



wwPDB EM Validation Summary Report ⓘ

Nov 3, 2024 – 05:05 am GMT

PDB ID : 5O31
EMDB ID : EMD-3731
Title : Mitochondrial complex I in the deactive state
Authors : Blaza, J.N.; Vinothkumar, K.R.; Hirst, J.
Deposited on : 2017-05-23
Resolution : 4.13 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.dev113
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

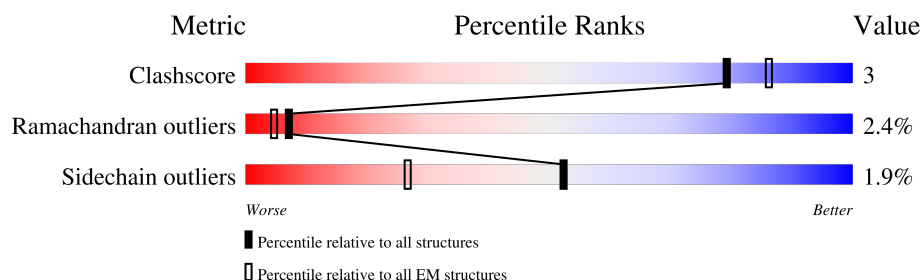
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.13 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	115	<div> <div>23%</div> <div>64%</div> <div>11%</div> <div>23%</div> </div>
2	B	179	<div> <div>8%</div> <div>71%</div> <div>8%</div> <div>18%</div> </div>
3	C	228	<div> <div>11%</div> <div>75%</div> <div>14%</div> <div>11%</div> </div>
4	D	430	<div> <div>18%</div> <div>84%</div> <div>12%</div> <div>.</div> </div>
5	E	217	<div> <div>.</div> <div>81%</div> <div>5%</div> <div>14%</div> </div>
6	F	464	<div> <div>6%</div> <div>87%</div> <div>.</div> <div>8%</div> </div>
7	H	318	<div> <div>18%</div> <div>79%</div> <div>14%</div> <div>7%</div> </div>
8	I	176	<div> <div>11%</div> <div>84%</div> <div>16%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
9	J	175	
10	K	98	
11	L	606	
12	M	459	
13	N	347	
14	O	320	
15	P	297	
16	S	98	
17	T	88	
17	U	88	
18	V	115	
19	W	128	
20	Y	141	
21	a	70	
22	b	80	
23	c	49	
24	e	105	
25	f	57	
26	g	125	
27	i	111	
28	j	52	
29	k	74	
30	l	120	
31	o	136	
32	p	169	

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Mol	Chain	Length	Quality of chain
33	q	145	
34	G	704	
35	s	75	
36	Q	133	
37	R	96	
38	r	112	
39	h	143	
40	d	116	
41	X	171	
42	m	128	
43	n	178	
44	Z	144	

2 Entry composition

There are 49 unique types of molecules in this entry. The entry contains 52703 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-ubiquinone oxidoreductase chain 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	88	Total	C	N	O	S	0	0
			691	474	100	114	3		

- Molecule 2 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	147	Total	C	N	O	S	0	0
			1159	740	203	202	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	204	Total	C	N	O	S	0	0
			1678	1086	286	303	3		

- Molecule 4 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	416	Total	C	N	O	S	0	0
			3229	2056	560	589	24		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	129	ARG	GLN	conflict	UNP P17694

- Molecule 5 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	186	Total	C	N	O	S	0	0
			1038	645	196	193	4		

- Molecule 6 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	425	Total	C	N	O	S	0	0
			2441	1508	467	460	6		

- Molecule 7 is a protein called NADH-ubiquinone oxidoreductase chain 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	296	Total	C	N	O	S	0	0
			2312	1557	357	376	22		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	176	Total	C	N	O	S	0	0
			1388	875	239	264	10		

- Molecule 9 is a protein called NADH-ubiquinone oxidoreductase chain 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	171	Total	C	N	O	S	0	0
			1211	814	179	207	11		

- Molecule 10 is a protein called NADH-ubiquinone oxidoreductase chain 4L.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	95	Total	C	N	O	S	0	0
			720	472	108	126	14		

- Molecule 11 is a protein called NADH-ubiquinone oxidoreductase chain 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	604	Total	C	N	O	S	0	0
			4538	3005	708	787	38		

- Molecule 12 is a protein called NADH-ubiquinone oxidoreductase chain 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	457	Total	C	N	O	S	0	0
			3549	2363	556	592	38		

- Molecule 13 is a protein called NADH-ubiquinone oxidoreductase chain 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	344	Total	C	N	O	S	0	0
			2592	1713	405	440	34		

- Molecule 14 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	314	Total	C	N	O	S	0	0
			1941	1225	353	360	3		

- Molecule 15 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	283	Total	C	N	O		0	0
			1415	849	283	283			

- Molecule 16 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	80	Total	C	N	O		0	0
			405	245	80	80			

- Molecule 17 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	75	Total	C	N	O		0	0
			378	228	75	75			
17	U	85	Total	C	N	O		0	0
			432	262	85	85			

- Molecule 18 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub-unit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	106	Total	C	N	O	S	0	0
			700	441	130	128	1		

- Molecule 19 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	W	111	Total	C	N	O	S	0	0
			817	516	154	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Y	138	Total	C	N	O	S	0	0
			1011	644	173	188	6		

- Molecule 21 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	a	64	Total	C	N	O	S	0	0
			480	312	86	77	5		

- Molecule 22 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	b	80	Total	C	N	O	S	0	0
			519	336	89	93	1		

- Molecule 23 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	c	46	Total	C	N	O	0	0
			320	211	56	53		

- Molecule 24 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	e	89	Total	C	N	O	S	0	0
			619	383	122	109	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
e	27	GLY	LYS	conflict	UNP Q02379

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	f	54	Total	C	N	O	S	0	0
			350	223	62	64	1		

- Molecule 26 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	g	97	Total	C	N	O	S	0	0
			677	438	120	117	2		

- Molecule 27 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	i	106	Total	C	N	O		0	0
			616	376	126	114			

- Molecule 28 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	j	52	Total	C	N	O		0	0
			260	156	52	52			

- Molecule 29 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	k	74	Total	C	N	O		0	0
			370	222	74	74			

- Molecule 30 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	l	118	Total	C	N	O	0	0
			590	354	118	118		

- Molecule 31 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	o	58	Total	C	N	O	S	0	0
			296	176	58	58	4		

- Molecule 32 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10,NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10,NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	p	169	Total	C	N	O	S	0	0
			1039	633	198	202	6		

- Molecule 33 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	q	138	Total	C	N	O	0	0
			696	420	138	138		

- Molecule 34 is a protein called NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	G	688	Total	C	N	O	S	0	0
			4151	2549	792	786	24		

- Molecule 35 is a protein called NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	s	41	Total	C	N	O	0	0
			234	148	42	44		

- Molecule 36 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
36	Q	123	Total	C	N	O	0	0
			749	476	143	130		

- Molecule 37 is a protein called NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	R	93	Total	C	N	O	S	0	0
			638	399	124	112	3		

- Molecule 38 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	r	88	Total	C	N	O	0	0
			575	363	116	96		

- Molecule 39 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	h	134	Total	C	N	O	0	0
			822	527	153	142		

- Molecule 40 is a protein called NADH dehydrogenase [ubiquinone] 1 subunit C2,NADH dehydrogenase [ubiquinone] 1 subunit C2.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	d	113	Total	C	N	O	S	0	0
			803	519	145	136	3		

- Molecule 41 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	X	164	Total	C	N	O	S	0	0
			1170	736	216	209	9		

- Molecule 42 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	m	118	Total	C	N	O	0	0
			904	579	168	157		

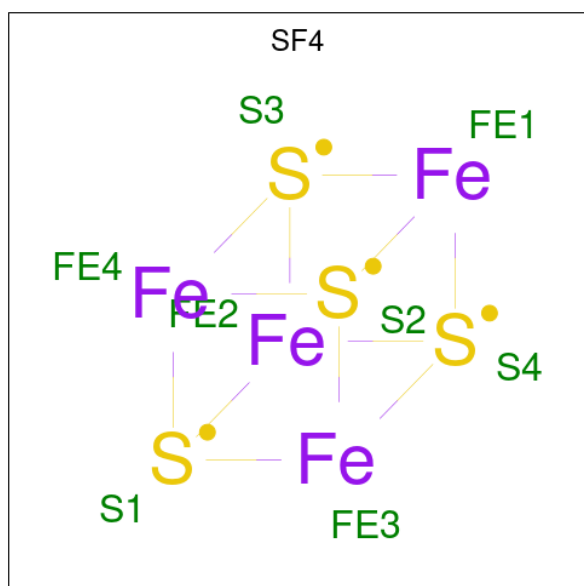
- Molecule 43 is a protein called NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	166	Total	C	N	O	S	0	0
			1124	707	217	197	3		

- Molecule 44 is a protein called NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Z	137	Total	C	N	O	S	0	0
			920	575	171	167	7		

- Molecule 45 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



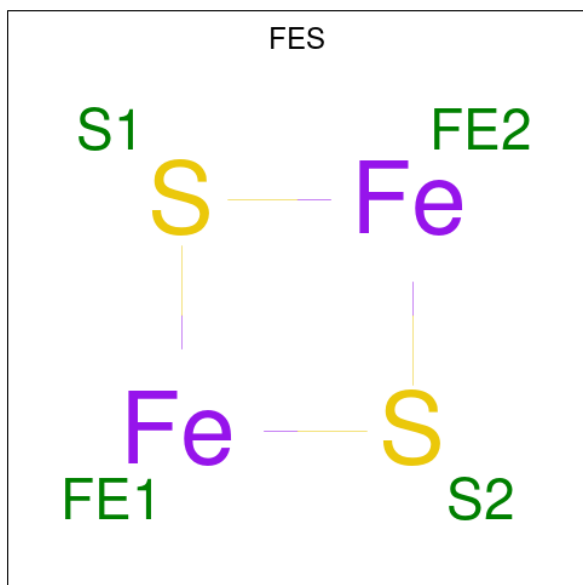
Mol	Chain	Residues	Atoms			AltConf
45	B	1	Total	Fe	S	0
			8	4	4	
45	F	1	Total	Fe	S	0
			8	4	4	
45	I	1	Total	Fe	S	0
			8	4	4	

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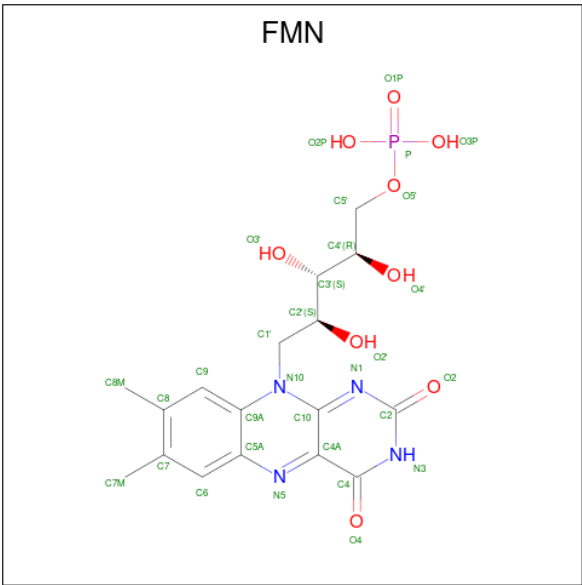
Mol	Chain	Residues	Atoms			AltConf
45	I	1	Total	Fe	S	0
			8	4	4	
45	G	1	Total	Fe	S	0
			8	4	4	
45	G	1	Total	Fe	S	0
			8	4	4	

- Molecule 46 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe_2S_2).



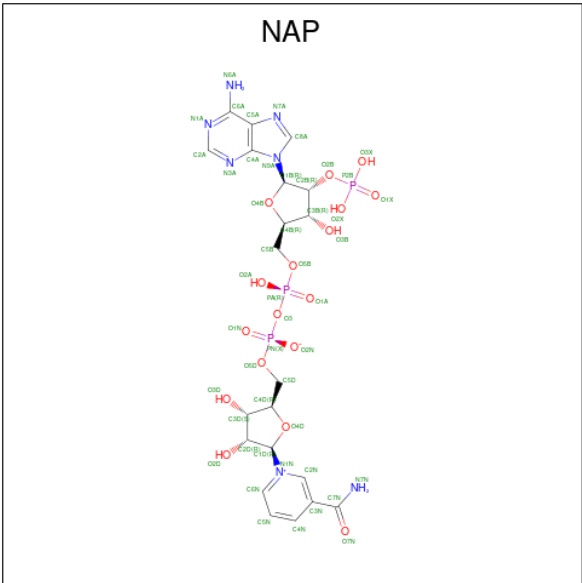
Mol	Chain	Residues	Atoms			AltConf
46	E	1	Total	Fe	S	0
			4	2	2	
46	G	1	Total	Fe	S	0
			4	2	2	

- Molecule 47 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $\text{C}_{17}\text{H}_{21}\text{N}_4\text{O}_9\text{P}$).



