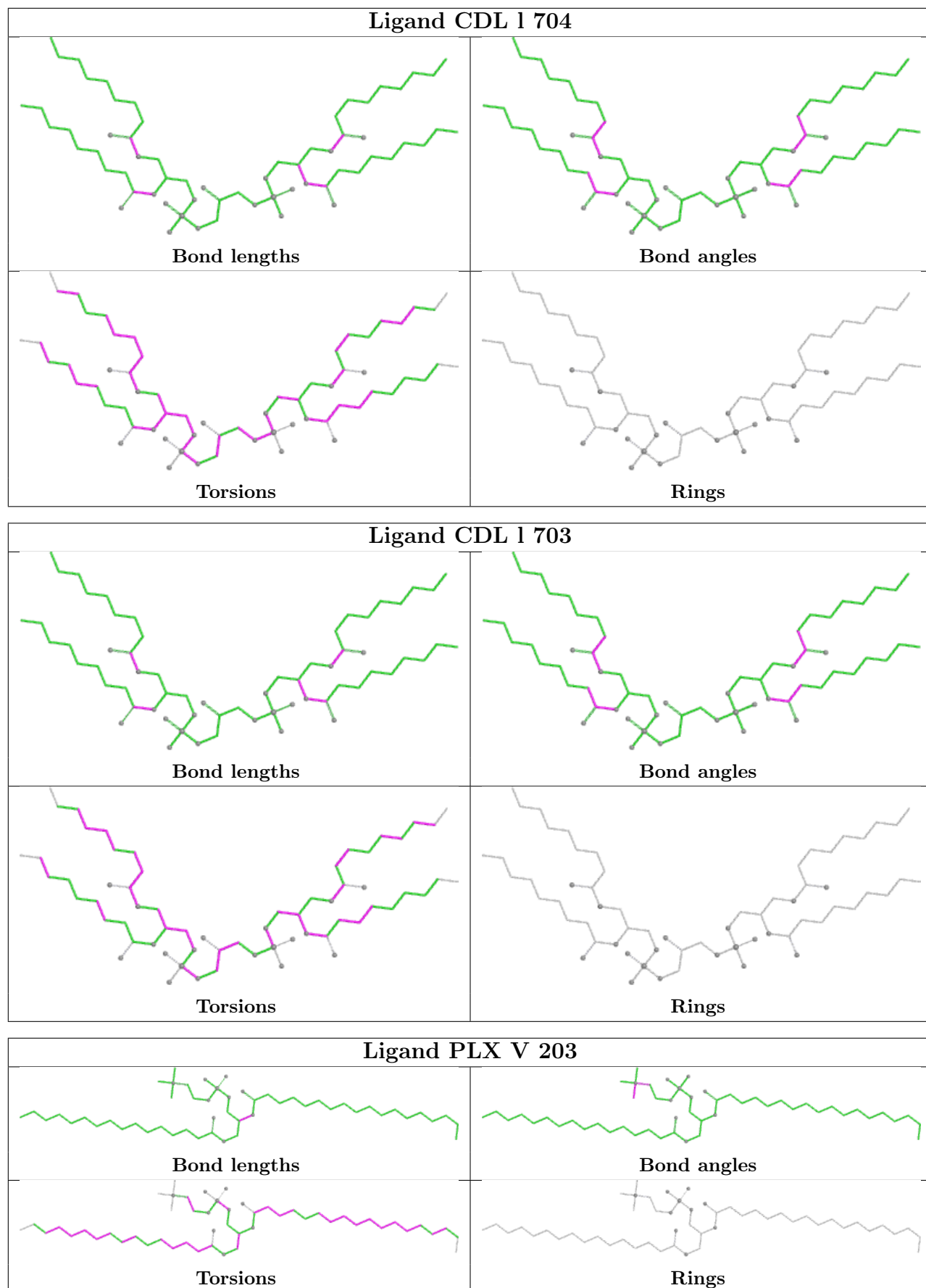
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

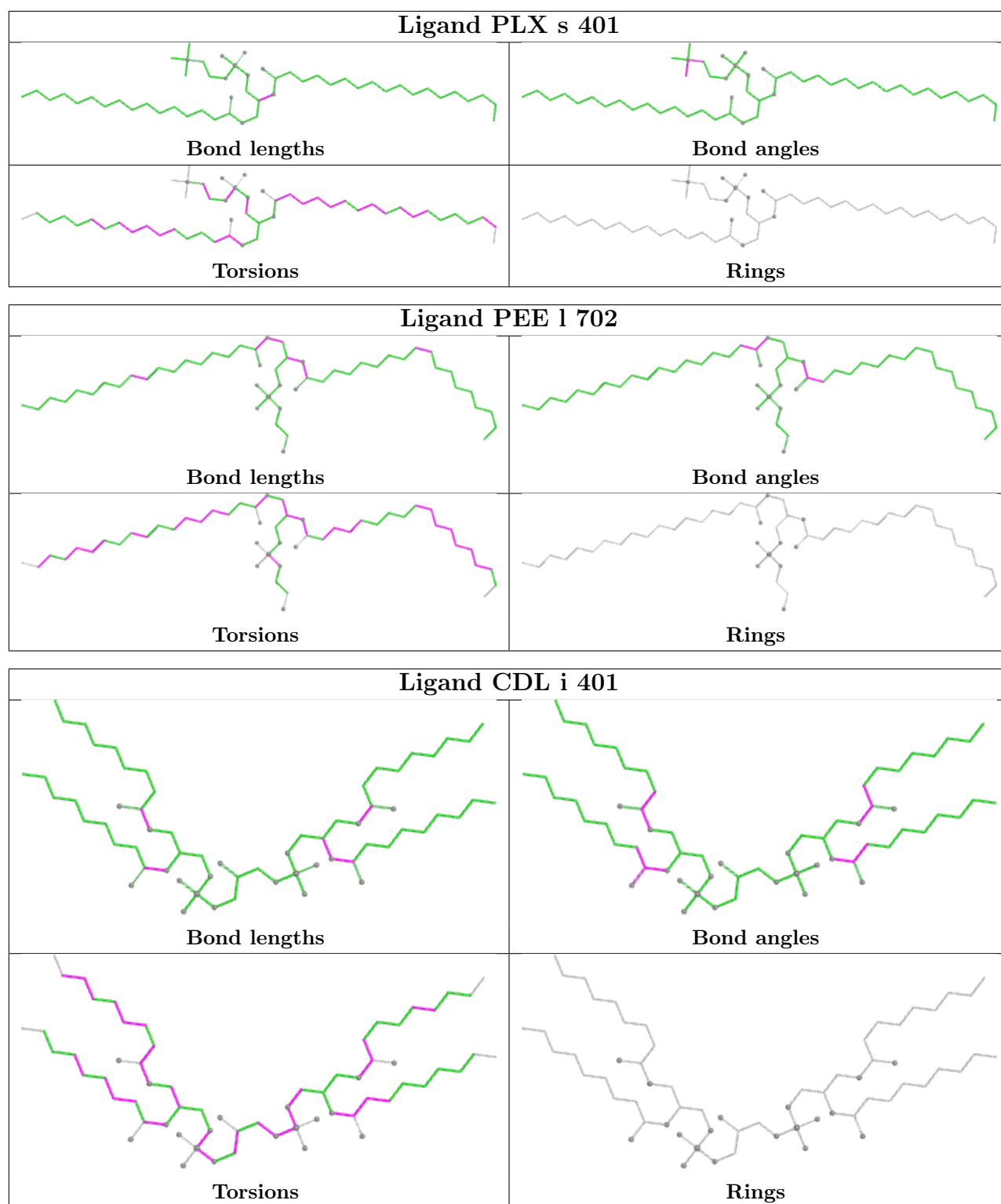


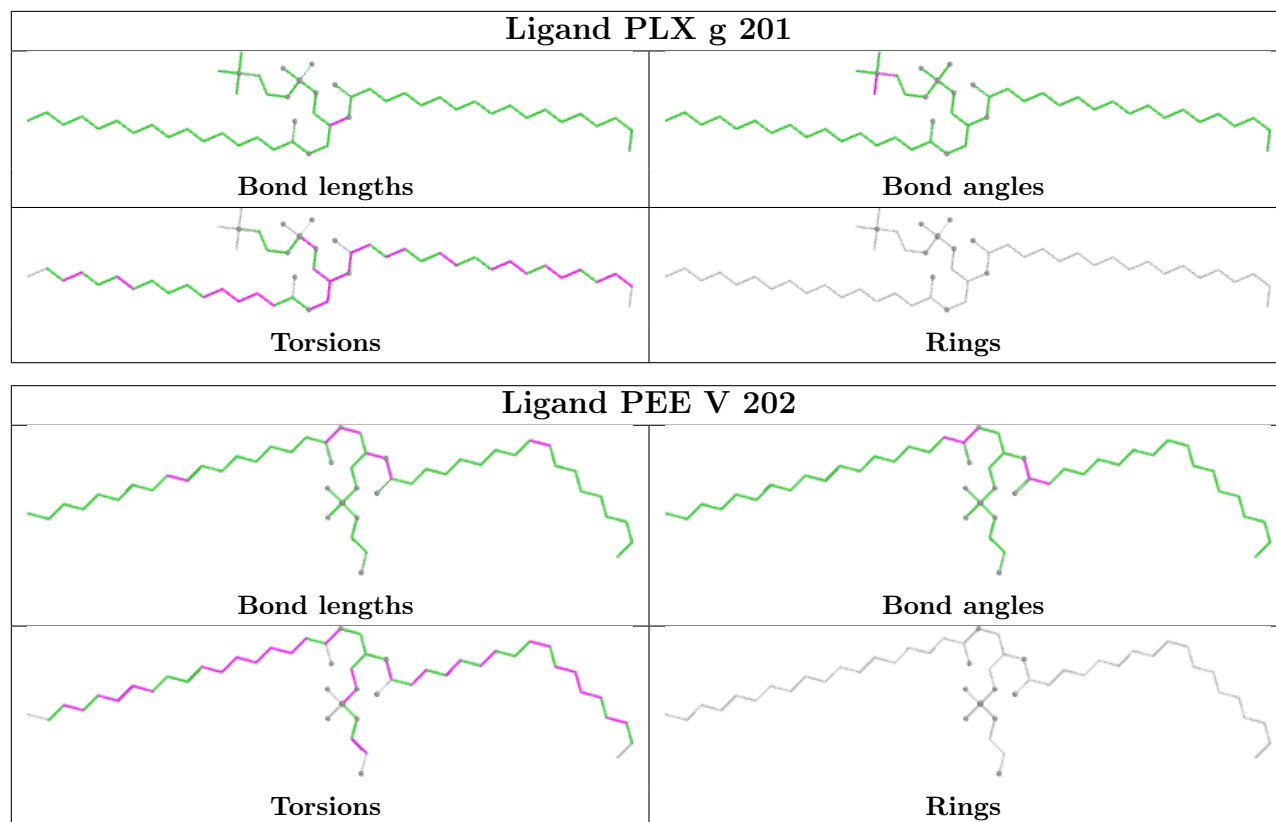












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

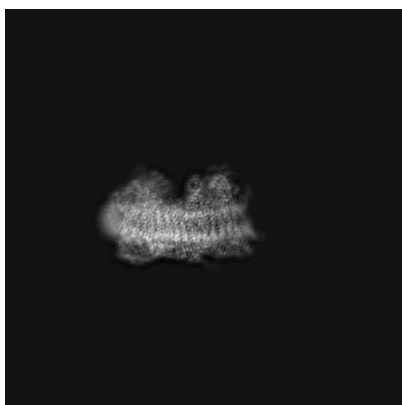
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6772. These allow visual inspection of the internal detail of the map and identification of artifacts.

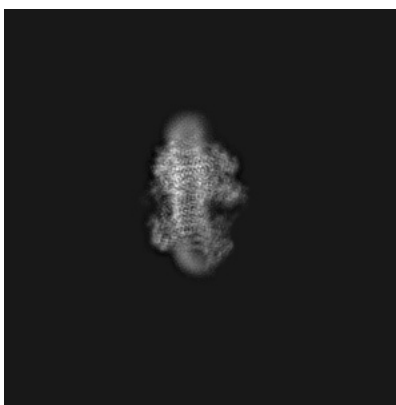
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