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

- Molecule 48 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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

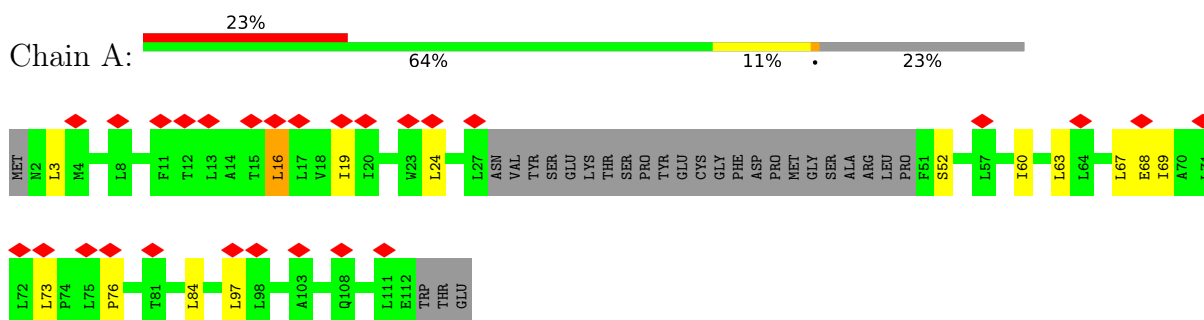
- Molecule 49 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
49	R	1	Total 1	Zn 1	0

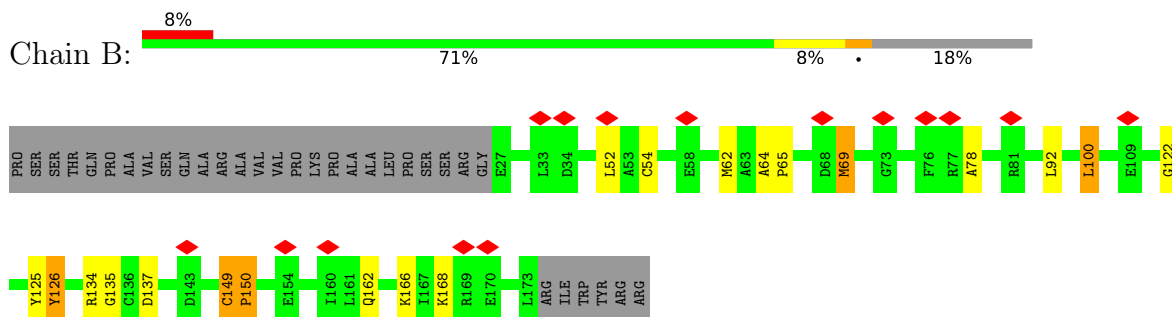
3 Residue-property plots [i](#)

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.

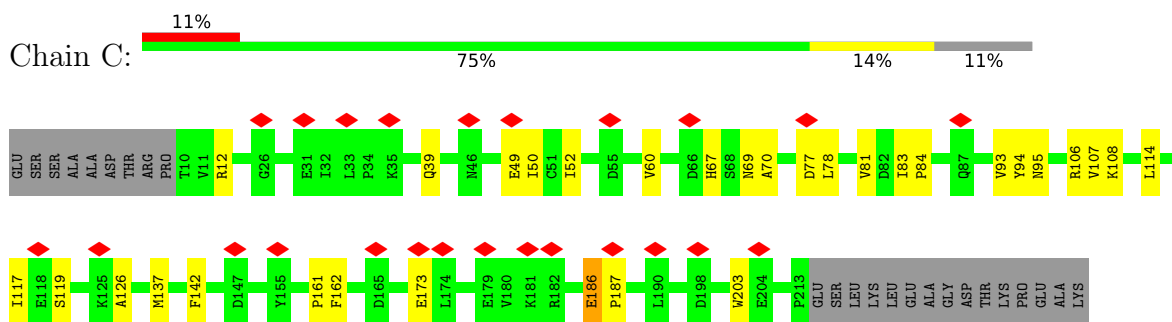
- Molecule 1: NADH-ubiquinone oxidoreductase chain 3



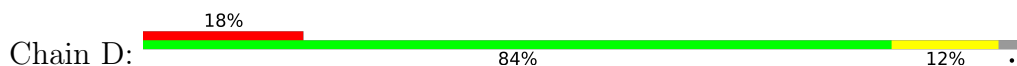
- Molecule 2: NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial



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



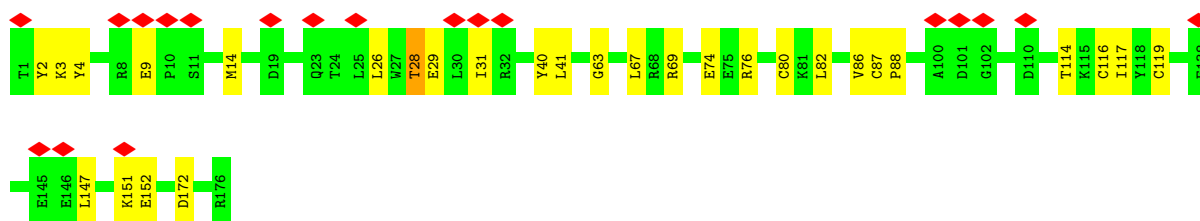
- Molecule 4: NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial



GLN
THR

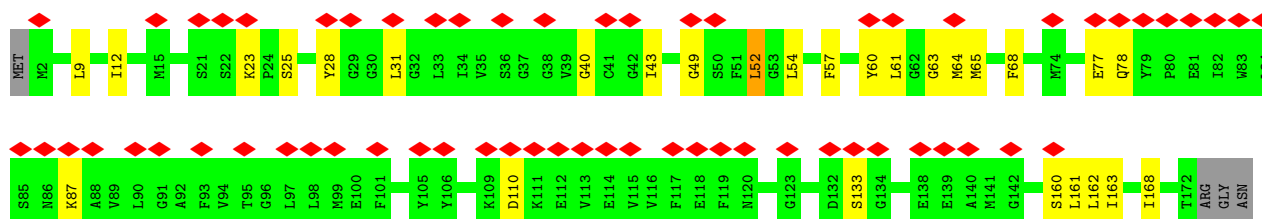
- Molecule 8: NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial

Chain I: 11% 84% 16%



- Molecule 9: NADH-ubiquinone oxidoreductase chain 6

Chain J: 35% 82% 15%



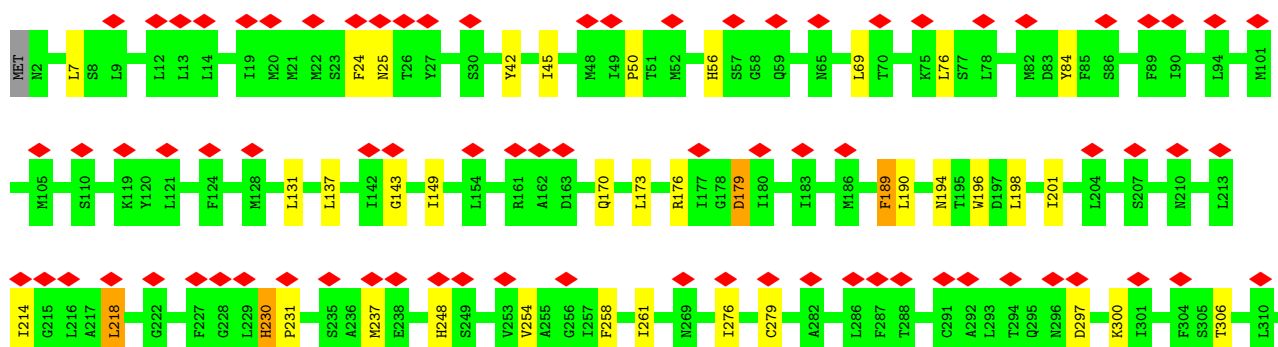
- Molecule 10: NADH-ubiquinone oxidoreductase chain 4L

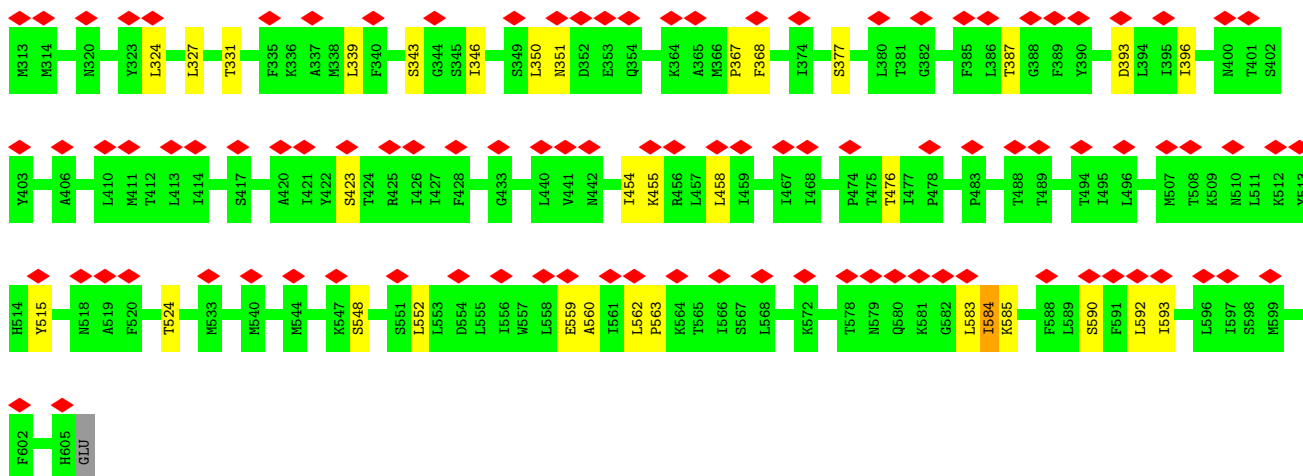
Chain K: 21% 79% 18%

GLN
CYS

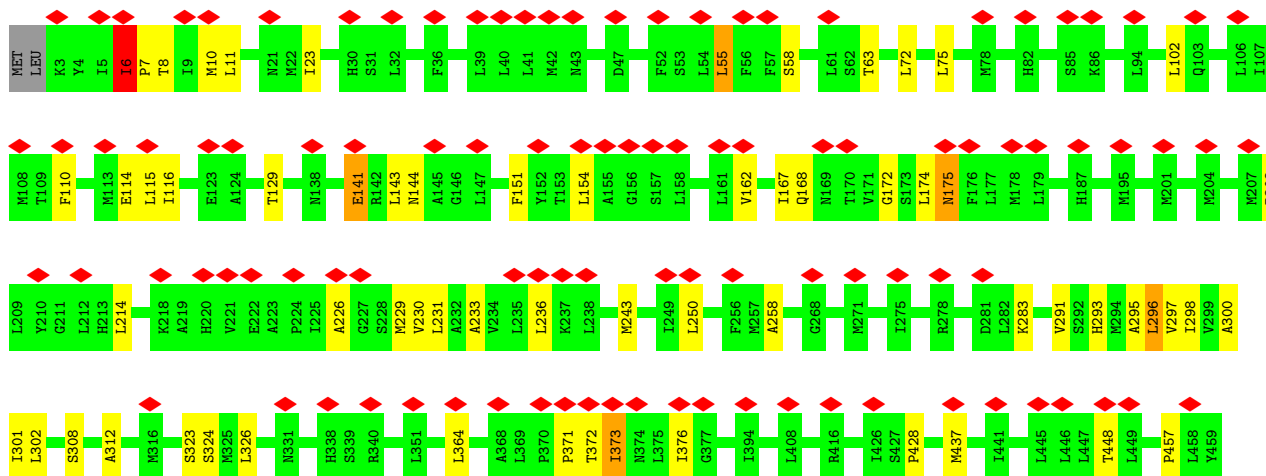
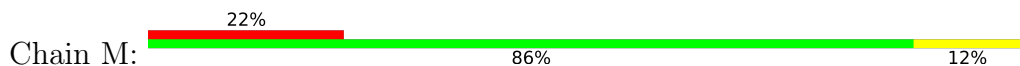
- Molecule 11: NADH-ubiquinone oxidoreductase chain 5

Chain L: 29% 88% 11%

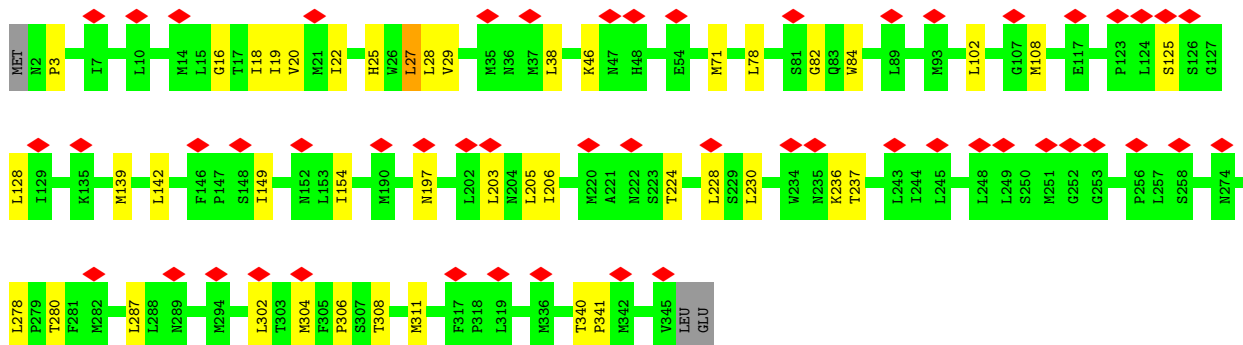
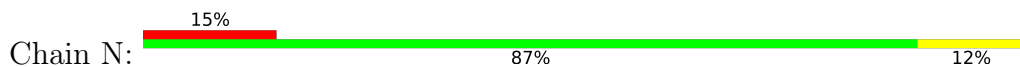




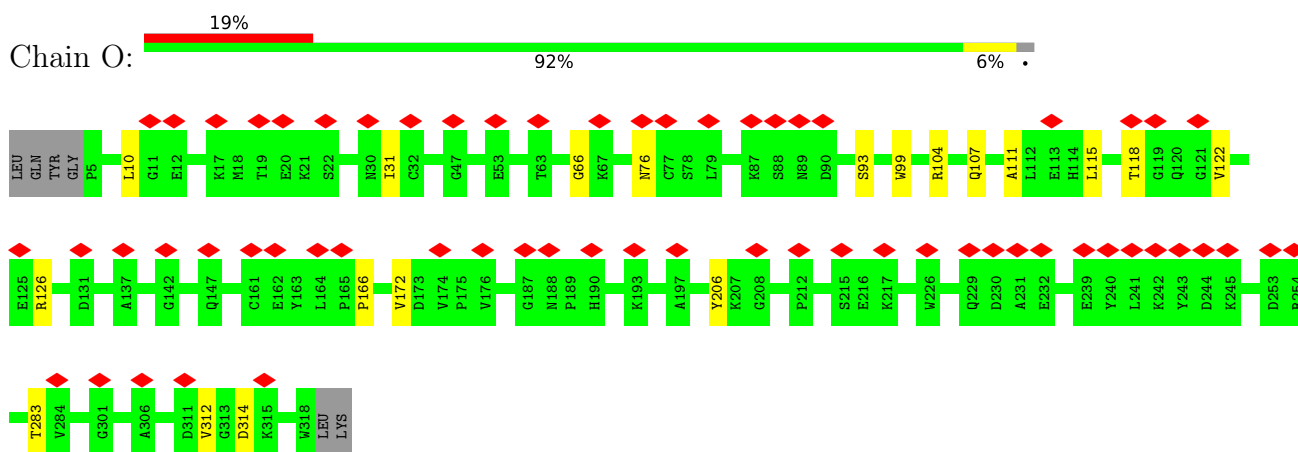
• Molecule 12: NADH-ubiquinone oxidoreductase chain 4



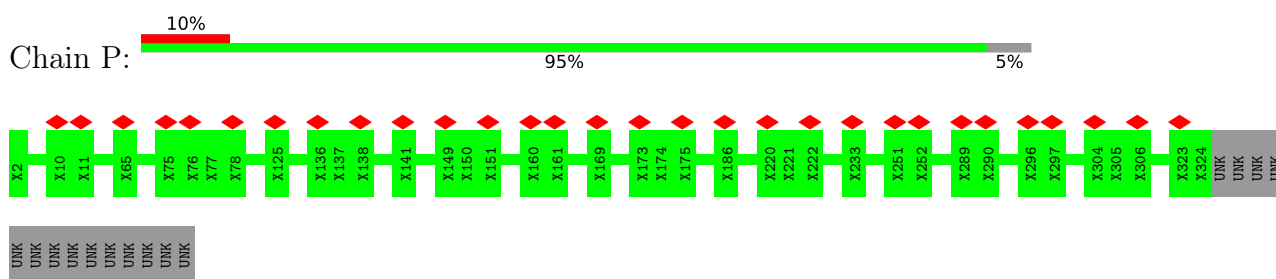
• Molecule 13: NADH-ubiquinone oxidoreductase chain 2



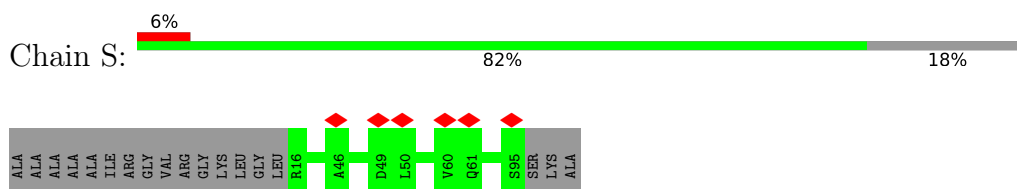
• Molecule 14: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial



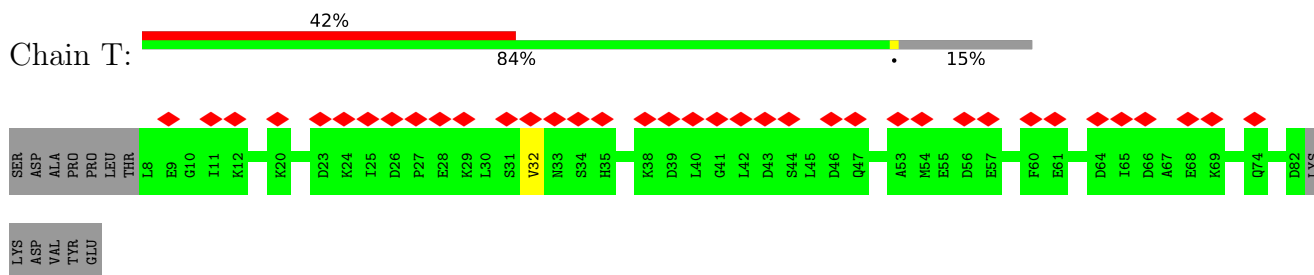
- Molecule 15: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9



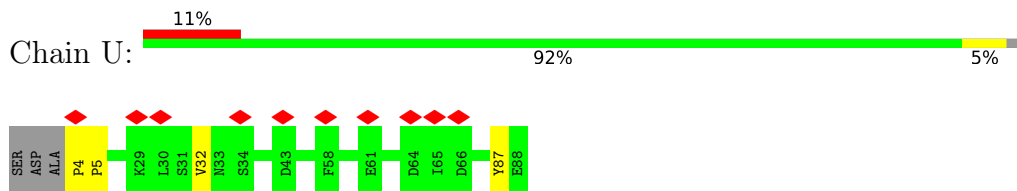
- Molecule 16: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2



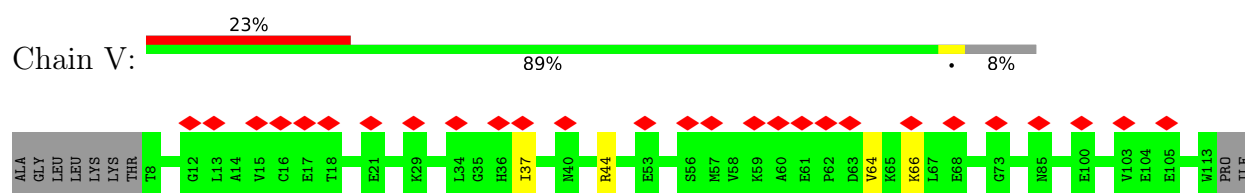
- Molecule 17: Acyl carrier protein, mitochondrial



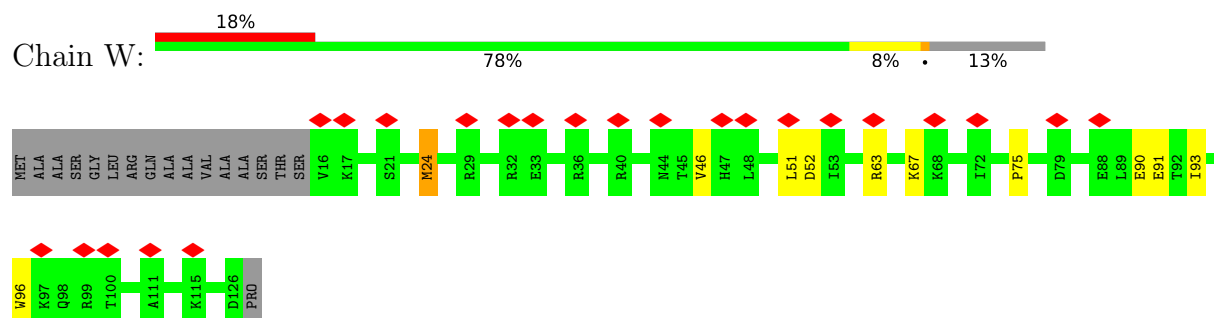
- Molecule 17: Acyl carrier protein, mitochondrial



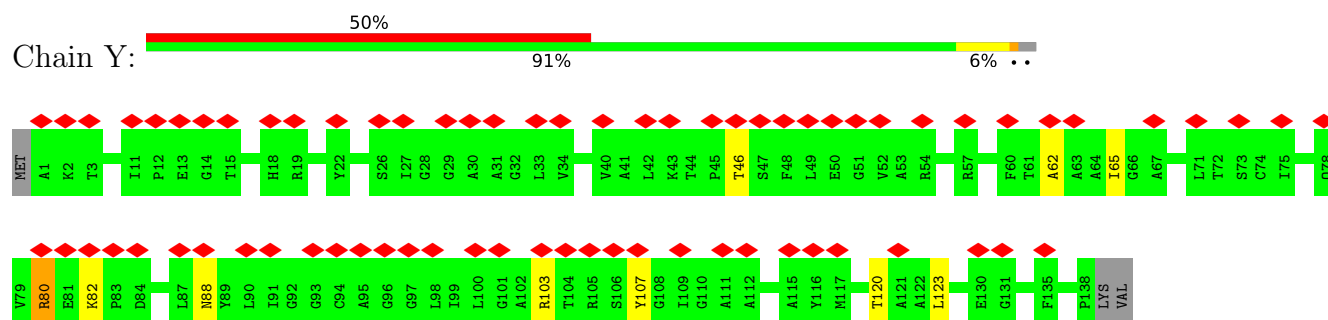
- Molecule 18: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5



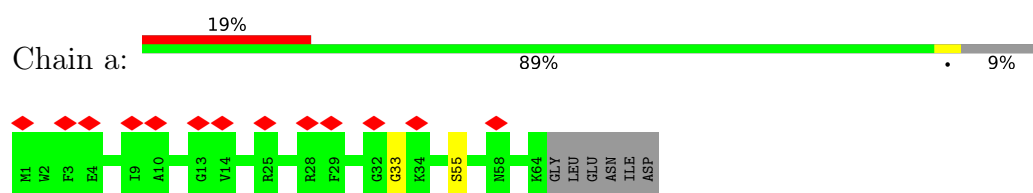
- Molecule 19: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6



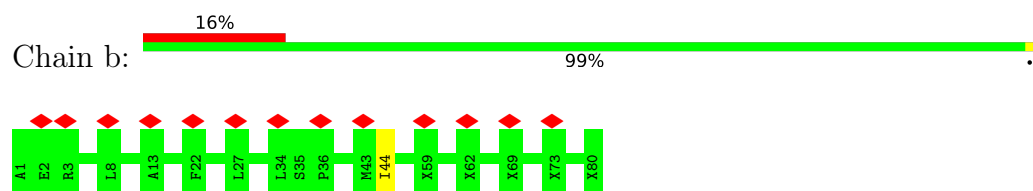
- Molecule 20: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11



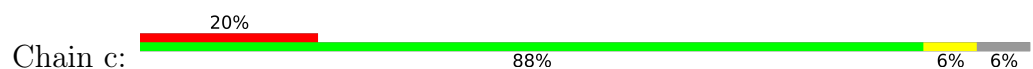
- Molecule 21: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1

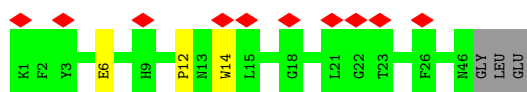


- Molecule 22: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3, NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3

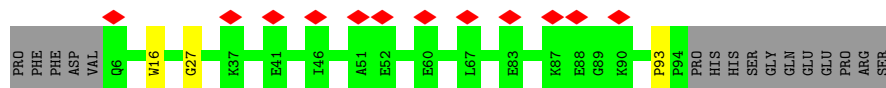
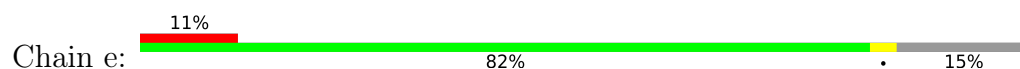


- Molecule 23: NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial

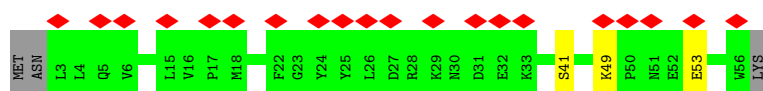
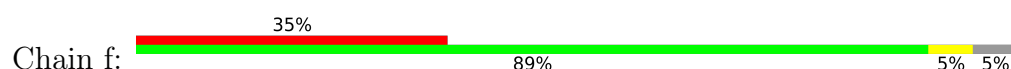