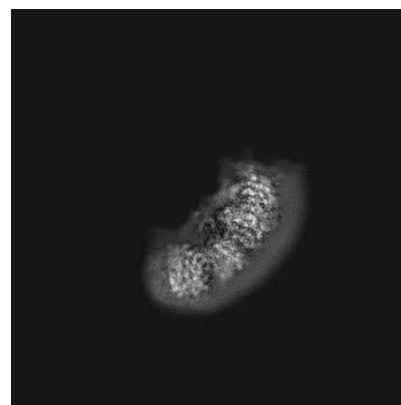
6.1.1 Primary map



X



Y

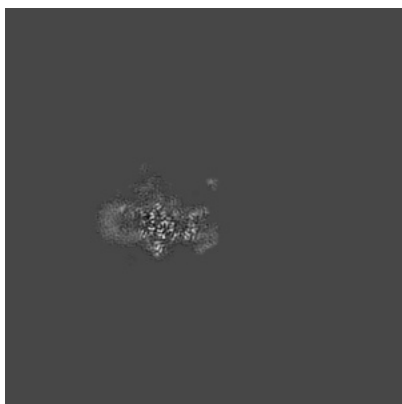


Z

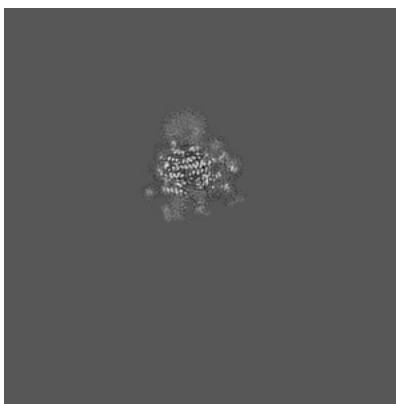
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

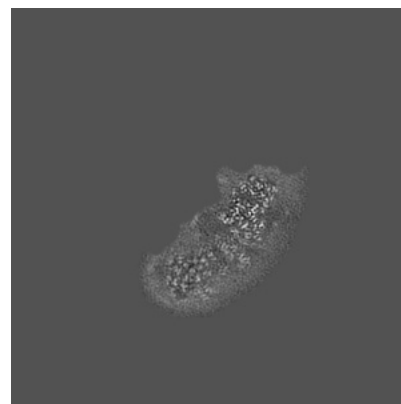
6.2.1 Primary map



X Index: 240



Y Index: 240

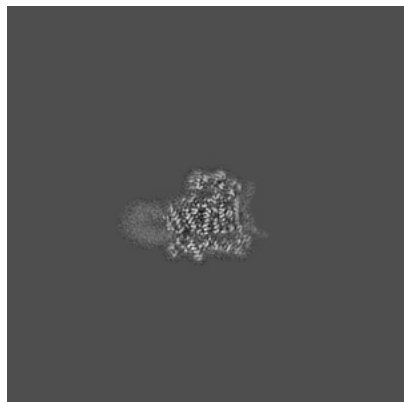


Z Index: 240

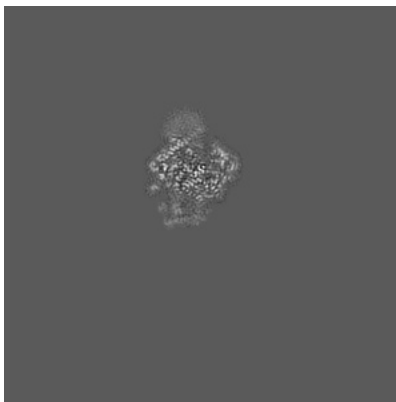
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