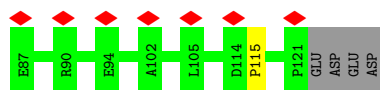
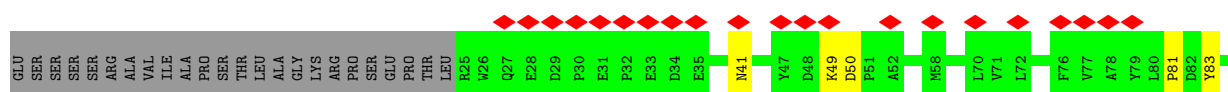
- Molecule 24: NADH dehydrogenase [ubiquinone] iron-sulfur protein 5



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



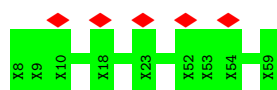
- Molecule 26: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial



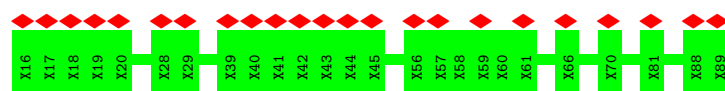
- Molecule 27: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6



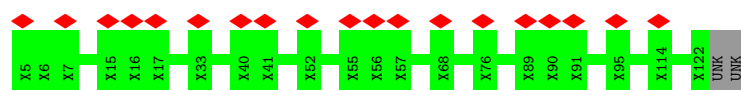
- Molecule 28: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2



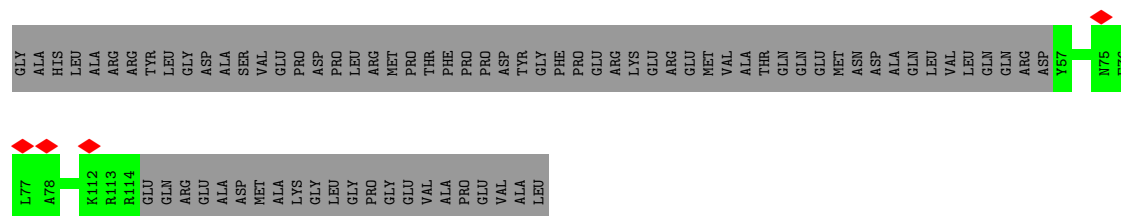
- Molecule 29: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3



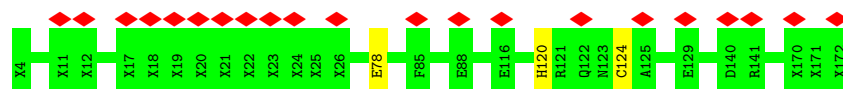
- Molecule 30: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8



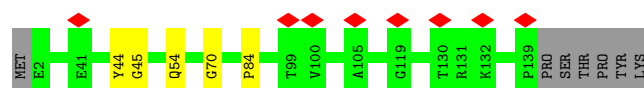
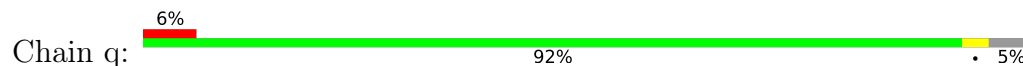
- Molecule 31: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7



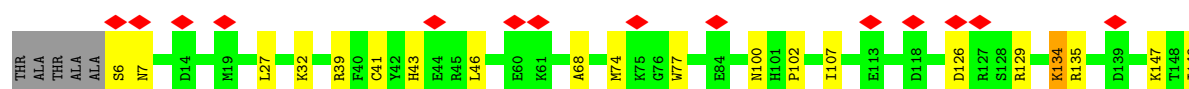
- Molecule 32: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10, NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10

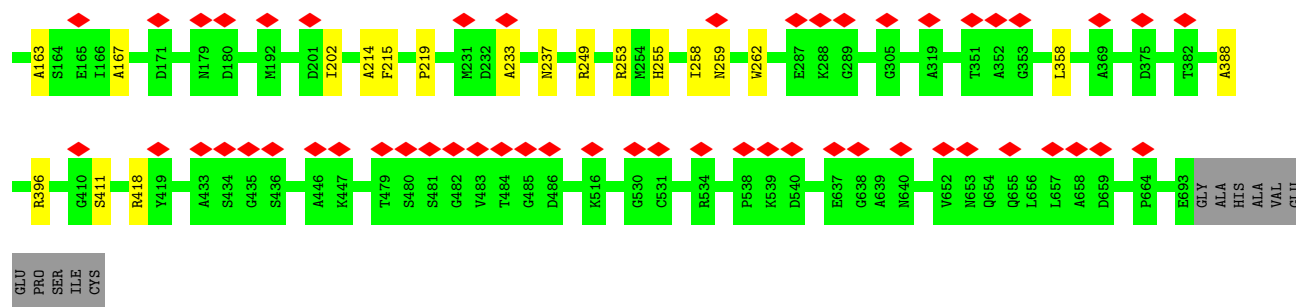


- Molecule 33: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12

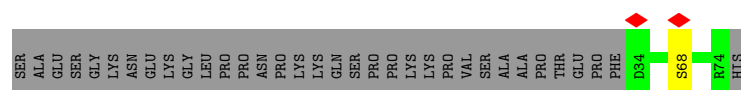


- Molecule 34: NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial

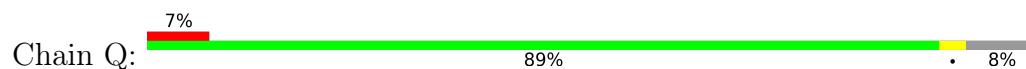




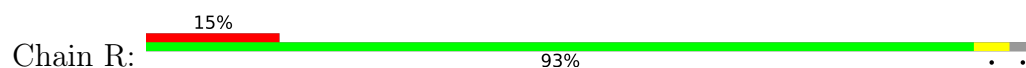
- Molecule 35: NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial



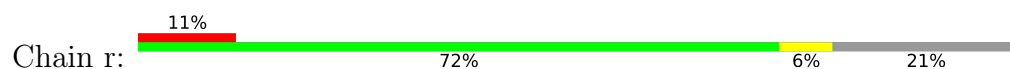
- Molecule 36: NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial



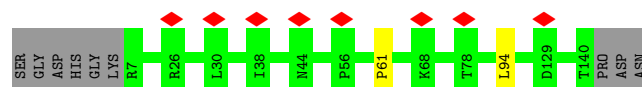
- Molecule 37: NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial



- Molecule 38: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7

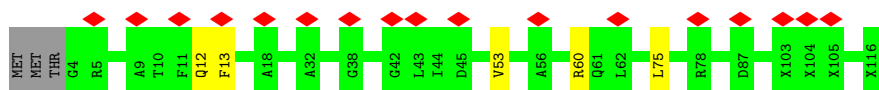


- Molecule 39: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial



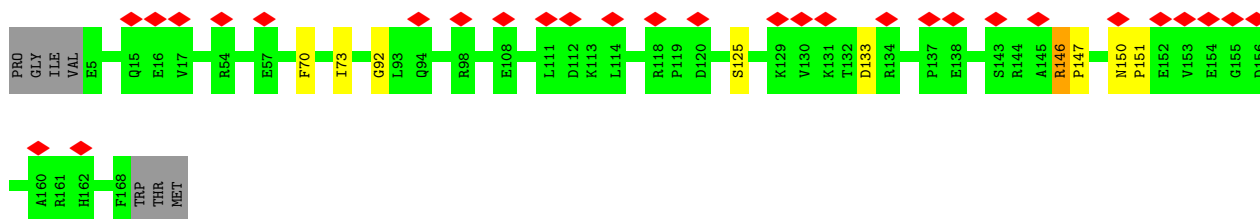
- Molecule 40: NADH dehydrogenase [ubiquinone] 1 subunit C2,NADH dehydrogenase [ubiquinone] 1 subunit C2

Chain d: 




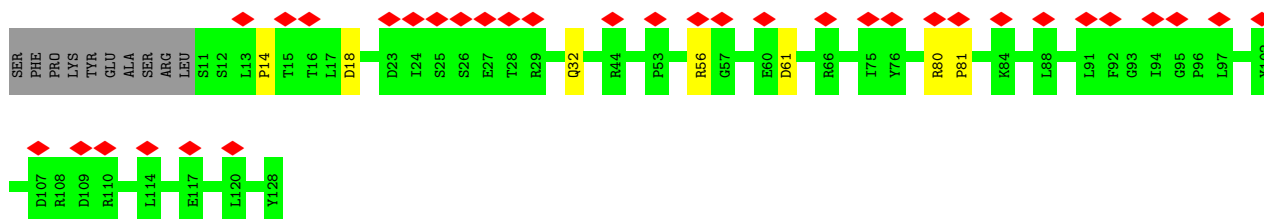
- Molecule 41: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8

Chain X: 




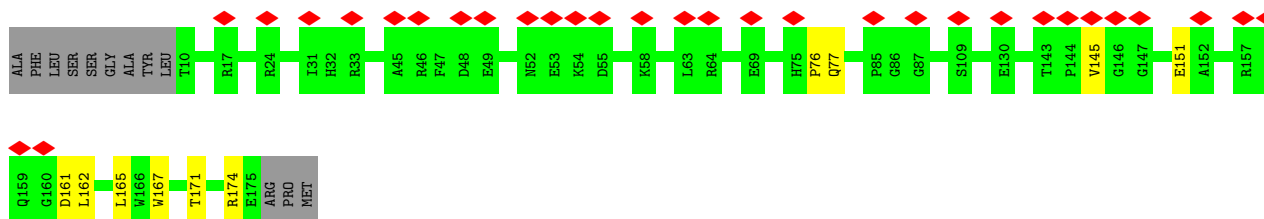
- Molecule 42: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4

Chain m: 




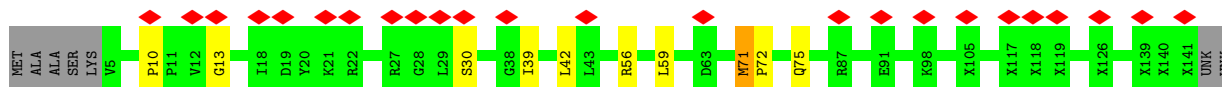
- Molecule 43: NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9

Chain n: 



- Molecule 44: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13,NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13

Chain Z: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	125006	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; CTF correction was done per particle after the CTF was estimated on the whole micrograph.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	3100	Depositor
Magnification	101499	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.450	Depositor
Minimum map value	-0.316	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.14	Depositor
Map size (Å)	496.8, 496.8, 496.8	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SF4, NAP, FES, FMN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/706	0.63	0/967
2	B	0.39	0/1187	0.63	0/1607
3	C	0.43	0/1728	0.61	0/2353
4	D	0.39	0/3304	0.59	0/4478
5	E	0.38	0/1062	0.54	0/1484
6	F	0.37	0/2488	0.51	0/3434
7	H	0.42	0/2378	0.60	0/3250
8	I	0.41	0/1419	0.63	0/1925
9	J	0.45	0/1239	0.55	0/1688
10	K	0.39	0/730	0.64	0/988
11	L	0.43	0/4653	0.59	0/6350
12	M	0.41	0/3638	0.62	0/4967
13	N	0.41	0/2656	0.61	0/3630
14	O	0.39	0/1983	0.53	0/2742
16	S	0.32	0/408	0.49	0/571
17	T	0.31	0/380	0.49	0/531
17	U	0.31	0/436	0.50	0/610
18	V	0.37	0/713	0.53	0/977
19	W	0.39	0/831	0.56	0/1128
20	Y	0.42	0/1031	0.55	0/1400
21	a	0.44	0/494	0.56	0/669
22	b	0.43	0/352	0.56	0/481
23	c	0.44	0/330	0.58	0/455
24	e	0.38	0/630	0.55	0/851
25	f	0.42	0/356	0.56	0/488
26	g	0.46	0/696	0.63	0/957
27	i	0.36	0/224	0.57	0/300
31	o	0.32	0/296	0.48	0/412
32	p	0.38	0/535	0.53	0/718
33	q	0.36	0/704	0.59	0/984
34	G	0.36	0/4212	0.53	0/5789
35	s	0.40	0/238	0.55	0/332

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	Q	0.39	0/768	0.52	0/1066
37	R	0.39	0/649	0.52	0/879
38	r	0.43	0/594	0.58	0/824
39	h	0.38	0/837	0.53	0/1157
40	d	0.45	0/730	0.54	0/992
41	X	0.41	0/1200	0.56	0/1634
42	m	0.42	0/926	0.58	0/1260
43	n	0.39	0/1163	0.52	0/1586
44	Z	0.39	0/718	0.55	0/967
All	All	0.40	0/49622	0.57	0/67881

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
2	B	0	1
12	M	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	149	CYS	Peptide
12	M	6	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	A	691	0	728	9	0
2	B	1159	0	1166	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	1678	0	1612	17	0
4	D	3229	0	3123	30	0
5	E	1038	0	623	2	0
6	F	2441	0	1628	5	0
7	H	2312	0	2426	23	0
8	I	1388	0	1323	11	0
9	J	1211	0	1165	14	0
10	K	720	0	761	13	0
11	L	4538	0	4480	32	0
12	M	3549	0	3674	31	0
13	N	2592	0	2632	21	0
14	O	1941	0	1366	4	0
15	P	1415	0	303	0	0
16	S	405	0	197	0	0
17	T	378	0	176	0	0
17	U	432	0	207	1	0
18	V	700	0	582	1	0
19	W	817	0	743	5	0
20	Y	1011	0	1020	3	0
21	a	480	0	440	0	0
22	b	519	0	408	0	0
23	c	320	0	277	0	0
24	e	619	0	513	0	0
25	f	350	0	260	0	0
26	g	677	0	559	0	0
27	i	616	0	300	0	0
28	j	260	0	58	0	0
29	k	370	0	77	0	0
30	l	590	0	125	0	0
31	o	296	0	134	0	0
32	p	1039	0	582	0	0
33	q	696	0	338	0	0
34	G	4151	0	3048	16	0
35	s	234	0	138	0	0
36	Q	749	0	496	1	0
37	R	638	0	565	1	0
38	r	575	0	425	0	0
39	h	822	0	644	0	0
40	d	803	0	659	0	0
41	X	1170	0	969	3	0
42	m	904	0	832	0	0
43	n	1124	0	862	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Z	920	0	704	7	0
45	B	8	0	0	0	0
45	F	8	0	0	0	0
45	G	16	0	0	0	0
45	I	16	0	0	0	0
46	E	4	0	0	0	0
46	G	4	0	0	0	0
47	F	31	0	19	0	0
48	P	48	0	25	0	0
49	R	1	0	0	0	0
All	All	52703	0	43392	220	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 3.