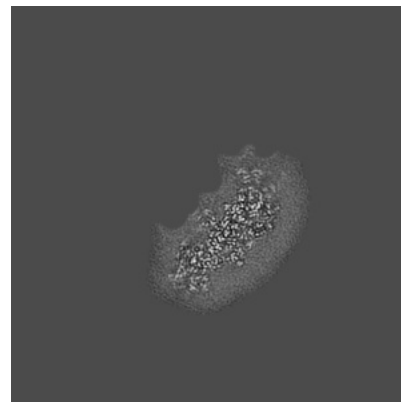
6.3.1 Primary map



X Index: 290



Y Index: 232

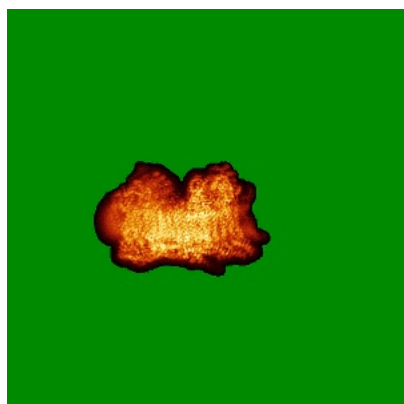


Z Index: 207

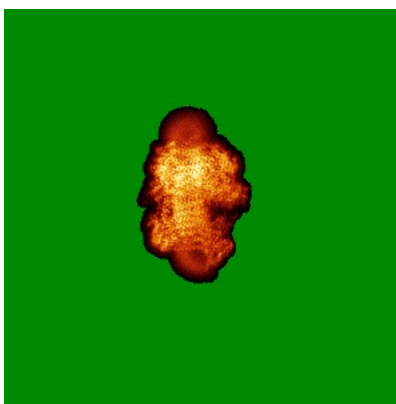
The images above show the largest variance slices of the map in three orthogonal directions.

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

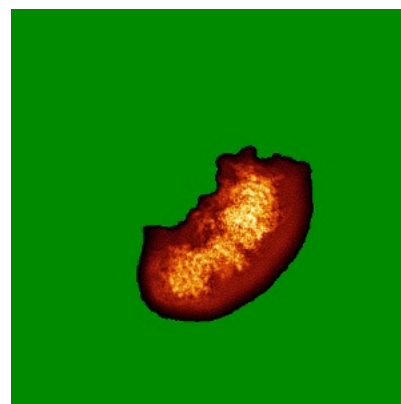
6.4.1 Primary map



X



Y

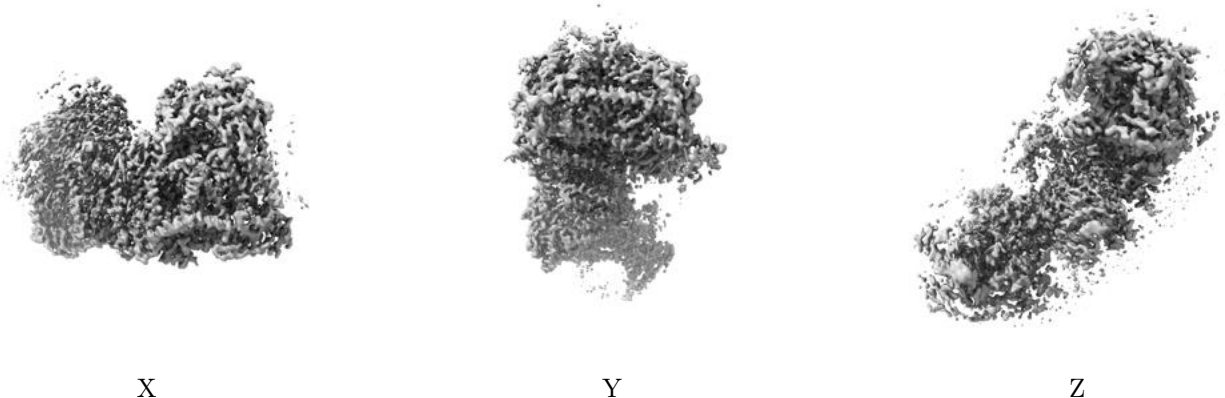


Z

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 0.0677. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