The worst 5 of 220 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)
44:Z:71:MET:H	44:Z:72:PRO:HD2	1.55	0.71
4:D:112:MET:H	4:D:145:THR:HG21	1.59	0.68
11:L:189:PHE:HB3	11:L:196:TRP:HB3	1.77	0.66
5:E:152:PRO:HD2	5:E:163:ASP:HA	1.81	0.62
12:M:143:LEU:HD21	13:N:302:LEU:HD11	1.82	0.61

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	84/115 (73%)	79 (94%)	4 (5%)	1 (1%)	11 43
2	B	145/179 (81%)	124 (86%)	19 (13%)	2 (1%)	9 40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	202/228 (89%)	175 (87%)	23 (11%)	4 (2%)	6	34
4	D	412/430 (96%)	364 (88%)	41 (10%)	7 (2%)	7	37
5	E	184/217 (85%)	157 (85%)	20 (11%)	7 (4%)	2	22
6	F	423/464 (91%)	381 (90%)	33 (8%)	9 (2%)	5	32
7	H	292/318 (92%)	264 (90%)	20 (7%)	8 (3%)	4	28
8	I	174/176 (99%)	144 (83%)	22 (13%)	8 (5%)	2	20
9	J	169/175 (97%)	150 (89%)	13 (8%)	6 (4%)	3	23
10	K	93/98 (95%)	87 (94%)	5 (5%)	1 (1%)	12	45
11	L	602/606 (99%)	535 (89%)	54 (9%)	13 (2%)	5	32
12	M	455/459 (99%)	412 (90%)	32 (7%)	11 (2%)	5	30
13	N	342/347 (99%)	311 (91%)	26 (8%)	5 (2%)	8	39
14	O	312/320 (98%)	277 (89%)	24 (8%)	11 (4%)	3	23
16	S	78/98 (80%)	75 (96%)	3 (4%)	0	100	100
17	T	73/88 (83%)	66 (90%)	6 (8%)	1 (1%)	9	40
17	U	83/88 (94%)	72 (87%)	9 (11%)	2 (2%)	5	30
18	V	104/115 (90%)	88 (85%)	15 (14%)	1 (1%)	13	47
19	W	109/128 (85%)	93 (85%)	14 (13%)	2 (2%)	7	35
20	Y	136/141 (96%)	125 (92%)	7 (5%)	4 (3%)	3	26
21	a	62/70 (89%)	58 (94%)	2 (3%)	2 (3%)	3	25
22	b	44/80 (55%)	38 (86%)	6 (14%)	0	100	100
23	c	44/49 (90%)	41 (93%)	0	3 (7%)	1	14
24	e	87/105 (83%)	78 (90%)	7 (8%)	2 (2%)	5	31
25	f	52/57 (91%)	46 (88%)	3 (6%)	3 (6%)	1	16
26	g	95/125 (76%)	72 (76%)	17 (18%)	6 (6%)	1	15
27	i	25/111 (22%)	23 (92%)	2 (8%)	0	100	100
31	o	56/136 (41%)	50 (89%)	6 (11%)	0	100	100
32	p	67/169 (40%)	60 (90%)	4 (6%)	3 (4%)	2	20
33	q	136/145 (94%)	111 (82%)	20 (15%)	5 (4%)	2	23
34	G	686/704 (97%)	621 (90%)	59 (9%)	6 (1%)	14	50
35	s	39/75 (52%)	34 (87%)	4 (10%)	1 (3%)	4	29
36	Q	121/133 (91%)	107 (88%)	12 (10%)	2 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	R	91/96 (95%)	79 (87%)	10 (11%)	2 (2%)	5	32
38	r	84/112 (75%)	66 (79%)	13 (16%)	5 (6%)	1	16
39	h	132/143 (92%)	111 (84%)	20 (15%)	1 (1%)	16	53
40	d	93/116 (80%)	84 (90%)	6 (6%)	3 (3%)	3	25
41	X	162/171 (95%)	142 (88%)	16 (10%)	4 (2%)	4	29
42	m	116/128 (91%)	93 (80%)	18 (16%)	5 (4%)	2	20
43	n	164/178 (92%)	135 (82%)	19 (12%)	10 (6%)	1	16
44	Z	93/144 (65%)	82 (88%)	8 (9%)	3 (3%)	3	25
All	All	6921/7837 (88%)	6110 (88%)	642 (9%)	169 (2%)	7	30

5 of 169 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	150	PRO
3	C	12	ARG
4	D	388	ARG
6	F	423	ARG
7	H	92	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	73/101 (72%)	69 (94%)	4 (6%)	18	42
2	B	124/150 (83%)	116 (94%)	8 (6%)	14	37
3	C	179/204 (88%)	175 (98%)	4 (2%)	47	65
4	D	332/371 (90%)	327 (98%)	5 (2%)	60	75
5	E	36/183 (20%)	36 (100%)	0	100	100
6	F	97/368 (26%)	92 (95%)	5 (5%)	19	43
7	H	250/275 (91%)	248 (99%)	2 (1%)	79	84
8	I	143/151 (95%)	138 (96%)	5 (4%)	31	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	J	112/142 (79%)	109 (97%)	3 (3%)	40	60
10	K	83/86 (96%)	81 (98%)	2 (2%)	44	63
11	L	463/534 (87%)	454 (98%)	9 (2%)	52	69
12	M	387/413 (94%)	381 (98%)	6 (2%)	58	74
13	N	277/316 (88%)	273 (99%)	4 (1%)	62	75
14	O	102/283 (36%)	101 (99%)	1 (1%)	73	81
16	S	4/81 (5%)	4 (100%)	0	100	100
17	T	3/81 (4%)	3 (100%)	0	100	100
17	U	5/81 (6%)	5 (100%)	0	100	100
18	V	49/101 (48%)	48 (98%)	1 (2%)	50	68
19	W	71/114 (62%)	71 (100%)	0	100	100
20	Y	99/102 (97%)	98 (99%)	1 (1%)	73	81
21	a	41/59 (70%)	41 (100%)	0	100	100
22	b	36/36 (100%)	35 (97%)	1 (3%)	38	59
23	c	26/45 (58%)	26 (100%)	0	100	100
24	e	46/94 (49%)	45 (98%)	1 (2%)	47	65
25	f	22/54 (41%)	22 (100%)	0	100	100
26	g	51/112 (46%)	51 (100%)	0	100	100
27	i	20/31 (64%)	20 (100%)	0	100	100
31	o	5/119 (4%)	5 (100%)	0	100	100
32	p	50/62 (81%)	50 (100%)	0	100	100
33	q	9/131 (7%)	9 (100%)	0	100	100
34	G	226/588 (38%)	221 (98%)	5 (2%)	47	65
35	s	9/69 (13%)	9 (100%)	0	100	100
36	Q	31/119 (26%)	31 (100%)	0	100	100
37	R	52/79 (66%)	51 (98%)	1 (2%)	52	69
38	r	32/96 (33%)	30 (94%)	2 (6%)	15	37
39	h	45/124 (36%)	44 (98%)	1 (2%)	47	65
40	d	62/84 (74%)	60 (97%)	2 (3%)	34	55
41	X	95/154 (62%)	95 (100%)	0	100	100
42	m	79/114 (69%)	77 (98%)	2 (2%)	42	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	n	78/160 (49%)	78 (100%)	0	100	100
44	Z	63/83 (76%)	63 (100%)	0	100	100
All	All	3967/6550 (61%)	3892 (98%)	75 (2%)	52	69

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
14	O	115	LEU
40	d	60	ARG
20	Y	103	ARG
34	G	215	PHE
6	F	415	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
23	c	34	GLN
34	G	237	ASN
34	G	100	ASN
34	G	255	HIS
7	H	5	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 1 is monoatomic - leaving 10 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	$\# Z > 2$
45	SF4	G	802	34	0,12,12	-	-	-		
45	SF4	I	201	8	0,12,12	-	-	-		
47	FMN	F	501	-	33,33,33	1.64	5 (15%)	48,50,50	1.40	8 (16%)
45	SF4	B	201	2	0,12,12	-	-	-		
45	SF4	G	801	34	0,12,12	-	-	-		
45	SF4	F	502	6	0,12,12	-	-	-		
46	FES	G	803	34	0,4,4	-	-	-		
48	NAP	P	501	-	45,52,52	0.92	3 (6%)	56,80,80	1.23	5 (8%)
46	FES	E	301	5	0,4,4	-	-	-		
45	SF4	I	202	8	0,12,12	-	-	-		

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
46	FES	E	301	5	-	-	0/1/1/1
45	SF4	G	802	34	-	-	0/6/5/5
45	SF4	I	201	8	-	-	0/6/5/5
47	FMN	F	501	-	-	9/18/18/18	0/3/3/3
45	SF4	B	201	2	-	-	0/6/5/5
45	SF4	G	801	34	-	-	0/6/5/5
46	FES	G	803	34	-	-	0/1/1/1
48	NAP	P	501	-	-	7/31/67/67	0/5/5/5
45	SF4	I	202	8	-	-	0/6/5/5
45	SF4	F	502	6	-	-	0/6/5/5

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	F	501	FMN	C9A-C5A	5.82	1.50	1.41
47	F	501	FMN	C8-C7	3.88	1.50	1.40
48	P	501	NAP	C5A-C4A	2.71	1.48	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	F	501	FMN	C4A-N5	2.61	1.35	1.30
47	F	501	FMN	C10-N10	2.46	1.42	1.37

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	P	501	NAP	N3A-C2A-N1A	-3.62	123.03	128.68
48	P	501	NAP	C3D-C2D-C1D	3.33	105.98	100.98
48	P	501	NAP	PN-O3-PA	-3.23	121.76	132.83
47	F	501	FMN	C4A-C10-N1	-3.11	117.52	124.73
47	F	501	FMN	C4'-C3'-C2'	2.66	118.89	113.36

There are no chirality outliers.