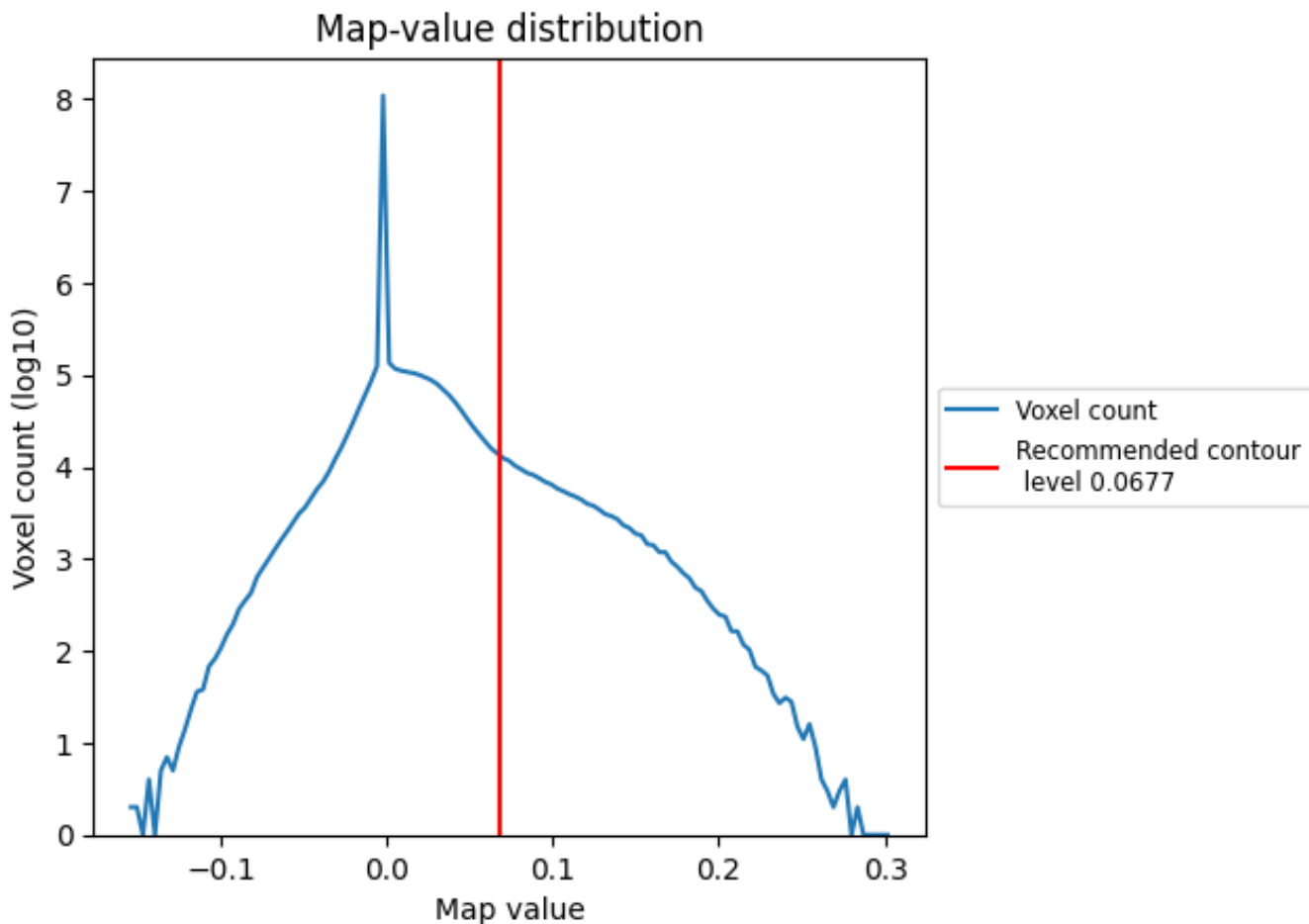
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

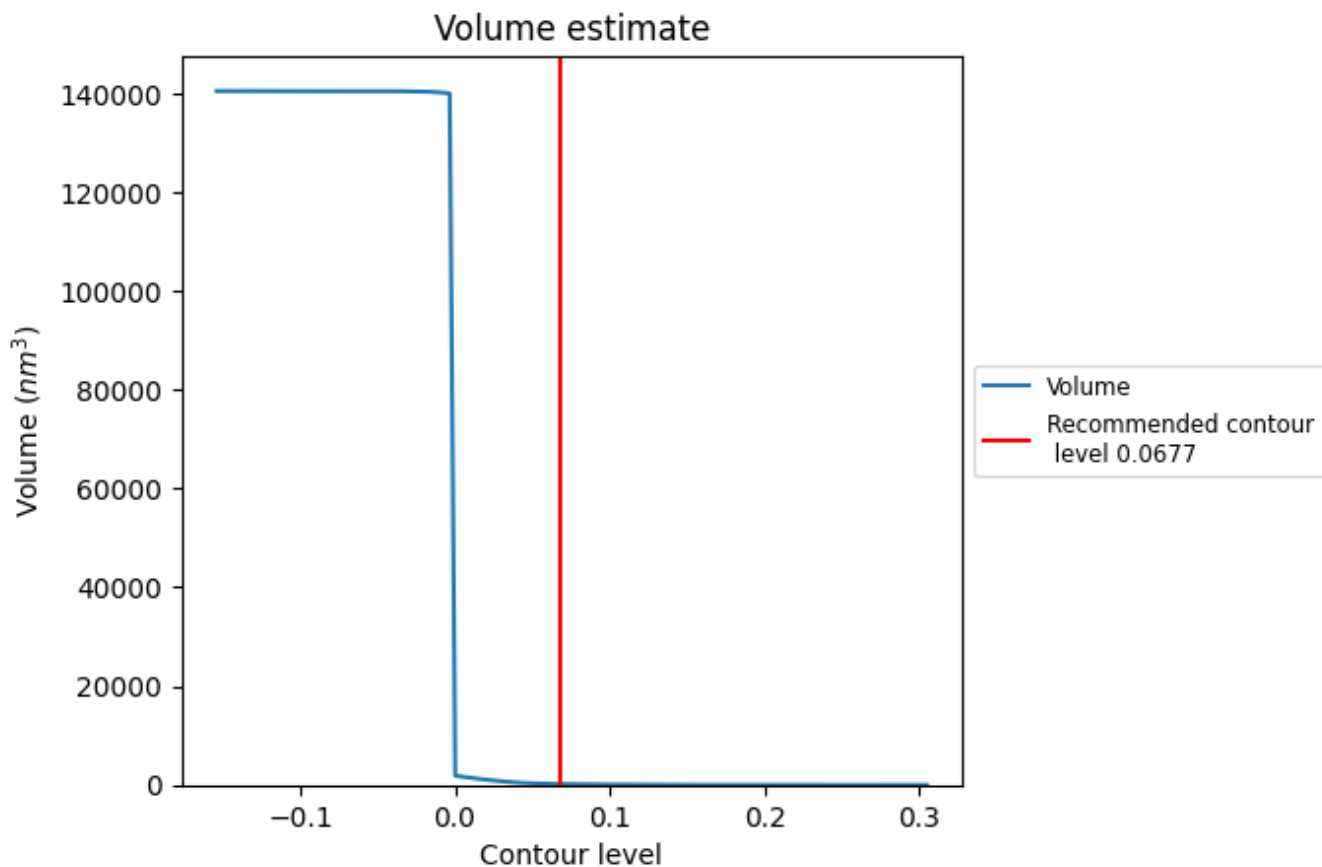
This section contains the results of statistical analysis of the map.

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.

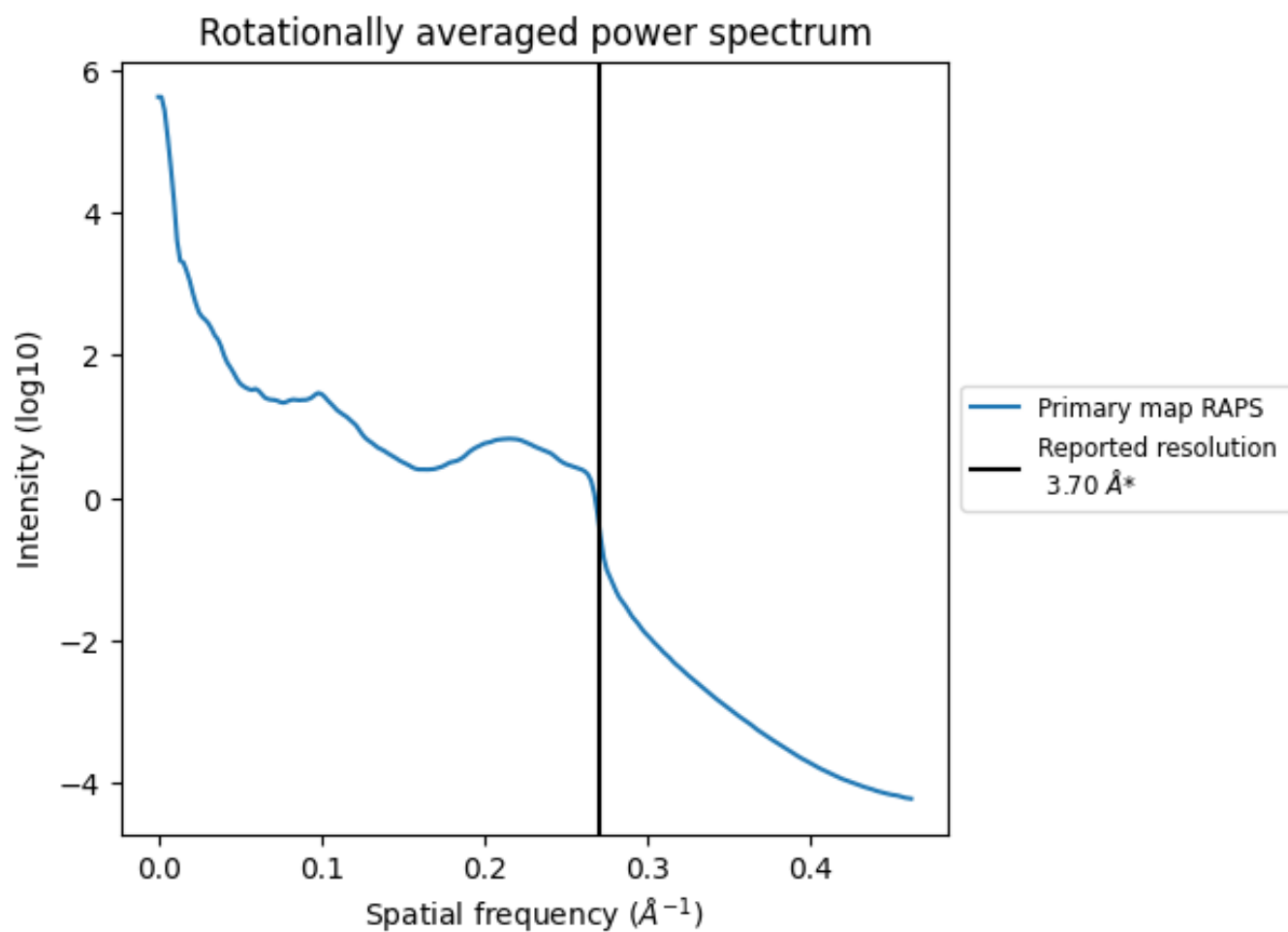
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 198 nm³; this corresponds to an approximate mass of 179 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](#)