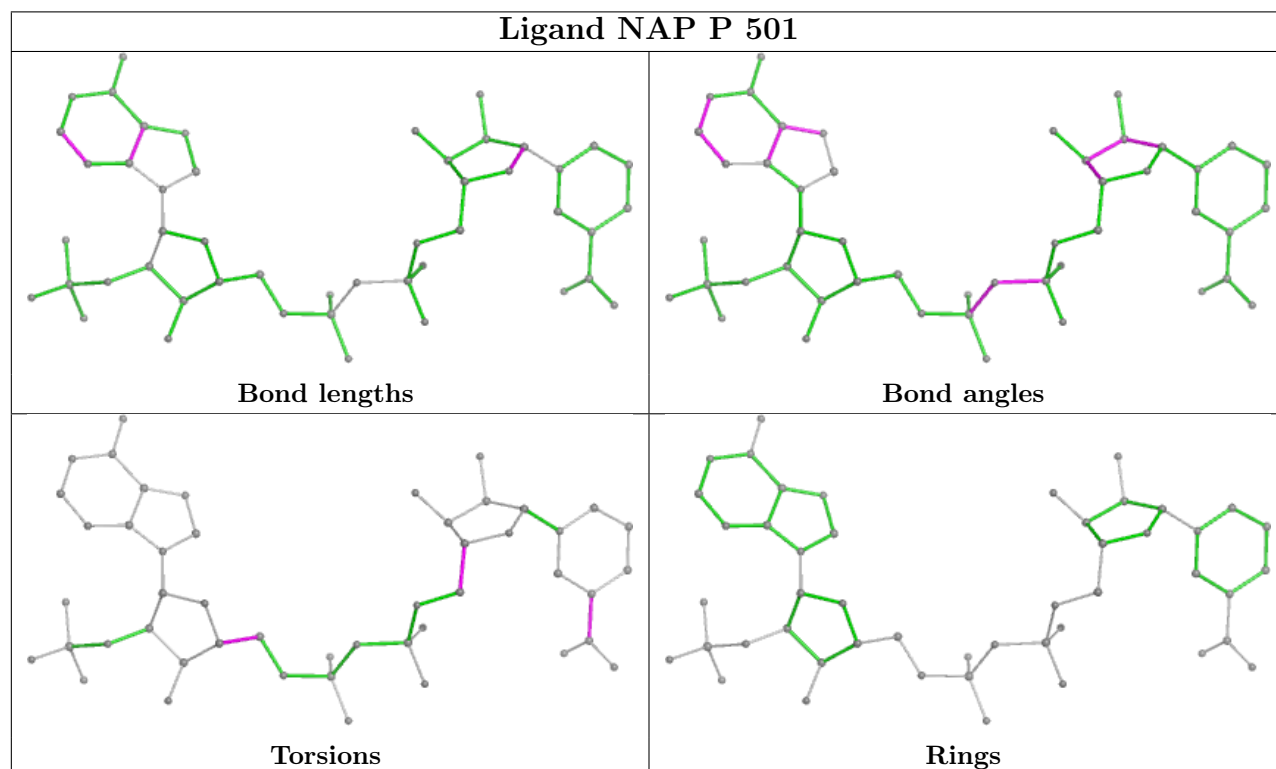
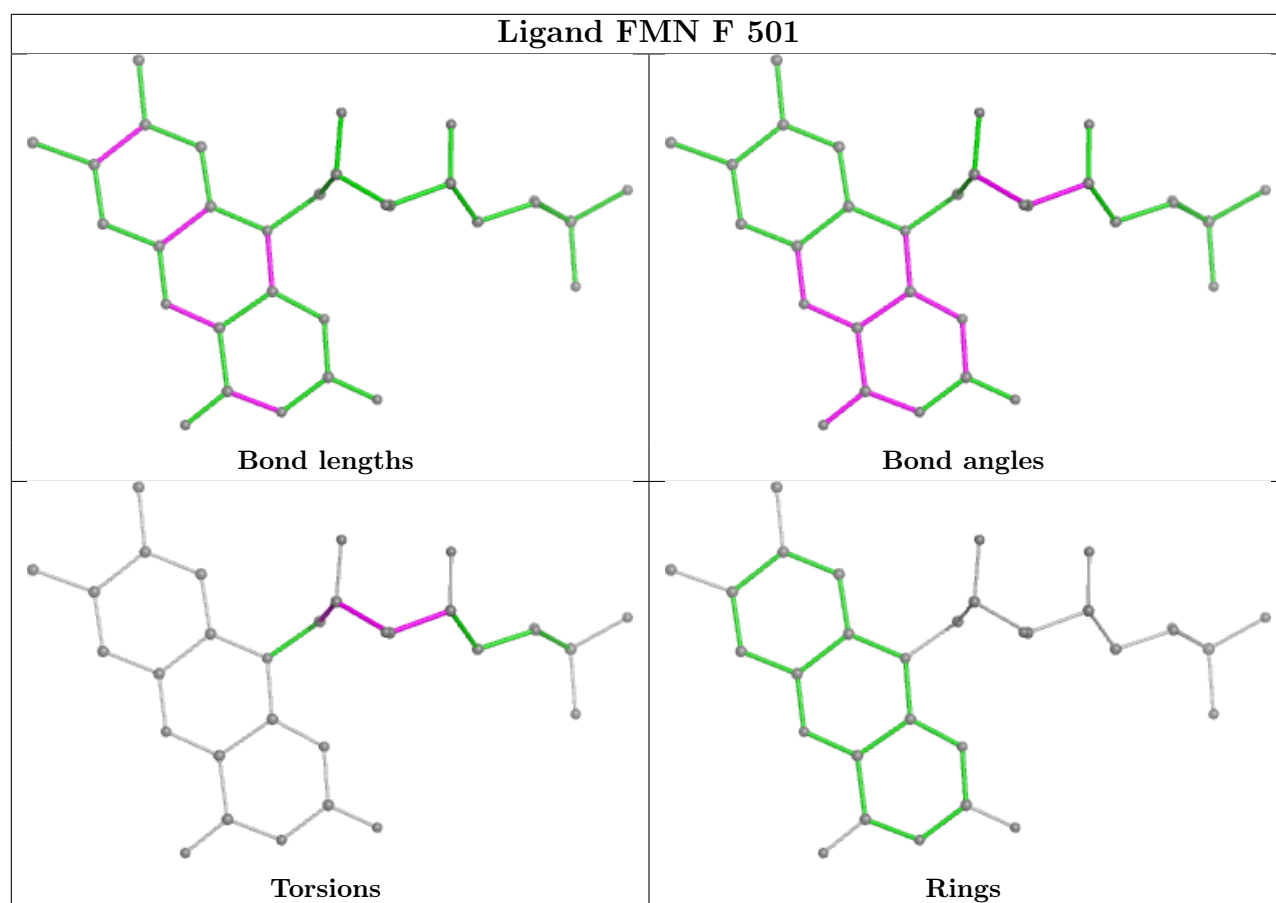
5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
47	F	501	FMN	N10-C1'-C2'-O2'
47	F	501	FMN	N10-C1'-C2'-C3'
47	F	501	FMN	C1'-C2'-C3'-O3'
47	F	501	FMN	C1'-C2'-C3'-C4'
47	F	501	FMN	C2'-C3'-C4'-C5'

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
15	P	2
27	i	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	P	186:UNK	C	200:UNK	N	21.75
1	P	252:UNK	C	280:UNK	N	19.92
1	i	32:PRO	C	40:UNK	N	15.54

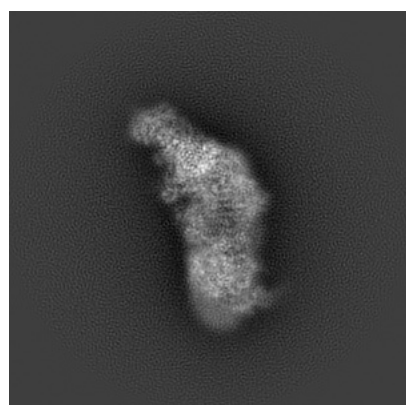
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3731. These allow visual inspection of the internal detail of the map and identification of artifacts.

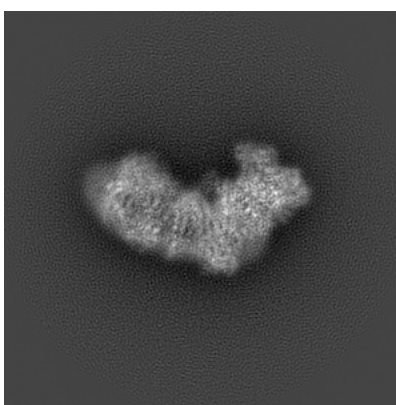
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

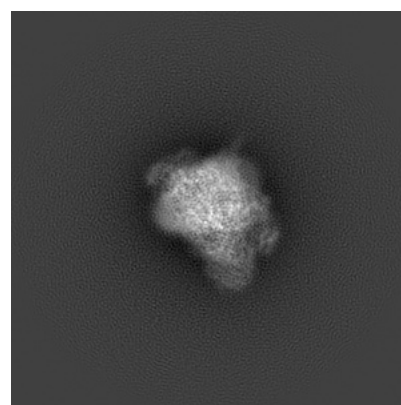
6.1.1 Primary map



X



Y

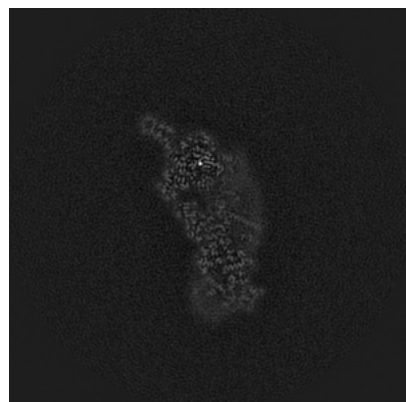


Z

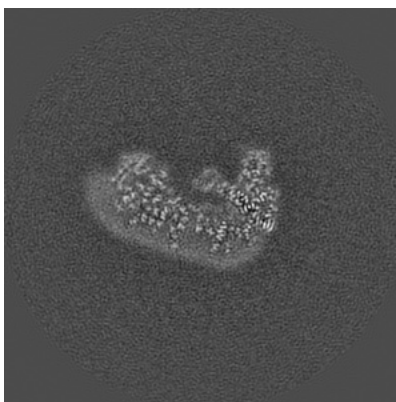
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

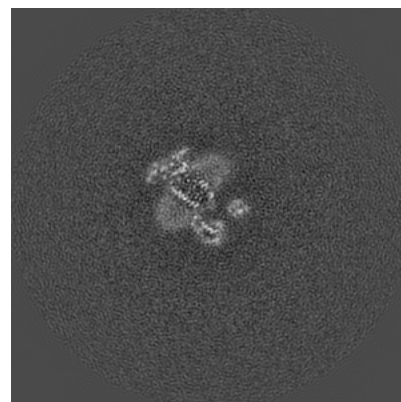
6.2.1 Primary map



X Index: 180



Y Index: 180



Z Index: 180

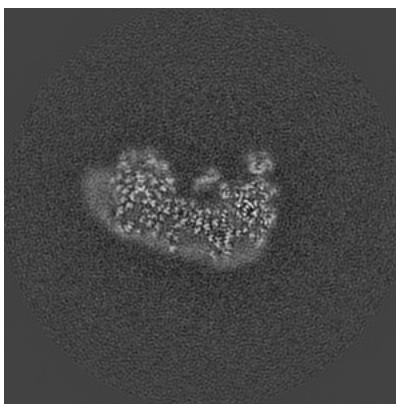
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

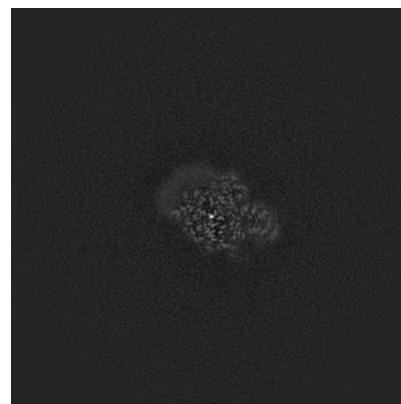
6.3.1 Primary map



X Index: 185



Y Index: 184

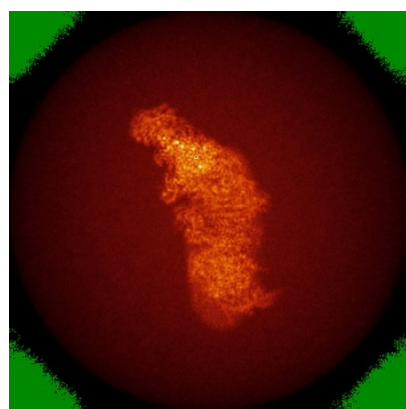


Z Index: 219

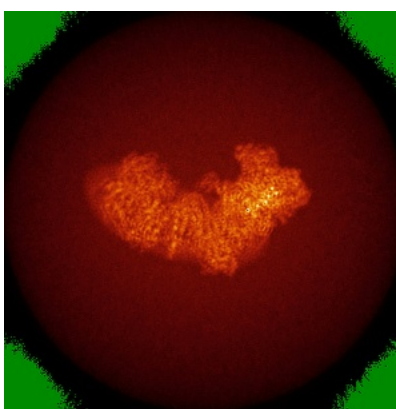
The images above show the largest variance slices of the map in three orthogonal directions.