*Reported resolution corresponds to spatial frequency of 0.270\AA^{-1}

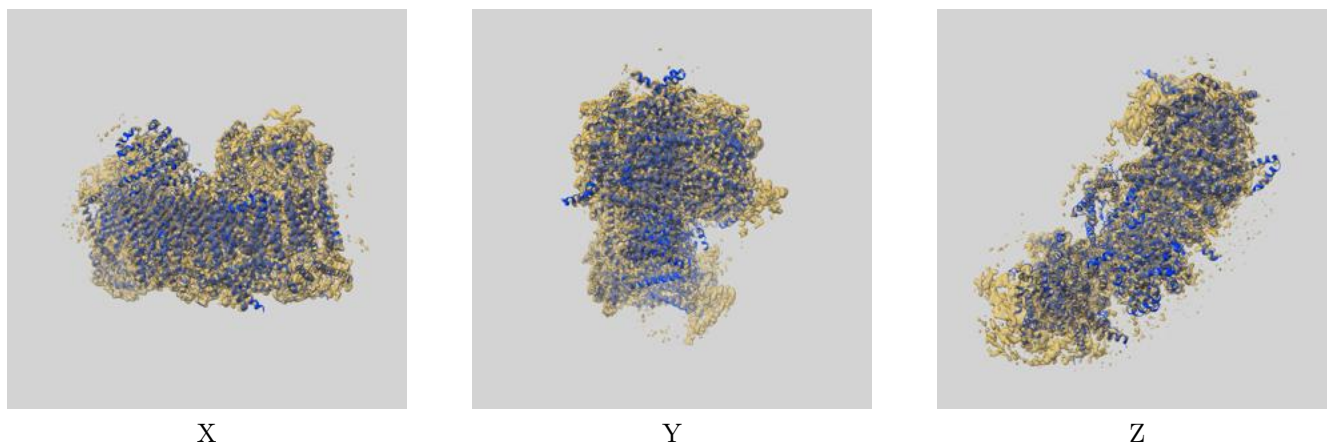
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

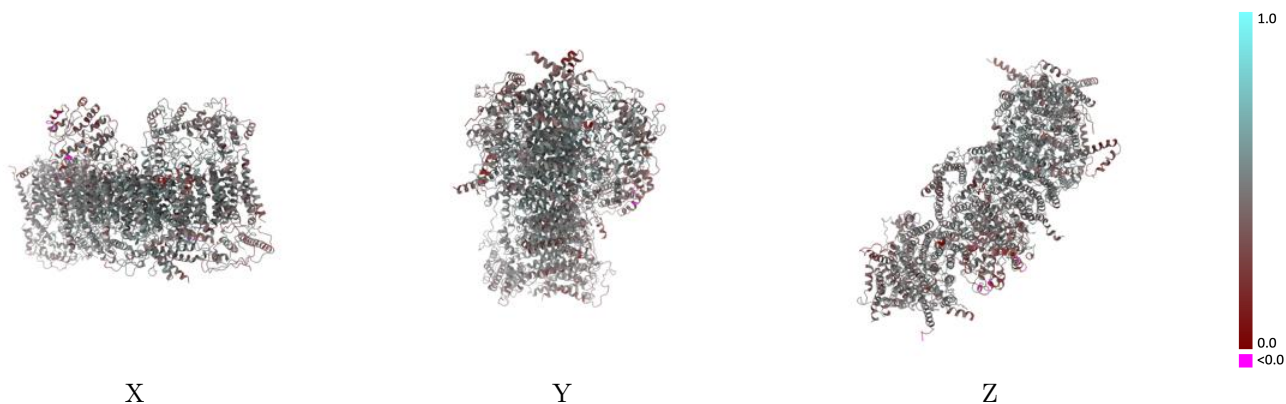
This section contains information regarding the fit between EMDB map EMD-6772 and PDB model 5XTC. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



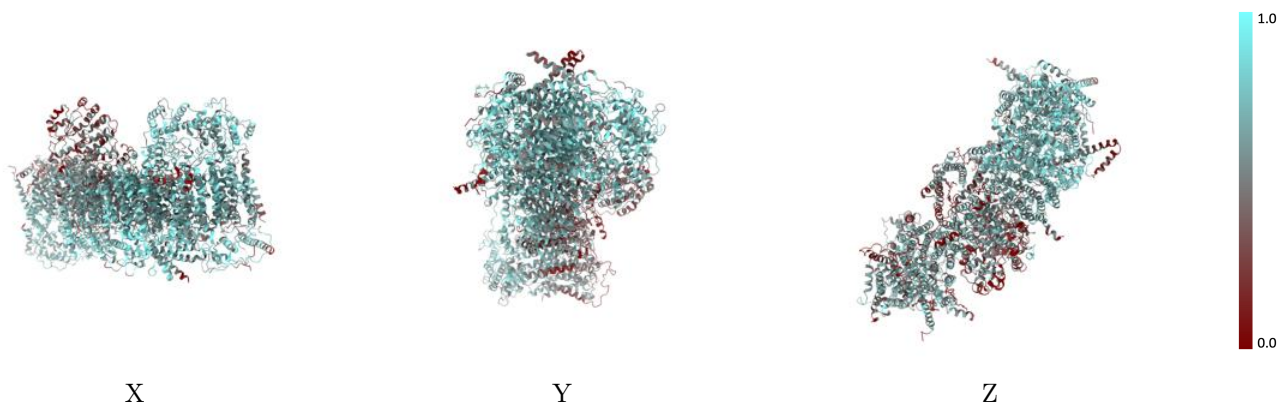
The images above show the 3D surface view of the map at the recommended contour level 0.0677 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