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

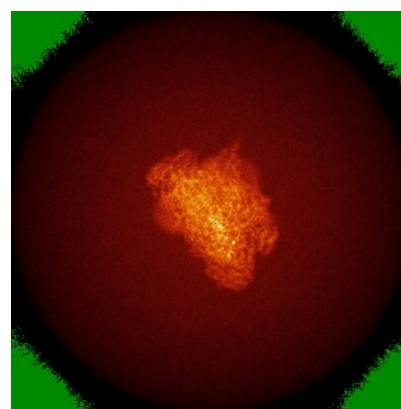
6.4.1 Primary map



X



Y

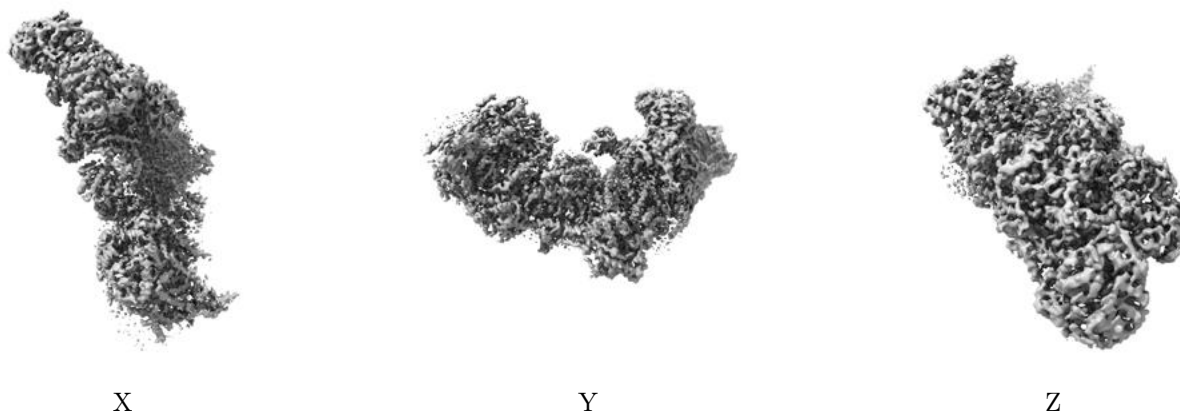


Z

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

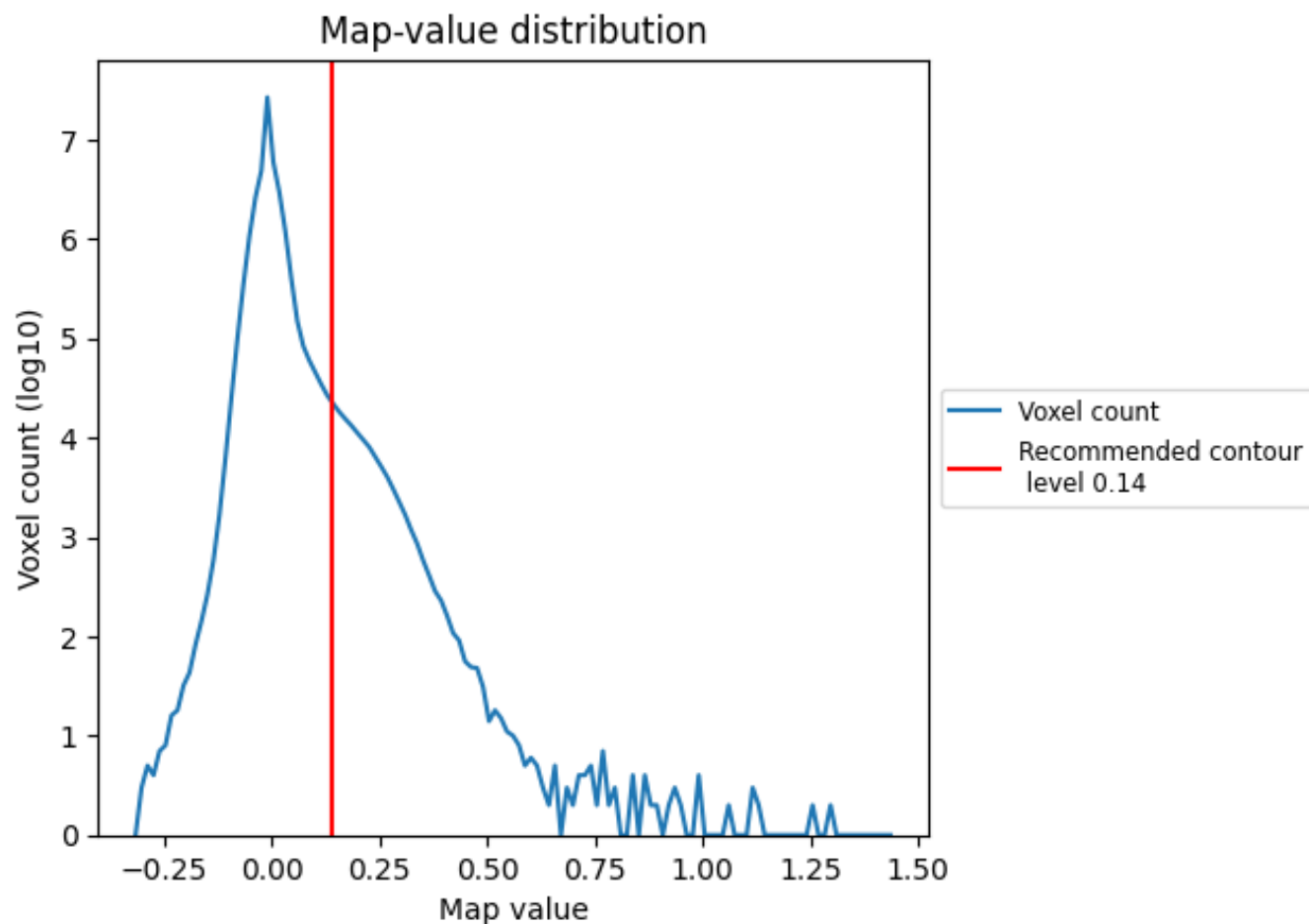
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

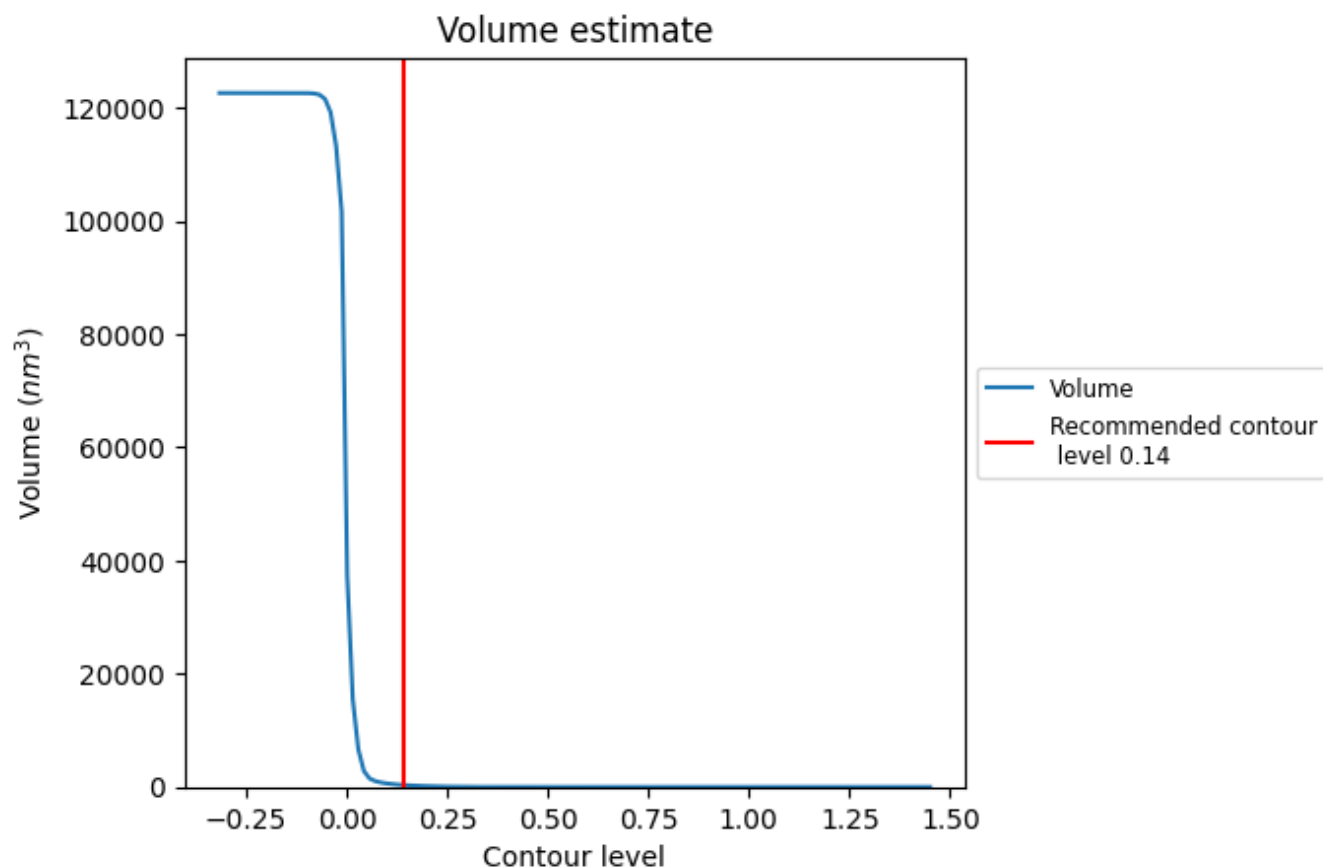
This section contains the results of statistical analysis of the map.

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.

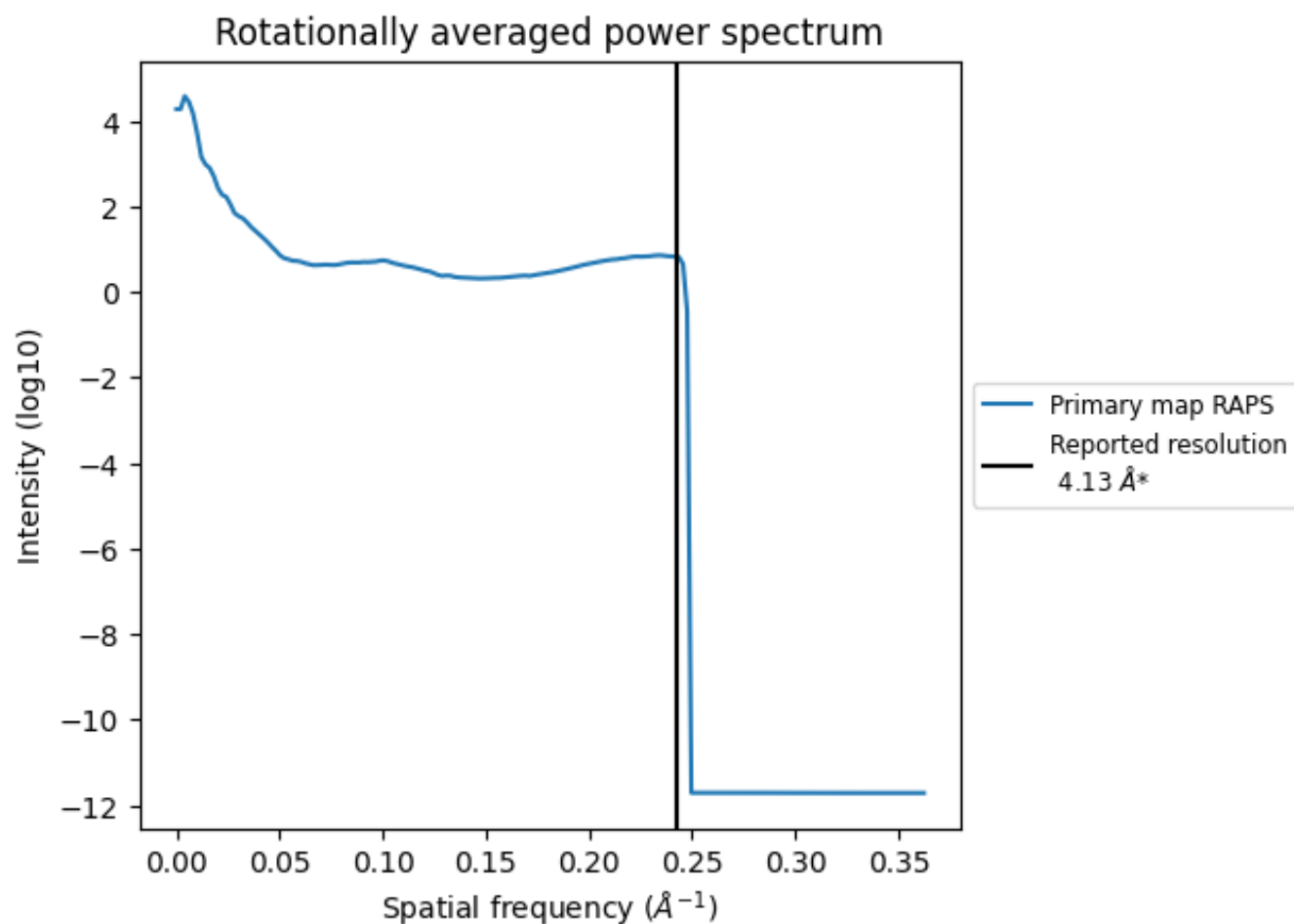
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 341 nm^3 ; this corresponds to an approximate mass of 308 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

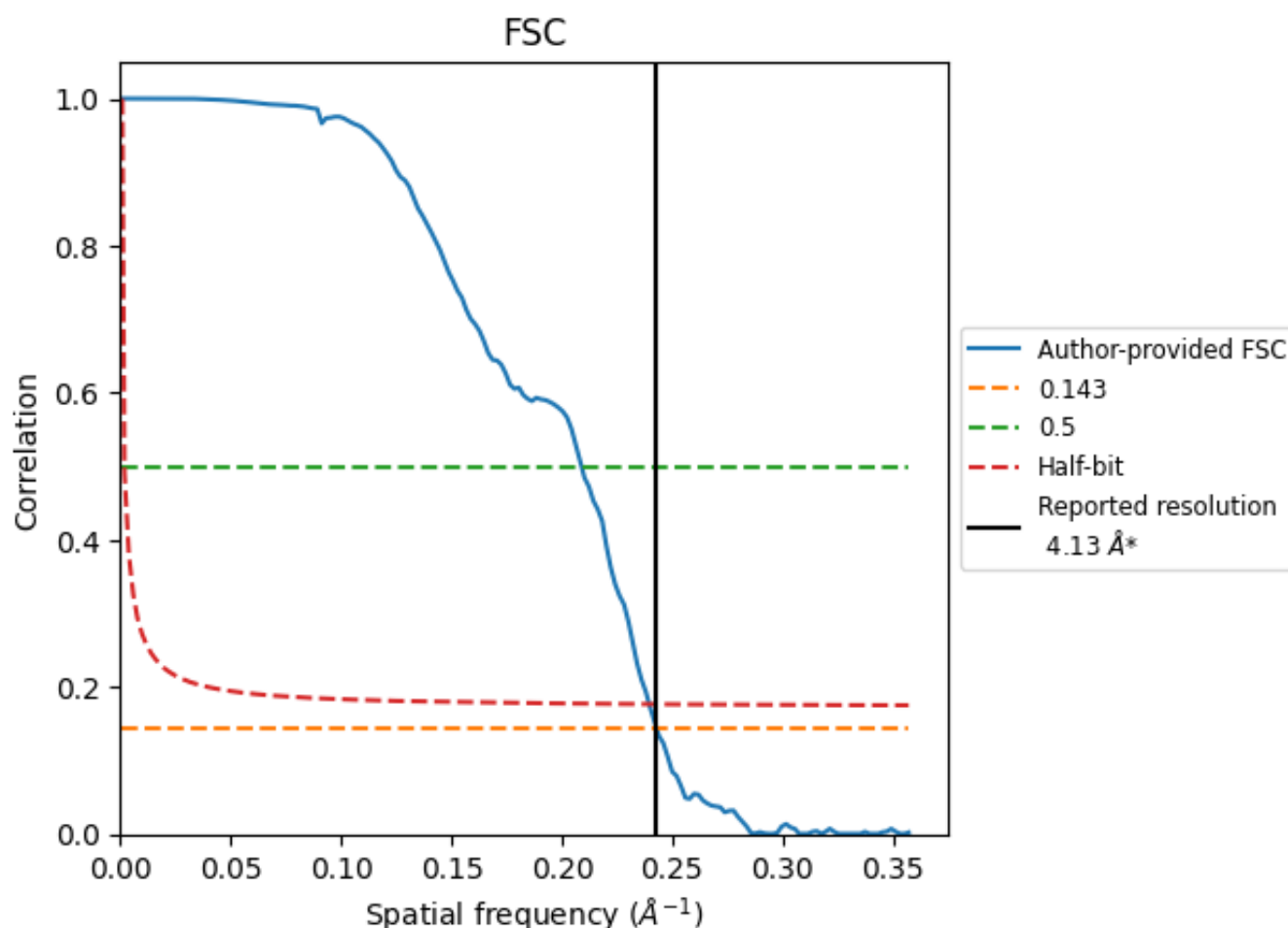


*Reported resolution corresponds to spatial frequency of 0.242 \AA^{-1}

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 0.242 Å⁻¹

8.2 Resolution estimates [i](#)

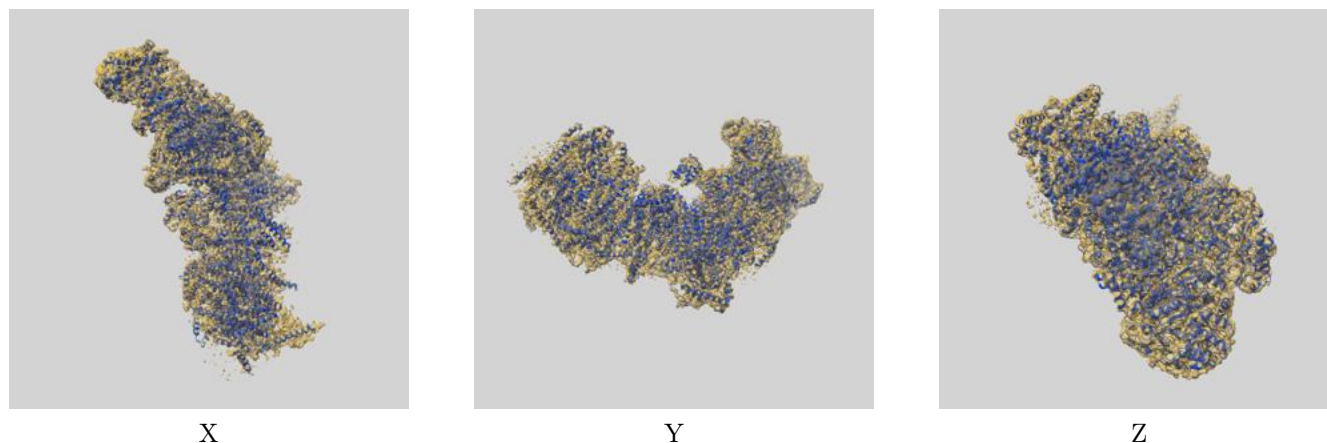
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.13	-	-
Author-provided FSC curve	4.12	4.79	4.17
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

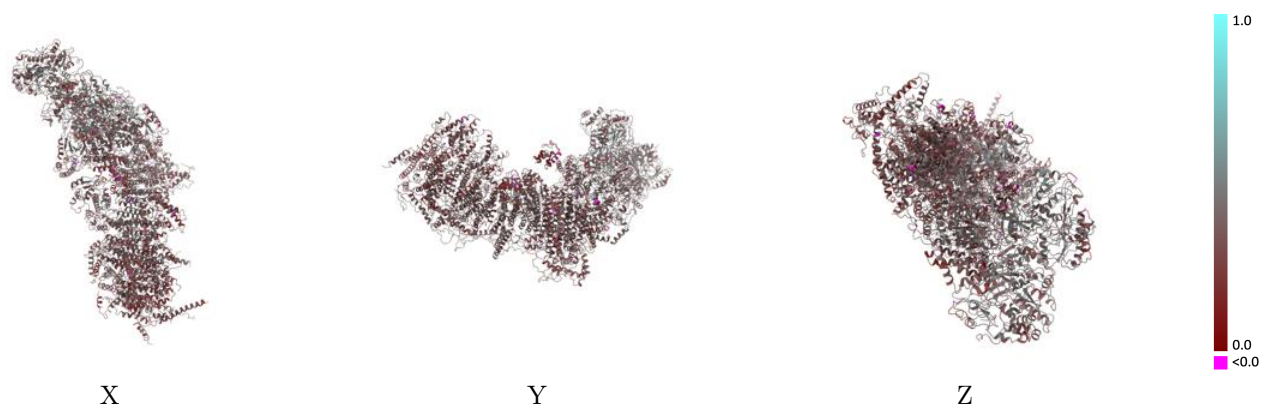
This section contains information regarding the fit between EMDB map EMD-3731 and PDB model 5O31. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



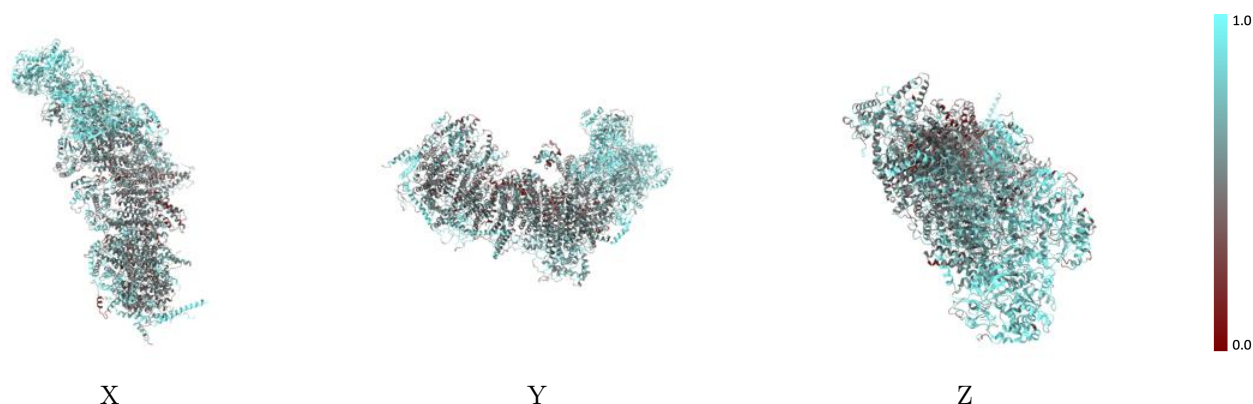
The images above show the 3D surface view of the map at the recommended contour level 0.14 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



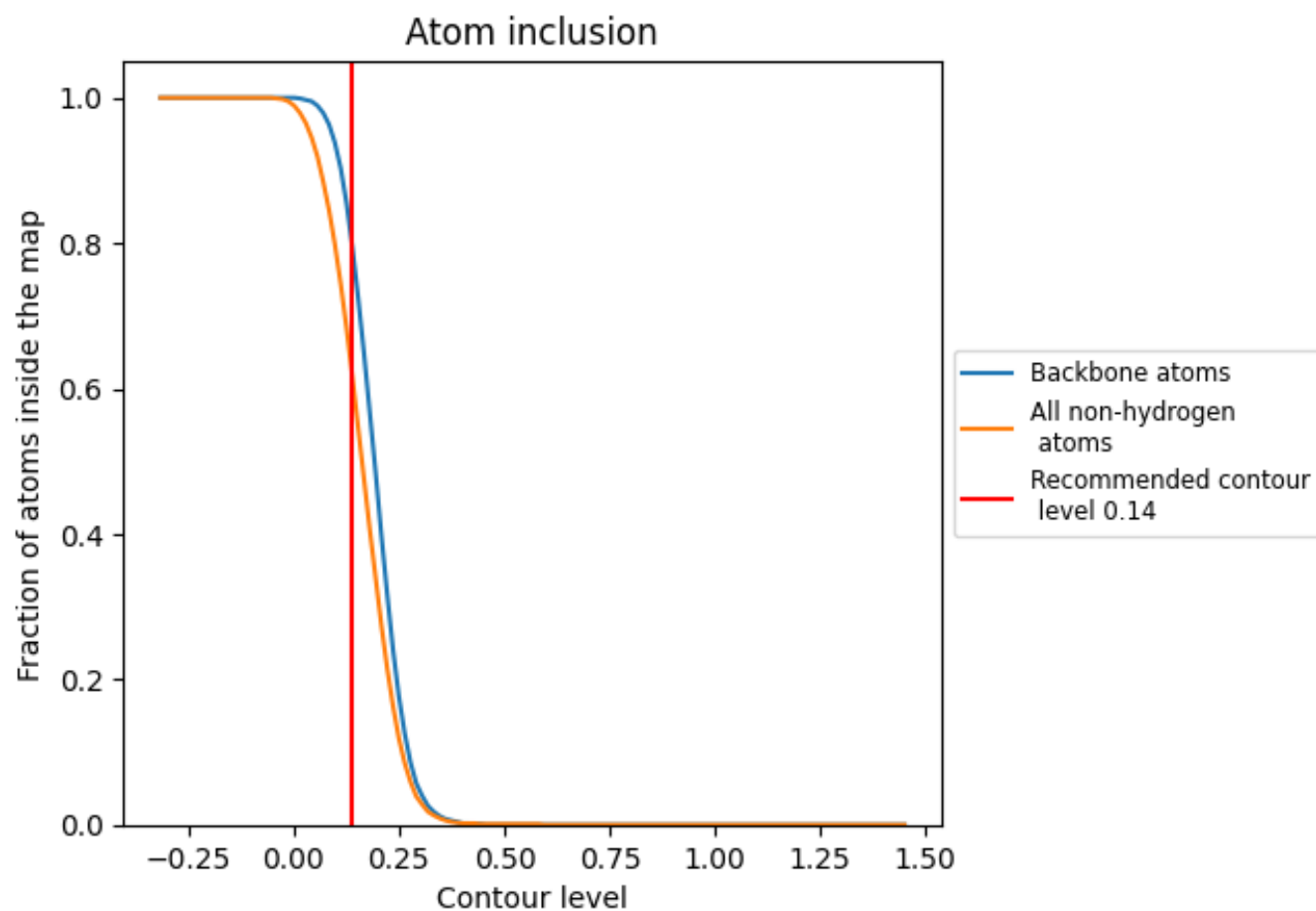
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.14).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 79% of all backbone atoms, 61% 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 (0.14) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6140	 0.3520
A	 0.4960	 0.3340
B	 0.6270	 0.3750
C	 0.6200	 0.3630
D	 0.5790	 0.3670
E	 0.8250	 0.3910
F	 0.7540	 0.3810
G	 0.7150	 0.4050
H	 0.5480	 0.3440
I	 0.6600	 0.3640
J	 0.4490	 0.3140
K	 0.5040	 0.3370
L	 0.5000	 0.3090
M	 0.5320	 0.3380
N	 0.5570	 0.3570
O	 0.6280	 0.3600
P	 0.7590	 0.3960
Q	 0.7600	 0.4360
R	 0.6500	 0.3840
S	 0.8000	 0.3670
T	 0.4730	 0.2310
U	 0.7080	 0.3610
V	 0.6000	 0.3240
W	 0.5680	 0.3170
X	 0.6160	 0.3260
Y	 0.3870	 0.2820
Z	 0.6200	 0.3070
a	 0.5780	 0.3040
b	 0.5900	 0.3400
c	 0.5680	 0.3070
d	 0.6090	 0.3510
e	 0.6270	 0.3740
f	 0.5350	 0.3320
g	 0.5290	 0.3170
h	 0.7120	 0.3780



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Chain	Atom inclusion	Q-score
i	 0.6000	 0.3200
j	 0.7610	 0.3600
k	 0.6190	 0.3300
l	 0.7030	 0.3560
m	 0.5360	 0.3130
n	 0.6340	 0.3350
o	 0.8350	 0.3210
p	 0.6790	 0.3570
q	 0.7960	 0.4070
r	 0.7190	 0.3920
s	 0.7850	 0.3820