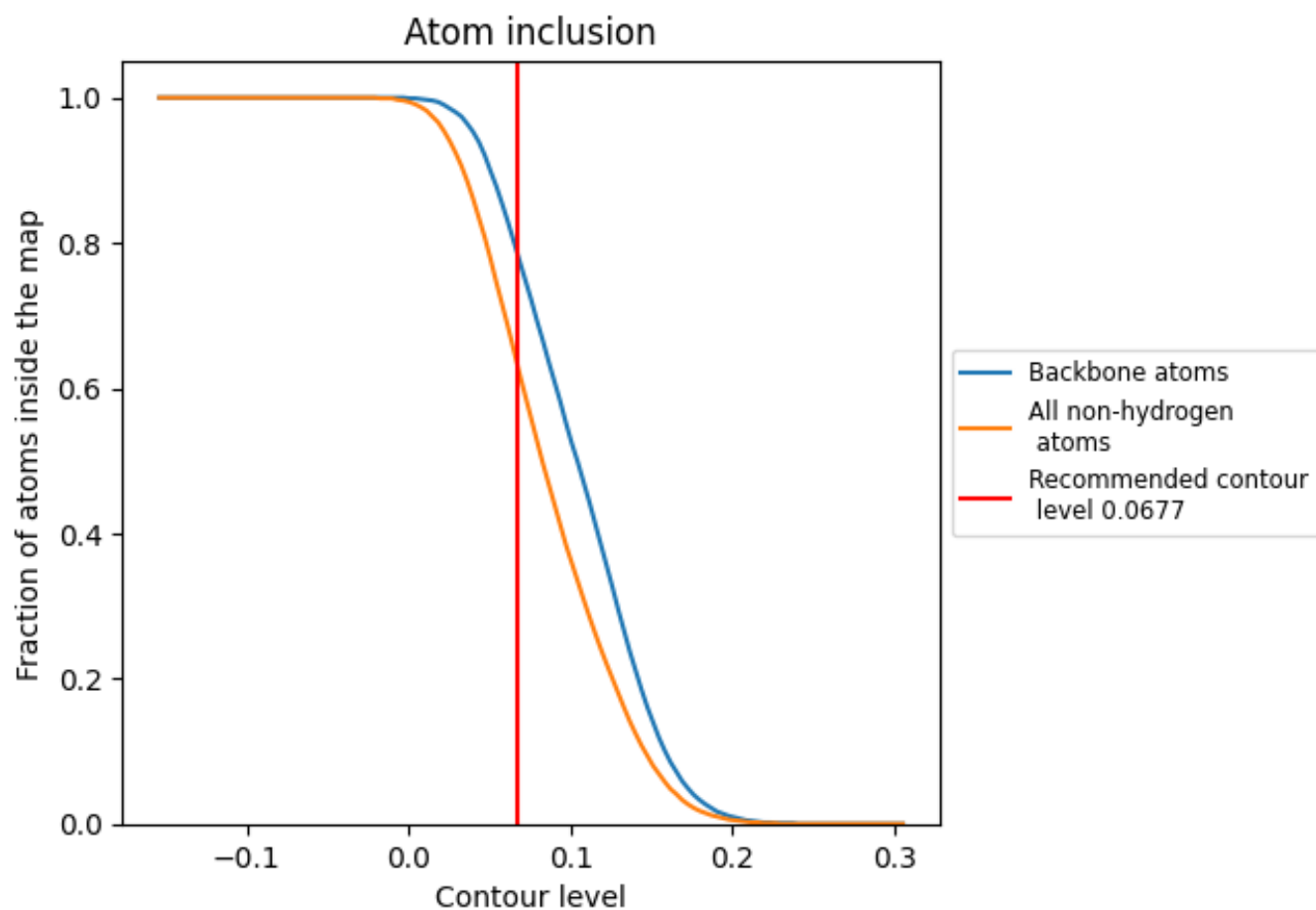
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0677).





























































9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 63% 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 (0.0677) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6260	 0.4550
Q	 0.1600	 0.3760
S	 0.6490	 0.4460
U	 0.5820	 0.4320
V	 0.4690	 0.4430
W	 0.6980	 0.4530
X	 0.6870	 0.4460
Y	 0.7120	 0.4390
Z	 0.6150	 0.4280
a	 0.7780	 0.4990
b	 0.5620	 0.4050
c	 0.7210	 0.4830
d	 0.7260	 0.4660
e	 0.6580	 0.4670
f	 0.5350	 0.3810
g	 0.6660	 0.4870
h	 0.7160	 0.4550
i	 0.6630	 0.4960
j	 0.4020	 0.3850
k	 0.5780	 0.4600
l	 0.6490	 0.4770
m	 0.5340	 0.4350
n	 0.6050	 0.4470
o	 0.6720	 0.4730
p	 0.7260	 0.4700
r	 0.7260	 0.5070
s	 0.5710	 0.4410
u	 0.6960	 0.4390
v	 0.6050	 0.3870
w	 0.3810	 0.3740

